

Complete detail of the core proteome of *C. pneumonia*

>core/0/1/Org1_Gene58

MKSLPVYVSGIKVRNLKNVSIHFNSEIEVLLTGVSGSGKSSIAFDTLYAAGRKRYISTLPTFFATTITTLPNPKV
EEIHGLSPTIAIKQNHFSHYSHATVGSTTELFSLHALLFTLEGQARDPKTKEVLDLYSKEKVLSTIMELSEGVI
SILAPLLRKDIAAIEHYAQQGFTKVRNCGTIHPIYSFLTSGIPEDCSVDIVIDTLIKSENNIARLKVSLFTALEFGE
GHCSVLSDEELMTFSTKQQIDDVITYTPLTQQFLSPHALESRCSLCQSGSIFISIDNPLLIDENLSIKENCCSFAGN
CSSYLYHTIYQALADALNFNLETPWKDLSPEIQNIFLRGKNNLVLPVRLFDQTLGKKNLTYKVWRGVLDIG
DKVRYTTKPSRYLSKGMSAHSCSLCKGTGLGDYASVATWEGKTFTEFQQMSLNNWHVFFSKVKSPSLSIQEI
LQGLKQRLSFLIDLGLGYLTPNRALATLSGGEQERTAIKHLGGELFGITYILDEPSIGLHPQDTEKLIGVIKKL
RDQGNTVILVEHEERMISLADRIIDIGPGAGIFGGEVLFNGKPEDFLMNSSSLTAKYLRQELTIPIESREAPTS
WLLLTEATIHNLKNLSIRLPLARLIGVTGVSGSGKSSLINNTLVPAIESFLKQENPKNLHFEWGCIGRLIHITRDL
PGRSQRSIPLTYIKAFDDIRELFA SQPRSLRQGLTKAHFSFNQPQGACIQCQGLGTMISDDDTPIPCSECQGKR
YHSEVLEILYEGKNIADILDMTAYEAEKFFISHPKIHEKIHALCSLRDYLPLGRPLSTLSGGEIQRKLKLAHELL
FASPKQTLVYVLDDEPTTGLHTHDIQALIEVLLSLTYLGHTVLVIEHNMHVVKVCDYVLELGPEGDDLGGYLLA
SCTPKDLIQLNTPAKALAPYIEGSLDIPVVKSEPPSSPKSCDILIKDAYQNNLKHIDLALPRNSLIAIAGPGASG
KHSLVFDILYASGNIAAYAEFPPYIRQGLLKETPLPSVGEVKGLSPVISVRKCSSSNRSYHTIASALGLSNGLEK
LFAILGEPFSPLTEEKLSKTTPTQTIIDSLLKSYKDDYVTITSPIPLGSDLEIFLQEKQKEGFIKLYSEGNLYDLDER
LPLNLEPAIVIQHTKVSPKNSSSLLSAISVAFSLSSEIWIYISQKKQRKLSYSLGWKDKKGRLYPEITHQLLSSD
HPEGRC LTCGGRGEILKISLEEHKEKIAHYTPLEFFSLFFPKSYMKPVQKLLKDENASQPLKLLTTKEFLNFCR
GSSEFPGMNALLMEQLD TESDSPLIKPLLALTSCPACKGSGLNDYANYVRINNTSLLDIYQEDATFLESFLNTI
GTDDTRSIIQDLMNRLTFISKVGLSYITLGQRQDTLSDGENYRLHLAKKISINLTNIVYLFEEPLSGLHPQDLPTI
VQLLKELVANNNTVIATDRSCSLIPHADHAIFLPGSGPQGGFLMDSDEVCPSVDLHANVPQTEVCPKAPLS
ISKANHTRGSDRTLKVNL SIHHIQNLKVSAPLHALVAIGGVSGSGKTSLLLEGFKKQAELLIAGTTTTFSDLVV
IDSHPIASSQRSDISTYFDIAPSLRAFYASLTQAKALNISSTMFSTNTKQGQCSDCQGLGYQWIDRAFYALEKR
PCPTCSGFRIQPLAQEVLYEGKHFGELLHTPIETVALRFPFIKKIQKPLKALLDIGLYLPYGQKLSSLSVSEKTA
LKTAYFLYQTPETPTLFLIDELFSSLDPIKKQHLPEKLRSLNSGHSVIYIDHDVKLLKSADYLIIEIGPGSGKQGG
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>core/1/1/Org1_Gene389

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SSSSSSSGSASAVVAADPKGGAAFY SNEANGTLTFTTDSGNPGSLTLQNLKMTGDGA AIYSKGPLVFTGLKN
LTFTGNESQKSGGAAYTEGALT TQAIVEAVTFTGNTSAGQGGAIYVKEATLFNALDSLKFEKNTSGQAGGGI
YTESTLTISNITKSIEFISNKASVPAPAPEPTSPAPSSLINSTTIDTSTLQTRAASATPAVAPVAAVTPTPISTQETA
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IYAVGQVTLEDIANLKMTNNTCKGEGGAIYTKKALTINNGAILTTFSGNTSTDNGGAIFAVGGITLSDLVEVR
FSKNKTGNYSAPITKAASNTAPVVSSSTTAASPAVPA AAAAPVTNAAKGGALYSTEGLTVSGITSILSFENNEC
QNQGGGAYVTKTFQCSDSHRLQFTSNKAADEGGGLYCGDDVTLTNLTGKTLFQENSSEKHGGGLSLASGKS
LTMTSLESFCLNANTAKENGGGANVPENIVLTFTYTPTPNEPAPVQQP VYGEALVTGNTATKSGGGIYTKNA
AFSNLSSVTFDQNTSSENGGALLTQKAADKTDCSFTYITNVNITNNTATGNNGGIAGGKAHFDRIDNLT VQSN

QAKKGGGVYLEDALILEKVITGSVSQNTATESGGGIYAKDIQLQALPGSFTITDNKVETSLTTSTNLYGGGIYS
SGAVTLTNISGTFGITGNSVINTATSQDADIQGGGIYATTSLINQCNTPIFSNNSAATKKTSTTKQIAGGAIFS
AAVTIENNSQPIIFLNNSAKSEATTAATAGNKDSCGGAIAANSVTLTNNPEITFKGNYAETGGAIGCIDLTNGS
PPRKVSIADNGSVLFQDNSALNRGGAIYGETIDISRTGATFIGNSSKHDGSAICCSTALTLAPNSQLIFENNKVT
ETTATTKASINNLGAAIYGNNETS DVTISLSAENGSIFFKNNLCTATNKYCSIAGNVKFTAIEASAGKAISFYDA
VNVSTKETNAQELKLNEKATSTGTILFSGELHENKSYIPQKVTFAHGNLILGKNAELSVVSFTQSPGTTITMGP
GSVLSNHSKEAGGIAINNVIIDFSEIVPTKDNATVAPPTLKLVSRTNADSKDKIDITGTVTLDPNGNLYQNSY
LGEDRDITLFNIDNSASGAVTATNVTLQGNLGAKKGYLGTWNLDPNSSGSKIILKWTFDKYLRWPYIPRDNH
FYINSIWGAQNSLVTVKQGILGNMLNNARFEDPAFNNFWASAIGSFLRKEVSRNSDSFTYHGRGYTAAVDAK
PRQEFILGAAFSQVFGHAESEYHLDNYKHKGSGHSTQASLYAGNIFYFPAIRSRPILFQGVATYGYMQHDTT
YYPSSIEEKNMANWDSIAWLFDLRFSVDLKEPQPHSTARLTFYTEAEYTRIRQEKFTELDYPRSFSACSYGNL
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>core/2/1/Org1_Gene739

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EKISSDTKENRKDLETEDPSKKSGLKEVSSDLPKSPETA VAAISEDLEISENISARDPLQGLAFFYKNTSSQSISE
KDSSFQGIIFSGSGANSGLGFENLKAPKSGAAVYS DRDIVFENLVKGLSFISCESLEDGSAAGVNIVVTHCGDV
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FVYSNNENTALWKENQALSGGAISSASDIDIQGNCSAIEFSGNQSLIALGEHIGLTD FVGGGALAAQGTTLR
NNAVVCVKNTSKTHGGAILAGTVDLNETISEVAFKQNTAALTGGALSANDKVIIANNFGEILFEQNEVRNH
GGAIYCGCRSNPKLEQKDSGENINIIGNSGAITFLKNKASVLEVMTQAEDYAGGGALWGHNVLLDSNSGNIQ
FIGNIGGSTFWIGEYVGGGAILSTDRVTISNNSGDVVFKGNGQCLAQKYVAPQETAPVESDASSTNKDEKSL
NACSHGDHYPPKTVEEEVPPSLLEEHPVVSSTDIRGGGAILAQHIFITDNTGNLRFSGNLGGGEESSTVGDLAI
VGGGALLSTNEVNVCSNQNVVFS DNVT SNGCDSGGAILAKKVDISANHSVEFVSNGSGKF GGAVCALNESV
NITDNGSAVSFSKNRTRLGGAGVAAPQGSVTICGNQGNIAFKENFVFGSENQRSGGGAIANSSVNIQDNAGD
ILFVSNSTGSYGGAI FVGSLVASEG SNPRTL TITGNSGDILFAKNSTQTAASLSEKDSFGGGAIYTQNLKIVKNA
GNVSFYGNRAPSGAGVQIADGGTVCLEAFGGDILFEGNINFDG SFNAIHL CGNDSKIVELSAVQDKNIIFQDAI
TYEENTIRGLPKDVSPLSAPSLIFNSKPQDDSAQHHEGTIRFSRGVSKIPQIAAIQEGTLALSQNAELWLAGLK
QETGSSIVLSAGSILRIFDSQVDSSAPLP TENKEETLVSAGVQINMSSPTPNKDKAVDTPVLADIISITVDLSSFV
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VSLPSITPATYGHTGVWSESKMEDGRLVVGWQPTGYKLNPEKQ GALVLNNLWSHYTDLRALKQEIFAHTI
AQRME LDFSTNVWGSGLG VVEDCQNIGEFDFGKHHLTG YALGLDTQLVEDFLIGGCFSQFFGKTESQSYKA
KNDVKS YMGAA YAGILAGPWLKGA FVYGNINNDLT TDYGT LGISTG SWIGKGFIAGTSIDYRYIVNPRRFIS
AIVSTVVPFVEAEYVRIDLPEISEQGKEVRTFQKTRFENV AIPFGFALEHAYS RGSRAEVNSVQLAYVFDVYR
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>core/3/1/Org1_Gene886

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LSQYPDLRKSTLYKYSITHVKPKKGFVVKLVENLRPDLHKNKDDGGAAADSRLDFAGYGVKHYQTDALLG
VSGVNSVEWQRLASLIMSVKNDILNDVGSREPIDKAQRSALVVSGKDIGGEIQPGGILDISRDILAICGYGMNV
GVEAKKAIDQYKKWYLNSSTFIAWNPQLPAIAQSYLLEQQRHLDYAAKIFQDLSALTTAHGTGQALEDLDSL
LCYYDQLIESKGVGEKIIASIHQKHLDLAMQDSCDQEHLKKWSNLYHVFSTIKEFTEGKLEQNEVVSRIQRL
RGKLEKSKCSILGNCRNTAEYATKSEKKLADYLLQIGDREPFLTGMHKAIAATGKAIQGKVEGVISQHPEKQIM
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GNRLQEAISSSEGVSQGLMMLNSLLNRDEKINKNIESSRKNLVAIAKQARSDARNIDSQGLAPLIQRNRASLDNI
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DAVAEDVSGTHRLHHQVLKRRCADLKNMISQLQKSINKWGMAKAIVLGIVAVLFCVLSAIFIGQNILSLLILS
CVGLLLTQVCPLIFDRISKSKEFEKQVLETAQSLIPATKILPSEFNKDLNRLAKLQDNLNLEGFGPTWARNIV
SDLEGIPTKEKSLKDLTKEFRKDSKNLNKRIKRRFKEGLGQEAPVVRPTIPQDIRGAEVFAELHRELEHLQKQ
KEEISIRGDALVQERMGLCLEKSKYDNEKAHAAAMTKKVGLQONIDRLQKNNETYVRIQNFFRTLIEKLG
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MQASFRERILLNPDGAKHGEAERTLASREEMKLTGLSYLTPFVRFSSPESTQSGYNQILKVREQLFDIEQRLQ
NQETVSPEDYAAVQAALAAAYVRKHESLIVSTYGLGAQEGQTSSKVTTLMRDLHAVEELVEMGVETYRLNRS
DQILHRVHSLVHSHLRDSDSSNGIIDVVKKLFELLNNGNNPNNDPECQKYMQILLDAPVSLLYGAFKSFKNE
FLLNFTELNIANSTKAAEEEEAKRYVEEKGRGFETYWEEAKQRLEAIAAELDDLNRNQETLLEQEIRLANLKISIF
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LGLLGREEAA

>core/4/1/Org1_Gene326

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GGTATFTDNASVTLQKNTSEKDGAAVSAYSIDLAKTTTAAALLDQNTSTKNGGALCSTANTTVQGNSGTVTFS
SNTATDKGGGIYSKEKDSTLDANTGVVTFKSNTAKTGGAWSSDDNLALTGNTQVLFQENKTTGSAAQANNP
EGCGGAICCYLATATDKTGLAISQNQEMSFTSNTTTANGGAIYATKCTLDGNTTLTFDQNTATAGCGGAIYT
ETEDFSLKGSTGTVTFTNTAKTGGALYSKGNSSLTGNTNLLFSGNKATGPSNSSANQEGCGGAILAFIDSGS
VSDKTGLSIANNQEVSLTSNAATVSGGAIYATKCTLTGNGSLTFDGNTAGTSGGAIYTETEDFTLTGSTGTVT
FSTNTAKTGGALYSKGNNSLSGNTNLLFSGNKATGPSNSSANQEGCGGAILSFLESASVSTKKGLWIEDNENV
SLSGNTATVSGGAIYATKCALHGNTTLTFDGNTAETAGGAIYTETEDFTLTGSTGTVTFTNTAKTAGALHTK
GNTSFTKNKALVFSGNSATATATTTTDQEGCGGAILCNISESDIATKSLTLTENESLSFINNTAKRSGGGIYAPK
CVISGESINFDGNTAETSGGAIYSKNLSITANGPVSTNNSSGGKGGAIIYADSGELSLEAIDGDITFSGNRATE
GTSTPNSIHLGAGAKITKLAAAPGHTIYFYDPITMEAPASGGTIEELVINPVVKAIVPPPQPKNGPIASVPVVPV
APANPNTGTIVFSSGKLPSQDASIPANTTTILNQKINLAGGNVVLKEGATLQVYSFTQQPDSTVFMDAGTTLE
TTTTNNTDGSIDLKNLSVNLDALDGKRMITIAVNSTSGGLKISGDLKFHNNEGSFYDNPGLKANLNLPLDLS
STSGTVNLDDFNPISSMAAPDYGYSWTLVPKVGAGGKVTLVAEWQALGYTPKPELRATLVPNSLWNA
YVNIHSIQEIATAMSDAPSHPGIWIGGIGNAFHQDKQKENAGFRLISRGYIVGGSMTPQEYTFVAFAFSQLFG
KSKDYVVSDIKSQVYAGSLCAQSSYVIPLHSSLRRHVLSKVLPELPGETPLVLHGQVSYGRNHHNMTTKLAN
NTQGKSDWDSHSFAVEVGGSLPVDLNYRYLTSYSPYVKLQVSVNQKGFQEVAADPRIFDASHLVNVSIPM

GLTFKHESAKPPSALLLTGAYVDAYRDHPHCLTSLTNGTSWSTFATNLSRQAFFAEASGHLKLLHGLDCFA
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>core/5/1/Org1_Gene410

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SFVSYSSENEQEMASSILQRVYSACTFPKQKDCSCSYPSIWETAPKEQLLQYAKNLSSGFEVFSSRLSAFCQQS
FSSNQDRLAFLSRLSSLSNDAIDVEDQKLLKSVYETLSQTACIRSLDCPYIEGLRLDCSESSLFFSSIEYCPKER
KIFLTLHSDLLAQRSTLSKEQRLDFDSRLAVEKQKLSKNLTVQVEDYNNGFSFQWMDKDTQGKIILQGERLL
QGIAEHLTALTLHRPAAESCDLIPENFPVFCRQPRESEAFGCYIFSPNTDCKHFSKGSVYILLKGLRSIVAKYQQ
GGGKELQSFEKDLQNLYNCFSHTEAISWTLGEDQVLEIRHPLQQFLDVWGEFVIGKEGCAFLEVKDIQDRL
ATVNQIEKNRQSDLVRWHEQYRHAKCSMDLQERLSAPIPYQNLFLENMKLNMRFKSRGENILRLGIDFVGG
RQLLSFKDHQGKQLTDKEDILKVSDELCARLNKLGVSEIELRREGDYIHLSPGSSSTISSEILGTSKMSFHV
NERFSSYSASRYEVQRFLDYLWFTSQAQGKTSPEEINTFASALFNEEVDVPPSVHEAITKLKSEGLAFSPSGCE
TPSTDLDTTFSMIAIGKDAEQKANPLVIVFRNYALDGASLKDIRPEFAAGEGYVLNFSVKDTSPKKMAEKLSP
TESFHTWTSAYCQEGISGTANGQYSANRGWRMAVVIDGYMVSSPILNVPLKNHASVSGKFTHREVSKLASD
LKSGAMSFVPEVLSEETISSDLGKKQCTQGIISACCGLAMLIVLMSVYYRFGGVIASGAVLLNLLLIWAALQY
LDAPLTLISGLAGIVLAMGMAVDANVLVFERIREEFLLSQSLKKSVEKGYTKAFGAIFDSNLTTVLASALLFFL
DTGPIKGFALTILGIFSSMFTALFMTKFFFMLWMNKTQHTQLHMMNKFVGIKHDFLRGCKKLWAVSGSVF
LLGCVALGFGAWNSVLGMDFKGGYAFTFNPKEHGISDVAQMRGKVVHKLQEAGLSSRDFRIQTFGSSEKIKI
YFSDKALSITKADTSLSPKINDHELALAVGLLSETGLDFSTETLNETQNFWSKVSSKLSKKMRYQATIGLLGA
LAIIILYVSLRFEWQYAFSAVCALIHDLATCAVLFIHFFLKQIDQLQAIGALMTVLGYSLNNTLIIFDRIRED
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MVRKENRSK

>core/6/1/Org1_Gene885

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IDPGKTDLTCKQLLNDAAQYREVVEKWGKDAFVAKMGGEAIYDLLKSEDQLSLLKDLKERLRKTKSQQARM
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VIVRNEKRMLQEAVDALFDNGRHGHPVMGAGNRPLKSLSEMLKGKNGRFRQNLLGKRVDYSGRSVIIVGPE
LKFNQCGLPKEMALELFEPFIIKRLKDQGSVYTIRSAAKKMIQRGAPEVWDVLEIIKGHVPVLLNRAPTLHRLGI
QAFEPVLIEGKAIRIHPLVCAAFNADFDGDQMAVHVPLSVEAQLEAKVLMMA PDNIFLPSSGKPV AIPSKDM
TLGLYYLMADPTYFP EEHGGKTKIFKDEIEVLRALNNGGFIDDVFGDRRDETGRGIHIHEKIKVRIDGQIIETTP
GRVLFNRIVPKELGFQNYSMPSKRISSELILQCYKKVGLEATVRFLDDLKDLGFIQATKAAISMGLKDVRIPDIK
SHILKDAYDKVAIVKKQYDDGIITEGERHSKTISIWTEVSEQLSDALYVEISKQTRSKHNPLFLMIDSGARGNK
SQLKQLGALRGLMAKPNGAIIESPITSNFREGLTVLEYSISSHGARKGLADTALKTADSGYLTRRLVDVAQDV
IITEKDCGTLNHIEISAIGQGSEELLPLKDRIYGR TVAEDVYQPGDKSRLLAQSGDVLNSVQAE AID DAGIETIK
IRSTLTCESPRGVCAKCYGLNLANGRLIGMGEAVGIIAAQSIGEPGTQLTMRTFHLGGIAATSSTPEIITNSDGIL
VYMDLRVVLGQEGHNLVLNKKGALHVVGDEGRTLNEYKKLLSTKSIESLEVFPVELGVKILVADGTPVSQG
QRIAEVELHNPIICDKPGFIKYEDLVEGISTEKVVNKNTGLVELIVKQHRGELHPQIAIYDDADLSELVGTYAI

PSGAISVEEGQRVDPGMLLARLPRGAIKTKDITGGLPRVAELVEARKPEDAADIAKIDGVVDFKGIQKNKRIL
VVCDEMTGMEEEHLIPLTKHLIVQRGDSVIKGGQLTDGLVVPHEILEICGVRELQKYL VNEVQEVYRLQGVD
INDKHIEIIVRQMLQKVRITDPGDTTLLFGEDVNKKEFYEENRRTEEDGGKPAQAVPVLG GITKASLGTESFIS
AASFQDTTRVLTDAACCSKTDYLLGFKENVIMGHMIPGGTGFETHKRIKQYLEKEQEDLVDFDVSETECVC

>core/7/1/Org1_Gene46

MLKCPERSVSVKKKEDIPDLPNLIEIQIKSYKQFLQIGKLAERENIGLEEVFREIFPIKSYNEATVLEYLSYNLGV
PKYSPEECIRRGITYSVTLKVRFRLTDETGKKEEVYMGTIPLMTDKGTFIINGAERVVVSQVHRSPGINFEQEK
HSKGNILFSFRIIPYRGSWLEAIFDINDLIYIHIDRKKRRRKILAITFIRALGYSSDADIIEEFFTIGESSLRSEK DFA
LLVGRILADNIIDEASSLVYGKAGEKLSTAM LKRMLDAGIASVKIAVDADENHPHIKMLAKDPTDSYEAALKD
FYRRLRPGEATLANARSTIMRLFFDPKRYNLGRVGRYKLN RKLGFSIDDEALSQVTLRKEDVIGALKYLIRL
KMGDEKACVDDIDHLANRRVRSVGELIQNQCRSGLARMEKIVRERMNLFDFSSDTLTPGKVVS AKGLASVL
KDFFGRSQLSQFMDQTNPVAELTHKRRLSALGPGGLNRERAGFEVRDVHASHYGRICPIETPEGPNIGLITSLS
SFAKINEFGFIETPYRIVRDGIVTDEIEYMTADVEEECVIAQASASLDEYNMFTEPVCWVRYAGEAFEADTSTV
THMDVSPKQLVSIVTGLIPFLEHDDANRALMG SNMQRQAVPLLKTEAPVVG TGLECRAAKDSGAIVVAEED
GVVDFVDGYKV VVAAKHNPTIKRTYHLKKFLRSNSGTCINQQPLCAVGDVITKGDVIADGPATDRGELALG
KNVLVAFMPWYGYNFEDAIHSEKLIREDAYTSIYIEEFELTARDTKLGKEEITRDIPNVSDEVLANLGEDGIIRI
GAEVKPGDILVGKITPKSETELAPEERLLRAIFGEKAADV KDASLTVPPGTGEGVMDVKVFSRKDRLSKSDDE
LVEEAVHLKDLQKGYKNQVATLKTEYREKL GALLNEKAPAAIHRRTAEIVVHEGLLFDQETIERIEQEDLV
DLLMPNCEMYEV LKGLLSDYETALQRLEINYKTEVEHIREGDADLDHG VIRQVKVYVASKRKLQVGDKMA
GRHGNKGVVSKIVPEADMPYLSNGETVQMILNPLGVPSRMNLGQVLETHLGYAAKTAGIYVKTPVFEGFPE
QRIWDMMIEQGLPEDGKSFLYDGKTGERFDNKVVIGYIYMLKLSHLIADKIHARSIGPYSLVTQQPLGGKAQ
MGGQRFGE MEVWALEAYGVAHMLQEILTVKSDDVSGRTRIYESIVKGENLLRSGTPESFNVLIKEMQGLGL
DVRPMVVDA

>core/8/1/Org1_Gene500

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LKSPEALLLELQWFQDLFKDDYFTEVQLHKMSEESIAGFKEE WLKQEYYS LIEKQIKVNTAVLEASKRLGIPT
VATNDIHYINANDWQAHEILLNVQSGETVRIAKQ NTHIPNPKRKVYRSREYYFKSPAQMAELFKDIPEVISNT
LEVAKRCDFTFDFSKKHYPYVPESLKTLSY TEEDRYQASAVFLKQLAEEALPKKYSSEVLAHIAKKFPHRD
PIDIVKERMDMEMAIIIPKGMCDYLLIVWDIIH WAKANGIPVGPGRGSGAGSVLLFLLGITEIEPIRFDLFFERFI
NPERLSYPDIDIDICMAGRERVINYA IERHGKDNVAQIITFGTMKAKMAVKDVGR TLDMALSKVNHI AKHIPD
LNTTLSKALETDPDLHQLYINDAES AQVIDMALCLEGSIRNTGVHAAGVIICGDQLTNHIPICISKDSTMITTQY
SMKPVESVGMLKVDLLGLKTLTSINIAMS AIEKKTGQSLAMATLPLDDATTFSL LHQGKTMGIFQMESKGMQ
ELAKNLRPDLFEEIIMGALYRPGPMDMIPSF INRKHGKEIIEYDHPLMESILKETYGIMVYQE QVMQIAGALA
SYSLGEGDVLRRAMGKKDFQQMEQEREKFCKRACN NGIDPELATVIFDKMEKFAAYGFNKSHAAAYGLITY
TTAYLKANYPKEWLAALLTCDSDDIEKIGKLIREAQ SMGIPILPPHINVSSNH FVATDEGIRFAMGAIKGIGRG
LIESIVEERDHHGPHYESIRDFIQ RSDLKKVSKKSIESLIDAGCFDCFD SNRDLLASVEPLYE AIAKDKKEAASG
VMTFFTLGAMDRKNEVPICLPKDIPTRSK KELLKKEKELLGIYLTEHPMDTVRDHLSRSLSVVLAGEFENLPHG
SVVRTVFIIDKVTTKISSKAQKKFAVLRVSDGIDS YELPIWPDMYEEQQELLEEDRLIYAILVLDKRSDSLRISC

RWMKDLSIVNENIIYECDQAFDRIKNQVQKMSFTMSTSGKETKAKGNKPNENGHTQALAPVTLSLDLNELR
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>core/9/1/Org1_Gene638

MVLEALAIFRQDAMQHLLKHRKEIVVDFCEDSYTIRIPDEEAPEGYWLSTLKLQDIDRLTFASCSCPDGECCL
HLMTAYFAVYDALGLHPLHDKFRHSFWYAVFSHFFLDSIPLQAQGEMVYTLESPHITLTIECLSEEVFQDWLR
TIHASEEPTVFTNKTFKLSALYRTAKKFFFLNEEGAELTIGENSQGFP SHFSLQWQGLVFKA EILDFPTLEDIFP
KLELAHTSLENVSHDISITNVTVC AEEAKVNFTLSPVIHKKDRENHPKTRIGSVEYVAKTHEMITGPKAIALPI
YAIPLLADKFKDQLLSLLCYDSLEYRLRYDIRLLRDASFSSAYLVTPGDLDNGSLIYPNYCYSPTKGLMQVV
GMLSPKQAFIVKSEQVEDFLNERGH LIQEPGFQTFINERPEGHLYTNVTEQGVLLFH YDVGDPSSSTEIRFGTWT
YYTNQGFFLEKKNDLPIQDGLIVEPQDIPAFIVKND AALRRLPNFFSSPPNLKDLLIEVHRQSRGKGLDLKPILV
GLGESRCWLFVGLYREDIGFS LIPTPLQGLCFLPRVIPPENVPQFLTQYAQHERILFPNPQTRPPESYELVIQSI
HRPHPASPLHLQLELKTNLGSPIGIALQGLKSKHTFLFTQAGFLDLKQNL FQFLKQFLSTQKC VIAENTVIANI
TDVFKLDALAPLSVTDDTIANPEDLQFFSQLKAACLPPIPQNL FSSDHQLRPYQNSGLLWMWFLYNHRLSGLL
CDEMGLGKTHQATALLDIVFQSSQPSARPKFLIVCPTSVLPHWEHILSNHLP GVSIFSFGPNKPSELPPADILL
TSYGTLRQNYDKFYKIAFTIVVFDEIHMAKNKSSQIHKILCRID AQMKLGLTGTP IENNLLFEFKGLLDIILPNYL
PSDALFKKLFTKRCSS EEEIIPSQDLLLLKLTRPFILRRTKKLVLPELPDKVESIIACSLSPDQEKLYMATLQRE
KSHIQKLETPEEPATNFLHIFALLNHLKQICDHPAVFFKDPDQYKNYESGKWN A FVKLLKESLNAGYKV VVF
SQYIHMIRIITLYLEEIGIKYASIQGKSLNRKEE IETFTTDPNCQVFVGSLLAAGTG INLTAGNVVIMYDRWWN
PAKENQALDRVHRIGQKNTVFIYKLITEDTLEERIH YLIEKKIRLLDKVIASQDSN ILMNLNREDLLTILSYKDE
HGTSDSEESPVDAPVEDDTGVLPPEDS

>core/10/1/Org1_Gene649

MLNFRKLRRDFSANILQDGKKLFEQGAVIDAKILSMNGETVCISAQVRGLYDNIYECEIEVDRSESDTVDSNC
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LREYVHAANALSANPFFLPLEYLEKDSAELAVLFVSVNEDTFAPANQPIEFQLVLR LPCRSKPFYISNIRTFLEG
VLYQEPIVLNRRFFFTMQSFNASDRKLIDLLIRYVRYPNHTTEEKLLKSAYLMPPALGVILAKMFEHQ LADR
GGGSLGEKESFSGLFCGNLEEPLCWSLTPAKMKFNLDFFDMPYKALLMTPVILVDDDEVQPEQTM LLESDAP
GIIHHFVYHRFSPQIKRAHLRSFSRLRDIAIPEALFGSFRENALPVFQEYAEIANVHLLNSFVTLPYVDEVRAIC
DMSYLDGELEAKLHFLYGSLRVPAASLALQYQDVRAFISDEGILARNLVEERKM LEEVFSGFIYDERDGAFR
VKSEKKIVEFMTETIPANQHRITFNCPENLSGQFIYDETIFELSFREGSDINYYEADLKVHG LLLKGVPLDLLWD
CISAKKRFLLELPKAGQQSKGTRRGKVN SGKLP CILVLDLEKIAPVVQIFNEIGFKVLDDL VQKCPLWSLTGISL
DQFEALPVNFSMSERLIEIQKQIRGEIEFDFQDVPQQIQATLSYQTEGVHWLERLRKMHLNGILADD MGLGK
TLQAIHAVTQSKLEKSGCSLIVCPTSLVYNWKEEFRKF NPEFRTLVIDGVPSQRRKQLTALADR DVAITSYNL
LQKDVELYKSFRFDYVVLDEAHHIKNRTTRNAKSVKMIQSDHRLILTGTP IENSLEELWSLFDFLMPGL LSSY
DRFVGKYIRTGNMGNKADNMVALKKKVSPFILRRMKEDVLKDLPPVSEILYHCHLTESQKELYQSYAASA
KQELSRLVKQEGFERIIHV LATLTRLKQICCHPAIFAKDAPEPGDSAKYDMLMDLLSSLVDSGHKT VVFSQY
TKMLGIIKKDLESRGIPFVYLDGSTKNRLDLVNQFNEDPSLLVFLISLKAGGTGLNLVGADTVIHYDMWWNP
AVENQATDRVHRIGQSRSVSSYKLVTLNTIEEKILTLQNRK KSLVKKVINS DDEVVSKLTWEEVLELLQI

>core/12/1/Org1_Gene955

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GSVPYLVAANVSERTYLKLMKLSKDWPLHVEAVVRRHYPQESVASDILGYVGPISLQEYKRVLTQELSQR
ECVRAVEEGEDPKLPEGLASIDQVRALLESVESNAYSLSNALVGKMGVEACWDSKLRGKIGKKPILVDRRGNF
IQEMEGAVPEAPGTLQLTLAELQAYADALLLEYEKTETFRSAKSLKKREKLPLFPWIKGGAIHALDPNNG
EILAMASSPRYRNNDNFVNAKVAEDSKAVRSSIYRWLENKEHIAEIYDRKVPLIRERRNPLTGLCYEEILPLTFD
CFLDFLFPENSVIKLQLKRNSFVGQAIEVQNLVTRLLSLFPYEEGTCPCSAIFDAVFPNEEGHILIQEVISLREQK
WIMECLNQHKADIEELKEALDQVFNELPANYDKILYTDILRLIVDPERFSPVLPSEVHRLSLSEFTTELQGRYVV
LRSFSTILEDAFIEVHFKSWRKSEFLQYLAARKQEEALRKQRYPTPYVDYLEEEKTRQYKMFCEHLDFTL
AYLFSKTPYKEGLEPYDILDLWINELDNGAHRALSWHEHYLFLKERVSHLSEHLPALFSTFREFNELQRPLL
GKYPISIVRNKRQTEQDLAASFYPVYGYGLRPHAYGQAATLGSIFKLVSAYSVLSQRILWGHNEEPANPLVI
IDKNSFGYRSSKPHVGFKDGTPIPTFRGGSLPGNDFMGRGFIDLVSALMSSNPYFSLLVGEGLDGEDLAD
AASLFGFGEKTGLGLPGEYAGRVPHDLAYNRSGLYATAIGQHTLVVTPLQTAVMLASLVNGGVVYVPKLLL
GEWEGEHVSYLSSKKKRTIFMPDAVVEVLKTGMRNVIWGQYGTARAIQSQFPQLLSRIIGKTSTAESIMRVG
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>core/13/1/Org1_Gene1027

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FPSSEIDLSPKLVNIDAVGKRDHLLYSLNQHRAPIFCVTTLKALLEKTRSPQATSQQHLDLAVGDVLDPEATTE
LCKSLGYSQVMLTSEKGEFSCRGGIVDIFPLSSPEPFRIEFWGEKIISIRSYNPSDQLSTGKVSISISPAYTEEAS
GGNYSHSLLDYFSTPPLYLFDNLEILEDFADISGTLSSLPDRFFSIGTLYDRISTSNQVYFSETPFPNVKNLKEN
RVIIIEAFHRNMEASRQAIPILYPEQIIQNDENPLLAFLQHLQEYMPPHGKPLKLAIYSTKTKSLKEARALAETV
ARGDVEIYEKTNLTSSFALVNEAFAAISLSEFASTKVLRRQKQORTHFSVTTEEVFVPIPGETVVHIIHNGIGKFL
GIEKKPNHLNIETDYLVEYADKARLYVPSNQAYLISRYVGTSDKAADLHHLNSSKWKRSDLTEKSLIVYA
EKLLQLEAQRSTTPAFVYPPHGESVIKFAETFPYEETPDQLKTIDQIYNMMSPKLMDRLICGDAGFGKTEVI
MRAAVKAVCDGHRQVIVMVPTTILATQHYETFKERMAGLPIEIAVLSRFSQAKVQKLICEQVASGQIDIIIIGTH
KLINKSLEFKNPGLLIIDEEQRFVGVKVDNLKERYPMIDCLTVSATPIPTLHMSLSGARDLSVIAMPPLDRLP
VSTFVMEHNTETLTAALRHELLRGGQAYVIHNRIESIYTLAETIRNLIPEARIGVAHGQMGAEGLSNIFTKFKN
QKTDILVATALIENGIDIPNANTILIDHADKFGMADLYQMKGRVGRWNKKAYCYFLVPHLDRLSGPAAKRL
AALNKQEYGGGMKIALHDLEIRGAGNILGTDQSGHIGTIGFNLYCKLLKKAVSALKKHTSPLLFNDDVKIEFP
YNSRIPDTYIETGSMRIEFYQKIGNAESSEELTAIQEEMRDRFGPLPQEICWLFALAEIRLFALQHGISSIKGTAN
ALYVQKCLSKSEQTKKTLPYALSPTPELLVKEVIESIERGFLINAS

>core/14/1/Org1_Gene994

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PPVRVATPMPLRPSSQGYWQCLNRMVSMVLRRAPLPLPAMQVDPILGDFNPHFVASYPNRIDNEPMYFQIKQ
FKKIAQNPDLPQQHRLAQLSLEQALYLNNDNYLNVNPGDGNCFYRAYAVGWLSALYEESSRNDIVFEQEA
TRLLDLPFASSSPANANLCAEMAELLQLCSTYCSFIDLYDGVILSQKHTATLIAFLRKLSAYAIRQQIAASSNEE
TARALFISDMQDDLLPSVLEFLAANRPYSELFQNLINHSALPYMQSRDKLFLLLEHLPALFLTDAELQKMSPE
DQQLRKQYEREIREAFKLSRRIADSGWDTERFNAIVKDHLPEAIRCQYSRFLATIENRRSGDLPWSPALSFFA

FLCTCPSVRFHKLCAIFYKSLEDIIIASAPPQRSIQEILQISNASLSYLNEDLDSSWQREVISSNIMTILTTHESLTL
ESSMPQLETLHKRIANLLKNVISTSFETPPLSNQPDLLSNLVNKLVAIHSKLELKEHFNTVCSARSLRLTRDE
GSGLSQEQLLYTQAVQLLFFILQHPQVNNRPETKDAVKELKMLLLPFLQYAFKKVENEKKLQKLLRSILGS
LVLKPPARYPSTPSNKKETFCKFWSRHPEVMVLDPILEKNCMQFLRATFPNYQLETEAILLEKEIESTFRNG
WNVFLTRLNLFGSKLGGSPSSPTALSDQFSKSFLIFCFLNNYPKLLQKKTPLAARLDAFQREASHRFTQVKDKL
LLSLKYGFPLATATINQYSRARDQLICNLLKNTVTASDGFCSRSGFRQSLIGYLHSLSSNELGDILDDVKEQAEA
NDVAAMTTVPLQPFVCLIMSDRDTVSEENIENFVAMHGFLNTISPERDARIFLIRFPNHYGCLLPNPRTEQDQ
NSKPDSSNP

>core/15/1/Org1_Gene890

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QLVLHHITNYLKQDLWKNVLFQEQFHLLAVRYNVTSKHTSSLVDKLLASYTQPISSYFSSRVERLEQISLWHQ
QIYNSLLEIPKQVFLDQLTAHISGFKKQPFSSILDDLHHFVDLLYTSETHSSLSFSSFKIAETFNFKHRLARYKPCA
AFTVLENMSWVERTLEFCNLDRIENTLLVDLQEYLKQNYTPWLSPDESVALEKLLSSSEAQPVVQALREQY
QLVLIDEFQDQDKQWSIFSNNLFIKFTGSLFLIGDPKQSIYEWRSADLPTYLTAKSSFSSEDKQLQLVNNYRST
PKLMEAINQIFGKISPFLEIPGYLPIEYHALNPQSSETFENPPHAPIHFFFYETIKDQALWIFSEALRLQKEQKIPL
GNMVVLVSDSNQAFELISYATIPVSFSKNKSIFHLTETHILTALLEAILHPENYEKISKILFSSLFGLSLDEVTTK
KEDFTIYFQSLHSYISHHGLLATFYRVMTTQGNVLFSSPRGDLIFQEMEKLCCGYLDTISSYPYHQLHLKNFSE
TGRWEEELAISSYSEDLETLKITTIHSSKGLEVDIVFCPGIEKSKKNKSSSELLREMYVACTRAKKQLYLPISTQ
PPSLQRSSALTNYVKLEGTQSSAYDLAIHLHQHPDLFSYSLPKDHGHATTVLNLPLLETFAKVTTPKTIFSFS
STKFLDTHKDSQSIPYSKLPISKQQLPLGEKTGILHKILESIFSLQDTEYLMSTIMRFIKHTHLEGFEETILK
LLSKTFFSPLTFSSQTFSLSQVLPNKIFRETSFLFLENQELWQGVIDLFFEHEGKYIIDWKTSLGETNSDYSKS
NLSIYIKQEKLQDYQGRIYVKA VRKFLNQFEIDDDVELGVIFIRGIDTQGNNGFFALNSSSEDIPNFPNPKAIQKCQAY
H

>core/16/1/Org1_Gene753

MVEVEEKHYTIVKRNGMFVFPFNQDRIFQALEAAFRDTRSLETSSPLPKDLEESIAQITHKVVKEVLAKISEGQ
VVTVERIQDLVESQLYISGLQDVARDYIVYRDQRKAERGNSSSIIAIRRDGGSAAKFNPMKISAALEKAFRATL
QINGMTTPPATLSEINDLTLRIVEDVLSLHGEEAINLEEIQDIVEKQLMVAGYYDVAKNYILYREARARARANK
DQDGQEEFVPQEETYVVQKEDGTTYLLRKTDLKRFWSACKRFPKTTDSQLLADMAFMNLYSGIKEDEVTT
ACIMAARANIEREPDYAFIAAELLTSSLYEETLGCSSQDPNLSEIHKHFKKEYILNGEEYRLNPQLKDYLDDAL
SEVLDSLSDQQFSYMGVQNLVDRYFNLHEGRRLETAQIFWMRVSMGLALNEGEQKNFWAITFYNLLSTFRY
TPATPTLFNSGMRHSQSSCYLSTVKDDLISHYKVISDNALLSKWAGGIGNDWDVDRATGAVIKGTNGKSQG
VIPFIKVANDTAIAVNQGGKRKGAMCVYLENWHLDYEDFLELRKNTGDERRRTHDINTASWIPDLFFKRLEK
KGMWTLFSPDDVPGLHEAYGLEFEKLYEYERKVESGEIRLYKKVEAEVLWRKMLSMLEYETGHPWITFKDP
SNIRSNQDHVGVVRCSNLCTEILLNCSESETAVCNLGSINLVEHIRNDKLDEEKLKETISIAIRILDNVIDLNFYP
TPEAKQANLTHRAVGLGVMGFQDVLVELNISYASQEAVEFSDECSEIIAYYAILASSLLAKERGTYASYSGSK
WDRGYLPLDTIELLKETRGEHNVLDVTSSKKDWTPVRDTIQKYGMRNSQVMAIAPTATISNIIGVTQSIEMMY
KHLFVKSNSLSGEFTIPNTYLIKKLKLGLWDAEMLDDLKYFDGSLLEIERIPNHLKKLFLTAFEIEPEWIIETS

RRQKWIDMGVSLNLYLAEPDGKKLSNMYLTAWKKGLKTTYLRSQAATSVEKSFIDINKRGIQPRWMKNK
SASTSIVVERKTTTPVCSMEEGCESCQ

>core/17/1/Org1_Gene910

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FSSTWKTMDASFMESVWWVFQSLYNQGLVYEGTKVVPFSTALGTPLSNFEASQNYKEVDDPSLVVRMPLQ
NDSASLLVWTTTPWTLPSNMAIAVGETLVYVRIQDKKSGEQWILSQGCVSRWFSNPEEFVILESFSGKDLVG
RTYEPPFTFFQSKREEGAFRVIAASFVEESEGTGVVHMAPAFGEGDFLVCKENHVPLVCPVDAHGSFTEEIPQ
YQGQYIKHADKEIIFLKKKEGRIFYHGTVKHRYPPFCWRTDTPLIYKAVNSWFVAVEKIKDKMLRANSSIHVW
PEHIQEGRFKWLLEGARDWAISRNRWGTPIPIWKSADGEILVVGSIREELELTGTQITDIHRHFIDDLNIVKD
GKPFHRIPYVFDWFDGAMPYAQNHYPFENQKETEEAFPADFIAEGLDQTRGWFYTLTVISAILFDRPAFRN
AIVNGIILAEDGNKMSKRLNNYPSPKYVLDTYGADALRLYLLHSVVVKAEDLRFSDKGIEGVLKQILLPLTNV
LSFFNTYAELYGFDPKSQDIEPAYTEIDQWILSNLYSVVGKVRRESMSQYHLNFAVEPFVTFIDDLTNWYIRRC
RRRFWEAEDTPDRRAAFSTLYEVLTVFCKVIAPFVPFLAEDIYQKLKLEKEPESVHLCDFPQVEMDKILPDLE
KHMHDIREIVGLGHSLRKEHKLKVRQPLANFYVVGSKDRLSLLKTFEGLIAEELNVKNVIFYEEAPSFIYTTV
KPNFRMLGKKVGSKMKEVQKALSELPNNAIDKLIQEETWVLTIDDREIALDGDDVVICRHTDPGYIARSSALF
SVILDCQLREPLIVEGIARELVNKINTMRRNQQLHVSDRIALRIKTTEAVHRAFLDYENYICEETLIAYDFTQD
SDFQGENWDINGHATQIEITVSSIDS

>core/18/1/Org1_Gene561

MNATKHCRASFSNSPRHLLAQLAEDITSTHQPFTKRWILVANATTGHWIKNQLVHVLSDHIFMGSTIFTASD
SIVKHLFLGSGCSQPNIPDYLTLPLINNILEEISKASKFENGREFLSPTTYETTKKLAAAFKQFHTFSQRPTKNA
SHYQELFQILESHFSSYEEMFTTILNNRTQEEDCSLHIFGYAHLPKHLAEFFINLSTYFPVYFYCFSPCREYFGD
LLSDRAIDFFWNQLPDSPIKNAWEHYVLSDRQALLANLAHKSQSSQNFFLDREIDYQEMFLPSKHDSSLGVIQ
NSILDLKPTSPQDFSQTKQTICIRALNIPREVQEVFCKVTELLHRGVSPEEIFILSSHIESYKVHLNAIFNPHVPI
YFTDEVDPRAEDLRNKILLSSILQTQGDLYILQLLTHPQLQQPIDQNKVPYLIKLSSEWGKISSKDRASGQ
QMKA LGDLILEEYPFHQEGGRVSQVEVWETTVPLIYFIQERINLYLSSSQHSYEDLFQNVFSCLEKIFVLSPEET
SFITTLRNSLFPTFATSSCSLLFFTFCLDFLLHFHKPSPLYDKPGPYIGSLSSLIPKGYVFILGANKTTSSDIFD
LLNRTTTHEELAFSSTEDEENFHFLQILVSTKHELHISYISSAAQFNLPSPFLNHIKETLDLPVETLPTQPYLSAFF
KNKACLHTSQEYNYS LAHAFYSKKALLPSLFIPTVKQVNL PQHLSLNEIIGIFSPLDLFLKTNYNLRISYPEHL
KKQQKLFPTKHQIEDFWNECFVDKEHDLIPSISPHAEELFTYYREKTILLRNGLDKDPKHSPYTVTFSSSIFEER
PYHESYLFPPLSLSFQGNPVQIHGTIHGVCNEGLYLCSIDPRDSLKKTTRTLGSLPETSSEQKQLLERYVALAV
LQMSQHLSSDSALIKLTSFNTKENHHPPFSDPEGYLRKVLEVYHLMSSQPIPLLSPLCWKTLDDDEEFHQAVL
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>core/19/1/Org1_Gene866

MSEHPLTLQSMIATILRFWSEQGCVIHQGYDLEVAGAGTFNPATFLRALGPEPYKAAYVEPSRRPQDGRYGVH
PNRLQNYHQLQVILKVPENFLSLYTESLRAIGLDLRDHDRIHDDWENPTIGAWGLGWEVWLNNGMEITQL
TYFQAIGSKPLDTISGEITYGIERIAMYLQKKTSIYDVLWNDTLTYGQITQASEKAWSEYNFDYANTEMWFKH
FEDFAEEALRTLKNGLSVPAYDFVIKASHAFNILDARGTISVTERTRYIARIRQLTRLVADSYVEWRASLNYPL

LSLSSTSEPKETSESVVPMISSTEDLLLEIGSEELPATFVPIGIQQLESARQVLT D H N I V Y E G L E V L G S P R R L A L
LVKNVAPEVVQKA FEKKGPMLTSLFSPDGDVSPQGQQFFASQGV DISHYQDLSRHASLAIRTVNGSEYLFLL
HPEIRLRTADILMQELPLLIQRMKFPKKMVWDNSGVEYARPIRWLVALYGEHILPITLGTHIASRNSFGHRQLD
PRKISSSPQDYVETLRQACVVVSQKERRMIIEQGLRAHSSDTISAIPLPRLIEEATFLSEHPFVSCGQFSEQFCA
LPKELLIAEMVNHQKYFPTHETSSGAISNFFIVVCDNSPNDTHIEGNEKALTPRLTDGEFLFKQDLQTPLTTFIEK
LKSVTYFEALGSLYDKVERLKAHQRVFSTFSSLAASEDLDAIQYCKADLVSAVVNEFPELQGIMGEYYLKH
ANLPTASAVAVGEHLRHITMGQKLSTIGTLLSLDRLDNLLACFILGLKPTSSHDPYALRRQSLEVLTLVSASR
LPIDLASLLDRLADHFPSTIEEKVWDKSKTIEILEFIWGRLKTFMGSLEFRKDEIAAVLIDSATKNPIEILDTAE
ALQLLKEEHTEKLA VITTTNRLKKILSSLKLSMTSSPIEVLGDRESNFKQVLDAFPGFPKETSAAHAFLEYFLSL
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>core/20/1/Org1_Gene998

MSRLDIFVFDSLIANQDQNLLEEIFCSEDTVLFKAYRTTALQSPLAAKNLNIARKVANYILADNGEIDTVKLVE
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RQAALTALFTYLRQDVGSCFATAPAILIHQEYPERFLKDLNDLISSGKLSRIVNQREIAVPINLSGCIGELFKPLR
ILDLYPDPLVKLSSSPGLKKAFSAANLIETLGDSEAQIQQLSHQYLMQKLQNVHETLTANDIHKSTLLHYYQL
QESTVRAIFFKEGLFSKEQVAFSTQHPRELSEIQRVYHYLHAYEEAKSAFIHDTQNPLLKAWEYTLATLADAS
QSTISNHIRLALGWKSEDPHSLVSLVTHFVEEEVENIRILVQQCEQTYHEARSQLEYIEGRMRNPLNNQDSQIL
TMDHMRFRQELNKALYEWDSAQEKAKKFLHLPEFLLSFYTKQIPLYFRSSYDAFIQEFAHLYANAPAGFRILF
THGRTHPNTWSPISINEFIRFLSEFFTSESELLGKHAVINLEKETSRLVHNITAMLHTDVFQEALLTRILEAY
QLPVPPSILNHL DQLSQTPWVYVSGGTVDTL LLDYFESSEPLTLTEKHPENPHELA AFYADALKDLPTGIKSYL
EEGSHSLLSSSPHVF SIIAGSPLFREAWDNDWYSYTWLRDVWVKQH QDFLQDTILPQLSIYAFIENFCNKYA
LQHVVHDFHDFCSDHSLTLPELYDKGSRFLSSLFTKDKTVALIYIRRLLYLMVREVVPYVSEQQLPEVLDNVSS
YLGISSRITYEKFRSLIEETIPKMTLLSSADLRHIYKGLLMQSYQKIYTEEDTYLR LTTAMRHHNLAYPAPLLFA
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>core/21/1/Org1_Gene333

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TSATPAITTVTTGASALQPTDSLTVENISQSIKFFGNLANFGSAISSSPTAVVKFINNTATMSFSHNFTSSGGGVI
YGGSSLLFENNSGCIIFTANSCVNSLKGVTPSSGTYALGSGGAICIPTGT FELKNNQGKCTFSYNGTPNDAGAI
YAETCNIVGNQGALLLDSNTAARNNGGAICAKVLNIQGRGPIEFSRNRAEKGGAIFIGPSVGDPAPAKQTSTLILA
SEGDI AFQGNMLNTKPGIRNAITVEAGGEIVSLSAQGG SRLVFYDPITHSLPTTSPSNKDITINANGASGSVVFT
SKGLSSTELL L PANTTTILLGTVKIASGELKITDNA VVNVLGFATQGGGQLTLGSGGT LGLATPTGAPAAVDFT
IGKLAFDPFSFLKRDFVSASVNAGTKNVTLTGALVLDEHDVTDLYDMVSLQSPVAIPIAVFKGATVTKTGFPD
GEIATPSHYGYQGKWSYTW SRPLIPAPDGGFPGGSPSANTLYAVWNSDTLVRSTYILDPERYGEIVSNSLW
ISFLGNQAFSDILQDVLLIDHPGLSITAKALGAYVEHTPRQGHEGFSGRYGGYQAALSMNYTDHTTLGLSFGQ
LYGKTNANPYDSRCSEQMYLLSFFGQFP IVTQKSEALISWKAAYGYSKNHLNTTYLRPDKAPKSQGQWHNN
SYYVLISAEHPFLNWCLLTRPLAQAWDL SGFISAEFLGGWQSKFTETGDLQRSFSRGKGYNVSLPIGCSSQWF
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>core/22/1/Org1_Gene750

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NSENHLCYTGVPFNMKGAMMSGEARLSEALNAAIFPSVTYGVNSGGEPREIVTLSHEDVRAFHQSQYSINR
CLFYFYGNIKPSRHLDLFLEEKLLRQATKLEKQAVSVPLQKRKFKEPVRNILTYPVDHQEEDKVLFGISWLTCSIL
EQQELLALHVLEIILMGTDASPLKSRLKSGFCKQTEMSIENDIREIPMTLVCKGCSPAGAQKLEALIFASLEEH
REGISENIVEGAVHQLELSRKEITGYSLPYGLSLFFRSGLLKQHGGSAEDGLRIHSLFSELRNSLKNSDYLAKLI
RKYFLDNPHFARVILLPDTELVAKDNKDEQQLLLSVSEKLTDENKEKIQQNVRELTESQEQLKEDLNGILPNLA
LDKVPTSGKEFPLIKEGLSQGEVLHHECFTNDIVFIDVVLDPPLSGEELPWLRLLVFLMLQLGCGGRSYKEHL
EFLLEHTGGVDVSYDFSPHANKNSFLSPSVSIRGKALSSKSEKLCGIVSDMLTSDVFTDIPRIRELLMQHNEAL
TNSVRNSPMSYAVSMACSGNSITGAMSYLTGLPYVKKIRELTKNFDQNIDEAVVILQRLYTKCFSGKRQIVI
SGSAHNYQQKDNKFYGLLDYLVIPPEPWENPSINLYVTSRGLHIPARAAFNALAFPIGDIAYDHPDAAALTV
AAEILDNVVLHTKIREQGGAYGSGAAANLSRGSFYCYSYRDPEIATTYKTFLKGVSEIASGNFTKEDIYEGAL
GVVQGLDMPVAPGSRASVAFYRLKSGRIPVLRQAFRRSVLEVTKEHICMVMMDKYLESTVQETTLISFAGEEM
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>core/23/1/Org1_Gene332

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YATTPMLFTNND SILFQYNRSAGFGAAIRGTSITIENTKK SLLFNGNGSISNGGALTGSAAINLINNSAPVIFSTN
ATGIYGGAIYLTGG SMLTSGNLSGVLFVNNSSRSGGAIYANGNVTF SNNSDLTFQNNNTASPQNSLPAPT PPTP
PAVTPLLGYGGAIFCTPPATPPPTGVSLTISGENSVTFLENIASEQGGALY GKKISIDSNKSTIFLGNTAGKGGAI
AIPESGELSLSANQGDILFNKNLSITSGTPTRNSIHFGKDAKFATLGATQGYTLYFYDPITSDDL SAASAAATV
VVNPKASADGAYSGTIVFSGETLTATEAATPANATSTLNQKLELEGGTLALRNGATLNVHNFTQDEKSVVIM
DAGTTLAT TNGANNTDGAITLNKL VINLDSLDGT KAAVVNVQSTNGALTISGTLGLVKNSQDCCDNHGMFN
KDLQQVPILELKATSNTVT TDFSLGTNGYQQSPYGYQGTWEFTIDTTHTVTGNWKKTG YLPHPERLAPLIP
NSLWANVIDLRAVSQASAADGEDVPGKQLSITGITNFFHANHTGDARSYRHMGGGYLINTYTRITPDAALSL
GFGQLFTKSKDYL VGHGHSNVYFATVYSNITKSLFGSSRFFSGGTSRV TYSR SNEKVKTSYTKLPKGRC SWS
NNCWLGELEG NLPITLSSRILNLKQIIPFVKA EVAYATHGGIQENTPEGRIFGHGHL LNVA VPVGVRFGKNSH
NRPDFYTHIVAYAPDVYRHNPDCDTTL PINGATWTSIGNNL TRSTLLVQASSHTSVNDVLEIFGHCGCDIRTS
RQYTLDIGSKLRF

>core/24/1/Org1_Gene643

MLGFLKRFFGSSQERILKKFQKLVDKVNIYDEMLTPLSDDEL RNKTAELKQRYQNGESLDSMLPEAYGVVK
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TVNDYLAQRDCEWVGSVLRWLGLTTGVLVSGTLLEKRKKIYQCDVVYGTASEFGFDYLRDNSIATRLEEQV
GRGYYFAIIDEVDSILIDEARTPLIISGPGEKHNPVYFELKEKVASLVYLQKELCSRIALEARRGLDSFLDVDILP
KDKKVLEGISEFCRSLWL VSKGMPLNRVLRRVREHPDLRAMIDKWDVYYHAEQNKEESLERLSELYIIVDEH
NNDFELTDKGMQQWVEYAGGSTEEFVMMDMGHEYALIENDET LSPADKINKKIAISEEDTLRKARAHGLRQ
LLRAQLLMERD VDYIVRDDQIVIIDEHTGRPQPGRRFSEGLHQAIEAKEHVTIRKESQTLATVTLQNFFRLYEK

LAGMTGTAITESREFKEIYNLYVLQVPTFKPCLRIDHNDEFYMTEREKYHAIVNEIATIHGKGNPILVGTESVE
VSEKLSRILRQNRIHTVLNAKNHAQEAIIAGAGKLGAVTVATNMAGRGTDIKLDNEAVIVGGLHVIGTTR
HQSRRIDRQLRGRCARLGDPGAAKFFLSFEDRLMRLFASPKLNTLIRHFRPPEGEAMSDPMFNRLIETAQKR
V
EGRNYTIRKHTLEYDDVMNKQRQAIYAFRHDVLHAESVFDLAKEILCHVSLMVASLVMSDRQFKGWTLPNL
EEWITSSFPIALNIEELRQLKDTDSIAEKIAAELIQEFQVRFDHMVEGLSKAGGEELDASAICRDVVRSMVMH
IDEQWRIHLVDMDLLRSEVGLRTVGQKDPLLEFKHESFLLFESLIRDITITARHLFRLELTVEPNPRVNNVIPT
VATSFHNNVNYGPLELTVVTDSEDQD

>core/26/1/Org1_Gene340

MSLNLERISPLLYLLDVTAKKIDTSNLIVEAMNLDEHYGYQGIWSPYWMETTTTTTSSTVPEQTNTNHRQLYV
DWTPVGYRPNPERHGEFIANTLWQSAYNALLGIRILPPQNLKEHDLEASLQGLGLLINQHNREGRKGFNRHT
TGAAATTSAKTAARHSFSLGFAQMFSKTRERQSPSTTSSHNYFAGLRFDSELLFRDFISTGLSLGYSYGDHML
CHYTEILKGSSKAFFNNHTLVASLDCTFLPARITRTLELQPFISAIALRCSQASFQETGDHIRKFHPKHPLTDLSS
PIGRSEWKTSHHIPMLWTTEISYVPTLYRKNPMEFTLLISNGTWTTQATPVSYNSVAAKIKNTSQLFSRVTL
SLDYSAQVSSSTVGQYLKAESHCTF

>core/27/1/Org1_Gene388

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VLCQNNISYGPGGALLLQGRKSKALFFRDNRGTILFLKNKAVNQDESHPGYGGAVSSISPGSPITFADNQEILF
QENEGELGGAIYNDQGAITFENNFQTTSFFSNKASFGGAVYSRYCNLYSQWGDTLFTKNAAAKVGGAIHAD
YVHIRDCKGSIVFEENSATAGGAIAVNAVCDINAQGPVRFINNSALGLNGGAIYMQATGSILRLHANQGDIEF
CGNKVRSQFHSHINSTSNFTNNAITIQGAPREFSLSANEGHRICFYDPIISATENYNSLYINHQRLLLEAGGAVIFS
GARLSPEHKKENKNKTSIINQPVRLCSGVLSIEGGAILAVRSFYQEGGLLALGPGSKLTTQGKNSEKDKIVITN
LGFNLLENLDSSDPAEIRATEKASIEISGVPRVYGHTESFYENHEYASKPYTTSIILSAKKLVTAAPSPEKDIQNLII
AESEYMGYGYQGSWEFSWSPNDTKEKKTIIASWTPTGEFSLDPKRRGSFIPTTLWSTFSGLNIAASNIVNNNYL
NNSEVIPLQHLCVFGGPVYQIMEQNPKQSSNNLLVQHAGHNVGARIPFSFNTILSAALTQLFSSSSQQNVADK
SHAQILIGTVSLNKSQALSRLSSFSYTEDSQVMKHVFPYKGTSRGSRWNYGWSGSVGMSYAYPKGIRYLK
MTPFVDLQYTKLVQNPVETGYDPRYFSSSEMNTNLSLPIGIALEMRFIGSRSSLFLQVSTSYIKDLRRVNPQSSA
SLVLNHYTWDIQGVPLGKEALNITLNSTIKYKIVTAYMGISSTQREGSNLSANAHAGLSLSF

>core/28/1/Org1_Gene831

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SF
PNASNFAADTCTGGAVLCSKNVTISKNGTAYFINNKAQSSGGAIQAAIINIKDNTGPCLFFNNAAGGTAGGAL
FANACRIENNSQPIYFLNNQSGLGGAIRVHQECILTKNTGSVIFNNNFAMEADISANHSSGGAIYCISC
SIKDNPGIAAFDNNTAARDGGAICTQSLTIQDSGPVYFTNNQGTWGGAIMLRQDGACTLFADQGDIIFYNNRHF
KDTFSNHVSVNCTRNVS�TVGASQGHSAFTYDPILQRYTIQNSIQKFNPNPPEHLGTILFSSAYIPDTSTSRDD
FISHFRNHIGLYNGTLALEDRAEWKVKFDQFGGTLRLGSRAVFSTTDEEQSSSSVGSVINNNLAINLPSILGN
RVAPKLWIRPTGSSAPYSEDNNPIINLSGPLSLLDDENLDPYDTADLAQPIAEVPLLYLLDVTAKHINTDNFY
PEGLNTQHYGYQGVWSPYWIETITTSSTSDTSSEDTVNTLHRQLYGDWTPGTGYKVNPNENKGDIALSAFWQ
SFHNLFATL

RYQTQQGQIAPTASGEATRLFVHQNSNNDKGFHMEATGYSLGTTSNTASNHSFGVNFSQLFSNLYESHSDN
SVASHTTTVALQINNPNWLQERFSTSASLAYSYSNHHIKASGYSGKIQTEGKCYSTTLGAALSCSLSLQWRSRP
LHFTPFQIAIAVRSNQTAQESGDKARKFSVHKPLYNLTVPLGIQSAWESKFRLPTYWNIELAYQPVLYQQNP
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>core/29/1/Org1_Gene734

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LFINPKFRQEDLDREKYAVHQEFAAHPLSDGRRVHRIQQLVAPQGHPCARFGCGNASTLTPVTTEKMAEWF
KLHYPENMCAIAYTSAPLSKAKKQFSKIFSQIPRSKNYERQEPFLPSGDTSSLKNLYINQAIQPTSNEIYWHI
YESSHPIPLGCYKALAEVLRNESKNSLVSLKNEQLITDLDEFFRSSLNTGEFYISYELTEKGDKHYSQVIDST
FQYLRVIQEHGIPNYTLEEISTINALNYCYSSKSPLFDLLCKQIVSLGNEDLSTYPYHSLVYPKYSSSEDESALLN
LVSDPEQARFVLSSKNSEHWEEATQLHDPIDMTYYVKALDGVQDYGKVQSLKPIALPKPNLFIPKEVTLPG
VHLLKKQEFPPAPALSYQDDKLTLYHCEDHYTAPKLSSQIRIRSPQISRSSPQFLVATELYCLAVNDQLLREY
YPATQAGLSFTSALGGDIDLRVSGYTTTVPALLNSILTSLPNLEISYETFLVYKKQLELYQGALLNCPVRSG
LDELASQVMKETYSNTTKLSALEKLSFSEFQAFASNLFNSVHLEVMVLGNLSEQQKKDYLEMLQVFTASRSS
HATKPFYYELQSQEISEIHHDYPLTANGMLLLLQDKSSPSIQGKVCAEMLFEWLHHITFEELRTQQQLGYMV
GARYREFASRPFGFLYIRSDAYSPEELLAKTSLFLNKVSASPEKFGISQEKFANIRKAYINKILEPEHSLDMMNS
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>core/30/1/Org1_Gene56

MTTEDFPKAYNFQDTEPELYVFWEKNGMFKAEESSDKPPYSVIMPPPNVTGVLHMGHALVNTLQDVLVRY
KRMSGFEVCWIPGTDHAGIATQAVVERHLQASEGKRRTDYSREDFLKHIWAWKEKSEKVVLSQLRQLGCSC
DWDRKRFTMEPLANRAVKKAFKTLFENGYYIRGYLVNWDVPLQTALADDEVEYEEKDGWLYYIRYRMV
GSQESIVVATTRPETS LGDTGIAVSPNDERYASWIGASVEVPFVNRQIPIIGDASVDPTFGTGAVKVTPAHDKD
DYL MGTNHHLP MINILTPSGGINENGGPFAGMAKEKAREEILIALEEQGLFVRKEPYKLRVGVSYRSGAVIEP
YLSKQWFVSVSEFRGALREFVESQDIKIFPKDFVKNYLSWVNHLRDWCISRQLWWGHRIPVWYHKNDDERV
LCYDGE GIPEEVAQDPDSWYQDPDVLDTWFSSGLWPLTCLGWPDENSPDLKKFYPTALLVTGHDILFFWVT
RMVLLCSSMSG EKPFSEVFLHGLIFGKSYKRYNDFGEWSYISGKEKLAYDMGEALPDGVVAKWEKLSKSKG
NVIDPLEMIATYGTDAVRLTLCSCANRGEQIDLDYRLFEEYKHFANKVWNGARFIFGHISDLQGKDLLAGIDE
DSLGLEDFYILDGFNQLIHQLEEAYATYAFDKVATLAYEFFRNDLCSTYIEIHKPTLFGKQGNEASQSTKRTLL
AVLLINVLGVLHPVAPFITESLFLRIQDTLGALPEGDGDAFTGHALRMLRSRACMEAPYPKAFDVKIPQDLRE
SFTLAQRLVYTIRNIRGEMQLDPRHLKAFVVCSDTTEIQSCIPILQALGGLESIQLLDKEPEKGLYSFGVVDTI
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FA

>core/31/1/Org1_Gene993

MRFFCFGMLLPFTFVLANEGLQLPLETYITLSPEYQAAPQVGFTHNQNQDLAIVGNHNDFILDYKYYRSNGG
ALTCKNLLISENIGNVFFEKNVCPNSGGAIYAAQNCTISKQNQYAFTTNLVSDNPTATAGSLLGGALFAINC SI
TNNLGQGTFVDNLALNKGALYTETNLSIKDNKGPIIHKQNRALNSDSLGGGIYSGNSLNIEGNSGAIQITSNSS
GSGGGIFSTQTLTISSNKKLIEISENSAFANNYGSNFPNGGGGLTTTFC TILNNREGVLFNNNQSQSNGGAIHAK

SIHKENGPVYFLNNTATRGGALLNLSAGAGNGSFILSADNGDIIFNNNTASKHALNPPYRNAIHSTPNMNLQI
GARPGYRVLFYDPIEHELPSSFPILFNFETGHTGTVLFSGEHVHQNFTDEMNFSSYL RNTSEL RQGV LAVEDG
AGLACYKFFQRGGTLLLGQGAVITTAGTIPTSPSTPTTVGSTITLNHIAIDLPSILSFQAQAPKIWIYPTKTGSTY
TEDSNPTITISGTLTLRNSNNEDPYDSLDSLHSLKVP LLYIVDVAAQKINSSQLDLSTLNSGEHYGYQGIWST
YWVETTTITNPTSLLGANTKHKLLYANWSPLGYRPHPERRGEFITNALWQSAYTALAGLHSLSSWDEEKGH
AASLQGIGLLVHQDKNGFKGFRSHMTGYSATTEATSSQSPNFSLGFAQFFSKAKEHESQNSTSSHHYFSGM
CIENTLFKEWIRLSVSLAYMFTSEHTHTMYQGLLEGNSQGSFHNHTLAGALSCVFLPQPHGESLQIYPFITALA
IRGNLAAFQESGDHAREFSLHRPLTDVSLPVGIRASWKNHHRVPLVWLTEISYRSTLYRQDPELHSKLLISQG
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>core/32/1/Org1_Gene327

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GNLSLTGNSQIIFTQNFSSDNGGVINTKNFLLSGTSQFASF SRNQAFTGKQGGVVYATGTITIENSPGIVSFSQN
LAKGSGGALYSTDNCSITDNFQVIFDGNSAW EAAQAQGG AICCTTTDKTVTLTG NKNLSFTNNTALTYGGAI
SGLKVSISAGGPTL FQSNISGSSAGQGGGGAINIASAGELALSATSGDITFNNNQVTNGSTSTRNAINIIDTAKV
TSIRAATGQSIYFYDPITNPGTAASTDTLNLNLADANSEIEYGG AIVFSGEKLSPT EKAIAANVTSTIRQPAVLA
RGDLVLRDGVTVTFKDLTQSPGSRILMDGGTTLSAKEANLSLNLGLAVNLSSLDGTNKAALKTEAADKNISLS
GTIALIDTEGSFYENHNLSASTYPLLELT TAGANGTITLGALSTLTLQEPETHYGYQGNWQLSWANATSSKI
GSINWTRTGYIPSPERKSNLPLNSLWGNFIDIRSINQLIETKSSGEPFERELWLSGIANFFYRDSMPTRHGRHIS
GGYALGITATTPAEDQLTFAFCQLFARDRNHITGKNHGD TYGASLYFHHT EGLFDIANFLWGKATRAPWVLS
EISQIPLSFD AKFSYLHTDNHMKTY YTDNSI IKG SWRND AFCADLGASLPFVISVPYLLKEVEPFVKVQYIYA
HQQDFYERHAEGRAF NKSELINVEIPIGVTFERDSKSEKGT YDLTLMYILDAYRRNPKCQTS LIASDANWMA
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>core/33/1/Org1_Gene339

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CNGDFTISQNQGTFFYVNNSVNNWGGALSTNGHCRIQSNRAPLLFFNNTAPSGGGALRSENTTISDNTRPIYF
KNNCGNNGGAIQTSVTVAIKNNSG SVIFNNNTALSGSINSNGNGSGGAIYTTNLSIDDNPGTILFNNNYCIRDGG
AICTQFLT IKNSGHVYFTNNQGNWGGALMLLQDSTCLLFAEQGNIAFQNN EVFLTTFGRYNAIHCTPNSNLQ
LGANKGYTTAFFDPIEHQHPTTNPLIFNPANHQGTILFSSAYIPEASDYENNFISSSKNTSEL RNVLSIEDRA
GWQFYKFTQKGGILKLGHAA SIATTANSETPSTSVGSQVIINN LAINLPSILAKGKAPTLWIRPLQSSAPFTEDN
NPTITLSGPLTLLNEENRDPYDSIDLSEPLQNIHLLSLSDVTARHINTDNFHPESLNATEHYGYQGIWSPYWVE
TITTTNNAS IETANTLYRALYANWTPLGYKVNPEYQGD LATTPLWQSFHTMFSLLSYNRTGDS DIERPFLEI
QGIADGLFVHQNSIPGAPGFRIQSTGYSLQASSETS LHQKISLGFAQFFTRTKEIGSSNNVSAHNTVSSLYVELP
WFQEA FATSTVLAYGYGDHHLHSLHPSHQEAEGTCYSHTLAAAIGCSFPWQQKSYLHLSPFVQAIAIRSHQ
TAFEEIGDNPRKFVSQKPFYNLTPLGIQGWQSKFHVPT EWTLELSYQPVLYQQNPQIGVTLLASGGSWDIL
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>core/34/1/Org1_Gene57

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KDPVYYTMPYIEGYTLKTLLKSVWQKESLSKELAEKTSVGAFLSIFHKICCTIEYVHSRGILHRDLKPDNILLG
LFSEAVILDWGAACVACGEEEDLLDIDVSKEEVLSSRMTIPGRIVGTPDYMAPERLLGHPASKSTDIYALGVVL
YQMLTSLFPYRRKKGKKIVLDGQRIPSPQEVAPYREIPPFLSAVVMRMLAVDPQUERYSSVTELKEDIESHLKG
SPKWTLTTALPPKKSSSWKLNEPILLSKYFPMLEVSPASWYSLAISNIESFSEMRLEYTLSKKGLNEGFGILLPT
SENALGGDFYQGYGFWLHIKERTLSVSLVKNSLEIQRCSDLESCKETFLIALEQHNHSLSLFVDGTTWLIHM
NYLPSRSGRVAIHVRDMEDILEDIGIFESSGSLRVSLAVPDAFLAEKLYDRALVLYRRIAESFPGRKEGYEARF
RAGITVLEKASTDNNEQEFALAIIEFSKLHDGVAAPLEYLGKALVYQRLQEYNIEIKSLLLALKRYSQHPEIF
RLKDHVVYRLHESFYKRDRLLALVFMLVLEIAPQAITPGQEEKILVWLKDKSRATLFCLLDPTVLELRSSKME
LFLSYWSGFIPHLNSLFHRAWQSDVRALIEIFYVACDLHKWQFLSSCIDIFKESLEDQKATEEIVEFSFEDLGA
FLFAIQSIFNKEDAEEKIFVSNDQLSPILLVYIFDLFANRALLESQGEAIFQALDLIRSKVPENFYHDYLRNHEIRA
HLWCRNEKALSTIFENYTEKQLKDEQHELFVLYGCVLALIQAEEAAKQHFDVCREDRIFPASLLARNYNRLG
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>core/35/1/Org1_Gene832

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GALNLTDNGTILFSQNVSNNEANNNGGAIKATLSISGNTSSITFTSNSAKKLGGAIYSSAAASISGNTGQLVFM
NNKGETGGGALGFEASSSITQNSSLFFSGNTATDAAGKGGAIYCEKTGETPTLTISGNKSLTFAENSSVTQGG
AICAHGLDLSAAGPTLFSNNRCGNTAAGKGGAIADSGSLSLSANQGDITFLGNTLTSTSAPTSTRNAIYLG
SAKITNLRAAQGQSIYFYDPIASNTTGASDVLINQPDNSPLDYSGTIVFSGEKLSADEAKAADNFTSILKQPL
ALASGTLALKGNVELDVNGFTQTEGSTLLMQPGTKLKADTEAISLTKLVVDLSALEGNKSVSIETAGANKTIT
LTSPLVFQDSSGNFYESHTINQFTQPLVVFTAATAASDIYIDALLTSPVQTPEPHYGYQGHWEATWADTSTA
KSGTMTWVTTGYNPNPERRASVVPDSLWASFTDIRTLQQIMTSQANSIYQQRGLWASGTANFFHKDKSGTN
QAFRHKSYGYIVGGSAAEDFSENIFSVAFQCFLGKDKDLFIVENTSHNYLASLYLQHRAFLGGLPMPSPSGSITD
MLKDIPLILNAQLSYSYTKNDMDTRYTSYPEAQGSWTNNSGALELGGSLALYLPKEAPFFQGYFPFLKFQAV
YSRQQNFKESGAEARAFDDGDLVNCSIPVGIRLEKISEDEKNNFEISLAYIGDVYRKNPRSRSTLMVSGASWT
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>core/37/1/Org1_Gene328

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IQSNYSCYFGQNFSNDNGGALQGSSISLSLNPNTFAKNKATQKGGALYSTGGITINNTLNSASFSENTAANN
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RASQGNITIYFYDPITTSITAALSDALNLNGPDLAGNPAYQGTIVFSGEKLSEAEAAEADNLKSTIQQPLTLAGG
QLSLKSGVTLVAKSFSQSPGSTLLMDAGTTLETADGITINNLVLNVDLSKETKKATLKATQASQTVTLGSL
LVDPGSGNVYEDVSWNNPQVFSCLTLTADDPANIHTDLAADPLEKNPIHWGYQGNWALSQWEDTATKSKAA
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HISAGYVVGATTTLASDNLITAAFCQLFGKDRDHFINKNRASAYAASLHLQHLATLSSPSLLRYLPGESESEQP
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KERN T T L V R S F D S G D L I N V S V P I G I T F E R F S R N E R A S Y E A T V I Y V A D V Y R K N P D C T T A L L I N N T S W K T T G T N L S
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>core/38/1/Org1_Gene330

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F K Q T T D N L T F L G N G H S L T F G F I D A G T H A G A A A S T T A N K N L T F S G F S L L S F D S S P S T T V T T G Q G T L S S A G G V N L
E N I R K L V V A G N F S T A D G G A I K G A S F L L T G T S G D A L F S N N S S T K G G A I A T T A G A R I A N N T G Y V R F L S N I A S T S G
G A I D D E G T S I L S N N K F L Y F E G N A A K T T G G A I C N T K A S G S P E L I S N N K T L I F A S N V A E T S G G A I H A K K L A L S S G G
F T E F L R N N V S S A T P K G G A I S I D A S G E L S L S A E T G N I T F V R N T L T T T G S T D T P K R N A I N I G S N G K F T E L R A A K N H T
I F F Y D P I T S E G T S S D V L K I N N G S A G A L N P Y Q G T I L F S G E T L T A D E L K V A D N L K S S F T Q P V S L S G G K L L L Q K G V T
L E S T S F S Q E A G S L L G M D S G T T L S T T A G S I T I T N L G I N V D S L G L K Q P V S L T A K G A S N K V I V S G K L N L I D I E G N I Y E S
H M F S H D Q L F S L L K I T V D A D V D T N V D I S S L I P V P A E D P N S E Y G F Q G Q W N V N W T T D T A T N T K E A T A T W T K T G F
V P S P E R K S A L V C N T L W G V F T D I R S L Q Q L V E I G A T G M E H K Q G F W V S S M T N F L H K T G D E N R K G F R H T S G G Y V I
G G S A H T P K D D L F T F A F C H L F A R D K D C F I A H N N S R T Y G G T L F F K H S H T L Q P Q N Y L R L G R A K F S E S A I E K F P R E I P
L A L D V Q V S F S H S D N R M E T H Y T S L P E S E G S W S N E C I A G G I G L D L P F V L S N P H P L F K T F I P Q M K V E M V Y V S Q N S F
F E S S D G R G F S I G R L L N L S I P V G A K F V Q G D I G D S Y T Y D L S G F F V S D V Y R N N P Q S T A T L V M S P D S W K I R G G N L S R
Q A F L L R G S N N Y V Y N S N C E L F G H Y A M E L R G S S R N Y N V D V G T K L R F

>core/39/1/Org1_Gene841

M Q R V L R L L F N L H H G E E K R A F L F F L L G L V W G I G C Y G T L S L A E G L F I E K L G S A E L P K I Y L G S S L I L C V L S S L I L Y N L
F K K H I S A T A L F L I P V S L S I L C N F Y L I L S S I F A I D P P R S P L F F Y R I V I W S L T I L S Y T S F W G F V D Q F F N L Q D G K R H F C I F
N A I I F L G D A I G S G I I A S L V H T I G I Q G I L I L F T A A L V L T F P I V F Y V S K S L K S L S D D H D L F I D T G H P P L S K A L K L C F Y D
K Y T F Y L L C F Y F L M Q L L A I A T E F N Y L K I F E I Q F A S K E E F E L V A H I G K C S L W I S L G N M C F A L F A Y S R I V K R L G V N N I
I L F A P L C F L S L F L F W T F K T T L S I A V L A M V V R E G V T Y A L D D N N L Q L L I Y G V P N K I R N Q I R I V V E S F I E P I G M L V W S
L V C F L S S Q Q Y V F C L I I S L I A T I L V C L V R S Y Y A K A I L K N L S A Q A L Q L T R S M Q D W I K S M T V K Q K R Q V E L F L L A H L
K H P S E R H Q T F A F Q H L L N L A S R S V L P S L L A H M N K L S L P N K L K T I E M V K S S L W A K D F L T L E L L K R W T S I F P H P A I
A S A I H L Y F A E H D L L H I T H I A E D L Y D T V G D R L L A A I L T V R R Q E A Y G P Y R D L A D K R L K E L L N S D Q P E D I V M G L T I
L K L E K N P Q N F P I L L D F L N T K N E D I L I V T C K A L H T S V R A N H K P Y C P E L L K R L R Q C S H N D E A S Q Y L L K T I S I A L D I S
F V K D L L M T T S Q L K N T S R K Y A E A M I G E L D K E V A P A F L Q V L T D E G T H N R C R I L A A K A L C K I D N W L L K K H A Y K I
V K S K A S K A L F Y S Y H G H Y I Q K K Y P T Y N L S L L A N T L N S N Y Y A E V N F M L S L L G I L G S M E H S G V L I R A L T S K N Q K I
K A Q A L E S L E K N C D S H L F S L L E P F V N Q P G M C Y S E K Y Y F K C G V I P L T L K E L L N M M E N S P S S L N K L T A Q Q L K E E L
S Y C D P D F Q S V N T I Y N Q E H E D F R T E E S E T L I S F L S I

>core/40/1/Org1_Gene893

M R F S L C G F P L V F S F T L L S V F D T S L S A T T I S L T P E D S F H G D S Q N A E R S Y N V Q A G D V Y S L T G D V S I S N V D N S A L N K
A C F N V T S G S V T F A G N H H G L Y F N N I S S G T T K E G A V L C C Q D P Q A T A R F S G F S T L S F I Q S P G D I K E Q G C L Y S K N A L
M L L N N Y V V R F E Q N Q S K T K G G A I S G A N V T I V G N Y D S V S F Y Q N A A T F G G A I H S S G P L Q I A V N Q A E I R F A Q N T A K
N G S G G A L Y S D G D I D I D Q N A Y V L F R E N E A L T T P I G K G G A V C C L P T S G S S T P V P I V T F S D N K Q L V F E R N H S I M G G
G A I Y A R K L S I S S G G P T L F I N N I S Y A N S Q N L G G A I A I D T G G E I S L S A E K G T I T F Q G N R T S L P F L N G I H L L Q N A K F L K
L Q A R N G Y S I E F Y D P I T S E A D G S T Q L N I N G D P K N K E Y T G T I L F S G E K S L A N D P R D F K S T I P Q N V N L S A G Y L V I K E
G A E V T V S K F T Q S P G S H L V L D L G T K L I A S K E D I A I T G L A I D I D S L S S S S T A A V I K A N T A N K Q I S V T D S I E L I S P T G N

AYEDLRMRNSQTFPLLSLEPGAGGSVTVTAGDFLPVSPHYGFQGNWKLAWTGTGNKVGEFFWDKINYKPRP
EKEGNLVPNILWGNAVDVRSLMQVQETHASSLQTDRLWIDGIGNFFHVSASEDNIRYRHNSGGYVLSVNN
EITPKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPVNVGILSRRFLQNPLMI
FHFLCAYGHATNDMKT DYANFPMVKNSWRNNCWAIECGGSMPLLVFENGRLFQGAIPFMKLQLVYAYQG
DFKETTADGRRFSNGSLTSISVPLGIRFEKLALPQDVL YDFSFSYIPDIFRKDPSCEAALVISGDSWLVPAAHVS
RHAFVGS GTGRYHFNDYTELLCRGSIECRPHARNYNINCGSKFRF

>core/41/1/Org1_Gene531

MKT VILNIGRKILQGIKKKKKKIGILSGLFFLDLVLLGVSSQRPTETSANVKHNL RDEKLAACPKN SAASLSAK
KSHTKKTTPGSIPSKVFSKFDATQDKTFQKTS GSAPPAKPTTLKELEERKKPRPERRTTADV KRSRFLPTQEV
EEPVPAASKEQLDSIQVWEEKQNYARRAVNAINLSIKKQLEEQTSTVTEKDVQPKTQATPHASKKNVASPST
SMPGIEKAATTVA VPQDKSEEEKVKERLTKRELTCEDLKDNGYTVNFEDISILELLQFVSKISGTNFVFDSNDL
QFNVTIVSHDPTSVDDLSTILLQVLKM HDLKVVEQGNNVLIYRNPHLSKLSTVVT DSSLKETCEAVV VTRVFR
LYSVSPSAAVNIIQPLL SHDAIVSASEATRHVHISDIAGNV DKVSDLLAALDCPGTSVDMTEYEVKYANPAALV
SYCQDVLGTLAEDDAFQMFIQPGTNKIFVSSPRLANKAEQLLKSLDVP EMAHTLDDPASTALALGGTGTTS
PKSLRFFMYKLKYQNGEVIANALQDIGYNLYVTTAMDEDFINTLNSIQWLEVNN SIVIIGNQGNVDRVIGLLN
GLDLPPKQVYIEVLILDT SLEKSWDFGVQWVALGDEQSKVAYASGLLNNTGIATPTKATVPPGTPNPGSIPLP
TPGQLTGFS DMLNSSSAFGLGIIGNVL SHKGKSFLT LGGLLSALDQDGD TVIVLNPRIMAQDTQQASFFVGQT
VPYQTTNTIIQETGTVTQNIDYEDIGVNLVVTSTVAPNNVVT LQIEQTISELHSASGSLTPVTDKTYAATRLQIP
DGCFLVMSGHIRDKTTKV VSGVPLLNSIPLIRGLFSRTIDQRQKR NIMMFIKPKVISSFEEGTRVTNKEGYRYN
WEADEGSMQVAPRHAPECQGPPSLQAESDFKIIEIEAQ

>core/43/1/Org1_Gene766

MSKDKKMKPEPKKNFPTVFFLLFGVVFGVVA FQNFLAGKKARVGF SHQIEHLVNLRLIVPEDSHKIALNDN
LVSF GGRFRDVQTQEGQLRYHYLELIDQGHRLDL DLQETSKSLTTLGKEVTNSILWFS AISGPIPEQGYAISY
PSEVSGSVLTEPLVVTGPATPQLINLHSLQERYPTLSRSPEALRTYGS DLYELIGKYLSPVLGIGSETLKRELKD
LYQQVEVSLTQETDTEAAYTLYGQVLSTLNRISSSLV VSEGGERFSQLRSVRLYREEWNKYHKLVEARDLNQ
AQLEKLRGELSQT VWFNNQELSSRSLEKQDPEVFGHWFAGAKEE WTA FKFNHSLSFKAPDQPRNLVLEKT
FKSQEPSPHYLGYLFTFLPIILVLLFVYLVFSRQMRGMSG SAMSFGKSPARMLLK GQNKVTFADVAGIEEAKE
ELIEIVDFLKNPNKFTSLGGRIPKGVLLIGPPGTGKT LIAKAVSGEADRPFFSIAGSDFVEMFVG VGASRIRDMF
EQAKRNAPCIIFIDEIDA VGRHRGAGIGGGHDEREQTLNQ LLVEMDGFGTNEG VILMAATNRPDVLDKALLR
PGRFDRRVVMNLPDIKGRFEILMVHAKRIKLDPTVDLMAVARSTPGASGADLENLLNEAALLAARKDRTAV
TAVDVAEARDKVLYG KERRSLEMDAEERKTTAYHESGHAVVGLCVQH GDPVDKVTIIPRGLSLGATHFLPE
KNKLSYWKKELYDQLAVLMGGRAAEEIFLGDISSGAQQDISQATKLVRSMVCEWGMSPQLGNVTYDERSD
GLTGYGGYHEKSYSEETA KTIDTEL RMLLDAAYQRALDIINEHKAEIELMTQMLIEFETLDSKDVKEIMDHT
WDPEKKRARLKEEGMLFKKSSDDLPPPPPKEDTLPGLGFNAT

>core/44/1/Org1_Gene273

MDSEFVGQVYSSDMDWIESMYQRFMNHETLDPSWKYFFEGYQLGQAASPSEASTKISGNETIAMLQEQKSQ
FLCTIYRYYG YLQSQISTLAPT TDSRFIQEKIAKIDLDEQVPSAGLLPKAQVSVRELIEALKKCYCGSLTLETLT
CTPELQEFVWNLMEKRQVERFAEQLLSYKDLCKATFFEEFLQIKFTGQKRFSLEGGETLVPMLEHLVHYGS

ALGISNYVLGMAHRGRLNVLTNVLGKPYRYVFMEFEDDPAARGLESVGDVKYHKGYVLKSHQKDRETTFV
MLPNASHLESVDPIVEGVVAALQHQGHAGKEQSSLAILVHGDAAFSGQGQVVYETLQLSRVPGYSTEGTLHIV
VNNYIGFTAVPRESRSTPYCTDIKMLGIPVFRVNSEDDVACIEAIEYALQVRERFSCDVIIDLCCYRKYGHNE
SDDPSVTAPLLYDQIKRKKSIREFRQYLLEGQFADISEETLASIEKEIQESLNREFQVLKGTDPPEFPKKECHH
CDRLNNGELILHDCDVSLDRETFLHMSRLCGFPDNFHPHPKIKTLLEKRMKMAEGGVGYDWAMAEELAFA
SLLIEGYNLRLSGQDSIRGTFSQRHLVWSDTVTGDYSPLYHLSAEQGSVEMYN SPLSEYAILGFEYGYAQQAL
LKTLLVLEAQFGDFANGAQIIFDQYISSGIQKWDLHSDIVLLLPHGYEGQGPEHSSSRIERYLQLAANWNFQV
VLPSTPVQYFRILREHAKRDL SPLVIFTPKLLLRYPQCVSSIEEFTEPGGFRAILEDADPNYDASILVLCSGKIY
YDYAEMLPQDRRKDFSCRLIESLYPLALEDLVSLIDKYSHLKHFWWLQEESKNMGAYDYMFMALQDILPEK
LLYIGRPRSSTASGSAKLSRQELVTCMETLFSLR

>core/45/1/Org1_Gene230

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SPESTSRRIRAKNRSSFSSEESESSAHIPVDTSEPAPVSIADPEPELEVVDDEVCDDESPEVHPVAEVLPEQPVLPET
PPQEKELEPKPVKPAEPKSVVMIKSKFGPTGKHINHLLAKTFKAPAKEEKVVAGSKSTKPVASDKTGKPGTSE
GGEQNNREKQFN PANRSPASGPKRDAGKKNLTDFRDRSKKSDESLK AFTGRDRYGLNEGGEEDRWKRRV
YKPKKHYDEASIQRPTHIKISLPITVKDLAAEMKLKASEVIQKLFHGMTYVVNDILDSETAVQFIGLEFGCTID
IDYSEQDKLCLSN DTVRDEIQSTDP SKLVIRSPIVAFMGHVDHGKTTLIDSLRKS NVAATEAGAITQHMG AFC
CSTPVGDITILDTPGHEAFS AMRARGAEVCDIVVLV VAGDEGIKEQTLEAIEHAKAADIAIVVAINKCDKPNF
NSETIYRQLSEINLLPEAWGGSTVTVNTSAKTGEGLSELLEMLALQAEVLELKADPSARARGLVIESELHKGL
GPVATVLIQNGSLKLGEALVFND CYGKVKTMHNEHNELMKEAGPSIPVLITGLSDIPKAGDPFFVVKNEKTA
RDIIARSAGQQRFALQQKKRPNFDSMLQNK KTLKLMIKADVQGSIEALVSSISKIKSEKVDVEILTNSVGEIS
ESDIRLAAASKAVLIGFHTGIESHA EPLIKSLGVRVELFTVIYHAIDAIKEIMTSLLDP IAAEEKDEGSAEIKEIFRS
SQVGSIIYGCIVTEGIMTRNHKVRVLRNKEILWKGT LSSLKRVKEDVKEVRKGLECGILLEGYQQAQIGDVLQ
CYEVIYHPQKL

>core/46/1/Org1_Gene682

MLSNTIRSNFLKFYANRHHTILPSSPVFPHNDPSILFTNAGMNQFKDIFLNKEKVSYSRATTSQKCIRAGGKHN
DLDNVGHTSRHLTFFEM LGNFSGFDYFKA EAIAFaweVSLSVFNFNPEGIYATVHEKDDEAFALWEAYLPTD
RIFRLTDKDNFWSMANTGPCGYCSELLFDRGPSFGNASSPLDDTDGERFLEYWNLVFM EFNRTSEG SLLALP
NKHVDTGAGLERLVSLIAGTHTVFEADV LRELIAKTEQLSGKVYHPDDSGAAFRVIADHVRSLSFAIADGLLP
GNTERGYVLRKILRRSVNYGRRLGFRNPFLAEIVPSLADAMGEAYPELKNSLSQIQKVL TLEESFFKTLDRG
GNLLQQVLKSSSSSSCISGEDAFKLKDTYGMPIDEISLLAKDYDYSVDMDTFHKLEQEAKERSRKNVVQSQG
TSESIYNELHLTSEFIGYDHLSCDTFIEAII SKDHIVSSLQEKQEGAIVLKVSPFYAEKGGQVGDSGEIFCSEGTFI
VTHTTSPKAGLIVHHGRISQGS LTVEAAVTAQVNRYRRKRIANNHTACHLLHKALEITLGDHIRQAGSYVDD
TKIRLDFTHPQAISPEDLLCIETLVNESIRENEPVDIREALYS DVMNSSEIKQFFGDKYSDVVRVVSAGHSHEL
CGTHAEATGDIGFFRITKEHAVAMGIRRIEAVTGEKAEATVHQQSEVLEEIATLLQVPRDQIVSRLTATLDER
KQQDKRLNELENSLIQTKLDKLIHNCHQRQGITCLVHHLAEHENHRLQQYAQCLHQRIPEKLISLWTTEKNG
KYIVLSRVSDDLITQGVHAQDLLKAVLTPCGGRWGGKDQSAQGSAPALPATEVLNETLWQWISTQLI

>core/47/1/Org1_Gene553

MSTFSIQNRLRTISGESTRIIKLDHKYSGFDPRSVPAINLEELNSGIYALRHLMNALQSENTNVAALLNPNTTIF
PTTSWTDYKHSRPQASSPRAPSSQTPTDIVSAAALALVLVIDGGLAELVASVTEIDL GALSTISTVRQLMASYL
GLTTLTAEQEKVVFSSSYVPSEKNLLEHVKQEKAAEIQAKQEEIKAVLEAKGVSTEEIEAILKEYPDIYAADFF
KEFIEEPLHTYRAKVGAPIQEMNENAIQLLTPPAITPDNVNEVNGMNTLSTILQAIDDAIKQAPALGGDQEIT
ILQTLVPLVDKTTFTKAEFDLIYTATQLPNTASLKLYLTDRQIAEYRGKITKVYQNSIQNLSETKRVVENNRSM
LETQLSMFQQAQNCFVTWISQANALNIAITNKYISAVLTTSMEMYGGLLCLSYMYERLADDEKAIFDKSVNE
YLPPIHVVGGSWVNGWIAKMAAYQELAEYSLGTAVTSQDQIKAYLQTRGNEFKATRHFFHNIGDQMYQFAN
ETVFGNCLTTANGAIQPDLGGFIREAMTNVGTVEADYVSNAQRILNEFNATAAHVLQLQLQIAELQKKADD
LDPGKASFTENRKFVAAAWITSESLGDALISMILNSQLPKQEAFLKPLIEEINFNLAANALNSLLQITNEFSTT
SVYYSLSSYLVSQKTGQNLFAGDYYETLLAAAREREYIYRDTARCKQAINLVNGLLQKINSLPGATSAQKQE
MLNATTYYQYSLSVTLNQLTVLESLLAGLKMTLQTTSNNKYDKSVFKIESFDDWIPTLAALESFLTSGFPNIS
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>core/48/1/Org1_Gene586

MKKSLIIVESPAKIKTLQKLLGSEFVFASSIGHIVDLPakeFGIDVDHDFEPQYQVLPDKQEVINHIRKLAACKCE
KVYLSPDPDREGEAIAWHIANQLPDSPLIQRVSFNaitKNAVTEALKHPRTIDMALVNAQQARRLLDRIVGYK
ISPILSRKLQQRSGISAGRVQSVALKLVDREKAIDAFVPVEYWNLRVLMQDPKTTKTFWAHLYAVQGKKW
EKEIPEGKTENDVLLINSEEKARHYAELLEKSSYTITRVEAKAKRRFAPPPFITSTLQQEASRHFRRFSASRTMSI
AQTLYEGVDLDSedSTGLITYMRTDSVRVDPEALTTVREYIQQTfGKEYLPEKANVYTTKKMTQDAHEAIRP
TDINLTPDKLKNKLSDDQFKVYNLIWKRFVASQITPAIYDTLAVQITTDTEIDLRASGSLLKFKGFLAVYEEKQ
DDENDQEEDHPLPPLHAQDALIKEEVSQEQAFTKPLPRFTEASLVKELEKSGIGRPSTYATIMNKIQSREYTTK
ENQRLRPTELGKIISQFLETNFPRI MDIGFTALMEDELELIADNKKPWKLLLQEFWTTFLPVVITAEKEAVIPRI
LTNIECSKCHKGKLVKIWSKNSYFYGCSEYPECDYRTSEEELAFNKEDYAEDTPWDSPCPLCGGVMKVRHG
RYGTFLGCEKYPECRGTISIHKKGEEIEQEEPIPCPAIGCNGKIFKKRSRYNKIFYSCSEYPECSVIGNSIDAVITK
YSGTEKIPYKKKTPTKKKSSAKTTKAAKTPSKKGKAKSSVKSSEKKTGPLFLPSPDLAKMIGNEPVSRGEAT
KKIWDYIKEHQLQAPENKKLLVPDNNLATIIGPNPIDMFQLSKHLSQHLLTKVSNDessASS

>core/49/1/Org1_Gene949

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VAWNPWADQGVVGISEVIERYGIPPGNIPDYLALVGDSSDNIPGLPGCGPKKAAALLKQFGSVEGLLENLDA
VKGLSQTMLSERQETLKLskRLALLDSNIPVPIESLTFPQHPVDEEKLIHFYIQQGFKTLVPSKQTEAATVDV
QIIKDAESLTNINLVQGGDIAFAVAYTGNHLLSLKLEGLALTQGGSGVFFIALEEgTKILPILKDFFLREDLTF
YGYNLKRDCHALLNAGIVIREISYDLALAEHLTNGGGKISFQSLLVNHGFTETAHRFAKEWGNsgLPiGRlPE
QPEQYFGEFVAYLPIIKDAILEEINRKNLNHILSDIEMPLEKVLFSMERAGVPLDVEELAILEALFETELAVLTE
EIYDLSGGPFNIKSPKQLSDILYNELGLRPIDKAKSTRAEVLEALRSEHPiIEKLLAFRTIEKLLSTYVKALPKQV
DSHTQRIHPSFDQTGAVTGRLACRDPNLQNIPIRSErgILLRKAfRLSEKNSYFLSADYSQIELRFLAHLsQDKS
LKFAFESGEDIHAFtasQVFHVPLEQVSKEQRMQAkTVNFGIVYgQQAfGLAKVLKISIGEAQELIqAYFSRY
PEIAHFVEETIQQAakDLRVTTMLGRERIIDSWNEFPgsRAASGRFAVNTRIqGSAAELIKLAMLDisQAIKQQ
QMKSrMLLQIHDELLFEVPEEEIEEMQRLVREKMESAMTLsvPIVVNIlIGKNWAEc

>core/50/1/Org1_Gene93

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EGEVDPKPSPGLQTLLRDAKQEAKTLGDEYISGDHLLLAFWSSNKEPFNSWKQTTKVSFKDLKNLITKIRRGN
RMDSPAESNFQGLEKYCKNLTALAREGKLDPVIGRDEEIRRTIQVLSRRTKNNPMLIGEPGVGKTAIAEGLA
LRLIQGDVPESLKGKQLYVLDMGALIAGAKYRGEFEERLKSVLKDVESGDGEHIIFIDEVHTLVGAGATDGA
MDAANLLKPALARGTLHCIGATTLENEYQKYIEKDAALERRFQPIFVTEPSLEDAVFILRGLREKYEIFHGVRIT
EGALNAAVLLSYRYIPDRFLPDKAIDLIDEAASLIRMQIGSLPLIDEKERELAALIVKQEAIKREQSPSYQEEA
DAMQKSIDALREELASRLGWDEEKKLISGLKEKKNSLESMTKFSEEEAERVADYNRVAELRYSPLIPLEEEIK
QDEASLNQRDNRLQEEVDERLIAQVVANWTGIPVQKMLEGEAEKLLILEESLEERVVGQPFVSAVSDSIR
AARVGLNDPQRPLGVFLFLGPTGVGKTELAKALADLLFNKEEAMVRFDMSSEYMEKHSISKLGSSPGYVGYE
EGGSLSEALRRRPYSVVLFDIEKADKEVLNILLQVFDDGILTDGKKRKVNCKNALFIMTSNIGSPELADYCS
KKGSELTKEAILS SVVSPVLKRYLSPEFMNRIDEILPFVPLTKEDIVKIVGIQMRRIAQRLKARRINLSWDDSVIL
FLSEQGYDSAFGARPLKRLIQKVILLKALLKGDIPDTSIELTMAKEVLVFKKVETPS

>core/51/1/Org1_Gene957

MAVRLIVDEGPLSGVIFVLEDGISWSIGRDSSANDIPIEDPKLGASQAIINKTDGSYYITNLDDTIPIVVNGVAIQ
ETTQLKNEDTILLGSNQYSFLSDEFDPQDLVYDFDIPEDNFSNDSGDLSDSNEQGKDLEPRQTSETNHSPKPKE
KLTKDQGSSDPITSGDQELADAFASAKAEKNQPRAKVAKKGLKESSNESLNPKEQNAKDSPKGEERTNKPQ
NAIMEDNGASPRQDPQPKSAEPSLKNTARDETPLKENKPVEEKANKKATPDSPEKKDQPEEGSKIEATPLDSQ
KESDKEAEEAFVQEEEEENLTEDNKEDSDSAADANDDTASDHTAEDNKETPKKVENEKSAVLSPFHVQDLF
RFDQTIFPAEIDDIACKNISVDLTQPSRFLKVLAGANIGAEFHLDGSKTYILGTDPTTCDIVFNDLSVSHQHAK
ITVGNDGGILIEDLDSKNGVIVEGRKIDKTSTLSSNQVVALGTTFLLLIDHHAPADTIVASLSPDDYSLFGRQQ
DAEALERQEAQEEEEKQKRATLPAGSFILTLFVGGLAILFGIGTASLFHTKEVVPLENIDYQEDLAQVINQFPT
VRYTFNKTNSQLFLIGHVKNSTDKSELLYKVDALSFVKSVDNDVIDDEAVWQEMNILLSKRPEFKGISMHSP
EPGKFIIITGYVKTEEAACLVDYLNHFNYLSLENKVVVETQMLKAIAGHLLQGGFANIHVAFVNGEVILT
YVNNDDAEKFRVAVVQELSGIPGVRLVKNFAVLLPAEEGIIDLNLRYPNRYRVTGYSRYGEISINVVVNGRILT
RGDVIDGMTVTSIQPNAIFLEKEGLKYKIDYNK

>core/52/1/Org1_Gene833

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NLQLPPSSSSSSSSSRNPSSSKSPLGHSLSGDKNEKLSALKAYGYDLTEMVRESKLDPVIGRSSEVERLILILCR
RRKNNPVLIGEAGVGKTAIVEGLAQKIILNEVPDALRKKRLITLDLALMIAGTKYRGQFEERIKAVMDEVKHK
GNILLFIDELHTIVGAGAAEGIDASNLKPALARGEIQCIGATTIDEYRKHIEKDAALERRFQKIVVHPPSVDE
TIEILRGLKKKYEEHHNVFITEEALKAAATLSDQYVHGRFLPDKAIDLLDEAGARVRVNTMGQPTDLMKLEA
EIENTKLAKEQAIGTQEYEKAAGLRDEEKKLRERLQSMKQEWENHKEEHQVPVDEEAVAQVVSQTGIPSA
RLTEAESEKLLKLEDTLRRKVIGQNDAVTSICRAIRRSRTGIKDPNRPTGSFLFLGPTGVGKSLLAQQIAIEMFG
GEDALIQVDMSEYMEKFAATKMMGSPPGYVGHEEGGHLTEQVRRRPYCVVLFDEIEKAHPDIMDLMLQILE
QGRLTDSFGRKVDFRHAIIMTSNLGADLIRKSIGEIGFLKSHMDYKVIQEKIEHAMKKHLKPEFINRLDESVI

FRPLEKESLSEIIHLEINKLDSRLKNYQMALNIPDSVISFLVTKGHSPEMGARPLRRVIEQYLEDPLAELLKES
CRQEARKLRATLVENRVAFEREEEEQEAAALPSPHLES

>core/53/1/Org1_Gene882

MKIPLRFLLLISLVPTLSMSNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVFKDSVVIENVPKTGET
QSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSEAANKTVTLSGFSALSFLKSPASTVTNGLGAIN
VKGNLSLLDNDKVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNSSSTRGGAIHTKNLTLSSGGETLFQNGT
APTAAGKGGAIADSGTLSISGDSGDIIFEGNTIGATGTVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGS
TSVADALNINSPDTGDNKEYTGTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQ
DANSKLIMDLGTSLVANTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVLAISDESFYQNGFLNEDH
SYDGILELDAGKDIVISADSRSIDAVQSPYGYQGKWTINWSTDDKKATVSWAKQSFNPTAEQEAPLVPNLLW
GSFIDVRSFQNFIELGTEGAPYEKRFVWAGISNVLHRSGRENQRKFRHVSGGAVVGASTRMPGGDTLSLGFA
QLFARDKDYFMNTNFAKTYAGSLRLQHDASLYSVVSILLGEGGLREILLPYVSKTLPESFYGQLSYGHTDHR
MKTESLPPPPRRSRRIILLGEDMSGLESWELELLLKIPAAEDFSKSTLHL

>core/54/1/Org1_Gene842

MFNKDEIIVPKNLEEEMKESYLRYSMSVIISRALPDIRDGLKPSQRRVLYAMKQLSLSPGAKHRKCAKICGDT
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VDIVPNYDETKHEPVVFPKFPNLLCNGSSGIAVGMATNIPPHNLGELIEATLLLLANPQASVDEILQVMPGPD
FPTGGIICGSEGIRSTYTTGRGKIKVRARLHVEENEDKHRESIIITEMPYNVNKSRLIEQIANLVNEKTLAGISDV
RDESDKDGIIRVVLEIKKGESSEIIINRLYKFTDVQVTFGANMLALDKNLPRTMSIHRMISAWIRHRKEVIRRT
RYELNKAETRAHVLEGYLKALSCLDALVKTIRESGNKEHAKERIIESFGFTEPQALAILRLYQLTGLEAEKI
QKEYEELLNKIAYYKQVLSDEGLVKDIIRNELQDLLKHHKVARRTTIEFDADDIRDIEDIITNESVIITISGDDY
VKRMPVKVFKEQRRGGHGVTFGDMKKGAGFLKAVYSAFTKDYLIFTNFGQCYWLKVVWLPEGERRAKG
KPIINFLEGIRPGEELAAILNIKNFDNAGFLFLATKRGVVKKVSLDAFSNPRKKGIRALEIDEGDELIAACHIVS
DEEKVMLFTHLGMVVRFPHEKVRPMGRTARGVRGVSLKNEEDKVVSCQIVTENQSVLIVCDQGFGKRSLVE
DFRETNRGGVGVRISILINERNGNVLGAIPVTDHDSILLMSSQGQAIRINMQDVRVMGRSTQGVRLVHLKEGD
ALVSMEKLSSNENDDEVLSGSEEECSDTVSLR

>core/55/1/Org1_Gene958

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ERATVAKSIPVAAIHEKPLSSTHASVQVTASTPAATGSGVGAYYNAVKKQKWAQDLIVELNTVMTTIMASVNS
KNPANKDVFDKLNTELQALVAAGNNLTEENFQTLYNFP EEIFTAIQRADTFTGGMKTDFTNQLAGKYGNQA
TLTQTFADGRVEGFKDILTAVQGVLTPEQFTIFAEIATELQALADHVGNFDEAGLQRIEDAGEKLAAVINSSD
LTRNDKIMFCQHITDLYSDQVAALGSFDTVLDASIYVNQHQGTMFSNLSSFVGSLIGTFAPIDLSSSQGDISSA
ALAGALQTARGLNSRFNELTAEQQKLINECIKSLVTFKCGEHLGAIWAYFTASTVVALNPTATMDHVKAAIL
EEAKELDNSSFQLASSIKSAMTSIVNSSGSFSVTVNSSTLQYTIYSEKNGKVEINQILLNYGSIGFLPEITKLAKT
NAESTARSYFRFKALAAVESENVQNKIEDLQSQLQQFTNMKTELFDGQLLSQASELRALPLPSAVASVLIDRY
MPKEVDYLNIEYKKLYYSNLGSSVGNSIIDAISQYVNGATYFNFASYVGQQPAVGAGGANAFPGSQAQAK
LDQERKQAALYLQETRGA LTVIEEQRARVLKDDKITNEQRSTILDSLRNYEDNINSISGSLVLLQNYLQPLSIA

GGSVAGTFEVKEGQEQWQARLQILEEALVSGLVGNMINGGMFPLQSTIQSDQQSFADMGQNFQLDLQMHLT
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>core/56/1/Org1_Gene867

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LSTGSFFIEECENTKELVDEICRLAPSEVLSCNKFYNKETAIVMQLQQHLKLTSTYADWAFEHKFASQKLTT
HFQVASLDGFGGLKGLVPAINAAGGLLSYIQDKLLLPTKHIAIPQTRGKQQKLLIDTASQVNLELLAPLNDPQG
KNSLLRIMDHTSTPMGGRLLRQILISPFYNPKEILVRQDAVEFFLRQVTLRKNIKTYLCQVRDIERLMTKVTTG
LAGPRDIGTLRDSFSAGA QIYEQLASATLPEFFIDKCSLDTKLASLIALLSKSLNGDLPLRVSDGNIFVDEFHND
LKRLRHNQEHSQEWIWEYQERIRKETGIKKLKICFAQALGY YIEVSSEFAPQLPKDFIRQRSRLHAERFTTIEL
QQFQDDMSNISEKLQTLETQFFKDLCSHILQRTEILALSQSLADLDYIISLADLAHAQGYCRPRVDMSDTLCI
YRGCHPVAKTLVDTGKFIPNDTEMRG SQTRMILLTGPNMAGKSTYIRQIALLVIMAQMGSYIPAKSAHIGVID
KIFTRIGAGDNLSKGMSTFMVEMAETANILHNATDRSLVILDEVGRGTSTYDGLAIAQAVVEYLLFTDKKKA
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RQLEGPESITRPAQDKMQQLTLF

>core/57/1/Org1_Gene1020

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QRIVNGYQEEAPDEWLR YGNPWEICRGEYLYPVRFYGRVIHYTDSRGKQVADLVD TQEVLAMAYDIPIPGY
GNDTVNSLRLWQAQSPRGFEFSYFNHGNYIQAIEDIALIENISRVLYPNDSITEGQELRLKQEYFLVSATIQDIIR
RYTKTHICLDNLADKVVVQLNDTHPALGIAEMMHILVDREELPWDKAWEMTTVIFNYTNHTILPEALERWP
LDLFSKLLPRHLEIIYEINSRWLEKVGSRYPKNDDKRRSLSIVEEGYQKRINMANLAVVGS AKVNGVSSFHSQ
LIKDTLFKEFYEFFPEKFINVTNGVT PRRWIALCNPRLSKLLNETIGDRYIIDLSHLSLIRSFAEDSGFRDHWKG
VKLKNKQDLTSRIYNEVGEIVDPNSLFDCHIKRIHEYKRQLMNILRVYVYNDLKENPNQDVVPTTVIFSGKA
APGYVMAKLIKLINSVADV VNQDSRVNDKLVFLPNYRVSM AEHIIPGTDLSEQISTAGMEASGTGNMKF
ALNGALTIGTMDGANIEMA EHIGKENMFIFGLLEEQIVQLRREYCPQTICDKNPKIRQVLDLLEQGGFFNSNDK
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PTKSCSGEGN

>core/58/1/Org1_Gene679

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CHESLQDHLLFELYTVTLHSGYENRKQDMLLAKEQG DYKKAIELAKELVA ALEKGSCSPHPEIVQIEKTFLQ
KTLLALQIKVAQEAQESCDALLTPYCLSEIAYTEAMDALVLRIARGEVSRTNEVDSVLLSHALQHLPFA REKA
IPELEVLI DHGAYLESTLLYYAYFSLLELYHQNKDFASLERLLEKGD AVFVPEHPYFPEY GFFLGAYFYAKGK
YESAEKVFLQIIDPAVKLGATFARAYEYLGCIAYVQNHYEKAEEYFLRAYKSWGREESGIGLFLAYAVQKKK
TACEDMLYHPKFSFTYRHLLDSLCSLSYPHGENKGSSAIQRVHRAVPELSEIYSRCIYDMIKYRNV TYTHPIIE
LAYNQVRNLEKRNLEEICRDAQDPEYDKALAFWGALQSGASVPRSLIESSDVDEARITIRCYEALYFHNPD AI
AMLPQAFSEECNSWQTALRLVWTLVRPKGAPNHAKYWDHLVLRPHGDSL YFFGYDLQEY LIGKEDALKHL

SVFAELFPKSSLLSLVYYLQGYSESSALRKVGWVFKALEEFTEISWSGEHMKTWAYIYYMVKLDLADTYISL
GNFSQAVHILEEVKEDWQVASHPKLHFLKGEDCYLAMELRWVEGLAYAYFQLHETAHLSNHLLEHVEKNLI
SPRSYRDYYGESLQRTLGLCQRFLGV

>core/59/1/Org1_Gene98

MRYDPNLIEKKWQQFWKEHRSFQANEDEDKVKYVLDMPYPSPGAGLHVGHLLIGYTATDIVARYKRARGF
SVLHPMGWDSFGLPAEQYAIRTGTHPKVTTQKNIANFKKQLSAMGFSYDEGREFATSDPDYYHWTQKLFLF
LYDQGLAYMADMAVNYCPELGTVLSNEEVENGFSIEGGYPVERKMLRQWILKITAYADKLLEGLDALDWP
ENVKQLQKNWIGKSEGALVTFHLTQEGSLEAFTTRLDTLLGVSFLVIAPEHPDLDSIVSEEQRDEVTAYVQES
LRKSERDRISSVKTKTGVTGNVYAKHPITGNLLPVWISDYVVLGYGTGVVMGVPAHDERDREFAEMFSLPIH
EVIDDNGVCIHSNYNDFCLNGLSGQEAKDYVINYLEMRSLGRAKTMYRLRDWLF SRQRYWGEPIPIIHFEDG
THRPLEDDELPLPPNIDDYRPEGFGQGPLAKAQDWVHIYDEKTGRPGCRETYTMPQWAGSCWYYLRFCDA
HNSQLPWSKEKESYWMPVDLYIGGAEHAVLHLLYSRFWHRVFDAGLVSTPEPFKKLINQGLVLASSYRIPG
KGYVSIEDVRENGTWISTCGEIVEVRQEKMSKSKLNGVDPQVLIIEYGADALRMYAMFSGPLDKNKTWSN
EGVGGCRRFLNRFYDLVTSSEVQDIEDRDGLVLAHKL VFRITEHIEKMSLNTIPSSFMEFLNDFSKLPVYSKRA
LSMAVRVLEPIAPHISEELWVILGNPPGIDQAAWPQIDESYLV AQTVTFVVQVNGKL RGRLEVAKEAPKEEVL
SLSRSVVAKYLENAQIRKEIYVPNKL VNFVL

>core/60/1/Org1_Gene12

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ADNKELTEELKAYSISIVSVIKDLLKLNPLFKEELQIFLGHSDFTEPGKLADFSVALTTATREELQEVLTTNM
HDIRDKALILLKKELDLSRLQSSINQKIEATITKSQKEFFLKEQLKTIKKELGLEKEDRAIDIEKFSERLRKRHPV
DYAMEVIQDEIEKLQTLETSSAEYTVCRNYLDWLTIIPWGIQSKEYHDLKKAIEVLNKDHYGLDEIKQRILELI
SVGKLSKGLKGSIIICLVGPPGVGKTSIGRSIAKVLHRKFFRFSVGGMRDEAEIKGHRRTYIGAMPGKMVQALK
QSQAMNPVIMIDEVDKIGASYHGD PASALLEVLDP EQNKDFLDHYLDVRVDLSNVLFILTANVLDTIPDPLD
RMEILRLSGYILEEKLQIAKKYLVPKARKEIGLTASEVNFQPEALKYMINNYAREAGVRTLNNGNIKKVLRKVA
LKIVQNQEKPKSKKITFKISSKNLQTYLGKPIFSSDRFYESTPVGVATGLAWTSLGGATLYIESVQVSSLKTD
HLTGQAGEVMKESSQIAWTYLHSALHRYAPGYTFFPKSQVHIHIPEGATPKDGPSAGITMVTSLLSLLLETPV
VNNLGMTGEITLTGRVLGVGGIREKLI AARRSRLNILIFPEDNRRDYEELPAYLKTGLKIHVSHYDDVLKVA
FPKLK

>core/61/1/Org1_Gene972

MKGTPQYHFIGIGGIGMSALAHILLDRGYEVSGSDLYESYTIESLKAKGARCFSGHDSHVPHDAVVVYSSSI
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YSGSSKIFVAEADESDGSLKHYPRAVVITNIDNEHLN NYAGNLDNLVQVIQDFSRKVTDLNKVFYNGDCPIL
KGNVQGISYGYSPECQLHIVSYNQKAWQSHFSFTFLGQEYQDIELNLPQHNAAAACGVALTFGIDINII
RKALKKFSGVHRRLERKNISESFLFLEDYAHHPVEVAHTLRSVRDAVGLRRVIAIFQPHRFSRLEECLQTFPKA
FQEADEVILTDVYSAGESPRESIILSDLAEQIRKSSYVHCCYVPHGDIVDYLRNYIRIHDVCVSLGAGNIYTIGE
ALKDFNPKKLSIGLVCGGKSCEHDISLLSAQHVS KYISPEFYDVSYFIINRQGLWRTGKDFPHLIEETQGDSPLS
SEIASALAKVDCLFPVLHGPFGEDGTIQGF FEILGKPYAGPSPSLAATAMDKLLTKRIASAVGVPVVPYQPLNL

CFWKRNPELCIQNLIETFSFPMIVKTAHLGSSIGIFLVRDKEELQEKISEAFLYDTDVFVEESRLGSREIEVSCIG
HSSSWYCMAGPNERCGASGFIDYQEKYGFDDGIDCAKISFDLQLSQESLDCVRELAERVYRAMQGKG SARIDF
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>core/62/1/Org1_Gene675

MIRERKKS RHPRLPTLPLAAKASLYLFFACFSGLSLWSFHRDQPCTQNWIGLLGWSFSSFLLYFFGAAAFFIPL
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YEGQSFC LKHLIGSVGTALIFGFV MLFSVLYLCGGIAL LKKKTFQDGVKKAFC SFFQTCFKNLKKLINRRNYL
PKPSVPFVSKNPF SCKTSQPSRRVSE TIILDGSGISPLQEEIPGSKKESFFLTPHPCKRFLT K FVEPQENKAKEGK
TIALSSTPTV VRESKGKERAALPKLKS LA VPENDLPQYHLLSKNREARPE SLQAELERKALILKQTLTSFGIDA
DLGNICSGPTLAAFEVLPHSGVKVQKIKSLENDIALKLQASSIRIIAPIPGKAAV GIEIPTFPFPQAVNFRDLLEDY
QKTNRKLQIPLLLGKKANGDNLWADLATMPHLIIAGTTGSGKSVCINTIVMSMIMTTLPSEIKLVIIDPKKVEL
TGYSQLPHMLSPVITESREVYNALVWL VKEMESRYEILRYLGLRNIQAFNSRTRNK TIEASYDREIRETMPFM
VGIIDELSDLLLSSSQDIETPIRLAQMARAVGIHLILATQRPSREVITGLIKANFPSRISFKVSNKVNSQIIIDEPG
AENLMGNGDMLVLLPSVFGTIRAQGAYICDEDINKVIQDLCSRFTQYVIPSFHAFDDSDSDNSGEKDPLFAQ
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>core/63/1/Org1_Gene194

MDPKEKNYDASAITVLEGLQAVRERPGMYIGDTGITGLHHLVYEVVDNSIDEAMAGYCSRIDVRILEDGGIVI
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DKKCYQMEFSRGIPVTPLQYVSVSDRQGTEIVFYDPDKIFSTCTFDRSILMKRLREL AFLNRGITIVFEDDRDVS
FDKVTFYFEGGIQSFSYLNQNKESLFSEPIYICGTRVGDDGEIEFEAALQWNSGYSELVYSYANNIPTRQGGT
HLTGFTALTRVINTYIKAHNLA KNNKLALTGEDIREGLTAVISVKVPNPQFEGQTKQKLGNSDVSSVAQQV
VGEALTIFFEENPQIARMIVDKVFVAAQAREAAKKARELTLRKSALDSARLPGLIDCLEKDPEKCEMYIVEG
DSAGGSAKQGRDRRFQAILPIRGKILNVEKARLQKIFQNQEIGTHIAALGCGIGADNFNLSKLRYRRIIIMTDAD
VDGSHIRTL LLLTFFYRHMTALIENECVYIAQPPLYKVSKKKDFRYILSEKEMDSYLLMLGTNESSILFKSTERE
LRGEALESFINVILDVESFINTLEKKAIPFSEFLEMYKEGIGYPLYLAPATGMQGGRYLYSDEEKEEALAQEE
THKFKIIELYKVAVFVDIQNLKEYGLDISSYLIPQKNEIVIGNEDSPSCNYSCTLEE VINYLKNLGRKGIEIQR
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>core/64/1/Org1_Gene840

MNKRTL L FVSLIGIAFVGCQIFFGYNEFRSCKNLA EKQRKISEQTLAAVESVGLSVASWDTDVNGEEHKNNY
AVRVGDKL FLLHNGEAAQSVYSSGESWSFVDHKCGFDNIHLALYRQQGSSFNPTNTGKVFLPTNHEGLPVL
VVEFRNNKEPLVFLGEYAQGRISNKDSTIFGTALVFWRSGSDYIPLGLYDSREEKLVS LDLPITRAVIFGNDQD
SAKSSDTANHYVLFNDYMQII VSEESGSIEGINLPFASTNNKSIVNEIGFDRDLASEKSPEALFPGLSSKL PDGQ
QAKNSIGGYYP LLRRGLLSDSKKLLPLEYHALNVVSGRELATPVALRYRVLSYTPHSIQLES LDRSVQKVYKL
PENPEEKPYVFETAITLTKETEDVWVTSGVPEVEIMSNASAPTIKYRVIKKNKGS LDKVKLPKVKEPLAVRRG
VYPQWILNSNGYFGIILTPLSEIASGYGSLYISGSTAPTRLSAISPKNQLYPVSKYPGYETLLPLPKDAGTHRFL
VYAGPLAEPTLKVL DKTITQEKGENPEYLD SISFRGVFAFITAPFAALLFIIMKFFKLVTGSWGISIILLTVFLKL
LLYPLNAWSIRSMRRMQILSPYIQQIQQKYKNEPKRAQMEIMGLYKTNKNVPITGCLPLLIQLPFLIAMFDLLK

SSFLLRGASFIPGWIDNLTAPDVLFSWQTSIWFIGNEFHLLPILLGIVMFLQQKVTSLHKKGPVTDQQKQQQV
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>core/65/1/Org1_Gene438

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VCGAPNCEAGLIVALALPGAKLFDSEGQAYTIKKSKLRGVESQGMCCGADELGLDELQIQERALLELPEATP
LGEDLATVLGNTSLEISLTPNLGHCASFLGLAREICHVTQANLVIPKEFSFENLPTTALDMGNDPDICPFFSYV
VITGISAQPSPIKLQESLQALKQKPINAIVDITNYIMLSLGQPLHAYDASHVALDSLVEKLSTPESLTLLNGET
VLLPSGVPVVRDDHSLGLGGVMGAKAPSFQETTTTTVIKAAAYFLPEALRASQKLLPIPSESAYRFTRGIDPQN
VVPALQAAIHYLEIFPEATISPIYSSGEICRELKEVALRPKTLQRILGKSFSIEILSQKLQSLGFSTTPQETSLLVK
VPSYRHDINEEIDLVEEICRTESWNIETQNPVSCYTPIYKLKRETAGFLANAGLQEFFTPDLLDPETVALTRKE
KEEISLQGSKHHTTVLRSSLLPGLLKSAATNLNRQAPSVQAFEIGTVYAKHGEQYQETQTLAILLTEDGESRSW
LPKPSLSFYSLKGWVERLLYHHHLSIDALTLESSALCEFHPYQQGVLRHKKQSFATLGQVHPELAKKAQIKHP
VFFAELNLDLLCKMLKKTTKLYKPYAIYPSSFRDLTLTPEDIPANLLRQKLLHEGSKWLESVTIISYQDKSL
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>core/66/1/Org1_Gene988

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YLKRGYFASSVDYSLEHNQEKGHIDVLIKINEGPCGKIKQLTFSGISRSEKSDIQEFIQTKQHSTTTSWFTGSGL
YHPDIVEQDSLAITNYLHNNGYADAIVNSHYDLDDKGNILLYMDIDRGSRYTLGHVHIQGFEVLPKRLLIEKQS
QVGPNDLYCPDKIWDGAHKIKQTYAKYGYINTNVDVLFIPHATRPIYDVITYEVSEGSPYKVGLIKITGNHTHK
SDVILHETSLFPGDTFNRLKLEDTEQRLRNTGYFQSVSVYTVRSQLDPMGNADQYRDIFVEVKETTTGNLGLF
LGFSSLDNLFGGIELSESNFDFGARNIFSKGFRCLRGGGEHLFLKANFGDKVTDYTLKWKPHFLNTPWILGI
ELDKSINRALSKDYAVQTYGGNVSTTYILNEHLKYGLFYRGSQTSLEKRRKFLGPNIDSNGFVSAAGVNL
NYDSVDSPTPTTGIRGGVTFEVSGLGGTYHFTKLSLNSSIYRKLTRKGILKIKGEAQFIKPYSNTTAEGVPVSE
RFFLGGETTVRGYKSFIIGPKYSATEPQGGLSSLLISEEFQYPLIRQPNISAFVFLDSGFVGLQEYKISLKDRLSS
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>core/67/1/Org1_Gene856

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AEFVELQQILCQEGRLLEFVINQTRYIGRDLFKREDSLYKLWEWLGYLPSGDVRGERLKKSAREVVDRFMRT
TCNIRKIAMTFDRHVYSVAKTAFEKAFGALETVCYYESMRESYREAFCEYEKAKLLGDEEKSAHAEQRFQDIK
NRWEDVKDAFFWVKEDGKIEIDDAIGNSCKWSERYEEHRITRARWYKVAEHQLFNATMRVKDSLREHNEA
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ESIDKHYQSCVREQELY

>core/68/1/Org1_Gene830

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ENPSQGV PETSSGPEPQRLFSLPSVKKQSGLGRLVQTVRDRIVLPSGAPPTDSEPLSLYELNLR LSSLRQELSDI
QSN DQLTPEEKAEATVTIQQLIQITEFQCGYMEATQSSVSLAEARFKGVETSDEINSLCSELTDP ELQELMSDG
DSLQNL LDETADDLEAALSHARLSFSLDDNPTPIDNNPTLISQEEPIYEEIGGAADPQRTRENWSTRLWNQIRE
ALVSL LGMILSILG SILHRLRIARHAAAEAVGRCCTCRGEECTSSSEEDSMSV GSPSEIDETERTGSPHDVPRRN
GSPREDSPLMNALVGWAHKHGAKTKESSESSTPEISISAPIVRGWSQDSSVSFIVMEDDHIFYDVPRRKDGIYD
VPSSPRWSPARELEEDVFGDYEVPITSAEPSKDKNIYMT PRLATPAIYDLPSRPGSSGSSRSPSSDRVRSSSPNR
RGVPLPPVPSPAMSEEGSIYEDMSGASGAGESDYEDMSRSPSPRGDLDEPIYANTPEDNPFTQRNIDRILQERS
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GESEYLEPLGGLVATTKILLQKGWPRGESNA

>core/69/1/Org1_Gene1003

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LNFLINGGRSLMMTAESESLDLFHVSKRLGYLP SGDVRGEGLKKS AKEIVARLMSLHCEIHKVAVAFDRNSY
AMAEKAFKALGALEESVYRSLTQSYRDKFLESERAKIPWNGHITWLRDDAKSGCAEKKLRDAEERWKKF
RKAVFWVEEDGGFDINNLLGDWGTVLDPYRQERMDEITFHEL YEKTTFLKRLHRKCALAKTTFEKKRSKKN
LQAVEEANARRLKYVRDWYDQEFQKAGERLEKLHALYPEVSVSIRENKIQETR SNLEKAYEAIEENYRCCVR
EQEDYWKEEEKREAEFRERGNKILSPEELESSLEQFDHGLKNFSEKLMELEGHILKLQKEATAEVENKILSDA
ESRLEIVFEDVKEMPCRIEEEIEKTLRMAELPLLPTKKA FEKACSQYNSCAEMLEKV KPYCKESLAYVTSKERL
VSLDEDLRRAYTECQKRFQGD SGLESEVRACREQLRERIQEFETQGLDLVEKELL CVSSRLRNTECDCVSGV
KKEAPP GKKFYAQYYDEIYRVRVQSRWMTMSERLREGVQACNKMLKAGLSEEDKVLKEEEYWL YREERK
NKEKRLVGTKIVATQQRVA AFESIEVPEIPEAPEEKPSLLDKARSLFTREDHT

>core/70/1/Org1_Gene883

MLFSKNFSTDNGGAI TAKTSLTGTTMSALFSENTSSKKGGAIQTSDALTITGNQGEVSFSDNTSSDSGAAIFT
EASVTISNNAKV SFIDNKVTGASSSTTGDMSSGAICAYKTSTD TKVTLTGNQMLLFSNNTSTTAGGAIYVKKL
ELASGGLTLFSRNSVNGGTAPKGGAI AIEDSGELSLSADSGDIVFLGNTVTSTTPGTNRSSIDLGTSAKMTALR
SAAGRAIYFYDPITTSSTTVTDVLKVNETPADSALQYTGNII FTGEKLSETEAADSKNLTSKLLQPVTLSGGT
LSLKHGVTLQTQAFTQQADSRLEMDVGTTLPEADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLL
DPTGTFYENHSLRNPQSYDILELKASGTVTSTAVTPDPIMGEKFHYGYQGTWGPIVWGTGASTTATFNWTKT
GYIPNPERIGSLVPNSLWNAFIDISSLHYLMETANEGLQGDR AFWCAGLSNFFHKDSTKTRRGFRHLSGGYVI
GGNLHTCSDKILSAAFCQLFGRDRDYFVAKNQGT VYGGTLYYQHNETYISLPCKLRPCSLSYVPTEIPVLFSG
NLSYTHTDNDLKT KYTTYPTVKGSWGNDSFALEFGGRAPICLDESALFEQYMPFMKLQFVYAHQEGFKEQG
TEAREFGSSRLVNLALPIGIRFDKESDCQDATYNLT LGYTVDLVRSNPDCTTTLRISGDSWKTFGTNLARQAL
VLRAGNHFCFNSNF EAFSQFSFELRGSSRNYNVDLGAKYQF

>core/71/1/Org1_Gene651

MTLQPSYINFTPNVTTALSGGKIDTSAIELSCSALFFQELQDKAQGLKHALGLVQELSAEALRPAQVQTSISYL
PTEESSRPGISAGIIDRTMPTFTDDEVKAILQNP NFETSKIFVEGLDKVFKSYLDSVTPPEGIDPSNPESAILNYIT
LLNNLKPKFAAGSTPTDADYNALYALPGDFVKEIEALKAADAPPKSKVHAFWQEIMTIYNNMQVLSYPVTD
YLVNQIADLSLNITAAQEVQQYLKNFY SILKDILNPGWTD PQATHYPADA EYNARDAGVIQSLLNLSGNYRQ

LTENMLPNTDTSPLPQEIIAQIRSFQNGVNGTIIASNTLLPTTMRDLTLLGVIYTYQCCATIFGMSYGTSTPAKQN
YIDAINQEKS YWQARANGFDVTS DQVFDQFATNIQSGTSYRGIDLFKNNKVNEINPIFLSQAASFLRYPYNLM
SRSMYQTIEDAANRSITALDGLISGWSTQIATFQTQKNSLDPSLLKYFDTMKANKESFVTTAPLQMVYSSLML
DKYLP TQQNVIASLGIQMTYSNKA AKYLNELIKEITTFQSADIYYSLSIYLKQMN LQAVADPIGKAVGV LNDE
KTRAMADITRCNKIKAAIDKMLVEIKADAELSKSQIRELVDTLTNFKSQSDDLIRNLSCLLGFLSGLTLKAVN
DPNATYEAFTAEIFTEPFNNWKRQLATFESFVIQGGQNGITPGGQQQLLQAMESSQQDFSTFNQNQQLALQLE
SSAMQQEWTLVSAALALLNQMVSKIARRIKS

>core/75/1/Org1_Gene620

MVFFRNSLLHLVALSGMLCCSSGVALTIAEKMASLEHSGRGADDYEGMASFNANMREYSLQLSKLYEEARK
LRASGTEDEALWKDLIRRIGEVRGYLREIEELWAAEIREKGGNLEDYALWNHPETTIYNLVTDYGTEDSIYLI
PQEIGAIIKIATLSKFVVPKESFEDCLTQILSRLGIGVRQVNSWIKELYMMRKEGCSVAGVFSSRKDLEALPETA
YIGFVLNSNVDAHTNQHV LKKFINPETTHVDVIAGRVWIFGSAGEVGELLKIYNFVQSESIRQEYRVIPLTKID
PGEMISILNAAFREDLTKDVSEESLGLRVVPLQYQGRSLFLSGTAALVQQALTLIRELEEGIENPTDKTVFWYN
VKHSDPQELAALLSQVHDFVSGENKASVGAADGCGSQLNASIQIDTTVSSSAKDGSVKYGNFIADSKTGTLI
MVVEKEVLPRIQMLLKKLDVPKKMVRIEVL LFERKLAHEQKSGLNLLRLGEEVCKKGCSPSVSWAGGTGILE
FLFKGSTGSSIVPGYDLAYQFLMAQEDVRINASPSVVTMNQTPARIAVVDEMSIAVSSDKDKAQYNRAQYGI
MIKMLPVINVGEEDGKSYITLET DITFDTTGKNHDDRPDVTRRNITNKVRIADGETVIIGGLRCKQMSDSHDGI
PFLGDIPGIGKLFGMSSTSDSLTEMFVFITPKILENPVEQQRKEEALLSSRPGEREEYYQALAASEAAARA AH
KKLEMFPASGVSLSQVERQEYDGC

>core/76/1/Org1_Gene708

MGYIESSTFRLYAEVIVGSNINKVLDYGV PENLEHITKGTAVTISLRGGKKVGVIIYQIKTTTQCKKILPILGLSD
SEIVLPQDLLDLFWISQYYFAPLGKTLKLFLPAISSNVIQPKQH YRVVLKQSKAKTKEILAKLEV LHPSQGAV
LKILLQHASPPGLSSLMETAKVSQSPIHSLEKL GILDIVDAAQLELQEDLLTFFPPAPKDLHPEQQSAIDKIFSSL
KTSQFHTHLLFGITGSGKTEIYLRATSEALKQ GKSTILLVPEIALTVQTVSLFKARFGKDVGV LHHKLSDS DKS
RTWRQASEGSLRILIGPRSALFCPMKNLGLIIVDEEHPAYKQTESPPCYHARDVAVMRGKLAHATVVLGSA
TPSLESYTNALSGKYVLSRLSSRAAAAHPAKISLINMNLEREKSKTKILFSQPVLKKIAERLEVGEQVLIFFNRR
GYHTNVSCTVCKHTLKCPC HCDMVLTFHKYANVLLCHLCNSSPKDLPQSCP KCLGTMTLQYRGSGTEKIEKIL
QQIFPQIRTIRIDS DTTKFKGSHE TLLRQFATGKADVLIGTQMIAKGMNFSAVTLAVILNGDSGLYIPDFRASEQ
VFQLITQVAGRSRSHLPGEILIQSFLPDHPTIHSAMRQDYS AFYSQEITGRELCEYPPFIRLIRCIFMGKCPKQT
WEEAHRVHNILKEQLESTNPLMPVTPCGHFKIKD TFRYQFLIKSAYVIPVNKKLHHALMLAKLSPKVKFMID
VDPMTTFF

>core/77/1/Org1_Gene78

MEKICGYLEQILVENKDSGDITAYIKIPNKTTPILIKGKLPQPLELGSP IQIYGVWSHSPSNTKYFQIHSYDSPLL
YEYRGVFHYLT SKLIKIGPKIAEKIIEKFQEKTCYVLDITPERLSEVSGISETRCVSICKQLCEQKILRK TLLFLQ
EYNIPIHYGVRIFFK KYQEK SIEKICEDPFLAREMEGIGFKTADFIAMKLGVP RNSESRLCAGIQHSLEELQEEG
HTCYPIELLIDVVA KLLNQDVFDTPITLEEIDTQILNMQKRKLLHIQDISGTLHVWTRYLHLAEKTIVSDLKRIL
FSSRRIRSIDGEKAIAWVEENLSIDLAEQQREAIKACFSEKLLIITGGPGTGKSTITQAILKIFEQVTHKIILAAPT
GKAAKRMTEITQKHSVTIHALLQYDFKTKSFRKNHDNPIDCDLIIVDESGMMDTHLLHHFLKALPDYTTLVFI

GDIHQLPSVGP GNILKDLITSNKMTVIRLNKIFRQVHDSGIVTNAHRVNEGELPILYSETGRRDFFQKDDQE
EALNHIIIHLVTKFVPQKYHIYPQDIQVLAPMKKGTLGIYNLNKALKHALNPKKANLHGRFQSYAVGDKVMQI
RNNYNKEVFNGDIGYVSTINFEDKAVVVRMEGKHVGYSFSELDLVLAYATSVHKYQGSSEPCIIPIHTSHF
MMLYRNLLYTAITRGKKLVILVGTKKAIAIATRNNRVQHRCTGLAEVLKELDTKKNYADL

>core/78/1/Org1_Gene930

MLSFFYKHQKKFIGIVIAVVCVSGTGVGWGRFSRKGSAAESTSRRTVFTTASGKRYVEKDFMAMKKFFAHEA
YPFTGNPRAWNFINEGLLTDYFLTTRVGEKLFVKVYHPGEKIFSKEKAYQPYRRFDAPFISSEEVWKSSAPQL
LEILKVFQQIENPISKEGFLARAKLFLEERRFPHYVLRQMLEYRRQMFALPPDEALSRGKDLRLFGYQTIQDW
FGDAYLSAAVELLIRFIDEQKKVLPRPSKQEARDDFYDKAKHAYTKISKNKEFSLGFEEFVNSYFQFLEISESE
FFNMYRDILLCKRALLLLQGGVSFDFQPLTTFFVQGKDSIQVEFFRLPKEYSFKTKQELKA FEVYLKLVSLPKS
DSL DVPNEILPIATIKAKEPRLVGRRFSIDYKRVALQDLAATVPMVEVLHWQQNSEHFQEILQQFPDVETCQS
YKDFQHLKPALRDKISLFRKEILRARPERILQSLQQVVPKQSQEVLLSAGKNSALPGISDGQQLAKVLLENEVL
DLYSQDAETYYTHIVNSSFEKEEVL PYREVLKRDLASQLLTSHGHLVDMERLESALRTRYPGEEGASLWQRR
LWKVVENHRLGRHLEGFSWSLDRSLKTF SRGDKELPQEFDRIFSMKVGDYSSVFMSPNEGPCYYQCLSHLL
YDRPASVDKLFLAKSQLDEELLGSYMERFIEQGVVR

>core/79/1/Org1_Gene564

MDYLEKLQVLIEEGQSANFLSLWEEYCFNDVVRGRELVEILEKVKSSSLASLFGKIVDTVVPWLEKIPEGKDK
DRVLQLILDQLQTSNSQMFFDIATEYVNKKYSGEENFNEALRVVGLRDGRDFQFSLSRFDLFMHMHKGNFVFH
QGGWGVGEVMGVSFLLQKVLIEFEGIMSAKDISFETA FKS LTPLSGDHFLSRRFGDPDGFEAFAKENPIEVVEI
LLRDLGPKTAKEIKDELVDLVIPEADWNRWWQSAKTKIKKGTRIISPDNPKEPYVLS DAGCSHMGQLERKLG
LSLNSAEKISLIYHFIRDLHSELKNIEIRKSLVKALQDL DVEEGNKSLLQRELLSEYLGIKDASIDKEYITSLE
DDTSRLLENMPIVALQKSFLSLVRKYSSFWQQVFMQILLYTTSPTMRDFVYKTIKNDPSSVEVLKKRLLDSA
HQPMMFPELFFVWFFLKLGNHEDGLFDPEDKEVLRLFLESALNFMYQVASTPHKELGKKLHHYLVGQRYLAVR
QMIEGASLPFLKELLLLSTKCPQFSSDLNVLQSLAEVVQPTLKKHKS NVEEENVLWSTSESFSRMKAKLQSL
VGKEMVDNAKEIEDARSLGDLRENSEYKFALEKRARLQEEIRVLSEEINRARILTKDLVFTDKVGVGCKVTL
KGDAGEVVEY TILGPWDADPDSCILSLQSKLAQNMLGKKLNDVVILQGKEYKISR IQSIWEEHGA

>core/80/1/Org1_Gene342

MVDKLIHPWDLDLLVSGRQKDPHKLLGILASEDSSDHIVIFRPGAHTVAIELLGELHHAVAYRSGLFFLSVPK
GIGHGDYRVYHQNGLLAHPYAF PPLWGEIDSFLFHRGTHYRIYERMGAIPMEVQGISGVLFVLWAPHAQR
VSVVGD FNF WHGLVNPLRKISDQGIWELFVPGLGEGIRYKWEIVTQSGNVIVKTD PYGKSFDPPPQGTARVA
DSESYSWSDHRWMERRSKQSEGPVTIYEVHLGSWQWQEGRPLSYSEMAHRLASYCKEMHYTHVELLPITEH
PLNESWGYQVTGYAPTSRYGTLQEFQYFVDYLHKENIGIILDWVPGHFPVDAFALASFDGEPLYEYTGHSQ
ALHPHWNTFTFDYSRHEVTN FLLGSALFWLDKMHIDGLRVDASMLYRDYGREDEGWTPNIYGGKENLE
SIEFLKHLNSVIHKEFSGLTFAEESTAFPGVTKDVDQGGGLGFDYKWNLGWMHDTFH YFMKDPMYRKYHQ
KDLTFS LWYAFQESFILPLSHDEVVHGKGS LVNKLPGDTWTRFAQMRVLLSYQICLP GKLLFMGGEFGQY
GEWSPDRPLDWELLNHHYHKTLRNCVSALNALYIHQPYLWMQESSQECFHWVDFHDIENNVIAYYRFAGS
NRSSALLCVHHFSASTFPSYVLRCEGVKHCELLNTDDESF GSGKGNRAPVVCQDQGVAWGLDIELPPLAT
VIYLVTF

>core/81/1/Org1_Gene879

MNKFKTYLQTALIAFFSFPALSGSFSSIAEEITQQVNHPGAELLSEGSYIPGLQTFRLGIKITASKGSHIYWKN
PGEIGSPLKISWQLPKGFVVEEEHWPTPKVFEEEGTTFFGYEDSALIVADVRAPEGYTPGQEVELRAQVEWLA
CGDSCLPGNVDLKLTLPYEEKEPSLYPDTHAEFTKTLHAQPRVLENDHSVQVAQKGNEIILNISKKINATKA
WVFSEKADKLFAYAETSYSGGTGTAWRLKVKNLSGVQKNEKLHGILLADHTGRPVESLTIHSEVLGQTGS
AVAGLSQYITILIMAFLLGGVLLNIMPCVLPLVTLKVYGLIKSAGEHRSSVIANGLWFTLGVVGCFWGLAGVAF
ILKVLGHNIGWGFQLQEPMFVATLIIVFFLFALSSLGLFEMGTMFANLGGKLQSSEMKSSNNKAVGAFFNGIL
ATLVTTTPCTGPFLGSVLGLVMSLSFLQQLLIFTAIGLGMASPYLVFSVFPKMLSVLPKPGGWMSTFKQLTGFM
LLVTVTWLWVIFGSETSTTSVVVLLGGLWLAGLGAWILGRWGTPVSPKKQRVCASLLFFAFLGGAISVSGLA
SHYFAEPQQTVSVNEDSLWQPFSLKLAQLRAQGRPVFVNFTAKWCLTCQMNKPVLYGDAVQKMFETHGI
VTLEADWTRKDPGITEELARLGRASVPSYVYYPGDNSAPVVLPEKITQNLLEDVVSRFVR

>core/82/1/Org1_Gene205

MIRSPLPFISSKRALNMLGLQDEFSCPEDVVDLFLFSEIELLAQQDEPSEGYLALSRSLLMMTHNHPKVVKRVIF
YGVSYGLKHKSMSIFIDVLTIDFLFEKLGISASDRLSLCSARTCINFELYSQTGEMKFLSEVVDNFRLEQLLK
MHPQLKNRLGWEHFRIGAKQEEVSLVASASVYQAVGRSFIELYHKHLELSDLACGMKCLALALDLSNNAH
IHADYAKGLVVLGTRQGKSLIERGMEHFSKAIFLSFSRDGDTLAYQNYRYSYALASVKLFDLTYKKEHFDQ
AMNILYQTVQAFPNLSGLWMVWGELLIRSGWLNSNMKYIEVGLEKLASLQKKTNDPIALSGLLATGIAILGL
YLEEPNLFKDSRHLISAMRTFPGNSALVHALGVVQLCSALYFNEDSHFASAISCFQSCLEWDLDATGMWQK
LFDAYFSWGIKKKSARLLRKAVDVASRLCSLRPEAFLFWSDRGLALKCLAEATIDEAYKEIFLSESLHYQRA
WDLGRLEILELWGQSHYLLAELQQSLFHYDEAYTLLTKVDLTLSSSRVKLILAAVLLGKGRLQDTPAEE
AREILEPLVEVYLEDENFLLLLGKVYLFLFWKNKNVCLGKLARTYLEKATSLGCPEAYYTLGKFYAVIKDVN
KAWGMVIRSAQYGVRITEAKWLNDPYLANLREIHAFREVVENQKGRLWLGNKTEMKRN

>core/83/1/Org1_Gene235

MNKLLNFVSRTLGGDTALNMINKSSDLILALWMMGVVLMIIPLPPPVDLMITINLSISVFLLMVALYIPSAQ
LSVFPSLLLITTMFRLGINISSRQILLKAYAGHVIQAFGDFVVGGNVVGFIIFLIITIIQFIVVTKGAERVAEVA
ARFRLDAMP GKQMAIDADLAGMIDATQARDKRAQIQKESELYGAMDGAMKFIKGDVIAGIVISLINIVGGL
TIGVAMHGMDLAQAAHVYTLLSIGDGLVSQIPSLLIALTAGIVTTRVSSDKNTNLGKEISTQLVKEPRALLA
GAATLGVGFFKGFPLWSFSILALIFVALGILLTTKSAAGKKGGGSGASTTVGAAGDGAATVGDNPDDYSLT
LPVILELGKDL SKLIQHKTSGQSFVDDMIPKMRQALYQDIGIRYPGIHVRTDPSLEGYDYMILLNEVPYVR
GKIPPHHVLTNEVEDNLSRYNLPFITYKNAAGLPSAWVSEDAKAILEKAAIKYWTPLEVILHLSYFFHKSSQE
FLGIQEVRS MIEFMERSFPDLVKEVTRLIPLQKLTEIFKRLVQEQISIKDLRTILESLSSEWAQTEKDTVLLTEYVR
SSLKLYISFKFSQGQSAISVYLLDPEIEEMIRGAIKQTSAGSYLALDPDSVNLIKSMRNTITPTPAGGQPPVLLT
AIDVRRYVRKLIETFPDIAVISYQEILPEIRIQPLGRIQIF

>core/84/1/Org1_Gene997

MYKRCVLDKILKGIVAGSLILLYWSSDLLERDIKSIKGNVRDIQEDIREISR VVKQQQTSQAIPAAPGVMLAPK
LVRDEAFALLFGDPSYPNLLSLDPYKQQTLPPELLGTNFHHPHGILRTAHVGKPENLSPFNGFDYVVGFDYDL CIPS
LASPHVGKYEEFSPDLAVKIEEHLVEDGSGDKEFHILRPNVFWRPIDPKALPKHVQLDEVFQRPHPVTAHDI

KFFYDAVMNPYVATMRAVALRSCYEDVVSVSSENDLKL VVRWKAHTVINEEGKEERKVL YSAFSNTLSLQ
PLPRFVYQYFANGEKIIEDENIDTYRTNSIWAQNFTMHWANNYIVSCGAYYFAGMDDEKIVFSRNPDFYDPL
AALIDKRFVYFKESTDLSLFQDFKTGKIDISYLPPNQRDNFY SFMKSSAYNKQVAKGGAVRETVSADRAYTYI
GWNCFSLFFQSRQVRCAMNMAIDRERIEQCLDGQGYTISGPFASSSPSYNKQIEGWHYSPEEAARLLEEEGW
IDTDGDGIREKVIDGVTVPFRFRLCY YVKSVT AHTIADYVATACKEIGIECSLLGLDMADLSQAFDEKNFDAL
LMGWCLGIPPEDPRALWHSEGAMEKGSANVVGFHNEEADKIIDRLSYEYDLKERNRLYHRFHEIIHEEAPYA
FLFSRHCSLLYKDYVKNIFVPTHRTDLIPEAQDETVNVTMVWLEKKEDPCLSTS

>core/85/1/Org1_Gene903

MKELRHESYNRALHKL SHQWVRYFLYTFVSCSFIVAIFTFAWLKVLYVPEYKAGEISRISLTAPMDFSLSWSA
HKFYKRTAHISEAFGKVYHLT LSPGSLLSKEGNADENTDYWFKKAADFLSTNFVDSSTQKCLKDL CIYPPLL
GKEKKTLEININSNKG NVIAQCFCCHKIFLIQENCPQPCFDAIMDILKIANFEVAVDKEMSGCVKGELLGKRCI
EKITKGTPILEKYQRIDDRDAKILKQLRAQLLSVHTL FSCRSLWGAIFVLLILLWGYGALKALCP EMLKSPQ
RFMLYIAILTSL L WCRGTEIFCAYWVS YLSYPPILPFTAVLLGYFLGLPIAGFSCTFLALLYTLGSDLWNNSW
FLSINLLCSWRILVSLHRVSRLSSVFWACMKLGGVAMGSLLMFRIFTNTISREALYADGIESFVYSLITAISVVA
LIPVFEASFGASTNFSLLTYLSPENALLKRLFKEAPGT YQHSVLVGS LAEAAAQAIGADSLYCLVA AHYHDIG
KLINPGFFSENQKILQQSGHSLSPLECAKMIMRHIPEGVNLARQAGLPESFIQVIEEHHGTSVIRSAYYSHMVE
NPSTGSFDEELFRYSGNKPSSKETTIIMIADSFEAASRSLKNASLPDLQRLIDQIIQGKLQDGQFSCSPVTLDELA
LISKSMVQTLYGALHSRMKYPEISYQISMDSCPKPSIGGT

>core/86/1/Org1_Gene981

MPEPLYTNKLITEKSPYLLLYAHTPVNWYPWGAEAFHIAAIENKPVFLSIGCKHSRWCQV MLQESYTNPEIAA
MLNEYFVN VKVDKEELPYVAKLYGD LAQMLAVSGDHQETVSWPLNVFLT PDLVPFFSVNYLGN EGKLG LP
SFPQIIDKLHFMWEDA EEREALVEQAMKVLEIASFLEG CVRKEILDESSLKRTVAALYQDIDPHYGGVKA FPK
RLPGLLLQFFLRYSLEYQESRGLFFVDRSLSMVALGGVRDHIGGGVYSYTIDDKWLIPAF EKRLIDNALMALN
YLEAWACLGKEEYRGIGKQILSYILSELYSPEVGAFYSSEQAENWGAGGQNFYTWSVEEISNALGEDAEIFCD
YYGISREGFFNGRNILHIPVHREIEELSEKYHRSIEAIEDIVDRSRDILKGIRAQRSHRSKDDL SLTFNNGWMIYT
FAYAGRLLGEVEYIEIGKKCGEFVRNSLYKHHEL YRRWREGEAKYRASLEDY GALILGVLALYESGCGSFWL
SFAEELMQEVVLSFRSEEGGFYSVDGRDSTLLIKQSPLSDGETISGNALICQCLLSLHLITEKKHYLT YAEDILQ
IAQAYAHTHKFSSLGLLIASQNYFSRKHV KVLIALGDQEDRSPVLKCLSGLFLPYLSLIWMTQENQE HLETVL
PEYEHCLIPKGDCTATTIYVLEVDQCKRFDLELFRYLISL

>core/88/1/Org1_Gene6

MKRCFLFLASFVLMGSSADAL THQEAVKKKNSYLSHFKSVSGIVTIEDGVLNIHNNLRIQANKVYVENTVGQ
SLKLVAHGNVMVNYRAKTLVCDYLEYYEDTDSCLLTNGRFAMYPWFLGGSMITLTPETIVIRKGYISTSEGP
KKDLCLSGDYLEYSSDSLLSIGKTTLRVCRIPILFLPPFSIMPMEIPKPPINFRGGTGGFLGSYLGMSYSPISRKH
SSTFFLDSFFKHGVMGFNLHCSQKQVPENVFNMKSYYAHLRAIDMAEAH DRYRLHGDFCFTHKHVNFSGE
YHLSDSWETVADIFPNNFMLKNTGPTRVDCTWNDNYFEGYLTSSVKVNSFQNaNQELPYLT LRQYPISYINT
GVYLENIVECGYLNFAFS DHIVGENFSSLRLAARPKLHKTVPLPIGTLSSTLGSSLIYYSDVPEISSRHSQLSAKL
QLDYRFL LHKS YIQRRHII EPVTFITETRPLAKNEDHYIFSIQDAFHSLNLLKAGIDTSVLSKTNPRFPRIHAKL
WTTHILSNTESKPTFPKTACELSLPFGKKNTVSLDAEWIWKKH CWDHNMNIRWEWIGNDNVAMTLES LHRSK

YSLIKCDRENFILDVSRPIDQLLDSPLSDHRNLILGKLFVRPHPCWNYRLSLRYGWHRQDTPNYLEYQMILGT
KIFEHWQLYGVYERREADSRFFFFLKLDPKKPPF

>core/89/1/Org1_Gene977

MNFQTISINLTEGKILVFETGKIARQANGAVLVRSGETCVFASACAVDLDKVDLPLRVQYQEKFSSTGKTL
GGFIKREGRPSEKEILVSRLIDRSLRPSFPYRLMQDVQVLSYVWSYDGGVLPDPLAICAASAALAISDIPQSNIV
AGVRIGCIDNQWVINPTKTELASSTLDLVLGATENAILMIEGHCDFFTEEQVLDAIEFGHKHIVTICKRLQLWQ
EEIGKSKNLSAVYPLPAEVLTAVKECAQDKFTELFNIKDKKVHAATAHEIEENILEKLQREDDDLFSSFNIAA
CKTLKSDTMRALIRDREIRADGRSLTTVRPITIETSYLPRTHGSCLFTRGETQTLAVCTLGSEAMAQRYEDLNG
EGLSKFYLYQYFFPPFSVGEVGRIGSPGRREIGHGKLAEKALSHALPDSATFPYTIRIESNITESNGSSSMASVCG
GCLALMDAGVPISSPIAGIAMGLILDDQGAILSDISGLEDHLGDMDFKIAGSGKGITAFQMDIKVEGITPAIMK
KALSQAKQGCNDILNIMNEALSAPKADLSQYAPRIETMQIKPTKIASVIGPGGKQIRQIIETGVQIDVNDLGV
VSISASSASAINKAKEIIEGLVGEVEVGKTYRGRVTSVVAFGAFVEVLPGKEGLCHISECSRQRIENISDVVKEG
DIIDVKLLSINEKGQLKLSHKATLE

>core/90/1/Org1_Gene399

MSNQEFDLSAIRNIGIMAHIDAGKTTTTERILFYAGRTHKIGEVHEGGATMDWMAQEGERGITITSAATTVFW
LGAKINIIDTPGHVDFTIEVERSLRVLDGAVAVFDAVSGVEPQSETVWRQADKYGVPRIAFVNKMDRMGAD
YFAAVESMKEKLGANAFVHCPIGSESQFVGMVDLISQKALYFLDDTLGAKWEEKIESEDLKERCAELRANL
LEELATIDESNEAFMMKVLEDPDSITEDEIHQVMRKGVIENKINPVLCGTAFKNKGVQQLNVIVKWLPSPLD
RGNIRGINLKTQDEISLEPRRDGPLAALAFKIMTDPYVGRITFIRIYSGTLKKGSAILNSTKDKKERISRLEMH
ANERTDRDEFTVGDIGACVGLKFSVTGDTLCDDNQEIVLERIEFPDPVIDMAIEPKSKGDREKLAQALSSLSEE
DPTFRVSTNEETGQTIISGMGELHLDILRDRMIREFKVEANVGKPVQVSYKETITVSGNSETKYVKQSGGRGQY
AHVCLEIEPNEPGKGNEVSVKIVGGVIPKEYIPAVIKGIEEGLNTGVLAGYGLVDVKVSIVFGSYHEVDSSEM
AFKICGSMMAVKDACRKAKPVILEPIMKVAVITPEDHLGDVIGDLNRRRGKILGQESSRGMAQVNAEVLPLSEM
FGYTTSLSRLTSGRATSTMEDIAFAKVPQKIQEEIVKK

>core/92/1/Org1_Gene351

MYNLLHAHHDAASPDGRLVSHLKKLSPHIYEGEVLIENIPAYFLGFHLPQQCIQVNLKSSLAQLGVEAVLNHL
ELNKARKEARLHVLFMSQDPIATAMLELLEPGSFVCKLFAADDRRLVRSPCYLNRMFTHTDRTGSPLLRFGK
KLEHFITLEIINDRLVVFLPILPGTICYEETIYGFLPLMSKSLTRPHLKIRKFLPLYQMVTDRPPVPEDHKILLIKT
EPLHIRTVFARVVQDLLPQGLRHTAADILEPTTQESGDIYEFYGSTSEPIERIPLEFFTLEPYKEHSFFFYRDMLQ
ETLESPQEVFRVFESIPEGEDQAAMFISKGSELLELSQDSWIIKPRISPSDERHAREIQKHIEDQPCFPFLKAMET
DHITSQGVLFSTRYFPSASLKGMFLSNYSRYYLQHIYFQIPSPSTSGEFFSNRDRSFLDLFYFAGISVFWADLESKR
LLQYIKRRNKDVGMFVPKHQAEQFAQSYFIGIHGSCLIAAGDYDEFLRELLTGMHTLSQQFTIPEFPPQTPLAIL
TGGGSGAMELANRVATELSILSCGNLISLDTTNAIVEAKMSYAIPDLLERQADFHVLDLAVFVIGGMGTDFFEL
LLELISLKTGKKALVPVFLIGPVDYWKSKITALYNSNHAVGTIRGSEWVHNCLFCLSSAKAGIAIFRRYLNHTL
PIGPEHPVPEDGFVIV

>core/93/1/Org1_Gene763

MKRSRRNFEQALENLEKLKEISLATSND SYLNNPARFNQRKQTGSSVMEMKEALKNVENYLLEISCVSKSHA
DKALKESDFLIAGVQNVFSFLENQEDLYKSLLDEYSEVTKAYDEVKKNLKEVPTYDLSTDEETEEHKEPECFL
NNLVEVKRDRSYELFYMLDEQDKRFYNDALVQIHYKQKNLHETVNEGDP LTKTLLWNSEEVKNIASSLVIVN
DMPLRLFYQRALSHLDIEAVVKVHNAMALFFSRYEATMVFKSPKKHNIWYFND FLLFLREAWKDLNNNVI
DSQERKQTKLLASALSLGIFESKLVFEEASRYLYFNIQTKLENANGKKPLSPGQYLTDAYEELHRLISKYPNGP
LFKAMDRVLEHESRPYDPMILGILPSLEGTLKLHGKSIDIIRSPSPVTQSSILYANCNEEFLGFLNAKAHRSEVT
LVLNIQNRISRKERARSRVIEEALQE EHAPYVHA FSPPEPEELLQNLESIHGDIETFADFFSILQEEFHKPLLAS
SFFLTKE LKEFVGSFLKEKLTALKDIFFAKKKILFRNDKLLLLHLLSYLIVFKLIERTNPNSIVVVS KDGLDYVS
VFIAGFAFFSREAFWDEHSLKLLL TNVLSPTLVARDRLV FVSHIELLSKFVNCLKKNRQGFSS LKSFFKDDIEG
WEFTGYLHELTEVSHKHN L

>core/94/1/Org1_Gene607

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RHAAQATGVSGDGKIVIGMKVPDDPFAITVGFQYIDGHLQPLEAVRPQCSVYPNGITPDGTVIVGTNYAIGM
GSVAVKWVNGKVSELPM LPTLDSVASAVSADGRVIGGNRNINLGASVAVKWEDDVITQLPSLPDAMNAC
VNGISSDGSII VGTMV DVSWRNTAVQWIGDQLSVIGTLGGTTSVASAISTDGT VIVGGSENADSQTHAYAYK
NGVMSDIGTLGGFYSLAHAVSSDGSVIVGVSTNSEHRYHAFQYADGQMVDLGT LGGPESYAQGVSGDGKVI
VGRAQVPSGDWHAFLCPFQAPSPAPVHGGSTVVT SQNPRGMVDINATYSSLKNSQQQLQRLLIQHSAKVESV
SSGAPSFTSVKGAISKQSPAVQNDVQKGTFLSYRSQVHGNVQNQQLLTGAFMDWKLASAPKCGFKVALHY
GSQDALVERAALPYTEQGLGSSVLSGFGGQVQGRYDFNLGETVVLQPFMGIQVLHLSREGYSEKNVRFPVSY
DSVAYSAA TSFMGAHV FASLSPKMSTAATLGVERDLNSHIDEFKGSVSAMGNFVLENSTVSVLRPFASLAMY
YDVRQQQLVTL SVVMNQQLTGTL SLVSQSSYNLSF

>core/95/1/Org1_Gene17

MGVVQNQVISSIRDVLKL VWELRFAEHKMLLLSRQSGSGGTFQLSCAGHEL AGVLAGKSLIPGKDWSFPYY
RDQGFPIGLGCDLSEIFASFLARTTPNHSSARMMPYHYSHKKLRICCQSSVVG TQFLQAAGRAWAVKHSSAD
EVVYVSGGDGATSQGEFHEMLNFVALHQLPLITVIQNNHWAISVPFEDQCGADLASLGRCHQGLAVYEVDG
GNYTSLTETFSHAVDQARQH SVPALILIDV VRLSSHSNSDNQEKYRSALDLKLSMDKDPLILLEKEAINVFGLS
PFEIEEIKAEAEQEEVRKSCEIAEALPFPSKGST SHEVFSPTYTETLIDYENSESAQNLRNSEPKVMRDAISEALVEE
MTRDSGVIVFGEDVAGDKGGVFGVTRNLTEKF GPQRCFNSPLAEATIIGTAIGMALDGIHKPVVEIQFADYIW
PGINQLFSEASSIYYRSAGEWEVPLVIRAPSGGYIQGGPYHSQSIEGFLAHCPGIKVAYPSNAADAKALLKAAI
RDPNPVVFLEHKALYQRRIFSACPVF SHDYVLPFGKAAIVHPGKDLTIVSWGMP LVLSLEVAQELASRGISIEV
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NEVLPHKESILQAAKSLAEF

>core/96/1/Org1_Gene362

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GASPALQMLEFIGHTNAKADFQAIQAEYNLAE EFPPEVIEEASLFSQKHITQVLHSRKDLRDLLCFTIDSSTAR
DFDDAISLT YDHNNNYILGVHIADVSHYVTPHSHLDKEAAKRCNSTYFPGKVIPMLPSALSDNLCSLKP NVDR
LAVSVFMTFTKSGHLSDYQIFRSVIRSKYRMTYDEV DNIIEKKHSHPLSKILNEMATLSKKFSDIREERG CIRFV

LPSVTMSLDNLQEPVALIENHQTFSHKLIEEFMLKANEVVAHYHISHQGVSLPFRSHEPPNDENLLAFQELAKN
MGFDITFTPTQEPDYQYLLQTTTSAGHPLEQVLHSQFVRSMTASYSYENKGGHYGLKLDYYTHFTSPIRRYIDL
IVHRLLFNPLSIDQTHLEIIVRACSTKERVSAKAENSFENLKKTRFINKFLQECPKTTYHAYIITANHEGLSFVV
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KGTKKRAS

>core/98/1/Org1_Gene1000

MINKELDIGILGKIAGAIKQISIESIQKASSGHPGLPLGCAELAAAYLYGYVLRQNPRDPHWINRDRFVLSAGHG
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RPGHEIFNGKIYCLAGDGCMEGVCSFAGSLNLLNNLVVIYDYNVLDGYLNEISVEDTKKRFEAYG
WDVYEIDGYDFTHIHETFSIKRGQERPVLVIAHTIIGHGSPKEGTNKAHGSPLGVEGTHETKQFWHLPEEKFF
VPPAVKNFFAHKIQEDRKAQEQLDEVRVWSKQFPELHEEFVALTSHKLPKNLESVQSVEMPDSIAGRAAS
NKLIQVLVQHIPPYLIGGSADLSSSDGTWIANEKVIHTYDFSGRNIKYGVREFGMATIMNGLAYSQVFRPFGGT
FLVFSYMRNAIRLAALSKLPVIYQFTHDSIFVGEDGPTHQPVEQLMSLRAIPGLYVIRPADANEVRGAWIAG
LKHTGPTVIVLSRQALPTLPAHRPFKDGVRGAYIVLKESGEKPDYTLFATGSEVSLALSVAKELEHLDKQV
RVVSFPCWELFEAQDQVDYKQSIYVGGDLGIRVSIEAGSALGWYKYIGSEGLAIAMDRFGYSGASDDVSEECGF
TTEQILQRILSQ

>core/99/1/Org1_Gene282

MEKVSSYPSVPLPLGASKISPNRYRFALYASQATEVILALTDENSEVIEVPLYPDTHRTGAIWHIEIEGSDQSS
YAFRVHGPKKHGMQYSFKEYLADPYAKNIHSPQSFGSRKKQGDYAFCYLKEEPFPWDGDQPLHLPKEEMIY
EMHVRSTQSSSRVHAPGTFLGIIKIDHLHKLGINAVELLPIFEFDETAHPFRNSKFPYLCNYWGYAPLNFFS
PCRRYAYASDPCAPSREFKTLVKTLHQEGIEVILDVVFNHTGLQGTTCSLPWIDTPSYIYLDAAQGHFTNYSGC
GNTLNTNRAPTTQWILDILRYWVEEMHVDGFRFDLASVFSRGPSPQLQFAPVLEAISFDPLLASTKIIAEPWD
AGGLYQVGYFPTLSRWSEWNGPYRDNVKAFLNGDQNLIGTFASRISGSQDIYPHGSPTNSINYVSCHDGFTL
CDTVTYNHKHNEANGEDNRDGTANYSYNFGTEGKTEDPGILEVRERQLRNFFLTLMVSQGIPMIQSGDEY
AHTAEGNNNRWALDSNANYFLWDQLTAKPTLMHFLCDLIAFRKKYKTLFNRGFLSNKEISWVDAMGNPMT
WRPGNFLAFKIKSPKAHVYVAFHVGAQDQLATLPKASSNFLPYQIVAESQQGFVPQNVATPTVSLQPHTTLIA
ISHAKEVT

>core/100/1/Org1_Gene96

MKEENSQAHYLALCRELEDHDYSYYVLRPRISDYEYDMKLRKLEIERSHPEWKVLWSPSTRLGDRPSGTF
SVVSHKEPMLSIANSYSKEELSEFFSRVEKSLGTSPRYTVELKIDGIAVAIRYEDRVLVQALSRGNGKQGEDIT
SNIRTIRSLPLRPEDAPEFIEVRGEVFFSYSTFQIINEKQQQLEKTIFANPRNAAGGTLKLLSPQEVAKRKLEISI
YNLIAPGDNDSDHYENLQRCLEWGFPVSGKPRLCSTPEEVISVLKTIETERASLPMEIDGAVIKVDSLASQRVLG
ATGKHRYWALAYKYAPEEAETLLEDILVQVGRTGVLTPVAKLTPVLLSGSLVSRASLYNEDEIHRKDIRIGDT
VCVAKGGEVIPKVVRVCREKRPEGSEVWNMPEFCPVCHSHVVREEDRVSVRCVNPECVAGAIEKIRFFVGR
GALNIDHLGVKVITKLFELGLVHTCADLFQLTTEDLMQIPGIRERSARNILESIEQAKHVDLDRFLVALGIPLIG
IGVATVLAGHFETLDRVISATFEELLSLEGIGEKVAHAIAEYFSDSTHLNEIKKMQDLGVCISPYHKSGSTCFG
KAFVITGTLEGMSRLDAETAIRNCGGKVGSSVSKQTDYVVMGNNPGSKLEKARKLGVSILDQEAFTNLIHLE

>core/101/1/Org1_Gene53

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LSTAYNFDYYLVLGVVDLPRDRYTEIEAPRSVNELQVDLANLQREIRNRSDRLCDLYAYRREVLRGLCNYDN
EQRLHQAKECCEDLFDGKVFVAVAGWVIVDRIKELQSLCNRYQIYMERVVPDPDETIPTYLENKGVGMMGED
LVQIYDTPAYSDDKDPSTWVFFAFVLFFSMIVNDAGYGLLFLMSSLLFSWKFRKMKFSKHLRMLKMTAILG
LGCICWGTTTTTSFFGMSFSKTSVFREYSMTHVLALKKAEEYQLQMRPKAYKELTNEYPSLKAIRDPKAFLLAT
EIGSAGIESRYVVYDKFIDNLMELALFIGVVHLSLGMRLRYLRYRYSIGWILFMVSAYLYVPIYLGTVSLIHY
LFHVPYELGGQIGYYGMFGGIGLAVVLAMIQRSWRGVEEISVIQVFSVDLSYLRIYALGLAGAMMGATFNQ
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NSIV

>core/102/1/Org1_Gene361

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YFNDSQRASTKDAGRIAGLDVKRIIPEPTAAALAYGIDKVGDKKIAVFDLGGGTDFDISILEIGDGVFEVLSTNG
DTLLGGDDFDEVIKWMIEEFKKQEGIDLSKDNMALQRLKDAAEKAKIELSGVSSTEINQPFITMDAQGPKHL
ALTLTRAQFEKLAASLIERTKSPCIKALSDAKLSAKDIDDVLLVGGMSRMPAVQETVKELFGKEPNKGVNPD
EVVAIGAAIQGGVLGGEVKDVLLLDVIPLSLGIETLGGVMTTLVERNTTIPTQKKQIFSTAADNQPAVTIVVLQ
GERPMAKDNKEIGRFDLTDIPPAPRGHPQIEVSFDIDANGIFHVSADKDVASGKEQKIRIEASSGLQEDEIQRMV
RDAEINKEEDKKRREASDAKNEADSMIFRAEKAIKDYKEQIPETLVKEIEERIENVRNALKDDAPIEKIKEVTE
DLSKHMOKIGESMQSQSASAAASSAANAKGGPNINTEDLKKHSFSTKPPSNNGSSEDHIEEADVEIIDNDDK

>core/103/1/Org1_Gene929

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VAIRVSRDLRQDYFKALQQLPMTFFHDHDIGNLSNRVMTDSASIALAVNSLMINYIQAPITFILTLGVCLSISW
KFSILVCVAFPIFILPIVVIARKIKNLAKRIKQSQDSFSSVLYDFLAGVMTVKVFRTEKFAFTKYCEHNNKISAL
EEKSAAYGLLPRPLLHTIASLFFAFVVVIGIYKFAIPPEELIVFCGLLYLIYDPIKKFGDENTSIMRGCAAERFY
EVLNHPDLHSQKEREIEFLGLSNTITFENVSGYQEDKHILKNLSFTLHKGEALGIVGPTGSGKTTLVKLLPRL
YEVSQGKILIDSLPITEYNKGSLRNHIACVLQNPFLFYDTVWNNLTCGKDMEEEAVLEALKRAYADEFILKLP
KGVHVSVEESGKNLSGGQQQLRAIARALLKNASILILDEATSALDAISENYIKNIIGELKGQCTQIIAHKLTTLE
HVDRVLYIENGQKIAEGTKEELLQTCPEFLKMWELSGTKEYNRVFPDHKLVANPTDMAITT

>core/104/1/Org1_Gene664

MFSRLFFTSFSAEVVNTFFESGMSEDTSPLLSKQNRKLSHNLPLKSAYLSLGTYLIALLSFWLHAKNLSNLFVV
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LAPTTGWLVLLEDGNLQKVAINKIEVGNILRIKSGEVVPLDGEILHGSSSINLMHLTGEKVPKSCHPGSIVPAGA
HNMEGSFDLRVLRGTSDSTIAHIINLVIQAQNSKPRLLQRLDKYSSVYALSIFAACGIALLVPLFTSIPLLPQS
AFYRALAFLIAASPCALIIAIIPIAYLSAINACAKHGVLLKGGVILDRLVSCNSVMDKTGTLTGTGELTCIGCDYF

GSKNETFFPSVLALAEQSSSHPIAEAIVSYLMEQKVSSLPADRYLTPGEGVRGYFNEQEAFVGRVETGLGKVP
SEYLEDIEQKIYQAKQHGEICSLAYVGNSFALFYFRDIPRPQAKEIIQDLKDLGYPVSMILTGDHKVSAENTAEL
LGISEVFFDLTPEDKLAKIRELATQRQIMMVGDGINAPALAQATVGIAMGEAGSATAIEAADIVLLHDSLSS
LPWHIQAQKQTKKVVSQNLALALAHILLVSWPASLGIPLWLAVILHEGSTVIVGLNALRLLKS

>core/105/1/Org1_Gene609

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YQEFREFFPNNAVEYFISYYDYYQPEAYIARSDTYIEKSLLINDEIDKLRLSATRSILERDRTLIVSSVSCIYGIGS
PENYTSMALVLEVGKEYPRNILTAQLVKMHYQASPIQRSACFRERGSVIDIFPAYESELAALRLEFLNDTLTSIE
YSDPLTMIPKESVPSATLYPGSHYVIPEAIREQAIRTIQEELEERMAFFDDRPIEKDRIFHRTTHDIEMIKEIGFCK
GIENYSRHFTGAPPGAPPTCLLDYFPEDFLLIIDESHQTLPIRAMYRGDQSRKQSLVEYGFRLPSAFDNRPLT
YEEAQKYFRKVIYVSATPGDTEVQESSGHIVQQIIRPTGIPDPMPEIRPATGQVDDLLEEIRLRLSQKHEKILVIS
ITKKLAEDMAGFLSELEIPAAYLHSGIETAERTQILTDLRSGVIDVLIGVNLLREGLDLPEVSLVAILDADKEGF
LRSTSSLIQFCGRAARNINGKVIFYADQKTRSIEETLRETERRRQIQLDYNKEHNIVPKPIIKAIFANPILQTSKDS
ESPKESQRPLSKEDLEEQIKKYEALMQRAAKEFRFNEAAKYRDAMQACKEQLLYLF

>core/106/1/Org1_Gene430

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DPAVPQVVVDCEKRLGMLDRKLRREEEILYRSTAHLKDEERYEFLLELLEMRSLVADRLEFNRRSYERFVQG
IMTVRSEEGEKEISRLQDLISLQQQTVQDLRSRIDDEQKRCWTALQRINQSQKDIQRAHDREASQRACEGTEM
DCAERQQLEKDLRRQLKSMQEWIEMRGTIHQKEKAWRKQNAKLERLQEDLRLTGIAFDEQSLFYREYKEKY
LSQKLDQMOKILQEVNAEKSEKACLESVHDYEKQLEQKDANLKKAAAVWEEELGKQQQEDYEQTQEIRRL
STFILEYQDSLREAEKVEKDFQELQQRYSLQEEKQVKEKILEESMNHFADLFEKAQKENMAYKKKLADLE
GAAAPTEIGEDDDWVLTDSASLSQKKIRELVEENQELLKALAFKSNELTQLVADAVEAEKEISKLREHIEEQK
EGLRALDKMHAQAIKDCEAAQRKCCDLESLLSPVREDAGMRFELEVELQRLQEENAAQLRAEVERLEQEQQFQ
G

>core/107/1/Org1_Gene306

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QPFVAVDITKFHLCADPLAIPCHRDEIIQGILQFIEGQTYDDLCLKDKKSRYCKLYPLLDVSVHDRLSLWWK
GYATKHRLPTNALFFITDYQRSYPFGKLLGQVLHTLREIKDEKTGKAFPTGGMEAYFNHILEGDVGERKLLRS
PLNRDNTNRVIKLPKDGSDIYLTINPVIQTIAEEELERGVLEAKAQGGRLILMNSQTGEILALAQYPFFDPTNYK
EYFNNKERIEHTKVSFVSDVFEPGSIMKPLTVAIALQANEEASLKSQKKIFDPEEPIDVTRTLFPGRKGSPLKDI
SRNSQLNMYMAIQSSNVYVAQLADRIIQLSGVAWYQQKLLALGFGRKTGIELPSEASGLVPSPHRFHINGSL
EWSLSTPYSLAMGYNILATGIQMVQAYAILANGGYAVRPTLVKKIVSASGEEYHLPTKEKTRLFSEEITREVV
RAMRFTTLPGSGFRASPKHHSSAGKTGTTEKMIHGKYDKRRHIASFIGFTPVESSEGNFPPLVMLVSIDDPEY
GLRADGTKNYMGGRCAAPIFSRVADRTLLYLGILPDKKLRNCDEEAAALKRLYEEWNRSPKQGGR

>core/108/1/Org1_Gene554

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ATDEETAIAAEWETKNADAVKVGQAQITELAKYASDNQAILDSLGLTSFDLLQAALLQSVANNKAAELLK
EMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGN AIRDAYFAGQNASGAVENAKSNNSISNIDSAKAAIAT
AKTQIAEAQKKFPDSPILQEAQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAE
NETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAACAAGDDSAALADAQKALEAALGKAGQQQ
GILNALGQIASAAVVSAGVPPAAASSIGSSVKQLYKTSKSTGSDYKTQISAGYDAYKSINDAYGRARNDATR
DVINNVSTPALTRSVPRARTEARGPEKTDQALARVISGNSRTLGDVYSQVSALQSVMQIIQSNPQANNEEIRQ
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>core/109/1/Org1_Gene946

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SLDEVKQRQRALLLSYLSLHLGASSSRYEGKEEQLAALCLRQIENHENVYLGINDHGVAMDRDEEAYQFHI
RVVKALAHSLDAHTAYFSKDEALAMRIQLEKGMCGIGVVLKEDIDGVVVREIIPGGPAAKSGDLQLGDIIYR
VDGKDIEHLSFRGVLDCLRGGHGSTVVLDIHRGESDHTITLRREKILLED RRVDVSYEPYGDGVIGKVTLSHF
YEGENQVSSEQDLRRAIQGLKEKNLLGLVLDIRENTGGFLSQAIVSGLFMTNGVVVVSR YADGTMKCYRT
VSPKKFYDGPLAILVSKSSASAAEIVAQTLQDYGVALVVGDEQTYGKGTIQHQTITGDASQDDCFKVTVGKY
YSPSGKSTQLQGVKSDILIPSLYAEDRLGERFLEHPLPADCCDNVLHDPLTDLDTQTRPWFQKY YLPNLQKQE
TLWREMLPQLTKNSEQRLSSENSNFQAFLSQIKSSEKTDLSYGSNDLQLEESINILKDMILLQQCRK

>core/110/1/Org1_Gene811

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AAFSCGLTLEALNNISTDLSKFVVILNDNNMSISKNVGAMS RIFSRWLHHPATNKLTQVEKWLAKIPRYGD
SLAKHSRRLSQC VKNLFCPTPLFEQFGLAYVGPIDGHN VKKLIPILQSVRNLPFPILVHVCTTKGKGLDQAQN
NPAKYHGV RANFNKRESAKHLPAIKPKPSFPDIFGQTLCELGEVSSRLHV VTPAMSIGSRLEGFKQKFPERFFD
VGIAEGHAVTFSAGIAKAGNPVICSISTFLHRA LDNVFHDVCMQDLPVIFAIDRAGLAYGDGRSHHGIYDMS
FLRAMPQMIICQPRSQVVFQQLLYSSLHWSSPSAIRYPNIPAPHG DPLTGDPNFLRSPGNAETLSQGEDVLI AL
GTLCFTALS IKHQLLAYGISATVVDPIFIKPFNDLFSLLLMSH SKVITIEEHSIRGGLASEFNNFVATFNFKVDI
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>core/111/1/Org1_Gene964

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NRLLFPEDLDPNDYIDPVVSIYQEYQKKLIEANALDFD DLLFLT VRLLRESPEAQELYNQLWKALLIDEYQDT
NHAQYTLMQLLSKQHRNVFAVGDPDQSIYSWRGANIHNILNFENDYPNAKVLCLEENYRSYGNILNAANALI
KNNASRLEKELRSVKGPGEKIRLFLGSTDREEAD FVAAEILQLHRVGNIKLRDICIFYRTNSQSRTFEDALLRR
RIPYEIIGGLSFYKRKEIQDILAFLRIFISKSDIVAFDR TVNLPKRGIGSTTIFALTQYAIAQGLPILKACQQALDT
KDVKLSKKQQEGLQEYLALFPQIEHAYNTLSLRDFIESVVRITGYLEILKEDADTFKDRKSNLEELYHKALESE

QQNPKTHLELFLDDLALKGSDDDLNLTA DRVNLMTLHNGKGLEFRVSFLVGLLEEQLLPHANSLGGTYENIEE
ERRLCYVGITRAQDLLYLTTAQVRSLWGTVRMMKPSRFLKEIPKDYMIQVR

>core/112/1/Org1_Gene67

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GGLVVFTVGDLPIDADTKYFGLIPGKKRYIKRCMGRPGDFLYFYGGKIYGLDDAGKRIEFPSVHGLENL YH
VPYISFDGTTSSHTEGQKTIIDFKQFNQSYGRLIFPQTSMYGQFFDHKEWHQDEPNKLKDPHLSPVSYADLFG
MGNYAMVRILTEHQARTSHLLPNPGSPTKVYLEICHTANLSYPKPLL RHYEHQLSPAIQPMKTLLPLRKEHLH
LIRNNLTTSRFIVAQGCAYKYHQFKINTSGIAKAYAILLPKVPDGCYEYSKGEAYQIGFGEIRYK LKSSHPLTQ
LNDKQVIELFNCGINFSSIYNPVNPLQAPLPNRYAFFNQGNLYIMDSPVFIKNDPTLQKFVTSETEKQEGSSET
QPYIAFVDKGLPPEDFKEFVEFIHNFGIQVPKGHV LVLGDNYPMSADSREFGFVPMENLLGSPLCTFWPIGRM
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>core/113/1/Org1_Gene604

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PKNQEVF SVMQANVFDAKTQELQGILYTTFSAESLLKDLLINKQSYLTVKTAILSKYGVILKASDPALHLHTV
YPMTEKEKFCQVFLNDDPCPIDSELGPLTSLPDIGENFYSFKIKDTEIWGCIENVPSIDIAVLSYAKKEESFAPL
WRRARMYTAYFFCILLGSLIAFIVARRLSLPIRKLATAMIESRKNKNCLYTDDSLGFEINRLGHIFNAMVENLH
KQQHLAKTNFEMKENAQNALHLGEQAQQRLLPNTLPSYPHIELAKAYIPAITVGGDFFDV FVVGEGSKARLF
LIVADASGKGVNACGYSLFLKNMLRTFLSRSSSLQQA IQETSRLFYNNTKNSGMFVTL CVYCYHQTSNTMEY
YSCGHPPACYLDPDGETSWLFHPGMALGFLPEVANITSKL FHPKPGSLFVLYSDGITEAHNNNNNDMFGEERL
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>core/114/1/Org1_Gene614

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NPFKTELIRELPENEEISAYSQGEFFDLCRGPHLPSTAHVKAFKVLRTSAAYWRGDPSRESLVRIYGTSFPTSKE
LRAHLEQIEEAKKRDRHVLGAKLDLFSQQESSPGMPFFHPRGMIVWDALIRYWKQLHTAAGYKEILTPQLM
NRQLWEVSGHWDNYKANMYTLQIDDEDYAIKPMNCPGCMLYYKTRLHSYKEFPLRVAEVGHVHRQEASG
ALSGLMRVRAFHQDDAHVFLTPEQVEEETLNILQLVSTLYGTFGLEYHLELSTRPEKDTIGDDSLWELATDAL
NRALVQSGTPFIVRPGEGAFYGPKIDIHVKDAIQRTWQCGTIQLDMFLPERFELEYTTAQGTSVPVMLHRAL
FGSIERFLGILIENFKGRFPLWLSPEQVRIITVADRHIPRAKELEEAWKRLGLVVTLDDSSSVSKKIRNAQNM
QVNYMITLGDHEINENVLAVRTRDNRVINDVSVERFLNTILEEKNSLSLTALL

>core/117/1/Org1_Gene602

MDENRKVIVVGGGLAGLSAAMQLANLGIIVELVSLTKVKRSHSVCAQGGINAALNLKPEEEDSPYVHAYDTI
KGGDFLADQPPVLEMCLAAPRIIKMLDNFGCPFNRGPSGNLDVRRFGGTLYHRTVFCGASTGQQLMYTLDE
QVRRREHAGRVIKRENHEFVRLVTDHSGRACGIILMNLFN NRLEILRGDAVIIATGGPGVIFKMSTNSTFCTGA
ANGRLFLQGMAYANPEFIQHPTAIPGRDKLRLISESVRGEGGRVWVPGDSSKRIVFPDGSERPCGETGAPWY

FLEDMYPAYGNLVS RDVGARAILRVCEAGLGIDGRMEAYLDVTHLPEKTRHKLEVVLDIYKKFTGEDPNTV
PMRIFPAVHYSMGGAWVDWPAADDPDRDSRFRQMTNIPGCFNCGESDFQYHGANRLGANSLLSCLFAGLVS
GDEASRFIEAFGASQATSSDFDRALQQEKEENARLLSASGKENIFVLHEEIAKIMVRNVTVKRNNRDLQETM
DKLKEFRERLKNVSVLDSSPFANKSFHFVRQMGPMLLALAITKGALLRNEFRGSHYKPEPPERDDEHWLKT
TVAVYAPEEPEISYLPVDTRHVAPT LRDYTKSSTGKIELTNIPDNIRLPI

>core/118/1/Org1_Gene838

MTIIYFILAALALGILVLIHELGHLLVAKAVGMAVESFSIGFGPALFKKRIGGIEYRIGCIPFGGYVRIRGMERT
KEKGEKGKIDSVYDIPQGFFSKSPWK RILVLVAGPLANILLAVLAFSILYMNGGRSKNYSDCSKVVGWVHPV
LQAEGLLPGDEILTCNGKPYVGDKDMLTTSLLEGHLNLEIKRPGYLTVP SKEFAIDVEFDPTKFGVPCSGASY
LLYGNQVPLTKNSPMENSELRPNDRFVWMDGTLLFSMAQISQILNESYAFVKVARNDKIFFSRQPRVLASVL
HYTPYLRNELIDTQYEAGLK GKWSSLYTLPYVINSYGYIEGELTAIDPESPLPQPQERLQLGDRIL AIDGTPVSG
SVDILRLVQNHRSIIVQQMSPQELEEVS RDADKRFIASYHSEDLLQILNHLGESHPVEVAGPYRLLDPVQPR
PWIDVYSSES LDKQLEVAKKIKNKDKQRY YLERLDAEKQKPSLGISLKD LKVRYNPSPVVMLSNITKESLITL
KALVTGHLSPQWLSGPVGIVQVLHTGWSVGFSEVLFWIGLISMNLAVLNLLPIPVLDGGYILLCLWEIVTRRR
LNMKIVERILVPFTFLLIFFIFLTFQDLFRFFG

>core/119/1/Org1_Gene369

MRRSVCYVNP SIARAGQISTWKFLYSLATPLPAGTKCKFDLAGSGKPTDWEAPATDLSQTRNVIYAEMPEGE
IIEATAIPVKDNPVPQFEFTLPYELQVGETLTIVMGASPNHPQVDDAGNGAQLFAQRRKPFYLYIDPTGEGNY
DEPDVFSMDIRGNVLKKIEIFTPSYVVKNRFDITVRFEDEFGNLTNFSPEETRIELSYEHLRENLNWQLFIPET
GFVILPNLYFNEPGIYRIQLKNLSTQEIFISAPIKCFADSAPNLMWGLLHGESERVDSEENIETCMRYFRDDRAL
NFYASSSFENQENLSPDIWKLINQTVSDFNEEDRFITLSGFQYSGEPHLEGVRHILHTKETKSHSKHKEYKHIPL
AKLYKSTVNHDMISIPSFTASKEHGDFD FENFYPEFERVVEIYN AWGSSETTAALNNPFPIQGK DSEDPRGTVIE
GLKKNLRF GFVAGGLDDRGIYKDYFDSPQVQYSPGLTAI CNKYTRESLVEALFARHCYATTGPRIVLSFNITS
APMGSELSTGSKPGLNVNRHISGHVAGTALLKTVEIIRNGEVLHTFFPD SNLDYEYDDMVPLSSVTLKDPNG
KAPFVFFYYLRVTQADNAMA WSSPIWVDLN

>core/120/1/Org1_Gene913

MESEKDIGAKFLGDYRILYRK GQSLWSEDLLAEHRFIKKRYLIRLLL PDLGSSQPFMEAFHDVVVKLAKLNHP
GILSIENVSESEGR CFLVTQE QDIPILSLTQYLKSIPRKLTELEIVDIVSQLASLLDYVHSEGLAQEEWNLD SVYI
HILNGVPKVILPDLGFASLIKERILDGFISDEENRESKIKERVLLHTSEGKQGREDTYAFGAITYYLLFGFLPQGI
FPMPSKVFSDFIYDWDFLISSCLSCFMEERAKELFPLIRKKTLGEELQNVVTNCIESSLREVDPDPLESSQNLPQA
VLKVGETKVSHQQKESA EHLEFVLVEACSIDEAMDTAIESESSSGVEEEGYSLALQSLLVREP VVSRYVEAEK
EPPKPQPILTEMV LIEGGEFSRGSVEGQRDEL PVHKVILHSFFLDVHPVTNEQFIRYLECCGSEQDKYYNELIRL
RDSRIQRRSGRLVIEPGYAKHPVVGVTWYGASGYAEWIGKRLPTEAEWEIAASGGVAALRYPCGEEVEKSR
ANFFTADTTTVMSYPPNPYGLYDMAGNVYEW CQDWYGYDFYEISAQEPESPQGPAQGVYRVLRGGCWKSL
KDDLRC AHRHRNNPGAVNSTYGFRC AKNIN

>core/121/1/Org1_Gene779

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MGIREAIESLRFGRGSATDYSAAVRSLSRSAAFGDAVPSGIAMKLRRPSGLIRSTPVRWRYTPEHIGDFSLV
APLIPEHKPQLPTQSCVLF RSGVNSQSSSSSLFSSYMVPYFWEELRVQNKQRFD SNHHIGSRNGFLPTFGPILW
EQDKGPYRSYIFKAKDSQGNPHRIGFLRISSYVWTDLEGLEEDHKDSPWELFGEIIDHLEKETDALIIDQTHNP
GGSVFYLYSLLSMLTDHPLDTPKHRMIFTQDEVSSALHWQDLLEDVFTDEQAVAVLGETMEGYCMDMHAV
ASLQNFSSQSVLSSWVSGDINLSKPMPLLGFAQVRPHPKHQYTKPLFMLIDEDDFSCGDLAPAILKDN GRATLI
GKPTAGAGGFVFQVTFPNRSGIKGLSLTGSLAVRKDGEFIENLGVAPHIDLGFTSRDLQTSRFTDYVEAVKTIV
LTSLSENAKKSEEQTSPQETPEVIRVSYPTTTSAS

>core/122/1/Org1_Gene853

MFGTLVSTLCCPANSE RDWEDHEVNCIYIASTSDTQLEAVQGGMHITELRGEPVRVLYETGHLYAFARENTC
HSRLEVSH TVRAMTYFWDRFFSRHWNVGRRFLVFYQGN GGAYVQAALDSSMHTQDIYVLGLSPTVYIRGN
YHVQH YRVRGFWPSCLD SLAACAE NTSVLPYGESSDGIFYPSLFSHTFDNAIRYGERCLLVCSEGMGMLPET
QQQTSPLTSLEGGHEVALVLNPQQNPEALS IASRLMHEERGGRLSNYMPGRSSNPFMTSMYVLVRLNTLAQ
IYLMSPYYSFQSN DIVCLIFISSAAVETVSYIFLTVTDSTCGRRYL RVPRLVCTGLRNLALPTTLELLILSYPRS
VEGV PFNVRFILGYMCTTRVVFFAWN LILHWPFRCLRHGIQLFVHRSIIIGHTLGARITDLTLASMRYAIVFPSI
VSSCLLTALAHANTNILALDPYRLIESGDLRRPAFNDDDEMQQADNPWDAYSIGLVINTCIYMLILFANLIFMV
YSVRRYHRSRR

>core/123/1/Org1_Gene268

MTLITPAINSSRRKTH TVRIGNLYIGSDHSIKTQSM TTTLTDDIDSTVEQIYALAEHNCDIVRVTVQGIKEAQAC
EKIKERLIALGLNIPLVADIHFFPQAAMLVADFADKVRINPGNYIDKRNMFKGTKIYTEASYAQSLLRLEEKFA
PLVEKCKRLGKAMRIGVNHGSLSERIMQKYGDTIEGMVASAIEYIAVCEKLN YRDVVFSMKSSNP KIMVTAY
RQLAKDLDARGWLYPLHLGVTEAGMGVDGIIKS AVGIGITLLAEGLGDTIRCSLTGCPTTEIPVCD SLLRHTKI
YLDLPEKKNPFSLQHSENFVSAAEKPAKTTLWGDVYGVFLKLYPHHLTDFTPEELLEHLGVNPVTKEKAFTT
PEGVVVPPELKDAPITDVLREHFLVFHHHQVPCLYEHNEEIWDSPAVHQAPFVHFHASDPFIHTSRDFFEKQG
HQGKPTKL VFSRDFDNKEEA AISIATEFGALLDGLGEAVVLDLPNLPLQDVLKIAFGTLQNAGVRLVKTEYI
SCPMCGRTLFDLEEVTTRIRKRTQHLPGLKIAIMGCIVNGPGEMADADFGFVGSKTGMIDLYVKHTCVKAHIP
MEDAEELIRLLQEHGVWKDPEETKLT V

>core/124/1/Org1_Gene457

MWTHPIAYDVIVVGAGHAGCEAA YCSAKMGVSVLMLTSNLD TIAKLSCNPAVGGIGKGHIVREIDALGGIM
AEVTDQSGIQFRILNQTKGPAVRAPRAQVDKQLYHIHMKRLLENT PGLHIMQATVESLLDKEGVISGVTTKE
GWMFSGKTVVLSSGTFMRGLIHIGDRNFSGGRLGDPSSQGLSEDLKKRGFPISR LKTGTPPRLASSINFSCME
EQPGDLGVGFVHRTEPFQPLPQLSCFITH TMEKTKAIISANLHRSALYGGCIEGVGP RYCPSIEDKIVKFSDKE
RHHVFLEPEGLHTQEIYANGLSTSM PFVQYDMIRSVLGLENAIITR PAYAIEYDYIHGNVIHPTLESKLIEGLF
LCGQINGTTGYEEAAAQGLIAGINAVNKVFNRPPFIPSRQESYIGVMLDDLT TQILDEPYRMFTGRAEHRLLLL
QDNACARLSHYGYELG LLSEERYELVKKQNQLLEEEKVRLQKTFRQY GQSVVSLAKALSRPEVSYDMLREA
FPNDIRDLGAVLNASLEMEIKYSGYIDRQKILIQSLEKAESLLIPEDLDYKQITALSLEAQEKLAKFTPRTL GSA
SRISGIASADIQVLMIALKKHAHH

>core/125/1/Org1_Gene87

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KKFSVERKLDQLYIYAHLIHDQDITNPEGESDYQSIVYLYTLFSQEISWIQPALIALSEEKVAALLSSSVLAPYR
FYLEKIFRLSPHTGTANEEKILASSFAALNVSNKAFSSLSDAEIPFGIAKDSNGEEHPLSHALASLYMQSPDQEL
RRTAYLAQFQRYDYRNTFANLLNGKVQAHLFEAKARNYPSCLEASLFQHNIPTTVYINLINETKKHTSLINR
YFNLKKEALNLKEHFHYDVYAPISQTTSKNYSYEEGVDLVCKSLLPLGTHYVEILRNGLLSNRWVDRYENKH
KRSGAYSSGCYDSAPYILLNYTNTLYDVS VIAHEAGHSMHSYFSREAQPYHDAQYPLFLAEIASTFNEMLLM
EALSKSDQSKEDKIVIITKTLDTIFATLFRQTFFAAFEYEIHSAAEQGTPLTEEFLSATYGNLQKEFYGGVVTSD
SLSALEWARIPHFYYNFYVYQYATGIIAALSFAEKILTQEPGALELYLKFLKSGRSDFPLNILKKSGLDMTTSA
PLDKAFAFITKKIDLLSSLLSED

>core/126/1/Org1_Gene572

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QKLYREVIEQLAYWQEEKTRALAPLLNISIEQLLTDFLLDYISAHSLIEQKMFPEGRVILNRNINRLKHECEW
NAKTYDRIALLSRSYFLELVESKSADIYFDYYEMVLFYLLKKIYILEQCPYAELLPEEELVSLIMEHV FILPKDK
LYPLIQLLEMWQKHVHPNSSLVVQILVDRFSTHMEGAIRFCEALVSFSGLEELHQQIITTFEELLSNKVQQIK
TEEAKQCVALHILDPSISISEKLALSSDTLQNIVSGDDEQHTKLRNYLDLWEAIQSYDIDRQQLVHHLVYGA
KDLWKKGGNDEKALNLLQLVLRFTSYDIECESVFLFIKQAYKQALSSHAIRLLKLEKFISEANIPSIVISEAE
KANFLADAEYLF AHEDYDKCYLYSMWLT KVAPSPQSYRLAGLCLMENKRYDEALEFLCMLSPNDSINDYK
TQKALAF CQKHQSKDRAAS

>core/127/1/Org1_Gene864

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WATHGVPTEINAH PHVDEGRSCAVVHNGI IENFKELRRELTAQG ISFASDTDSEIIVQLFSLYYQESQDLVFSF
CQTLAQLRGSVACALIH KDHPTILCASQESPLILGLGKEETFIASDSRAFFKYTRHSQALASGEFAIVSQGKEP
EVYNLELKKIHKDVRQITCSEDASDKSGYGYMLKEIYDQPEVLEGLIQKHMDEEGHILSEFLSDVPIKSFKEI
TIVACGSSYHAGYLAKYIIESLV SIPVHIEVASEFRYRRPYIGKDTLGILISQSGETADTLAALKELRRRNIA YLL
GICNPESAIALGV DHCLFLEAGVEIGVATTKAFTSQ LLLL VFLGLKLANVHGALTHAEQCSFGQGLQSLPDL
CQKLLANESLH SWAQPYSYEDKFLFLGRRLMYPVVM EAALKLKEIAYIEANAYPGGEMKHGP IALISKGTPV
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LAKGMEIDCPRNLA KSVTVE

>core/128/1/Org1_Gene741

MIPSGLVYLLYPLGFLASLFFGSAFSIQWWLSKKRKEVYAPRSFWILSSIGATLMIVHGTIQSQFPVTVLHVINL
IYYLRNLNITSSRPISFRATLVLMALSVV FVTLPFLYVNMEWMASPNIFHLPLPPAQLSWHLIGCLGLAIFSGRF
LIQWFYIESNNTKDFPLLFWKIGLLGGLLALVYFIRIGDPINILCYGCGLFPSIANLRLFYKEQRSTPYLDTHCFL
SAGEASGDILGGKLIQSIKSLYPNIRFWGVGGPAMRQEG LQPILNMEEFQVSGFAEVLGSLFRLYRNYRKILKT
ILKHKPATLIFIDFPDFHLLLIKLRKHG YRGKIIHYVCPSIWAWRPKRKRILEQHLDMLLLILPFEEGLFKNTSL
ETVYLGHPLVEEISDYKEQASWKEKFLNSDRPIVA AAFPGSRRGDISRNLRIQVQAFLNSSL SQTHQFVSSSSA

KYDEIIEDTLKAEGCQHSQIIPMNFYELMRSCDCALAKCGTIVLETALNQTPPTIVMCRLRPFDFTFLAKYIFKIL
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LPAV

>core/129/1/Org1_Gene603

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TIPGKPLLHYLILVEDVASWDSTTTSGLLVSFYPMFLQKDLFQSLHITKGNICLVNKYGEVLFCQDSESSFV
FSLDLPNLPQFQARSPSAIEIEKASGILGGENLITVSINKKRYLGLVLNKIPIQGTYTLSLVPVSDLIQSALKVPL
NICFFYVLAFLLMWWIFSKINTKLNKPLQELTFCMEAAWRGNHNVRFEPPQYGYEFNELGNIFNCTLLLLLNS
IEKADIDYHSGEKLQKELGILSSLQSALLSPDFPTFPKVTFSQHLRRRQLSGHFNGWTVQDGGDTLLGIIGLA
GDIGLPSYLYALSARSLFLAYASSDVSLQKISKDTADSFSKTTEGNEAVVAMTFIKYVEKDRSLELLSLSEGAP
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HSADGTLTILSFS

>core/130/1/Org1_Gene722

MRIEDFSLKLIPSSPGVYLMKDVHDQVLYIGKAKNLKNRLASYFHEKGDSRERIPFLMKKTASIEIVVSNETE
ALLENLIKQHHPKYNVLLKDDKTFFCLAISLSHWPKEAIRTKAITSSQRQLIFGPYVSAEACHTLLEVISQ
WFPLRTCSDREFALRKRPCILYDMKRCLAPCVGYCTPEEYQGTLDKAILFLKGKIEEVVKDLEKVIQKASDNL
EFEQAANYRRTLSLIKQAMAKQQVEKFHFQNI DALGLYRHKQRTILTLLTVRSGKLLGARHFSFFENAQEDQ
DLLSSFILQYYVSQPYIPKEILTPLPLEFPTLSYVLNAESPRLRSPKTGYGKELLDLAYRNAKAYAATTLPSST
LPYQDFQNILRMSQYPYRIECYDNAHMQGAHATGVYIVFENNGFDPKQYRTFSIDSEKTQNDLALLEEVLLR
RFHSLTTALPDMIVVDGGKTHYNKTKKIIQTLNLTGIQVVIAKEKSNHSRGLNKEKIFCETFPFGSLPPTSNL
LQFFQILRDEAHRFAISKHRKKRGKALFEQEKIPGIGEVKRKRLLQKFKSWKQVMLSSQEELEAIPGLTKKDIA
VLLARQKDFNKSD

>core/131/1/Org1_Gene256

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QQIEDYIGLDTTNIIACSAKTGQGIPAILKAIIDLVPKKAPAE TELKALVFDSHYDPYVGIMVYVRIISGELKKG
DRITFMAAKGSSFEVLGIGAFLPKATFIEGSLRPGQVGFFIANLKKVKDKIGDVTVTCKHPAKTPLEGFKEIN
PVVFAGIYPIDSSDFDTLKD DALGRLQLNDSALTIEQESSHSLGFGFRGFLGLLHLEIIFERIIREFDLDIIATAPS
VIYKVVLKNGKVL DIDNPSGYPDPAIIEHVEEPWVHVNIITPQEYLSNIMNLCCLKRGICVKTEMLDQHRLVL
AYELPLNEIVSDFNDKLKSVTKGYGSFDYRLGDYRKGSIIKLEVLIN EEPIDAFSCLVHRDKAESRGRSICEKL
VDVIPQQLFKIPIQA AINKKVIARETIRALSKNVTAKCYGGDITRKRKLWEKQKKGKKRMKEFGKVSIPNTAFI
EVLKLD

>core/132/1/Org1_Gene1021

MVMVWSTNIKHEGLKSWIDEVAKLTTPKDIRLCDGSDTEYDELCTLMESTGTMIRLNPEFHPNCFLVRSSAD
DVARVEQFTFICTSTEAEAGPTNNWRDPQEMRRELHQLFRGCMQGR TLYIVPFCMGPLDSPFSIVGVELTDSF
YVVC SMKIMTRMGDDVLRSLGTSGKFLKCLHSVGKPLSPGEADVSWPCNPKSMRIVHFQDDSSVMSFGSGY

GGNALLGKKCVALARLASYMAKSQGWLAEHMLIIGITNPEGKKKYFSASFPSACGKTNLAMLMPKLPGWKIE
CIGDDIAWIRPGRDGRLYAVNPEYGFFGVAPGTSERTNPNALATCRSNSIFTNVALTADGDVWWEGLTEQPP
EPLTDWLKGKPKPGGSPAHPNSRFTAPLRQCPSLDPEWNSPQGVPLDAIIFGGRRSEITPLVYEALSWEHGV
TIGAGMSSTTTAAIVGQLGKLRHDPFAMLPFCGYNMAYYFQHWLSFAENRSLKLPKIFGVNWFRKNNQGEF
LWPGFSENLRVLEWIFQRTDGLEDIAERTPIGYLPNIQKFNLNGLNLDLQTVQELFSVDAEGWLAEEVENIGEY
LKIFGSDCPQQITDELLRIKSELKEK

>core/133/1/Org1_Gene542

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SKQGSTKDPDGTFSFTPDPSIFPEFTFNHDFLKD KIRQYTYLHSGLEIRFNDEVFISHNGLKDLFDAEITEPPLY
SPLFFQNEDLTFIFSHLEGNTERYFSFVNGQETLDGGTHLTAFKEAIVKGVNEFFGKTFVSNDIREGIVGCIAIKI
ASPIFESQTKNKL GNTQIRSSLIKDVKEAIVQALRKDKVAPELLLEKIKFNEKTRKNIQFIKQDLKSKQKKVHY
KIPKLRDCKFHYNDRSLYGEASSIFLTEGESASASILASRNPLTQAVFSLRGKPMNVFSLEETKMYKNDEL FYL
ATALGITQNEIQHLRYNKVILATDADVDGMHIRNLLITFFLKTLLPLVENNHLEFILETPLFKVRNKT TTTLYYYS
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NLITDF

>core/134/1/Org1_Gene26

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INLFTIRRTTQGLVQVLR AHLPHPGDPMRVVVGCDTRHNSIEFAQETAKVLAGNGCEVFLFQYPEPLALVSFT
VRYERAIGGVMITASHNPPNYNGYKVYMASGGQVLPPLDQEIVAACSAVNEILSVPSIDHPNIHLIGKEYEAL
YRDTLKQLQLYPEANRISGRSLSISYSPLHGTGISLVPHVLKDWGFLSVHLVEKQAIGDGDFTVQLPNPEDPE
ALTLGIEQMLANDDDLFIATDPDADRVGVVCLEDGQP YRFNGNQMASLLADHILGAWSKTRHLGEHDKLV
KSLVTTEMLSAIAKH YHVDLINVG TGFKYIGEKIESWRNSTNKFVFGAEESYGCLYGTHVEDKD AIIASALIA
EAALQQKLQGKTLCDALLSLYETYGYFANKTESVVFSAKTDEQEIRKKLSHLEEISSANFFSGKYQVEKFENY
KQGIGFNLLSKDSYAL TLPKTSMLCYFSGGGRVIIRPSGTEPKIKFYFEMSTHYPERVTDKEIQKQREAESFQ
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>core/135/1/Org1_Gene50

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GALVTFSGHLLEAELGPGLLQGIFDGLQNRLEVLAEDSSFLQRGKHVNAISDHNLWNYTPVASVGDTLRRGD
LLGTVPEGRFTHKIMVPFSCFQEVTLTWVISEGTYNAHTVVA KARDAQGKECAFTMVQRWPIKQAFIEGEKI
PAHKIMDVGLRILDTQIPVLKGGTFCTPGPFGAGKTVLQH HLSKYAAVDIVILCACGERAGEVVEVLQEFPHL
IDPHTGKSLMHRTCIICNTSSMPVAARESSIYLGVTIAEYYRQMGLDILLADSTSRWAQALREISGRLEEIPGE
EAFPAYLSSRIA AFYERGGAITTKDGSEGSTICGAVSPAGGNFEETVQSTLAVVGAF CGLSKARADARRYP
SIDPLISWSKYLNQVGQILEEKVSGWGGAVKKA AQFLEKGSEIGKRMEVVGEEGVSMEDMEIYLKAELYDF
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RLLEKTMVQMA

>core/136/1/Org1_Gene276

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PLCQALLTVWEQFFSAPENQNREFLVIFYGDASPYIQQALTQSRHSPRIVVVGISPTVFIQGD FRVHNYRVSGD
FFSSLDCRGTRAENTTILPYSSGLEGVFLPSIRCPSFTWAVRFGEQCLVANRGEDVEDRGGLSQDAERSQLPHS
ERDLAVVIDSTDPSSMSRLVEWLNQGSPSSDMEINPYPQRCPDVALSALY AISRVSGLAQEWILASVHEGLDL
QICYSLILMHTTFAVRYFFLLFTNYPQSRERFRTARIVAQSLYLPSILVLVFD CGNVLRKLWMPQEILRAIFISA
STISGSIVFVECTRW MGRGLRHRVQQFVQQRVIGSGLPVGTVRASYRDRAGFIIGFLQTVHGGLYLPVSIMVL
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>core/137/1/Org1_Gene978

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GATKFQLLIKLRIPHALPHIFSGLKIAIGSAGFAAIAGEWVASQSGLGILMLESRRNYEMELAFAGLATLSILTL
SLFQITLLIEKLIFSLFRVKRMSLKHKSVAKKALSVLALIPIMLIPWKGN SKSPDKKNLTSLTLLLDWTPNPNH
IPLYAGVAKGYFKQHGLDLQLQKNTDSSSAVPHVLFEQVDMALYHALGIMKTSIKGMPIQIVGRLIDSSLQGF
LYRSQDPIYKFEDLNGKVLGFCLNNSRDLNRLLET LNRNGVVPSEVKNVSSDLISPMLLNKIDFLYGA FYNIE
GVKLQTLGMPVKCFLSDTCDLPTGPQLIVFTKKGTKASEPEIVEAFQKALQESIIFSKDHPEDAFKLYAKETKS
IPKNLYQEYLQWEETFPLLAQSQDPLSKDLVDK LLETIHKQYPELASEVAKFSLNDLYNP SLPEEQSV

>core/138/1/Org1_Gene723

MYTEESLDNLRHSIDIVDLSEHIHLKRSGATYKACCPFHTEKTPSFIVNPAGAHYHCFGCGAHGDAIGFLMQ
HLGYSFTEAILVLSKKFQVDLVLQPKDSGYTPPQGLKEELRHINSEAE TFFRYCLYHLPEARHALQYLYHRGF
SPDTIDRFHLGYGPEQSLFLQAMEERKISQEQLHTAGFFGNKWFLFARRIIFPVHDALGHTIGFSARKFLENSQ
GGKYVNTPETPIFKKSRILFGLNFSRRRIAKEKKVILVEGQADCLQMIDSGFNCTVAAQGTAFTEEHVKELSK
LGVLKVFLLFDSDEAGNKAALRVGDLCQTAQMSVFVCKLPQGHDPDSFLMQRGSSGLIALLEQSQDYLTFLI
SEKMSSYPKFGPREKALLVEEAIRQIKHWGSPILVYEHLKQLASLMMVPEDMVLSLANPQVTAEPQNIPIKQK
VPKIH PHIVMETDILRCMLFCGSNTKILYTAQFYFVPEDFKHPECRKLFAFMISYYEKYRKNVPFDEACQVLS
DSQILQLLTKRRLNTEALDTIFVQSLQKMADRRWREQCKPLSLNQN IQDKKLEILEDYVQLRKDRTHITLLDPE
SELIP

>core/139/1/Org1_Gene341

MSTSPISNDPRYLSLSNATEKTSLLANSRSLSPVPNSLVPSNPEDTGLRKSIFTHSVTLFAGLVVLLVAVSVVV
VALTVLAPGVPQAILLGIAISGVGIGGFSIMKSLVYMVRDYMSPRMQESSRIKSALAVGTGFTVMGLVMKVG
ANFVPPGGYGGLVGS LGSSAYS RGSQTTLASF SHYIYTKFFRSEKVAKGEKLTEAETIKEAKKLHYITLSIATIG
VGLAVLGILLAIAGTVLLGGAPATIAIILAPPLISIGLTTVLQ TILHSSIGKWRAFLTQEKKDLFVDTS LKDIRLE
KLPPSEVEESETSQSVIEVPDSEGIAETRISAEEIDTRLSLTTRQKVIFALATLLLLASIAAFIVTGFGGLTVMQVL
LVASVGSASVASVTLP MVSSGFSYVAYQLKARLNISKLRWKEAKNKKRVRQFLIESGVIASDREFNQMWKTV
YKKQIQKTDAAIREEV RNFEKGGEVNSALVGGILLGVGTGIMLLALVPAFAPIVPGILALGGSTLGIAGSILMR
KFVNWLYDELVKLYERRRRNRRELLYGPESKMRSIATDLVVEALAASHDHLFDLDGPVDFIDVDVDIDGAA

>core/140/1/Org1_Gene409

MTNSDNASAAGLLWAHPKEDPAFLGMIIKEFHLPPTVAQIFISRGFQTIQEIHKFLYSHLSSLYDPGLFLDMSK
AVERLLLARDRKEHVMYIGSDSDVDGMTGVALLVEFLRDIDVHVSFFLGAILKQHGETSTLIAKLKEEGITLL
ITVDCGITAGKEVSDITRQGIDVIITDHHMPTGKIPHC VATLNPKLRDHTYPNREL TGVGVAFKLARGVLNALI
SRNLVPK SQSLKKLLDLVTLGTITDVGVLLGENRVMVRYGIKEIARGARPGLNKL CALCGVEKSEVTSTDIV
LKIAPKLNSLGRLLDDPAKGVELLLTQDDERVDALIMELDNINRERQRIEAEVFQDVQEILNSNPEILKQAAIVL
SSTAWHARVIPIISARLAKTYNKPVVIIAIQRGIGKGSARTIGSFLLGVLLKCCSSLLLSYGGHDF AAGVIMKED
KVEDFKKKFVHLVNSSLKKGDTLPHLEIDAYADFDAIDYDLLASMELFEPFGKGNLMPIFYSKVRQVRYPKV
LPGNHLKLYLSQKERNLEGVAFGLGRHADALKASWHYPLEIAYTPRLSQTSGSGVIHLLVRDFRISSEPRFSD

>core/141/1/Org1_Gene240

MSFLRRHISLFRSQKQLIDVFAPVSPNLELAEIHRRVIEDQGPALLFHNVISSFPVLTNLFGTKHRVDQLFSQA
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LVYTESPTLTTPNLGMYRVQRFNQNTMGLHFQIQKGGGMHLYEAEQKKQNLPSVSVFLSGNPFLTLSAIAPLP
ENVSELLFATFLQGAKLLYKKTNDHPHPLLYDAEFILVGESPAKRRPEGPFGDHFGYYSLQHDFFEFHCHKI
YHRKDAIYPATVVGKPYQEDFYIGNKLQEYLSPLFPLVMPGVRRLKSYGESGFHALTA AVVKERYWRESLTT
ALRILGEGQLSLTKFLMVTDQEVPLDRFSVLETLERLQPDRLIIFSETANDTLDYTGPSLNKGSKGIFMGIG
KAIRDLP HGYQGGKIHGVDIAPFCRGCLVLETSLEDRCIKSLLHHPDLKSWPLIILADNLRETIQSEKDFLWR
TFTRCAPANDLHALHSHFATHRPNYNFPFVIDALMKPSYPKEVEVDPSTKQKVSERWHAYFPNKETFYI

>core/142/1/Org1_Gene496

MKYRTHRCNELTSNHIGENVQLAGWVHRYRNHGGVV FIDLRDRFGITQIVCREDEQPELHQRLDAVRSEWV
LSVRGKVCPRLAGMENPNLATGHIEVEVASFEVLSKSQNLPSIADDHINVNEELRLEYRYLDMRRGDIIEKL
LCRHQVMLACRNFMDA QGFTEIVTPVLGKSTPEGARDYLVP SRIYPGKFYALPQSPQLFKQLLMVGGLDRYP
QIATCFRDEDLRADRQPEFAQIDIEMSF GDTQDLLPIIEQLVATLFATQGIEIPLAKMTYQEAKDSYGTDKP
DLRFDLKLKDCRDYAKRSSFSIFLDQLAHGGTIKGFCVPGGATMSRKQLDGYTEFVKRYGAMGLVWIKNQE
GKVASNIAKFMDEEVFHELFAFYFDAKDQDILLLIAAPESVANQSLDHLRRLIAKERELYSDNQYNFVWITDFP
LFSLEDGKIVA EHHPTAPLEEDIPLLETDPLAVRSSSYDLVLNGYEIASGSQRIHNPDLQSQIFTILKISPESIQE
KFGFFIKALSFGTPPHLGIALGLDRLVMVLTA AESIREVIAFPKTQKASDLMMNAPSEIMSSQLKELSIKVAF

>core/143/1/Org1_Gene259

MSGKKDGV RGMIFVPLSILVLIFLPLPQILLDFGLCISFALSLLTVCWVFTLNSSNSAKLFPPFFLYLC LLRLGLN
LASTRWIVSSGTASSLIVSLGSFFSLGSLWAATFACLLFFVNFLMVSKGSERIAEVR SRFFLEALPAKQMALD
SDLVSGRASYKAVKKQKNALIEEGDFFSAMEGVFRFVKGDAIISCILLVNVVSVTCLYYTSGYALEQMWFT
VLGDALVSQVPALLTSCAAATLISKIDKEESLLNYLFEYYKQLRQHFRVVSLLIFSLCCIPSSPKFPIVLLASLL
WLAYRKEEPASEDSCIERAFSYVEGACPKEQESQFYQVYRAASEEVFEDLGVR LPVLTSLRIERPWL RVFGQ
NVYLD EMTPEAVLPFLRNIAHEALNAEVVQKYLEESERVFGIAVEDIVPKKISLSSLVVL SRRLLVRERSLKL F
PKILEAVAVYQNSGDSLEILAEKVRKSLGYWIGRSLWDQKQTLEVITIDFHVEELINSSYSKSNPVMQENVIRR
VDSLLERSVFKDFRAIVTSCETRFEMKKMLDPHFPDLLVLSHDELPKEIPISFLGIVSDEVLP

>core/144/1/Org1_Gene228

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KSEGVIPMSEFIDSSEGLVLGAEEVYLDQAEDEEGKVVLRSREKATRQRQWEYILAHCEECSIVKGQITRKVK
GGLIVDIGMEAFLPGSQIDNKKIKNLDDYVGKVCFEKILKINVERRNIVVSRRELLEAERISKKAELIEQISIGEY
RKGVVKNITDFGVFLDLGDIDGLLHITDMTWKRIRHPSEMVELNQELEVIILSVDKEKGRVALGLKQKEHNP
WEDIEKKYPPGKRVLGKIVKLLPYGAFIEIEEGIEGLIHISEMSWVKNIVDPSEVVNKGDEVEAIVLSIQKDEGK
ISLGLKQTERNPWDNIEEKYPIGLHVNAEIKNL TNYGAFVELEPGIEGLIHISDMSWIKKVSHPSELFKKGNSV
EAVILSVDKESKKITLGVKQLSSNPWNEIEAMFPAGTVISGVVTKITAFGAFVELQNGIEGLIHVSELSDKPFA
KIEDIISIGENVSAKVIKLDPDHKKVSLSVKEYLADNAYDQDSRTELDFKDSQGPKERKKKGGK

>core/145/1/Org1_Gene618

MSTRRPIQLLDPLTINQIAAGEVIENSVS VVKELIENSLDAGADEIEIETLGGGQGAIIRDNGCGFRAEDIPIALQ
RHATSKIREFSDIFSLNSFGFRGEALPSIASISKMEIQSSIEGDEGVRTVIHGGDIVSCEPCARQLGTTVIVNSLFY
NVPVRRGFQKSMQSDRLGIRKLIENRILSTANIGWSWISEGHHEIQIAKQQGFQERVAYVMGDHFMQDALT
DKEANGVRIVGVLGSPSFHRPTRQGQKIFINDRPIESLFISKKVGDAYALLPLHRYPVFVLKLYLPSSWCFDN
VHPQKIEARILKEELVGDCIKEAIVETLACPPGILCRTHQEIEESDSVPLPMFRMLETSQVEEESVEFDQNLFA
YSSSEDVSLEKQEYTSRGPKSQMDWIYSSDVRFSLTSLGRVLAEDLEGVHIIFTAAARKHLFFLSLMQENSRM
YQSQALLIPLRLQVTPEEAFFFSHHGRTLCDLGIEISQVGPCVFSIESTPTVIGEEELKEWLLLLAARGSTDINSE
ALTALMKETLTQATFSKHQHVFVDVSWLKLLWSVGKPEKGFDGARIRRLILDSDFMEG

>core/146/1/Org1_Gene242

MAVSGGGGVQPSSDPGKWNPALQGEQAEGPSPLKESIFSETKQASSAAKQESLVRSGSTGMYATESQINKAK
YRKAQDRSSTSPKSKLKGTFSKMRASVQGFMSGFGSRASRVSAKRASDSGEGTSLLPTEM DVALKKGNRISP
EMQGFFLDASGMGGSSSDISQLSLEALKSSAFSGARSLSLSSSESSSVASFGSFQKAIEPMSEEKVNAWTVARL
GGEMVSSLLDPNVETSSLVRRAMATGNEG MIDLSDLGQEEVSTAMTSPRAVEGKVKVSSSDSPEANPTGIPN
SNTLRAEKEAEKQESREQLSEDQMMLARAMAGLLTGAAPQEVLSNSVWSGPSTVFPPPKFSGTLPTQRSGD
KSKHKSPGIEKSTNHTNFSPLREGTVKSAEVKSLPHPESMYRFPKDSIVSREEPEAVVKESTAFKNPENSSQNF
LPIAVESVFPKESGTGGALGSDAVSSSYHFLAQRGVSL LAPLPRATDDYKEKLEAHKGPGGPPDPLIYQYRNV
AVEPPIVLRSPQPFSGSSRLSVQGKPEAASVHDDGGGGNSGGFSGDQRRGSSGQKASRQEKKGKKLSTDI

>core/147/1/Org1_Gene441

MQKHPSFYQRFLSAYYKNLLASLSWKFFISVALIGIYAPLFASSKPLLVTWHGEIFFPLLRYLFFPGYYTKPVD
LFFNVLMVTFPFFILSFKLTRGWLRRWLLGLCIISQCMIFAWAYSGKVQDPALAENLKKMRAEKVRENISKV
NSEMVMLLPKDTRTWEMERRY MSTYEQLGILIKAKYRKKQEASVKKYQVAFEEKRQSPMPTLRHLEMKNE
GICLKRLQQRVDKMQRPYEMAQQA WN RATDN YRPFLMALTRIEHELRLADYNNWGPEDLCIAYANVEKR
AEPYKKSLLAIRQVLEDYAKLRS AISFIQDKRLWIEKESEDLRILINPFFSSFWEDDAGGSREM NKYVPWWQ
LSRVTRKDLLAALVFGIRIALV VAGIGITALAIGIMIGLVSGYFGGTVD MILSRFTEIWETMPVLFILMLVISIT
QQKSLLLNTVLLGCFSWTGFSRYVRIEVLKQRDRGYVLAATNLGYSHYYIMVHQILPNAIVPVISLVPFAMM
AMISCEAGLTFLGLGEESSASWGNLMREGVTGFPAESAVLWPPAILTMLLIAIALIGDGVRDALDPRLQDS

>core/148/1/Org1_Gene986

MTDFPTHFKGPKLNPIKVNPNFFERNPKVARVLQITAVVLGIIALLSGIVLIIGTPLGAPISMILGGCLLASGGAL
FVGGTIATILQARNSYKKAVNQKKLSEPLMERPELKALDYSDDLKEVWDLHHSVVKHLKKLDNLSETQRE
VLNQIKIDDEGPSLGECAAMISENYDACLKMLAYREELLKEQTQYQETRFNQNLTHRNKVLLSILSRITDNIS
KAGGVFSLKFSTLSSRMSRIHTTTTIVILALSAVVSVMVVAALIPGGILALPILLAVAISAGVIVTGLSYLVRQIL
SNTKRNQRQDFYKDFVKNVDIELLNQTVTLQRFLFEMLKGVLEEEEEVSLEGQDWYTQYITNAPIEKRLIEEIR
VTYKEIDAQTKMKMTDLEFLENEVRSGRLSVASPEDPSETPIFTQGKEFAKLRRQTSQNISTIIYGPDNENIDPE
FSLPWVPKKEEEIDHSLEPVTKLEPGSREELLVEGVNPTLRELMRIALLQQQLSSVRKWRHPRGEHYGNVI
YSDTELDRIQMLEGAFYNHLREAQEEITQSLGDLVDIQNRILGIIVEGSDSRTEEEPQE

>core/149/1/Org1_Gene33

MANPTQSRPPSPEISIEEELQELAGSSNTETISNTPPPSCAATAEEVSLFIEGGRRNSEDEEGPLGSCEVYDVVC
ITNQGDPEVRDHEVRVMYINGSGRTQHEGILDAMNICDLRGEPVRFIHNSGYGLGSCFLGIRNRIPPRDNVISQ
AIQARWNEFFIFAENANRDYIVLFSGNGGLYLQVALDNSIYSHHILCVGIGSSYYIQGNRVHNYRVTGDWTT
LLDRRGATAVNTTTLPYADSAEGLFLPSVRCPSYQWALRCGEQCLIMDNNQQVGFRPQDSSSEIALVNLNQ
DHSTWTRLIEWIDRGDSQAVLELNPQPSHCRDIALTALYATTRISSLLQECLMISVTYAPEVFVTYAIVTGYSI
MTLRYFILLLTNRPGCRRHFRVLRALALGLQSLGFLTVLDDHINVTRRVNRRPPLISVIFCTASFATGSFIYVDL
TRMFFTSLRSRLQLFVQRRLTGRGLPLRRVFNHLDSLRF SQNALITFHGGLFMPLIIGFFNQLVIQVPRVVIRP
NTTAVYDLNQTSQEAWDSDGDLAIGQTINFLLCMILLVINTFFFVRSVRRNLHRRPHR

>core/150/1/Org1_Gene576

MFMTQNSQATEVSSEESQKKLEELVALAKEQGFIYEEINEILPMSFDTPEQIDQVLIFLTGMDIQVLNQID
VERQKEKKKEAKELEGLARRTEGTPDDPVRMYLKEMGTVPLLTRREEVEISKRIEKAQVQIERIILRFYSAK
EASIAHYLISGKERFDKIISEKEVEDKTHFLKLLPKLITLLKEEDTYLENLLSLKQPDLSKQEA AKLND SLEK
CRIRTQAYLRFCFHC RHNVTEDFGEVVFKAYDSFLHLEQQINDLKVRAERNKF AA AKLAAKRKLYKREVA A
GRTLEEFKKDVRMLQRWMDKSQEAKKEMVESNLRLVISIAKKYTNRGLSFLDLIQEGNMGLMKAVEKFEY
RRGYKFSTYATWWIRQAVTRAADQARTIRIPVHMIETINKVLRGAKKLMMETGKEPTPEELAEELGLTPDR
VREIYKIAQHPISLQAEVGESESSFGDFLED TAVESPAEATGYSMLKDKMKKEVLKTLTDRERFVLIHRFGLL
DGKPKTLEE VGSAFNVTREIRIRQIEAKALRKM RHP RSKQLRAFLDLLEEEKTGTSKVKSLKSK

>core/151/1/Org1_Gene901

MDTQSSIGNEEWRIAGTSIVSGMALGKVFFLGTSPHVLRELTL PQEEVEHEIHRYYKALNRSKSDIVALEQEV
TGQQGLQEVSSILQAHLEIMKDPLLTEE VVNTIRKDRKNAEYVFSSVMGKIEESLTAVRGMPSVVDRVQDIH
DISNRVIGHLCCQHKSSLGESDQNLIIFSEELTPSEVASANSAYIRGFVSLVGAATSHTAIVSRAKSIPYLANISE
ELWNI AKRYNGKLVLIDGYRGELIFNP KPATLQSCYKKELSVVAHTSQRLVRKSLHPVSSHAGSDKDVEDLL
ENFPQTSIGLFRSEFLAVILGRLPTLREQVDLYEKLARFP GDSPSVLRLFD FGEDKPCPGIKNKKERSIRWLLDY
SVILEDQLQAIKASLQGSIKVLIPGVSDVSEIIEVKKKWETIQTRFPKGHKVSWGTMIEFPSAVWMIEEILPEC
DFLSIGTNDLVQYTLGISRESALPKHLNVTLP PAVIRMIHHVLQAAKQNQVPVSICGEAAGQLSLTPLFIGLGV
QELSVAMPVINRLRNHIALLELNSCLEITEALLQAKTCSEVEELLNRNNKITS

>core/152/1/Org1_Gene1022

MVKVPWAFKNFIPKLYTSIKEGYSFNTFKKDFQAGITVGILAFPFAIAIAIGVGVSPIQGLLASIIGGLLASAMG
GSNVLISGPSSAFISILYCLSAKYGAEALFTVTLLAGVFLIAFGLTGLGTFIKYMPYPVVTGLTTGLAIIIFSSQIK
DFLGLQMGANIPADFLPKWIAYWDHLWTWDSKSAVGLFTLLIMYFRNYKPRYPGVMIAIVTATTLVWLL
KIDIPTIGSRYGTLPTAIPLPKIPQLSITKILQLMPDALTIAVLSGLETLLSAVVADGMTGWRHQSNQCLVAQGV
ANIGTSLFSGIPVTGSLSRSTAASIKSEATTPIAGIVHSIFICIFILLLLAPLTVKIPLTCLAAVLILIAWNMSEIHFIH
LFTAPKKDIVVLLTVFILTVMTTITA AVQVGMMLAAFLFMKQMSDLSDVISTAKYFDKDSDFLSKA EVPQNT
EIYEINGPFFFGIADRLKNLLNDIEKPPKIFILCMTRVPTIDASAMHALEEFFLECDRQGTLLLLAGVKKTPLAD
LKRYHLDELIGVDHIFSNIKSALLFAQALTNLESKTSTRHLV

>core/153/1/Org1_Gene899

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HSSDPQTRKSTVIGAGLAGSSEALDVLSQAMETADPLQQLVLSAVSGHLGKTSDDLFLKALASYPVIRLEA
AYRLANLKNTKVIDHLHSFIHKLPEEIQCLSA AIFLRLETEESDAYIRDLLAAKKS AIRSATALQIGEYQQKRFL
PTLRNLLTSASPQDQEAILYALGKLKDGQSYNYKQQLQKPDVDVTLAAAQALIALGKEEDALPVIKKQALE
ERPRALYALRHLPSEIGIPIALPIFLKTKNSEAKLNVALALLELGCDTPKLLEYITERLVQPHYNETLALSFSKG
RTLQNWKR VNIIVPQDPQERERLLSTTRGLEEQILTFLFRLPKEAYLPCIYKLLASQKTQLATT AISFLSHTSHQ
EALDLLFQA AKLPGEPIIRAYADLAIYNLTKDPEKKRSLHDYAKKLIQETLLFVDTENQRPHPSMPYLR YQVT
PESRTKLMLDILETLATSKSSEDIRLLIQLMTEGDAKNFPVLAGLLIKIVE

>core/154/1/Org1_Gene358

MKTSQLFYKTSKNANKSAAVLSNELLEKAGYLFKVSKGVYTYTPLLWRVVS KMMNIIREELNAIGGQELLLP
LLHNAELWQHTGRWEAFTSEGLLYTLKDREGKSHCLAPTHEEVICSFVAQWLSSKRQLPLHLYQIATKFRDE
IRPRFGLIRSRELLMEDSYTFSDSPEQMNEQYEKLRSAYS KIFDRLGLAYVIVTADGGKIGKGKSEEFQVLCSL
GEDTICVSGSYGANIEAAVSIPPQHAYDREFLPVEEVATPGITTIEALANFFSIPLHKILKTLVVKLSYSNEEKFI
AIGMRGDRQVNLVKVASKLNADDIALASDEEIERVLGTEKGFIGPLNCPIDFFADETTSPMTNFVCAGNAKD
KHYVNVNWDRDLLPPQYGDFLLAEEGDTCPENPGHPYRIYQGIEVAHIFNLGTRYTDSFEVNFQDEHGQTQQ
CWMGTYGIGVGRTLAACVEQLADDRGIVWPKALAPFSITIAFNGGDTV SQELAETIYHELQSQGYEPLDDR
DERLGFKLKDSDLIGIPYKLILGKSYQSSGIFEIESRSGEKYTVSPEAFPTWCQNHLA

>core/155/1/Org1_Gene560

MTVSVKKKSFRALVTTHFLTIINDNLYKFLLAFFLLEGKLTENAKILSCVSFFFALPFLLLAPLAGSLADRQ
KRNILATRFIEILCTILGT YFFFIQS VVG GYVVLILMACHTTIFGPAKL GILPEMLPSEQLSQANGIMTAATYTG
SILGSCLAPLLVDVTHRLGVNSYVWPTLMCVIVSIISTLISFCIRPSNVKNVKQKITLV SFKDLWKVLKDTRMI
HYLTVSIFLGSFFLLIGAYTQLEIIPFVEFTLKYPKHYGAYLFPIVALGVGTGSYITGKISGDKIKIGYVPLAAIGL
ALVFMGLYAFACSILFVLFFLLALGFLGGVYQVPLHAYVQYASPEHKRGQILAANNFLDFFGVLV AAGVIRV
LGSNLGLSPETSFFYIGWFVLAVSIWTLWIWREHVYRLLLGIILRRQLGYYLKI HQSSSPKCYFVAVQSYREIR
RVLAALTKTVRSRVII LDQKL VPGWRAWLLSWCVPTV VSSVRDNDSEAQDAWAVLQANHLKTS LKKFPDV
SVVCLGLPKNVERFTSILQEQQIDLHP IQLVQKEGKKRVIYTLVFP HA

>core/156/1/Org1_Gene416

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LIEIAGAGFINFTFSPVFLNQQLEHFKDALKLGFQVSQPKKIIIDFSSPNIAKDMHVGHLRSTIIGDSLARIFSYVG
HDVLRNLNHIGDWGTAFGMLITYLQENPCDYSLEDLTSLYKKAYVCFTNDEEFKKRSQQNVVALQAKDPQA
IAIWEKICETSEKAFQKIYDILDIVVEKRGESFYNPFLPEIIEDLEKKGLLTVSNDAKCVFHEAFSIPFMVQKSDG
GYNYATTDLAAMRYRIEEDHADKIIIVTDLGQSLHFQLLEATAIAAGYLQPGIFSHVGFGLVLDPPQGKKLKTR
SGENVKLRELLDTAIEKAEEEALREHRPELTDEAIQERAPVIGINAIKYSDLSSHRTSDYVFSFEKMLRFEGNTA
MFLLYAYVRIQGIKRRRLGISQLSLEGPPEIQEPAEELLALTLLRFPEALESTIKELCPHFLT DYLYNLTHKFNGFF
RDSHIQDSPYAKSRLFLCALAEQVLATGMHLLGLKTLERL

>core/157/1/Org1_Gene947

MSKLIRRVTVLALTSMASCFASGGIEAAVAESLITKIVASAETKPAPVPMATAKKVRLVRRNKQPVEQKSRG
AFCDKEFYPCEEGRCQPVEAQQESCYGRLYSVKVNDDCNVEICQSVPEYATVGSPYPPIELAIGKKDCVDVVI
TQQLPCEAEFVSSDPETTPSTDGKL VWKIDRLGAGDKCKITVWVKPLKEGCCFTAATVCACPELRSYTKCGQ
PAICIKQEGPDCACLRCPVCYKIEVVNTGSAIARNVTVDNPVPDGYSHASGQRVLSFNLGDMRPGDKKVFVTV
EFCPQRRGQITNVATVTYCGGHKCSANVTTVVNEPCVQVNISGADWSYVCKPVEYSISVSNPGDLVLHDVVI
QDTLPSGVTVLEAPGGEICCNKVWRIKEMCPGETLQFKLVVKAQVPGRFINQVAVTSESNCGTCTSCAETT
THWKGLAATHMCVLDTNDPICVGENTVYRICVTNRGSAEDTNVSLILKFSKELQPIASSGPTKGTISGNTVVF
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>core/158/1/Org1_Gene847

MELLSLNKSYFEIQRRLRYRPEILTLETIRSKHIQETSSPPSPPELQKHIPNLCRIPEVSIYTEQETSSKPLKIGVL
LSGGQAPGGHNVVIGLFDALRVFNPKTRLFGFIKGPLGLTRGLYKDLDISVIYDYNNMGGFDMSSSREKIKT
EEQKKNILNTVKQLKLDGLLIIGGNSNTDTAMLAEYFLAHNCKT SVIGVPKTIDGDLKNCWIETSLGFHTSC
RTYSEMIGNLAKDALSAKKYHHFIRLMGQQASYTTLECGLQTLPNIALISELIATRKISLKQLSEQLALGLVRR
YKSGKNYSTVLIPEGLIEHIFDTRKLIDELNVLLANGDSSIEKILSKLSPETLKT FHLFPKDIANQLLLARDSHGN
VRVSKIAATEELLAVMVKKEIEKIKPHMEFHSVSHFFGYEARAGFPSNFD CNYGIALGIISALFLVRQKTGYMIT
INNLAQSYTEWQGGATPLYKMMHLENRCGTETPVIKTDSVDPKSPAVQHLLQQSDSCLVEDLYRFPGPLQYF
GKEELIDQRPLTLLWENQTHSPLL

>core/159/1/Org1_Gene813

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VIQDILRVLSRRARNYKILVYPVTVQGNSAAHEISKAIEVMNAENLADVLIHARGGGSIEDLWAFNEEILVKAI
HASTIPIVSAVGHETD YTLCDFASDVRAPTPSAAAEIVCKSSEEQVQVFEGYLRHLLSHSRQLLTSKKQQLLP
WRRFLDRAEFYT TAQQQLDSIEIAIQKGVQGGKI HESKQRYDNISRWLQGD LVSRMTCRLQSLKKMLSQALSH
KALSLQVRCHQLKKS LTYPRQIQQASQKLS PWRQQLDTLISRRLHYQKEEYFHKHTRLKHAHNVLEQQ LRS
HVQKLELLGRRLSRGCELNLQNQKIA YANVKETLATILERRYENSVARYSALKEQLHSLNPKNVLKRGYAM
LDFDNENSAMISVDSLQENARVRIQLQDGEAILTVTNIEICKLIK G

>core/160/1/Org1_Gene973

MDNSDNSFHTLETEQGSFLNDELAVEEVASTESTEISDATLCFADEIQELPSPEKKVAFILNKMREALTGSSQG
SDLRLFWDLRKQCLPLFNEIEDTAKRADHWRCYIELTKEGRHLKGLQDEEGSFVVGQIDLAITCLEKDILKFQ
EGTEDKIFKDREDNFLESQALDKHQAFYKQHHTSLLWLSSFSSKIIDLKELINVGMRLKSKFFQRLSNLG
NQVFPKRKELIEKVSQTFAEDVDAFVAKYFIGSDKETLKKTVFFLRKEIKNLQHAARKLFVSSHVFAETRLKL
SKCWDQLKGMEKEIRQEQGRLRVVSAENSKEVRQMLAEVSSLLIEGNDLSKVRKDLEGISKKIRALDLTHDD
VISLKKEMQQLFDQLREKQDAAEHSYQEQLAKDKQVKKEAARSLAERITTFSTKTCSEGNITSESREEWQTLK
ELLGKMSFLPPPEKISLDNQLNLALQTIVNFEEQQLSSPDSREKLVNMRQVLKQRRERRQELKDKLEQDKKL
LGSSGLDFDRAMQYSALVEEDKRALEELDASILELKQQIQQL

>core/161/1/Org1_Gene911

MPQKVLITSALPYANGPLHFGHIAGVYLPADVYARFRLLGDDVLYICGSDEFGIAITLNADREGLGYQEYV
DMYHKLHKDTFEKLGFDLFFSRTTNPFHAELVQDFYSQLKASGLIENRISEQLYSEQEQRFLADRYVEGTCP
RCGFDHARGDECQSCGADYEAILDIPKSKISGVLEVKKETEHSYFLLDRMKDALLSFIQGCYLPDHVRKFV
VDYIEHVRSRAITRDLSWGIPVPDFPGKVIFYVWFDAPIGYISGTMEWAASQGNPDEWKRFWLEDGVEYVQFI
GKDNLPFHSVVPAMELGQKLDYKKVDALVSEFYLLLEGRQFSKSEGNVYVMDKFLSSYSCLKLRYVLAAT
APETSDSEFTFLDFKTRCNSELVGKFGNFIRVLAFAEKNHYDKLSYHSVVLEDSDFLEEARQLVRDAEK
CYREYSLRKATSVIMSLAALGNVYFNQQAPWKLLKEGTRERVEAILFCACYCQKLLALISYPIIPESAVAIWE
MISPKSLENCNLDTMYARDLWKEEILDVINEEFHLKSPRLFFTVE

>core/162/1/Org1_Gene140

MHPLYVDLDTIISSYSPPLPKEFQEAASLIAVPDTSKPKVPVPGVKTLFPQTYHLPLYLKFBVQGENVVHTPLKVG
VMFSGGPAPGGHNVIQGLFNSLKDFHPDSSLVGFVNNGDGLTNNKSIDITEEFLSKFRNSSGGFNCIGTGRKKIV
TPEAKEACLKTAALDLDGLVIIGDGSNTATAILAEYFAKRRPKTSIVGVPKTIDGDLQHTFLDLTFGFDAT
KFYSSIISNISRDALSCKAHYHFIKLMGRSASHIALECALQTHPNIALIGEEIAEKNLPLKTIHKICSVIADRAAM
EKYYGVILPEGIIIEFIPEIINLITEIESLSEYEDKISRSPESQRLLKSFPAPIIEQILNDRDAHGNVYVSKISVDKLL
IHLVSNHLQQYFPNVPFNAISHFLGYEGRSGLPTKFDNTYGYSLGYGAGILVRNHCNGYLSTIESLACPFMKW
KLRAIPVVKMFTVKQQADGTLQPKIKKYLVDIGSTAFRKFKLYRKIWALEDYSYRFLGPLQIETPPMHSDNFP
PLTLLLNHNFWQRHQGCIEIPDTTY

>core/163/1/Org1_Gene555

MSRKDNEVSLARSIFNILSGTFCSRITGIFREIAMATYFGADPIVAAFVLGFRTVFFLRKILGGLILEQAFIPHFE
FLRAQSLDRAAFFRRFSRLIKGSTIIFTLLIEAVLWVVLQYVEEGTYDMILLTMILLPCGIFLMMYNVNGALL
HCENKFFGVGLAPVVVNIIWIFFVIAARHSDPRERIIGLSVALVIGFFFEWLITVPGVWKFLLEAKSPPQEHDVS
RALLAPLSLGLTSSIFQLNLLSDICLARYVHEIGPLYLMYSLKIYQLPIHLFGFGVFTVLLPAISRCVQREDHER
GLKLMKFVLTLTMSVMIIMTAGLLLLALPGVRVLYEHGLFPQSAVYAIVRVLRGYGASIIPMALAPLVSVLFY
AQRQYAVPLFIGITALANIVLSVLGRWVLKDVSGISYATSITAWVQLYFLWYYSSKRLPMYSKLLWESIRR
SIKVMGTTMLACMITLGLNILTQTTYVIFLNPLTPLAWPLSSITAQAIAFLSESCIFLAFLFGFAKLLRVEDLINL
ASFEYWRGQRGLLQRQHVMQDTQN

>core/164/1/Org1_Gene85

MAAKNIKYNEEARKKIHKGVKTLAEAVKVTLGPKGRHVVIDKSFGSPQVTKDGVTVAKEIELEDKHENMGA
QMVKEVASKTADKAGDGTTTATVLAELIYSEGLRNVTAGANPMDLKRIGDKAVKVVDDELKKISKPVQHH
KEIAQVATISANNDSEIGNLIAEAMEKVGKNGSITVEEAKGFETVLDVVEGMNFNRYGLSSYFSTNPETQECV
LEDALILIYDKKISGIKDFLPVLQQVAESGRPLLIIEEIEGEALATLVNRLRAGFRVCAVKAPGFGDRRKAM
LEDIAILTGGQLVSEELGMKLENTTLAMLGKAKKVIVTKEDTTIVEGLGNKPDIQARCDNIKKQIEDSTSDYD
KEKLQERLAKLSGGVAVIRVGAATEIEMKEKKDRVDDAQHATIAAVEEGILPGGGTALVRCIPTLEAFLPML
ANEDEAIGTRIILKALTAPLKQIASNAGKEGAIIICQQVLARSANEGYDALRDAYTDMIDAGILDPTKVTRSALE
SAASIAGLLLTTEALIADIPEEKSSSAPAMPSSAGMDY

>core/165/1/Org1_Gene349

MFGSESLRYQLLIQDFAKVSEEGIGLLESKEYSLLQAKLVLRALAQNSSFDDWFRSFKKCQISYPELAHDRDV
LEEFGIQVLREGIENPSVTVRVSVLAIGLARDFRLVPLLLQSCNDDSAIVRSLALQVAVNYGSESLKKAIVEL
ARNDDSIHVRITAYQVVALLQIEELLPFLRERAENKLVDSEVERREAWKACLELSSQFLETGVAKDDIDQALFT
CEVLRNGMLPETTEIFTELLSVEHPEVQESLLLSALAWSHQLQNHKEFLSKVRHVMCTSPFAKVRFAQAAALL
HLHGDPLGRDSLVEGLRSPQPLVCEAASAALCSLGIHGVPLAKEHLESLSRKAANLSILLVSREDIERAGD
VIARYLSNPEMCWAIEYFLWDAQWNLRGDTFPLYSDMIKREIGRKLIRLLAVARYSQAKAVTATFLSGQQA
QGWSFFSGMFWEEGDVKTSEDLVTDACFAAKLEGALASLCQKKDQASLQRVSQLYNDSRWQDKLAILESV
AFSENLDVAPFLDCCHHEAPSLRSAAAGALFSIFK

>core/166/1/Org1_Gene488

MLRIFCFVISWCLIAFAQPDLSGFVSILGAACGYGFFWYSLEPLKKPSLPLRTLTVSCFFWIFTIEGIHFSWMLS
DQYIGKLIYLVWLTILITLSVLFSGFSCLLVAIVRQKRTAFLWSLPGVWVAIEMLRFYGIFSGMSFDYLGWPM
TASAYGRQFGGFLGWAGQSFVAVIENMSFYCLLLKKPHAKMLWVLTLLLPYTFGAIHYEYLKHAFQQDKR
ALRVAVVQPAHPPIRPKLSPIVVWEQLLQLVSPQQPIDLLIFPEVVVPFGKHRQVYPYESCAHLLSSFAPLPE
GKAFLSNSDCATALSQHFQCPVIIGLERWVKKENVLYWYNLSAEVISHKGISVGYDKRILVPGGEYIPGGKFGS
LICRQLFPKYALGCKRLPGRRSGVVQVRGLPRIGITICYEETFGYRLQSYKRQGAELLVNLNDGWYPESRLP
KVHFLHGMRLNQEFGMPCVRACQTGVTAAVDSLGRILKILPYDTRETKAPSGVLETSPLPFNYKTLYGYCGD
YPMILIAFCAVSYLGGGFLGYRLLAKKEIR

>core/167/1/Org1_Gene455

MQSSEVKPFSRLRAYLCPIYKSEFSKFVPLFLLAFFVGFNYCLLKNMKDTLVIVGSDAGAEVIPFLKVWGIVP
GAVIVTMVYGWLGSRYPRTDVFYCFMAAFLGFFFLFAVIIYPVGDSLHLNSLADKLQELLPQGLRGFIVMVR
YWSYSIYYVMSELWSSVVLMLFWGLANQITTITEAGRFYALINTGLNLSSICAGEISYWMGKQTFVAYSFA
CDSWHSVMLNLTMLITCSGLIMIWLRYRIHHLTIDTSIPPSRRVLAEEGAATANLKEKKKPKAKARNLFLHLI
QSRYLGLLAIIVLSYNLVIHLFEVVWKDQVSQIYSSHVEFNGYMSRITTIGVVSVLA AVLTTGQCIRKWGWT
VGALVTPVLMLVSGLLFFGTIFAAKRDIFGGVLGMTPLALAAWTGGMQNVLSRGTKFTFFDQTKEMAFIP
LSPEDKNHGKAAIDGVVSRIGKSGGSLIYQGLLVIFSSVAASLNVIALVLLIIMVVWIAVVAYIGKEYYSRAAD
AVATLKQPKEPSSSIVREAQESVEQEEMAVL

>core/168/1/Org1_Gene706

MHDQRNRGHNNHNLRLRPGSTLLEAFLILCSEHEEGIACFDEHLGSLSYRELRNAIIAVAIKVSKFSEDRVGV
MMPASIGAFIAYFGILLAGKTPVMMNWSQGLRELRACTKTVEVRRVLTSSQQFIKHLTEVQGFVEYFPDLMY
MEDVRKRLSWWEKCRIGLYSKCSVPWLLRIFGVSGVESDDTAVILFTSGTEKLPKAVPLTHKNLMENQEACL
KFFDPNTQDVMLAFLPPFHAYGFNSCGLFPLLMGVHVVFASNPLNPKKLVEFIDDKKVTFFGSTPVFFDYILK
TAKKQNSCLESRLRVVIGGDALKDTLYEETKKLQPQIALYQGYGATECSPVISITTKESPRKSECVGMPIEGM
DVLIISKETHIPVSSGEQGLIVVRGNSVFSGYLGNEHQSFVSLGGDQWYLTGDLGHIGPSGDLFLEGRLSRFV
KIGGEMVSLEALESILHEHFTENQNEAGSLVVCGIPGDKVRLCLFTTLATTIHEVNDILKSAETSSIVKISYVH
QVESIPILGIGKPDYVSLNALAVSLFG

>core/169/1/Org1_Gene166

MPFKCIFLTGGVVSSLGKGLTAASLALILERQRLNVAMKLDPYLNVDPGTMNPFEGEIIYVTDDGVETDLD
LGHYHRFSSAALSRHSSATSGQIYARVIKREREGDYLGSTVQVIPHITNEIIQVILDAAKEHSPDVLIVEIGGTIG
DIESLPFLEAIRQFRYDHSEDCLNIHMTYVPYLQAADEVKSKPTQHSVQTLRGIGIIPDAILCRSEKPLTQEVKS
KISLFCNVPNRAVFNVIDVKHTIYEMPLMLAQEKIANFIGEKLKLATVPENLDDWKVLVNQLSQDLPKVKIG
VVGKYVQHRDAYKSIFEALTHAALRLGHAAEIIPIIDAEDENLTMELSQCDACLVPGGFGVRGWEGKIAAAKF
CREQGIPYFGICLGMQVLVVEYARNVLNLDQANSLEMDPNTPHPIVYVMEGQDPLVATGGTMRLGAYPCLL
KPGSKAHKAYNESSLIQERHRHRYEVNPDYIQSLEDHGLRIVGTCPQGLCEIIEVSDHPWMIGVQFHPEFVSK
LISPHPLFIAFIEAALVYSKDASHV

>core/171/1/Org1_Gene131

MRKISVGICITILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNLSG
NIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLS
IDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPH
YYNQSQVETKTITIHFIPDANTA AKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLT FNIN
KFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSHYPEHQKQEMAQRQAYAKKLFKEALEELQ
ITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMA
FLTIFAYPSGVPPYAINHKDFLEILQNIEQEQDHQKRSELVSQASLYLETFHIIPIYHDAFQFAMNKKLSNLGV
SPTGVVDFRYAKEN

>core/172/1/Org1_Gene568

MLGKEEEFTCKQKQCLSHFVTNLTSDFV FALKNLPEVVKGALFSKYSRSVLGLRALLLKEFLSNEEDGDVCDE
AYDFETDVQKAADFYQRVLDNFGDDSVGELGGAHLAMENVSILA AKVLEDARIGGSPLEKSTRYVYFDQKV
RGEYLYYRDPILMTSAFKDMFLGTCDFLFD TYSALIPQVRAYFEKLYPKDSKTPASAYATSLRAKVLD CIRGL
LPAATLTNLGFFGNRFRWQNLIHKLQGHNL AELRRLGDESLTELMKVIPSFVSRAEPHHHHHQAMMQYRRA
LKEQLKGLAEQATFSEEMSSSPSVQLVYGDPDGIYKVAAGFLFPYSNRSLTDLIDYCKKMPHEDLVQILESSV
SARENRRHKSPRGLECVFEGFDILADFGAYRDLQRHRTL TQERQLLSTHHGYNFPVELLDTPMEKSYREAME
RANETYNEIVQEFPEEAQYMVPMAYNIRWFFHV NARALQWICELRSQPQGHQNYRTIATGLVREVVKFNPM
YELFFKFVDYSDIDLGRNLNQEMRKEPTT

>core/173/1/Org1_Gene849

MFVGGGLVSFLLPIPDLECANNVTKTYDKKASVISRDLKLQEDCQKFWNLDPYKLESLCAYQVLYHDDYSSK
RIRELFPQIQKDEVPIFATMILTLGKVDRGFSPEEISLIQKLSYPGLSLASLRGSTEIDPNTDLARALVVSEFSGD
LGKNRADYYSNCLDILALRIHAERQRYLDQSPCVPGTSEFHKATIEAINTILFYEEAVRYPSKKEMFSDEFSFL
SSVTDRKFGVCLGVSSLYFSLSQRLDLPLEAVTPPGHIYLRYPQGGEVNIETTAGGRHLPTASYCDCLDLEDLQ
VRTPEEMIGLTFMNQGSFALQKKKYKEAEEAYKKAQEYLGDEELQELLGFVQILGGKKKEGKSLIGKSPRAS
QKGSVAYDYLKGRINIPTLALLFSYPGSNYEEIASYEEELKKAMKSSMPCCEGQRRLASVAFHLGKTAEAVA
LLEKCVEDIPNDLSHLRLCKILCDRHEYTKALKYFIIAERLMEDQGFLKKNRSFALFYEVKKIISKVAPQKA
NTLLLMESER

>core/174/1/Org1_Gene8

MSIVLDKIGKSLGTRILFDDVSVVFNPGNCYGLTGPNAGAGKSTLLKIIMGMIETRGSSISLPKKVGILRQNIDSF
HDTTVLDCVIMGNTRLWEALQRRDNLYLQEFTDAIGMELGEIEEIIIGEENGYRADSEAEELLTGIGIPNEMFD
KKMAMIPIDLQFRVLLCQALFGHPEALLLDEPTNHLDLYSINWLGNFLKDYEGLTVIVVSHDRHFLNTITTHIA
DIDYDTIIYPGNYDDMVEMKTASREQEKADIKSKEKKISQLKEFVAKFGAGSRASQVQSRLREIKKLQPQEL
KKSNIQRPYIRFPLSDKSSGKVVLSEAITKDYGDHQQVIHPFSLEIYQGDKLGIIGNGLGKTTLMKLLAGVEA
PSSGSIKLGHQAICSYFPQNHSDVLADCGQETLFEWLRNRKTGINDQEIRSVLGKMLFGGDDAFKQIQALSGG
ETARLLMAGMMLNHNVLILDEANNHLDLESVSALSWAINDYKGTAIFVSHDRGLIQDCATKLLIFDKDKIT
FFDGTMDVDTAGHKQLL

>core/175/1/Org1_Gene845

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AQKSLETGLIQAKDDLTLVITLEQPFYFLTLIARPVFSPVHHTLRESYKKGTPPSTYISNGPFVLKKHEHQNYL
ILEKNPHYDHESVKLDRTVLKIIPDASTATKLFKSKSIDWIGSPWSAPISNEDQKVLSQEKILTYSVSSTLLIY
NLQKPLIQNKALRKAIAHAIDRKSILRLVPSGQEAUTLVPPNLSQLNLQKEISTEERQTKARAYFQEAETLSE
KELAELSILYPIDSSNSSIIAQEIQRQLKDTLGLKIKIQGMEYHCFLKKRRQGDFFIATGGWIAEYVSPVAFLSIL
GNPRDLTQWRNSDYEKTLEKLYLPHAYKENLKAEMIIEETPIIPLYHGKYIYAIHPKIQNTFGSLLGHTDLK
NIDILS

>core/176/1/Org1_Gene861

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GLGILVTRLILSTIRKVDAMGYDAAVKEEQYLSRIRELESENREIRDRNRAVEDQCAHLSEENKDRLDPEYLH
GMTERLIASLEIENQALVAENILLKDOWNASLSRDFRAYKQKFPLGALEPWKEDIACIMEQNLFLKPECIAMVK
SLPLETQRLFLYPKGFQSLVNRFAPRSRFFQTPKYEYNSRNENEDGKVAAVCARLKKEFFSAVLGACSYEELG
GICERAVALKETLPLPEAVYDTLVQEFPNLLTAESLWKEWCFYSYPYLRPYLSVDYCKRFLVQLFEELCLKLF
TTGSPEDQALVRLFSYYRNHIAVLASFLPPPETGGSVFVLLPKQENLLWSQIEVLATRYLKDTFVRNSEWT
GSFEMMFSYNEMCKEISEGRIRFAEDYETRHSEEFPPSPLSEEGEREGEEFLPPCSEEEVSVLERPDLDVDSMWV
WHPPVVKGPL

>core/177/1/Org1_Gene714

MTARA EYLDHEDFLYRSHKLQELSELGVVLYPYEFPGVFSCEDIKKTFASQELGNSEAAMSRSTPRVRFAGR
LVLFRAMGKNAFGQILDHNQTIQVMFNREFTSVHGLSEDAEITPIKFIEKKLDLGDILGIDGYLFFTHSGELTV
LVETVTL LCKSLSLPDKHAGLS DKEVRYRKRWLDLISSREVSDTFVKRSYIHKLRNYMDAHGFLEVETPILQ
NIYGGAEAKPFTTTMEALHSEMFLRISLEIALKKILVGGAPRIYELGKVFRNEGIDRTHNPEFTMIEAYAAAYMD
YKEVMVFVENLVEHLVRAVNHDNTSLVYSYWKHGPQEVDFAKWPWRMTMKESIATYAGIDVDVHSDQKLK
EILKKKTTFPETAFATASRGMLIAALFDELVSDNLIAPHHITDHPVETTP LCKTLRSGDTAFVERFESFCLGKEL
CNAYSELNDPIRQRELLEQQHTKKELLPDSECHPIDEEFLEALCQGMPPAGGFGIGVDRLVMILTNAASIRDVL
YFPVMRRFDAEKTN

>core/178/1/Org1_Gene132

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LAESYTI SEDGTRYTFKIKNILWSNGDPLTAQDFVSSWKEILKEDASSVYLYAFLPIKNARAIFDDTESPENLG
VRALDKRHLEIQLETPCAHFLHFLTLP IFFPVHETLRNYSTSFEEMPITCGAFRPVSLEKGLRLHLEKNPMYHN
KSRVKLHKIIVQFISNANTAAILFKHKKLDWQGPPWGEPIPEISASLHQDDQLFSLPGASTTWLLFNIQKKPW
NNAKLRKALS LAIDKDM LTKVVYQGLAEPTDHILHPRLYPGTYPERKRQNERILEAQQLFEEALDELQMTRE
DLEKETLTFSTFSFSYGRICQMLREQWKKVLKFTIPIVGQEFTTIQKNFLEGNYS LTVNQWTA AFIDPMSYLM I
FANPGGISPYHLQDSHFQTL LKITQEHHKHLRNQLIIEALDYLEHCHILEPLCHPNLR IALNKNIKNFNLFVRR
TSDFRFIEKL

>core/179/1/Org1_Gene238

MNV LKYTKHSPSAHAWK LIGTSPKHGIYLP LFSIHTKNSCGIGEF LDIPLISWCQKQGFSVIQ LLLPLNDTGEDT
SPYNSISSVALNPLFLSLSSLPNIDTIPEVAKKLQDMHELCSTPSVS YTVKEKKWAFLREYYQKCKSSLEGN
SNFSEFLESERYWLYPYGTFRAIKHHMHGEPINNWP KSLTDQENFPDLTKKFHDEVLF FSYLQFLCYQQ LCEV
KAYADQH HVLLKGDL PILISKDSCDVWYFRDYFSSSR SVGAPPDLYNSEGQNWHLPIYNFSQLAKDDYIWW
KERLRYAQN FYSVYRLDHIIGFFRLWIWDSSGRGRFIPDNPKDYIKQGTEILSTMLGASSMLPIGEDLGIIPQDV
KTTLTHLGICGTRIPRWERNWESDSAFIPLKDYNPLSVTTLSTHDSDTFAQWWLNSPKEAKQFAKFLHLPFQK
TLTTETQIDILKLSHESASIFHINLFNDYLALCPDLVSKNLQRERINTPGTISKKNWSYRVRPSLEELAIHKKFN
GYIEKILTGL

>core/180/1/Org1_Gene980

MERKRFIDCDSTKILQELALNPLDLTAPGVLSAERIKKFSLLGGGFTFSFATERLDDAILAALISLAEERGLHES
MLAMQQGQVVNYIEGFPSEMRPALHTATRAWVTDSSFTGEAEDIAVRSRVEAQRLKDFLTKVRSQFTTIVQI
GIGGSELGPKALYRALRAYCPTDKHVHFISNIDPDNGAEVLDTIDCAKALVVVVS KSGTTIETAVNEAFFADY
FAKKGLSFKDHFIAVTCEGSPMDDTGKYLEVFHLWESIGGRFSSTSMVGGVVLGFAYGF EVFLQLLQGASA
MDQIALQPNARENLPMLSALISIWNRNFLGYPT EAVIPYSSGLEFFPAHLQCCMESNGKSIAQDGRRVGFST
SPVIWGEPTNGQHSFFQCLHQGTDIIPVEFIGFEKSQKGEDISFQGT TSSQKLFANMIAQAIALACGSENTNPN
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EAASLLTLFNIKFR

>core/181/1/Org1_Gene252

MTKTEEKPF GKLR SFLWPIH THELKKV LPMFLMFFCITFN YTVLRDTKDTLIVGAPGSGAEAI PFIFKFWLVVPC
AII FMLIYAKLSNLSKQALFYAVGTPFLIFFALFPTVIYPLRDV LHPTEFADRLQAILPPG LLGLVAILRNWTF A
AFYVLAELWGSVMLSLMFWG FANEITKIHEAKRFYALFGIGANISLLASGRAI VWASKLRASVSEG VDPWGI
SLRLLMAMTIVSGLVLMASYWWINK NVLTDPRFYNPEEMQKGKKGAKPKMNMKDSFLYLARSPYILL LAL
LVIAYGICINLIEVTWKSQ LKLQYPNMNDYSEFMGNFSFWTGVVSVLIMLFVGGNVIRKFGWLTGALVTPVM
VLLTGIVFFALVIFRNQASGLVAMFGTTPLMLAVVVGAIQNLSKSTKYALFDSTKEMAYIPLDQE QKVKGK
AAIDVVAARFGKSGGALIQG LLVICGSIGAMTPYLA VILLFI IAIWLVSATKLNKLF LAQSALKEQEVAQEDS
APASS

>core/182/1/Org1_Gene592

MVWVFKSQFEGLSALKRGVHALTKAVTPAFGPRGYNVVIKKGKAPIVLTKN GIRIAKEIILQDAFESLGVKLA
KEALLKVVEQTGDGSTTALVVIDALFTQGLKGIAAGLDPQEIKAGILLSVEMVYQQ LQRQAIELQSPKDV LH
VAMVAANHDTVLTGTVVATVISQADLKGVFSSKDSGISKTRGLGKRVKSGYLSPYFVTRPETMDV VWEELV
LILSHSLVSLSEELIRYLELISEQNTHPLVIIAEDFDQNVLR TLILNKLNRNGLPVC AVKAPGSREL RQVVLEDLAI
LTGATLIGQESENCEIPVSLDVLGRVKQVMITKETFTFLEGGGDAEIIQARKQELCLAIARSTSESECQELEERL
AIFIGSIPQVQITADTDTEQRERQFQLESALRATKAAMKGGIVPGGGVAF LRAAHAIEVPANLSSGMTFGFETL
LQAVRTPLKVLAQNCGRSSEEV IHTILSHENPRFGYNGMTDTFEDLVDAGICDPLIVTTSSLKCAVSVSCLLLT
SSFFISSRTKT

>core/183/1/Org1_Gene5

MYQENLRLLERLLYNSVQKSYADRLFSYEKTKMVHDTPLIPWEEDKEKCAEAEKAFLEQQKILLDYGKSIFW
LNENDEINLNDPWSWGLNTVRTRKVFQEVD DSERWNHKVLIQKLEDDYEKLLEESSKESTEANKKLLSDLV
DRLEDAKTKFFLKQEEVETRVKDLRARYGGTVDPKQDTEAKKKVELEASLETFLDSIESELVQCLEDQDIY
WKEQDVKDLARTQELEEQDIEAKREEAAEDLRSLNERLKKSKTMLDRAKWHIENAEDSITWWTSQIEMKD
MKARLKILKEDITSVLPEIDEIETCLSLEELPLLTRELLTKSYLKFKICSETLLKMTSVFENNIYVQEYEVQLQ
NLGFKLQGISQRF GKQDDFANLEEQVALQKKRLRELTQNFEIQGFNFMKEDFKAAAKDLYIRSTAEQKMN
FDVPCMELFRRYHEEVNKPLLELMYNCADSYRDAKKKCLSLRLDEKELLQKEIKKEEFYQKKQQRHADRSR
HTTYQKLRIAEELALELKKKI

>core/184/1/Org1_Gene996

MVARGLCDFPTLVPNERLPIGPFFVPQHTSGAKGKEFAKRNF SIISGLDDILKLCILQRRPFALQWDNLSVKSD
YEEAGPAIGIRSLEPQVSQISPAHGRLCSTLVQWAPILGSEEQLVWLEETMKRLKFPKSLGSKDAVIVDSEMP
VNANPTQEIPAASETVESSPVAPGNTTDTMPAASGTTDTTSGVSEAAAAEATVDSTPGTEEEPSFSRLYALVV
QNVYPPEPPKEPEVMFTDEEKSLILEATRARMELDLYNGYLADYELSKDEIQKHVPDLPENWRTNWRWSE
RLYKFFFKTKKEGLEEIFLNKELGNMILARGLAATQSQARIKVFNSLVAWLLQSFNVGRSCTAKPLPTSKLDL
FKSEFESKPKNNILTEFLVASDEEILFKGLRVLEPGIEGWYDHPDQAGEIRSVLEGLVQAGRISGYWENQPFGR
FVLRGVGERRTELVELLES LVASGEIMQFFESSDEEGAFIIDNEPSKTAMLKQRFKSCVRTKLVG SFADESLPR
GRFTILV

>core/185/1/Org1_Gene826

MVSL LHKFLENASGKKGQSLASTAYLAALDHLLNAFPSIGERIIDE LKSQRSH LKMIASENYSSLSVQLAMGN
LLTDKYCEGSPFKRFYSCCENVDAIEWECVETAKELFAADCACVQPHSGADANLLAVMAILTHKVQGPAVS
KLGYKTVNELTEEEYTLLKAEMSSCVCLGPSLNSGGHLTHGNVRLNVMSKLMRCFPYDVNPDTECFDYAEI
SRLAKEYKPKVLIAGYSSYSRRLNFAVLKQIAEDCGSVLWVDMAHFAGLVAGGVFVDEENPIPYADIVTTTT
HKTLRGRGGLVLATREYESTLNKACPLMMGGPLPHVIAAKTVALKEALSVDFFKKYAHQVVNNARRLAER
FLSHGLRLLTGGTDNHMMVIDLGSLGISGKIAEDILSSVGIAVNRNSLPSDAIGKWDTS GIRLGT PALTTLG MG
IDEMEEVADIIVKVLNRIRLSCHVEGSSKKNKGELPEAIAQEARDRVRLNLLRFPLYPEIDLEALV

>core/186/1/Org1_Gene686

MSEQEKL SNYNADKKLFSGIDKLFQIVKGSYGPKQSLSPTSFFKERG FYAISQTELSNSYENLGVDFAKAMVN
KIHKEHSDGATTGLILLHAILQESYAALEKGISTHKL IASLKLQGEKLQEALQQQSWPIKDALKVRNIIFSSLH
MPTIADHFYNAFSVVGPEGLISITKERENDKTSMDVFGFKIPAGYASTYFVSDTASRLTRIAHPLILITDRKIS
MIHSLLPLLQEISEQNQHIIFCEDIDPDVLATLVVNKLQGLLQVTVV TIPQLSTTNQELAEDIALFTGTHICPCQ
EASHVLAPEMVTLGSCLSIEISESQTTLIGGLHIPEVLTLKTRQLAEEIRTTSCLETKKRLIKSTNRLQSSVAILPT
DEDNEPLYTLALKIMESALSRGYVPGGGVALFYASLT LGTPKDDADENSIAISLLQKACCAPLKLLATNADLD
GDAVIAKLSSLGTTSLGISVFSREIEDLIAGGILDSLATTSTILAQALDTAILVLSSKILILENQYEISTL

>core/187/1/Org1_Gene736

MENEILLNIESKEIRY AHLKNGQLFDLTIERKKVRQLKGNIYRGRVTNILRN IQSAFINIDERENGFIHISDILENS
KKFEQMFDMDVDALPEEASEAPLLSSEEAPIEEFLKLDSPVLVQVVKEPIGSKGARLTSNISIPGRYL VLLPNSP
HRGVS RKIEDPHMREQ LKQLIRSFEMPQDMGLICRTASTTASTEALINEAHDLLLTWKTILEKFYSTEQPCLLY
SETDILKKA VITCIDKNYKRL LIDDYATYQKCKHMLKKYSPDASIKIEYYRDSIPMFERFNIEKEIDKATRRKI
WLSSGGYLFFDKTEAMHTIDVNSGRSTQLESGVEETLVQINLEAAEEIARQLRLRNVGGLVIIDFIDMKSRKN
QRRVLERLKEHMKYDAARCTILSMSEFGLVEMTRQRNRESLMQTLFTLCPYCSGNAIIKTPESVVIEIERDLK
KVINHKEHSHLCLV VHPEIASYMKQENDDNEMINLAKQLKAKLQINTSDSVHLNHYQFFSLITGESIDL

>core/188/1/Org1_Gene203

MFNLFFFTANKETTASHELIYRKNQSFSLSPVTILCLLAISVLLLLGVVFALVGCHVLAAPLGLLVWGCAASV
CSMMAIVSLMCLYKGGKPLIEPSNEEKIDPTKDLEIKDPESLKPVPVEGQSLPKERKTVSFKAKIPSIVEDDFKP
YVIQSTFYHQNKVYSKPIAERMQSLEKEITTLIVDFPRALEESSKSSGSLLRGVISEIKNLFLPRFLSRKVKYSLT
ACLRRLGSIVEEYASSDLLILLTKPEPLNMVTQQLIAHLNSLKTEKRKLTPHMQKL VLSINFWFYGWSLEEK
CIEKIVAYDPNLLTDELKAHLEAGNIVQFLLSFQSSEM QREFRALFPSDAQELPSAKDGSNYVPAINSEYMY
DFKDLSVLKKSLSERLAFCEKIPSPSSWNFTSSVASHYKDFSLLFTFFSNQQSVILQNPFLLI ELLHENPKCQTF L
KGLLEKAMPMSNWAALFRPMLMGMLCSGIARKKELKIIAEHLGVPFKEITQAIASGKILDLLQHLFDF

>core/189/1/Org1_Gene331

MTILRNFLTCSALFLALPAAAQVVYLHESDGYNGAINNKSLEPKITCYPEGTSYIFLDDVRISNVKHDQEDAG
VFINRSGNLFFMGNRCNFTFHNLMTEGFGA AISNRVGDTTLT LSNFSYLAFTSAPLLPQQGGA IYSLG SVM IEN
SEEVTF CGNYSSWSGAAIYTPYLLGSKASRPSVNLSGNRYLVFRDNVSQGYGGAISTHNLTLTTRGPSCFENN
HAYHDVNSNGGAIAIAPGGISISVKS GDLIFKGNTASQDGNTIHN SIHLQSGAQFKNLR AVSES G VYFYDPIS
HSESHKITDLVINAPEGKETYE GTISFSGLCDDHEVCAENLTSTILQDVTLAGGTLSLSDGVTLQLHSFKQEA

SSTLTMSPGTTLLCSGDARVQNLHILIEDTDNFVPVRIRAEDKDALVSLEKLKVAFEAYWSVYDFPQFKEAFT
IPLLELLGPSFDSLLLGETTLERTQVTTENDAVRGFWSLSWEEYPPSLDKDRRITPTKKTVFLTWNPEITSTP

>core/190/1/Org1_Gene168

MTNVVQETIGGLNSPRTCPCPCILVIFGATGDLTARKLLPALYHLTKEGRLSDQFVCVGFARREKSNELFRQEM
KQAVIQFSPSELDIKVWEDFQQRLFYHRSEFDNNMGYTSLKDSLEDLDKTYGTRGNRLFYLSTPPQYFSRIEN
LNKHKLFYKNQDQGKPWSRVIIKPFGRDLDSAKQLQQCINENLNENSVYHIDHYLGKETVQNILTTFRANTI
FESCWNSQYIDHVQISLSETIGIGSRGNFFEKSGMLRDMVQNHMMQLLCLLTMEPPTTFDADEIRKEKIKILQR
ISPFSEGSSIVRGQYGPQTVQGVSVLGYREEENVDKDSRVETYVALKTVINNPRWLGVPFYLRAGKRLAKKS
TDISIIFKKSPYNLFAAECSRCPENDLLIIRIQPDEGVALKFNCKVPGTNNIVRPVKMDFRYDSYFQTTTPEAY
ERLLCDCIIGDRTLFTGGDEVMAWKLFTPVLEEWDQDSSPSFPNYPAGSSGPKEADALIERDGRSWRPL

>core/191/1/Org1_Gene782

MSSWLSQASEVLLNQDPYIPDAPRSQESSVPKISYSITVAPQEAQKSLPKFFTQKFQSQCKSEPPITHHKTFIIAT
PRERILRFGSSSFESQLHNTSQAQTSSPWNLFQKNSTEASKALMQELTMPKSPEKTSEKALDKNLSSKQEGSC
KNFDTLHLQQLKLFQTVDSLVSQSLDSEQQELLQSRREERSETYANQQSSEKKIETKVQIKDLCKDLFSQDQ
DSNQKQKKSPFQQDTSRKNRIAKAAQAVPVIPPSIGVFTLSYLLTKQGILSDFSSYGCHKDSVESTQRELDAL
HEKRIETIKVSIEKEKRERLWGSLSDIIGWLAPFVSIIGIVAILSGGGIFAFAGFFAGLISLVIKCLEKLKFWDW
LEKHLPIKNEELRRKIITIIQWVVYLTPVILSICTLKVENLGFSPHIEGAIKGIQPAIESTMAALRCAILFSQAEIYK
LKGKLTQIQLDIELKSFDRDDHYERSQELLDNMESSFEALSRIILNYMRELDQVYLHSLRG

>core/192/1/Org1_Gene938

MAVGGVGGSRSPPIPPNRRNSEDGKVSPKDNLGEHTVSSSDSSLASQGPTIEERKAQLGGTDKIPLPSVKEPG
DSQTSGRSGVLQRIWKGVKGVFKKTPQARPEVSSPRLPSHVQHGQRLPGLEGFRDRIQKRSENPEADLGKMK
RSYSDGDLDRVGHDSNEDSTEDSRSEGGEPPSSKSSSFLSGVRGATSTVQGALGDAKEKVSFAFGEQAAGAIRS
APGNIRTRFQRSSEGDLSNVNKAACHLRKALENLEKVAPEQVSPEVASRVQSLLARMEQLTHQEPPTVEDLI
TFVESNVGSDSVEYASIVPQDGSQAPAETAETGGVEGSAAQGAWKALRDFVVSIFQAVASFFRAIASRLS
SARRESAVDDLASESNTQWFVEQEGVSNPSAAPSLSFAEEIARRAAEMSNRNAQSLEKLESIGNVTDPIVQQG
LGLARSFAPEGQ

>core/193/1/Org1_Gene97

MADILVIGANPTGLILANMLIQHGISVKVIDHRASPEDPSFLDCRKLPVILSCSSLELLHNSEMLGDFIQANHKI
FGARYHWKKRTLLFKFSQATDSPVPFSLSTTYQSLEQHLIDEFLKRGGVIDWSTRPVTLVDNSIFIESTKVSQN
FENREIYNPKWIIACEADNNLDIRDLVKSQLRARRINREVIFINCDEGEPPFEEDHIIHLLPITKNFLNFVFYNPQEK
TKQLCLPQGTHSISPCLKQKLLYTYNLVISDENFHIKTSHHAFPEHGNVFLGSLSNLTLSSYLNGINTNIAHA
FNLAWKLLPVLKKAALKHLVITKEQEDGNILPYISPTTEKRAKKLPFSRFYTPALMYFLKGCRKFNTTGEEY
YYPHQALKYRSSDIKMSPDKEIHGPGPGMRAIDARLENGSFLLDPLKSSKHLLIFFKDIPLDKEALQEEYG
EWIEICNVKEPRILNLYHANPNSLFIIRPDRIYIGYRTHTFKLHELISYLLRIFASEKTS

>core/194/1/Org1_Gene406

MNWENVVRVAPSTGDPHVGTAYMALFNEIFAKRFKGKMILRIEDTDRTRSRQDYEENIFSALRWCGIQW
DEGPDVGGPYGPYRQSERTKIYQGYVETLLKTDCAYKCFATPQELAEMRAVASTLGYRGGYDRRYRYSPE
EVASREAAGQPYTIRLKVPLSGECVFEDYSKGRVVFPWADVDDQVLVKSDFPTYHFANVIDDHLMGITHV
LRGEEWLSSTPKHLLLYEAFGWEPVFLHMPLLLNPDGTKLSKRKNPTSIFYRDSGYVKEAFVNFLTLMGY
SMEGDEEVYSLERIIETFNPRRIGKSGAVFDIQKLDWMNKHLYLNHEGSPECLLKELQGWLLNDEFFLKILPLC
QSRITTLAEFINLTSFFFSGLLEYRVEELLQALSPEKAAILLYSYVKYLEKTDQWTKETCYLGSKWLAQAFN
VHHKKAIIPLLYVAITGKKQGLPLFDSIEILGKPRARARLVYAEKLLGGVPPKLAATVDKFMQREDFEEATFD
L

>core/195/1/Org1_Gene956

MDCRGGIPLPEPQVIGGYHVKKILSKKLRSRVVHGLHPETRHSTVIKVFSPSPSFTSRSVYNFLKEAQLHQIT
HPNIVKFHRYGKWQDCLYIAMEYIEGISLREYILAQFISLPQAIDIIFDIAQALEHLHSRNILHKDIKPENILITPQ
GKIKLIDFGLADWDTEIQRHPSVIGTPYYMSPEQRQGESHPASDIYALGLLAYELILGHLSLGRVFLSLVPE
RISKILAKALQSPNNRYSSTREFIQDIHHYRMSGDMQEDLRIKDHTVALYEQLQTQRFWLAPETLRFDPDFISG
VLYHQGYPLYPHAYDTLLEGDVFNWLWGYSPISNATIALSVVKSLSVCQQLQRPLLDRCVCEINECLIRMKIPI
DEMGISILCLEISKENKELSWVACGKTVFWIKRQGRVVQDFESFSPGLGKITSLQIRETKVAWEIGDEAVVCTL
ELEESVASLKTLSLAELQDRRQKAIFCPIESIHGGIQRQHGSNSPSTLISLKRIR

>core/196/1/Org1_Gene314

MLKKFINSWLKLCQQDKYQRFTPIVDAIDTFCYEPIETPSKPPFIRDSVDVKRWMMMLVVIALFPATFVAIWN
GLQSIVYSSGNPVLMEQFLHISGFGSYLSFVYKEIHIVPILWGLKIFIPLLTISYVVGGTCEVLFAVVRGHKIAE
GLLVTGILYPLTLPTIPYWMAALGIAFGIVVSKELFGGTGMNILNPALSGRAFLFFTFPAKMSGDVWVGSNP
GVIKDSLMMKNSSTGKVLIDGFSQSTCLQTLNSTPPSVKRLHVDAIAANMLHIPHVPTQDVIHSQFSLWTETH
PGWVLDNLTLTQLQTFVTAPVAEGGLGLLPTQFDSAYAITDVIYGIGKFSAGNLFWGNIGSLGETSTFACLLG
AIFLIVTGIASWRTMAAFGIGAFLTGWLFKFISVLIVGQNGAWAPARFFIPAYRQLFLGGLAFGLVFMATDPVS
SPTMKLGKWIYGFFIGFMTIVIRLINPAYPEGVMLAILLGNVFAPLIDYFAVRKYRKRGV

>core/197/1/Org1_Gene917

MKFEFSVALKYLIPIGRGRLYSAIVSLFSVGIISLVVWLSIVFISVIHGLEQRWIEDLSQLHSPITILPSDTYYSSYY
YQIDKHSSLSNYTTKTLGEKIASPQVDPYPDPESDYLLPETFPLKDCDLGGQQKDPVKMTLES LGPYLQSQHGK
VIEFEQGVGYLDIKTSLKLQKPQPRNLTHFLTYP SKLSYEDKVL PYDETDTY TSAELNPFNRSPSGWQQDFHHL
EELYRGASIILPSTYKDSGYKVGDTGVFSTYSIENEKETQYTVHVIGFYNPGLSPLGGRTVFIDPDLARSIRSQS
EGLGMSNGFHLFFPDTKRIVFVKKQIENILTSLGVDDYWEISSLHDYDYFQPILDQLQSDQVFLFVCILILIVA
CSNIVTMSMLLVNNKKKEIGILKAMGTSSRSLKIIFACCGAFSGACGVVIGTIFAII TLKNLQFIVKALNYLQGR
ETFNTAFFGQNLPSNVHPQAIYFLGLGTLLLAAVSGALPARKVAKMHVSEILKAD

>core/198/1/Org1_Gene279

MVLFHAQASGRNRVKADAIVLPFWHFKDAKNAASFEEFEP SYLPALENFQGKTGEIELLYSSPKAKEKRIV
LLGLGKNEELTSDVVFQTYATLTRVLRKAKCSTVNILPTISELRLSAEEFLVGLSSGILSLNYDYPRYNKVDR
NLETPLSKVTVIGIVPKMADAIFRKEAAIFEGVYLTRDLVNRNADEITPKKLAEVALNLGKEFPSIDTKVLGKD
AIAKEKMGLLLAVSKGSCVDPHFIVVRYQGRPKSKDHTVLIGKGVTFDSGGLDLKPGKSMLTMKEDMAGG

ATVLGILSALAVLELPINVTGIIPATENAIDGASYKMGDVYVGMSSGLSVEICSTDAEGRLLILADAITYALKYCK
PTRIIDFATLTGAMVVSLGEEVAGFFSNNDVLAEDLLEASAETSEPLWRLPLVKKYDKTLHSDIADMKNLGS
NRAGAITAALFLQRFLEESSVAWAHLDIAGTAYHEKEEDRYPKYASGFGVRSILYYLENSLSK

>core/199/1/Org1_Gene781

MTVSYQSISTPPPEGEFDIFVDGNATEEAVVAAEVQVALPAGEQYAMLRATSELFCGILTQSECALTQALPPK
EKPLQEEQFLVKNGILMRSTSLPNLKPQSQQTSLASHRNPLAQQTSSNSTGKASTETTSSSPFFSCKAPEG
DSSVDKTFTVSVQTPKAQEQQEASASQSQAQFHVRSYSSSTIKEHSAKEKVSQSTKSAETQKHTQTKSDATLS
PMSLYSTLHKEVPQALSSTKSQQKDEEHRDQRQQEGYEQEQEQEKGKKTPWCTVESLQQTSSSNQVYESY
TPIIPDPIVEFALSESQLSVLAGKRVTNLDVLRICTELMKLMKSRANDTMTRLEERELMEREAEHLAASYSR
QAKYARWLGIATATLGILGAIAPMVGEISGDSILGFVQRISGRFKDATAKTFFKGIGKVFTSLSQLTEAASKVH
ELSESAVRAVAEYRKEVFRMRQDEVTRTIEEVKDNWKSMDNFLLNILQTEHDAARSLYQ

>core/200/1/Org1_Gene621

MAASILSQELLDILPYTFLKKHCLLPIEESSEAITIAHATATSVIAQDEVKLLIKKPVRFVLKEESEILQRLQQLY
SNREGNVSDMLLTMKKEEDGTTISEEEDLLETTDITPVVRLLNWILKEAIEERASDIHFEPCEDSMRIRYRIDGVL
HDRHSPPSHLRSALTTRLKVLAKMDIAEHRLPQDGRIKIHIGGQEVDMRVSTVPVIYGERVVLRILDKRVIL
DIAGLHMPKGTEILFKDTITAPEGILLVTGPTGSGKTTTLYSVLQELKGPLTNIMTIEDPPEYKLPGIAQIAVKP
KIGLTFARGLRHLLRQDPDILMVGEIRDQETAIEIAQAALTGHLVVSTLHTNDAISAIPRLLDMGIESYLLSATL
VGVVAQRLVRTICPYCKVAYTPENQEKSFLASLGKDTEMPLYRGQGCVHCFRSGYKGRQGIYEFLRPNTLFR
SEVASNRPHYHILRETAEQNGFLPILEHGIALAVSGETTLAEVLRVTKRCD

>core/201/1/Org1_Gene207

MNKKHASFSSRLGFIFSMIGIAVGAGNIWRFPRVAAQNGGGAFLILWLCFLFLWSIPLIIIELSIGKLTKKAPIGA
LIKTAGKKFAWAGGFITLVTTCILAYYSTIVGWGLSYFYAVSGKIHGNDFAKLWTSHYQSSIPLWAHLTSL
GLAYLVIRKGIVHGIEKCNKILIPAFFLCTIALLLRAVTLPGAVQGQKQLFSCDKSCFSNYKVWIEALTQNAWD
TGAGWGLLLVYAGFASKKTGVVSNGALTAICNNLVSLIMGIIIFSTCASLDILGTTQLQDGAGASSIGITFIYLP
ELFTRLPGGIYLTTLFSSIFFLAFSMAALSSMISMLFLLSQTLEFGIKPYISETLATIIAFVLGIPSALSLTFFSNQ
DTVWGVALIVNGLIFIYAALVYGFPKLKKEVINAAPGDLRLNKAFDYIIKYLLPIEGILLGWYFYEGFLPENG
QWWNPISLYSLGSLVLQWSLGLIILWKFNKQLYLRFSRYNHEIL

>core/203/1/Org1_Gene442

MLKYILKRLVLIPLTLFAIVSINFVILNAAPGDVLEEKSRDALGEAGKSDKMRSYKGPDRYLQFREHYGLTLPI
FFNTRPKITHKKIQTALQELANANNTTPSAKNAAKSLVYWGDCAKFVMPALLFEADDASRDDKYRHIAADL
FIRGGVLQGFVGPNLSPEQRAQNKEIAESNAFLVRQLNEEDLDTKVEALKGWFQDHGGTEVFCYSSKQFWK
TFFLETRFARYMSRVLRDLFGTLRNDAAKTVISEVIKRLRCSLVLSILPMIVGFVLCQIFGMIMALKRNRWIDH
SLNFIFLILFSIPVFVAVPWILDNFVINKTIPFTTIPMPYSGLRSPPEVFNELSTLGRIFDLVSHGFLPFCVSYGAL
AAQSRLSRSIFLEVLSQDFICAAKARGLRWFDILYKHVGKNAAVSIVTSLASSLGTLLGGALVVETLNFNIDGFG
NFFYQAILNRDHNVVLFVSVLVGSALSLVGYLLGDICYVLLDPRVQLEGRRI

>core/204/1/Org1_Gene881

MHTEFAPFLEDLVHQQVISPLDIAFASKHISSDFEESFVFLAVSSALWRYGHPFLSLEENRIRPSLGGISETDLY
RGFHNLPKEVRDKLFVVVSGRLYLRSLYTIRSKLLDKLSLLCSATPNYFPPSIDSSILSEEQNFIFNKITQGCFSI
VSGGPGTGKTFLAAQLILSLVKQQPKLRIAIVSPTGKATSHIRQILMKYNIFDDMVLMQTVHHFLQEYAYRRY
NSIDVLLVDEGSMVTFDLLYSLVQTLQGYEKDKKLYTSSLIILGDTNQLPPIGIGVGNPLQDLIGYFHENTFFL
KTSHRAKTGVVDQLTQSVLRGEMISFSPLPSISSAIEVLKNRFVKSLRQSEARLCVLTTPMRHGPWGVNLNTM
IHQRLARSDPDLRIPIMVTSRYETWGLFNGDTGLLCLKTQKLHFPQHEPIDSRALSQYVYNYVMSVHKSQGSE
YDEVIVIIPKGSEVFGVSILYTAITRAKYRVSVWGDPELHKIIKKNY

>core/205/1/Org1_Gene1009

MNLDKSHFDINSANFLEEFKAFISFPSISADSDHLQDCENCAHFLVDHVNKIFDVELWETPGHPPIIYASYKSE
DPLSPTLMMLYNHYDVQPAQLSDGWKGDPFILREENGNYARGASDNKGQCFYTLKALQHYYESQGNFPLNII
WLIEGEEESGSLALFTWLEKKKEALRADYLLIVDGGFLSEKHPYVSIGARGIVSMKISLEEGNKDMHSGVLGG
IAYNTNRALSEILSSLHHPDNSIAIEGFYDDLALPSDSRDPDLPKSDTLRECEENLGFRPQGYEASYSPEESALR
PTVEINGISGGYTGPFGKTVIPYRATAYLSCRLVPNQDPDKAAHQVIHHLKQQVPSSLKFSYEILPGGSRGWRS
SANLPIVKVLQEIYSDLYNEECLRLVMPATIPIGPLLGEAAQTSPICGTSYLSDDIHAAEEHFSMDQLKKGFLSI
CQLLDKLPKIKE

>core/206/1/Org1_Gene877

MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTMESDATIAGASGKDKTSSTTKT
ETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSIEEASKSMESTLESLSLSAAQMKEV
EAVVVAALSGKSSGSAKLETPELPGVTPRSEVIEIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLG
LEKQAIKIDKEREYQEMKAAEQKSKDLEGTMDTVNTVMIAVSVAITVISIVAAIFTCGAGLAGLAAGAAVG
AAAAGGAAGAAAATTVATQITVQAVVQAVKQAVITAVRQAITAAIKAAVKSGIKAFIKTLVKAIKAISKGI
SKVFAKGTQMIAKNFPKLSKVISSLTSKWVTVGVGVVVAAPALGKGIMQMQQLSEMQQNVAQFQKEVGKLQ
AAADMISMFTQFWQQASKIASKQTGESNEMTQKATKLGAQILKAYAAISGAIAAGAA

>core/207/1/Org1_Gene892

MYRYSALELAKAVTLGELTATGVTQHFFHRIEEAEGQVGAFISLCKEQALEQAELIDKKRSRGEPLGKLAGV
PVGIKDNIHVTGLKTTCASRVLENYQPPFDATVVERIKKEDGIILGKLMDEFAMGSTTLYSAFHPTHNPWDL
SRVPGGSSGGSAAAVSARFCPVALGSDTGGSIRQPAAFCGVVGFKPSYGAVSRYGLVAFASSLDQIGPLANT
VEDVALMMDVVFSGRDPKDATSREFFRDSFMSKLSTEVPKIVIGVPRTFLEGLRDDIRENFFSSLAIFEGEGTHLV
DVELDILSHAVSIYYILASAEAAATNLARFDGVRYGYRSPQAHTISQLYDLRSRGEFGKEVMRRILLGNYVLSA
ERQNVYYKKATAVRAKIVKAFRTAFEKCEILAVPVCSSPAFEIGEILDVPTLYLQDIYTVAMNLAYLPAIAVPS
GFSKEGLPLGLQIIGQQGQDQVCQVGYSFQEHAQIKQLFSKRYAKSVVLGGQS

>core/208/1/Org1_Gene1011

MNGCWEDLKQTIFWVGEHDCTDIETVRKSCMWLDRIYADKILREKEEKMERHELPHATMVRKASGHAYA
KAKAAFEKERSNENQRKVVDVEKWLSKGLAEFRNQESRRARERLRELQTLYPEVSVEERVLERQRTKKVNL
ENLYADIEKKYHHCVREQEYHWEVENKEAEYRENGEKVLSAEVSECLQRLEDCLTWSKKLTKAESVF
EMKFDATEKLGKVLSDVTNRLEILCEDAEEMIFRIEIEIEMTLRMVELPLLFMKNTFEKASLQYNSCKEMLA
KVEPQCKESPTYRSSQERLERLNQDLQTAYTNCQERLQGFSDLESKVRTCRDHLREQMKHFEVQGLNFINEE

LLWVGAEFLTQARLDLVATVPYMEFYLYYHNKREKVRSQWMAKTERYREIRQAFQGVMMKEDLLAEDTIL
KEEDYWLLRDDWLLRDERKNRQRRLLCNKIAAAQQRVKGF

>core/209/1/Org1_Gene79

MLGILLIASGIIFLAVAIPGLSSAVALGLGCGMTALGTVLLITGLVLLIRSEKLALQVEIKQARTRVNNELDQL
SQYVFYFYTENVLDNLKRWSYRDLGFVRQAQEEVTNLEQDIEEIFLTRDIRNALDNEEFFMTHAKQCLAQVGE
SLFQDASIDEFINLAHLSEIRQHLDINDPRWSMITKKVKGTVVRFIYVSTMYKQIKSNFEKSDFGQLRKMLLN
NYKTIEEVLYQSFQKGYNRAALLSEKTRIIHTSSLLHWEKDEDDKHLNKNECASRLNFKKFRTFLGLSEED
VIDFTGASGWDCSKLPRKEVPLDGGKKKLRFKRTFADEQVGDWDRTTSLEHMTPQEEDPLDRLMDQVEQE
ATSVLKDQDRYWKEIETSEAKFRSLPREDDFEKQSQIDSYIRDLDDHLSVWANQLSAAEDALIEVTDVQEHG
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>core/210/1/Org1_Gene817

MTFPCGNCNCYYRETPPPNPGGEDIPLQEGGQSGSQGGRVITQQPGTGGREMGISLGSDNVLMVEQAGSLL
NNLLDSARMQRLGHYCYRTGTPWCREHCPGFLQWIWGGCCACCLETVDDPDNPSAQFLQQLIQQYGPICVG
MSFQQLPHTCTQKIEQGEPLGDGDKQEVENGCKLHRELLKAAQPRCMGESLVKLLQNNGLGEDMQQTTPWS
LILQAVSEGALSFTSSDNPPTCWILQPEQQPCPPPPTDEEQLGAVGGAPAPQQKKHPAQECRVCTCKLNFR
LLQKLSRLEVLSLESGYKGPLGQAAKQIVDLIKKSLKRLVASDLATFLGPGIGLSLESQVFEVLVLLCLLSKGY
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>core/211/1/Org1_Gene740

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KIVEQSVGKAPLPNPFLNRLVAISPQESQEAARKIPDLCSQLKKVLKSLGVLTPEWKHMLKYFEGLKNEHDS
NPDKKTFPILIKLLIEALTGKSSLPKTPSTKEKMQAALFIASSCKTCKPTWGEVITRSLNRLYSIANEGDNQLLI
WVQEFKERELMSIQDGDAAEEYRFAAQQHGERYTEAIEQVLRNESAAKLQWHVINTMKFFHGKNLGLVTE
HLQDTLGAALTQRQTTVDTHQGREDADLSAALFLNKYLNLSGNQLVNSVFKSMQKADPETKALIREFALDILYA
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>core/212/1/Org1_Gene3

MSAVYADWESVIGLEVHVELNTASKLFSSALNRFGEPTNTNISTVCTGLPGSLPVLNQSAVEKAVLFGCAVE
GEISLLSRFDRKSYFYPDSPRNQITQFEHPIIRGGRIKAIVQGEERYFELAQTHIEDDAGMLKHFGFAGVDYN
RAGVPLIEIVSKPCMFCPEDAVAYATSLVSLLDYIGISDCNMEEGSIRFDVNVSVRPKGSPELRNKVEIKNMNS
FAFMAQALEAEKQRQIDEYLNQPNKDPKLVIPAAATYRWDPEKKKTVMRLKESAEDYKYFPEPDLPTLQLTE
SYIERIRKTLPELPYDKYHRYIQEYGLSEDIASILISDKNIATFFEYACKDCKNFRSLSNWVTVEFGGRCKTLGV
KLPSSGIFPEGVAQLVNAIDQGVITGKIAKEIADLMMESPGKNPEEILKEKPELLPMSDEGELQKIIAEVVLANP
ESIVDYKNGKTKALGFLVGQIMKRTAGKAPPKRVNELLLELDKG

>core/213/1/Org1_Gene1002

MITKQLRSWLAVLVGSGLLALPLSGQAVGKKESRVSELPQDVLLKEISGGFSKVATKATPAVVYIESFPKSQA
VTHPSPGRRGPYENPFDYFNDEFFNRFFGLPSQREKPKSKEAVRGTGFLVSPDGYIVTNNHVVEDTGKIHVTL
HDGQKYPATVIGLDPKTDLAVIKIKSQNLPLYLSFGNSDHLKVGDWAIAGNPFGLQATVTVGVISAKGRNQL
HIADFEDFIQTDAAINPGNSGGPLLNDGQVIGVNTAIVSGSGGYIGIGFAIPSLMANRIIDQLIRDGQVTRGFLG
VTLQPIDAELAACYKLEKVYGALVTDVVKGSPADKAGLKQEDVIIAYNGKEVDSL SMFRNAVSLMNPDTRI
VLKVVREGKVIEIPVTVSQAPKEDGMSALQRVGIRVQNLT PETAKKLGIAPETKGILIISVEPGSVAASSGIAPG
QLILAVNRQKVSSIEDLNRTLKDSNNENILLMVSQGDVIRFIALKPEE

>core/214/1/Org1_Gene18

MWNRCQVFSSFFFRYPISSWLIRLRASCECFQQRHPIFLCGLYWLAGITSRGHPECSALILIFLGMFLPRNPKQ
WLPLASAWIISLMLTPAPFLHDGPISGTFVIHHAGGQGTYTGEALCIQTPCGKRAHHLSCQILSESRLLEKKVY
ELEGTLHHTSQIVFKSNACYKEIPRSRFYIMKEKCRESSCHFLNHRFPSSEVGPFASSLLLGTPLPQNLRDLFRQ
KGLSHLFAISGWHFSLCATTWMLCALLPLKIKKILSFIVLTSACIFPMSLSVWRSWISVTLLCFSWCFSGSCS
GLNRLGAGFILCSIFFSPFSPTFVLSFLATLGILLFFPKIFSFLYTPWTQFLSPFWLYPIRYLAMTLAISLSAQLFIV
LPIMQYFGSLPLEGLLYNLIVPFTILPIIVFLIATIILPCCSPITEALIQGFLSHPWLHNPNIKTL SFAPVPPWMLTL
ASLILFFIGILRTNVSPYASISATSYRFIETL

>core/215/1/Org1_Gene644

MLKIAILGRPNVGKSSLFNRLCKRSLAIVNSQEGTTRDRLYGELHAFGVPAQVIDTGGVDHNSDYFQKHIYN
QALTGAKEADVLLLVIDIRCGITEEDAHLAKLLLPLKKPLILVANKADSRQEELQIHETYKLGIRDIVVTSTAH
DKHIDTLLQRIKLVANLPEPREEEEEGLEELSVDEHEESEAAALPSNTFPDFSEVFTEGFSPEEPTIPESPQQAPK
TLKIALIGRPNVGKSSIINGLLNEERCII DNTPGTTRDNIDILYSHKDRQYLFIDTAGLRKMKSVKNSIEWISSR
TEKAISRADICLLVIDATQKLSSYEKRILSLISKRKKPHIILINKWDLLEEVRMEHYCKDLRATDPYLGQAKML
CISATTKRNLKKIFSAIDELHHVVS NKVPTPIVNKTLASALHRNHPQVIQGRRLRIYYAIQKTTTPLQFLFINA
KSLLTKHYEYYLKNTLKSSFNLYGIPFDLEFKEKPKRHN

>core/216/1/Org1_Gene784

MNMPVPSAVPSANITLKEDSSTVSTASGILKTATGEVLVSCTALEGSSSTDALISLALGQIILATQQELLQSTN
VHQLLFLPPEVVELEIQVVDLLVQLEHAETITSEPQETQTQSRSEQTL PQQSSSKQSALSPRSLKPEISDSKQQQ
ALQTPKDSAVRKHSEAPSPETQARASLSQASSSSQ RSLPPQESAPERTLLEQQKASSFSPLSQFSAEKQKEALT
TSKSHELYKERDQDRQQREQHDRKHDQEEDAESKKKKKKRGLGVEAVAEEPGENLDIAALIFSDQMRPPAE
ETSKKETTFKKKLSPMSVFSRFIPSKNPLSVGSSIHGPIQTPKVENVFLRFMKLMARILGQAEAEANELYMRV
KQRTDDVDTLTVLISKINNEKKDIDWSENEEMKALLNRAKEIGVTIDKEKYTWTEEEKRLLKENVQMRKEN
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>core/217/1/Org1_Gene859

MTSRTKSSKNLGTIALAGMVVSSIIGGGIFSLPQNMAATAGAGAVILSWILTGFGMFFIANTFRILSTIRPDLKE
GIYMYSREGFGPYIGFTIGWGYWLCQIFGNVGYAVITMDALNYFFPPYFQGGNTLPAILGGSILIWVFNFIVLK
GIRQASIINVIGTIFKIIPLIIFIILTAFFFKLAVFKTDFWGHAVTKAQPSLGSVSSQLKGTMVLTLWAFIGIEGAV
VMSGRAKNPLSVGQATVLGFLGCLTIYILFSLLPFGSLFQHQ LANIPNPSTAGVLDILVGKWGEVLMNVGLIIA
VLSSWLSWTIIVAEIPFSAAKNGTFPEIFTIENKEKSPSVSLYITSSVMQLAMLLVYFSSNAWNTMLSITGVMV

LPAYLASAAFLFKLSKSKTYPKKGSIKAPLAMITGILGVVYSLWLIYAGGLKYLFMALVLLALGIPFYIDAGK
KKKNAKTFFAKKEIVGMTFIGLLALTAIFLFSTGRIKI

>core/218/1/Org1_Gene59

MITRTKIICTIGPATNSPEMLAKLLDAGMNVARLNFSHGSHETHGQAIGFLKELREQKRVPLAIMLDTKGPEIR
LGNIQPISVSQGQKLRLVSSDIDGSAEGGVSLYPKGIFPFVPEGADVLIDDGYIHAVVVSSEADSLELEFMNS
GLLKSHKSLSIRGVDVALPFMTEKDIALDFGVEQNMDVVAASFVRYGEDTMRKCLADLGNPKMPIIAKI
ENRLGVENFSKIAKLADGIMIARGDLGIELSVVEVPNLQKMMAKVSRETGHFCVTATQMLES MIRNVLPTRA
EVSDIANAIYDGSSAVMLSGETASGAHPVAAVKIMRSVILETEKNLSHDSFLKLDDSNSALQVSPYLSAIGLA
GIQIAERADAKALIVYTESGSSPMFLSKYRPFPIIAVTPSTSVYYRLALEWGVYPMLTQESDRAVWRHQACI
YGIEQGILSNYDRILVLSRGACMEETNNLTLTIVNDILTGSEFPET

>core/219/1/Org1_Gene522

MGESVKVFLEEREDYPYGFVTPIESQGLTRGLSEETIEEIAALRNEPQFIIDFRLQAYRYWKQLHEPAWARLH
YGP IAYDDIVYFSSPKQKKPLGRLEDADPEILDTFKKLGIPLDEQKRLN VENVAVDLVFDSVSIGTTFKEALE
KAGVIFCSLGEAIQEHPNLVKKYLGSVVSHRDNFFAALNAAVFSDGSFVYVPKGVKCPMDISTYFRINNKEA
GQFERTLIVVEDGGYASYLEGCTAPAYSSNQLHAAVVELVAHEHAVIRYSTVQNWYAGDKKTGKGGIYNFV
TKRGLCAGYRSKISWSQVEVGAAITWKYPSCILKGDES VGEFYSVALTSGKMQADTGT KMLHVGKRTTSTV
ISKGISSESKNTFRSLVSLGKKA EHSSNYTQCDSMLIGKASGAYTDPKIVVENSTSSIEHEATT SKLREDQLLY
LRSRGLSPEEAVSLVIHGFCREIIEQLPLEFAQEASKLLLIKLENSVG

>core/220/1/Org1_Gene305

MDLKELLHGVQAKIYGKVRPLEVRNLTRDSRCVSVGDIFIAHKGQRYDGNDFAVDALANGAIAIASSLYNPF
LSVVQIITPNLEELEAELSAKY YEYPSSKLHTIGVTGTNGKTTVTCLIKALLDSYQKPSGLLG TIEHILGEGVIK
DGFTTPTPALLQKYLATMVRQNRDAVVMEVSSIGLASGRVAYTNFDTAVLTNITLDHLD FHGTFETYVAAK
AKLFSLVPPSGMVVINTDSPYASQCIESAKAPVITYGIESAADYRATDIQLSSSGTKYTLVYGDQKIACSSSFIG
KYNVYNLLAAISTVHASLRCDLEDLLEKIGLCQPPPGRLDPVLMGPCPVYIDYAHTPDALDNVLTGLHELLPE
GGRLIVVFGCGGDRDRSKRKLMAQVVERYGFAVVTSDNPRSEPPEDIVNEICDGFYSKNYFIEIDRKQAITYA
LSIASDRDIVLIAGKGHEAYQIFKHQTVAFDDKQTVCEVLASYV

>core/222/1/Org1_Gene257

MQTNIGLIGLAVMGKNLVNLN MIDHGFSVSVYNRTPEKTRDFLKEYPNHREL VGFESLEDFVNSLERPRKIML
MIQAGKPV DQSIHALLPFLEPGDVIIDGGNSYFKDSERRCKELQEKGILFLGVGISGGE EGARHGPSIMPGGNP
EAWPLVAPIFQSIAAKVQGRPCCSWVGTGGAGHYVKAVHNGIEYGD IQLICEAYGILRDFLKL SATAVATILK
EWNTLELESYLIRIASEVLAL KDPEGIPVIDTILDVVGQKGTGKWT AIDALNSGVPLSLIIGAVLARFLSSWKEI
REQAARNYPGTPLIFEMPHDPSVFIQDVFHALYASKIISYAQGFMLLGEASKEYNWGLDLGEI ALMWRGGCII
QSAFLDVIHKGFAANPENTSLIFQEYFRGALRHAEMGWRRTVVTAIGAGLPIPC LAAAITFYDGYRTASSSMS
LAQGLRDYFGAHTYERNDRPRGEFYHTD WVHTKTTERVK

>core/223/1/Org1_Gene543

MRDVSELFRTTHFMHYASYVILERAIPHILDGLKPVQRRLWTLFLMDDGKMHKVANIAGRTMALHPHGDAP
IVEALVVLANKGYLIDTQGNFGNPLTGDPHAAARYIEARLSPLARETLFNTDLIAFHDSYDGREKEPDILPAKL
PVLLLHGVDGIAVGMTTKIFPHNFAELLLKAQIAILNDKKFTVFPDFPSGGLMDPSEYQDGLGSITLRASIDIIND
KTLVVKQICPQSTTETLIRSIENAAKRGTIKIDTIQDFSTDVPHIEIKLPKGSRAKEMPLLLFEHTECQVILYSKPT
VIYENKPVECSISEILKLHTTALQGYLEKELLLLQEQLTLDHYHKTLEYIFIKHKLYDSVREVLAINKKISADDL
HQAHLHALEPWLHELATPVTQDTSQLASLTIKKILCFNEEACTKELLAIEKKQAAIQKDLGRIKEVTVKYLK
GLLERHGLGERKTQITNFKTAKTSILKQQTLI

>core/224/1/Org1_Gene792

MLCATVSGPSFCEAKQQILKSLHLVDIHELRLDLINELDDQELHTLITTAQNPILTFRQHKEMSTALWIKLYSL
AKLEPKWMDIDVSLPKTALQTIRKSHPKIKLILSYHTDKNEDLDAIYNEMLATPAEIKIVLSPENSSEALNYI
KKARLLPKPSTVLCMGTHGLPSRVLSPLISNAMNYAAGISAPQVAPGQPKLEELLSYNYSKLSEKSHIYGLIG
DPVDRSISHLSHNFLLSKLSLNATYIKFPVTIGEVVTTFFSAIRDLPFSGLSVTMPLKTAIFDHVDALDASAQLCE
SINTLVFRNQKILGYNTDGEGVAKLLKQKNISVNNKHIAIVGAGGAAKAIAATLAMQGANLHIFNRTLSSAA
ALATCCKGKAYPLGSLENFKTIDIINCLPPEVTFPWRFPPIVMDINTKPHSPYLERAQKHGSLIIHGYEMFIEQ
ALLQFALWFPDFLTPESCDSEFRNYVKNFMAKV

>core/225/1/Org1_Gene321

MMSRLRFRLAALGIFFILLVPNSVSAKTIVASDKEKVGVLVYDNSVEAFQQILDCIDHANFYVELCPCMTGGR
TLKEMVDHLEARMDLVPELCSYIIIQPTFTDAEDQKLLKALKERHPNRFFYVFTGCPPSTSILAPNVIEMHIKLS
IIDGKYCILGGTNFEFEMCTPGDEVPEKVDNPRFLVSGVRRPLAFRDQDIMLRSTAFGLQLREEYHKQFAMW
DYAAHHMWFIDNPEQFAGACPPLTLEQAEETVFPGFDKHEDLVLDSSKIRIVLGGPHDKQPNPVTQEYLKLI
QGARSSVKLAHMYFIPKDELLNALVDVSHNHGVHLSLITNGCHELSPAITGPYAWGNRINYFALLYGKRYPL
WKKWFCEKLKPYERVSIYEFAIWETQLHKKCMIIDDEIFVIGSYNFGKKSDAFDYESIVVIESPEVAAKANKV
FNKDIGLSIPVSHGDIFSWSYFHSVHHTLGHLLQLTYMPA

>core/226/1/Org1_Gene728

MRIVQVAVEFTPIVKVGGLGDAVASLSKELAKQNDVEVLLPHYPLISKFSSSQVLSERSFYEFGLGKQQASAI
YSYEGTLTIIITLDSQIELFSTTSVYSENNVVRFSFAAAAAAYLQEADPADIVHLHDWHVGLLAGLLKNPLN
PVHISKIVFTIHNFGYRGYCSTQLLAASQIDDFHLSHYQLFRDPQTSVLMKGALYCSDYITTVSLTYVQEINDY
SDYELHDAILARNSVFSGIINGIDEDVWNPKTDPALAVQYDASLLSEPDLFTKKEENRAVLYEKLGISSDYFP
LICVISRIVEEKGPEFMKEIILHAMEHSYAFILIGTSQNEVLLNEFRNLQDCLASSPNIRLILDFNDPLARLTYAA
ADMICIPSHREACGLTQLIAMRYGTVPVLRKTGGLADTVIPGVNGFTFFDTNNFNEFRAMLSNAVTTYRQEP
DVWLNLIESGMLRASGLDAMAKHYVNLYQSLLS

>core/227/1/Org1_Gene974

MAFSHIEGLYFYNTASQKKELFFPNHTPVRLYTCGPTVYDYAHIGNFRITYVFEDILKRTL VFFGYSVTHVMNI
TDVEDKTIAGASKKNIPLQEYTPYTEAFFEDLDTLNARADFYPHATHYIPQMIQAITKLLEQGIAYIGQDAS
VYFSLNRFPNYGKLSHLDLSSLRCCSRISADEYDKENPSDFVLWKAYNPERDGVIIYWESPFGKGRPGWHLEC
SIMAMELLGDSLDIHAGGVDNIFPHHENEIAQSEALSGKPFARYWLHSEHLLIDGKKMSKSLGNFLTLDLLH
QEFTGQEVRYMLLQSHYRTQLNFTEEALLACRHALRRLKDFVSRLEGVDLPGESPLPRTL DSSSQFIEAFSRA

LANDLNVSTGFASLFDVHEINTLIDQGHFSKADSLYILDTLKKVDTVLGVLPLTTSVCIPETVMQLVAEREEA
RKTKNWAMADTLRDEILAAGFLVEDSKSGPRVKPL

>core/228/1/Org1_Gene939

MDTIDTPGEGSQSFGNSLGARFDLPRKEQDPSQALAVASYQNKTDSQVVEEHLDELISLADSCGISVLETRS
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VQLAQARYLLPRLKRLWGHLNRQKSGGGSGGFVKGEGEKQIELDRRMVRERIHKLKSAQLKAVIKQRAERRK
VKSRRGIPTFALIGYTNSGKSTLLNLLTAADTYVEDKLFATLDPKTRKCVLPGGRHVLLTDTVGFIRKLPHL
VAAFKSTLEAAFHEDVLLHVVDASHPLALEHVQTTYDLFQELKIEKPRIITVLNKNVDRLPQGSIPMKLRLLSPL
PVLISAKTGEGIQNLLSLMTEIIQEKS LHVTLNFPYTEY GKFTL CDAGV VASSRYQEDFLVVDAYLPKELQK
KFRPFISYVFPEDCGDDEGRGPVLESSFGD

>core/229/1/Org1_Gene204

MDSRTSHLDDELSFKLEKAFTCLSTDIHSHDLSKIVIEYNPIDLAYAVSCLPSESRAILYKNLSCITAKVAFIINT
DSASRWAIFRRLSDSEVCALIEQMPPDEAVWVLDDIPDRRYRRILELIDSKKALKIRDLQKHGRNTAGRLMTN
EFAFLMETTVKDVSA CIRSNPGIDLTRLVFVLDFK GELQGVVTD RSLIINPPMSLKQIMNQIEHKVLPDATR
EEVVDLVERYKIAALPVVDEENFLIGAITYEDVVEAIEDIADETIARMAGTTEDVGYQTCHVVQRFLLRAPWL
LVTFLAGLISASVMAYFQKISPALLALIIFFIPLINGMSGNVGVQCSTILVRSMATGTLSFGRRRETIFKEMSIGL
LTGVVLGILCGLVVYLMGFLGLNIFSGGGIQLGVT VATGV LGASLTATTLGVLS PFFFAKLGVDPALASGPV
TALNDIMSMIIFFLIAGGINFLFFN

>core/230/1/Org1_Gene844

MNKKKRFLSLLFLTAVLLGIWFSPHPASINSNAWQLFAIFTTITIMGIIFQPVPMGAIAIIGISTLLLLTQTLTLEQG
LSGFHNPIAWLVFLSFSIAKGIIKTGLGERIAYFFVSALGKSPLGLSYGLVITDFFLAPAIPSVTARAGGILYPVV
TSLSDSFGSSAEKGTQDLIGSFLIKVAYQSSVITSAMFLTAMAGNPLVAALAGHVGVSLSWVLWAKAAIIPGL
LSLFLMPIILYKLYPPKITSCEEAIKRLRLKEMGPLKKEEKTILMIFFLVVLWTFGDLLGISATTAALIGLSL
LILTNIWDWQKDVIANTTAWETFIWFGALIMMASFLNQLGFIPLVGDSAAALVSGLSWKIGFPLFLIYFYSHY
LFASNTAHIGAMYPIFLAVSISLGTNPIFAALTLAFASNLFGGLTHYGSGPAPLYFGSHL VTVQEWWRS GFALS
IVNIVIWIGIGSLWWKALGLI

>core/231/1/Org1_Gene1006

MTTKSLGSFNSVISKNKIHFIISLGCSRNLVDSEVMLGILLKAGYESTNEIEDADYLILNTCAFLKSARDEAKDY
LDHLIDVKKENAKIIVTGCMTSNHKDELKPWM SHIHYLLGSGDVENILSAIESRESGEKISAKSYIEMGEVPRQ
LSTPKHYAYLKVAEGCRKRCAFCIIPSIK GKLR SKPLDQILKEFRILVNKSVKEIILIAQDLGDY GKDLSTDRSS
QLESLLHELLKEPGDYWLRLMYLYPDEVSDGIIDLMQSNPKLLPYVDIPLQHINDRILKQMRRTTSREQILGFL
EKLRAKVPQVYIRSSVIVGFPGETQEEFQELADFIGEGWIDNLGIFLYSQEANTPAAELPDQIPEKV KESRLKIL
SQIQKRNVDKHNQKLIGEKIEAVIDNYHPETNLLLTARFYGQAPEVDPCIIVNEAKLVSHFGERC FIEITGTAG
YDLVGRVVKKSQNQALLKTSKA

>core/232/1/Org1_Gene200

MHSHSKPTKPLGTFTVGMLSLAVVISLRNLPLTAKHGLSTLFFYGLAVICFMIPYALISAELASFKPQGIYIWA
RDALGKWWGFFAIWMQWFHNMTWYPAVLAFIASTIVYKINPELAHNKVYIATVILAGFWILTFNFLGITSS
ALFSSICVIIGTLIPGVILVSLALFWIFSGNPISLSWGNLLPNFSNVSSLVLLAGMLLALCGLEANANLASDM
VNPRKNYPKAVFIGAIAITLILVLGSLSIAIVIPKEEISLVSGLVKTFTLFFDKYNLSWMTGIVVVM TIAGSLGE
LNAWMFAGTKGLFISTQNDCLPRLFKKVNSKNVPTNMLFQGIVVTIFTLLFLCLDSADLVYWILTALSVQM
YLAMYICLFLAGPILRIKEPRAQRLYSVPGKFLGICTMSILGILSCAFALWVSFLPPRELAQISEGSKIGYTTFLL
LAFSLNCLIPFGIYFTHKRLSKKS

>core/233/1/Org1_Gene824

MDKSTGVPLPSPPHSKESEMIVLGCMLTGCVHYLNLAANQLYEEDFYYLEHKIIFRVLQDAFKQDKPIDVHLA
GEELKRHNQITVIGGPSYLITLAEFAGTAAYLEEYVDIIRSKSILRKMISTAKEIEKRALEQPKNVAEALDEAQN
SFFKISQSTSVSQYTLVADKLRGLTTTTDKPYLVQLQERQELFLQNAQGDNKSFFTGIPTHFIDLDQLIHGFSPS
NLMILAAPAMGKTALALNIAENLCFQNRPLIGIFSLEMTVDQLIHRMICSRSSEVDSKKISIGDLSGHDQFQIVS
VINEMQEHTLLIDDQPLKVSDDLARARRMKESYDIQFLIIDYLQLLSGSGTLRATESRQTEISEISRMLKTLAR
ELNIPILCLSLSRKVEDRANHRPMMSDLRESGSIEQSDSLVMFLLRREYYDPNDKPGTAELIIAKNRHGSIGS
VPLVFEKELARFRNYSAFECIS

>core/234/1/Org1_Gene566

MKITVNRGLDLSLQGSPKESGFYNKIDPEFVSIDLRPFQPLSLKLKVEQGDVCSGAPIAEYKHFNPNTYITSHV
SGVVTAIRRGNKRSLLDVIKKKTPGPTSTEYTYDLQTLRSDDLSEIFKENGLFALIKQRPFDIPAIPQTQTPRDVFIN
LADNRPFTSPPEKHLALFSSREEGFYVFFVGVRAIAKLFGLRPHIVFRDRLTLPTQELKTIAHLHTVSGFPFSGS
PSIIHHSVAPITNEKEVVFTLSFQDVL TIGHLFLKGRILHEQVTALAGTALKSSLRRYVITTKGASFSSLINLNDI
SDNDTLISGDPLTGRCLKKEEPPFLGFRDHSISVLHNPTKRELFSFLRIGFNKPTFTKTYLSGFFKKKRTYTNPD
TNLHGETRPIIDTDIYDKVMPMRIPVVPLIKAVITKNFDLANELGFLEVCGEDFALPTLIDPSKTEMLTIVKESLI
EYAKESGILTPHQD

>core/236/1/Org1_Gene452

MKEERSSEILPRVKETKKHAYVSMQEKSCVGECAVVASESEEAESVTVTKIAKLQRMGIEELNILARQYGVK
NIGSLTKSQVVFEIVKAKSERPDELLIGEGVLEVLPDGFGLRSPTYNYLPSAEDIYVSPAQIRRFDLKKGDTIIG
TIRSPKEKEKYFALLKVDKINGSTPDKAKERVLFENLTPLYPNQRIVMEMGKDHLAERVLDLTAPIGKGQRG
LIVAPPRSGKTVILQSIHAHAIVNNPDIVLIVLLIDERPEEVTDMIRQVRGEVVASTFDEQPERHIQVAEMVIEK
ARRLVEHGNDVVILLDSITRLARAYNTVQPHSGKILTGGVDASALHKPKRFFGAARNIEGGGSLTILATALIDT
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HLLGLRLKKTNSNAEFLLSLKE

>core/237/1/Org1_Gene963

MNFKLPHYHIGLTKAENNTIKIAILQKTCKGWIVCHCEQIPEGKTWSLPKKYFAAPTTFSLQGS DILVKSSSSS
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ADIFFLAEQSPKSLPAYLLIYGGSSEVTCIFVKNHAI AVARSFSNHSTKKSCDDIHATLQYIQETFPQTVLPAIH
VAQISPNLQKILEQKLSLPLVVCQSMTYGVEDEDWEIYGDTIAAAHHGASRRPLTFPYDATSVSPA AQKHWL
LRSSLLIGKYALMATVVVSLGSVLKLKSLSSSASNHFACPEEGVLP RSLRAAEKTVKAIGKKNSASNYPLL

PTIPTSEQTLKFLALGKSSPSIKFSYFSYTMSTSYPSKDNPSLPYSALVEVKGGQPEDIPQFLKKISSHPKLQHV
SESLEDQRSFKLQFTLSS

>core/238/1/Org1_Gene655

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AGQPLPLAFMTSPLNTRQTRSFFESNDYFHLDPNQVDFFCQPLWPLLTLSGDLFLEDMDTLALGPNGNGCIAT
LLYTSGVWEKWKNAAGIEMVSVIPIDNPLALPFDVELCGFHAMSNNNEVTIKAALRQTAIEDVGILVKSHDSGK
TSVIEYSEIPQNERFALNEDGKLKYCLANIGLYCLSMDFIRHAAYQQPLLYKVHKKHAKQLGHTSLNEKNAWK
FEEFIFDLFCYSDHCQTLVYPRQECFAPLKNLEGNHSPDTRQALSDRERQLFHKVTGKKLSPNTTTFEADDF
YYPSTSTSLHWENKAFFEEPFFEAS

>core/239/1/Org1_Gene969

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DGYTIDYPAMAKRKNTVVQGIRQGLEGLIRSNKITVLKGTGSLVSSTEVKVIGQDTTIIKANHIILATGSEPRPF
PGVPFSSRILSSTGILELEVLPPKLAIIIGGGVIGCEFASLFHTLGVEITVIEALDHILAVNNKEVSQTVTNKFTKQ
GIRILTKASISAIEESQNQVRITVNDQVEEFDYVLVAIGRQFNTASIGLDNAGVIRDDRGVIPVDETMRTNVPNI
YAIGDITGKWLLAHVASHQGVIAAKNISGHHEVMDYSAIPSVIFTHPEIAMVGLSLQEAQQNLPAKLTKFPF
KAIGKAVALGASDGFAAIVSHEITQQILGAYVIGPHASSLIGEMTLAIRNELTLPCIYETVHAHPTLSEVWAEG
ALLATNHPLHFPPKS

>core/240/1/Org1_Gene31

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EREKATSRFVNESQLSSARKRYCTPSSAAPSLFLETEIVRAPVERTKELQDNEIHIPVVQVQTNPKQNTKTTK
QLASQASIQQSEGTEQSLRELAQGASLPVLVRSNPEVSVQRQKEELLKELVAERRQCKRKSVRQALEARSLT
KKVARGGSVTSTLRYDPEKAAEIKSRRNCKVSPEAREQKYSSCKRDARANGKQDKTTPSEDASQEEQQTGA
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VGALIIANATESQTTSDPTPTPTP

>core/241/1/Org1_Gene223

MRAWEEFLLLQEKEIGTNTVDKWLRLSLKVLCFDACNLYLEAQDSFQITWFEHHRHKVKSGLVNNNNKPIRV
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YLFSGPEGSGKTHLMQSAISVLRSEGGKILYVSSDLFTEHLVSAIRSGEMQKFRSFYRNIDALFIEDIEVFSGKSA
TQEEFFHTFNSLHSEGKLIVVSSSYAPVDLVAVEDRLISRFEGVVAIPIHPLVQEGLRSFLMRQVERLSIRIQET
ALDFLIYALSSNVKTLHALNLLAKRVMYKKLSHQLLYEDDVKTLLKDVLEAAGSVRLTPLKIIRNVAQYYG
VSQESILGRSQSREYVLPRQVAMYFCRQKLSLSYVRIGDVFSRDHSTVISSIRLIEQKIEENSHDIHMAIQDISKN
LNSLHKSLEFFPSEEMII

>core/242/1/Org1_Gene777

MRQEKDSL GIVEVPEDKLYGAQTMRSRNFFSWGPELMPYEVIRALVWIKKCAAQANQDLGFLDSKHCDMIV
AAADEILEGGFEEHFPLKVWQTGSGTQSNMNVNEVIANLAIRHHGGVLGSKDPIHPNDHVNKSQSSNDVFPT
AMHIAAVISLKNKLIPALDHMIRVLDKVEEFRHVDVKIGRTHLMDAVPMTLGQEFSGYSSQLRHCLIESIAFSL
AHL YELAIGATAVGTGLNVPEGFVEKIIHYLRKETDEPFIPASNYFSALSCHDALVDAHGSLATLACALTKIAT
DLSFLGSGPRCGLGELFFPENEPGSSIMPGKVNPTQCEALQMVCAQVLGNNQTVIIGGSRGNFELNVMKPVII
YNFLQSVDLLSEGMR AFSEFFVKGLKVNKARLQDNINNSLMLVTALAPVLGYDKCSKAALKAFHESISLKEA
CLALGYLSEKEFDRLVVPENMVGNH

>core/243/1/Org1_Gene940

MNFSLFLFFLIAIQGICLYVGRRGSKKVEDRESYFLAGRSLKIFPLMMTFIATQIGGGVLLGAAEEAF CYGYGG
ILYPLGVALGLIFLGMGPGKRLAEGSLTTVVSIFEV FYGSKKLRKIAFLLSAGSLFFILVAQVIALDRLFSSFPFG
KYVTVAFWIVLASYTSTGGFRGVVRTDVIQAGFLLIAVLVCGVSVWLSVPKSLSVLDPFQSLPCA KLSNWIF
MPMLFMLVEQDMVQRCVAASSPKRLQWAAVGAGLVLLLFNFIPLFLGSLGAKAGLKAGCPLIDTIA YFCNPS
LAAVMAAAIGVAILSTADSLMNAVSQLIAEEYPTLKAPYYRYLV LGLAVAAPLVAIGFTNIVDVLISYSLSV
CCLSVPGFYLLAPKGRRVSGAAAWAGVLVGALGYGWVQIVSLGMFGELLA WIGSLVAFSFGFIEITWKN
KVKTQT

>core/244/1/Org1_Gene743

MQQSVRKLFGTDGVRGRANFEPMTVETTVLLGKAVARVLREGRSGKHRVVVGKDTRLSGYMFENALIAGL
NSMGIETLVLGPIPTPGVAFITRAYRADAGIMISASHNPYRDNGIKIFSLEGFKISDVLEQRIETMVSEADFGPLP
EDHAVGKNKRVIDAMGRYVEFVKATFPKGRTLKGLKIVLDCAHGASYKVAPS VFEELDAEVICYGCEPTGIN
INEHCGALFPQVIQKAVIEHQ AHLGIALDGDGDRIIMVDEKGHIVDGD MILSICAGDLKKRSALPHNRVVATI
MTNFGVLKYLEGLGLQVFTSPVGDRHVLHAMLEHEVTLGGEQSGHMIFLDYNTTGDGIVSALQVLRIMIESE
SMLS DLTAPIVKSPQTLINAVREKIPIETIPLIERTLRDVQDALGPSGRILLRYSGTENICRVMVEGHKKHQV
DCLAKALADVIDAELGTGSRE

>core/245/1/Org1_Gene417

MQIAQVFGCGR LNGEVKVSGAKNAATKLLVASLLSDQKCTLRNVPDIGDVSLTVELCKSLGAHVSWDKETE
VLEIYTPEIQCTRVPPTFSNVNRIPILLGALLGRCPEGVYVPTVGGDAIGERTLNFHFEG LKQLGVQISSDSSG
YYAKAPRGLKGNYIHLPYPSVGATENLILAAIHAKGRTVIKNVALEAEILDVLFLQKAGADITTDNDRTIDIF
GTGGLGSVDHTILPDKIEAASFGMAAVVSGGRVFVRNAKQELLIPFLKMLRSIGGGFLVSESGIEFFQERPLVG
GVVLETDVHPGFLTDWQQPFAVLLSQAQGSSVIHETVHENRLGYLHGLQHMGAECQLFHQCLSTKACRYAI
GNFPHSAVIHGATPLWASHLVIPDLRAGFAYVMAALIAEGGGSIIENTHLLDRGYTNWVGKLRSLGAKIQIFD
MEQEELTTSPKSLALRDASL

>core/246/1/Org1_Gene672

MLYFIEQLNKLSTSF CVFPMILLGGFLT WKLRGLQFHGLKLGFNLMLQNKLDDSSSKANEVSSYEAVAGIL
AGNFGTGNIAGMAVALACGGPGALVWVWLAALLGAIVQYAGSYLGSKYRKPEGNTGEFIGGPIACLAFGM
RKKILAGFFALFTIMT AFCAGNCVQVSCIVPLCAEGTPGKLLVGILLALVVIPVL AGGNNRILRFSARVIPFIAG
FYCISCGIILFQHASAILPAIKLICSSAFGIKAGLAGIGGYTLSQVISTGINRAVMATDCGSGMVSILQANTKSKN
PVVDGLVTLVPPVIVMVVCSITMLVLIVSGAYSSGAQGTLMVMSAFKNSLGSLSGVIVILAMALFGYTTILTW

FACAEKSLQYMIPGRRANLWLKAIYVLIIPLGGVIDMRMIWALSDTGFSGMVILNCIALIALLKDVLSTNRDV
ALLKERECSVADPVRNLDA

>core/247/1/Org1_Gene680

MFNVNFKFLEGLHQAPRYTSYPTALEWEPSDAAPALLAFQRIRENPPQLSLYFHIPFCQSMCLYCGCSVVLN
RREDIVEAYINTLIQEMKLVVETIGFRPQVSRIHFGGGTPSRLSRELFTLLFDHIHKLFDLSHAEEIAIEVDPRSL
RNDMEKADFFQNVGFNRVSLGVQDTQADVQEAVRRRQSHEESLKAYEKFKELAFAQSINIDLIYGLPKQTKES
FSKTIQDILAMYPDRLALFSFASVPWIKPHQKAMKASDMPSPMEEKFAIYSQSRHLLTKAGYQAIGMDHFSLP
HDPLTLAFKNKTLIRNFQGYSLPPEEDLLGLGMTSTSFIRGIYLNQAKTLEEYHNTVLRGTFATVKSILTEDD
RIRKWAHKLMTFTINKEEFFNLFGYEFDTYFIESRDLISMETTGLIHNSPGSLKVTPLGELFVRVIATAFDH
YFLNKVSKKECFASI

>core/248/1/Org1_Gene468

MTTLRQFFLITELRQKLFYTFALLTACRVGVFIPVPGINGELAVAYFKQLLGSGQNLFQLADIFSGGAFAQMT
VIALGVVPYISASIIVQLFLVFMALQREMRESSDQGKRRIGRLTRLFTVALAVIQSLLFAKFALRMNLTIPGIV
LPTLLSSKFLGVPWIFYITTVVVMTTGTLLLMWIGEQISDKGIGNGISLIILGILSSFPSVLGSIVNKLNLGSQD
SSDLGLISILILALVFVFLITLIIIEGVRKIPVQYARRVIGRREVPGGGSYLPLKVNYAGVIPVIFASSLLMFPA
TIGQFIASESSWMKRIAALLAPGSLVYSICYVLLIIFFTYFWTATQFHPEQIASEMKKNNAFIPGIRQGKPTQHY
LEYTMNRVTLLGALFLAAIAILPSLLGCLLRVDSNVSYFLGGTAMLIVVGVVLDTMKQVDAFLLMRRYDSVL
KTDRTKGRH

>core/250/1/Org1_Gene499

MNVWTKFFQPPKHIKEIEDQEVVKKKYKYWRIRIFYSMFIGYIFYFTRKSFTFAMPTLIADLGFDKAQLGIIG
STLYFSYGISKFVSGVMSDQSNPRYFMAIGLMTGLTNIFFGMSSSIVLFALWWGLNGWFQGWGWPPCARLL
THWYAKSERGTWWSVWSTSHNIGGALIPILTGFIIDYSGWRGAMYVPGILCIGMGLVLINRLRDTPQSLGLPPI
EKYKRDPHHAHHEGKSASEGTEEIERELSTREILFTYVLTNQWLWFLAAASFFIYVRMAVNDWSALFLIETK
HYAAVKANFCVSLFEIGGLFGMLVAGWLSDKISKGNRGP MNVLFSLGLLFAILGMWF SRSHNQWWVDGTL
LFVIGFFLYGPQMMIGLAAAELSHKKAAGTASGFTGWFA YFGATFAGYPLGKVTDVWG WKGFFIALLACAS
IALLLFLPTWNATEKNTRSKA

>core/251/1/Org1_Gene119

MKKVLIANRGEIAVRIIRACHDLGLSTVAVYSLADQEALHVLLADEAICIGEPQAAKSYLKISNILAACEITGA
DAVHPGYGFLSENANFASICESCGLTFIGPSSESIAMMGDKIAAKSLAKKIKCPVIPGSEGIIEDESEGLKIAEKI
GFPIVIKAVAGGGGRGIRIVKEKDEFYRAFSAARAEAEAGFNNPNVYIEKFIENPRHLEIQVIGDTHGNYVHLG
ERDCTIQRRRQKLIEETPSPILNAEIRVKVGKVAVDLARSAGYFSVGTVEFLDKDKKFYF MEMNTRI QVEHT
ITEEVTGIDL VKEQIHVAMGNKLPWKQKNIEFSGHIIQCRINAEDPTNNFSPSPGRLDYYLPPAGPSIRVDGAC
YSGYAIPPPYDSMIAKVIAKGKNREEAIAIMKRALKEFHIGGVQSTIPFHQFMLDNPKFLESNYDINYIDNLLA
QGNSFFKEF

>core/252/1/Org1_Gene24

MATKTKTQWTCNQCGATAPKWLGQCPGCHNWNLSLVEEYVPQARSGTSSRSSTSAIALSSIELENESRIFIDHA
GWDRILGGGVVRGSLTLLGGDPGIGKSTLLLQTAERLASQKYKVLVVCGEESVTQTSRAKRLNISSPLIYLF
PETNLDNIKQQIATLEPDILIISIQIIFNPTLNSAPGSVAQVREVTYELMQIAKSAQITTFIIGHVTKSGEIAGPRV
LEHLVDTVLYFEGNSHANYRMIRSVKNRFGPTNELLLSMHADGLKEVSNPSGLFLQEKTGPTTGSMIPIIEG
SGALLIELQALVSSSPFANPVRKTAGFDPNRFSLLLAVLEKRAQVKLFTMDVFLSITGGLKIIIEPAADLGALLA
VASSLYNRLLPNNSIVIGEVLGGGEIRHVAHLERRIKEGKLMGFEGAILPEGQISSLPKEIRENFRLQGVTIKD
AIRLLL

>core/253/1/Org1_Gene670

MLKILKIKVLVFPLALLMGCNSIGYAGPQGSQTNSQTKVKIGSEVWIEQKLRQYPELLWLTESGGAPLLTST
PIDMAYSEKLFNKKVPALDIAIRSMIHLHLLIQGSRQSYMQLSQILPSEEGMTFKQFQTAHKQLLFFLNPKS
FDNTRLRILETAIVLRHVGCSAKAVTTFKPYFTDSCPQSFYAKALHVLRTFPELCPSYARLSPEQQEVLLSLRRL
GNYDSLNLTEVPSAQLLSAWRTRRSLAILDLYLYCLDTCGDKNCSQEFYINFAPLLSMLQQHATIEEAFSRY
FTYRANRLGFEGTSRTDMLVRLATLMNLSPEASTLAWSFKNLPSDEAENLVNSFYTVQGEHIPLTFRGLPS
LVAGLSVATHGSTVSPENRLRQLYSTMLSLLVKSLRSHREMLNKQLLPQGTVLDFSETTLSSGGLDVFAESIA
VRIHLNGAVSINL

>core/254/1/Org1_Gene126

MRKRHSFDSTSTKKEAVSKAIQKIIKIMETTDPSLNVETPNAEIESILQEIKEIKQKLSKQAEDLGLLEKYCSQE
TLNLENTNASLKL SIGSVIEELASLKQLVEESIEESLGQQDQLIQSVLIEISDKFLSSIGETLSGNLDMNQNVIQ
GLLIKENPEKSEAASVGYVQTLLEPLSKRIGETHKKVATHDVNISSLQFHMMSVAGGRFRGHIDMNGYRVLG
LGEPKNGEDAVSKDYLERIVSSQLTIDKVEDKPITKPNKGKLLYSQGTSPKLESPLPLGLLTSGISGFTWKSAS
KSNDGSFPFSALRHKETESDTCFQITSTTLSGNQAGTYTWSLSLKVLVPSIFQIEKPEVQLSLVYSYEDWLPID
NIFNMSQPRTIPLALLGQTMLAGQKYDILELAAHQTNQTLMISPNC SRFSLQLKQTNQFENSPVDFYIVHAAH
SCHWSGF

>core/255/1/Org1_Gene311

MLTCNECTTWEQFLNYVKTRCSKTAFENWISPIQVLEETQEKIRLEVNPVIFVQNYLLDNYKRDLC SFVPLDVH
GEPALEFVVAEHKKPSAPVASQKESNEGISEVFEETKDFELKLNL SYRFDNFIEGPSNQFVKSAAVGIAGKPGR
SYNPLFIHGGVGLGKTHLLHAVGHYVREHHKNLRIHCITTEAFINDLVYHLKSKSVDKMKNFYRSLDLLLVD
DIQFLQNRQNFEEFECNTFETLINLSKQIVITSDKPPSQLKL SERIARM EWGLVAHV GIPDLETRVAILQHKAE
QKGLLIPNEMAFYIADHIYGNVRQLEGAINKLTAYCRLFGKSLTETTVRETLKELFRSPTKQKISVETILKSA
TVFQVKLNDLKGNSRSKDLVLARQIAMYLAKTLITDSLVAIGAAF GKTHSTVLYACKTIEHKLQNDETLKRQ
VNLCKNHIVG

>core/256/1/Org1_Gene733

MILPPYSYSLKIGAAVLFFCSILHTFLTPWLYTLCQSYEHKKLVFPECWKRYARLSE LFRILSRVEIVFFLWAVP
LFFWFLYTEGYRISMAFYNSRNYGFAVFIMVILILLESRPVYFAELVLSSIAKLGKTS PKSWWWTLMIAPPL
SCLLKETGAMII GATLLMRHFYVFSPSRRFAYATMGLLFSNISIGGLTSYVSSRALFLIFPALKWEHSSFFLSHFA
WKAIVAILISTTIYYFIFRKEFKKFPDIPSDKDPSVEKVPWWIICVNIIFVGSILSRSTPLFMGALLLFYLG FQKFT
IFYQDPINLSKVCYVGLFYAGLVVFGDLQEWWVLNLMQGLSDFGYMTVSYTLSIFLDNALVNYLVHNL SVA

TDCYHYLVVAGCMAAGGLTLVSNIPNIVGYLILRSAFPSSTIHMGWFLGALGPSIISLGVFWLLKNVPEFLYC
FFR

>core/257/1/Org1_Gene578

MSEPRFVCLSLGSNLGNRFKNLQIARTLLGEQAVLGLRSSVILETEALLPGSPPEWDLPYFNSVLVGETTSL
RELLVTIKQIEKVVGRAEESPPWSPRTIDVDILLYGDESFCCDHTEITIPLSNLLSRPFLIALIASLCPYRRFCTQG
SPYHNFTFGELAHHLPSPPGMIRRSLSPTDMLMGVVNVTNDSMSDGGMFLDPEKAVAQAIEKLFTGAAVIDF
GAQATNPKVKQFLSVDQEWERLEPVLRLKETWSNRKQYPIISLDTFYPEIILRAMDIYPIQWINDVSGGSQS
MAEVARDCELSLVMNHSSSLPVDPKNILSFSVPIGEQLLSWGEKQLKMFSDVGLNANQVIFDPGIGFGKGAA
QSLATLYEIAKFKRLGCPILIGHSRKSFLSLFGNHDPKDRDWETVGLSILLQQQGVDYLRVHNVAAHQKALS
VAACEACAPI

>core/258/1/Org1_Gene385

MNRLLSLLSVFDDFFWSYVAFILIIVLGVSFWSKSRFFQFTKFSQFCKLFRYYSQNPQERETKQGVHPLKVFFA
SAGGNIGIGNVVGIVTAACIGGPGALFWVWIAGIFGSIVKYSEVYLGIFRKLDRDGVYQGGPMYFLIKAFKT
PVVSVIVAILLCIYGVEIYQFSVITDSLHWCWNLPKVYPMLGLLFLVFYAIRGGLQRIGKICSIVLPFFMLLYCA
LSLYILVKEFHTLPHLLSTVFSSAFKQGSALGGFAGCTVATTIHQGISRAAYSGDIGIGFDSIIQSESSAKDPSTQ
AQLSIVGIAIDNICTLSLLMVLASGSWSLGLENASQVVEHTLASYFPMVKFFLPTFFFVTGYTTIISYFLVGKK
CAKFLYGNTGAKIYTLYGLLILPLFCFLSQNTALLIMSVSGALLLCFNLLGVFILRKEVIFPARAASLTETSLST
E

>core/259/1/Org1_Gene248

MLSCVFSDTIFLSSFLAVTLICMTTALWGTILLISKQPLLSESLSHASYPGLLVGALMAQYVFSLQASIFWIVLF
GCAASVFGYGIIVFLGKVCKLHKDSALCFVLVVFFAIGVILASYVKESSPTLYNRINAYLYGQAATLGFLEAT
LAAIVFCASLFALWWWYRQIVVTTFDKDFAVTCGLKTVLYEALSILFISLVIVSGVRSVGIVLISAMFVAPSLG
ARQLSDRLSTILLSAFFGGISGALGSYISVAFTCRAIIGQQAVPVTLPTGPLVVICAGLLAGLCLLFSPKSGWVI
RFVRRKHFSFSKDQEHLKVFVWHISHNRLNENISVRDFVCSYKYQEYFGPKPFPRWRVQILEWRGYVKKEQDY
YRLTKKGRSEALRLVRAHRLWESYLVNSLDFSKESVHELAEIEHVLTEELDHTLTEILNDPCYDPHRQIIPNK
KKEV

>core/260/1/Org1_Gene852

MINSLSQKLSSIFSFLVSSRRINEENISESIREVRLALLDADVNYHVVKDFISKVKEKILGEEIWKHVSPGQQFIR
CLHEELVAFLSDGREEFTIQKTPSIILLCGLQGAGKTTTAAKLADYVIKNKKAKKVLVPCDLKRFAAVDQL
KILVAQTKAEFYQSQENKPIDVVVKALAYAKENGHDFVILDTAGRLNIDNELMEELTAIQKVSQANERLFVM
NVAMGQDVLATVQAFDQSLDLTGVILSMTDGDARAGAVFSIKHVLGKPIKFEGCGERIQDLRSFDPQSMAER
ILGMDGTINFKEMREYISEEEDAELGKKLVTAIFTYEDYYKQMKAFRRMGPLRKLGMMPGFNNAKPSQ
KEIEDSEQMKRTEAIIISMTPEERKELVELDMSRMKRIASGCGLTLGDVNQFRKQMSQSKKFFKGMSKGK
MEQVRKKMSGGNQWR

>core/261/1/Org1_Gene62

MDALILSRIQFGLFITFHLYLVPLSMGLSMMLVIMEGLYLVTKKQIYKQMTWFWVGIFALT FVLGVVTGIMQI
FSFGSNWANFSEYTGNI FGTLGSEGVFAFFLESGFLGILLFGRHKVSKKMHHFSTCMVALGAHMSAFWIICA
NSWMQTPSGYEMVMHKGKLPALTSFWGVVFSPTTIDRFIHAVLGTWLSGVFLVISVSAYYLWKKRHHEFA
KQGMKIGTICAVIVLVLQLWSADVTARGVAKNQPAKLAAFE GIFKTEEYTPIWAFGYVDMEKERVIGLPIPG
ALSFLVHRNIKTPVTGLDQIPRDEWPNVQAVFQLYHLMIMLWGVMVALTLISWSAYKGWRWALKPFFLVIL
TFSVLLPEICNECGWCAAEMGRQPWVVQGLLKTDAVSPIVQANQIVQSLVIFSLVFIALLT LFITVLCKKIKH
GPEEENDLTEFEVK

>core/262/1/Org1_Gene687

MRAMLLEDWVSLMLS DVSCPKCDKKITGFAIDSQQVQPGDLFFALPGNATDGHQFLKHAATAGAVAAVVS
HDYQGDSFGLELIRVDDTKSALQEAGSNQCNLFQGTLVGITGSVGKTTTKEFSKITLSSYKTHASPKSYNSQL
TVPLSLLMAEGDEDVMILEMGVSEPGNMQDLLRIVQPEIAVITHINDQHAMHFPQGIQEILKEKSYILQKSKL
QLLPKDSPPYYLDRSCSPTAEKFSFSFNDPLADFCYKAISGDSVVIQTPEENYCLPIAFSYKPAYTNLLIAVALS
WILEVPEEGVIRSLPELKLPPMRFEHSMRNGMQVINDAYNACPEAMIAALDALPLPSDGGKIILILGHMAELG
RYSEEGHALVAEKAASRGDMIFFIGEKWIPVQSVLKSYSCEVSFFSSAQDVKDILKQVARYGDVILLKGSRAL
ALESLLACF

>core/263/1/Org1_Gene253

MSNITSPVIQNNRSCNYYFELKNSTTIHIVISAILLCGALIAFLCVAAPVSYILSGALLGLGLLIALIGVILGIKKIT
PMISSKEQVFPQELVNRIRAHYPKFVSDFVSEAKPNLKD LISFIDLLNQLHSEVGSSTNYNVSEELQQKIDTFEG
IARLKNEVRTASLKRLESAASSRPLFPSPKILQKVFPFFWLGEFISAGSKVVELHRVKKIGGSLEEDLSDYIKP
EMLPTYWLIPLDFRPTNSSILNLHTLVLARVLTRDVFQHLKYAALNGEWNLNHSDLNTMKQQLFAKYHAAY
QSYKHL SQPSLQEDEFYNLLLCIFKHRYSWKQMSLIKTVPADLWENLCCLTLDHTGRPQDMEFASLIGTLYT
QGLIHKESEAFSSLTLLSLDQFKTIRRQSTNIAMFLENLATHNSTFRSLPPITVHPLKRSVFSQPEEDESSLIG

>core/264/1/Org1_Gene898

MVITNLSINADTIYGKNPINIVASAANKNITLTGTLALVNADGAFYENHTLQDSQDYSFVKLSPGAGGTIITQD
ASQKPLEVAPSRPHYGYQGHWNVQVIPGTGTQPSQANLEWVRTGYLPNPERQGSLVPNSLWGSFVDQRAIQ
EIMVNSSQILCQERG VWGAGIANFLHRDKINEHGYRHSGVG YLVGVGTHAFSDATINA AFCQLFSRDKDYV
VSKNHGTSYSGVVFLEDTLEFRSPQGFYTDSSSEACCNQVVTIDMQLSYSHRNNDMKTKYTTTYPEAQGSWA
NDVFGLEFGATTYYYPNSTFLFDYYSPFLRLQCIYAHQEDFKETGGEVRHFTSGDLFNLA VPIGVKFERFSDC
KRGSYELTFAYVPDVIRKDPKSTATLASGATWSTHGNNLSRQGLQLRLGNHCLINPGIEVF SHGAIELRGSSR
NYNINLGGKYRF

>core/265/1/Org1_Gene795

MLTYKVSPSSVYGN AFIPSSKSHTLRAILWASVAEGKSIINYLDSPDTEAMICACKQMGASIKKFPQILEIVG
NPLAIFPKYTLIDAGNSGIVLRFM TALACVFSKEITVTGSSQLQRRPMAPLLQALRNFGASFHFSSDKSVLPFT
MSGPLRSAYS DVEGSDSQFASALAVACSLAEGPCSFTIIEPKERPWFDSLWWLEKLHLPYSCSDTTYSFPGSS
HPQGFSYHVTGDFSSAA FIAAAAALLSKSLQPIRLRNLDILDIQGDKIFFSLMQNLGASIQYDNEEILVFPSSFSGG
SIDMDGCIDALPILTVLCCFADSPSHLYNARS AKDKESDRILAITEELQKM GACIQPTHDGLLVNPSPLYGAVL

DSHDDHRIAMALTIAALYASGDSRIHNTACVRKTFPNFVQTLNIMEARIEECHDNYSMWSTHKRKVFARESF
G

>core/266/1/Org1_Gene615

MTSGVSGSSSQDPTLAAQLAQSSQKAGNAQSGHDTKNVTKQGAQAEVAAGGFEDLIQDASAQSTGKKEATS
STTKSSKGEKSEKSGKSKSSTSVASASETATAQAVQGPGLRQNNYDSPSLPTPEAQTINGIVLKKGMGTLAL
LGLVMTLMANAAGESWKASFQSQNQAIRSQVESAPAIGEAIKRQANHQASATEAQAKQSLISGIVNIVGFTV
SVGAGIFSAAKGATSALKSASFAGETGASAAGGAASKALTSASSSVQQTMASTAKAATTAASSAGSAATKA
AANLTDDMAAAASKMASDGASKASGGLFGEVLNKNPNWSEKVSRRGMNVVKTQGARVASFAGNALSSSMQ
MSQLMHGLTAAVEGLSAGQTGIEVAHHQRLAGQAEQAQAEVLKQMSSVYGQQAGQAGQLQEQAMQSFNTA
LQTLQNIADSQTQTTSIAFN

>core/267/1/Org1_Gene22

MTLQPYQASSRKYRPQIFREILGQSSVAVLKNALVFNRAAHAYLFSGIRGTGKTTLARILAKALNCVHLS
GEPCNQCFSCKEIASGSSLDVLEIDGASHRGIEDIRQINETVLFTPVKAKFKIYIIDEVHMLTKEAFNALLKTLE
EPPQHVKFFFATTEIHKIPGTILSRCQKMHLQRIPEKTILEKLSLMAQDDHIEASQEALAPIARAAQGSLRDAES
LYDYVISLFPKSLSPDTVAQALGFASQDSLRTLDNAILQRDYATALGIVTDFLNSGVAPVTFLHDLTLFYRNLL
LTNSTTSKFSSQYKTEQLLEIIDFLGESAKHLQNTIFEQTLETVIIHIIRIYQRPVLSSELISIKSRQFEGLRNIKEP
TLTQQVSAPQPQPTYKEQSFLEKKNQPAEKGKISVEVKSSASIKSAAVDTLLQFAVVEFSGILRQ

>core/268/1/Org1_Gene640

MLKHDTIAAIATPPGEGSIAVVRLSGPQAIVIADRIFSGSVASFASHTIHLGQVIFEETLIDQALLLLMRSPRSFT
GEDVVEFQCHGGFFACSQILDALIALGARPALPGEFSQRAFLNGKIDLVQAEAIQNLIVAENIDAFRIAQTHFQ
GNFSKKIQEIHTLIEALAFLEVLADFPEEEQPDLLVPQEKIQNALHIVEDFISSFDEGQRLAQGTSILLAGKPNV
GKSSLLNALLQKNRAIVTHIPGTTRDILEEQWLLQGKRIRLLDTAGQRTTDNDIEKEGIERALSAMEEADGIL
WVIDATQPLEDLPKILFTKPSFLLWNKADLTPPPFLDTSLPQFAISAKTGEGLTQVKQALIQWMQKQEAGKTS
KVFLVSSRHHMILQEVARCLKEAQQNLYLQPPEIIALELREALHSIGMLSGKEVTESILGEIFSKFCIGK

>core/269/1/Org1_Gene648

MPRSLSNEQFSVDLEESPGCIVSALVKVSPEVLNKLNKQALKKKIKKEITLPGFRKGKAPDDVIASRYPTNVRK
ELGELVTQDAYHALSTVGDRRPLSPKAVRSNSITQFDLQEGAKVEFSYEAFPAISDLPWENLSLPQEEAASEIS
DSDIEKGLTNIGMFFATKTPVERPSQEGDFISISLHVSKSNDENASSAAIFENKYFKLSEEEMTDAFKEKFLGIS
TGHRVVETITSPEIQSFLRGDTLTFTVNAVIEVSIPEIDDEKARQLQAESLDDLKAKLRIQLEKQAKDKQLQKR
FSEAEDALAMLVDFELPTSLLEERISLITREKLLNARLIQYCSDEELEKRKSELIKEAEEDATKALKLLFLTHKI
FSDEKLTISREELQYMMDVCSRERFGQQPPKDISNDTLQELVMSARDRLTYSKAIEHVLRKAELLASTPSA

>core/270/1/Org1_Gene535

MDQLTTDFDTLMSQLGDVNLTTVVGRITEVVGMLIKAVVPNVRVGEVCLVKRNGMEPLVTEVVGFTQSFAF
LSPLGELSGVSPSSEVIPTGLPLHIRAGNLLGRVLNGLGEPIDVETKGPLQNVDQTFPIFRAPPDPLHRAKLKQ
ILSTGVRCIDGMLTVARGQRIGIFAGAGVGKSSLLGMIARNAEEADVNVIALIGERGREGREFIEGDLGEEGM
KRSVIVVSTSDQSSQLRLNAAYVGTAIAEYFRDQGKTVVLMMDSVTRFARALREVGLAAGEPPARAGYTPS

VFSTLPRLLERSGASDKGTITAFYTVLVAGDDMNPEVVADEVKSILDGHIVLSNALAQAYHYPAIDVLASISRL
LTAIVPEEQRRRIIGKAREVLAKYKANEMLRIGEYRRGSDREIDFAIDHIDKLNRFLLKQDIHEKTNYYEEAAQQL
RAIFR

>core/271/1/Org1_Gene642

MWLVLWALAASLAIALVAKGYRFRVYFRRYAVQVIREVRLSMELKEWALAEQQLLPILKKRSYRRQCLFE
YMRILRKMQRFESEKLLAEAKKLGLRGPYFFLEIAYKAYRFGAFKECAQAFASVPQDLFEEEDAKEYASAL
VRLGDLDAACSLIEPWISPLSHQETFTVMGHIYFTSKRYKDAIDFYNRANALGVCPEVTYNLAQAYRITSSY
AKAGKLFRKLLSNPVYKEEALFNIGLCEQKLGRPGKALLIYQSSDLWSRGDALLMKYAAMAAMDQRDYVL
AEPWELALRCSTFAKDYKCGLGYGFSLCRLRKYGDAERVYCNLIQNFPECLTACKALAWLCGVGYATLLG
SEGLMYAKKAVELDHSCETLELLSACEARCGNFDAAYEIQSFLSSRDTSLQEKQRRSQILRILRKKLPLNDH
HIVEVDALLAA

>core/272/1/Org1_Gene449

MIENDFPEASNFESSHFYRDKVGVILCGGEGKRLSPLTNCRCCKPTVSFGGRYKLDIPISHAISAGFSKIFVIGQ
YLTYTLQQHLFKTYFYHGVLDQDIHLLAPEARQGDQIWYQGTADAIKKNLLYFEDTEIEYFLILSGDQLYNM
DFRSIVDTAIRTHVDMVLVAQPIPEKDAYRMGVLDIDSEGKLIDFYKEKPQEKEVLKRFQLSSEDRIHKLTEDS
GDFLGSMGIYLFRRDSLFSLLREEEGNDFGKHLIQAQMKRGQVQTLLYNGYWADIGTIESYYEANIALTQKP
HAEKRGLNCYDDNGMIYSKNHHLPGAITDSMISSLLCEGCVINTSHVSRSVLGIRSKIGENSVVDQSIIMGN
ARYGSPSPSLGIGKDCEIRKAIIDENCCIGNGVKLQNLKGYIKYDSPDKKLFVRDNIIVPQGTHIPDNYIF

>core/273/1/Org1_Gene89

MLNCSNQKHTVTFEEACQVFPGGVNSPVRACRSVGVTPPIVSSAQGDIFLDTHGREFIDFCGGWGALIHGHSH
PKIVKAIQKTALKGTSYGLTSEEEILFATMLLSSLKLKEHKIRFVSSGTEATMTAVRLARGITNRSIIKFIGGYH
GHADTLLGGISTTEETIDNLTSLIHTPSPHSLISLPYNNSQLHHVMEALGPQVAGIIFEPICANMGIVLPKAEF
LDDIHELCKRFGSLSIMDEVVTGFRVAFQGAQDIFNLSPDITIYGKILGGGLPAAALVGHRSLDHLMPGTFIQ
AGTMSGNFLAMATGHAAIQLCQSEGFYDHLSQLEALFYSPIEEEIRSQGFPVSLVHQGTMFSLFFTESAPTTFD
EAKNSDVEKFQTFYSEVFDNGVYLSPSPLEANFISSAHTENLTYAQNIIDSLIKIFDSSAQRFF

>core/274/1/Org1_Gene588

MFQQKQKLSLKYLPRLMQQGLQMLQSPLTELSSYVVQEIIDNPFFDLSSLEEEEWSPCYRPTNSTFSYLNQTP
GPQESLYTRLLPQIEEAFSTAEERFIAHQIAGNLSDEGLFLRNPEDFAQELELPLEKIHKVWDTIQNLSPEGIASP
SLQSYWMKLLRNSSHQQAYSIVRDCYPLMTNCEFAPIMKKFSLSLSELRNILKKALGSIPWCPAAACTVKPM
VSTPLPDIYLFYSSGSWKIEVSTRGLPSIKLNKETFFHYEHLPKKEEQKNLSQQILSAKWLIKNLKREQTLLQV
METLLPKQEDFLLGKIPAPYPLGIKDLAEDLSFHSTIFRAIENKAVAAPIGIFPLKHLFPRGIHQDSSHSENVL
QWIRQWIATEQTPLSDSVISDRITAKGIPCARRTVAKYRAQLKILPANKRKKLFYIRSSNSHFRDRQF

>core/275/1/Org1_Gene804

MSKIVYKFGGTSLATAENICLVCDIICKDKPSFVVVSAIAGVTDLLVDFCSSSLREREEVLRKIEGKHEEIVKNL
AIPFPVSTWTSRLLPYLQHLEISDLDFARILSLGEDISASLVRAVCSTRGWDLGFLEARSVILTDDSYRRASPNL
DLMKAHWHQLELNQPSYIIQGFISNGLGETVLLGRGGSDYSATLIAELARATEVRIYTDVNGIYTMDBPKVIS

DAQRIPELSFEEMQNLASFGAKVLYPPMLFPCMRAIGIPFVTSTFDPEKGGTWVYAVDKSVSYEPRIKALSLS
QYQSFCSDYTVLGCGLLEEILGILESHGIDPELMIAQNNVVGFMDDDIISQEAQEHLVDVLSLSSVTRLHHS
VALITMIGDNLSSPKVVSTITEKLRGFQGPVFCFCQSSMALSFVVAASELAEGHIEELHNDYVKQKAIVAT

>core/276/1/Org1_Gene51

MQTIYTKITDIKGNLITVEAEGARLGELATITRSDGRSSYASVLRFDLKKVTLQVFGGTSGSLSTGDHVTFLGRP
MEVTFGSSLLGRRLNGIGKPIDNEGECFGEPIEIA TPTFNPVCRIVPRSMVRTNIPMIDVFNCLVKSQKIPIFSSSG
EHHNALLMRIAQAQTDADIVVIGGMGLTFVDYSFFVEESKKLGFADKCVMFHKAVDAPVECVLVPDMALAC
AEKFAVEEKKNVLVLLTDMTAFADALKEISITMDQIPANRGYPGSLYSDLALRYEKA VEIADGG SITLITVTT
MPSDDITHPVPDNTGYITEGQFYLRNNRIDPFGSL SRLKQLVIGKVTREDHGD LANALIRLYADSRKATERMA
MGFKLSNWDKKLLAFSELFETRLMSLEVNIPLLEEALDIGWKILAQSFTSEEVG IKAQLINKYWP KACL SK

>core/277/1/Org1_Gene1010

MISFRLLLLSGLCALGISSYAETPKETTGHYHRYKARIQKKHPESIKESAPSETPHHNSLLSPVTNIFC SHPWKD
GVSVSNLLTSVEKATNTQISLDFSILPQWFYPHKALGQTQALEIPSWQFYFSPSTTWTLYDSPTAGQGIVDFS Y
TLIHYWQTNGVDANQAAGTASSMNDYSNRENNLAQLTFSQTFPGDFLT LAIGQYSLY AIDGTLYDNDQYSG
FISYALSQNASATYSLGSTGAYLQFTPNSEIKVQLGFQDSYNIDGTNFSIYNLT KSKYNFYGYASWTPK PSCGD
GQYSVLLYSTRKVPEQNSQVTGWSLNAAQHIEKLYLFGRINGATGTALPINRSYVLGLVSENPLNRHSQDL
LGIGFATNKVNAKAISNVNKLRRYESVMEAFATIGFGPYISLTPDFQLYIHPALRPERRTSQVYGLRANLSL

>core/278/1/Org1_Gene99

MMLRGVHRIFKCFYDVVLVCAFVIALPKLLYKMLVYGKYKKSLAVRFG LKKPHVPGEGLVWFHGASVGE
VRLLLPVLEKFCEEFPGWRC LVTSC TELGVQVASQVFIPMGATVSILPLDFSIIKSVVAKLRPSLVVFSEGDC
WLNFIIEAKRIGATTLVINGRISIDSSKRFKFLKRLGKNYFSPVDGFLLQDEVQKQRFLSLGIPEHKLQVTGN IK
TYVAAQTALHLERETWRDRLRLPTDSKLVLGSMHRSDAGKWLPVVQKLIKEGVSVLWVPRHVEKTKDVE
ESLHRLHIPYGLWSRGANFSYVPVVVVDEIGLLKQLYVAGDLAFVGGTFDPKIGGHNLLEPLQCEVPLIFGPH
ITSQSELAQRLLLSGAGLCLDEIEPIIDTVSFLNNQEVREAYVQKGKVFVKAETASFDRTWRALKSYIPLYKN
S

>core/279/1/Org1_Gene506

MKRPFPTYLCIIFYGSCASLSLHAGLSFPEVRGATAAVVHADSGKV FYDKDIDAVIYPASMTKIAT ALFILKHY
PTVLDTLIKVKQDAIASITPQAKKQSGYRSPPHWLETDGSTIQLHLREELLGWDLFHALLVCSANDAANVLA
MACCGSVEKFMDKLNFFLKEEIGCTHTHFNNPHGLHHPNHYT TTRDLISIMRCALKEPPFRGVISTTSYKIGAT
NLHGERILSPTNKLLLPGSTYHYPPALGGKTGTTKTAGKNLIMAAEKNRLLVTIATGYSGPVS DLYQDVIAL
CETVFNEPLL RKELVPPSDCLQLEIANLGKLS CPLPEGLYYDFYASEDREPLSVSFIAHADAFPIEQGDLLGHW
VFYDDEGKKISSQPFYAPCRFERTIKPWKLYMKRVFTSYRTYMSITMLLMYFRIRKHKRKYKNLKHYSKI

>core/280/1/Org1_Gene971

MKRAIIIGAGISGLAAGWWLHKKFPQAEILVLDKEAYAGGFVRTESPQGFSFDLGPKGFLTRGDGEYTLKLIH
ELGLQNSLIFSDRAAKNRFVYYRGKAHKISTWTLLRKGLLPSLIKDFRAPCYTQDSSVQDFLKRHSSQNFTSYI
LDPLITAIRAGHSSILSTHMAFPELAKREASSGSLLRSYLKNRSPKSKTD RYLASLSPSMGTLITT IQEKL PAT

WKFSTSVTHIDCSPKEACVTTTPSETFFADMVIYTGPLQQLPVLLPNYGIENTLSKRVL PWNLSSISLGWHHANFS
LPKGYGMLFADELPLL GIVWNSQIFPQATPGKTVLSLLIEGKWRESEAHAF AIAALSEYLNINQKPD AFALFSS
QDGIPQHAVGFLERKERILPHLPGNLKIVGQNIAGPGLNRCIASAYHAICDLHTEETLAQPQSSL

>core/281/1/Org1_Gene133

MFSRWITLFLLFISLTGCSSYSSKHKQSLIPIHDDPVAFSPEQAKRAMDLSIAQLLFDGLTRETHRESNDLELAI
ASRYTVSEDFCSYTFFIKDSALWSDGTPITSEDIRNAWEYAQENSPHIQIFQGLNFSTPSSNAITIHLDSPNPDPF
KLLAFPAFAIFKPENPKLFSGPYTLVEYFPGHNIHLKKNPNYYDYHCVSINSIKLLIIPDIYTAIHL LN RGKVDW
VGQPWHQGIPWELHKQSQYHYTYTPVEGAFWLCLNTKSPHLNDLQNRHRLATCIDKRSIIEEALQGTQQPAE
TLSRGAPQPNQYKKQKPLTPQEKLVLTYPSDILRCQRIAEILKEQWKAAGIDLILEGLEYHLFVNKRKVQDYA
IATQGTGVAYYPGANLISEEDKLLQNFEIPIYYLSYDYL TQDFIEGVIYNASGAVDLKYTYFP

>core/282/1/Org1_Gene229

MNKNLVAIFDYMEKEKGIQRSTIIGAIESALKIAAKKTLRDDANISVNINSRTGDIEVFCEKEIVEICQNPSKEIP
LDKAREYDPDCQIGQYMDVPFVSDNFGRIA AHAARQIIGQKL RHAERDVIYEEYRHRVNETLSGVVKRFAKG
SNLIIDL GKVEAILPTRFY PKTEKHKIGDKIY ALLYEVQESENGGA EVILSRSHA EFVKQLFIQEVPELEEGSVEI
VKIAREAGYRTKLAVRSSDPKTD PVGAFVGMGRGSRVKNIIRELNDEKIDIVNYS PVSTELLQNLLYPIEQKIAI
LEDDKVIAIVNDADYATVIGKRGINARLISHILDYELEVQRMSEYNKLL EIQLQLAEFDSPHLDQPLEMEGI
SKLVIQNLEHAGYDTIRRVLLASANDLASVPGISLELAYKILEQVSKYGESKVDEKPEIED

>core/283/1/Org1_Gene925

MSMTIVPHALFKNHCECHSTFPLSSRTIVRIAIASLFCIGALAALGCLAPPVSYIVGSVLAFIAFVILSLVILALIF
GEKKLPPTPRIIPDRFTHVIDEAYGLSISAFVREQQVTLAEFRQFSTALLCNISPEEKIKQLPSELRSKVESFGISR
LAGDLEKNNWPIFEDLLSQTCP LYWLQKFISAGDPQVCRDLGVPRECYGY YWLGPLGYSTAKATIFCKETHH
ILQQLTKEDVLLKNKALQEKWDTGEVKAIVERIYTTYTARGTLKTEAGGLTKETISKELLLL SLHGYSFDQL
QLITQLPRDAWDWLCFVDNSTAYNLQLCALVGALSSQNLLDESSIDFDVNLGLYVIQDLKEAVQA F SASDEP
KKELGKFLLRHLSSVSKRLESVLRQGLHRIA LEHGNARARVYDVNFVTGARIHRKTSIFFKD

>core/284/1/Org1_Gene657

MNHLNKEKLHIHNWQPYRACGLLSKVSGN LIEVDGLSACL GELCKISSTKDPNLLAEVIGFHNHTTLLMSLSP
LHSVALGTEVLPLRRPSLHLS DHLLGRVLD AFGNPIDKKEDLPKTHRKP LLSLPPSPMMRQPIDQIFPTGIKAI
DAFLT LGKGQRIGVFSEPGSGKSSLLSAIALGSKSTINVIALIGERGREVREYIEKHSNALKQQR TIIIAAPAHET
APTKVIAGRAAMTIAEYFREQGHEVL FIMDSL SRWIAALQEVALARGETLSAHQYAASVFHHVSEFTERAGN
NDKGSITALYAILYYPKHPDIFTDY LKSLLDGHFFLTSQGKALASPPIDILSSLSRSAQALALPHHYAAAERLRS
LLKVYNEALDIIHLGAYTPGQDEELDKAVKLLPSIKAFLAQLSSYCYLDNTLKQLEALADS

>core/285/1/Org1_Gene774

MLKPMYVLSKRLYRWVNQLIKLGD LVKNSRSFSVEWVFISALLIFGCLGCASVVKVSLVPFLLLFSFLAFPLI
LCFRGKGYALLLG VFTLYVAKYVVGETLYVSFWLSGLGVSFLLAFGLFLQG VWLAQEEEMVKGKEQLRL
SEDLDAQRSAYEDLLLTKS QEKEFLDARAQGLDRELTECQELLKAAYQKQEYLTIDLKILADQKNSWLEDY
AELHNKYIELVSKNGDVVFPWVAEPSVGESQGSERVDVSRWVSALQEKEESLERLRNEILVEKQRCS DYEHR

CQELGLLLQNFTALERRCEELQNLLNQKETQINELHQLVCKSEEKVSVEPSAHAETSCVEEKQYKGLYSQLQ
EQFLEKSETLSLVRKKLFAVQEKYLTLLKKKEELTKQDISFDDISMIQGLLERIEILEEEVSHLEELVSRSLSL

>core/286/1/Org1_Gene597

MLRQLCFQVFFFCFASLVYAAEELEVVRSEHITLPIEVSCQTDTKDPKIQKYLSSLTEIFCKDIALGDCLQPTAA
SKESSSPLAISRLHVPQLSVVLLQSSKTPQTLCSFTISQNLSDVRQKIHHAADTVHYALTGIPGISAGKIVFALS
SLGKDQKLKQGELWTTDYDGKNLAPLTTECSLSITPKWVGVGSNFPYLYVSYKYGVPKIFLGSLENTEGKKV
LPLKGNQLMPTFSPRKKLLAFVADTYGNPDLFIQPFSLTSGPMGRPRLLNENFGTQGNPSFNPEGSQLVFISN
KDGRPRLYIMSLDPEPQAPRLTTKKYRNSSCPAWSPDGKKIAFCSVIKGVRQICIYDLSSGEDYQLTTSPTNKE
SPSWAIDSRHLVFSAGNAEESELYLISLVTKKTNKIAIGVGEKRFPSWGAFFPQQPIKRTL

>core/287/1/Org1_Gene676

MTWLSGLYFICIASLIFCAIGVILAGVILLSRKLFIVHPCCLKINDNEELTKTVESGQTLLVSLSSGIPSPCG
GKATCKQCKVRVVKNADEPLETDRSTFSKRQLEEGWRLSCQCKVQHDMSLEIEERYLNASSWEGTVISNDN
VATFIKELVVAVDPNKPIPFKPGGYLQITVPSYKTNSSDWKQTMapeyySDWEHFHFLDQVIDNSQLPADSA
NKAYSLASYPaelptikfniriATPPFINGKPNSEIPWGVCSsyVfSLKPGDKITVSGPYGESFMKDDDRPLIFLI
GGAGSSFGRSHILDLLLNNKHSKREIDLWYGARSLKENIYQEEYENLERQFPNFHYHLVLSEPLPEDIAAGWDK
DDPTKTNFLFRAFNLGQLSRLDNPEDYLYYVCGPPLHNSSILKLLGDYGVERSsiILDDFGS

>core/288/1/Org1_Gene497

MTVTLPKGVFDIFPYLADAKQLWRHTSLWHSVEKAIHTVCMLYGFCEIRTPIFEKSEVFLHVGEESDVVKKE
VYSFLDRKGRSMTLRPEGTAAVVRSFLEHGASHRSDNKFYYILPMFRYERQQAGRYRQHHQFGVEAIGVRH
PLRDAEVLALLWDFYSRVGLQHMQIQLNFLGGSETRFRYDKVLRAYLKESMGELSALSQQRFSTNVLRILDS
KEPEDQEIRQAPPILDYVSDEDLKYFNEILDALRVLEIPYAINPRLVRGLDYYSDDLVEATTTTFQEVSYALGGG
GRYDGLISAFGGASLPACGFGVGLERAIQTLLAQKRIEPQFPKLRILPMEPDADQFCLEWSQHLLRRLGIPTEV
DWSHKKVKGALKAASTEQVSFVCLIGERELISQQLVIKNMSLRKEFFGTKEEVEQRLLYEIQNTPL

>core/289/1/Org1_Gene125

MFRKLFPFSKKKTGQKQRLRNNGLLQAIQSIKVLLHNEASKEACVLSYYGLLTCVPILVFFLRLSQHLFTNLN
WKEWLIKFPDYKKPIVAIVEAAYHATESNIGLVLVGSFFVFCWAGILMLLSLEDGLNKIFRTSWTPISLKRVL
SYFVITLVSPMIFIHVCgswiyITQIMPIQYAKLFSLSHSMTALYFISRFVPYLLLYLALFCCYAFLPRVAIQKTSa
LISTLIIGSVWIVFQKAFFSLQVSIFNYSFTYGALVALPSFLLLLYIYTMiYLFGGALTFIiQNRGCTFiFLGDKILP
SCYLQLITSTYILALTTRQFNEGLSPLTAQFIAKQSKVPIGEVSQCLDVLEKEGFLFPYNNGYQPVFNFSelTIK
DIADKLLHREIFKKFNPDLGITFIENSFQNIQNASKNKENLTLSEIARRIK

>core/290/1/Org1_Gene742

MVCENNILSGRGLELLKKKSNIltTPTiYsvSNHNIKLKDFSPHALSVIKTLRKAGYIAYIVGGCIRDLLLNTTP
KDFDISTSAKPEEIKaIFKNCILVGKRFRLAHIRFSKQiEVSTFRSGSTDEDVLITKDNLWGTPEEDVLRRDFTI
NGLFYDPEHEEiIDYTGGVNDLRNRYLRTIGDPFTRFKQDPVRMLRLLKILSRSPFTVETQTQEALIAcRQELIK
SSQARVFEELIKMLNSGAakNFFQLLIENHLLeILFPYMDKAFRLNRALEEQTATYLKALDDKILKKEAEYDR

HQLMAIFLPLVNFNVRYKHQHPYLSLTSVFDYIKNFLEQFFADSFTSCSKNFILTALILQMQYRLTPLIPTK
KALFFNKKLLHHTRFLEALSLEIRSIVYPKLDKVYVAWIRHHQTLKCKKDSHSQK

>core/291/1/Org1_Gene221

MISLLKMPKLSPTMEVGTIVKWHKKSNDQVSFGDVIVEISTDKAILEHTANEDGWIREILRHEGEKIVIGTPIA
VLSTEANEPFNLEELLPKTEPSNLEASPKGSSEEVSPATTPQAASATFTAFTKPEPPLSSPLVFKHVGTTNNLS
PLARQLAKEKNIDVSSIQSGPGGRIVKKDLEKAPPKSIAGFGYPESPEVPPGSYHEENLSPIREVIAARLQAAK
ISIPHFYVRQQVYASPLLNLLKELQAQGIKLSINDCIVRACALALKEFPSINSGFNSVDNKIVRFDTIDISIAVAIP
DGIITPIIRCADRKNLGMISAEIKSLALKARNQSLQDTEYKGGSFVSNLGMTGITEFTAIVNPPQAAILAVGSV
TEQALVLDGEITIGSTCNLTLSVDHRVIDGYPAAMFMKRLQKILEAPAVLLN

>core/293/1/Org1_Gene968

MFEAVIADIQAREILDSRGYPTLHVKVTSTGSGVEARVPSGASTGKKEALEFRDTSPPRYQGKGVQLQAVKN
VKEILFPLVKGCSVYEQSLIDSLMMDSDGSPNKETLGANAILGVSLATAHAAAATLRRPLYRYLGGCFACSLP
CPMMNLINGGMHADNGLEFQEFMIRPIGASSIKEAVNMGADVFTLTKLLHERGLSTGVGDEGGFAPNLAS
NEEALELLLLAIEKAGFTPCKDISLALDCAASSFYNVKTGTYDGRHYEEQIAILSNLCDRYPIDSIDGLAEED
YDGWALLTEVLGEKVQIVGDDLFVTNPILILEGISNGLANSVLIKPNQIGTLTETVYAIKLAQMAGYTTIISHR
SGETTDTTIADLAVAFNAGQIKTGSLRSERVAKYNRLMEIEEELGSEAIFTDSNVFAYEDSEE

>core/294/1/Org1_Gene962

MDIKKLFCLFLCSSLIAMSPIYGKTGDYEKLTLTGINIIDRNGLSETICSKEKLKKYTKVDFLAPQPYQKVMMR
YKNKRGDNVSCLTAYHTNGQIKQYLECLNNRAYGRYREWHVNGNIKIQAIEVIGGIADLHPSAESGWLFDQT
TFAYNDEGILEAAIVYEKGLLEGSSVYYHTNGNIWKECPYHKGVPPQGKFLTYTSSGKLLKEQNYQQGKRHG
LSIRYSEDSEEDVLAWEEYHEGRLLKAEYLDPQTHEIYATIHEGNGIQAIYGKYAVIETRAFYRGKPYGKVTR
FDNSGTQIVQTYNLLQGAKHGEEFFYPETGKPKLLLNWHEGILNGIVKWTWYPGGTLESCHELNNKKSGLL
TIYYPEGQIMATEEYDNDLLIKGEYFRPGDRHPYSKIDRGCGTAVFFSSAGTITKKIPYQDGKPLL

>core/295/1/Org1_Gene909

MKKTMMVIDTSVFIYDPEALFSFENTRIIPFPVIEELEAFGKFRDESAKNASRALSNIRLLLENAKTKVTDGVLLP
SGSELRIEVAPLSNDDRRGKLLTLELLKIIAKREPMVFVTKSLGRRVRAEALQIESRDYESKRFSFRSLYRGFRE
LQVSQEDIENFYKNGYLDLPLDVVPSPNEYFFMSAGENHFALGRYYVSEGKIIALKAMDKSVWGIKPLNTEQ
RCALDLLLRDDVKLVTLIGQAGSGKTILALAAAMHKVFDKETYNKVLVSRPIVPMGRDIGFLPGLKEDKLM
HWMQPIYDNMEVLFSINQMGNSSSEALQALMDAKKLEMEALTYIRGRSLPKAFIIDEAQNLTPHEIKTIISRAG
KGTKIVLTGDPTQIDSLYFDENSNGLTYLVGKFHHLALYGHMFMTRTERSELAAAAATIL

>core/296/1/Org1_Gene666

MLDIKIIRKTPEECETRLRKKDPKISLEPVLSLDKEVRQLKTDSETLQAQRRLLSQDIHKAKTQGV DATNLIQE
VETLAADLEKIEQHLDQKNAQLHELLSHLPNYPADDIPVSEDKAGNQVIKSVGDLPIFSFPPKHHLELNQELDI
LDFQAAAKTTGSGWPAYKNRGVLEWALLTYMLQKQAAHGFQLWLPPLLVKKEILFGSGQIPKFDGQYYR
VEDGEQYLYLIPTAEVVLNGFRSQDILTEKELPLYAACTPCFRREAGAAGAQERGLVRVHQFHKVEMFAFT

TPNQDDIAYEKMLSIVEEMLTELKLPYRLSLLSTGDMSFTASKTIDAEVWLPQGKAFYEVSSISQCTDFQSRRS
GTRYKDSQGKLQFVHTLNGSGLATPRLLVAILENNQQADGSVVIPEVLRPYLGGLEILLPKDQ

>core/297/1/Org1_Gene512

MLPLIIFVLLCGFYTSWNIGANDVANAVGPSVSGSVLTLRQAVVIAAIFEFFGALLLGDRVAGTIESSIVSVTN
PMIASGDYMYGMTAALLATGVWLQLASFFGWPVSTTHSIVGAVIGFGLVLGKGTHIYWNSVGIILISWILSPF
MGGCVAYLIFSIRRHIFYKNDPVLAMVRVAPFLAALVIMTLGTVMISGGVILKVSSTPWA VSGVLVCGLLSY
IITFYYVHTKHCSYISDTPKKGSLTYRLKERGGNYGRKYL VVERIFAYLQIIVACFMAFAHGSNDVANAIAPV
AGVLRQAYPASYSYTLIRLMAFGGIGLVIGLAIWGWRIETVGCKITELTPSRGFSVGMGSALTIALASILGL
PISTTHVVVGAVLGIGLARGIRAINLNIKDIVLSWFITLPAGALLSILFFFALRALFH

>core/298/1/Org1_Gene1025

MIMGLQSRLQHCHIEVSQNSNFDSQVKQFIYACQDKTLRQSVLKIFRYHPLLKIHDIARAVYLLMALEEGEDLG
LSFLNVQQYPSGAVELFSCGGFPWKGLPYPAEHAEFGLLLLQIAEFYEESSQAYVSKMSHFQQALFDHQGSVF
PSLWSQENSRLLEKTTLSQSFLFQLGMQIHPEYSLEDPALGFWMQRTRSSSAFVAASGCQSSLGAYSSGDV
GVIAYGPCSGDISDCYYFGCCGIAKEFVCQKSHQTTEISFLTSTGKPHPRNTGFSYLRDSYVHLPIRCKITISDK
QYRVHAALAEATSAMTFSIFCKGKNCQVVDGPRLRSCSLDSYKGPNDIMILGENDAINIVSASPMEIFALQ
GKEKFWNADFLINIPYKEEGVMLIFEKKVTSEKGRFFTKMN

>core/299/1/Org1_Gene797

MDKQSSGNSGCIWHPFTQSALDSTPIKIVRGEGAYLYAESGTRYLDAISSWWCNLHGHGHPYITKKLCEQAQ
KLEHVIFANFTHEPALELVSKLAPLLPEGLERFFFSDNGSTSIEIAMKIAVQYYYNQNKAKSHFVGLSNAYHG
DTFGAMSIAGTSPTTVPFHDLFLPSSTIAAPYYGKEELIAQAQAKTVFSESNIAAFIYEPLLQGAGGMLMYNPEG
LKEILKLAKHYGVLCIADEILTGFGRTGPLFASEFTDIPDIICLSKGLTGGYLPLALTVTTKEIHDAFVSQDRM
KALLHGHTFTGNPLGCSAALASLDLTLSECLQQRQMIERCHQEFQEAHGSLWQRCEVLGTVLALDYPAEAT
GYFSQYRDHLNRFFLERGVLLRPLGNTLYVLPPYCIQEEDLRIYSHLQDALCLQPQ

>core/300/1/Org1_Gene900

MAEISTPSLPDSSIVSQKTPPVPDPDSSPDHIPTIPTQAPFKPQRKKETPSSIVNAIAFAILAFLSCLGGVFAICLGC
SLEITVPLFILTAVFIAFTLLYFIHYLEKPKIPEPLTPPPSPTLRAPTLTPEIPAPAPGIPLPPTLPKVDRTKLTCNP
DIHYPSTYDPKACFSLLKQLFSLDPETRPEDRKYSNKLASILRSKEKSGFRFHCFCGHFSDHKILNKKSGAVV
ISSHSSMDFSTTLGRAFAVTTCLQRSCWEKIKNNIPTPEKHLPIGSCVSGPWDVEEGAQLYTSHLIVINPPTLET
LIKEKMRRAITLKDFSMEKFAFTNLVLA YLQCFDICIEHNLESVQLEVFGLNNLSADQEEFTTWESCCHLALLE
SVRILLASKEEYALS NVSVNSISQVPLQTACRALFLN

>core/301/1/Org1_Gene959

MKKQVYQWLASVVLLALTISGYAELPLSEQKVKSHTYTTLDEVKDYL SKRGFVETRKQDGVLR IAGDVRAR
WLYFREDIKNPSDKDKYNPLPVNRYRSEFYLYIDYRAERNWLSSKMNWTAIAGGENTAAGVDINRAFLGYR
FYKNPETRTDFFMEIGRSGLDLFESEVQFQRNFDGLHIYWTRELSKDYQYQVIVHGGPFVVMNMTKKHYAW
VVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWL VGKRSQVPWINGQKKPLYL

YGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFW
FAQAIAANYDPKEANGFTNYKGFSALYMYGITDSLFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF

>core/302/1/Org1_Gene837

MQSWLQSLQERNILENFTAGLESVEGPAAAYLGFDPTAPALHIGHWIGICFLKRLAALGITPIALVGGATGMV
GDPSGKQSERSLLQTSEVFDNSQKITACLQRYLPGVTLVNNADWLQEISLIDFLRDIGKHFRLGQMLVKDTIK
QRVHSDEGISYTEFSYLILQSYDFYHLFKNYGTILQCGGSDQWGNITSGIDFIRRKGLGQAYGLTYPLLNAQ
GKKIGKTESGTVWLSDLTSPFELYQYLLRLPDDTIPKIARTLTLLSNEEIQDIDRRVQTDPVAVKEFVAQDILS
AIHGDLGLEEALSVTRSMHPGNLSSLSEKDFHELFAAGMGASLDKSEVLGKRWLDLFLVLGLCKSKGEIRRLI
EQKGVYINNVPIANEHSVCEEQDICYGHYVLLAQGKKRKLVLVLN

>core/303/1/Org1_Gene829

MTVAEVKGTFLVCLGCRVNQYEVQAYRDQLTILGYQEVLDSEIPADLCIINTCAVTASAESSGRHAVRQLC
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FCSYCIIPYLRGRSVSRPAEKILAEIAGVVDQGYREVVIAGINVGDYCDGERSLASLIEQVDQIPGIERIRISSIDP
DDITEDLHRAITSSRHTCPSSHLVLQSGSNSILKRMNRKYSRGDFLDCVEKFRASDPRYAFTTDVIVGFPGESD
QDFEDTLRIIEDVGFIVHSPFSARRRTKAYTFDNQIPNQVIYERKKYLAEVAKRVGQKEMMKRLGETTEVL
VEKVTGQVATGHSPYFEKVSFPVVGTVAINTLVSVRLDRVEEEGLIGEIV

>core/304/1/Org1_Gene646

MNKKNLTICSFCGRSEKDVEKLIAGPSVYICDYCIKLCSGILDKKPSSTISSAPVSETPSQPSDLRVLTPKEIKKH
IDEYVIGQERAKKTIAVAVYNHYKRIRALLHNKQVSYGKSNVLLLGP TGSGKTIAKTLAKILDVPFTIADAT
TLTEAGYVGEDVENIVLRLQLAADYDVARAERGIIYIDEIDKIGRTTANVSITRDVSGEGVQQALLKIVEGTTA
NVPPKGGRKHPNQEYIRVNTENILFIVGGAFVNLDKIIAKRLGKTTIGFSDDQADLSQKTRDHLLAKVETEDLI
AFGMIPEFVGRFNCIVNCEELSLDELVAILTEPTNAIVKQYMELFAEENVKLVFKKEALYAIKKAKQAKTGA
RALGMILENLLRDLMFEPDPTVEAIIHQEDTIAENKAPIIIRRTPEAIA

>core/305/1/Org1_Gene60

MIKFLSQLFIRHWPRKVVS LGFAIIWILVGQSVTITRTL TNVPVRIVDLHPDQTVLGLQKSGFLNKKVSLTITG
NKNTVQDLRPSNLEVVISAA NHTESWIATIDKHNLSVDHEINIRKDIHSVDANDIFVRLTQYVTE DILLTITKP
IGSPPKGYEYLDVWP KYLNQKVSGPKEYINALKEQGLELTFNLNKISFEELERNRIAQGS HDEIIFPIPK EWKKI
LIPFENTFMDLNDPQADFLRLFLKRECIPLNLNPVFLFFPVTFIQTMNPLEYSLDPVPPIILNHGIHQINIPLYV
KDVSQRQLDVVKNNMVL TIVMPSPQDPSSINWAEFLDEKTLTENTFLQTIIAQEHGILHDIALIDEAGIRHRFRE
YLRKLALFTADGEPLNLIAEIKNNKVVIQTKTKETTKLYKKEW

>core/306/1/Org1_Gene778

MLKLQLCALFLFGYLAIVFEHIVRVNKS AIALAMGGLMWLVCFSHIPMADHMILVEEIADMSQVIFFLFSAM
AIVELIDAHKGFSVIVKFCRIQSRTLLLWALIGLSFFLSAALDNLT SIIIIISILKRLVKAREDRLLLGAICVIAVNA
GGAWTPLGDVTTTMLWINNKITSWGIIRALFVPSLVCVLVAGFCGQFFLRKRGSTLIAKDVELQSAPPKSLWII
FIGLGSLLMVPVWKACLGLPPFMGALLGLGLVWLTSDWIHS PHGEDRYHLRVPHILTKIDISSITFFIGILLAVN

ALSFANLLTDFSLWMDKIFSRNVVAIVIGLLSSVLDNVPLVAATMGMYTLPLDDTLWKLIAYAAGTGGSILII
GSAAGVAFMGLEKVDLWYFKRISWIALASYFGGLFSYFVLES LNFFI

>core/307/1/Org1_Gene146

MSSAIARDCFPSPSPQPSSTLGVHPPKYKSLILSVSLIVLGVLLLCVGMLLL VN AIFSFSVLT VGLGGAGVFLGS
LLLILGLIFFVSYHRKLSEATRSLEQKITLEYQPWADLRKELNEVQEWSN FLLDEWEDFKEVVAQHK SQFATF
EGDLLLFGREVEKYETIWKELDGRDVALLTELKNIWGPLEFLRKKGDRLQCEIDKLRKEVMKV GKSGLKLA
CELTKFKSALKDVKIEQECYRDKRKVEKLEVFPEGYRRELLEVLKTRLSVEKEIQLFEEVVS AFEEKLASLHR
TVFSEEELQEALDKAKAELLDIQVRKSVVEDLSCEPTLIQYHLLRLYE VQCRIVEQFLTQTFSSEQEKVLEEYE
ALKARIRKTLRVKLDQVRANVAFVASTTDLLSESESLDGND SVFEDAHD DFLD

>core/309/1/Org1_Gene668

MIETREEVGSANFVSLERAIEDLRAGKFVIVVDEASREDEGDLIAGEKITVEKMTFLLQHTTG VVCAALSQER
LLSLDLPPMVKDNRCRFTKPTFTVSVDAAHGVTTGVSAADR TKV VQLLADPKSKPEDFISPGHFFPLASSPGGV
LK RAGHTESTVDLMELAGLQPCGVLAELVNEDYSMMRLPQILEFARKHNIAVIPVTSIIAHRMLSDRLVSKIS
SARLP TIYGDFTIHVYESLLEGMQHLALVKGNVAGKSNVLVRVHSECVTGDILGSKRCD CGEQLSSAMSYIA
EKGTGVLVYLRGQEGRGIGLGHKVRAYALQDNGYD TVDANLAMGFPVDSREYGIGA QILVDLKLTTIKLIT
HNPQKYFGLQGFGLSITERVPLPVRISEDNEQYLRTKQERMGHWLDLPCCNNRVQ

>core/310/1/Org1_Gene876

MLCYSPTYVTDL YRISLSAEESLGGIRAFPQAESLLGGACALNFPDLEERLPDLRKELLFLGSNDRPDACGGK
FSLQLASSKECYIAALKERVYLNVTNSSRGPVYSFSPKGVPTELWIECF SVSVDGRVEVKVRLQGLHKELISKP
RDCETLFLNPPANKLDCWEIAGFRVDASFPVKQKIRRIGVDKFLLMHGGAEYADKATKERVDFVSSDEENYS
RYLAVGDVLLWDGNCWQTCGEFQGASSRAPLFEVKRIDDKVM IADLWNVGGTQRQTISLVKGVPSPIEINE
VIREIEFTGMRSWSKPIVLVGGQRLILSPDDWILRTAKGW EKLSRADQIQDYVTGKVTGPLL VFEKLEKDLRG
FVLRGHMFNAQRTL VETISLPLKQGFEP AVASQEVSSNTRSAAAH PGATNRGGS

>core/311/1/Org1_Gene931

MSQPPINPLGQPQVPAAASPSGQPSVVKRLKTSSTGLFKRFITVPDKYPKMRYVYDTGIIALAAIAILSILLTAS
GNSLVLYALAPALALGALGV TLLISDILDSPKAKKIGEAITAIVVPII VLAIAAGLIAGAFVASSGTMLVFANPM
FVMGLITVGLYFMSLNKLTLDYFRREHLLRMEKKTQETAEPILVTPSADDAKKIAVEKKKDL SASARMEEHE
ASQRQDARHRRIGREAQGSFFYSSRNPEHRRSFGSLSRFKTKPSDAASTRPASISPPFKDDFQPYHFKDLRSSSF
GSGASSAFTPIMPASSRSPNFSTGTVLHPEPVYPKGGKEPSIPRVSSSSRRSPRDRQDKQQQQQNQDEEQKQQS
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>core/312/1/Org1_Gene689

MCQRILILGTGITGKSVARFLYQQGHYLGADNSLESLSVDHLHDRLLMGASEFPENIDL VIRSPGIKPYHPW
VEQAVSLKIPVVTDIQVALKTPEFQRYPSFGITGSNGKTTTTLFLTHLLNTLGIPAIAMGNIGLPILDHMGQPGV
RVVEISSFQLATQEEHIPALSGSVFLNFSRNHLDYHRNLDAYF DAKLRIQKCLRQDKTFWVWEECSLGNSYQI
YSEEIEEILDKGDA LKPIYLHDRDNYCAAYALANEVGWVSPEGFLKAIRTFEKP AHRLEYLGKKDGVHYIND

SKATTVTAVEKALMAVGKDVIVILGGKDKGGDFPALASVLSQTTKHVIAMGECRQTIADALSEKIPLTLSKD
LQEAVSIAQTIAQEGDTVLLSPGCASFDQFQSFKERGAYFKLLIREMQAVR

>core/313/1/Org1_Gene700

MSKKRVVVTGFGVVSCLGNEVDTFYDNLLAGVSGVRPITSFPCEDYATRFAGWIPEFNPEPYVDKKQARRV
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PALIAMDFGLMGPNYSISTACATGNYCIDAAYQHLVSGRADMIICGGTEAAVNRI GLEGFIANRALSERNDAP
DQASRPWDRDRDGFVLGEGAGILVLETLESALRRDAPIFAEMLGSYVTCDAFHITAPRDDGEGITACVLGAL
NSAGIPKERVNYVNAHGTSTPLGDLSEVLAVKKAFGSHVRNLRMNSTKSLIGHCLGAAGGVEAVVAIQAILT
GKLHPTINLDNPIAEIEDFDVVANKAQDWDIDVAMSNSFGFGGHNSTILFSRYVP

>core/314/1/Org1_Gene520

MLVSIETFSSIASGSPVQKAAEACYTQYSKQPSSKEVLSSFSWIQELSLFPDRYNLATGASELIKQHWLHNNHS
LAFECILINGKYEPSLSQLPEGVIVCGIDEARGSLSSFMQGFVDNKHPLAFLNAVCSSEDRGVVIYIPEEMQTS DP
IFVRHISFPTVSDHDVIFSPRIVVILGQRASAIQISHDVDLEMVGSSKTIVNGVTELFVGEGADLTVFMVPGYS
EEDTLWSSTIATVEKDAICRMTQNLLESCQGFGWFDNTSYIVGKKGHAESLVLVQSPRKTWVNNLMSHDAE
ETVSRQNIKSILYSGHFLFEGTISISSQGDLSDANQKHDTLLSSEARVSTFPRLEIETDEVKASHGATVGPLDP
QQIFYMRSRGMTEAEAQEKLIHGFLKQGLVSDTFLGSSFQLNQTS

>core/315/1/Org1_Gene872

MRYHKYFRYVNSWVFLVVLTLMLLSVVVISSMDPTAMLVTSSKGLLTNKSIMQLRHFALGWVVFICAYFD
YHLFKRWAWVLYFFMICALVGLFFVPSVQNVHRWYRIPFIHMSVQPSEYGKL VIVIMLSYILES RKADITSKT
TAFLACLVALPFFLILKEPDLGTALVLCPVTLTIFYLSNVHSLLVKFCTVVATIGIIGSLLIFSGIVSHQKV KPY
ALKVIKEYQYERLSPSNHHQRASLISIGLGGIRGRGWKTGEFAGRGWLPYGYTDSVFSALGEEFGLLGLLFTL
GLFYCLICFGCRTVAVATDDFGKLLAAGITVYLAMHV LINISM MCGLLPITGVPLILISYGGSSVISTMASLG V
LQSIYSHRFAKY

>core/316/1/Org1_Gene377

MKLWMKIFIGLVGVTLGLVLEDKAIFFKPIGDIFLNLLSMVVYPLVFCSMVLGIASISDMKKLGRIGIKSVGL
YLGTTALAIVIGLCFAWIFSPGN GCDFAQAQSMDSAVTVIDSNKTAAYFLSIIAQVFPSNPVRSFAEGNILQIIIF
AIFLGIALRLSGERGRPVERFIDGFSEIMLRMVNMIMSFAPYGVGASMAWISGNHGLGV LWQLGKFIIAYYLA
CLFHATLVFGGLVRFGCKMSFSKFLSSMMDAISCAVSTASSSATLPVTMRCVSKNLGVSAEVS GFVLPLGAT
VNMNGTAIFQGMAAVFIAQAYNCPLSLSSLLLLVVTATFSAVGSAGVPGGGMITLGSVLASVGLPIQGIAILA
GIDRLRDIVGTPMNILGDVAVVATYVASGEGELSPYESIKQESVETT

>core/317/1/Org1_Gene591

MKKIFYSFVLLSCIFPYVGCAQVFVGLDRIFSEGEYTRCIQGKKIALISHSAAINSRGQDALSVFYSRKHDCTVE
ILCTLEHGYYGATPTETVGNQPSRYPNLRSVSLYGVKEVPKEVAEHCDVFVYDVQDIGVRSYSFVTVLMQIV
KASERYGKQLIVLDRPNPMGGRIVDGPLPNPTTSGSLAIPYCYGMTPGELALFFKKTYAPNANVVVIPMKGW
NRSMTFDETGLIWMP TSPQMPDPQSPFFYAATGILGALSVASIGVGYTL PFKVLGAPWMDGEKVADELNRM

KLPGVLFLPFFYEPFFGKYKMEMCSGVLLVLQDPKIFYPVETQCTIWGVLKALYPKQVEQTLKSIERIPARRSS
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>core/318/1/Org1_Gene874

MKKNASHKTNDKKSLSIWSIGGSIFAMFFGAGNIVFPLALGYHYNAHPWSAYFGMMLTAVCVPLLGLVSML
FYSGDYQKFFFSIGRIPGMIFITAIILLIGPFGGIPRAIAVSHATLISLSEHKSAFIPSLPIFSAICCVLIYIFSCKLSRL
IQWLGSVFFPIMLVTLWVIIRSFMIPTHPMVQEFIPNARQAWLAGFIEGFNTMDLLAAFFFCISVLISLRQLVA
EEKHPTEEEIPLSFQGISKKNKRSLALGFFLAAILLGMTYLG FVLSAARHAGLLVNVSKGHILGRISAIALGPNS
ILAGVSVFIACLTTEIALVGIVADFLARVVSFKKLNYSASAVICTLIPTYLISILNFETISHLLLPLLQLSYPALIVLA
CGNIAYKLWNFRYSPVLFYLTLSLTIVLKLVN

>core/319/1/Org1_Gene160

MDKETLENIYRHFRYRFLKLNILPAFLGLLLLCSPNTLNYTQVDVIFSDRLCSCLLIFLAIASLTKRSLLWLGAP
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EARYLTASSLGITSSQSSNLLLLYSSIMTVYSLLVVLSLAGSERRWHTRPKIVIATALALTGVIIITLLPIILHQLR
YDCWLCLCLTIEPALAVVFAYDETRATLRYISQFLGDKRALTRASFFGSEYYKHTLSWEERTVLPLRKAYKQ
AFEGISFPINQLLAILVATVFVKVNSSMGLPTFPRNFLNICCWFIIVLFILAFaesLRHLRWMNLIFSAAILFSPVL
FHIPVESPMFLPIIVTGLILILSIGKRRRTKRKL

>core/320/1/Org1_Gene287

MIPTMLMFFHICFTLCSGFISLSQIALFSLPTSLISHYKRSKSKKQQRVATLLLHPHLLITLIFCDIGLNIAIQNCF
AILFGDAASWWFTVGLPLAITLILGEILPKAVALPFNTQIASSVAPLILCVTKIFKPLLHWGIVGINYVVQWILS
KQQIDIIQPQELKEVLQSCKDFGVVNQEEsRLLYGYLSLSDCSVKERMQPRQDILFYDIQTPLENLYLLFSKQH
CSRVPICNDNLQNLLGICTARSLLLHDKPLQSSDDLPLKKPYMPETISAKMALCQMAAEDETGMIIIDEY
GSIEGLITQEDLFEIVAGEIVDQRDNKILYTTSGADVIIASGTLELREFSEIFDINLPTNNNIATIGGWLIEQIGTIP
TTGMKLSWNNLLFQVLDAAPNRIRRVYIRKLYD

>core/321/1/Org1_Gene846

MDESDGEEASKDSAFSASFSEYFVKSSTRESKNTVTHSTASRTLYILRQDCSYDPRALKVDDEFWVEKRL
DAKNPDSLNAFVKEVGTHYVASVTYGGIGFQVLKMSYLQVEELEKEKISISVAAASSLLKSKTSNATEKGYS
SYQSESSAQTVFLGGTVLPDLQQDKLDFKDWSEsIPNEIPLAISVSSITDLIPELFPSEDAQVLSQKKSALGQV
ILNYLESHKPKEEGPKPVQITSGFNSSSSVFTLQAAKAPKTVSFPYIDYWSTIPYLFPTLKETSGAQPLSFYLR
DDIFEQQNLVHNTSYILASTSVRLGYFGDSYRDYDALSFYGSWPQAYFDWAGYKDRCTWTLEKLNTTGDLF
IRSGDEIRLKHNTSGKYLATTSMsDGYQTLTCTTQTSDSVFIITV

>core/322/1/Org1_Gene751

MNLPVSLACLLLSGCVFFLGVFVSSSLYARKKRAFLEKIQKLEHENQLLQTSNLNLSRHQEQLIEDFSNRLALSS
HKLIKDMKEEAQNYFGDTSKSFQSILSPIQTTLTTFKQSLETFETKHAEDRGRLEKEISQLLAVEKKLEHETHV
LTDILKHPSRGRWGIEQLERILELAGMLKYCDYDSQTSAQGAFRADIIIRLPQDRCLIIDAKAPISDSYFSVE
EIDKGDLDVKIKEHIKTLKSKSYWEKFHQsPEYVILFLPGESLFNDAIRLAPELMEIGASSNVILSSPLTLLALLK

TIAYMWKQENLQKQIQEVSLGKELHRRRLQVVFTHFQKIGKNLNQTVQSYNDMTSSFQYRVLP TLRKFEGLE
TSSSHQIEEPTPIESLATSFPHTCDIDTNLAVIESLEKQD

>core/323/1/Org1_Gene828

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MHFLDSRTQVVIEKNRAYLFSLPVDSSLSEAITNFVRDLPFICAVEICERPYGECITRSSAERPLLPKEKTLGMPI
FCGKEGVWLPQNTILFSPLIADPRQVTNSAGIRFNEKVVGNRVGATIFGGDFILLRLFDVSRFHVDCDFGIQGG
VFSVFDLDHPESCMVNSDFFVAGLWSGAIDKWSFRFRLWHLSSHLGDEFILTHPNFPRFNLSDEGVDLFISFR
YTPQIRLYGGCGYIVSRDLTFPERPFYCEWGAELRPFGLREGNLHAQPIFAMHFRCWEEQKFGLDQSYILGME
WAKFQEIGRKIRAVLEYHQGFSKEGQFIREPCNYYGFRLTYGF

>core/324/1/Org1_Gene645

MTTIAIEAAKKVLIKL RNAGYQAYFVGGCVRDMLMNRPLEDIDIATNASPTIVSTIFPDVISIGVAFGIIVVKQD
GRLFEVATFRSDGEYKDGRHPDRIIFSSMREDALRRDFTVNGMYYPFEDKVDFDVEGTRDIEKKVIRAIGHP
RLRFSEDKLRILRAIRFSSSLGFTLDPTTERAIKEAPALVNSVSPERIWQELKKMLKRQPYGALSLLLKLKVLIF
IFPELRDIPYSLRRTTIEFARKFNPTHFPEILFLLPLFQGVSEEAATVAFGRRLISNKELKLIESWYEALPHFQNQS
GNRVFWAHFLASPTAPLFLELFSALQKDPSRQQHFISRVQELESRLQFILRIKTSSPVVSAPDLIAKGISPGRLL
GDLLREAEILSIENECLDKEKILLLLQEKGFWK

>core/325/1/Org1_Gene519

MKNLKEDFPIFAAKAKENEPFIYLD SAATTQKPQQVIDAVANFYTSSYATVNRAIYSSSRNVTEAYA AAVREK
VRKWVSAASDSEIVFTRGTTAGLNLLAISVNDLWIPKGGVVLVSEAEHHANVLSWEIACRRRGSLVKKIRVH
DSGLIDLDDLEKLLNEGAQFVSIPHVSNTGCVQPLQQVAELVHRYDAYLAVDGAQGAPHLPIDVQLWDVD
FYVFSSHKIYGPTGIGVLYGKKDLLDQLPPVEGGGDMVAIYDHQNPEYLPAPMKFEAGTPNIAGVLGLGAAL
DYLDGLSAKFIYDKEIALTTYLHKELLEIPGVEILGPSIEEPRGALIGMTIDGAHPLDLGFLDLRGIAVRTGHQ
CAQPAMERWNVGHVLRVSLGIYNDEDDIDQFILVLQDSL DKIRR

>core/326/1/Org1_Gene145

MVVVALFILGIFFLSGSLAFLVHTSCGVLLGAALPILCIGLVLLAVALIVFLCHKHKTRQDL DYYDQDLDSLVI
HKKEIPNDISELRVTFEKLQNL FQFHTKDFS DLSQELQGKFINCMEKWL TLEDEVTKFLIVRDRFLETRRNFTT
FGEQVKGIQSNIFDLHEEKSSLYLELYRLRKDLQVLLNFFLLPPGILKVDYDEIEAIKGLFIRLTSRLDKLDVKA
QERKKFINEMSREFKEVEKA FDIVDRATKKLMDRAKKESPARLFMGRTESLLEMKKNEEALKNQGLDPENL
SHPELFSPYQQLLILNYLNSEIVLHHYEFLISGTVTSGLTLEECENRMRAASTGLNALLVRKLQFRGAIKSAYF
EKLTEIEKELRSLQDVIKSLELELIHKIKDIVTEET

>core/327/1/Org1_Gene264

MTDSNPLPSYTDASLYRTPAKHSYPIRLPLNRTDRIEKILKIVTLTLALACALGFSIAAGILAMPIFS AVVVITLA
IAAVSLYSLLKKPKLYEILPQIEPESEQSSLSPPQPPEQQDLPLQIDPLDPESLPEVSLADLTPPEELTAITVTP
GYEALLEQNWDLLPSLAAVDPSFTTETPQQPCFIWKLKDSKLIFISTSGDIAVPRIKTQGRVMIVNAANENISR
EGGGTNKALSLATSLQCWNASRLPRAHSRSGSQLQPGECRS AKWENS DHTSNDHVP GKAHFLAQLLGPEAA

KCNNDPKQAFEVSKKAFHNLFQEAEIIGVDVIQLPLIGCNLFAPSRLNLGKTRAEWIEAIKLALITSLQDFGW
EQDNQEEQKIIILTDKDQPPHPPRFDLTP

>core/328/1/Org1_Gene921

MKKQRSHYTKNNLLLLLSILVGLGLGSVQSPWIVYSAECIANTFLKFLRLLSIPLVFCALGSTITSIQNFNTMVT
LGKRILYYTLLTTVIAASIGLLLFFLLRPQMITQDALATTTKCNPLGYLDVLSDTLPENIFKPFLQGNVISAACL
AVLLGTASLFLQEKEKHFNQFFNSFFSIFLNLARGLKLLPIAMLGFSVILFKELKDQSNLTMFAKYLLCVIG
ANLAQGFIPLPILLKINKVSPLKVAKAMSPALVTAFSSKSSAATLPLTMELAEDDLKINKNLSRFSFPLCSVIN
MNGCAAFILITVLFVATSNGMIISPLMSLGWIFIATLAAIGNAGVPMGCYFLTLSLLTSMNVPLSILGLILPFYT
VIDMIETSLNVWSDCCVVSLAN

>core/329/1/Org1_Gene288

MTNSALFWIGVNIICIVLQGFYSMMEMACVSFNRVRLQYYLTKDHKKARYINFLIRRPYRLFQTVMLGVNIA
LQVGSESSRNCYRALGITPDYAPFTQIFIVVIFAELLPLTISRKIPEKLALWGAPILYYSHYIFYPLIQLIGSLTEGL
YYLLNIRKEKLNSTLSRDEFQKALETHHEEQDFNTIATNIFSLSATCADQVCQPLEQVTMLPSSANVKDFCRTI
KNTDINFIPVYHKARKNVIGIAHPKDFVNKALDEPLINNLHSPWFITAKSKLIRILKEFRDNRSSVAVVLNASG
EPIGILSLNAIFKILFNTTANIAHLKPKTISVIERTFPGNSRIKDLQKELDIQFPQYPVETLAQLVLQLLDSPA EVGT
SVIINNLLLEVKEMSLSGIKTVSIKNLLS

>core/330/1/Org1_Gene511

MDKLTVQDLSPEEKKVLVRVDFNVPMQDGKILDDIRIRSAMPTINYLLKKHAAVILMSHLGRPKGQGFQEEY
SLQPVVDVLEGYLGHVPLAPDCVGEVARQAVAQLSPGRVLLLENLRFHIGEEHPEKDPTFAAELSSYGDFY
VNDAFGTSHRKHASVYVVPQAFPGRAAAGLLMEKELEFLGRHLLTSPKRPFTAILGGAKISSKIGVIEALLNQ
VDYLLLAGGMGFTFLQALGKSLGNSLVEKSALDLARNVLKIAKSRNVTIVLPSDVKAAENLQSKEYSVISIDQ
GIPPHLQGFDIGPRTTEEFIRIINQSATVFWNGPVGVEVPPFDSGSIAIANALGNHPSAVTVVGGGDAAAVVA
LAGCSTKVSHVSTGGGASLEFLEQGFLPGTEVLSPSKS

>core/331/1/Org1_Gene870

MSTMQNCPHFGVCGGCSFPQSNYSDSLKKKEELLHQLFAPLVPSDMIAPIPCSPSLRGRNKMEFSFFQTYEGE
KSLGFISSTKPKKGIPVTTCLLIHEQTMDILKLTREWWDKHPELMAYFPPKNKGSLCTLTVRTGSPQQNFMVI
LTTSGTPEYRVNEACIDEWKEILLSSSLNIASIYWEEKVAARGISTYYETKLLYGAPSIQQKLSLPSDGNSASFS
LRPRSFFQPQITQAAKIIETAKEFINPEGSETLLDLYCGAGTIGIMLSPYVKNVIGVEIIPDAVASAQENIKANNK
EDCVEVYLEDAKAFCKRNENCKAPDVIIIDPPRCGMQSKVLKYILRIGSPKIVYISCNPKTQFQECADLISGGY
RIKKMQPIDQFPYSTHLENIILLEREIDL

>core/332/1/Org1_Gene575

MLLVRKWLHTCFKYWIYFLPVVTLLLPLVCYPFLSISQKIYGYFVFTTISSLGWFFALRRRENQLKTA AVQLL
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KMQVDSLIQECGEKTEEVTNLNRELAETLAYQQALNDEYQATFSEQRNMLDKRQIYIGKLENKVQDLMYEI
RNLLQLES DIAENIPSQESNAVTGNISLQLSSELKKIAFKAENIEAASSLTASRYLHTDTSVHNYSLECRQLFDS

LREENLGMLFVYARQSQRAVFANALFKTWTGYCAEDFLKFGSDIVISGGKQWMEDLHSSREECSGRLVIKT
KSRGHLPPFRYCLMALNKGPLCYHVLGVLYPLHKEVLQS

>core/333/1/Org1_Gene64

MRMLQISMLLLALGTAINSPAIIYAADSQSVSFPEQLPSSFTGEIKGNHVRMRLAPHTDGTIIREFSKGDLVAVI
GESKDYYVISAPPGITGYVFRSFVLDNVVEGEQVNVRLPSTSAPVLVRLSRGTQIQPASQEPHGKWLEVVLP
SQC VFYVAKNFVANKGPIELYTQREGQKKIAMDLINSALNFAHIELEKSLNEIDLEAIYKKINLVQSEEFKDVP
GIQGLIQKALEEIQDAYLSKSLESQNTSIASSQCSTPKVSSSEVTTSLLSRHIRKQTALKTAPLTQGRENLEYSLF
RIWASMQQGNDHSEALTQEA FYRAEQKKKQVLAGVLEVYPHVVKNNPGDYLLKAQENTIAFLYGTSINLEQ
WLGKRVTVECLPRPNNHFAFPAYYVVGIKEAS

>core/334/1/Org1_Gene236

MAASGGTGGLGGTQGVNLA AVEAAAAKADAAEVVASQEGSEMNIQQSQDLTNPAAATR TKKKKEEFQT
LESRKKG EAGKA EKKSESTEEKPD TDLADKYASGNSEISGQELRGLRDAIGDDASPEDILALVQE KIKDPALQ
STALDYL VQTTPPSQGKLKEALIQARNTHTEQFGR TAIGAKNILFASQEYADQLNVSPSGLRSLYLEVTGDTH
TCDQLLSMLQDRYTYQDMAIVSSFLMKGMATELKRQGPYVPSAQLQVLM TETRNLQAVLTSYDYFESRVPI
LLDSLKAEGIQTPSDLNFVKVAESYHKIINDKFPTASKVEREVRNLIGDDVD SVTGVLNLFFSALRQTSSRLFS
SADKRQQLGAMIANALDAVNINNEDYPKASDFPKPYPWS

>core/335/1/Org1_Gene843

MVYFMVFSPPSES VVKANSVVR SNFCYFLENKFVSPSESTEVMFSEIMKGRVPDIESLFD RPTDMMMTGFKA
AQNLGNLFNSFGILIMCFSQCKSCQTPEKETS AIVLGATLLFFVIALILGPTLGALVYCA YKVYTLGKMIYSLN
KAKAKVLRHPAQNVFHRAAGVATIRSSEEAVKACKLYKSAMIGSLVVS LIASLALIALTAGIVLV LFFVAPGA
APVITAAMMGCCAAGGGALLISLLGLWIAIVRKAKHQEACVGH LTNVVLHTAVSEALLHDPSHFQTNALAR
DLFLTDCLSHYGH LFSNEEVAQLVQGGAPGGGSRPSQHYGGSSDYQNR RGNGNFGGSHFGGGGGFAGSHF
GAGYPTAPT MPSAPPPFPPPAYDTIYG

>core/336/1/Org1_Gene359

MLSVTIVLVGLEMARSKVSKRDSKILDILFATTELYLKTGQPVGSKTLKESFCSDLSTATIRNYFAELEAEGFL
KKNHTSGGRIPTDLALRH YVDHQEECPAEISAPIFDKISQLPSES RNIKD LQKATELLGEILDLP TFFSSPRFEN
DSVTNIQITQVDKQRAV TILSTEFQGIFTDTLWLPEACD TLSIKRIEKFLQNYIRKLPTNEELSKKEEHL SMSLY
NEVVVRYLTRYCNFSEEDLYQTGMSKLLKYEAFKDPEVLALGLSLFENRRQMCELLNIGMHKGRATAFIGK
ELSDILGTSNPGCSVITIPYYMNR SPLGALGILGPINLPYKEALPLLKLFANKINETLTQSFYKFKLSFRRPLTSN
CKLSNEPILRTEYSSIKLLPSKETL

>core/337/1/Org1_Gene354

MRRNPHFSLLKPQYLFSEISKKLAQFRKENPEISVIDLSIGDTTQPLCRSITQAIKEFCVSQEKQETYRGYGPET
GLEKLRTKIASEVYENRISPEEIFISDGAKPDIFRLFSFFGSEKTLGLQDPVYPAYRDIAHITGIRDIIP LACRKET
GFIPELPNQQLDILCLCYPNNPTGTVLTFQQLQALVNYANQHGTVLIFDAAYS AFVSDPSLPKSIFEIPEAKYC
AIEINSFSKSLGFTGMRLAWNVIPKELTYDNNEPMINDWKRLFATT FNGASLLMQEAGYYGLDLFPTPPAISL

YLTNAQKLKKSLETAGFSVHGGDHAPYLWVELPEGISDEEAFDFFLHQYHIAVTPGHGFGSCGQGFVRFSAL
TQPQNIALACDRLCTASLKETMVLA

>core/338/1/Org1_Gene744

MSNKVLGGSLLIAGSAIGAGVLAVPVLTAKGGFPPATFLYIVSWLFSMASGLCLLEVMTWMKESKNPVNML
SMAESILGHVGKISICLVYLFLFYSLLIAYFCEGGNILCRVFNCQNLGISWIRHLGPLGFAILMGPIIMAGTKVID
YCNRRFFMFGLTVAFGIFCALGFLKIQPSFLVRSSWLT TinaAFPVFFLAFGFQSIPTLYYYMDKKVGDVKKAILI
GTLIPLVLYVLWEVVVLGAVSLPILSQAKIGGYTAVEALKQAHRSWAFYIAGELFGFFALVSSFVGVGVALGVM
DFLADGLKWNKKSHPF SIFLTFIPLAWAVCYPEIVLTCLKYAGGFGA AVIIGVFPTLIVWKGRYGKQHHRE
KQLVPGGKFALFLMFL LIVINVVSIYHEL

>core/339/1/Org1_Gene255

MVNIQPVYRNTQVNYSQATQFSVCQPALSLIIVSVVAAVLAIVALVCSQSLLSIELGTALVLVSLILFASAMFM
IYKMRQEPKELLIPKKIMELIQEHYPSIVVDFIRDQEVSIYEIHHLLISILNKTNVFDKAPVYLQEKLLQFGIEKFK
DVHPSKLPNFEEILLQHCHPLHWLGRLVYPMVSDVTPGTYGYYWCGPLGLYENAPSLFERRSLLLLKKISFGEF
ALLEDGLKKNTWSSSELVQIRQNLFTTRYADKEEVDEAELNADYEQFDSLLHLIFSHKLS

>core/340/1/Org1_Gene563

MSFFNHIPTFSPDAILGLQNVFFADKRPEKVNLVIGVYEHPPQKRYGGLSCIRKAQTVILEEEQNKSYPISGLQI
FLDEMRELVFGAVDPSAIVGFQSLGGTGALHLGARLLSVAKGSGKVYVPEQTWSNHIRIFSQEGLEVIRYPYY
SKEQKQLLFEPLIAFLKEVEKNSVILLHGCCHNPTGVDFTEDMWKELAILMKERELIPFFDTAYQGFAHGIEL
DRKPIEIFISEGNTVLVAASSSKNFALYGERVGYFAVHSTFTDELVKIHSFLEEKIRGEYSSPQRWGVEIVSTILS
NPYLKEEWQSELNFIRESLGKMRTFRVQALRKVAGHTFDLLSQHGFFAYPGFSDKQVFLREQHAVYTTAG
GRMNLNGITEKNIDHVVSFIQAYEL

>core/341/1/Org1_Gene144

MVVSIIYSEILSFSELTSCKHSLFPFGPIETASIRIHHVFNVVIVCLIIILGTLFVCLGMVFLGVFSTYLLGMSSMILG
LLISISGLALLKFKERYGLEPKELFGVEGGFDKKLPSEIIQMMDQIADLARELDLEQKKDTLIRGFSARLDVLE
GSKTEKKQILKIGVPRNLSEIQERAQE QNSILEQCKEALLFRRKSAQEIFKKLYDRKAAFWR SYREDLWCYSEI
HVSKKALS NLYIGDVFEGTAPHFLMEAYAMC RTAKNLRNYVKVCVEDMRVNEEKKRAKQLSVSELLCCCT
EIETDLENETNLFTSDSEDL EEYQIHCIRVTMLHALWAIYNDEVVSRKPIDTLDRVRARMAVEDCIETFEELQ
MCVVHTKTLELEIAQLYVDILLEA

>core/343/1/Org1_Gene39

MSKETFQRNKPHINIGTIGHVDHGKTTLTAAITRALSGDGLASFRDYSSIDNTPEEKARGITINASHVEYETPN
RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSATDGAMPQTKEHILLARQVGVPYIVVFLNKVDMISQE
DAELIDL VEMELSELEEKG YKGCPIIRGSALKALEGDANYIEKVRELMQAVDDNIPTPEREIDKPFLMPIEDV
FSISGRGT VVTGRIERGIVKVSDKVQLVGLGETKETIVTGVEMFRKELPEGRAGENVGLLLRGIGKNDVERG
MVVCQPNSVKPHTKFKSAVYVLQKEEGGRHKPFFSGYRPQFFR TTDVTGVVTLPEGTEMVMPGDNVELDV
ELIGTVALEEGRFAIREGGRTIGAGTISKINA

>core/344/1/Org1_Gene1007

MFEFRFPKIGETSSGGSSIVRWLKNLGDHVARDEPLIEVSTDKIATELPSPKAGRLVRFCVNEGDEVASGDVLG
LIELEEISEADDESTSCPLTSCETKSEAGSSSSSVWFSPA VLSLAQREGIGLDNLQKIAGTGKGGRVTRQDLEA
YISESQQVSIPEIFQGEVNRIPMSPLRRAIASSLSKSSDEVPHASLVVDVDVTDLMHLISGERQRFLDTHGVKLT
ITSFIVQCLAQTLRQFPLLNGSLDGT TIVMKKSVNVGVAVNLNKEGVVVPVIHNCQDRGLVSIKALADLSSR
ARLNKLDPSEVQDGSVTVTNFGMTGALIGMPIIRYPEVAILGIGTIQKR VVVRDDDSLAVRKMVYVTLTFDH
RVLDGIYGSEFLTSLKNRLESVTMG

>core/345/1/Org1_Gene16

MDYYISILGISKTASAEI KKA YRKLAVKYHPDKNPGDAAAEKRFKEVSEAYEVLSDPQKRDSYDRFGKDGPF
AGAGGFGGAGGMGNMEDALRTFMGA FGGEFGGGSFFDGLFGGLGEAFGMRS DPAGARQGASKKVHINLTF
EEAAHGVEKELVVS GYKSCETCSGQGAVNPQG I KSCERCKGSGQVVQSRGFFSMAS TCPEC GGEGRIITDPCS
SCRGGQGRVKDKRSVHVHIPAGVDSGMRLKMEGYGDAGQNGAPSGDLYVFIDVESHVPVFERRGDDLILELPIG
FVDAALGMKKEIPTLLKTEGSCRLTVPEGIQSGTILKVRNQGF PNVHGKGRGDLLVRISVETPQNLSEEQKEL
LRTFASTEKAENFPKKRSFLDKIKGFFSDFTV

>core/346/1/Org1_Gene123

MSSPVNNTPSAPNIPIAPTTPGIPTTKPRSSFIEKVIIVAKYILFAIAATSGALGTILGLSGALTPGIGIALLVIFV
SMVLLGLILKDSISGGEERRLREEVSRFTSENQRLTVITTTLETEVKDLKAAKDQLTLEIEAFRNENGNLKT TA
EDLEEQVSKLSEQLEALERINQLIQANAGDAQEISSELKKLISGWDSKVVEQINTSIQALKVLLGQEWVQEAQ
THVKAMQEIQALQAEILGMHNQSTALQKSVENLLVQDQALTRVVGELLESENKLSQACSA LRQEIEKLAQ
HETSLQQRIDAMLAQEQNLAEQVTALEKMKQEAQKA ESEFIACVRDRTFGRRET PPTTPVVEGDESQEEDE
GGTPPVSQPSSPVDRATGDGQ

>core/347/1/Org1_Gene622

MPRYRYTYLDPKERRKRGYLEALHIQEAREKLAQENIQVLDIREVALRRMSIKSTELIVFTKQLLLLLRSGLPL
YESLVSLRDQYHEQKMGLLLTSFMETLRSGGSLSQAMAAHPNIFDHFYCSGVAAGESVGNLEGCLQNIIVVL
EERAQITKKMVGALSYPVLLVFSFAVMLFFLLGVIPSLKETFENMEVKGLTKIVFGVSDCLSAYRYLFLGFA
SALITVGILMRHRIPWKKILEKLLFALPGTKKFVVKVAVNRFCSVASAILKGGGT LIEGLDLGCD AIPYDRLKT
DMRDIVQAVIGGGSLSQELAQRSWVPKLAIGMIALGEESGDLADVLGYVAHIYNEDTQKTLASITSWCQPVI
LIFLGGLIGVIMLAILIPLTSNIQTL

>core/348/1/Org1_Gene652

MHPKIEKRNSLPLTAVAPVFEESYHPSVATTVDYVDATTLSRH LTVLKDV I KEARNLDLGKAFLTSMKQGFI
NTGT ELAIIQASLADQSSRESRKKEEKIFHQHLGKAAPQAATATSGVQPTADPVADKMPLQSAFAYVLLDKYI
PAQEEALYALGRELNLSGYAQNLFSPLLDMIKSFNSAPINYNLGSYISQTSGTANFAYGYEMILSRYNNEVSQ
CRLDIAS TVKAKAALANMSASVKANVSLTDAQKKQIEDIIASYTKSLDVIHTQLTDVMTNLASITFVPGLNKY
DPSYRIVGGDLSIIALQNDEKVLVDGKVDITTAVNEGGLLNFFTTVLTDVQNYGDLAQTQQQLMLDLELKAM
QQQWSLVSASLKLLNGMYTTVISGFKN

>core/349/1/Org1_Gene524

MKKLLKSALLSAAFAGSVGSLQALPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFD
RILKVDAPKTFSMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG
YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGCATLGAEFQYAAQ
SKPKVEELNVICNVSQFSVNPKPGYKGVAFFPLPTDAGVATATGTKSATINYHEWQVGASLSYRLNSLVPYIG
VQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVG
ATLVDADKWSLTAEARLINERAAHVSGQFRF

>core/350/1/Org1_Gene992

MMKQGVGQDAKELYTFLSRGNEHYQPCLWFSLEEELGFLFDAKMLCAPLSEDHYCHSYLVDLVDQHLKDL
ILSMFLDPQNISAGELLKVSINVGDSSFPLQQKDFLSMVLRLDETGKNVVVVFKGVLSLPATQVCKLVEELNSK
DYSYLNIFSCHGDSSPQLLFRKELEGTSGRYFTVICALYLGDTDMRSLQLASERIMVSREFDLVDAYAARCKL
LKIDHTNWRPGTFSRHADFADAVDVSAGFNSREFKLITQANQGILESSELPLPSKTFWEGFLAFCDRVTVTRH
FIPMLDAAIKQAVWTHKHPSLIDKECEALDLKTQCLPSIVSYLEYVTNSHEKTSKGPFIQKEIADCSPLKEALF
PGSDEDVPSTSEDPSDDHPSDLEDS

>core/351/1/Org1_Gene509

MGTPISGNDGDRNTISDPLEESAAEEGDSLEDREVSESATQVIETIADTGIPEATPSEGTSNDLNSDLVDRVEY
EARGSLTTMLARIRKAVSQIWMHVKTKRHPKEQGVRSLGDIPCDLLKATRLPKETAEPYFYALETALASC
RSFFFHVFLRLFTLLRRQHPEAPLDLCGTDPISEAAVAFALILRSCCKWVATDAVQEGLPLEVIEEAGMYNA
FSLEATTTVEEVSKRLSELLYSDKRIDGLANVRGITKIITSPYLGAGQCVSVVDNLKTYDLGRNYTQVLACAS
QIDEFADKGENEALVMKDILYLVRQDRSKELGDFLMMWSEEHASEVNYDVVLAILEVNLPILEEDYRSHPLA
YQKKLNYVICQFFCSERLTSIEPKD

>core/352/1/Org1_Gene367

MLHILLAIFCILLFLAFGLTQPSCHGSSKFLKTLNQRFFKDKGREYPPFPSAPTILATLLCILYGALGTKLYTLLP
PKTAHKDLLFWPLYSLSALIAYGFLPPWISTKVPKETTAHLRFLASVFQLGLFPLQLLFYRRRPNQVRSSTSF
QSQLSEALSAFDNLIVREVMIPKVDIFALPEETTLQEALVLVSEEGYSRVPVYKKNLDNITGILLVKDLLLLYT
SSHDLSQPISSVAKPPFYAPEIKKASSLLQEFRQKHRHLAIIVNEYGFTEGIATMEDIIEEIIIEIADEHDVQENTP
YKKIGSSWIVDGRMNISDAEEYFNLKIDHENSYDTLGGHV FHKVGAVPQKGMRIHHENFDIEIITCTERNVGK
LKITPRKRKFNIS

>core/353/1/Org1_Gene431

MAIKNILVVDDEPLLRDFLSELLTSQGFIPDTAENLRNALQMIRSRDYDLVISDMSMPDGSGLDLIKIKQSSPH
TPVLVVTAYGSIENAVEAMHQGAFNYLTKPFSSEALFAFISKAEEELKNLVHENLFLHSQTTTPDSHPLIAESKA
MKDLLAIAKKAASSSANIFIHGESGCGKEVLSFFIIHNSPRANHPYIKVNCAAI PETLLESELF GHEKG AFTGA
TTKAGRFELAHKGTLLLDEITEVPVNLQAKLLRAIQEKEIEHLGGTKTLSVDVRILATSNRKLKEAIDDKSFR
QDLYYRLNVIPLHLPLLRDRQDDILPLANYFLNKFCRMNNTPLKTLSPKAQELLNYPWPGNIRELSNVLERV
VILENTSLLTEDMLALA

>core/354/1/Org1_Gene746

MHLHEYQAKDLLASYDVPIPPYWVVSSEEEGELLITKSGLDSAVVKVQVHAGGRGKHGGVIVAKSSAGILQ
AVAKLLGMHFTSNQTADGFLPVEKVLISPLVAIQREYYVAVIMDRKHRCPVLMMLSKAGGMDIEEVAHSSPEQ
ILTLPLTSYGHIYSYQLRQATKFMeweGEVMHQGVQLIKKLAKCFYENDVSLLEINPLVLTLEGELLVLDSKI
TIDDNALYRHPNLEVLYDPSQENVRDVLAKQIGLSYIALSGNIGCIVNGAGLAMSTLDILKLHGGNAANFLDV
GGGASQKQIQEAVSLVLSDSVKVLFINIFGGIMDCSVVASGLVAVMETRDQVVPTVIRLEGTNVELGKEIVQ
QSGIPCQFVSSMEEGARRAVELSM

>core/355/1/Org1_Gene691

MKWFVISCLLGIFSLGLIMVFDTSsAEVLDRSLECSTHKALIRQVTYLILGLGVASLLYMMEWDRFLKISPVLL
SGAALALICVFIPGLGICRNGARRWLGFQGLTIQPSEFVKYLVPIVALYFLTFSSLYQKQLKMFLKLTAILFIPIL
LIAIEPDNGSAAVISASLIPVFIMTSVRLRYWLLPLLCVLIAGGALAYRMPYVRYRLNVYLHPELDIKGRGHQP
YQAKIAAGSGKLLGKGPASLQKLTYLPEAQNDYIAAIYAEFGFLGMLVLILLYMCFVYGGYAIKASSLE
GAALAMVITLIISMQAfMNLGVVSGLLPSKGVNLPFFSQGGSSLIANMCGVTLLLKVYDEENSKSSLGCRRFR
RPHCPSSLGKGSFFS

>core/356/1/Org1_Gene827

MSSVNQSSGTPNPEEVTSPESTEENKNVVSSDEAQATHAVALPIVTQLSLPEGVGTSSSEETASNPKVDEIVAEEV
SSSRAVADQISSLVERVGELLDDLKGAQSLFTSFQSELKNCLPAWKSSTRRLETRGAGDNADIARLELFRSDY
EAVLGHANQFHGKAHLILSKLTDVHHKLQGLSREDLSLAFDNNDRVLEHLGSLGLDVAEGNWSLSCERGI
PRLVLTADSMVLVQIKKVNLPtVEELRTLQGTTESSDPRVEESLSCCERLLNELRRLWANFVGFISSCYDNIVF
VLMWIVRRINLLPGLGCLPFHNPdASQEDQRSSSGERSTRRERLSRRSDLSEEEMIVRAEGESIHPESPHGDGR
NQPSRGDKQDSdSEEETEL

>core/357/1/Org1_Gene660

MEKPQNRKAPRIFWLNNQVAIPPSERVKESYALHSDIFSLPPGSALKLAEKTEESIRQLVGLKDShIFRVPHFP
HVVHIVLAALVENLSMFQGRNHIILPAHDQQLINSLCRHQGLGTTYDWVTVNHEGRIVEEQLIETLSPRSLLF
SLSAAHGLTGVIQPLDPLLSLCKDRRILLHLDISDILGRAPLTPEILNADIITFSSAALGGMGSIGGIFIRKSLERV
FSSWFPpHTSASLCFSAVAAMQTACEERISALPLFTFHTSNLCKKLIQELQSVLPSIQLAFSEVQNRLPNIVVAA
IPDIPAESLAFHLHQQGIYPSLGYERFQPLAQVLQNCGISPFLCHSALHFSLTERSKDLEFSKLARAMHDAIKHL
TPLLGSSS

>core/358/1/Org1_Gene508

MILDFQFSIGYYLRVLELAIRDGTRILAYDRKRLLLDawPVNDPLPTNYDTSVSTIRQVIHELFSWSAISYSISS
RLLAIIELRLHEEKpQTGWLYRLFFPSKYHIKKAIVDKLCMFKSLILFESKRPVDKIVQAANKVFSKGKSNFSS
WEDFTHEVTvSEVQTPLAGEVQRRLAADASLQMIIEALTTLLEGHTAYLPLSLELLNQFIGEKAQPLKTLSEK
SYVLLRELIQLFSLSAEDFQTIIMSISDSLSEVLANSIGNQPLTFHGKTFVGLWQETALASPEDSKLALGFLAE
VLRKVIVEKKLHVSKSDNTTPEEVGNIYSIRDQNPALWdkMITMLLMRWLLDYDRDIGIALRKAAEYYNPHF
SFWRQFLRLWQRRP

>core/360/1/Org1_Gene170

MSAMISLSSSHEASIASNTQVRDVLVSLAMDEFVEHNTEILPIKVFLARGTLSSTAIIDDLKDVVETEGEHHFQ
VYSNISLKMiyQRFFEKIFGIGCCPLLLVTDShHTDPCGALITGIFAAVLFTVLAIVFGPTLGILCYSAYKIYQLT
KKISSLSRTHTEVINSVQKSDPFIHRSGAVAAAAASQSTIKACKVFRQSTLIFFVLGLIITISLAALIVGLVFALFF
LDPGAPAVMTAAMIGCCAAGGTGILLSVIGFLLASVYSVQKSQEGVHHMHTALLRCIVSNTIIQMPYLPITPG
TKKVLTSIRRYQQFFSDDEYRDIESEVPLNRQTTPPPSYETLFHEEGSDGSSNVIPRESPPAYSTIDSSNSPFPSS
SPPPYR

>core/361/1/Org1_Gene1028

MSETIITTPHVVKLISNFFQKKLFSSISTAYPLVIITDVSVQQHLLGPILDHIKMLGYQVIVLTFPPGEPNKTWET
FISLQYQLVDQNISPKSSIIIGGGTVLDMTGFLAATYCRGLPLYLIPTTITAMVDTSIGGKNGINLRGIKNRLGT
FYLPKEVWMCQFLSTLPREEWYHGIAEAIKHGFIADAYLWEFLNSHSMKMLFSSSQILHEFIKRNCQIKAAIVA
EDPYDRSLRKILNFGHSIAHAETLAKGTVNHGQAVSVGMMIETRISLAEGVMKTPQLIDQLERLLKRFNLPST
LKDLQSIVPEHLHNSLYSPENIIYTLGYDKKNLSQHELKMIMIEHLGRAAPFNGTYCASPNMEILYDILWSECH
VMRHC

>core/362/1/Org1_Gene799

MLCQQFLIEALARRKSKHTYRSLSLNSHLIDFTSNDYLGFASSPELRKEYITKLHAIESLGATGSRLLTGHSQL
CQRIEEQLAAYHNFESCLIFNTGYTANLGLLYALATDQDRILHDLYIHASIYDGIRLSKAQSFPPHNNDLNHLE
KRLASSHLGRTFVCVESVYSLHGSVAPLQAISEL CERYSAYLIVDEAHAVGVFGDQGEGLVSALGLQDKVLA
TVYTFGKALGTHGAAIAGSSILKDYLINFCRPFIYTTAQPPHALTAIELAYEHNQRAFNQREHLSALIHFFREK
AQNGLQLMKDNTTTPIQSICVSGSHRARQAALQIQNSGYDVRPIVSPTVKQREELLRICLHAFNTKNEIDHLL
HTLEQIFLCNVSSL

>core/363/1/Org1_Gene206

MSCFNLTSTNESLRPISPKASFPKQGWQSYFRSALRKHRSDTLSVSVCKVNKYDANL FVRLTVIALAVVGVL I
LFSIMLASIQGTLVITSWPLVTAAILIPTILLTGGMYLHRLGKKVDVISGVCIPPF SRRCWVPISSSH TLEKFDEK
HVSACSYLDISTLSADGSGIAAVYQCPPLL FRAFPFCGIPCAMPFVALLRMIYNLIRFLVVPFYIIFRMIYEHFFC
KHLPEDDRFIYKDVAREMGRSLAAFLKAPFYASACMIGAFYSLLDPLAGRVLMGSVERDWNDNVILARSVS
LANEAHSLFRFEGGGGRKGLGQHAFYMLCCQPQSVFLFDKGEIVSGAHPSIQLPERRGLDTSGRYPHISVIPD
SGNDSAKNFIV

>core/364/1/Org1_Gene954

MGINPSGNRSPDDVWVRGAQGDSSSTQGTGATNSNLGAHNVTSTSQPVASKAKQLWQTVREFFLGKKSP
DSSQGASGPAMQSPSGPTIRPTRPAPPPPTTG GANAKRPATHGKGRAPQPPTAGSSSGSEQPTAMSSEVAKLV
SELKDAVHSHAESQKVLKKVSQELQTKWTDWENNRGPDYLLHGYRVIARALQQTYTEQSMLIEGTLSTGPV
PQAVTVAKDAVTQTVRGAIKNLENPKPGNDPDGVLMQVVISL GIEGPTLDPGESIQNFLETRVSDFGGDDSDI
DYTSDIARLGSALDRVRENHPNEMPRIWIALARELGA AVHSHATSVRIANAGKNHTRDVVRMANESSRLLQ
GMKVL SVGAWANTMTVLIGDLFE

>core/365/1/Org1_Gene711

MIPSPTPINFRDDTILETDPKPSLIMFSSKKTEIASERRKAHPTLTKVLGTIWNIVKFIISIILFLPLALLWVLKKT
CQFFILPSSIISSQMSKTAVAIRRMFTLSHIKQLLSLKEISAADRVVIQYDDLVDLSLAIKIPHALPHRWILYSQGN
SGLMENLFDGRDSSLHQLAKATGSNLLVFNYPGIMSSKGEAKRENLVKSYQACVRYLRDEETGPKANQIIAF
GYSLGTSVQAAAALDREVTGSDGTSWIVVKDRGPRSLADVANQICKPIASAIKLVGWNIDSVKPSERLRCPEI
FIYNSNHDQELISDGLFERENCVATPFLELPEVKTSGTKIPIPERDLLHLNPLSPNVVDRLAAVISNYLDSNRK
SQQPD

>core/366/1/Org1_Gene924

MKHLAVLGSTGSIGRQTLEIVRRYPSEFKIISMASYGNNLRLFFQQLEEFAPLAAAVYNEEVYNEACQRFPHM
QFFLGQEGLTQLCIMDTVTTVVAASSGIEALPAILESMKKKGKALALANKEILVCAGELVSKTAKENGIVLPI
DSEHNALYQCLEGRITIEGIKKLILTASGGPLLNKSLEELSCVTQDVLNHPWIMMGSKVTVDSSTLVNKGLEII
EAYWLFGLNIEILAVIHPQSLIHGMVEFLDGSVISIMNPPDMLFPIQYALTAPERFASPRDGMDFSKKQTLEFF
PVDEERFPSIRLAQQVLEKQGSSGSFFNAANEVLVRRFLCEEISWCDILRKLTTLMCHKVYACHSLEDILEVD
GEARALAQEI

>core/367/1/Org1_Gene606

MKDLGTLGGTSSTAKTVSPDGKVMGRSQIADGSWHAFMCHTDFSSNNVLFDLDDNTYKTLRENGRQLNSIF
NLQNMMLQRASDHEFTEFGRSNIALGAGLYVNALQNLPSNLAAQYFGIAYKIRPKYRLGVFLDHNFSHVNP
NFNVSHNRLWMGAFIGWQSDALGSSVKVSFGYGKQKATITREQLENTEAGSGESHFEGVAAQIEGRYGKS
LGGHVRVQPFLGLQFVHITRKEYTENAVQFPVHYDPIDYSTGVVYLGIGSHIALVDSLHVGTMRMGMEQNFAA
HTDRFSGSIASIGNFVFEKLDVTHTRAFAEMRVNYELPYLQSLNLILRVNQQLQGVMGFSSDLRYALGF

>core/368/1/Org1_Gene667

MEDFSEQQLFFMRRAIEIGEKGKITAPPNPWVGCVVVQENRIIGEGFHAYAGGPHAEELAIQNASMPISGSDV
YVSLEPCSHFGSCPPCANLLIKHKVSRVFVALVDPDPKVAGQGIAMLRQAGIQVYVGIGESEAQASLQPYLY
QRTNFPWTILKSAASVDGQVADSQGKSQWITCPEARHDVGKLRAESQAILVGSRTVLSDDPWLTARQPQG
MLYPKQPLRVVLDSRGSVPPTSKEVFDKTSPTLYVTTERCPENYIKVLDSLDPVLLTESTPSGVDLHKVYEYL
AQKKILQVLVEGGTTLHTSLLKERFVNSLVLYSGPMILGDQKRPLVGVVLGNLLESASPLTLKSSQILGNSLKV
VWEISPQVFPIRN

>core/369/1/Org1_Gene712

MNLSNRSDILSGIFSNPHPVSYFSSTHAKQLSDFSCKHPILTKIVTIIVKIFKLLIGLIIPPLGIYWLCQLVCSLALF
PRSSMLYSVLKTCFKKYRLEQEIQDYFVKNLDPSFKDPAVSESKRITIQDHLTIDTLAIHFSTARPKRWLLISL
GSGDFLEDMIGLKDSLFLSWKELAKLLGANILIYNYPGVKSSTGKLNLENLATAHNLCAKYLQDKIQGPGAN
EIITYGYSLGGVVQSAALQKNPFTNSETSWVAVKDRAPHSLPAAANSFFGPIGKLIAVLARWKMDAEKNSRE
LPCPEILVYSADRFRPSEVGDDTALLPEFTLAHAIKRTPFARSKKFIGEVLNLLHSSPLKHPTIQKLAEAILESLSR
KN

>core/370/1/Org1_Gene92

MNTSLKRPLKSHFDVVGSLRPEHLKKTRESLKEGSISLDQLMQIEDIAIQDLIKKQKAAGLSFITDGEFRRAT
WHYDFMWGFHGVGHHRATEGVFFDGERAMIDDTYLTDKISVSHHPFVDHFKFVKALEDEFTTAKQTLPPA

QFLKQMIFPNNIEVTRKFYPTNQELIEDIVAGYRKVIRDLYDAGCRYLQLDDCTRGGGLVDPRVCSWYGIDEK
GLQDLIQYLLINNLVIADRPDDL VVNLHVCRGNYHSKFFASGSYDFIAKPLFEQTNVDGYYLEFDHERSGDF
SPLTFISGEKTVCLGLVTSKTPTLENKDEVIARIHQAADYLPLERLSLSPQCGFASCEIGNKLTEEEQWAKVAL
VKEISEEVWK

>core/371/1/Org1_Gene465

MSDNAHNLLYDKFELPEAVKMLPVEGLPIDKHARFIAEPLERGMGHTLGNALRRALLIGLEAPAIISFAMTGV
LHEYMAIEGVIEDVTNIILNLKGALLKKYPMQDSSLGRTTQVLKASISIDASDLAAANGQKEVTLQDLLQEGD
FEAVNPDQVIFTVTQPIQLEVVLRIFAFRGYTPSERIVLEDKGVYEIVLDAAFSPVTLVNYFVEDTRVGQDTEF
DRLVLIVETDGRVTPKEALAFSTQILTKHFSIFENMDEKKIVFEEAISIEKENKDDILHKLILGINEIELSVRSTNC
LSNANIETIGELVIMPEPRLLQFRNFGKKSLCEIKNKLKEMKLELGMDLTQFGVGLDNVKEKMKWYAEKIRA
KNTKG

>core/372/1/Org1_Gene275

MNGKAPLALYIHIPFCTKKCRYCSFYTIPYKSESVSLYCNAVIQEGLRKLAPIQETHFIETVFFGGGTPSLVSPL
DLKRILKELAPHAREITLEANPENLTVSYLRQLQETPINRISVGVQTFDDSIQLLGRTHSSSAITALQECQNH
GFSNLSIDLIYGLPTQSLEIFLSDLHQALTLPITHISLYNLTIDPHTSFYKHKILVPTIAQEEILAEMSLAENLLL
SQGFQRYELASYAKPDYPAKHNLYYWTDPRFLGLGVSAQYLHGERSKNYSHISHYLRAVRKNLPTQETSEI
LPKKERIKEALALRLRLLLEGADLAEFPSTLISMLTQDVKLQNLFSVHGQCLALNRQGRLFHDTIAEEIMGYSF

>core/373/1/Org1_Gene408

MSIAIAREQYAAILDMHPKPSIAMFSSEQARTSWEKRQAHPYLYRLLEIHWGVVKFLLGLIFFIPLGLFWVLQK
ICQNFILLGAGGWIFRPICRDSNLLRQAYAARLFSASFQDHVSSVRRVCLQYDEVFIDGLELRPNAPDRWM
LISNGNSDCLEYRTVLQGEKDWIFRIAEESQSNILIFNYPGVMKSQGNITRNNVKSQACVRYLRDEPAGPQ
ARQIVAYGYSLGASVQAEALSKEIADGSDSVRFVVKDRGARSTGAVAKQFIGSLGVWLANLTHWNINSEK
RSKDLHCPELFIYGKDSQGNLIGDGLFKKETCFAAPFLDPKNLEECGKKIPVAQTGLRHDHILSDDVIKEVAG
HIQRHFDN

>core/374/1/Org1_Gene150

MALKFHLIHQSKKSQARVGGIETSHGVIDTPAFVPVATHGALKGVIDHSDIPLLCNTYHLLLHPGPEAVAKL
GGLHQFMGRQAPIITDSGGFQIFSLAYGSVAEEIKSCGKKKGMSLVKITDEGAWFKSYRDGRKLFLSPELSV
QAQKDLGADIIPLDELLPFHTDQEYFLTSCSRTYVWEKRSLEYHRKDPRHQSMYGVHGGLDPEQRRIGVRF
VEDEPFDGSAIGGSLGRNLQEMSEVVKITTSFLSKERPVHLLGIGDLPSIYAMVGFGIDSFDSSYPTKAARHGLI
LSKAGPIKIGQQKYSQDSSITDPSCSCLTCLSGISRAYLRHLFKVREPNAAIWASIHNLHHMQQVMKEIREAIL
KDEI

>core/375/1/Org1_Gene713

MAPIHGSNAFVEDILHSHPSQATYFSSTRAQKLHEFKDRHPVLTRIASVIKIFKVLIGLIILPLGIYWLCQTLCT
NSILPSKNLLKIFKKQPNTKTLKTNYLHALQDYSSKNRVASMRRVPILQDNVLIDTLEICLSQAPTNRWMLISL
GSDCSLEEIACKEIFDSWQRFAKLIGANILVYNYPGVMSSSTGSSSLKDLASAHNICTRYLKDKEQGPGAKEIIT

YGYSLGGLIQAEALRDQKIVANDDTTWIAVKDRCPLFISPEGFHSCRRIGKLVARLFGWGTKAVERSQDLPCLEIFLYPTDSLRRSTVRQNKLLAPELTLAHAIKNSPYVQNKEFIEVRLSSDIDPIDSKTRVALATPILKKLS

>core/376/1/Org1_Gene265

MSTTEPNLTNVNLTMLISSESMPTQLASHKLKGLDLVAFILIIGIAVSSGTAAILGIPLLFLTALAVLAFSILLY
FLLREPKSPISVTHQPTPIIKDSDLPPVPPLALTPVPTEAVLEEPPPLSPRTHQTLLQENWDRIPDLQANTDMPFI
AADNQTGYAWHLKNSNLTLISTLGPIEKPRYKTQGIVMIVNAATPNMANNVKGTSALAKATSVRCWENSK
KSPDPLRSKQPLQLGECRSKAKWENLNGTTNAGKAGLPQFLGQLLGPKASDYNYNPNDAFTFCRQAYLNCLN
EAKRRKTTVVQLPLLSSHFPKDEETSLRLQWIDGVKLALIDALQTFGSEAENQNQPWVIILTTLARHPLI
TP

>core/377/1/Org1_Gene532

MAVAADSSASWLKSRNNFLSSLGKTEEQVAAPPEFPKELCQHKIREKFRLEDVQVSIKFRGSITAVEATKEFGV
HLLIQPMVVQPWEVENLLFLTSEEDLQELMVAVFDDASLASYFYEKDKLLGFHYFVAEACKLFEELQWVP
SLSAKVGGDAIFTATSLQGSFQVVDISRLDGKNVRCRLLLPEDTFQSCQKFFSGLHDESDLHNIDQTQQISLS
VEVGYSQLTQEEWHQVVPGSFIMLDSCLYDPETEESGALLTVQKHQFFGGRFLTPSSGEFKITSYPNLTHEDP
PLPENQASAAPLPGYSRLVVEVARYSLAVSEFIKLNLSILSLGNHPAYGVDIILDGAKVGRGEIIALGDVLGI
RVLEV

>core/378/1/Org1_Gene289

MIYLDNNAMTPPERGLLEFLQKTFLIEGTYANPSSVHQLGKKSRQLVLEASHWMQKVLSFQGRVLYTSGATE
SLNLAIASLPKDSHVITSGSEHPAILEPLKHSSLSVSYLNPEEGRCVLTIEQIERAVTPKTSAILGWVNSETGAK
ADIAAIAHFAQERQLQFIVDATANVGKERIVLPSGVTMAAFSGHKFHALSGIGALLVSPGVKLHPQLWGGGQ
QGGLRAGTENLWGIASLLYIFKYLDLHQRISQEILTHRNGFEKAIAKARIPDVHIHCADQPRANNVSAIAFPPL
EGEVLQIALDIEGVACGYGSACSSGATAPFKSLVSMGVDEELTLATLRFSSFHLLLQEDVERAVGIIIEKVVERL
KNS

>core/379/1/Org1_Gene707

MTTSDVIDFVTNDFLGFARSPTIYCEVSKRFQIHCQQFPHEKLGIRGSRLMVGPSVIDDLESKIASYHGAPNA
FIVNSGYMANLGLCHHVSRSTDVLLWDEEVHMSVVHLSLSAISGQHHTFHNNLEHLESLLQCYRISSKGRIFI
FVSSVYSFRGTLAPLEQIIALSCKKYHAHLIVDEAHAMGIFGDDGKGLCHALGYENFYAVLVITYGKALGTMG
ASLLTSSEVKYDLMQNSPPLRYSTSLSPHTLISIGTAYDFLASEGEIARKQVFKLKEHFHECFDSDHAPGCVQPIF
LPHTCLEEAISVLETTGIHVGVVAFAKHPFLRVNLHAYNTVDEVNLLAQVMKPYLEKSSHRVHINHEFHLWR
ELCQH

>core/380/1/Org1_Gene891

MMLVYCFDPSVPTSPEHRLMAALDRWFFLGGHVRILTLEGNHYRAFQENMSISTVEKILKLISYLLIPIVLIA
LLIRCFLHSRFGCNWKCDLSLARVPHDVQPFNDFQLFNNQERLNIWKNRRYVSGIDVLMVPVDYLRSQFPG
FKEIPEAIRCENYVSDGQFSEESKTSYLRAMLTDIVGYILSLDETYWTNVILKIRAMCITFESFPGKEADPNYSP
RVTHHYFDESWKALARHVLGEGNMVNRLDEALIRTEKPGKEGECITKQFLKDYCKKHLEVMSCPDFIESLV

DEKIREFRCP SILNSAVCDVIDRKCQEHLKAIINEANRRLPGMKNSSFTMRGNQVLFYTIFSPPKLPPAASSVY
F

>core/381/1/Org1_Gene370

MTTCLPQPPKTSPLYSIFEKLDAQERLSSDALHLLLLTNKEDQRTLWNFADQVRKQRVGDTVYYSSSTLYLY
PTNFCDFSCFKCSFYAKPGDPKGWLYSPDDLQIQNIKTPITEVHIVGGCFPSCNLQYYSDLFTKIKEYDPQIH
IKALTAIEYAYLSDLDNLSIRDVLLTLKDAGLDSIPGGGAELVDKIRNFLAPKRLSSSDFLNIHKMAHQGLIHS
NITMLCYHKEGPEDLVTHMVKVRDLQDETQGFKNFILLKFAQENNVLGKRLRKSGQGHAIPKSLMAVARIF
LDNFSNMKALWNYLGIEAALDLLSCGANDLSSTHMGEKVFQMASSKEPIKMDAEGMAALITQQGRTPCLTN
SSHV

>core/382/1/Org1_Gene1013

MRRQVREIMQQTIVIVAMSGGVDSSVVAYLFFKKFTNYKVIGLFMKNWEEDSEGGLCSSTKDYEDVERVCLQ
LDIPYYTVSFAKEYRERVFARFLKEYSLGYTPNPDILCNREIKFDLLQKKVQELGGDYLATGHYCRLNTELQE
TQLLRGCDPQKDQSYFLSGTPKSALHNVLFPLGEMNKTEVRAIAAQAALPTAEKKDSTGICFIGKRPFKEFLE
KFLPNKTGNVIDWDTKEIVGQHQAHAHYTIGQRRGLDLGGSEKPCYVVGKNIEENSIYIVRGEDHPQLYLRE
LTARELNWFTPPKSGCHCSAKVRYRSPDEACTIDYSSGDEVKVRFSQPVKAVTPGQTIAFYQGDTCLGSGVID
VPMIPSEG

>core/383/1/Org1_Gene293

MTKIAFSEKAKNFPVEALKKWFEEKNRSLPWRDNPTPYSVWVSEVMLQQTRAEVVIDYFNQWMERFPTIES
LAAAKEEDVIKLWEGLGYYSRARHLLEGARMVMEEFHGKIPDDAISLAQIRGVGPYTVHAILAFAFKRRAAA
VDGNVLRVLSRIFLIETSIDLESTRTWVSRIAQALLPHKSPEVIAEALIELGACICKKVPQCHRCPPVRQACGAW
RENKQFVLPVRHARKKVIFLHRLVAIVLYDGSLVVEKRRPKEMMAGLYEFPYIEVEPEEGLQDIEGFTKKME
LSLESPLEFLGNLKEQRHAFTNHKVHLCPIIFKATSLPQFGELHLLSDIDHLAFSSGHKKIKDALLIYLGDVRSR
ESIGV

>core/384/1/Org1_Gene422

MQENLDKRLEALRTEISLAARSLFDLDDKKQKELQVLEESSEENFWQDSVHAGKISEQIVSLRRQIQEYQELK
SKIDAIEFFLEDADALEDPAICEDLEKEFLFCEKKLAVWETQRLLSGEADKNSCFLTINAGAGGTESCDWVEM
LFRMYSRWATKHQWALEVVDRLDGEVVGIKHVTVKFSGMYAYGYAKAERGVHRLVRISPFDSNGKRHTSF
ASVDVFPEIDDQIKIEIRPNDLRIDTFRSSGAGGQHVNVTESAVRITHLPSGVVWSCQNERSQIQNRESCMKML
QAKLYQQVLQERLEKQSLDRKDKKEIAWGSQIRNYVFQPYTLVKDVRTGHETGNVQAMLDGELLDEFIKAY
LAEFGEVS

>core/385/1/Org1_Gene34

MAVEGRVNSSQALNQDCQEVLANQSKGLLRCRILSIVVAVITFIAGVVLIALTASILTSVPYLALGVFLLIV
TLGCIIFALCSEKIKKVPPTPISHKEEIIAWFEERKNIDMEKEKEDPEHFGRTATDIPMRSALDQFNHSCHHIHES
PALTETYRSHQDVLLFKDWCPVTLPDVTSEEEVLIRS SVGSYLLMEACVPKVSMLIDELHNKCLKSPSERECLF
IDKKT LQRKASFLFTQKDLATFFLAYTRVNDGHLAPFRAGAKWILIHVRLRRQHNQNDFFTPGHSCYYARL

AFNQTQRLYHQLFNVEKLRSIYANMDKDPLCHPWAFIPIYDLLKTEDHGDGFLEQQEDREYPSRAAQDQFW
G

>core/386/1/Org1_Gene650

MSPHRNLFKLKNFSNRLYNRALGRFDKVFNFSSGNVIGDLGTANTLVYVRGRGIVLSEPSVVAVDAQTHAVL
AVGHKAKAMLGKTPRKIMAVRPMKDGVIADFEIAEGMLKALIKRVTPSRSVFRPRILIAVPSGITGVEKRAVE
DSALHAGAQEVLIEEPMAAAIGVDLPVHEPAASMIIDIGGGTTEIAIISLGGIVESRSLRIAGDEFDECIINYMR
RTYNLMIGPRTAEIKITIGSAYPLGDQELEMEVRGRDQVAGLPITKRINSVEIRECLAETPIQQIIECVRLTLEKC
PPELSADLVERGMVLAGGGALIKGLDKALSKNTGLSVITAPHLLAVCLGTGKALEHLDQFKKRKGNLV

>core/387/1/Org1_Gene888

MKFVVSRLNELGNLIKKIQSVVPQNTPIPVLTHTVLIETYNDELVFTATDLTVSTRCVTKAKVYEKGAISIPSKRF
FQLVKELTEANLEISSSAGEMAQITSGSSCFRLLSMEKEDFPMLPDIQNALRFSLPAEQLKTMLQRTSFAVSRE
ESRYVLTGVLLAIANGVATIVGTDGKRLAKIDAEVTLDKSFSGEYIPIKAVEEIIKMCSDGEATIFLDQDKIA
VECDNTLLITKLLSGEFPDFSPVISTESNVKLDLHREELITLLKQVALFTNESSHSVKFSFLPGELTLTANCTKV
GEGKVSMVAVNYSGELLEIAFNPFFFLDILKHSKDELVSLGISDSYNPGIITDSASGLFVIMPMRLHDD

>core/388/1/Org1_Gene764

MLIWKRHLLTRFWFALTSLVLALIFYASIHSLHTLKGASTAASGASVKLSILYYLAQISLKAFLMPQLVA
VATTSTLFAMQNKREIILLQASGLSLKSLMHPLLLSGAVIMMVLYANFQWLHPICEKISITKENMDRGTDDKE
QGKIPALYLKDQTVLLYSSIEPKTLTLNNVFWIKDPKTIYTMEKLAFTTSLPIGLNVTQFFANDSENLELKEFF
DMKEFPEIEFNFYENPFSLKFSAGNKNRLSEFFKAIPWNATGLGLSTQVPQRILSLLAQFYVVLISPLACMAAII
LSAYLCLRFSRTPTVTLAYLIPLGTVNIFFVFLKAGIVLASSSVLPTLPVMAFPLIVLFLLTNYAYAKLQ

>core/389/1/Org1_Gene411

MKFPRISISDLIPTQMVIWVRGGGNVHYVPNAQNLPKKILGGVLACFGLALLGCAAFAGVCQTIFPCIGLMI
LGLVLLGFAYLQYSKGWSRFRPLFRETKVFEKPINWLGCSSLQSWKKIRPGCYYPGCPQVEICEGSQEIV
TKIFQKKS DRNTSIFLIQEMDQIALRQGIEKSSLSRKTF AIDPSVVSLLSEIQREEQQYLDPKVISWSSEDQASD
RTHPKSAIYVNISDAAQEPQGRCYIDAYTKAFFTVLDQIGDPNIVKKHTIYVLTPILGVPDALPKEEQENLKL
SQAFLYSAEQVAKRMREEKQDSIRIKFIFTDPTSPTSLSLYFSPHHSSTPHSVTPISLSGFVGEQESYTF

>core/390/1/Org1_Gene878

MSKKIKVLGHLTLCTLFRGVLCAAALSNIGYASTSQESPYQKSIEDWKGYTFTDLELLSKEGWSEAH AISGNG
SRIVGASGAGQGSVTAVIWESH LIKHLGTLGGEASSAEGISKDGEVVVGWSDTREGYTHAFVFDGRDMKDL
GTLGATYSVARGVSGDGSIIVGVSATARGEDYGWQVGKWEKGKIKQLKLLPQGLWSEANAISEDGTVIVG
RGEISRNHIVAVKWNKNAVYSLGTLGGSVASAE AISANGKVIVGWSTTNNGETHAFMHKDETMHDLGTLG
GGFSVATGVSADGRAIVGFS AVKTGEIHAFYYAEGEMEDLTTLGGEARVFDISSEGNDIIGSIKTDAGAERA
YLFHIIHK

>core/391/1/Org1_Gene378

MKKRFPSTLFLFYRRVTIAISLEGILGWGWLGSLLSKVFAFLVACWNRFSWSTPYRARSTVISVGNIVVGGAG
KTPTVLWLAEALRLRGYSCGVLSRGYKSQSSRQKKLTVVDSKVHSASYVGDEPLLMAEKLPEGSVWVHKD
RRISAARAAEKFGILLDDGLQYRKLHKDVEIAVVNGQDPLGGRAFFPKGRLRDFPLRLKTVDAIIVNGGGKE
AGTVVKRVSNAPOIFVKPTIASVWVTHNGERIPKEALRELRVGVFCGLGFPQGFLNMLREEGIHILGKYLLPD
HAAITKKELNYFCQQMAMRQGQGLLCTEKDSVKLPRLSGEVSLPIAKVEMRLSVNQDDTLSSLNMIEQIHK
NRGN

>core/392/1/Org1_Gene429

MNVPDSKNLHPPAYELLEIKARITQSYKEASAILTAIPDGILLSETGHFLICNSQAREILGIDENLEILNRSFTD
VLPDTCLGFSIQEALLESKVPKTLRLSLCKESKEKEVELFIRKNEISGYLFIQIRDRSDYKQLENAIERYKNIAEL
GKMTATLAHEIRNPLSGIVGFASILKKEISSPRHQMLSSIISGTRSLNNLVSSMLEYTKSQPLNLKIINLQDFFS
SLIPLLSVSFPNCKFVREGAQPLFRSIDPDRMNSVWVNLVKNVETGNSPITLTLHTSGDISVTNPGTIPSEIMD
KLFTPFFTTKREGNGLGLAEAQKIIRLHGGDIQLKTSDSAVSFFIIPELLAALPKERAAS

>core/393/1/Org1_Gene233

MSHTECGIVGLPNVGKSGLFNALTGAQVASCNYPFCTIDPNVGIVPVIDERLEALAKISNSQKIIYADMKFVDI
AGLVKGASDGAGLGNRFLSHIRETHAIAHVVRCFDDPDVTHVSGKVNPVEDIEVINLELIFSDFSSAKNIHSLK
EKLAKGKREVGALLPLFDTHAHLEKGLPLRTLTLTPEQIVALKPYPFLTMKPMFYIANVDESSLPDMDNDYV
AAVREVAAKENSKVVPICVRIEEEIVSLPIEERLEFLMSLGLEKSGLHRLVRAAYDTLGLISYFTTGPQESRAW
TVVRGSSAWEAAGEIHTDIQKGFIRAIEVITFEDMIECQGRAAAARELGKLLHIEGRDYIVQDGDTMLFLHN

>core/394/1/Org1_Gene272

MTTEVRIPNIAESISEVTVASLLVTEGALIQENQGLLEIESDKVNQLIYAPVSGRIFWEVSEGDVVPVGGVVGKI
EPAGEGEELGDSQSKETIEAEIICFPQSGVRQSPENKTFIPLRDQMDQGSQGLSAGDRGETRERMTSIRKTISR
RLLSALHESAMLTTFNEVYMTPLFHLRKEKQEEFLSRYGKLGFMSSFFVKAVLEALKAYPRVNAYIDGEEIV
YRHYYDISIAVGIDRGLVVPVIRDCDKLSNGEIEQKLADLALRAREGLLAIAELEGGGFTITNGGVYGSLLSTPI
INPPQVGILGMHKIEKRPVVDNEIVIADMMYVALSYDHRLIDGKEAVGFLVKVKEGLENPASLLDL

>core/395/1/Org1_Gene507

MVPFRQHHAYQLLKQLHTSAISEADRVSYFYFKQNRSLGSKDRQWIQNIIFNILRHRRLLETILDSGEQVTPEA
LVAKVNEGVLENLDSYSAIPWPVRYISDDLAHFLVQDYGEEQAEEIAKIWLTEAPITIRVNTDKISVKELQEK
LEYPPSPGELPEALHFSKRHPLQSTEAFFRGFFFIQDENSQRISQGISLTDKDIVLDFCAGAGGKSLIFAQKAKH
VVINDSRKAILQTAKHRLLRAGARNFSLADQLRLGSFSVVIVDAPCSGTGVFRRHPEHKWQFSKKLLLNYVR
VQKSILKQASAYVGPRGRLVYITCSLLKEENEAHVAYMHSLGWKEVHRKTLPLQVGKGDAFFTSHFQKI

>core/396/1/Org1_Gene810

MKLYQTLRGIVLVSTGCIFLGMHGGYAAEVPVTSSGYENLLESKEQDPSGLAIHDRILFKVDEENVVTALDVI
HKLNLLFYNSYPHLIDSFPARSQYYTAMWPVVLESVIDEFLMVADAKAKRIATDPTAVNQEIEEMFGRDLSP
LYAHFEMSPNDIFNVIDRTLTAQRVMGMMVRSKVMLKVTPGKIREYYRKLEEEASRKVIWKYRVLTIKANT
ESLASQIADKVRARLNEAKTWDKDRLTALVISQGGQLVCSEEFSSRENSLSQSHKQELDLIGYPKELCGLPKA

HKSGYKLYMLLDKTSGSIEPLDVMESEKIKQHLEFALEAESVEKQYKDRLRKRYGYDASMIKLLSEEAPPLFSL
LL

>core/397/1/Org1_Gene437

MAFKRKTRWLWQVLILSVGLNMLFLLLFYSAIFRKDIYKLHLFSGPLIAKSSRKVYLSEDFLNEISQASLDDLI
SLFKDERYMYGRPIKLWALSVAIASHHIDITPVLKPLTYTELKGSSVRWLLPNIDLKDFPVILDYLRCHKYPY
TSKGLFLLIEKMVQEGWVDEDCLYHFCSTPEFLYLRTLLVGADVQASSVASLARMVIRCGSERFFHFCNEESR
TSMISATQRQKVLKSYLDCEESLAALLLLVHDSVVLHEFCDEDELEKVIRLMPQESPYSQNFFSRLQHSPRRE
LACMSTQRVEAPRVQEDQDEEYVVQDGDSDLWLIKRFGIPMDKIIQKNGLNHHRLFPKGVLKLPKQS

>core/398/1/Org1_Gene1023

MAVVSTPFFNRNLWYRLLSSRFSLWKSYPFRFFLDYLDAGLLSDFLDHQAVIDKFFETHFSYYPVSGFVAP
HQYLSLLQDRYFPIASVMRTLKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ
RIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQET
LFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVLCQ

>core/400/1/Org1_Gene73

MKIDILSLFPGYFDGPLQTSILGRAIKQRLLDVQLTNLRDFGLGKWKQVDDTPFSGGGMLLMAEPVTSAIRSV
RKENSKVIYLS PQGALLTAEKSRELAASHLILLCGHYEGIDERAIESEVDEEISIGDYVLTNGGIAALVLIDAV
SRFIPGVLGNQESAERDSLENGLLEG PQYTRPREFEGKEVPEVLLQGDHKAISQWRLEQSERRTYERRPDLYL
NYLYKRSIDHKFDEETTTNRDHFCKDKISVVLEV NKLKRAKNFYCKVFGLDAMSCENKFCLPHEGKTIFWLR
EVQAEKKNIVTSLSLDCACEEDFCYLLRRWELFGGKLEKQADEHAVWALAQDLGDHAWIFSWHRMK

>core/401/1/Org1_Gene234

MGEKTEKATPKRLRDARKKGQVAKSQDFPSAVTFIVSMFTA FSLSTFFFKHLGGFLVSMLSQAPTRHDPVITL
FYLKNCLMLILTASLPLLGAVAVVGIVGFLIVGPTFSTEVFKPDIKKFNPIENIKQKF KIKTLIELIKSILKIFGA
ALILYITLKS KVS LIETAGVSP IITAQIFKEIFYKAVTSIGIFFLIVAILDLVYQRHNF AKELKMEKFEVKQEFKD
TEGNPEIKGRRRQIAQEIA YEDSSSQVKHASTVVS NPKDIAVAIGYMPEKYKAPWIIAMGINLRAKRILDEAEK
YGIPIMRNVPLAHQLLDEGKELKFIPESTYEAIGEILLYITSLNAQNPNKNTNQP DHL

>core/402/1/Org1_Gene217

MSEAPVYTLKQLAELLQVEVQGNIE TPISGVEDISQAQPHHIAFLDNEKYSSFLKNTKAGAILSRSQAMQHA
HLKKNFLITNESPSLTFQKCIELFIEPVTSGFPGIHPTAVIHPTARIEKNVTIEPYVVISQHAHIGSDTYIGAGSVIG
AHSV LGANCLIH PKVVIRERVLMGNRVVVQPGAVLGSCFGYITNAFGHHKPLKHLGYVIVGDDVEIGANTT
IDRGRFKNTVIHEGTKIDNQVQVAHHVEIGKHSIIVAQAGIAGSTKIGEHVIIGGQTGITGHISIA DHVIMIAQTG
VTKSITSPGIYGGAPARPYQETHRLIAKIRNLPKTEERLSKLEKQVRDLSTPSLAEIPSEI

>core/403/1/Org1_Gene944

MSGPSRTESSQVSVLSYVPRDKEIAPKKQFTIAKISTLAILASLALGALVAGISLTIVLGNPVFLALLITTALFSV
VTFLVYHQMTSKVSSNWQKVLEQNFKPLGKAWQEKNVDCYSNEMQFYNNHLNPKFKVAIQTDASQPFQPT
FLTGLRVIEKNQSTGIIFNPVGPTNLIDNTATNLSTILYSTLKDKSVWDTCKQREGDPAKGEDPFPSPTEVRVVK

LPNEALDQTFNLNLSSAEKKSILPTFLGHVCGPKSEELPNQQEYYRQALLAYENCLKAAIESHAAIIVALPLFTS
VYEVPP EEILPKEGTFYWDNQTQAFCKRALLDAIQNTALRYPQRSLLVILQDPFNTIESQSRSEE

>core/404/1/Org1_Gene793

MKNSFGSLFSFTTWGESHGPSIGVVIDGCPAGLELHESDFVPAMKRRRPGNPGTSSRKENDIVQILSGVYK GK
TTGTPLSLQILNTDVDSSPYENSERLYRPGHSQYTYEKKFGIVDPNGGGRSSARETACRVAAGVVAEKFLAN
QNIFTLAYLSSLGSLTLPHYLKISPELIHKIHTSPFYSPLPNEKIQEILTSLHDDSDSLGGVISFITSPIHDFLGEPLF
GKVHALLASALMSIPAAKGFEIGKGFASAQMRGSQYTDPFVMEGENITLKSNNCGGTGGLGITIGVPIEGRIAF
KPTSSIKRPCATVTKTKKETTYRTPQTGRHDPCVAIRAVPVVEAMINLVLADLVLYQRCSKL

>core/405/1/Org1_Gene530

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HSKLSFAFSSEFGFLTTPNPKNCGTGLKSQCFLHIPALLYSKEFTNLIDEEVEIITSSLLLGV TGFPGNIVVLSNRC
SLGLTEELLSSLRITASKLSVAEVA AAKKRLSEENSGDLKNLILRSLGLLTHSCQLELKETLDALSWIQLGIDLG
LIKVTENHPLWNPLFWQIRRAHLALQKQAEDSRDLQKDTISHLRASVLKELTKGLSPESF

>core/406/1/Org1_Gene692

MMKKIRKVALAVGGSGGHIVPALSVKEAFSREGIDVLLLGKGLKNHPSLQQGISYREIPSGLPTVLNPIKIMSR
TSLCSGYLKARKELKIFD PDLVIGFGSYHSLPVLLAGLSHKIPLFLHEQNLVPGKVNQLFSRYARGIGVNFSP
VTKHFRCPAEEVFLPKRSFSLGSPMMKRCTNHTPTICVVGGSQGAQILNTCVPQALVKLVNKYPNMYVHHIV
GPKSDVMKVQH VYNRGEVLCCVKPFEEQLLDVLLAADLVISRAGATILEEILWAKVPGILIPYPGAYGHQEV
NAKFFVDVLEGGT MILEKELTEKLLVEKVTFALDSHNREKQRNSLAAYSQQRSTKTFHAFICECL

>core/407/1/Org1_Gene70

MKKKVAEYLNRLAEVEIKISNPEIFSNSKEYSALSKEHSYLLELKNAYDKILNLEKVLADDDKQALAEKDPEM
VVMLEEGINENKVELEKLNKILESLLVPPDPDDDLNVIMELRAGTGGEAAALFVGDCVRMYHLYASSKGWK
YEVLSASESDLKGYKEYVMGISGTGVKRLQYEAGTHRVRVPETETQGRVHTSAITIAVLPEPSEEDTELLI
NEKDLKIDTFRASGAGGQHVNVTD SA VRITHLPTGVVVTCQDERSQHKNKDKAMRILKARIRDAEMQKRHN
EASAMRSAQVGSGDRSERIRTYNFSQNRVTDHRIGLTLYNLDKVMEGDLDPITTAMVSHAYHQLLEHGN

>core/408/1/Org1_Gene976

MPILWKVLIFRYLKTA AFCTLSLICISIISSLQEIVAYIAKDVPYDTVLRRLMAYQIPYLLPFILPGSCFVSAFSLFR
KLSDNNHMTFLRASGASQSIIMFPVLMVSGAICCLNFYTCSELASICRYQTCKEIANMAMTSPALLQTLQKK
ENNRIFIAVDHCAKSKFDNVIVALKGNNEISHVGIKSIIPD TT KDTV KAKDVVFISKLPDSL TESSSPSSQRFYIE
TLDELLIPKITSTLFAGKSYLKTRTDYLPWKQLVKQSLKHPHLPETLRRVAIGFLCITLTYAGMILGIHKPRFRK
SIALYFIFPILDILLIVGKNTKNLPLAFMLFVFPQLVSWVVF AARAYRESRGYA

>core/409/1/Org1_Gene294

MSLLSGHRLEGFPPIAEVMAACDRCSMD FCEILKSQSMDLWADAASCVDGLLQDPFWSTAIASGIAKSSLQE
TEFECESKVMVLSSWGEQGAQVCSPFNLERICMSFP SLKVFSLKKNGCENMGIQLSASCMNLLMSIFFVATN

GGSTPIWITKENLMALVALVLSHYQCYFVPATGDPQQRGNILGNPEVNAILARGMGMRVDLERKRGGESSSSR
YLELAARCFENSLTKTSLSDANNVQERDKCLLQMSTSLMHTAGLNLQRPPVPTPSGVT AHPQPQDPVVT
QPSLLGARERSPVSSRGRFPVVLPLSVISPRSHPGRVERRDLEDEEEVVMF

>core/410/1/Org1_Gene619

MSHDRILRAQRALSEHNLDAILVEKSEDLAYFLHDEAIAIGILLIGQQEVMFFVYRMDKDLYSHIQRVPLTFLT
QDVVADLSLYVQKQRYQKIGFDSASTVYHKFAQRQVLPCLWEPLECFTEKIRSIKSEEEIRRMQEAALGSA
GYDYVLTLLREGITEKEVVRQLRAFWAEAGAEGPSFPPIIAFGEHSAPHSIPTDRPLKKGDIVLIDIGVLLNGY
CSDMTRMTALGTPHPKLLESYPVVVEAQKRAMALCKEGVLWGDIDAEAVRVLREHHLDTYFIHGIGHGVG
RHIHEYPCSPRGSQVKLESGMTITVEPGVYFPGIGGIRIEDTLCIDKNKNFSLTARPVISELVCL

>core/411/1/Org1_Gene923

MNKRQKDKLKICVIISTLILVGIFARAPRGDTFKTFLKSEEAIYYSNQCNDMRKILCDAIEHADEEIFLRIYNLS
EPKIQQSLTRQAQAKNKVTIYYQKFKIPQILKQASNVTLVEQPPAGRKLMMHQKALSIDKKDAWLGSANYTNL
SLRLDNNLILGMHSSELCDLIITNTSGDFSIKDQTGKYFVLPQDRKIAIQAVLEKIQTAQKTIQVAMFALTHSEII
QALHQAKQQRGIHVDIIIDRSHSKLTFKQLRQLNINKDFVSINTAPCTLHHKFAVIDNKTLLAGSINWSKGRFSL
NDESLIILENLTKQQNQKLRLMIWKDLAKHSEHPTVDDEEKEIIEKSLPVEEQEAA

>core/412/1/Org1_Gene961

MNLPDRKKALEAAVAYIEKQFGAGSIMSLGRHSATHEISTIKTGALSDDLALGIHGVPKGRVIEIFGPESGKT
TLATHIVANAQKMGGVAAYIDAEHALDPSYASLIGVNIDDLMISQPDCEGALSIAELLARSGAVDVIVIDSV
AALVPKSELEGDIGDVHVGLQARMMSQALRKLTATLSRSQTCVFINQIREKIGVSFGNPETTTGGRALKFY
SIRLDIRRIGSIKGSNDSDIGNRIKVKVAKNKLAPPFRIAEDILFNEGISSAGCILDALVEYNIIEKKGSWFNYQE
KKLGQGREFVREELKRNRLKFKEIEKRIYDVIAANKTPSVHANETPQEVPAQTVEA

>core/413/1/Org1_Gene697

MNLCKRISFEEGLELFVSSPIERLQERADAIKERYPSNEVTYVLDANPNYTNICKIDCTFCAFYRKPKSPDAY
LLSFDEVRSLLQRYVSSGVKTVLLQGGVHPGLGIDYLEELVRITVQEFPSPHFFSAVEIEHACRVSGISIEQG
LQRLWDAGQRTIPGGGAEILSERVRKIISPKKMQPGGWINLHKL A HLMGFRTTATMMFGHVENPEDILHLQ
TLRDAQDSCPGFYSPFWSYKPGNTALRRNVPQQASIETYRILALGRIFLDNFDHVAASWFGEGKSLGAKAL
HYGADDFGGVILDES VHKATGWSIQSSEEEICNIIRSEGFIPVERNTFYQHISCTVSSL

>core/414/1/Org1_Gene703

MKYSLNFKEIKIDDYERVIEVTC SKVRLHAIIAHQTA VGPALGGVRASLYSSFEDACTDALRLARGMTYKAI
SNTGTGGGKSVIILPQDAPSLTEDMLRAFGQAVNALEGTICAEDLGVSINDISIVAEETPYVCGIADVSGDPSI
YTAHGGFLCIKETAKYLWGSSSLRGKKIAIQGIGSVGRRLQLSLFFEGAELYVADVLERAVQDAARLYGATIV
PTEEIHAECDIFSPCARGNVIRKDNLADLNCKAIVGVANNQLEDSSAGMMLHERGILYGPDYLVNAGGLLN
VAAAIEGRVYAPKEVLLKVEELPIVLSKLYNQSKTTGKDLVALSDSFVEDKLLAYTS

>core/417/1/Org1_Gene199

MLNIHDILGNDDENLLSYQCKHITKDKLTLPSHDFVDKVFGLSDRNNRVLRLSLQTMFSHGRLANSGYLSILPV
DQGIEHSAGASFAINPIYFDPENIVKLAIESGCSAVASTYGTLSLLSRKYAHKIPFMLKLNHNELLSYPTKYHQI
FFTQVEAAYSMGA VAVGATVYFGSETSNEEIVAVSNAFAKARSLGLATVLWCYLRNPAFVANGVDYHTAA
DLTGQADHLGATLGADIVKQKLPTCQGGFKAINFGKTDERVYSELSSNHPIDLCRYQVLNSYCGKVGLNSG
GPSGKNDFTEAARTAVINKRAGGMGLILGRKAFQRPLSEGIQLLNLVQDIYLDPNITIA

>core/418/1/Org1_Gene688

MIPLIPMFLKQSLFFSLALTGMTTLVLTVALGVPMKWLKRKNYRDYIHKEYCEKLEMLHKDKAEVPTGGG
VLLFISLIASLLVWLPWGKFSTWFFIILLTCYAGLGWYDDRIKIKRKQGHGLKAKHKFMVQIAIAAFTLIALPY
IYGSTEPLWTLKIPFMEGMLSPLFWLGKVFCLGLALVAIIGTSNAVNLTDGLDGLAAGTMSFAALGFIFVALR
SSTIPIAQDVAYVLAALVGACIGFLWYNGFPAQLFMGDTGSLLLGGLLGSCAVMLRAECILVVIGGVFVAEA
GSVILQVLSCLRLKKRLFLCSPLHHHYEYQGLPETKIVMRFWIFSFCAGLGIAAVLWR

>core/419/1/Org1_Gene789

MRIAVLGAGYAGLSVTWHLHLSQGTATIDLFDPIPLGEGASGMSSGLLHAFTGKKALKPPLADQGINATHA
LITEASKALNPVIVISQGILRPAIDEDQAQLFTERVEEFPEVEWWEKARCEISIPSMVIPPNLGALFIKSGVTLN
NDLYIQGLADACMKLGTQFYDELIEDLADIEEFYDHIIVTPGANASILPELKDMPVNVKVGQLLEISWPKDLA
MLSFSINAHKYMVANTQKNTCILGATFEHNQPEETPDPAIAYQEIMPPVLSLFPGLKDAQVLHCYAGMRSSS
KSRLPVISRIREKLWFLGGLGSKGLLYHGITGDMLAQAVLRKSTAYIAKEFLFTI

>core/420/1/Org1_Gene715

MILLQNIKRCSLKQLKVLATLLLSLSLPTLEAAENRDSDSIVWHLDYQEALQKSKEAELPLL VIFSGSDWNGP
CMKIRKEVLESPEFIKRVQGKFVCVEVEYLKHRPQVENIRQQNLALKSKFKINELPCMILLSHEEREIYRIGSFG
NETGSNLGDSLCHIVESDSLLRRAFPMMTSLSELQRYYRLAEELSHKEFLKHALELGVRSDDYFFLSEKFR
LLVEVGKMDSEECQRIKKRLNKPNEKQTHFTVALIEFQELAKRSRAGVRQDASQVIAPLESYISQFGQQD
KDNLWRVEMMIAQFYLDSDQWHHALQHA EVAFEAAPNEVRSHISR SLEYIRHQ S

>core/421/1/Org1_Gene397

MYLQEKFKAQQVPLVLRELLSCSDSINDSDPIYRMVFDSNDTTISYKVGDALGVLPENSKEVSEHVLQLLGYS
PTTLVNVKKTSEKVSQAQKFIQGYVDLDKIPAKLNSFFPDKDPKITLYDAIQEYRPQIPIELFAESVFLLPRFYSI
ASSPDLHPKSIELLVKHVSYPGKYQKRFGVCSSFLCSELQVNDSAYIFVQPTKHFTLSTQTEGKPLVMIGAGT
GIAPYKAFLEERLFNKDPGNNLLFFGERKEKVN FYREFWNHAE EGGK LKLFLAFSRERDQKVYVQDLLRIQ
KDEV RKAYEEGGFF FVCGRKVLGIEVKHALEEILGKDTLASLRKEHRYVVDVY

>core/422/1/Org1_Gene218

MDVSRKINRHTQFYVDSIDGVIKNFDHKPSEDKSRDHEELEEKLLTITKRIVASAQEFQNRKTDSKNYYLKK T
QWLPFKNEELEQTKELFAMLTSMKKIAQLFFYSPGCSSDWVEFTEVICH LND SIGLGGVLLCCGLFEQQCEH
VVTVNKKLDLPLLLGTTVVNSLRYYLT YRNISLLNCQSMSELGKELGDVLKQHGVAFTLIFKEIVDIDLLNYV
KLIQGLKRSGNIQARIYDNDVPTLPSVSSSPIALRYSLANTIRGLALHVD FSSLKFISPSILSNTEHTAKALNSGG
ECFIFSNLDEFNLGMKIVMQLLRTGKISPEILNKNIMKILMIKRRVRSLYI

>core/423/1/Org1_Gene754

MEADILDGKLKRVEVSKKGLVNCNQVDVNQLVPIKYKWAWEHYLNGCANNWLPTEVPMARDIELWKSDE
LSEDERRVILLNLGFFSTAESLVGNNIVLAIFKHITNPEARQYLLRQAFEEAVHTHTFLYICESLGLDEGEVFNA
YNERASIRAKDDFQMTLTVDVLDPNFSVQSSEGLGQFIKNLVGYYIIMEGIFYSGFVMILSFHRQNKMTGIGE
QYQYILRDETIHLNFGIDLINGIKEENPEVWTTTELQEEIVALIEKA VELEIEYAKDCLPRGILGLRSSMFIDYVRH
IADRRLERIGLKP IYHSRNPFPWMSETMDLNKEKNFFETRVT EYQTAGNLSW

>core/426/1/Org1_Gene63

MELSLTSLPLAWYVILGVAVFAYSFGDGF DLGLGAVY LKAKEDKERRILLNSIGPVWDGNEVWLVIIVGGL
FAGFPACYATLLSIFYMPIWTLVLLYIFRGCSLEFRSKSESVS WKIFWDIIFICSGTAISFFLGTIVGNLILGLPLSP
DTSYASLSWILFFRPYAALCGAVVASAFAIHGSCFALMKTSDSLNARIAQQFPYILSSFLVFYVLFLGASLISIP
KRFDAPPTYPLILLIALTSCCCVAAKTSVSKKRYGYAFIYSTLNLLSLILSAATLTFPNILLSTVDPQYSYTIYN
SAVETKTLKSLLIIVLIGLPFIITYTCYIYRVFRGKT NFPSIY

>core/427/1/Org1_Gene653

MNSKMLKHLRLATLSFSMFFGIVSSPAVYALGAGNPAAPVLPGVNPEQTGWCAFQLCNSYDLFAALAGSLK
FGFYGDYVFSESAHITNVPVITSVTTSGTGTTPTITSTTKNVDFDLNNSISSSCVFATIALQETSPAAIPLLDIAF
TARVGGLKQYYRLPLNAYRDFTSNPLNAESEVTDGLIEVQSDYGIVWGLSLQKVLWKDGVSVFVGVSADYRH
GSSPINYIIVYNKANPEIYFDATDGNLSYKEWSASIGISTYLNDYVLPYASVSIGNTSRKAPSDSFTELEKQFTN
FKFKIRKITNFDRVNFCFGTTCCISN NFYYSVEGRWGYQRAINITSGLQF

>core/428/1/Org1_Gene748

MMEVYSFSPSVRTSFQHRVMAALDNWFFLGGRRLKVVS LDSCNSGQACEEYVPISTTEKVLKILSYLLIPV
ALLIRYLLHSNFTAKVSQKPWLKTLQLGIDIKSFILPGSHVNTMDSATLFKAIRLEGKRVDVEYHRLHSSDKV
VFYIPAQKLPDDLRLTHWLPEKETR KTEYVRHMLAHVMGYLTSQGKERLQQVVQDSRSSTSLGAEKVLQYR
FIDHPQSQGEFQRLLENITTKGSEDKEVVQSDLFDMAFQCWWPQFISVIQSPTFSEELVHEMSQKLDLDCIYP
EDDEFEQKFLNTLLKAVLHHGFEGISVASMGVIFLICPDSLALQIPFLRNQK

>core/429/1/Org1_Gene610

MNKKKRVLTGDRPTGKLHLGHVGSIKNRLELQNSPEYDCFFIADLHTLTTKIRKEEVLDVDNHIYEV LAD
WLSVGIDPTKSIIYLQSAIPEIYELHLLFSMLISINRVMGIPSLKDMARNASIEEGSLSYGLIGYPILQSADILLAK
AQFVPVGKDNEAHVELTRDIARNFNRLYGQVFPEPEVLQGELTSLVGIDGQGKMSKSANNAIYLSDS DATITE
KVRKMYTDPNRIRATTPGRVEGNPLFIYHDIFNPHKDEV EEFKARYRQGCIKDIEVKARLAEELIHFLKPIKER
RSEFLSKPLALQNVLEDGTHKMREVAKVTMEEVHDKFGF SHKWRSLLK

>core/430/1/Org1_Gene130

MLTLGLESSCDETACAIVNEDKQILANIIASQDIHASYGGVPELASRAHLHIFPQVINKALQQANLLIEDMDL
IAVTQTPGLIGSLSVG VHF GK G IAGAKKSLIGVNHVEAHL YAAYMAAQNVQFPALGLVVS GAHTAAFFIENP
TSYKLIGKTRDDAIGETFDKVGRFLGLPYPAGPLIEKLAL EGSSEDSYPFSPAKVPNYDFSFSGLKTAVLYAIKG

NNSSPRSPAPEISLEKQRDIAASFQKAACTTIAQKLPTIIKEFSCRSILIGGGVAINEYFRSAIQTACNLPVYFPPA
KLCSDNAAMIAGLGGENFQKNSSIPEIRICARYQWESVSPFSLASP

>core/431/1/Org1_Gene83

MENAMSSSFVYNGPSWILKTSVAQEVFKKHGKGIQVLLSTSVMLFIGLGVCAFIFPQYLIVFVLTIALLMLAIS
LVLFLLIRSVRSSMVDRLWCSEKGYALHQHENGPFLLDVKRVQQILLRSPYIKVRALWPSGDIPEDPSQAAVLL
LSPWTFSSVDVEALLPSPQEKEGKYIDPVLPKLSRIERVSLLVFLSAFTLDDLNEQGVNPLMNNEEFLFFINK
KAREHGIQDLKHEIMSSLEKTGVPLDPSMSFQVSQAMFSVYRYLRQRDLTTSELRCFHLLSCFKGDVVHCLA
SFENPKDLADSDFLEACKNVEWGEFISACEKALLKNPQGISIKDLKQFLVR

>core/432/1/Org1_Gene219

MDSSAPYNIASQGTEKSTVERILDLYGPASCIKFLKQMVLIREFEARGEAYLEGLVGGFYHSYAGQEAVATA
AIANTGLDPWVFSSYRCHALAILLNIPLQEIAAELLGKETGCALGRGGSMHMCNPNPGGFGIVGGQIPLAAG
AAFTIKYQEKNRVSLCFIGDGAVAQGVFHETLNFVSLHQLPLMLIENNGWSMGTSLNRAVAKQPIAESQG
SSYDIRAVTVNGFDLFNSLLGFREAYRYMVDTESPVLVECLCSRFRGHSISDPNLYRSKEEMQCLFKKDPIVL
AKDWLIRLEVLTEEEFQNIHQECKTAVLEAFSNAKLSSDPSVTTLEEGVYA

>core/433/1/Org1_Gene105

MKLYSISSDVDTPWIFQLMSKVDSYLFLGGNRIKVVSIVMQEPNLIIGKVENVRISTIVKILKILSFLIFPLILIAL
ALHYFLHAKYANHLLVSKILERAPQYVPIPGRSGDTASHYKLTTLPVVSQKNLQAMGSNPLEVEAALRTTKP
SFFCVPKAKYRQHIISSHGIRFSLDLEQLADDINLDSVSWPTEYLNSTMDFCADKRVIQNVQNLRTGTIYNSV
GKRSLLKFMLQHLFIDGITQENPEALPNNTSGRLTLFPSVRYIYSHFTPQNPTIWPQVFFRQGPLDEDRGGGFEI
LEQLQELGVRFPICPSQGPDPNPNFQGFQGIYIYWEDSYQPNKEV

>core/434/1/Org1_Gene696

MLPFEFENNTSSPECVCLDPQKLFVKLFKRTIVLLSGPTGSGKTDVSLALAPMIDGEIVSVDSMQVYQGMD
IGTAKVSLKARQEIPHHIDIRHVQEPFNVVDFYYEAIQACQNILSRNKVPILVGGSGFYFHAFLSGPPKGPA
DPQIREQLEAIAEEHGVSALYEDLLLKDPEYAQTITKNDKNKIIRGLEIIQLTGKKVSDHEWDIVPKASREYCC
RAWFLSPETEFLKNNIQMRCEAMLQEGLLVEVRGLLNQGIENPSAFKAIGYREWIEFLDNGEKLEEYEETKR
KFVNSNSWHYTKKQKTWFKRYSIFRELPTLGLSSDAIAQKIAKDYLLYS

>core/435/1/Org1_Gene659

MFFQNLAKKLTALGISPLGCLLIGGVVSCAILFGRSSNPSLAPTQVKTEKTSGNWLKLTQMGNPKLIESLTKK
EQLEKDLTSFHPIASAKVAIALSTEDDVMSPHLHSVILTLRKEESLTPSLLFSITDYLCSSLPGLKREHISLSDNL
GNLYIPESITVNSLFIHTLENYLGIKIFKEHFALAYHAKAEKPTLQLTLNENYIAHLTKEESEKIVAHTKHLY
QNYDDSYDIVIETLPFARLQNKKSFPKVLIGSMILVISLMIVALASFYLARHAYERSPEPRKIKRGINISKLL
IIQKESPEKIALILSYLDPKKAALLNRLPEDLKHQVLKYKL

>core/436/1/Org1_Gene920

MSEQHSPIISVQDVSKKLGDHILLSKVSFSVYPGEVFGIVGHSGSGKTTLLRCLDFLDMPSTSGSISVAGFDNSLP
TQKFSRRNFSKNVAYISQNYGLFSSKTVFENIAYPLRIHHEMSKSEVEEQVYDTLNLNLYHRHDAYPGNLS

GGQKQKVAIARAIVCQPEVVLCDEITSALDPKSTENIIERLLQLNQERGITLVLVSHEIDVVKKICSHVLVMHQ
GAVEELGTTEELFLNSENSITNELFHEDINIAALSSCYFAEDREEVLRNLNFSKELAIQGIISKVIQTGLVSINILSG
NINLFRKSPMGFLIIVLEGEVEQRKKAKELLIELGVVIKEFY

>core/437/1/Org1_Gene355

MTILRKLSQYLFFFSLFCSFIYVATCGSQPDSVSSPKIAIFLSFPHPLEDCSKSCIETLKDFENLPEIVVLNAEDSI
VKARKIARSLHTDKNVVAIVTLGTIATKVMSHIETQKPVIYAAVPDRESLTLPKNTMNIYGVNDTLDINQYCF
AIQAVATNAQSIVYLPSEPFPSDLQKEIVKKLHASGIEVIEISITSSTFKTRIRQAIDKRPSAIFIPLSPLSHKEGT
AFLQEILKEKIPIITDDTSLISEGACIACSVDYKKSGKQIAKIVHHLLYNNHDVDSLKIIAQRLSPTTTFNEDIK
YLGIKLHKTERNQFLSFKSKKLEKSEKGKNVAVS

>core/438/1/Org1_Gene762

MEMKEEIEAVKQQFHSELDQVNSSQALADLKVRYLGKKGIFRSFSEKLKQCTDKAKLGLINDFKTYVEDLL
QEKSLVLLASEQAEAFSKEKIDSSLPGDSQPSGGRHILKSILDDVVDIFVHLGFCVREAPNIESEANNFTLLNFT
EDHPARQMHDTFYLNATTVLRTHTSNVQARELKKQOPPIKVVAPGLCFRNEDISARSHVLFHQVEAFYVDH
NVTFSDLTAILSAFYHSFFQRKTELRFHSYFPFVEPGIEVDVSCECCGKGCALCKHTGWLEVAGAGMIHPQV
LRNGNVDPEIYSGYAVGMGIERLAMLYGVSDIRLFSENDLRFLQQFS

>core/439/1/Org1_Gene261

MATISPISLTVDHPLVDTKKKSCSNFDKIQRILLITAIFAVLVTIGTLLIGLLLNIPIYFLTGISFIAVVLSNFILY
KRATTLLKPRACGKHKEIKPKRVSTNLQYSSISIAINRSKENWEHQPKDLQNLPAAPSALLTDNPYEIWKAKHS
LFSLVSLLPGGNPEHLLISASENLGKTLLIETSQNAPISSYVDTTPSPKSLLEAIQETRVEINTELPAGDSGER
LYWQPDFRGRVFLPQIPTTPEAIYQYYYALYVTYIQTAINNTQIIQIPLYSLREHLYSRELPPQSRMQQSLAMI
TAVKYMAELHPEYPLTIACVERSLAQLPQESIEDLS

>core/440/1/Org1_Gene523

MEEAAKHLAKEFLCSGINLFLSGEYEQAEKRLKETLELDSTAALAYCYLGIIALETGRVSEALNWCSKGLASE
PGDSYLRICYGVALDRGNQYEAIEQYSAYVALHPDDVECWFSLSVYHRLKRLQEALDCFDKILALDPW
NPQSLYNKAVILSEMDDEAESIRLLEVAVAKNPLYWKAWVKLGFLLSRSKRWDKATEAYERVVQLRPDLSD
GHYNLGLCYLTLDKTRLALKAFQEALFLNAEDADAHFYVGLAHLDLKQMREAYEAFNSALSINLEHERAHY
LLGYLHHMQGETDKATKELLFLQKKDSTFAPLLQKTVVSDPSSMQFERRLDNIS

>core/441/1/Org1_Gene541

MVLGVVGISYREAALKERERAIQYLQSFENLFLAQRFLGKGGAFIPLLTCHRAELYYYSESPEIAQAALLSEL
TSQGIRPYRHRGLSCFTHLFQVTSIGDSLIFGETEIQGQVKRAYLKGSKERELPFDLHFLFQKALKEGKEYRSRI
GFPDHQVTIESVVQEILLSYDKSIYTNFLFVGYSINRKVAAYLYQHGYHRITFCSRQQVTAPYRTLSRETLSF
RQPYDVIFFGSSESASQFSDLSCESLASIPKRIVFDNFVPRFTLWKETPTGFVYLDIDFISECVQKRLQCTKEGV
NKAKLLL TCAAKKQWEIYEKKSSHITQRQISSPRIPSVLSY

>core/442/1/Org1_Gene81

MFPSANQESRTRNVPLGIFHGLVACLYWGIVFVIPNFLGSFGDLDIVLTRYTIFGIFSLIACAIIKNPSVIKKTPLYI
WRKSLLWTLLINPVYYFGITLGIRYVGSAITVVIASLAPTAVLYHSNTKQKELPYSLLFAISSVIITGVILTHLSA
LNLPTAASPLYLSILGVIAVILSTSLWVIYVIRNQSLEKHPNLTPDTWSYLIGISALIICLPMIILDLGITHVTHN
LISHTPGSERLLFLLCSAMGIFSSAKALIAWNKASLNLSPALLGAILIFEPIFGLVLTLYLSQSLPSLQEGIGIFL
MLGGSLLCLVLFGRKVQKSLENSQVSSSNE

>core/443/1/Org1_Gene967

MKKTCCQNYRSIGVVFSVVLFLVLTQTFLAGHFIDIGTSGLYSWARGVSGDGRVVVGYEAGNAFKYVDGEK
FLLEGLVPRSEALVFKASYDGSVIIIGISDQDPSCRAVKWVNGALVDLGIFSEGMQSFAEGVSSDGKTIVGCLY
SDDTETNFAVKWDETGMVVLNLPEDRHSCAWDASEGGSVIVGDAMGSEEIAKAVYWKDGEQHLLSNIPG
AKRSSAHAVSKDGSFIVGEFISEENEVHAFVYHNGVIKDITLGGDYSVATGVS RDGKVIVGHSTRTDGEYR
AFKYVDGRMIDLGTLLGGSASFAFGVSDDGKTIVGKFETELGECHAFIYLLDD

>core/444/1/Org1_Gene284

MTHQVAVLHQDKKFDVSLRPKGLEEFYQQHHLKERLDLFLCAALQRGEVPGHCLFFGPPGLGKTSLAHIVA
YTVGKGLVLASGPQLIKPSDLLGLLTSLQEGDVFFIDEIHRMGKVAEEYLYSAMEDFKVDITIDSGPGARSVR
VDLAPFTLVGATTRSGMLSEPLRARFAFSARLSYYSQDLKEILVRSSHLLGIEADSSALLEIAKRSRGTPRLA
NHLLRWVRDFAQIREGNCINGDVAEKALAMLLIDDWGLNEIDIKLLTTIIDYYQGGPVGKIKTSLSAVGEDIKT
LEDVYEPFLILKGFIKKTTPRGRMVTQLAYDHLKRHAKNLLSLGEGQ

>core/445/1/Org1_Gene562

MSYSLRNKKTICVYIIIALGILSFRSIPQEVYDKIRSSFVSLHVKFFPKIKQAPSSHLANLELENLVLKERVASL
EEKLKLVEVSNHTPPLFPEILTPYFHKLVEGKVYVRDYTHWSSSCWVNVGKTHGIKKNSPVLSGNVLVGLVD
YVGEHQSRIRLITDVGMKPSVVAMRGDIQSWWIKHSLRELIRQVEQISHAYILEKDKYEKISQLQELDSLQGE
GENQALLRGILSGVGGALWKEGSLCLEGEGFYFSEGKTLLPGDILVTTGLDGVFPGLLVARVTKVKAPRDG
ACTFKIEAQSLEEKLMELDQLFILPPLEFNPNDRPDIFGLLWD

>core/446/1/Org1_Gene463

MKVVINGFGRIGRLVLRQILKRNSSVEVLAINDLVPGDALTYLFKFDSTHGRFPEDVRCEADHLIVGKRKIQF
LSERNVQNLPPWKDLGVDLVIECTGLFTKKEDA EKHIQAGAKRVLISAPGKGDIPTFVMGVNHNKTFNPEKDFV
ISNASCTTNCLAPIAKVLLDNFGITEGLMTTVHAATATQLVVDGPSKKDWRGGRGCLQNIIPASTGAAKAVT
LCLPELK GKLTGMAFRVPIEDVSVDLTVRLDKSTTYDDICKAMKQASETDLKGILDYTD EQVVSSDFIGSEY
SSIFDALAGIALNDRFFKLVAWYDNETGYATRIVDLLEYVEKNSK

>core/447/1/Org1_Gene393

MFVDQITLELRAGKGGNGVVAWRKEKYLPGGPGYGGNGGNGGSGVIIIEATTSVYSFEAYRNIRFLKAPDGQS
GATNNRTGRSGKDLIVSVPTGTLLRDAETGEILHDFTVDGERLLVSQGGKGGKGNTEFFKTSVNRAPT KATPG
KPGEIRQVELELKLIADIGLVGFPNAGKSTLFNTLAHTEVKVGAYPFTTLAPSLGLVLCKDRLYQKPWIIADIP
GIIEGAHQNKGLGLDFLRHIERTLLLLFVIDVSKRERNSPEEDLETILHELHSHQPDFEKKDMLVALNKIDDLL
PDEQEECLQS FQKRFPSTYTFVLISGLTGEGVDGLYRFFTQRLAV

>core/448/1/Org1_Gene214

MWFSVNKNKKAIIWATGSYLPEKVLSNADLEKMVDTSDEWIVTRTGIKERRIAGPQEYTSMLGAIAAEKAI
ANAGLSKDQIDCIIFSTAAPDYIFPSSGALAQAHLGIEDVPTFDCQAACTGYLYGLSVAKAYVESGTYNHVLLI
AADKLSSFVDYTDNRNCTVLFGDGGAACVIGESRPGSLEINRLSLGADGKLGELLSLPAGGSRCPASKETLQSG
KHFIAMEGKEVFKHAVRRMETAAKHSIALAGIQEEDIDWFVPHQANERIIDALAKRFEIDESRVFKSVHKYGN
TAASSVGIALDELVHTESIKLDDYLLLVAFGGGLSWGAVVLKQV

>core/449/1/Org1_Gene585

MAAPIFIKNILLRSSIVYAPLAGFSDYPYRCMSALYQPGLMFCCEMVKVEGILYAPERTSKLLDYNENMRPIGA
QLCGSNPETSGEAAKILEGLGFDLIDLNCGCPTDKITKDGSGSGLLKTPELIGRILDKIINSVSIPVTVKIRSGWD
MEHINVEDTVRIIRDAGASAVFVHGRTRAQGYHGPSKQEYISRAKAAAGKEFPVFGNGDIFSPEAAQAMLTT
GCDGVLVARGTLGAPWIGKQIQDYLTGGSYEKIPFIKRKAAFLEHMRLVEDYYQSETKFLSETRKLCGHYLIS
AAKVRFLRSSLAKATSYQEVYQLVNDYEEADSSLETfVKC

>core/450/1/Org1_Gene37

MSTPLSSGGISPSDQYVPQELFCDRLLSSSRNSPDSNASGDSPIVSPISALVALTDLKLVYPYNQNSFSWTTRLK
NAVEKIGLFLQRNWKYILLYILAWALILVCHHTVALTLTIWLGVGLGIGVVFGIFTATCLDKENKHRHVNSL
WNLINHGILQLDPNGTRQILLATMIASISALIYAVPQAVGLVIGFSIGNQLSINTVYGARLGDEATYAIRKAH
KKRIENIEQAINQHQIIKHQMINQKQLNALIEINRNNQTDPATANLLASLKLNLNQPMPCFSMPECGVTSSYL
DLNNNSPDDIARADQCIMTSLSQTLQQIKKEPDRIIESNH

>core/451/1/Org1_Gene632

MVRRSISFCLFFLMTLLCCTSCNSRSLIVHGLPGREANEIVLLVSKGVAAQKLPQAAAATAGAATEQMWDI
AVPSAQITEALAILNQAGLPRMKGTSLLDLFAKQGLVPSELQEKIRYQEGLSEQMASTIRKMDGVVDASVQIS
FTTENEDNLPLTASVYIKHRGVLDNPNSIMVSKIKRLIASAVPGLVPENVSVVSDRAAYS DITINGPWGLTEEI
DYVSVWGIILAKSSLTKFRLIFYVLILILFVISCGLLWVIWKTHTLIMTMGGTKGFFNPYPYTKNALEAKKAEG
AAADKEKKEDADSQGESKNAETSDKDSSDKDAPEGSNEIEGA

>core/452/1/Org1_Gene654

MKQHIGYLGMGIWGFCLASLLANKGYPVVAWSRNPDLIKQLQEERRHPLAPNVVISPNLSFTTDMKEAIHNA
FMIVEGVTSAGIRPVAEQLKQITDLSVPFVITSKGIEQNTGLLLSEIMLEVLGDSVTPYLGYLSGPSIAKEVLNG
SPCSVVVSAYDSQTLKQIHEAFSLPTFRVYPNTDIKGAALGGALKNVIAIACGIAEGLSFGNNAKAGLVTRGL
HEMRKLAAIMDCKPETLNGLAGLDLCVTCFSESSRNLRFGHLLAQGLTFEQAKAKIGMVVEGAYTALSAY
QVAKHHKIDMPITTTGIYRVLYENLDLKEGIALLLQRNTKEEFL

>core/453/1/Org1_Gene444

MKPLGFQENLEALCNKTSRQLLKYLKQILFVCGASLLIALEFSFFLYFFLFSGKTVIPAFCLACFFLTLFVCLV
TRLYLLSGKGDFFDLASEYLQGAVPPNKR SQNIVEEQSHLAAAATKLSINLQNQEYSLLSEIFKFLPKHDLIR
KFSCFCFWKDYFLFRECLLQKAIEAYIKVVQAIPVDLSAHVSLADAYVALSGLYADPRKYPEFDANYWIPSG

RYSAEIQEKFFATARRAIEEFQILNEYAPGNAWVHAQLAYSYHDLQMPMEEIQEYEIVLKLKPNDVETMSKL
GILYFQQGMNAKGLRIYEEIKKRDYKKSQKLIKFGVEYKY

>core/455/1/Org1_Gene625

MQPFIFTLLCLTSLVSLVAFDAANARKRCACAQTIERGENFFSIKRSACAEIEYQEKSRRHASAIERISKDKGKV
TPKQIAKVATKKKQRYRLLQVPFSRPPNNSRYNLYALLSEPPECYSDTASWYAIFIRLLRRAYVDTGNVPPGS
EYAIANALISNKQEILERGAQLGPDVIETLTLPPEQAEIFYKMLKGSSNSQSLLNFLHYEEKSLGHCKNLIFM
DPLLLEAVLDHPDAYRETSLLRDGIWEAVKRQEHAIQEHGQAAALELFKTRTDFRLELRDKMQLLLSRYDLL
PLLNKKMFYDYLGSAGDYFLVDPDTKAISRCRCPSKSIKL

>core/456/1/Org1_Gene952

MATNAIRSTGSAASKMLLPVAKEPAAVSSFAQKGIYCIQQFFTNPGNKLAKFVGATKSLDKCFKLSKAVSDC
VVGSLLEEAGCTGDALTSARNAQGMLKTTREVVALANVLNGAVPSIVNSTQRCYQYTRQAFELGSKTKERKT
PGEYSKMLLTRGDYLLAASREACTAVGATTYSATFGVLRPLMLINKLTAKPFLDKATVGNFGTAVAGIMTIN
HMAGVAGAVGGIALEQKLFKRAKESLYNERCALENQSQLSGDVILSAERALRKEHVATLKRNVLTLLEKA
LELVVDGVKLIPLPITVACSAAISGALTAASAGIGLYSIWQKTKSGK

>core/457/1/Org1_Gene803

MRIAVLGVTGLVGQKFVALLHKWYRDWVIAEVVASNSKYGQSYGDACIWQEPIGMPPEMVRDLPIRKIEEV
QSDIVVSFLPSSAESMEAYCLSQGKVVFSNASTYRMHSSVPIIPEVNSDHFQLLEEQPYPGKIITSPNCCVSGIT
LALAPLRKFSLDHVHIVTLQSASGAGYPGVPSDLLANTVPHIVGEEKILRETVKILGSSKQPLPCKLSVTVH
RVPVAYGHTLSLHVTFSKDVDLDEILYSYQEKNEFPNTYQLYDNPWSPQARKHLSHDDMRVHLGPITYGG
DFRTIKMNVLIHNLVRGAAGTLLASMENYFFDYLKREMCLR

>core/458/1/Org1_Gene454

MKTLWHFVSKAFLSIVGLCCGVVLAFFVIFALIASSLGNGDATFVSLPDAQGEVKDLGKTAPIIAVIEMKDVI
ASSKNTAKTIQNILEGFEEKAPLKDRVKGIVIDMDCPGGEVFEIDRIYSMLRFWKERKGFPIIYVNGLCASGGY
YVSCAATKIYATSSSLIGSIGVRSGPFFNVKEGLNRYGVESDLLTAGKDKAPMNPYTPWTSHDREERQATLDF
LYGQFVDIVTQNRPLLTKELVHTLGARIFSPEKAKQEGYIDVVGATKEQVLQDIVAVCKIEDNYRVIGSGGD
GWWKRVASAAASSPLVTGMIKHDILPLSHDAAYIPPYLAL

>core/460/1/Org1_Gene567

MSSLTLRRPRNRKTAAIRDLLAETHLSPKDLIAPFFVKYGNNIKEEIPSLPGVFRWSLDLLLKEIERLCTYGL
RAVMLFPPIPDDLKDAYGSYSSNPKNILCHSIHEIKNAFPHLCLISDIALDPYTTHGHDGIFLNGEVLNDESVRIF
GNIATLHAEMGADIVAPSDMMDGRIGYIRSKLDQSGYSKTSIMSYSVKYASCLYSPFRDALSSHVTS GDKKQ
YQMNPKNVLEALLESSLDEEEGADILMVKPAGLYLDVIYRIRQNTCLPLAAYQVSGEYAMILSAFQQGWLD
KETLFHESLIAIKRAGADMIISYSAPFILELLHQGFEF

>core/461/1/Org1_Gene101

MNIYQFSPGASPNWQASLMAQLNSYFCLGGETVTRIISLRPSGLILAKKEKAVVSTA EKILKILSFILFPLVLIAL
AIRYLLYNKFNKDLDRVFFIPTEITKAEELIIAKNPALVKEAALTVSPLFYSLPKKYQLMKVETP

>core/462/1/Org1_Gene102

MLLEDLDTDSIPWPKLYLSEDFDFAYYPESKAIIDTVAKLEKNNPGEEFCLESKKILARYLLEQLFKLETGLNF
PTSTIDGGRESFLIEFSHETKKPTVWAFIYFYYYHSNGPKLEKDFKQAGCEVHNRLNLGLKYRPQAGAQN
GRNGGPYGPIGFLIVWEENYGSVLKDHGFIKDN

>core/463/1/Org1_Gene735

MQFSRYLRYAFDNQYLPEPLYQKFSVFHQNYIDAATKKAAADQAEVLCLQWVKVIIEDLKNPFIFPPYHKKI
RAPIDLFRLSIDFFSLVIDDKNSRILNLHRLKEIEEYIARGDNVLLANHQTECDPQLMYALGKTHPELMEN
MIFVAGDRVTS DPLARPF SMGCDLLCIYSKRHIATPPELREEKLLHNQKSMQILKTLLNEGKFIYVAPAGGR
DRKNAEGRLYPSEFSPESIEVFRLLAKASNQTTHFYPFALKTYDILPPPKIENAIGEQR AIF FAPVFFNFGAELF
FDALCSKEELIHCDKHAQRTLRAEKVFSIVKNLYEEL

>core/464/1/Org1_Gene800

MREETVSW SLEDIREIYHTPVFELIHKANAILRSNFLHSELQTCYLISIKTGGCVEDCAYCAQSSRYHHTVTPEP
MMKIVDVVERAKRAVELGATRVCLGAAWRNAKDDRYFDRVLAMVKSITDLGAEVCCALGMLSEEQAKKL
YDAGLYAYNHNLDSSPEFYETIITTRSIEDRLNTLDVVNKS GISTCCGGIVGMGESEEDRIKLLHVLATRDHIP
ESVPVNLLWPIDGTPLQDQPPISFWEVLR TIATARVVFPRSMVRLAAGRAFLTVEQQTL CFLAGANSIFYGDK
LLTVENNDIDEDAEMIKLLGLIPRPSFGIERGNPCYANNS

>core/465/1/Org1_Gene343

MIDIMQHFKPYTMVPGQKLPIPGSLLYAQVFPTLWRLFSSKHEILNEQTLQVQGPKRFAVFQDLHRGGLAV
TSERYKYLLPSGECTQSIKGLPSAAQAGPLLSLGVHKHADWQKVRCRRDLKEILPLWFRFAAMAPKGSY
RDLETTAIGSLVKTAHQ RVLHRETTEIAPALLSIALAGFSECFLPRS YDEEFQGILPQDGDPEGGV PFELLSYSF
GMIQDIFLRHQGQLVEILPALPPEFPCGRLIHVALPNLGTLSIVWTKKTIRQVELHAEYSGEVFLKFCSSLCSAR
LREWSERRLSGSKRLSLGETLEIKAGTTYLWDCFBK

>core/466/1/Org1_Gene681

MSAFFDLLKSQTASHPIWLLRQVGRYMPPYQELKGSQSLKTFFHNTEAIVEATLLGPSLLHVDAAILFADILS
ILDGFAVTYDFAPGPRIQFSPEQPFTFTSDPQTIFS YLLDAIRTLKQKLPVPLIVFAASPFTLACYLIDGGASKDF
SKTMSFLYVYPEKFDQLISTHIEGTAIYLKTQMDAGAAAVQLFESSRLPSALFTRYVTEPNRRLIAKLKEQAI
PVSLFCRCFEENFYTLQATQADTLHPDYHVDLHRIQKNLMLS LQGNLDP AIFLLPQEKLLHYVEAFLVPLRTY
PNFIFNSGHGILPETPLENVQLVVS YVQRQL

>core/467/1/Org1_Gene376

MPSPMISTDVCQDILGKQKEAVDFFFQAFQPK EAMQLAEKILGHSGWVFFSGVGKSGCVARKLVATLQSLSE
RALFFSPVDLLHGDLGLVSPGDIVCLFSKSGETQELLDTVPHLKSRRAILVAITSM PYSNLAALSDLVVILPSV
AELDPFNLIPTNSTTCQMIFGDFLAMLLFHSRGVSLSTYGKNHPSGQVGMKANGKVKDFMFPKTEVPFCHLG
DKVSFSLEVFSAYGCGCVCIVDPQFRLMGIFTDGD LRRSLASYGGEVLSLSLEKVM TANPRCITEDSDIAIALQ
LMESSPVAVLPVLDNEENRHVTGLLHMHTLAKAGLL

>core/468/1/Org1_Gene788

MAFKEVVRVAVTGGKGQIAYNFLFALAHGDVFGVDRGVDLRIYDVPGTERALSGVRMELDDGAYPLLHRL
RVTTSLNDAFDGIDAAFLIGAVPRGPGMERGDLLKQNGQIFSLQGAALNTAAKRDAKIFVVGNPVNTNCWIA
MKHAPRLHRKNFHAMRLDQNRMHSM LAHRAEVPLEEVS RVVIWGNHSAKQVPDFTQARISGKPAAEVIG
DRDWLENILVHSVQNRGSAVIEARGKSSAASASRALAEAARSIFCPKSDEWFSSGVCSDHNPYGIPEDLIFGFP
CRMLPSGDYEIIPGLPWEPFIRNKIQISLDEIAQEKASVSSL

>core/469/1/Org1_Gene220

MPKHKLTLEIREALREAIDEEMSRDPNVCILGEEVGDYNGAYKVTKGLLDKWGPKRVIDAPISEAAFSGIGIGA
ALSGLRPIIEFM SWNFSFVALDQIISHAAKMHFMTGGKFSVPIVFRGPNGAAAQVSCQHSHCVESLYANIPGLI
IIAPSNPYDAKGLLKSAIRNNNPVLFLENELEYNLKGEVPTEEYLVPIGKAHRVQEGNDLTIITYSRMVSITKEA
CSLAKKRWGLSIEIIDLRTIKPLDISTILSSVRKTSRCIVIEEGHYFAGISSEIIALITEHVFDSLDAPPLRVCQKETP
MPYSKILEQATLPNVNRILDTIEKVMR

>core/470/1/Org1_Gene47

MSNQFDQLKKLSTIVCDSGDPELVKASGSQDATTNPSLILKVAQEPKFQELLNEAVVWGIRQNGDDLQTLSFI
LDKIQVNFALIEIKNIPGRISLEIDARLSFNVEAMVQRAVFLSQLFEAMGGDKKRLLVKIPGTWEGIRAVEFLE
AKGIACNVTLIFNLVQAIAAAKAKATLISPFVGRIYDWWIAAYGDEGYSIDADPGVASVSNIYAYYKKFGIPT
QIMAASFRTKEQVLALAGCDLLTISPKLLDELKKSQHPVKKELDPAEAKKLDVQPIELTESFFRFLMNEDAMA
TEKLAEGIRIFAGDTQILETAITEFIKQIAAEGA

>core/471/1/Org1_Gene445

MTTPAYLLANFGGPRHAKDLQEFLISLLTDRDVTGTFLPRVLHRHLFTFIAKKRVPKVLPQYQSLQNWSPYIF
DTETLAKTLSEILRAPVIPFHRYLPSTHEKTLLALRTLHTRHVIGIPLPHFTYSVTGSIVRFFMKHVP EIPISWIP
QFGSDSKFVSLITCHIRDFLQKLGILEKECCFLFSVHGLPVRYISQGDPYSKQCYESFSAITTNFKQSENFLCFQS
KFGPGKWLS PSTAQLCQNIDTDKPNVIVVPFGFISDHLETLYEIERDYLPLLRSRGYRALRIPAIYSSPLWVSTL
VDIVKENSTVVAEELIKSGKKHTGIR

>core/472/1/Org1_Gene250

MDAKMGYIFKVMRWIFCFVACGITFGCTNSGFQNANSRPCILSMNRM IHDCVERVVGNRLATAVLIKGSLDP
HAYEMVKGDKD KIAGSAVIFCNGLGLEHTLSLRKHLENNPNSVKLGERLIARGAFVPLEEDGICDPHIWMDL
SIWKEAVIEITEVLIEKFPEWSAEFKANSEELVCEMSILDSWAKQCLSTIPENLRYLVSGHNAFSYFTRRYLATP
EEVASGAWRSRCISPEGLSPEAQISVRDIMAVVDYINEHDVSVVPEDTLNQDALKKIVSSLKKSHLVRLAQK
PLYSDNVDDNYFSTFKHNVCLITEELGGVALECQR

>core/473/1/Org1_Gene372

MMTYPVPQNPLLLRILRLMDAFSKSDDERDFYLD RVEGFILYIDLDKDQEDLNKIYQELEENAERYCLIPKLT
FYEVKKIMETFINEKIYDIDTKEKFLEILQSKNAREQFLEFIYDHEAELEKWQQFYVERSRIIEWLRNNKFHF
VFEEDLDFTKNVLEQLKIH L F DAKVGKEITQARQLLSNKAKIYYSNEALNPRPKRGRPPKQSAKVETETTISD
IYTKVPQAARRFLFLPEITSPSSITFSEKFDTEEEFLANLRGSTRVEDQLNLNLNLSERFASLKELSAKLG YDSLST
GDFFGDDDEKVVT KTKGSKRGRKKSS

>core/474/1/Org1_Gene704

MHSELPNYQNIVESVVTEITTQLLNYSRSEHRLVPFWEKSDGSFITAADYGSQYYLKQQLAKAFNPFIGEETL
YPDQDNEKIPEILKFTRLLTSSVSRDDLSTLVPPPSPTSLFWLVDPIDGTAGFIRHRAFAVAISLIYEYRPILSVM
ACPAYNQTFKLYSAAKGHGLSIVHSQNLDRRFVYADRKQTKQFCEASLAALNQQHHATRKLSTGLPNTSPS
RRVESQYKYALVAEGAVDFFIRYPFIDSPARAWDHVPGAFLVEEAGGRVTDALGAPLEYRKESLVLNNHAVI
LASGDQETHETTLAALQNQLNVVPTDKLIAL

>core/475/1/Org1_Gene546

MKTVTSFTVCKENSGRLDKYLTEVHPKYSRAFYQEHILSGLVQINGQINTRVATRLNCGDIVTIDIQEKEELLE
LLPEAIPLDKVYEDGMILVINKPRDMVVHPAPGHFHGTLVHALLHEIGERLKEEFPEEPWRPGIVHRLDKDTS
GLIITAKTRQAKKVSELFSTKRLKKSILAVCIGKPRSTTIHTHISRHQNKREMTVSSQGKEAVTHCQVLAF
NGKLSFVALSPETGRTHQLRVHMKHLGTPILGDPVYGIPSMNSSYGLDKQQLHAYSVDFTHPETRQFCSLKA
GLPEDMRSLLIKEFRNETTILNKNLLESILKEQ

>core/476/1/Org1_Gene190

MTIDMHCDLLSHPHFCRKDPAVRCSPEQLLSGGVRQQVCAIFVPHSRGEPNCDKQNSLFFSLPNQYPDIGLLS
YEEENGSSSQKKSLSLIRSIENASALGDDTAPLGTLLAKLIHLTKQGPLAYLGIVWKGDNRFGGGTEAPKRL
SNDGKVLLDIMYELGVPIDLSHCSDKLAEDILDYADKLPNLAVIASHSNFRSVLDHRRNLVDAHAKEIVRRK
GVIGLNLVRSYVGDSLGDLEKHVLHAENLGILSSIVLGSDDFFYANEDENFFFNECSSAEAHPLVNQLIHRIFSK
GKAESILSSRAEKFLKQVIVEQVNPKITDVKL

>core/478/1/Org1_Gene850

MIEFAFVPHTSVTADRIEDRMACRMNKLSTLAITSCLVLISVCIMIGILCISGTVGTYAFVVGIIFSVLALVACV
FFLYFFYFSSEEFKCASSQEFRFLPIPAVVSALRSYEYISQDAINDVIKDTMQLSTLSSLLDPEAFFLEFPYFNSLI
VNHSMEADRLSREAFLLIGEITWKDCETKILPWLKDPNITPDDFWKLLKDHFDLKDFKKRIATWIRKAYPE
IRLPKKHCLDKSIYKGCCKFLLLAENDVQYQRLHVKVCYFSGEFPAMVLGLGSEVPMVLGLPKVPKDLTWE
MFMENMPVLLQSKREGHWKISLEDVASL

>core/479/1/Org1_Gene302

MELLPHEKQVVEYEKAIAEFKEKNKNSLLSSSEIQKLEKRLDKLKEKIYSDLTPWERVQICRHPSRPRTVNYI
EGMCEEFFVELCGDRTFRDDPAVVGGFVKIQGQRFVLIGQEKGCDTASRLHRNFGMLCPEGFRKALRLGKLA
EKFGLPVVFLVDTPGAYPGLTAEERGQGWAIKKNLFELSRLATPVIIIVIGEGCSGGALGMAVGDSVAMLEH
SYYSVISPEGCASILWKDPKKNSEAAASMLKMHGENLKQFGIIDTVIKEPIGGAHHPALVYSNVREFIIQEWLR
LKDLAIEELLEKRYEKFRSIGLYETTSESPEA

>core/480/1/Org1_Gene514

MASNPILQIEDLSITLAKQRQQYPIVQSLSTINEGQTLAIIGESGSGKSVSAHAILRLLPCPPFSVSGQVNFQGH
NLLTASRSIQKKIIGTEISMIFQNPQASLNPVFTIEQQFREIIHTHALTAEVAKEKMLYALEETGFHDPRLCLNL
YPHQLSGGMLQRICIAMALLCSPKLLIADEPTTALDVSQYQILQLLKTQKKTGMSLLIITHNMGVVAETAD

DVLVLYAGRMVECAPAVQMFHNPSHPYTRDLLASRPSLQPQQLGSFNPPIGQPPHYTAFPSGCRYHPRCSKIL
NRCSAEAEPIYPVREGHKVRCWLYDD

>core/481/1/Org1_Gene247

MALGSPSPYYGVSFQFFSVFFSRLFSGSLFTGSLYIDDIQIIVFLAISCAGAFAGTFLVLRKMAMYANAVSHTVL
FGLVCVCLFTHQLTTLSLGTTLAAMATAMLTGFLIYFIRNTFKVSEESSTALVFSLLFSLSLVLLVFMTKNAH
IGTELVLGNADSLTKEDIFPVTIVILANAVITIFAFRSLVCSSFDSVFASSLGIPIRLVDYLIIFQLSACLVGAFKA
VGVLMAFLIIPSLIAKVIAKSIRSLMAWSLVFSIGTAFLAPASSRAILSAYDLGLSTSGISVVFLTMMYIVVK
FISYFRGYFSKNFEKISEKSSQY

>core/482/1/Org1_Gene515

MTTNFPQPLIQATSLTKHYKRSFWFQGKTIASRPVDDVSFSLYSRRAVGLIGESGSGKSTLALALAGLLPLTS
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LSEEFYRYPHQLSGGQQQRVSIARALLGVPQLICDEIVSALDLSIQAQILNMLAELQKKLSLTYLFISHDLAV
VRSFCTEVFIMYKGQIVEKGNTKRIFSDPQHYPYTRMLLNAQLPETPDQRQSKPIFQEYHKDSEESCSTGCYFY
NRCPQKQEACKSEIIPNQGDAAHTYRCIH

>core/483/1/Org1_Gene558

MEKKYYALAYYYITRVDNPHEEIALHKKFLEDLDVSCRIYISEQGINGQFSGYEPHAELYMQWLKERPNFSKI
KFKIHHIKENIFPRITVKYRKELAAALGCEVDLSKQAKHISPQEWHEKLQENRCLILDVRNNYEWKIGHFDNAT
LPDIQTFREFPEYAEKLAQECDPETTPVMMYCTGGIRCELYSPVLLEKGFKEVYQLDGGVIAYGQQVGTGKW
LGKLFVFDDRLAIPIDESDPDVAPIAECCHCQTPSDAYYNCANTDCNALFLCCDECIHQHQGCCGEECSQSPR
VRKFDSSRGNKPFRAHLCEISENSESASCCLI

>core/484/1/Org1_Gene439

MKQLLFCVCVFAMSCSAYASPRRQDPSVMKETFRNNYGIIVSGQEWVKRGSDGTITKVLKNGATLHEVYSG
GLLHGEITLTFPHTTALDVVQIYDQGRLVSRKTFFVNGLPQSQEELFNEGDGTFVLTRWPDNNDSDTITKPYFIET
TYQGHVIEGSYTSFNGKYSSSIHNNEGVRVSFSSNNILLSEETFNEGVMVKYTTTFYPNRDPESITHYQNGQPHG
LRLTYLQGGIPNTIEEWRYGFQDGTTIVFKNGCKTSEIAYVKGVKEGLELRYNEQEIVAAEEVSWRNDFLHGER
KIYAGGIQKHEWYYRGRSVSKAKFERLNAAG

>core/486/1/Org1_Gene484

MNLKVVFYFGTPTFAATVLQDLLHHKIQITAVVTRVDKPQKRSAQLIPSPVKTIALTHGLPLLQPSKASDPQFIE
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GDMANITRVPIGPDMTSGELADALASQGAEVLIKTLQQIESGQLQLVSQDAALATIAPKLSKEEGQVPWDKP
AKEAYAHIRGVTPAPGAWTLFSFSEKAPKRLMIRKASLLAEAGRYGAPGTVVVTDRQELAIACSEGAICLHE
VQVEGKGSTNSKSFLNGYPAKKLKIVFTLNN

>core/488/1/Org1_Gene315

MSKGSSKHTVRINQTWYIVSFILGLSLFAGVLLSTIYYVLSPIQEQAATFDRNKQMLLAAHILDFKGRFQIQEK
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QSPLPFYVILENTSRTENMSGADVAKDLSTVQALIFPISGFGLWGPIHGYLGVKNDGDTVLTAWYQQGETP
GLGANITNPEWQEQQFYGKKIFLQDSSGTTNFATTDLGLEVVKGSVRTTLGDSPKALSAIDGISGATLTCNGVT
EAYVQSLACYRQLLINFSNLTHEKKTGE

>core/489/1/Org1_Gene462

MRLLSILKLHLFSLRSSSSLSPHYHSCSRSMHLHLLCRWKDADIMEWQQICNILSGVCSRMSGKLVSLQKETQ
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SVQRTEISEGRRLCYEHKIKQLEEQLQRYVSQHGAPSIEIEEDKSSAAYAEINRLKKSLIDLQQEKDIYIKTYHS
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DHLKGLLGKEPESEVDVVFSESKSLGS

>core/490/1/Org1_Gene738

MEVQIGIDLMGGDHSPLVVWQVLVDVLKSQSSTIPFAFTLFASEEIRKQIQEEFISDLPQEKFPKIISAENFVAM
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VGANISVKPEEMVGFARMGLAYRQCLGDSKIPTIGLLNIGSEERKGTEAHRQTFRMLRETFGAEFLGNIESGA
VFDGAADIVVTDGFTGNIFLKTAEGVFEFLQRILGDKLEADIQRRLDYTFYPGSVVCGLSKLVKCHGKACGS
SLFHGILGSINLAQARLCKRILSNLI

>core/491/1/Org1_Gene424

MLISISLATLPILAFSWASFIENWLRRTAIPWRLPKKHAHLHGLRIAQISDLHFHKRVPEKFLNKVSKSIKNFSP
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LFSSPSYRYDPNLTPQEPHPDLLKLLKNTPLTLLHNTTHVIPNTLNIVGLGDLFARQFHPEQAFKNYDPSLPGL
LLSHNPDGITRLQQYPGDFVLSGSHGPGQVTLSPWPKFARKFFERLSGLENPYLARGYFVTKEGKQLYVNRGL
GGLKRIRFCSPPEICYITCSYD

>core/492/1/Org1_Gene765

MVLSSDLLRDDKQLDLFFASLDVKKRYLLALSGGSDSLFLFYLLKERGVSTAVHIDHGWRSTSAQEAKELE
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LTNLKAMAERSYVEDVLLLRPLLHIPKSSLKEALDARGISYLQDPSNEDERYLRARMRKKLFPWLEEVFGKNI
TFPLLTLGEESAELSEYLEKQAQPFFSAATHQDSQGELPCPDCLIQQAFLCKWVMKKFFNNAGIAVSRHFLQ
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>core/493/1/Org1_Gene502

MKFLLYVPLLLVLVSTGCDAPVSFEPFSGKLSTQRFEPQHSAEEYFSQGQEFLLKGNFRKALLCFGIITHHFP
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MNADEDALRIYDEILTAFPSKDLGAQALYSKAALLIVKNDLTEATKTLKKLTLQFPLHLSSEAFVRLSEIYLQ
QAKKEPHNLQYLHFAKLNEEAMKKQHPNHPLNEVVSANVGAMREHYARGLYATGRFYEKKKKAEEAANIY
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>core/494/1/Org1_Gene357

MNRRKARWVVALFAMTALISVGCCPWSQAKSRCSIDKYIPVVRNLLEVCGLPEAENVEDLIESSSAWVLTPE
ERFSGELVSICQVKDEHAFYNDLSLLHMTQAVPSYSATYDCAVVFGGPLPALRQRLDFLVREWQRGVRFKKI
VFLCGERGRYQSIEEQEHFFDSRYNPFPTENWESGNRVTPSSEEEIAKFVWMQMLLPRAWRDSTSGVRVTF
LLAKPEENRVVANRKDTLLLFRSYQEAFFGRVLFVSSQPFIGLDACRVGQFFKGESYDLAGPGFAQGVLKYH
WAPRICLHTLAEWLKETNGCLNISEGCFG

>core/495/1/Org1_Gene848

MRKVAFLVSCFLSVAIGASAAPVRVPGFPQIPEDLVQIKTEVCPKQEVCLAVTIKCDDHNLIGVLHLPNTPTPE
GGFPTVVLFHGFGRGTKFGGLTGAYRKLGRKFAAAGIATLRVDMAGCGDSEGVAEEVPIETYLRDAQTILETV
QEHPDLNAYRLGISGFSLGCHIAFELAKIYNPRDLNIKALSVWAPIADGGILLKELYENFSKHGEGDIISVGKDF
GFGPPPIIVCSGDVDLLIRIQDHVTANSLPTKPYILHQQGIDDTLVSRTQQTLFKNTAPGRMTFISYPNTGHNLA
TAPDLDMILDQIVSHFQRTL

>core/496/1/Org1_Gene324

MFKLLFHIAAFAGHVLSTPIFIVQDACGIDEEACKNPPPRPFSAQVQYLKVNDKFKKLPHQTIGYRQYDGT
LCTLPITEHSGLLFSTGYIGADIQWKSSLPISETDPNGLGWATFQDTSFYNYVLLSLGAYTSLKNWQWSIILS
GLVDPKNIEMGYGLYQGVLSGKYQATEKLSAIFGVINETGLHQEKAWPLVGVSYKATDQLTLNCIYPVNFSI
DYRSTSVCNLGLAYRLTRFRKKLHKNHLISSRGIFEYQGREIEANVKLTPWPGSFIKGFYGWSIGNDISIADHD
NNNKTSHTFKTSAFFGGSAVMNF

>core/497/1/Org1_Gene142

MLVELEALKREFAHLKDQKPTSDQEITSLYQCLDHLEFVLLGLGQDKFLKATEDEDVLFESQKAIDAWNALL
TKARDVLGLGDIGAIYQTIEFLGAYLSKVNRRAFCIASEIHFLKTAIRDLNAYYLLDFRWPLCKIEEFVDWGN
DCVEIAKRKLCTFEKETKELNESLLREEHAMEKCSIQDLQRKLSDIIEHLDVSLFCFSKTPSQEEYQKDCLYQS
RLRYLLLLLYEYTLCKTSTDFQEQARAKEEFIREKFSLLELEKGIGKQTKELEFAIAKSKLERGCLVMRKYEAA
AKHSLDSMFEEETVKSPRKDTE

>core/498/1/Org1_Gene277

MTLPMQKSLTSFDDFSQAYA EKVPAIALIGSALEDDKDALIELLVSESFKELGGQGLMPATLMSWTETFALFQ
EHETLGIIHA EKFP L ATKEFLSR YARNPQPHLTILIFTTKQECFRELSKALPSALSLSLFGWPADRQKRIRLLL
QRAERVGISCSQSLASFLRALASTSLPDILSEFDKLLCSVGKKTSLDHSDIKELVVKKEKASLWKFRDSLLKR
DPVEGHQQLHFLLEDGEDPLGIITFLRTQCLYGLRSIEEGSKENKHRMFVLYGKERLHQALNSLFYAETLIK
NVQDPIVAVETLVIRMVNL

>core/499/1/Org1_Gene134

MFSYIKNRILFNLLSLWIVLTLTFLVMKTIPGDPFNDEGCNVLSEEVLTQTLKSRYGDKPLYQQYTQYLHSHIAK
LDFGNSLVYKDRKVTNIISTAFPISAILGLQSLFSLIGGGIALGTIAALKKKKQRRYILGASILQISIPAFIFATLLQ
YVFAVKIPLLPIACWGSFTHTILPTLALAVTPMAFIIQLTYSSVSAALNKDYVLLAYAKGLSPLKVVIKHILPYA
IFPTISYSAFLT TTTVITGTFAIENIFCIPGLGKWFICSIKQRDYPVALGLSVFYGTFLMLSSLLSDLIQSIIDPQIRYA
HGKEKKRK

>core/500/1/Org1_Gene246

MAMLPKFFLVLLCLGLCSCSQKTTTIEGEQMTIFYRIVLGTSLSAKEKASLSQQIDRCFHKIDSIYNNWNPYSE
LSIINRAPADVPIITLSVELSEFLDQVDTLYKLSEGRFDPTVGPLKTLWLLHLKSQTLPPKDVWEQHYKDMGW
QHLEFQSNTKTLIKKNPHVQIDLCGVVKGYYAVDCLNEICNTFCPNNYVEWGGEIKTSGHHPSGRPWRIFSEA
AGTILDIDDMAIATSGNHIQKWCVEGKIYTHILDTRTGKPLELSSYPYQSVSVVHPSCAYADAIATVLMTFDSK
IEAKQWAEHHILTYINDGASS

>core/501/1/Org1_Gene945

MWRVVLRFLIIFILGRVVFPLRASESFSWETSTCLTVLGIPFIDIILTNEDEFVAQCGLQIGTISSTNNAKIKEIFLI
YKEKFPEASISFKRKEPLNLSQSHLSDLGILCMRNGETYAEGMANKENGPAKQPKDLRLVLRCPNQPDITLL
YSEKEAEKGIETNTCLCNQGYTLLDGQLILYGDSIEKFLKETKRKNNHTLVDLCDSSQVVTTFLLGRFWSLLNY
VQVFLSEDSAKILAGIPDLAATQLLSHTVPLLFIYTNDSDIIEQKESSTYNTQDLTEPILGFLFGYINRGSM
EYCFNCAQSSLGET

>core/502/1/Org1_Gene9

MIASIYSFLDYLMVKSSASPHLTRNYCLDLNGLKIFLEERGNLAPSSPLQLATEKRKVSELPPSLFTKEHVRM
YIAKLIENGKAKRTIKRCLSSIKSFAHYCVIQKILLENPAETIHGPRLPKELPSPMTYAQVEVLMATPDISKYHG
LRDRCLMELFYSSGLRISEIVAVNKQDFDLSTHLIRIRGKGKKERIIPTVSNAIQWIIQIYLNHPDRKRLEKDPQA
IFLNRFGRRISTRSDRSFQEYLRSSGLSGHITPHTIRHTIATHWLESMDLTKTIQALLGHSSLETTTIVYTQVSV
KLKKQTHQEAHPHA

>core/503/1/Org1_Gene227

MIHSRLIIIGSGPSGYTAAIYASRALLHPLLFEFFSGISGGQLMTTTEVENFPGFPEGILGPKLMNNMKEQAVR
FGTKTLAQDIISVDFSVRPFILKSKEETYSCDACIIATGASAKRLEIPGAGNDEFWQKGVTAACVCDGASPIFK
NKDLYVIGGGDSALEEALYLTRYGSHVYVHRRDKLRASKAMEARAQNNEKITFLWNSEIVKISGDSIVRSV
DIKNVQTQEITTREAAGVFFAIGHKPNTDFLGGQLTLDESGYIVTEKGTSTSVPGVFAAGDVQDKYYRQAV
TSAGSGCIAALDAERFLG

>core/504/1/Org1_Gene780

MRKLILCNPRGFCSGVVRAIQVVEVALEKWGAPIYVKHEIVHNRHVVNALRAKGAIFVEELVDVPEGERVY
SAHGIPPSVRAEAKARKLIDIDATCGLVTKVHSAKLYASKGYKIILIGHKKHVEVIGIVGEVPEHITVVEKVA
DVEALPFSSDTPLFYITQTTLSDDVQEISSALLKRYPSIITLPSSSICYATTNRQKALRSVLSRVNYVYVVGDV
NSSNSNRLREVALRRGVPADLINNPEDIDTNIVNHSGDIAMTAGASTPEDVVQACIRKLSSLIPGLQVENDIFA
VEDVVFQLPKELRCS

>core/505/1/Org1_Gene636

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LPQATTEVLASDFQGNVSALHTLLDSGITYNHNHNVETVARLSPLVRHKATYARSMFMLEQAANYLPDLKIKS

GIMVGLGEMEGEVKQTLQDLASIGVRIVTIGQYLRPSRKHLQVKSYVTPETFDYYRRVGEAMGLFVYAGPFV
RSSFNADMILASVQDKASA

>core/507/1/Org1_Gene213

MKKRYAFLFPGQGSQYVGMGQDLYMEYPEVRELFDFANERLGFSLTSIMFEGPEDLLMETVHSQLAIYLHS
MAVVKVLSQRSSIQPSLVSGLSLGEYTALVASDRISVLDGLELVRKRGQLMNEACNQSPGAMAALLGLPSEV
IEENITSLGQGIWIANYNAPKQLVVAGIAEKVDQAIELFRDLGCKKAVRLKVSGAFHTPLMQVAQDGLAPDI
YALCMKDSSLPLVSHVVGKSLVNTEEMRECLARQMTSPTLWYQSCYHIESEVDEFLELGPVKVLAGLNRSIG
ISKPITSLGTFAQIEKFLSEV

>core/508/1/Org1_Gene413

MLNSNKFKSKTGAYGDLFQRVHVHSLVLTFLVLLLYSSLFPLTSFALGFITATCGAVGTYEYSSMAKAKMHY
PLSTFSAIGSFLFLALSFLSIRWGHSLPGFFDALPWTLIVVWVWSIFRVRKSTIGALQLSGVTLFSILYVGPIRL
FLHVLYSFIHTQEPYLGIIWWASFLIATTKGADIFGYFFGKAFGNKKIAPQISPNTVVGVFVAGCLGATLISFIF
LQIPTRFASYFPMPIPLGLALGITGFFGDIIESIFKRDAHLKNSNKLKAVGGMLDTLDSLLLSTPIAYLFLIT
QSKEFIG

>core/509/1/Org1_Gene28

MRLFSYDKPKIKVQKIKADGFSGWLKCNHCHEMIHANELGQNYNCCPKCSYHYRITAIERVKLLADKDSWR
PLYTDLKSQDPLEFIDTDYANRLEKARKNTTESEGVIVGICTIGLHPVALAVMDFNFMAGSMGAVVGEKLT
RLIEEAIETRLPVIIVSASGGARMQESVFSLMQMVKTSAAALAKLHEAGLPYISVLTNPTSGGV TASFAALGDIII
AEPKALICFAGPRVVAQVIGEDLPEGAQKSEFLLEHGMIDKIVERKELKTTLQTLDDYFLAQEYTGKSKAPR
DLSKRLKEIFLLTDDSE

>core/510/1/Org1_Gene922

MEIAYSLTSSFSVDSVTVGFFDGCHLGHSNLLSILTSYSGSSGVITFDSHPQTVLSLNHTKLINTKEERLQLLQT
FPIDWLGVLTFDLNFANQSAEEFLTLLHRNLKCKRLILGYDSCIGKEQQSNTEALDTIGKPLGIEVIKIPPYRMD
NIVVSSKAIRQFLSAGNLECAHRFLGHPYAISGKITEGSGIGGSLGFATINLPREESLIPLGVYACEIRYDSTTCQ
GVMNLGTAPTFGRESLYAEAHIFSFAENLYGKEVSIIPRKFLREEKKFQSKETLIRAIEKDILDAQDWFAKGSF
NYEGTA

>core/511/1/Org1_Gene10

MSSRELIILGCSSQQPTRTRNQGAYLFRWNGEGLLFDPGEGTQRQFIFANIAPTTVNRIFVSHFHGDHCLGLGS
MLMRLNLDKVSHPHICYYPASGKKYFDRLRYGTIYHETIQVVEHPISEEGIVEDFGSFRIEAQRLQHQVDTLG
WRITEPDTIKFLPKESRGIRGLIIQDLIRDQEISIGGSTVYLSVSYVRKGDSIAIIADTLPCQAAIDLAKNSCM
MLCESTYLEQHRHLAESHFHMTAKQAATLAKRAATQKLILTHFSARYLNLDIFYKEASAVFPNVSVAQEYR
SYPFPKNPLLNK

>core/512/1/Org1_Gene629

MRSIFRFSLCFFTLVSCCFADASLYENSCPSRCQPTPPSNSNPLNVVQQPVAASSVPSYMPPLNADDVLPRD
HLSDGFSFDTPDITTQAILIFLALSPFLVMLLTSYLKIIITLVLLRNALGVQQTPPSQVLNGLIALILSIYVMFPT

GVAMYKDARKEIEANTIPQSLFTAEGAETVFVALNKSKEPLRSFLIRNTPKAQIQSFYKISQKTFPSEIRAHHTA
SDFVIIIIPAFIMGQIKNAFEIGVLIYLPFFVIDLVTANVLVAMQMMMLSPLSISLPLKLLIVMVDGWTLTLLQGL
MISFK

>core/513/1/Org1_Gene757

MKEAAPMHFPFPVRRSVWLNRYSTFRIGGPANYFKAIHTIEEAREVIRFLHSINYPFLIIGKGSNCLFDDRGRFD
GFVLYNAIYGKQFLEDARIKAYSGLSFAALGKATAYNGYSGLEFAAGIPGSVGGAI FMNAGTNESDISSVVRN
VETINSEGELCSYSVEEELS YRSSRFHRQQEFILSATFQLSKKQVSADHSKSILQHRLMTQPYTQPSAGCIFRN
PEGTSAGKLIDAAGLKGLAIGGAQISPLHANFIINTGKATSDEVKQLIAIIQSTLKTQGIDLEHEIRIIPYQPKIHS
PVSEK

>core/514/1/Org1_Gene999

MSLFLVFLTAFIWSSSFALSKLVMNASAPIFATGARMVIAGAILALAAWFRGGFVGISKKIFLYIVLLALTGFY
LTNIFEFIGLQSLSSSKTCFIYGLSPLMSALFSYIQLKEKVTLKKVLGLSLGLVSYICYLTFGGGGDDSQPWTW
QIGLPELLILGAASLASFGWTLLRQIEKQSTLSVTAINAYAMLIAGMLSIMHSAVVEPWRLPVQDISQFLYAT
LALVVISNLICYNLYAKLLRKYSSTFLSFCSLVMPLYSGFYGWILLGEKGVSLGLVLAVAFMVAGCRLIYHEE
FRQGYIVS

>core/515/1/Org1_Gene641

MQKPQYIDRITKKKVIEPIFYEKTMLFLYNSKL GKKLSVFLSTHPIFSRIYGWLQRCSWTRRQIRPFMNRYKIS
EKELTKPVADFTSFNDFFTRKLKPEARPIVGGKEVFITPVDGRYLVYPNVSEFDKFIVKSKAFSLPKLLGDHEL
TKLYAHGSIVFARLAPFDYHRFHPCDCLPQKTRCVNGALFSVHPLAVKDNFILFCENKRTVTVLETEQFGNV
LYLEV GAMNVGSIVQTFSPNQTYAKGDEKGFFAFGGSTVILLFLPNAIRFDNDLLKNSRMGMFETRCLMGQSL
GRSQREEI

>core/516/1/Org1_Gene786

MTMPSTQFHTTILEQFSLFLSVDRGLCQQSIAAYRQDISSFLTISAISSPQDISQNSVYIFAEELYRRKEAETTLA
RRLIALKVFFLFLKDQQLLPYPPIIEHPKIWKRLPSVLT PQEVDALLAVPLQMEKNPRHLAFRDTAILHTLYST
GVRVSELCDLRLGHVSDDCIRVTGKGSKTRLVPLGSRAREAIDAYLCPFRDQYQKKNPHEDHLFLSTRGHKL
ERSCVWRIHNYAKQVTSKPVSPHSLRHAFATHLLDNKADLRVIQEMLGHARIASTEYVYTHVAADSLIEKFL
AHHPRNL

>core/517/1/Org1_Gene296

MLKIDLTGKVAFVAGIGDDQGYGWGIAKLLAEAGATIIVGTWVPIYKIFSQSWELGKFNESRKLSNGTLLEIA
KIYPMDASFDSPEDVPEDIAENKRYKGITGFTISEVAEQVKKDFGHIDILVHSLANSPEISKSLLET SRKGYLAA
LSASSYSFVSLLSHFGSIMNRGGSTISLTYLASMRAVPGYGGGMSSAKAALES DTKTLAWEAGRRWGIRVNT
ISAGPLASRAGKAIGFIERMVDYYQEWAPIPEAMNAEQVGAVAAFLASPLASAITGETLYVDHGANVMGIGP
EMFPKDS

>core/518/1/Org1_Gene815

MPPPFVVTLT TSAQNNLRDQLKEKNFIFSQPQNTVFQARSNTVTCTLYPSGKLVIQKGKSEEFIEFFLEPEILHT
FTHARVEQDLRPRLGVDES GKGDFFGPLCIAAVYASNAEILKKLYENKVQDSKNLKDTKIASLARIIRSLCVC
DVIIYPEKYNELYGKFQNLNTLLAWAHATVINNLAPKPAGDVFAISDQFAASEYTLLKALQKKETDITLIQK
PRAEQDVVVAAASILARDAFVQSIQKLEEQYQVQLPKGAGFNVKAAGREIAKQRGKELLAKISKTHFKTFDE
ICSGK

>core/519/1/Org1_Gene192

MHLEENQGW EALLRKVYHQEVPPAILLHGFTLPVLQDKAEQLASEILLSSSPGSEHKVSQKIHPDIYQFFPEG
KGRLHSIDLPRGIKKQIYISPF EANYKIYIIHEADRMTLAAISAF LKVFE EPPKHAVIILT TAKVQRLPKTIISRLS
IFIERGEKILCSKETFSYLF RY AQCEIPVTEVSQIIKESSETDKQVLRDKVQR FMEV LLELYRDRYTLNLGLKAS
ALNYPEHVKEILQLPLLPLDKVLLIVESACRSLNNSSSAASVLEWVAIQLVSLQYKEKELVSVSPGQDLSN

>core/520/1/Org1_Gene186

MRLNYFLNLVNF KY SIFSILFLSASTVFALSINEISQNL SFKEGFKISVFGAIAFVFARTTGIVVNQCIDRFIDKKN
TRTSKRVL PANLVSLNFAWVLSLFC SFLFLCKILRIFSLGIASLTLMIVYPYMKRVTF FCHWGLGLVYTVAI
LMNFCAFAESGLSMRLCFLALLWGGSVGMVIAANDIYAIEDTEFDRE EGLRSVPAHYGEKKAVEIAKVN LW
VSYLAYIFSGFVGSLDKEFYFTAIIPLVVILKVVRMYSNYSKKDQEGESKFFLANIAIALSFLVSMTLFWSLSR

>core/521/1/Org1_Gene308

MSERAHIPVLVEECLALFAQRPPQTFRDVTLGAGGHAYAFLEAYPSLTCYDGSDRDLQALAI AEKRLET FQD
RVSF SHASFEDLANQPTPRLYDGV LADLGVSSMQLDTL SRGFSFQGEKEELDMRMDQTQELSASDV LNSLKE
EELGRIFREYGE EPQWKSAKA VVHFRKHKKILSIQDVKEALLGVFPHYRFHRKIHPLTLIFQALRVYVNGED
RQLKSLTSAISWLAPQGRLVIISFCSSEDRPVKWFFKEAEASGLGKVITKKVIQPTYQEVRRNPRSRSAKLRC
FEKASQ

>core/522/1/Org1_Gene965

MSRHEICPEVSHKKGKYYSTFIFRCIHSLAGIAFTFFLCEHLFTNMLASSYFSQGKG FVAMVNGFHKIPGLKII E
VAGLVLPFLCHAIIGIVYLFQGKSNCYSGDGRPHLRYAKNYSYTWQRWTAWILLFGIAFHVVHLRFIRYPVH
VDIHGTTYAYAVDIQPSRYDVIVRGTKGFLTNLNP NTEASSIEVSRHDLGGADAALLSERNSYLLTPSAGTAFLY
VVRDALGSLFIALLYTILVIAAAFHGFNGLWTFCCRWGVVVS LRMQGVLRIVCYLAMTVVTFMGVSAVWN
LYSVA

>core/524/1/Org1_Gene163

MRRFLFLILSSLPLVAFSADNFTILEEKQSPLSRVSIIFALPGVTPVSFDGNCPIPWFSH SKKTLEGQRIYYSGDSF
GKYFVVSALWPNKVSSAVVACNMILKHRVDLILIIGSCYSRSQDSRFGSVLVSKGYINYDADVRPFFERFEIPD
IKKSVFATSEVHREAILRGGE EFISTHKQEIEELLKTHGYLKSTTKTEHTLMEGLVATGESFAMSRNYFLSLQK
LYPEIHGFDSVSGAVSQVCYEYSIPCLGVNILLPHPLESRSNEDWKHLQSEASKIYMDTLLKSVLKELCSSH

>core/525/1/Org1_Gene184

MSHGPRPTKFSFPLYFSKTL SWFILGGFLAACGVQMVLVPNELIDGGIVGLSIIASHFLGHKALPFCLVLFNL PF
VFLAFKQIGKYFVIQMLTAVIIFSCSLWLIDQLPSWLGMSPFVFKGSEMETVVLGGAIIGVGCGLIIRHGGSTD

GTEILGIIINKKKGYTVGQIILFVNFFIFALSGIVYKNWHTAFVSFLTGYGIATKVMMDMVILGLEDTKSVTIITSSP
RKLGHILMETLGIGLTYIHAEGGYSGEPRNLLYVVVERLQLSQLKEIVHREDPSAFIAIENLHEVINGRRT

>core/526/1/Org1_Gene685

MQEKPRHVHRIIHISDVHFHVLVPVNPVHCFNKRLKGLLRKVFGLVHFQATTIGQRFPKVVRSLGADSVICITGD
FSLTAMDGEFLLAKHFVETLAKHSSVYLLPGNHDVYTLKSLAQQTIFYTHFPNDQLQQNKVSFHKITDHWL
ILLDCSCLNGWFSANGVVHLAQISAIETFLLSLSPEENVIIANHYPLLSSQNPSHDLINNTHLQNVLKKYPKVR
YLHGHEHQAADVNCADTSPSYILNSGSISLPTNSRFHVIDLYPEKYQVHTMILKNLLDFDAPLEIANEATWDC
QKL

>core/527/1/Org1_Gene297

MEKLLVTDIDGTITHQSHHLDKKVYERLYALHQAGWKLFFLTGRYYKYAARLFSDFDAPYLLGCQNGASV
WSSTSSNLLYSKSLPSDLLCILQDCMEGATALFSVESGAPYGDHYRFSPTPIAQLHEYVDPRYFPNAKEREI
LFETRSLKDDYAFPSFAAAKVFGRLDEVIRIQKELERQEALTSVATMTLMRWPFDFRYAILFLTDKSVSKGKA
LDRVVNILYDGKKPFVMAVGDDANDLDLIERGDFKIVMSSAPEEMHVVHADFLAPPADKNGILSAWEAGVRY
YDDLMSL

>core/528/1/Org1_Gene501

MKKLILYFAAFVASLFCGVFLWDRVPCAQKIMRLAADHSSEVFSKSCRFVRKISGFEELQVFERHVSPEQALA
LFPEYRDGKSFVELAFIPHTLMHVRFKEEPVKKHIISQEGEILWSLVNGEMVLHTGTWTCSKGFRECLLLHA
GKQDMRVIQTLATLGGTTSRESLAQALALKNIRAERVIKECQKKKLIFASGNQIGTHFQQFQPIRGCTTTLNN
NPVWLQKPRHAAVFPAQYSEDRVRHLVKMIFGDNFLIVRSSMVYVPVYKISLVSADNSVRVEYINAVTGKSF
QDL

>core/529/1/Org1_Gene747

MFHSLSKNTPIITQGITGKAGSFHTEQCLAYGTNFVGGVTPGKGGTLWLDLPVYDSVLEAKQATGCRATMIF
VPPPYAAEAILEAEAEAGIELIVCITEGIPVRDMLEVARVMDNSTSQLIGPNCPGIHKPGECKIGIMPGYIHLPGNI
GVVSRSGTLTYEAVWQLTQLKIGQSICVGIGGDPLNGTSFIDVLQALEEDPYTELILMIGEIGGSAEEEEAAWI
QAHCTKPVVAFIAGVTAPKGKRMGHAGAIISGNSGDAKSKIQVLRESGVTTVVESPAHIGKTVDAVLRAKEL

>core/530/1/Org1_Gene683

MSKHTSESRIAQDMLERYSGSSVKQFCPYLLLTFNSYYIQTFAKLHGVPVFEGSMFSAAHAPHLKTSILDFKL
GSPGAALTIDLCSFLPDLKAALMLGMCGLRSHYQVGDFVPVASIRGEGTSDAYFPPEVPALANFVVQKAT
TEVLEDKKANYHIGITHTTNIRFWEFNKKFRKKLYETKAQSAEMECATLFAAGYRRNLPIGALLLISDLPLRK
EGIKTKSSGNFIFNTYTEDHILTGQEVIENTLEKVMLKRAASDHKKDQQYRGLPHMEVGEADDTMASGSETSD
SDY

>core/531/1/Org1_Gene556

MKVLPPPSIPLLGAHTSTAGGLKNAIYEGRDIGASTVQIFTANQRQWQRRALKEEVIEDFKAALKETDLSYIM
SHAGYLINPGAPDPVILEKSRIGIYQEILDCITLGISFVNFHPGAALKSSKEDCMNKIVSSFSQSAPLFDSSPPLV

VLETTAGQGTLIGSNFEELGYLVQNLKNQIPIGVCVDTCHIFAAGYDITSPQGWEDVLNEFDEYVGLSYLRA
FHLNDSMFPLGANKDRHAPLGEGYIGKESFKFLMTDERTRKIPKYLETPGGPENWQKEIGELLKFSKNRDS

>core/532/1/Org1_Gene392

MLSSLIRDSFPLILLPTFLAALGASVAGGVMGTIYVVKRIVSISGSISHAILGGIGLTLWIQYKLHLSFFPMYGA
IVGAIFLALCIGKIHLKYQEREDSLIAMIWSVGMAIGIIFISRLPTFNGELINFLFGNILWVTPSDLYSLGIFDLLV
LGIVVLCHTRFLALCFDERYTALNHCSVQLWYFLLLVLTAITIVMLIYVMGTILMLSMLVLPVAIACRFSYKM
TRIMFISVLLNILCSFSGICIAYCLDFPVGPTISLLMGLGYTASLCVKKRYNPSTPSPVSPEINTNV

>core/533/1/Org1_Gene775

MKRNDPCWCGSGRKWKQCHYPQPPKMSPEALKQHYASQYNILLKTPEQKAKIYNACQITARILDELCKASQ
KGVTTNELDELSQELHKKYDAIAAPFHYGSPPFPKTICTSLNEVICHGIPNDIPLKDGDIMNIDVSCIVDGYYG
DCSRMVMIGEVEIKKKICQAALECLNDSIAILKPGIPLCEIGEAEARADTYGFSVVDQFVGHGVGIEFHENPY
VPHYRNRSMIPLAPGMIFTIEPMINVGKKEGVVDPKNQWEARTCDNQPSAQWEHTIAITETGYEILTLLND

>core/534/1/Org1_Gene805

MHLLTATVTPFFPNGTIDFASLERLLSFQDAVGNGVVLLGSTGEGLSLTKKEKQALICFACDLQLKVPLFVGT
SGTLLEEVLDWIHFCDLPISGFLMTTPYTKPKLCGQILWFEAVLNAAKHPAILYNIPSRAATPLYLDTV KAL
AHHPQFLGIKDSGGSVEEFQSYKSIAPHIQLYCGDDVFWSEMAACGAHGLISVLSNAWPEEAREYVLNPQE
DYRSLWMETCRWVYTTTNPIGIKAILAYKKAITHAQLRLPLSIEDFDLENVSPAVESMLAWPKLRTSVFSYS

>core/535/1/Org1_Gene1008

MFKFFRNKLQSLFKKNISLDLIEDAESLFYEADFGTELTEELCARLRWTKKADASTIKDLITVLLRESLEGLPS
QASQSSQTRPIVSLLLGTNGSGKTTTAAKLAHYKERSESVMLVATDTFRAAGMDQARLWANELGCGFVSG
QPGGDAAAIAFDGIQSAIARGYSRVIIDTSGRLHVHGNLMKELSKIVSVCCKALEGAPHEIFMTVDSTLGNNAI
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>core/536/1/Org1_Gene180

MKRRNLQKILPNASTPSTNVAENTGIKDQNLFLDQATLNV DGNVDIENFLETRDLKVADTITSPCEFTVGGGL
SAESSQFKATTLSKGLEITSEDQDGRVPKFTNVSDPQSPRDALTYNYYRNTGCQALNLYTYSSSQPTTVGKP
IETVCQNPNPETYRISASAKIYDAVTRFPYIQFKAPGIYQVTIQIRRESGQHSGLDNPNLYLNL MIGNNKTLLCA
SDTRGYSGGHRTSIAVTGTFTLTEIVATPPHDYPWLFLETTIGLDIKSMSTCVIWFPPQANFAEVD

>core/537/1/Org1_Gene889

MQIPRSIGTHDGSFHAEV TACALLIIFDLVDENKIIRS RDPVVL SKCEYVCDVGGVYSIENKRFDH HQVS YDG
SWSSAGMILHYLKEFGYMDCEEYHFLNNTLVHGVDEQDNGRFFSKEGFCSFS DIKIYNPREEEETNSDADFS
CALHFTIDFLCRLRKKFYDRVCRGIVREAMETEDMCLYFDRPLAWQENFFFLGGEKHPAAFVCFPSCDQWI
LRGIPPNLDRRMEVRVPF PENWAGLLGKELSKVSGIPGAVFCHKGLFLSVWTNRESCQRALRLTLQDRGII

>core/538/1/Org1_Gene627

MGISLPELFSNLGSAYLDYIFQHPPAYVWSVFLLLLARLLPIFAVAPFLGAKLFPSPIKIGISLSWLAIIFPKVLA
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VTIIFWLVGHRIVISLLLQTLFVIPIHSFFPAEMMSLSAPIWITMIKMCQLCLVMTIQLSAPAALAMLMSDLFL
GIINRMAPQVQVIYLLSALKAFMGLLFLTLAWWFIHKQIDYFTLAWFKEVPIMLLGSNPQVL

>core/539/1/Org1_Gene569

MLHALD TYRPSIESAIEKALEGFGPIGHP IRS PVEYALQGGGKRLRPGLVCMMAQGLGLNHDVMD SALAVEF
VHTSTLIADDLPCMDNDDERRGRPTVHKAFDEATALLASYALIPAAYSHLRLNAKKLKEQGCDPREIDIA YNI
IGDITDKNIGCSGVLGGQYDDMFFSNRGQEHVQSIMIKKTGSLFEIACISGWLFGGGDPQFAPIITSFSNNFGLL
FQIKDDFSDLQKDSQQIGLNYALLFGEKAALELLARSQNNCLELLDRLSAGGLKNSSEFETIISLGSF

>core/540/1/Org1_Gene179

MSNPTPKTKISIPTFVRFN IQSINLTEDQKKTTFTVGGKVT TENTVVRGDLTCTDGGLTCQSDLT IQKDINIRPT
STNSMVF DGRNLNSNSPLSYKNSQGQDITDYEKMSSGKPQEYVPFGYYKRTQIMMAQRAAHSSGYVGGGSV
PSGSYVPWNKFDQTSTQKTSGTEIYIDPNDSTKL VFEVNNKVPKLF R ISVIMAKHGSWLDNGTGADILLAANE
YEQGGGRINVTDLAMTTSRGSSYYETRPLQVVCVTYYAQNNGYFTFQNRAGGGRLVSFFSWNIVALPYVE

>core/541/1/Org1_Gene819

MLKIQKKRMCVSVVITVGAIVGFFNSADAAPKKKKIPIQILYSFTKVSSYLKNEDASTIFCVDVDRGLLQHRY
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TLHSLLRQNLSFQKR SIASESFLKIDSAPSDASVFYKGVLF RGETAIVDALSQLFAQLDLSPKKIIFLGEDPEV
VQAVGSACIGWGMNFLGLVYYPAQESLFSYVHPYSTATELQEAQGLQVISDEVAQLTLNALPKMN

>core/542/1/Org1_Gene11

MSHLIPSLRNSVTSYFHKPQPIKQAAPSKSIRDICNIA YLIICVLVVVVVLVGAMLCMFIPSVGIPLCLSSLALLV
LLSIFNPCLINWISTKKTKEIAPKDASESQPTKSASRKGSPQLSPHHDHEPKNFIRTQLEKGVNYVTNFKSGEE
SPHISDEHHSRQSKRSSEIESSDESSPELHRKAKGKAPHTATTKESKTSTTESSKKKKTKHSLHRTTSSIHKR
SAPKPMVPSKKRKPVLLKKT VPLPIEDLEHQSSGNESSDSSSPPPVQRKAILPWFCQPTDP

>core/543/1/Org1_Gene71

MEIKKAIQEGTAYLDYYGVPLSDCEALYILMDLLEVSSRAKLFDLVGISETMLMEYRKRLALRGQRCPTAYL
NGAVSFLGLRLRVDSRVLIPRTETELLA EYIINYLLSHSEIQT FYDICCGSGCLGLAIKKSCPHVEVVLSDVCPQ
AVAVANENAKSNGLDVKILLGDLSAPYTRPADAFVCNPPYLSFNEIIHIDPEVRCYEPWKALVGGSTGLEFYQ
RIAQELPKIVTSTGVGWLEIGSSQGESIKNIFSKHGIYGR LHQDLSGRDRIFLEMDGRDPVSSGAYS

>core/544/1/Org1_Gene224

MAVIYWDRSKIVWSFEPWSRLTWYGVFFTVGIFLACLSARYLALSYYGLKDHL SFSKSQLRVALENFFIYSI
LFIVPGARLAYVIFYGWSFYLQHPEEIIQIWHGGLSSHGGVLGFL LWAAIFSWIYKKKISKLTFLFLTDLCGSVF
GIAAFFIRLGNFWNQEI VGTPTSLPWGVVFS DPMQGVQGVVHPVQLYEGISYLVVSGILYFLSYKRYLHLGK
GYVTSIACISVAFIRFFAEYVKSHQGKVLAE DCLLTIGQILSIPLFLFGVALLIICSLKARRHRSHI

>core/545/1/Org1_Gene245

MLLRGIPAAEKILQRLKEEISQSPTSPGLAVVLIGNDPASEVYVGMKVKKATEIGIISKAHKLPDSTLSSVLKL
IERLNQDPSIHGILVQLPLPKHLDSEVILQAISPDKDVDGLHPVNMGKLLLGNFDGLLPCTPAGIHELLNYYEIP
LRGRHAAIVGRSNIVGKPLAALMMQKHPQTNCTVTVLHSQSENLEILKTADIIAALGAPLFIKETMVAPHA
VIVDVGTTRVPADNAKGYTLLGDVDFNNVVTKCAAITPVPGGVGPMTVAMLSNTWRCYQNFS

>core/546/1/Org1_Gene516

MTEEISKDTIIEVAIDDIRVSPFQPRRVFSNEELQELIASIKAVGLIHPPVVREICTGDRVLYYELIAGERRWRAM
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RLLALSKTIQESLLQGQITLGHAKVILTLEDPILREKLNEIIIQEHLAVREAELIAKQLISEEGSSIELKPTPLDMA
ESSKQHEELQQRLSDLCGYKVQIKTRGSKATVSFHLQNTQDLQKLEAWLSSHGTLSESLS

>core/547/1/Org1_Gene919

MPDKKAQITFSLPEVMSAIHQGKIVALPTDTVYGFVLSLYAPEAEERLYALKDREPSKAFALYVNSIEDIENIS
GYPLSPTAKKLAQLFPGAITLVVKHRNPRFPKETLAFRIVDHSVVREIVDHCGLTIGTSANLSEFPSALTAQEIF
ADFADHDLCIFDGPCSHGLESTVVASDPLYIYREGLISRSVIENIAGTEAKIFHRTSHAFSKHIKIYTVKNQEQL
VSFLSGSLDFKGVVCEHPKPKNFYTRLREALKKKTPSIVFIYDINTSDYPELFPFLSPYYIE

>core/548/1/Org1_Gene918

MKNNINNNECYFKLDSTVDGDLLAANLKTFTDQAAGISSTETFSVQGNATFKDQVSATGLTSGTTYNLNAQ
NFTSSQISIDFKNNRLSNCALPKEDCDPVPANYVRSPEYFFCSKPLIGDFDFNSGESYLPLTGSEYTLYQSRNVN
SIFRFIGWKQSTRELTVGGNTAIQFLAAGTYIVSFTVGKRWGWNNRWGGAIYINNGLGQVQCESTIYSGGGY
ATIGTLGTSIYRASVDVAPNPNDPNASDRYRAGIFYLSNGGSSAGIGNYSFSLLYYPDDR

>core/549/1/Org1_Gene347

MHEVLILTFTYPLPRTLKQHPDEVHTVPISPNLSFGEGSPILIAGPCTLESYEHTVSSALTVKEAGAQVFRGSIR
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IILKRSPAATLEEWLCAA EYILASSPCPGVILCERGIRTFEHSTRYTLDLNTVALLKEISSLPVIVDP SHAAGKR
SLVLPLASAGLSVGADGLMIEVHAHPEKALCDAKQKITPEELHLFAKKHFCPSESRAHAIS

>core/550/1/Org1_Gene173

MKHYSFSPSADFFSKQGAIETQVLFGERVLVKGSTCYAYSQLFHNELLWKPYPGHSFRSTLVPCTPEFHIHP
NVSVVSVD AFLDPWGIPLPFGTLLHVNSQNTVIFPKDILNHMNTIWGSGTPQCDPRHLRRLNYNFFAELLIKD
ADLLL NFPYVWGGRSVHESLEKPGVDCSGFINILYQAQGYNVPRNAADQYADCHWISSFENLPSGGLIFLYP
KEEKRISHVMLKQDSSTLIHASGGGKKVEYFILEQDQKFLDSTYLFRRNNQRGRAFFGIPRKRKAFL

>core/551/1/Org1_Gene136

MDNYLLNIKDLTITSTNPKRTLIENTLSLQKKNRNLALVGESGSGKTTITKAILGFLPENCLIKTGSILFEDIDIT
KLSPKELHKIRGQKIATILQNAMGSLTPSMRIGMQIIETLRQHHKMNKEEA YNKAMQLLTDVCIPNPKYSFSQ
YPFELSGGMRQRVVIAIALASQPKLILADEPTTALDSMSQAQVLRILRNIQQQKQATILLVTHNLSLVKELCND
ICIIKD GKLIETGTVEEIFLSPKHPYTLKLLNAVSKIPIKKTSSPILKNKFQPLMSMQGGL

>core/552/1/Org1_Gene135

MENLSSAPSRSIWKSIIQNKMLVLGLTTLIILMLGALLLPWFYQDYEQTSKDLVSPCSRFPFGTDTLGRCMF
ARTLRGLRSLLIATLATLIDVCVGLLWATVAISGGKKIDFLMMRTTEILFSLPRIPIIILLVIFHHGLLPLILAM
TITGWIPISRIIYGQFLLLKNKPFVLSAKAMHASTFHILKKHLLPNTLAPIISTLIFTIPNAIYTEAFISFLGLGIQPP
QASLGTLVKEGINAIDYYPWLFFFPSLMIALSISFNLIGEGAKTLCLEEGSHG

>core/553/1/Org1_Gene115

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RRRTSHDGPKNRAVLNLIKSSGRRCNAIGLEMTEEDFVIARRREGVYSLYPVEVCSYPQGNPFVIAYAWIADE
SACSKEVLPVKGYYSLVWESVSSSDSLNAFGDSFAEDYLRSTFLANGTSILCVHESYKKVPPQP

>core/554/1/Org1_Gene480

MFKKFKPVTPTGTRQLVLPADFELTTRGELRGTKSKRSLRPNNKLSFFKKSSGGRDNLGHISCRHRGGGAKQL
YRVVDFKRNDGITAKVVTVEYDPNRSAYIALLSYEDGEKRYILAPKGIQRGDVVVSGEGSPFKPGCCMTLK
SIPLGLSVHNIEMRPSSGGKLVRSAGLAAQVIAKSPGYVTLKMPSGEFRMLNEGCRATIGEVSADHNLRVD
GKAGRRRWMGVRPTVRGTAMNPVDHPHGGGEGRHNGYIPRTPWGKVTGLKTRDKNKSNKWIVKDRRK

>core/556/1/Org1_Gene485

MASIHPTAIIPEGAKIGKDVVIEPYVVIKATVTLCDNVVVKSAYAYIDGNTTIGKGTTIWPSAMIGNKPQDLKYQ
GEKTYVTIGENCEIREFAIITSSTFEGTTVSIGNNCLIMPWAHVVAHNCTIGNNVVLSNHAQLAGHVQVGDYAIL
GGMVGVBHQFVRIGAHAMVVGALSIGRRDVPPTYTIGSGNPYQLAGINKVGLQRRQVPFATRLALIKAFKKIYRA
DGCFFESLEETLEEYGDIEVKNFIEFCQSPSKRGIERSIDKQALEEESADKEGV LIES

>core/557/1/Org1_Gene526

MSDFSMETLKTTLRQQTGVLTKCKEAEACGGNLEEAVVYLRKLGLASAGKKEHRETKEGIIAAKTDANGT
ALIEVNVETDFVANNAVREFVSNLLNDILKYKVDTEALSQAASSQDPSLSVDELRAVTMQTVGENIRISRV
AYFPKATNSTVGIYSHGNGKTVALTMLSGSSTADSLAKDIAMHVVAAPQFLSKESVPAEAIAKEKEVIASQI
QGKPQEVIEKIVTGKLNTEFFQEACLLEQPFIKNADLSIQSLIDDFSKTSGSSVAIEQFILWKIGA

>core/558/1/Org1_Gene487

MLERTQRTLKREVRYSVGVIHLGKSSTLHLQPAQTNTGIVFQRQSASGNYENVPALLDHVYTTGRSTTL SRG
SAVIATVEHLMAALRSNNIDNLIQCSGEEIPIGDGSSNVFVELIDQAGICEQEDKVSIALRLTRPVYYQH QDIFL
AAFPSDELKISYTLHYPQSSTIGTQYKSLVINEESFRQEIAPCRTFALYNELCFLMEKGLIGGGCLDN AVVFKD
DGIISRGQLRFADEPVRHKILDIGDLSLVGRPFVAHVLA VSGHSSNIAFGKKILEALEL

>core/559/1/Org1_Gene573

MATAHLGRQALLHLRSWTPAIRASGNLFRQQSMSLHNNVLFAGDIVGAIKNSTAISRHALGSSHYAHAALQK
TEGFLGAADGVNTAVAGAMLWGQLLNGSMIFETDEETGELRRRCNEADAEGCMTQKLQRRSALTITGKVAR
LASKTLGTATFLHEMDVVS LGANANKIGCKVTSCNLVATGCSL TESSISLYRILSTRPETISDPENRNKPSAEF
AARSKAIRNAFI AWLGDVVDLVCDALGTL SFLPAILGVHAVLIMAILGLISCVIN FVKDYAKIG

>core/560/1/Org1_Gene183

MVLMNKRLKIILTNDGITA KGM SCLVSALLEANIGDIYIAAPQAEQSGKSMAISLNQVVCASPYAYPQPVKE
AWAVGGSPTDCVRLGLRTL FESVSPDLVISGINCGNNICKNAWYSGTIGAAKQALVDGIPSMALSQDNHISFF
QQDKAPEILKALVIYLLSQPFCLTGLNINFPTSPGGSSWEGMRLVPPGDEFFYEYPQYLGSVNKNQYYVGKIS
GVRIGEHPSEELACMLENHISVSPIFSQNSPIGLMTLEEFQKTQENFNASLLSSELTTKIF

>core/561/1/Org1_Gene533

MELKKTAESLYSAKTDNHTVYQNSPEPRDSRDVKVFSLEGKQTRQEKTSSKGNTRTESRKFADEEKRVDD
EIAEVGSKEEEQESQEFCLAENAFAGMSLIDIAAAGSAEAVVEVAPIAVSSIDTQWIENIILSTVESMVISEINGE
QLVELVLDASSSVPEAFVGANLTLVQSGQDLSVKFSSFVDATQMAEADLVTNNPSQLSSLVSALKGHQLTL
KEFSVGNLLVQLPKIEEVQTPLHMIASITIRHREEKDQRDQNQKQKQDDKEQDSYKIEEARL

>core/563/1/Org1_Gene860

MRQSFDELSQNAFKNIFNKQRF CFIFCSLCCFGFVFALFLKLCSRLAPEISLSTLGLGAFFCAFSVICASAIIVQF
LLHKESQGETSKLCCA IKNTWSSLWLSLLVSMPPFIAMVAVVTVAMLSSFLGSLPWVGKLFHTVLIFIPYLSA
TALILLFLGSFSLFFCIPVLHNQESIDYRKILLECFRGNILRQFIGVVIALVPLALCSWLALDSFYLMTHLVEIAD
IHTWSFLAQMFVLIVPIALILTPAVSFFFNFSSFSFYLAKEEEKALVK

>core/564/1/Org1_Gene390

MHKVIVFIFLTL YSLKSYGNDVIDKPHVLVSIAPYKFLVEQIAEETCFVYAIVTNHYDPHTYELPPQIKELRQ
GDLWFRIGEAFEKTCERNLTCQQVDLSQNVSLIQGKPCCNQHTTNYDHTWLSPKNLKVQVETIVTTLSKKY
PQHATLYQSNGEKLLLALDQ LNEEILTITSKAKQRHILVSHGAFGYFCRDYNFSQHTIEKSSHVEPSPKDVAR
VFRDIEQYKISSVILLEYSGRRSSAMLADRFHMHTVNLDPYAENVLVNLKTIATTFSSL

>core/565/1/Org1_Gene950

MYFTRDPIIETVITSREGYKLSVRNTKHFSQDPFMVEAIEVISLGNICFFRNCDHSPFLVPAGDYEVMEVRDT
KINLKA VGLDRGVKIAGGREALIKLTKSTPLPVIDEKPLADSP EEGTEPTSPSKKEKKEARKDSFKGEKWKEK
KKLSRRRNHKEIAEVTGASQEILDTVKEELWEESQENEIVEQKKFSLPPPAKLISEVISQTVVDPVVT SADLN
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>core/566/1/Org1_Gene982

MTRSSPAQLSRFLSEIQNKPKKSLSQNFLVDQ NIVKKIVATSEVIPQDWVLEIGPGFGALTEELIAAGAQVIAIE
KDPMFAPSLEELPIRLEIIDACKYPLDQLQEYTTLGKGRVVANLPYHITTPLLTKLFLEAPDFWKT VTVMVQD
EVARRIVAQPGGKDYGSLTIFLQFFADIHYAFKVSASCFYPKPQVQSAVIHMKVKETLPLSDEEIPVFFTLTRT
AFQQRKVLANTLKG LYPKEQVEQALKEGLLLNVRPEVLSLNDYLALFHKMQAG

>core/567/1/Org1_Gene525

MESQSCKLTIKDLMSAGAHFGHQTRRWNP KMKLYIFEEKNGLYIINLAKTLQQLRNALPHIRKVIQDNKTVL
FVGTKKQAKCVIREAAIEAGEFFIAERWLGGMLTNMTTIRNSIKTLDKIEKDLSRNQAYLTKKEAALLAKRH
QKLLRNLEGIRYMKKAPGLLVVVDPSYEKIAVA EAKKLGIPVLALVDTNCDPTPIDHVIPCNDDSLKSIRLIIN
VIKENIIEAKHKLGI EIVSPVKSLEV PDL SAFESSQDDESDEENREEDLLAKKFDGEAN

>core/569/1/Org1_Gene631

MTANTFGTLDILMKHSEDDLSRFLPKNLLVESPHPEEIPLKSLSFTMSWLPTIHPSWITIAMKEFPPEIQGQLL
AWLPEPLVQEILPLPGISIAPHRCAPFGAFYLLDMLSCKIRPCGITEEIFLPASSANAILYYTGPKIALINCLGL
YSIAKELKHILDKVVIERVKNALSPTEKLFLTYCQSHPMKHLETTNFLSSWTTDAELRQFVHKQGLEFLGKAL
TKENASFLWYFLRRLDVGRAYIVEQTLKWTYDHPYVDYFKSRLEQCMKVLVK

>core/570/1/Org1_Gene380

MDYKLLDSGDGNKLECFGPVTLIRPSSIAVWPKSRLPELWSQAQLQYVREGERGAWKNFKRLPEEWEVAFSD
VRCLLKRTPFHGLGVFPEHMGFWPALKQAIEKHKERQVLNLFAYTGAGSIFAAKCGARVTHVDASQA AVR
WAQRNVEKNAFPERRIFWVIEDVISFLKKEIRRNKKYQVILLDPPSYGRGPDGEVFKIDKDLFPLLSLCSKLLA
DDASYFLLTSHTPGHTPEFLRAIARRSVPTLVSEAWSCGESFCGEGVGALPSGSFVQWIA

>core/571/1/Org1_Gene104

MITGVVLEKHEQRTMFSLTLLNNFTTFGLLHTPLHYNPPYPIVILLHGLASDKTGSKRSHVRLAQELTRLGIAA
LRVDLLGHGDCEGELMDFSLENYKQNIREIIEYTHSLLHIDQERLAIFGSSLGGTLALQTLPPFNKIKALAVWA
PTISGELMAAEAQKNAPEVITMSQKGAITYAGMTLNPDFYTQFLKIDIVKELMPSARNLPPILYMQGEQDLLV
SINHRTLFTFAFANQDKPITILTYPDVDHAFPAESSALSDLTQWLKRELTSGE

>core/572/1/Org1_Gene551

MLLGFLCDCPCASWQCAAVANCYDSVFMSRPEHKPNIPYITKATRRGLRMKTLAYLASLKDARQLAYDFLK
DPGSLARLAKALIAPKEALQEGNLFFYGCSNIEDILEEMRRPHRILLGFSYCQPKACPEGRFNDACRYDPSH
PTCASC SIGTMMRLNARRYTTVIPTFIDIAKHLHTLKKRYPGYQILFAVTACELSLKMFGDYASVMNLKGVG
IRLTGRICNTFKAFKLAERGVKPGVTILEEDGFEVLARILTEYSSAPFPRDFCEIH

>core/573/1/Org1_Gene820

MRRYLFMVLAALCLYRAAPLEAVVIKITDAQAVLKFAREKTLVCFNIEDTVVFPKQMVGQSAWLYNRELDLK
TTLSEEQAREQAFLEWMGISFLVDYELVSANLRNVLTGLSLKRSWVLGISQRPVHLIKNTLRILRSFNIDFTSC
PAICEDGWL SHPTKDTTFDQAMAIEKNILFVGS LKNGQPMDAALEVLLSGISSPPSQIHYVDQDAERLRSIGAF
CKKANIYFIGMLYTPAKQRVESYNPKLTAIQWSQIRKNLSDEYYESLLSYVKS KG

>core/574/1/Org1_Gene1005

MKVKINDQLICIPPFISARWSQIAFIESQEGENKDQGT LRLHLIDGKIISIPNLDQSIIDIAFQEHLLYLETSQSGKE
DSRDDD KLGVGVLMNVLQQITKGNDIQVLPKNLISPLFSGTNPIEAILQHTPEHKDHPDAPTDVLEKMADVIR
VLSGNNATLLPRPEPHCNCMHCQIGRVMNEEDTLAVSDKDLTFRTWDIMQSGDKLYIVTNPLNPSDQFSVYL
GPPIGCTCGEPNCEHIKAVLYT

>core/575/1/Org1_Gene283

MKLLKNVLLGLFFSMSISGFSEVKVSDTFVKQDTVVEPKIRVLLSNESTTALIEAKGPYRIYGDNVLLDTAIQG
QRCVVHALYEGIRWGEFY PGLQCLKIEPVDDTASLFFNGIQYQGS LYVHRKDNHCIMVSNEVTIEDYLKSVL
SIKYLEELDKEALSACIILERTALYEKLLARNPQNF WHVKAEEEGYAGFGVTKQFYGVEEAIDWTARLVVDS
PQGLIIDAQGLLQSNVDRLAIEGFNARQILEKFYKD VDFV VIESWNEELDGEIR

>core/576/1/Org1_Gene197

MKKKLSLLVGLIFVLSSCHKEDAQNKIRIVASPTPHAEELLESQEEAKDLGIKLIKLPVDDYRIPNRLLLDKQV
DANYFQHQAFLLDDECERYDCKGELVVIKVVHLEPQAIYSKKHSSLERLKSQKKLTIAIPVDRNTAQRALHLL
EECGLIVCKGPANLNMTAKDVCCKENRSINILEVSAPLLVGSLLPDVDAAVIPGNFAIAANLSPKKDSLCELDL
SVSKYTNLVVIRSEVDGSPKMIKLQKLFQSPSVQHFFDTKYHGNILTMTQDNG

>core/577/1/Org1_Gene344

MVRDIQSESIGKLVFLGTGNPEGIPVPFCSCRVCQNTGIHRLRSSVLIQYQNKTLVIDAGPDFRTQMLVAGVSE
LDGVFLTHPHYDHIGGIDDLRAWYIVTQRSPLVLSASTYRFLNKAKEYLFATPNVESSLPAVLEFTILNEDCG
QEEFQGIPYTYVSYYQKSCHVTGFRFGNLAYLTDLCSYDAKIFSYPDNDVETLILSAGPSETPIPFQGHKSSHLT
VEEAKAFANHAGIKNLIITHISHCLEAERDQHPEVTFAYDGMENVLWTL

>core/578/1/Org1_Gene868

MIRRRFKTLFPPGPQYSLCYASILIVLSSLVCVPTFCWLFLPELSLSKFNPSPIRNLFLVSSTLSKVPPTAIAEHLR
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SLNLPQIFFSQEDLKMQLPKPKMLFTKILLKELAMESPKIIDLSLSDAYPGEIIVTLSSGSLRLPIKTLDRALD
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>core/579/1/Org1_Gene548

MFNNKMILIAGPCVIEGEDITLEIAGKLQSILAPYSDRIQWFFKSSYDKANRSSLNSFRGPGLTEGLRILAKVKE
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GNNKILLTERGCSFGYNNLVSDMRSIPVLSRSGFPVIFDATHSVQLPGALSTESGGLTEFVPTLSRAALAAGAH
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>core/580/1/Org1_Gene426

MTKVALLIAYQGTAYSGWQQQPNDLSIQEVISSLKKITKTRTPLIASGRTDAGVHAYGQVAHFRAPDHPLF
ANANLTKKALNAILPKDIVIRDVALFDDNFHARYLAIAKEYRYSRLAKPLPWQRHFCYTPRHPFSTELMQE
GANLLIGTHDFASFANHGRDYNSTVRTIYTLDIVDKGDSLSIICRGNGFLYKMRNLVGALLDVGKGAYPPE
HLLDILEQKNRREGPSAAPAYGLSLHHVCYSSPYNNFCCEQCSVSTSNEG

>core/582/1/Org1_Gene906

MTQYYFLSSFLPTQLPESVPLFSISDLDDLLYLNLSENDLCNYGLLKRFFDFENFAFFWAGKPIPFSGEVTQE
NIERMLSSQQWSDDNDFEDFFKDFLMNHKSSQDRLNHFSDLFREFLSYHQTNSSKFLQDYFRFQQQLRVVLA
GFRARVLNMDVSYVLRDEDSSDPVVLEVLMQKDSPNYELPEEFSDLQGVLDYGLLPHTLNRALALYQFHK
LEGFCSDSYFDGNVILARCATYMFAIRNSLASVEKGREIINHIEKAIKW

>core/583/1/Org1_Gene124

MHSKFLSRRKKNSSHKEETSWDCIASSYNKIVQDKGHYYHRETILPQLPSLTLGSKSSVLDIGCGQGFLERA
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EPLGQFFIVLNHPCFRIPRASSWHYDENKKAISRHDYRLSPMKIPIMAHPGQKDSPSTLSFHFPLSYWFKELSS
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>core/584/1/Org1_Gene970

MTLPLEPMIFWSSLSAKVMKKFLTPHCAGTFSEEDAEAKEAHLVTGKQGHRLMGNCVTFYWLVDDKKNNGVI
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EQCLEIPLEDGSLPLQNSPMNLDNFEDANPYSQSDWEALTHEQKLYALRATIAEKIGPYIAMDGGEVTVESLEN
FIVTIAYSGNCSGCPSSLGSTLNSIGQLLRAYIYPELQVKVDESSLNLSHP

>core/585/1/Org1_Gene674

MQGFFPLASGSKGNSAYLGTDSCKILIDLGVSKQVVTRELLSMNIDPEDIQAIFVTHEHSDHISGIKSFVKAYN
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WITHELYDCDYLLIESNHSPELVRQSQRPDVYKKRVLSKLGHISNQECGQLLQKIITPKLKKLYLAHLSTECNT
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>core/586/1/Org1_Gene752

MAGLDLEARGKRRVVTNPAITAFGLCCGLFIIFKSVLRTSSSVELFHRLQGLSLLLISAMIADFSDGAIARIMKA
ESAFGAQFDSLSDAVTFGIAPPLIAIKSLDGIYVGNFFSSLLITSIIYSLCGVLRLVRYNLFSSQKTVDVSKPYCFI
GLPIPAAAASIVSLALFLASDFFPDLPAQLRVGLLSFALLFIGGLMISPWKFPGVKHFRFNVSSFLLVVTIGLAA
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>core/587/1/Org1_Gene19

MKKPDNDSTFDVRSFFPFDVLCIEQLRKEMSWEVVSAKIPRLPRGWYELMGLSKEDRIDFCLDFWCSVLGIE
HKESPSICRFFSLLETIEVYIYRLEKEPYQLKMFYVFRDGRCGFQGEPLLDLFGHHRLPPLGDRHYEKFFSIHN
GFGKWEDEGIFPMRSLAKVQKLRQQLVVMNKMQAEDNCYSLGIFPFYGYEEPFAIYQSFFFDPEIRRDLPSP
NVLLNEESLEHRSLETIELLHLSKSYPSFLSWLENYLHSEEVYNE

>core/590/1/Org1_Gene379

MDCIGKHNPLVKEALALKRSRCRKSSWFLVEGAREIQKALRTGYLCQHVFCSHLSSEKEKEFLYELKRNSTK
ILYCLDSTLAQLSFKEHDSFVAVIQKRVWNKEDFLIQRKNAQPFYLIIEQVEKPGNVGAILRIADGAGVDGVI
LCNPIVDLYNPVVRSSLGAVFSLPILSISREEGKELFKQEGWTVFVTSPRAETMYFSKNYLGPTALVFGSEKD
GLTEDWFSEDFSEIALPMLGESDSLNLATSVAAYAYEVVRQRWVN

>core/591/1/Org1_Gene802

MGSSMHVGVIGCSGRTGKVIVSALEQSSEYTLGPGFSRSSALTLFQVIAHNDVLVDFSHPLLTKEVVAHLLISP
KPLIIGTTGFP GKCKEAHDSLEELTHIVPVVCPNASLGAYIHKRLVMLLSQLCNPQFDIRIRETHHRYKKDSL
SGTAQDLLDTIQQVKQEDWGEEYEVGQRDSSKKTIEVQSSRVGDIPGEHEVAFISSGEQILVRHTVFSRNVFG
RGILSILDWLKTLNPQPLYSLGDTLELVLRNEHCLLKKTTDH

>core/592/1/Org1_Gene587

MEKLEFVTSLSPPDDDLITFNKQGLIAGPEEEKVAFLVRSNAMLDAGPETPASFPESLREQFDIFPEYVEVLYS
NEGLDVWEAGCTWILNNEVTIQLRKHHRKASRWLGMYSRDEVLAHEAVHAVRMKFHEPVFEEVLAYQTSR
WGWRRFFGPLFRSPGESYLLFFITLGLGISLWYPAGILIMLVLP MYFLMRLCMAQSYLYRAMKKIRKMLGV
PPLWVLLRLTDKEIKMFAKEPIPVLEHYARKRKLENVRWKQIYQSYFV

>core/593/1/Org1_Gene371

MSNQLQPCISLGCVSYINSFPLSLQLIKRNDIRCVLAPPADLLNLLIEGKLDVALTSSLGAISHNLGYVPGFGIA
ANQRILSVNLYAAPTFFNSPQPRIAATLESRSSIGLLKVLCRHLWRIPTPHILRFITTKVLRQTPENYDGLLLIGD
AALQHPVLPGFVITYDLASGWYDLTKLPFVFALLHSTSWKEHPLPNLAMEEALQQFESSPEEVLKEAHQHTG
LPPSLLQEYYALCQYRLGEEHYESFEKFREYYGTLYQQARL

>core/594/1/Org1_Gene304

MKLT KYLNTKQLRSMISRLFVRYSLPMSKQLSFFALCVLGSHPIFAQTPNPPQVRVRSEVIFIDPGHGGKDQGT
ASKELHYEEKSLTSLALT VQSYLKRMGYKPQLTRSSDVYVDLGKRVALSNRGQGDVFISHCNHSSNAAAF
GTEVYFYNGKVGSPTRNRMSEVLGKNILAAMEKNGILKSRGLKTANFVVIRDTSMPAVLVETGFLSNSRERA
ALQDARYRMHVAKGIAEGVHNFLSGPSFQKPKQNI AKIRKPQIQAN

>core/597/1/Org1_Gene61

MPFDITYYTTPLEIILIWVMLNYLLKFFWGTRAMDVVFGLLAFLFLFVLADKLHLPIIRRLMLHVVNIAAIVV
FIIFQPEIRLALSRI RFHGKKFFIDTQE QFVEQLAASIYQLSERQIGALVVLENKDSFDEYLSFSSVKINATFSEEL
LETIFEPSSPLHDGAVILRGDILAYARVVLPLAHDTTQLSRSMGTRHRAALGASQRSDALIITVSEENGSVLSLR
DGLLTRGVKIDRFKAVLRSILSPKEHKRKP LFSWIWKR

>core/599/1/Org1_Gene137

MTTLLSIKDLSTIRGKKILNHINLNLIKGSYLTIVGPSGSGKSSLALTILDLLKPTTGTITFHMDPKIPRARKVQ
VIWQDIDSSLNPCMSIKGIISEPLNIIGTYSKAEQNKEIYNVLDLVNLPKSVLHLKPYKLSGGQKQRI AIAKALV
SKPELLICDEPLSSDLTNQSLILDLFQTIKKEYQNTLLFITHDMSAAYYIADTIAVMDQGSLVEHACREKIFST
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>core/600/1/Org1_Gene791

MKTWLFFTFLFSCSSFYASCRYAEVRSIHEVAGDILYDEENFWLILDLDLDDTLLQGGEALSHSIWWSKAIQGLQ
KQGTPQEAEWA EVVPFWIEIQEMGTVQPIESAIFLLIEKIQKQGKTT FVYTERPKTAKDLTLKQLHMLNVSL E
DTAPQPQAPLPKNLLYTSGILFSGDYHKGPGLDLFLEICTPLPAKIIYIDNQKENVLRIGDLCQKYGIAYFGITY
KAQELHPPIYFDNIAQVQYNYSKLLSNEAAALLLRHQMHE

>core/601/1/Org1_Gene598

MMKYLPYIAITACIHGGILLLVFASPLPKRRLQPKAFQEKLVTIQPKPPVPTPSVVVDPAKTIRPSVATQPQKQ
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VDKIEKSETSLKNISWPSTAQLTMHSELKATQEDELCELFRT HIALPSKGYVRIKLVLSPNGEIQECSFLSEVSA
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>core/602/1/Org1_Gene601

MDLADAHVHLSDDAFEEDINSVLQRAQDSGVSLVVNVTTTEKELNRSFAYAERFPKIRFCHVGGTPPQDQDQ
DIEEDYRNFHAAAHSKKLAAIGEVLGYCFATEEGIARQKEVLQRYLALSLECELPLVVHCRGAFNDFFRML
DQYYHNDPRSRPGMLHCFTGTLEEAQELISRGWFSISGIVTFKNAQDLRDLVVELPLEHLLIETDAPFLAPVP
YRGKKNEPAHVLHTINAVANVKGMFPQELAAALAYKNVLRFLHG

>core/603/1/Org1_Gene13

MFLQFFHPIVFSdqslsflpylgkssgiiekcsnivehyhlhlggdtsviitgvsgatflsVDHALPISKSEKIHKILS
YILILPLILALFIKIVLRILFFKYRGLILDVKKEDLKKTLTPDQENLSLPLSPPTTLKKIHALHILVRSGKTYNELI
QEGFSFTKITDLGQAPSPKQDIGFSYNSLLPNFYFHSLVSVPNISGEERALNYHKEQQEEMAVKLKTMQACSF
VFRSLHLPSMQTKDKKAGFGLLTFFPWKIYPL

>core/605/1/Org1_Gene300

MILTAAFSPCPNDIFLFRSFLKDPQFRPLLNQVTIADIETLNTLALQRRLSLMKMSAALFPLVSDYYNLMDVG
NTLGYNSGPVLSLDPECSLDTLATPGEMTTAHALCKLYYPKAKLIPMPYDKILSAILQGKVDGGALIHEERFS
YDLQLTLRADFGELWRRKTIFPLPLGCLAIAKYVPMATVDALTAALRKSLICSLKDPITAGAKAVEYSKNKN
VTVIHRFIGTYINKETFQLSKTGKKALHMLWKANeccqyt

>core/606/1/Org1_Gene346

MIKQIGRFFRAFIIMPLSLTSCESKIDRNRIWIVGTNATYPPFEYVDAQGEVVGFdidLAKAISEKLGKQLEVR
EFAFDALILNLKKHRIDAILAGMSITPSRQKEIALLPYYGDEVQELMVVSKRSLETpVLPtQYSSVAVQTGTf
QEHYLLSQPGICVRSFDSTLEVIMEVRYGKSPVAVLEPSVGRVVlKDFPNLVATRLELPPECWVLGCGLGVA
KDRPEEIQTiQQAiTDLKSEGVIQSLTKKWQLSEVAYE

>core/607/1/Org1_Gene82

MLRNQVLVYCSEGVSPYYLRHTIRFLKYYSTQEGAFDILRVDGNFLIKNPfWEETTRLLVFPGGADRPYHRV
LHGLGTARIFQYVSEGGNfLGICAGAYFGSKMIYfYEPEGAPLQGARDLGFFPGTAKGPAYRGNFsYVSPSGV
RVSPQLFSDfGLGYAMfNGGCFfEGSEGYPGVNIESRYDDLPGKPASIVSRIVSKGLAVLSGPHIEYLPHYCR
MVKENVQKTREFLQRERTTLDRYCQNLVQRLRQPAFSKADC

>core/608/1/Org1_Gene249

MNVKDETFWSVHNLCVNYEHAaVLYHISfSLGKGSLTAILGPNGAGKSTLLKASLGLIKPSSGTvYFFNqKF
KKVRQRIAYMPQRASVDWDFPMTVLDLALMGcYSYKGMWGRISSDDRREAfHILERVGLESVADRQIGQLS
GGQQQRAFLARALMQKADLYLMDELfSAIDMASFKTSVGVLQELRDQGKTIVVHHDLShVRQLFDHVVl
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>core/609/1/Org1_Gene495

MNRRWNLVLATVALALSVASCDVRSKDKDKDQGS�VEYKDNKDTNDIELSDNqKLSRTFGHLLARQLRKS
EDMFFDIAEVAKGLQAELVCKSAPlTETeYEEKMAEVQKLvFEKKSkenLSLAEKFLKENSknAGVVEVQP
SKLQYKIIKEGAGKAISGKPSALLHYKGSFINGQVFSSSEGNNEPILLPGQTIPGFALGMQGMKEGETRVLYI
HPDLAYGTAGQLPPNSLLIFEINLIQASADEVAaVPQEGNQGE

>core/611/1/Org1_Gene966

MENLETFILKIYRGVPGKQYwESFELPLHPGENVISALMEIEKRPVNILGEKvNPVVWEQGCLEEVCgSCSILV
NGVPRQACTALIqEYIDATQSREIVLAPLTkFPLIRDLIVDRSIMFDNLERIQGWVAADIEGETFGPQVTQEQQ
ELLYALSQCMTCGCCTEACPQIDNKSDFIGPAAISQARYfNTYPGDkQSKKRWRALMGKGgieGCGQAHNC
VRVCPKKLPLTESISAMGREISKfSLRSLfSALFkkkk

>core/613/1/Org1_Gene927

MSKFILLLSLGVAALASKNFFIWPAPSGKTPLKLRQVLFGGALLVFSSLVALSVSSQTAELLSTMTGISLAFALFYLLFLPKDITRAILFSGERPVKTSWRALGSAIRMWIIIPVTQLIGIMMSKFLTLVLPMQEIHTQEVTQEVQNSLPITGHYISMILNLGVLTPIFGEEVFFRGILQTFLKNKMTRIAAVLCSSIIFSFIHIEHSLGSWVFPVLFVFSLSAGFLYEKDRHILSPIALHGLFNLTSLFLGIK

>core/614/1/Org1_Gene373

MAFYSPSTISKYFIYSGAGNRFLGETLPEVEDVRFLCQETRVDGFLYLKPSSCADAQLIIFNSDGSRPTMCGNGLRCAIAHLASQKGKSDISVSTDSGLYSGYFYSWDRVLVDMTLADWRASVHRLESRPDPLPKEVVCIHGTGPHAVVILPEISTLDLSILGPFLRYHQTFSPDGVNVNFVQILGHCQLRVRTYERGVEGETAACGTGALASALVVSNSYGWKESIQTHTWGGELMTVSQNRGRVYLQGSVTRDL

>core/615/1/Org1_Gene84

MFKLLKNLFLIGCCIVGYFWMRKESIVEQWLSNRLHTQVTVGRVSIRTSGIKIRHICIHNPASERFPYAAEIEYADVRFSSISMLLTQKLEISELIIHGANFTIFPYDSHGTKTNWSLVWKNFHPQKETPSNLWIDRAPVLIRRCFLNTRLYGRLRANH KDIPHLSPVPSLEFHSHTSSAKELPKLSEALPSLLYLAL EESLYHLNLP GDIIKPLSQQA HKHFYS SYPQFQDRLNDINTPGTPT EEIIGFIRGLFFH

>core/616/1/Org1_Gene65

MVSPLSLFHKMLLENWTPVEEPFPWPPAEKNQKIFAWALNQSKLIFVSTSGNIAQPRLVTDSMSMMIVNAANRTMSRDGAGTNQVL SAAVSVD SWGLSQRPLNPERQGTPLNEGECRAGMWRNADGSNHTGKQGKPHYLAQLLGPKAVDHHNKSQA AFDRCKNAYLNCFSLAQTLGVTF LQIPLISSGIYAPPENRKKPNSEENKVRMRWIHAVKCALVAAMQEFGN EPGNTDRRMLIVLTDLKTPAITDPKKKSHL

>core/617/1/Org1_Gene258

MKTQQTQNIIEVWNFYWETQEIEYRDSLIEFYLPVKSVVHRLISGMPSHVKTEDLYASGVEGLVRAVERYNPERSRRFEGYAVFLIKAAIIDDLRKQDWVPRSVHQKANKLSGAMDSL RQSLGKEPTDLELCEYLNISQQELSGWFVSARPALIVSLNEEWPSQSDEGAGMALEERIPDERAETGYDVVDKQEFSLCLANAIQELEEKERKVMALYYEELVLKEIGKVLGVSESRVSQIHSKALLKLRAALSAFR

>core/618/1/Org1_Gene317

MWLGAYTWLNVFGILLQAAFIQNILLANFLGMCSYLACSTRVSTANGLGMSVALVLTVTGSINWVHAFITGPKALTWISPSLASVNLGFLELIIFIVVIAAFTQILELLEKVSRLYLSLGF LPLIAVNCAILGGVLFGITRSYPFIPMMIFSLGAGCGWWLAIVILATI KEKLAYS DIPKNLQGMGISFITTGLIAMAFMSLTGIDISKPSAKIQRAPLETEVVENTTNPLKESSSKHQPSISKARTQRRSL

>core/619/1/Org1_Gene521

MLKIKHLHASCNDVKILDDFNLNIQPGTMHVIMGPNGAGKSTLAKILAGDESVLVSSGEIALQEQNLLSMLPEERSRAGLFGVGFQMPPEIPGVNNKMFLRDAYNARRRANQEGDISIDEFN TLLSTVLETYEYNATTDLFLDRNVNEGFSGGERKRNEICQMLVLEPEMVLLDEPD SGLDVDALRLICRVLEKYRELHPTSSLCIVTHNP KLGNLIRPDVVHLLLDGRVALSGDVSLMHELEAKSYQEVTKRVAWR

>core/621/1/Org1_Gene613

MKTIAVNSFKGGTAKTSTTLHLGAALAQYHQARVLLIDFDAQANLTSGLGDPDCYDSLAVVLQGEKEIQE
VIRPIQDTQLDLIPADTWLERIEVSGNLAADRYSHERLKYVLGVSVDKYDYVIIDTPPSLCWLTESALIAADYA
LICATPEFYSVKGLERLAGFIQGISARHPLTILGVALSFWNCRGKNNSAFAELIHKTFPGKLLNTKIRRDITVSE
AAIHGKPVFATSPSARASEDYFNLTKEILLILRDI

>core/622/1/Org1_Gene857

MTRQSYVLGNWKMHKTIQEAKKEYVQTLASLLQGEPLSCTIGIASPFTSLRAIHEMINTTGAFLWLGAQNVHP
ELSGAFTGEISLPMLKEVGVEFVLVGHSERRHIFGESDAFIASKVKSVAQAGLVPVLCVGESLEVREEGKAHQ
VIKKQLLLGLEQMDNGSEFLIAYEPVWAIGTGKVAEASDVQDIHMFCEVVAAERFSEATAEEISILYGGSVKV
DNAQRFGQCSDVDGLLVGGASLEGQSFFEVAKNFNV

>core/623/1/Org1_Gene375

MHDALLSILAIQELDIKMIRLMRVKKEHQKELAKVQSLKSDIRRKVQEKELEMENLKTQIRDGENRIQEISEQI
NKLENQQAAVKKMDEFNALTQEMTTANKERRSLEHQLSDLMDKQAGGEDLIVSLKESLASTENSSSVIEKEI
FESIKKINEEGKALLEQRTELKHATNPPELLSIYERLLNNKKDRVVVPIENRVCSGCHIVLTPQHENLVRKKDRL
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>core/624/1/Org1_Gene165

MKPEESECLCIGVLPARWNSSRYPGKPLAKIHGKSLIQRTYENASQSSLLDKIVVATDDQHIIDHVTDFGGYA
VMTSPTCSNGTERTGEVARKYFPKAEIIVNIQGDEPCLNSEVVDALVQKLRSPEAELVTPVALTTDREEILTE
KKVKCVFDSEGRALYFSRSPFILKKATPVYLHIGVYAFKREALFRYLQHSSTPLSDAEDLEQLRFLEHGGKI
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>core/625/1/Org1_Gene705

MLIKLWRATYEGMYTFLVGALLKLRYRMQVEGWDTLNINPKQGCLFLANHVAEVDPIILEYLFWSRFHVRP
MAVEYLFHSRVVQWFLNSVRSIPIQLVPGKESKRSLERMNVCYEEASRALNRGESLLYPSGRLSRTGKEEI
VNQYSAYVLLHRVMECNVVLVRVSGLWGSAFSRYKQNSTPKLGPAFKEAFRALLRRGIFFMPKRFBKITLC
QVDHLFLKQFPTKQDLNTFLASWFNQGDDNLPIEVPYA

>core/626/1/Org1_Gene434

MQICVTGVVLRSRPLGKNHTLTTLFTPEGLFTFFAKQGQTLQCDYRETLVPISLGKTYLHRNGSRLPKLTHGD
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TPACSLCKASLPYACYRYQGHKLCKKHQHKQAISIEKEEQILQAIHAKQFSELLAIAEFPIAIAEKIFYLFDSL
QEEKKSERNSSDPYHEILRLSKVVHPY

>core/627/1/Org1_Gene518

MLIVLAFRQVFFSHSRSQLDRLKNYLRLLKQNFALTLPKERTSKGHSLMLTFDFASFDFYTNIFPFLEEQKIPAV
VGVASRYIPSNAAQDLHPSHRLKPSETLAFQDEIFSNYMPFCCQNELIEMAKSPYIQLASSGFAIRNLMNNPPY
LTTEILLSRHHIETITGAKPLAFLFPFGKSDPTSRKLAADHYPYSFLLGNTINRKLKTHNIYRLDIKPMQYVCPS
LFQSSRYLKNWIKESKQLYLKKQLPKR

>core/628/1/Org1_Gene139

MLMDISHILEDLAYDEGILPREAIEAAIVKQMQITPYLLHILHDATQRVPEIVNDGSYQGHLIYAMYLLAQFRE
SRALPLIIKLFAFEDDTPHAIAGDVLTEDLPRILASVCNDDSLIKELIETPKINPYVKAAASGLVTLVGAGKIPR
DKVIRYFAELLNRYLEKQPSFAWDNLIAGICTLYPGELFYPISKAFDGGGLVDTSFISMEDVENIIHEETVESCIH
TLCSSSTELINDTLEEMEKWLEDFPIEP

>core/629/1/Org1_Gene88

MNVADLLSHLETLLSSKIFQDYGPNGLQVGDPQTPVKKIAVAVTADLETIKQAVAAEANVLIVHHGIFWKG
MPYPITGMIHKRIQLLIEHNIQLIAYHLPLDAHPTLGNNWRVALDLNWHDLKPFSGSLPYLGVQGSFSPIDIDS
FIDLLSQYYQAPLKGSALGGPSRVSSAALISGGAYRELSSAATSQVDCFITGNFDEPAWSTALESNINFLAFGH
TATEKVGPKSLAEHLKSEFPISTTFIDTANPF

>core/630/1/Org1_Gene68

MKKQGKTLFLFLSFLFSTAFSGLFASQTSSLRTIQENIFLAKTGDYTVLSRGSQRTFVLVKSTTPKTVWIEIHH
FPCIAHKERPSLEQASWKTVIHQLESQSQVFVVSLSSEGSQFFSLNTRTKSLEPVGKSTTVPAFLQIFDLPLSPAP
ANVIKTKGKENKPWSPKVSFEGAPLTSISVNAWQGLWPKDRGPLSETGILMYFTQPDISVFPLWVSIETPKGT
SIVRAVDIGHGATSPYVYSLPDSKTQ

>core/632/1/Org1_Gene412

MSLATNNAESKFPSLQRLPNHVAIIMDGNRRWYKKHREECGHTHTSGHYYGAKVLPNILNAVLDLGIKVLTL
LYTFSTENFGRPKEEIQEIFNIFYTQLDKQLPYLMENEICLRIGDLSKLPKGIQTKINHVSMTASFRLVLA
VNYGGKDELVRAFKKLHVDILNKKISSDDLSESLISSYLDTSGLTDPDLLIRTGEMRVSNFLLWQIAYTELYI
TDTLWPDFTPQDLFEAINVYQQRSRGGK

>core/633/1/Org1_Gene612

MGNLKTLLSRFKKNTPTKMEALARKRMEGDPSPLAVRLSNPTLSSKEKEQLRHLLQHYNFREQIEEPDLTQ
LCTLSAEVKQIHHQSULLHGERITKVRDLLKSYREGAFSSWLLTYGNRQTPYNFLVYYELFTLLPEPLKIEM
EKMPRQAVYTLASRQGPQEKKEEIRNYRGERKSELLDRIRKEFPLVETDCRKTSPVKQALAMLTGKSQILTK
CTSLSSDEQIILEKLIKKEKVKSNLFPDTKV

>core/634/1/Org1_Gene446

MKIKFSWKVNFLICLLAVGLIFFGCSRVKREVLVGRDATWFPKQFGIYTSDTNAFLNDLVSEINYKENLNINIV
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VLVAQNIPDAVISLYQHVPALAEALTSNCYDALLAPVIEVTALLETAYKGRLKIISKPLNADGLRLAILKGTNG
DLLEGFNAGLVKTRRSGKYDAIKQRYRLP

>core/635/1/Org1_Gene490

MSLLKDTVFTCLDCEMTGLDVKKDRIIEIAAVRFTFDSVISSIEFLINPERVVSAESQRVHHISNAMLRLDQPKIA
EVFPQIKAFFKEGDYIVGHSVGFDLQVLAQEMERIGETFLSKYTIIDTLRLAKEYGDSPNNSLES LAVHFNVPIY
DGNHRAMKDVEININIFKHLCKRFRITLEQLKQVLAKPIKMKYMPLGKHKGRCFSEIPLAYLQWASKMDFDS
DLLFSIRHEIKHRQKGTGFSQVNNPFMEL

>core/636/1/Org1_Gene212

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KIGSAGQTNAAAAGIIAFTKSLAKEVAARNIRVNC LAPGFIETDMTSVLNDNLKAEWLKSIPLGRAGTPED
VARVALFLASQLSSYMTAQTLVVDGGLTY

>core/637/1/Org1_Gene665

MTQDPHDHFKSRTPEDHIKHVRDKHRVCKGEPHTTFKGFFYHLANNALSTGVFIFFIRTLFFLIPTNRALQVKS
LISLGVGWTFYHGCLKARKAWAYMELSHRSMLEEKNEIEENFEQEKIELRILFENQGFKDPLLQEMVEYVCS
DSTLLLDTMIREELYIRKEDLPHPLIQGGSRI LGGLCGLAIFLPLVLCISYTLAGVFSALMVLVLSFLKAKILKN
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>core/638/1/Org1_Gene269

MTLSFHTHPLNYWTFEEFDGLPIRHGVFSKQKDAEGTVFAAKNPEIASALQSPKYCDLHQRHGTSVRCVTPT
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FVAIGPSIGPDYAIYPDYATLFPRSFLPFMNPKNHFDLRAIARKQLTNLGISKDRIFISDLCTYTEHDAFFSSRYL
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>core/639/1/Org1_Gene527

MAKQTRRVLFKISGEALSKDSSNRIDEMRLSRLVSELRAVRNNDIEIALVIGGGNILRGLAEQKELQINRV SAD
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LRACELNVDVLIKATMHVDGVYDKDPRLFPDAVKYDFVSYKDFLSNQLGVMDAS AISLCMDSHIPRVFSFL
QHSLEKALFDPTIGTLVSEDVNHVCSPRH

>core/640/1/Org1_Gene48

MKFFILFILIVAQFPAFSAQPRTQVSASHSKQAKARRTSRIRSSAATNASVSRYKTRAAARKKIGKFEKKPSLSP
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KEATSGDAILEKALEALQENK

>core/641/1/Org1_Gene448

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QSYTEQDEKIFLRELGR LKRAFAALPKEVTEVIVMTHYPPISSDGTGPISFLEADGRVSLCLFGHIHKVQRPI
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>core/642/1/Org1_Gene580

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WNGFFPLYNYVGKPD CFGRALKMTYSNLLDGLSAAAVLCMGEGDEQTPIAIIIEAPKITFHSSPTTLQDMSTL
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>core/643/1/Org1_Gene834

MDFDYFGLSDIGRVRARNEDFWQVNLMSQVVAIADGVGGRLGGDIASQEAVTSLMELIDEQQSKLMGYED
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ENQLKNRYGLPKQSDKVYSYRHILT NVLGSRPYVMPDIRNLPCEKEDLYCLCSDGLTNMVPDIDIRDILNQPA
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>core/644/1/Org1_Gene391

MTIRILAEGLAFRYGSKGPNIIHDVSFSVYDGDFIGIIGPNGGGKSTLTMLILGLLTPTFGSLKTFPSHSAGKQTH
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QRVLLARALASYPEILILDEPTTNIDPDNQQRILSILKKLNRTCTILMVTHDLHHTTNYFNKVFYMNKTLTSLA
DTSTLTDQFCCHPYKNQEFSCSPH

>core/646/1/Org1_Gene979

MSYFNYQKNSVVLRLSLGLLAKFFSRLLYRVFFSFREGIYLFSSLYLKYPRLFFYDLGKYVYSLRHCPYAKLGR
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MHRKLSSGFALFDTEEFKNVVLSQLASYVYFYGSSFSRLLNEIILKLSEMAPGSVVISISFPLDSFSRGKECFFT
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>core/647/1/Org1_Gene182

MSTLLLNPWMKAGKRIESLVRKALYTHTMLANHRKIVVALSGGKDSL TLLLMLKAISGRGFPDLDLHAVNI
GGKYSCGAENVKPYLTRICDQLCIPFRTIPSPYAPETPECYPCSQARRLLFQAAKEIGASAIAFGHHRDDL VQ
TALLNLLHKA EFAGMLPVLD MVHFGVTILRPLIFTPEFWIRKFAKENG FARVTCRCPVVS LRSKAEQSLKLE
EVFPLARHNIALAIQEHGSSKSQKI

>core/648/1/Org1_Gene191

MTDYSFFRRKIGNIEAIECPGNPQDPPIILCHGYGSLADNL TFFPSICSFSKLRPTWIFPNGILPLENDFRGS RACF
PLNVLLLQELSRLYANGVGNLQEKYDELFDVDLET PKEALEELILNLNRPYNEIIGGFSQGAILATHLVLT SQ
NPYAGALIFAGARLFNQGWEEGLKQCAQVPFLQSHGYEDEILPYHLGAHLNDLLLTKLNGQFVSFHHGGHEIP
SVVFQKMQVTPVNWIDPARG

>core/650/1/Org1_Gene550

MPILSVCNLVKKYNKKPVTNDVSFQINPGEIVGLLGPNGAGKTTAFYLT VGLIRPDSGKIIFKNVDVTKKTMD
HRARLGIGYLAQEPTIFKELTVQDNLICILEIYKARKQQSHLLNTLVDDLQLGSLHKKAGT LSGGERRRLEI
ACVLALNPSVLLLDEPFANVDPLVIQNVKYLIKILAGRGIGILITDHNAKELLSIADRCYLIIDGKIFFEGSSSQM
ISNPMVKQHLYLGDSFSY

>core/651/1/Org1_Gene322

MKVRIVDSGKSSAASHMAKDRDLLES LQDGELILHLYEWENPCSLTYGHFMRPEKFLLSNYADLGLDAAVR
PTGGGFVFHKG DYAFSVLMSATHPSYSSSVLENYHTVNSFVAKVLEKVFRIQGMLAPEDENSSSRDSGNFCM
AKTSKYDVLFGDKKIGGAAQRKVQQGFLHQGSLFLSGSSSEFYQRFLKPEVLEEIIIEQIQIHAF FPLGLEAADE
VLQEARQQVKEAFIKLFCGEGL

>core/652/1/Org1_Gene835

MTLYLLPNTLGTRAVETLPSVIGELVHRLDGLIVESDRGGRAFLSLWKIPEVHKFPLAILSKHARLPKAWDFY
LEPIVKHGENWGLISDAGLPCIADPGASLVRRARALGIPVQAFSGPCSITLALMLSGLPSQSFTFLGYLPQSPKE
RVKSIKKAATSKEVSTSVCIETPYRNVYTFESLLDTLPSYAELCVASDLSGPSELVLTRQVQSWRTTEDLGSV
KQSITKVPTIFLFHIPN

>core/653/1/Org1_Gene419

MAGHSKWANTKHKERADHKKKGKIFSRIIKELISAVKLGGADPKSNARLRMVIQKAKENNIPNENIERNLKK
ATSAEQKNFEEVITYELYGHGGVGIIVEAMTDNKNRTASDMRIAINKRGGSLVEPGSVLYNFARKGACTVAK
SSIDEEVIFSIAIEAGAEDLDTEDEENFLVICAPSELASVKEKLISQGATCSEDRLIYLPLRLVDCDEKDGEANL
ALIDWLEQIEDVDDVYHNMS

>core/654/1/Org1_Gene492

MDISGAVKQKLLQFLGKQKKPELLATYLFYLEQALSLRPVVFVRDKIIFKTPEDAVRILEQDKKIWRETEIQIS
SEKPQVNENTKRIYICPFTGKVFADNVYANPQDAIYDWLSSCPQNMEKQGGVRIKRFLVSEDPDVIKEYAVPP
KEPIIKTVFASAITGKLFHSLPPLLEDFISSYLRPMTLEEYVQNQTKFQLESSFLSLLQDALVEDKIAAFIESLADD
TAFHVYISQWVDTEE

>core/655/1/Org1_Gene745

MGLYDRDYIQDSRVQGTFA SRVYGWMTAGLIVTSCVALGLYFSGLYRSLFSFWVWCFATLGVSFFINSKI
QTL SVSAVGGLFLLYSTLEG MFFGTLLPVYAAQYGGGVIWAAFGSAALVFGLAAVYGAFTKSDLTKISKIMT
FALIGLLLVTLVFAVSMFVSMPLIYLLICYLGLVIFVGLTAADAQAIRRISS TIGDNNTLSYKLSLMFALKMY
CNVIMVFWYLLQIFSSSGNRD

>core/656/1/Org1_Gene904

MHPPIDITAIEAKLNFTFTQPKLLEIALTHPSYKNESAVQIEDSERLEFLGDAVLGLIVTEHLFLLFPSMDEGTLS
TARASLVNAKACCRYTTVLGIGDYLLIGKGEKIQSERGRLSAYANLFESILGAVYLDGGLSPARKLTVPLPP
REEILPLMSGNPKNLLQQFTQKQFRVLPVYQSTAVTDAQGNVSYQIQVLVNQE VWGEGNASSKKEAEKIAA
QQALDTYGKNKNQNTMDV

>core/657/1/Org1_Gene995

MEPSTNKPDCCKIFDSIASKYDRNTILSLGMHHFWNRSLIQILGSGYSLLDLCAGTGKVA KRYIAAHPQASV
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ELTPPKKTHPTYSAHKLYLRVVPWIGKSVSKDPDAYSYSLSKSIQQLPKDHDLEDLFSKSGFYIAKKKKLFLG
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>core/658/1/Org1_Gene928

MDVLIFYDTETTGTQIERDRIIEIAAYNSVTDESFLT YVNPEIPIPEASKIHGITTDVLSAPKFPEAYEGFRKF
CGEDSILVAHNNDGFD FPLLGKECRRHSLEPLTNRTIDSLKWAQKYRPDLPKHNLQYLRQVYGFAENQAHR
ALDDVVILHKVFTSLIGDLPPQQVLDLLQQSYHPKVFKMPFGKYKGQPLVDIPKSYFEWLENQGALDKPENK
DIKAAIAL LHQPT

>core/659/1/Org1_Gene589

MQNATIDQLPVSWQEQLPLCWREQLKEEWSKPYMQQLLIFLKQEYKEHTVYPEENCVFSALRSTPFDQVRV
VILGQDPYPGKGQAHGLSFSVPEGQRLPPSLINIFRELKTDLGIENHKGCLQSWANQGILLNNTVLTVRAGEPF
SHAGKGWELFTDAIVTKLIQERTHIIFVLWGAAARKKCELLFNSKHQHAVLSSPHPSPLAAHRGFFGCSHFSKI
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>core/660/1/Org1_Gene232

MDLAVELKEGILLVDPKPGRTSFSLIRALTKLIGVKKIGHAGTLDPFATGVMVMLIGRKFTRLSDILLFEDKEY
EAIAHLGTTTDSYDCDGKVVGRSKIPSLEEVLAAEYFQGEIQQLPPMFSAKKVQGKKLYEYARKGLSIERH
HSTVQVHLQITKYEYPLLHFVVSCSKGTYIRSAHELGTMLGCGAYLEQLRRLRSGRFSIDECIDGNLLDHPDF
DISPYLRDAHGNSL

>core/661/1/Org1_Gene571

MIGDKIILFVTEDLSLSSQLKDLASQRSYQILVSPVFPTSFESVAIFCEYLLLPEQIFSPGIFPEEDLIVLFDTFQE
EAITKVLNQGATGYLLRPITAKVLDAVIRAFRLRQHEVLEHSIPDTMTFGDHTFRVLNLVIESPEGSVYLTSEA
GILKKLLINRGHLCLRKNLLAEIKGNTKEIARNVDVHIASLRKKLGPYGSKIVTIRGVGYLFSDDDSIPLQNH
NTAHPNEE

>core/662/1/Org1_Gene873

MTKVRLNKFLASAGVASRRKCDEIIFSGSVTVNGRVAEGPFVLVDPEDKVQVGGTSVHLTKKVYFMVHKAI
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RDVSA
KDLGKLMEGTFIDGKHVRPVSVTKIRRGTVKIVVSEGKKHEIRLFADAAGLPILELKRIRIGSLVLGGLRYGEY
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>core/663/1/Org1_Gene162

MLQAHRLCYSCDNQVILKDASFQASPGTITIILGSSGVGKTTLFRLLAGFLPLQEGELLWNGSPLNRKDVA
YMQKEALLPWRTALKNMTLSTELGINTSHNALSNERLEEIIHNFDLGQLLDRLYDELSSGGQRQRIALAAQCL
SL
KPILLDEPFSSLDVLLKEQLYQDIVALAKKENKTVLLVTHDFHDVSCLGDVLYVIKNKTLTPVPLDPSMRPL
NNGLCFIKDLKKHLYT

>core/664/1/Org1_Gene770

MRVIFPDKHNNFPNLSKLLKKLPSVILVTSCIAPFFSYIINKFFGIPGLLEILALSVKGIQKHFWQFLTYPLITAD
SLSLNKDQSFEITQRLLLRNVLDFFLFYKAIQHLIRKLGAFSVLVVISGQALIIGAVLWGFMALIHSSQSFFGPE
SIICGVLTQIFLDPEKRFTIGPTPLSVSIKWGFLFVLGFYCCILIFSGAFLLLASMLAIVLAILFCKKEKIPNPYT
TSLRF

>core/665/1/Org1_Gene458

MPTTNCIFDLRGHSILHQLQIEEALLRVANQNFCIINSGAKDSIVLGISRNLNQDVHISRAQADHIPIIRRYSGG
GTVFIDSNTLMVSWIMNSSEASAQPQELLAWTYGIYSPLLPNTFSIRENDYVLGHKKIGGNAQYIQRHRWVH
HTTFLWDIDLKLSYYLPQPQPTYRNQRSHEEFLLTLRPWFPSRDDFLERIKASGSLLFTWEEFLDNELEEIL
AQPHRKATTVLN

>core/666/1/Org1_Gene23

MLSVCYSDPCLSDFCQGKRPLRIASRNSNLAQAQVHECISLLRSWYPKLWFQLSTTETTGDREKKIPLHLVEN
SYFFTDGVDALVHKGVCDLAIHSAKDLPETPSLPVVAITRCLHPADLLVYADHYVHEPLPLSPRLGSSSLRRS
AVLKQLFPQGQILDIRGTIEERLDQLHRGHYDAIVLAKAASRLHLHHAYSIELPPPYHALQGSLAITAKDHA
GKWKQLFTPIHCHSS

>core/667/1/Org1_Gene630

MKFFSLIFKDDDVSPNKKVLSPEAFSAFLDAKELLETKADSEAYVAETEQKCAQIRQEAKDQGFKEGSESW
SKQIAFLEEETKNLRIRVREALVPLAIASVRKIIGKELELHPETIVSIISQALKELTQNKHIIISVNPKDLPLVEKSR
PELKNIVEYADSLILTAKPDVTPGGCHETEAGIINAQLDVQLDALEKAFSTILKAKNPVDEPSETSSSTDSSSL
NDQDKKE

>core/668/1/Org1_Gene690

MNRRDMVITAVVVNAILLVALFVTSKRIGVKDYDEGFRNFASSKVTQAVVSEEKVIEKPVVAEVPSRPIAKET
LAAQFIESKPVIVTTPVPVSETPEVPTVAVPPQPVRETVKEEQAPYATVVVKKGDFLERIARANHTTVAKL
MQINDLTTTQLKIGQVIKVPTSQDVSNEKTPQTQTANPENYYIVQEGDSPWTIALRNHIRLDDLLKMNDLDEY
KARRLKPGDQLRIR

>core/669/1/Org1_Gene1026

MFFIVCFGLIHKKHTILPPKAHIPTNAKHFTIGNPYAPINITVFEEPPSCSACAEFTTEVFPLLKKHYIDTGEISF
TLIPVCFIRGSKPAAQALLCIYHHDPRQADIDAYMEYFHRILTYPKEEGSHWATPEVLTKLAEGLKINSGRSVN
PKGLEQCIASGQYNEQIKKNLYGSQVLGGQLATPTAVVG DYLIEDPTFHEIERAIQHIRQLQAVEGDHDD

>core/670/1/Org1_Gene600

MVHFSHNPIIQAYTEADFFGKSIFFCLLILSVCTWTVLHQKLAIQKNFLKAGKSLKDFLIKNRHAPLSLDIHPEL
SPFADLYFTIKRGTTLELLDKNRQSAPDRGPILSSEDIQSLETLLGAIMPKYKALLHKNSFIPATTISLAPFLGLLG
TVWGILVAFTHISSGSSGNSAIMEGLATALGTTIIGLFVAIPSLIAFNYLKAHSSSELISEIEQTAYLLLNSIEVKYR
NTNL

>core/671/1/Org1_Gene43

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ILVFASGNKVKEAVEAGADFMGSDDLVEKIKSGWLEFDVAVATPDMMREVGKLGKVLGPRNLMPTPKTGT
VTTDVAKAISELRKGKIEFKADRAGVCNVGVGKLSFESSQIKENIEALSSALIKAKPPAAKGQYLVSFTISSTM
GPGISIDTRELMA

>core/672/1/Org1_Gene91

MEKDLHLHEKKCLAHEAATQVTSGMILGLGSGSTAKEFIFALAHRIQTESLAVHAIASSQNSYALAKQLAIPL
LNPEKFSSDLTVDGADEVDPQLRMIKGGGGAIFREKILLRAAKRSIILVDESKLVVVLGKFRVPLEISRFRSA
IIEIRHLGYEGEWRLQDTGDLFITDSSNYIYDIFSPNSYPNPEKDLLKLIQIHGVIEVGVFVIEKVEVWSSNSQGL
ISKKYSV

>core/673/1/Org1_Gene164

MLQSCCKALLSIVVSILAFHPIPGMGVEAKSGFLGKVGWFSKKEIQEEARILPVKDSLWKRYDYTSSSGFS
VEFPGEPDHSGQIVEVPQSEITIRYDTYVTETHPDNTVYVVSVWEYPEKVDISRPELNLQEGFSGMMQALPES
QVLFMQARQIQGHKALEFWIVCEDVYFRGMLISVNHTLYQVFMVYKNKNPQALDKEYEAFSQSFKITKIREP
RTIPSSVKKKVSL

>core/674/1/Org1_Gene187

MALDEINNQNNPSQQIASSTSQTSKINQDRKTFACVTLLVVATLMILSGIVLLFTIGSLGLSVPLSGILGTFVAV
TVGAVLFITGLTILVRKSLGIEQKNEDLNFLKIKTPTPPARPLMSKFSVTCSTTSIVLGMALLIGAVVSVFFLTG
YLQLGLCAGLVGLGTALFVAGLARMSPRSLADQEGSGSADSQSNIVGIGEPKAAQEQKWYKMAVVRGEDGI
PTAIRLTPEK

>core/675/1/Org1_Gene617

MSKPSPRNANQPQKPSASFNKKTRSRLAELAAQKKAKADDLEQVHPVPTEEEIKKALGNIFEGLSNGLDLQQI
LGLSDYLL EEIYTVAYTFYSQGKYNEAVGLFQLLAAAQPQNYKYMLGLSSCYHQLHLYNEAAFGFFLAFDA
QPDNPIPPYYIADSLKLQQPEESNNFLDVTMDICGNNPEFKILKERCQIMKQSIEKQMAGETKKAPTCKPAG
KSKTTTNKKSGKKR

>core/676/1/Org1_Gene427

MYLEDYDVFFFDLDGLLDVTEPCFYRAFLQACAEFSLEVHWDFSTYYSHTTLGTEIFSKKFIEQYPQAEYM
AEIFAKRLQIYYKSLEHAGPALMPGVEAFIELVLSLNKTFGVVTNSPRDATHTLRTMYPILNKFLFWVTRENY
ARPKPYGDSYDYAYRTFAREGMKVIGFEDSVKGLRALSKIPATLVCINSMAEITPEDYPELKGKEFFSYPSFD
VLTEHCSQQKLL

>core/677/1/Org1_Gene801

MNTSHRKTLVFSYLSSTFTLLLVLNLVLSSKLIPTTFFNFIIPGGLILYPLTFLISDVVNEIFGPKKARVMIFSAFI
ANLLASSIVQIFMFFPVASPEMQTAWHCLFDLSPLRFLASLLAFIVSQQLDIVLYTFFKNRTPNSSLWLRSNGS
TWISQIPDFTIVDTCILYFGMGLSFPQTLNIMFYSYIYKITFCVLTTPLFYLAVNTIRKFLGMPSTKIAN TVPLIN
QP

>core/678/1/Org1_Gene122

MKKQESVLVGPSIMGADLTCLGVEAKKLEQAGSDFIHIDIMDGHFVPNLTFGPGIIAAINRSTDLFLEVHAMIIY
NPFEFIESFVRSGADRIIVHFEASEDIKELLSYIKKCGVQAGLAFSPDTSIEFLPSFLPFCDVVVLMSVYPGFTGQ
SFLPNTIEKIAFARHAIKTLGLKDSCLEVDGGIDQQSAPLCRDAGADILVTASYLFEADSLAMEDKILLLRGEN
YGVK

>core/679/1/Org1_Gene148

MKGFLSVNELIFGFQTFSSVVVLGVFFASRGKAWLTGWLSLLSSIMNVFVLKQIHLWGFEVTSADVYVIGLLT
CLNYAREHYEKNDINDAMLCSWVISIAFLVLTQLHLFLIPSPNDSSQEHFLALFSSTPRIVVASLVTLIFVQIVDI
KLFTFLQRVFSKKYFAMRSTISLLFSQLIDTIIFSFLGLYGLVSNLCDVMIFAMLVKGIVITLAIPTLTVTKAVLD
RRSS

>core/680/1/Org1_Gene432

MRPHRKHVSSKSLALKQSASTHVEITTKAFRLSMPLKQLILEKSDHLPPMETIRVVLTSHKDKLGTEVHVVAS
HGKEILQTKVHNANPYTAVINAFKKIRTMANKHSNKRKDR TKHDLGLAAKEERIAIQEEQEDRLSNEWLPVE
GLDAWDSLKTLGYVPASAKKKISKKKMSIRMLSQDEAIRQLESAAENFLIFLNEQEHKIQCIYKKHHDGNYVLI
EPSLKPGFCI

>core/681/1/Org1_Gene661

MALLILLRHGQSVWNEKNLFSGWVDIPLSQQGIEEAFSAGRAIQNLPIDCIFTSTLVRSLMTALLAMTNHHSK
KIPYIVHEDPKAKEMSRIYSAEEENNMIPLYQSSALNERMYGELQGKNKKQTAEQFGEERVKLWRRSYKTAP
PQGESLYDTKQRTLPHYFEKNILPQLQNGKNVVFVSAHGNSLRSLIMDLEKLSEEEVLSLELPTGKPVVYQWKN
HKIEKHPEFFG

>core/682/1/Org1_Gene161

MSSQPLVTTSSSLSRVYVLTGEEKVACYKKAFNHIWHGAPAILAAALLMFCIFGFVLGSILLGAPLEGASILY
DVILPWLLPSILVFVLLVLPLNIYAYSHHKQVLALHERITQSNYKEIYDHCEKEKKTTPNKKALSLYIESQVLVP
EYSKRFSSMILGKTLKIIPKKDSPESLKHDELIQKALERAKENIYMKNQREKRDEREAKKEAKNASKTNPLW
EGLGT

>core/683/1/Org1_Gene176

MSLLIEAKNLSKTIQQNQNISILTDVSLSLHAGETISITGASGNGKTTLLHLLGTLDVPSSGSLRFFDKDLKNQ
DLANFRNQHIGFVFQNFYLLEDDTVLKNVLMPALIARKNISKGSPVYTRALELLDLVNLEDKVRTRCSKLSG
GEKQRVAIARALINEPAILLADEPSGNLDEETSEQIHNLLLEQASALCGILIVTHNKH LASRCSREGVLSNGKLF
FHNS

>core/684/1/Org1_Gene127

MTIRVRNLAYSVNKKKILDGVTFSLERGHITLFVGKSGSGKTMILRALAGLVQPTQGDIWIEGEAPALVFQQP
ELFSHMTVLGNCTHPQIHIGRSTEEAREKAFELLHLLDIEEVAKNYPDQLSGGQKQRVAIVRSLCMDKHTLL
FDEPTSALDPFATASFRHLLLETLRDQELTVGLTTHDMQFVHSCLDRIYLIDQGTVAGVYDKRDGELDSGHPLS
KYIHS AQ

>core/685/1/Org1_Gene854

MDLKLDEVASLLDVSEHTVLQWLKEGAIPSYSMNNEYRFSREEIEDWLLHNQALMIQERGEDKEALKDLSL
KYSLYKAHRRGGVLCDVVVHSKEEALQYASKYIAQKFQLDESVLFEMLSHRENLMSTGIGEGIALPHA KDFLI
NAYYDIVVPMFLAEPIEYGALDGKPVGILFFLFACQDKSHLNLVNKIVHLGMSLNARSFFKNYPNKDQLLAY
VKEWESQTH

>core/686/1/Org1_Gene948

MILRISTVSLLTSCSFSKNSRTCFVTPERITSQKDCPVLLHPKSTTISPLYDWIPP NREVITAYSFYCRGQGNSII
TPEGVLYDCDGLHHSITKEEFRIYHPRLIEVVRLLQQDHPKVSII EAFCCPKHFHFLEASGISLSQLHLQGTAAT
FALDPPLPMEKLLATIKKLYKNSDPSLSNFIVTEATLTNP ELRLTQQDLGSHTEITVEILDNLQNKETLSSA

>core/687/1/Org1_Gene709

MENSQNFHDTLCQLLDYSEELYPTLASLLNVTLPNTAISASVSSIPEKAVEVPNAEPQPITPPPTNLSQEKT
PSDWKCVPLHPDLSQNAILKEKYPALKDCSLPAPKIPCSIFVYEENNEEVLFNRLAKILTQQLFPTKLT
LIHAKTNIFVNNPNFFLALAPLNVIRYKIPTTDYHQSLTQNGCIFLPLYSSLEYEKDSQLKRNLWAILNRLPFAYTPKSS

>core/688/1/Org1_Gene755

MKPQDLSPFLWKERRPCIQDGVLYVPRHYFEHQNFSTSYHQEFFQNHTSIACELCSGNGDWVVAQAQKDP
QVLWIAVEQRFDRVRKIWSKMINHQINLRIVCGTAETFFQYYVPDQFLQRLVVNFDPWPCKMRHRKHRL
LQPSFVQEISRLQDSAVFALATDDKTYLLESIEALQTHLAPRMETPYIYKMTDTYGNSWFENLWRTKGQEIFY
TEFIKKAGI

>core/689/1/Org1_Gene536

MIDPVECFPNLDGDAEAQSITQNSGTPLASELKKDISPFALGSYAAPKDTTLVQGFKPNPMAMMQDQNSNLI
DPQLQEALAESEELQEINNLKGRLWDFRSTFEDSQTTAQFADEHFQAVGVIIIDLINEDLNTIAEHTQQDARKE
DKEEGSVTRKIHDWVSSGEEVLNRALLYFSDRDGNRESLANFLKVQYAVQQRATQRAELFASIVGTSVSSVKTI
MTTQLG

>core/690/1/Org1_Gene581

MTSWIELLDKQIEDQHMLKHEFYQRWSEGKLEKQQLQAYAKDYLLHIKAFPCYLSALHARCDDLQIRRQIL
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QVCVEKIRGLKEYFGVSARGYAYFTVHQEADIKHASEEKEMLQTLVGRENPD AVLQGSQEVLDLWNFLSS
FINSTEPCK

>core/691/1/Org1_Gene482

MVLLSKFDFSGNKIGEEVADSLFADEGDGLQLIKDYIVAIRANKRQWSACTRNRSEVSHSTKKPFKQKGTG
NARQGCLASPPFRGGGIVFGPKPKFNQHVIRNRKERKAAIRLLLAQKIQTNKLTVVDDTVFVDALTA
PKTQSALRFLKDCNVECRSILFIDHLDHVEKNENLRSLRNLTA VKGFVYGININGYDLASAHNIVISKKALQEL
VERLVSETKD

>core/692/1/Org1_Gene513

MQTLARLFGQSPFAPLQAHLEMVVSCVEYMLPIFTALRDGRYEELLEMAKLVSDKEYQADCIKNDMRNHL
PAGLFMPISRAGILEIISIQDSIADTAEDVAILLTIRRLNFYPSMETLFFRFLEKNLEAFELTMTLLHEFN
QLLESSFGGRKADKARLLVGRVAKSEHESDVLQRELMQIFFSDDFIPEKEFYLWLQVIRRTAGISDSSEK
LAHRINMTLEEK

>core/693/1/Org1_Gene796

MSTTTVKHFIHTASRWEPLKEIVASNYWHAQWINTLSFLENSGAKKISASEHPTEVKEEVLKHAAEEFRHG
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LYPLYHDILKEAQSKITVKSIILEEQGHLQEMERELKDLPHGEEELGYACQFEGELCLQFVERLEQMIFDP
SSSTFTKF

>core/694/1/Org1_Gene156

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>core/695/1/Org1_Gene364

MKKYFITGLVILLPLAITIAIVTMIMNFLTQPFVGLASEFFEKFSFYTKHRALLKFVLQIILLFGLFFATVLLGFLTRIMIFKSLLSIYDKILHRIPHIKTVYKAAQQVMTTIFGSKSGSFKQVVMVFPNANVQCIGLVAGDAPTVCCTGEKEDDPLVTVFIPTTPNPTSGFLTFRKSDIVFLDMKIEDAFKYIISCGVLSTPMACSSPLPDELHQDQGS

>core/696/1/Org1_Gene823

MGQKGCPIGFRTGVTKKWRSWLWYGNKQEFGKFLIEDVRIRQFLRKKPSCQGAAGFVVRMSGKIEVTIQTARPGLVIGKKGAEVDLLKEELRALTGKEVWLEIAEIKRPELNAKLVLADNIARQIERRVSFRRAMKKAMQSVMDAGAVGVKIQVSGRLAGAEIARSEWYKNGRVPLHTLRADIDYATACAETTYGIIGIKVWINLGENSSSTTPNNPAAPSAAA

>core/697/1/Org1_Gene942

MTLYLGLNQKTARKYQAHYLPILTLFPYAKSTPQNKRALQFLPQATHVILTSPSSTHLFLSRMTSLLSKATLTKTYLCIGESTKERLLSFLGQVKYVVATQEIAEGIFPLLQALPSSARILYPHSSLARPVIREFLYNRFTFFSYPHYTVKPRKLKKNILSKYKKIILTSPSTVRAFAKIFPRFPEKTYWCQGRMTLQEFQKFSSQKQVSLLETLGKSRTSP

>core/698/1/Org1_Gene559

MLMMLMMIIGITGGSGAGKTTLTQNIKEIFGEDVSVICQDNYYKDRSHYTPEERANLIWDHPDAFDNDLLISDIKRLKNNEIVQAPVDFDFVLGNRSKTEIETIYPSKVILVEGILVFENQELRDLMDIRIFVDTDADERILRRMVRDVQEQQGDSVDCIMSRYLMSVKPMHEKFIEPTRKYADIIVHGNRYRQNVVTNILSQKIKNHLENALESDETYVMVNSK

>core/699/1/Org1_Gene198

MQSDLIQILLKETVNTLYMVSTAFFFSICAIGGMLGLGLFCTSPKSLNPKKSLYATISMILSFLTAIPFAILIVILFPIRWIVGTSLGPTASIVPLTIGAIPFVVITIVVDAFRNSALNYLESAVALGIPKRNILFGILLPESYPQLIFSLKSLVVHLISCSTLAGFVGGGGLGQLLLQYGYRFEWSVTTSVLVITLVLIESVRILGDFWGRRVLKYRGIL

>core/700/1/Org1_Gene871

MSTVTTEPCSSIHISLNNDWRDSQPYSLDRASELLHFRFLPSLVFSNWKVEQQIETLCHKSEKRRLISPLAKWLGKLHKQDLLCPPAPPVSVCWINAHVGYGVFARDEIAPWTYIGEYTGILRHRQAIWMDENDYCFRYPMPLFTLRYFTIDSGKQGNVTRFINHSEQPNAEAIGVFSEGLFHVIIRTIAPIYAGQEICYHYGPLYWKHRKKREEFIPEEE

>core/701/1/Org1_Gene483

MRSHISVMGKKEGMIHIFDKDGSLVACSVIRVEPNVVTQIKTKESDGYFSLQIGAEEMNAPAHTITKRVSKPKLGHLRKAGGRVFRFLKEVRGSEEALNGVSLGDAFGLEVFEDEVSSVDVRGISKGKGFGQGVMMKKFGFRGGPGSHGSGFHRHAGSIGMRSTPGRCFPGSKRPSHMGAEENVTVKNLEVIKVDLEKKVLLVKGAIPGARGSIVIVKHSSRT

>core/702/1/Org1_Gene798

MQRIIVGIDTGVGKTIVSAILARALNAEYWKPIQAGNLENSDSNIVHELSGAYCHPEAYRLHKPLSPHKAAQI
DNVSIEESHICAPKTTSNLIETSGGFLSPCTSKRLQGDVFSSWSCSWILVSQAYLG SINHTCLTVEAMRSRNLN
ILGMVVNGYPEDEEHWTQEIKLPIIGTLAKEKEITKTIISCYAEQWKEVWTSNHQGIQGVSGTPSLNLH

>core/703/1/Org1_Gene301

MNAVNTPKKILCIVADYREISPLIEQLDFTQINEHLYSYRCTDYHLDLYIVHVWGSTAVLNALQSYCQAYTDY
DLWINPGFVGACSP EIPLGQCYTIEKIANLTDTTPVLS EDPPIYFDALPDSL PKSSLVTSPVLYHYGFHKTFKL
LDMEGYAIASQAAEH HIPC SFLKITS DYTVP GD C PFSRLEEVSQKLTQTLVELLPELMERAIPP KLLLPCP

>core/704/1/Org1_Gene345

MLGSLPCYPGAGNIEEYKNRYFYCQLCAEVVSPYVVPVIVVDVQGAPPTGILQVLRCKQHKKFQGLPVHGPI
SLWALEPVGKGAPQLESAMYELCSQVRNFDICSI SVSWVFGGLCIFAGLIVGVMVEAPLIAGLSAWVIPCIIGG
GAILCLFAILMAYLGRGRVREWLNL SHEYITQCHCRQIQAH SQNYSVITEYPATCALSQPITKLPNGSRRDN

>core/705/1/Org1_Gene128

MDHWLAIARLLL R GCGYTLCVSGIGILCGSILGLLIGTVTSLYFPSKLT KLLANSYVTVIRGTPLFIQILIIYFGLP
EVLPIEPTPLVAGIIALSMNSAAYLAENIRGGINSLSIGQWESAMVLGYKKYQIFVYIIYPQVFKNILPSLTNEFV
SLIKESSILMVVGVP ELTKVTKDIVSRELNP MEMYLICAGLYFLMTTSFSCISRLSEKRRSYDN

>core/706/1/Org1_Gene671

MKRVIYKTIFCGLTLLTSLSSCLDPKGYNLETKN SRDLNQESVILKENRET PSLVKRLSRRSRRLFARRDQTQ
KDTLQVQANFKTYAEKISEQDERDLSFVVSAAEKSSISLALSQGEIKDALYRIREVHPLALIEALAENPALIEG
MKKMQGRDWIWNFLTQLSEVFSQAWSQGVISEEDIAAFAS TLGLDSGTVASIVQGERWP ELVDIVIT

>core/707/1/Org1_Gene517

MQKL VHNIWKKFYSFSSAIAICIVLASFLSLKIVSNTYKHSQAKRNSILL LTRAAEVAVSQGFLPSKSALSSLEQ
AYHLGGESMKPYAGFLASCFYIHNEPLRGAYYAGLAYNNSQALQLPHPIQKLLKEISEAQADQLYDVALSKS
YQLLQTANSSPEYPTLSFLTLLRVIELKELLHQDVSQDFAALKSSPLFHQFERMYSDGEWTLSKRFGKKG

>core/708/1/Org1_Gene414

MIITIDGPSGTGKSTTAKALADHLHFNYCNTGKMYRTLAYARLQSPWATLPLTKFLEPPFSFTFATGQPLESF
FNGHLLTSELTTQEVANAASELSQLPEVRAFMQDLQRRYAQLGNCVFEGRDMGSKVFPNADLKIFLTSSPEV
RAQRRLKDLPEGTL SPEQLQAELVKRDAADAQRAHDPLVIPENGIVIDSSDLTIRQVLEKILALLFRNEL

>core/709/1/Org1_Gene291

MRKMLVLLASLGLL SPTLSSCTHLGSSGSYHPKLYTSGSKTKGVIAMLPVFHRPGKSLEPLPWNLQGEFTEEI
SKRFYASEKVFLIKHNASPQTVS QFYAPIANRLPETIIEQFLPAEFIVATELLEQKTGKEAGVDSVTASVRVRV
DIRHHKIALIYQEII ECSQPLTTLVNDYHRYGWNSKHFDSTPMGLMHSRLFREVVARVEGYVCANYS

>core/710/1/Org1_Gene702

MSKKPLYVAHPWHSPTLTQDNYESLCCYIEITPYDSVKFELDKATGLLKVDRPQKFSNFCPCLYGLLPQTYC
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DISDCPGTVLDMIQHYFLTYKATPNHLIKGSPAKIEIVGIYGKKEAQKVIQLAHEDYLSYIGDTAEVN

>core/711/1/Org1_Gene510

MSVNPSGNSKNDLWITGAHDQHPDVKESGVTSANLGSHRVTASGGRQGLLARIKEAVTGFFSRMSFFRSGAP
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KTGGTNAKRPATHGKGPAQPQPKTGGTNAKRAATHGKGPAQPQPKGILKQPGQSGTSGKKRVSWSEDED

>core/712/1/Org1_Gene75

MNTSISEIQRFLSMIAFEKELVSEDFSVVAGIDEAGRGPLAGPVVASACILPKGKVFPGVNDSKKLSPKQRAQV
RDALMQDPEVCFGIGVISVERIDQVNILEATKEAMLQAISLPISPDILLVDGLYLPHDIPCKKIIQGDAKSASIA
AASILAKEHRDDLMLQLHRLYPEYGFDRHKGYGTSLHVEAIRRYGPSPCHRKSFSPIKQMCAIV

>core/713/1/Org1_Gene172

MTKGSVFIIMGPPGSGKGTQSQYLANRIGLPHISTGDLLRAIIREGTPNGLKAKAYLDKGAFVPSDFVWEILKE
KLQSQACSKGCIIDGFPRTLTDAHLLDSFLMDVHSNYTVIFLEISEDEILKRVCSRFLCPSCSRIYNTSQGHTEC
PDCHVPLIRSDDTPEIIKERLTKYQERTAPVIAYYDSLGLKLCRVSSSENKEDLVFEDILKCIYK

>core/714/1/Org1_Gene316

MTSKKSYKSYFFDPLWSNNQILAILGICSALAVTTTVQTAITMGIAVSIVTGCSSFFVSLLRKFTPDSVRMITQ
LIIISLFVIVIDQFLKAFFFDISKTLVSFVGLIITNCIVMGRSESLARHVTPIPAFLDGFASGLGYGWVLLVIGVIRE
LFGFGTLMGFRIIPQFVYASETHPDGYQNLSMLVLAPSAFFLLGIMIWLVNIRDSKKRKR

>core/715/1/Org1_Gene14

MYFYKYVIIIDTSGYYPFLACVDNQQVLEHWSLPVGPDLGIVLEFLFKSKNLSFQGVAAVALGPGNFSATRIGIS
FAQGLAMAKNVPLLGYSSLEGYLLSKDEKKALMLPLGKRGGVLTLSSEIPEEGLNEKRRGVGPGALLSYEEA
SDYCVAHGYYHVISPNPQLFASSFSDKITVEEVAPSVEQIRRHVISQFMFVEYDKQLSPDYRSYSCIF

>core/716/1/Org1_Gene323

MATSVAPSPVPESSPLSHATEVLNLPNAYITQPHPIPAAPWETFRSKLSTKHTLCFALTLLLTLGGTISAGYAG
YTGNWIIICGIGLGIIVLTLILALLLAIPKKNKQTGTKLIDEISQDISSIGSGFVQRYGLMFSTIKSVHLPPELTTQNQ
EKTRILNEIEAKKESIQNLELKITECQNKLAQKQPKRKSSQKSFMRSIKHLSKNPVILFDC

>core/717/1/Org1_Gene415

MIFRICKFFTWVAFSLFYKLKVYGVKKNFIKGPAIIAVNHNSFLDPIALHMCVHECIYHLARASLFNIPWLWK
QWGCFPVRQDEGNSAAFKIASRLFNKRKKLVITYPEGARSPDGQLQPGKVIGIMMAAKSRVPIIPVYIRGTFEA
FNRHQKIPHVWKTITCVFGTPMYFDDIIQNPEIKNKETYQIITNQTMNKIAELKAWYESGCKGDVP

>core/718/1/Org1_Gene425

MIKSSLILLSGGQGTRFGSKIPKQYLPLNGTPLVLHSLKILSSLPQIAEVIVVCDPSYQETFQEYPVSFAIPGERR
QDSVFSGLQQVSYPWVIIHDGARPFYIPDEIHDLLETAEKIGATALASPIPYTIKQRNPVRTLDRDNLAIHHTPQ
CIKTEILREGLALAKEKQLTLVDDIEAAEIIGKPSQLVFNKHPQIKISYPEDLTIAQALL

>core/719/1/Org1_Gene450

MMNYEDAKLRGQAVAILYQIGAIFGKHILASGEETPLYVDMRLVISSPEVLQTVATLIWRLRPSFNSSLLCG
VPYTALTLATSISLKYINIPMVLRRKELQNVDPSDAIKVEGLFTPGQTCLVINDMVSSGKSIETAVALEENGLV
VREALVFLDRRKEACQPLGPQGIKVSSVFTVPTLIKALIAYGKLSSGDLTLANKISEILEIES

>core/720/1/Org1_Gene557

MARYCGPKNRVARRFGANIFGRSRNPLLKKPHPPGQHGMQRKKKSDYGLQLEEKQKLKACYGMIMEKQLV
KAFKEVIHKQGNVAQMFLERFECRLDNMVYRMGFAKTIFAAQQLVAHGHLVNGRRVDRRSFFLRPGMQIS
LKEKSKRLQSVKDALESKDESSLPSYISLDKTGFKGELLVSPEQDQIEAQLPLPINISVVCEFLSHRT

>core/721/1/Org1_Gene639

MKQFILRTLNALFPNPKPSLEGWSSPFQLLIAILLSGNSTDKAVNSVTPQLFAKAPDAQSILDLP PGKLYQLIAP
CGLGERKSAYIYQLSQILVRDFHGEPPNDMALLTQLPGVGRKTASVFLGIAYGKPTFPVDTHILRLAQRWKIS
EKKSPSAAEKDLARFFGHENTPKLHLQLIYYARQYCPALHHKIDNCPICSYLAKEANSTRT

>core/722/1/Org1_Gene52

MSVQVKLTKNSFRLEKQKLARLQTYLPTLKLKALLQAEVQNAVKDAAECDKDYVQAYERIYAFELFSIP
LCTDCVEKSFEIQSIDNDFENIAGVEVPIVREVTLPASYSLLGTPIWLDTMLSASKELVVKKVM AEVSKERLK
ILEEELRAVSIRVNLFEKKLIPETTKILKKIAVFLSDRSITDVGVKMAKKKIELRKARGDEC V

>core/723/1/Org1_Gene49

MANLNADGKLKQICDALRLDTLKP AEDEAAALLHNAKEQAKRIIQEAQEEARKILETAEERAHQKIKQGEVA
LSQAGKRALEALKQAVENKIFRESLVEWLEHVTTDPEVSTKLIQALVQALEAQGVSGNLTAYIGKHSVPRAV
NELLGKAVTTKLRKKS VVVGSVFVGGVQLKVEEKNWVLDLSSSALLEIFTRYLQKDFREMIFQGS

>core/724/1/Org1_Gene570

MTYLASSIFSPEDFLYPEIISK AHYTDILDLDMDQMLENHVFSGIHGTVESGVTLKNIEKIEIAEDAYVESGAYI
VGPCILGSQTEVRHGAYLRGNVITGSR CVVGHCTEIKNSYLGHHTKAAHFAYLGDSVLSSEVN LGAGVRCA
NFRLDGRNIYVRSTSDKSKKIDTGRRKLGAFLGKGVAIGCNVVINPGQHILPHTRIRPGQVI

>core/726/1/Org1_Gene27

MSFVPYSLPELPYDYDALEPVISSEIMILHHQKHQIYINN LNAALKRLDAAETQQNLNELIALEPALRFNGGG
HINHSLFWETLAPIDQGGGQPPKHELLSLIERFWGTMDNFLKKLIEVAAGVQGS GWAWLGFCPAKQELVLQ
ATANQDPLEPLTGKLPLLGV DVWEHAYYLQYKNVRMDYLKAFPQIINWGH IENRFSEIISSK

>core/727/1/Org1_Gene460

MYDYIRGTLTYVHTGAIVIECQGIGYHIAITERWAIECIRALHQDFLVFTHVIFRETEHLLYGFHSREERECEFRILISFSGIGPKLALAILNALPLKVLCSVVRSEDIRALASVSGIGKKTAEKLMVELKQKLPDLLPLDSRVETSQTHTTSSCLEEGIQALAAALGYSKIAAERMIAEAIKDLPEGSSSLTDILPIALKKNFSGVVKD

>core/728/1/Org1_Gene880

MKIVIASHHGYKIRETKTFLKRLGDFDIFSLSDFPDYKLPQEQEDSITANALTKGIHAANHLCWVIADDTMLRVPALNGLPGPLSANFAGVGGAYDKDHRKKLLDLMSSLESLVDRSAYFECCVVLVSPNQEIFKTYGICEGYISHQEKGSSEGGYDPIFVKYDYKQTFAELEDVKNQVSHRAKALQKLAPHLQSLFEKHLLTRD

>core/729/1/Org1_Gene727

MGLPNYITFSRLFITPIFMILYLKGKWFGITPVVLPYVLLALLAISELTDIDGYVARKFSQVTDLGKLLDPMADSIYRISIIYLTFTQPPVNLPLLLVFIFLARDSVISTLRTVCAFRGRVVAARASGKLKAILQGVSFLLVMIPHSLGLLSQNGLEIFASVTVSIIAVYSIASGIEYFWMNKNFLSQRAKTKDSEKNHESKD

>core/730/1/Org1_Gene193

MFIVIEGGEGSGKSSLAKALGDQLVAQDRKVLLTREPGGCLIGERLRDLILEPPHLELSRCCELFLFLGSRAQHIEQVIIPALRDGYIVICERFHDSTIVYQGIAEGLGADFDVADLCSKVVGTPFLPNFVLLLDIPADIGLQRKHRQKVFDKFEKKPLSYHNRIREGFLSLASADPSRYLVLDARESLSLIDKVMLHTQLGLCT

>core/731/1/Org1_Gene76

MNKILVDSFSPDHQKCCPKLFTISAPAGVGKTTLVRMLEQEFSSAFAETISVTTRKPREGEVPGKDYHFVSHEEFQRLLEDQALLESWVFLFGECYGTSMLEIERIWSLKGHAVAVIDIQGALFIRSRMPSVSIFIAPPSQEELERRLASRGSEEGSQRKERLEHSLIELAAANQFDYVIINDDLNQAYRVLKSIFIAEEHRNIL

>core/732/1/Org1_Gene595

MHAKLSFFILLSLLFSGIDCSRLHAAGRSPSLQGVLAIEDISAKLASHEVEIVMLSERLDEQDSKCQKWTAAKPETLAQKIRELESDQKALAKTLAVLTTSVKDLQTNLQSKLQEIQKDHRALAQDLRLVRRSLLALVDSSSPGAYADFSDPVPENIYIVREGDSLAKKIKYKLSVTELKKINKLDSDAIYAGQRLCLQRNKQ

>core/733/1/Org1_Gene278

MIGAQQKQSGKKTASRAVRKPAKKVAAKRTVKKATVRKTAVKKPAVRKTAAKKTVAKKTTAKRTVRKTVAKKPAVKKVAAKRVVKKTVAKKTTAKRAVRKTVAKKPVARKTTVAKGSPKAAACALACHKNHKHTSSCKRVCSSTATRKHGSKSRVRTAHGWRHQLIKMMSR

>core/734/1/Org1_Gene209

MTSPIPFQSSGDASFLAEQPQQLPSTSESQVLTQLLTMMKHTQALSETVLQQQRDRLPTASIIQVGGAPTGGAGAPFQPGPADDDHHPIPPPVVPAQIETEITTIRSELQLMRSTLQQSTKGARTGVLVVTAILMTISLLAIHIIILAVLGFTGVLPQVALLMQGETNLIWAMVSGSIICFIALIGTLGLILTNKNTPLPAS

>core/735/1/Org1_Gene647

MTLVPYVVEDTGRGERAMDIYSRLLKDRIVMIGQEITEPLANTVIAQLLFLMSEDPKKDIQIFINSPGGYITAG
LAIYDTIRFLGCDVNTYCIGQAASMGALLSAGTKGKRHALPHSRMMIHQPSGGIIGTSADIQLQAAEILTLKK
HLANILSECTGQPVEKIIEDSERDFFMGAEAAISYGLIDKVVTSAKETNKDTSST

>core/736/1/Org1_Gene453

MLKLLKVSITGDLSSGKTEACQVFQELGAYVVSAD EISHSFLIPHTRIGRRVIDLLGSDVVVDGAFDAQIAA
KVFYNSVLLQGLEAILHPEVCRIIEEQYHQSIQDGNYPFVAEVPLLYEIHYAKWFDSVILVMANEDIRRERFM
KKTGRSSEDFDQRCRFLNVEEKLAQADVVENNGTKKELHQKIEEYFYALKGAL

>core/737/1/Org1_Gene776

MLILLNLSLLFYVLFDSPGSIPVFVALLKNFSRKKQQRVILRECLFALGALILFVTFGRSFFQFLDISLYAFQIIG
GFLFLT VSIKMMLAPMPEKAKDDTSKTEPIFFPLAFPVITGPAVITALLSYMEEGIYSREIIFTAMIIAWAFSLFT
LLCSSFFDRLFGNFGLLALERLFGIALLLMSVNLMLKGISIAFNIGFYIG

>core/738/1/Org1_Gene381

MFSGIIQELGEVCFFEAQGNGLSLGIKSTPLFVTPLVTGDSVAVDGVCLTLTSCNESKIFFDVIPETLACTTLGE
KRCSDQVNLEAALKMGDSIGGHLLSGHVFGTAEIFLIKENRYYFRGSKELSQYLFEEKGFIAIDGISLTLVSVDS
DTFSVGLIPETLQRTTLGKKREGERVNIEIDMSTKIQVDTVKRILASSGKD

>core/739/1/Org1_Gene756

MFAYRTLTHNVVQVSHEIFKTTVVPGDTVIDATCGNGNDSLFLARLLQGEGRLVVYDIQKEALSNALLLFE
THLSEQERSVIEMKEQSHEHILEKDVKLIHYNLGYLPKGNKEITTLARTTEISLEYALNIVRPDGLITVVCYPGH
PEGEKETHSVESLAQRLHPKEWCVSSFFYVANRCRAPRLFIFQRQGSSESSVDKG

>core/740/1/Org1_Gene215

MTRYPDYLSKLIFFLRKLPGIGFKTAEKLAFELISWDSEQLKILGNAFHNVASERSHCPLCFTLKESEADCHF
CREERDNQSLCIVASPKDVFFLERSKVFKGRYHVLGSLLSPITGKHIENERLSILKSRIETLCPKEIILAI DATLEG
DATAFLKQELQHFSVNISRLALGLPIGLSFDYVD SGTLARAFSGRHSY

>core/741/1/Org1_Gene435

MGFACRYLFFFI VLFASGSFGNQLLSVPCWLSEEE SFYTHRFDFS KSYPD MENMEIQAQRKKRVEFNLTGEFP
KLET LNYQGSFGHLRAKCRGVYPVLYALNFSCSSCKMDMDFRGKWNRSSTITISNQKESINLKL PKDVG VIV
NTKTSLKGNVCPGSTFIKQGWGVWNKIYHNDLVGFSEVT LIFNV SSEG GTITFS

>core/742/1/Org1_Gene503

MRLFSLGTIY LFFSLALSSCCGY SILNSPYHLSSLGKSLLQERIFI APIKEDPHGQLCSALTYELSKRSFAISGRSS
CAGYTLKVELLNGIDKNIGFTYAPNKLGDKTHRHFIVSNEGRLSLSAKVQLINNDTQEV LIDQC VARESVD FDF
FEPDLGTANAHEFALGQFEMHSEAIKSARRILSIRLAETIAQQVYYDLF

>core/743/1/Org1_Gene915

MNWVPKTIDHVDPESEIDIRKVVSCYKLIKECQPEFRSLISELLGVIRCGLRLLKRSKYKEQARTVSDADPLF
CLTRSYQDGYLTPLRAGPRDLINHYIHLRRRENPKHFFSPKHPCYYARLAFNESVCVYRELFDIRLTKMYV
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>core/744/1/Org1_Gene726

MRIASLLSLLMIFPIFGESRPGSEDGNSNTQEIVGSQDTQVCLYHSYEQGLQASRIEGKPLVIVVLCNSGDD
GQACTIGLSETCEEVLSVLSGSIFSELANFVVLVPSGVNPLIYPPIEDPILAEIVKFKELFKDESFTGLSIIVGV
TPEGPGDIIIVSPVSLTVEEEEETLPSEQTTEVESTSELQSEDPAIA

>core/745/1/Org1_Gene403

MSSNLHPVGGTGTGAAAPESVLNIVEEIAASGSVTAGLQAITSSPGMVNLLIGWAKTKFIQPIRESKLFQSRAC
QITLLVLGILLVVAGLACMFIFHSQLGANAFWLIIIPAAIGLIKLLVTSLCFDEACTSEKLMVFQKWAGVLEDQL
DDGILNNSNKIFGHVKTEGNTSRATTPVLNDGRGTPVLSPLVSKIARV

>core/746/1/Org1_Gene7

MSLPLVLGSSSPRRKFILEKFRVPFTVIPSNFDESKVSYSGDPIAYTQELAAQKAYAVSELHSPCDCIILTGDITV
SYDGRIFTKPQDKADAIQMLKTLRNQTHDVVTSIAVLHKGKLLTGSETSQISLTMIPDHRIESYIDTVGTLNNC
GAYDVCHGGLILKKVHGCVYNVQGLPIQTLKYLLEELNIDLWDYSI

>core/747/1/Org1_Gene363

MLQEHFFLSEDVITLAQQLGHKLITTHEGLITSGYIVETEAYRGPDDKACHAYNYRKTQRNRAMYLKGGSA
YLYRCYGMHLLNVVTGPEDIPHAVLIRAILPDQGKELMIQRRQWRDKPPHLLTNGPGKVCQALGISLENNR
QRLNTPALYSISKEKISGTLTATARIGIDYAQEYRDVPWRFLSPEDSGKVLS

>core/748/1/Org1_Gene593

MTLSLVGKEAPDFVAQAVVNGETCTVSLKDYLGYVVLFFYPKDFTYVCPTELHAFQDALGEFHTRGAEVI
GCSVDDIATHQQWLATKKKQGGIEGITYPLLSDEDKVISRSYHVLKPEEELSFRGVFLIDKGGIIRHLVVNDLP
LGRSIEEELRTLDAIFFETNGLVCPANWHEGERAMAPNEEGLQNYFGTID

>core/749/1/Org1_Gene312

MFRRTGKGPFDVQTLYEEETSSPSSYSPYSRSETPPETPSLFDNPKASEARPLNHNLT EESSLPQWSSTPRTES
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ELRGGAIIKGDIIQANTLCVDEGVRLGYLAAGITDHSEERDL

>core/750/1/Org1_Gene790

MAYGTRYPTLAFHTGGIGESDDGMPPQPFETFCYDSALLQAKIENFNIVPYTSVLPKELFGNIVPVDTCVKSFK
HGAVLEVIMAGRGAALSDGTHAIATGIGICWGKDKNGELIGGWAAEYVEFFPTWINDEIAETHAKMWLKK
LQHELDLRSIAKHSEFQFFHNYINIKQKFGFCLTALGFLNFENAEPKVN

>core/751/1/Org1_Gene583

MKKWISILILSFLSLLSILPVLAITINHVKISQRWSDLNSQILTLKVIRDHEDQVIKHNARISKDRNNLSIESLNAS
CKQLRPLSKERERLNKLNSNSLLAQSKEVWERKRALEKSNHQLVWNCEQMHNDFAFVRLEQATEMDNEDI
ESLFSLFNPENPVAPLVFFTCWKMTKQTTPLGNEVWLTHAEAISRWI

>core/752/1/Org1_Gene596

MNIHSLWKLCTLLALLALPACSLSPNYGWEDSCNTCHHTRRKKPSSFGFVPLYTEEDFNPNTFGEYDSKEEK
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KEHLRKQGISADRLSTISYGKEHPLNSGHNELAWQQNRRTFEFKIHAR

>core/753/1/Org1_Gene313

MVLFSLLPFKLCYGCQAPGAYFCSNCLEKLLVEDREGRCLHCFRYLGSSETRLCSQCSPSSQLQAFSLYLPSQ
TALSVYARACEGKRPALQFFSKSIAFELASLDETSPSCIAYITSTISRKIVVEVAKLEKLLRIPLWPWLPKKRQIE
KLPKGEGICFLSAYPLSQKWMQTIVGGSASPLVSISLFLSQNDQ

>core/754/1/Org1_Gene185

MKRYVVGISGASGVILAVKLIKELVNAKHQVEVHISPSGRKTLYYELGCQSFDAKFSEENLEYIHTHSIQAISS
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MPMWYFKPQSVEDLENALVGKILAYLNIPSDLTKQWSNPE

>core/755/1/Org1_Gene663

MKVIYYEIEEIPSTNTMAKSYMHLWDPYALTVISTKCQTAGTGKFGKSWKSSKGDLLNTFCFFITDLHIDVSR
LFRLGTEAVVALCKDLGITEAKIKWPNDVLVHGEKLCGVLPETLPVEGLLGVVLGIGLNGNTTKQALKDVG
QPATSLQEILGHPIDLETTRELLIHLLGVLQENLPDSLATKSNRGN

>core/757/1/Org1_Gene374

MADGEVHKLRDIEKELLEARRVFFSEPVTEKSASDAIKKLWYLELKDPGKPIVFVINSPPGGSVDAGFAVWDQ
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YVEATNQPRDIEKAIDRDMWMTANEAKDFGLLDGILFSFNDL

>core/758/1/Org1_Gene35

MIKKFFIYSLIFSCSFSAPLKGICNEDVSSQSRIEEDPEVLITQLNELIETPIEEGKEIRNELQAISDGQKSSEEIEES
CGTSDSEGLSEKTDKESSNEYVLDDFFDSMVQRLEGISKMCQSGQVAQIIDCFNREFDIRNRELELKNRELELRE
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>core/759/1/Org1_Gene285

MSIKEDKWIREMALNADMIHPFVNGQVNVNEETGEKLISYGLSSYGYDLRLSREFKVFTNVYNSVVDPKCFT
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IYANEGIAQVLFFESSTTCEVSYADRKGGKYQKQQGITVPCV

>core/760/1/Org1_Gene684

MVRVSTSEFRVGLRIEIDGQPYLILQNDFVKPGKGQAFNRIKVKNFLTGRVIERTYKSGESVETADIVERSMRL
LYTDQEGATFMDDETFEQEVVFWEKLENIRQWLLEDTIYTLVLYNGDVVAVEPPIFMELSIAETAPGVRGDT
ASGRVLKPAVTNTGAKIMVPIFIDEGELVKVDTRTGSYESRVSK

>core/762/1/Org1_Gene987

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>core/763/1/Org1_Gene814

MIRRLEYYGSPILRKKSSPIAEITDEIRNLVSDMCDTMEAHRGVGLAAPQVGKNVSLFVMCVDRETEDGELIF
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>core/764/1/Org1_Gene759

MALNFKINRQIRAPKVRLLIGSAGEQLGILAIKDALDLAREAGLDLVEVASNSEPPVCKIMDYGKYRYGLTKKE
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>core/766/1/Org1_Gene447

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>core/768/1/Org1_Gene865

MELVVTSRETGKKSFLKKIRQQGGIPAVVYSAGKSLANITVDALVFKKFLSNLESGALSSTVFSLSYEGRIKA
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>core/770/1/Org1_Gene121

MVLSSQLSVGMFISTKDGLYKVTSVSKVAGPKGESFIKVALQAADSDVVIERNFKATQEVKEAQFETRLEY
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>core/771/1/Org1_Gene360

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>core/772/1/Org1_Gene611

MAAKTKTLEEDNVFLLLEGNLKRIFATPIGYTTFREFFQNVVFNCCANGQQEIANFFFEMLINGKLTQELAPQQ
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ARLLEAQKNPVGEKNLQEIQEEITSLKNHFDELTKALQ

>core/773/1/Org1_Gene420

MVETVLHNFQRYLSKYLYRVFRFPCRKKTFLSSHRVLARPSFPVDYCPGKIYDLQEIYEELNAQLFQGALRLQ
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>core/775/1/Org1_Gene807

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>core/776/1/Org1_Gene472

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>core/777/1/Org1_Gene41

MYKWYVVQVFTAQEKVKKALEDKFESSGMTDFIQEIILPIENVMEVKKGEHKVVEKYIWPGYLLVKMHLT
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FHDKGRLSVMVSIFGRETRVDDLEFWQVEEVAPGQSE

>core/778/1/Org1_Gene433

MSLLNLPSSQDSASEDSTSQSQIFDPIRNRELVSTPEEKVRQRLLSFLMHKLNYPKKLIIEKELKTLFPLLMRK
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>core/779/1/Org1_Gene309

MVEIFNYSTSIYEQHASNNRIVSDFRKEIQMEGISIRDVAKHAQILDMNPKPSALTSLLQTNQKSHWACFSPPN
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QGKVLLKALDLGVKSTNVMIDYVISRIFQFVQG

>core/780/1/Org1_Gene151

MSKESIRSYSEISTPTPIFRETPSKEGVAYKLQLRSPAKDCILRNRVSLKGALLRSIPFYGSFLGAKRIHSAWSA
KDAPCTTRVYHYLVGGLELLGLGVVVLACKVLATALKFLFSKASSKIKQMKWREKARNLAAKDTVQSIKEF
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>core/781/1/Org1_Gene582

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>core/782/1/Org1_Gene474

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>core/784/1/Org1_Gene729

MAKLIVAIGNPRHGYANTRHNAGFLLADRLVEELQGPPFKPLSKCHALMTLVESSSGPLVFIKPTTFVNLSGK
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ELSNFVLGKFSEENLQLGSIFVEASTLFTWCSKF

>core/785/1/Org1_Gene528

MSVLQDTEKKMAAALDFFHKEVKSFRITGKAHPALVETVVVDVYGTTMRLSDIASISVADLRQLVISPYDGN
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DVVKGNEKKIQELTDKFCKQLDELTKQKEAEIASI

>core/786/1/Org1_Gene658

MTTPQSPGSLSQSHLPHPHDPWDTEPTSLPEDPNDKASQELHSLVHLFRKLSIHLLESEVEKTVQQQLKPDLELA
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SGFKIETPNGILRQEISEELDHLLSVLTA

>core/787/1/Org1_Gene407

MACEQHEGCYEEEREIEIDIKSDTKWVSITQAAKLHNVTQAIYVAIKQKKLKASKETRWEIDIKDLEEY
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>core/789/1/Org1_Gene794

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PVDHVDHSSKSSLEQASQDLITLLKS

>core/790/1/Org1_Gene208

MSAPIPTPQELSDQITCLNVQYQQVSELARENKGDIEGLKTLTAALTADAGIQPSADEIYSLQTAAALILSASE
KPGSGPSGSTEGSVTVQSPCKFKKVLAVVLTHALIAIAVLIACIIACGGFPLLSALNLYTIGACVSLPIASTS
VALICLCTFVANSLIKPVITVRTR

>core/791/1/Org1_Gene396

MDRDNEVPLPKPKWIYRTGIGQDSHRFLPESSTKPCILGGIIFDHCPGFQANSDDIIFHAICNAISSVTNKIILG
KVADELLQTRGITDSGIYLEEALKSLKPNQKISHVAITIEGSRPKFLCKLSALRQNIQVMNLTPTDIGITATSG
EGLSDFGCGDGVQCFCVLTVMHEYCD

>core/793/1/Org1_Gene662

MGYVFYVIAGSIFLGISLGAYCQLYYSVKSVLFSWYLLTVYALEKRHALLALSQLVGEEDAQSQKEIDFLSQ
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KLRQRAPLRLASKLFRFLDVPSIRFSS

>core/794/1/Org1_Gene975

MDCVDNLKLYIFRLKLPDTERISYSISPEYIREKGEEELLSPIEVEGSLGRIDSDQWILSLSLKTQLGLCCPVC
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EYL

>core/795/1/Org1_Gene991

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>core/796/1/Org1_Gene771

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>core/797/1/Org1_Gene772

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>core/798/1/Org1_Gene440

MADDTLIPKLMKNSLSQACSEGLLIAKYPPLQVIVHFDNNLVVKTHLSVAPVFSCFLGPAAHKAMQEIVLW
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>core/799/1/Org1_Gene325

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>core/800/1/Org1_Gene783

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>core/802/1/Org1_Gene244

MSVHITPRKCFILCSMFTLPTLFPKAHLILFSPIYVLCFYCFSKDKGLVLALGCGVLSDLALGSRGVFLLLYP
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CAINSGIHKMISFFRRLVCY

>core/803/1/Org1_Gene529

MVHSPTHQCYHCQQPATICYTEIDKDKVIRSYVCATCPCPSHYYNNEHLSLSKGVGVLTLECGNCKTVWHS
KQDDEQLLGCHQCYTNFNQITSKLKSERVSSSFTMEKGQGS LHIGRAPGEASNTNPLLKLIALNEALQDTL
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>core/804/1/Org1_Gene421

MTAEKQNTGILGLEIRYTLPSDATYMLKWLNDPKILRGFP IQTEAEIRETVNFWVGFYRYHSSLTAVYNGNV
AGVATLVLNPYVKVSHHALISIIVGEEFRNKGIGTALLNNLIHLAKTRFKLEVLYLEVYEGNPALHLYQRFGF
VEVGRQNR FYKDEIGYLA KTTMEKDL

>core/805/1/Org1_Gene216

MKKLLFSTLLVLGSTSAAHANLGYVNLKRCLEESDLGKKETEELEAMKQQFVKNAEKIEEELTSIYNKLQD
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>core/806/1/Org1_Gene80

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RVVVDDSYFEEEEK EEQKVDNRKKEQD

>core/807/1/Org1_Gene579

MCKNRGVRGIVACDPRGVIGLEGKLPWHYPEDLQFFSETIQKFPIVMGRK TWETLPRKYFVDRAVVVFSHEK
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>core/808/1/Org1_Gene44

MKQEK TLLLQEVEDKISAAQG FILLRYLRFTAAYSREFRNSLSGVSAEFEVLKKRIFFKAIEAAGLEVDCSDTD
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>core/809/1/Org1_Gene55

MQRLGLSNLFHCLLLFLRYYYSKLVFGLTVLLAAISVICLLGCSEPSLSSFTEYVVGPEYSAAAQLSIEQSCHDE
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>core/810/1/Org1_Gene732

MKQQLLLLEDVDGLGRSGDLITARPGYVRNYLIPKKKAVIAGAGTLRLQAKLKEQRLIQAAADKADSERIAQ
ALKDIVLEFQVRVDPDNNMYGSVTIADIIAEAAKKNIFLVRKNFPHAHYAIGNLGKKNIPLKLKEEVTATLLV
EVTSDNEYVTVLAQGKQTEENQEG

>core/811/1/Org1_Gene196

MIINVRAPAFGITSVQQFSTNFQAAIPILNIVIGCSRISSTYAEDIEEVAQEKLEKSTHSKSSTSVNLWAHRVRGV
VEILGGGIVILALEITALVLQVIIKLIKCLIDVLCVCLFGLGVCVVAIIIGAIAFCV VVVVKYLGFCSQGEELEPIE
VKTLISPDKPYPTVVYV

>core/812/1/Org1_Gene461

MSELIIGVDPGTIVAGYAIIAVEQRYQLRPYSYGAI RLSSD MPLPMRYKTLFEQLSGVLDDTQPNAMVLETQF
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>core/813/1/Org1_Gene456

MRQFCNLLSLSRLWLALYFCQEKLHIRLLAIVGAMLSDVLDGYLARRYKATSRLGSILDPITDKVFVFVCITV
LYMEGSLSIAHLFFICARDLFLIIFVCYLSLVKGWKGYDYGSLFWGKIFTVVQFIILLGVTAGGEIPWTGLVPL
VALGFLYFLERIMDYKKQFLR

>core/814/1/Org1_Gene384

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LLRIFVILGLLAYLFFKKKSIQSTTQTALVLLCAGAINVGDIIIFYGHIVDFISFNYKQWAFPTFNVADVLISLGT
LLL VYKFYFPTKQTEKKR

>core/815/1/Org1_Gene534

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VLQIKSYIKVAVQLSEEEKVNKQKEVLAASKELEKAEVNLAKRRKEEEKTRLHKEEWMKEALKEEARA
EEKEQDEMGQLLFQLRQKKKRESGGS

>core/816/1/Org1_Gene251

MAVEQSHIKEEIEKLIGKAIKRVCGNKENDLCRYLPGPSGGYMHFTLKKMKSAAPEQLLKM LKTFISETP
RTINPKPRAPRGSKKRRDFINFTKTDIERVLELARQVGDKDLLARFSPKKPLTSLKRELIRSIRNGIVSVELWNA
YVEAVKAVSSPNLEVTSPFV

>core/817/1/Org1_Gene120

MDLKQIEKLMIAMGRNGMKRFAIKREGLELELERDRTREGNRQEPVFYDSRLFSGFSQERPIPTDPKKDTIKET
TTENSETSTTTSSGDFISSPLVGTFYGGSPAPDSPSFVKPGDIVSEDTIVCIVEAMKVMNEVKAGMSGRVLEVLIT
NGDPVQFGSKLFRIAKDAS

>core/819/1/Org1_Gene181

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QKAAVVGKFHQITKNKEVMSKKALKKAQAKEEKLVTETKLQQHNFEILNTGENLAPPMESTATLNQDTNFCVCE
DFIPTQEDFRISENSQKPPVEED

>core/820/1/Org1_Gene281

MSRQNAEENLKNFAKELKLPDVAFDQNNTCILFVDGEFSLHLYEEHSDRLYVYAPLLDGLPDNTQQRKLALY
EKLLEGSM LGGQMAGGGVGVATKEQLILMHCVLDMKYAETNLLKAFAQLFIETVVKWRTVCADICAGREP
SVDTMPQMPQGGGGMQPPPTGIRA

>core/821/1/Org1_Gene710

MKFWLQGCAFGCLLLTLPCAARRRASGENLQQTRPIAAANLQWESYAEALEHSKQDHPICLFFTGS DW
CMWCIKMQDQILQSSEFKHFAGVHLHMVEVDFFPQKNHQPEEQRQKNQELKAQYKVTGFPELVFIDAEGKQL
ARMGFEPGGGAAYVSKVKSALKLR

>core/822/1/Org1_Gene400

MSRRHSAEKRDIPGDPIYGSVILEKFINKVMMHGKKS VARKIVYSALERFGKKLNLENVLEGFGEALENAKPI
LEVRSRRVGGATYQVPVEVASERRNCLAMQWIIKHARSKPGKSMEVGLATELIDCFNKQGATIKKREDTHR
MAEANKAFAHYKW

>core/823/1/Org1_Gene470

MSLSKNSHKEDQLEEKVLVNNRCSKVVKGGRKFSFSALILVGDGKGRLGYGFAKANELTDAIRKGGEAAKK
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KALTGLSPRKDLLRRGA AIND

>core/826/1/Org1_Gene549

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SSSGGMKTLYLSLFRN

>core/827/1/Org1_Gene725

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AQCQAVLPLETKN

>core/828/1/Org1_Gene773

MSITTLGTLPTVNTINSSRPPLEPLNTPKIGAVLFSIYELLLQAIEIRQQTVLTSQQQLNDNTNIQQQLNQETNQI
KYAIVSAGAKEDEITRVQNQNQNYSAQRSNIQDELVTTRQNGQIILSHASTNINIIQQSSQDSSFIKTTNSIGST
VNQLNKPLG

>core/829/1/Org1_Gene299

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LLHLLNRDIDIPGFGMDDEEQGLIFYRLVLPCLNGEIHDtLLRIYIDTIKLVCDSFSHAIGLISSGNMNLDELRRQ
ALQEQQEKrne

>core/831/1/Org1_Gene758

MATLSPEKFSGSPISISKEFPQQKMREILQMLYALDMAPSAEDSLVLLMSQTAVSQKHVLVALNQTKSILEK
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SLNENSLSI

>core/832/1/Org1_Gene280

MMFGHFAGYLGADPEERMTSKGKRVITLRLGVKTRVGMKDETVWCKCNIWHNRYDKMLPYLKKGSGVIV
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MYAGYGQEQQYVCEDVPF

>core/834/1/Org1_Gene149

MSKKVFFESYEDFANVASSWPksLRALVQGRYFVDSELKETPYRIHDFKKTPIHHRLYRSLPIISTIGGIIRLIEA
HSGPIHPRDKMKYRFEVLQAVIEILGLGVLLlVFDIIGCFLAFLVAIILSLLLYCNSTFTCVQNLsfTERMLEGIG
EAVNFLA

>core/835/1/Org1_Gene298

MFFNLfSLVfKLsDELALAETIQEPISVHEMFPGSMKLEMfKMLGSLILLLTIFGFGVWAFKKFVRSRSHGFGG
SSQIKILERRSLTPKTSIYLIRVVNKTLVIAETPEKITLLTEFPpDtdINHLLQENNKQSSSSATSDFLSKAIQKIqK
KQQTnQD

>core/837/1/Org1_Gene30

MPSYCQNQQDFSLfSLLSPRLVMFLGKHSRDEILQDLTDLVDAAGLLEDKQAFFDALVRRENIMSTGIGMGV
AIPHGKLESCSNFFIAIGIHTQGILWDAIDGALVRLVFLIGGPENAEYLKLLSTLTLSLREESRRQQLLQVNT
IEEVMNVFVGM

>core/838/1/Org1_Gene626

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QDTsnKPS

>core/839/1/Org1_Gene366

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RKKHALLTA

>core/841/1/Org1_Gene720

MLPISILLFYVILGCLSAYIADKKKRN VIGWFFAGAFFGFIGLVVLLLLPSRRNALEKPQNDPFDNSDLFDDLK
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VPSLQQALKEASK

>core/842/1/Org1_Gene241

MRIIRFDPYGALSAQSI AKDSRQNSPLVEKISEEIATNEAIRLALLAIGDREQEEKQRHRYKLLGQKQAKVLL
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TASTLFYQKDEEA

>core/843/1/Org1_Gene721

MEKQNLKLDVKEIEFPETVFSRDIETRVIQVIILHCLAKINGVSLLGGNLIDALFGRDIERMKG IYVEQDSKNHL
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LENSEG

>core/844/1/Org1_Gene113

MIMTTISNSPSPALNP ELSLIPPTLVSSGTQTSLAYTIPAQGRRSTLR IILDIFIILGLATIISTFIVIFFLNGLNLLS
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>core/845/1/Org1_Gene494

MRVV LHCPDIPQNTGNIGRTCVALGAELILVRPLGFSLADKFVKRAGMDYWDKLQLTVVDSIEEALHDVPED
QIFCLSTKG SASYTEFSLPSSGTYYVFGSESKGLPKEILKKYYKNCLRIPMQQDIRSLNLATSVGIVLYEVVRQKT
VALQKNPTV

>core/846/1/Org1_Gene768

MEKDIFFMQQAFKEARKAYDQDEVPGCVIVKDDKIIARAHNSVEKLKDATAHA EILCIGSAAQDLDNWRL
LDTVLYCTLEPCLMCAGAIQLARIPRIVWAAPDVRLGAGGSWVNIFTEEHPFHTVSCTGGVCSEEA EHLMKK
FFVEKRREKSEK

>core/847/1/Org1_Gene262

MGYLPVSATDVL FESPAAPLINSANTQNQKLI ELKGKQQAESSPRTITSVILEVLLVIGCCLIVLSLLAIRPALQF
TLETGHPAAIAVLAVSGTILLVAVIILFCFLAAVPFAAKKTYKYVKTVDDYASW HSHQQTPTLTGTIFSGIVYAE
SQAQL

>core/848/1/Org1_Gene489

MLKKKPVSFSCIDGHIYKIFPNDLNANNTVFGLLMSLLDRLALVVAERHTESVCVTA FVDALRFYAPAYMG
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DRRRQARLELK

>core/849/1/Org1_Gene669

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>core/850/1/Org1_Gene637

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>core/851/1/Org1_Gene25

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>core/852/1/Org1_Gene486

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LVDKESI

>core/853/1/Org1_Gene382

MQCPFCNHGELKVIDSRNAPEANAIKRRRECLKCSQRFTTFETVELTLQVLKRDGRYENFQESKLIHGLNAAS
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>core/854/1/Org1_Gene989

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MKRRHH

>core/855/1/Org1_Gene225

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>core/856/1/Org1_Gene167

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LTL

>core/857/1/Org1_Gene701

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YLFSS

>core/858/1/Org1_Gene673

MQLLSPAFAYGAPIPKKYTCQGAGISPPLTFVDVPGAAQSLALIVEDPDVPKEIRSDGLWIHWIVYNLSTTITN
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EKS

>core/859/1/Org1_Gene175

MEKRKDTKTTIVKSSETTKSWYVVDAAGKTLGRLSSEVAKILRGKHKVTTYTPHVAMGDGVIVINAEKVRLT
GAKKGQKIYRYTGYISGMREIPFENMMARKPNYIIEHAIKGMMPRTRLGKKQLKSLRIVKGDSYETFESQK
PILLDI

>core/860/1/Org1_Gene36

MEFICPLQHARCLKKQHKIIEELFPEPFQKDHLYLKLMENSSSRDAFDKKRMLKENLVVGCQSDLYLYEVYQ
DGILFFFTYTKALMSSGIASLFTEVYSGETPSTILTCKPIFFQRLTPYLSFGRLNGGESLYMRMKQIAVQYLKPP
QT

>core/861/1/Org1_Gene537

MADLEVFAQDFALLFEAGLLAIKQGDEDSARKLFQSLHILNPNHYGHDLGLALISLHKMDLFD AEERLSALIK
GNEDNWSIKAFLSLTHMLIVLHQSSFEVRRESLESCLKFADQVIANCKIESTRALAQSVLDWHDTLVAKSA
GPLG

>core/863/1/Org1_Gene274

MKSERLKKLESELHDLTQWMQLGLVPKKEISRHQEEIRILEHKKIYEEKERLQLLKENGEIEEYVTPRRSPAKTV
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W

>core/864/1/Org1_Gene271

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KKRG

>core/865/1/Org1_Gene875

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LTSGKGQTVSLAYTSQGIGYRIPYGYNVDIRQEVRGDNLKMKVCLADVVELFPDQKQAVSVQRCLCVTL

>core/866/1/Org1_Gene129

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TRHLVLSIRHNASLIVIRTVPGSASWIAALLDQGLKDEILGTLAGDDTIFVTPIDEGRLPLLMVSIANLLQVFLD

>core/867/1/Org1_Gene237

MQNQYEQLLES LAPLLNTTLAPDKNNSCLIRFSDTHVPVQIEEDGNSGDLAVSTLLGTLPENVFRERIFKAALS
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>core/868/1/Org1_Gene693

MEEFVAYIVKNLVTNPEAVEIRSIEDEDNESIKLEIRVAAEDIGKII GRRGNTIHALRTILRRVCSRLKKKVQIDL
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>core/869/1/Org1_Gene90

MSLEKELLEETPLVLLNFYKLV SFCNYAGMILGTEKKFAIYGHVSMGQAFQGADTEGHSPQRPF AHDLLNF
VFSGFDIQVLRVVINDYKDNV FYTRLFLEQKDREFLYVVDVDARPSDSIPLAL THKIPILCVKSVF DAVVPYEE

>core/870/1/Org1_Gene147

MNPVTFDRIQVDFIPEDTSLRINSYIVAGGLLILGVVLSILSVICLDIGLVGLSAGAAFTLGLGCLIFALFLFSFL
ILLLSQEKRVPDVL SLYLEKEVPQYETPLYKEDLESERDMSAISERLGII EKLRIA EKFRYSDSVFV

>core/871/1/Org1_Gene29

MTVFCELDSGGELPEYTTPGAAGADLRANIEEPIALLPGQRALIPTGIKAEIPEGYELQVRPRSGLALKHGITVL
NSPGTIDSDYRGEIRVILINFGDSTFII EPKMRIAQVVLSPVVQATFVVKQESLAETARGSGGFGHTGAS

>core/872/1/Org1_Gene504

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>core/873/1/Org1_Gene459

MEQTLSIIKPDSVSKAHIGEILSIFEQSGLRIAAMKMMHLSQTEAEGFYFVHRERPFFQELVDFMVSGPVVVLV
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>core/874/1/Org1_Gene469

MIKLES LFDISERKRRKKLLGRGPSSGHGKTSGRGHKGDGSRSGYKRRFGYEGGGVPLYRRVPTRGF SHKRF
DKCVEEITTGRLAELFQEGEAITLDALKAKKAIARQAVRVK VILKGDLEKTFVWQDTAVVLSQGVQNLLGIT

>core/875/1/Org1_Gene171

MACSIFFRMSQGDYDDEPLSKKTACLVDTMLYPVIAVVCVVSVVLLILKVLFLLLSFPFKLCSASSALPGE
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>core/876/1/Org1_Gene816

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>core/877/1/Org1_Gene505

MSLDFFEEFYHQ SILNTGTSFPEGYL NIAEILSYPHCTDANTDFLCSQSDNDFHIAESKDKLTLFNADFAIWLVP
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>core/878/1/Org1_Gene464

MQHARKKFRVGR TSSHNR CMLANMLKSLIHYERIETTL PKAKELRRHADKMITLAKKNSLAARRIAIGRLM
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>core/879/1/Org1_Gene565

MNSKSAQKIIDS IKQILTIYNIDFDPSFGSSLSSDSDADYEYLITKTQEKIQELDKRAQEILTQTGMSKEQMEVF
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>core/880/1/Org1_Gene310

MLDNEWKAILGWGDDELEELRISGYSFLRQGHYSKAILFFEALVILDPLSIYDHQTLGGLYLQIGENSQALAV
LDQALRMQGDHLPTLLNKTKALFCLGRIEEATAIATYLSSCPIPAIANDAEALLMSYSKATKKNAALVR

>core/881/1/Org1_Gene491

MGRYRRVSHSSQETLLLGT ELGQVLVPGAVLLLFGDYGAGKTEFVRGIVSGYLGDTIAEEVASPSFSILHVG
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>core/882/1/Org1_Gene42

MSVKKVIKIIKLQIPGGKANPAPPIGPALGAAGVNIMGFCKEFNAATQDKPGDLLPVVITVYADKTFTFITKQP
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>core/883/1/Org1_Gene54

MIDMSVVG PALVLGLAMIGSAIGCGMAGVASHAVMSRIDE GHGKLIGMSAMPSSQSIYGFILMLLMQAAIKN
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>core/885/1/Org1_Gene716

MHPLTLPKQSRVLKRKQFLYITRSGFCCRG SQATFYVVP SRHPGTCRMGITVSKKFGKAHERNSFKRVVREV
FRHVRHQLPNCQIVVFPKGHKQRPVFSKLLQDFINQIPEGLHRLGKTKATTGGE CTPKSEKCVTAPR

>core/886/1/Org1_Gene478

MLMPKRTKFRKQQKGQFAGLSKGATFVDFGEYAMQTLERGWVTSRQIEACRVAINRYLKRRGKVWIRIFPD
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>core/887/1/Org1_Gene210

MNLIDRAFLKKTIIFQSLDMDLLLTIADKTETIIFKPGSNVFSIGQPGFSFYIIVEGYITISKEKLESPLNLKPLDC
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>core/888/1/Org1_Gene152

MVNRYKSSAEFSADHYYDDNLVRMGYKRNLRLGLAPVENEVCLFEENNLLSVMASIPIMGSILGLGRLHSV
WSTQDPKDSKISIHFTALGILETLGLGIHVLLIKITITILLILFTPCLLCYFMYSAAYSDFHPI

>core/889/1/Org1_Gene158

MINFIRSYALYFAWAISCAGTLISIFYSYILNVEPCILCYQRICLFPLTVILGISAYREDSSIKLYILPQAVLGLGI
SIYQVFLQEIPGMQLDICGRVSCSTKIFLSYVTIPMASVVAFGAIVCLLVLTCKYRG

>core/890/1/Org1_Gene599

MKYRFTEEIEEEPLVNLTPOLIDIVFVILMAFIVAVPLIKLDSIALAPGTQEQLSSENDSIAVIKVFADHSLTLN
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>core/891/1/Org1_Gene174

MAKSTIQESVATGRRKQAVSSVRLRPGSGKIDVNGKSFEDYFPLEIQRTTILSPLKKITEDQSQYDLIIRVSGGG
IQGQVIATRLGLARALLKENEENRQDLKSCGFLTRDPRKKERKKYGHKKARKSFQFSKR

>core/892/1/Org1_Gene577

MIAIERYQLISKFRMWLFLGCSVEERHFKQPVLISVTFSYNEVPSACLSDKLSDACCYLEVTSLEEIANTKPY
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>core/893/1/Org1_Gene157

MPYYANTLEFIQGTQSLCPLFKYGFVRHHYKGQLEIEDASHDWDFLEPPSTWKRTLLAAIPILGSVIGLGRIFS
IWSIREPQDSQEYKSIFWHTLCAVLEILGLGIVALILKILATFIMAMPGLKRVATFLFYS

>core/894/1/Org1_Gene473

MGMTSDSIADLLTRIRNALMAEHLVVDVEHSMREAIKILKHKGFVAHYLVKEENRKRMRVFLQYSDD
RKPVIHQKRVSKPSRRVYVSAKIPYVFGNMGISVLSTSQGVMEGSLARSKNIGGELLCLVW

>core/895/1/Org1_Gene466

MVKNQAQAKKSVKRKQLKNIPSGVVHVKATFNNTIVSITDPAGNVISWASAGKVGYSGRKSSAFAATVAA
QDAAKTAMNSGLKEVEVCLKGTGAGRESAVRALISAGLVVSVIRDETPVPHNGCRPRKRRRV

>core/896/1/Org1_Gene698

MNFVSTLTGSDFYAPVLEKLEEFADTTGQVILFSSSPDFIVHPIAQLGISSWYASCYRDQSAEQTIYKKCLT
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>core/898/1/Org1_Gene189

MSQCQSSSTSTWEWMKSFVPNWKNPTPPLSPIPSEDEFILAYEPFVLPKTDPENAQANPPGTSTPNVENGIDDL
NPLLGQPNEQNNANNPGTSGSNPTSLPAPERLPETEENSQEEEQGSQNNEDLIG

>core/899/1/Org1_Gene540

MLEKLIKNFATYMGITSTLELDADGAYVLPISVVKVRAQQNADNEIVLSASLGALPPSADTAKLYLQMMIG
NLFGRETGGSALGLDSEGNVVMVRRFSGDTTYDDFVRHVESFMNFSETWLSDLGLGKQ

>core/900/1/Org1_Gene292

MRDHAFSKLIGTVRAMVVEGRCPWSLQQSLVSMVEHILGECQEFHEAVLQGKTVQEVGSEAGDVLTLVLIL
CFLLEREGVLASEDVANEAMEKLRRRAPYIFAEDYKPVSIIEADRLWELAKHREKNEST

>core/901/1/Org1_Gene905

MDYKSQLVFSCPCCKGNVCFSVFNLDVILTCNVCSSSTYTFDSVIRNEIRQFVALCKRIHDANSILGNATVSVS
VEDNQMDIPFQLLFSRFPVVLNLSLDGKKIAIRFLFDALNTSILHQESDLIS

>core/902/1/Org1_Gene335

MREEGSVSFREYFRAYMCDKIVAQKNFLFTLDAVIKQAGWRSQEKLNLFYVESQALGREIKVSLEEYIQSMV
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>core/903/1/Org1_Gene45

MTTESLETLVEKLSNLTVLELSQLKKLLEEKWDVTASAPVVAAGGGGEAPVAAEPTEFAVTLEDVPADK
KIGVLKVVREVTGLALKEAKEMTEGLPKTVKEKTSKSDAEDTVKKLQDAGAKASFKGL

>core/904/1/Org1_Gene594

MKFTVALFGAEAKGSYDTAYFCRSLVDLHNYLGDVSSPGITLAIKTLLSDYNVYFRVREEGYCVDSYFFGL
HFLNTQTTLKNIIAIGLPGVGNQHIIASRSLCQKHNSLLLFFDHDLYDLLTFNQPF

>core/905/1/Org1_Gene914

MRAGGSLVTTPKEGQRLRSPEQLRVLDDLVSQSYPNHLHAIELDCGAIPQDLIGATYIITFADFSAYILSLRSY
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>core/906/1/Org1_Gene154

MLIGRYSSDDQFTEATKNTPTIIKLG FVRDNLEGLTNPISIVSETSSSIKDSVLRSLPILGSILGCARLYSTLSTN
DPLDETQEKIWHTIFGALETGLGILILLFKIIFVILHCIFHLVIGFCK

>core/908/1/Org1_Gene383

MPLSDDEIEQFKRLLMKAKLSHTLEGNAQEVKKPNEATGYSQHQADQGTDTFDRRTISLEVTTKEYELLRQ
INRALEKINESSYGICDVS GEEIPLARLIAIPYATMTVKAQEQFEKGLLSGN

>core/909/1/Org1_Gene471

MESSLCKKSLMKRRRALRVRKVLKGSPTKPRLSVVKTNKHIYVQLIDDSIGKTLASVSTLSKLNKSQGLTKK
NQEVAKVLGTQIAELGKNLQLDRVVFDRGPFKYHGIVSMVADGAREGGLQF

>core/910/1/Org1_Gene401

MPTINQLIRKRRKSSLARKKSPALQKCPQKRGVCLQVKTKTPKKPNSALRKVAWVRLSNGQEVIA YIGGEGH
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>core/911/1/Org1_Gene678

MALKDTAKKMKDLLDSIQHDLAKAEKGNKAAAQRVRTDSIKLEKVAKLYRKESIKA EKSGLLKRKPSTKAP
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>core/912/1/Org1_Gene623

MKRQKRKQSITLIEMMVVITLIGIIGGALAFNMRGSIHKGKVFQSEQNCAKVYDILMMEYATGGSSLKEIIAH
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>core/913/1/Org1_Gene656

MRDRLGSLSLILKVKIHKYLDTLHNQKRLALTVSRNIQATNKRIADLHLERYEHFISRDNIKHYDILLEYLKTL
QSSLYKQQSESLRFLEIHHQQLQELINRRKII EKIKNNKYSKDQEIGT

>core/914/1/Org1_Gene467

MPRIIGIDIPAKKKLKISLTYIYGIGSARSDEIHKKLKDPEARASELTEEEVGRLNSLLQSEYTVEGDLRRRVQS
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>core/915/1/Org1_Gene476

MIQQESQLKVADNTGAKKVKCFKVLGGSRRRYATVGDVIVCSVRDVEPNSSIKKGDVIKAVIVRTRRHITRK
DGSTLKFDTNSCVIIDDKGNPKGTRIFGPVAREIRD RGFIKISSLAPEVI

>core/917/1/Org1_Gene226

MEIIHIGTDIIEISRIREAIATHGNRLN RIFTEAEQKYCLEKTDPIPSFAGRFAGKEAVAKALGTGIGSVVAWKD
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>core/918/1/Org1_Gene74

MVNLLKELEQEQCRNDLPEFHVGD TIRLATKISEGGKERVQVFQGTVMARRGGGSGETVSLHRVAYGEGME
KSFLSNSPRIVSIEIVKRGKVARARLYYLRGKTGKA AKVKEFVGPRSSKK

>core/919/1/Org1_Gene761

MVRATGSVASRRRRKRILKQAKGFWGDRKGHIRQSRSSVMRAMAFNYMHRKDRKGDFRSLWIARLNVASR
IHSLSYSRLINGLKCANISLNRKMLSEIAIHNPEGFAEIANQAKKALEATV

>core/920/1/Org1_Gene153

MRELNAFELTQPEEYRNRWVLMPCCLKRFCRTQHAKVWSYRCVHEASLYEKNCFLLTYDDKHLPQYGS
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>core/921/1/Org1_Gene222

MATVAQTPQTTQPQPSVSHKATHRYCSWVFFKPILVSLGLLASLTTLGLVIASGVTLISLGIGIVLAIQIVLAGI
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>core/922/1/Org1_Gene231

MTENRRIKRVNALLQEAIKVKLDVKHPKISNLWITVTRVSLSKDLHSARVYVSVMPHENTKEEAEALKV
SAGFIAHRASKNVVLKYFPELHFYLLDDIFSPQDYIENLLWQIQEKEKS

>core/923/1/Org1_Gene616

MNKKPKKTKKAVQSKAAPVKRVPEESQEAAIQLELAVSDLYKELPLAQTFASLTDKNQINSIIAALSGTLES
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>core/924/1/Org1_Gene386

MDNYLLGSLIFCCVLLSIGMCTIFVMTICFLRQLNKILKNIHRVTILNFEAKILAPMLGKKLLCGWLKKRKN
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>core/925/1/Org1_Gene699

MDSFCFDLLKVAAKAIDDKKGNNLVVLDVRTISEFTDYFVFVEGSVNVHVKALANTIVEELKKQKVSPLHVE
GITDGNWVVVIDYGFIVVHVVFSEIRGKYRLEELWKDGFIVTSKLLAS

>core/926/1/Org1_Gene266

MPVSSAPLPTSHRPSSGNLGLMEPNKALKAKHQDKTTKTIKLLVKILVAILVIEVLGHIAAFFIPGTPPICLIILG
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>core/927/1/Org1_Gene72

MALKIRLRQQGRRNHVVYRLVLADVESPDRGKYIELLGWYDPHSSINYQLKSERIFYWLERGAQLSSKAEAL
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>core/928/1/Org1_Gene1004

MTVLFYAFLFIFLFLCVILCGLILVQESKSMGLGSSFGVDSGDSVFGVSTPDILKKVTSWCAVAFICGCLLLSFS
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>core/929/1/Org1_Gene677

MLSRIVTCFLFLLSSLPLFAEEEEAAQSKNTFVQPAVMLAIAILFFYFILWRPEQKRRKAMEKRKNDLAKGDKV
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>core/930/1/Org1_Gene368

MSDIQKEEHGSTTIFHLHGKLDGISSPEVQENISQSLAAGSKNIILDCAHLDYMSSAGIRVLLQSYHQVGQHSG
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>core/932/1/Org1_Gene195

MFLKRKKRGGSQVQNKRTASPIKHAKHYLHNYLQELQKIMAARPHDAIDAWNQVFRDKYKGMSQAIGFRD
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>core/933/1/Org1_Gene286

MSKVSVRKKNWGFRLLEEVMIKSWWVIFSILIGGFVYDRAIQELRTEELRLQSKVSSLCQDILSAQEKQRQLQ
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>core/934/1/Org1_Gene320

MWYS DYHVWILPVHERVVRLGLTEKMQKNLGAILHVDLPSVGS LCKEGEVLVILESSKSAIEVLSPVSGEVID
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>core/936/1/Org1_Gene730

MGKKENQLYEGAYVFSVTLSEEARRKALDKVISGITNYGGEIHKIHDQGRKKLAYTIRGAREGYYYFIYFSVS
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>core/937/1/Org1_Gene694

MTAVLILTSFPSEESARSLARHLITERLASCVHVFPKGTSTYLWEGKLCES EHHIQKSIDIRFSEICLAIQEFSG
YEVPEVLLFPIENGDP RYLNWL TILSYPEKPPLSD

>core/938/1/Org1_Gene479

MFKATARYIRVQPRKARLAAGLMRNLSVQEAEELGFSQLKAGRCLKKVLNSAVANAELHENIKRENLSVT
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>core/939/1/Org1_Gene475

MKKQNIRVGDKVFILAGNDKGKEGKVLSLTEDKVVVEGVNVRIKNIKRSQQNPKGKRISIEAPIHISNVRLTIA
GEPAKLSVKVTEQGRELWQRRPDGTSQLYRLVRGKKG

>core/940/1/Org1_Gene318

MTTLPKYVPRSRQNPDTLTFLKRYSSVLLHSENSLSYRIFAKVLAILLTS LAVAFVTLFSCEGSQRLCALYI
GIALAICVLLTIVVYCIASKIATA CKPPSISR IEIV

>core/943/1/Org1_Gene481

MKDPYDVIKRHYVTEKAKMLEHLSAGTGEGKKKGSFCKDPKFVFIVSHDATKPLIAQALEAIYVDKNVKVK
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>core/945/1/Org1_Gene350

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>core/946/1/Org1_Gene695

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>core/947/1/Org1_Gene943

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>core/948/1/Org1_Gene69

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>core/949/1/Org1_Gene20

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>core/950/1/Org1_Gene836

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>core/952/1/Org1_Gene443

MDEITPNYPLLRQDSLWNRVRVSWRADLSVSSRYEIASAAILGLLVAFCASAAVSIIFTANPLAQVFIDGCLA
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>core/954/1/Org1_Gene395

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>core/955/1/Org1_Gene545

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>core/956/1/Org1_Gene428

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>core/957/1/Org1_Gene398

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>core/958/1/Org1_Gene267

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>core/959/1/Org1_Gene436

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>core/961/1/Org1_Gene493

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>core/962/1/Org1_Gene86

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>core/963/1/Org1_Gene319

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>core/964/1/Org1_Gene719

MAKKSSVAREAKRRRLVEANFKKRSDLRKIVKSLSVSEEEKENARISLNKMKRDTSPTRLHNRCLLTGRPRG
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>core/965/1/Org1_Gene2

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>core/967/1/Org1_Gene387

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>core/968/1/Org1_Gene303

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>core/969/1/Org1_Gene574

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>core/970/1/Org1_Gene785

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>core/971/1/Org1_Gene544

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>core/972/1/Org1_Gene908

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>core/974/1/Org1_Gene584

MLSyllRTAINVYSFLILAYIFASWVPDCQSARWYQLVSKCVD PFLNFFRRFVPRIGFIDPSPFVGLLCLGILPF
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>core/975/1/Org1_Gene243

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>core/976/1/Org1_Gene77

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>core/977/1/Org1_Gene402

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IALGILLINCVC DLKQYLTSS

>core/978/1/Org1_Gene21

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>core/979/1/Org1_Gene307

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>core/980/1/Org1_Gene628

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>core/982/1/Org1_Gene451

MLIRLFLGISLPKGFPLYLEPPLVLATFQGTQFVGTYSEATNPLYIDNLNLNYHYTQELLYKAVPCNYKSIYRE
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>core/983/1/Org1_Gene1

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SCSSGGCHSHHSDKN

>core/988/1/Org1_Gene260

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>core/989/1/Org1_Gene356

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>core/990/1/Org1_Gene404

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>core/991/1/Org1_Gene767

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>core/992/1/Org1_Gene239

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>core/993/1/Org1_Gene822

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>core/994/1/Org1_Gene116

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>core/996/1/Org1_Gene423

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>core/997/1/Org1_Gene724

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LEIESLLAQNEVM

>core/998/1/Org1_Gene477

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>core/999/1/Org1_Gene812

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>core/1000/1/Org1_Gene538

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>core/1001/1/Org1_Gene394

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>core/1003/1/Org1_Gene40

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>core/1004/1/Org1_Gene539

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>core/1005/1/Org1_Gene731

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>core/1009/1/Org1_Gene211

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>core/1012/1/Org1_Gene547

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>core/1013/1/Org1_Gene1015

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>core/1014/1/Org1_Gene590

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LVPSE

>core/1015/1/Org1_Gene769

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>core/1016/1/Org1_Gene869

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>core/1018/1/Org1_Gene552

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>core/1019/1/Org1_Gene858

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>core/1021/1/Org1_Gene38

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>core/1023/1/Org1_Gene985

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>core/1028/1/Org1_Gene498

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>core/1031/1/Org1_Gene825

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>core/1033/1/Org1_Gene760

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>core/1034/1/Org1_Gene348

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>core/1037/1/Org1_Gene405

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>core/1045/1/Org1_Gene737

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>core/1046/1/Org1_Gene953

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>core/1050/1/Org1_Gene15

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>core/1054/1/Org1_Gene290

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>core/1056/1/Org1_Gene932

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>core/1058/1/Org1_Gene365

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>core/1059/1/Org1_Gene177

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>core/1067/1/Org1_Gene787

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>core/1068/1/Org1_Gene984

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>core/1069/1/Org1_Gene718

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>core/1070/1/Org1_Gene717

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>core/1073/1/Org1_Gene1014

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>core/0/2/Org2_Gene73

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>core/1/2/Org2_Gene462

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>core/2/2/Org2_Gene856

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PEQDGTLPPLPEIIIPKGTKLHSNAIDLKIIDPTNVGYENHALLSSHKDIPLISLKTAEGMTGTPTADASLSNIKID
VSLPSITPATYGHTGVWSESKMEDGRLVVGWQPTGYKLNPEKQ GALVLNNLWSHYTDLRALKQEIFAHTTI
AQRME LDFSTNVWGSG LGVVEDCQNIGEFDGFKHHLTG YALGLDTQLVEDFLIGGCFSQFFGKTESQSYKA
KNDVKSYMGAAYAGILAGPWLKGA FVYGNINNDLT TDYGT LGISTG SWIGKGFIAGTSIDYRYIVNPRRFIS
AIVSTVVPFVEAEYVRIDLPEISEQGKEVRTFQKTRFENV AIPFGFALEHAYS RGSRAEVNSVQLAYVFDVYR
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>core/3/2/Org2_Gene120

MASSSNNSTKQDGIPSWVNPVQWNRASQVGDQEANSLTPEAQTSRSWFS DRKHFLEVL DVSL EEMENNDL
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LSQYPDLRKSTLYKYSITHVKPKKGFVGKLVENLRPD LHKNKDDGGAAADSRLDFAGYGVKH YQTDALLG
VSGVNSVEWQRLASLIMSVKNDILNDVGSREPIDKAQRSALV VSGKDIGGEIQPGGILDISRDILAICGYGMNV
GVEAKKAIDQYKKWYLNSSTFIAWNPQLPAIAQSYLLEQQRHLDYAAKIFQDLSALT TAHTGQALEDLDSL
LCYYDQLIESKGVGEKIIASIHQKHLDLAMQDSCDQEHLKKWSNLYHVF SITIKEFTEGKLEQNEVVSRIQRL
RGKLEKSKCSILGNCR TNAEYATKSEKKLADYLLQIGDREPFLTGMHKA IATGKAIQGKVEGVISQHP EKQIM
MLRCSIERLEGMLRREDWGAILQKNEDEV LALKSTME AQLQGFKDLVGTWEGKYQEFKKNKLSKVLVYDF
TKSYSNLLNRLEVLHAESSTDDLVLHVD RMSEDLKKTIEEIDGNLFQVTPEELSLLAREYQGLMNELPLIVQE
GNRLQE AISSEGVSQGLM LLLNSLLNRDEKINKNIESSRKNLVAIAKQARS DARNIDSQGLAPLIQRN RASLDNI
LQNM YLFNGSIRNIHALDTETLVATSSNMFSAMHTFDWNIYTNLLDVLEIQSKPAPAPMENPDLP GALPEEVQ
DAVAEDVSGTHRLHHQVLKRRCADLKNMISQLQKSINKWGM AKAIVLGIVAVLFCVLSAIFIGQNILSLLILS
CVGLLLTQVCPLIFDRISK SKEFEKQVLETAQSLIPATKILPSEFN NKDLNRLAKLQDNLNLEGF GPTWARNIV
SDLEGIPTKEKSLKDLTKEFRKDSKNLNKRIKRRFKEGLGQEAPVVRPTIPQDIRGA EVFAELHREHLQKQ
KEEISIRGDALVQERMGLCLEKSKYDNEKAHAAAMTKKVGKLQNI DRLQKNNETYVRIQNFFRTLIQEKLGR
DTVQEIDVVKEAKELHELA AIIYGNTSGKSQKQRAKKQFKENVLHIAGKGQLELLEAYLNV TASQGLCRHQ
MQASFRERILLNPDGAKHGEAERTLASREEM LKTLGLSYLTPFVRFS SPESTQSGYNQILKVREQLFDIEQRLQ
NQETVSPEDYAAVQAALAAAYVRKHESLIVSTYGLGAQEGQTSSKVTTLMRDLHAVEELVEMGVETYRLNRS
DQILHRVH SVLHSHLRDCDSSGNGIIDVVKLFELLNNNGNNPNDPECQKYMQILLDAPV SLLYGAFKSFKN
EFLLNFTELN IANSTKAAEEEEAKRYVEEKGRGFETYWEEAKQRLEAIAAE LDDL RNQETLLEQEIRLANLKISI
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LLGLLGREEAA

>core/4/2/Org2_Gene382

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GGTATFTDNASVTLQKNTSEKDGAAVSAYSIDLAKTTTAAALLDQNTSTKNGGALCSTANTTVQGNSGTVTFSS
SNTATDKGGGIYSKEKDSTLDANTGVVTFKSNTAKTGGAWSSDDNLALTGNTQVLFQENKTTGSAAQANNP
EGCGGAICCYLATATDKTGLAISQNEQSFTSNTTTANGGAIYATKCTLDGNTTLTFDQNTATAGCGGAIYT
ETEDFSLKGSTGTVTFSTNTAKTGGALYSKGNSSLTGNTNLLFSGNKATGPSNSSANQEGCGGAILAFIDSGS
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SLSGNTATVSGGAIYATKCALHGNTTLTFDGNTAETAGGAIYTETEDFTLTGSTGTVTFSTNTAKTAGALHTK
GNTSFTKNKALVFSGNSATATATTTTDQEGCGGAILCNISESDIATKSLTLTENESLSFINNTAKRSGGGIYAPK
CVISGSESINFDGNTAETSGGAIYSKNLSITANGPVSFTNNSGGKGGAIYIADSGELSLEAIDGDITFSGNRATE
GTSTPNSIHLGAGAKITKLAAAPGHTIYFYDPITMEAPASGGTIEELVINPVVKAIVPPPQPKNGPIASVPVVPV
APANPNTGTIVFSSGKLPSQDASIPANTTTILNQKINLAGGNVVLKEGATLQVYSFTQQPDSTVFMDAGTTLE
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STSGTVNLDDFNPIPSMAAPDYGYQGSWTLVPKVGAGGKVTLVAEWQALGYTPKPELRATLVPNSLWNA
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NTQGKSDWDSSHFAVEVGGSLPVDLNYRYLTSYSPYVKLQVSVNQKGFQEVAADPRIFDASHLVNVSIPM
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SGSCELRSSRSYNANCGTRYSF

>core/5/2/Org2_Gene485

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SFVSYSSENEQEMASSILQRVYSACTFPKQKDCSCSYPSIWETAPKEQLLQYAKNLSSGFEVFSSRLSAFCQQS
FSSNQDRLAFLSRLSSLSNDAIDVEDQKLLKSVYETLSQTACIRSLDCPYIEGLRLDCSESSLFFSSIEYCPKER
KIFLTLHSDLLAQRSLSKEQRLDFDSRLAVEKQKLSKNLTVQVEDYNNGFSFQWMDKDTQGKIILQGERLL
QGIAEHLTALTLHRPAAESCDLIPENFPVFCRQPRESEAFGCYIFSPNTDCKHFSKGSVYILLKGLRSIVAKYQQ
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ATVNQIEKNRQSDLVRWHEQYRHAKCSMDLQERLSAPIPYQNLFLENMKLNMRFKSRGENILRLGIDFVGG
RQLLSFKDHQKQLTDKEDILKVSDEL CARLNKLGVSEIELRREGDYIHLSVPGSSSTISSSEILGTSKMSFHVV
NERFSSYSASRYEVQRFLDYLFWTSQAQGKTSPEEINTFASALFNEEVDVPPSVHEAITKLKSEGLAFSPSGCE
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TESFHTWTSAYCQEGISGTANGQYSANRGWRMAVVIDGYMVSSPILNVPLKNHASVSGKFTHREVSKLASD
LKSGAMSFVPEVLSEETISSDLGKKQCTQGIISACGLAMLIVLMSVYYRFGGVASGAVLLNLLLIWAALQY
LDAPLTLISGLAGIVLAMGMAVDANVLVFERIREEFLLSQSLKKSVEKGYTKAFGAIFDSNLTTLVASALLFFL
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YFSDKALSYTKADTSLSPKINDHELALAVGLLSETGLDFSTETLNETQNFWSKVSSKLSKKMRYQATIGLLGA
LAIILLYVSLRFEWQYAFSAVCALIHDLATCAVLFIHFFLKKIQIDLQAIGALMTVLGYSLNNTLIIFDRIRED

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MVRKENRSK

>core/6/2/Org2_Gene60

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LKFNQCGLPKEMALELFEPFIKRLKDQGSVYTIRSAAKMIQRGAPEVWDVLEEIIKGHPVLLNRAPTLHRLGI
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IRSTLTCESPRGVCAKCYGLNLANGRLIGMGEAVGIIAAQSIGEPGTQLTMRTFHLGGIAATSSTPEIITNSDGIL
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QRIGEVELHNIPICDKPGFIKYEDLVEGISTEKVVNKNTGLVELIVKQHRGELHPQIAIYDDADLSELVGTYAI
PSGAISVEEGQRVDPGMLLARLPRGAIKTKDITGGLPRVAELVEARKPEDAADI AKIDGVVDFKGIQKNKRIL
VVCD EMTGMEEH LIPLTKHLIVQRGDSVIKGQQLTDGLVVPHEILEICGVRELQKYL VNEVQEVYRLQGVD
INDKHIEIIVRQMLQKVRITDPGDTLLFGEDVNKKEFY EENRRTEEDGGKPAQAVP VLLGITKASLGTESFIS
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>core/7/2/Org2_Gene59

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LLVGRILADNIIDEASSLVYGKAGEKLSTAM LKRMLDAGIASVKIAVDADENHP IIKMLAKDPTDSYEAALKD
FYRRLRPGEATLANARSTIMRLFFDPKRYNLGRVGRYKLN RKLGFSIDDEALSQVTLRKEDVIGALKYLIRL
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KDFFGRS QLSQFMDQTNPVAELTHKRRLSALGPGGLNRERAGFEVRDVHASHYGRICPIETPEGPNIGLITSLS
SFAKINEFGFIETPYRIVRDGIVTDEIEYMTADVEEECVIAQASASLDEYNMFTEPVCWVRYAGEAFEADTSTV
THMDVSPKQLVSIVTGLIPFLEHDDANRALMGSNMQRQAVPLLKTEAPVVG TGLECRAAKDSGAIVVAEED
GVVDFVDGYKV VVA AAKHNPTIKRTYHLKKFLRSNSGTCINQQPLCAVG DVITKGDVIADGPATDRGELALG
KNVLVAFMPWYGYNFEDAIIESEKLIREDAYTSIYIEEFELTARDTKLGKEEITRDIPNVSDEVLANLGEDGIIRI
GAEVKPGDILVGKITPKSETELAPEERLLRAIFGEKAADV KDASLTVPPGTEGVVMDVKVFSRKDRLSKSDDE
LVEEAVHLKDLQKGYKNQVATLKTEYREKL GALLNEKAPAAIIHRRTAEIVVHEGLLFDQETIERIEQEDLV
DLLMPNCEMYEVLKGLLSDYETALQRLEINYKTEVEHIREGDADLDHGVIRQVKVYVASKRKLQVGDKMA
GRHGNKGVVSKIVPEADMPYLSNGETVQMILNPLGVPSRMNLGQVLETHLGYAAKTAGIYVKTPVFEGFPE
QRIWDMMIEQGLPEDGKSFLYDGKTGERFDNKVVIGYIYMLKLSHLIADKIHARSIGPYSLVTQQPLGGKAQ

MGGQRFGEVWALEAYGVAHMLQEILTVKSDDVSGRTRIYESIVKGENLLRSGTPESFNVLIKEMQGLGL
DVRPMVDA

>core/8/2/Org2_Gene583

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LKSPEALLLELQWFQDLFKDDYFTEVQLHKMSEESIAGFKEEWLKQEYYSLEIKQIKVNTAVLEASKRLGIPT
VATNDIHYINANDWQAHEILLNVQSGETVRIAKQNTHIPNPKRKVYRSREYYFKSPAQMAELFKDIPEVISNT
LEVAKRCDFTFDFSCKKHYPYVPESLKTLSYTEEDRYQASAVFLKQLAEEALPKKYSSEVLAHIAKKFPHRD
PIDIVKERMDMEMAIIIPKGMCDYLLIVWDIIHWAKANGIPVGPGRGSGAGSVLLFLLGITEIEPIRFDLFFERFI
NPERLSYPDIDIDICMAGRERVINYAIERHKGKDNVAQIITFGTMKAKMAVKDVGRTLDMALSKVNHIAXHIPD
LNTTLSKALETDPDLHQLYINDAESAQVIDMALCLEGSIRNTGVHAAGVIIICGDQLTNHIPICISKDSTMITTQY
SMKPVESVGMLKVDLLGLKTLTSINIAMSIAIEKKTGQSLAMATLPLDDATTFSLHQQKTMGIFQMESKGMQ
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SYSLGEGDVLRRAMGKKDFQQMEQEREKFCKRACNNGIDPELATVIFDKMEKFAAYGFNKSHAAAYGLITY
TTAYLKANYPKEWLAALLTCDSDDIEKIGKLIREAQSMGIPILPPHINVSSNHFVATDEGIRFAMGAIKGIGRG
LIESIVEERDHHGPYESIRDFIQRSDLKKVSKKSIESLIDAGCFDCFDNSNRDLLASVEPLYEAIKDKKEAASG
VMTFFTLGAMDRKNEVPICLPKDIPTRSKKELLKKEKELLGIYLTEHPMDTVRDHLSRSLSVVLAGEFENLPHG
SVVRTVFIIDKVTTKISSKAQKKFAVLRVSDGIDSYELPIWPDMYEEQQELLEEDRLIYAILVLDKRSDSLISC
RWMKDLSIVNENIIECDQAFDRIKNQVQKMSFTMSTSGKETKAKGNKPNENGHTQALAPVTLSLDLNLNR
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>core/9/2/Org2_Gene743

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TIHASEEPTVFTNKTFLKSALYRTAKKFFFLNEEGAELTIGENSQGFPESHFSLQWQGLVFKAIEILDFPTLEDIFP
KLELAHTSLENVSHDISITNVTVCAAEAKVNFTLSPVIHKKDRENHPKTRIGSVEYVAKTHEMITGPKAIALPI
YAIPLLADKFKDQLLSLLCYDSLEYRLRYDIRLLRDASFSSAYLVTPGDLDNGSLIYPNYCYSPTKGLMQVV
GMLSPKQAFIVKSEQVEDFLNERGHILIQEPGFQTFINERPEGHLYTNVTEQGVLLFHVDVGDPSSTEIRFGTWT
YYTNQGFFLEKKNDLPIQDGLIVEPQDIPAFIVKNDAAALRRLPNFFSSPPNLKDLLIEVHRQSRGKGLDLKPILV
GLGESRCWLFVFLYREDIGFSLIPTPLQGLCFLPRVIPPENVPQFLTQYQAHERILFPNPQTRPPESYELVIQSI
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TDVFKLDALAPLSVTDDTIANPEDLQFFSQLKAACLPPIPQNLFFSSDHQLRPYQNSGLLWMWFLYNHRLSGLL
CDEMGLGKTHQATALLDIVFQSSQPSARPKFLIVCPTSVLPHWEHILSNHLPGVISFSFHGPNKPSLPPADILL
TSYGTLRQNYDKFYKIAFTIVVFDEIHMAKNKSSQIHKILCRIDAQMKGGLTGTPIENNLLFEKGLLDIILPNYL
PSDALFKKLFTKRCSSSEELIIPSDLLKLTRPFILRRTKKLVLPELPDKVESIIACSLSPDQEKLYMATLQRE
KSHIQKLETPEEPATNFLHIFALLNHLKQICDHPAVFFKDPDQYKNYESGKWNFAVKLLKESLNAGYKVVVV
SQYIHMIRIITLYLEEIGIKYASIQGKSLNRKEEIEFTTDPNCQVFGVGSLLAAGTGINLTAGNVVIMYDRWWN
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HGTSDSEESPVDAPVEDDTGVLPPEDS

>core/10/2/Org2_Gene754

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LREYVHAANALSANPFFLPLEYLEKDSAELAVLFVSVNEDTFAPANQPIEFQLVLRLLPCRSKPFYISNIRTFLEG
VLYQEPIVLNGRRFFFTMQSFNASDRKLIDLLIRYVRYPNHTTEEKLLKSAYLMPPALGVILAKMFEHQLADR
GGGSLGEKESFSGLFCGNLEELCWSLTPAKMKFNLDFFDMPYKALLMTPVILVDDDEVQPEQTMLES DAP
GIIHHFVYHRFSPQIKRAHLRSFSRLRDIAIPEALFGSFRENALPVFQEYAEIANVHLLNSFVTLPLYVDEVRAIC
DMSYLDGELEAKLHFLYGLSLRVPAASLALQYQDVRAFISDEGILARNLVEERKMLEE VFSGFIYDERDGAFR
VKSEKKIVEFMTETIPANQHRITFNCPENLSGQFIYDETIFELSFREGSDINY YEADLKVHGLLKGVPLDLLWD
CISAKKRFLLEPKAGQQSKGTRRGKVN SGKLP CILVLDLEKIAPVVQIFNEIGFKVLDDL VQKCPLWSLTGISL
DQFEALPVNFMSERLIEIQKQIRGEIEFDFQDVPQQIQATLSYQTEGVHWLERLRKMHLN GILADDMGLGK
TLQAIHAVTQSKLEKSGCSLIVCPTSLVYNWKEEFRKFNP EFRTLVIDGVPSQRRKQLTALADR DVAITSYNL
LQKDVELYKSFRFDYVVLDEAHHIKNR TTRNAKSVKMIQSDHRLILTGTPIENSLEELWSLFD FLM PGLSSY
DRFVGKYIRTGNMGNKADNMVALKKKVSPFILRRMKEDVLKDLPPVSEILYHCHLTESQKELYQSYAASA
KQELSRLVKQEGFERIHHVLA TLTRLKQICCHPAIFAKDAPEPGDSAKYDMLMDLLSSLVDSGHKTVVFSQY
TKMLGIIKKDLESRGIPFVYLDGSTKNRLDLVNQFNEDPSLLVFLISLKAGGTGLNLVGADTVIHYDMWWNP
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>core/12/2/Org2_Gene609

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LAVNQLQYDVSVA YGAIRDLPTRAWRVDEHGHKQLIPVRKHYIMCLSELLSQELHLDREAIEDAIHAKASVL
GSVPYLVAANVSERTYLKLKMLSKDWPGLHVEAVVRRHYPQESVASDILGYVGPISLQEYKRV TQELSQR
ECVRA YEEGEDPKLPEGLASIDQVRALLESVESNAYS LNALVGKMGVEACWDSKLRGKIGKKPILVDRRGNF
IQEMEGAVPEAPGTKLQLTLSAELQAYADALLLEYEKTETFRSAKSLKKREKL PPLFPWIKGGAIALDPNNG
EILAMASSPRYRNND FVNAKVAEDSKAVRSSIYRWLENKEHIAEIYDRKVPLIRERRNPLTGLCYEEILPLTFD
CFLDFLPENSVIKLQLKRNSFVGQAIEVQNLVTRLLSLFPYEEGTCPCSAIFDAVFPNEEGHILIQEVISLQEQK
WIMECLNQHKADIEELKEALDQVFNELPANYDKILYTDILRLIVDPERFSPVLPSEVHRLSLSEFTELQGRYVV
LRSAFSTILED AFIEVHFKSWRKSEFLQYLA AKRQEEALRKQRYPTPYVDYLEEEKTRQYKMFCQEHLDTFL
AYLFSKTPYKEGLEPYDYDILDLWINELDN GAHRALSWHEHYLFLKERVSHLSEHLPALFSTFRE FNELQRPLL
GKYPISIVRNKRQTEQDLAASFYPVYGYGYLRPHAYGQAATLGSIFKLVSAYSVL SQRILWGHNEEPANPLVI
IDKNSFGYRSSKPHVGFFKDGTPIPTFFRGGSLPGNDFMGRGFIDL VSALEMSSNPYFSLLVGEGLGDPEDLAD
AASLFGFGEKTGLGLPGEYAGRVPHDLAYNRSGLYATAIGQHTLVVTP LQTAVMLASLVNGGVVYVPKLLL
GEWEGEHVSYLSSKKKRTIFMPDAVVEVLKTGMRNVIWGQYGTARAIQSQFPPQLLSRIIGKTSTAESIMRVG
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>core/13/2/Org2_Gene1020

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LCKSLGYSQVMLTSEKGEFSCRGGIVDIFPLSSPEPFRIEFWGEKIISIRSYNPSDQLSTGK VSKISISPAYTEEAS
GGNYSHSLLDYFSTPPLYLFDNLEILED DFADISGTLSSLPDRFFSIGTLYDRISTSNQVYFSETPPFNVKNLKEN

RVIIIEAFHRNMEASRQAIPILYPEQIIQNDENPLLAFLQHLQEYMPPHGKPLKLAIYSTKTKSLKEARALAETV
ARGDVEIYEKTGNLTSSFALVNEAFAAISLSEFASTKVLRRQKQRTTHFSVTTEEVFVPIPGETVVHIIHNGIGKFL
GIEKKPNHLNIETDYL VLEYADKARLYVPSNQAYLISRYVGTSDKAADLHHLNSSKWKRSRDLTEKSLIVYA
EKLLQLEAQRSTTPAFVYPPHGESVIKFAETFPYEETPDQLKTIDQIYNDMMSPKLMDRLICGDAGFGKTEVI
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KLINKSLEFKNPGLLIIDEEQRFQVGVKVDNLKERYPMIDCLTVSATPIPRTLHMSLSGARDLSVIAMPPLDRLP
VSTFVMEHNTETLTAALRHELLRGGQAYVIHNRIESIYTLAETIRNLIPEARIGVAHGQMGAEEDLSNIFTKFKN
QKTDILVATALIENGIDIPNANTILIDHADKFGMADLYQMKGRVGRWNKKAYCYFLVPHLDRLSGPAAKRL
AALNKQEYGGGMKIALHDLEIRGAGNILGTDQSGHIGTIGFNLYCKLLKKAVSALKKHTSPLLFNDDEVKIEFP
YNSRIPDTYIETGSMRIEFYQKIGNAESSEELTAIQEEMRDRFGPLPQEICWLFALAEIRLFALQHGISSIKGTAN
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>core/14/2/Org2_Gene413

MIKKRAIFERMFPIPPPHCPPNNKNNFYHLTTDTKDPLLLRILRTIGYVLLHIITLGLLLLIHYYKHHRVVRKEG
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PPVRVATPMPLRPSSQGYWQCLNRMVSMVLRRAPLPLPAMQVDPILGDFNPHFVASYPNRIDNEPMYFQIKQ
FKKIAQNPDLPQQHRRLAQLSLEQALYLNDNYLNVNPGDGNCFYRAYAVGWLSALYEESSRNDIVFEQEA
TRLLDLPFASSSPANANLCAEMAELLQLCSTYCSFIDLYDGVILSQKHTATLIAFLRKLSAYAIRQQIAASSNEE
TARALFISDMQDDLLPSVLEFLAANRPYSELFQNLIDHSALPYMQSRDKLFLLLEHLPALFLTDAELQKMSPE
DQQLRKQYEREIREAFAKLSRRIADSGWDTERFNAIVKDHLPEAIRCQYSRFLATIENRRSGDLPWSPALSFFA
FLCTCPSVRFHKLCAIFYKSLEDIIIASAPPQRSIQEILQISNASLSYLNEDLDSSWQREVISSNIMTILTTHESTL
ESSMPQLETLHKRIANLLKNVISTSFETPLSNQPDLLSNLVNKLVAIHSKLELKEHFNTVCSARSRLRTRDE
GSGLSQEQLLYTQAVQLLFFILQHPQVNNRPETKDAVKELKMLLLPFLQYAFKKVENEKKLQKLLRSILGS
LVLKPPARYPSTPSNKKETFCFKFWSRHPEVMVLDPILEKNCMQFLRATFPNYQLETEAILLEKEIESTFRNG
WNVFLTRLNLFSGSKLGSPSSPTALSDQFSKSFLIFCFLNNYPKLLQKKTPLAARLDAFQREASHRFTQVKDKL
LLSLKYGFPLATATINQYSRARDQLICNLLKNTVTASDGFCSRSGFRQSLIGYLHSLSSNELGDILDDVKEQAEA
NDVAAMTTVPLQPFVCLIMSDRDTVSEENIENFVAMHGFNTISPERDARIFLIRFPNHYGCLLPNPRTEDQ
NSKPDSSNP

>core/15/2/Org2_Gene652

MKPFNIFDSNSSIQGKFFLEASAGTGKTFTIEQIVLRALIEGSLTHVEHALAITFTNASTNELKVRIKDNLAQTL
RELKAVLNSQPASLPTYLDINCNVKQIYMQVRNALATLDQMSLFTIHGFCNFVLEQYFPKTRLIHKNPALTHS
QLVLHHITNYLKQDLWKNVLFQEYFHLAVRYNITSKHTSSLVDKLLASYTQPISSYFSSRVERLEQISLWHQ
QIYNSLLEIPKQVFLDQLTAHISGFKKQPFISLDDLHHFVDLLYTSETHSSLSFFKIAETFNFKHRLARYKPCA
AFTVLENMSWVERTLEFCNLDRIFNTLLVDLQEYLKQNYTPWLSPDESVALEKLLSSSEAQPVVQALREQY
QLVLIDEFQDQDKQWSIFSINLFIKFTGSLFLIGDPKQSIYEWRSADLPTYLTAKSSFSQKQLVLNNYRST
PKLMEAINQIFGKISPFLEIPGYLPIEYHALNPQSSETFENPPHAPIHFFFYETIKDQALWIFSEALRLQKEQKIPL
GNMVVLVSDSNQAFELISYATIPVSFSKNKSIFHLTETHILTALLEAILHPENYEKISKILFSSLFGLSLDEVTTK
KEDFTIYFQSLHSYISHHGLLATFYRVMTTQGNVLFSSPRGDLIFQEMEKLKCGYLDTISSYPYHQLLHLKNFSE
TGRWEEELAISSYSEDLETLKITTIHSSKLEYDIVFCPGIEKSKKNKSSSELLREMYVACTRAKKQLYLPISTQ
PPSLQRSSALTNYVKLEGTQSSAYDLAIHLHQEHPDLFSYSLPKDHGHATTVLNLPLLETFAKLVTPPKTIFSFS

STKFLLDTHKDSQSIPYSKLPISKQQLPLGEKTGILHKILESISQFSLQDTEYLMSTIMRFIKHHTHLEGFEETILK
LLSKTFFSPLTFSSQTFSLSQVLPNKIFRETSFLFLENQELWQGVIDLFFEHEGKYIIDWKTSFLGETNSDYSKS
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H

>core/16/2/Org2_Gene874

MVEVEEKHYTIVKRNGMFVFPFNQDRIFQALEAAFRDTRSLETSSPLPKDLEESIAQITHKVVKEVLAKISEGQ
VVTVERIQDLVESQLYISGLQDVARDYIVYRDQRKAERGNSSSIIAIIRRDGGSAKFNPMKISAALEKAFRATL
QINGMTPPATLSEINDLTLRIVEDVLSLHGEEAINLEEIQDIVEKQLMVAGYYDVAKNYILYREARARARANK
DQDGQEEFVPQEETYVQKEDGTTYLLRKTDLEKRFSWACKRFPKTTDSQLLADMAFMNLYSGIKEDEVTT
ACIMAARANIEREPDYAFIAAELLTSSLYEETLGCSSQDPNLSEIHKKHFKKEYILNGEEYRLNPQLKDYDLDAL
SEVLDSLSDQQFSYMGVQNLVDRYFNLHEGRRLTAQIFWMRVSMGLALNEGEQKNFWAITFYNLLSTFRY
TPATPTLFNSGMRHSQ LSSCYLSTVKDDL SHIYKVISDNALLSKWAGGIGNDWDV RATGAVIKGTNGKSQG
VIPFIKVANDTAIAVNQGGKRKGAMCVYLENWHLDYEDFLELRKNTGDERRRTHDINTASWIPDLFFKRLEK
KGMWTLFSPDDVPGLHEAYGLEFEKLYEEYERKVESGEIRLYKKVEAEVLWRKMLSMLEYETGHPWITFKDP
SNIRSNQDHVGVVRCSNLCTEILLNCSESETAVCNLGSINLVEHIRNDKLDEEKLKETISIAIRILDNVIDLNFYP
TPEAKQANLTHRAVGLGVMGFQDVLVELNISYASQEA VEFSDCESEIIAYYAILASSLLAKERGTYASYSGSK
WDRGYLPLDTIELLKETRGEHNVLDVTSSKKDWTPVRDTIQKYGMRNSQVMAIAPTATISNIIGVTQSIEMYP
KHLFVKSNLSGEFTIPNTYLIK KKLKELGLWDAEMLDDLKYFDGSLLEIERIPNHLKKLFLTA FEIEPEWIIETS
RRQKWIDMGVSLNLYLAEPDGKKLSNMYLTAWKKGLKTTYLRSQAATSVEKSFIDINKRGIQPRWMKNK
SASTSIVVERKTPVCSMEEGCESCQ

>core/17/2/Org2_Gene84

MTADEVGKNSFAKKEEQVLKFWKDNQIFEKSLQNRQGKTLYSFYDGPPFATGLPHYGHLLASTIKDVVGRY
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FSSTWKTMDASFMESVWWVFQSLYNQGLVYEGTKVVPFSTALGTPLSNFEASQNYKEVDDPSLVVRMPLQ
NDSASLLVWTTTPWTLPSNMAIAVGETLVYVRIQDKKSGEQWILSQGCVSRWFSNPEEFVILESFSGKDLVG
RTYEPPFTFFQSKREEGAFRVIAASFVEESEGTGVVHMAPAFGEGLVCKENHVPLVCPVDAHGSFTEEIPQ
YQGQYIKHADKEIIFLKKKEGRIFYHGTVKHRYPPFCWRTDTPLIYKAVNSWFVAVEKIKDKMLRANSSIHVW
PEHIQEGRFGKWLEGARDWAISRNRVWGTPPIWKSADGEILVVGSI RELEELTGTQITDIHRHFIDDLNIVKD
GKPFHRIPIYVFDWFD SGAMPYAQNHYPPFENQKETEEAFPADFIAEGLDQTRGWFYTLTVISAILFDRPAFRN
AIVNGIILAEDGNKMSKRLNNYPSPKYVLDTYGADALRLYLLHSVVVKAEDLRFSDKGIEGV LKQILLPLTNV
LSFFNTYAELYGFDPKSQDIEPAYTEIDQWILSNLYSVVGKVRESMSQYHLNFAVEPFVTFIDDLTNWYIRRC
RRRFWEAEDTPDRRAAFSTLYEVLTVFCKVIAPFVPFLAEDIYQKLKLEKEPESVHLCDFPQVEMDKILPDLE
KRMHDI REIVGLGHSLRKEHKLKVRQPLANFYVVGSKDRLSLLKTFEGLIAEELNVKNVIFYEEAPSFIYTTV
KPNFRMLGKKVGSKMKEVQKALSEL PNNAIDKLIQEETWVLTIDDREIALDGDVVICRHTDPGYIARSSALF
SVILDCQLREPLIVEGIARELVNKINTMRRNQQLHVSDRIALRIKTTEAVHRAFLDYENYICEETLIIAYDFTQD
SDFQGENWDINGHATQIEITVSSIDS

>core/18/2/Org2_Gene651

MNATKHCRAFSNSPRHLLAQLAEDITSTHQKPFTRWILVANATTGHWIKNQLVHVLSDHIFMGSTIFTASD
SIVKHLFLGSGCSQPNIPDYLTLPLINNILEEISKASKFENGREFLSPTTYETTKKLAAAFKQFHTFSQRPTKNA
SHYQELFQILESHFSSYEEMFTTILNNRTQEEDCSLHIFGYAHLPKHLAEFFINLSTYFPVYFYCFSPCREYFGD
LLSDRAIDFFWNQLPDSPIKNAWEHYVLSDRQALLANLAHKSQSSQNFFLDREIDYQEMFLPSKHDSSLGVIQ
NSILDLKPTSPQDFSQTKQTICIRALNIPREVQEVFCKVTELLHRGVSPEEIFILSSHIESYKVHLNAIFNPHVPI
YFTDEVDPRAEDLRNKILLSSILQTQGDLYILQLLTHPQLQQPIDQNKVPYLIKLSSEWGKISSKDRASGQ
QMKALGDLILEEYPPFHQEGGRVSQVEVWETTVPYLIYFIQERINLYLSSSQHSYEDLFQNVFSCLEKIFVLSPEET
SFITTLRNSLFPTFATSSCSLLFFTDCLDFLLHFHKPSPLYDKPGPYIGSLSSLSLIPKGYVFILGANKTTSSDIFD
LLNRRTTTHEELAFSSTEDENFHLQILVSTKHELHISYISSAAQFNLPSPFLNHIKETLDLPVETLPTQPYLSAFF
KNKACLHTSQEYNYSLAHAFYSKKALLPSLFIPTVKQVNLQHLSLNEIIGIFSPLDLFLKTNYNLRISYPEHL
KKQQKLFPKHKQIEDFWNECFVDKEHDLIPSISPHAEELFTYYREKTILLRNLGDKDPKHSPYTVTFSSSIFEER
PYHESYLFPPSLSFQGNPVQIHGTIHGVCNEGLYLCSIDPRDSLKKTTRTLGSLPETSSEQKQLLERYVALAV
LQMSQHLSSDSALIKLTSFNTKENHHPFSDPEGYLRKVLEVYHLMSSQPIPLLPLCCKWKTLDDEEKFHQAVL
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>core/19/2/Org2_Gene1007

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TYFQAIGSKPLDTISGEITYGIERIAMYLQKKISYDVLWNDTLTYGQITQASEKAWSEYNFDYANTEMWFKH
FEDFAEEALRTLKNGLSVPAYDFVIKASHAFNILDARGTISVTERTRYIARIRQLTRLVADSYVEWRASLNYPL
LSLSSTSEPKETSESVVPMISSTEDLLEIGSEELPATFVPIGIQQLESARQVLTQHNIVYEGLEVLGSPRRAL
LVKNVAPEVVQKAFAEKKGPMLTSLFSPDGDVSPQGGQFFASQGVDSHYQDLRSHASLAIRTVNGSEYLFLL
HPEIRLRTADILMQELPLLIQRMKFKPKMVWDNSGVEYARPIRWLVALYGEHILPITLGTIIASRNSFGHRQLD
PRKISSPQDYVETLRQACVVVSQKERRMIEQGLRAHSSDTISAIPLPRLIEEATFLSEHPFVSCGQFSEQFCA
LPKELLIAEMVNHQKYFPTHETSSGAISNFFIVVCDNSPNDTIEGNEKALTPRLTDGEFLFKQDLQTPLTTFIEK
LKSVTYFEALGSLYDKVERLKAHQRFVSTFSSLAASEDLDAIQYCKADLVSAVVNEFPELQGIMGEYYLKH
ANLPTASAVAVGEHLRHITMGQKLSTIGTLLSLDLRLDNLACFILGLKPTSSHDPYALRRQSLEVLTLVSASR
LPIDLASLLDRLADHFPSTIEEKVWDKSKTIHEILEFIWGRLKTFMGSLEFRKDEIAAVLIDSATKNPIEILDTAE
ALQLLKEEHTEKLAVITTTNRLKKILSSLKLSMTSSPIEVLGDRESNFKQVLDAFPGFPKETSAAHAFLEYFLSL
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>core/20/2/Org2_Gene997

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RQAALTALFTYLRQDVGSCFATAPAILHQEYPERFLKDLNDLISSGKLSRIVNQREIAVPINLSGCIGELFKPLR
ILDLYPDPLVKLSSSPGLKKAFAANLIETLGDSEAQIQQLSHQYLMQKLQNVHETLTANDIHKSTLLHYYQL
QESTVRAIFFKEGLFSKEQVAFSTQHPRELSEIQRVYHYLHAYEEAKSAFIHDTQNPLLKAWEYTLATLADAS
OPTISNHIRLALGWKSEDPHSLVSLVTHFVEEEVENIRILVQQCEQTYHEARSQLEYIEGRMRNPLNNQDSQIL
TMDHMRFRQELNKALYEWDSAQEKAKKFLHLPEFLLSFYTKQIPLYFRSSYDAFIQEFALHYANAPAGFRILF
THGRTHPNTWSPISINEFIRFLSEFFTSESELLGKHAVINLEKETSRLVHNITAMLHTDVFQEALLTRILEAY
QLPVPPSILNHLQDLSQTPWVYVSGGTVDTLLLDYFESSEPLTLTEKHPENPHELAIFYADALKDLPTGIKSYL

EEGSHSLSSSPTHVFSIIAGSPLFREAWDNDWYSYTWLRDVVVKQHQDFLQDTILPQLSIYAFIENFCNKYA
LQHVVDHDFHDFCSDHSLTLPELYDKGSRFLSSLFTKDKTVALIYIRRLLYLMVREVPYVSEQQLPEVLDNVSS
YLGISSRITYEKFRLIEETIPKMTLLSSADLRHIYKGLLMQSYQKIYTEEDTYLRLTTAMRHHNLAYPAPLLFA
DSNWPSIYFGFILNPGTTEIDLWKFNAGLQGGQPLDNIQELFATSRPWTLYANPIDYGMPPPPGYRSRLPKEFF

>core/21/2/Org2_Gene390

MPLSFKSSSFCLLACLCSASCAFAETRLGGNFVPPITNQGEEILLTSDFVCSNFLGASFSSSFINSSSNLSLLGKG
LSLTFTSCQAPTNSNYALLSAAETLTFKNFSSINFTGNQSTGLGGLIYGKDIVFQSIKDLIFTTNRVAYSPASVT
TSATPAITTVTTGASALQPTDSLTVENISQSIKFFGNLANFGSAISSSPTAVVKFINNTATMSFSHNFTSSGGGVI
YGGSSLLFENNSGCIIFTANSCVNSLKGVTTPSSGTYALGSGGAICPTGTFFELKNNQGKCTFSYNGTPNDAGAI
YAETCNIVGNQGALLLDSNTAARNNGGAICAKVLNIQGRGPIEFSRNRAEKGGAIFIGPSVGDPKQKTSTLTLA
SEGDIQFQGNMLNTKPGIRNAITVEAGGEIVSLSAQGGSRVLFYDPITHSLPTTSPSNKDITINANGASGSVVFT
SKGLSSTELLPLANTTTILLGTVKIASGELKITDNAVVNVLGFATQGGGQLTLGSGGTLGLATPTGAPAAVDFT
IGKLAFDPFSFLKRDFVSASVNAGTKNVTLTGALVLDEHDVTDLYDMVSLQSPVAIPIAVFKGATVTKTGFPD
GEIATPSHYGYQGKWSYTWSRPLLIPAPDGGFPGGSPSANTLYAVWNSDTLVRSTYILDPERYGEIVSNSLW
ISFLGNQAFSDILQDVLLIDHPGLSITAKALGAYVEHTPRQGHEGFSGRYGGYQAALSMNYTDHTTLGLSFGQ
LYGKTNANPYDSRCSEQMYLLSFFGQFPVITQKSEALISWKAAYGYSKNHLNTTYLRPDKAPKSQGGQWHNN
SYYVLISAEHPFLNWCLLTRPLAQAWDLSGFISAEFLGGWQSKFTETGDLQRSFSRGKGYNVSLPIGCSSQWF
TPFKKAPSTLTIKLAYKPDYRVNPHNIVTVVSNQUESTSISGANLRRHGLFVQIHDVVDLTEDTQAFNLNYTFDG
KNGFTNHRVSTGLKSTF

>core/22/2/Org2_Gene871

MKAGDTYRNFIKSKCDLPEIESKLLAEHKPTGASIMMIVNNDENNVFNICFRTCPQTSNGVAHVLEHMLVC
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NSENHLCYTGVVFNEMKGAMMSGEARLSEALNAAIFPSVTYGVNSGGEPREIVTLSHEDVRAFHQSQYSINR
CLFYFYGNIKPSRHLDLFLEEKLLRQATKLEKQAVSVPLQKRKFKEPVRNILTYPVDHQEEDKVLFGISWLTCSIL
EQQELLALHVLEIILMGTDASPLKSRLKSGFCKQTEMSIENDIREIPMTLVCKGCSGAGAKLEALIFASLEEII
REGISENIVEGAVHQLELSRKEITGYSLPYGLSLFFRSGLLKQHGGSADGLRIHSLFSELRNSLKNSDYLAKLI
RKYFLDNPHFARVILLPDTELVAKDNKDEQQLLLSVSEKLTDENKEKIQQNVRELTESQEQLKEDLNGILPNLA
LDKVPTSGKEFPLIKEGLSQGEVLHHECFNDIVFIDVVDIPPLSGEELPWLRLLVFLMLQLGCGGRSYKEHL
EFLLEHTGGVDVSYDFSPHANKNSFLSPSVSIRGKALSSKSEKLCGIVSDMLTSVDFTDIPRIRELLMQHNEAL
TNSVRNSPMSYAVSMACSGNSITGAMSYLTTGLPYVKKIRELTKNFDQNIDEAVVILQRLYTKCFSGKRQIVI
SGSAHNYQQKDNKFYGLLDYLIVPEPWENPSINLYVTSRGLHIPARAAFNALAFPIGDIAYDHPDAAALTV
AAEILDNVVLHTKIREQGGAYGSGAAANLSRGSFYCYSYRDPEIATTYKTFLKGVSEIASGNFTKEDIYEGAL
GVVQGLDMPVAPGSRASVAFYRLKSGRIPVLRQAFRRSVLEVTKEHICMVMMDKYLESTVQETTLISFAGEEM
LRNNVLTLDKDFPIVPAI

>core/23/2/Org2_Gene389

MKTSIRKFLISTTLAPCFASTAFTVEVIMPSENFDGSSGKIFPYTTLSDPRGTLCIFSGDLYIANLDNAISRTSSSC
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YATTPMLFTNNDLSILFQYNRSAGFGAAIRGTSITIENTKKSLLFNGNGSISNGGALTGSAAINLINNSAPVIFSTN

ATGIYGGAIYLTGGSMILTSGNLSGVLFVNNSSRSGGAIYANGNVTFSSNNDLTFQNNTAS PQNSLPAPTPPPTP
PAVTPLLGYGGAIFCTPPATPPPTGVSLTISGENSVTFLENIASEQGGALYGKKISIDSNKSTIFLGNTAGKGGAI
AIPESGELSLSANQGDILFNKNLSITSGTPTRNSIHFGKDAKFATLGATQGYTLYFYDPITSDDL SAASAAATV
VVNPKASADGAYSGTIVFSGETLTATEAATPANATSTLNQKLEGGTLALRNGATLNVHNFTQDEKSVVIM
DAGTTLATTTNGANN TDGAITLNLKLVINLDSLDGTAAVVNVQSTNGALTISGTLGLVKNSQDCCDNHGMFN
KDLQQVPILELKATSNTVT TTTDFSLGTNGYQQSPYGYQGTWEFTIDTTTHTVTGNWKKTGYPHPERLAPLIP
NSLWANVIDLRAVSQASAADGEDVPGKQLSITGITNFFHANHTGDARSYRHMGGGYLINTYTRITPDAALSL
GFGQLFTKSKDYL VGHGHSNVYFATVYSNITKSLFGSSRFFSGGTSRV TYSR SNEKVKTSYTKLPKGRC SWS
NNCWLGELEGNLPITLSSRILNLKQIIPFVKA EVAYATHGGIQENTPEGRIFGHGHLNVA VPVGVRFGKNSH
NRPDFYTHIVAYAPDVYRHNPDCDTLPINGATWTSIGNNLTRSTLLVQASSHTSVNDVLEIFGHCGCDIRTS
RQYTLDIGSKLRF

>core/24/2/Org2_Gene748

MLGFLKRFFGSSQERILKKFQKLVDKVNIYDEMLTPLSDDEL RNKTAELKQRYQNGESLDSMLPEAYGVVK
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TVNDYLAQRDCEWVGSVLRWLGLTTGVLVSGTLLEKRKKIYQCDVVYGTASEFGFDYLRDNSIATRL EEQV
GRGYYFAIIDEVDSILIDEARTPLIISGPGEKHNPVYFELKEKVASLVYLQKELCSRIALEARRGLDSFLDVDILP
KDKKVLEGISEFCRSLWL VSKGMPLNRVLRVREHPDLRAMIDKWDVYYHAEQNKEESLERLSELYIIVDEH
NNDFELTDKGMQQWVEYAGGSTEEFVMMDMGHEYALIENDETLPADKINKKIAISEEDTLRKARAHGLRQ
LLRAQLLMERDVDYIVRDDQIVIIDEHTGRPQPGRRFSEGLHQAIEAKEHVTIRKESQTLATVTLQNNFRLYEK
LAGMTGTAITESREFKEIYNLYVLQVPTFKPCLRIDHNDEFYMTEREKYHAIVNEIATIHGKGNPILVGTESVE
VSEKLSRILRQNRIEHTVLNAKNHAQEA EIIAGAGKLGAVTVATNMAGRGTDIKLDNEAVIVGGLHVIGTTR
HQSRRIDRQLRGRCARLGDPGA AKFFLSFEDRLMRLFASPKLNTLIRHFRPPEGEAMSDPMFNRLIETAQKRV
EGRNYTIRKHTLEYDDVMNKQRQAIYAFRHDVLHAESVFDLAKEILCHVSLMVASLVMSDRQFKGWTLPNL
EEWITSSFPIALNIEELRQLKDTDSIAEKIAAELIQEFQVRFDHMVEGLSKAGGEELDASAICRDVVR SVMVMH
IDEQWRIHLVDMDLLRSEVGLRTVGQKDPLLEFKHESFLLFESLIRDIRITIA RHLFRLELTVEPNPRVNNVIPT
VATSFHNNVNYGPLELTVVTDSEDQD

>core/26/2/Org2_Gene400

MSLNLERISPLLYLLDVTAKKIDTSNLIVEAMNLDEHYGYQGIWSPYWMETTTTTTSSTVPEQTNTNHRQLYV
DWTPVGYRPNPERHGEFIANTLWQSAYNALLGIRLPPQNLKEHDLEASLQGLGLLINQH NREGRKGF RNHT
TGAAATTSAKTAARHSFSLGFAQMFSKTRERQSPSTTSSHNYFAGLRFD SLLFRDFISTGLSLGYSYGDH HML
CHYTEILKGSSKAFFNNHTLVASLDCTFLPARITRTLELQPFISAIALRCSQAS FQETGDHIRKFHPKHPLTDLSS
PIGFRSEWKTSHHIPMLWTTEISYVPTLYRKNP EMFTLLISNGTWTTQATPVSYNSVA AKIKNTS QLFSRVTL
SLDYSAQVSSSTVGQYLKAESHCTF

>core/27/2/Org2_Gene461

MKQMRLWGFLFLSSFCQVSYLRANDVLLPLSGIHSGEDLELFTLRSSSPTKTTYSLRKDFIVCDFAGNSIHKPG
AAFLNLKGD LFFINSTPLAALT FKNH LGARGAGLFSES NVTFKGLHSLVLENNESWGGVLT TSGDLSFINNTS
VLCQNNISYGP GGALLLQGRKSKALFFRDNRGTILFLKNKAVNQDESHPGYGGAVSSISP GPSPITFADNQEILF
QENEGELGGAIYNDQGAITFENN FQTTSFFSNKASFGGAVYSRYCNLYSQWGD TLFKNAAAKVGGAIHAD

YVHIRDCKGSIVFEENSATAGGAIAVNAVCDINAQGPVRFINNSALGLNGGAIYMQATGSILRLHANQGDIEF
CGNKVRSQFHHSHINSTSNFTNNAITIQGAPREFSLSANEGHRICFYDPIISATENYNSLYINHQRLLLEAGGAVIFS
GARLSPEHKKENKNKTSIINQPVRRLCSGVLSIEGGAILAVRSFYQEGGLLALGPGSKLTTQGKNSEKDKIVITN
LGFNLNLDSSDPAEIRATEKASIEISGVPRVYGHTESFYENHEYASKPYTTSIILSAKKLVTAPSRPEKDIQNLI
AESEYMGYGYQGSWEFSWSPNDTKEKKTIIASWTPTGEFSLDPKRRGSFIPTTLWSTFSGLNIA SNIVNNNYL
NNSEVIPLQHLCVFGGPVYQIMEQNPKQSSNNLLVQHAGHNVGARIPFSFNTILSAALTQLFSSSSQQNVADK
SHAQILIGTVSLNKSQALSRLSSFSYTEDSQVMKHVFPYKGTSRGSRWNYGWSGSGVMSYAYPKGIRYLK
MTPFVDLQYTKLVQNPVETGYDPRYFSSSEMTNLSLPIGIALEMRFIGSRSSLFLQVSTSYIKDLRRVNPQSSA
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>core/28/2/Org2_Gene401

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PNASNFADTCTGGAVLCSKNVTISKNGTAYFINNKA KSSGGAIQAAIINIKDNTGPCLFFNNAAGGTAGGAL
FANACRIENNSQPIYFLNNQSGLGGAIRVHQECILTKNTGSVIFNNNFAMEADISANHSSGGAIYCISCSIKDNP
GIAAFDNNTAARDGGAICTQSLTIQDSGPVYFTNNQGTWGGAIMLRQDGACTL FADQGDIIFYNNRHFKDTF
SNHVSVNCTRNVS LTVGASQGH SATFYDPILQRYTIQNSIQKFNP NPEHLGTILFSSTYIPDTSTSRDDFISHFRN
HIGLYNGTLALEDRAEWKVYKFDQFGGTLRLGSRVFTTDEEQSSSSVGSVININNLAINLPSILGNRVAPKL
WIRPTGSSAPYSEDNNPIINLSGPLSLLDDENLDPYDTADLAQPIAEVPLLYLLDVTAKHINTDNFYPEGLNTT
QHYGYQG VWSPYW IETITTS DTSSEDTVNTLHRQLYGDWTP TGYKVN PENKGDIALSAFWQSFHNL FATLR
YQTQQGQIAPTASGEATRLFVHQNSNND AKGFHMEATGYS LGTTSNTASNHSFGVNFSQLFSNLYESHSDNS
VASHTTTVALQINNPWLQERFSTSASLAYSYSNHHIKASGYSGKIQTEGKCYSTTLGAALSCSLSLQWRSRPL
HFTPFQIAIAVRSNQTA FQESGD KARKFSVHKPLYNLTVPLGIQSAWESK FRLPTYWNIELAYQPVL YQQNPEI
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>core/29/2/Org2_Gene851

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LFINPKFRQEDLDREKYAVHQEFAAHPLSDGRRVHRIQQLVAPQGHPCARFGCGNASTLTPVTTEKMAEWF
KLHYPENMCAIAYTSAPLSKAKKQFSKIFSQIPRSKNYERQEPFLPSGDTSSLKNLYINQAIQPTS NLEIYWHI
YESSHIPPLGICYKALAEVLRNESKNSLVSLKNEQLITDL DVEFFRSSLNTGEFYISYELTEKGDKHYSQVIDST
FQYLR YIQEHGIPNYTLEEISTINALNYCYSSKSPLFDLLCKQIVSLGNEDLSTYPYHSLVYPKYSSEDESALLN
LVSDPEQARFVLSSKNSEHWEEATQLHDPIFDMTY YVKALDGVQDYGKVQSLKPIALPKPNLFIPKEVTLP
VHLLKKQEFPFAPALSYQDDKLTLYHCE DHYYTAPKLSSQIRIRSPQISRSSPQFLVATELYCLAVNDQLLREY
YPATQAGLSFTSALGGDIDLRVSGYTTTVPALLNSILTSLPNLEISYETFLVYKKQLLELYQGALLNCPVRSG
LDELASQVMKETYSNTTKLSALEKLSFSEFQAFASNLFNSVHLEV MVLGNLSEQQKKDYLEMLQVFTASRSS
HATKPFYYELQSQEISEIHHDYPLTANGMLLLLQDKSSPSIQGKVCAEMLFEWLHHITFEELRTQQQLGYMV
GARYREFASRPFGFLYIRSDAYSPEELLAKTSLFLNKVSASPEKFGISQEKFANIRKAYINKILEPEHSLDMMNS
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>core/30/2/Org2_Gene71

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DWDRKRFTMEPLANRAVKKAFKTLFENGYYIRGYLVNWDVPLQTALADDEVEYEEKDGWLYYIRYRMV
GSQESIVVATTRPETS LGDTGIAVSPNDERYASWIGASVEVPFVNRQIPIIGDASVDPTFGTGAVKVTPAHDKD
DYLMTGNHHLPMINILTPSGGINENG GPFAGMAKEKAREEILIALEE QGLFVRKEPYKLRVGVSYRSGAVIEP
YLSKQWFVSVSEFRGALREFVESQDIKIFPKDFVKNYLSWVNHLRDWCISRQLWWGHRIPVWYHKND DERV
LCYDGEGIP EEAQDPDSWYQDPDVLDTWFSSGLWPLTCLGWPDENSPDLKKFYPTALLVTGHDILFFWVT
RMVLLCSSMSG EKPFSEVFLHGLIFGKSYKRYNDFGEWSYISGKEKLAYDMGEALPDGVVAKWEKLSKSKG
NVIDPLEMIATYGTDAVRLTLCSCANRGEQIDLDYRLFEEYKHFANKVWNGARFIFGHISDLQGKDLLAGIDE
DSLGLEDFYILDGFNQLIHQLEEAYATYAFDKVATLAYEFFRNDLCSTYIEIHKPTLFGKQGNEASQSTKRTLL
AVLLINVLGVLPVAPFITESLFLRIQDTLGALPEGDGDAFTGHALRMLRSRACMEAPYPKAFDVKIPQDLRE
SFTLAQRLVYTIRNIRGEMQLDPRHLKAFVVCSDTTEIQSCIPILQALGGLESIQLLDKEPEKGLYSFGVVDTI
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FA

>core/31/2/Org2_Gene398

MRFFCFGM LLPFTFVL ANEGLQLPLETYITLSPEYQAAPQVGFTHNQNQDLAIVGNHND FILDYKYYRSNGG
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TNNLGQGT FVDNLALNKG GALYTETNLSIKDNKGPIIHKQNRALNSDSLGGGIYSGNSLNIEGNSGAIQITSNSS
SGSGGIFSTQTLTISSNKKLIEISENSAFANNYGSNFPNGGGGLTTTFC TILNNREGVLFNNNQSQSNGGAIHAK
SIIKENGPVYFLNNTATRGGALLNLSAGSGNGSFILSADNGDIIFNNNTASKHALNPPYRNAIHSTPNMNLQIG
ARPGYRVLFYDPIEHELPSSFPILFNFETGHTGTVLFSGEHVHQNF TDEMNFSSYL RNTSELRQGVLAVEDGA
GLACYKFFQRGGTLLLGQGA VITTAGTIPTSPSTPTTVGSTITLNHIAIDLPSILSFQAQAPKIWIYPTKTGSTYT
EDSNPTITISGTLTLRNSN NEDPYDSLDSLHSEKVP LLYIVDVAAQKINSSQLDLSTLNSGEHYGYQGIWSTY
WVETTTITNPTSLLGANTKHKLLYANWSPLGYRPH PERRGEFITNALWQSAYTALAGLHSLSSWDEEKGHA
ASLQGIGLLVHQDKNGFKGFRSHMTGYSATTEATSSQSPNFSLGFAQFFSKAKEHESQNSTSSH HYFSGMCI
ENTLFKEWIRLSVSLAYMFTSEHTHTMYQGLLEGNSQGSFHNHTLAGALSCVFLPQPHGESLQIYPFITALAIR
GNLAAFQESGDHAREFSLHRPLTDVSLPVGIRASWKNHHRVPLVWLTEISYRSTLYRQDPELH SKLLISQGTW
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>core/32/2/Org2_Gene383

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GNLSLTGNSQIIFTQNFSSDNGGVINTKNFLLSGTSQFASF SRNQAF TGKQGGVVYATGTITIENSPGIVSFSQN
LAKGSGGALYSTDNCSITDNFQVIFDGNSAWEAAQAQGG AICCTTTDKTVTLTGKNLSFTNNTALTYGGAI
SGLKVSISAGGPTL FQSNISGSSAGQGGGGAINIASAGELALSATSGDITFNNNQVTNGSTSTRNAINIIDTAKV
TSIRAATGQSIYFYDPITNPGTAASTDTLNLNLADANSEIEYGGAI VFSGEKLSPT EKAIAANVTSTIRQPAVLA
RGDLVLRDGVTVTFKDLTQSPGSRILMDGGTTLSAKEANLSL NGLAVNLSSLDGTNKAALKTEAADKNISLS
GTIALIDTEGSFYENHN LKSASTYPLLELT TAGANGTITLGALSTLTLQEPETHYGYQGNWQLSWANATSSKI
GSINWTRTGYIPSPERKSNLPLNSLWGNFIDIRSINQLIETKSSGEPFERELWLSGIANFFYRDSMPTRHGF RHIS
GGYALGITATTPAEDQLTFAFCQLFARDRNHITGKNHGD TYGASLYFHHT EGLFDIANFLWGKATRAPWVLS

EISQIPLSFDKFSYLHTDNHMKTYT DNSIIGSWRND AFCADLGASLPFVISVPYLLKEVEPFVKVQYIYA
HQQDFYERHAEGRAF NKSELINVEIPIGVTFERDSKSEKGT YDLTLMYILDAYRRNPKCQTS LIASDANWMA
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>core/33/2/Org2_Gene399

MFGMTPAVYSLQ TDSLEKFALERDEEFRTSFP LLDSLSTLTGFSPITTFVGNRHNS SQDIVLSNYKSIDNILLW
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CNGDFTISQNQGTFFYVNN SVNNWGGALSTNGHCRIQSNRAPLLFFNNTAPSGGGALRSENTTISDNTRPIYF
KNNCGNNGGAIQTSVTVAIKNNSGSVIFNNNTALSGSINSGNGSGGAIYTTNLSIDDPGTILFNNNYCIRDGG
AICTQFLT IKNSGHVYFTNNQGNWGGALMLLQDSTCLLFAEQGNIAFQNNNEVFLTTFGRYNAIHCTPNSNLQ
LGANKGYTTAFFDPIEHQHPTTNPLIFNPANHQGTILFSSAYIPEASDYENNFISSSKNTSELRNGVLSIEDRA
GWQFYKFTQKGGILKLGHAA SIATTANSETPSTSVGSQVIINNLA INLPSILAKGKAPTLWIRPLQSSAPFTEDN
NPTITLSGPLTLLNEENRDPYDSIDLSEPLQNIHLLSLSDVTARHINTDNFHPESLNATEHYGYQGIWSPYWVE
TITTTNNASIETANTLYRALYANWTPLGYKVNPEYQGD LATTPLWQSFHTMFSLLRSYNRTGDS DIERPFLEI
QGIADGLFVHQNSIPGAPGFRIQSTGYSLQASSETSLHQKISLGFAQFFTRTKEIGSSNNVSAHNTVSSLYVELP
WFQEA FATSTVLAYGYGDHHLHSLHPSHQEAEGTCYSHTLAAAIGCSFPWQQKSYLHLSPFVQAIAIRSHQ
TAFEEIGDNPRKFVSQKPFYNLTLP LGIQGKWQSKFHVPT EWTL ELSYQPVLYQQNPQIGVTLLASGGSWDIL
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>core/34/2/Org2_Gene72

MERYDIVRIIGKGGMGEVYLAYDPVCSRKVALKKIREDLAENPLLKRRFLREARIAADLIHPGVVPVYTIYSE
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LFSEAVILDWGA AVACGEEEDLLDIDVSKEEVLSSRMTIPGRIVGTPDYMAPERLLGHPASKSTDIYALGVVL
YQMLT LSFYRRKKGKKIVLDGQRIPSPQEVAPYREIPPFLSAVVMRMLAVDPQERYSSVTELKEDIESHLKG
SPKWTLTTALPPKSSSWKLNEPILLSKYFPMLEVSPASWYSLAISNIESFSEMRLEYT LSKKGLNEGFGILLPT
SENALGGDFYQGYGFWLHIKERTLSVSLVKNSLEIQ RCSQDLESDKETFLIALEQHNHSLSLFVDGTTWLIHM
NYLPSRSGRVAIIVRDMEDILEDIGIFESSGSLRV SCLAVPDAFLAEKLYDRALVLYRRIAESFPGRKEGYEARF
RAGITVLEKASTDNNEQEFALAI EEF SKLHDGVAAPLEYLGKALVYQRLQEYN EEEKSLLLALKRYSQHPEIF
RLKDHVVYRLHESFYKRDR LALVF MILVLEIAPQAITPGQEEKILVWLKDKSRATL FCLLDPTVLELRSSKME
LFLSYWSGFIPHLNSLFHRAW DQSDVRALIEIFYVACDLHKWQFLSSCIDIFKESLEDQKATEEIVEFSFEDLGA
FLFAIQSIFNKEDA EKIFVSNDQLSPILLVYIFDLFANRALLESQGEAIFQALDLIRSKVPENFYHDYLRNHEIRA
HLWCRNEKALSTIFENYTEKQLKDEQHELFVLYG CYLALIQGAEAAKQHFDVCREDRIFPASLLARNYNRLG
LPKDALS YQERRLLL RQKFLYFHCLGNHDERDLCQTM YHLLTEEFQL

>core/35/2/Org2_Gene384

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GALNLT DN GTILFSQNVSN EANNNGGAITTKT LSI SGNTSSITFTSNSAKKLGGAIYSSAAASISGNTGQLVFM
NNKGETGGGALGFEASSSITQNSSLFFSGNTATDAAGKGGA IYCEKTGETPTLTISGNKSLTFAENSSVTQGG
AICAHGLDLSAAGPTLFSNNRCGNTAAGKGGAIAIADSGSLSLSANQGDITFLGNTLTSTSAPTSTRNAIYLG S
SAKITNLRAAQGQSIYFYDPIASNTTGASDVL TINQPDNSPLDYSGTIVFSGEKLSADEAKAADNFTSILKQPL

ALASGTLALKGNVELDVNGFTQTEGSTLLMQPGTKLKADTEAISLTKLVVDLSALEGNKSVSIETAGANKTIT
LTSPLVFQDSSGNFYESHTINQAFTQPLVVFTAATAASDIYIDALLTSPVQTPEPHYGYQGHWEATWADTSTA
KSGTMTWVTTGYNPNPERRASVVPDSLWASFTDIRTLQQIMTSQANSIYQQRGLWASGTANFFHKDKSGTN
QAFRHKSYGYIVGGSAAEDFSENIFSVAFQCQLFGKDKDLFIVENTSHNYLASLYLQHRAFLGGLPMPSPSGSITD
MLKDIPLILNAQLSYSYTKNDMDTRYTSYPEAQGSWTNNSGALELGGSALALYLPKEAPFFQGYFPFLKFQAV
YSRQQNFKESGAEARAFDDGDLVNCSIPVGIRLEKISEDEKNNFEISLAYIGDVYRKNPRSRTSLMVSGASWT
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>core/37/2/Org2_Gene385

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IQSNYSCYFGQNFSNDNGGALQGSSISLSLNPNTFAKNKATQKGGALYSTGGITINNTLNSASFSENTAANN
GGAIYTEASSFISSNKAISFINNSVTATSATGGAIYCSSTSAPKPVLTLSDNDELNFIGNTAITSGGAIYTDNLVL
SSGGPTLFGKNNSAIDTAAPLGGAIAIADSGSLSLALGGDITFEGNTVVKGASSSQTTTRNSINIGNTNAKIVQL
RASQGNTIYFYDPITTSITAALSDALNLNGPDLAGNPAYQGTIVFSGEKLSEAEAAEADNLKSTIQQPLTLAGG
QLSLKSGVTLVAKSFSQSPGSTLLMDAGTTLETADGITINNLVLNVDLKETKKATLKATQASQTVTLSGSL
LVDPSGNVYEDVSWNNPQVFSCLTLTADDPANIHITDLAADPLEKNPIHWGYQGNWALSWQEDTATKSKAA
TLTWTKTGYNPNPERRGTLVANTLWGSFVDVRSIQQLVATKVRQSQETRGIWCEGISNFFHKDSTKINKGFR
HISAGYVVGATTTLASDNLITAAFCQLFGKDRDHFINKNRASAYAASLHLQHLATLSSPSLLRYLPGSESEQP
VLFDAQISYIYSKNTMKTYTQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIKVEASYIHQDSF
KERNTTLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVADVYRKNPDCTTALLINNTSWKTTGTNLS
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>core/38/2/Org2_Gene387

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ENIRKLVVAGNFSTADGGAIKGASFLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIASSTG
GAIDDEGTSILSNNKFLYFEGNAAKTTGGAICNTKASGSPELIISNNKTLIFASNVAETSGGAIHAKKLALSSGG
FTEFLRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTDTPKRNAINIGSNGKFTELRAAKNHT
IFFYDPITSEGTSSDVLKINNGSAGALNPYQGTILFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQKGV
LESTSFQSEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYES
HMFSDQLFSLKITYDADVDNVDISSLIPVPAEDPNSEYGFQGWNVNWTDTATNTKEATATWTKTGF
VPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFVWSSMTNFLHKTGDENRKGFRHTSGGYVI
GGAHTPKDDLFTFAFCHLFARDKDCFIAHNSRITYGGTLFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREIP
LALDVQVSFSHSDNRMETHYTSLEPEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSF
FESSDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDSWKIRGGNLSR
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>core/39/2/Org2_Gene248

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NAIIFLGDAIGSGIIASLVHTIGIQGILILFTAALVLTPIVFYVSKSLKSLSDDDHDLFIDTGHPPPLSKALKLCFYD
KYTFYLLCFYFLMQLLAIAATEFNLYLKIFEIQFASKEEFELVAHIGKCSLWISLGNMCFALFAYSRIVKRLGVNNI
ILFAPLCFLSLFLFWTFKTTLSIAVLAMVVREGVTYALDDNNLQLLIYGVPNKIRNQIRIVVESFIEPIGMLVWS
LICFLSSQQYVFCIIISLIATILVCLVRSYYAKAILKNLSAQALQLTRSMQDWIKSMTVKQKRQVELFLLAHLK
HPSERHQTFAFQHLLNLASRSVLPSELLAHMNKLSLPNKLKTIEMVKSSLWAKDFLTLELLKRWTSIFPHPAIAS
AIHLYFAEHDLLHITHIAEDLYDTVGDRLLAAILTVRRQEAYGPYRDLADKRLKELLNSDQPEDIVMGLTILK
LEKNPQNFPILLDFLNTKNEDILIVTCKALHTSVRANHKKPYCPELLKRLRQCSDHNDASQYLLKTISIALDISFV
KDLLMTTSQLKNTSRKYAEAMIGELDKEVAPAFQLVLTDEGTHNRCRILAAKALCKIDNWLLKKHAYKIVK
SKASKALFYSYHGHYIQKKYPTYNLSLLANTLNSNYAEVNFMLSLLGILGSMEHSGVLIRALTSKNQKIK
QALESLEKNCDSHLFSLLEPFVNQPGMCYSEKYYFKCGVIPLTLKELLNMMENSPSSLNKLTAQQLKEELSYC
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>core/40/2/Org2_Gene5

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MLLNNYVVRFEQNQSKTKGGAISGANVTIVGNYDSVSFYQNAATFGGAIHSSGPLQIAVNQAEIRFAQNTAK
NGSGGALYSDGDIDIDQNA YVLFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNH SIMGG
GAIYARKLSISSGGPTLFINNISYANSQNLGGAIAIDTGGEISLSAEKGTITFQGNRTSLPFLNGIHLLQNAKFLK
LQARNGYSIEFYDPITSEADGSTQLNINGDPKNKEYTG TILFSGEKSLANDPRDFKSTIPQNVNLSAGYLVIKE
GAEVTVSKFTQSPGSHLVLDLGT KLASKEDIAITGLAIDIDSLSSSSTA AVIKANTANKQISVTD SIELISPTGN
AYEDLRMRNSQTFPLLSLEPGAGGSVTVTAGDFLPVSPHYGFQGNWKLAWTGTGNKVGEFFWDKINYKPRP
EKEGNLVPNILWGN AVDVRSLMQVQETHASSLQTDRGLWIDGIGNFFHVSASEDNIRYRHNSGGYVLSVNN
EITPKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPVNVNGILSRRFLQNPLMI
FHFLCAYGHATNDMKT DYANFPMVKNSWRNNCWAIECGGSMPLL VFENGRLFQGAIPFMKLQLVYAYQG
DFKETTADGRRFSNGSLTSISVPLGIRFEKLALSQDVL YDFSFSYIPDIFRKDPSCEAALVISGDSWLVPAAHVS
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>core/41/2/Org2_Gene617

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EEPVPAASKEQLDSIQVWEEKQNYARRAVNAINLSIKKQLEEQTSTVTEKDVQPKTQATPHASKKNVASPST
SMPGIEKAATTVA VPQDKSEEEKVKERLTKRELTCEDLKDNGYTVNFEDISILELLQFVSKISGTNFVFDSNDL
QFNVTIVSHDPTSVDDLSTILLQVLKM HDLKVVEQGNVLIYRNPHLSKLSTVVT DSSLKETCEAVVVTRVFR
LYSVSPSAAVNIIQPLL SHDAIVSASEATRHVIISDIAGNVDKVSDLLAALDCPGTSVDMTEYEVKYANPAALV
SYCQDVLGTLAEDDAFQMFIQPGTNKIFVSSPRLANKAEQLLKS LDVPEMAHTLDDPASTALALGGTGTT
PKSLRFFMYKLKYQNGEVIANALQDIGYNLYVTTAMDEDFINTLNSIQWLEVNN SIVIIGNQGNVDRVIGLLN
GLDLPPKQVYIEVLILDT SLEKSWDFGVQWVALGDEQSKVAYASGLLNNTGIATPTKATVPPGTPNPGSIPLP
TPGQLTGFS DMLNSSSAFGLGIIGNVL SHKGKSFLT LGGLLSALDQDGD TVIVLNPRIMAQDTQQASFFVGQT
VPYQTTNTIIQETGTVTQNIDYEDIGVNLVVTSTVAPNNVVT LQIEQTISELHSASGSLTPVTDKTYAATRLQIP
DGCFLVMSGHIRDKTTKV VSGVPLLNSIPLIRGLFSRTIDQRQKR NIMMFIKPKVISSFEEGTRVTNKEGYRYN
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>core/43/2/Org2_Gene888

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PSEVSGSVLTEPLVVTGPATPQLINLHSLQERYPTLSRSP EALRTYGSDLYELIGKYLS PVLGIGSETLKRELKD
LYQQVEVSLTQETDTEAAYTLYGQVLSTLNRISSSLVVSEGGERFSQLRSVRLYREEWNKYHKLVEARDLNQ
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FKSQEPSPHYLGYLFTFLPIILVLLFVYLVFSRQMRGMSG SAMSFGKSPARMLLK GQNKVTFADVAGIEEAKE
ELIEIVDFLKNPNKFTSLGGRIPKG VLLIGPPGTGKT LIAKAVSGEADRPFFSIAGSDFVEMFVG VGASRIRDMF
EQAKRNAPCIIFIDEIDAVGRHRGAGIGGGHDEREQTLNQLLVEMDGFGTNEG VILMAATNRPDVL DKALLR
PGRFDRRVVMNLPDIKGRFEILMVHAKRIKLDPTVDLM AVARSTPGASGADLENLLNEAALLAARKDRTAV
TAVDVAEARDKVLYGKERRSLEMDAEERKTTAYHESGHAVVGLCVQH GDPVDKVTIIPRGLSLGATHFLPE
KNKLSYWK KELYDQLAVLMGGRAAEI FLGDISSGAQQDISQATKLVRSMVCEWGMSPQLGNVTYDERSD
GLTGYGGYHEKSYSEETA KTIDTELRMLLDAAYQRALDIINEHKA EIELMTQMLIEFETLDSKDVKEIMDHT
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>core/44/2/Org2_Gene322

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CTPELQEFVWNLMEKRQVERFAEQLLRSYKDLCKATFFEEFLQIKFTGQKRFSLEGGETLVPMLEHLVHYGS
ALGISNYVLGMAHRGRLNVL TNVLGKPYRYVFMEFEDDPAARGLESVGDVKYHKGYVLKSHQKDRETTFV
MLPNASHLESVDPIVEGVVAALQH QGHAGKEQSSLA ILVHGDAAFSGQG VVYETLQLSRVPGYSTEGTLHIV
VNNYIGFTAVPRESRSTPYCTDI AKMLGIPVFRVNSEDDVACIEAIEYALQVRERFSCDVIIDLCCYRKYGHNE
SDDPSVTAPLLYDQIKRKSIRELFRQYLLEGQFADISEETLASIEKEIQESLNREFQVLKGTDPPEFPKKECHH
CDRLNNGELILHDCDVSLDRET L FHMSSRLCGFPDNFHPHPKIKTLLEKRMKMAEGGVGYDWAMAEELAF A
SLLIEGYNLRLSGQDSIRGTFSQRHLVWSDTVTGD TYSPLYHLSAEQGSVEMYNSPLSEYAILGFEYGYAQQ A
LKTLLVWEAQFGDFANGAQIIFDQYISSGIQK WDLHSDIVLLLPHGYEGQGPEHSSSRIERYLQLAANWNFQV
VLPSTPVQYFRILREHAKRDL SLPLVIFTPKLLLRYPQCVSSIEEFTEPGGFRAILEDADPNYDASILVLCSGKIY
YDYAEMLPQDRRKDFSC LRIESLYPLALEDLVSLIDKYSHLKHFWLQEESKNMGAYDYMFMALQDILPEK
LLYIGRPRSSTASGS AKLSRQELVTCMETLFS LR

>core/45/2/Org2_Gene271

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PPQEKELEPKPVKPAEPKSVVMIKSKFGPTGKHINHLLAKTFKAPAKEEKVVAGSKSTKPVASDKTGKPGTSE
GGEQNNREKQFN PANRSPASGPKRDAGKKNLTDFRDRSKKSDESLKAFTGRDRYGLNEGGEEDRWKRKR V
YKPKKH YDEASIQRP THIKISLPITVKDLAAEMKLKASEVIQKLFHGMTYV VNDILDSETAVQFIGLEFGCTID
IDYSEQDKLCLSN DTVRDEIQSTDP SKLVIRSPIVAFMGHVDHGKTTLIDSLRKS NVAATEAGAITQHMGAF C
CSTPVG DITILDTPGHEAFS AMRARGAEVCDIVVLV VAGDEGIKEQTLEAIEHAKAADIAIVVAINKCDKPNF
NSETIYRQLSEINLLPEAWGGSTVTVNTSAKTGEGLSELLEMLALQAEVLELKADPSARARGLVIESELHKGL
GPVATVLIQNGSLKLGEALVFND CYGKVKTMHNEHNELMKEAGPSIPVLITGLSDIPKAGDPFFVVKNEKTA

RDIEARSAGQQRFALQQKKRPNFDSMLQNKKTLKLMIKADVQGSIEALVSSISKIKSEKVDVEILTNSVGEIS
ESDIRLAAASKAVLIGFHTGIESHAEPLIKSLGVRVELFTVIYHAIDAIKEIMTSLLDPIAEEKDEGSAEIKEIFRS
SQVGSIIYGCIVTEGIMTRNHKVRVLRNKEILWKGTLSSLKRVKEDVKEVRKGLECGILLEGYQQAQIGDVLO
CYEVIYHPQKL

>core/46/2/Org2_Gene792

MLSNTIRSNFLKFYANRHHTILPSSPVFPHNDPSILFTNAGMNQFKDIFLNKEKVSYSRATTSQKCIRAGGKHN
DLDNVGHTSRHLTFFEMLGNFSGFDYFKAEAIFAWEVSLSVFNFNPEGIYATVHEKDDEAFALWEAYLPTD
RIFRLTDKDNFWSMANTGPCGYCSELLFDRGPSFGNASSPLDDTDGERFLEYWNLVFMENRTSEGSLALP
NKHVDTGAGLERLVSLIAGHTTVFEADVLELIAKTEQLSGKVYHPDDSGAAFRVIADHVRSLSAIADGLLP
GNTERGYVLRKILRRSVNYGRRLGFRNPFLAEIVPSLADAMGEAYPELKNSLSQIQKVLLEEESFFKTLDRG
GNLLQQVLKSSSSSSCISGEDAFKLKDTYGMPIDEISLLAKDYDYSVDMDTFHKLEQEAKERSRKNVVSQSG
TSESIYNELHLTSEFIGYDHLSCDTFIEAIIKDHIVSSLQEKQEGAIVLKVSPFYAEKGGQVGDSGEIFCSEGTFI
VTHTTSPKAGLIVHHGRISQGSALTVEAAVTAQVNRYRRKRIANNHTACHLLHKALEITLGDHIRQAGSYVDD
TKIRLDFTHPQAISPEDLLCIETLVNESIRENEPVDIREALYSVDMNSSEIKQFFGDKYSDVVRVVSAGHSHEL
GGTHAEATGDIGFFRITKEHAVAMGIRRIEAVTGEKAEATVHQQSEVLEEIATLLQVPRDQIVSRLTATLDER
KQQDKRLNELENSLIQTKLDKLIHNCHQRQGITCLVHHLAEHENHRLQQY AQCLHQRIPEKLISLWTTEKNG
KYIVLSRVSDDLITQGVHAQDLLKAVLTPCGGRWGGKDQSAQGSAPALPATEVLNETLWQWISTQLI

>core/47/2/Org2_Gene642

MSTFSIQNRLRTISGESTRIIKLDHKYSGFDPRSPAINLEELNSGIYALRHLMNALQSENTNVAALLNPNTIF
PTTSWTDYKHSRPQASSPRAPSSQTPTDIVSAAALALVLVIDGGLAELVASVTEIDL GALSTISTVRQLMASYL
GLTTLTAEQEKVV FSSSYVPSEKNLLEHV KQEKAAEIQAKQEEIKAVLEAKGVSTEEIEAILKEYPDIYAADFF
KEFIEEPLHTYRAKVGAPIQEMNENAIQLLPTPPAITPDNVNEVNGMNTLSTILQAIDDAIKQAPALGGDQEIT
ILQTLVPLVDKTTFTKAEFDLIYTATQLPNTASLKLYLTDRQIAEYRGKITKVYQNSIQNLSETKRVVENNRSM
LETQLSMFQQAQNCFTWISQANALNIAITNKYISAVLTTSMEMYGGLLCLSYMYERLADDEKAIFDKSVNE
YLPPIHIVGGSWVNGWIAKMAAYQELAEYSLGTAVTSQDQIKAYLQTRGNEFKATRHFFHNIGDQMYQFAN
ETVFGNCLTTANGAIQPD LGGFIREAMTNVGTVEADYVSNAQRILNEFNATAAHVLQLQLQIAELQKKADD
LDPGKASFTENRKFVAAAWITSESLGDALISMILNSQLPKQEAFLKPLIEEINFNNLAANALNSLLQITNEFSTT
SVYYSLSSYLVSQKTGQNLFAGDYETLLAAAREREYIYRDTARCKQAINLVNGLLQKINSLPGATSAQKQE
MLNATYYQYSLSVTLNQLTVLESLLAGLKMTLQTTSNNKYDKSVFKIESFDDWIPTLAALESFLTSGFPNIS
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>core/48/2/Org2_Gene681

MKKSIIIVESPAKIKTLQKLLGSEFVFASSIGHIVDLPakeFGIDVDHDFEPQYQVLPDKQEVINHIRKLAACKCE
KVYLSPDPDREGAIAWHIANQLPDSPLIQRVSFNAITKNAVTEALKHPRTIDMALVNAQQARRLLDRIVGYK
ISPILSRKLQQRSGISAGRVQSVALKL VVDREKAIDAFVPVEYWNLRVLMQDPKTTKTFWAHLYAVQGKKW
EKEIPEGKTENDVLLINSEEKARHYAELLEKSSYTITRVEAKAKRRFAPPPFITSTLQQEASRHFRFSASRTMSI
AQTLYEGVDLDSSTGLITYMRTDSVRVDPEALTTVREYIQQTFGKEYLPEKANVYTTKKMTQDAHEAIRP
TDINLTPDKLKNKLSDDQFKVYNLIWKRFVASQITPAIYDTLAVQITTDTEIDLRASGSLLKFKGFLAVYEEKQ
DDENDQEEDHPLPPLHAQDALIKEEVSQEQAFTKPLPRFTEASLVKELEKSGIGRPSTYATIMNKIQSREYTTK

ENQRLRPTELGKIISQFLETNFPRI MDIGFTALMEDELELIADNKKPWKLLLQEFWTTFLPVVITAEKEAVIPRI
LTNIECSKCHKGKLVKIWSKNSYFYGCSEYPECDYRTSEEELAFNKEDYAEDTPWDSPCPLCGGVMKVRHG
RYGTFLGCEKYPECRGITISIHKKGEEIEQEEPIPCPAIGCNGKIFKKRSRYNKIFYSCSEYPECSVIGNSIDAVITK
YSGTEKIPYKKKTPTKKKSSAKTTKAAKTPSKKGKAKSSVKKSSSEKKTGPLFLPSPDLAKMIGNEPVSRGEAT
KKIWDYIKEHQLQAPENKKLLVPDNNLATIIGPNPIDMFQLSKHLSQHLTKVSNDESSASS

>core/49/2/Org2_Gene531

MKKLFLVDASGFIFRAYFALPEMKNHQGQATQAVFGFIRSLNKLIFESPEYMISSVFDGPNNKQSRQAIYADY
KSNRQKKFEDIPPQIALVKEYCSLIGLAYLEKESVEADDVIASIAKKAREENYKVYVCTADKDLLQLVNDHV
VAWNPWADQGVVGISEVIERYGIPPGNIPDYLALVGDSSDNIPGLPGCGPKKAAALLKQFGSVEGLLENLDA
VKGLSQTMLSERQETLKL SKRLALLDSNIPIVPIESLTFPQHPVDEEKLIHFYIQQGFKTLVPSKQTEAATVDV
QIIKDAESLTNILNLVQGGDIAFAVAYTGNHLLSLKLEGLALTQGSGVFFIALEEETGKILPILKDFFLREDLTF
YGYNLKRDCHALLNAGIVIREISYDLALAEHLTNGGGKISFQSLLVNHGFTETAHRFAKEWGNISGLPIGRLPE
QPEQYFGEFVAYLPIIKDAILEEINRKNLNHILSDIEMPLEKVLFSMERAGVPLDVEELAILEALFETELAVLTE
EIYDLSGRPFNIKSPKQLSDILYNELGLRPIDKAKSTRAEVLEALRSEHPHIEKLLAFRTIEKLLSTYVKALPKQV
DSHTQRIHPSFDQTGAVTGRLACRDPNLQNIPIRSERGILLRKAFLRSEKNSYFLSADYSQIELRFLAHLSDK
LKFASFESGEDIHAFTASQVFHVPLEQVSKEQRMQA KTVNFGIVYGGQAFGLAKVLKISIGEAQELIQAYFSRY
PEIAHFVEETIQQA KDLRVTTMLGRERIIDSWNEFFPGSRAASGRFAVNTRIQQSAAELIKLAMLDISQAIKQQ
QMKSRMLLQIHDELLFEVPEEEIEEMQRLVREKMESAMTSLVPIVVNIIIGKNWAEC

>core/50/2/Org2_Gene115

MEKFSDAVSEALEKAFELAKSSKHTYVTENHLLLALLENTESLFYLVIKDIHGNPGLLNTAVKDALSREPTVV
EGEVDPKPSPGLQTLLRDAKQEAKTLGDEYISGDHLLLAFWSSNKEPFNSWKQTTKVSFKDLKNLITKIRRG
RMDSPSAESNFQGLEKYCKNLTAAREGKLDPVIGRDEEIRRTIQVLSRRTKNNPMLIGEPGVGKTAIAEGLA
LRLIQGDVPESLKGKQLYVLDMGALIAGAKYRGEFEERLKSVLKDVESGDGEHIFIDEVHTLVGAGATDGA
MDAANLLKPALARGTLHCIGATTLNEYQKYIEKDAALERRFQPIFVTEPSLEDAVFILRGLREKYEIFHGVRIT
EGALNAAVLLSYRYIPDRFLPKAIDLIDEAASLIRMQIGSLPLPIDEKERELAALIVKQEAIKREQSPSYQEEA
DAMQKSIDALREELASRLGWDEEKKLISGLKEKKNSLES MKFSEEEAERVADYNRVAELRYS LIPQLEEEIK
QDEASLNQRDNRLQEEVDERLIAQVVANWTGIPVQKMLEGAEKLLILEESLEERVVGQPFVAVSAVSDSIR
AARVGLNDPQRPLGVFLFLGPTGVGKTELAKALADLLFNKEEAMVRFDMS EYMEKH SISKLIGSSPGYVGYE
EGGSLSEALRRRPYSVVLFDIEKADKEVLNILLQVFDDGILTDGKKRKVNCKNALFIMTSNIGSPELADYCS
KKGSELTKEAILS VVSPVLKRYLSPEFMNRIDEILPFVPLTKEDIVKIVGIQMRRIAQRLKARRINLSWDDSVIL
FLSEQGYDSAFGARPLKRLIQKV VILLSKALLKGDIKPDTSIELTMAKEVLVFKKVETPS

>core/51/2/Org2_Gene627

MAVRLIVDEGPLSGVIFVLEDGISWSIGRDSSANDIPIEDPKLGASQAIINKTDGSYYITNLDDTIPIVVNGVAIQ
ETTQLKNEDTILLGSNQYSFLSDEFDPQDLVYDFDIPEENFSNDSGDLSDSNEQGKDLEPRQTSETNHSPKPKE
KLTKDQGSSDPITSGDQELADAFASAKAEKNQPRAKVAKKGLKESSNESLNPKEQNAKDSPKGEERTNKPQ
NAIMEDNGASPRQDPQPKSAEPSLKNTARDETPLKENKPVEEKANKKATPDSPEKKDQPEEGSKKEGSKIEA
TPLDSQKESEDKEAEFAVQEEEEENLTEDNKEDSDSAADANDDTASDH TAEDNKETPKKVENEKSAVLSPFH
VQDLFRFDQTIFPAEIDDI AKKNISVDLTQPSRFLKVL AGANIGA EFHLD SGKTYILGTDPTTCDIVFNDLSVS

HQHAKITVGNDGGILIEDLDSKNGVIVEGRKIDKTSTLSSNQVVALGTTFLFLIDHHAPADTIVASLSPDDYSL
FGRQQDAEALERQEAQEEEEKQKRATLPAGSFILTLFVGGLAILFGIGTASLFHTKEVVPLENIDYQEDLAQVI
NQFPTVRYTFNKTNSQLFLIGHVKNSTDKSELLKYVDALSFKSVDDNVIDDEAVWQEMNILLSKRPEFKGIS
MHSPEPGKFIITGYVKTEEQAACLVDYLNHFNYLSLLENKVVVETQMLKAIAGHLLQGGFANIHVAFVNGE
VILTYVNNDDAEKFRAVVQELSGIPGVRLVKNFAVLLPAEEGIIDLNLRYPNRYRVGTGYSRYGEISINVVVN
GRILTRGDVIDGMTVTSIQPNAIFLEKEGLKYKIDYNK

>core/52/2/Org2_Gene376

MFEEKFTNRAKQVIKLAKKEAQRLNHNLYGTEHILLGLLKLGQGVAVNVLRNLGIDFDTARQEVERLIGYGPE
IQVYGDPAALTGRVKKSFSANEEASLLEHNYVGTEHLLLGLHQSDSVALQVLENLHIDPREVRKEILRELETF
NLQLPPSSSSSSSSSRNPSSSKSPLGHSLSGDKNEKLSALKAYGYDLTEMVRESKLDPVIGRSSEVERLILILCR
RRKNNPVLIGEAGVGKTAIVEGLAQKIILNEVPDALRKKRLITLDLALMIAGTKYRGQFEERIKAVMDEVKHH
GNILLFIDELHTIVGAGAAEGAIDASNILKPALARGEIQCIGATTIDEYRKHIEKDAALERRFQKIVVHPPSVDE
TIEILRGLKKKYEEHNVFITEEALKAAATLSDQYVHGRFLPDKAIDLLDEAGARVRVNTMGQPTDLMKLEA
EIENTKLAKEQAIGTQEYEKAAGLRDEEKKLRERLQSMKQEWENHKEEHQVPVDEEAVAQVVSQTGIPSA
RLTEAESEKLLKLEDTLRRKVIGQNDVAVTSICRAIRRSRTGIKDPNRPTGSFLFLGPTGVGKSLLAQQIAIEMFG
GEDALIQVDMSEYMEKFAATKMMGSPPGYVGHEEGGHLTEQVRRRPYCVVLFDEIEKAHPDIMDMLMLQILE
QGRLTDSFGRKVDFRHAIIMTSNLGADLIRKSGEIGFGLKSHMDYKVIQEKIEHAMKKHLKPEFINRLDESVI
FRPLEKESLSEIHHLEINKLDSRLKNYQMALNIPDSVISFLVTKGHSPEMGARPLRRVIEQYLEDPLAELLKES
CRQEARKLRATLVENRVAFEREEEEQEAALPSPHLES

>core/53/2/Org2_Gene9

MKIPLRFLILSLVPTLSMSNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVFKDSVVIENVPKTGET
QSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSEAANKTVTLSGFSALSFLKSPASTVTNGLGAIN
VKGNLSLLDNDKVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNSSSTRGGAIHTKNLTLSSGGETLFQGNT
APTAAGKGGAIADSGTLSISGDSGDIIFEGNTIGATGTVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGS
TSVADALNINSPDTGDNKEYTGTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQ
DANSKLIMDLGTSLVANTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAIKDESIFYQNGFLNEDH
SYDGILELDAGKDIVISADSRSIDAVQSPYGYQGKWTINWSTDDKKATVSWAKQSFNPTAEQEAPLVPNLLW
GSFIDVRSFQNFIELGTEGAPYEKRFVWAGISNVLHRSGRENQRKFRHVSGGAVVGASTRMPGGDTLSLGFA
QLFARDKDYFMNTNFAKTYAGSLRLQHDASLYSVVSILLGEGGLREILLPYVSKTLPSCSFYQGLSYGHTDHR
MKTESLPPPPPTLSTDHTSWGGYVWAGELGTRVAVENTSGRGFFQEYTPFVKVQAVYARQDSFVELGAISR
FSDSHLYNLAIPLGIKLEKRFAEQYYHVAMYSPOVCRSNPKCTTTLLSNQGSWKTKGSNLARQAGIVQASG
FRSLGAAAEFLGNGFGFEWRGSSRSYNVDAGSKIKF

>core/54/2/Org2_Gene229

MFNKDEIIVPKNLEEEMKESYLRYSMSVVISRALPDIRDGLKPSQRRVLYAMKQLSLSPGAKHRKCAKICGDT
SGDYHHPGESVIYPTLVRMAQNWAMRYPLVDGQGNFGSIDGDPPAAMRYTEARLTHSAMYLMEDLDKDT
VDIVPNYDETKHEPVVFPKFPNLLCNGSSGIAVGMATNIPPHNLGELIEATLLLLANPQASVDEILQVMPGPD
FPTGGIICGSEGIRSAYTTGRGKIKVRARLHVEENEDKHRESIIITEMPYNVNKSRLIEQIANLVNEKTLAGISDV
RDESDKDGIRVVLEIKKGESSEIIINRLYKFTDVQVTFGANMLALDKNLPRMTMSIHRMISAWIRHRKEVIRRRRT

RYELNKAETRAHVLEGYLKALSCLDALVKTIRESGNKEHAKERIIESFGFTEPQALAILRLYQLTGLEAEKI
QKEYEELLNKIAYYKQVLSDEGLVKDIIRNELQDLLKHHKVARRTTIEFDADDIRDIEDIITNESVIITISGDDY
VKRMPVKVFKEQRRGGHGVGTGDMKKGAGFLKAVYSAFTKDYLLIFTNFGQCYWLKVWQLPEGERRAKG
KPIINFLEGIRPGEELAAILNIKNFDNAGFLFLATKRGVVKKVSLDAFSNPRKKGIRALEIDEGDELIAACHIVS
DEEKVMLFTHLGMVVRFPHEKVVRPMGRTARGVRGVSLKNEEDKVVSCQIVTENQSVLIVCDQGFGKRSLVE
DFRETNRGGVGVR SILINERNGNVLGAIPVTDHDSILLMSSQGQAIRINMQDVRVMGRSTQGVRLVHLKEGD
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>core/55/2/Org2_Gene641

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KNPANKDVFDKLNTELQALVAAGNNLTEENFQTLYNFPPEEIFTAIQRADTFTGGMKTDFTNQLAGKYGNQA
TLTQTFADGRVEGFKDILTAVQGVLTPEQFTIFAEIATELQALADHVGNFDEAGLQRIEDAGEKLA VINSSD
LTRNDKIMFCQHITDLYSDQVAALGSFDTVLDASIYVNQHQTMTFSNLSSFVGSGLIGTFAPIDLSSSQGDISSA
ALAGALQTARGLNSRFNELTAEQQKLINECIKSLVTFKCGEHLGAIWAYFTASTVVALNPTATMDHVKAAIL
EEAKELDNSSFLASSIKSAMTSIVNSSGSFSVTVNSSTLQYTIYSEKNGKVEINQILLNYGSTGFLPEITKLAKT
NAESTARSYFRFKALAAVESENVQNKIEDLQSQLQQFTNMKTELFDGQLLSQASELRALPLPSAVASVLIDRY
MPKEVDYLNEIYKKLYYSNLGSSIGNSIIDAISQYVNGATYFNFASYVGQQPAVGAGGANAFPGSQESAQAK
LDQERKQAALYLQETRGA LTVIEEQRARVLKDDKITNEQRSTILDSL RNYEDNINSISGSLVLLQNYLQPLSIA
GGSVAGTFEVKEGQE QWQARLQILEEALVSGLVGNMINGGMFPLQSTIQSDQQSFADMGQNFQLDLQMHLT
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>core/56/2/Org2_Gene838

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LSTGSFFIEECENTKELVDEICRLAPSEVLSCNKFYNKETAIVMQLQQHLKLTSTYADWAFEHKFASQKLTT
HFQVASLDGFG LKGLVPAINAAGGLLSYIQDKLLLPTKHIAIPQTRGKQQKLLIDTASQVNLELLAPLNDPQG
KNSLLRIMDHTSTPMGGRLLRQILISPFYNPKEILVRQDAVEFFLRQVTLRKNIKTYLCQVRDIERLMTKVTTG
LAGPRDIGTLRDSFSAGA QIYEQLASATLPEFFIDKCSLDTKLASLIALLSKSLNGDLPLRVSDGNIFVDEFHND
LKRLRHNQEHSQEWIWEYQERIRKETGIKKLKICFAQALGY YIEVSSEFAPQLPKDFIRRQSRLHAERFTTIEL
QQFQDDMSNISEKLQ TLETQFFKDLCSHILQLRTEILALSQSLADLDYIISLADLAHAQGYCRPHVMSDTLCI
YRGCHPVAKTLVDTGKFIPNDTEMRGSQTRMILLTGPNMAGKSTYIRQIALLVIM AQMGSYIPAKSAHIGVID
KIFTRIGAGDNLSKGMSTFMVEMAETANILHNATDRSLVILDEVGRGTSTYDGLAIAQAVVEYLLFTDKKKA
KTLFATHYKELTTLEDHCPHVENFHAGVKDKAGQPVFLYEILKGHSQKSFGIHVARLAGFPLCVVSRAQQIL
RLEGPE SITRPAQDKMQQLTLF

>core/57/2/Org2_Gene1013

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QRIVNGYQEEAPDEWLRYGNPWEICRGEYLYPVRFYGRVIHYTDSRGKQVADLVDTQEV LAMAYDIPIPGY
GNDTVNSLRLWQAQSPRGFEFSYFNHGNYIQAIEDIALIENISRVLYPNDSITEGQELRLKQEYFLVSATIQDIIR

RYTKTHICLDNLADKVVVQLNDTHPALGIAEMMHILVDREELPWDKAWEMTTVIFNYTNHTILPEALERWP
LDLFSKLLPRHLEIIYEINSRWLEKVGSRYPKNDDKRRSLSIVEEGYQKRINMANLAVVGS AKVNGVSSFHSQ
LIKDTLFKEFYEFFPEKFINVTNGVTPRRWIALCNPRLSKLLNETIGDRYIIDLSHLSLIRSFAEDSGFRDHWKG
VKLKNKQDLTSRIYNEVGEIVDPNSLFDCHIKRIHEYKRQLMNILRVIYVYNDLKENPNQDVVPTTVIFSGKA
APGYVMAKLIKLINSVADVNNQDSRVNDKLVFLPNYRVSM AEHIIPGTDLSEQISTAGMEASGTGNMKF
ALNGALTIGTMDGANIEMA EHIGKENMFIFGLLEE QIVQLRREYCPQTICDKNPKIRQVLDLLEQGGFFNSNDK
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PTKSCSGEGN

>core/58/2/Org2_Gene788

MKKLYHPTLFLRPLIRLSLIFALSLTLISGNFPQQKSFGHCCADMHSALISGKNCEELFADFIERV LADRET LTA
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CHESLQDHLLFELYTVTLHSGYENRKQDMLLAKEQG DYKKAIELAKELVA ALEKGSCSPHPEIVQIEKTFLQ
KTLLALQIKVAQEAQESCDALLTPYCLSEIAYTEAMDALVLR IARGEVSRTNEVDSVLLSHALQHLPFAREKA
IPELEV LIDHGAYLESTLLYYAYFSLLELYHQNKDFASLERLLEKGD AVFVPEHPYFPEY GFFLGAYFYAKGK
YESAEKVFLQIIDPAVKLGATFARAYEYLGCIAYVQNHYEKAE EYFLRAYKSWGREESGIGLFLAYAVQKKK
TACEDMLYHPKFSFTYRHLLDSLCSLSYPHGENKGSSAIQ RVHRAVPELSEIYSRCIYD MIKYRNV TYTHPIIE
LAYNQVRNLEKRNLEEICRDAQDPEYDKALAFW GALQSGASVPRSLIESSDVDEARITIRCYEALYFHNPD AI
AML PQAFSEECNSWQTALRLVWTLVRPKGAPNHAKYWDHLVLRPHGDSL YFFGYDLQEY LIGKEDALKHL
SVFAELFPKSSLLSLVYYLQGYSESSALRKVGW FVKALEEFTEISWSGEHMKTWAYIYYMVKLDLADTYISL
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SPRSYRDYYGESLQRTLGLCQRFLGV

>core/59/2/Org2_Gene123

MRYDPN LIEKKWQQFWKEHR SFQANED EDKV KYYVLDMFPYPSGAGLHVGH LIGYTATDIVARYKRARGF
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LYDQGLAYMADMAVN YCPELGTVLSNEEVENGF SIEGGYPVERKMLRQWILKITAYADK LLEGLDALDWP
ENVKQLQKNWIGKSEGALVTFH LTQEGSLEAFTTRLDTLLGV SFLVIAPEHPDLDSIVSEEQRDEVTAYVQES
LRKSERDRISSVKTKTG VFTGN YAKHPITGNLLPVWISDYVVLGYGTGVVMGVP AHDERDREFAEMFSLPIH
EVIDDNGVCIHSNYNDFCLNGLSGQEAKDYVINYLEM RSLGRAKTMYRLRDWLF SRQRYWG EPIPIIH FEDG
THRPLEDDELPLLPNID DYRPEGFGQGPLAKAQDWVHIYDEKTGRPGCRETYTMPQWAGSCWYYLRFCDA
HNSQLPWSKEKESYWMPVDLYIGGA EHAVLHLLYSRFWHRVFYDAGLVSTPEPFKKLINQGLVLASSYRIPG
KGYVSIEDVREENG TWISTCGEIVEVRQEKMSKSKLNGVDPQVLIEEY GADALRMYAMFSGPLDKNKTWSN
EGVGGCRRFLNRFYDLVTSSEVQDIEDRDGLVLA HKLVFRITEHIEKMSLNTIPSSFMEFLNDFS KLPVYSKRA
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SLSRSVVAKYLENAQIRKEIYVPNKL VNFVL

>core/60/2/Org2_Gene17

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ADNKELTEELKAYSISIVSVIKDLLKLNPLFKEELQIFLGHSDFTEPGKLADFSVALTTATREELQEVL ETTNM

HDRIDKALILLKKELDL SRLQSSINQKIEATITKSQKEFFLKEQLKTIKKELGLEKEDRAIDIEKFSERLRKRHVP
DYAMEVIQDEIEKLQTLETSSAEYTVCRNYLDWLTII PWGIQSKEYHDLKKA EIVLNKDHYGLDEIKQRILELI
SVGKLSKGLKGSII CLVGP PGVGKTSIGRSIAKVLHRKFFRFSVGGMRDEAEIKGHRRTYIGAMPGKMVQALK
QSQAMNPVIMIDEVDKIGASYHGDPASALLEVLDP EQNKDFLDHYLDVRVDLSNVLFILTANVLDTIPDPLLD
RMEILRLSGYILEEKLQIAKKYLVPKARKEIGLTASEVNFQPEALKYMINNYAREAGVRTLN GNIIKKVLRKVA
LKIVQNQEKP KSKITFKISSKNLQTYLGKPIFSSDRFYESTPVGVATGLAWTSLGGATLYIESVQVSSLKTDM
HLTGQAGEVMKESSQIAWTYLHSALHRYAPGYTFFPKSQVHIHIPEGATPKDGPSAGITMVTSLLSLLETPV
VNNLGMTGEITLTGRVLGVGGIREK LIAARRSRLNILIFPEDNRRDYEELPAYLKTGLKIHVSHYDDVLKVA
FPKLK

>core/61/2/Org2_Gene804

MKGTPQYHFIGIGGIGMSALAHILLDRGYEVSGSDLYESYTIESLKAKGARCFSGHDSSHVPHDAVVVYSSSI
APDNVEYLTAIQRSSRL LHRAELLSQLMEGYESILVSGSHGKTGTSSLIRAIFQEAQKDPSYAIGGLAANCLNG
YSGSSKIFVAEADESDGSLKHYPRAVVITNIDNEHLNNYAGNLDNLVQVIQDFSRKVTDLNKVFYNGDCPIL
KGNVQGISYGYSPECQLHIVSYNQKAWQSHFSFTFLGQEYQDIELNLPQGHNAANAAAACGVALTFGIDINII
RKALKKFSGVHRRLERKNISESFLFLEDYAHHPVEVAHTLRSVRDAVGLRRVIAIFQPHRFSRLEECLQTFPKA
FQEADEVILTDVYSAGESPRESIILSDLAEQIRKSSYVHCCYVPHGDIVDYLRNYIRIHDVCVSLGAGNIYTIGE
ALKDFNPKKLSIGLVC GGKSCEHDISLLSAQHVS KYISPEFYDVSYFIINRQGLWRTGKDFPHLIEETQGDSPLS
SEIASALAKVDCLFPVLHGPFGE DGTIQGF FEILGKPYAGPSLSLAATAMDKLLTKRIASAVGVPPVVPYQPLNL
CFWKRNPELCIQNLIETFSFPMIVKTAHLGSSIGIFLVRDKEELQEKISEAFLYD TDVFVEESRLGSREIEVSCIG
HSSSWYCMAGPNERCGASGFIDYQEKYGF DGIDCAKISFDLQLSQESLDCVRELAERVYRAMQGKG SARIDF
FLDEEGNYWLSEVNPIPGMTAASPFLQAFVHAGWTQE QIVDHFII DALHKFDKQQTIEQAFTKEQDLVKR

>core/62/2/Org2_Gene783

MIRERKKS RHPRLPTLPLAAKASLYLFFACFSGLSLWSFH RDQPCTQNWIGLLGWSFSSFLLYFFGAAAFFIPL
YFLWLSFLYFRRTPRPLFFYKAA AFLSLPFC SAILLSMLSPVGTLPALLDTRL PKFILGNNPPVS YVGGIPFYLF
YEGQSFC LKHLIGSVGTALIFGFV MLFSVLYLCGGIAL LKKKTFQDGVKKAFC SFFQTCFKNLKKLINRRNYL
PKPSVPFVSKNPF SCKTSQPSRRVSE TIILDG SISPLQEEIPGSKKESFFLTPHPCKRFLTKFVEPQENKAKEGK
TIALSSTPTVVRESKGKERAALPKLKS LAVPENDLPQYHLLSKNREARPESLQAELERKALILKQTLTSFGIDA
DLGNICSGPTLAAFEVLPHSGVKVQKIKSLENDIALKLQASSIRIIAPIGKAAV GIEIPTFPFQAVNFRDLLEDY
QKTNRKLQIPLLLGKKANGDNLWADLATMPHLIIAGTTGSGKSVCINTIVMSMIMTTLPSEIKLVIIDPKKVEL
TGYSQLPHMLSPVITESREVYNALVWL VKEMESRYEILRYLGLRNIQAFNSRTRNK TIEASYDREIRETMPFM
VGIIDELSDLLLSSSQDIETPIIRLAQMARA VGIHLILATQRPSREVITGLIKANFPSRISFKVSNKVNSQIIIDEPG
AENLMGNGDMLVLLPSVFGTIRAQGA YICDEDINKVIQDLCSRFTQYVIPSFHAFDDSDSDNSGEKDPLFAQ
AKTLILQTGNASTTFLQRK LKIGYARAASLIDQLEEARIIGPSEGA KPRQILIQNPLEG

>core/63/2/Org2_Gene230

MDPKEKNYDASAITVLEGLQAVRERPGMYIGDTGITGLHHLVYEVVDNSIDEAMAGYCSRIDVRILEDGGIVI
VDNGRGIPIEVHERESAKQGREVSALEVVLTVLHAGGKFDKDSYKVSGGLHGVGVSCVNALSEKLVATVFK
DKKCYQMEFSRGIPVTP LQYVSVSDRQGTEIVFY PDPKIFSTCTFDRSILMKRLREL AFLNRGITIVFEDDRDVS
FDKVTFYEGGIQS FVS YLNQNKESLFSEPIYICGTRVGDDGEIEFEAALQWNSGYSELVYSYANNIPTRQGGT

HLTGFSTALTRVINTYIKAHNLAKNKLALTGEDIREGLTAVISVKVPNPQFEGQTKQKLGNSDVSSVAQQV
VGEALTIFFEENPQIARMIVDKVFVAAQAREAAKKARELTRKSALDSARLPGLIDCLEKDPEKCEMYIVEG
DSAGGSAKQGRDRRFQAILPIRGKILNVEKARLQKIFQNQEIGTHIAALGCGIGADNFNLSKLYRRIIIMTDAD
VDGSHIRTLTLLTFFYRHMTALIENECVYIAQPPLYKVSKKKDFRYILSEKEMDSYLLMLGTNESSILFKSTERE
LRGEALESFINVILDVESFINTLEKKAIPFSEFLEMYKEGIGYPLYLAPATGMQGGRYLYSDEEKEEALAQEE
THKFKIIELYKVAVFVDIQNLKEYGLDISSYLIPQKNEIVIGNEDSPSCNYSCYTLEEVINYLNKLGKRGIEIQR
YKGLGEMNADQLWDTTMNPEQRTLHVSLKDAVEADHIFTMLMGEEVPPRREFIESHALSIRINNLDI

>core/64/2/Org2_Gene264

MNKRTLLFVSLIGIAFVGCQIFFGYNEFRSCKNLAEKQRKISEQTLAAVESVGLSVASWDTDVNGEEHKNNY
AVRVGDKLFLHNGEAAQSVYSSGESWSFVDHKCGFDNIHLALYRQQGSSFNPTNTGKVFLPTNHEGLPVL
VVEFRNNKEPLVFLGEYAQGRISNKDSTIFGTALVFWRSGSDYIPLGLYDSREEKLVSLDLPITRAVIFGNDQD
SAKSSDTANHYYVLFNDYMQIIVSEESGSIEGINLPFASTNNKSIVNEIGFDRDLASEKSPEALFPGLSSKLPDGQ
QAKNSIGGYYP LLRRGLLSDSKLLPLEYHALNVVSGRELATPVALRYRVLSTPHSIQLES LDRSVQKVYKL
PENPEEKPYVFETAITLTKETEDVWVTSGVPEVEIMSNASAPTIKYRVIKKNKGSLDKVKLPKVKEPLAIRRG
VYPQWILNSNGYFGIILTPLSEIASGYGSLYISGSTAPTRLAISPKNQLYPVSKYPGYETLLPLPKDAGTHRFL
VYAGPLAEPTLKVLDKTITQEKGENPEYLDSSIFRGVFAFITAPFAALLFIIMKFFKLVTGSWGISIILLTVFLKL
LLYPLNAWSIRSMRRMQILSPYIQQIQKYKNEPKRAQMEIMGLYKTNKVN PITGCLPLLIQLPFLIAMFDLLK
SSFLLRGASFIPGWIDNLTAPDVLFSWQTSIWFIGNEFHLLPILLGIVMFLQQKVTS LHKKG PVT DQQKQQQV
MGNMMAILFTAMFYNFPSGLNIYWLSSMILGVVQQWITNKILDSKHLKNEVV LNNKKHR

>core/65/2/Org2_Gene514

MRIPITLLQTYFSEPLSTKEILEACDHIGIEAEIENTTLYSFASVITAKILHTIPHPNADKLRVATLTDGEKEHQV
VCGAPNCEAGLIVALALPGAKLFDSEGQAYTIKKSKLRGVESQGMCCGADELGLDELQIQERALLELPEATP
LGEDLATVLGNTSLEISLTPNLGHCASFLGLAREICHVTQANLVIPKEFSFENLPTTALDMGNDPDICPFFSYV
VITGISAQPSPIKLQESLQALKQKPINAIVDITNYIMLSLGQPLHAYDASHVALDSL RVEKLSTPESLTLLNGET
VLLPSGVPVVRDDHSLGLGGVMGAKAPSFQETTTTTVIKAAAYFLPEALRASQKLLPIPSSESAYRFTRGIDPQN
VVPALQAAIHYLEIFPEATISPIYSSGEICRELKEVALRPKTLQRILGKSFSIEILSQKLQSLGFSTTPQETSLLVK
VPSYRHDINEEIDLVEEICRTESWNIETQNPVSCYTPYIKLKRETAGFLANAGLQEFTPDLLDPETVALTRKE
KEEISLQGSKHTTVLRSSLLPGLLKSAATNLNRQAPSVQAFEIGTVYAKHGEQYQETQTLAILLTEDGESRSW
LPKPSLSFYSLKGWVERLLYHHHLSIDALTLESSALCEFHPYQQGV LRIHKQSFATLGQVHPELAKKAQIKHP
VFFAELNLDLLCKMLKKTTLKYKPYAIYPSSFRDLTLTPEDIPANLLRQKLLHEGSKWLESVTIISYQDKSL
ETRKNVSLRLVFQDYERTLSNQDIEEEYCRLVALLNELLTDTKGTINS

>core/66/2/Org2_Gene255

MLIMRNKVILQISILALIQTPLTLFSTEKVKEGHVVVDSITIITEGENASNKHPLPKLKTRSGALFSQLDFDEDLR
ILAEKYDSVEPKVEFSEGKTNIALHLIAKPSIRNIHISGNQVPEHKILKTLQIYRNDL FEREKFLKGLDDLRTY
YLKRGYFASSVDYSLEHNQEKGHIDVLIKINEGPCGKIKQLTFSGISRSEKSDIQEFIQTKQHSTTTSWFTGAGL
YHPDIVEQDSLAITNYLHNNGYADAIVNSHYDLDDKGNILLYMDIDRGSRYTLGHVHIQGFEVLPKR LIEKQS
QVGPNDL YCPDKIWDGAHKIKQTYAKYGYINTNV DVLFI PHATRPIYDV TYEVSEGSPYKVGLIKITGNTHTK
SDVILHETSLFPGDTFNRLKLEDTEQRLRNTGYFQSVSVYTVRSQ L DPMGNADQYRDIFVEVKETTTGNLGLF

LGFSsLDNLFGGIELSESNFDFLGARNIFSKGFRCLRGGEHLFLKANFGDKVTDYTLKWTKPHFLNTPWILGI
ELDKSINRALSKDYAVQTYGGNVSTTYILNEHLKYGLFYRGSQTSLHEKRRKFLGPNIDSNKGFVSAAGVNL
NYDSVDSRPTPTTGIRGGVTFEVSGLGTYHFTKLSLNSSIYRKLTRKGILKIKGEAQFIKPYSNNTAEQVPVSE
RFFLGGETTVRGYKSFIIGPKYSATEPQGGLSSLLISEEFQYPLIRQPNISAFVFLDSGFVGLQEYKISLKDLRSS
AGFGLRFDVMNNVPVMLGFGWPFPRPTETLNGEKIDVSQRFFFFALGGMF

>core/67/2/Org2_Gene30

MLLLISGALFLTLGIPGLTAGVSFGLGIGLSALGGVLVVSGLLCLLVKREVSKVCPEEIPAVQPEETPEGVPVTP
FEKPALDEAQKEQKTQKILDQLPQELDQLDRYIQEAFACLGPLKDLKYEDQGFLQDVKEEFQVDFVQKDMI
AEFVELQQILCQEGRLLEFVINQTRYIGRDLFKREDSLYKLWEWLGYLPSGDVRGERLKKSAREVVDRFMRT
TCNIRKIAMTFDRHVYSVAKTAFEKAFGALETVCYYESMRESYREAFCEYEKAKLLGDEEKSAHAEQRFQDIK
NRWEDVKDAFFWVKEDGKIEIDDAIGNSCKWSERYEEHRITRARWYKVAEHQLFNATMRVKDSLREHNEA
RVAFEKERSKENQRQVQKKKEKRLRDLKELHDQELPRAQERLRELQALYPEIAVSVVEARREVASDLEKAH
ESIDKHYSQSCVREQELY

>core/68/2/Org2_Gene402

MASGIGGSSGLGKIPPKDNGDRSRSPSPKGELGSHEISLPPQEHGEEGASGSSSHIHSSSSFLPEDQESQSSSSAAS
SPGFFSRVRSGVDRALKSFGNFFSAESTSQARETRQAFVRLSKTITADERRDVSSSAAATEARVAEDASVSG
ENPSQGVPETSSGPEPQRLFSLSVKKQSGLGRLVQTVRDRIVLPSGAPPTDSEPLSLYELNLRSLRQELSDI
QSNDQLTPEEKAEATVTIQQLIQITEFQCGYMEATQSSVSLAEARFKGVETSDEINSLCSELTDPQLQELMSDG
DSLQNLLDETADDLEAALSHTRLFSFLDDNPTPIDNNPTLISQEEPIYEEIGGAADPQRTRENWSTRLWNQIRE
ALVSLGMLSILGSILHRLRIARHAAAEAVGRCCTCRGEECTSSSEEDSMSVSGSPSEIDETERTGSPHDVPRRN
GSPREDSPLMNALVGWAHKGHGAKTKESSSESSTPEISISAPIVRGWSQDSSVSFIVMEDDHIFYDVPRRKDGIYD
VPSSPRWSPARELEEDVFGDYEVPITSAEPSKDKNIYMTPLATPAIYDLPSRPGSSGSSSRSPSSDRVRSSSPNR
RGVPLPPVPSPAMSEEGSIYEDMSGASGAGESDYEDMSRSPSPRGDLDEPIYANTPEDNPFTQRNIDRILQERS
GGASASPVEPIYDEIPWIHGRPPATLPRPENTLTNVSLRVSPGFGPEVRAALLSESVSAMVMAESIVPPTTEPGD
GESEYLEPLGGLVATTKILLQKGWPRGESNA

>core/69/2/Org2_Gene990

MLLLISGALFLTLGIPGLSAAISFGLGIGLSALGGVLMISGLLCLLVKREIPTVRPEEIPGVSLAPSEEPALQAA
QKTLAQLPKELDQLDTDIQEVFACLRKLDKSKYESRSFLNDAKKELRVFDFVVEDTLSEIFELRQIVAQEGWD
LNFLINGGRSLMMTAESESLDLFHVSKRLGYLPSGDVRGEGLKKSACEIVARLMSLHCEIHKVAVAFDRNSY
AMAEKAFKALGALEESVYRSLTQSYRDKFLESERAKIPWNGHITWLRDDAKSGCAEKKLRDAEERWKKF
RKAVFWVEEDGGFDINNLLGDWGTVLDPYRQERMDEITFHELYEKTTFLLKRLHRKCALAKTTFEKKRSKKN
LQAVEEANARRLKYVRDWDYDQEFQKAGERLEKLHALYPEVSVSIRENKIQETRSLNEKAYEAIENYRCCVR
EQEDYWKEEEKREAEFRERGNKILSPEELESSLEQFDHGLKNFSEKLMELEGHILKLQKEATAEVENKILSDA
ESRLEIVFEDVKEMPCRIEEEIEKTLRMAELPLLPTKKAFAKACSQYNSCAEMLEKVKPYCKESLAYVTSKERL
VSLDEDLRRAYTECQKRFQGDSEVRACREQLRERIQEFETQGLDLVEKELLCVSSRLRNTECDCVSGV
KKEAPPGKKFYAQYYDEIYRVRVQSRWMTMSERLREGVQACNKMLKAGLSEEDKVLKEEEYWLYREERK
NKEKRLVGTKIVATQQRVAAFESIEVPEIPEAPEEKPSLLDKARSLFTREDHT

>core/70/2/Org2_Gene974

MLFSKNFSTDNGGAITAKTSLTGTMTSALFSENTSSKKGGAIQTSDALTITGNQGEVSFSDNTSSDSGAAIFT
EASVTISNNAKVSFIDNKVTGASSSTTGDMSSGAICAYKTSTDTKVTLTGNQMLLFSNNTSTTAGGAIYVKKL
ELASGGLTLFSRNSVNGGTAPKGGAIATEDSGELSLSADSGDIVFLGNTVTSTTPGTNRSSIDLGTSAKMTALR
SAAGRAIYFYDPITTSSTTVTDVLKVNETPADSALQYTGNIFTGEKLSETEAADSKNLTSKLLQPVTLSGGT
LSLKHGVTLQTQAFTQQADSRLEMDVGTTLPEADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLL
DPTGTFYENHSLRNPQSYDILELKASGTVTSTAVTPDPIMGEKFHYGYQGTWGPIVWGTGASTTATFNWTKT
GYIPNPERIGSLVPNSLWNAFIDISSLHYLMETANEGLQGDRFWCAGLSNFFHKDSTKTRRGFRHLSGGYVI
GGNLHTCSDKILSAAFCQLFGRDRDYFVAKNQGTVYGGTLYYQHNETYISLPCKLRPCSLSYVPTEIPVLFSG
NLSYTHTDNDLTKTYTTYPTVKGSWGNDSFALEFGGRAPICLDESALFEQYMPFMKLQFVYAHQEGFKEQG
TEAREFGSSRLVNLALPIGIRFDKESDCQDATYNLTGTYVDLVRSNPDCTTTLRISGDSWKTFGTNLARQAL
VLRAGNHFCFNSNF EAFSQFSFELRGSSRNYNVDLGAKYQF

>core/71/2/Org2_Gene756

MTLQPSYINFTPNVTTALSGGKIDTSAIELSCSALFFQELQDKAQGLKHALGLVQELSAEALRPAQVQTSISYL
PTEESSRPGISAGIIDRTMPTFTDDEVKAILQNPNFETSKIFVEGLDKVFKSYLDSVTPPEGIDPSNPESAILNYIT
LLNNLKPKFAAGSTPTDADYNALYALPGDFVKEIEALKAADAPPKSKVHAFWQEIMTIYNNMQVLSYPVTD
YLVNQIADLSLNITAAQEVQQYLKNFYSLKIDILNPGWTDPAATHYPADA EYNARDAGVIQSLNLSGNYRQ
LTENMLPNTDTSLPQEIIAQIRSFQNGVNGTHIASNTLLPTTMRDLTLLGVIYTYQCCATIFGMSYGTSTPAKQN
YIDAINQEKS YWQARANGFDVTS DQVFDQFATNIQSGTSYRGIDLFKNNKVNEINPIFLSQAASFLRYPYNLM
SRSMYQTIEDAANRSITALDGLISGWSTQIATFQTQKNSLDPSLLKYFDTMKANKESFVTTAPLQMVYSSLML
DKYLPQQNVIASLGIQMTYSNKA AKYLNELIKEITTFQSADIYYSLSIYLKQMNLQAVADPIGKAVGVLNDE
KTRAMADITRCNKIKAAIDKMLVEIKADAELSKSQIRELVDLTNFKSQSDDLIRNLSCLLGFLSGLTLKAVN
DPNATYEAFTAEIFTEPFNNWKRQLATFESFVIQGGQNGITPGGQQQLLQAMESSQQDFSTFNQNQQLALQLE
SSAMQQEWTLVSAALALLNQMVSKIARRIKS

>core/75/2/Org2_Gene724

MVFFRNLLHLVALSGMLCCSSGVALTIAEKMASLEHSGRGADDYEGMASFNANMREYSLQLSKLYEEARK
LRASGTEDEALWKDLIRRIGEVRGYLREIEELWAAEIREKGGNLEDYALWNHPETTIYNLVTDYGTEDSIYLI
PQEIGAIIATLSKFVVPKESFEDCLTQILSRLGIGVRQVNSWIKELYMMRKEGCSVAGVFSSRKDLEALPETA
YIGFVLNSNVDAHTNQHVLLKKFINPETTHVDVIAGRVWIFGSAGEVGELLKIYNFVQSESIRQEYRVIPLTKID
PGEMISILNAAFREDLTKDVSEESLGLRVVPLQYQGRSLFLSGTAALVQQALTLIRELEEGIENPTDKTVFWYN
VKHSDPQELAALLSQVHDFVSGENKASVGAADGCGSQLNASIQIDTTVSSSAKDGSVKYGNFIADSKTGTLI
MVVEKEVLPRIQMLLKKLDVPKMMVRIEVLLFERKLAHEQKSGLNLLRLGEEVCKKGCSPSVSWAGGTGILE
FLFKGSTGSSIVPGYDLAYQFLMAQEDVRINASPSVVTMNQTPARIAVVDEMSIAVSSDKDKAQYNRAQYGI
MIKMLPVINVGEEDGKSYITLETDITFDTTGKNHDDRDPVTRRNITNKVRIADGETVIIGGLRCKQMSDSHDGI
PFLGDIPGIGKLFMSSTSDSLTEMFVFITPKILENPVEQQERKEEALLSSRPGEREEYYQALAASEAAARAAH
KKLEMFPASGVSLSQVERQEYDGC

>core/76/2/Org2_Gene821

MGYIESSTFRLYAEVIVGSNINKVLDYGVPENLEHITKGTAVTISLRGGKKVGVYQIKTTTQCKKILPILGLSD
SEIVLPQDLLDLFWISQYYFAPLGKTLKLFLPAISSNVIQPKQHVRVVLKQSKAKTKEILAKLEVLHPSQGAV
LKILLQHASPPGLSSLMETAKVSQSPIHSLEKLGILDIVDAAQLELQEDLLTFFPPAPKDLHPEQQSAIDKIFSSL
KTSQFHHTLLFGITGSGKTEIYLRATSEALKQGKSTILLVPEIALTVQTVSLFKARFGKDVGVLLHHKLSDSK
RTWRQASEGSLRILIGPRSAFCPMKNLGLIIVDEEHPAYKQTESPPCYHARDVAVMRGKLAHATVVLGSA
TPSLESYTNALSGKYVLSRLSSRAAAHAPAKISLINMNLEREKSKTKILFSQPVLKKIAERLEVGEQVLIFNRR
GYHTNVSCTVCKHTLKCPCPHCDMVLTFHKYANVLLCHLCNSSPKDLPQSCPKCLGTMTLQYRGSGETEKIEKIL
QQIFPQIRTIRIDSDDTKFKGSHETLLRQFATGKADVLTQMIAGMNFSAVTLAVILNGDSGLYIPDFRASEQ
VFQLITQVAGRSGRSHLPGEILIQSFLPDHPTIHSAMRQDYSAFYSQEITGRELCEYPPFIRLIRCIFMGKCPKQT
WEEAHRVHNILKEQLESTNPLMPVTPCGHFKIKDTFRYQFLIKSAYVIPVNKKLHHALMLAKLSPKVKFMID
VDPMTTFF

>core/77/2/Org2_Gene98

MEKICGYLEQILVENKDSGDITAYIKIPNKTTPILIKGKLPQPLELGSPIQIYGVWSHSPSNTKYFQIHSYDSPLL
YEYRGVFHYLTSLIKGIGPKIAEKIIEKFQEKTCYVLDITPERLSEVSGISETRCVSICKQLCEQKILRKTLFLQ
EYNIPIHYGVRIFKKYQEKSIKICEDPFLAREMEGIGFKTADFIAMKLGVPNRNSESRLCAGIQHSLEELQEEG
HTCYPIELLIDVVAKLLNQDVFDTPITLEEIDTQILNMQKRKLLHIQDISGTLHVWTRYLHLAEKTIVSDLKRIL
FSSRRIRSIDGEKAIAWVEENLSIDLAEQQREAIKACFSEKLLIITGGPGTGKSTITQAILKIFEQVTHKIILAAPT
GKAAKRMTEITQKHSVTIHALLQYDFKTKSFRKNHDNPIDCDLIIVDESGMMDTHLLHHFLKALPDYTTLVFI
GDIHQLPVSGPGNLIKDLITSNKMTVIRLNKIFRQVHDSGIVTNAHRVNEGELPILYSETGRDRLFFQKDDQE
EALNHHIHLVTKFVPQKYHIYPQDIQVLAPMKGTLGIYNLNKALKHALNPKANLHGRFQSYAVGDKVMQI
RNNYNKEVFNGDIGYVSTINFEDKAVVVRMEGKHVGYSFSEDDLVLAYATSVHKKYQGSSEPCIIPIHTSHF
MMLYRNLLYTAITRGKKLVILVGTKKAIAIATRNNRVQHRCTGLAEVLKELDTKKNYADL

>core/78/2/Org2_Gene995

MLSFFYKHQKKFIGIVIAVVCVSGIGVGWGRFSRKGSAAESTSRRTVFTTASGKRYVEKDFMAMKKFFAHEAY
PFTGNPRAWNFINEGLLTDYFLTTRVGEKLFLLKVFYHPGEKIFSKEKAYQPYRRFDAPFISSEEVWKSSAPQLLE
ILKVFQQIENPISKEGFLARAKLFLEERRFPHYVLRQMLEYRRQMFALPPDEALSRGKDLRLFGYQTIQDWFG
DAYLSAAVELLIRFIDEQKKVLPRPSKQEARDDFYDKAKHAYTKISKNEFSLGFEEFVNSYFQFLEISESEFF
NMYRDILLCKRALLLLQGGVSFDFQPLTTFVQGKDSIQVEFFRLPKEYSFKTKQELKA FEVYLKLVSLPKSD
SLDVPNEILPIATIKAKEPRLVGRRFSIDYKRVALQDLAATVPMVEVLHWQQNSEHFQEILQQFPDVETCQSY
KDFQHLKPALRDKISLFTRKEILRARPERILQSLQQVPKQSQEVLLSAGKNSALPGISDGQQLAKVLLENEVLD
LYSQDAETYYTIIVNSSFEKEEVLPYREVLKRD LASQLLTSHGHLVDMERLESALRTRYPGEEGASLWQRR
WKVVENHRLGRHLEGSFSWSLDRSLKTFSRGDKELPQEFDRIFSMKVG DYSSVFMSPNEGPCYYQCLSHLLY
DRPASVDKLFLAKSQLDEELLGSYMERFIEQGVVR

>core/79/2/Org2_Gene655

MDYLEKLQVLIIEGQSANFLSLWEEYCFNDVVRGRELVEILEKVKSSSLASLFGKIVDTVVPPLWEKIPEGKDK
DRVLQLILDQLTSNSQMFFDIATEYVNKKYSGEENFNEALRVVGLRDGRDFQFSLSRFDLFMHMHKGNFVFH
QGGWGVGEVMGVSFLQKQVLIEFEGIMSAKDISFETA FKSLTPLSGDHFLSRRFGDPDGFEAFAKENPIEVVEI
LLRDLGPKTAKEIKDELVDLVIPEADWNRWWQSAKTKIKKGTRIISPDNPKEPYVLS DAGCSHMGQLERKLG

LSLNSAEKISLIYHFIRDLHSELKNIEIRKSLVKALQDL DVEEGNKS LILQRELL LSEYLG IKDASIDKEYITS LSE
DDTSRLLENMPIVALQKSFLSLVRKYSSFWQQVFMQILLYTTSPTMRDFVYKTIKNDPSSVEVLKKRLLDSA
HQPMMFPELVFWFFLKLGNHEDGLFDPEDKEVLRFLFLESALNFMYQVASTPHKELGKKLHHYLVGQRYLAVR
QMIEGASLPFLKELLLLSTKCPQFSSSDLNVLQSLAEVVQPTLKKHKSNVEEENVLWSTSESFSRMKAKLQSL
VGKEMVDNAKEIEDARSLGDLRENSEYKFALEKRARLQEEIRVLSEEINRARILTKDLVFTDKVGVGCKVTL
KGDAGEVVEYITILGPWDADPDSCILSLQSKLAQNM LGKKLNDVVILQGKEYKISR IQSIWEEHGA

>core/80/2/Org2_Gene405

MVDKLIHPWDLDLLVSGRQKDPHKLLGILASEDSSDHIVIFRPGAHTVAIELLGELHHAVAYRSGLFFLSVPK
GIGHGDYRVYHQNGLLAHPYAFPPLWGEIDSFLFHRGTHYRIYERMGAIPMEVQGSGVLFVLWAPHAQR
VSVVGDFNFHGLVNPLRKISDQGIWELFVPGLGEGIRYKWEIVTQSGNVIVKTDOPYGKSFDPPPQGTARVA
DSESYSWSDHRWMERRSKQSEGPVTIYEVHLGSWQWQEGRPLSYSEMAHRLASYCKEMHYTHVELLPITEH
PLNESWGYQVTGYAPTSRYGTLQEFQYFVDYLHKENIGIILDWVPGHFPVDAFALASFDGEPLYEYTGHSQ
ALHPHWNTFTFDYSRHEVTN FLLGSALFWLDKMHIDGLRVD AVASMLYRDYGREDEGWTPNIYGGKENLE
SIEFLKHLNSVIHKEFSGLTFAEESTAFPGVTKDVDQGG LGFDYKWN LGWMHDTFH YFMKDPMYRKYHQ
KDLTFSLWYAFQESFILPLSHDEVVHGKGSLVNKLPGDTWTRFAQMRVLLSYQICLP GKLLFMGG EFGQY
GEWSPDRPLDWELLNHHYHKTLRNCVSALNALYIHQPYLWMQESSQECFHWVDFHDIENNVIAYYRFAGS
NRSSALLCVHHFSASTFPSYVLRCEGVKHCELLLNTDDESF GSGKGNRAPVVCQDQGVAWGLDIELPLAT
VIYLVTF

>core/81/2/Org2_Gene973

MNKFKTYLQTALIAFFSFPA LSGSFSSIQAE EITQQVNHPGAELLSEGSYIPGLQTFRLGIKITASKGSHIYWKN
PGEIGSPLKISWQLPKGFVVEEHWPTPKVFEEEGTTF FGYEDSALIVADVRAPEGYTPGQEVELRAQVEWLA
CGDSCLPGNVDLKLTLPYEEKEPSLYPDTHAEFTKTLHAQPRVLENDHSVQVAQGGKNEIILNISKKINATKA
WVNSEKADKLFAYAETSYSGGTGTAWRLKVKNLSGVQKNEKLHGILLADHTGRPVESLTIHSEVLGQTGS
AVAGLSQYITILIMAFLGGVLLNIMPCVLPLVTLKVYGLIKSAGEHRSSVIANGLWFTLGVVGC FWGLAGVAF
ILKVLGHNIGWGFQLQEPMFVATLIIVFFLFALSSLG LFMGTMFANLG GKLQSSEM KSSNKA VGAFFNGIL
ATLVTTTPCTGPFLGSVLGLVMSLSFLQQLLIFTAIGLGMASPYLVFSVFPKMLSVLPKPGGWMSTFKQLTGFM
LLVTVTWL VWIFGSETSTTSVVVLLGGLWLAGLGAWILGRWGTPVSPKKQRVCASLLFFAFLGGAISVSGLA
SHYFAEPQQT VSVNEDSLWQPF SLEKLAQLRAQGRPVFNFTAKWCLTCQMNKPVLYGDAVQKMFETHGI
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>core/82/2/Org2_Gene242

MIRSPLPFISSKRALNMLGLQDEFSCPEDVVDL FSEIELLAQQDEPSEGYLALSRSLMMTHNHPKVVKRVIF
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MHPQLKNRLGW EHFRI GAKQEEVSLVASASVYQAVGRSFIELYHKHLESLDACGMKCLALALDLSPNNAH
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AREILEPLVEVYLEDENFLLLLGKVYLFLFWKNKNVCLGKLARTYLEKATSLGCPEAYYTLGKFYAVIKDVN
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>core/83/2/Org2_Gene276

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>core/84/2/Org2_Gene519

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>core/85/2/Org2_Gene31

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>core/86/2/Org2_Gene939

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>core/88/2/Org2_Gene10

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>core/89/2/Org2_Gene889

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>core/90/2/Org2_Gene472

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IDTPGH
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SETV
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KYGV
PRIAF
VVKMD
RMDR
MGAD
YFAAV
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KLGAN
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NKIN
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KNKG
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YSGT
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RLLE
MH

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>core/92/2/Org2_Gene419

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KLEHFITLEIINDRLVVFLPILPGTICYEETIYGFLPLMSKSLTRPHLKIRKFLPLYQMVTDRPPVPEDHKILLIKT
EPLHIRTVFARVVQDLLPQGLRHTAADILEPTTQESGDIYEFYGSTSEPIERIPLEFFTLEPYKEHSFFFYRDMLQ
ETLESPQEVFRVFESIPEGEDQAAMFISKGSSELLELSQDSWIIPRISPSDERHAREIQKHIEDQPCFPFLKAMET
DHITSQGVLFSTRYFPSASLKGMFLSNYSRYYLQHIYFQIPSPTSGEFFSNRDRSFLDLFYFAGISVFWADLESKR
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>core/93/2/Org2_Gene884

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NNLVEVKRDRSYELFYMLDEQDKRFYNDALVQIHYKQNKLHETVNEGDP LTKTLLWNSEEVKNIASSLVIVN
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LFKAMDRVLEHESRPYDPMILGILPSLEGTLKLHGKSIDIIRSPSPVTQSSILYANCNEEFLGFLNAKAHRSEVT
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>core/94/2/Org2_Gene705

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GSVAVKWVNGKVSELPMPLD TLDVSAVASADGRVIGGNRNINLGASVAVKWEDDVITQLPSLPDAMNAC
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>core/95/2/Org2_Gene22

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GNYTSLTETFSHAVDQARQHSVPALILIDVRLSSHSNSDNQEKYRSALDLKLSMDKDPLILLEKEAINVFGLS
PFEIEEIKAEAEQEEVRKSCEIAEALPFPSKGSTSHFVSPYTETLIDYENSESAQNLRNSEPKVMRDAISEALVEE
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>core/96/2/Org2_Gene430

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>core/98/2/Org2_Gene793

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NKLIQVLVQHIPPYLIGGSADLSSSDGTWIANEKVIHTYDFSGRNIKYGVREFGMATIMNGLAYSQVFRPFGGT
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LKHTGPTVIVLSRQALPTLPAHRPFKDGIGRGAYIVLKEGKPDYTLFATGSEVSLALSVAKELEHLDKQV
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>core/99/2/Org2_Gene332

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>core/100/2/Org2_Gene119

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>core/101/2/Org2_Gene68

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>core/102/2/Org2_Gene429

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YFNDSQRASTKDAGRIAGLDVKRIIPEPTAAALAYGIDKVGDKKIAVFDLGGGTDFDISILEIGDGVFEVLSTNG
DTLLGGDDFDEVIKWMIEEFKKQEGIDLSKDNMALQRLKDAAEKAKIELSGVSSTEINQPFITMDAQGPXHL
ALTLTRAQFEKLAASLIERTKSPCIKALSDAKLSAKDIDDVLLVGGMSRMPAVQETVKELFGKEPNKGVNPD
EVVAIGAAIQGGVLGGEVKDVLILLDVIPLSLGIETLGGVMTTLVERNTTIPTQKKQIFSTAADNQPATVIVVLQ
GERPMAKDNKEIGRFDLTDIPPAPRGHPQIEVSFDIDANGIFHVSAKDVASGKEQKIRIEASSGLQEDEIQRMV
RDAEINKEEDKKRREASDAKNEADSMIFRAEKAIDYKEQIPETLVKEIEERIENVRNALKDDAPIEKIKEVTE
DLSKHMQKIGESMQSQSASAAASSAANAKGGPNINTEDLKKHSFSTKPPSNNGSSEDHIEEADVEIIDNDDK

>core/103/2/Org2_Gene354

MKLLLKAVLRHKNHLVILGCSLLAILGLTFSSQMEIFSLGMIKTGPD AFLFGRKESGKLVKVSELSQKDILE
NWQAISKDSETLTVSDATTYIAEHGKSTASLTSKLSKFVRNYIDVSRFRGLAIFLICVAIFKAVTLFFQRFLGQV
VAIRVSRDLRQDYFKALQQLPMTFFHDHDIGNLSNRVMTDSASIALAVNSLMINYIQAPITFILTLGVCLSIW
KFSILICVAFPIFILPIVVIARKIKNLAKRIQKSQDSFSSVLYDFLAGVMTVKVFRTEKFAFTKYCEHNNKISALE
EKSAAYGLLPRPLLHTIASLFFAFVVVIGIYKFAIPPEELIVFCGLLYLIYDPIKKFGDENTSIMRGCAAERFYE
VLNHPDLHSQKEREIEFLGLSNTITFENVSFQYQEDKHILKNLSFTLHKGEALGIVGPTGSGKTTLVKLLPRLY
EVSQGGKILIDSLPITEYNKGSLRNHIACVLQNPFLFYDTVWNNLTCGKDMEEEA VLEALKRAYADEFILKLPK
GVH SVLEESGKNLSGGQQQLAIARALLKNASILILDEATSALDAISENYIKNIIGELKGQCTQIIAHKLTTLEH
VDRVLYIENGQKIAEGTKEELLQTCPEFLKMWELSGTKEYNRVFPDHKLVANPTDMAITT

>core/104/2/Org2_Gene771

MFSRLFFTSFSAEVVNTFFESGMSEDTSPLLSKQNRKLSHNLPLKSAYLSLGTLYLIALLSFWLHAKNLSNLFVV
FTFFLAGTPALIKSLDNICQKVVNIDILMTSAAFGSIFIGGALEGALLVLFAISEALGQMVSGKAKSTLVSLKQ
LAPTTGWL VLEDGNLQKVAINKIEVGNILRIKSGEVVPLDGEILHGSSSINLMHLTGEKVPK SCHPGSIVPAGA
HNMEGSFDLRVLRGTSDSTIAHIINLVIQAQNSKPRLQQRLDKYSSVYALSIFAACGIALLVPLFTSIPLGPQS
AFYRALAFLIAASPCALIIAIIPIAYLSAINACAKHGVLLKGGVILDRLVSCNSVVM DKTGTLTGTGELTCIGCDYF
GSKNETFFPSVLAL EQSSSHPIAEAIVSYLMEQKVSSLPADRYLTVPGEGVRGYFNEQEAFVGRVETGLGKVP
SEYLEDIEQKIYQAKQHGEICSLAYVGN SFALFYFRDIPRPAKEIIQDLKDLGYPVSM LTGDHKVSAENTA EI
LGISEVFFDLTPEDKLAKIRELATQRQIMMVGDGINDAPALAQATVGIAMGEAGSATAIEAADIVLLHDSLSS
LPWIIQKAKQTKKVVSQNLALALAILLVSWPASLGIPLWLAVILHEGSTVIVGLNALRLLKS

>core/105/2/Org2_Gene710

MTFQLHAPFAPCGDQPEAIARLSAGVRNQVKSQVLLGTTGSGKTFTIANVVANVNLPTLVLAHNKTLAAQL
YQEFREFFPNNAVEYFISYYDYYQPEAYIARSDTYIEKSLLINDEIDKLRLSATRSILERRDTLIVSSVSCIYGIGS
PENYTSMALVLEV GKEYPRNILTAQLVKMHYQASPIQRS AFRERGSVIDIFPAYESE LALRLEFLNDTLTSIE
YSDPLTMIPKESVPSATLYPGSHYVIP EAIREQAIRTIQEELEERMAFFDDRPIEKDRIFHRTTHDIEMIKEIGFCK
GIENYSRHFTGAPPGAPPTCLLDYFPEDFLLIIDESHQTL PQIRAMYRGDQSRKQSLVEYGFRLPSAFDNRPLT
YEEAQKYFRKVIYVSATPGDTEVQESSGHIVQQIIRPTGIPDPMPEIRPATGQVDDLLEEIRLRLSQKHEKILVIS
ITKKLAEDMAGFLSELEIPAAYLHSGIETAERTQILTDLRSGVIDVLIGVNLLREGLDLPEVSLVAILDADKEGF
LRSTSSLIQFCGRAARNINGKVIFYADQKTRSIEETLRETE RRRQIQLDYNKEHNIVPKPIIKAIFANPILQTSKDS
ESPKESQRPLSKEDLEE QIKKYEALMQRAAKEFRFNEAAKYRDAMQACKEQLLYLF

>core/106/2/Org2_Gene506

MATPAQKSPTFQDPSFVRELGSNHPVFSPLTLEERGEMAIARVQQCGWNHTIVKVSLIILALLTILGGGLLVGL
LPAVPMFIGTGLIALGAVIFALALILCLYDSQGLPEELPPVPEPQQIQIEDLRNETREVLEGTLLLEVLLKDRDAK
DPAVPQVVVDCEKRLGMLDRKLRREEEILYRSTAHLKDEERYEFLLELLEMRSLVADRLEFNRRSYERFVQG
IMTVRSEEGEKEISRLQDLISLQQQTVQDLRSRIDDEQKRCWTALQRINQSQKDIQRAHDREASQRACEGTEM
DCAERQQLEKDLRRQLKSMQEWIEMRGTIHQEKA WRKQNAKLERLQEDLRLTGIAFDEQSLFYREYKEKY
LSQKLD MQKILQEVNAEKSEKACLES LVHDYEKQLEQKDANLKKAAAVWEEELGKQQQEDYEQTQEIRRL

STFILEYQDSLREA EKVEKDFQELQQRY SRLQEEKQVKEKILEESMNH FADLFEKAQKENMAYKKKLADLE
GAAAPTEIGEDDDWVL TDSASLSQKKIRELVEENQELLKALAFKSNELTQLVADAVEAEKEISKLREHIEEQK
EGLRALDKMHAQA IKDCEAAQRKCCDLESLLSPVREDAGMRFELEVELQRLQEEN AQLRAEVERLEQE QFG
G

>core/107/2/Org2_Gene359

MSYRK RSTLIVLGVFALYALLVLRYYKI QICEGDHWA AEALGQHEFCVRDPFRRGTFFANTTVRKGD KDLQ
QPF AVDITKFHLCADPLA IPECHRDEIIQGILQFIEGQTYDDL SLKLDKKSRYCKLYPLLDVSVHDRLSLWWK
GYATKHRLPTNALFFITDYQRSYPFGKLLGQVLHTLREIKDEKTGKAFPTGGMEAYFNHILEGDVGERKLLRS
PLNRLDTNRVIKLPKDGSDIYLTINPVIQTIAEEELERGVLEAKA QGGRLILMNSQTGEILALA QYPFFDPTNYK
EYFNNKERIEHTKVSFVSDVFEPGSIMKPLTV AIALQANEEASLKSQKKIFDPEEPIDVTRTLFPGRKGSPLKDI
SRNSQLNMYMAIQKSSNVYVAQLADRII QSLGVAWYQQKLLALGFGRKTGIELPSEASGLVPSPHRFHINGSL
EWSLSTPYSLAMGYNILATGIQMVQAYAILANGGYAVRPTLVKKIVSASGEEYHLPTKEKTRLFSEEITREVV
RAMRFTTLPGGSGFRASPKHHSSAGKTGTTEKMIHGKYDKRRHIASFIGFTPVESSEGNFPPLVMLVSI DDPEY
GLRADGTKNYMGGRCAAPIFSRVADRTL LYL GILPDKKLRNCDEEAAALKRLYEEWNRSPKQGGTR

>core/108/2/Org2_Gene643

MVNPIGPGPIDETERTPPADLSAQGLEASAANKS AEAQRIAGAEAKPKESKTDSVERWSILRS AVNALMSLAD
KLGIASSNSSSSTSRSADVDSTTATAPT PPPPTFDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNIKDTA
ATDEETAIAAEWETKNADAVKVGAQITELAKYASDNQAILDSL GKLT SFDLLQAALLQSVANNKAAELLK
EMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGN AIRDAYFAGQNASGAVENAKSNN SISNIDSAKAAIAT
AKTQIAEAQKKFPDSPILQEA EQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAE
NETASILMSGFRQMIHMFNTENPDSQAAQ QELAAQARA AKAAGDSDAAAALADAQKALEAALGKAGQQQ
GILNALGQIASAAVVSAGVPPAAASSIGSSVKQLYKTSKSTGSDYKTQISAGYDAYKSINDAYGRARNDATR
DVINNVESTPALTRSVPRARTEARGPEKTDQALARVISGNSRTLGDVYSQVSALQ SVMQIIQSNPQANNEEIRQ
KLTS AVTKPPQFGYPYVQLSNDSTQKFI AKLES LFAEGSRTAAEIKALS FETNSLFIQQVLVNIGSLYSGYLQ

>core/109/2/Org2_Gene996

MKKLVRLCVVLLSLLPNVLFSSDLLREEGIKKMMDKLIEYHVDAQEVSTDILSRSLSSYIQSFDPHKSYLSNQE
VAVFLQSPETKKRLLKNYKAGNFAIYRNINQLIHESILRARQWRNEWVKNPKELVLEASSYQISKQPMQWSK
SLDEVKQRQRALLSYLSHLAGASSSRYEGKEEQLAALCLRQIENHENVYLGINDHGVAMDRDEEAYQFHI
RVVKALAHSLDAHTAYFSKDEALAMRIQLEKGMCGIGVVLKEDIDGVVREIIPGGPAAKSGDLQLGDIIYR
VDGKDIEHLSFRGVLDCLRGHGSTVVLDIHRGESDHTIALRREKILLED RRV DVSYEPYGDGVIGKVTLHSF
YEGENQVSSEQDLRRAIQGLKEKNLLGLVLDIRENTGGFLSQA IKVSGLFMTNGVVVVSRYADGTMKCYRT
VSPKKFYDGPLAILVSKSSASAAEIVAQTLQDYGVALVVGDEQTYGKG TIQHQTITGDASQDDCFKVTVGKY
YSPSGKSTQLQGVKSDILIPSLYAEDRLGERFLEHPLPADCCDNVLHDPLTDLDTQTRPWFQKY YLPNLQKQE
TLWREMLPQLTKNSEQR LSENSNFQAFLSQIKSSEKTDLSYGSNDLQLEESINILKDMILLQQCRK

>core/110/2/Org2_Gene942

MTSSSCPLLDLILSPADLK KLSISQLPGLAE EIRYRIISVLSQTGGHLSSNLGIVELTIALHYVFSSPKDKFIFDVG
HQTYPHKLLTGRNNEGFDHIRNDNGLSGFTNP TESDHD LFFSGHAGTALS LALGMAQTTPLESRTHVIPILGD

AAFSCGLTLEALNNISTDLSKFVVILNDNNMSISKNVGAMSRIFSRWLHHPATNKLTKQVEKWLAKIPRYGD
SLAKHSRRLSQCCKNLCPTPLFEQFGLAYVGPIDGHNVKKLIPILQSVRNLPFIPILVHVCTTKGKGLDQAQN
NPAKYHGVNANFNKRESAKHLPAIKPKPSFPDIFGQTLCELGEVSSRLHVVTAMSIGSRLEGFKQKFFPERFFD
VGIAEGHAVTFSAGIAKAGNPVICSISTFLHRAIDNVFHDVCMQDLPVIFAIDRAGLAYGDGRSHHGIYDMS
FLRAMPQMIICQPRSQVVFQQLLYSSLHWSSPSAIRYPNIPAPHGDPLTGDPNFLRSPGNAETLSQGEDVLIHAI
GTLCTALSIAKHQLLAYGISATVVDPIFIKPFNDLFSLLMSHSHKVITIEEHSIRGGLASEFNNFVATFNFKVDI
LNFAIPDTFLSHGSKEALTKSIGLDESSMTNRILTHFNFRSKKQTVGDVRV

>core/111/2/Org2_Gene684

MTCISELNEAQRKAVTAPLNPVLVLGAGAGKTRVVITYRILHLINQGIAPREILAVTFTNKAARELKERIVNQ
CASTNEFDVPMVCTFHSLGVFILRRSINLLNRENNFTIYDQSDAEKLIKHALQQHNLKPNLASKIAHVSQAK
NRLLPEDLDPNDYIDPVVSIYQEYQKKLIEANALDFDILLFTVRLLRESPEAQELYNQLWKALLIDEYQDT
NHAQYTLMQLLSKQHRNVFAVGDPDQSIYSWRGANIHNLNFENDYPNAKVLCLEENYRSYGNILNAANALI
KNNASRLEKELRSVKGPGEKIRLFLGSTDREEADFAAEILQLHRVGNIKLRDICIFYRTNSQSRTFEDALLRR
RIPYEIIGGLSFYKRKEIQDILAFIRIFISKSDIVAFDRTVNLPKRGIGSTTIFALTQYAIAQGLPILKACQQALDT
KDVKLSKKQQEGLEQYLAFLPQIEHAYNTLSLRDFIESVVRITGYLEILKEDADTFKDRKSNLEELYHKALESE
QQNPKTHLELFLDDLALKGSDDDLNLTA DRVNLMTLHNGKGLEFRVSFLVGLLEEQLLPHANSLGGTYENIEE
ERRLCYVGITRAQDILLYLTAAQVRSWGTVRMMKPSRFLKEIPKDYMIQVR

>core/112/2/Org2_Gene85

MKQHYSLNKSRHILRSTYKLLKSKKLAHSPADKKQLQELLEQLEEAIFEHDQETASDLAQQALAFSNRYPNS
FGRKTYELIKALLFAGVVAFLVRQFWFELYEVPTGSMRPTILEQDRILVSKTTFGLHCPFAKKPLAFNPESVTR
GGLVVFTVGDLPDADTKYFGLIPGKKRYIKRCMGRPGDFLYFYGGKIYGLDDAGKRIEFPSVHGLENLYH
VPYISFDGTTSSHTGQKTIIDFKQFNQSYGRLIFPQTSMYGQFFDHKEWHQDEPNKLKDPHLSPVSYADLFG
MGNYAMVRILTEHQARTSHLLPNPGSPTKVYLEICHTANLSYPKPLLRHYEHQLSPAIQPMKTLLPLRKEHLH
LIRNNLTTSRFIVAQGCAYKYHQFKINTSGIAKAYAILLPKVPDGCYEYSKGEAYQIGFGEIRYKLKSSHPLTQ
LNDKQVIELFNCGINFSSIYNPNPLQAPLPNRYAFFNQGNLYIMDSPVFIKNDPTLQKFVTSETEKQEGSSET
QPPIAFVDKGLPPEDFKEFVEFIHNFQVPGKHVVLVLDNYPMSADSREFGVPMENLLGSPLCTFWPIGRM
GRLTGVSAPTTLSGYLVSGIALATGLSLIGYVYYQKRRRLFPKKEEKNHKK

>core/113/2/Org2_Gene702

MIPFTKTIGFRLWLACAVAIAPLGINIVWLNLDQYRTIVSAISTALKENAAFKANTLTQIVPLNVDVLSLFS
LDLDAGIPETPNVLLSNEMQKVFGGIYNEISLIKVFNGDKIVVASSIPEHLGENYNHKIDIPKNTPFLAALKQS
PKNQEVFSVMQANVFDAKTQELQGILYTTFAESLLKDLLINKQSYLTVKTAILSKYGVILKASDPALHLHTV
YPDMTKEKFCQVFLNDDPCPIDSELGPLTSLPDIGENFYSFKIKDTEIWGCIENVPSIDIAVLSYAKKEESFAPL
WRRARMYTAYFFCILLGSLIAFIVARRLSLPIRKLATAMIESRKNKNCLYTDDSLGFEINRLGHIFNAMVENLH
KQQHLAKTNFEMKENAQNALHLGEQAQQRLLPNTLPSYPHIELAKAYIPAITVGGDFFDVVVGEGSKARLF
LIVADASGKGVNACGYSLFLKNMLRTFLSRSSSLQQAQIETSRLFYNNNTKNSGMFVTL CVYCYHQTSTNTMEY
YSCGHPPACYLDPDGETSWLHFGMALGFLPEVANITSKLFHPKPGSLFVLYSDGITEAHNNNNNDMFGEERL
QAAIQGLTGKSAADAVHRLMLSVKTFVGNSHQHDDITLLILKVLES

>core/114/2/Org2_Gene715

MIQVTCNQKNEYEVLEGTAAELAKQLKNSHQFIGVLINERPRDLSTHLNEGDTLVFLTSEDPEGREIFLHTSA
HLLAQAVLRLWPDIAIPTIGPVIDHGFYDFANLSISESDFPLIEDTVKQIVDEKLAISRFTYGDKQQALAQFPQ
NPFKTELIRELPENEEISAYSQGEFFDLCRGPHLPSTAHVKAFAKVLRTSAAAYWRGDPSRESLVRIYGTSFPTSKE
LRAHLEQIEEAKKRDHRVLGAKLDLFSQQESSPGMPFFHPRGMIVWDALIRYWKQLHTAAGYKEILTPQLM
NRQLWEVSGHWDNYKANMYTLQIDDEDYAIKPMNCPGCMYYKTRLHSYKEFPLRVAEVGHVHRQEASG
ALSGLMRVRAFHQDDAHVFLTPEQVEEETLNILQLVSTLYGTFGLEYHLELSTRPEKDTIGDDSLWELATDAL
NRALVQSGTPFIVRPGEGAFYGPBKIDHVKDAIQRTWQCGTIQLDMFLPERFELEYTTAQGTKSVPMVLMHRL
FGSIRFLGILIENFKGRFPLWLSPEQVRIITVADRHIPRAKELEEAWKRLGLVVTLDDSSSESVSKKIRNAQNM
QVNYMITLGDHEINENVLAVRTRDNRVINDVSVERFLNTILEEKNSLSLTALL

>core/117/2/Org2_Gene700

MDENRKVIVVGGGLAGLSAAMQLANLGIIVELVSLTKVKRSHSVCAQGGINAALNLKPEEEDSPYVHAYDTI
KGGDFLADQPPVLEMCLAAPRIIKMLDNFGCPFNRGPSGNLDVRRFGGTYHRTVFCGASTGQQLMYTLDE
QVRRREHAGRVIKRENHEFVRLVTDHSGRACGIILMNLFNRLLEILRGDAVIIATGGPGVIFKMSTNSTFCTGA
ANGRLFLQGMAYANPEFIQIHPTAIPGRDKLRLISESVRGEGGRVWVPGDSSKRIVFPDGSERPCGETGAPWY
FLEDMYPAYGNLVSRDVGARAILRVCEAGLGIDGRMEAYLDVTHLPEKTRHKLEVVLDIYKKFTGEDPNTV
PMRIFPAVHYSMGGAWVDWPAADDPDRDSRFRQMTNIPGCFNCGESDFQYHGANRLGANSLLSCLFAGLVS
GDEASRFIEAFGASQATSSDFDRALQQEKEENARLLSASGKENIFVLHEEIAKIMVRNVTVKRNNRDLQETM
DKLKEFRERLKNVSVLDSSPFANKSFHFVRQMGPMLELALAITKGALLRNEFRGSHYKPEFPERDDEHWLKT
TVAVYAPEEPEISYLPVDTRHVAPTLRDYTKSSTGKIELTNIPDNIRLPI

>core/118/2/Org2_Gene291

MTIIFYFILAALALGILVLIHELGHLLVAKAVGMAVESFSIGFGPALFKKRIGGIEYRIGCIPFGGYVRIRGMERT
KEKGEKGKIDSVYDIPQGFFSKSPWKRLVLVAGPLANILLAVLAFSILYMNGGRSKNYSDCSKVVGWVHPV
LQAEGLLPGDEILTCNGKPYVGDKDMLTTSLLEGHLNLEIKRPGYLTVPKSKEFAIDVEFDPTKFGVPCSGASY
LLYSNQVPLTKNSPMENSELRPNDRFVWMDGTLLFSMAQISQILNESYAFVKVARNDKIFFSRQPRVLASVL
HYTPYLRNELIDTQYEAGLKGWSSLYTLVPYVINSYGYIEGELTAIDPESPLPQPQERLQLGDRILAIIDGTPVSG
SVDILRLVQNHRSIIVQQMSPQELEEVSNSRDADKRFIASYHSEDLLQILNHLGESHPVEVAGPYRLLDPVQPR
PWIDVYSSSESLDKQLEVAKKIKNKDKQRYLYLERLDAEKQKPSLGISLKDLDKVRYNPSPVVMVLSNITKESLITL
KALVTGHLSPQWLSGPVGIVQVLHTGWSVGFSEVLFWIGLISMNLAVLNLLPIPVLDGGYILLCLWEIVKRRR
LNMKIVERILVPFTLLIIFIFLTFQDLFRFFG

>core/119/2/Org2_Gene437

MRRSVCYVNPISARAGQISTWKFLYSLATPLPAGTKCKFDLAGSGKPTDWEAPATDLSQTRNVIYAEMPEGE
IIEATAIPVKDNPVPQFEFTLPYELQVGETLTIVMGASPNHPQVDDAGNGAQLFAQRRKPFYLYIDPTGEGNY
DEPDVFSMDIRGNVLKKIEIFTPSYVVKNKRFDITVRFEDEFGNLTNFSPEETRIELSYEHLRENLNWQLFIPET
GFVILPNLYFNEPGIYRIQLKNLSTQEIFISAPIKCFADSAPNLMWGLLHGSESRVDSEENIETCMRYFRDDRAL
NFYASSSFENQENLSPDIWKLINQTVSDFNEEDRFITLSGFQYSGEPHLEGVRHILHTKETKSHSKHKEYKHIPL
AKLYKSTVNHDNISIPSFTASKEHGFDFENFYPEFERVVEIYNWGSSETTAALNNPFPIQGKDSIEDPRGTVIE

GLKKNLRFGFVAGGLDDRGYKDYFDSPQVQYSPGLTAHCNKYTRESLVEALFARHCYATTGPRIVLSFNITS
APMGSELSTGSKPGLNVNRHISGHVAGTALLKTVEIIRNGEVLHTFFPDSNNLDYEYDDMVPLSSVTLKDPNG
KAPFVFFYYLRVTQADNAMA WSSPIWVDLN

>core/120/2/Org2_Gene118

MESEKDIGAKFLGDYRILYRKQSLWSEDLAEHRFIKKRYLIRLLL PDLGSSQPFMEAFHDVVVKLAKLNHP
GILSIENVSESEGRCLVTQE QDIPILSLTQYLKSIPRKLTELEIVDIVSQLASLLDYVHSEGLAQEEWNLD SVYI
HILNGVPKVILPDLGFASLIKERILDGFISDEENRESKIKERVLLHTSEGKQGREDTYAFGAITYYLLFGFLPQGI
FPMPSKVFSDFIYDWDFLISSCLSCFMEERAKELFPLIRKKT LGEELQNVVTNCIESSLREVDPDPLESSQNLPQA
VLKVGETKVSHQKESA EHLEFVLVEACSIDEAMDTAIESESSSGVEEEGYSLALQSLLVREP VVSRYVEAEK
EPPKPQILTEMVLIEGGEFSRGSVEGQRDEL PVHKVILHSFFLDVHPVTNEQFIRYLECCGSEQDKYYNELIRL
RDSRIQRRSGRLVIEPGYAKHPVVGVTWYGASGYAEWIGKRLPTEAEWEIAASGGVAALRYPCGEEIEKSRA
NFFTADTTTVM SYPPNPYGLYDMAGNVYEW CQDWYGYDFYEISAQEPESPQGPAGVYRVLRGGCWKSLK
DDLCAHRHRNNPGAVNSTYGFRC AKNIN

>core/121/2/Org2_Gene903

MKKGKLGAI VFGLLFTSSVAGFSKDLTKDNAYQDLNVIEHLISLKYAPLPWKELLFGWDLSQQTQQARLQLV
LEEKPTTNYCQKVLSNYVRSLNDYHAGITFYRTESAYIPYVLKLSEDGHVFVVDVQTSQGDIYLGDEILEVDG
MGIREAIESLRFGRGSATDYSAAVRSLTSRSAAF GDAVPSGIAMKLRRPSGLIRSTPVRWRYTPEHIGDFSLV
APLIPEHKPQLPTQSCVLF RSGVNSQSSSSSLFSSYMPYFWEELRVQNKQRFD SNHHIGSRNGFLPTFGPILW
EQDKGPYRSYIFKAKDSQGNPHRIGFLRISSYVWTDLEGLEEDHKDSPWELFGEIIDHLEKETDALIIDQTHNP
GGSVFYLYSLLSMLTDHPLDTPKHRMIFTQDEVSSALHWQDLLEDVFTDEQAVAVLGETMEGYCMDMHAV
ASLQNFSQSVLSSWVSGDINLSKPMPLLGFAQVRPHPKHQYTKPLFMLIDEDDFSCGDLAPAILKDN GRATLI
GKPTAGAGGFVFQVTFPNRSGIKGLSLTGSLAVRKDGEFIENLGVAPHIDLGFTSRDLQTSRFTDYVEAVKTIV
LTSLSENAKKSEEQTSPQETPEVIRVSYPTTTSAS

>core/122/2/Org2_Gene48

MTTPPPSRSSSPPPYDWIELQDLGNTNNN SSRATPPPPEVGGELPPYFSASN FVVIERGAPSLPSPQQLLSLPEYS
RQPPPGYFDE TASITSRTSEEMFGTLVSTLCCPAN SERDWEDHEVN CIYIASTSDTQLEAVQGGMHITE LRGEF
VRVLYETGHL YAFARENTCHSRLEVSH TVRAMTYFWDRFFSRHWNVGR RFLVFYQGNGGAYVQAALDSS
MHTQDIYVLGLSPTVYIRGN YHVQH YRVRGFWPSCLDSLAA CAENTSVLPYGESSDGIFYPSLFSHTFDNAIR
YGERCLLVCEGMGMLPETQQQTSPLTSLEGGHEVALVLNPQQNPEALS IASRLMHEERGGRLESNYMPGRS
SNPFMTSMYVLVRLNTLAQIYLMSPYYSFQSN DIVCLIFISSAAVETVSYIFLTVTDSTCGRRYL RVPRLVCTG
LRNLALPTTLELLILSYPR SVEGV PFNVRFILGYMCTTRVFFAWNLILHWPFRCLRHGIQLFVHRSIIGHTLG
ARITDLTLASMRYAIVFPSIVSSCLLTALAHANTNILALDPYRLIESGDLRRPAFNDD EMQQADNPWDAYSIGL
VINTCIYMLILFANLIFMVYSVRRYHRSRR

>core/123/2/Org2_Gene317

MTLITPAINSSRRKTHTVRIGNLYIGSDHSIKTQSM TTTLTDDIDSTVEQIYALAEHNCDIVRVTVQGIKEAQAC
EKIKERLIALGLNIPLVADIHFFPQAAMLVADFADKVRINPGNYIDKRNMFKGTKIYTEASYAQSLRL EEFKFA
PLVEKCKRLGKAMRIGVNHGSLSERIMQKYGDTIEGMVASAIEYIAVCEKLN YRDVVFSMKSSNP KIMVTAY

RQLAKDL DARGWLYPLHLGVTEAGMGVDGHIKSAVGIGTLLAEGLGDTIRCSLTGCPTTEIPVCD SLLRHTKI
YLDLPEKKNPFS LQHSNFVSAAEKPAKTTLWGDVYGVFLKLYPHHLTDFTPEELLEHLGVNPVTKEKAFTT
PEGVVVPPELKDAPITDVLREHFLVFHHHQVPCLYEHNEEIWDSPAVHQAPFVHFHASDPFIHTSRDFF EKQG
HQGKPTKL VFSRDFDNKEEA AISIATEFGALLLDGLGEAVVLDLPNLPLQDVLKIAFGTLQNAGVRLVKTEYI
SCPMCGRTLFDLEEVTTRIRKRTQHLPGLKIAIMGCIVNGPGEMADADFGFVGSKTGMIDLYVKHTCVKAHIP
MEDAEELIRLLQEHGVWKDPEETKLT V

>core/124/2/Org2_Gene535

MWTHPIAYDVIVVGAGHAGCEAA YCSAKMGVSVLMLTSNLDTI AKLSCNPAVGGIGKGHIVREIDALGGIM
AEVTDQSGIQFRILNQTKGPAVRAPRAQVDKQLYHIHMKRLLENTPGLHIMQATVESLLDKEGVISGVTTKE
GWMFSGKTVVLSSGTFMRGLIHIGDRNFSGGRLGDPSSQGLSEDLKKRGFPISRLKTGTPPRL LASSINFSCME
EQPGDLGVGFVHRTEPFQPPLPQLSCFITH TMEKTKAIISANLHRSALYGGCIEGVGPRYCPSIEDKIVKFSDKE
RHHVFLEPEGLHTQEIYANGLSTSM PFDVQYDMIRSVLGLENAIITRPAYAIEYDYIHGNVIHPTLESKLIEGLF
LCGQINGTTGYEEAAAQGLIAGINAVNKVFNRPPFIPSRQESYIGVMLDDLTTQILDEPYRMFTGRAEHRLLLL
QDNACARLSHYGYELGLLSEERYELVKKQNQLLEEEKVRLQKTFRQY GQSVVSLAKALSRPEVSYDMLREA
FPNDIRDLGAVLNASLEMEIKYSGYIDRQKILIQSLEKAESLLIPEDLDYKQITALSLEAQEKLAKFTPRTL GSA
SRISGIASADIQVLMIALKKHAHH

>core/125/2/Org2_Gene109

MTTELKTEALPTRTQVDPKHCWDTTLMYANREEWKKDFDL CSSGKDRSPIWPEFSPSHYQIDNPESLLELLS
KKFSVERKLDQLYIYAHLIHDQDITNPEGESDYQSIVYLYTLFSQEISWIQPALIALSEEKVAALLSSSVLAPYR
FYLEKIFRLSPHTGTANEEKILASSFAALNVS NKAFFSSLSDAEIPFGIAKDSNGEEHPLSHALASLYMQSPDQEL
RRTAYLAQFQRYDYRNTFANLLNGKVQAHLFEAKARNYPSCLEASLFQHNIPTTVYINLINETKKHTSLINR
YFNLKKEALNLKEHFHYDVYAPISQTT SKNYSYEEGVDLVCKSLLPLGTHYVEILRNGLLSNRWVDRYENKH
KRSGAYSSGCYDSAPYILLNYTNTLYDVS VIAHEAGHSMHSYFSREAPYHDAQYPLFLAEIASTFNEMLLM
EALSKSDQSKEDKIVIITKLTDTIFATLFRQTFFAAFEYEIHSAAEQGTPLTEEFLSATYGNLQKEFYGGVVTSD
SLSALEWARIPHFYNFYVYQYATGIIAALSFAEKILTQEPGALELYLKFLKSGRSDFPLNILKKSGLDMTTSA
PLDKAFAFITKKIDLLSSLLSED

>core/126/2/Org2_Gene663

MFRCILFGIFLLTCFSSGGVLYYLFCSHDFSIGPKEKSRSVWIEEEKEFTDSVLHHLPSQH QHLHILCFQGFLQ
KQKFSQA EKIFSKVYDEAQDGPFLFKEEILGSRLINSFFLEKTDVMETILCLLNQRCPNSPYH LFKALVCYK
QKLYREVIEQLAYWQEEKTRALAPLLNISIEQLLTDFLLDYISAHSLIEQKMFPEGRVILNRNINRLLKHECEW
NAKTYDRIAILLSRSYFLELVESKSADIYFDYYEMVLFYLKKIYILEQCPYAELLPEEELVSLIMEHVFILPKDK
LYPLIQLLEMWQKH YVHPNSSLVVQILVDRFSTHMEGAIRFCEALVSFSGLEELHQQIITTFEELLSNKVQQIK
TEEAKQCVAL LHILDPSISISEKLALSSDTLQNIVSGDDEQHTKL RNYLDLWEAIQSYDIDRQQLVHHLVYGA
KDLWKKGGNDEKALNLLQLVLRFTSYDIECESV VFLFIKQAYKQALSSHA IARLLKLEKFISEANIPSIVISEAE
KANFLADAEYLF AHEDYDKCYLYSMWLTKVAPSPQSYRLAGLCLMENKRYDEALEFLCMLSPNDSINDYK
TQKALAF CQKHQSKDRAAS

>core/127/2/Org2_Gene861

MCGIFGYLGNQDGVSVILEGLAKLEYRGYDSAGLAAVVEQELFIRKTVGRVQELSNLFQEREIPTASVIGHTR
WATHGVPTEINAHPHVDEGRSCAVVHNGIENFKELRRELTAQGIFASDSTDSEIIVQLFSLYYQESQDLVFSF
CQTLAQLRGSVACALIHKDHPTILCASQESPLILGLGKEETFIASDSRAFFKYTRHSQALASGEFAIVSQGKEP
EVYNLELKKIHKDVRQITCEDASDKSGYGYMLKEIYDQPEVLEGLIQKHMDEEGHILSEFLSDVPIKSFKEI
TIVACGSSYHAGYLAKYIIESLVSTPVHIEVASEFRYRRPYIGKDTLGILISQSGETADTLAALKELRRRNIAYL
LGICNPESAIALGVDHCLFLEAGVEIGVATTKAFTSQLLLLVLGLKLANVHGALTHAEQCSFGQGLQSLPD
LCQKLLANESLHWAQPYSYEDKFLFLGRRLMYPVVMEEAALKLKEIAYIEANAYPGGEMKHGPIALISKGTP
VIAFCGDDIVYEKMIGNMMEVKARHAHVIAIAPESREDIAAVSDQQIFVPDCHFLAAPVLYTIVGQVMAYAM
ALAKGMEIDCPRNLAKSVTVE

>core/128/2/Org2_Gene858

MIPSGLVYLLYPLGFLASLFFGSAFSIQWWLSKKRKEVYAPRSFWILSSIGATLMIVHGTIQSQFPVTVLHVINL
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LIQWFYIESNNTKDFPLLFWKIGLLGGLLALVYFIRIGDPINILCYGCGLFPSIANLRLFYKEQRSTPYLDTHCFL
SAGEASGDILGGKLIQSIKSLYPNIRFWGVGGPAMRQEGQLPILNMEEFQVSGFAEVLGSLFRLYRNYRKILKT
ILKHKPATLIFIDFPDFHLLIKKLRKHGYRGKIIHYVCPISIAWRPCKRKRILEQHLDMLLLILPFEEGLFKNTSL
ETVYLGHPLVEEISDYKEQASWKEKFLNSDRPIVAAFPGSRRGDISRNLRIQVQAFLNSSLSQTHQFVSSSSA
KYDEIIEDTLKAEGCQHSQIIPMNFRYELMRSCDCALAKCGTIVLETALNQTPTIVMCRLRPFDFTFLAKYIFKIL
LPAYSLPNIIMNSVIFPEFIGGKKDFHPEEIATALDLLNQHGSKEKQKEDCRKLCKVMTTGQIASEEFLKRIFDT
LPAV

>core/129/2/Org2_Gene701

MKHTFTKRVLFFFFLVIPIPLLLNLMVVGFFSFSAAKANLVQVLHTRATNLSIEFEKKLTIHKLFLDRLANTLA
LKSYASPSAEPYAQAYNEMMALSNITDFSLCLIDPFDGSVRTKNPGDPFIRYLKQHPKMKKLSAAVGKAFL
TIPGKPLLHYLILVEDVASWDSTTTSGLLVSFYPMFSLQKDLFQSLHITKGNICLVNKYGEVLFCAQDSESSFV
FSLDLPNLPQFQARSPSAIEIEKASGILGGENLITVSINKKRYLGLVLNKIPIQGTYTLSLVPVSDLIQSALKVPL
NICFFYVLAFLLMWWIFSKINTKLNKPLQELTFCMEAAWRGNHNVRFEPPQYGYEFNELGNIFNCTLLLLLNS
IEKADIDYHSGEKLQKELGILSSLQSALLSPDFPTFPKVTFSQHLRRRQLSGHFNGWTVQDGGDTLLGIIGLA
GDIGLPSYLYALSARSLFLAYASSDVSQKISKDTADSFSKTTEGNEAVVAMTFIKYVEKDRSLELLSLSEGAP
TMFLQRGESFVRLPLETHQALQPGDRLICLTGGEDILKYFSQLPIEELLKDPLNPLNTENLIDSLTMMLNNETE
HSADGTLTILSFS

>core/130/2/Org2_Gene837

MRIEDFSLKLIPSSPGVYLMKDVHDQVLYIGKAKNLKNRLASYFHEKGDSRERIPFLMKKTASIEITIVVSNETE
ALLENNLIKQHHPKYNVLLKDDKTFFCLAISLSHWPKEAIRTKAITSSQRQLIFGPYVSAEACHTLLEVISQ
WFPLRTCSDFEALRKRPCILYDMKRCLAPCVGYCTPEEYQGTLDKAILFLKGKIEEVVKDLEKVIQKASDNL
EFEQAANYRTLSLIKQAMAKQQVEKFHFQNI DALGLYRHKQRTILTLLTVRSGKLLGARHFSFFENAQEDQ
DLLSSFILQYYVSQPYIPKEILTLPLEFPTLSYVLNAESPRLRSPKTGYGKELLDLAYRNAKAYAATTLPSS
LPYQDFQNILRMSQYPYRIECYDNAHMQGAHATGVYIVFENNGFDPKQYRTFSIDSEKTQNDLALLEEVLLR
RFHSLTTALPDMIVVDGGKTHYNKTKKIIQTLNLTGIQVVIAKEKSNHSRGLNKEKIFCETFPPEGFSLPPTS
NL

LQFFQILRDEAHRFAISKHRKKRGKALFEQEKIPGIGEVKRKRLLQKFKSWKQVMLSSQEELEAIPGLTKKDIA
VLLARQKDFNKS

>core/131/2/Org2_Gene304

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YQLNLIDTPGHVDFSIEVSRSLSACEGALLIVDAAQGVQAQSLANVYLALERDLEIIPVLNKIDLPAADPVRIA
QQIEDYIGLDTTNIACSAKTGQGIPAILKAIIDLVPPPKAPAETELKALVFDSHYDPYVGIMVYVRIISGELKKG
DRITFMAAKGSSFEVLGIGAFLPKATFIEGSLRPGQVGFFIANLKKVKDKVIGDVTVTCKHPAKTPLEGFKEIN
PVVFAGIYPIDSSDFDTLKDALGRLQLNDSALTIEQESSHSLGFGFRCGFLGLLHLEIIFERIIREFDLDIIATAPS
VIYKVVLKNGKVLDIDNPSGYPDPAIEHVVEEPWVHVNIITPQEYLSNIMNLCCLKRGICVKTEMLDQHRLVL
AYELPLNEIVSDFNDKLKSVTKGYGSFDYRLGDYRKGSIIKLEVLNINEPIDAFSCLVHRDKAESRGRSICEKL
VDVIPQQLFKIPIQAAINKKVIARETIRALSKNVTAKCYGGDITRKRKLWEKQKKGKKRMKEFGKVSIPNTAFI
EVLKLD

>core/132/2/Org2_Gene1014

MVMVWSTNIKHEGLKSWIDEVAKLTTPKDIRLCDGSDTEYDELCTLMESTGTMIRLNPEFHPNCFLVRSSAD
DVARVEQFTFICTSTEAEAGPTNNWRDPQEMRRELHQLFRGCMQGRPLYIVPFCMGPLDSPFSIVGVELTDSP
YVVCMSKIMTRMGDDVLRSLGTSGKFLKCLHVSVGKPLSPGEADVSWPCNPKSMRIVHFQDDSSVMSFGSGY
GGNALLGKKCVALARLASYMAKSQGWLAEHMLIIGITNPEGKKKYFSASFPSACGKTNLAMLMPKLPGWKIE
CIGDDIAWIRPGRDGRLYAVNPEYGFFGVAPGTSERTNPNALATCRSNSIFTNVALTADGDVWWEGLTEQPP
EPLTDWLKGPWKPGGSPAHPNSRFTAPLRQCPSLDPEWNSPQGVPLDAIIFGGRRSEIPLVYEALSWEHGV
TIGAGMSSTTTAAIVGQLGKL RHDPFAMLPFCGYNMAYYFQHWLSFAENRSLKLPKIFGVNWFRKNNQGEF
LWPGFSENLRVLEWIFQRTDGLEDIAERTPIGYLPNIQKFNLNGLNLDLQTVQELFSVDAEGWLAEEVENIGEY
LKIFGSDCPQQITDELLRIKSELKEK

>core/133/2/Org2_Gene630

MAAYTEASILSLASLDHIRLRAGMYIGRLGNGSQKEDGIYTLFKEVVDNGIDEFIMGHGKSLKISASDKQISIQ
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SKQGSTKDPDGTFSFTPDPSIFPEFTFNHDFLKDKIRQYTYLHSGLEIRFNDEVFISHNGLKDLFDAEITEPLY
SPLFFQNEDLTFIFSHLEGNTERYFSFVNGQETLDGGTHLTAFKEAIVKGVNEFFGKTFVSNDIREGIVGCIAIKI
ASPIFESQTKNKLGNTOIRSSLIKDVKEAIVQALRKDKVAPELLLEKIKFNEKTRKNIQFIKQDLKSKQKKVHY
KIPKLRDCKFHYNDRSLYGEASSIFLTEGESASASILASRNPLTQAVFSLRGKPMNVFSLEETKMYKNDELFLY
ATALGITQNEIQHLRYNKVILATDADVDGMHIRNLLITFFLKTLLPLVENNHLEFILETPLFKVRNKTTLTYYS
EQEKMQUALQQFGKKDSSLEITRFKGLGEISPKEFAAFIGPEIRLTPVTITSLESISSILQFYMGKNTKERKQFIMD
NLITDF

>core/134/2/Org2_Gene36

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INLFTIRRTTQGLVQVLAHLPHPGDPMRVVVGCDTRHNSIEFAQETAKVLAGNGCEVFLFYQYPEPLALVSFT
VRYERAIGGVMITASHNPPNYNGYKVYMASGGQVLPPLDQEIVAACSAVNEILSVPSIDHPNIHLIGKEYEAL
YRDTLKQLQLYPEANRISGRSLSISYSPLHGTGISLVPHVLKDWGFLSVHLVEKQAIGDGDFTVQLPNPEDPE

ALTLGIEQMLANDDDDLFIATDPDADRVGVVCLEDGQPYRFNGNQMASLLADHILGAWSKTRHLGEHDKLV
KSLVTTEMLSAIAKHVHVDLINVGTGFKYIGEKIESWRNSTNKFVFGAEESYGCLYGTHVEDKDIIASALIA
EAALQQKLQGKTLCDALLSLYETYGYFANKTESVVFSAKTDEQEIRKKLSHLEEISSANFFSGKYQVEKFENY
KQGIGFNLLSKDSYALTLPKTSMCLYYFSGGGRVIIRPSGTEPKIKFYFEMSTHYPERVTDKEIQKQREAESFQ
HLDDFIFDFKEKFSNL

>core/135/2/Org2_Gene65

MVTVSEQTAQGHVIEAYGNLLRVRFDGYVRQGEVAYVNVNDNTWLKAEVIEVADQEVKVQVFEDTQGACR
GALVTFSGHLLEAELGPGLLQGIFDGLQNRLEVLAEDSSFLQRGKHVNAISDHNLWNYTPVASVGDTLRRGD
LLGTVPEGRFTHKIMVPFSCFQEVTLTWVISEGTYNHTVVAKARDAQGKECAFTMVQRWPIKQAFIEGEKI
PAHKIMDVGLRILDTQIPVLKGGTFCTPGPFGAGKTVLQHHLISKYAAVDIVILCACGERAGEVVEVLQEFPHL
IDPHTGKSLMHRTHICNTSSMPVAAARESSIYLGVTIAEYYRQMGLDILLADSTSRWAQALREISGRLEEIPGE
EAFPAYLSSRIAAFYERGGAITTKDGSEGSLTICGAVSPAGGNFEEPVTQSTLAVVGAFGLSKARADARRYP
SIDPLISWSKYLNQVGQILEEKVSGWGGA VKKAAQFLEKGSEIGKRMEVVGEEGVSMEDMEIYLKAELYDF
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RLLEKTMVQMA

>core/136/2/Org2_Gene325

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PLCQALLTVWEQFFSAPENQNREFLVIFYGDASPIYQALQTSRHSRIVVVGISPTVFIQGDVRVHNYRVSGD
FFSSLCDRGTRAENTTILPYSSGLEGVFLPSIRCPSFTWAVRFGEQCLVANRGEDVEDRGGLSQDAERSQLPHS
ERDLAVVIDSTDPSSMSRLVEWLNQGSPPSDMEINPYPQRCPDVALSALYASRVSGLAQEWILASVHEGLDL
QICYSILMHTTFAVRYFFLLFTNYPQSRERFRTARIVAQSLYLPSILVLVFD CGNVLRKLWMPQEILRAIFISA
STISGSIVFVECTRW MGRGLRHRVQQFVQQRVIGSGLPVGTVRASYRDRAGFIIGFLTQTVHGGLYLPVSIMVL
NQIAIQVPRILVRPNNTAVYDLHNKSAEENWSSGDVLAVGQTLNFILCAFVLVNLWFFVKSVLRHSRRRRR

>core/137/2/Org2_Gene900

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GATKFQLLIKLRIPHALPHIFSGLKIAIGSAGFAA IAGEWVASQSGLGILMLESRRNYEMELAFAGLATLSILTL
SLFQITLLIEKLIFSLFRVKRMSLKHKSVAKKALS V LALIPIMLIPWKGN SKSPDKKNLTSLTLLLDWTPNPNH
IPLYAGVAKGYFKQHGLDLQLQKNTDSSSAVPHVLFEQVDMALYHALGIMKTSIKGMPIQIVGRLIDSSLQGF
LYRSQDPIYKFEDLNGKVLGFCLNNSRDLNRLLET LNRNGVVPSEVKNVSSDLISPMLLNKIDFLYGA FYNIE
GVKLQTLGMPVKCFLSDTCDLPTGPQLIVFTKKG TKASEPEIVEAFQKALQESIIFSKDHPEDAFKLYAKETKS
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>core/138/2/Org2_Gene839

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SPDTIDRFHLGYGPEQSLFLQAMEERKISQEQLHTAGFFGNKWFLFARRIIFPVH DALGHTIGFSARKFLENSQ

GGKYVNTPETPIFKKSRILFGLNFSRRRIAKEKKVILVEGQADCLQMIDSGFNCTVAAQGTAFTEEHVKELSK
LGVLKVFLLFDSDEAGNKAALRVGDLQCQTAQMSVVFCKLPQGHDPDSFLMQRGSSGLIALLEQSQDYLTFLI
SEKMSSYPKFGPREKALLVEEAIKQIKHWGSPILVYEHLKQLASLMMVPEDMVLSLANPQVTAEPQNIPIKQK
VPKIHPIHVMETDILRCMLFCGSNTKILYTAQFYFVPEDFKHPECRKLFAFMISYYEKYRKNVPFDEACQVLS
DSQILQLLTKRRLNTEALDTIFVQSLQKMADRRWREQCKPLSLNQNIQDKKLEILEDYVQLRKDRTHITLLDPE
SELIP

>core/139/2/Org2_Gene404

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VALTVLAPGVPQAILLGIAISGVGIGGFSIMKSLVYMVRDYMSPRMQESSRIKSALAVGTGFTVMGLVMKVG
ANFVPGGYGGLVGS LGSSAYS RGSQTTLASF SHYIYTKFFRSEK VAKGEKLTEAETIKEAKKLHYITLSIATIG
VGLAVLGILLAIAGTVLLGGAPATIAIILAPPLISIGLTTVLQ TILHSSIGKWRAFLT TQEKKDLFVDTSLKDIRLE
KLPPSEVEESETSQSVIEVPDSEGIAETRISAEEDTRL SLTTRQKVIFALAT LLLLASIAAFIVTGFGGLTVMQVL
LVASVGSASVSLTPMVSSGFSYVAYQLKARLNISKLRWKEAKNKKRVRQFLIESGVIASDREFNQMWKTV
YKKQIQKTDAAIREEVNFEKGGEVNSALVGGILLGVGTGIMLLALVPAFAPIVPGILALGGSTLGIAGSILMR
KFVNWLYDELVKLYERRRRNRRELLYGPESKMRSIATDLVVEALAASHDHLFDLDGPVDFIDVDVDIDGAA

>core/140/2/Org2_Gene484

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ITVDCGITAGKEVSDITRQGIDVIITDHHMPTGKIPHC VATLNPKLRDHTYPNREL TGVGVAFKLARGVLNALI
SRNLVPKSQGS LKLLDLVTLGTITDVGVLLGENRVMVRYGIKEIARGARPGLNKL CALCGVEKSEVTSTDIV
LKIAPKLNSLGRLLDDPAKGVELLLTQDDERVDALIMELDNINRERQRIEAEVFQDVQEILNSNPEILKQAAIVL
SSTAWHARVIPIISARLAKTYNKPVVIIAIQRGIGKGSARTIGSFLLGV LKKCSSLLSYGGHDF AAGVIMKED
KVEDFKKKFVHLVNSSLKKGDTLPHLEIDAYADFDAIDYDLLASMELFEPFGKGNLMPIFYSKVRQVRYPKV
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>core/141/2/Org2_Gene281

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LVYTESPTLTTPNLGMYRVQRFNQNTMGLHFQIQKGGGMHLYEAEQKKQNL PVS VFLSGNPFLTLSA IAPLP
ENVSELLFATFLQGAKLLYKKTNDHPHPLLYDAEFILVGESPA GKRRPEGPFGDHFGYYS LQHD FPEFHCHKI
YHRKDAIYPATVVGKPYQEDFYIGNKLQEYLSPLFPLVMPGVRR LKSYGESGFHALTA AVVKERYWRESLTT
ALRILGEGQLSLTKFLMVTDQEVPLDRFSV VLETILERLQPDRDLIIFSETANDTL DYTGPSLNKGSKGIFMGIG
KAIRDLP HGYQGGKI HGVQDIAPFCRGCLVLETSLEDRCIKSLLHHPDLKSWPLIILADNLRETIQSEKDFLWR
TFTRCAPANDLHALHSHFATHRPNYNFPFVIDALMKPSYPKEVEVDPSTKQKV SERWHAYFPNKETFYI

>core/142/2/Org2_Gene579

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LCRHQVMLACRNFMDAQGFTEIVTPVLGKSTPEGARDYL VPSRIYPGKFYALPQSPQLFKQLLMVGGLDRYF

QIATCFRDEDLRADRQPEFAQIDIEMSFGDTQDLLPIIEQLVATLFATQGIEIPLPLAKMTYQEAKDSYGTDKP
DLRFDLKLKDCRDYAKRSSFSIFLDQLAHGGTIKGFCVPGGATMSRKQLDGYTEFVKRYGAMGLVWIKNQE
GKVASNIAKFMDEEVFHELFAFYFDAKDQDILLLIAAPESVANQSLDHLRRLIAKERELYSDNQYNFVWITDFP
LFSLEDGKIVAEEHPFTAPLEEDIPLLETDPLAVRSSSYDLVLNGYEIASGSQRIHNPDLQSQIFTILKISPESIQE
KFGFFIKALSFGTPPHLGIALGLDRLVMVLTAESIREVIAFPKTQKASDLMMNAPSEIMSSQLKELSIKVAF

>core/143/2/Org2_Gene307

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SDLVSGRASYKAVKKQKNALIEEGDFFSAMEGVFRFVKGDAIISCILLVNVVSVTCLYYTSGYALEQMWFT
VLGDALVSQVPALLTSCAAATLISKIDKEESLLNYLFEYYKQLRQHFRVVSLIFSLCCIPSSPKFPIVLLASLL
WLAYRKEEPASEDSCIERAFSYVEGACPKESQFYQVYRAASEEVFEDLGVRLPVLTSLRIERPWLRFVFGQ
NVYLDGMTPEAVLPFLRNIAHEALNAEVLVQKYLEESERVFGIAVEDIVPKKISLSSLVVLRSLLVRERSLKL
PKILEAVAVYQNSGDSLEILAELKVRKSLGYWIGRSLWDQKQTLVITIDFHVEELINSSYSKSNPVMQENVIRR
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>core/144/2/Org2_Gene269

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GGLIVDIGMEAFLPGSQIDNKKIKNLDDYVGKVCEFKILKINVERRNIVSRRELLEAERISKKAELIEQISIGEY
RKGVVKNITDFGVFLDLGDIGLLHITDMTWKRIRHPSEMVELNQELEVIILSVDKEKGRVALGLKQKEHNP
WEDIEKKYPPGKRVLGKIVKLLPYGAFIEIEEGIEGLIHISEMSWVKNIWDPSEVVNKGDEVEAIVLSIQKDEGK
ISLGLKQTERNPWDNIEEKYPIGLHVNAEIKNLNTNYGAFVELEPGIEGLIHISDMSWIKKVSHPSSELFKKGNSV
EAVILSVDKESKKITLGVKQLSSNPWNEIEAMFPAGTVISGVVTKITAFGAFVELQNGIEGLIHVSELSDKPFA
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>core/145/2/Org2_Gene721

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NVPVRRGFQKSMQSDRLGIRKLIENRILSTANIGWSWISEGHHEIQIAKQQGFQERVAYVMGDHFMQDALT
DKEANGVRIVGVLGSPSFHRPTRQGQKIFINDRPIESLFISKKVGDAYALLPLHRYPVFVLKLYLPSSWCDFN
VHPQKIEARILKEELVGDCIKEAIVETLACPPGILCRTHQEIEESDSVPLPMFRMLETSDVQEEESVEFDQNLFA
YSSDEVSLKQEYTSRGPKSQMDWIYSSDVRFLLTSLGRVVLAEDLEGVHIIFTAAARKHLFFLSLMQENSRM
YQSQALLIPLRLQVTPEEAFFFSHHGRTLCDLGIEISQVGPCVFSIESTPTVIGEEELKEWLLLLAARGSTDINSE
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>core/146/2/Org2_Gene284

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EMQGFFLDASGMGGSSSDISQLSLEALKSSAFSGARSLSLSSSESSSVASFGSFQKAIEPMSEEKVNAWTVARL
GGEMVSSLLDPNVETSSLVRRAMATGNEG MIDLSDLGQEEVSTAMTSPRAVEGKVKVSSSDSPEANPTGIPN

SNTLERAEKEAEKQESREQLSEDQMMLARAMAGLLTGAAPQEVLSNSVWSGPSTVFPPPKFSGTLPTQRSGD
KSKHKSPGIEKSTNHTNFSPLREGTVKSAEVKSLPHPESMYRFPKDSIVSREEPEAVVKESTAFKNPENSSQNF
LPIAVESVFPKESGTGGALGSDAVSSSYHFLAQRGVSL LAPLPRATDDYKEKLEAHKGPGGPPDPLIYQYRNV
AVEPPIVLRSPQPFSGSSRLSVQGKPEAASVHDDGGGGNSGGFSGDQRRGSSGQKASRQEKKGKKLSTDI

>core/147/2/Org2_Gene517

MQKHPSFYQRFLSAYYKNLLASLSWKFFISVALIGIYAPLFASSKPLLVTWHGEIFFPLRLRYLFFPGYYTKPVD
LFFNVLMVTFPFFILSFKLTRGWLRRWLLGLCIISQCMIFAWAYSGKVQDPALAENLKKMRAEKVRENISKV
NSEMVMMLPKDTRTWEMERRY MSTYEQLGILIKAKYRKKQEASVKKYQVAFEEKRQSPMPTLRHLEMKNE
GICLKRLQQRVDKMQRPYEMAQQA WN RATDN YRPFLMALTRIEHELRLADYNNWGQPEDLCIAYANVEKR
AEPYKKSLLAIRQVLEDYAKLRS AISFIQDKRLWIEKESEDRLILNPFSSFWEDDAGGSREM NKYVPWWQ
LSRVTRKDLLAALVFGIRIALV VAGIGITIALAIGIMIGLVSGYFGGTVD MILSRFTEIWETMPVLFILMLVISIT
QQKSLLLNTVLLGCF SWTGFSRYVRIEVLKQRDRGYVLAATNLGYSHYYIMVHQILPNAIVPVISLVPFAMM
AMISCEAGLTFLGLGEESSASWGNLMREGVTGFPAESAVLWPPAILTMLLIAIALIGDGV RDALDPRLQDS

>core/148/2/Org2_Gene44

MTDFPTHFKGPKLNPIKVNPNFFERNPKVARVLQITAVVLGIIALLSGIVLIIGTPLGAPISMILGGCLLASGGAL
FVGGTIATILQARNSYKKA V NQKKLSEPLMERPEL KALDYS LDLKEVWDLHHSVVKHLKKLDLNL SKTQRE
VLNQIKIDDEGPSLGECAAMISENYDACLKMLAYREELLKEQTQYQETRFNQNLTHRNVLLSILSRITDNIS
KAGGVFSLKFSTLSSRMSRIHTTTT VILALSAVV SVMVVAALIPGGILALPILLAVAISAGVIVTGLSYLVRQIL
SNTKRNRQDFYKDFVKNVDIELLNQTVTLQRFLFEMLKGV LKEEEEVSLEGQDWYTQYITNAPIEKRLIEIR
VTYKEIDAQTKKMKTDLEFLENEVRSGRLSVASPEDPSETPIFTQGKEFAKLRRQTSQNISTIIY GPDNENIDPE
FSLPWMPKKEEIDHSLEPVTKLEPGSREELLLVEGVNPTLRELNMRIALLQQQLSSVRKWRHPRGEHYGNVI
YSDTELDRIQMLEGAFYNHLREAQEEITQSLGDLVDIQNRILGIIVEGDSDSRTEEEPQE

>core/149/2/Org2_Gene45

MANPTQSRPPSPEISIEEELQELAGSSNTETISNTPPPSCAATAEEVSLFIEGGRRNSEDEEGPLGSCEVYDVVC
ITNQGDPEVRDHEVRVMYINGSGRTQHEGILDAMNICDLRGEPVRFIHNSGYGLGSCFLGIRNRIPPRDNVISQ
AIQARWNEFFIFAENANRDYIVLFSGNGGLYLQVALDNSIYSHHILCVGIGSSYYIQGN YRVHNYRVTGDWTT
LLDRRGATAVNTTTLPYADSAEGLFLPSVRCPSYQWALRCGEQCLIMDNNQQVGFRPQDSSSEIALV VNLNQ
DHSTWTRLIEWIDRGDSQAVLELNPQPSHCRDIALTALYATTRISSLLQECLMISVTYAPEVFVTYAIVTGYSI
MTLRYFILLLTNRPGCRRHFRVLRLAALGLQSLGFLT VLLDHINVTRRVNRRPPLISVIFCTASFATGSFIYVDL
TRMFFTSLRSRLQLFVQRRLTGRGLPLRRVFNHLDSLRF SQNALITFHGGLFMPLIIGFFNQLVIQVPRVVIRP
NTTAVYDLNQTSQEAWDSGDVLAIGQTINFLLCMILLVINTFFFVRSVRRNLHRRPHR

>core/150/2/Org2_Gene668

MFMNTQNSQATEVSSEEEESQKKLEELVALAKEQG FITYEEINEILPMSFDTPEQIDQVLIFLTGMDIQVLNQID
VERQKEKKKEAKELEGLARRTEGTPDDPVRMYLKEMGTVPLL TREEVEISKRIEKAQVQIERIILRF RYSAK
EASIAHYLISGKERFDKIISEKEVEDKTHFLKLLPKLITLLKEEDTYLENLLLSLKQPDLSKQEAAKL NDSLEK
CRIRTQAYLR CFHCRHNVTEDFGEVVFKAYDSFLHLEQQINDLKVRAERNKF AA AKLAAAKRKLYKREVAA
GRTLEEFKKDVRMLQRWMDKSQEAKKEMVESNLRLVISIAKKYTNRGLSFLDLIQEGNMGLMKAVEKFEY

RRGYKFSTYATWWIRQAVTRAIADQARTIRIPVHMIETINKVLRGAKKLMMETGKEPTPEELAEELGLTPDR
VREIYKIAQHPISLQAEVGESESSFGDFLEDTAVESPAEATGYSMLKDKMKEVLKTLTDRERFVLIHRFGLL
DGKPKTLEEVGSAFNVTRERIRQIEAKALRKMHPISKQLRAFLDLLEEEKTGTSKVKSLKSK

>core/151/2/Org2_Gene27

MDTQSSTGNEEWRIAGTSIVSGMALGKVFFLGTSPLVRELTLPEEEVEHEIHRYYKALNRSKSDIVALEQEV
TGQQGLQEVSSILQAHLEIMKDPLLTEEVVNTIRKDRKNAEYVFSSVMGKIEESLTAVRGMPSVVDRVQDIH
DISNRVIGHLCCQHKSSLGESDQNLIIFSEELTPSEVASANSAYIRGFVSLVGAATSHTAIVSRAKSIPYLANISE
ELWNIAKRYNGKLVLIDGYRGELIFNPKPATLQSCYKKELSVVAHTSQRLVRKSLHPIVSSHAGSDKDVEDLL
ENFPQTSIGLFRSEFLAVILGRLPTLREQVDLYEKLARFPGDSPSVLRLFDGFKPCPGIKNKKERSIRWLLDY
SVILEDQLQAIKASLQGSIKVLIPGVSDVSEIIEVKKKWEITRTRFPKGHKVSWGTMIEFPSAVWMIEEILPEC
DFLSIGTNDLVQYTLGISRESALPKHLNVTLPNAVIRMIHHVLQAAKQNQVPVSICGEAAGQLSLTPLFIGLGV
QELSVAMPVINRLRNHIALLELNSCLEITEALLQAKTCSEVEELLNRNNKITS

>core/152/2/Org2_Gene1015

MVKVPWAFKNFIPKLYTSIKEGYSFNTFKKDFQAGITVGILAFPPAIAIAIGVGVSPIQGLLASIIGLLASAMG
GSNVLISGPSSAFISILYCLSAKYGAELFTVTLLAGVFLIAFGLTGLGTFIKYMPYPVVTGLTTGLAIIFSSQIK
DFLGLQMGANIPADFLPKWIAIYWDHLWTWDSKSAVGLFTLLIMIYFRNYKPRYPGVMIAIVTATTLVWLL
KIDIPTIGSRYGTLPTAIPLPKIPQLSITKILQLMPDALTIAVLSGLETLLSAVVADGMTGWRHQSNQQLVAQGV
ANIGTSLFSGIPVTGSLSRTAASIKSEATTPIAGIVHSIFICIFILLAPLTVKIPLTCLAAVLILIAWNMSEIHFIH
LFTAPKKDIVLLTVFILVTMTTITAAVQVGMMLAAFLFMKQMSDLSDVISTAKYFDKDSDFLSKAIEVPQNT
EIYEINGPFFFGIADRLKNLLNDIEKPPKIFILCMTRVPTIDASAMHALEEFFLECDRQGTLLLLAGVKKTPLAD
LKRYHLDDELIGVDHIFSNIKSALLFAQALTNLESKTSTRHLV

>core/153/2/Org2_Gene11

MGLFHLTLFGLLLCSLPISLVAKFPESVGHKILYISTQSTQQALATYLEALDAYGDHDFVLRKIGEDYLKQSI
HSSDPQTRKSTIIGAGLAGSSEALDVLSQAMETADPLQQLVLSAVSGHLGKTSDDLFFKALASPYPVIRLEA
AYRLANLKN TKVIDHLHSFIHKLPEEIQCLSAAIFLRLETEESDAYIRDLLAAKKSARSATALQIGEYQQKRFL
PTLRNLLTSASPQDQEAILYALGKLKDGQSYNYIKKQLQKPDVDVTLAAAQALIALGKEEDALPVIKKQALE
ERPRALYALRHLPSIGIPIALPIFLKTKNSEAKLNVALALLELGCDTPKLLEYITERLVQPHYNETLALSFSKG
RTLQNWKRVNIIVPQDPQERERLLSTTRGLEEQILTFLFRLPKEAYLPCIYKLLASQKTQLATTASFLSHTSHQ
EALDLLFQAAKLPGEPHIRAYADLAIYNLTKDPEKKRSLHDYAKKLIQETLLFVDTENQRPHPSMPYLRVQVT
PESRTKLMLDILETLATSKSSEDIRLLIQLMTEGDAKNFPVLAGLLIKIVE

>core/154/2/Org2_Gene426

MKTSQLFYKTSKNANKSAAVLSNELLEKAGYLFKVSKGVYTYTPLLWRVVSKMMNIIREELNAIGGQELLLP
LLHNAELWQHTGRWEAFTSEGLLYTLKDREGKSHCLAPTHEEVICSFVAQWLSSKRQLPLHLYQIATKFRDE
IRPRFGLIRSRELLMEDSYTFSDSPEQMNEQYEKLRSAYS KIFDRGLAYVIVTADGGKIGKGKSEEFQVLCSL
GEDTICVSGSYGANIEAAVSIPPQHAYDREFLPVEEVATPGITTIEALANFFSIPLHKILKTLVVKLSYSNEEKFI
AIGMRGDRQVNLVKVASKLNADDIALASDEEIERVLGTEKGFIGPLNCPIDFFADETTSPMTNFVCAGNAKD
KHVYVNVNWDRLDLPQYGDFLLAEEGDTCPENPGHPYRIYQGIEVAHIFNLGTRYTDSFEVNFQDEHGQTQQ

CWMGTYGIGVGRTLAACVEQLADDRGIVWPKALAPFSITIAFNNGDTSQELAETIYHELQSQGYEPLDDR
DERLGFKLKDSDLIGIPYKLILGKSYQSSGIFEIESRSGEKYTVSPEAFPTWCQNHLA

>core/155/2/Org2_Gene650

MTVSVKKKSFRALVTTHFLTIINDNLYKFLLAFFLLEGKTLTENAKILSCVSFFFALPFLLLAPLAGSLADRFQ
KRNIILATRFIEILCTILGTYFFFIQSVVGGYVVLILMACHTTIFGPAKLGILPEMLPSEQLSQANGIMTAATYTG
SILGSC LAPLLVDVTHRLGVNSYVWPTLMCVIVSIISTLISFCIRPSNVKNVKQKITLVSFKDLWKVLKDTRMI
HYLTVSIFLGSFFLLIGAYTQLEIIPFVEFTLKYPKHYGAYLFPIVALGVGTGSYITGKISGDKIKIGYVPLAAIGL
ALVFMGLYAFACSILFVLFFLLALGFLGGVYQVPLHAYVQYASPEHKRGQILAANNFLDFFGVLVAAGVIRV
LGSNLGLSPETSFFYIGWFLAVSIWTLWIWREHVYRLLLGIIILRRQLGYLYLKIHQSSSPKCYFVAVQSYREIR
RVLAALTKTVRSRVIILDQKLVPGWRAWLLSWCVPTVVS SVRDNDSEAQDAWAVLQANHLKTSKKKFPDV
SVVCLGLPKNVERFTSILQEQQIDLHPIQLVQKEGKKRVIYTLVFPHA

>core/156/2/Org2_Gene491

MSTLLSILSVICSQAIAKAFPNLEDWAPEITPSTKEHFGHYQCNDAMKLARVLKKAPRAIAEAIVAELPQEPFS
LIEIAGAGFINFTFSPVFLNQQLEHFKDALKLGFQVSQPKKIIIDFSSPNIAKDMHVGHLRSTIIGDSLARIFS YVG
HDVLRNLNHIGDWGTAFGMLITYLQENPCDYSLEDLTSLYKKAYVCFTNDEEFKKRSQQNVVALQAKDPQA
IAIWEKICETSEKAFQKIYDILDIVVEKRGESFYNPFLPEIIEDLEKKGLLTVSNDAKCVFHEAFSIPFMVQKSDG
GYN YATTDLAAMRYRIEEDHADKIIIVTDLGQSLHFQLLEATAIAAGYLQPGIFSHVGFGLVLDPQGKKLKTR
SGENVKLRELLDTAIEKAEEALREHRPELTDEAIQERAPVIGINAIKYSDLSSHRTSDYVFSFEKMLRFEGNTA
MFLLYAYVRIQGIKRRRLGISQLSLEGPEIQEPAEELLALTLLRFPEALESTIKELCPHFLT DYLYNLTHKFNGGF
RDSHIQDSPYAKSRLFLCALAEQVLATGMHLLGLKTLERL

>core/157/2/Org2_Gene478

MSKLIRRVTVLALTSMASCFASGGIEAAVAESLITKIVASAETKPAPVPM TAKKVRLVRRNKQPVEQKSRG
AFCDKEFYPCEEGRCQPVEAQQESC YGRLYSVKVNDDCNVEICQSVPEYATVGSPYP IELAIGKKDCVDVVI
TQQLPCEAEFVSSDPETTP TSDGKL VWKIDRLGAGDKCKITVWVKPLKEGCCFTAATVCACPELRSYTKCGQ
PAICIKQEGPDCACLRCPVCYKIEVVNTGSAIARNVTVDNPVPDGYSHASQRVLSFNLGDMRPGDKKVFTV
EFCPQRRGQITNVATVTYCGGHKCSANVTTVVNEPCVQVNISGADWSYVCKPVEYSISVSNPGDLVLHDVVI
QDTLPSGVTVLEAPGGEICCNKV VWRIKEMCPGETLQFKLVVKAQVPGRFTNQVAVTSESNCGTCTSCAETT
THWKGLAATHM CVLDTNDPICVGENTVYRICVTNRGSAEDTNVSLILKFSKELQPIASSGPTKGTISGNTVVF
DALPKLGSKESVEFSVTLKGIAPGDARGEAILSSDTLTSPVSDTENTHVY

>core/158/2/Org2_Gene129

MELLSLNKSYFEIQRRLRYRPEILTLLETIRSKHIQETSSPPSPPELQKHIPNLCRIPEVSIYTEQETSSKPLKIGVL
LSGGQAPGGHN VVIGLFDALRVFNPKTRLFGFIKGPLGLTRGLYKDLDISVIYDYNNMGGFDMLSSSREKIKT
EEQKKNILNTVKQLKLDGLLIIGGNSNTDTAMLA EYFLAHNCKT SVIGVPKTIDGDLKNCWIETSLGFHTSC
RTYSEMIGNLAKDALSAKKYHHFIRLMGQQASYTTLE CGLQTLPNIALISELIATR KISLKQLSEQLALGLVRR
YKSGKNYSTVLIPEGLIEHIFDTRKLIDELNVLLANGDSSIEKILSKLSPETLKT FHLFPKDIANQLLLARDSHGN
VRVSKIA TEELLAVMVKKEIEKIKPHMEFHSVSHFFGYEARAGFPSNFD CNYGIALGIISALFLVRQKTGYMIT

INNLAQSYTEWQGGATPLYKMMHLENRCGTETPVIKTDSVDPKSPAVQHLLQQSDSCLVEDLYRFPGPLQYF
GKEELIDQRPLTLLWENQTHSPFQALYSTSGKRSL

>core/159/2/Org2_Gene944

MSSPPQAVASLTERIKTLLESNFCQIIVKGELSNVSLQPSGHLVYFGIKDSQAFLNGAFFHFKSKYYDRKPKDGD
AVIIHGKLAVYAPRGQYQIVAHALVYAGEGDLQKFEETKRRLTAEGYFATEKKKPLPFAPQCIGVITSPTGA
VIQDILRVLSRRARNYKILVYPVTVQGNSSAAHEISKAIEVMNAENLADVLIARGGGSIEDLWAFNEEILVKAI
HASTIPIVSAVGHETDYLCDFAVDVRAPTPSAAAEIVCKSSEEQVQVFEGYLRHLLSHSRQLLTSKKQQLLP
WRRFLDRAEFYTAAQQQLDSIEIAIQKGVQGGIHEKQRYDNISRWLQGDVSRMTCRLQSLKKMLSQALSH
KALSLQVRCHQLKKSLTYPRQIQQASQKLSPWRQQLDTLISRRLHYQKEEFHKKHTRLKHAHNVLEQQRLS
HVQKLELLGRRLSRGCELNLQNQKIAYANVKETLATILERRYENSVARYSALKEQLHSLNPKNVLKRGYAM
LDFDNENSAMISVDSLQENARVRIQLQDGEAILTVTNIEICKLIK

>core/160/2/Org2_Gene810

MDNSDNSFHTLETEQGSFLNDELAVEEVASTESTEISDATLCFAEKKVAFILNKMREALTGSSQGSDLRLFW
LRKQCLPLFNEIEDTAKRADHWRCYIELTKEGRHLKGLQDEEGSFVVGQIDLAITCLEKDILKFQEGTEDKIFK
DREDNFLESQALDKHQAQFYKQHHTSLLWLSSFSSKIIDLKELINVGMRLKSKFFQRLSNLGNQVFPKRK
ELIEKVSQTFADVDFAVAKYFIGSDKETLKKTVFFLRKEIKNLQHAARKLRFVSSHVFAETRLKLSKCDWLK
GMEKEIRQEQRRLRVSAENSKEVRQMLAEVSSLLIEGNDLSKVRKDLLEGISKKIRALDLTHDDVISLKKEM
QQLFDQLREKQDAAEHSYQEQLAKDKQVKKEAARSLAERITTFSTKTCSEGNITSESREEWQTLKELLGKMSF
LPPPEKISLDNLNLALQTIVNFFEEQLSSPDSREKLVNMRQVLKQRRERRQELKDKLEQDKKLLGSSGLDF
DRAMQYSALVEEDKRALEELDASILELKQQIQQL

>core/161/2/Org2_Gene97

MPQKVLITSALPYANGPLHFGHIAGVYLPADVYARFRLLGDDVLYICGSDEFGIAITLNADREGLGYQEYV
DMYHKLHKDTFEKLGFDFFSRTTNPFHAELVQDFYSQKASGLIENRISEQLYSEQEQRFLADRYVEGTCP
RCGFDHARGDECQSCGADYEAIDLIGPKSKISGVELVKKETEHSYFLLDRMKDALLSFIQGCYLPDHVRKFV
VDYIEHVRSRAITRDLSWGIPVPDFPGKVIFYVWFDAPIGYISGTMEWAASQGNPDEWKRFWLEDGVEYVQFI
GKDNLPFHSVVFPAMELGQKLDYKKVDALVSEFYLLRQFSKSEGNVDMDKFLSSYSCLKLRYVLAAT
APETSDSEFTFLDFKTRCNSELVGKFGNFINRVLAFAEKNHYDKLSYHSVLEDSDRAFLEEARQLVRDAEK
CYREYSLRKATSVIMSLAALGNVYFNQQAPWKLLKEGTRERVEAILFCACYCQKLLALISYPIIPESAVAIWE
MISPKSLENCNLDTMYARDLWKEEILDVINEEFHLKSPRLFFTVE

>core/162/2/Org2_Gene171

MHPLYVDLDTIISYSPPLPKEFQEAASLIAVPDTSKPKVVPVGVKTLFPQTYHLPYLKFVQGENVVHTPLKVG
VMFSGGPAPGGHNVIQGLFNSLKDFHPDSSLVGVNNGDGLTNNKSIDITEEFSLKFRNSSGGFNCIGTGRRKIV
TPEAKEACLKTAEALDGLVIIGGDGSNTATAILAEYFAKRRPKTSIVGVPKTIDGDLQHTFLDLTFGFDAT
KFYSSIISNISRDALSCKAHYHFIKLMGRSASHIALECALQTHPNIALIGEEIAEKNLPLKTIHKKICSVIADRAAM
EKYYGVILPEGIIIEFIPEIINLITEIESLSEYEDKISRSPESQRLKSFPAPIIEQILNDRDAHGNVYVSKISVDKLL
IHLVSNHLQQYFPNVPFNAISHFLGYEGRSGLPTKFDNTYGYSGLYGAGILVRNHCNGYLSTIESLACPFMKW

KLRAIPVVKMFTVKQQADGTLQPKIKKYLVDIGSTAFRKFKLYRKIWALED SYRFLGPLQIETPPEMHSDNFP
PLTLLLNHNFWQRHQGCIEIPDTTY

>core/163/2/Org2_Gene645

MSRKDNEVSLARSIFNILSGTFCSRITGIFREIAMATYFGADPIVAAFVLGFRTVFFLRKILGGLILEQAFIPHFE
FLRAQSLDRAAFFFRFRSRLIKGSTIIFTLLIEAVLWVVLQYVEEGTYDMILLTMILLPCGIFLMMYNVNGALL
HCENKFFGVGLAPVVVNIIWIFFVIAARHSDPRERIIGLSVALVIGFFFEWLITVPGVWKFLLEAKSPPQEHDVS
RALLAPLSLGLTSSIFQLNLLSDICLARYVHEIGPLYLMYSLKIYQLPIHLFGFGVFTVLLPAISRCVQREDHER
GLKLMKFVLTLTMSVMIIMTAGLLLLALPGVRVL YEHLFPQSAVYAIVRVLRGYGASIIPMALAPLVSVLFY
AQRQYAVPLFIGIGTALANIVLSVLGRWVLKDVSGISYATSITAWVQLYFLWYYSSKRLPMYSKLLWESIRR
SIKVMGTTMLACMITLGLNILTQTTYVIFLNPLTPLAWPLSSITAQAIAFLSESCIFLAFLFGFAKLLRVEDLINL
ASFEYWRGQRGLLQRQHVMQDTQN

>core/164/2/Org2_Gene107

MAAKNIKYNEEARKKIHKGVKTLAEAVKVTLGPKGRHVVIDKSFGSPQVTKDGVTVAKEIELEDKHENMGA
QMVKEVASKTADKAGDGTTTATVLAEAIYSEGLRNVTAGANPMDLKRGRIDKAVKVVVDELKKISKPVQHH
KEIAQVATISANNDSEIGNLIAEAMEKVGKNGSITVEEAKGFETVLDVVEGMNFNRGYLSSYFSTNPETQECV
LEDALILIYDKKISGIKDFLPVLQQAESGRPLLIIEEIEGEALATLVNRLRAGFRVCAVKAPGFGDRRKAM
LEDIAILTGGQLVSEELGMKLENTTLAMLGKAKKVIVTKEDTTIVEGLGNKPDIQARCDNIKKQIEDSTSDYD
KEKLQERLAKLSGGVAVIRVGAATEIEMKEKKDRVDDAQHATIAAVEEGILPGGGTALVRCIPTLEAFLPML
ANEDEAIGTRIILKALTAPLKQIASNAGKEGAII CQQVLARSANEGYDALRDAYTDMIDAGILDPTKVTRSALE
SAASIAGLLLTTEALIADIPEEKSSSAPAMPSAGMDY

>core/165/2/Org2_Gene416

MFGSESLRYQLLIQDFAKVSEEGIGLLESKEYSLLQAKLVLRALAQNSSFDDWFRSFKKQCISYPELAHDRDV
LEEFIQVLREGIENPSVTVRVSVLAIGLARDFRLVPLLLQSCNDDSAIVRSLALQVAVNYGSESLKKAIVEL
ARNDDSIHVRITAYQVVALQIEELLPFLRERAENKLVDsverREAWKACLELSSQFLETGVAKDDIDQALFT
CEVLRNGMLPETTEIFTELLSVEHPEVQESLLLSALAWSHQLQNHKEFLSKVRHVMCTSPFAKVRFQAAALL
HLHGDPLGRDSLVEGLRSPQPLVCEAASAALCSLGIHGVPLAKEHLESLSRKAANLSILLVSREDIERAGD
VIARYLSNPEMCWAIEYFLWDAQWNLRGDTFPLYSDMIKREIGRKLIRLLAVARYSQAKAVTATFLSGQQA
QGWSFFSGMFWEEGDVKTSEDLVTDACFAAKLEGALASLCQKKDQASLQRVSQLYNDSRWQDKLAILESV
AFSENLDVAPFLDCCHHEAPSLRSAAAGALFSIFK

>core/166/2/Org2_Gene571

MLRIFCFVISWCLIAFAQPDLSGFVSILGAACGYGFFWYSLEPLKKPSLPLRTL FVSCFFWIFTIEGIHFSWMLS
DQYIGKLIYLVWLT LITILSVLFSGFSCLLV AIVRQKRTAFLWSLPGVWVAIEMLRFYGIFSGMSFDYLGWPM
TASAYGRQFGGFLGWAGQSFAVIAVNMSFYCLLLKKPHAKMLWVLTLLPYTFGAIHYEY LKHAFQQDKR
ALRVAVVQPAHPPIRPKLKSPIVVWEQLLQLVSPIQPIDLLIFPEVVVPFGKHRQVYPYESCAHLLSSFAPLPE
GKAFLSNSDCATALSQHFQCPVIIGLERWVKKENVLYWYN SAEVISHKGISVG YDKRILVPGGEYIPGGKFGS
LICRQLFPKYALGCKRLPGRRSGVVQVRGLPRIGITICYEETFGYRLQSYKRQGAELLVNL TNDGWYPESRLP

KVHFLHGMLRNQEFGMPCVRACQTGVTA AVDSLGRILKILPYDTRETKAPSGVLETS LPLFNYKTLYGYCGD
YPMILIAFCAVSYLGGGFLGYRLLAKKEIR

>core/167/2/Org2_Gene533

MQSSEVKPFSRLRAYLCPIYKSEFSKFVPLFLLAFFVGFNYCLLKNMKDTLVIVGSDAGAEVIPFLKVGIVP
GAVIVTMVYGWLGSRYPRTVFYCFMAAFLGFFFLFAVIIYPVGDSLHLNSLADKLQELLPQGLRGFIVMVR
YWSYSIYYVMSELWSSVVL SMLFWGLANQITTITEAGRFYALINTGLNLSSICAGEISYWMGKQTFVAYSFA
CDSWHSVMLNLTMLITCSGLIMIWL YRRIHHLTIDTSIPPSRRVLAEEGAATANLKEKKKPKAKARNLFLHLI
QSR YLLGLAIIVLSYNLVIHLFEV VWKDQV SQIYSSHVEFNGYMSRITTLLIGVVSVLAAVLLTGQCIRKWGWT
VGALVTPLVMLVSGLLFFGTIFA AKRDISIFGGVLGMTPLALAAWTGGMQNVLSRGTKFTFFDQTKEMAFIP
LSPEDKNHGKAAIDGVVSRIGKSGGSLIYQGLLVIFSSVAASLNVIALLIIMVVWIAVVAYIGKEYYSRAAD
AVATLKQPKEPSSSIVREAQESVEQEEMAVL

>core/168/2/Org2_Gene819

MHDQRNRGHNHNHNLRLRPGSTLLEAFLILCSEHEEGIACFDEHLGSLSYRELRNAIIA VAIKVSKFSEDRVGV
MMPASIGAFIAYFGILLAGKTPVMMNWSQGLRELRACTKTVEVRRVLT SQQFIKHLTEVQGFVEYPPFDLMY
MEDVRKRLSWWEKCRIGLYSKCSVPWLLRIFGVSGVESDDTAVILFTSGTEKLPKAVPLTHKNLMENQEACL
KFFDPNTQDVMLAFLPPFHAYGFNSCGLFPLLMGVHVVFASNPLNPKKLVEFIDDKKVTFFGSTPVFFDYILK
TAKKQNSCLESRLV VIGGDAL KDTLYEETKKLQPQIALYQGYGATECSPVISITTKESPRKSECVGMPIEGM
DVLIISKETHIPVSSGEQGLIVVRGNSVFSGYLGNHEHQSFVSLGGDQWYLTGDLGHIGPSGDLFLEGRLSRFV
KIGGEMVSLEALESILHEHFTENQNE DAGSLVVC GIPGDKVRLCLFTTLATTIHEVNDILKSAETSSIVKISYVH
QVESIPILGIGKPDYVSLNALAVSLFG

>core/169/2/Org2_Gene197

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LGHYHRFSSAALSRHSSATSGQIYARVIKREREGDYLGSTVQVIPHITNEIIQVILDAAKEHSPDVLIVEIGGTIG
DIESLPFLEAIRQFRYDHSEDCLNIHMTYVPYLQA ADEVKSKPTQHSVQTLRGIGIIPDAILCRSEKPLTQEVKS
KISLFCNVPNRAVFNVIDVKHTIYEMPLMLAQEKIANFIGEKLKLATVPENLDDWKVLVNQLSQDLPKVKIG
VVGKYVQHRDAYKSIFEALTHAALRLGHAAEIIPIDAEDENLTMELSQCDA CLVPGGFGVRGWEGKIAAAKF
CREQGIPYFGICLGMQVLVVEYARNVLNLDQANSLEMDPNTPHPIVYVMEGQDPLVATGGTMRLGAYPCLL
KPGSKAHKAYNESSLIQERHRHRYEVNPDYIQSLEDHGLRIVGTCPPQGLCEIIEVSDHPWMIGVQFHPEFVSK
LISPHPLFI AFIEAALVYSKDASHV

>core/171/2/Org2_Gene161

MRKISVGICITILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNL SG
NIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLS
IDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQR TLQSKSLPIASGAFYPKNIKQKQWIKLSKNPH
YYNQSQVETKTITIH FIPDANTA AKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLT FNIN
KFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKLFKEALEELQ
ITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMA

FLTIFAYPSGVPPYAINHKDFLEILQNIEQEQDHQKRSELVSQASLYLETFHIIPIYHDAFQFAMNKKLSNLGV
SPTGVVDFRYAKEN

>core/172/2/Org2_Gene659

MLGKEEEFTCKQKQCLSHFVTNLTSDFVFAKLNLPVVKGALFSKYSRSVLGLRALLLKEFLSNEEDGDVCDE
AYDFETDVQKAADFYQRVLDNFGDDSVGELGGAHLAMENVSILAAKVLEDARIGGSPEKSTRYVYFDQKV
RGEYLYYRDPILMTSAFKDMFLGTCDFLDFTYSALIPQVRAYFEKLYPKDSKTPASAYATSLRAKVLDCIRGL
LPAATLTNLGFFGNRFRWQNLHKLQGHNLAE LRRLGDESLTELMKVIPSFVSRAEPHHHHHQAMMQYRRA
LKEQLKGLAEQATFSEEMSSSPSVQLVYGDPDGIYKVAAGFLFPYSNRSLTDLIDYCKKMPHEDLVQILESSV
SARENRRHKSPRGLECEVEFGFDILADFGAYRDLQRHRTLQTQERQLLSTHHGYNFPVELLDTPMEKSYREAME
RANETYNEIVQEFPEEAQYMVPMAYNIRWFFHVNARALQWICELRSQPQGHQNYRTIATGLVREVVKFNPM
YELFFKFVDYSDIDLGRNLNQEMRKEPTT

>core/173/2/Org2_Gene962

MFVGGGLVSFLLPIPDLECANNVTKTYDKKASVISRDLKLQEDCQKFWNLDPYKLESLCAYQVLYHDDYSSK
RIRELFPQIQKDEVPIFATMILT LGKVDRGFSPEEISLIQKLSYPGLSLASLRGSTEIDPNTDLARALVVSEFSGD
LGKNRADYYSNCLDILALRIHAERQRYLDQSPCVPGTSEFHKATIEAINTILFYEEAVRYPSKKEMFSDEFSFL
SSVTDRKFGVCLGVSSLYFSLSQRLDPLEAVTPPGHIYLRYPQGGEVNIETTAGGRHLPTASYCDCLDLEDLQ
VRTPEEMIGLTFMNQGSFALQKKKYKEAEEAYKKAQEYLGDEELQELLGFVQILGGKKKEGKSLIGKSPRAS
QKGSVAYDYLKGRINIPTLALLFSYPGSNYEEIASYEEELKKAMKSSMPCCEGQRRLASVAFHLGKTAEAVA
LLEKCVEDIPNDLSLHLRLCKILCDRHEYTKALKYFIIAERLMEDQGFLKKDNRSFALFYEVKKIISKVAPQKA
NTLLLMESER

>core/174/2/Org2_Gene13

MSIVLDKIGKSLGTRILFDDVSVVFNPGNCYGLTGPNAGAGKSTLLKIIMGMIETRGSSISLPKKVGILRQNIDSF
HDTTVLDCVIMGNTRLWEALQRRDNLYLQEFTDAIGMELGEIEEIIIGEENGYRADSEAEELLTGIGIPNEMFD
KKMAMIPIDLQFRVLLCQALFGHPEALLLDEPTNHLDLYSINWLGNFLKDYEGTVIVVSHDRHFLNTITTHIA
DIDYDTIIIPGNYDDMVEMKTASREQEKADIKSKEKKISQLKEFVAKFGAGSRASQVQSRLREIKKLQPQEL
KKSNIQRPYIRFPLSDKSSGKVVL SLEAITKDYGDHQVIHPFSLEIYQGDKLGIIGNGLGKTTLMKLLAGVEA
PSSGSIKLGHQAICSYFPQNHSDVLADCGQETLFEWLRNRKTGINDQEIRSVLGKMLFGGDDAFKQIQALSGG
ETARLLMAGMMLNHNVLILDEANNHL DLESVSALSWAINDYKGTAIFVSHDRGLIQDCATKLLIFDKDKIT
FFDGTMDVDYTAGHKQLL

>core/175/2/Org2_Gene961

MKMHRLKPTLKS LIPNLLFLLLTLSSCSKQKQEPLGKHLVIAMSHDLADLDPRNAYLSRDASLAKALYEGLT
RETDQGIALALAE SYTL SKDHKVYTFKLRPSVWSDGTPLTAYDFEKS IKQLYFE EFSPSIHTLLGVIKNSSAIHN
AQKSLETLGIQAKDDLTLVITLEQPPFYFLT LIARPVFSPVHHTLRESYKKGTPPSTYISNGPFVLKKHEHQNYL
ILEKNPHYD HESVKLDRVTLKIIPDASTATKLFKSKSIDWIGSPWSAPISNEDQKVLSQEKILTYSVSSTLLIY
NLQKPLIQNKALRKAIAHAIDRKSILRLVPSGQEA VTLVPPNLSQLNLQKEISTEERQTKARAYFQEAKETLSE
KELAELSILYPIDSSNSSIIAQEIQRQLKDTLGLKIKIQGMEYHCFLKKRRQGDFFIATGGWIAEYVSPVAFLSIL

GNPRDLTQWRNSDYECTLEKLYLPHAYKENLKRAEMIIEEETPIIPLYHGKYIYAIHPKIQNTFGSLLGHTDLK
NIDILS

>core/176/2/Org2_Gene914

MPGSVSSPPLSPVIVRERVSSSSGSDLIQPHAVLKISILIFALVTILGIVLVVLSSALGALPSLVLTVSGCIAIAVGL
IGLGILVTRLILSTIRKVDAMGYDAAVKEEQYLSRIRELESENREIRDNRNRAVEDQCAHLSEENKDLRDPEYLH
GMTERLIASLEIENQALVAENILLKDOWNASLSRDFRAYKQKFPLGALEPWKEDIACIMEQNLFKPECIAMVK
SLPLETQRLFLYPKGFQSLVNRFAPRSRFFQTPKYEYNSRNENEDGKVAAVCARLKKEFFSAVLGACSYEELG
GICERAVALKETLPLPEAVYDTLVQEFPNLLTAESLWKEWCFYSYPYLRPYLSVDYCKRLFVQLFEELCLKLF
TTGSPEDQALVRLFSYYRNHIPAVLASFGLPPPETGGSVFVLLPKQENLLWSQIEVLATRYLKDTFVRNSEWT
GSFEMMFSYNEMCKEISEGRIRFAEDYETRHSEEFPPSPLSEEGERGEEFLPPCSEEEVSVLERPDLDVDSMWV
WHPPVPKGPL

>core/177/2/Org2_Gene828

MTARAEYLDHEDFLYRSHKLQELSELGVVLYPYEFPGVFSCEDIKKTFFASQELGNSEAAMSRSTPRVRFAGR
LVLFRAMGKNAFGQILDHNQTIQVMFNREFTSVHGLSEDAEITPIKFIEKKLDLGDILGIDGYLFFTHSGELTV
LVETVTLCKSLLSLPDKHAGLSDKEVRYRKRWLDLISSREVSDTFVKRSYIHKLIRNYMDAHGFLEVETPILQ
NIYGGAEAKPFTTTMEALHSEMFLRISLEIALKKILVGGAPRIYELGKVFRNEGIDRTHNPEFTMIEAYAAAYMD
YKEVMVFVENLVEHLVRAVNHNTSLVYSYWKHGPQEVDFKAPWIRMTMKESIATYAGIDVDVHSDQKLLK
EILKKKTTFPETAFAFATASRGMLIAALFDELVSDNLIAPHHITDHPVETTPCKTLRSGDTAFVERFESFCLGKEL
CNAYSELNDPIRQRELLEQQHTKKELLPDSECHPIDEEFLEALCQGMPPAGGFGIGVDRLVMILTNAASIRDVL
YFPVMRRFDAEKTN

>core/178/2/Org2_Gene162

MLRFFAVFISTLWLITSGCSPSQSSKGIFVVMKEMPRSLDPGKTRLIADQTLMRHLYEGLVEEHSQNGEIKPA
LAESYTISEDGTRYTFKIKNILWSNGDPLTAQDFVSSWKEILKEDASSVYLYAFLPIKNARAIFDDTESPENLG
VRALDKRHLEIQLETPCAHFLHFLTLPFIFFPVHETLRNYSTSFEEMPITCGAFRPVSLEKGLRLHLEKNPMYHN
KSRVKLHKIIVQFISNANTAAILFKHKKLDWQGPPWGEPIPEISASLHQDDQLFSLPGASTTWLLFNIQKKPW
NNAKLRKALSLAIDKDMLTKEVVYQGLAEPTDHILHPRLYPGTYPERKRQNERILEAQQLFEEALDELQMTRE
DLEKETLTFSTFSFSYGRICQMLREQWKKVLKFTIPIVGQEFFTIQKNFLEGNYSLTVNQWTAAFIDPMSYLM
FANPGGISPYHLQDSHFQTLLIKITQEHHKHLRNQLIIEALDYLEHCHILEPLCHPNLRIALNKNIKNFNLVRR
TSDFRFIEKL

>core/179/2/Org2_Gene279

MNVLYKTKHSPSAHAWKLIGTSPKHGIYLPFSIHTKNNSCGIGEFLDLIPLISWCQKQGFSVIQLLPLNDTGEDT
SPYNSISSVALNPLFSLSSLPNIDTIPEVAKKLQDMHELCASTPSVSYSYQVKEKKWAFLREYYQKCKSSLEGN
SNFSEFLESERYWLYPYGTFRRAIKHHMHGEPINNWPKSLTDQENFPDLTKKFHDEVLFSSYLQFLCYQQLCEV
KAYADQHHVLLKGDLPIISKDSCDVWYFRDYFSSSRSVGAPPDLYNSEGQNWHLPIYNFSQLAKDDYIWW
KERLRYAQNFYSVYRLDHIIGFFRLWIWDSSGRGRFIPDNPKDYIKQGTEILSTMLGASSMLPIGEDLGIIPQDV
KTTLTHLGICGTRIPRWERNWESDSAFIPLKDYNPLSVTTLSTHDSDTFAQWWLNSPKEAKQFAKFLHLPFQK

TLTTETQIDILKLSHESASIFHINLFNDYLALCPDLVSKNLQRRERINTPGTISKKNWSYRVPSLEELAIHKKFN
GYIEKILTGL

>core/180/2/Org2_Gene912

MERKRFIDCDSTKILQELALNPLDLTAPGVLSAERIKKFSLLGGGFTFSFATERLDDAILAALISLAEERGLHES
MLAMQQGQVVNYIEGFPSEMRPALHTATRAWVTDSSFTGEAEDIAVRSRVEAQRLKDFLTKVRSQFTTIVQI
GIGGSELGPKALYRALRAYCPTDKHVHFISNIDPDNGAEVLDTIDCAKALVVVVSXSGTTIETAVNEAFFADY
FAKKGLSFKDHFIAVTCEGSPMDDTGKYLEVFHLWESIGGRFSSTSMVGGVVLGFAYGFEVFLQLLQGASA
MDQIALQPNARENLPMLSALISIWNRNFLGYPTAVIPYSSGLEFFPAHLQQCCMESNGKSIAQDGRRVGFST
SPVIWGEPTNGQHSFFQCLHQGTDIIPVEFIGFEKSQKGEDISFQGTSSQKLFANMIAQAIALACGSENTNPN
KNFDGNNRPSSVLVSSQLNPYSLGELLSYYENKIVFQGLCWGINSFDQEGVSLGKALANRVLELLEGADASNFP
EAASLLTLFNIKFR

>core/181/2/Org2_Gene298

MTKTEEKPFGLRSFLWPIHTHELKKVLPMLMFFCITFNYTVLRDTKDTLIVGAPGSGAEAIPIKFWLVVPC
AIIIFMLIYAKLSNLSKQALFYAVGTPFLIFFALFPTVIYPLRDVLPTEFADRLQAILPPGLLGLVAILRNWTF
AFYVLAELWGSVMLSMLFWGFANEITKIHEAKRFYALFGIGANISLLASGRAIWASKLRASVSEGVPDWGI
SLRLLMAMTIVSGLVLMASYWWINKNVLTDPFRFYNPPEEMQKGGKAKPKMNMKDSFLYLARSPYILLAL
LVIAYGICINLIEVTWKSQKLQYPNMNDYSEFMGNFSFWTGVVSVLIMLFVGGNVIRKFGWLTGALVTPVM
VLLTGIVFFALVIFRNQASGLVAMFGTTPLMLAVVVGAIQNILSKSTKYALFDSTKEMAYIPLDQEQKVKGK
AAIDVVAARFGKSGGALIQGGLVICGSIGAMTPYLA VILLFIIAIWLVSATKLNKLFLAQSALKEQEVAQEDS
APASS

>core/182/2/Org2_Gene689

MVWVFKSQFEGLSALKRGVHALTKAVTPAFGPRGYNVVIKKGKAPIVLTKNIGIRIAKEIILQDAFESLGVKLA
KEALLKVVEQTGDGSTALLVIDALFTQGLKGIAAGLDPQEIKAGILLSVEMVYQQQLQRQAIELQSPKDV LH
VAMVAANHDTVLTGTVVATVISQADLKGVFSSKDSGISKTRGLGKRVKSGYLSPYFVTRPETMDVVWEEALV
LILSHSLVSLSEELIRYLELISEQNTHPLVIIAEDFDQNVLRRTLILNKLNRNGLPVCVAPGSRELRQVVLEDLAI
LTGATLIGQESENCEIPVSLDVLGRVKQVMITKETFTFLEGGGDAEIIQARKQELCLAIARSTSESECQELEERL
AIFIGSIPQVQITADTDTEQRERQFQLESALRATKAAMKGGIVPGGGVAFLRAAHAIEVPANLSSGMTFGFETL
LQAVRTPLKVLAQNCGRSSEEVIIHTILSHENPRFGYNGMTDTFEDLVDAGICDPLIVTTSSLKCAVSVSCLLLT
SSFFISSRTKT

>core/183/2/Org2_Gene8

MYQENLRLLERLLYNSVQKSYADRLFSYEKTKMVHDTPLIPWEEDKEKCAEAEKAFLEQQKILLDYGKSIFW
LNENDEINLNDPWSWGLNTRVTRKVFQEVDSDSERWNHVKVLIQKLEDDYEKLLKESSKESTEANKKLLSDLV
DRLEDAKTKFFLKKQEEVETRVKDLRARYGGTVDPKQDTEAKKKVELEASLETFLDSIESELVQCLEDQDIY
WKEQDVKDLARTQELEEQDIEAKREEAAEDLRSLNERLKKSKTMLDRAKWHIENAEDSITWWTSQIEMKD
MKARLKILKEDITSVLPEIDEIETCLSLEELPLLTTRELLTKSYLKFKICSETLLKMTSVFENNIYVQEYEVQLQ
NLGFKLQGISQRFQKQDDFANLEEQVALQKKRLRELTQNFEIQGFNFMKEDFKAAAKDLYIRSTAEQKMN

FDVPCMELFRRYHEEVNKPLLELMYNCADSYRDAKKKLCSLRLDEKELLQKEIKKEEFYQKKQQRHADRSR
HTTYQKLRIAEELALELKKKI

>core/184/2/Org2_Gene440

MVARGLCDFPRTLVPNERLPIGPFFVPQHTSGAKGKEFAKRNFISIISGLDDILKLCILQRRPFALQWDNLSVKSD
YEEAGPAIGIRSLEPQVSQISPAHGRLCSTLVQWAPILGSEEQLVWLEETMKRLKFPKSLGSKDAVIVDSEMPV
VNANPTQEIPAASETVESSPVAPGNTTDTMPAASGTTDTTSGVSEAAAAEAAVDSTPGTEEEPSFSRLYALVV
QNVYPPEPPKEPEVMFTDEEKSLILEATRARRMELDLNGYLADYELSKDEIQKHVPDLPENWRTNWRWSE
RLYKFFFKTKKEGLEEIFLNKELGNMILARGLAATQSQARIKVFNSLVAWLLQSFNVGRSCTAKPLPTSCLDL
FKSEFESKPKNILTEFLVASDEEILFKGLRVLEPGIEGWYDHPDQAGEIRSVLEGLVQAGRISGYWENQPFGR
FVLRGVGERRTELVELLESLVASGEIMQFFESSDEEGAFIIDNEPSKTAMLKQRFKSCVRTKLVGSAFADSLPR
GRFTILV

>core/185/2/Org2_Gene956

MVSLHLHKFLENASGKKGQSLASTAYLAALDHLLNAFPSIGERIIDELKSQRSHLKMIASENYSSLSVQLAMGN
LLTDKYCEGSPFKRFYSCCENVDAIEWECVETAKELFAADCACVQPHSGADANLLAVMAILTHKVQGPVAVS
KLGYKTVNELTEEEYTLLKAEMSSCVCLGPSLNSGGHLTHGNVRLNVMSKLMRCFPYDVNPDTECFDYAEI
SRLAKEYKPKVLIAGYSSYSRRLNFAVLKQIAEDCGSVLWVDMAHFAGLVAGGVFVDEENPIPYADIVTTTT
HKTLRGRPGGLVLATREYESTLNKACPLMMGGPLPHVIAAKTVALKEALSVDFKKYAHQVVNNARRLAER
FLSHGLRLLTGGTDNHMMVIDLGSLGISGKIAEDILSSVGIAVNRNSLPSDAIGKWDTS GIRLGT PALTTLGMG
IDEMEEVADIIVKVLNRIRLSCHVEGSSKKNKGELPEAIAQEARDVRNLLLRFP LYPEIDLEALV

>core/186/2/Org2_Gene797

MSEQEKLSNYNADKKLFSGIDKLFQIVKGSYGPKQSLSPTSFFKERGFY AISQTELSNSYENLGVDFAKAMVN
KIHKEHSDGATTGLILLHAILQESYAALEKGISTHKLIALSKLQGEKLQEALQQQSWPIKDALKVRNIIFSSLH
MPTIADHFYNAFSVVGPEGLISITKERENDKTSMDVVFQGFKIPAGYASTYFVSDTASRLTRIAHPLILITDRKIS
MIHSLPLLQEISEQNQHLIIFCEDIDPDVLATLVVNKLQGLLQVTVVTIPQLSTTNQELAEDIALFTGTHICPCQ
EASHVLAPEMVTLGSLSIEISESQTTLIGGLHIPEVLTALKTRQLAEEIRTTSCLETKKRLIKSTNRLQSSVAILPT
DEDNEPLYTLALKIMESALSRGYVPGGGVALFYASLTGTPKDDADENSIAISLLQKACCAPLKLLATNADLD
GD AVIAKLSSLGTTSLGISVFSREIEDLIAGGILDSLATTSTILAQALDTAILVLSSKILILENQYEISTL

>core/187/2/Org2_Gene853

MENEILLNIESKEIRY A HLKNGQLFDLTIERKKVRQLKGNIYRGRVTNILRNIQSAFINIDERENGFIHSDILENS
KKFEQMFDMDVDALPEEASEAPLLSSEEAPIEEFLKLDSPVLVQVVKKEPIGSKGARLTSNISIPGRYL VLLPNSP
HRGVSRKIEDPHMREQLKQLIRSFEMPQDMGLICRTASTTASTEALINEAHDLLL TWKTILEKFYSTEQPCLLY
SETDILKKAVITCIDKNYKRLIDDYATYQKCKHMLKKYSPDASIKIEYYRDSIPMFERFNIEKEIDKATRRKI
WLSSGGYLFFDKTEAMHTIDVNSGRSTQLESGVEETLVQINLEAAEEIARQLRLRNVGGLVIIDFIDMKSRKN
QRRVLRLKEHMKYDAARCTILSMSEFGLVEMTRQRNRESLMQTLFTLCPYCSGNAIKTPESVVIEIERDLK
KVINHKEHSHLCLV VHPEIASYMKQENDDNEMINLAKQLKAKLQINTSDSVHLNHYQFFSLITGESIDL

>core/188/2/Org2_Gene240

MFNLFFFTANKETTASHELIYRKNQSFSLSPVTILCLLAISVLLLLGVVFALVGCHVLAAPLGLLVWGCAASV
CSMMAIVSLMCLYKGGKPLIEPSNEEKIDPTKDLEIKDPESLKVPVVEGQSLPKERKTVSFKAKIPSIVEDDFKP
YVIQSTFYHQNKVYSKPIAERMQSLEKEITTLIVDFPRALEESSKSSGSLRGVISEIKNLFLPRFLSRKVKYSLT
ACLRRLGSIVEEYASSDLLILLTKPEPLNMVTQQLIAHLNSLKTEKRKLTPHMQKLVLINFWFYGWSLEEK
CIEKIVAYDPNLLTDELKAHLEAGNIVQFLLSFQSSEMQRERFALFPSDAQELPSAKDGSNYVPAINSEYMY
DFKDLSVLKKSLSERLAFCEKIPSPSSWNFTSSVASHYKDFSLLFTFFSNQQSVILQNPFLLIELLHENPKCQTFL
KGLLEKAMPMSNWAALFRPMLMGMLCSGIARKKELKIIAEHLGVPFKEITQAIASGKILDLLQHLFDF

>core/189/2/Org2_Gene388

MTILRNFLTCSALFLALPAAAQVVYLHESDGYNGAINNKSLEPKITCYPEGTSYIFLDDVRISNVKHDQEDAG
VFINRSGNLFFMGNRCNFTFHNLMTEGFGAAISNRVGDTTLTLSNFSYLAFTSAPLLPQQGQAIYSLGSVMIEIN
SEEVTFCGNYSSWSGAAIYTPYLLGSKASRPSVNLSGNRYLVFRDNVSQGYGGAISTHNLTLTTRGPSCFENN
HAYHDVNSNGGAIAIAPGGSISISVKSGLIFKGNTASQDGNTIHNSIHLQSGAQFKNLRAVSESGVYFYDPIS
HSESHKITDLVINAPEGKETYEGETISFSGLCDDHEVCAENLTSTILQDVTLAGGTLSLSDGVTQLHSHFKQEA
SSTLTMSPGTTLLCSGDARVQNLHILIEDTDNFVPVRIRAEDKDALVSLEKLKVAFEAYWSVYDFPQFKEAFT
IPLELLGPSFDSLLLGETTLERTQVTTENDAVRGFWSLSWEEYPPSLDKDRRITPTKKTVFLTWNPEITSTP

>core/190/2/Org2_Gene199

MTNVVQETIGGLNSPRTCPCPILVIFGATGDLTARKLLPALYHLTKEGRLSDQFVCVGFARREKSNELEFRQEM
KQAVIQFSPSELDIKVWEDFQQRLFYHRSEFDNNMGYTSLKDSLEDLDKTYGTRGNRLFYLSTPPQYFSRIEN
LNKHKLFYKNQDQGKPWSRVIIKPFGRDLDSAKQLQQCINENLNENSVYHIDHYLGKETVQNILTTRFANTI
FESCWNSQYIDHVQISLSETIGIGSRGNFFEKSGMLRDMVQNHMMQLLCLLTMEPPTTFDADEIRKEKIKILQR
ISPFSEGSSIVRGQYGPQTVQGVSVLGYREEENVDKDSRVETYVALKTVINNPRWLGVPFYLRAGKRLAKKS
TDISIIFKKSPYNLFAAECSRCPENDLLIIRIQPDEGVALKFNCKVPGTNNIVRPVKMDFRYDSYFQTTTPEAY
ERLLCDCIIGDRTLFTGGDEVMAWKLFTPVLEEWDQDSSPSFPNYPAGSSGPKEADALIERDGRSWRPL

>core/191/2/Org2_Gene907

MSSWLSQASEVLLNQDPYIPDAPRSQESSVPKISYSITVAPQEAQKSLPKFFTQKFQSQCKSEPPITHHKTFIAT
PRERILRFGSSFESQLHNTSQAQTSSPWNLFSSQKNSTEASKALMQELTMPKSPEKTSEKALDKNLSSKQEGSC
KNFDTLHLQQLKLFQTVDSLVSQSLDSEQQELLQSRREERSETYANQQSSEKKIETKVQIKDLCKDLFSQDQ
DSNQKQKKSPFQQDTSRKNRIAKAAQAVPVIPPPSIGVFTLSYLLTKQGILSDFSSYGCHKDSVESTQRELDAL
HEKRIETIKVSIEKEKRERLWGSLSDIIGWLAPFVSIIGIVAILSGGGIFAFAGFFAGLISLVKCLEKLKFWDW
LEKHLPIKNEELRRKIITHIQWVVYLTPVILSICTLKVENLGFSPHIEGAIKGIQPAIESTMAALRCAILFSQAEIYK
LKGKLTQIQLDIELKSFDRDDHYERSQELLDNMESSFEALSRLNYMRELDQVYLHSLRG

>core/192/2/Org2_Gene403

MAVGGVGGSRSPSPIPPNRRNSEDGKVSPKDNLGEHTVSSSDSSLASQGPTIEERKAQLGGTDKIPLPSVKEPG
DSQTSGRSGVLQRIWKGVKGVFKKTPQARPEVSSPRLPSHVQHGRQLPGLEGFRDRIQKRSENPEADLGKMK
RSYSDGDLDRVGHDSNEDSTEDSRSEGGEPSKSSSFLSGVRGAVSKVHGALGDIKGFQRSASEDDLTTQG
EDSAGDTVKERRSEEAEASSKSSSFLSGVRGATSTVQGALGDAKEKVSAFGEQAAGAIRSAPGNIRTRFQRSS
SEGDLNVNKAACHLRKALENLEKVAPEQVSPEVASRVQSLLARMEQLTHQEPPTVEDLITFVESNVGSDSV

EYASIVPDGGSQAPAETAETGGVEGSAAQGAWKALRDFVVSIFQAVASFFRAIASRLSSARRESAVDDL
ASESNTQWFVEQEGVSNPSAAPSLSFAEEIARRAAEMSNRNAQSLEKLESGNVTDPVIQQGLGLARSFAPEGQ

>core/193/2/Org2_Gene121

MADILVIGANPTGLILANMLIQHGISVKVIDHRASPEDPSFLDCRKLPVILSCSSLELLHNSEMLGDFIQANHKI
FGARYHWWKRTLLFKFSQATDSPVPFSLSTTYQSLEQHLIDEFLKRGGVIDWSTRPVTLVDNSIFIESTKVSQN
FENREIYNPKWIIACEADNNLDIRDLVKSQLRARRINREVIFINCDEGEPEEDHIIHLLPITKNFLNFVFYNPQEK
TKQLCLPQGTHSISPKLKQKLLYTYNLVISDENFHIKTSHHAFPEHGNVFLGSLSNTLLLSYLNGININTNIIAA
FNLAWKLLPVLKKAALKHLVITKEQEDGNILPYISPTTEKRAKKLPFSRFYTPALMYFLKGCRKFNTTGEEY
YYPHQALKYRSSDIKMSPDKEIHGPGPGMRAIDARLENGSFLLDPLKSSKHLIIFFKDIPDLKEALQEEYG
EWIEICNVKEPRILNLYHANPNSLFIIRPDRYIGYRTHTFKLHELISYLLRIFASEKTS

>core/194/2/Org2_Gene481

MNWENVRVRVAPSPTGDPHVGTAYMALFNEIFAKRFKGMILRIEDTDRTRSRQDYEENIFSALRWCGIQW
DEGPDVGGPYGPYRQSERTKIYQGYVETLLKTDCAYKCFATPQELAEMRAVASTLGYRGGYDRRYRYLSPE
EVASREAAGQPYTIRLKVPLSGECVFEDYSKGRVVFPWADVDDQVLVKSDFPTYHFANVIDDHLMGITHV
LRGEEWLSSTPKHLLLYEAFGWEPVFLHMPLLLNPDGTKLSKRKNPTSIFYRDSGYVKEAFVNFLTLMGY
SMEGDEEVYSLERIITFNPRRIGKSGAVFDIQKLDWMNKHLYLNHEGSPECLLKELQGWLLNDEFFLKILPLC
QSRITTLAEFINLTSFFSGLLEYRVEELLQALSPEKAAILLYSYVKYLEKTDQWTKETCYLGSKWLAQAFN
VHHKKAIIPLLYVAITGKKQGLPLFDSIEILGKPRARARLVYAEKLLGGVPPKLAATVDKFMQREDFEEATFD
L

>core/195/2/Org2_Gene618

MDCRGGIPLPEPQVIGGYHVKKILSKKLRSRVVHGLHPETRHSTVIKVFSPSPSFTSRSVYNFLKEAQSLHQIT
HPNIVKFHRYGKWQDCLYIAMEYIEGISLREYILAQFISLPQAIDIIFDIAQALEHLHSRNILHKDIKPENILITPQ
GKIKLIDFGLADWDTEIQRHPSVIGTPYYMSPEQRQGESHSPASDIYALGLLAYELILGHLSLGRVFLSLVPE
RISKILAKALQPSNNRYSSTREFIQDIHHYRMSGDMQEDLRIKDHTVALYEQLQTQRFWLAPETLRFPDFISG
VLYHQGYPLYPHAYDTLLEGDVFNLWLGYSPISNATIALSVVKSVCQQDLQRPLLDVCEINECLIRMKIPI
DEMGISILCLEISKENKELSWIACGKTVFWIKRQGRVVQDFESFSPGLGKITSLQIRETKVAWEIGDEAVVCTL
ELEESVASLKTLSLAELQDRRQKAIFCPIESIHGGIQSRQHGSNSPSTLISLKRIR

>core/196/2/Org2_Gene367

MLKKFINSWLKLCQQDKYQRFTPIVDAIDTFCYEPIETPSKPPFIRDSVDVKRWMLLVVIALFPATFVAIWNS
GLQSIVYSSGNPVLMEQFLHISGFGSYLSFVYKEIHIVPILWEGLKIFIPLLTISYVVGGTCEVLFAVVRGHKIAE
GLLVTGILYPLTLPTIPYWMAALGIAFGIVVSKELFGGTGMNINPALSGRAFLFFTFPAKMSGDVWVGSNP
GVIKDSLMMKNSSTGKVLIDGFSQSTCLQTLNSTPPSVKRLHVDAIAANMLHIPHVPTQDVIHSQFSLWTETH
PGWVLDNLTLTQLQTFVTAPVAEGGLGLLPTQFDSAYAITDVIYGIGKFSAGNLFWGNIIIGSLGETSTFACLLG
AIFLIVTGIASWRTMAAFGIGAFLTGWLFKFISVLIVGQNGAWAPARFFIPAYRQLFLGGLAFGLVFMATDPVS
SPTMKLGKWIYGFFIGFMTIVIRLINPAYPEGVMLAILLGNVFAPLIDYFAVRKYRKRGV

>core/197/2/Org2_Gene209

MKFEFSVALKYLIPGRGRLYSAIVSLFSVGIISLVVWLSIVFISVIHGLEQRWIEDLSQLHSPITILPSDTYYSSYY
YQIDKHSSLSNYTTKTLGEKIASPQVDPYPEDSYLLPETFPLKDCDLGGQQKDPVKMTLES LGPYLQSQHGK
VIEFEQGVGYLDIKTSLKLQKPQPRNLTHFLTYP SKLSYEDKVL PYDETDTYSAELNPFNRSPSGWQQDFHHL
EELYRGASIILPSTYKDSGYKV GDTGVFSTYSIENEKETQYTVHVIGFYNPGLSPLGGRTVFIDPDLARSIRSQS
EGLGMSNGFHLFFPNTKRIVFVKQIENILTSLGVDDYWEISSLHDYDYFQPILDQLQSDQVLFVLCILILIVA
CSNIVTMSMLLVNNKKKEIGILKAMGTSSRSLKIIFACCGAFSGACGVVIGTIFAHTLKNLQFIVKALNYLQGR
ETFNTAFFGQNL PNSVHPQAIYFLGLGTLLLA AVSGALPARKVAKMHVSEILKAD

>core/198/2/Org2_Gene329

MVLFHAQASGRNRVKADAIVLPFWHFKDAKNAASFEEFEP SYLPALENFQGKTGEIELLYSSPKAKEKRIV
LLGLGKNEELTSDVVFQTYATLTRVLRKAKCSTVNILPTISELRLSAEEFLVGLSSGILSLNYDYPRYNKVDR
NLETPLSKVTVIGIVPKMADAIFRKEAAIFEGVYLTRDLVNRNADEITPKKLAEVALNLGKEFPSIDTKVLGKD
AIAKEKMGLLLAVSKGSCVDPHFIVVRYQGRPKSKDHTVLIGKGVTFDSGGLDLKPGKSMLTMKEDMAGG
ATVLGILSALAVLELPINVTGIIPATENAIDGASYKMGDVYVGM SGLSVEICSTDAEGRILADAITYALKYCK
PTRIIDFATLTGAMVVSLGEEVAGFFSNNDVLAEDLLEASAETSEPLWRLPLVKKYDKTLHSDIADMKNLGS
NRAGAITAALFLQRFLEESSVAWAHLDIAGTAYHEKEEDRYPKYASGFGVRSILYYLENSLSK

>core/199/2/Org2_Gene906

MTVSYQSISTPPPEGEFDIFVDGNATEEAVVAAEVQVALPAGEQYAML RATSEL CFGILTQSECA LTQALPPK
EKPLQEEQFLVKNGILMRSTSLPNLKPGQSQQTSLASHRNPLAQQSTSSNSTGKASTETTSSSFPFFSCKAPEG
DSSVDKTFTVSVQTPKAQEQQEASASQSQAQFHVRSYSSSTIKEHSAKEKVSQSTKSAETQKHTQTKSDATLS
PMSLYSTLHKEVPQALSSTKSQQKDEEHRDQRQQEGYEQE QE EGKKKTPWCTVESLQQTSSSNQVYESY
TPIIPDPIVEFALSESQLSVLAGKRVTNLDVLRICTELMKLMKSRANDTMTRLEERELMEREAEHLAASYSR
QAKYARWLGIATATLGILGAIAPMVGEISGDSILGFVQRISGRFKDATAKTFFKGIGKVFTSLSQLTEAASKVH
ELSESAVRVAEYRKEVFRMRQDEVTRTIEEVKDNWKSMDNFLLNILQTEHDAARSLYQ

>core/200/2/Org2_Gene725

MAASILSQELLDILPYTFLKKHCLLPIEESSEAITIAHATATSVIAQDEVKLLIKKPVR FVLKEESEILQRLQQLY
SNREGNVSDMLLTMKEEDGTTISEEEDLLETTDTIPVVRLLNWILKEAIEERASDIHFEPCEDSMRIRYRIDGVL
HDRHSPPSHLRSALTTRLKVLAKMDIAEHRLPQDGRIKIHIGGQEVD MRVSTVPVIYGERVVLRILDKRNVIL
DIAGLHMPKGTEILFKDTITAPEGILLVTGPTGSGKTTTLYSVLQELKGPLTNIMTIEDPPEYKLPGIAQIAVKP
KIGLTFARGLRHLLRQDPDILMVGEIRDQETA EIAIQAALTGHLVVSTLHTNDAISAIPRLLDMGIESYLLSATL
VGVVAQRLVRTICPYCKVAYTPENQEKSFLASLGKDTEMPLYRGQGCVHCFRSGYKGRQGIYEFLRPNTLFR
SEVASNRPHYILRETAEQNGFLPILEHGIALAVSGETTLAEVLRVTKRCD

>core/201/2/Org2_Gene245

MNKKHASFSSRLGFIFSMIGIAVGAGNIWRFP RVAAQNGGGAFLILWLCFLFLWSIPLIIIELSIGKLTKKAPIGA
LIKTAGKKFAWAGGFITLVTTCILAYYSTIVGWGLSYFYAVSGKIH LGNDFAKLWTSHYQSSIPLWAHLTSL
GLAYLVIRKGIVHGIEKCNKILIPAFFLCTIALLLRAVTLPGAVQG IKQLFSCDKSCFSNYKVWIEALTQNAWD
TGAGWGLLLVYAGFASKKTGVVSNGALTAICNNLVSLIMGIIIFSTCASLDILGTTQLQDGAGASSIGITFIYLP
ELFTRLPGGIYLTTLFSSIFFLAFSMAALSSMISMLFLLSQT LAEFGIKPYISETLATIIAFVLGIPSALSLTFFSNQ

DTVWGVALLIVNGLIFIYAALVYGFPKLKKEVINAAPGDLRLNKAFDYIIKYLLPIEGILLLGWYFYEGLFPENG
QWWNPISLYSLGSLVLQWSLGLIILWKFNKQLYLRFSRYNHEIL

>core/203/2/Org2_Gene518

MLKYILKRLVLIPLTLFAIVSIN FVILNAAPGDVLEEKSRDALGEAGKSDKMRSYKGPDRYLQFREHYGLTLPI
FFNTRPKITHKKIQTALQELANANNTTPSAKNAAKSLVYWGDCAKFVMPALLFEADDASRDDKYRHIAADL
FIRGGVLQGFVGP NLSPEQRAQNKEIAESNAFLVRQLNEEDLDTKVEALKGWFQDHGGTEVFCYSSKQFWK
TFFLETRFARYMSRVLRLDFGTLRND AHKTVISEVIKRLRCSLVLSILPMIVGFVLCQIFGMIMALKRNRWIDH
SLNFIFLILFSIPVFVAVPWILDNFVINKTIPFTTIPMPYSGLRSPPEVFNELSTLGRIFDLVSHGFLPFCVASYGAL
AAQSRLSRSIFLEVLSQDFICAAKARGLRWFDILYKHVGKNAAVSIVTSLASSLGTLGGALVVETLFNIDGFG
NFFYQAILNRDHN VVLFVSVLVGSALS LVGYLLGDICYVLLDPRVQLEGRRI

>core/204/2/Org2_Gene664

MHTEFAPFLEDLVHQQVISPLDIAFASKHISDFEESFVFLAVSSALWRYGHPFLSLEENRIRPSLGGISETDLY
RGFHNLPKEARDKLFVVVSGRLYLRSLYTIRSKLLDKLSLLCSATPNYFPPSIDSSILSEEQNFIFNKITQGCFSI
VSGGPGTGKTFLAAQLILSLVKQQPKLR IAVSPTGKATSHIRQILMKYNIFDDMVLMQTVHHFLQEYAYRRY
NSIDVLLVDEGSMVTFDLLYSLVQTLQGYEKDKKLYTSSLIILGDTNQLPPIGIGVGNPLQDLIGYFHENTFFL
KTSHRAKTGVVDQLTQSVLRGEMISFSPLPSISSAIEVLKNR FVKSLRQSEARLCVLT PMRHGPWGVLNLNTM
IHQRLARSDPDLRIPIMVTSRYETWGLFNGDTGLLCLKTQKLHFPQH EPIDSRALSQYVYNYVMSVHKSQGSE
YDEVIVIIPKGSEVFGVSILYTAITRAKYRVSVWGD PETLHKIIKKS NY

>core/205/2/Org2_Gene994

MNLDSKHFDINSANFLEEF AKFISFPSISADSDHLQDCENCAHFLVDHV NKFIDVELWETPGHPPIIYASYKSE
DPLSPTLMLYNHYDVQPAQLSDGWKGDPFILREENG NLYARGASDNKGQCFYTLKALQHYYESQGNFPLNII
WLIEGEEESGSLALFTWLEKKKEALRADYLLIVDGGFLSEKHPYVSIGARGIVSMKISLEEGNKDMHSGVLGG
IAYNTNRALSEILSSLHHPDNSIAIEGFYDDLALPSDSDRPDLPKSDTLRECEENLGFRPQGYEASYSPEESALR
PTVEINGISGGYTGP GFKTVIPYRATAYLSCRLVPNQDPDKAAHQVIHHLKQQVPSSLKFSYEILPGGSRGWRS
SANLP IVKVLQEIYSDLYNEECLRLVMPATIPIGPLLGEAAQTSP IICGTSYLSDDIHAAEEHFSMDQLKKGFLSI
CQLLDKLPKIKE

>core/206/2/Org2_Gene718

MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAGASGKD KTSSTTKT
ETAPQQGVAAGKESSESQKAGADTGVS GAAATTASNTATKIAMQTSIEEASKSMESTLESLSL SAAQMKEV
EAVVVAALSGKSSGS AKLETPELPKPGVTPRSEVIEIGLALAKAIQTLGEATKSALS NYASTQAQADQTNKLG
LEKQAIKIDKERE EYQEMKAAEQKSKDLEGTMDTVNTVMIAVSVVAITVISIVAAIFT CGAGLAGLAAGAAVG
AAAAGGAAGAAAATT VQITVQAVVQAVKQAVITAVRQAITAAIKA AVKSGIKAFIKTLVKAIKAIKSKI
SKVFAKGTQMI AKNFPKLSKVISSLTSKWVTVGVGVVVAAPALGKGIMQMQLSEMQQNVAQFQKEVGKLG
AAADMISMFTQFWQQASKIASKQTGESNEMTQKATKLGAQILKAYAAISGA IAGAHKTNNF

>core/207/2/Org2_Gene3

MYRYSALELAKAVTLGELTATGVTQHFFHRIEEAEGQVGAFISLCKEQALEQAELIDKKRSRGEPLGKLAGV
PVGIKDNIHVTGLKTTCASRVLENYQPPFDATVVERIKKEDGIILGKLNMDEFAMGSTTLYSAFHPTHNPWDL
SRVPGGSSGGSAAAVSARFCPVALGSDTGGSIRQPAAFCGVVGFKPSYGAVSRYGLVAFASSLDQIGPLANT
VEDVALMMDVFSGRDPKDATSREFFRDSFMSKLSTEVPKVIGVPRTFLEGLRDDIRENFFSSLAIFELEGTHLV
DVELDILSHAVSIYYILASAEAATNLARFDGVRYGYRSPQAHTISQLYDLSRGEGFGKEVMRRILLGNYVLSA
ERQNVYYKKATAVRAKIVKAFRTAFEKCEILAMPVCSSPAFEIGEILDPVTLYLQDIYTVAMNLAYLPAIAVP
SGFSKEGLPLGLQIIGQQGQDQVCQVGYSFQEHAQIKQLFSKRYAKSVVLGGQS

>core/208/2/Org2_Gene1004

MNGCWEDLKQTIFWVGEHDCTDIETVRKSCMWLDTRYADKFIKREKEEKMERHELPHATMVRKASGHAYA
KAKAAFEKERSNENQRKVKDVEKWLSKGLAEFRNQESRRARERLRELQTLYPEVSVEERVLERQRTKKVNL
ENLYADIEKKYHHCVREQEYHWEVENKEAEYRENGEKVLSAEVSECLQRLEDCLTWSKKLTKAESVF
EMKFDATEKLGKVLSDVTNRLEILCEDAEEMIFRIEEIEMTLRMVELPLLFMKNTFEKASLQYNSCKEMLA
KVEPQCKESPTYRSSQERLERLNQDLQTAYTNCQERLQGFSDLESKVRTCRDHLREQMKHFEVQGLNFINEE
LLWVGAEFLTQARLDLVATVPYMEFYLYHNIKREKVRSQWMAKTERYREIRQAFQGVMKEDLLAEDTIL
KEEDYWLLRDDWLLRDERKNRQRRLLCNKIAAAQQRVKGF

>core/209/2/Org2_Gene99

MLGILLIASGIIFLAVAIPGLSSAVALGLGCGMTALGTVLLITGLVLLIRSEKLALAEQVEIKQARTRVNNELDQL
SQYVFYTENVDNLKRWSYRDLGFVRQAQEEVTNLEQDIEEIFLTRDIRNALDNEEFFMTHAKQCLAQVGE
SLFQDASIDEFINLAHLSEIRQHLDINDPRWSMITKKVKGTVVRFIYVSTMYKQIKSNFEKSDFGQLRKMLLN
NYKTIEEVLYQSFQKGYNRAALLSEKTRIIHTSSLLHWEKDEDKHLNIKNECASRLNFKKFRTLFLGLSEED
VIDFTGASGWDCSKLPRKEVPLDGGKKKLRFKRTFADEQVGWDWRTTSLEHMTPQEEDPLDRLMDQVEQE
ATSVLKDQDRYWKEIETSEAKFRSLPREDDFEKQSQIDSYIRDLDDHLSVWANQLSAAEDALIEVTDVQEHG
NREMLKNIQQGLELIEDAVKATLPRVDFIQELLEKEELPLVAARMSLENS

>core/210/2/Org2_Gene949

MTFPCGNCNCYYRETPPPNPGGEDIPLEGGQSGSQGGRVITQQPGTGGREMGISLGSDNVLGMVEQAGSLL
NNLLDSARMQRLGHYCYRTGTPWCREHCPGFLQWIWGGCCACCLETVDDPDNPSAQFLQQLIQQYGPICVG
MSFQQLPHCTQKIEQGEPLGDGDKQEVENGCKLHRELLKAAQPRCMGESLVKLLQNNGLGEDMQQTTPWS
LILQAVSEGALSFVTSSDNPPTCWILQPEQQPCPPPTDEEQLQGAVGGAPAPQKKHPAQECRVCTCKLNFRT
LLQKLSRLEVLSESGYKGPLGQAAKQIVDLIKKSLKRLVASDLATFLGPGIGLSLESQVFEVLVLLCLLSKGY
LPLDPLHPEQTVLDPRVQGPWQRILRKVLVTTTAGENIWRQTQGEAPRQAPPPDPWDDDEIERDGIVTGGG
FGIPCQCLRCWRKLPTEKRPNRWL

>core/211/2/Org2_Gene857

MHMSNPISLFSPAELIAKYNLIPKTSPIYPRRTELIILEENACQTRLTNVAQVLHPSSLFSMSKKILNPCGCSGGP
LCWVILNILAFIITSVLFHILLPVNLIVAGLRLFMPLPPKKIVEDLSEPTTEETNEVIQPFIFALQALLFEDNKLRSF
KIVEQSVGKAPLPNPFLNRLVAISPQESQEAMRKIPDLCSQLKKVLKSLGVLTPEWKHMLKYFEGLKNEHDS
NPDKKTFPILIKLLIEALTGKSSLPKTPSTKEKMQAALFIASSCKTCKPTWGEVITRSLNRLYSIANEGDNQLLI
WVQEFKERELMSIQDGDDAEEYRFAAQQHGERYTEAIEQVLRNESAAKLQWHVINTMKFFHGKNLGLVTE

HLQDTLGALTLRQTTVDTHQGREDADLSAALFLNKYLNSGNQLVNSVFKSMQKADPETKALIREFALDILYA
SLRLPQTSAHTEVFSTLLMDPETYEPNKACIAYLLYVLKIIEL

>core/212/2/Org2_Gene4

MSAVYADWESVIGLEVHVELNTASKLFSSALNRFGEPTNTNISTVCTGLPGSLPVLNQSAVEKAVLFGCAVE
GEISLLSRFDRKSYFYPDSPRNFQITQFEHPIIRGGRIKAIVQGEERYFELAQTHIEDDAGMLKHFGEFAGVDYN
RAGVPLIEIVSKPCMFCPEDAVAYATSLVSLLDYIGISDCNMEEGSIRFDVNVSVRPKGSPELRNKVEIKNMNS
FAFMAQALEAEKQRQIDEYLNQPNKDPKLVIPAATYRWDPEKKKTVLMRLKESAEDYKYFPEPDLPTLQLTE
SYIERIRKTLPELPYDKYHRYIQEYGLSEDIASILISDKNIATFFEVACKDCKNFRSLSNWVTVEFGGRCKTLGV
KLPSSGIFPEGVAQLVNAIDQGVTGKIAKEIADLMMESPGKNPEEILKEKPELLPMSDEGELQKIIAEVVLANP
ESIVDYKNGKTKALGFLVGQIMKRTAGKAPPKRVNELLLLLLELDKG

>core/213/2/Org2_Gene870

MITKQLRSWLAVLVGSSLLALPLSGQAVGKKESRVSELPQDVLLKEISGGFSKVATKATPAVVYIESFPKSQA
VTHPSPGRRGPYENPFDFYNDEFFNRFFGLPSQREKPSKEAVRGTGFLVSPDGYIVTNNHVVEDTGKIHVTL
HDGQKYPATVIGLDPKTDLAVIKISQNLPLYLSFGNSDHLKVGDWAIAGNPFGLQATVTVGVISAKGRNQL
HIADFEDFIQTDAAINPGNSGGPLLNDGQVIGVNTAIVSGSGGYIGIGFAIPSLMANRIIDQLIRDGQVTRGFLG
VTLQPIDAELAACYKLEKVYGALVTDVVKGSPADKAGLKQEDVIIAYNGKEVDSLSMFRNAVSLMNPDTRI
VLKVVREGKVIEIPVTVSQAPKEDGMSALQRVGIRVQNLTPETAKKLGIAPETKGILIISVEPGSVAASSGIAPG
QLILAVNRQKVSSIEDLNRTLKDSNNENILLMVSQGDVIRFIALKPEE

>core/214/2/Org2_Gene24

MWNRCQVFSSFFFRYPISSWLIRLRASCECFQQRHPIFLCGLYWLAGITSRGHPECSALILIFLGMFLPRNPKQ
WLPLASAWIISLMLTPAPFLHDGPISGTFVIHHAGGQGTTYGEALCIQTPCGKRAHHLSCQILSESRLKLVY
ELEGTLHHTSQIVFKSNACYKEIPRSRFYIMKEKCRESSCHFLNHRFPSSEVGPFASSLLLGTPLPQNLRLFRQ
KGLSHLFAISGWHFSLCATTWMLCALLPLKIKILSFIVLTSACIFPMSLSVWRSWISVTLLCFSWCFSGSCS
GLNRLGAGFILCSIFFSPFSPTFVLSFLATLGILLFFPKIFSFLYTPWTQFLSPFWLYPIRYLAMTLAISLSAQLFIV
LPIMQYFGSLPLEGLLYNLIVPFTILPIIVFLIATILPCCSPITEALIQGFLSHPWLHNPNILKTLFSAPVPPWMLTL
ASLILFFIGILRTNVSPYASISATSYRFIETL

>core/215/2/Org2_Gene749

MLKIAILGRPNVGKSSLFNRLCKRSLAIVNSQEGTTRDRLYGELHAFGVPAQVIDTGGVDHNSDYFQKHIYN
QALTGAKEADVLLLVIDIRCGITEEDAHLAKLLLPLKKPLILVANKADSRQEELQIHETYKLGIRDIVVTSTAH
DKHIDTLLQRIKLVANLPEPREEEEEGLEELSVDEHEESEAAALPSNTFPDFSEVFTEGFSPEEPCTIPESPQQAPK
TLKIALIGRPNVGKSSIINGLLNEERCIIIDNTPGTTRDNIDILYSHKDRQYLFIDTAGLRKMKSVKNSIEWISSR
TEKAISRADICLLVIDATQKLSSYEKRILSLISKRKKPHIILINKWDLLEEVRMEHYCKDLRATDPYLGQAKML
CISATTKRNLKKIFSAIDELHHVVSUNKVPTPIVNKTLASALHRNHPQVIQGRRLRIYYAIQKTTTPLQFLLFINA
KSLLTKHYEYYLKNTLKSSFNLYGIPFDLEFKEKPKRHN

>core/216/2/Org2_Gene909

MNMPVPSAVPSANITLKEDSSTVSTASGILKTATGEVLVSCTALEGSSSTDALISLALGQIILATQQELLQSTN
VHQLFLPPEVVELEIQVVDLLVQLEHAETITSEPQETQTQSRSEQTLPPQSSSKQSALSPRSLKPEISDSKQQQ
ALQTPKDSAVRKHSEAPSPETQARASLSQASSSSQSRSLPPQESAPERTLLEQQKASSFSPLSQFSAEKQKEALT
TSKSHELYKERDQDRQQREQHDRKHDQEEDAESKKKKKKRGLGVEAVAEEPGENLDIAALIFSDQMRPPAE
ETSKKETTFKKKLPSMVSFVSRFIPSKNPLSVGSSIHGPIQTPKVENVFLRFMKLMARILGQAEAEANELYMRV
KQRTDDVDTLTVLISKINNEKKDIDWSENEEMKALLNRAKEIGVTIDKEKYTWTEEEKRLLKENVQMRKEN
MEKITQMERTDMQRHLQEISQCHQARSNVLKLLKELMDTFIYNLRP

>core/217/2/Org2_Gene917

MTSRTKSSKNLGTIALAGMVVSSIIGGGIFSLPQNMAATAGAGAVILSWILTGFGMFFIANTFRILSTIRPDLKE
GIYMSREGFGPYIGFTIGWGYWLCQIFGNVGYAVITMDALNYFFPPYFQGGNTLPAILGGSILIWVFNFIVLK
GIRQASIINVIGTIFKIPLIIFIILTAFFFFKLAVFKTDFWGHAVTKAQPSLGSVSSQLKGTMLVTLWAFIGIEGAV
VMSGRAKNPLSVGQATVLGFLGCLTIYILFSLLPFGSLFQHQLANIPNPSTAGVLDILVGKWGEVLMNVGLIIA
VLSSWLSWTHIAEIPFSAAKNGTFPEIFTIENKEKSPSVSLYITSSVMQLAMLLVYFSSNAWNTMLSITGVMV
LPAYLASAAFLFKLSKSKTYPKKGSIKAPLAMITGILGVVYSLWLIYAGGLKYLFMALVLLALGIPFYIDAGK
KKKNAKTFFAKKEIVGMTFIGLLALTAIFLFLTGRIKI

>core/218/2/Org2_Gene74

MITRTKIICTIGPATNSPEMLAKLLDAGMNVARLNFHSHGSHETHGQAIGFLKELREQKRVPLAIMLDTKGPEIR
LGNIPQPISVSQGQKLRLVSSDIDGSAEGGVSLYPKGIFPFVPEGADVLIDDGYIHAVVVSSEADSLELEFMNS
GLLKSHKSLSIRGVDVALPFMTEKDIALDFGVEQNMDDVVAASFVRYGEDIETMRKCLADLGNPKMPIIAKI
ENRLGVENFSKIAKLADGIMIARGDLGIELSVVEVPNLQKMMAKVSRETGHFCVTATQMLES MIRNVLPTRA
EVSDIANAIYDGSSAVMLSGETASGAHPVA AVKIMRSVILETEKNLSHDSFLKLDDSNSALQVSPYLSAIGLA
GIQIAERADAKALIVYTESGSSPMFLSKYRPFPIIAVTPSTSVYYRLALEWGVYPMLTQESDRAVVRHQACI
YGIEQGILSNYDRILVLSRGACMEETNNLTIVNDILTGSEFPET

>core/219/2/Org2_Gene607

MGESVKVFLEEREDYPYPGFVTPIESQGLTRGLSEETIEEIAALRNEPQFIIDFRLQAYRYWKQLHEPAWARLH
YGPIAYDDIVYFSSPKQKKPLGRLEDADPEILDTFKKLGIPLDEQKRLNVENVAVDLVFDSVSIGTTFKEALE
KAGVIFCSLGEAIQEHPNLVKKYLGSVVSHRDNFFAALNAAVFSDDGSFVYVPKGVKCPMDISTYFRINNKEA
GQFERTLIVVEDGGYASYLEGCTAPAYSSNQLHAAVVELVAHEHAVIRYSTVQNWYAGDKKTGKGGIYNFV
TKRGLCAGYRSKISWSQVEVGAAITWKYPSCILKGDES VGEFYSVALTSGKMQADTGTKMLHVGKRTTSTV
ISKGISSESKNTFRSLVSLGKKAHSSNYTQCDSMLIGKASGAYTDPKIVVENSTSSIEHEATTSKLREDQLLY
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>core/220/2/Org2_Gene358

MDLKELLHGVQAKIYGKVRPLEVRNLTRDSRCVSVGDIFIAHKGQRYDGNDFAVDALANGAIAIASSLYNPF
LSVVQIITPNLEELEAELSAKYEYPPSKLHTIGVTGTNGKTTVTCLIKALLDSYQKPSGLLG TIEHILGEGVIK
DGFTTPTPALLQKYLATMVRQNRDAVVMEVSSIGLASGRVAYTNFDTAVLTNITLDHLDHFHGT FETYVAAK
AKLFSLVPPSGMVVINTDSPYASQCIESAKAPVITYGIESAADYRATDIQLSSSGTKYTLVYGDQKIACSSSFIG
KYNVYNLLAAISTVHASLRCDLEDLLEKIGLCQPPPGRLDPVLMGPCPVYIDYAHTPDALDNVLTGLHELLPE

GGRLIVVFGCGGDRDRSKRKLMAQVVERYGFAVVTSDNPRSEPPEDIVNEICDGFYSKNYFIEIDRKQAITYA
LSIASDRDIVLIAGKGHEAYQIFKHQTVAFDDKQTVCEVLASYV

>core/222/2/Org2_Gene305

MQTNIGLIGLAVMGKNLVLNMIDHGFSVSVYNRTPEKTRDFLKEYPNHRELVGFESELEDFVNSLERPRKIML
MIQAGKPVDQSIHALLPFLEPGDVIIIDGGNSYFKDSERRCKELQEKGILFLGVGISGGEEGARHGPSIMPGGNP
EAWPLVAPIFQSIAAKVQGRPCCSWVGTGGAGHYVKAVHNGIEYGDIQLICEAYGILRDFLKL SATAVATILK
EWNTLELESYLIRIASEVLALKDPEGIPVIDTILDVVGQKGTGKWT AIDALNSGVPLSLIIGAVLARFLSSWKEI
REQAARNYPGTPLIFEMPHDPSVFIQDVFHALYASKIISYAQGFMLLGEASKEYNWGLDLGEI ALMWRRGGCII
QSAFLDVIHKGFAANPENTSLIFQEYFRGALRHAEMGWRRTVVTAIGAGLPIPCLA AAITFYDGYRTASSSMS
LAQGLRDYFGAHTYERNDRPRGEFYHTDWVHTKTTERVK

>core/223/2/Org2_Gene631

MRDVSELFRTHFMHYASYVILERAIPHILDGLKPVQRRLLWTLFLMDDGKMHKV ANIAGR TMALHPHGDAP
IVEALVVLANKGYLIDTQGNFGNPLTGDPHAAARYIEARLSPLARETLFNTDLIAFHDSYD GREKEPDILPAKL
PVLLLHGVDGIAVGM TTKIFPHNFAELLKAQIAILNDKKFTVFPDFPSGGLMDPSEYQDGLGSITLRASIDIIND
KTLVVKQICPQSTTETLIRSIENAAKRGTIKIDTIQDFSTDVPHIEIKLPKGSRAKEMLP LLFEHTECQVILYSKPT
VIYENKPVECSISEILKLHTTALQGYLEKELLLLQEQLTLDHYHKTLEYIFIKHKL YDSVREVLAINKKISADDL
HQA V LHALEPWLHELATPVTKQDTSQLASLTIKKILCFNEEACTKELLAIEKKQAAIQKDLGRIKEVTVKYLK
GLLERHGH LGERKTQITNFKTAKTSILKQQT LI

>core/224/2/Org2_Gene921

MLCATVSGPSFCEAKQQILKSLHLVDIHELRLDLINELDDQELHTLITTAQNPILTFRQHKEMSTALWIQKLYSL
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KKARLLPKPSTVLCMGTHGLPSRVLSPLISNAMNYAAGISAPQVAPGQPKLEELLSYNYSKLSEKSHIYGLIG
DPVDRSISHL SHNFLLSKLSLNATYIKFPVTIGE VVTFFSAIRDLPFSGLSVTMPLKTAIFDHVDALDASAQLCE
SINTLVFRNQKILGYNTDGEGVAKLLKQKNISVNNKHIAIVGAGGAAKAIAATLAMQGANLHIFNRTLSSAA
ALATCCKGKAYPLGSLENFKTIDIINCLPPEVTFPWRFPPIVMDINTKPHPSPYLERAQKHGSLIIHGYEMFIEQ
ALLQFALWFPDFLTPESCDSFRNYVKNFMAKV

>core/225/2/Org2_Gene374

MMSRLRFRLAALGIFFILLVPNSVSAKTIVASDKEKVGVLVYDNSVEAFQQILDCIDHANFYVELCPCMTGGR
TLKEMVDHLEARM DLVPELCSYIIIQPTFTDAEDQKLLKALKERHPNRFFYVFTGCPPSTSILAPNVIEMHIKLS
IIDGKYCILGGTNFE EFMCTPGDEVPEKV DNPRLFVSGVRRPLAFRDQDIMLRSTAFGLQLREEYHKQFAMW
DYIAHMHMWFIDNPEQFAGACPPLTLEQAEETVFPGFDKHEDLVLDSSKIRIVLGGPHDKQPNPVTQEYKLKI
QGARSSVKLAHMYFIPKDELLNALVDVSHNHGVHLSLITNGCHELSPAITGPYAWGNRINYFALLYGKRYPL
WKKWFCEKLPYERVSIYEFAIWETQLHKKCMIIDDEIFVIGSYNFGKKSDAFDYESIVVIESPEVA AAKANKV
FNKDIGLSIPVSHGDIFS WYFHSVHHTLGHLQLTYMPA

>core/226/2/Org2_Gene844

MRIVQVAVEFTPIVKVGGLGDAVASLSKELAKQNDVEVLLPHYPLISKFSSSQVLSERSFYYEFLGKQQASAI
YSYEGTLTLTIITLDSQIELFSTTSVYSENNVVRFSFAAAAAAYLQEADPADIVHLHDWHVGLLAGLLKNPLN
PVHISKIVFTIHNFGYRGYCSTQLLAASQIDDFHLSHYQLFRDPQTSVLMKGALYCSDYITTVSLTYVQEINDY
SDYELHDAILARNSVFSGIINGIDEDVWNPKTDPALAVQYDASLLSEPDVLF TKKEENRAVLYEKLGISSDYFP
LICVISRIVEEKGPEFMKEIILHAMEHSYAFILIGTSQNEVLLNEFRNLQDCLASSPNIRLILDFNDPLARLTYAA
ADMICIPSHREACGLTQLIAMRYGTVP LVRKTGGLADTVIPGVNGFTFFDTNNFNEFRAMLSNAVT TYRQEP
DVWLNLIESGMLRASGLDAMAKHYVNLYQSLLS

>core/227/2/Org2_Gene829

MAFSHIEGLYFYNTASQKKELFFPNHTPVRLYTCGPTVYDYAHIGNFR TYVFEDILKRTL VFFGYSVTHVMNI
TDVEDKTIAGASKKNIPLQEY TQPYTEAFFEDLDTLNIARADFYPHATHYIPQMIQAITKLLEQGIAYIGQDAS
VYFSLNRFPNYGKLSHLDLSSLRCCSRISADEYDKENPSDFLWKAYNPERDGV IYWESPFGKGRPGWHLEC
SIMAMELLGDSL DIHAGGVDNIFPHHENEIAQSEALSGKPFARYWLHSEHLLIDGKKMSKSLGNFLTLRDLLH
QEFTGQEVRYMLLQSHYRTQLNFTEEALLACRHALRRLKDFVSRLEGVDLPGESPLPRTL DSSSQFIEAFSRA
LANDLNVSTGFASLFD FVHEINTLIDQGHFSKADSLYILDTLKKVDTVLGVLP LTTSV CIPETVMQLVAEREEA
RKTKNWAMADTLRDEILAAGFLVEDSKSGPKVKPL

>core/228/2/Org2_Gene408

MDTIDTPGEQGSQSFGNSLGARFDLPRKEQDPSQALAVASYQNKTDSQVVEEHLDELISLADSCGISVLETRS
WILKTPSASTYINVGKLEEIEEILKEFPSIGTLIIDE EITPSQQRNLEKRLGLVVLDRTELILEIFSSRALTA EANIQ
VQLAQARYLLPRLKRLWGHLSRQKSGGGSGGFVKGEGEKQIELDRRMVRERIHKL SAQLKAVIKQRAERRK
VKSRRGIPTFALIGYTNSGKSTLLNLLTAADTYVEDKLFATLDPKTRKCVLP GGRHVLLTDTVGFIRKLPHTL
VAAFKSTLEAAFHEDVLLHVVDASHPLALEHVQTTYDLFQELKIEKPRIITVLN KVDRLPQGSIPMKLRLLSPL
PVLISAKTGEGIQNLLSLMTEHQEKS LHVTLNFPYTEY GKFTELCDAGVVASSRYQEDFLVVEAYLPKELQKK
FRPFISYVFPEDCGDDEGRGPVLESSFGD

>core/229/2/Org2_Gene241

MDSRTSHLDDELSFKLEKAFTCLSTDIHSHDL SKIVIEYNPIDLAYAVSCLPSESRAILYKNL SCITAKVAFIINT
DSASRWAIFRRLSDSEVCALIEQMPPDEAVWVLDDIPDRRYRRILELIDSKKALKIRD LQKHGRNTAGRLMTN
EFFAFLMETTVKDV SACIRSNPGIDLTRLVFVLDFK GELQGVVTDRSLIINPPMSLKQIMNQIEHKVLPDATR
EEVVDLVERYKIAALPVVDEENFLIGAITYEDVVEAIEDIADETIARMAGTTEDVGYQTCHVVQRFLLRAPWL
LVTLFAGLISASVMAYFQKISPALLALIIFFIPLINGMSGNVGVQCSTILVRSMATGTLSFGRRRETIFKEMSIGL
LTGVVLGILCGLVVYLMGFLGLNIFSGGGIQLGVT VATGVLGASLTATTLGVLS PFFFAKLGVDPALASGPV
TALNDIMSMIIFFLIAGGINFLFFN

>core/230/2/Org2_Gene170

MNKKKRFLSLLFLTAVLLGIWFSPHPASINSNAWQLFAIFTT TIMGIIFQPVPMGAIAIIGISTLLLTQT LTLEQG
LSGFHNPIAWLVFLSFSIAKGIIKTGLGERIAYFFVSALGKSPLGLSYGLVITDFFLAPAIPSVTARAGGILYPV
TSLSDSFGSSAEKGTQDLIGSFLIKVAYQSSVITSAMFLTAMAGNPLVAALAGHVGVSLSWVLWAKAAIIPGL
PSLFLMPIILYKLYPPKITSCEEAI RSAKLRLKEMGPLKKEEKTILMIFFLVVLWTFGDLLGISATTAALIGLSL
LILTNI LDWQKDVIANTTAWETFIWFGALIMMASFLNQLGFIPLVGDSAAALVSGLSWKIGFPLLLIIFYSHY

LFASNTAHIGAMYPIFLAVSISLGTNPIFAALTLAFASNLFGGGLTHYGSGPAPLYFGSHLVTVQEWWRSGFALS
IVNIVIWIGIGSLWWKALGLI

>core/231/2/Org2_Gene993

MTTKSLGSFNSVISKNKIHFIISLGCSRNLVDSEVMLGILLKAGYESTNEIEDADYLILNTCAFLKSARDEAKDY
LDHLIDVKKENAKIIVTGCMTSNHKDELKPWMSHIHYLLGSGDVENILSAIESRESGEKISAKSYIEMGEVPRQ
LSTPKHYAYLKVAEGCRKRCAFCIIPSIK GKLR SKPLDQILKEFRILVNKSVKEIILIAQDLGDY GKDLSTDRSS
QLESLLHELLKEPGDYWLRMLYLYPDEVSDGIIDLMQSNPKLLPYVDIPLQHINDRILKQMRRTTSREQILGFL
EKLRAKVPQVYIRSSVIVGFPGETQEEFQELADFIGEGWIDNLGIFLYSQEANTPAAELPDQIPEKVKESRLKIL
SQIQKRNVDKHNQKLIGEKIEAVIDNYHPETNLLLTARFYGQAPEVDPCHVNEAKLVSHFGERCFIEITGTAG
YDLVGRVVKKSQNQALLKTSKA

>core/232/2/Org2_Gene237

MHSHSKPTKPLGTFTVGMLSLAVVISLRNLPLTAKHGLSTLFFYGLAVICFMIPYALISAELASFKPQGIYIWA
RDALGKWWGFFAIWMQWFHNMTWYPAVLAFIASTIVYKINPELAHNKVYIATVILAGFWILTFNFLGITSS
ALFSSICVIGTLIPGVILVSLALFWIFSGNPISLSWGNLLPNFSNVSSLVLLAGMMLALCGLEANANLASDM
VNPRKNYPKAVFIGAIAITLILVLGSLSIAIVIPKEEISLVSGLVKTFTLFFDKYNLSWMTGIVVMTIAGSLGE
LNAWMFAGTKGLFISTQNDCLPRLFKKVNSKNVPTNMLFQGIVVTIFTLLFLCLDSADLVYWILTALSVQM
YLAMYICLFLAGPILRIKEPRAQRLYSVPGKFLGICTMSILGILSCAFALWVSFLPPRELAQISEGSKIGYTTFL
LAFSLNCLIPFGIYFTHKRLSKKS

>core/233/2/Org2_Gene954

MDKSTGVPLPSPPHSKESEMIVLGCMLTGCVHYLNLAANQLYEEDFYYLEHKIIFRVLQDAFKQDKPIDVHLA
GEELKRHNQITVIGGPSYLITLAEFAGTAAYLEEYVDIIRSKSILRKMISTAKEIEKRALEQPKNVAEALDEAQN
SFFKISQSTSVSQYTLVADKLRLGLTTTTDKPYLVQLQERQELFLQNAQGDNKSFFTGIPTHFIDLDQLIHGFSPS
NLMILAAPAMGKTALALNIAENLCFQNRPLIGIFSLEMTVDQLIHRMICSRSSEVDSKKISIGDLSGHDFQRIVS
VINEMQEHTLLIDDQPGLKVSDLRARARRMKESYDIQFLIIDYLQLLSGSGTLRATESRQTEISEISRMLKTLAR
ELNIPILCLSLSRKVEDRANHRPMMSDLRESGSIEQSDSLVMFLLRREYYDPNDKPGTAELIIAKNRHGSIGS
VPLVFEKELARFRNYSAFECIS

>core/234/2/Org2_Gene657

MKITVNRGLDLSLQGSPKESGFYNKIDPEFVSIDLRPFQPLSLKLKVEQDAVCSGAPIAEYKHPNTYITSHV
SGVVTAIRRGNKRSLLDVIKKTPGPTSTEYTYDLQTLRSDDLSEIFKENGLFALIKQRPFDIPAIPQTTPRDVFIN
LADNRPFPSPEKHLALFSSREEGFYVFVVGVAIAKLFGLRPHIVFRDRLTLPTQELKTIAHLHTVSGPFPSGS
PSIIHHSVAPITNEKEVVFTLSFQDVLTIHGLFLKGRILHEQVTALAGTALKSSLRRYVITTKGASFSSLINLNDI
SDNDTLISGDPLTGRCLCKKEEPFLGFRDHSISVLHNPTKRELFSFLRIGFNKPTFTTKTYLSGFFKKKRTYTNPD
TNLHGETRPIIDTDIYDKVMPMRIPVVPLIKAVITKNFDLANELGFLEVCGEDFALPTLIDPSKTEMLTIVKESLI
EYAKESGILTPHQD

>core/236/2/Org2_Gene529

MKEERSSEILPRVKETKKHAYVSMQEKSCVGECAVVASESEEAESVTVTKIAKLQRMGIEELNILARQYGVK
NIGSLTKSQVVFEIVKAKSERPDELLIGEGVLEVLPDGFGLRSPTYNYLPSAEDIYVSPAQIRRFDLKKGDTIIG
TIRSPKEKEYFALLKVDKINGSTPDKAKERVLFFENLTPLYPNQRIVMEMGKDHLAERVLDLTAPIGKGQRG
LIVAPPRSGKTVILQSIHAHAIVNNPDIVLIVLLIDERPEEVTD MIRQVRGEVVASTFDEQPERHIQVAEMVIEK
ARRLVEHGNDVVILLDSITRLARAYNTVQPHSGKILTGGVDASALHKPKRFFGAARNIEGGGSLTILATALIDT
GSRMDEVIFEEFKGTGNMELVLDRLSDRRTYPAIDLIKSGTRKEELLYHPSELERVYLFRQAIADLTTIDAM
HLLLGRLKKTNSNAEFLLSLKE

>core/237/2/Org2_Gene678

MNFKLPVYHIGLTKAENNTIKIAILQKTCKGWIVCHCEQIPEGKTWSLPKKYFAAPTTFSLQGS DILVKSSSSS
LKNRKNILKVALTNLEASLALPWESLIVQPQLGKPTDRGETPLTLWIAQKNTLKKELSFLSQAQIFPDKLSCRA
ADIFFLAEQSPLKSLPAYLLIYGGSEEVTCIFVKNHAIAVARSFSNHSTKKSCDDIHATLQYIQETFPQTVLPAIH
VAQISPNLQKILEQKLSLPLVVCQSM TYGVEDEDWEIYGDTIAAAHHGASRRPLTFPYDATSVSPA AQKHWL
LRSSLLIGKYALMATVVVSLG SVLKLKSLSSSASNHFACPEEGVLPRSLKAAEKT VKAIGKKNSASNYPLL
PTIPTSEQTLKFLALGKSSPSIKFSYFSYTM TSYP SKDNPSLPYSALVEVKGGQGPEDIPQFLKKISSHPKLQHV
SESLEDQRSFKLQFTLSS

>core/238/2/Org2_Gene760

MTESVYSPSAMHVNSLADKLKAINQEHI LDIWPSLSPKQQQRLFQQLTSVDIDFFRKQQQLLSSPTAILKDFHP
ITSFASSGEDPERAHAGTTLLKEKKVACVVL AGGQGSRLKCDGPKGLFPVSPIKKKPLFQLVAEKVRAASKL
AGQPLPLAFMTSPLNTRQTRSFFESNDYFHLDPNQVDFFCQPLWPLLTLSGDLFLEDMDTLALGPNGNGCIAT
LLYTSGVWEKWKNAGIEMVSVIPIDNPLALPFDVELCGFHAMSNNEVTIKAALRQTAIEDVGILVKSHDSGK
TSVIEYSEIPQNERFALNEDGKLKYCLANIGLYCLSMDFIRHAAYQQLPLYKVHKKHAKQLGHTSLNEKNAWK
FEEFIFDLFCYSDHCQTLVYPRQECFAPLKNLEGNHSPD TVRQALSDRERQLFHKVTGKKLS PNTTTFEAD F
YYPSTSTSLHWENKAFFEEPFEAS

>core/239/2/Org2_Gene741

MTQEFDCVVIGAGPSGYVAAITAAQSKLR TALIEEDQAGGTCLNRGCIPSKALIAGANVVSHIKHAEQFGIHV
DGYTIDYPAMAKRKNTVVQGIRQGLEGLIRSNKITVLKGTGSLVSSTE VKVIGQDTTIKANHIILATGSEPRPF
PGVPFSSRILSSTGILELEVL PKKLAIIGGGVIGCEFASLFHTLGVEITVIEALDHILAVNNKEVSQTVTNKFTKQ
GIRILTKASISAIEESQNQVRITVNDQVEEFDYVLVAIGRQFNTASIGLDNAGVIRDDRGVIPVDETMRTNVPNI
YAIGDITGKWLLAHVASHQGVIAAKNISGHHEVMDYSAIPSVIFTHPEIAMVGLSLQEAEQQNLPAKLTKFPF
KAIGKAVALGASDGFAAIVSHEITQQILGAYVIGPHASSLIGEMTLAIRNELTLPCIYETVHAHPTLSEVWAEG
ALLATNHPLHFPPKS

>core/240/2/Org2_Gene42

MMSSKRTSKIAVLSILLTFTHSIGFANANSSVGLGT VYITSEVVKKPQKG SERKQAKKEPRARKGYLVPSSRT
LSARAQKMKNSSRKESGGCNEISANSTPRSVKLRRNKRAEQKAAKQGFSAFSNLTLKSLLPKLPSKQKTSIH
EREKATSRFVNESQLSSARKRYCTPSSAAPSLFLETEIVRAPVERTKELQDNEIHIPVVQVQTNPK EQNTKTTK
QLASQASIQQSEGTEQSLRELAQGASLPVLVRSNPEVSVQRQKEELLKELVAERRQCKRKS VRQALEARSLT
KKVARGGSVTSTLRYDPEKAAEIKSRRNCKVSPEAREQKYSSCKRDARANGKQDKTTPSEDASQEEQQTGA

GLVRKTPKSQVASNAQNFYRNSKNTNIDSYLTANQYSCSSEETDWPCSSCVSKRRTHNSISVCTMVVTVIAMI
VGALIIANATESQTTSDPTPTPTP

>core/241/2/Org2_Gene263

MRAWEEFLLLQEKEIGTNTVVDKWLRSLKVLCFDACNLYLEAQDSFQITWFEEHIRHKVKSGLVNNNNKPIRV
HVTSDKAAPFYKEKQMQQEKTAYFTMHYGSVNPEMTFSNFLVTPENDLPFRVLQEFTKSPDENGGVTFNPI
YLFSGPEGSKTHLMQSAISVLRSEGGKILYVSSDLFTEHLVSAIRSGEMQKFRSFYRNIDALFIEDIEVFSGKSA
TQEEFFHTFNSLHSEGKLIVVSSSYAPVDLVAVEDRLISRFEWGVAIPIHPLVQEGLRSFLMRQVERLSIRIQET
ALDFLIYALSSNVKTLLHALNLLAKRVMYKKLSHQLLYEDDVKTLLKDVLEAAGSVRLTPLKIIRNVAQYYG
VSQESILGRSQSREYVLPRQVAMYFCRQKLSLSYVRIGDVFSRDHSTVISSIRLIEQKIEENSHDIHMAIQDISKN
LNSLHKSLEFFPSEEMII

>core/242/2/Org2_Gene901

MRQEKDSL GIVEVPEDKLYGAQTMRSRNFFSWGPELMPYEVIRALVWIKKCAAQANQDLGFLDSKHCDMIV
AAADEILEGGFEEHFPLKVWQTGSGTQSNMNVNEVIANLAIRHHGGVLGSKDPIHPNDHVNKSQSSNDVFPT
AMHIAAVISLKNKLIPALDHMIRVLDKVEEFRHDVKIGRTHLMDAVPMTLGQEFSGYSSQLRHCLESIAFSL
AHLIELAIGATAVGTGLNVPEGFVEKIIHYLRKETDEPFIPASNYFSALSCHDALVDAHGSLATLACALTKIAT
DLSFLGSGPRCGLGELFFPENEPGSSIMPGKVNPTQCEALQMVCAQVLGNNQTVIIGGSRGNFELNVMKPVII
YNFLQSVDLLSEGMRAFSEFFVKGLKVNKARLQDNINNSLMLVTALAPVLGYDKCSKAALKAFHESISLKEA
CLALGYLSEKEFDRLVVPENMVGNH

>core/243/2/Org2_Gene959

MNFSLFLFFLIAIQGICLYVGRRGSKKVEDRESYFLAGRSLKIFPLMMTFIATQIGGGVLLGAAEEAFICYGYGG
ILYPLGVALGLIFLGMGPGKRLAEGSLTTVVSIFEVIFYGSKKLRKIAFLLSAGSLFFILVAQVIALDRLFSSFPFG
KYVTVAFWIVLASYTSTGGFRGVVRTDVIQAGFLLIAVLVCGVSVWLSVPKSLSVLDPPFQSLPCAKLSNWIF
MPMLFMLVEQDMVQRCVAASSPKRLQWAAVGAGLVLLLFNFIPLFLGSLGAKAGLKAGCPLIDTIAYFCNPS
LAAVMAAAIGVAILSTADSLMNAVSQLIAEEYPTLKAPYYRYLVGLAVAAPLVAIGFTNIVDVLILSYSLSV
CCLSVPGFYLLAPKGRRVSGAAAWAGVLVGALGYGWVQIVSLGMFGELLAWVGSLVAFSFGFIEITWK
NKVKTQT

>core/244/2/Org2_Gene860

MQQSVRKLFGTDGVRGRANFEPMTVETTVLLGKAVARVLREGRSGKHRVVVGKDTRLSGYMFENALIAGL
NSMGIETLVLGPIPTPGVAFITRAYRADAGIMISASHNPYRDNGIKIFSLEGFKISDVLEQRIETMVSEADFGPLP
EDHAVGKNKRVIDAMGRYVEFVKATFPKGRTLKGLKIVLDCAHGASYKVAPSVFEELDAEVICYGCEPTGIN
INEHCGALFPQVIQKAVIEHQAHLGIALDGDGDRIIMVDEKGHIVDGDMLSICAGDLKKRSALPHNRVVATI
MTNFGVLKYLEGLGLQVFTSPVGDRHVLHAMLEHEVTLGGEQSGHMIFLDYNTTGDGIVSALQVLRIMIESE
SMLSDLTAPIVKSPQTLINVAVREKIPIETIPLIERTLRDVQDALGPSGRILLRYSGTENICRVMVEGHKKHQV
DCLAKALADVIDAELGTGSRE

>core/245/2/Org2_Gene492

MQIAQVFGCGRNLNGEVKVS GAKNAATKLLVASLLSDQKCTLRNVPDIGDVSLTVELCKSLGAHVSWDKETE
VLEIYTPEIQCTRVPPTFSNVNRIPILLGALLGRCPEGVYVPTVGGDAIGERTLNFHFEGLKQLGVQISSDSSG
YYAKAPRGLKGNYIHLPPYPSVGATENLILAAIHAKGRTVIKNVALEAEILDVLFLQKAGADITTDNDRTIDIF
GTGGLGSVDHTILPDKIEAASFMAAVVSGGRV FVRNAKQELLIPFLKMLRSIGGGFLVSESGIEFFQERPLVG
GVVLETDVHPGFLTDWQQPFAVLLSQAQGSSVIHETVHENRLGYLHGLQHMGAECQLFHQCLSTKACRYAI
GNFPHSAVIHGATPLWASHLVIPDLRAGFAYVMAALIAEGGGSIIENTHLLDRGYTNWVGKL RSLGAKIQIFD
MEQEELTTSPKSLALRDASL

>core/246/2/Org2_Gene779

MLYFIEQLNKLSTSF CVFPMILLGGFLT WKLRGLQFHGLKLGFNLMLQNKLDDSSSKANEVSSYEAVAGIL
AGNFGTGNIAGMAVALACGGPGALVWVWLAALLGAIVQYAGSYLGSKYRKPEGNTGEFIGGPIACLAFGM
RKKILAGFFALFTIMTAF CAGNCVQVSCIVPLCAEGTPGKLLVGILLALVVIPVLAGGNNRILRFSARVIPFIAG
FYCISCGIILFQHASAILPAIKLICSSAFGIKAGLAGIGGYTLSQVISTGINRAVMATDCGSGMV SILQANTKSKN
PVVDGLVTLPVPVIVMVVCSITMLVLIVSGAYSSGAQGTLMVMSAFKNSLGSLSGVIVILAMALFGYTTILT W
FACAEKSLQYMIPGRRANLWLKAIYVLIIPLGGVIDMRMIWALS DTGFSGMVILNCIALIALLKDVLSTNRDV
ALLKERECSVADPVRNLDA

>core/247/2/Org2_Gene790

MFNVNFKFLEGLHQ PAPRYTSYPTALEWEP SDAAPALLAFQRIREN PQPLSLYFHIPFCQSMCLYCGCSVVLN
RREDIVEAYINTLIQEMKLVVETIGFRPQVSRIHFGGGTPSRLSRELFTLLFDHIHKLFDLSHAEEIAIEVDPRSL
RNDMEKADFFQNVGFNRVSLGVQDTQADVQEA VRRRQSHEESLKAYEKFELAFQSINIDLIYGLPKQT KES
FSKTIQDILAMY PDRLALFSFASVPWIKPHQKAMKASDMPSMEEKFAIYSQSRHLLTKAGYQAIGMDHFSLP
HDPLTLAFKNKTLIRNFQGYSLPPEEDLLGLGMTSTSFIRGIY LQNAKTLEEYHNTVLRGTFATV KSKILTEDD
RIRKWAIHKLMCTFTINKEEFFNLFGYEFDTYFIESRDR LISMETTGLIHNSPGSLKV TPLGELFVRVIATAFDH
YFLNKVSKKECF SASI

>core/248/2/Org2_Gene547

MTTLRQFFLITELRQKLFYTFALLTACRVGVFIPVPGINGELAVAYFKQLLGSGQNLFQLADIFSGGAFAQMT
VIALGVVPYISASII VQLFLVFMPALQREMRESSDQGKRRIGRLTRLFTVALAVIQSLLFAKFALRMNLTIPGIV
LPTLLSSKLF GVPWIFYITT VVVMTTGTLLLMWIGE QISDKGIGNGISLIIALGILSSFPSVLGSI VNKNLG SQD
SSDLGLISILILALVFVFLITTI IIEGVRKIPVQYARRVIGRREVPGGGSYLPLKVNYAGVIPVIFASSLLMFPA
TIGQFIASESSWMKRIAALLAPGSLVYSICYVLLIIFFTYFWTATQFHPEQIAS EMKKNNAFIPGIRQGKPTQHY
LEYTMNRVTLLGALFLAAIAILPSLLGCLLRVDSNVSYFLGGTAMLIVVGVVLD TMKQVDAFLLMRRYDSVL
KTDRTKGRH

>core/250/2/Org2_Gene582

MNVWTKFFQPPKHIKEIEDQEVVKKKYKYWRIRIFYSMFIGYIFYFYFTRKSFTFAMPTLIADLGFDKAQLGIIG
STLYFSYGISK FVSGVMSDQSNPRYFMAIGL MITGLTNIFFGMSSSIVLFALWWGLNGWFQGWGWPPCARLL
THWYAKSERGTWWSVWSTSHNIGGALIPILTGFIIDYSGWRGAMYVPGILCIGMGLVLINRLRDT PQSLGLPPI
EKYKRDPHHAHHEGKSASEGTEEIERELSTREILFTYVL TNQWLWFLAAASFFIYVRMAVNDWSALFLIETK
HYAAVKANFCVSLFEIGGLFGMLVAGWLS DKISKGNRGP MNVLFSLGLLFAILGMWF SRSHNQWWVDGTL

LFVIGFFLYGPMIGLAAAELSHKKAAGTASGFTGWFAYFGATFAGYPLGKVTDVWGWKGFFIALLACAS
IALLLFLPTWNATEKNTRSKA

>core/251/2/Org2_Gene148

MKKVLIANRGEIAVRIIRACHDLGLSTVAVYSLADQEALHVLLADEAICIGEPQAAKSYLKISNILAACEITGA
DAVHPGYGFLSEANANFASICESCGLTFIGPSSESIAMMGDKIAAKSLAKKIKCPVIPGSEGIIEDESEGLKIAEKI
GFPVIVKAVAGGGGRGIRIVKEKDEFYRAFSAARAEAEAGFNNPNVYIEKFIENPRHLEIQVIGDTHGNYVHLG
ERDCTIQRRRQKLIEETPSPILNAEIRVKVGKVAVDLARSAGYFSVGTVEFLDKDKKFYFMMNTRIQVEHT
ITEEVTGIDL VKEQIHVAMGNKLPWKQKNIEFSGHIIQCRINAEDPTNNFSPSPGRLDYYPAGPSIRVDGAC
YSGYAIPPYDYSMIAKVIAKGKNREEAIAIMKRALKEFHIGGVQSTIPFHQFMLDNPKFLESNYDINYIDNLLA
QGNSFFKEF

>core/252/2/Org2_Gene33

MATKTKTQWTCNQCGATAPKWLGQCPGCHNWNLSVEEYVPQARSGTSSRSSTSAIALSSIELENESRIFIDHA
GWDRILGGGVVRGSLTLLGGDPGIGKSTLLLQTAERLASQKYKVLVVCGEESVTQTSRAKRLNISSPLIYLF
PETNLDNIKQQIATLEPDILIISIQIIFNPTLNSAPGSVAQVREVTYELMQIAKSAQITTFIIGHVTKSGEIAGPRV
LEHLVDTVLYFEGNSHANYRMIRSVKNRFGPTNELLILSMHADGLKEVSNPSGLFLQEKTGPTTGSMIPIIEG
SGALLIELQALVSSSPFANPVRKTAGFDPNRFSLLLAVLEKRAQVKLFTMDVFLSITGGLKIIIPAADLGALLA
VASSLYNRLLPNNSIVIGEVLGGEIRHVAHLERRIKEGKLMGFEGAILPEGQISSLPKEIRENFRLQGVTIKD
AIRLLL

>core/253/2/Org2_Gene777

MLKILKIKVLVFPLALLMGCNSIGYAGPQGSQTNSQTKVKIGSEVWIEQKLRQYPELLWLTESGGAPLLTST
PIDMAYSEKLFNKKVPALDIAIRSMIHLHLLIQGSRQSYMQLSQILPSEEGGMTEFKQFQTAHKQLLFFLNPKS
FDNTRLILETAIVLRHVGCSAKAVTTFKPYFTDSCPQSIFYAKALHVLRTFPELCPSYARLSPEQQEVLLSLRRL
GNYDSLNLTEVPSAQLLSAWRTRSLAILDLYLYCLDTCGDKNCSQEFYINFAPLLSMLQQHATIEEAFSRY
FTYRANRLGFEGTSRTDMLVRLATLMNLSPEASTLAWSFKNLPSDEAENLVNSFYTVQGEHIPLTFRGLPS
LVAGLSVATHGSTVSPENRLRQLYSTMLSLLVKSLSHREMLNKQLLPQGTVLDFSETTLSSGGLDVFAESIA
VRIHLNGAVSINL

>core/254/2/Org2_Gene156

MRKRHSFDSTSTKKEAVSKAIQKIIKIMETTDPSLNVETPNAEIESILQEIKEIKQKLSKQAEDLGLLEKYCSQE
TLNLENTNASLKL SIGSVIEELASLKQLVEESIEESLGQQDQLIQSVLIEISDKFLSSIGETLSGNLDMNQNVIQ
GLLIKENPEKSEAASVGYYVQTLLEPLSKRIGETHKKVATHDVNISSLQFHMMSVAGGRFRGHIDMNGYRVLG
LGEPKNGEDAVSKDYLERIVSSQLTIDKVEDKPITKPNKGKLLYSQGTSPKLESPLPLGLLTSGISGFTWKSAS
KSNDGSFPFSALRHKETESDTCFQITSTLSGNQAGTYTWSLSLKVLVPSIFQIEKPEVQLSLVYSYEDWLPID
NIFNMSQPRTIPLALLGQTMLAGQKYDILELAAHQTNQTLMISPNC SRFSLQKQTNQFENSPVDFYIVHAAH
SCHWSGF

>core/255/2/Org2_Gene364

MLTCNECTTWEQFLNYVKTRCSKTAFENWISPIQVLEETQEKIRLEVPNIFVQNYLLDNYKRDLCSEFVPLDVH
GEPALEFVVAEHKKPSAPVASQKESNEGISEVFEETKDFELKLNLSYRFDNFIEGPSNQFVKSAAVGIAGKPGR
SYNPLFIHGGVGLGKTHLLHAVGHYVREHHKNLRIHCITTEAFINDLVYHLKSKSVDKMKNFYRSLDLLLVD
DIQFLQNRQNFEEFECNTFETLINLSKQIVITSDKPPSQLKLSERIIARMEWGLVAHVGIPDLETRVAILQHKAE
QKGLLIPNEMAFYIADHIYGNVRQLEGAINKLTAYCRLFGKSLTETTVRETLKELFRSPTKQKISVETILKSA
TVFQVKLNDLKGNSRSKDLVLARQIAMYLAKTLITDSLVAIGAAGFGKTHSTVLYACKTIEHKLQNDETLKRQ
VNLCKNHIVG

>core/256/2/Org2_Gene850

MILPPYSYSLKIGAAVLFFCSILHTFLTPWLYTLCQSYEHKKLVFPECWKRYARLSEFRILSRVEIVFFLWAVP
LFFWFLYTEGYRISMAYFNSRNYGFAVFIMVILILLESRPVYFAELVLSSIAKLGKTSPKSWWWTLMIAPLL
SCLLKETGAMIIGATLLMRHFYVFSRRAFAYATMGLLFSNISIGGLTSYVSSRALFLIFPALKWEHSFFLSHFA
WKAIVAILISTTIYYFIFRKEFKKFPDIPSDKDPSVEKVPWWIICVNIIFVGSILSRSTPLFMGALLFYLGFKFT
IFYQDPINLSKVCYVGLFYAGLVVFGDLQEWVVLNMQGLSDFGYMTVSYTSLIFLDNALVNYLVHNLSVA
TDCYHYLVVAGCMAAGGLTLVSNIPNIVGYLILRSAPSSTIHMGWLFLGALGPSIISLGVFWLLKNVPEFLYC
FFR

>core/257/2/Org2_Gene670

MSEPRFVCLSLGSNLGNRFKNLQIARTLLGEQAVLGLRSSVILETEALLPGSPPEWDLPYFNSVLVGETTSL
RELLVTIKQIEKVVGRAEESPPWSPRTIDVDILLYGDESFCDDHTEITIPLSNLLSRPFLIALIASLCPYRRFCTQG
SPYHNFTFGELAHHLPSPPGMIRRSLSPTDMLMGVVNVTNDSMSDGGMFLDPEKAVAQAELFTEGAAVIDF
GAQATNPKVKQFLSVDQEWERLEPVLRLKETSWSNRKQYPIISLDTFYPEIILRAMDIYPIQWINDVSGGSQS
MAEVARDCELSLVMNHSSSLPVDPKNILSFSVPIGEQLLSWGEKQLKMFSDVGLNANQVIFDPGIGFGKGAA
QSLATLYEIAKFKRLGCPILIGHSRKSFLSLFGNHDPKDRDWETVGLSILLQQQGVVDYLRVHNVAAHQKALS
VAACEACAPI

>core/258/2/Org2_Gene458

MNRLLSLLSVFDDFFWSYVAFILIIVLGVFSWKSRRFFQFTKFSQFCKLFRYYSQNPQERETKQGVHPLKVFFA
SAGGNIGIGNVVGIVTAACIGGPGALFWVWIAGIFGSIVKYSEVYLGIFRKLDRDGVYQGGPMYFLIKAFKT
PVVSVIVAILLCIYGVEIYQFSVITDSLAHCWNLPKVYPMLGLLFLVFYAIRGGLQRIGKICSIVLPFFMLLYCA
LSLYILVKEFH TLPHLLSTVFSSAFKGQSALGGFAGCTVATTIHQGISRAAYSGDIGIGFDSIIQSESSAKDPSTQ
AQLSIVGIAIDNLICTLSLLMVLASGSWSLGLENASQVVEHTLASYFPMVKFFLPTFFFVTGYTTIISYFLVGKK
CAKFLYGNTGAKIYTLYGLLILPLFCFLSQNTALLIMSVSGALLLCFNLLGVFILRKEVIFPARAASLTETSLST
E

>core/259/2/Org2_Gene294

MLSCVFSDTIFLSSFLAVTLICMTTALWGTILLISKQPLLSESLSHASYPGLLVGALMAQYVFSLQASIFWIVLF
GCAASVFGYGIIVFLGKVCKLHKDSALCFVLVFFFAIGVILASYVKESSPTLYNRINAYLYGQAATLGFLEAT
LAAIVFCASLFALWWWYRQIVVTTFDKDFAVTCGLKTVLYEALSIFISLVIVSGVRSVGIVLISAMFVAPSLG
ARQLSDRLSTILISAFFGGISGALGSYISVAFTCRAIIGQQA VPVTLPTGPLVVICAGLLAGLCLLFSPKSGWVI
RFVRRKHFSFSKDQEHLKVFVWHISHNRLNISVRDFVCSYKYQEYFGPKPFPRWRVQILEWRGYVKKEQDY

YRLTKKGRSEALRLVRAHRLWESYLVNSLDFSKESVHELAEIEHVLTEELDHTLTEILNDPCYDPHRQIIPNK
KKEV

>core/260/2/Org2_Gene90

MINSLSQKLSSIFSFLVSSRRINEENISESIREVRLALLDADVNYHVVKDFISKVKEKILGEEIWKHVSPGQQFIR
CLHEELVAFLSDGREEFTIQKTPSIILLCGLQGAGKTTTAAKLADYVIKNKKAKKVLVVPCLDKRFAAVDQL
KILVAQTKAEFYQSQENKPINVVVKALAYAKENGHDFVILDTAGRLNIDNELMEELTAIQKVSQANERLFVM
NVAMGQDVLATVQAFDQSLDLTGVLSTMDGDARAGAVFSIKHVLGKPIKFEGCGERIQDLRSFDPQSMAER
ILGMDGTINFKEMREYISEEEDAELGKKLVTAFTYEDYYKQMKAFRRMGPLRKLLGMMPGFNNAKPSQ
KEIEDSEQMKRTEAIIISMTPEERKELVELDMSRMKRIASGCGLTLGDVNQFRKQMSQSKKFFKGMSKGK
MEQVRKKMSGGNQWR

>core/261/2/Org2_Gene78

MDALILSRIQFGLFITFHLYFVPLSMGLSMMLVIMEGLYLVTKKQIYKQMTWFWVGIFALTFVLGVVTGIMQI
FSFGSNWANFSEYTGNI FGTLGSEGVFAFFLESGFLGILLFGRHKVSKKMHFFSTCMVALGAHMSAFWIICA
NSWMQTPSGYEMVMHKGKLI PALTSFWGVVFSPTTIDRFIHAVLGTWLSGVFLVISVSAYYLWKKRHHEFA
KQGMKIGTICAVIVLVLQLWSADVTARGVAKNQPAKLAAFEGIFKTEEYTPIWAFGYVDMEKERVIGLPIPG
ALSFLVHRNIKTPVTGLDQIPRDEWPNVQAVFQLYHLMIMLWGVMVALTLISWSAYKGWRWALKPFFLVIL
TFSVLLPEICNECGWCAAEMGRQPWVVQGLLTKKDAVSPIVQANQIVQSLVIFSLVFIALLTLFITVLCKKIKH
GPEEENDLTEFEVK

>core/262/2/Org2_Gene798

MRAMLLEDWVSLMLSDVSCPKCDKKITGFAIDSQQVQPGDLFFALPGNATDGHQFLKHAATAGAVAAVVS
HDYQGDSFGLELIRVDDTKSALQEAGSNQCNLFQGTLVGITGSVGKTTTKEFSKITLSSYKTHASPKSYNSQL
TVPLSLLMAEGDEDVMILEMGVSEPGNMQDLLRIVQPEIAVITHINDQHMHFPQGIQEILKEKSYILQKSKL
QLLPKDSPYYLDRSCSPTAEKFSFSFNDPLADFCYKAISGDSVVIQTPEENYCLPIAFSYKPAYTNLLIAVALS
WILEVPEEGVIRSLPELKLPPMRFEHSMRNGMQVINDAYNACPEAMIAALDALPLPSDGGKIILILGHMAELG
RYSEEGHALVAEKAASRGDMIFFIGEKWIPVQSVLKSYSCEVSFFSSAQDVKDILKQVARYGDVILLKGSRAL
ALESLLACF

>core/263/2/Org2_Gene300

MSNITSPVIQNNRSCNYYFELKNSTTIHIVISAILLCGALIAFLCVAAPVSYILSGALLGLGLLIALIGVILGIKKIT
PMISSKEQVFPQELVNRIRAHYPKFVSDFVSEAKPNLKDLSIFIDLLNQLHSEVGSSTNYNVSEELQQKIDTFEG
IARLKNEVRTASLKRLESAASSRPLFPSPKILQKVFPFFWLGEFISAGSKVVELHRVKKIGGSLEEDLSDYIKP
EMLPTYWLIPLDFRPTNSSILNLHTLVLARVLTRDVFQHLKYAALNGEWNLNHSDLNTMKQQLFAKYHAAY
QSYKHLSPSLQEDEFYNLLLCIFKHRYSWKQMSLIKTVPADLWENLCCLTLDHTGRPQDMEFASLIGTLYT
QGLIHKESEAFSSLTLLSLDQFKTIRRQSTNIAMFLENLATHNSTFRSLPPITVHPLKRSVFSQPEEDESSLIG

>core/264/2/Org2_Gene998

MVITNLSINADTIYGKNPINIVASAANKNITLTGTLALVNADGAFYENHTLQDSQDYSFVKLSPGAGGTIITQD
ASQKPLEVAPSRPHYGYQGHWNVQVIPGTGTQPSQANLEWVRTGYLPNPERQGSVPNSLWGSFVDQRAIQ

EIMVNSSQILCQERGVWGAGIANFLHRDKINEHGYRHSVGVLVGVGTHAFSDATINA AFCQLFSRDKDYV
VSKNHGTSYSGVVFLEDTLFRSPQGFYTDSSSEACCNQVVTIDMQLSYSHRNNDMKT KYTTYPEAQGSWA
NDVFGLEFGATTYYYYPNSTFLFDYYSPFLRLQCTYAHQEDFKETGGEVRHFTSGDLFNLA VPIGVKFERFSDC
KRGSYELTLAYVPDVIRKDPKSTATLASGATWSTHGNLSRQGLQLRLGNHCLINPGIEVF SHGAIELRGSSR
NYNINLGGKYRF

>core/265/2/Org2_Gene924

MLTYKVSPSSVYGNAFIPSSKSHTLRAILWASVAEGKSIYNYLDSPDTEAMICACKQM GASIKKFPQILEIVG
NPLAIFPKYTLIDAGNSGIVLRFMTALACVFSKEITVTGSSQLQRRPMAPLLQALRNFGASFHFSSDKSVLPFT
MSGPLRSAYS DVEGSDSQFASALAVACSLAEGPCSFTIIEPKERPWFDSLWLEKLHLPYSCSDTTY SFPGSS
HPQGFSYHVTGDFSSAAFIAAAALLSKSLQPIRLRNLDILDIQGDKIFFSLMQNLGASIQYDNEEIL VFPSSFSGG
SIDMDGCIDALPILTVLCCFADSPSHLYNARSAKDKESDRILAITEELQKMGACIQPTHDGLLVNPSPLYGAVL
DSHDDHRIAMALTIAALYASGDSRIHNTACVRKTFPNFVQTLNIMEARIEECHDNYSMWSTH KRKVFARESF
G

>core/266/2/Org2_Gene717

MTSGVSGSSSQDPTLAAQLAQSSQKAGNAQSGHDTKNVTKQGAQAEVAAGGFEDLIQDASAQSTGKKEATS
STTKSSKGEKSEKSGKSKSSTSVASASETATAQAVQGP KGLRQNNYDSPSLPTPEAQTINGIVLKKGMGT LAL
LGLVMTLMANAAGESWKASFQSQNQAIRSQVESAPAIGEAIKRQANHQASATEAQAKQSLISGIVNIVGFTV
SVGAGIFSAAKGATSALKSASF AKETGASAAGGAASKALTSASSSVQQTMASTAKAATTAASSAGSAATKA
AANLTDDMAAAASKMASDGASKASGGLFGEVLNKNPNWSEKVS RGMNVVKTQGARVASFAGNALSSSMQ
MSQLMHGLTAAVEGLSAGQTGIEVAHHQRLAGQAEQA EVLKQMSSVYGQQAGQAGQLQEQAMQSFNTA
LQTLQNIADSQTQT TSAIFN

>core/267/2/Org2_Gene29

MTLQPYQASSRKYRPQIFREILGQSSVAVLKNALVFNRAAHAYLFSGIRGTGKTTLARILAKALNCVHLS ED
GEPCNQCFSCKEIASGSSLDVLEIDGASHRGIEDIRQINETVLF TPVKAKFKIYIIDEVHMLTKEAFNALLKTLE
EPPQHVKFF FATTEIHKIPGTILSRCQKMHLQRIPEKTILEKLSLMAQDDHIEASQEALAPIARAAQGS LRDAES
LYDYVISLFPKSLSPDTVAQALGFASQDSLRTL DNAILQRDYATALGIVTDFLNSGVAPVTFLHDLTLFYRNLL
LTNSTTSKFSSQYKTEQLLEIIDFLGESAKHLQNTIFEQT FLETVIIHIIRIYQRPVLSELISSIKSRQFEGLRNIKEP
TLTQQVSAPQPQPTYKEQSFLEKKNQPA AEGKIISVEVKSSASIKSAAVDTLLQFAVVEFSGILRQ

>core/268/2/Org2_Gene745

MLKHDTIAAIATPPGEGSIAVVRLSGPQAIV IADRIFSGSVASFASHTIHLGQVIFEETLIDQALLLLMRS PRSFT
GEDVVEFQCHGGFFACSQILDALIALGARPALPGEFSQRAFLNGKIDLVQAEAIQNLIVAENIDAFRIAQTHFQ
GNFSKKIQEIHTLIIEALAFLEVLADFPEEEQPDLLVPQEKIQNALHIVEDFISSFDEGQRLAQGTSLILAGKPNV
GKSSLLNALLQKNRAIVTHIPGTTRDILEEQWLLQ GKRIRLDLAGQRTTDNDIEKEGIERALSAMEEADGIL
WVIDATQPLEDLPKILFTKPSFLLWNKADLTPPPFLDTS LPQFAISAKTGEGLTQVKQALIQWMQKQEAGKTS
KVFLVSSRHMHMILQEVARCLKEAQQNLYLPPEIIALELREALHSIGMLSGKEVTESILGEIFSKFCIGK

>core/269/2/Org2_Gene753

MPRSLSNEQFSVDLEESPGCIVSALVKVSPEVLNKLNKQALKKKIKKEITLPGFRKGKAPDDVIASRYPTNVRK
ELGELVTQDAYHALSTVGDRRPLSPKAVRSNSITQFDLQEGAKVEFSYEAFPAISDLPWENLSLPQEEAASEIS
DSDIEKGLTNIGMFFATKTPVERPSQEGDFISISLHVSKSNDENASSAAIFENKYFKLSEEEMTDAFKEKFLGIS
TGH RVVETITSPEIQSFLRGDTLTFTVNAVIEVSIPEIDDEKARQLQAESLDDLKAKLRIQLEKQAKDKQLQKR
FSEAEDALAMLVDFELPTSLLEERISLITREKLLNARLIQYCSDEELEKRKSELIKEAEEDATKALKLLFLTHKI
FSDEKLTISREELQYMMDVCSRERFGQQPPKDISNDTLQELVMSARDRLTYSKAIEHVLRKAELLASTPSA

>core/270/2/Org2_Gene622

MDQLTTDFDTLMSQLGDVNLT TVVGRITEVVGMLIKAVVPNVRVGEVCLVKRNGMEPLVTEVVGFTQSF AF
LSPLGELSGVSPSSEVIPTGLPLHIRAGNLLGRVLNGLGEPIDVETKGPLQNVDQTFPIFRAPPDPLHRAKL RQ
ILSTGVRCIDGMLTVARGQRIGIFAGAGVGKSSLLGMIARNAEEADVNVIALIGERGREGVREFIEGDLGEEGM
KRSVIVVSTSDQSSQLRLNAAYVGTAIAEYFRDQGKTVVLMMDSVTRFARALREVGLAAGEPPARAGYTPS
VFSTLPRLLERSGASDKGTITAFYTVLVAGDDMNEPVADEVKSILDGHIVLSNALAQAYHYPAIDVLASISRL
LTAIVPEEQRRIGKAREVLAKYKANEMLRIGEYRRGSDREIDFAIDHIDKLNRF LKQDIHEKTNYYEEAAQQL
RAIFR

>core/271/2/Org2_Gene747

MWL VILWALAASLAIALVAKGYRFRVYFRRYAVQVIREVRLSMELKEWALAEQQLLPILKKRSYRRQCLFE
YMRILRKMQRFESEKLLAEAKKLGRGPYFFLEIA YKAYRFGAFKECAQAFASVPQDLFEEEDA AKYASAL
VRLGDLDAACSLIEPWISPLSHQETFVTMGHIYFTSKRYKDAIDFYNRANALGVC PVEVTYNLAQAYRITSSY
AKAGKLFRKLLSNPVYKEEALFNIGLCEQKLGRPGKALLIYQSSDLWSRGDALLMKYAAMAAMDQRDYVL
AEP CWELALRCSTFAKDYKCGLGYGFSLCRLRKYGDAERVYCNLIQN FPECLTACKALAWLCGVGYATLLG
SEEGLMYAKKAVELDHSCETLELLSACEARCGNFDAAYEIQSFLSSRDTSLQEQRRSQILRILRKKLPLNDH
HIVEVDALLAA

>core/272/2/Org2_Gene526

MIENDFPEASNFESSHFYRDKVGVII LCGGEGKRLSPLTNCRCCKPTVSFGGRYKLIDIPISHAISAGFSKIFVIGQ
YLTYTLQQHLFKTYFYHGV LQDQIHLLAPEARQGDQIWYQGTADAI RKNLLYFEDTEIEYFLILSGDQLYNM
DFRSIVDTAIRTHVDMVLVAQPIPEKDAYRMGVLDIDSEGKLIDFY EKPQEKEVLKRFQLSSEDRIHKL TEDS
GDFLGSMGIYLFRRDSLFSLLREEEGNDFGKH LIQAQMKRGQVQTLLYNGYWADIGTIESYYEANIA LTQKP
HAEKRGLNCYDDNGMIYSKNHHLPGAIITDSMISSLLCEGCVINTSHVSR SVLGIRSKIGENSVVDQSIIMGN
ARYGSPSPSLGIGKDCEIRKAIIDENCCIGNGVKLQNLKGYIKYD SPDKKLFVRDNIIIVPQGTHIPDNYIF

>core/273/2/Org2_Gene111

MLNCSNQKHTVTFEEACQVFPGGVNSPV RACRSVGVTPPIVSSAQGDIFLDTHGREFIDFCGGWGALIHGHSH
PKIVKAIQKTALKGTSYGLTSEEEILFATMLLSSLKLKEHKIRFVSSGTEATMTAVRLARGITNRSIIKFIGGYH
GHADTLLGGISTTEETIDNLTSLIHTPSPHSLLISLPYNN SQILHHVMEALGPQVAGIIFEPICANMGIVLPKAEF
LDDIIELCRFGSLSIMDEVVTGFRVAFQGAQDIFNLSPDITIY GKILGGGLPAAALVGHR SILDHLMPEGTIFQ
AGTMSGNFLAMATGHAAIQLCQSEGFYDHLSQLEALFYSP IEEEEIRSQGFPVSLVHQGTMFSLFFTESAPT NFD
EAKNSDVEKFQTFYSEVFDNGVYLSPSPLEANFISSAHT EENLTYAQNIIIDSLIKIFDSSAQRRF

>core/274/2/Org2_Gene683

MFQQKQKLSLKYLP SLRMQQGLQMLQSPLTELSSYVVQEIIDNPFFDLSSLEEEEWSPCYRPTNSTFSYLNQTP
GPQESLYTRLLPQIEEAFSTAEERFIAHQIAGNLSDEGLFLRNPEDFAQELELPLEKIHKVWDTIQNLSPEGIASP
SLQSYWMKLLRNSSHQQAYSIVRDCYPLMTNCEFAPIMKKFSLSLSELRNILKKALGSIPWCPAAACTVKPM
VSTPLPDIYLFYSSGSWKIEVSTRGLPSIKLNKETFFHFYEHLPKKEEQKNLSQQILSAKWLIKNLRKREQTLLQV
METLLPKQEDFLLGKIPAPYPLGIKDLAEDLSFHSTIFRAIENKAVAAPIGIFPLKHLFPRGIHQDSSHSKENVL
QWIRQWIATEQTPLSDSVISDRITAKGIPCARRTVAKYRAQLKILPANKRKKLFYIRSSNSHFRDRQF

>core/275/2/Org2_Gene933

MSKIVYKFGGTSLATAENICLVCDIICKDKPSFVVVSAIAGVTDLLVDFCSSSLREREEVLRKIEGKHEEIVKNL
AIPFPVSTWTSRLLPYLQHLEISDLDFARILSLGEDISASLVRAVCSTRGWDLGFEARSVILTDDSYRRASPNL
DLMKAHWHQLELNQPSYIIQGFIGSNGLGETVLLGRGGSDYSATLIAELARATEVRIYTDVNGIYTMDPKVIS
DAQRIPELSFEEMQN LASFGAKVLYPPMLFPCMRAGIPIFVTSTFDPEKGGTWVYA VDKSVSYEPRIKALSLS
QYQSFCSDYTVLGCGLLEEILGILESHGIDPELMIAQNNVVGFMDDDIISQEAQEHLVDVLSLSSVTRLHHS
VALITMIGDNLSSPKVVSTITEKLRGFQGPVFCFCQSSMALSFVVA SELAEGHIEELHNDYVKQKAIVAT

>core/276/2/Org2_Gene66

MQTIYTKITDIKGNLITVEAEGARLGELATITRSDGRSSYASVLRFDLKKVTLQVFGGTSGLSTGDHVTFLGRP
MEVTFGSSLLGRRLNGIGKPIDNEGECFGEPIEIA TPTFNPVCRIVPRSMVRTNIPMIDVFNCLVKSQKIPIFSSSG
EHHNALLMRIA AQTDADIVVIGGMGLTFVDYSFFVEESKKLGFADKCV MFIHKAVDAPVECVLVPDMALAC
AEKF AVEEKKNVLVLLTDMTAFADALKEISITMDQIPANRGYPGSLYSDLALRYEKA VEIADGG SITLITVTT
MPSDDITHPVPDNTGYITEGQFYLRNNRIDPFGSL SRLKQLVIGKV TREDHGD LANALIRLYADSRKATERMA
MGFKLSNW DKKLLAFSELFETRLMSLEVNI PLEEALDIGWKILAQSFTSEEVG IKAQLINKYWP KACL SK

>core/277/2/Org2_Gene919

MISFRLLLLSGLCALGISSYAETPKETTGHYHRYKARIQKKHPESIKESAPSETPHHNSLLSPVTNIFCSHPWKD
GISVSNLLTSVEKATNTQISLDFSILPQWFYPHKALGQTQALEIPSWQFYFSPSTTWTLYDSPTAGQGIVDFSYT
LIHYWQTNGVDANQAAGTASSMNDYSNRENNLAQLTFSQTFPGDFLTLAIGQYSLYAIDGTLYDNDQYSGFI
SYALSQNASATYSLGSTGAYLQFTPNSEIKVQLGFQDSYNIDGTNFSIYNLTKSKYNFYGYASWTPKPS CGDG
QYSVLLYSTRKVPEQNSQVTGWSLNAAQHIHEKLYLFGRINGATGTALPINRSYVLGLVSENPLNRHSQDLL
GIGFATNKVN AKAISNVNKLRRYESVMEAFATIGFGPYISLTPDFQLYIHPALRPERRTSQVYGLRANLSL

>core/278/2/Org2_Gene124

MMLRGVHRIFKCFYDVVLVCAFVIALPKLLYKMLVYGKYK KSLAVRFG LKKPHVPGEGLVWFHGASVGE
VRLLLPVLEKFCEEFPGW RCLVTSC TELGVQVASQVFIPMGATVSILPLDFSIIKSVVAKLRPSLVVFSEGDC
WLNFIIEAKRIGATTLVINGRISIDSSKRFKFLKRLGKNYFSPVDGFLLQDEVQKQRFLSLGIPEHKLQVTGNIK
TYVAAQTALHLERETWRDRLRLPTDSKL VILGSMHRSDAGKWLPVVQKLIKEGVSVLWVPRHVEKTKDVE
ESLHRLHIPYGLWSRGANFSYVPVVVVDEIGLLKQLYVAGDLAFVGGTFDPKIGGHNLLEPLQCEVPLIFGPH
ITSQSELAQRLLLSGAGLCLDEIEPIIDTVSFLNNQEVREAYVQKGKVFVKAETASFDRTWRALKSYIPLYKN
S

>core/279/2/Org2_Gene589

MKRPFPTYLCIIFYGSCASLSLHAGLSFPEVRGATAAVVHADSGKVFYDKDIDAVIYPASMTKIATALFILKHY
PTVLDTLIKVKQDAIASITPQAKKQSGYRSPPHWLETDGSTIQLHLREELLGWDLFHALLVCSANDAANVLA
MACCGSVEKFMDKLNFFLKEEIGCTHTHFNNPHGLHHPNHYYTTTRDLISIMRCALKEPPFRGVISTTSYKIGAT
NLHGERILSPTNKLLLPGSTYHYPPALGGKTGTTKTAGKNLIMAAEKNRLLVTIATGYSGPVSDLYQDVIAL
CETVFNEPLLRLKELVPPSDCLQLEIANLGKLSCPLPEGLYYDFYASEDREPLSVSFIAHADAFPIEQGDLLGHW
VFYDDEGKKISSQPFYAPCRFERTIKPWKLYMKRVFTSYRTYMSITMLLMYFRIRKHRKYKNLKHYSKI

>core/280/2/Org2_Gene789

MKRAIIIGAGISGLAAGWWLHKKFPQAEILVLDKEAYAGGFVRTESPQGFSFDLGPKGFLTRGDGEYTLKLIH
ELGLQNSLIFSDRAAKNRFVYYRGKAHKISTWTLLRKGLLPSLIKDFRAPCYTQDSSVQDFLKRHSSQNFTSYI
LDPLITAIRAGHSSILSTHMAFPELAKREASSGSLLRSYLKNRSPKSKTDTRYLASLSPSMGTLITTIEKLPAT
WKFSTSVTHIDCSPKEACVTTTPSETFFADMVIYTGPLQQLPVLLPNYGIEENLSKRVLPWNLSISLGWHHANFS
LPKGYGMLFADELPLLGIWNSQIFPQATPGKTVLSLLIEGKWRESEAHAFIAAALSEYLNINQKPDALFSS
QDGMPQHAVGFLEKERILPHLPGNLKIVGQNIAGPGLNRCIASAYHAICDLHTEETLAQPQSSL

>core/281/2/Org2_Gene163

MFSRWITLFLFISLTGCSSYSSKHKQSLIPIHDDPVAFSPEQAKRAMDLSIAQLLFDGLTRETHRESNDLELAI
ASRYTVSEDFCSYTFFIKDSALWSDGTPITSEDIRNAWEYAQENSPHIQIFQGLNFTSPSSNAITIHLDSPNPDPF
KLLAFPAFAIFKPENPKLFSGPYTLVEYFPGHNIHLKKNPNYYDYHCVSINSIKLLIIPDIYTAIHLNLRGKVDW
VGQPWHQGIPWELHKQSQYHYTYTPVEGAFWLCLNTKSPHLNDLQNRHRLATCIDKRSIIIEALQGTQQPAE
TLRGAPQPNQYKKQKPLTPQEKLVLTPSDILRCQRIAEILKEQWKAAGIDLILEGLEYHLFVNKRKVQDYA
IATQTGVAYYPGANLISEEDKLLQNFEIPIYYLSYDYLTDQDFIEGVIYNASGAVDLKYTYFP

>core/282/2/Org2_Gene270

MNKNLVAIFDYMEKEKGIQRSTIIGAIESALKIAAKKTLRDDANISVNINSRTGDIEVFCEKEIVEICQNPSKEIP
LDKAREYDPDCQIGQYMDVPFVSDNFGRIAHAARQIIGQKLRLHAERDVIYEEYRHRVNETLSGVVKRFAKG
SNLIIDLKGVAILPTRFYPKTEKHKIGDKIYALLYEVQESENGGAEVILSRSHAEFVKQLFIQEVPELEEGSVEI
VKIAREAGYRTKLAVRSSDPKTDVPVGAFFVGMRGSRVKNIIRELNDEKIDIVNYSVPSTELLQNLLYPIEQKIAI
LEDDKVIAIVNDADYATVIGKRGINARLISHILDYELEVQRMSEYNKLLIEIQLQLAEFDSPHLDQPLEMEGI
SKLVIQNLEHAGYDTIRRVLLASANDLASVPGISLELAYKILEQVSKYGESKVDKPEIED

>core/283/2/Org2_Gene301

MSMTIVPHALFKNHCECHSTFPLSSRTIVRIASLFCIGALAALGCLAPPVSYIVGSVLAFIAFVILSLVILALIF
GEKKLPPTPRIIPDRFTHVIDEAYGLSISAFVREQQVTLAEFRQFSTALLCNISPEEKIKQLPSELRSKVESFGISR
LAGDLEKNNWPIFEDLLSQTCPYWLQKFISAGDPQVCRDLGVPRECYGYYWLGPLGYSTAKATIFCKETHH
ILQQLTKEDVLLKKNKALQEKWDTDEVKAIVERIYTTYTARGTLKTEAGGLTKETISKELLLSLHGYSFDQL
QLITQLPRDAWDWLCFVDNSTAYNLQLCALVGALSSQNLLDESSIDFDVNLGLYVIQDLKEAVQAFAFSASDEP
KKELGKFLRLHSSVSKRLESVLRQGLHRIAIEHGNARARVYDVNFVTGARIHKTSIFFKD

>core/284/2/Org2_Gene762

MNHLNKEKLHIHNWQPYRACGLLSKVSGNLIEVDGLSACLGECKISSTKDPNLLAEVIGFHNHTTLLMSLSP
LHSVALGTEVLPLRRPPSLHLSDHLLGRVLDAFGNPIDKKEDLPKTHRKPLLSLPPSPMMRQPIDQIFPTGIKAI
DAFLT LGKGQRIGVFSEPGSGKSSLLSAIALGSKSTINVIALIGERGREVREYIEKHSNALKQQRTHIAAPAHET
APTKVIAGRAAMTIAEYFREQGHEVL FIMDSL SRWIAALQEVALARGETLSAHQYAASVFHHVSEFTERAGN
NDKGSITALYAILYYPKHPDIFTDYLSLLDGHFFLTSQGKALASPPIDILSSLSRSAQALALPHHYAAAERLRS
LLKVYNEALDIIHLGAYTPGQDEELDKAVKLLPSIKAFLAQPLSSYCYLDNTLKQLEALADS

>core/285/2/Org2_Gene897

MLKPMYVLSKRLYRWVNQLIKLGDLVKNSRSFSVEWVFISALLLIFGCLGCASVVKVSLVPFLLLSFLAFPLI
LCFRGKGYALLLGVFVTLYVAKYVVGETLYVSFWLSGLGVSFLLAFGLFLQG VWLAQEEEMVKGKEQLRL
SEDLDAQRSAYEDLLLTKSQEKEFLDARAQGLDRELTECQELLKAAYQKQEYLTIDLKILADQKNSWLEDY
AELHNKYIELVSKNGDVVFPWVAEPSVGESQGSERVDVSRWVSALQEKEESLERLRNEILVEKQRCSDYEHR
CQELGLLLQNFTALERRCEELQNLLNQKETQINELHQLVCKSEEKVSVEPSAHAETSCVEEKQYKGLYSQLQ
EQFLEKSETLSLVRKKLFAVQEKYLT LKKKEELTKQDISFDDISMIQGLLERIEILEEEVSHLEELVSRSLSL

>core/286/2/Org2_Gene694

MLRQLCFQVFFFCFASLVYAEELVVVRSEHITLPIEVSCQTDTKDPKIQKYLSSLTEIFCKDIALGDCLQPTAA
SKESSSPLAISRLHVPQLSVLLQSSKTPQTLCSTISQNL SVDQRQKIHAADTVHYALTGIPGISAGKIVFALS
SLGKDQKLKQGELWTTDYDGKNLAPLTTECSLSITPKWVG VGSNFPYLYVSYKYGVPKIFLGSLNTEGKKV
LPLKGNQLMPTFSRKKLLAFVADTYGNPDLFIQPFSLTSGPMGRPRLLNENFGTQGNPSFNPEGSQ L VFISN
KDGRPRLYIMSLDPEPQAPRLLTKKYRNSSCPAWSPDGKKIAFCSVIKGVRQICIYDLSSGEDYQLTTSPTNKE
SPSWAIDSRHLVFSAGNAEESELYLISLVTKKTNKIAIGVGEKRFPSWGAFPPQPIKRTL

>core/287/2/Org2_Gene784

MTWLSGLYFICIASLIFCAIGVILAGVILLSRKLFIKVHPCKLKINDNEELTKTVESGQTLLV SLLSSGIPIPSPCG
GKATCKQCKVRVVKNADEPLETDRSTFSKRQLEEGWRLSCQCKVQHDM SLEIEERYLNASSWEGTVISNDN
VATFIKELVVAVDPNKPIPKPGGYLQITVPSYKTNSSDWKQTM APEYYS DWEHFH LFDQVIDNSQLPADSA
NKAYSLASYP AELPTIKFNIRIATPPFINGKPNSEIPWGVCS SYVFS LKPGDKITVSGPYGESFMKDDDRPLIFLI
GGAGSSFGRSHILDLLLNKHSKREIDLWYGARSLKENIYQEEYENLERQFPNFHYHLVLSEPLPEDIAAGWDK
DDPTKTNFLFRAFNLGQLSRLDNPEDYLYYVCGPPLHNSSILKLLGDYGVERS SIILDDFGS

>core/288/2/Org2_Gene580

MTVTLPKGVFDIFPYLADAKQLWRHTSLWHSVEKAIHTVCMLYGFCEIRTPIFEKSEVFLHVGEESDVVKKE
VYSFLDRKGRSMTLRPEGTA AVVRSFLEHGASHRSDNKFYYILPMFRYERQQAGRYRQHHQFGVEAIGVRH
PLRDAEVLALLWDFYSRVGLQHMQIQNLFLGGSETRFRYDKVL RAYLKESMGELSALSQQRFSTNVLRILDS
KEPEDQEIRQAPPILDYVSDEDLKYFNEILDALRVLEIPYAINPRLVRGLDYYS DLVFEATTTTQEVSYALGGG
GRYDGLISAFGGASLPACGFGVGLERAIQTLLAQKRIEPQFPHKLRLIPMEPDADQFCLEWSQHLRRLGIPTEV
DWSHKKVKGALKAASTEQVSFVCLIGERELISQQLVIKNMSLRKEFFGTKEEVEQRLLYEIQNTPL

>core/289/2/Org2_Gene154

MFRKLFPFSSKKKTGQKQRLRNNGLLQAIQSIKVLLHNEASKEACVLSYYGLLTCVPILVFFLRLSQHLFTNLN
WKEWLIIFPDYKKPIVAIVEAAYHATESNIGLVLVGSFFVFCWAGILMLLSLEDGLNKIFRTSWTPISLKRLV
SYFVITLVSPMIFIHVCGSWIYITQIMPIQYAKLFSLSHSM TALYFISRFVPYLLLYLALFCCY AFLPRVAIQK TSA
LISTLIIGSVWIVFQKAFFSLQVSIFNYSFTYGALVALPSFLLLLYIYTM IYLFGGALTFI IQNRGCTFIFLGDKILP
SCYLQLITSTYILALTTRQFNEGLSPLTAQFIAKQSKVPIGEVSQCLDVLEKEGFLFPYNNGYQPVFNFSELTIK
DIADKLLHREIFKKFNPDLGITFIENSFQNIFNQASKNKENLTLSEIARRIK

>core/290/2/Org2_Gene859

MVCENNILSGRGLELLKKKSNITLTPTIYSVSNHNIKLDKDFSPHALSVIKTLRKAGYIAYIVGGCIRDLLLNTTP
KDFDISTSAPKEEIKAFKNCILVGKRFRLAHIRFSKQIIEVSTFRSGSTDEDLITKDNLWGTPEEDVLRRDFTI
NGLFYDPEHEEIIDYTGGVNDLRNRYLRTIGDPFTRFKQDPVRMLRLLKILSRSPFTVETQTQEALIA CRQELIK
SSQARVFEELIKMLNSGA AKNFFQLLIENHLL EILFPYMDKAFRLNRAL EEQ TATY LKALDDKILKKEAEYDR
HQLMAIFLPLVNFNVRYKHQKHPYLSLTSVFDYIKNFLEQFFADSFTSCSKNFILTALILQM QYRLTPLIPTK
KALFFNKLLHHTRFLEALSLEIRSIVYPKLDKVYVAWIRHHQTLKCKKDSHSQK

>core/291/2/Org2_Gene261

MISLLKMPKLSPTMEVGTIVKWHKKSNDQVSFGDVIVEISTDKAILEHTANEDGWIREILRHEGEKIVIGTPIA
VLSTEANEPFNLEELLPKTEPSNLEASPKGSSEEVS PATTPQAASATFTA VTFKPEPPLSSPLVFKHV GTTNLS
PLARQLAKEKNIDVSSIQSGPGGRIVKKDLEKAPPKSIAGFGYPESPEVPPGSYHEENLSPIREVIAARLQAAK
ISIPHFYVRQQVYASPLLNLLKELQAQGIKLSINDCIVRACALALKEFPSINSGFNSVDNKIVRFD TIDISIAVAIP
DGIITPIIRCADRKNLGMISAEIKSLALKARNQSLQDTEYKGGSFVSNLGMTGITEFTAIVNPPQAAILAVGSV
TEQALVLDGEITIGSTCNLTLSVDHRVIDGYPAAMFMKRLQKILEAPAVLLLN

>core/293/2/Org2_Gene709

MFEAVIADIQAREILDSRGYPTLHVKVTTSTGSGVEARVPSGASTGKKEALEFRD TDS PRYQGGKGV LQAVKN
VKEILFPLVKGCSVYEQSLIDSLMMDSDGSPNKETLGANAILGVSLATAHAAAATLRRPLYRYLGGCFACSLP
CPMMNLINGGMHADNGLEFQEFMIRPIGASSIKEAVNMGADV FHTLKKLLHERGLSTGVGDEGGFAPNLAS
NEEALELLLLAIEKAGFTPGKDISLALDCAASSFYNVKTGTYDGRHYEEQIAILSNLCDRYPIDSIEDGLAEED
YDGWALLTEVLGEKVQIVGDDL FVTNPELILEGISNGLANSVLIKPNQIGTLTETVYAIKLAQMAGYTTIISHR
SGETTDTTIADLAVAFNAGQIKTGSLRSERVAKYNRLMEIEEELGSEAIFTDSNVFSYEDSEE

>core/294/2/Org2_Gene676

MDIKKLFCLFLCSSLIAMSPIYGKTGDYEKLTLTGINIIDRNGLSETICSKEKLKKYTKVDFLAPQPYQKV MRM
YKNKRGDNVSCLTAYHTNGQIKQYLECLNNRAYGRYREWHVNGNIKIQA EVIGGIADLHPSAESGWLF DQT
TFAYNDEGILEAAIVYEKGLLEGSSVYYHTNGNIWKECPYHKGVPQGKFLTYTSSGKLLKEQNYQQGKRHG
LSIRYSEDSEEDVLAWEEYHEGRLLKAEYLDPQT HEIYATIHEGNIGIQA IYGYAVIETRAFYRGEPYGVK VTR
FDNSGTQIVQTYNLLQGAKHGEEFFYPETGKPKLLL NWHEGILNGIVKTWYPGGTLESCKELVNNKKSGLL
TIYYPEGQIMATEEYDNDLLIKGEYFRPGDRHPYSKIDRGCGTAVFFSSAGTITKKIPYQDGKPLL N

>core/295/2/Org2_Gene81

MKKT MVIDTSVFIYDPEALFSFENTRIIPFPVIEELEAFGKFRDESAKNASRALSNIRLLLLENAKTKVTDGVLLP
SGSELRIEVAPLSNDDRRGKLLTLELLKIIAKREPMVFVTKSLGRRVRAEALQIESRDYESKRFSFRSLYRGFRE
LQVSQEDIENFYKNGYLDLPLDVSSPNEYFFMSAGENHFALGRYYVSEGKIIALKAMDKSVWGKPLNTEQ
RCALDLLLRDDVKLVTLIGQAGSGKTILALAAAMHKVFDKETYNKVLVSRPIVPMGRDIGFLPGLKEDKLM
HWMQPIYDNMEVLFSINQMGNSSSEALQALMDAKKLEMEALTYIRGRSLPKAFIIDEAQNLTPHEIKTIISRAG
KGTKIVLTGDPTQIDSLYFDENSNGLTYLVGKFHHLALYGHMFMTRTERSELAAAAATIL

>core/296/2/Org2_Gene773

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VETLAADLEKIEQHLDQKNAQLHELLSHLPNYPADDIPVSEDKAGNQVIKSVGDLPIFSFPPKHHLELNQELDI
LDFQAAAKTTGSGWPAYKNRGVLLIEWALLTYMLQKQAAHGFQLWLPPLLVKKEILFGSGQIPKFDGQYYR
VEDGEQYLYLIPTAEVVLNNGFRSQDILTEKELPLYAACTPCFRREAGAAGAQERGLVRVHQFHKVEMFAFT
TPNQDDIAYEKMLSIVEEMLTELKLPYRLSLLSTGDMSFTASKTIDAEVWLPGQKAFYEVSSISQCTDFQSRRS
GTRYKDSQGKQLQFVHTLNGSGLATPRLLVAILENNQQADGSVVIPEVLRPYLGGLEILLPKDQ

>core/297/2/Org2_Gene597

MLPLIIFVLLCGFYTSWNIGANDVANAVGPSVGSGVLTLRQAVVIAAIFEFFGALLLGDRVAGTIESSIVSVTN
PMIASGDYMYGMTAALLATGVWLQLASFFGWVSTTHSIVGAVIGFGLVLGKGTHIYWNSVGIIISWILSPF
MGGCVAYLIFSFIIRRHIFYKNDPVLAMVRVAPFLAALVIMTLGTVMISGGVILKVSSTPWAVSGVLVCGLLSY
IITFYVHTKHCSYISDTPKKGSLTYRLKERGGNYGRKYLVERIFAYLQIIVACFMAFAHGSNDVANAIAPV
AGVLRQAYPASYSYTLIRLMAFGGIGLVIGLAIWGWRIETVGCKITELTPSRGFSVGMGSALTIALASILGL
PISTTHVVVGAVLGIGLARGIRAINLNIKDIVLSWFITLPAGALLSILFFFALRALFH

>core/298/2/Org2_Gene1018

MIMGLQSRLQHCIEVSQNSNFDSQVKQFIYACQDKTLRQSVLKIFRYHPLLKIHDIARAVYLLMALEEGEDLG
LSFLNVQQYPSGAVELFSCGGFPWKGLPYPAEHAEFGLLLLQIAEFYEESSQAYVSKMSHFQQALFDHQGSVF
PSLWSQENSRLLEKTTLSQSFLFQLGMQIHPEYSLEDPALGFWMQRTRSSSAFVAASGCQSSLGAYSSGDV
GVIAYGPCSGDISDCYYFGCCGIAKEFVCQKSHQTTEISFLTSTGKPHPRNTGFSYLRDSYVHLPIRCKITISDK
QYRVHAALAEATSAMTFSIFCKGKNCQVVDGPRLRSCSLDSYKGPNDIMILGENDAINIVSASPMEIFALQ
GKEKFWNADFLINIPYKEEGVMLIFEKKVTSEKGRFFTKMN

>core/299/2/Org2_Gene926

MDKQSSGNSGCIWHPFTQSALDSTPIKIVRGEGAYLYAESGTRYLDAISSWWCNLHGHGHPYITKKLCEQAQ
KLEHVIFANFTHEPALELVSKLAPLLPEGLERFFFSDNGSTSIEIAMKIAVQYYYNQNKAKSHFVGLSNAYHG
DTFGAMSIAGTSPTTVPFHDLFLPSSTIAAPYYGKEELAIAQAKTVFSESNIAAFIYEPLLQGAGGMLMYNPEG
LKEILKLAKHYGVLCIADEILTGFGRTGPLFASEFTDIPDIIICLSKGLTGGYLPLALTVTTKEIHDAFVSQDRM
KALLHGHTFTGNPLGCSAALASLDLTLSECLQQRQMIERCHQEFQEAHGSLWQRCEVLGTVLALDYPAEAT
GYFSQYRDHLNRFFLERGVLLRPLGNTLYVLPPYCIQEEDLRIIYSHLQDALCLQPQ

>core/300/2/Org2_Gene23

MAEISTPSLPDSSIVSQKTPPVPDPDSSPDHIPTIPTQAPFKPQRKKETPSSIVNAIAFAILAFLSCLGGVFAICLCG
SLEITMPLFILTAVFIAFTLLYFIHYLEKPKIPEPLTPPPSPTLRAPTLTPEIPAPAPGIPLPPTLPKVDRTKLTCNP
DIHYPSTYDPKACFSLKQLFSLDPETRPEDRKYSNKLASILLRSKEKSGFRFHCFCGHFSDKILNKKSGAVV
ISSHSSMDFSTTLGRAFAVTTCLQRSCWEKIKNNIPTPEKHLPIGSCVSGPWDVEEGAQLYTSHLIVNPPTLET
LIKEKMRRAITLKDFSMKEAFTNLVLAYLQCFDICIEHNLESVQLEVFGLNNLSADQEEFTTWESCCHLALLE
SVRILLASKEEYALSNVSVNSISQVPLQTACRALFLN

>core/301/2/Org2_Gene644

MKKQVYQWLASVLLALTISGYAELPLSEQVKVSHTYTTLDEVKDYLKRGFVETRKQDGVLRAGDVRAR
WLYFREDIKNPSDKDKYNPLPVNRYRSEFYLYIDYRAERNWLSSKMNWTAIAGGENTAAGVDINRAFLGYR
FYKNPETRTDFFMEIGRSGLDLFESEVQFQSNFDGLHIYWTRELSKDYPYQVIVHGGPFVVMNTKKHYAW
VVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKCVWQWLVGKHSQVPWINGQKKPLYL
YGAFLMNPLAKATKTTLNGKENLAWFIGGTGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFW
FAQAIAANYDPKEANGFTNYKGFSALYMYGITDSLFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF

>core/302/2/Org2_Gene1000

MQSWLQSLQERNILENFTAGLESVEGPAAAYLGFDPTAPALHIGHWIGICFLKRLAALGITPIALVGGATGMV
GDPSGKQSERSLLQTSEVFDNSQKITACLQRYLPGVTLVNNADWLQEISLIDFLGDIGKHFRLGQMLVKDTIK
QRVHSDEGISYTEFSYLILQSYDFYHLFKNYGTILQCGGSDQWGNITSGIDFIRRKGLGQAYGLTYPLLTNAQ
GKKIGKTESGTVWLDSDLTSPFELYQYLLRLPDDTIPKIARTLTLLSNEEIQDIDRRVQTDPAVKEFVAQDILS
AIHGDLGLEEALSVTRSMHPGNLSSLSEKDFHELFAAGMGASLDKSEVLGKRWLDLFLVLGLCKSKGEIRRLI
EQKGVYINNVPIANEHSVCEEQDICYGHYVLLAQGKKRKLVLVLN

>core/303/2/Org2_Gene407

MTVAEVKGTFLVLCLGCRVNQYEVQAYRDQLTILGYQEVLDSEIPADLCIINTCAVTASAESSGRHAVRQLC
RQNPTAHIVVTGCLGESDKEFFASLDRQCTLVSNKEKSRLIEKIFSDDTFPEFKIHSFEGKSRAFIKVQDGCNS
FCSYCIIPYLRGRSVSRPAEKILAEIAGVVQGYREVVIAGINVGDYCDGERSLASLIEQVDRIPGIERIRISSIDP
DDITEDLHRAITSSRHTCPSSHLVLQSGSNSILKRMNRKYSRGDFLDCVEKFRASDPYAFATTDVIVGFPGESD
QDFEDTLRIIEDVGFIVHSPFSARRRTKAYTFDNQIPNQVIYERKKYLAEVAKRVGQKEMMKRLGETTEVL
VEKVTGQVATGHSPYFEKVSFPVVGTVAINTLVSVRLDRVEEEGLIGEIV

>core/304/2/Org2_Gene751

MNKKNLTICSFCGRSEKDVEKLIAGPSVYICDYCIKLCSGILDKKPSSTISSAPVSETPSQPSDLRVLTPKEIKKH
IDEYVIGQERAKKTIAVAVYNHYKRIRALLHNKQVSYGKSNVLLLGPTGSGKTLIAKTLAKILDVPFTIADAT
TLTEAGYVGEDVENIVLRLQLAADYDVARAERGIIYIDEIDKIGRTTANVSITRDVSGEGVQQALLKIVEGTGA
NVPPKGGRKHPNQEYIRVNTENILFIVGGAFVNLDKIIAKRLGKTTIGFSDDQADLSQKTRDHLAKVETEDLI
AFGMIPEFVGRFNCIVNCEELSLDELVAILTEPTNAIVKQYMELEAFENVKLVFKKEALYAIKKAKQAKTGA
RALGMILENLLRDLMEIPSDPTVEAIIHQEDTIAENKAPIIIIRRTPEAIA

>core/305/2/Org2_Gene76

MIKFLSQLFIRHWPRKVVS LGFAIIWILVGQSVTITRTL TNVPVRIVDLHPDQTVLGLQKSGFLNKKVSLTITG
NKNTVQDLRPSNLEVVIS AANHTE SWIATIDKHNLSVDHEINIRKDIHSVDANDIFVRLTQYVTE DILLTITKP
IGSPPKGYEYLDVWP KYLNQKVSGPK EYINALKEQGLELTFNLNKISFEELERNRIAQGS HDEIIFPIK EWKKI
LIPFENTFMDLNDPQADFLRLFLKRECIPLNLNLPVFLFFPVTFIQTMNPLEYSLDPVPPIILNHGIHQINIPLYV
KDVS RQFLDVVKNNMVL TIVMPSPQDPSSINWAIEFLDEKTLENTFLQTIIAQEHGILHDIALIDEAGIRHRFRE
YLRKLALFTADGEPLNLIAEIKNNKVVIQTKTKETTKLYKKEW

>core/306/2/Org2_Gene902

MLKLQLCALFLFGYLAIVFEHIVRVNKS AIALAMGGLMWLVCFSHIPMADHMILVEEIADMSQVIFFLFSAM
AIVELIDAHKGFSVIVKFCRIQSRTL LLWALIGLSFFLSAALDNLT SIIIIISILKRLVKAREDRLLLGAICVIAVNA
GGAWTPLGDVTTTMLWINNKITSWGIIRALFVPSLVCVLVAGFCGQFFLRKRGSTLIAKDVELQSAPPKSLWII
FIGLGSLLMVPVWKACGLPPFMGALLGLGLVWLTSDWIHSPHGEDRYHLRVPHILTKIDISSITFFIGILLAVN
ALS FANLLTDFSLWMDKIFSRNVVAIVIGLLSSVLDNVPLVAATMGMYTLPLDDTLWKLIAYAAGTGGSILII
GSAAGVAFMGLEKVDFLWYFKRISWIALASYFGGLFSYFVLES LNFFI

>core/307/2/Org2_Gene177

MSSAIARDCFPSPSPQPSSTLGVHPPKYKSLILSVSLIVLGVLLLCVGMLLL VNAIFSFSVLT TVGLGGAGVFLGS
LLLILGLIFFVSYHRKLSEATRSLEQKITLEYQPWADLRKELNEVQEW SNFLLDEWEDFKEVVAQHKSQFATF
EGDLLLFGREVEKYETIWKELDGRDVALLTELKNIWGPLEFLRKKGDRLQCEIDKLRKEVMKVGKSGLKLA
CELT KFKSALKDVKIEQECYRDKRKVEKLEVFPEGYRRELLEVLKTRLSVEKEIQLFEEVVS AFEEKLASLHR
TVFSEEELQEALDKAKAELLDIQVRKSVVEDLSCEPTLIQYHLLRLYE VQCRIVEQFLTQTFSSEQEKVLEEYE
ALKARIRKTLRVKLDQVRANVAFVASTTDLLSESES LDGNDSVFEDA HDDFLD

>core/309/2/Org2_Gene775

MIETREEVGSANFVSLERAIEDLRAGKFVIVVDEASREDEGDLIIAGEKITVEKMTFLLQHTTG VVCAALSQER
LLSLDLPPMVKDNRCRFKTPFTVSVDAAHGVTTGVSAADRTKV VQLLADPKSKPEDFISPGHFFPLASSPGGV
LK RAGHTESTVDLMELAGLQPCGVLAELVNEDYSMMRLPQILEFARKHNI AVIPVTSIIAHRMLSDRLVSKIS
SARLP TIYGDFTIHVYESLLEGMQHLALVKG NVAGKSNVLVRVHSECVTGDILGSKRCD CGEQLSSAMS YIA
EKGTGVLVYLRGQEGRGIGLGHKVRAYALQDNGYDTVDANLAMGFPVDSREY GIGAQILVDLKLTTIKLIT
HNPQKYFGLQGFGLSITERVPLPVRISEDNEQYLRTKQERMGHWLDLPCCNNRVQ

>core/310/2/Org2_Gene723

MLCYSPNYVTDLYRISLSAEESLG GIRAFPQAESLLGGACALNFPDLEERLPDLRKELLFLGSNDRPDACGGK
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RDCETLFLNPPANKLDCWEIAGFRVDASFPVKQKIRRIGVDKFLLMHGGAEYADKATKERVDFVSSDEENYS
RYLA VGDVLLWDGNCWQTCGEFQGASSRAPLFEVKRIDDKVM IADLWNVGGTQRQTISLVKGVPSPIEINE
VIREIEFTGMRSWSKPIVLVGGQRLILSPDDWVLRTAKGWEKLSRADQIQDYVTGKVTGPLL VFEKLEKDLR
GFVLRGHMFNAQRTL VETISLPLKQGFEP AVASQEVSSNTRSAAAH PGATNRGGS

>core/311/2/Org2_Gene381

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VMGLITVGLYFMSLNKLTLDYFRREHLLRMEKKTQETAEPILVTPSADDAKKIAVEKKKDLASARMEEHEA
SQRQDARHRRIGREAQGSFFYSSRNPEHRRSFGSLSRFKTKPSDAASTRPASISPPFKDDFQPYHFKDLRSSSF
SGASSAFTPIMPASSRSPNFSTGTVLHPEPVYPKGGKEPSIPRVSSSSRRSPRDRQDKQQQQQNQDEEQKQSK
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>core/312/2/Org2_Gene800

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RVVEISSFQLATQEEHIPALSGSVFLNFSRNHLDYHRNLDAYFDAKLRIQKCLRQDKTFWVWEECSLGNYSYQI
YSEEIEEILDKGDALKPIYLHDRDNYCAAYALANEVGVWSPEGFLKAIRTFEKPAHRLEYLGKKDGVHYIND
SKATTVTAVEKALMAVGKDVIVILGGKDKGGDFPALASVLSQTTKHVIAMGECRQTIADALSEKIPLTSLKD
LQEAVSIAQTIAQEGDVTLLSPGCASFDQFQSFKERGAYFKLLIREMQAVR

>core/313/2/Org2_Gene813

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PALIAMDFGLMGPNYSISTACATGNYCIDAAYQHLVSGRADMIICGGTEAAVNRI GLEGFIANRALSERNDAP
DQASRPWDRDRDGFVLGEGAGILVLETLESALRRDAPIFAEMLGSYVTCDAFHITAPRDDGEGITACVLGAL
NSAGIPKERVNYVNAHGTSTPLGDLSEVLAVKKAFGSHVRNLRMNSTKSLIGHCLGAAGGVEAVVAIQAILT
GKLHPTINLDNPIAEIEDFDVVANKAQDWDIDVAMSNSFGFGGHNSTILFSRYVP

>core/314/2/Org2_Gene605

MLVSIETFSSIASGSPVQKAAEACYTQYSKQPSSKEVLSSFSWIQELSLFPDRYNLATGASELIKQHWLHNNHS
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DPFITYAMVAAKKAIAMSRWDKDHLPSPDVRGCVIVGSGMGGLSTLDQGMERLLVIHKKLSPPFIPYIITNMA
PALIAMDFGLMGPNYSISTACATGNYCIDAAYQHLVSGRADMIICGGTEAAVNRI GLEGFIANRALSERNDAP
DQASRPWDRDRDGFVLGEGAGILVLETLESALRRDAPIFAEMLGSYVTCDAFHITAPRDDGEGITACVLGAL
NSAGIPKERVNYVNAHGTSTPLGDLSEVLAVKKAFGSHVRNLRMNSTKSLIGHCLGAAGGVEAVVAIQAILT
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>core/315/2/Org2_Gene970

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RKADITSKT
TAFLACL VVALPFFLILKEPDLGTALVLCVTLTIFYLSNVHSLLVKFCTVVATIGIIGSLLIFSGIVSHQVKVPY
ALKVIKEYQYERLSPSNHHQRASLISIGLGGIRGRGWKTGEFAGRGWLPYGYTDSVFSALGEEFGLLGLLFTL
GLFYCLICFGCRTVAVATDDFGKLLAAGITVYLAMHV LINISMMCGLLPITGVPLILISYGGSSVISTMASLGV
LQSIYSHRFAKY

>core/316/2/Org2_Gene450

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AIFLGIALRLSGERGRPVERFIDGFSEIMLRMVNMIMSFAPYGVGASMAWISGNHGLGVWLWQLGKFIIAYYLA
CLFHATLVFGGLVRFVGCKMSFSKFLSSMMDAISCAVSTASSSATLPVTMRCVSKNLGVSAEVSGFVLP LGAT
VNMNGTAIFQGMMAVFIAQAYNCPLSLSSLLLLVVTATFSAVGSAGVPGGGMITLGSVLASVGLPIQGIAILA
GIDRLRDIVGTPMNILGDAVVATYVASGEGELSPYESIKQESVETT

>core/317/2/Org2_Gene688

MKKIFYSFVLLSCIFPYVGCAQVFVGLDRIFSEGEYTRCIQGKKIALISHSAAINSRGQDALSVFYSRKHDCTVE
ILCTLEHGYGATPTETVGNQPSRYPNLRVSLSLYGVKEVPKEVAEHCDVFVYDVQDIGVRSYSFVTVLMQIV
KASERYGKQLIVLDRPNPMGGRIVDGPLPNPTTSGSLAIPYCYGMTPGELALFFKKTYAPNANVVVIPMKGW
NRSMTFDETG LIWMP TSPQMPDPQSPFFYAATGILGALSVASIGVGYTL PFKVLGAPWMDGEKVADELNRM
KLPGVLFLPFFYEPFFGKYKMEMCSGVLLVLQDPKIFYPVETQCTIWGV LKALYPKQVEQTLKSIERIPARRSS
ICNLFGGDEFLSISHKERYIWPLRRLCKESRESFHQLRSSCLLSEYAES

>core/318/2/Org2_Gene971

MKKNASHKTNDKKSLSIWSIGGSIFAMFFGAGNIVFPLALGYHYNAHPWSAYFGMMLTAVCVPLLGLVSM L
FYSGDYQKFFFSIGRIPGMIFITAIILLIGPFGGIPRAIAVSHATLISLSEHKSAFIPSLPIFSAICCVLIYIF SCKLSRL
IQWLGSVFFPIMLVTL LWIIRSFMIPTHPMVQE FIPNARQAWLAGFIEGFNTMDLLAAFFFC SIVLISLRQLVA
EEKHPTEEEIPLSFQGISKKNKRSLALGFFLAAILLGMTYLG FVL SAA RHAGLLVNVSKGHILGRISAIALGPNS
ILAGVSVFIACLTTEIALVGIVADFLARVVSFKKLN YASAVICTLIPTYLISILNFETISHLLLPLLQLSYPALIVLA
CGNIAYKLWNFRYSPVLFYLTLSLTIVLKL VN

>core/319/2/Org2_Gene191

MDKETLENIYRHFRYRFLKLNILPAFLGLLLLCSPNTLN YTQVDVIFSDRLCSCLLIFLAIASLTKRSLLWLGAP
LGIWVTLFACVAGRSPTIFANDTLIGFAILAVVCISPTRPEALEVGPTLPEGFSYNPSAGGRRAAVLFLSLLGWL
EARYLTASSLGITSSQSSNFLLYSSIMTVYSLLVVL SLAGSERRWHTRPKIVIATALALTGV IILTLLPIILHQLR
YDCWLCLCLTIEPALAVVFAYDETRATLRYISQFLGDKRALTRASF FGSEYYKHTLSWEERTV LPLRKAYKQ
AFEGISFPINQLLAILVATVFVKVNSSMGLPTFPRNFLNICCWFIIVLFILAF AESLRHLRWMNLIFSAAILFSPVL
FHIPVESPMFLPIIVTGLILILSIGKRRRTKRKL

>core/320/2/Org2_Gene337

MIPTMLMFFHICFTLCSGFISLSQIALFSLPTSLISHYKRSKSKKQQRVATLLLHPHLLITLIFCDIGLNIAIQNCF
AILFGDAASWWFTVGLPLAITLILGEILPKAVALPFNTQIASSVAPLILCVTKIFKPLLHWGIVGINYVVQWILS
KQQIDIIQPQELKEVLQ SCKDFGVVNQEE SRLLYGYLSLSDCSVKERMQPRQDILFYDIQTPLENLYLLFSKQH
CSRVPICNDNLQNLLGICTARSLLLHDKPLQSSDDLPL LKKPYMPETISAKMALCQMAAEDET LGMIIDEY
GSIEGLITQEDLFEIVAGEIVDQRDNKILYTTSGADVIIASGTLELREFSEIFDINLPTN NNIATIGGWLIEQIGTIP
TTGMKLSWNNLLFQVLDAAPNRIRRVYIRKLYD

>core/321/2/Org2_Gene143

MDESDGEEASKDSAFSASFVKSSTRESKNTVTHSTASRTLYILRQDCSYDPRALKVDDEFWVEKRL
DAKNPDSLNAFVKEVGTHYVASVTYGGIGFQVLKMSYLQVEELEKEKISISVAAASSLLKSKTSNATEKGYS
SYQSESSAQTVFLGGTVLPDLQQDKLDFKDWSESIPIPLAISVSSITDLIPELFPSEDAQVLSQKKSALGQV
ILNYLESHKPKEEGPKPVQITSGFNSSSSVFTLQAAKAPKTVSFPYIDYWSTRIPYLFPTLKETSGAQPLSFYLR
DDIFEQQNLVHNTSYILASTSVRLGYFGDSYRDYDALSFYGSWPQAYFDWAGYKDRCTWTLEKLNTTGDLF
IRSGDEIRLKHNTSGKYLATTSMDSGYQKLTCTTQTSDSVFIITV

>core/322/2/Org2_Gene872

MNLPVSLACLLLSGCVFFLGVFVSSSLYARKKRAFLEKIQKLEHENQLLQTSNLNLSRHQEQLIEDFSNRLALSS
HKLIKDMKEEAQNYFGDTSKSFQSILSPIQTTLTTFKQSLETFETKHAEDRGRLEKISQLLAVEKKLEHETHV
LTDILKHPGSRGRWGEIQLERILELAGMLKYCDYDSQTTSAQGAFRADIIIRLPQDRCLIIDAKAPISDSYFSVE
EIDKGDLDVKIKEHIKTLKSKSYWEKFHQSPYVILFLPGESLFNDAILAPELMEIGASSNVILSSPLTLLALLK
TIAYMWKQENLQKQIQEVSLGKELHRRQLQVVFTHFQKIGKNLNQTVQSYNDMTSSFQYRVLPTLRKFEGLE
TSSSHQIEEPTPIESLATSFPHTCDIDTNLAVIESLEKQD

>core/323/2/Org2_Gene958

MKTAFHSCYSWFCWLFSLVLFVGGIAGGEPLCPDCKYETKSVLRSDQLPDHLWNYENDCYLTGYVQSLLD
MHFLDSRTQVVIEKNRAYLFSLPVDSSLSEAITNFVRDLPFICAVEICERPYGECITRSSAERPLLPEKTLGMPI
FCGKEGVWLPQNTILFSPLIADPRQVTNSAGIRFNEKVVGNRVGATIFGGDFILLRLFDVSRFHVDCDFGIQGG
VFSVFDLDHPESCMVNSDFFVAGLWSGAIDKWSFRFRLWHLSSHLGDEFILTHPNFPRFNLSDEGVDLFISFR
YTPQIRLYGGCGYIVSRDLTFPERPFYCEWGAELRPFGLREGNLHAQPIFAMHFRCWEEQKFGLDQSYILGME
WAKFQEIGRKIRAVLEYHQGFSKEGQFIREPCNYYGFRLTYGF

>core/324/2/Org2_Gene750

MTTIAIEAAKKVLIKLNRNAGYQAYFVGGCVRDMLMNRPLEDIDIATNASPTIVSTIFPDVISIGVAFGIIVVKQD
GRLFEVATFRSDGEYKDGRHPDRIIFSSMREDALRRDFTVNGMYYPFEDKVDFVEGTRDIEKKVIRAIGH
RLRFSEDKLRILRAIRFSSSLGFTLDPTTERAIKEAPALVNSVSPERIWQELKKMLKRQPYGALSLLLKLKVLIF
IFPELRDIPYSLRRTTIEFARKFNPTHFPEILFLLPLFQGVSEEAATVAFGRRLRISNKLKLIESWYEALPHFQ
GNRVFWAHFLASPTAPLFLELFSALQKDPQRQHFISRVQELESRLQFILRIKTSSPVVSAPDLIAKGISPGRLL
GDLLREAEILSIENECLDKEKILLLLQEKGFWK

>core/325/2/Org2_Gene604

MKNLKEDFPIFAAKAKENEPFIYLDAAATTQKPQQVIDAVANFYTSSYATVNRAIYSSSRNVTEAYAAVREK
VRKWVSAASDSEIVFTRGTAGLNLALSVNDLWIPKGGVVLVSEAEHHANVLSWEIACRRRGSVKKIRVH
DSGLIDLDLEKLLNEGAQFVSIPHVSNTGCVQPLQQVAELVHRYDAYLAVDGAQGAPHLPIDVQLWDVD
FYVFSSHKIYGPTGIGVLYGKKDLLDQLPPVEGGGDMVAIYDHQNPEYLPAPMKFEAGTPNIAGVLGLGAAL
DYLDGLSAKFIYDKEIALTTYLHKELLEIPGVEILGPSIEEPRGALIGMTIDGAHPLDLGFLDLRGIAVRTGHQ
CAQPAMERWNVGHVLRVSLGIYNDEDDIDQFILVLQDSLDKIRR

>core/326/2/Org2_Gene176

MVVVALFILGIFFLSGSLAFLVHTSCGVLLGAALPILCIGLVLLAVALIVFLCHKHKTRQDLDDYYDQDLDSLVI
HKKEIPNDISELRVTFEKLQNLQFHTKDFSDLSQELQGKFINCMEKWLLEDEVTKFLIVRDRFLETRRNFTT
FGEQVKGIQSNIFDLHEEKSSLYLELYRLRKDLQVLLNFFLLPPGILKVDYDEIEAIKGLFIRLTSRLDKLDVKA
QERKKFINEMSREFKEVEKAFFDIVDRATKKLMDRAKKESPARLFMGRTESLLEMKKNEEALKNQGLDPENL
SHPELFSPYQQLLILNYLNSEIVLHHYEFLISGTVTSGLTLEECENRMRAASTGLNALLVRKLQFRGAIKSAYF
EKLTEIEKELRSLQDVIKSLELELIHKIKDIVTEET

>core/327/2/Org2_Gene313

MTDSNPLPSYTDASLYRTPAKHSYPIRLPLNRTDRIEKILKIVTLTLALACALGFSIAAGILAMPIFSAVVVITLA
IAAVSLYSLLKKPKLYEILPQIEPESEQSSLSPSPQPPEQQDLPLQIDPLDPESLPEVSLADLTTPPEELTAITVTP
GYEALLEQNWDLPLSLAAVDPSFTTETPQQPCFIWKLKDSKLIFISTSGDIAVPRIKTQGRVMIVNAANENISR
EGGGTNKALSLATSLQCWNASRLPRAHSRSGSQLQPGECRSKAWENS DHTSNDHVPKGKAHFLAQLLGPEAA
KCNNDPKQAFEVSKKAFHNLFQEA EIIGVDVIQLPLIGCNLFAPSRLNLGKTRAEWIEAIKLALITSLQDFGW
EQDNQEEQKIILTDKDQPPHIPPRFDLTTP

>core/328/2/Org2_Gene244

MKKQRSHYKKNL LLLLLSILVGLGLGSVQSPWIVYSAECIANTFLKFLRLLSIPLVFCALGSTITSIQNFNTMV
TLGKRILYYTLLTTVIAASIGLLLFLLRPQMITQDALATTTKCNPLGYLDVLSDTLPENIFKPFLQGNVISAAC
LAVLLGTASLFLQEKEKHFNQFFNSFFSIFLN LARGGLKLLPIAMLGFSVILFKELKDQSNLTMFAEYLLCVI
GANLAQGFIVLPILLKINKVSPLKVAKAMSPALVTAFFSKSSAATLPLTMELAEDDLKINKNLSRFSFPLCSVIN
MNGCAAFILITVLFVATSNGMIISPLMSLGWIFATLAAIGNAGVPMGCYFLTSLTSMNVPLSILGLILPFYT
VIDMIETSLNVWSDCCVSLAN

>core/329/2/Org2_Gene338

MTNSALFWIGVNIICIVLQGFYSMMEMACVSFNRVRLQYYLTKDHKKARYINFLIRRPYRLFGTVMLGVNIA
LQVGSESSRNCYRALGITPDYAPFTQIFIVVIFAELLPLTISRKIPEKLALWGAPILYYSHYIFYPLIQLIGSLTEGL
YYLLNIRKEKLNSTLSRDEFQKALETHHEEQDFNTIATNIFSLSATCADQVCQPLEQVTMLPSSANVKDFCRTI
KNTDINFIPVYHKARKNVIGIAHPKDFVNKALDEPLINNLHSPWFITAKSKLIRILKEFRDNRSSVAVVLNASG
EPIGILSLNAIFKILFNTTNIAHLKPKTISVIERTFPGNSRIKDLQKELDIQFPQYPVETLAQLVLQLLDSPA EVGT
SVIINNLLLEVKEMSLSGIKTVSIKNLLS

>core/330/2/Org2_Gene596

MDKLTVQDLSPEEKKVLVRVDFNVPMQDGKILDDIRIRSAMPTINYLLKKHAAVILMSHLGRPKGQGFQEEY
SLQPVVVDVLEGYLGHHVPLAPDCVGEVARQAVAQLSPGRVLLLENLRFHIGEEHPEKDPTFAAELSSYGDFY
VNDAFGTSHRKHASVYVVPQAFFPGRAAAAGLLMEKELEFLGRHLLTSPKRPFTAILGGAKISSKIGVIEALLNQ
VDYLLLAGGMGFTFLQALGKSLGNSLVEKSALDLARNVLKIAKSRNVTIVLPSDVKAAENLQSKEYSVISIDQ
GIPPHLQGFDIGPRTTEEFIRIINQSATVFWNGPVGVEVPPFDSGSIAIANALGNHPSAVTVVGGGDAAAVVA
LAGCSTKVSHVSTGGGASLEFLEQGFLPGTEVLSPSKS

>core/331/2/Org2_Gene786

MSTMQNCPHFGVCGGCSFPQSNYSDSLKKKEELLHQLFAPLVPSDMIAPIPCSPSLRGRNKMESFFQTYEGE
KSLGFISSTKPKKGIPVTTCLLIHEQTMDILKLTREWWDKHPELMAYFPPKNKGSLCTLVVRTGSPQQNFMVI
LTTSGTPEYRVNEACIDEWKEILLSSSLNIASIYEEKVAARGISTYYETKLLYGAPSIQQKLSLPSDGNSASFS
LRPRSFFQPQITQAAKIIETAKEFINPEGSETLLDLYCGAGTIGIMLSPYVKNVIGVEIIPDAVASAQENIKANNK
EDCDEVYLEDAKAFCKRNENCKAPDVIIIDPPRCGMQSKVLKYILRIGSPKIVYISCNPKTQFQECADLISGGY
RIKKMQPIDQFPYSTHLENIILLEREIDP

>core/332/2/Org2_Gene667

MLLVRKWLHTCFKYWIYFLPVVTLPLVCYPFLSISQKIYGYFVFTTISSLGWFFALRRRENQLKTAAVQLL
QTKIRKLTENNEGLRQIRESLKEHQESAQLQIQSQKLKNSLFHLQGLLVKTKGEGQKLETLLLHRTEENRCL
KMQVDSLIECEKTEEVQTLNRELAETLAYQQALNDEYQATFSEQRNMLDKRQIYIGKLENKVQDLMYEI
RNLLQLES DIAENIPSQESNAVTGNISLQLSSELKKIAFKAENIEAASSLTASRYLHTDTSVHNYSLECRQLFDS
LREENLGMLFVYARQSQRVAFANALFKTWTGYCAEDFLKFGSDIVISGGKQWMEDLHSSREECSGRLVIKT
KSRGHLPPFRYCLMALNKGPLCYHVLGVLYPLHKEVLQS

>core/333/2/Org2_Gene80

MRMLQISM LLLALGTAINSPAIIYAADSQSVSFPEQLPSSFTGEIKGNHVRMRLAPHTDGTIREFSKGDLVAVI
GESKDYYVISAPPGITGYVFRSFVLDNVVEGEQVNVRLPSTSAPVLVRLSRGTQIQPASQEPHGKWLEVVLP
SQC VFYVAKNFVANKGPIELYTQREGQKKIAMDLINSALNFAHIELEKSLNEIDLEAIYKKINLVQSEEFKDVP
GIQGLIQKALEEIQDAYLSKSLESQNTSIASSQCSTPKVSSEVTTSLLSRHIRKQTALKTAPLTQGRENLEYSLF
RIWASMQQGNDHSEALTQEA FYRAEQKKKQVLAGVLEVYPHVVKNNPGDYLLKAQENTIAFLYGTSINLEQ
WLGKRVTVECLPRPNNHFAFPAYYVVGIKEAS

>core/334/2/Org2_Gene277

MAASGGTGGLGGTQGVNLA AVEAAAAKADAAEVVASQEGSEMNMIIQQSQDLTNPAAATR TKKKEEFQT
LESRKKG EAGKA EKKSESTE EKPDTDLADKYASGNSEISGQELRGLRDAIGDDASPEDILALVQEKIKDPALQ
STALDYL VQTTPPSQGKLKEALIQARNTHTEQFGRTAIGAKNILFASQEYADQLNVSPSGLRSLYLEVTGDTH
TCDQLLSMLQDRYTYQDMAIVSSFLMKGMATELKRQGPYVPSAQLQVLMTETRNLQAVLTSYDYFESRVPI
LLDSLKAEGIQTPSDLNFVKVAESYHKIINDKFPTASKVEREVRNLIGDDVD SVTGVLNLF FSALRQTSSRLFS
SADKRQQLGAMIANALDAVNINNEDYPKASDFPKPYPWS

>core/335/2/Org2_Gene201

MVYFMVFSPSSES VVKANSVVR SNFCYFLENKFVSPSESTEVMFSEIMKGRVPDIESLFDRPTDMMMTGFKA
AQNLGNLFNSFGILIMCFSQCKSCQTPEKETS AIVLGATLLFFVVALILGPTLGALVYCA YKVYTLGKMIYSLN
KAKAKVLRHPAQNVFHRAAGVATIRSSEEAVKACKLYKSAMIGSLVVS LIASLALIALTAGIVLV LFFVAPGA
APVITAAMMGCCAAGGGALLISLLGLWIAIVRKAKHQEACVGHLTNVVLHTAVSEALLHDP SHFQTNALAR
DLFLTDCLSHYGHLFSNEEVAQLVQGGAPGGGSRPSQHYGGSSDYQNR RGNGNFGGSHFGGGGGFAGSHF
GAGYPTAPT MPSAPPPFPPPAYDTIYG

>core/336/2/Org2_Gene427

MLSVTIVLVGLEMARSKVSKRDSKILDILFATTELYLKTGQPVGSKTLKESFCSDLSTATIRNYFAELEAEGFL
KKNHTSGGRIPTDLALRHYVDHQEECPAEISAPIFDKISQLPSESERNIIKDLQKATELLGEILDLPFFSSPRFEN
DSVTNIQITQVDKQRAVTILSTEFQGIFTDTLWLPEACDTLSIKRIEKFLQNYIRKLPNTNEELSKKEEHLMSLSY
NEVVVRYLTRYCNFSEEDLYQTGMSKLLKYEAFKDPEVLALGLSLFENRRQMCELLNIGMHKGRATAFIGK
ELSDILGTSNPGCSVITIPYYMNRSPLGALGILGPINLPYKEALPLLKLFANKINETLTQSFYKFKLSFRRPLTSN
CKLSNEPILRTEYSSIKLLPSKETL

>core/337/2/Org2_Gene421

MRRNPHFSLLKPQYLFSEISKKLAQFRKENPEISVIDLSIGDTTQPLCRSITQAIKEFCVSQEKQETYRGYGPET
GLEKLRTKIASEVYENRISPEEIFISDGAKPDIFRLFSFFGSEKTLGLQDPVYPAYRDIAHITGIRDIPLACRKET
GFIPELPNQQLDILCLCYPNNPTGTVLTFQQQLQALVNYANQHGTVLIFDAAYSASFVSDPSLPKSIFEIPEAKYC
AIEINSFSKSLGFTGMRLAWNVIKELTYDNNPEMINDWKRLFATTENGASLLMQEAGYYGLDLFPTPPAISL
YLTNAQKLKKSLETAGFSVHGGDHAPYLWVELPEGISDEEAFDFFLHQYHIAVTPGHGFGSCGQGFVRFSAL
TQPQNIALACDRLCTASLKETMVLA

>core/338/2/Org2_Gene862

MSNKVLGGSLLIAGSAIGAGVLAVPVLTAKGGFFPATFLYIVSWLFSMASGLCLLEVMTWMKESKNPVNML
SMAESILGHVGKISICLVYLFLFYSLLIAYFCEGGNILCRVFNCQNLGISWIRHLGPLGFAILMGPIIMAGTKVID
YCNRRFFMFGLTVAFGIFCALGFLKIQPSFLVRSSWLTTINAFPVFFLAFGFQSIPTLYYYMDKKVGDVKKAILI
GTLIPLVLYVLWEVVVLGAVSLPILSQAKIGGYTAVEALKQAHRSWAFYIAGELFGFFALVSSFVGVALGVM
DFLADGLKWNKKSHPFISIFFLTFIPLAWAVCYPEIVLTCLKYAGGFGA AVIIGVFPTLIVWKGRY GKQHHRE
KQLVPGGKFALFLMFLININVVSIIYHEL

>core/339/2/Org2_Gene303

MVNIQPVYRNTQVNYSQATQFSVCQPALSLIIVSVVA AVLALVALVCSQSLLSIELGTALVLVSLILFASAMFM
IYKMRQEPKELLIPKKIMELIQEHYPSIVVDFIRDQEVSIYEIHHLISILNKTNVFDKAPVYLQEKLLQFGIEKFK
DVHPSKLPNFEEILLQHCHPLHWLGRLVYPMVSDVTPGTGYGYWCGPLGLYENAPSLFERRSLLLLKKISFGEF
ALLEDGLKKNTWSSSELVQIRQNLFTTRYADKEEVDEAELNADYEQFDSLHLHLIFSHKLS

>core/340/2/Org2_Gene654

MSFFNHIPTFSPDAILGLQNVFFADKRPEKVNLVIGVYEHPPQKRYGGLSCIRKAQTVILEEEQNKSYLPISGLQI
FLDEMRELVFGAVDPSAIVGFQSLGGTGALHLGARLLSVAKGSGKVYVPEQTWSNHIRIFSQEGLEVIRYPY
SKEQKQLLFEPLIAFLKEVEKNSVILLHGCCHNPTGVDFTEDMWKELAILMKERELIPFFDTAYQGFAHGIEL
DRKPIEIFISEGNTVLVAASSSKNFALYGERVGYFAVHSTFTDELVKIHSFLEEKIRGEYSSPQRWGVEIVSTILS
NPYLKEEWQSELNFIRESLGKMRTFRVQALRKVAGHTFDLFSQHGFFAYPGFSDKQVFLREQHAVYTTAG
GRMNLNGITEKNIDHVVSFIQAYEL

>core/341/2/Org2_Gene175

MVVSIIYSEILSFSELTSCKHSLFPFGPIETASIRIHHVFNVVIVCLIIILGTLFVCLGMVFLGVFSTYLLGMSSMILG
LLISIGLALLKFKERYGLEPKELFGVEGGFDKKLPSEIIQMMDQIADLARELDLEQKKDTLIRGFSARLDVLE
GSKTEKKQILKIGVPRNLSEIQERAQEQNSILEQCKEALLFRRKSAQEIFKKLYDRKAAFWRYSYREDLWCYSEI

HVSKKALSPLYIGDVFEGTAPHFLMEAYAMCRTAKNLRNYVKVCVEDMRVNEEKKRAKQLSVSELLCCCT
EIETDLENETNLFTSDSEDLVEEYQIHCIQRTMLHALWAIYNDEVVSRKPIDTLDRVRARMAVEDCIETFEELQ
MCVVHTKTLELEIAQLYVDILLEA

>core/343/2/Org2_Gene52

MSKETFQRNKPINIGTIGHVDHGKTTLTAAITRALSGDGLASFRDYSSIDNTPEEKARGITINASHVEYETPN
RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSATDGAAMPQTKEHILLARQVGVPYIVVFLNKVDMISQE
DAELIDL VEMELSELLEEKGYKGCPIIRGSALKALEGDANYIEKVRELMQAVDDNIPTPEREIDKPFLMPIEDV
FSISGRGTVVTGRIERGIVKVSDKVQLVGLGETKETIVTGVEMFRKELPEGRAGENVGLLLRGIGKNDVERG
MVVCQPNSVKPHTKFKSAVYVLQKEEGGRHKPFFSGYRPQFFFRTTDTGTGVVTLPEGTEMVMPGDNVELDV
ELIGTVALEEGMRFAIREGGRTIGAGTISKINA

>core/344/2/Org2_Gene1003

MFEFRRPKIGETSSGGSIVRWLKNLGDHVARDEPLIEVSTDKIATELPSPKAGRLVRFCVNEGDEVASGDVLG
LIELEEISEADDESTSCPPTSCETKSEAGSSSSSVWFSPA VLSLAQREGIGLDNLQKIAGTGKGGRVTRQDLEAY
ISESQVSIPEIFQGEVNRIPMSPLRRAIASSLSKSSDEVPHASLVVDVDVTDLMNLISGERQRFLDTHGVKLT
TSFIVQCLAQTLRQFPLLNGSLDGTIVMKKSVNVGVAVNLNKEGVVVPVIHNCQDRGLVSIKALADLSSR
ARLNKLDPSEVQDGSVTVTNFGMTGALIGMPIIRYPEVAILGIGTIQKRVRVVRDDDSLAIKRMVYVTLTFDHR
VLDGIYGSEFLTSLKNRLESVTMG

>core/345/2/Org2_Gene21

MDYYSILGISKTASAEIKKAYRKLAVKYHPDKNPGDAAAEKRFKEVSEAYEVLSDPQKRDSYDRFGKDGPF
AGAGGFGGAGGMGNMEDALRTFMGAFGGEGFGGGSFFDGLFGGLGEAFGMRSDPAGARQGASKKVHINLTF
EEAAHGVEKELVVSGYKSCETCSGQGAVNPQGKSCERCKGSGQVVQSRGFFSMASCTCECGGEGRIITDPCS
SCRGGQGRVKDKRSVHVHIPAGVDSGMRLKMEGYGDAGQNGAPSGDLYVFIDVESHPVFERRGDDLILELPIG
FVDAALGMKKEIPTLLKTEGSCRLTVPEGIQSGTILKVRNQGFNPVHGKGRGDLLVRISVETPQNLSEEQKEL
LRTFASTEKAENFPKRSFLDKIKGFFSDFTV

>core/346/2/Org2_Gene152

MSSPVNNTPSAPNIPAPPTPGIPTTKPRSSFIEKVHIVAKYILFAIAATSGALGTILGLSGALTPGIGIALLVIFV
SMVLLGLILKDSISGGEERRLREEVSRFTSENQRLTVITTTLETEVKDLKAAKDQLTLEIEAFRNENGNLKT
EDLEEQVSKLSEQLEALERINQLIQANAGDAQEISSELKKLISGWDSKVVEQINTSIQALKVLLGQEWVQEAQ
THVKAMQEQIQALQAEILGMHNQSTALQKSVENLLVQDQALTRVVGELLESENKLSQACSA LRQEIEKLAQ
HETSLQQRIDAMLAQEQNLAEQVTALEKMKQEAQKAESEFIACVRDRTFGRRETPTPTTPVVEGDESQEED
GGTPPVSQPSSPVDRATGDGQ

>core/347/2/Org2_Gene726

MPRYRYTYLDPKERRKRGYLEALHIQEAREKLAQENIQVLDIREVALRRMSIKSTELIVFTKQLLLLLRSGPL
YESLVSLRDQYHEQKMGLLLTSFMETLRSGGSLSQAMAAHPNIFDHFYCSGVAAGESVGNLEGCLQNIIIVL
EERAQITKKMVGALSYPVLLVFSFAVMLFFLLGVIPSLKETFENMEVKGLTKIVFGVSDCLSAYRYLFLGFA
SALITVGILMRHRIPWKKILEKLLFALPGTKKFVVKVAVNRFCSVASAILKGGGTLEGLDLGCDAIPYDRLKT

DMRDIVQAVIGGGSLSQELAQRSWVPKLAIGMIALGEESGDLADVLGYVAHIYNEDTQKTLASITSWCQPVI
LIFLGGLIGVIMLAILIPLTSNIQTL

>core/348/2/Org2_Gene757

MHPKIEKRNSLPLTAVAPVFEEASYHPSVATTVDYVDATTLSRHLLTVLKDVIKEARNLDLGKAFLTSMKQGF
NTGTELAIIQASLADQSSRESRKKEEKIFHQHLGKAAPQAATATSGVQPTADPVADKMPLQSAFAYVLLDKYI
PAQEEALYALGRELNLSGYAQNLFSPLLMIKSFNSAPINYNLGSYISQTSGTANFAYGYEMILSRYNNEVSQ
CRLDIASVKAKAALANMSASVKANVSLTDAQKKQIEDIIASYTKSLDVIHTQLTDVMTNLASITFVPGLNKY
DPSYRIVGGDLSIIALQNDEKVLVDGKVDITTA VNEGGLLNFFTTVLTDVQNYGDLAQTQQQLMLDLELKAM
QQQWSLVSASLKLLNGMYTTVISGFKN

>core/349/2/Org2_Gene610

MKKLLKSALLSAAFAGSVGSLQALPVGNPSPDLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFD
RILKVDAPKTFMSGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG
YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGCATLGAEFQY AQ
SKPKVEELNVICNVSQFSVNPKPKGYKGVAFFPLPTDAGVATATGTKSATINYHEWQVGASLSYRLNSLVPYIG
VQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVG
ATLVDADKWSLTAEARLINERAAHVSGQFRF

>core/350/2/Org2_Gene395

MMKQGVGQDAKELYTFLSRGNEHYQPCLWFSLEEELGFLFDEKMLCAPLSEDHYCHSYLVDLVDQHLKDLI
LSMFLDPQNISAGELLKVSINVGDSFSPLQKQDFLSMVL RDETGKNVVVVFKGVLSLPATQVCKLVEELNSK
DYSYLNIFSCHGDSSPQLLFRKELEGTSGRYFTVICALYLGDTDMRSLQLASERIMVSREFDLV DAYAARCKL
LKIDHTNWRPGTFSRHADFADA VDVSAGFNSREFKLITQANQGILES GELPLPSKTFWEGFLAFCDRVTVTRH
FIPMLDAAIKQAVWTHKHPSLIDKECEALDLKTQCLPSIVSYLEYVTNSHEKTSKGPFIQKEIADCSPLKEALF
PGSDEDVPSTSEDPSDDHPSDLEDS

>core/351/2/Org2_Gene593

MGTPISGNDGDRNTISDPLEESAEEGDS DLED RVSESATQVIETIADTGIPEATPSEG TNSDLNSDLVDRVEY
EARGSLLTMLARIRKAVSQIWMHVKTKRHPKEQGVRSLGDIPCDLLKATRLPKETAEP PFYF YALETALASC
RSFFFHVFLRLFTLLRRQHPEAPLDLCGTDPI SPEAAVAFALILRSCCKWVATDAVQEGLPLEVIEEAGMYNA
FSLEATTTVEEVSKRLSELLYSDKRIDGLANVRGITKIITSPYLGAGQC VSVVDNLKTYDLGRNYTQVLACAS
QIDEFADKGENEALVMKDILYLVRQDRSKELGDFLMMWSEEHASEVNYDVVLAILEVNLPILEEDYRSHPLA
YQKKLNYVICQFFCSERLTSIEPKD

>core/352/2/Org2_Gene435

MLHILLAIFCILLFLAFGLTQPSCHGSSKFLKTLNQ RFFKDKGREYPPFPSAPTILATLLCILY GALGTKLYTLLP
PKTAHKDLLFWPLYSLSALIAYGFLPPWISTKVPKETTAHLRFLASVFQLGLFPLQLLFYRRRPNQQVRSSTSF
QSQLSEALS AFDNLIVREVMIPKVDIFALPEETTLQEALVLVSEEGYSRVPVYKKNLDNITGILLVKDLLLYT
SSHDLSQPISSVAKPPFYAPEIKKASSLLQEFRQKHRHLAIIVNEYGFTEGIATMEDIIEEII GEI ADEHDVQENTP

YKKIGSSWIVDGRMNISDAEEYFNLKIDHENSYDTLGGHVFHKVGAVPQKGMRIHHENFDIEIITCTERNVGK
LKITPRKRKFNIS

>core/353/2/Org2_Gene507

MAIKNILVVDDEPLLRDFLSELLTSQGFIPDTAENLRNALQMIRSRDYDLVISDMSMPDGSGLDLIKIIKQSSPH
TPVLVVTAYGSIENAVEAMHQGAFNYLTKPFSSEALFAFISKAEELEKNLVHENLFLHSQTTPDSHPLIAESKA
MKDLLAIAKKAASSSANIFIHGSGCGKEVLSFFIHHNSPRANHPIYKVNCAAIPTLLESELFGEKGAFTGA
TTKKAGRFEALAHKGTLLLDLDEITEVPVNLQAKLLRAIQEKEIEHLGGTKTLSVDVRLATSNRKLKEAIDDKSFR
QDLYYRLNVIPLHLPPLRDRQDDILPLANYFLNKFCRMNNTPLKTLSPKAQELLNYPWPGNIRELSNVLERV
VILENTSLLTEDMLALA

>core/354/2/Org2_Gene865

MHLHEYQAKDLLASYDVPPIPPYWVVSSEEEGELLITKSGLDSAVVKVQVHAGGRGKHGGVIVAKSSAGILQ
AVAKLLGMHFTSNQTADGFLPVEKVLISPLVAIQREYYVAVIMDRKHRCPLVMLSAGGMDIEEVAHSSPEQ
ILTLPLTSYGHIYSYQLRQATKFMeweGEVMHQGVQLIKKLAKCFYENDVSLLEINPLVLTLEGELLVLDSKI
TIDNALYRHPNLEVLYDPSQENVRDVLAKQIGLSYIALSGNIGCIVNGAGLAMSTLDILKLHGGNAANFLDV
GGGASQKQIQEAVSLVLSDES VKVLFINIFGGIMDCSVVASGLVAVMETRDQVVPTVIRLEGTNVELGKEIVQ
QSGIPCQFVSSMEEGARRAVELSM

>core/355/2/Org2_Gene802

MKWFVISCLLGIFSLGLIMVFDTSAEVLDRSLECSHKAIRQVTYLILGLGVASLLYMMEWDRFLKISPVLL
SGAALALICVFIPGLGICRNGARRWLGFGQLTIQPSEFVKYLVPIVALYFLTFSSLYQKQLKMFLKLTAILFIPIL
LIAIEPDNGSAAVISASLIPVFIMTSVRLRYWLLPLLCVLIAGGALAYRMPYVRYRLNVYLHPELDIKGRGHQP
YQAKIAAGSGKLLGKGPASLQKLTYLPEAQNDYIAAIYAEEFGFLGMLVLILLYMCFVYGGY AIAIKASSLE
GAALAMVITLIISMQA FMNLGVVSGLLPSKGVNLPFFSQGGSSLIANMCGVTLLLKVYDEENSKSSLGCRRFR
RPHCPSSLGKGSFFS

>core/356/2/Org2_Gene425

MSSVNQSSGTPNPEEVTSPESTEENKNVVSSDEAQATHAVALPIVTQLSLPEGVGTSSSEETASNPRVDEIVA
SSSRAVADQISSLVERVGELLDDLKGAQSLFTSFQSELKNCLPAWKSSTRRLETRGAGDNADIARLELFRSDY
EAVLGHANQFHGKAHLILSKLTDVHHKLQGLSREDLSLAFDNNDRVLEHLGSLGLDVDAEGNWSLSCERGI
PRLVLTADSMVLVQIKKVNLPTEELRTLQGTTESSDPRVEESLSCERLLNELRRLWANFVGFISSCYDNIVF
VLMWIVRRINLLPGLGCLPFHNPDASQEDQRSSSGERSTRRERLSRRSDLSEEEMIVRAEGESIHPESPHGDGR
NQPSRGDKQDSDSEEETEL

>core/357/2/Org2_Gene766

MEKPQNRKAPRIFWLNNQVAIPPSERVKESYALHSDIFSLPPGSALKLAEKTEESIRQLVGLKD SHIFRFPVPHF
HVHVHIVLAALVENLSMFQGRNHIILPAHDQQLINSLCRHQGLGTTYDWVTVNHEGRIVEEQ LIETLSPRSLLF
SLSAAHGLTGVIQPLDLLSLCKDRRILLHLDISDILGRAPLTPEILNADIITFSSAALGGMGSIGGIFIRKSLERV
FSSWFPHTSASLCFSAVAAMQTACEERISALPLFTFHTSNLCKKLIQELQSVLPSIQLAFSEVQNRLPNIVVAA

IPDIPAESLAFHLHQGGIYPSLGYERFQPLAQVLQNCGISPFLCHSALHFSLTERSKDLEFSKLARAMHDAIKHL
TPLLGSSS

>core/358/2/Org2_Gene592

MILDFQFSIGYYLRVLELAIRDGTRILAYDRKRLLLDWVPVNDPLPTNYDTSVSTIRQVIHELFSWSAISYSISS
RLLAIHELRLHEEKPQTGWLYRLFFPSKYHIKKAIVDKLCMFKSLILFESKRPVDKIVQAANKVFSKGKSNFSS
WEDFTHEVTVSEVQTPLAGEVQRRLAADASLQMIIEALTTLEGHTAYLPLSLELLNQFIGEKAQPLKTLSEK
SYVLLRELIQLFSLSAEDFQTIIMSIISDSLSEVLANSIGNQPLTFHGKTFVGLWQETALASPEDSKLALGFLAE
VLRKVIVEKKLHVSKSDNTTPEEVGNIYSIRDQNPALWDKMITMLLMRWLLDYDRDIGIALRKAAEYYNPHP
SFWRQFLRLWQRRP

>core/360/2/Org2_Gene202

MSAMISLSSSHEASIASNTQVRDVLVSLAMDEFVEHNTEILPIKVFLARGTLSSTAIDDLKDVVETEGEHHFQ
VYSNISLKMIIYQRF FEKIFGIGCCPLLLVTD SHHTDPCGALITGIFAAVLFTVLAIVFGPTLGILCYSAYKIYQLT
KKISSLSRTHTEVINSVQKSDPFIHRSGAVAAAAASQSTIKACKVFRQSTLIFFVLGLIITISLAALIVGLVFALFF
LDPGAPAVMTAAMIGCCAAGGTGILLSVIGFLLASVYSVQKSQEGVHHMHTALLRCIVSNTIIQMPYLPITPG
TKKVLTQSIRRYQQFFSDDEYRDIESEVPLNRQTTPPPSYETLFHEEGSDGSSNVIPRESPPAYSTIDSSNSPFPSS
SPPPYR

>core/361/2/Org2_Gene1021

MSETHITTPHVVKLISNFFQKKLFSSISTAYPLVIITDVSQQHLLGPILDHIKMLGYQVIVLTFPPGEPNKTWET
FISLQYQLVDQNISPKSSIIIGGGTVLDMTGFLAATYCRGLPLYLIPTTITAMVDTSIGGKNGINLRGIKNRLGT
FYLPKEVWMCQPFLSTLPREEWYHGIAEAIKHGFIADAYLWEFLNSHSMKMLFSSSQILHEFIKRNCQIKAAIVA
EDPYDRSLRKILNFGHSIAHAETLAKGTVNHGQAVSVGMMIETRISLAEGVMKTPQLIDQLERLLKRFNLPST
LKDLQSIVPEHLHNSLYSPENIITLGYDKKNLSQHELKMIMIEHLGRAAPFNGTYCASPMEILYDILWSECH
VMRHC

>core/362/2/Org2_Gene928

MLCQQFLIEALARRKSKHTYRSLSLNSHLIDFTSNDYLGFASSPELRKEYITKLHAIESLGATGSRLLTGHSQ
CQRIEEQLAAYHNFESCLIFNTGYTANLGLLYALATDQDRILHDLYIHASIYDGIRLSKAQSFPFNHNDLNHLE
KRLASSHLGRTFVCVESVYSLHGSAVPLQAISELCERYSAYLIVDEAHAVGVFGDQGEGLVSALGLQDKVLA
TVYTFGKALGTHGAAIAGSSILKDYLINFCRPFYITTAQPPHALTAIELAYEHNQRAFNQREHLSALIHFFREK
AQNLGLQLMKDNTTTPIQSICVSGSHRARQAALQIQNSGYDVRPIVSPTVKQREELLRICLHAFNTKNEIDHLL
HTLEQIFLCNVSSL

>core/363/2/Org2_Gene243

MSCFNLTSTNESLRPISPKASFQGWQSYFRSALRKHRSDTLSVSVCKVNKYDANL FVRLTVIALAVVGVLI
LFSIMLASIQGTLVITSWPLVTAAILIPTILLTGGMYLHRLGKKVDVISGVCIPPF SRRCWVPISSHTLEKFDEK
HVSACSYLDISTLSADGSGIAAVYQCPPLLFRAPFCFGIPCAMPFVALLRMIYNLIRFLVVPFYIIFRMIYEHFFC
KHLPEDDRFIYKDVAREMGRSLAAFLKAPFYASACMIGAFYSLDPLAGRVLMGSVERDWNNDNVILARSVS

LANEAHSLFRFEGGGGRKGLGQHAFYMLCCQPQSVFLFDKGEIVSGAHPSIQLPERRGLDTSGRYPHISVIPD
SGNDSAKNFIV

>core/364/2/Org2_Gene594

MGINPSGNRSPDDVWVRGAQGDSSSTQGTGATNSNLGAHNVTSTSQPVASKAKQLWQTVREFFLGKKSP
DSSQGASGPAMQSPSGPTIRPTRPAPPPPTTGGANAKRPATHGKGRAPQPPTAGSSSGSEQPTAMSSEVAKLV
SELKDAVHSHAESQKVLKKVSQELQTKWTDWENNRGPDYLLHGYRVIARALQQTYTEQSMLEGTSSSTGPV
PQAVTVAKDAVTQTVRGAIKNLENPKPGNDPDGVLMQVVISLIEGPTLDPGESIQNFLETRVSDFGGDDSDI
DYTSDIARLGSALDRVRENHPNEMPRIWIALARELGA AVHSHATSVRIANAGKNHTRD VVRMANESSRLQ
GMKVLSVGAWANTMTVLIGDLFE

>core/365/2/Org2_Gene824

MIPSPTPINFRDDTILETDPKPSLIMFSSKKTEIASERRKAHPTLKFVLGTIWNIVKFIISIILFLPLALLWVLKKTC
QFFILPSSIISQSMSTAVAIRRMTFLSHIKQLLSLKEISAADRVVIQYDDLVDLSLAIKIPHALPHRWILYSQGN
SGLMENLFDRGDSSLHQLAKATGSNLLVFNYPGIMSSKGEAKRENLVKSYQACVRYLRDEETGPKANQIIAF
GYSLGTSVQAAALDREVTDGSDGTSWIVVKDRGPRSLADV ANQICKPIASAIKLVGWNIDSVKPSERLRCPEI
FIYNSNHDQELISDGLFERENC VATPFLELPEVKTSGTKIPIPERDLLHLNPLSPNVVDRLAAVISNYLDSENRK
SQQPD

>core/366/2/Org2_Gene292

MKHLAVLGSTGSIGRQTLEIVRRYPSEFKIISMASYGNNLRLFFQQLLEEFAPLAAAVYNEEVYNEACQRFPHM
QFFLGQEGLTQLCIMDTVTTVVAASSGIEALPAILESMKKGKALALANKEILVCAGELVSKTAKENGIVLPI
DSEHNALYQCLEGRITIEGIKKLILTASGGPLLNKSLEELSCVTQDVLNHPINWNGMSKVTVDSSTLVNKGLEII
EAYWLFLENVEILAVIHPQSLIHGMVEFLDGSVISIMNPPDMLFPIQYALTAPERFASPRDGMDFSKKQTLEF
FPVDEERFPSIRLAQQVLEKQGSSGSFFNAANEVLVRRFLCEEISWCDILRKLTTLMECHKVYACHSLEDILEV
DGEARALAEI

>core/367/2/Org2_Gene704

MKDLGTLGGTSSTAKTVSPDGKVMGRSQIADGSWHAFMCHTDFSSNNVLFDL DNTYKTLRENGRQLNSIF
NLQNMMLQRASDHEFTEFGRSNIALGAGLYVNALQNLPSNLAAQYFGIAYKIRPKYRLGVFLDHNFSHVPN
NFNVSHNRLWMGAFIGWQSDALGSSVKVSFGYGKQKATITREQLENTEAGSGESHFEGVAAQIEGRYGKS
LGGHVRVQPFLGLQFVHITRKEYTENAVQFPVHYDPIDYSTGVVYLGIGSHIALVDSLHVGTTRMGMEQNFAA
HTDRFSGSIASIGNFVFEKLDVTHTRAFAEMRVNYELPYLQSLNLILRVNQPLQGVMGFSSDLRYALGF

>core/368/2/Org2_Gene774

MEDFSEQQLFFMRRAIEIGEKGRITAPPNPWVGCVVVQENRIIGEGFHAYAGGPHAEELAIQNASMPISGSDV
YVSLEPCSHFGSCPPCANLLIKHKVSRVFVALVDPDPKVAGQGIAMLRQAGIQVYVGIGESEAQASLQPYLY
QRTHNFPWTILKSAASVDGQVADSQGKSQWITCPEARHDVGKLRAESQAILVGSRTVLSDDPWL TARQPQG
MLYPKQPLRVLD SRGSPPTSKVFDKTSPTLYVTTERCPENYIKVLDSLDPVLLTESTPSGVDLHKVYEYL
AQKKILQVLVEGGTTLHTSLLKERFVNSLVLYSGPMILGDQKRPLVGVLGNLLESASPLTLKSSQILGNSLKV
VWEISPQVFPIRN

>core/369/2/Org2_Gene825

MNLSNRSDILSGIFSNPHVSYFSSTHAKQLSDFSKKHPILTKIVTIIVKIFKLLIGLIIPPLGIYWLCQLVCSLALF
PRSSMLYSVLKTCFKKYRLEQEIQDYFVKNLDPSFKDPAVSESKRITIQDHLTIDTLAIHFSTARPKRWLLISL
GSGDFLEDMIGLKDSLFLSWKELAKLLGANILIYNYPGVKSSTGKLNLENLATAHNLCAYLQDKIQGPGAN
EIITYGYSLGGVVQSAALQKNPFTNSETSWVAVKDRAPHSLPAAANSFFGPIGKLIAVLARWKMDAEKNSRE
LPCPEILVYSADRFPRSEVGDDTALLPEFTLAHAIKRTPFARSKKFIGEVNLLHSSPLKHPTIQKLAEAIKESLSR
KN

>core/370/2/Org2_Gene114

MNTSLKRPLKSHFDVVGSLRPEHLKKTRESLKEGSISLDQLMQIEDIAIQDLIKKQKAAGLSFITDGEFRRAT
WHYDFMWGFGHGVGHHRATEGVFFDGERAMIDDTYLTDKISVSHHPFVDHFKFVKALEDEFTTAKQTLPPA
QFLKQMIFPNNIEVTRKFYPTNQELEDIVAGYRKVIRDLVDAGCRYLQLDDCTRGGGLVDPVCSWYGIDEK
GLQDLIQQYLLINNLVIADRPDDLNVNLHVCRGNYHSKFFASGSYDFIAKPLFEQTNVDGYYLEFDHERSGDF
SPLTFISGEKTVCLGLVTSKTPTLENKDEVIARIHQAADYLPLERLSLSPQCGFASCEIGNKLTEEEQWAKVAL
VKEISEEVWK

>core/371/2/Org2_Gene544

MSDNAHNLLYDKFELPEAVKMLPVEGLPIDKHARFIAEPLERGMGHTLGNALRRALLIGLEAPAIISFAMTGV
LHEYMAIEGVIEDVTNIIILNLKGALLKKYPMQDSSLGRTTQVLKASISIDASDLAAANGQKEVTLQDLLQEGD
FEAVNPDQVIFTVTQPIQLEVVLRIFAQGRGYTPSERIVLEDKGVYEIVLDAAAFSPVTLVNYFVEDTRVGQDQDF
DRLVLIVETDGRVTPKEALAFSTQILTKHFSIFENMDEKKIVFEEAISIEKENKDDILHKLILGINEIELSVRSTNC
LSNANIETIGELVIMPEPRLQFRNFGKKSLCEIKNKLKEMKLELGMDLTQFGVGLDNVKEKMKWYAEKIRA
KNTKG

>core/372/2/Org2_Gene324

MNGKAPLALYIHIPFCTKKCRYCSFYTIPYKSESVSLYCNAVIQEGLRKLAPIQETHFIETVFFGGGTPSLVSPL
DLKRILKELAPHAREITLEANPENLTVSYLRQLQETPINRISVGVQTFDDSLQLLGRTHSSSAITALQECQNH
GFSNLSIDLIIYGLPTQSLEIFLSDLHQALTLPITHISLYNLTIDPHTSFYKHKILVPTIAQEEILAEMSLLAENLLL
SQGFQRYELASYAKPDYPAKHNLYYWTDPRFLGLGVSAQYLHGERSKNYSHISHYLRAVRKNLPTQETSEI
LPKKERIKEALALRLRLLEGADLAEFPSTLISMLTQDVKLQNLFSVHGQCLALNRQGRLFHDTIAEEIMGYSF

>core/373/2/Org2_Gene483

MSIAIAREQYAAILDMHPKPSIAMFSSEQARTSWEKRQAHPYLYRLLLEIHWGVVKFLLGLIFFIPLGLFWVLQK
ICQNFILLGAGGWIFRPICRDSNLLRQAYAARLFSASFQDHVSSVRRVCLQYDEVFIDGLELRPNAPDRWM
LISNGNSDCLEYRTVLQGEKDWIFRIAEESQSNILIFNYPGVMKSQGNITRNNVKSQYACVRYLRDEPAGPQ
ARQIVAYGYSLGASVQAEALSKEIADGSDSVRWVVKDRGARSTGAVAKQFIGSLGVWLANLTHWNINSEK
RSKDLHCPELFIYGKDSQGNLIGDGLFKKETCF AAPFLDPKNLEECGKKIPVAQTGLRHDHILSDDVIKEVAG
HIQRHFDN

>core/374/2/Org2_Gene181

MALKFHLLHQSKKSQARVGGIETSHGVIDTPAFVPVATHGALKGVIDHSDIPLLCNTYHLLLHPGPEAVAKL
GGLHQFMGRQAPIITDSGGFQIFSLAYGSVAEEIKSCGKKKGMSLVKITDEGAWFKSYRDGRKLFLSPELSV
QAQKDLGADIIIPLDLPPFHTDQEYFLTSCSRTYVWEKRSLEYHRKDPRHQSMYGVHGGLDPEQRRIGVRF
VEDEPFDGSAIGGSLGRNLQEMSEVVKITTSFLSKERPVHLLGIGDLPSIYAMVGFIDSFDSSYPTKAARHGLI
LSKAGPIKIGQQKYSQDSSIDPSCSCLTCLSGISRAYLRHLFKVREPNAI WASIHNLHMQQVMKEIREAIL
KDEI

>core/375/2/Org2_Gene826

MAPIHGSNAFVEDILHSHPSQATYFSSTRAQKLHEFKDRHPVLTRIASVIIKIFKVLIGLIILPLGIYWLCQTLCT
NSILPSKNLLKIFKKQPNKTKLKNYLHALQDYSSKNRVASMRRVPILQDNVLIDTLEICLSQAPTNRWMLISL
GSDCSLEEIACKEIFDSWQRFKLGANILVYNYPGVMSSTGSSSLKDLASAHNICTRYLKDKEQGPMAKEIIT
YGYSLGGLIQAEALRDQKIVANDDTTWIAVKDRCPLFISPEGFHSCRRIGKLVARLFGWGTKAVERSQDLPC
EIFLYPTDSLRRSTVRQNKLLAPELTLAHAIKNSPYVQNKEFIEVRLSSDIDPIDSKTRVALATPILKKLS

>core/376/2/Org2_Gene314

MSTTEPNLTNVNLTMLISSESMPTQLASHKLKGLDLVAFILIIGIAVSSGTAAILGIPLLFILTALAVLAFSILLY
FLLREPKSPISVTHQPTPIIKDIDLPPVPPLALTPVPTEAVLEEPPLSPRTHQTLLQENWDRIPLQANTDMPFI
AADNQTYAWHLKNSNLTLISTLGPKEPRYKTQGIVMIVNAATPNMANNVKGTSALAKATSVRCWENSK
KSPDPLRSKQPLQLGECRSKAWENLNGTTNAGKAGLPQFLGQLLGPKASDYNYNPNDAFTFCRQAYLNCLN
EAKRRKTTVVQLPLLSSHFPKDEETSLRLQWIDGVKLALIDALQTFGSEAENQNQPWVILTTLARHPLI
TP

>core/377/2/Org2_Gene619

MAVAADSSASWLKSRNNFLSSLGKTEEQVAAPFEPKELCQHKIREKFRLEDVQVSIKFRGSITAVEATKEFGV
HLLIQPMVVQPWEVENLLFLTSEEDLQELMVAVFDDASLASYFYEKDKLLGFHYFVAEACKLFEELQWVP
SLSAKVGGDAIFTATSLQGSFQVVDISLRDLGKNVRCRLLLPEDTFQSCQKFFSGLHDESDLHNIDQTQQISLS
VEVGYSQLTQEEWHQVVPGSFIMLDSCLYDPETEESGALLTVQKHQFFGGRFLTPSSGEFKITSYPNLTHEDP
PLPENPQASAAPLPGYSRLVVEVARYSLAVSEFIKLNLSILSLGNHPAYGVDIILDGAKVGRGEIILGDLVLI
RVLEV

>core/378/2/Org2_Gene339

MIYLDNNAMTPPERGLLEFLQKTFLIEGTYANPSSVHQLGKKSRQLVLEASHWMQKVLSFQGRVLYTSGATE
SLNLAIASLPKDSHVITSGSEHPAILEPLKHSSLSVSYLNPEEGRCVLTIEQIERAVTPKTSAILGWVNSETGAK
ADIAAIAHFAQERQLQFIVDATANVGKERIVLPSGVTMAAFSGHKFHALSGIGALLVSPGVKLHPQLWGGGQ
QGGLRAGTENLWGIASLLYIFKYLDLHQRISQEILTHRNFGFEKAIKARIPDVHIHCADQPRANNVSAIAFPPL
EGEVLQIALDIEGVACGYGSACSSGATAPFKSLVSMGVDEELTLATLRFSSHLLLQEDVERAVGIIKVVVERL
KNS

>core/379/2/Org2_Gene820

MTTSDVIDFVTNDFLGFARSPTIYCEVSKRFQIHCQQFPHEKLGIRGSRLMVGPSVIDDLESKIASYHGAPNA
FIVNSGYMANLGLCHHVSRSTDVLLWDEEVHMSVVHLSLSAISGQHHTFHNNLEHLESLLQCYRISSKGRIFI

FVSSVYSFRGTLAPLEQIIALSKKYHAHLIVDEAHAMGIFGDDGKGLCHALGYENFYAVLVITYGKALGTMG
ASLLTSSEVKYDLMQNSPPLRYSTSLSPHTLISIGTAYDFLASEGEIARKQVFKLKEHFHECFDSHAPGCVQPIF
LPHTCLEEAISVLETTGIHVGVVAFAKHPFLRVNLHAYNTVDEVNLLAQVMKPYLEKSSHRVHINHEFHLWR
ELCQH

>core/380/2/Org2_Gene867

MMLVYCFDPSVPTSPEHRLMAALDRWFFLGHRARILTLEGNHYRAFQENMSISTVEKILKLISYLLIPIVLIA
LLIRCFLHSRFGCNWKCDLS DARVPHDVQPFNDFQLFNNQERLNIWKNRRYVSGIDVLMVPVDYLRSQFPG
FKEIPEAIRCENYVSDGQFSEESKTSYLRAMLTDIVGYILSLDETYWTNVILKIRAMCITFESFPGKEADPNYSP
RVTHHYFDES WKALARHVLGEGNMVNRLDEALIRTEKPGKEGECITKQFLKDYCKKHLEVMSCPDFIESLV
DEKIREFRCP SILNSAVCDVIDRKCQEHLKAIINEANRRLPGMKNSSFTMRGNQVLFYTIFSPPKLPPAASSVY
F

>core/381/2/Org2_Gene438

MTTCLPQPPKTSPLYSIFEK LDAQERLSSDALHLLLLTNKEDQRTLWNFADQVRKQRVGDTVYYSSSTLYLY
PTNFCDFSCFKCSFYAKPGDPKGWLYSPD DLLQQIQNIKTPI TEVHIVGGCFPSCNLQYYSDLFTKIKEYDPQIH
IKALTAIEYAYLSDLDNLSIRDVLLTLKDAGLDSIPGGGAEILVDKIRNFLAPKRLSSSDFLNIHKMAHQLGIHS
NITMLCYHKEGPEDLVTHMVKVRDLQDETQGFKNFILLKFAQENNVLGKRLRKSQGQGHAIPLKSLMAVARIF
LDNFSNMKALWNYLGIEAALDLLSCGANDLSSTHMGEKVFQMASSKEPIKMDAEGMAALITQQGRTPCLTN
SSHV

>core/382/2/Org2_Gene1006

MRRQVREIMQQTIVIVAMSGGVDSSVVAYLFFKKFTNYKVIGLFMKNWEEDSEGGLCSSTKDIEDVERVCLQ
LDIPYYTVSFAKEYRERV FARFLKEYSLGYTPNPDILCNREIKFDLLQKKVQELGGDYLATGHYCRLNTELQE
TQLLRGCDPQKDQSYFLSGTPKSALHNVLFP LGEMNKTEVRAIAAQAALPTAEKKDSTGICFIGKRPFKEFLE
KFLPNKTGNVIDWD TKEIVGQHQAHAHYTIGQRRGLDLGGSEKPCYVVGKNIEENSIYIVRGEDHPQLYLRE
LTARELNWFTPPKSGCHCSAKVRYRSPDEACTIDYSSGDEVKVRFSQPVKAVTPGQTIAFYQGDTC LGSGVID
VPMIPSEG

>core/383/2/Org2_Gene345

MTKIAFSEKAKNFPVEALKKWF EKNKRSLPWRDNPTPYSVVWSEV MLQQTRAEVVIDYFNQWMERFPTIES
LAAAKEEDVIKLWEGLGYYSRARHLLLEGARMVMEEFHGKIPDDAISLAQIRGVGPYTVHAILAF AFKRRAAA
VDGNVLRVLSRIFLIETSIDLESTRTWVSRIAQALLPHKSPEVIAEALIELGACICKKVPQCHRC PVRQACGAW
RENKQFVLPVRHARKKVIFLHRLVAIVLYD GSLVVEKRRPKEMMAGLYEFPYIEVEPEEGLQDIEGFTKKME
LSLESPLEFLGNLKEQRHAFTNHKVHLCPIIFKATSLPQFGELHLLSDIDHLAFSSGHKKIKDALLIYLG DVRSR
ESIGV

>core/384/2/Org2_Gene497

MQENLDKRLEALRTEISLAARSLFDL DKKQKELQVLEESSEENFWQDSVHAGKISEQIVSLRRQIQEYQELK
SKIDAIEFFLEDADALEDPAICEDLEKEFLFCEKKLAVWETQRLLSGEADKNSCFLTINAGAGGTESCDWVEM
LFRMYSRWATKHQWALEVVDRLDGEVVG IKHVTVKFSGMYAYGYAKAERGVHRLVRISPFD SNGKRHTSF

ASVDVFPEIDDDQIKIEIRPNDLRIDTFRSSGAGGQHVNVTESAVRITHLPSGVVVSCQNERSQIQNRESCMKML
QAKLYQQVLQERLEKQSLDRKDKKEIAWGSQIRNYVFQPYTLVKDVRTGHETGNVQAMLDGELLDEFIKAY
LAEFGEVS

>core/385/2/Org2_Gene46

MAVEGRVNSSQALNQDCQEVLANQSKGLLRCRILSIVVAVITFIAGVVLIALTASILTSVPYLALGVFLLIV
TLGCIIFALCSEKIKKVPPTPISHKEEIIAWFEERKNIDMEKEKEDPEHFGRTATDIPMRSALDQFNHSCHHIHES
PALTETYRSHQDVLLFKDWCPVTLPDVTSEEEVLIRSVVGSYLLMEACVPKVSMLIDELHNKCLKSPSERECLF
IDKKTTLQRKASFLFTQKDLATFFLAYTRVNDGHLAPFRAGAKWILIHVRLRRQHNQNDFFTPGHSCYYARL
AFNQTQRLYHQLFNVEKLRSIYANMDKDPLCHPWAFIPIYDLLKTEDHGDGFLEQQEDREYPSRAAQDQFW
G

>core/386/2/Org2_Gene755

MSPHRNLFKLKNFSNRLYNRALGRFDKVFNFSSGNVIGDLGTANTLVYVRGRGIVLSEPSVVAVDAQTHAVL
AVGHKAKAMLGKTPRKIMAVRPMKDGVIADFEIAEGMLKALIKRVTPSRSVFRPRILIAVPSGITGVEKRAVE
DSALHAGAQEVLIEEPMAAAIGVDLPVHEPAASMIIDIGGGTTEIAIISLGGIVESRSLRIAGDEFDECIINYMR
RTYNLMIGPRTAEEIKITIGSAYPLGDQELEMEVRGRDQVAGLPITKRINSVEIRECLAETPIQQIIECVRLTLEKC
PPELSADLVERGMVLAGGGALIKGLDKALSKNTGLSVITAPHLLAVCLGTGKALEHLDQFKKRKGNLV

>core/387/2/Org2_Gene290

MKFVVSRNELGNLIKKIQSVVPQNTPIPVLTHTVLIETYNDELVFTATDLTVSTRCVTKAKVYEKGAISIPSKRF
FQLVKELTEANLEISSSAGEMAQITSGSSCFRLLSMEKEDFPMLPDIQNALRFSLPAEQLKTMQLQRTSFAVSRE
ESRYVLTGVLLAIANGVATIVGTDGKRLAKIDAEVTLDKSFSGEYIPIKAVEEIIKMCSDGEAAIFLDQDKIA
VECDNTLLITKLLSGEFPDFSPVISTESNVKLDLHREELITLLKQVALFTNESSHSVKFSFLPGELTLTANCTKV
GEGKVSMVAVNYSSELLEIAFNPFFFLDILKHSKDELVSLGISDSYNPGIITDSASGLFVIMPMRLHDD

>core/388/2/Org2_Gene885

MLIWKRHLLTRFWFALTSLVLALIFYASIHSLHTLKGASTAASGASVKLSILYYLAQISLKAFLMPQLVA
VATTSTLFAMQNKREIILLQASGLSLKSLMHPLLLSGAVIMMVLYANFQWLHPICEKISITKENMDRGTDDKE
QGKIPALYLKDQTVLLYSSIEPKTLTLNNVFWIKDPKTIYTMEKLAFTTSLPIGLNVTQFFANDSENLELKEFF
DMKEFPEIEFNFYENPFSKLFSAGNKNRLSEFFKAIPWNATGLGLSTQVPQRILSLLAQFYVVLISPLACMAAII
LSAYLCLRFSRTPTVTLAYLIPLGTVNIFVFLKAGIVLASSSVLPTLPVMAFPLIVLFLLTNYAYAKLQ

>core/389/2/Org2_Gene486

MKFPRISISDLIPTQMVIWWRGGGNVHYVPNAQNLPKKILGGVLACFGLALLGCAAFAGVCQTIFPCIGLMI
LGLVLLGFAYLQYSKGWSRFRPLFRETKVFEKPINWLGCSSLQSWKKIRPGCYYPGCPQVEICEGSQEIV
TKIFQKKS DRNTSIFLIQEMDQIALRQGIEKSSLSRKTF AIDPSVVSSLLSEIQREEQQYLDPKVISWSSDQASD
RTHPKSAIYVNISDAAQEPQGRCYIDAYTKAFFTVLDQIGDPNIVKKHTIYVLTPILGVPDALPKEEQENLKL
SQAFLYSAEQVAKRMREEKQDSIRIKFIFTDPTSPTSLSLYFSPHSSSTPHSVTPISLSGFVGEQESYTFA

>core/390/2/Org2_Gene706

MSKKIKVLGHLTLCTLFRGVLCAAALSNIGYASTSQESPYQKSIEDWKGYTFTDLELLSKEGWSEAHAVSGN
GSRIVGASGAGQGSVTAVIWESH LIKHLGTLGGEASSAEGISKDGEVVVGWSDTREGYTHAFVFDGRDMKD
LGTLGATYSVARGVSGDGSIIVGVSATARGEDYGWQVGVKWEKGKIKQLKLLPQGLWSEANAISEDGTIV
GRGEISRNHIVAVKWNKNAVYSLGTLGGSVASAEAISANGKVIVGWSTTNGETHAFMHKDETMHDLGTL
GGGFSVATGVSADGRAIVGFSAVKTGEIHAFYYAEGEMEDLTTLGGEEARVFDISSEGNDIIGSIKTDAGAER
AYLFHIIHK

>core/391/2/Org2_Gene451

MKKRFPSTLFLFYRRVTIAISLEGILGWGWLGSLLSKVFAFLVACWNRFSWSTPYRARSTVISVGNIVVGGAG
KTPTVLWLAELRLRGYSCGVLSRGYKSQSSRQKKLTVVDSKVHSASVVGDEPLLMAEKLPEGSVWVHKD
RRISAARAAEKFGILLDDGLQYRKLHKDVEIAVVNGQDPLGGRAFFPKGRLRDFPLRLKTVDAIIVNGGGKE
AGTVVKRVSNAPQIFVKPTIASVWVTHNGERIPKEALRELRVGVFCGLGFPQGFLNMLREEGIHILGKYLLPD
HAAITKKELNYFCQQMAMRQGQGLLCTEKDSVKLPRLSGEVSLPIAKVEMRLSVNQDDTLSLLNMIEQIHK
NRGN

>core/392/2/Org2_Gene505

MNVPD SKNLHPPAYELLEIKARITQSYKEASAILTAIPDGILLSETGHFLICNSQAREILGIDENLEILNRSFTD
VLPDTC LGFSIQEALLES LKVPKTLRLSLCKESKEKEVELFIRKNEISGYLFIQIRDRSDYKQLENAIER YKNIAEL
GKMTATLAHEIRNPLSGIVGFASILKKEISSPRHQ RMLSSIISGTRSLNNLVSSMLEYTKSQPLNLKIINLQDFFS
SLIPLLSVSFPNCKFVREGAQPLFRSIDPDRMNSV VWNLVKNAVETGNSPITLTLHTSGDISVTNPGTIPSEIMD
KLFTPF FTTKREGNGLGLAEAQKIIRLHGGDIQLKTS DSAVSFFIIPELLAALPKERAAS

>core/393/2/Org2_Gene274

MSHTECGIVGLPNVGKSGLFNALTGAQVASCNYPFCTIDPNVGIVPVIDERLEALAKISNSQKIIYADMKFVDI
AGLVKGASDGAGLGNRFLSHIRETHAIAHVVR CFDDPDVTHVSGKVNPVEDIEVINLELIFSDFSSAKNIH SKL
EKLAKGKREVGALLPLFDTHAHLEKGLPLRTLELTPEQIVALKPY PFLTMKPMFYIANVDESSLPDMDNDYV
AAVREVA AKENSKVVPICVRIEEEIVSLPIEERLEFLMSLGLKESGLHRLVRAAYDTLGLISYFTTGPQESRAW
TVVRGSSAWEAAGEIHTDIQKGFIRA EVITFEDMIECQGRAAARELGK LHIEGRDYIVQDGD TMLFLHN

>core/394/2/Org2_Gene321

MTTEVRIPNIAESISEVTVASLLVTEGALIQENQGLLEIESDKVNQLIYAPVSGRIFWEVSEGDVVPVGGVVGKI
EPAGEGEELGDSQSKETIEAEIICFPQSGVRQSP PENKTFIPLRDQMDQGSQGLSAGDRGETRERMTSIRKTISR
RLLSALHESAMLTTFNEVYMTPLFHLRKEKQEEFLSRYGVKLGFM SFFVKAVLEALKAYPRVNAYIDGEEIV
YRHHYDISIAV GIDRGLVVPVIRDCDKLSNGEIEQKLADLALRAREGLLAIAELEGGGFTITNGGVYGSLLSTPI
INPPQVGILGMHKIEKRPVVDNEIVIADMMYVALSYDHRLIDGKEAVGFLVKVKEGLENPASLLDL

>core/395/2/Org2_Gene591

MVPFRQHHAYQLLKQLHTSAISEADRVSY YFKQNRSLGSKDRQWIQNIIFNILRHRRLLET LILDSGEQVTPEA
LVAKVNEGVLNLD SYSAIPWPVRY SISDDL AHFLVQDYGEEQAEEIAKIWLTEAPITIRVNTDKISVKELQEK
LEY PSSPGELPEALHFSKRHPLQSTEAFRRGFFEIQDENSQRISQGISLTDKDIVLDFCAGAGGKSLIFAQKAKH

VVINDSRKAILQTAKHRLLRAGARNFSLADQLRLGSFSVVIVDAPCSGTGVFRRHPEHKWQFSKKLLLNYVR
VQKSILKQASAYVGPRGRLVYITCSLLKEENEAHVAYMHSLGWKEVHRKTLPLQVGKGDAFFTSHFQKI

>core/396/2/Org2_Gene940

MKLYQTLRGIVLVSTGCIFLGMHGGYAAEVPVTSSGYENLLESKEQDPSGLAIHDRILFKVDEENVVLTALDVI
HKLNLLFYNSYPHLIDSFPARSQYYTAMWPVVLESVIDEFLMVADAKAKRIATDPTAVNQEIEEMFGRDLSP
LYAHFEMSPNDIFNVIDRTLTAQRVMGMMVRSKVMLKVTPGKIREYYRKLEEEASRKVIWKYRVLTIKANT
ESLASQIADKVRARLNEAKTWDKDRLTALVISQGGQLVCSEEFSSRENSELSQSHKQELDLIGYPKELCGLPKA
HKSGYKLYMLLDKTSGSIEPLDVMESKIKQHLFALEAESVEKQYKDRLRKRYGYDASMIKLLSEEAPPLFS
LL

>core/397/2/Org2_Gene513

MAFKRKTRWLWQVLILSVGLNMLFLLLFYSAIFRKDIYKLHLFSGPLIAKSSRKVYLSEDFLNEISQASLDDLI
SLFKDERYMYGRPIKLWALSVAIASHHIDITPVLSKPLTYTELKGSSVRWLLPNIDLKDFPVILDYLRCHKYPY
TSKGLFLLIEKMVQEGWVDEDCLYHFCSTPEFLYLRTLLVGADVQASSVASLARMVIRCGSERFFHFCNEESR
TSMISATQRQKVLKSYLDCEESLAALLLVHDSDVVLHEFCDEDELEKVIRLMPQESPYSQNFFSRLQHSPRRE
LACMSTQRVEAPRVQEDQDEEYVVQDGDSDLWIAKRFGIPMDKIIQKNGLNHHRLFPKGVLKLPKQKS

>core/398/2/Org2_Gene1016

MAVVSTPFFNRNLWYRLLSSRFSWLKSYCPRFFLDYLEAFGLLSDFLDHQAIVKFFFELETHFSYYPVSGFVAP
HQYLSLLQDRYFPIASVMRTLDDKNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ
RIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQET
LFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVLCQ

>core/400/2/Org2_Gene92

MKIDILSLFPGYFDGPLQTSILGRAIKQRLLDVQLTNLRDFGLGKWQVDDTPFSGGGMLLMAEPVTSAIRSV
RKENSKVIYLSPOGALLTAEKSRELAASHLILLCGHYEGIDERAIESEVDEEISIGDYVLTNGGIAALVLIDAV
SRFIPGVLGNQESAERDSLLEGLLEGPYTRPREFEGKEVPEVLLQGDHKAISQWRLEQSERRTYERRPDLYL
NYLYKRSIDHKFDEETTTNRDHFCDKISVVLEVNKLKRAKNFYCKVFGLDAMSCENKFCLPHEGKTIFWLR
EVQAEKKNIVTSLSLDCACEEDFCYLLRRWELFGGKLLLEKQADEHAVWALAQDLGDHAWIFSWHRMK

>core/401/2/Org2_Gene275

MGEKTEKATPKRLRDARKKGQVAKSQDFPSAVTFIVSMFTAFLSLSTFFFKHLGGFLVSMLSQAPTRHDPVITL
FYLKNCLMLILTASLPLLGAVAVVGIVGFLIVGPTFSTEVFKPDIKKFNPIENIKQKFKIKTLIELIKSILKIFGA
ALILYITLKSQVSLIETAGVSPITTAQIFKEIFYKAVTSIGIFFLIVAILDLVYQRHNAKELKMEKFEVKQEFKD
TEGNPEIKGRRRQIAQEIAIEDSSSQVKHASTVVSNNPKDIAVAIGYMPEKYKAPWIIAMGINLRAKRILDEAEK
YGIPIMRNVPLAHQLLDEGKELKFIPESTYEAIGEILLYITSLNAQNPNKNTNQPDL

>core/402/2/Org2_Gene257

MSEAPVYTLKQLAELLQVEVQGNIEPISGVEDISQAQPHHIAFLDNEKYSSFLKNTKAGAILSRSQAMQHA
HLKKNFLITNESPSLTFQKCIELFIEPVTSGFPGIHPTAVIHPTARIEKNVTIEPYVVISQHAHIGSDTYIGAGSVIG

AHSVLGANCLHPKVVIRERVLMGNRVVVQPGAVLGSCFGYITNAFGHHKPLKHLGYVIVGDDVEIGANTT
IDRGRFKNTVIHEGTKIDNQVQVAHHVEIGKHSIIVAQAGIAGSTKIGEHVIIGGQTGITGHISIADHVIMIAQTG
VTKSITSPGIYGGAPARPYQETHRLIAKIRNLPKTEERLSKLEKQVRDLSTPSLAEIPSEI

>core/403/2/Org2_Gene447

MSGPSRTESSQVSVLSYVPRDKEIAPKKQFTIAKISTLAILASLALGALVAGISLTIVLGNPVFLALLITTALFSV
VTFLVYHQMTSKVSSNWQKVLEQNFKPLGKAWQEKNVDCYSNEMQFYNNHLNPKFKVAIQTDASQPFQPT
FLTGLRVIEKNQSTGHIIFNPVGPTNLIDNTATNLSTILYSTLKDKSVWDTCKQREGGPAKGEDPFSPTEV RVVK
LPNEALDQTFNLNLSSAEKKSILPTFLGHVCGPKSEELPNQQEYYRQALLAYENCLKAAIESHAAIVALPLFTS
VYEVPP EEILPKEGTFYWDNQTQAFCKRALLDAIQNTALRYPQRSLLVILQDPFNTIESQSRSEE

>core/404/2/Org2_Gene922

MKNSFGSLFSFTTWGESHGPSIGVVIDGCPAGLELHESDFVPAMKRRRPGNPGTSSRKENDIVQILSGVYK GK
TTGTPLSLQILNTDVDSSPYENSERLYRPGHSQYTYEKKFGIVDPNGGGRSSARETACRVAAGVVAEKFLAN
QNIFTLAYLSSLGSLTLPHYLKISPELIHKIHTSPFYSPLPNEKIQEILTSLHDDSDSLGGVISFITSPIHDFLGEPLF
GKVHALLASALMSIPAAKGFEIGKGFASAQMRGSQYTDPFVMEGENITLKSNNCGGTG GITIGVPIEGRIAF
KPTSSIKRPCATVTKTKKETTYRTPQTGRHDPCVAIRAVPVVEAMINLVLADLVLYQRCSKL

>core/405/2/Org2_Gene616

MTLPNDLLETLVKRKESPQANKVWPVTTFSLARNLSVSKFLPCLSKEQKLEILQFITSHFNHIEGFGEFIVLPLK
DTPLWQKEFLLEHFLLPYDLVGNPEGEALVVSRS GDFLAAINFQDHLVLHGIDFQGNVEKTL DQLVQLDSYL
HSKLSFAFSSEFGFLTTPNPKNCGTGLKSQCFLHIPALLYSKEFTNLIDEEVEIITSSLLLGVTFPGNIVVLSNRC
SLGLTEELLSSLRITASKLSVAEVA AKKRLSEENSGDLKNLILRSLGLLTHSCQLELKETLDALSWIQLGIDL G
LIKVTENHPLWNPLFWQIRRAHLALQKQAEDSRDLQKDTISHLRASVLKELTKGLSPESF

>core/406/2/Org2_Gene803

MMKKIRKVALAVGGSGGHIVPALSVKEAFSREGIDVLLL GKGLKNHPSLQQGISYREIPSGLPTVLNPIKIMSR
TSLCSGYLKARKELKIFDPDLVIGFGSYHSLPVLLAGLSHKIPLFLHEQNLVPGKVNQLFSRYARGIGVNFSP
VTKHFRCPAEEVFLPKRSFSLGSPMMKRCTNHTPTICVVGGSQGAQILNTCVPQALVKLVNKYPNMYVHHIV
GPKSDVMKVQH VYNRGEVLCCVKPFEEQLLDVLLAADLVISRAGATILEEILWAKVP GILIPYPGAYGHQEV
NAKFFVDVLEGGTMILEKELTEKLLVEKVTFALDSHNREKQRNSLAAYSQQRSTKTFHAFICECL

>core/407/2/Org2_Gene88

MKKKVAEYLNRLAEVEIKISNPEIFSNSKEYSALSKEHSYLLELKNA YDKILNLEKVLADDKQALAEKDP EM
VVMLEEGINENKVELEKLNKILESLLVPPDPDDDLNVIMELRAGTG GEEAALFVGDCVRMYHLYASSKGWK
YEVLSASESDLKGYKEYVMGISGTGVKRL LQYEAGTHR VQRPETETQGRVHTSAITIAVLPEPSEEDTELLI
NEKDLKIDTFRASGAGGQHVNVTD SAVRITHLPTGVVVTCQDERSQHKNKDKAMRILKARIRDAEMQKRHN
EASAMRSAQVGSGDRSERIRTYNFSQNRVTDHRIGLTLYNLDKVMEGDLDPITTAMVSHAYHQLLEHGN

>core/408/2/Org2_Gene886

MPILWKVLIFRYLKTAAFCTLSLICISIISSLQEIVAYIAKDVPHYDTVLRLMAYQIPYLLPFILPGSCFVSAFSLFR
KLSDNNHMTFLRASGASQSIIMFPVLMVSGAICCLNFYTCSELASICRYQTCKEIANMAMTSPALLLQTLQKK
ENNRIFIAVDHCAKSKFDNVIVALKGNNEISHVGIKSIIPDTTKDVTAKADVVFISKLPDSLTESSSPSSQRFYIE
TLDELLIPKITSTLFAGKSYLKTRTDYLPWKQLVKQSLKSHLPETLRRVAIGFLCITLTYAGMILGIHKPRFRK
SIALYFIFPILDILLIVGKNTKNLPLAFMLFVFPQLVSWVVFARRAYRESRGYA

>core/409/2/Org2_Gene346

MSLLSGHRLEGFPPIAEVMAACDRCSMDFCCEILKSQSMDLWADAASCVDGLLQDPFWSTAIASGIAKSSLQE
TEFECESKVMVLSSWGEQGAQVCSPFNLERICMSFPSLKVFSLKKNGCENMGIQLSASCMNLLMSIFFVATN
GGSTPIWITKENLMALVALVLSHYQCYFVPATGDPQQRGNILGNPEVNAILARGMGMRVDLERKRGGESSSR
YLELAARCFENSLTKTSLSDANNVQERDKCLLQMSTSLMHTAGLNLQRPPVPTPSGVT AHPQPQDPVVT
QPSLLGARERSPVSSRGRFPVVLPLSVISPRSHPGRVERRDLEDEEEVVMF

>core/410/2/Org2_Gene722

MSHDRILRAQRALSEHNLDAILVEKSEDLAYFLHDEAIAIGILLIGQQEVMFFVYRMDKDLYSHIQRVPLTFLT
QDVVADLSLYVQKQRYQKIGFDSASTVYHKFAQRQVLPCLWEPLECFTEKIRSIKSEEEIRRMQEAAALGSA
GYDYVLTLLREGITEKEVVRQLRAFWAEAGAEGPSFPPIIAFGEHSAPHSIPTDRPLKKGDIVLIDIGVLLNGY
CSDMTRMTALGTPHPKLLESYPVVVEAQKRAMALCKEGVLWGDIDAEAVRVLREHHLDTYFIHGIGHGVG
RHIHEYPCSPRGSQVKLESGMTITVEPGVYFPGIGGIRIEDTLCIDKNKNFSLTARPVISELVCL

>core/411/2/Org2_Gene282

MNKRQKDKLKICVIISTLILVGIFARAPRGDTFKTFLKSEEAIYSNQCNE DMRKILCDAIEHADEEIFLRIYNLS
EPKIQQSLTRQAQAKNKVTIYYQKFKIPQILKQASNVTLVEQPPAGRKL MHQKALSIDKKDAWLGSANYTNL
SLRLDNNLILGMHSSELCDLIITNTSGDFS IKDQTGKYFVLPQDRKIAIQAVLEKIQT AQKTIQVAMFALTHSEII
QALHQAKQQRGIHVDIIIDRSHSKLTFKQLRQLNINKDFVSINTAPCTLH HKFAVIDNK TLLAGSINWSKGRFSL
NDESLIILENLTKQQNQKL RMIWKDLAKHSEHPTVDDEEKEIIEKSLPVEEQEAA

>core/412/2/Org2_Gene674

MNLPDRKKALEAAVAYIEKQFGAGSIMSLGRHSATHEISTIKTGALS LLDLALGIHGVPKGRVIEIFGPESGKT
TLATHIVANAQKMGGVAAYIDAEHALDPSYASLIGVNIDDL MISQPDCGEDALSIAELLARSGAVDVVIDSV
AALVPKSELEGDIGDVHVGLQARMMSQALRKLTATLSRSQTC AVFINQIREKIGVSFGNPETTTGGRALKFY S
SIRLDIRRIGSIKGS DNSDIGNRIKVKVAKNKLAPPFRIA EFDILFNEGISSAGCILD LAVEYNIIEKKGSWFNYQE
KKLGQGREFVREELKRN RKLFEIEKRIYDVIAANKTPSVHANETPQEVPAQTVEA

>core/413/2/Org2_Gene809

MNLCKRISFEEGLELFVSSPIERLQERADAIKERYPSNEVTVLDANPNYTNICKIDCTFCAFYRKPKSPDAY
LLSFDEVRSLLQRYVSSGVKTVLLQGGVHPGLGIDYLEELVRITVQEFP SIHPHFFSAVEIEHACRVSGISIEQG
LQRLWDAGQRTIPGGGAEILSERVRKIISP KKMQPGGWINLHKL AHLMGFRTTATMMFGHVENPEDILHLQ
TLRDAQDSCPGFY SFIPWSYKPGNTALRRNVPQQASIETY YRILALGRIFLDNFDHVAASWFGEGKSLGAKAL
HYGADDFGGVILDES VHKATGWSIQSSEEEICNIIRSEGFIPVERNTFYQHISCTVSSL

>core/414/2/Org2_Gene816

MKYSLNFKKIDYERVIEVTCSEKVRHLHAIHQTAVGPALGGVRASLYSSFEDACTDALRLARGMTYKAI
SNTGTGGGKSVIILPQDAPSLTEDMLRAFGQAVNALEGTYICAEDLGVSINDISIVAEETPYVCGIADVSGDPSI
YTAHGGFLCIKETAKYLWGSSSLRGKKIAIQGIGSVGRRLQLSLFFEGAELYVADVLERAVQDAARLYGATIV
PTEEIHAECDIFSPCARGNVIRKDNLADLNCKAIVGVANNQLEDSSAGMMLHERGILYGPDYLVNAGGLLN
VAAAIEGRVYAPKEVLLKVEELPIVLSKLYNQSKTTGKDLVALSDSFVEDKLLAYTS

>core/417/2/Org2_Gene236

MLNIHDILGNDDENLLSYQCKHITKDKLTLPSHDFVDKVFGLSDRNNRVLRLSLQTMFSHGRLANSGLYSILPV
DQGIEHSAGASFAINPIYFDPENIVKLAIESGCSAVASTYGTLSLLSRKYAHKIPFMLKLNHNELLSYPTKYHQI
FFTQVEAAYSMGAVAVGATVYFGSETSNEEIVAVSNAFAKARSLGLATVLWCYLRNPAFVANGVDYHTAA
DLTGQADHLGATLGADIVKQKLPTCQGGFKAINFGKTDERVYSELSSNHPIDLCRYQVLNSYCGKVGLNSG
GPSGKNDFTEAARTAVINKRAGGMGLILGRKAFQRPLSEGIQLNLVQDIYLDPNITIA

>core/418/2/Org2_Gene799

MIPLIPMFLKQSLFFSLALTGMTTLVLTVALGVPVMKWLKRKNYRDYIHKEYCEKLEMLHKDKAEVPTGGG
VLLFISLIASLLVWLPWGKFSTWFFIILLTCYAGLGWYDDRIKIKRKQGHGLKAKHKFMVQIAIAAFTLIALPY
IYGSTEPLWTLKIPFMEGMLSPLFWLGKVFCLGLALVAIIGTSNAVNLTGDLGLAAGTMSFAALGFIFVALR
SSTPIAQDVAYVLAALVGACIGFLWYNGFPAQLFMGDTGSLLGGLLGSCAVMLRAECILVVGGVFVAAEA
GSVILQVLSCLRLKKRLFLCSPLHHHYEYQGLPETKIVMRWFWSFVCAGLGIAAVLWR

>core/419/2/Org2_Gene916

MRIAVLGAGYAGLSVTWHLHLSQGTATIDLFDPIPLGEGASGMSSGLLHAFTGKKALKPPLADQGINATHA
LITEASKALNPVIVISQGILRPAIDEDQAQLFTERVEEFPKEVEWWEKARCEISIPSMVIPPNLGALFIKSGVTLN
NDLYIQGLADACMKLGTQFYDELIEDLADIEEFYDHIIVTPGANASILPELKDMPVNVKVGQLLEISWPKDLA
MLSFSINAHKYMVANTQKNTCILGATFEHNQPEETPDPAIAYQEIMPPVLSLFPGLKDAQVLHCYAGMRSSS
KSRLPVISRIREKLWFLGGLGSKGLLYHGITGDMLAQAVLRKSTAYIAKEFLFTI

>core/420/2/Org2_Gene830

MILLQNIKRCSLKQLKVLATLLLSLSLPTLEAAENRDSIVWHLDYQEALQKSKEAELPLLVIKSGSDWNGP
CMKIRKEVLESPEFIKRVQGKFVCVEVEYLKHRPQVENIRQQNLALKSKFKINELPCMILLSHEEREIYRIGSFG
NETGSNLGDSLCHIVESDSLLRRAFPMMTSLSLSELQRYYRLAEELSHKEFLKHALELGVRSDDYFFLSEKFR
LLVEVGKMDSEECQRIKKRLLNKDPKNEKQTHFTVALIEFQELAKRSRAGVRQDASQVIAPLESYISQFGQQD
KDNLWRVEMMIAQFYLDSDQWHHALQHA EVAFEAAPNEVRSHISRSLYIRHQS

>core/421/2/Org2_Gene470

MYLQEKFKAAQQVPLVLRELLSCSDSINDSDPIYRMVFDSNDTTISYKVGDALGVLPENSKEVSEHVLQLLGYS
PTTLVNVKKTSEKVSQAQKFIQGYVDLDKIPAKLNSFFPKDPKITLYDAIQEYRPQIPIELFAESVFPLPRFYSI
ASSPDLHPKSIELLVKHVSYPGKYQKRFGVCSSFLCSELQVND SAYIFVQPTKHFTLSTQTEGKPLVMIGAGT

GIAPYKAFLEERLFNKDPGNNLLFFGERKEKVNFYREFWNHAE EEGKLLFLAFSRERDQKVYVQDLLRIQ
KDEVRKAYEEGGFFVCGRKVLGIEVKHALEEILGKDTLASLRKEHRYVVDVY

>core/422/2/Org2_Gene258

MDVSRKINRHTQFYVDSIDGVIKNFDHDKPSEDKSRDHEELEEKLLTITKRIVASAEFQNRKTDSKNYYLKKT
QWLPFKNEELEQTKELFAMLTSMDDKIAQLFFYSPGCSSDWVEFTEVICHNLNDSIGLGGVLLCCGLFEQQCEH
VVTVNKKLDLPLLLGTTVVNSLRYYLTYRNLNLCQSMSELGKELGDVLKQHGVAFTLIFKEIVDIDLLNYV
KLIQGLKRSGNIQARIYDNDVPTLPSVSSSPIALRYS LANTIRGLALHVD FSSLKFISPSILSNTEHTAKALNSGG
ECFIFSNLDEFNLGMKIVMQLLRTGKISPEILNKNIMKILMIKRRVRSLYI

>core/423/2/Org2_Gene875

MEADILDGKLKRVEVSKKGLVNCNQVDVNQLVPIKYKWAWEHYLNGCANNWLPTEVPMARDIELWKSDE
LSEDERRVILLNLGFFSTAESLVGNNIVLAIFKHITNPEARQYLLRQAFEEAVHTHTFLYICESLGLDEGEVFNA
YNERASIRAKDDFQMTLTVDVLDPNFSVQSSEGLGQFIKNLVGYYIIMEGIFYSGFVMILSFHRQNKMTGIGE
QYQYILRDETIHLNFGIDLINGIKEENPEVWTTTELQEEIVALIEKA VELEIEYAKDCLPRGILGLRSSMFIDYVRH
IADRRLERIGLKPIYHSRNPFPWMSETMDLNKEKNFFETRVT EYQTAGNLSW

>core/426/2/Org2_Gene79

MELSLTSLPLAWYVILGVAVFAYSFGDGF DLGLGAVYLKAKEDKERRILLNSIGPVWDGNEVWLVIIVGGL
FAGFPACYATLLSIFYMPIWTLVLLYIFRGCSLEFRSKSES VSWKIFWDIIFICSGTAISFFLGTIVGNLILGLPLSP
DTSYASLSWILFFRPYAALCGAVVASAF AIHGSCFALMKTSDSLNARIAQQFPYILSSFLVFYVFLGASLISIP
KRFDAPPTYPLILLIALTSCCCVAAKTSVSKKRYGYAFIYSTLNLLSLILSAATLTFPNILLSTVDPQYSYTIYN
SAVETKTLKSLLIHVLIGLPFIITYTCYIYRVFRGKT NFPSIY

>core/427/2/Org2_Gene758

MNSKMLKHLRLATLSFSMFFGIVSSPAVYALGAGNPAAPVLPGVNPEQTGWCAFQLCNSYDLFAALAGSLK
FGFYGDYVFSESAHITNVPVITSVTTSGTGTTPTITSTTKNVDFDLNNSISSSCVFATIALQETSPAAPLLDIAF
TARVGGLKQYYRLPLNAYRDFTSNPLNAESEVTDGLIEVQSDY GIVWGLSLQKVLWKDGVSVFVGVSADYRH
GSSPINYIIVYNKANPEIYFDATDGNLSYKEWSASIGISTYLNDYVLPYASV SIGNTSRKAPSDSFTELEKQFTN
FKFKIRKITNFDRVNF CFGTTCCISN NFYYSVEGRWGYQRAINITSGLQF

>core/428/2/Org2_Gene868

MMEVYSFSPSVRTSFQHRVMAALDNWFFLGGRRLKVVS LDSCNSGQACEEYVPISTTEKVLKILSYLLIPIVII
ALLIRYLLHSNFTAKVSQKPWLKTLQLGIDIKSFILPGSHVNTMDSATLFKAIRLEGKRVDVEYHRLHSSDKV
VFYIPAQKL PDDLRLTHWLPEKETRKTEYVRHMLAHVMGYLTSQGKERLQQVVQDSRSSTSLGAEKVLQYR
FIDHPQSQGEFQRLLENITTKGSEDKEVVQSDLFDMAFQCWWPQFISVIQSPTFSEELVHEMSQKLDLDCIYP
EDDEFEQKFLNTLLKAVLHHGFEGISVASMGVIFLICPDSLALQIPFLRNQK

>core/429/2/Org2_Gene711

MNKKKRVLTGDRPTGKLHLGHWVGSIKNRLELQNSPEYDCFFIADLHTLTTKIRKEEVLDVDNHIYEV LAD
WLSVGIDPTKSIHYLQSAIPEIYELHLLFSMLISINRVMGIPSLKDMARNASIEEGSLSYGLIGYPILQ SADILLAK

AQFVPVGKDNEAHVELTRDIARNFNRLYGQVFPEPEVLQGELTSLVGIDGQGKMSKSANNAIYLSDS DATITE
KVRKMYTDPNRIRATTPGRVEGNPLFIYHDIFNPHKDEVVEEFKARYRQGCIDIEVKARLAEELIHF LKPIKER
RSEFLSKPLALQNVLEDGTHKMREVAKVTMEEVHDKFGFSGHKWRSLLK

>core/430/2/Org2_Gene160

MLTLGLESSCDETACAIVNEDKQILANIIASQDIHASYGGVPELASRAHLHIFPQVINKALQQANLLIEDMDL
IAVTQTPGLIGSLSVGVFHGKGIAIGAKKSLIGVNHVEAHLYAAYMAAQNVQFPALGLVVSGAHTAAFFIENP
TSYKLIGKTRDDAIGETFDKVGRFLGLPYAGPLIEKLALEGSEDSYPFSPAKVPNYDFSFSGLKTAVLYAIKG
NNSSPRSPAPEISLEKQRDIAASFQKAACTTIAQKLPTIIKEFSCRSILIGGGVAINEYFRSAIQTACNLPVYFPPA
KLCSDNAAMIAGLGGENFQKNSSIPEIRICARYQWESVSPFSLASP

>core/431/2/Org2_Gene104

MENAMSSSFVYNGPSWILKTSVAQEVFKKHGKGIQVLLSTSVMLFIGLGVCAFIFPQYLIVFVLTIALLM LAIS
LVLFLLIRSVRSSMVDRLWCSEKGYALHQHENGPFLDVKRVQQILLRSPYIKVRALWPSGDIPEDPSQAAVLL
LSPWTFSSVDVEALLPSPQEKEGKYIDPVLPKLSRIERVSLLVFLSAFTLDDLNEQGVNPLMNNEEFLFFINK
KAREHGIQDLKHEIMSSLEKTGVPLDPSMSFQVSQAMFSVYRYLRQRDLTSELRCFHLLSCFKGDVVHCLA
SFENPKDLADSDFLEACKNVEWGEFISACEKALLKNPQGISI KDLKQFLVR

>core/432/2/Org2_Gene259

MDSSAPYNIASQGTEKSTVERILDLYGPASCIKFLKQMVLIREFEARGE EAYLEGLVGGFYHSYAGQEAVATA
AIANTGLDPWVFSSYRCHALAILLNIPLQEIAAELLGKETGCALGRGGSMMHMC GPNFPGGFGIVGGQIPLAAG
AAFTIKYQEQKNRVSLCFIGDGAVAQGVFHETLNFVSLHQLPLMLIENNGWSMG TSLNRAVAKQPIAESQG
SSYDIRAVTVNGFDLFNSLLGFREAYRYMVDTESPVLVECLCSRFRGHSISDP NLYRSKEEMQCLFKKDPIVL
AKDWLIRLEVLTEEEFQNIRQECKTAVLEAFSNAKLSSDPSVTTL EEGVYA

>core/433/2/Org2_Gene131

MKLYSISSDVDTPWIFQLMSKVDSYLFLGGNRIKVVSIVMQEPNLIIGKVENVRISTIVKILKILSFLIFPLILIAL
ALHYFLHAKYANHLLVSKILERAPQYVPIPGRSGDTASHYKL TTLVPVSQKNLQAMGSNPLEVEAALRTTKP
SFFCVPKYRQIISSHGIRFSLDLEQLADDINLDSVSWPTEYLNSTMDFC SKADKRVIQNVQNLRTGTYINSV
GKRSLLKFMLQHLFIDGITQENPEALPNNTSGRLTLFPSVRYIYSHFTPQNPTIWPQVFFRQGPLDEDRGGGFEI
LEQLQELGVRFPICPSQGPDPNPNFQGFQGIRIYWEDSYQPNKEV

>core/434/2/Org2_Gene808

MLPFEFENNTSSPEC DVCLDPQKLFVKLFKRTIVLLSGPTGSGKTDVSLALAPMIDGEIVSVDSMQVYQGMD
IGTAKVSLKARQEIPHHLIDIRHVQEPFNVVDFYYEAIQACQNILSRNKVPILVGGSGFYFHAFLSGPPKGPAA
DPQIREQLEAIAEEHGVSALYEDLLLKDPEYAQTITKNDKNKIIRGLEIIQLTGKKVSDHEWDIVPKASREYCC
RAWFLSPETEFLKNNIQMRCEAMLQEGLLEEVRGLLNQGI RENPSAFKAIGYREWIEFLDNGEKLEEYEETKR
KFVSNSWHYTKKQKTWFKRYSIFRELPTLGLSSDAIAQKIAKDYLLYS

>core/435/2/Org2_Gene764

MFFQNLAKKLTALGISPLGCLLIGGVVSCAILFGRSSNPSLAPTQVKTEKTSGNWLKLTQMGNPKLIESLTKK
EQLEKDLTSFHPIASAKVAIALSTEDDVMSPHLHSVILTLRKEESLTPSLLFSITDYLCSSLPGLKREHISLSDNL
GNLYIPESITVNSLFIHTLENYLGIKIFPKEHFALAYHAKAEKPTLQLTLNENYIAHLTKEESEKIVAHTKHLY
QNYDDSYDIVIETLPFARLQNKKSFPKVLIGSMILVISLMIVALASFYLARHAYERVSPEPRKIKRGINISKLLE
IIQESPEKIALILSYLDPKKA EALLNRLPEDLKHQVLKYKL

>core/436/2/Org2_Gene235

MSEQHSPISVQDVSKKLGDHILLSKVSFSVYPGEVFGIVGHSGSGKTTLLRCLDFLDMPSTSGSISVAGFDNSLP
TQKFSRRNFSKKVAYISQNYGLFSSKTVFENIAYPLRIHHSEMSKSEVEEQVYDTLNFLNLYHRHDAYPGNLS
GGQKQKVAIARAIVCQPEVVLCDEITSALDPKSTENIIRLLQLNQERGITLVLVSHEIDVVKKICSHVLVMHQ
GAVEELGTTEELFLNSENSITNELFHEDINIAALSSCYFAEDREEVLRNLNFSKELAIQGIISKVIQTGLVSINILSG
NINLFRKSPMGFLIIVLEGEVEQRKKAKELLIELGVVIKEFY

>core/437/2/Org2_Gene422

MTILRKLSQYLFSSFLFCFSFIYVATCGSQPDSVSSPKIAIFLSFPHPLLEDCKSKSCIETLKDFENLPEIVVLNAEDSI
VKARKIARSLHTDKNVVAIVTLGTIATKVM SHIETQKPVIIAAVPDRESLTLPKNTMNIYGVNDTLDINQYCF
AIQAVATNAQSIVYLPSEPFPSDLQKEIVKKLHASGIEVIEISITSSTFKTRIRQAIDKRPSAIFIPLSPLSHKEGT
AFLQEILKEKIPIITDDTSLISEGACIACSVDYKKSGKQIAKIVHHLLYNNHDVDSL RKIIAQRLSPTTTFNEDIK
YLGIKLHKTERNQFLSFKSKKLEKSEKGKNVAVS

>core/438/2/Org2_Gene883

MEMKEEIEAVKQQFHSELDQVNSSQALADLKVRYLGKKGIFRSFSEKLKQCTDKAKLGS LINDFKTYVEDLL
QEKSLVLLASEQAEAFSKEKIDSSLPGDSQPSGGRHILKSILDDVVDIFVHLGFCVREAPNIESEANNFTLLNFT
EDHPARQMHDTFYLNATTVLRTHTSNVQARELKKQOPPIKV VAPGLCFRNEDISARSHVLFHQVEAFYVDH
NVTFSDLTAILSAFYHSFFQRKTELRF RHSYFPFVEPGIEVDVSCECCGKGKALCKHTGWLEVAGAGMIHPQV
LRNGNVDPEIYSGYAVGMGIERLAM LKYGVSDIRLFSENDLRFLQQFS

>core/439/2/Org2_Gene309

MATISPISLTVDHPLVDTKKKSCSNFDKIQSRILLITAIFAVLVTIGTLLIGLLL NIPVIYFLTGISFIAVVLSNFILY
KRATTLKPRACGKHKEIKPKRVSTNLQYSSISIAINRSKENWEHQPKDLQNL PAPSALLTDNPYEIWKAKHS
LFSLVSLLPGGNPEHLLISASENLGKTLLIEETSQNAPISSYVDTTSPKSL LNEAIQETRVEINTELPAGDSGER
LYWQPDFRGRVFLPQIPTTPEAIYQYYYALYVTYIQTAIN TNTQIIQIPLYSLREHLYSRELPPQSRMQQSLAMI
TAVKYMAELHPEYPLTIACVERSLAQLPQESIEDLS

>core/440/2/Org2_Gene608

MEEAAKHLAKEFLCSGINLFLSGEYEQA EKRLKETLELDSTAALAYCYLGIIALETGRVSEALNWCSKGLASE
PGDSYLR YCYGVALDRGNQYEA AIEQYSAYVALHPDDVECWFSLSVYHRLKRLQEALDCFDKILALDPW
NPQSLYNKAVILSEMDDEAESIRLLEVA VAKNPLYWKA WVKLGFLLSRSKRWDKATEAYERVVQLRPDLS
GHYNLGLCYLTLDKTRLALKAFQEALFLNAEDADAHFYVGLAHLDLKQMREAYEAFNSALSINLEHERAHY
LLGYLHHMQGETDKATKELLFLQKKDSTFAPLLQKTVVSDPSSMQFERRLDTIS

>core/441/2/Org2_Gene629

MVLGVVGISYREAALKERERAIQYLQSFEKNLFLAQRFLGKGGAFIGLLTCHRAELYYYSESPEIAQAALLSEL
TSQGIRPYRHRGLSCFTHLFQVTSGIDSLIFGETEIQQQVVKRAYLKGSKERELPFDLHFLFQKALKEGKEYRSRI
GFPDHQVTIESVVQEILLSYDKSIYTNFLFVGYSINRKVAAYLYQHGYHRITFCSRQQVTAPYRTLSRETLSF
RQPYDVIFFGSSESASQFSDLSCESLASIPKRIVFDNFVPRTFLWKETPTGFVYLDIDFISECVQKRLQCTKEGV
NKAKLLLTCAAKKQWEIYEKKSSHITQRQISSPRIPSVLSY

>core/442/2/Org2_Gene102

MFPSANQESRTRNVPLGIFHGLVACLYWGIVFVIPNFLGSFGDLDIVLTRYTIFGIFSLIACAIGNPSVIKKTPLYI
WRKSLWTLINPVYYFGITLGIRYVGSAITVVIASLAPTAVLYHSNTKQKELPYSLLFAISSVIITGVILTHLSA
LNLPTAASPLYSILGVIAVILSTSLWVIYVIRNQSLLEKHPNLTPDTWSYLIGISALIICLPMIILDLCGITHVTHN
LISHTPGSERLLFLLCSAMGIFSSAKALIAWNKASLNLSPALLGAILIFEPIFGLVLTLYLSQSLPSLQEGIGIFL
MLGGSLLCLVLFGRKVQKSLENSQVSSSNE

>core/443/2/Org2_Gene707

MKKTCCQNYRSIGVVFVSVVLFVLTQTFLAGHFIDIGTSGLYSWARGVSGDGRVVVGYEGGNAFKYVDGEK
FLLEGLVPRSEALVFKASYDGSVIIIGISDQDPSCRAVKWVNGALVDLGIFSEGMQSFAEGVSSDGKTIVGCLY
SDDTETNFAVKWDETGMVVLPNLPEDRHSCAWDASEDGSVIVGDAMGSEEIAKAVYWKDGEQHLLSNIPG
AKRSSAHAVSKDGSFIVGEFISEENEVHAFVYHNGVIKDITLGGDYSVATGVSRDGKVIVGHSTRTDGEYR
AFKYVDGRMIDLGTLLGGSASFAGVSDDGKTIVGKFETELGECHAFIYLLDD

>core/444/2/Org2_Gene334

MTHQVAVLHQDKKFDVSLRPGLEEFYQHHLLKERLDLFLCAALQRGEVPGHCLFFGPPGLGKTSLAHIVA
YTVGKGLVLASGPQLIKPSDLLGLLTSLQEGDVFFIDEIHRMGKVAEEYLYSAMEDFKVDITIDSGPGARSVR
VDLAPFTLVGATTRSGMLSEPLRARFAFSARLSYYSQDLKEILVRSSHLLGIEADSSALLEIAKRSRGTPLRA
NHLLRWVRDFAQIREGNCINGDVAEKALAMLLIDDWGLNEIDIKLLTTIIDYYQGGPVGKTLTSAVGEDIKT
LEDVYEPFLILKGFIKKTTPRGRMVTQLAYDHLKRHAKNLLSLGEGQ

>core/445/2/Org2_Gene653

MSYSLRNKKTKICVYIIIALGILSFRSIPQEVYDKIRSSFVSLHVKFFPKIKQAPSSHLANLELENLVLKERVASL
EEKLKLYEVSNTHTPPLFPEILTPYFHKLVGKVVYRDYTHWSSSCWVNVGKTHGIKKNSPVLSGNVLVGLVD
YVGEHQSRIRLITDVGMKPSVVAMRGDIQSWWIKHSLRELIRQVEQISHAYILEKDKYEKISQLQELDSLQGE
GENQALLRGILSGVGGALWKEGSLCEGEGFYFSEGKTLLPGDILVTTGLDGVFPGLLVARVTKVKAPRDG
ACTFKIEAQSLLEKLMELDQLFILPPLEFNPNDRPDIFGLLWD

>core/446/2/Org2_Gene542

MKVVINGFGRIGRLVLRQILKRNSSVEVLAINDLVPGDALTYLFKFDSTHGRFPEDVRCEADHLIVGKRKIQF
LSERNVQNLPWKDLGVDLVIECTGLFTKKEDAEKHIQAGAKRVLISAPGKGDIPTFVMGVNHKTFNPEKDFV
ISNASCTTNCLAPIAKVLLDNFGITEGLMTTVHAATATQLVVDGPSKKDWRGGRGCLQNIIPASTGAAKAVT

LCLPELKGKLTGMAFRVPIEDVSVVDLTVRLDKSTTYDDICKAMKQASETDLKGILDYTDEQVVSSDFIGSEY
SSIFDALAGIALNDRFFKLVAWYDNETGYATRIVDLLEYVEKNSK

>core/447/2/Org2_Gene466

MFVDQITLELRAGKGGNGVVAWRKEKYLPKGGPYGGNGGNGGSVIIEATTSVYSFEAYRNIRFLKAPDGQS
GATNNRTGRSGKDLIVSVPTGTLLRDAETGEILHDFTVDGERLLVSQGGKGGKGNTFFKTSVNRAPTKATPG
KPGEIRQVELEKLIADIGLVGFPNAGKSTLFNTLAHTEVKVGAYPFTTLAPSLGLVLCKDRLYQKPWIIADIP
GIIEGAHQNKGLGLDFLRHIERTLLLLFVIDVSKRERNSPPEEDLETLIHELHSHQPDFEKKDMLVALNKIDDLL
PDEQEECLQSFQKRFPSYTFVLISGLTGEGVDGLYRFFTQRLAV

>core/448/2/Org2_Gene253

MWFSVNKNKKAIIWATGSYLPEKVLSNADLEKMVDTSDEWIVTRTGIKERRIAGPQEYTSMLGAIAAEKAI
ANAGLSKDQIDCIIFSTAAPDYIFPSSGALAQAHLGIEDVPTFDCQAACTGYLYGLSVAKAYVESGTYNHVLLI
AADKLSSFVDYTDNRNCTCVLFGDGGAACVIGESRPGSLEINRLSLGADGKLGELLSLPAGGSRCPASKETLQSG
KHFIAMEGKEVFKHAVRRMETAAKHSIALAGIQEEDIDWFVPHQANERIIDALAKRFEIDESRVFKSVHKYGN
TAASSVGIALDELVHTESIKLDDYLLLVAFGGGLSWGAVVLKQV

>core/449/2/Org2_Gene680

MAAPIFIKNILLRSSIVYAPLAGFSOPYRCMSALYQPGLMFCCEMVKVEGILYAPERTSKLLDYNENMRPIGA
QLCGSNPETSGEAAKILEGLGFDLIDLNCGCPTDKITKDGS GSGLLKTPELIGRILDKIINSVSIPVTVKIRSGWD
MEHINVEDTVRIIRDAGASAVFVHGRTRAQGYHGPSKQEYISRAKAAAGKEFPVFGNGDIFSPEAAQAMLTT
GCDGVLVARGTLGAPWIGKQIQDYLTGTSYEKIPFIKRKA AFLEHMRLVEDYYQSETKFLSETRKLCGHYLIS
AAKVRFLRSSLAKATSYQEVYQLVNDYEEADSSLET FVKC

>core/450/2/Org2_Gene50

MSTPLSSGGISPSDQYVPQELFCDRLLSSSRNSPDSNASGDSPIVSPPIALVALTDLKLV PYNQNSFSWTTRLK
NAVEKIGLFLQRNWKYILLYILAWALILVCHHTVALTLTIWLGVGLGIGVVFGIFTATCLDKENKHRHVNSL
WNLINHGILQLDPNGTRQILLATMIASISALIYAVPQAVGLVIGFSIGNQLSINTVYGARLGDEATY AIDRKAH
KKRIENIEQAINQHQIIKHQMINQKQLNALIEINRNNQTD PATANLLASLKLNLNQPMPCFSMPECVGTSSYL
DLNNNSPDDIARADQCIMTLSQTLQQIKKEPDRIIESNH

>core/451/2/Org2_Gene736

MVRRSISFCLFFLMTLLCCTSCNSRSLIVHGLPGREANEIVLLVSKGVAAQKL PQAAAATAGAATEQMWDI
AVPSAQITEALAILNQAGLPRMKGTSLLDLFAKQGLVPSELQEKIRYQEGLSEQMASTIRKMDGVVDASVQIS
FTTENEDNLPLTASVYIKHRGVLDNPN SIMVSKIKRLIASAVPGLVPENVS VSDRAAYS DITINGPWGLTEEI
DYVSVWGIILAKSSLTKFRLIFYVLILILFVISCGLLWVIWKTHTLIMTMGGTKGFFNPTPYTKNALEAKKAEG
AAADKEKKEDADSQGESKNAETSDKDSSDKDAPEGSNEIEGA

>core/452/2/Org2_Gene759

MKQHIGYLGMGIWGFCLASLLANKGYPVVAWSRNPDLIKQLQEERRHPLAPNVVISPNLSFTTDMKEAIHNA
FMIVEGVTSAGIRPVAEQLKQITDLSVPFVITSKGIEQNTGLLLSEIMLEVLGDSVTPYLG YLSGPSIAKEVLNG

SPCSVVVSAYDSQTLKQIHEAFSLPTFRVYPNTDIKGAALGGALKNVIAIACGIAEGLSFGNNAKAGLVTRGL
HEMRKLAAIMDCKPETLNGLAGLDLCVTCFSESSRNLRFGHLLAQGLTFEQAKAKIGMVVEGAYTALSAY
QVAKHHKIDMPITGTIYRVLYENLDLKEGIALLLQRNTKEEFL

>core/453/2/Org2_Gene521

MKPLGFQENLEALCNKTSRQLLKYLKQILFVCGASLLIALEFSFFLYFFLFSGKTVIPAFCLACFFLTFLVCLV
TRLYLLSGKGDFEDLASEYLQGAVPPNKRSQLNIVEEQSHLAAAATKLSINLQNQEYSLSEIFKFLPKHDLIR
KFSCFCFWKDYFLFRECLLQKAIEAYIKVVQAIPVDLSAHVSLADAYVALSGLYADPRKYPEFDANYWIPSG
RYSAEIQEKFFATARRAIEEFQILNEYAPGNAWVHAQLAYSYHDLQMPMEEIQEYEIVLKLKPNDVETMSKL
GILYFQQGMNAKGLRIYEEIKKRDYKKSQKLIKFGVEYKY

>core/455/2/Org2_Gene729

MQPFIFTLCLTSLVSLVAFDAANARKRCACAQTIERGENFFSIKRSACAEIEYQEKSRRHASAIERISKDKGKV
TPKQIAKVATKKKQRYRLLQVPFSRPPNNSRYNLYALLSEPPECYSDTASWYAIFIRLLRRAYVDTGNVPPGS
EYAIANALISNKQEILERGAQLGPDVIETLTLPEEQAEIFYKMLKGSSNSQSLLNFLHYEEKSLGHCKLNLIFM
DPLLLEAVLDHPDAYRETSLLRDGIWEAVKRQEHAIQEHGQAAALELFKTRTDFRLELRDKMQLLLSRYDLL
PLLNKKMFDYTLGSAGDYFLVDPDTKAISRCRCPSKSIKL

>core/456/2/Org2_Gene566

MATNAIRSAGSAASKMLLPVAKEPAAVSSFAQKGIYCIQQFFTNPGNKLAKFVGATKSLDKCFKLSKAVSDC
VVGSLLEEAGCTGDALTSARNAQGMLKTTREVVALANVLNGAVPSIVNSTQRQCYQYTRQAFELGSKTKERKT
PGEYSKMLLTRGDYLLAASREACTAVGATTYSATFGVLRPLMLINKLTAKPFLDKATVGNFGTAVAGIMTIN
HMAGVAGAVGGIALEQKLFKRAKESLYNERCALENQSQSLSGDVILSAERALRKEHVATLKRNVLTLLEKA
LELVVDGVKLIPLPITVACSAAISGALTAASAGIGLYSIWQKTKSGK

>core/457/2/Org2_Gene932

MRIAVLGVTGLVGQKFVALLHKWYRDWVIAEVVASNSKYGQSYGDACIWQEPGMPPEMVRDLPIRKIEEV
QSDIVVSFLPSSAESMEAYCLSQGKVVFSNASTYRMHSSVPIIPEVNSDHFQLLEECPYPGKIITSPNCCVSGIT
LALAPLRKFSLDHVHIVTLQSASGAGYPGVPSLDLLANTVPHIVGEEKILRETVKILGSSKQPLPCKLSVTVH
RVPVAYGHTLSLHVTFSKDVDLDEILYSYQEKNEFPNTYQLYDNPWSPQARKHLSHDDMRVHLGPITYGG
DFRTIKMNVLIHNLVRGAAGTLLASMENYFFDYLKREMCLR

>core/458/2/Org2_Gene532

MKTLWHFVSKAFLSIVGLCCGVVLAFFVIFALIASSLGNGDATFVSLPDAQGEVKDLGKTAPIIAVIEMKDVI
ASSKNTAKTIQNILEGFEKAPLKDRVKGIVIDMDCPGGEVFEIDRIYSMLRFWKERKGFPIIYVNGLCASGGY
YVSCAATKIYATSSSLIGSIGVRSGPFFNVKEGLNRYGVESDLLTAGKDKAPMNPYTPWTSHDREERQATLDF
LYGQFVDIVTQNRPLLTKELVHTLGARIFSPEKAKQEGYIDVVGATKEQVLQDIVAVCKIEDNYRVIGSGGD
GWWKRVASAAASSPLVTGMIKHDILPLSHDAAAYIPPYLAL

>core/460/2/Org2_Gene658

MSSLTISRPRRRNRKTAAIRDLLAETHLSPKDLIAPFFVKYGNNIKEEIPSLPGVFRWSLDLLLKEIERLCTYGL
RAVMLFPIIPDDLKDAYGSYSSNPKNILCHSIHEIKNAFPHLCLISDIALDPYTTHGHGDFLNGEVLNDESVRIF
GNIATLHAEMGADIVAPSDMMDGRIGYIRSKLDQSGYSKTSIMSYSVKYASCLYSPFRDALSSHVTSGDKKQ
YQMNPKNVLEALLESSLDEEEGADILMVKPAGLYLDVIYRIRQNTCLPLAAYQVSGEYAMILSAFQQGWLD
KETLFHESLIAIKRAGADMIISYSAPFILELLHQGF

>core/461/2/Org2_Gene126

MNIYQFSPGASPNWQASLMAQLNSYFCLGGETVTRIISLRPSGLILAKKEKAVVSTAEEKILKILSFILFPLVLIAL
AIRYLLYNKFNKDLDRVFFIPTEITKAEELIIAKNPALVKEAALTVSPLFYSLPKKYQLMKVETP

>core/462/2/Org2_Gene127

MLLEDLDTDSIPWPKLYLSEDFDFAYYPESKAIIDTVAKLEKNNPGEEFCLESKKILARYLLEQLFKLETGLNF
PTSTIDGGRESFLIEFSHETKKPTVWAFIYFYYYHSNGPKLEKDFKQAGCEVHNRLNLGLKYRPQAGAQN
GRNGGPYGPIGFLIVWEENYGSVLKDHGFIKDN

>core/463/2/Org2_Gene852

MQFSRYLRYAFDNQYLPEPLYQKFSVFHQNYIDAATKKAADQAEVLCLQWVKVIIEDLKNPFIFPPYHKKI
RAPIDLFRLSIDFFSLVIDDKNSRILNLHRLKEIEEYIARGDNVLLANHQTECDPQLMYALGKTHPELMEN
MIFVAGDRVTSDPLARPFMSMGCDLLCIYSKRHIATPPELREEKLLHNQKSMQILKTLLNEGKFIYVAPAGGR
DRKNAEGRLYPSEFSPESIEVFRLLAKASNQTTHFYPFALKTYDILPPPKIENAIGEQRRAIFFAPVFFNFGAELF
FDALCSKEELIHCDKHAQRTLRAEKVFSIVKNLYEEL

>core/464/2/Org2_Gene929

MREETVSWSLEDIREIYHTPVFELIHKANAILRSNFLHSELQTCYLISIKTGGCVEDCAYCAQSSRYHHTHTVPEP
MMKIVDVVERAKRAVELGATRVCLGAAWRNAKDDRYFDRVLAMVKSITDLGAEVCCALGMLSEEQAKKL
YDAGLYAYNHNLDSSPEFYETIITRSYEDRLNTLDVVNKSISTCCGGIVGMGESEEDRIKLLHVLATRDHIP
ESVPVNLLWPIDGTPLQDQPPISFWEVLR TIATARVVFP RSMVRLAAGRAFLTVEQQTL CFLAGANSIFYGDK
LLTVENNDIDEDAEMIKLLGLIPRPSFGIERGNPCYANNS

>core/465/2/Org2_Gene406

MIDIMQHFKPYTMVPGQKLPIPGSLLYAQVFPTLWRLFSSKHEILNEQTLQVQGPKRFAVFQDLHRGGLAV
TSERYKYLLPSGECTQSIKGLPSAAQAGPLLSLGVHKHADWQKVRCRRDLKEILPLWFRFAAMAPKGSY
RDLETTAIGSLVKTAHQRVLHRETTEIAPALLSIALAGFSECFLPRSYDEEFQGILPQDGDPEGGVFPFELLSYF
GMIQDIFLRHQGQLVEILPALPPEFPCGRLIHVALPNLGTLSIVWTKKTIRQVELHAEYSGEVFLKFCSSLCSAR
LREWSERRLSGSKRLSLGETLEIKAGTTYLWDCFHK

>core/466/2/Org2_Gene791

MSAFFDLLKSQTASHPPIWLLRQVGRYMPPIYQELKGSQSLKTFFHNTEAIVEATLLGPSLLHVDAAILFADILS
ILDGFAVTYDFAPGPRIQFSPEQPFTFTSDPQTIFSYLLDAIRTLKQKLPVPLIVFAASPFTLACYLIDGGASKDF
SKTMSFLYVYPEKFDQLISTIIEGTAIYLKTQMDAGAAAVQLFESSLRLPSALFTRYVTEPNRRLIAKLKEQAI

PVSLFCRCFEENFYTLQATQADTLHPDYHVDLHRIQKNLMLSLQGNLDP AIFLLPQEKLLHYVEAFLVPLRTY
PNFIFNSGHGILPETPLENVQLVVS YVQRQL

>core/467/2/Org2_Gene449

MPSPMISTDVCQDILGKQKEAVDFFFQAFQPK EAMQLAEKILGHSGWVFFSGVGKSGCVARKLVATLQSLSE
RALFFSPVDLLHGDLGLVSPGDIVCLFSKSGETQELLDTVPHLKSRRAILVAITSM PYSNLAALSDLVVILPSV
AELDPFNLIPTNSTTCQMIFGDFLAMLLFHSRGVSLSTYGKNHPSGQVGMKANGKVKDFMFPKTEVPFCHLG
DKVSFSLEVFSAYGCGCVCIVDPQFRLMGIFTDGD LRRSLASYGGEVLSLSLEKVM TANPRCITEDSDIAIALQ
LMESSPVAVLPVLDNEENRHVTGLLHMHTLAKAGLL

>core/468/2/Org2_Gene915

MAFKEVVRVAVTGGKGQIAYNFLFALAHG DVFVGVDRLRIYDVPGTERALSGVRMELDDGAYPLLHRL
RVTTSLNDAFDGIDAAFLIGAVPRGPGMERGDLLKQNGQIFSLQGAALNTAAK RDAKIFVVGNPVNTNCWIA
MKHAPRLHRKNFHAMLRLDQNRMHSM LAHRAEVPLEEVS RVVIWGNHSAKQVPDFTQARISGKPAAEVIG
DRDWLENILVHSVQNRGSAVIEARGKSSAASASRALAEAARSIFCPKSDEWFSSGVCSDHNPYGIPEDLIFGFP
CRMLPSGDYEIIPGLPWE PFIRNKIQISLDEIAQEKASVSSL

>core/469/2/Org2_Gene260

MPKHKTLEIREALREAIDEEMSRDPNVCILGEEVGDYNGAYKVTKGLLDKWGPKRVIDAPISEAAFSGIGIGA
ALSGLRPIIEFMSWNFSFVALDQIISHAAKM HFMTGGKFSVPIVFRGPNGAAAQVSCQHSHCVESLYANIPGLI
IIAPSNPYDAKGLLKS AIRNNNPVLFLENELEYNLKG EVPTEEYLVPIGKAHRVQEGNDLTIITYSRMVSITKEA
CSLAKKRWGLSIEIIDLRTIKPLDISTILSSVRKTSRCIVIEEGHYFAGISSEIIALITEHVFDSLDAPPLRVCQKETP
MPYSKILEQATLPNVNRILDTIEKVMR

>core/470/2/Org2_Gene61

MSNQFDQLKKLSTIVCDSGDPELVKASGSQDATTNPSLILKVAQE PKFQELLNEAVVWGIRQNGDDLQTL SFI
LDKIQVNFALEIINKNIPGRISLEIDARLSFNVEAMVQRAVFLSQLFEAMGGDKKRLLVKIPGTWEGIRAVEFLE
AKGIACNVTLIFNLVQAIAAAKAKATLISPFVGR IYDWWIAAYGDEGYSIDADPGVASVSNIYAYYKKFGIPT
QIMAASFRTKEQVLALAGCDLLTISPKLLDELKKSQHPVKKELDPAEAKKLDVQPIELTESFFRFLMNEDAMA
TEKLAEGIRIFAGDTQILETAITEFIKQIAAEGA

>core/471/2/Org2_Gene522

MTTPAYLLANFGGPRHAKDLQEFLISLLTDRDVTGTFLPRVLHRHLFTFI AKKRVPKVLPQYQSLQNWSP IYF
DTETLAKTLSEILRAPVIPFHRYLPSTHEKTLLALRTLHTRHVIGIPLFP HFTYSVTGSIVRFFMKHVPEIPISWIP
QFGSDSKFVSLITCHIRDFLQKLGILEKECCFLSVHGLPVRYISQGD PYSKQCYESFSAITTNFKQSENFLCFQS
KFGPGKWLS PSTAQLCQNIDTDKPNVIVVPFGFISDHLETLYEIERDYLPLLRSGYRALRIPAIYSSPLWVSTL
VDIVKENSTVVAEELIKSGKKHTGIR

>core/472/2/Org2_Gene296

MDAKMGYIFKVMRWIFCFVACGITFGCTNSGFQ NANSRPCILSMNRMIHDCVERVVGNRLATAVLIKGS LDP
HAYEMVKGDKDKIAGSAVIFCNGLGLEHTLSLRKHLENNPN SVKLGERLIARGAFVPLEEDGICDPHIWMDL

SIWKEAVIEITEVLIEKFPEWSAEFKANSEELVCEMSILDSWAKQCLSTIPENLRYLVSGHNAFSYFTRRYLATP
EEVASGAWRSRCISPEGLSPEAQISVRDIMAVVDYINEHDVSVVPEDTLNQDALKKIVSSLKKSHLVRLAQK
PLYSDNVDDNYFSTFKHNVCLITEELGGVALECQR

>core/473/2/Org2_Gene442

MMTYPVPQNPLLLRILRLMDAFSKSDDERDFYLDRVEGFILYIDLKQEDLNKIYQELEENAERYCLIPKLT
FYEYVKKIMETFINEKIYDIDTKEKFLEILQSKNAREQFLEFIYDHEAELEKWQQFYVERSIRIIEWLRNNKFHF
VFEEDLDFTKNVLEQLKIHLDFAKVGKEITQARQLLSNKAKIYYSNEALNPRPKRGRPPKQSAK VETETTISST
IYTKVPQAARRFLFLPEITSPSSITFSEKFDTEEEFLANLRGSTRVEDQLNLTNLSERFASLKELSAKLGYSLSLST
GDFFGDDDEKVVTKTKGSKRGRKKSS

>core/474/2/Org2_Gene817

MHSELPNYQNIVESVVTEITTQLLNYRSEHRLVPFWEKSDGSFITAADYGSQYYLKQQLAKAFNPFIGEETL
YPDQDNEKIPEILKFTRLLTSSVSRDDLSTLVPPPSPSTSLFWLVDPIDGTAGFIRHRAFAVAISLIYEYRPILSVM
ACPAYNQTFKLYSAAKGHGLSIVHSQNLDRRFVYADRKQTKQFCEASLAALNQHHATRKLSTGLPNTTPSP
RRVESQYKYALVAEGAVDFFIRYPFIDSPARAWDHVPGAFLVEEAGGRVTDALGAPLEYRKESLVLNNHAVI
LASGDQETHETTLAALQNQLNVVPTDKLIAL

>core/475/2/Org2_Gene634

MKTVTSFTVCKENSGRLDKYLTEVHPKYSRAFYQEHILSGLVQINGQINTRVATRLNCGDIVTIDIQEKEELLE
LLPEAIPLDKVYEDGMILVINKPRDMVVHPAPGHFHGTLVHALLHEIGERLKEEFPEEPWRPGIVHRLDKDTS
GLIITAKTRQAKKVSELFSTKRLKKSYLAVCIGKPRSTTIHTHISRHQNKRKEMTVSSQGKEAVTHCQVLAF
NGKLSFVALSPETGRTHQLRVHMKHLGTPILGDPVYGIPSMNSSYGLDKQQLHAYSVDFTHPETRQFCSLKA
GLPEDMRSLLIKEFRNETTILNKNLLESILKEQ

>core/476/2/Org2_Gene224

MTIDMHCDLLSHPHFCRKDPAVRCSPEQLLSGGVRQQVCAIFVPHSRGEPNCDKQNSLFFSLPNQYPDIGLLS
YEEEENGSSSQKKSLSLIRSIENASALGDDTAPLGTLLAKLIHLTKQGPLAYLGIVWKGDNRFGGGTEAPKRL
SNDGKVLLDIMYELGVPIDLSHCSDKLAEDILDYADKLPNLAVIASHSNFRSVLDHRRNLVDAHAKIVRRK
GVIGLNLVRSYVGDSLGDLEKHVLHAENLGILSSIVLGSDFFYANEDENFFFNECSSAEAHVPLNQLIHRIFSK
GKAESILSSRAEKFLKQVIVEQVNPKITDVKL

>core/478/2/Org2_Gene105

MIEFAFVPHTSVTADRIEDRMACRMNKLSTLAITSCLVLISSVCIMIGILCISGTVGTYAFVVGIHFSVLALVACV
FFLYFFYFSSEEFKCASSQEFRFLPIPAVVVSALRSYEYISQDAINDVIKDTMQLSTLSSLLDPEAFFLEFPYFNSLI
VNHSMKEADRLSREAFLLIGEITWKDCETKILPWLKDPNITPDDFWKLLKDHFDLKDFKKRIATWIRKAYPE
IRLPKKHCLDKSIYKGCCKFLLSENDVQYQRLLHKVCYFSGEFPAMVLGLGSEVPMVLGLPKVPKDLTWE
MFMENMPVLLQSKREGHWKISLEDVASL

>core/479/2/Org2_Gene355

MELLPHEKQVVEYEKAIAEFKEKNKNSLLSSSEIQKLEKRLDKLKEKIYSDLTPWERVQICRHPSRPRTVNYI
EGMCEEFFVELCGDRTFRDDPAVVGGFVKIQGQRFVLIGQEKGCDTASRLHRNFGMLCPEGFRKALRLGKLA
EKFGLPVVFLVDTPGAYPGLTAEERGQGWAIKKNLFELSRLATPVIIIVIGEGCSGGALGMAVGDSVAMLEH
SYYSVISPEGCASILWKDPKKNSEAASMLKMHGENLKQFGIIDTVIKEPIGGAHHPALVYSNVREFIIQEWLR
LKDLAIEELLEKRYEKFRSIGLYETTSSESGPEA

>core/480/2/Org2_Gene599

MASNPILQIEDLSITLAKQRQQYPIVQSLSFTINEGQTLAIIGESGSGKSVSAHAILRLLPCPPFSVSGQVNFQGH
NLLTASRSIQKKIIGTEISMIFQNPQASLNPVFTIEQQFREIIHTHLALTAEVAKEKMLYALEETGFHDPRLCLNL
YPHQLSGGMLQRICIAMALLCSPKLLIADEPTTALDVSQYQILQLLKTQKKTGMSLLIITHNMGVVAETAD
DVLVLYAGRMVECAPAVQMFHNPSHPYTRDLLASRPSLQPQQLGSFNPIPGQPPHYTAFPSGCRYHPRCSKIL
NRCSAEAEIYPVREGHKVRCWLYDD

>core/481/2/Org2_Gene293

MALGPSPYYGVVSFFQFFSVFFSRLFSGSLFTGSLYIDDIQIIVFLAISCAGAFAGTFLVLRKMAMYANAVSHTVL
FGLVCVCLFTHQLTTLISLGTTLAAMATAMLTGFLIYFIRNTFKVSEESSTALVFSLLFSLSLVLLVFMTKNAH
IGTELVLGNADSLTKEDIFPVTIVILANAVITIFAFRSLVCSSFDSVFASSLGIPIRLVDYLIIFQLSACLVGAFKA
VGVLMAFLIIPSLIAKVIKSIKSLMAWSLVFSIGTAFLAPASSRAILSAYDLGLSTSGISVVFLTMMYIVVK
FISYFRGYFSKNFEKISEKSSQY

>core/482/2/Org2_Gene600

MTTNFPQPLIQATSLTKHYKRSFWFQGKTIASRPVDDVSFSLYSRRVGLIGESGSGKSTLALALAGLLPLTS
GFLTNGTPIKLHSHKHGRHQLRSQVRLVFQNPQASLNPRKTILDSLGHSLLYHKLVPKEKVLATVREYLELVG
LSEEFYRYRPHQLSGGQQQRVSIARALLGVPQLIICDEIVSALDLSIQAQILNMLAELQKKLSLTYLFISHDLAV
VRSFCTEVFIMYKGQIVEKGNTKRIFSDPQHPYTRMLLNAQLPETPDQRQSKPIFQEYHKDSEESCSTGCYFY
NRCPQKQEACKSEIIPNQGDAAHTYRCIH

>core/483/2/Org2_Gene648

MEKKYYALAYYYITRVDNPHEEIALHKKFLEDLDVSCRIYISEQGINGQFSGYEPHAELYMQWLKERPNFSKI
KFKIHHIKENIFPRITVKYRKELAAALGCEVDLSKQAKHISPQEWHEKLQENRCLILDVRNNYEWKIGHFDNAT
LPDIQTFREFPEYAEKLAQECDPETTPVMMYCTGGIRCELYSPVLLEKGFKEVYQLDGGVIAYGQQVGTGKW
LGKLFVFDDRLAIPIDESDPDVAPIAECCHCQTPSDAYYNCANTDCNALFLCCDECIHQHQGCCGEECSQSPR
VRKFDSSRGNKPFRRHLCEISENSESASCCLI

>core/484/2/Org2_Gene515

MKQLLFCVCVFAMSCSAYASPRRQDPSVMKETFRNNYGIIVSGQEWVKRGSDGTITKVLKNGATLHEVYSG
GLLHGEITLTFPHTTALDVVQIYDQGRLVSRKTTFFVNLPSQEELFNEDGTFVLTRWPDNNDSDTITKPYFIET
TYQGHVIEGSYTSFNGKYSSSIHNGEGVRSVFSSNNILLSEETFNEGVMVKYTTTFYPNRDPESITHYQNGQPHG
LRLTYLQGGIPNTIEEWRYGFQDGTTFVFKNGCKTSEIAYVKGVKEGLELRYNEQEIVAAEEVSWRNDFLHGER
KIYAGGIQKHEWYYRGRSVSKAKFERLNAAG

>core/486/2/Org2_Gene567

MNLKV VYFGTPTFAATVLQDLLHHKIQITAVVTRVDKPQKRSAQLIPSPVKTIALTHGLPLLQPSKASDPQFIE
ELRAF NADV FIVVAYGAILRQIVLDIPRYGCYNLHAGLLPAYRGA APIQRCIMEGATESGNTVIRMDAGMDT
GDMANITRVP IGPDMTSGELADALASQGA EVLIKTLQQIESGQLQLVSQDAALATIAPKLSKEEGQVPWDKP
AKEAYAHIRGVT PAPGAWTLFSFSEKAPKRLMIRKASLLAEAGRYGAPGTVVVTD RQELAIACSEGAICLHE
VQVEGKGSTNSKSFLNGYPAKKLKIVFTLNN

>core/488/2/Org2_Gene368

MSKGSSKHTVRINQ TWYIVSFILGLSLFAGVLLSTIYYVLSP IQEQAATFDRNKQMLLAAHILDFKGRFQIQEK
KEWVPATFDKKTQLLEVATKKVSEVSYPELELYAERFVRPLL TDAQGKVFSFEKKNLNPIEFFEKYQESPPCQ
QSPLPFYVILENTSR TENMSGADVAKDLSTVQALIFPISGFGLWGPIHGYLGVKNDGDTVLTAWYQQGETP
GLGANITNPEWQE QFYGKKIFLQDSSGTTNFATTDLGLEVVKGSVRTTLGDSPKALS AIDGISGATLTCNGVT
EAYVQSLACYRQLLINF SNLTHEKKTGE

>core/489/2/Org2_Gene540

MRLLSILKLHLFSLRSSSSLSPHYHSCSR SMLHLLCRWKDADIMEWQQICNILSGVCSRMSGKL VSLQKETQ
DSCHQEHERIHLQYREQLSALEEEYRRREEAKNQDLEKLQQENTWLQNRLAEKLQQIRHQSDIIDEIKKELLQ
SVQRTEISEGRRLCYEHKIKQLEEQLQRYVSQHGAPSIEIEDKSSAAYAEINRLKKSLIDLQQEKDIYIKTYHS
EIAKLREKLQRQEGAQTSSEVCSIEKLTEVQTDLAEKKKAIALLQDIVEDQYCQLRDLHKEKGMAMPSNTKL
DHLKGLLGKEPESEVDVVFSESKSLGS

>core/490/2/Org2_Gene855

MEVQIGIDLMGGDHSPLV VVWQVLVDVLKSQSSTIPFAFTLFASEEIRKQIQEEFISDLPQEKFPKIISAENFVAM
EDSPLAAIRKKSSSMALGLDYLQEDKLD AFISTGNTGALVTLARAKIPLFPAVSRPALLVCVPTMRGHAVILD
VGANISVKPEEMVGFARMGLAYRQCLGDSKIPTIGLLNIGSEERKGTEAHRQTFRMLRETFG EAFLGNIESGA
VFDGAADIVVTDGFTGNIFLKTAEGVFEFLQRILGDKLEADIQRRLDYTFYPGSVVCGLSKLVIKCHGKACGS
SLFHGILGSINLAQARLCKRILSNLI

>core/491/2/Org2_Gene499

MLISISLATLPILAFSWASFIEPNWLRTTAIPWRLPKKHAHLHGLRIAQISDLHFHKRVPEKFLNKVSKSIKNFSP
DLIVFCGDLLCRARLEDKERLETFLNTLEAPLG VFAILGNHDYSSYISRNTKGEITCIPEEKS RPIQRAIIAVMQG
LFSSPSYRYDPNLTPQEPHPDLLKLLKNTPLTLLHNTTHVIPNTLNIVGLGDLFARQFHPEQAFKNYDPSLPGL
LLSHNPDGITRLQQYPGDFVLSGSHGPQVTLSWPKFARKFFERLSGLENPYLARGYFVTKEGKQLYVNRGL
GGLKRIRFCSPPEICYITCSYD

>core/492/2/Org2_Gene887

MVLSSDLLRDDKQLDLFFASLDVKKRYLLALSGGSDSLFLFYLLKERGV SFTAVHIDHGWRSTSAQEAKELE
ELCAREGV PFVLYTLTAE EQGDKDLENQARKKRYAFLYESYRQLDAGGIFLAHHANDQAETVLKRLL ESAH
LTNLKAMAERSYVEDVLLLRPLLHIPKSSLKEALDARGISYLQDPSNEDERYLRARMRKKLFPWLEE VFGKNI

TFPLLTLGEESAELSEYLEKQAQPFFSAATHQDSQGELPCPDCLIQQAFLCKWVMKKFFNNAGIAVSRHFLQ
MVYDHLSSCATLRMRNKIVIIKPGVVVID

>core/493/2/Org2_Gene585

MKFLLYVPLLLVLVSTGCDAPVSFEPFSGKLSTQRFEPQHSAEEYFSQGQEFLKKGNFRKALLCFGIITHHFP
RDILRNQAQYLIGVCYFTQDHPDLADKAFASYLQLPDAEYSEELFQMKYAIAQRFAQGKRKRICRLEGFPKL
MNADEDALRIYDEILTAFPSKDLGAQALYSKAALLIVKNDLTEATKTLKKLTLQFPLHLSSEAFVRLSEIYLQ
QAKKEPHNLQYLHFAKLNEEAMKKQHPNHPLNEVVSANVGAMREHYARGLYATGRFYEKKKKAEEAANIY
YRTAITNYPDTLLVAKCQKRLDRISKHTS

>core/494/2/Org2_Gene424

MNRRKARWVVALFAMTALISVGCCPWSQAKSRCSIDKYIPVVRNLLEVCGLPEAENVEDLIESSSAWVLTPE
ERFSGELVSICQVKDEHAFYNDLSLLHMTQAVPSYSATYDCAVVFGGPLPALRQRLDFLVREWQRGVRFKKI
VFLCGERGRYQSIEEQEHFFDSRYNPFTEENWESGNRVTPSSEEEIAKFVWMQMLLPRAWRDSTSGVRVTF
LLAKPEENRVVANRKDTLLLFRSYQEAFPGRVLFVSSQPFIGLDACRVGQFFKGESYDLAGPGFAQGVLYKH
WAPRICLHTLAEWLKETNGCLNISEGCFG

>core/495/2/Org2_Gene122

MRKVAFLVSCFLSVAIGASAAPVRVPGFPQIPEDLVQIKTEVCPKQEVCLAVTIKCDDHNLIGVLHLPNTPTPE
GGFPTVVLFHGFRTKFGGLTGAYRKLGRKFAAVGIATLRVDMAGCGDSEGVAEEVPIETYLRDAQTILETV
QEHPDLNAYRLGISGFSLGCHIAFELAKIYNPRDLNIKALSVWAPIADGGILLKELYENFSKHGEGDIISVGKDF
GFGPPPIIVCSGDVDLLIRIQDHVTANSLPTKPYILHQQGIDDTLVSRTQQTLFKNTAPGRMTFISYPNTGHNLA
TAPDLDMILDQIVSHFQRTL

>core/496/2/Org2_Gene379

MFKLLFHIAAFAGHVLSTPIFIVQDACGIDEEACKNPPRPFSAQVQYLKVNDKFKKLPHQTIGYRQYDGT
LCTLPITEHSGLLFSTGYIGADIQWKSSLPISETDPNGLGWATFQDTSFYNYVLLSLGAYTLSLKNWQWSIILS
GLVDPKNIEMGYGLYQGVLSGKYQATEKLSAIFGVINETGLHQEKAWPLVGVSYSYKATDQLTLNCIYPVNF
SI
DYRSTSVCNLGLAYRLTRFRKKLHKNHLLISSRGIFEYQGREIEANVKLTPWPGSFIKGFYGWSIGNDISIAD
DH
NNNKTSHTFKTSAFFGGSVMNF

>core/497/2/Org2_Gene173

MLVELEALKREFAHLKDQKPTSDQEITSLYQCLDHLEFVLLGLGQDKFLKATEDEDVLFESQKAIDAWNALL
TKARDVLGLGDIGAIYQTIEFLGAYLSKVNRRAFCIASEIHFLKTAIRDLNAYYLLDFRWPLCKIEEFVDWGN
DCVEIAKRKLCTFEKETKELNESLLREEHAMEKCSIQDLQRKLSIIIELHDSVSLFCFSKTPSQEEYQKDCLYQS
RLRYLLLLLYEYTLCKTSTDFQEQUARAKEEFIREKFSLLELEKGIKQTKELEFAIAKSKLERGCLVMRKYEAA
AKHSLDSMFEEETVKSPRKDTE

>core/498/2/Org2_Gene327

MTLPMQKSLTSFDDFSQAYA EKVP AIALIGSALEDDKDALIELLVSESFKELGGQGLMPATLMSWTETFALFQ
EHETLGIIHA EK FPLATKEFLSR YARNPQPHLTILIFTTKQECFRELSKALPSALSLSLFGW PADRQKRIIRLLL

QRAERVGISCSQSLASLFLRALASTSLPDILSEFDKLLCSVGKKTSLDHSDIKELVVKKEKASLWKFRDSLLKR
DPVEGHQQLHFLLEDGEDPLGIITFLRTQCLYGLRSIEEGSKENKHRMFVLYGKERLHQALNSLFYAETLIKN
NVQDPIVAVETLVIRMVNL

>core/499/2/Org2_Gene164

MFSYIKNRILFNLLSLWIVLTLTFLVMKTIPGDPFNDEGCNVLSEEVLQTLKSRYGDKPLYQQYTQYLHSIAK
LDFGNSLVYKDRKVTNIISTAFPISAILGLQSLFLSIGGGIALGTIAALKKKKQRRYILGASILQISIPAFIFATLLQ
YVFAVKIPLLPACWGSFTHILPTLALAVTPMAFIIQLTYSSVSAALNKDYVLLAYAKGLSPLKVVIKHILPYA
IFPTISYSAFLT TTTVITGTFAIENIFCIPGLGKWFICSIKQRDYPVALGLSVFYGTFLMLSSLLSDLIQSIIDPQIRYA
HGKEKKRK

>core/500/2/Org2_Gene288

MAMLPKFFLVLLCLGLCSCSQKTTTIEGEQMTIFYRIVLGTSLSAKEKASLSQQIDRCFHKIDSIYNNWNPNYSE
LSIINRAPADVPIITLSVELSEFLDQVDTLYKLSEGRFDPTVGPLKTLWLLHLKSQTLPPKDVWEQHYKDMGW
QHLEFQSNTKTLIKKNPHVQIDL CGVVKG YAVDCLNEICNTFCPNNYVEWGGEIKTSGHHPSGRPWRIFSEA
AGTILDIDDMAIATSGNHIQKWCVEGKIYTHILDTRTGKPLELSSYPIQSVSVVHPSCAYADAIATVLMTFDSK
IEAKQWAEHHILTYINDGASS

>core/501/2/Org2_Gene475

MWRVVLRLIIFILGRAVFPLRASESFSWETSTCLTVLGIPFIDIILT TNEDFVAQCGLQIGTISSTNNAKIKEIFLI
YKEKFPEASISFKRKEPLNLSQSHLSDLGILCMRNGETYAEGMANKENGPAKQPKDLRLVLRCPNQPD TLL
YSEKEAEKG IETNTCLCNQGYTLLDGQLILYGDSIEKFLKETKRKNNHTLV DLCDSQVVTTFLGRFWSLLNY
VQVFLSEDSAKILAGIPDLA QATQLLSHTVPLLFIYTND SIHIEQ GKESSFTYNQDLTEPILGFLFGYINRGSM
EYCFNCAQSSLGET

>core/502/2/Org2_Gene14

MIASIYSFLDY LKMVKSASPHTLRNYCLDLNGLKIFLEERGNLAPSSPLQLATEKRKVSEL PFSLFTKEHVRM
YIAKLIENGKAKRTIKRCLSSIKSFAHYCVIQKILLENPAETIHGPRLPKELPSPMTYAQVEVLMATPDISKYHG
LRDRCLMELFYSSGLRISEIVAVNKQDFDLSTHLIRIRGKGKKERIIPVTSNAIQWIIQIYLNHPDRKRLEKDPQA
IFLNRFGRRISTRSDRSFQEYLRRSGLSGHITPHTIRHTIATHWLES GMDLKT IQALLGHSSLETTTVYTQVSV
KLKKQTHQEAPHA

>core/503/2/Org2_Gene268

MIHSRLIIIGSGPSGYTAAIYASRALLHPLLFE GFFSGISGGQLMTTTEVENFPGFPEGILGPKLMNNMKEQAVR
FGTKTLAQDIISVDFSVRPFILKSKEETYSCDACIIATGASAKRLEIPGAGNDEFWQKGVTACAVCDGASPIFK
NKDLYVIGGGDSALEEALYLTRYGSHVYVVHRRDKLRASKAMEARAQNNEKITFLWNSEIVKISGDSIVRSV
DIKNVQTQEITTREAAGVFFAIGHKPNTDFLGGQLTLDESGYIVTEKGTSKTSVPGVFAAGDVQDKYYRQAV
TSAGSGCIAALDAERFLG

>core/504/2/Org2_Gene904

MRKLILCNPRGFCSGVVRAIQVVEVALEKWGAPIYVKHEIVHNRHVVNALRAKGAIFVEELVDVPEGERVY
SAHGIPPSVRAEAKARKLIDIDATCGLVTKVHSAAKLYASKGYKIILIGHKKKHVEVIGIVGEVPEHITVVEKVA
DVEALPFSSDTPLFYITQTTLSLDDVQEISSALLKRYPSIITLPSSSICYATTNRQKALRSVLSRVNYVYVVGDV
NSSNSNRLREVALRRGVPADLINNPEDIDTNIVNHSGDIAMTAGASTPEDVVQACIRKLSSLIPGLQVENDIFA
VEDVVFQLPKELRCS

>core/505/2/Org2_Gene740

MKCRPTLNTDQPRVRKKLPERFPKWLRPLPQGSAFHATDATIKRSGMPTVCEEALCPNRAECWSRKTATY
LALGDVCTRSCGFCNIGHSKTPPALDPTEPERIALSAKELGLKHVVITMVARDDLEDGGAQGLVDIIQKLREE
LPQATTEVLASDFQGNVSALHTLLDSGITIYNHNVETVARLSPLVRHKATYARSMFMLEQAANYLPDLKIKS
GIMVGLGEMEGEVKQTLQDLASIGVRIVTIGQYLRPSRKHLQVKSYVTPETFDYYRRVGEAMGLFVYAGPFV
RSSFNADMILASVQDKASA

>core/507/2/Org2_Gene252

MKKRYAFLFPGQGSQYVGMGQDLYMEYPEVRELFDFANERLGFSLTSMFEGPEDLLMETVHSQLAIYLHS
MAVVKVLSQRSSIQPSLVSGLSLGEYTALVASDRISVLDGLELVRKRGQLMNEACNQSPGAMAALLGLPSEV
IEENITSLGQGIWIANYNAPKQLVVAGIAEKVDQAIELFRDLGCKKAVRLKVSGAFHTPLMQVAQDGLAPDI
YALCMKDSSLPLVSHVVGKSLVNTEEMRECLARQMTSPTLWYQSCYHIESEVDEFLELGPVKVLAGLNRSIG
ISKPITSLGTFAQIEKFLSEV

>core/508/2/Org2_Gene488

MLNSNKFKSKTGAYGDLFQRVVVHSLVLTFLVLLLYSSLFPLTSFALGFITATCGAVGTYEYSSMAKAKMHY
PLSTFSAIGSFLFLALSFLSIRWGHSLPGFFDALPWTLIVWVWVSIFRVRKSTIGALQLSGVTLFSILYVGPIRL
FLHVLYSFIHTQEPYLGIIWWASFLIATTKGADIFGYFFGKAFGNKKIAPQISPNTVVGVFVAGCLGATLISFIFF
LQIPTRFASYFPMPAILPLGLALGITGFFGDIIESIFKRDAHLKNSNKLKAVGGMLDTLDSLLLSTPIAYLFLIT
QSKEFIG

>core/509/2/Org2_Gene38

MRLFSYDKPKIKVQKIKADGFSGWLKCNHCHEMIHANELGQNYNCCPKCSYHYRITAIERVKLLADKDSWR
PLYTDLKSQDPLEFIDTDITYANRLEKARKNTTESEGVIVGICTIGLHPVALAVMDFNFMAGSMGAVVGEKLT
RLIEEAIETRLPVIIVSASGGARMQESVFSLMQMVKTSAAALAKLHEAGLPYISVLTNPTSGGVTASFAALGDIII
AEPKALICFAGPRVVAQVIGEDLPEGAQKSEFLLEHGMIDKIVERKELKTTLQTLDDYFLAQEYTGKSKAPR
DLSKRLKEIFLLTDDSE

>core/510/2/Org2_Gene979

MEIAYSLTSSFSVDSVTVGFFDGCHLGHSNLLSILTSYSGSSGVITFDSHPQTVLSLNHTKLINTKEERLQLLQT
FPIDWLGVLTFDLNFANQSAEEFLTLLHRNLKCKRLILGYDSCIGKEQQSNTEALDTIGKPLGIEVIKIPPYRMD
NIVVSSKAIRQFLSAGNLECAHRFLGHPYAISGKITEGSGIGGSLGFATINLPREESLIPLGVYACEIRYDSTTCQ
GVMNLGTAPTFGRESLYAEAHIFSFAENLYGKEVSIIPRKFLREEKKFQSKETLIRAIEKDILDAQDWFAKGSF
NYEGTA

>core/511/2/Org2_Gene15

MSSRELIILGCSSQQPTRTRNQGAYLFRWNGEGLLFDPGEGTQRQFIFANIAPTTVNRIFVSHFHGDHCLGLGS
MLMRLNLDKVSHPHICYYPASGKKYFDRLRYGTIYHETIQVVEHPISEEGIVEDFGSFRIEAQRLQHQVDTLG
WRITEPDTIKFLPKESRGIRGLIIQDLIRDQEISIGGSTVYLSDVSYVRKGDSIAIADTLPCQAAIDLAKNSCM
MLCESTYLEQHRHLAESHFHMTAKQAATLAKRAATQKLILTHFSARYLNLDIFYKEASAVFPNVSVAQEYR
SYPFPKNPLLNK

>core/512/2/Org2_Gene733

MRSIFRFSLCFFTLVSVCCFADASLYENSCPSRCQPTPPSNSNPLNVVQQPVAASSVPSYMPPLNADDVLPRD
HLSDGFSFDTPDITTAAILIFLALSPFLVMLLTSYLKIIITLVLLRNALGVQQTPPSQVLNGIALILSIYVMFPT
GVAMYKDARKEIEANTIPQSLFTAEGAETVFVALNKSKEPLRSFLIRNTPKAQIQSFYKISQKTFPSEIRAHSTA
SDFVIIIAPAFIMGQIKNAFEIGVLIYLPFFVIDLVTANVLVAMQMMMLSPLSISLPLKLLIVMVDGWTLQLQGL
MISFK

>core/513/2/Org2_Gene878

MKEAAPMHFPFVRRSVWLNRYSTFRIGGPANYFKAIHTIEEAREVIRFLHSINYPFLIIGKGSNCLFDDRFGD
GFVLYNAIYGKQFLEDARIKAYSGLSFAALGKATAYNGYSGLEFAAGIPGSVGGAI FMNAGTNESDISSVVRN
VETINSEGELCSYSVEEELS YRSSRFHRQQEFILSATFQLSKKQVSADHKSILQHRLMTQPYTQPSAGCIFRN
PEGTSAGKLIDAAGLKGLAIGGAQISPLHANFIINTGKATSDEVKQLIAIIQSTLKTQGIDLEHEIRIIPYQPKIHS
PVSEK

>core/514/2/Org2_Gene716

MSLFLVFLTAFIWSSSFALSKLVMNASAPIFATGARMVIAGAILALAAWFRGGFVGISKKIFLYIVLLALTGFY
LTNIFEFIGLQSLSSSKTCFIYGLSPLMSALFSYIQLKEKVTLKKVLGLSLGLVSYICYLTFGGGGDDSQPWTW
QIGLPELLILGAASLASFGWTLLRQIEKQSTLSVTAINAYAMLIAGMLSIMHSAVVEPWRLPVQDISQFLYAT
LALVVISNLICYNLYAKLLRKYSSTFLSFCNLVMPLYSGFYGWILLGEKGVSLGLVLAVAFMVAGCRLIYHEE
FRQGYIVS

>core/515/2/Org2_Gene746

MQKPQYIDRITKKKVIEPIFYEKTMLFLYNSKLGGKLSVFLSTHPIFSRIYGWLQRCSWTRRQIRPFMNRYKIS
EKELTKPVADFTSFNDFFTRKLKPEARPIVGGKEVFITPVDGRYLVYPNVSEFDKFIVKSKAFSLPKLLGDHEL
TKLYAHGSIVFARLAPFDYHRFHPCDCLPQKTRCVNGALFSVHPLAVKDNFILFCENKRTVTVLETEQFGNV
LYLEV GAMNVGSIVQTFSPNQTYAKGDEKGFFAFGGSTVILLFLPNAIRFDNDLLKNSRMGFETRCLMGQSL
GRSQREEI

>core/516/2/Org2_Gene911

MTMPSTQFHTTILEQFSLFLSVDRGLCQQSIAAYRQDISSFLTISAISSQDISQNSVYIFAEELYRRKEAETTLA
RRLIAKVVFFLFLKDQQLLPYPIIHPKIWKRLPSVLTPQEV DALLAVPLQMEKNPRHLAFRDTAILHTLYST
GVRVSELCDLRLGHVSDDCIRVTGKGSKTRLVPLGSRAREAIDAYLCPFRDQYQKKNPHEDHLFLSTRGHKL

ERSCVWRIHNYAKQVTSKPVSPHSLRHAFATHLLDNKADLRVIQEMLGHARIASTEVYTHVAADSLIEKFL
AHHPRNL

>core/517/2/Org2_Gene348

MLKIDLTGKVAFAVAGIGDDQGYGWGIAKLLAEAGATIIVGTWVPIYKIFSQSWELGKFNESRKLSNGTLLEIA
KIYPMDASFDSPEDVPEDIAENKRYKGITGFTISEVAEQVKKDFGHIDILVHSLANSPEISKSLLETSRKGYLAA
LSASSYSFVSLLSHFGSIMNRGGSTISLTYLASMRAVPGYGGGMSSAKAALESDDTKTLAWEAGRRWGIRVNT
ISAGPLASRAGKAIGFIERMVDYYQEWAPIPEAMNAEQVGAVAAFLASPLASAITGETLYVDHGANVMGIGP
EMFPKDS

>core/518/2/Org2_Gene947

MPPPFVVTLTTSAQNNLRDQLKEKNFIFSQPQNTVFQARSNTVTCTLYPSGKLVIQKGKSEEFIEFFLEPEILHT
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DVIIYPEKYNELYGKFQNLNTLLAWAHATVINNLAPKPGADVFAISDQFAASEYTLLKALQKKETDITLIQK
PRAEQDVVVAASILARDAFVQSIQKLEEYQVQVQLPKGAGFNVKAAGREIAKQRGKELLAKISKTHFKTFDE
ICSGK

>core/519/2/Org2_Gene227

MHLEENQGWEEALLRKVYHQEVPPAILLHGFTLPVLQDKAEQLASEILLSSSPGSEHKVSQKIHPDIYQFFPEG
KGRlhsIDLPRGIKKQIYISPFEANYKIYIIHEADRMTLAAISAFLLKVFEPPKHAVIILTTAKVQRLPKTIISRLS
IFIERGEKILCSKETFSYLFYQAQCEIPVTEVSQIIKESSETDKQVLRDKVQRFMEVLLELYRDRYTLNLGLKAS
ALNYPEHVKEILQLPLLPLDKVLLIVESACRSLNNSSSAASVLEWVAIQLVSLQYKEKELVSVSPGQDLSN

>core/520/2/Org2_Gene220

MRLNYFLNLVNFKYSIFSILFLSASTVFALSINEISQNL SFKEGFKISVFGAIAFVFARTTGIVVNQCIDRFIDKKN
TRTSKRVL PANLVSLNFAWVLSLFC SFLFLCKILRIFSLGIASLTLMIVYPYMKRVTF FCHWGLGLVYTVAI
LMNFCAFAESGLSMRLCFLALLWGGSVGMVIAANDIYAIEDTEFDREEGLRSVPAHYGEKKAVEIAKVN LW
VSYLAYIFSGFVGSLDKEFYFTAIIPLVVILKVVRMYSNYSKKDQEGESKFFLANIAIALSFLVSMTLFWLSLR

>core/521/2/Org2_Gene361

MSERAHIPVLVEECLALFAQRPPQTFRDVTLGAGGHAYAFLEAYPSLTCYDGSDRDLQALAI AEKRLET FQD
RVSF SHASFEDLANQPTPRLYDGV LADLVSSMQLDTL SRGFSFQGEKEELDMRMDQTQELSASDV LNSLKE
EELGRIFREYGEEPQWKSAAKAVVHFRKHKKILSIQDVKEALLGVFPHYRFHRKIHP LTLIFQALRVYVNGED
RQLKSL LTS AISWLAPQGRLVIISFCSSEDRPVKWFFKEAEASGLGKVITKKVIQPTYQEVRRNPRSRSAKLRC
FEKASQ

>core/522/2/Org2_Gene699

MSRHEICPEVSHKKGKYYSTFIFRCIHSLAGIAFTFFLCEHLFTNMLASSYFSQGKGFVAMVNGFHKIPGLKII E
VAGLVLPFLCHAIIGIVYLFQGKSNCYSGDGRPHLRYAKNYSYTWQRWTAWILLFGIAFHVVHLRFIRYPVH
VDIHGTTYAYAVDIQPSRYDVIVRGTKGFLTNLNPNT EASSIEVSRHDLGGADAALLSERNSYLLTPSAGTAFLY

VVRDALGSLFIALLYTILVIAAAFHGFNGLWTFCCRWGVVVSRLRMQGVLRIVCYLAMIVVTFMGVSAVWNLYSVA

>core/524/2/Org2_Gene194

MRRFLFLILSSLPLVAFSADNFTILEEKQSPLSRVSIIFALPGVTPVSFDGNCPIPWFSHKKTLEGQRIYYSGDSFGKYFVVSALWPNKVSSAVVACNMILKHRVDLILIIGSCYSRSQDSRFGSVLVSKGYINYDADVRPFFERFEIPDIKKS VFATSEVHREAILRGGEFISTHKQEIEELLKTHGYLKSTTKTEHTLMEGLVATGESFAMSRNYFLSLQKLYPEIHGFDSVSGAVSQVCYEYSIPCLGVNILLPHPLESRSNEDWKHLQSEASKIYMDTLLKSVLKELCSSH

>core/525/2/Org2_Gene218

MSHGPRPTKFSFPLYFSKTLSWFILGGFLAACGVQMVLVPNELIDGGIVGLSIIASHFLGHKALPFCLVLFNLPFVFLAFKQIGKYFVIQMLTAVIIFSCSLWLIDQLPSWLGMSPFVFKGSEMETVVLGGAIIIGVGCGLIIRHGGSTDGTEILGIIINKKKGYTVGQIILFVNFFIFALSGIVYKNWHTAFVSFLT YGIATKVM DMVILGLEDTKSVTIITSSPRKLGHILMETLGIGLTYIHAEGGYSGEPRNLLYVVVERLQLSQLKEIVHREDPSAFIAIENLHEVINGRRT

>core/526/2/Org2_Gene796

MQEKPRHVRHIIHISDVHFHVLVPNPVHCFNKRLKGLLRKVFGLVHFQATTIGQRFKVVRS LGADSV CITGDFSLTAMDGEFLLAKHFVETLAKHSSVYLLPGNH DVYTLKSLAQQT FYTHFPNDQLQQNKVSFHKITDHWLILLDCSCLNGWFSANGVVHLAQISAIETFLLSLSP EENVIIANHYPLSSQNPS HDLINNTHLQNV LKKYPKVRLYLHGHEHQAAVYNCA DTSPSYILNSGSISLPTNSRFHVIDLYPEKYQVHTMILKNLLDFDAPLEIANEATWDCQKL

>core/527/2/Org2_Gene349

MEKLLVTDIDGTITHQSHHLDKKVYERLYALHQAGWKLFFLTGRYYKYAARLFSDFDAPYLLGCQNGASVWSSTSSNLLYSKSLPSDLLCILQDCMEGATALFSVESGAPYGDHYYRFSPTPIAQDLHEYVDPRYFPNAKEREILFETRSLKDDYAFPSFAAAKVFGLRDEVIRIQKELERQEALTSVATMTLMRWPFDFRYAILFLTDKSVSKGKALDRVVNILYDGKKPFV MASGDDANDLDLIERGDFKIVMSSAPEEMHVHADFLAPPADKNGILSAWEAGVRYYDDLMSL

>core/528/2/Org2_Gene584

MKKLILYFAAFVASLFCGVFLWDRVPCAQKIMRLAADHSSEVFSKSCR FVRKISGFEELQVFERHVSPEQALALFPEYRDGKS FVELAFIPHTLMHVRF SKEE PVKKHIISQEGEILWSLVNGEMVLHTGTW TCSKGFRECLLLHAGKQDMRVIQTLATLGGTTSRESLAQALALKNIRAERVIKECQKKKLIFASGNQIGTHFQQFQPIRGCTTTLNNP VWLQKPRHAAVFPAQYSEDVRHLVKMIFGDNFLIVRSSMVYVPVYKISLVSADNSVRVEYINAVTGKSFQDL

>core/529/2/Org2_Gene866

MFHSLSKNTPIITQGITGKAGSFHTEQCLAYGTNFVGGVTPGKGGTLWLDLPVYDSVLEAKQATGCRATMIFVPPPYAAEAILEAE EAGIELIVCITEGIPVRDMLEVARVMDNSTS QLIGPNCPGIIKPGECKIGIMPGYIHLPGNIGVVSRS GTLT YEAVWQLTQLKIGQSICVGIGGDPLNGTSFIDVLQALEEDPYTELILMIGEIGGSAEEEEAAAWIQA HCTKPVVAFIAGVTAPKGKRMGHAGAIISGNSGDAKSKIQVLRESGVTTVVESPAHIGKTVDAVLRAKEL

>core/530/2/Org2_Gene794

MSKHTSESRIAQDMLERYSGSSVKQFCPYLLL TNFSYYIQTF AKLHGVPVFE GSMFSAAHAPHLKTSILDFKL
GSPGAALTIDLC SFLPDLKAALMLG MCGGLRSHYQVGDYFVPVASIRGEGTSDAYFPPEVPALANFVVQKAT
TEVLEDDKANYHIGITH TTNIRFWEFNKKFRKKLYETKAQSAEMECATLFAAGYRRNLPIGALLLISDLPLRK
EGIKTKSSGNFIFNTYTEDHIL TGQEVIENLEKVMLKRAASDHKKDQQYRGLPHMEVGEADDTMASGSETSD
SDY

>core/531/2/Org2_Gene646

MKVLPPPSIPLLGAHTSTAGGLKNAIYEGRDIGASTVQIFTANQRQWQRRALKEEVIEDFKAALKETDLSYIM
SHAGYLINPGAPDPVILEKSRIGIYQEILDCITLGISFVN FHPGAALKSSKEDCMNKIVSSFSQSAPLFDSSPPLV
VLLETTAGQGTLIGSNFEELGYLVQNLKNQIPIGVCVDTCHIFAAGYDITSPQGWEDVLNEFDEYVGLSYLRA
FHLNDSMFPLGANKDRHAPLGEGYIGKESFKFLMTDERTRKIPKYLETPGGPENWQKEIGELLKFSKNRDS

>core/532/2/Org2_Gene465

MLSSLIRDSFPLLILLPTFLAALGASVAGGVMGTYIVVKRIVSISGSISHAILGGIGLTLWIQYKLHLSFFP MYGA
IVGAIFLALCIGKIHLYQEREDSLIAMIW SVGMAIGIIFISRLPTFNGELINFLFGNILWVTPSDLYSLGIFDLLV
LGIVVLCHTRFLALCFDERYTALNHCSVQLWYFLLL VLTAITIVMLIYVMGTILMLSMLVLPVAIACRFSYKM
TRIMFISVLLNILCSFSGICIA YCLDFPVGPTISLLMGLGYTASLCVKKRYNPSTPSPVSPEINTNV

>core/533/2/Org2_Gene898

MKRNDPCWCGSGRKWKQCHYPQPPKMSPEALKQHYASQYNILLKTPEQKAKIYNACQITARILDELCKASQ
KGVTTNELDELSQELHKKYDAIAAPFHYGSPPFPK TICTSLNEVICHGIPNDIPLKDGDIMNIDVSCIVDGYYG
DCSRMVMIGEVP EIKKKICQA ALECLNDSIAILKPGIPLCEIGE AIEARADTYGFSVVDQFVGHGVGIEFHENPY
VPHYRNRSMIPLAPGMIFTIEP MINVGKKEGVVD PKNQWEARTCDNQPSAQWEHTIAITETGYEILTLLND

>core/534/2/Org2_Gene934

MHLLTATVTPFFPNGTIDFASLERLLSFQDAVGNGV VLLGSTGEGLSLTKKEKQALICFACDLQLKVPLFVGT
SGTLLEEVL DWIHFCNDLPISGFLMTTPIYTKPKLCGQILWFEAVLNAAKHPAILYNIPSRAATPLYLDTV KAL
AHHPQFLGIKDSGGSVEEFQSYKSIAPHIQLYCGDDVFWSEMAACGAHGLISVLSNAWPEEAREYVLNPQE Q
DYRSLWMETCRWVYTTTNPIGIKAILAYKKAITHAQLRLPLSIEDFDLENVSPAVESMLAWPKLR TSVFSYS

>core/535/2/Org2_Gene864

MFKFFRNKLQSLFKKNISLDLIEDAESLFYEADFGTELTEELCARLRRTKKADASTIKDLITVLLRESLEGLPSQ
ASQSSQTRPIVSLLLGTNGSGKTTTAAKLAHY YKERSESVMLVATDTFRAAGMDQARLWANELGCGFVSGQ
PGGDAAAIAFDGIQSAIARGYSRVIIDTSGRLHVHGNLMKELSKIVSVCGKALEGAPHEIFMTVDSTLG NNAIE
QVRVFHDVVPLSGLIFTKVDGSAKGGTLFQIAKRLKIPTKFIGYGESLKD LNEFDLDFLNKLFPEVEKI

>core/536/2/Org2_Gene214

MKRRNLQKILPNASTPSTNVAENTGIKDQNLFLDQATLNVDGNVDIENFLETRDLKVADTITSPCEFTVGGGL
SAESSQFKATTLSKGLEITSEDQDGRVPKFTNVSDPQSPRDALTYNYYRNTGCQALNLYTYYSSSQPTTVGKP

IETVCQNPNPETYRISASAKIYDAVTRFPYIQFKAPGIYQVTIQIRRESGQHSGLDNPPLYNLNLMIGNNKTLLCA
SDTRGYSGGHRTSIAVTGTFTL TEIVATPPHDYPWLFLETTIGLDIKSMSTCVIWFPPQANFAEVD

>core/537/2/Org2_Gene418

MQIPRSIGTHDGSFHADEV TACALLIIFDLVDENKIIRS RDPVVL SKCEYVCDVGGVYSIENKRFDH HQVSYDG
SWSSAGMILHYLKEFGYMDCEEYHFLNNTLVHGVDEQDNGRFFSKEGFCFSFSIIKIYNPREEEETNSDADFS
CALHFTIDFLCRLRKKFQYDRVCRGIVREAMETEDMCLYFDRPLAWQENFFFLGGGEKHPAAFVCFPSCDQWI
LRGIPPNLDRRMDVRVPF PENWAGLLGKELSKVSGIPGAVFCHKGLFLSVWTNRESCQRALRLTLQDRGII

>core/538/2/Org2_Gene731

MGISLPELFSNLGSAYLDYIFQHPPAYVWSVFLLLLARLLPIFAVAPFLGAKLFPSPIKIGISLSWLAIIFPKVLA
DTQITNYMDNNLFYVLLVKEMIIGIVIGFVLAPFYAAQSAGSFITNQQGIQGLEGATSLISIEQTS PHGILYHYF
VTIIFWLVG GHRIVISLLLQTLEVIPIHSFFPAEMMSLSAPIWITMIKMCQLCLVMTIQLSAPAALAMLMSDLFL
GIINRMAPQVQVIYLLSALKAFMGLLFLT LAWVFIKQIDYFTLAWFKEVPIMLLG SNPQVL

>core/539/2/Org2_Gene660

MLHALDTYRPSIESAIEKALEGFGPIGHPIRSPVEYALQGGGKRLRPGLVCMMAQGLGLNHDVMDSALAVEF
VHTSTLIADDLPCMDND DERRGRPTVHKAFDEATALLASYALIPAAAYSHLRLNAKKLKEQGCDPREIDIA YNI
IGDITDKNIGCSGVLGGQYDDMFFSNRGQEHVQSIMIKKTGSLFEIACISGWLFGGGDPQFAPIITSFSNNFGLL
FQIKDDFSDLQKDSQQIGLNYALLFGEKAALELLARSQNNCLELLDRLSAGGLKNSSEFETHISSLG SF

>core/540/2/Org2_Gene213

MSNPTPKTKISIPTFVRFN IQSINLTEDQKKTTFTVGGKVTTENTVVRGDLTCTDGGLTCQSDLT IQKDINIRPT
STNSMVF DGRNLNSNSPLSYKNSQGQDITDYEKMSSGKPQEYVPFGYYKRTQIMMAQRAAHSSGYVGGGSV
PSGSYVPWNKFDQTSTQKTSGTEIYIDPN DSTKL VFEVNNKVPKLF RISRIVIMAKHGSWLDNGTGADILLAANE
YEQGGGRINVTDLAMTT SRGSSYYETRPLQVVCVTYYAQNNGYFTFQNRAGGGLRV SFFSWNIVALPYVE

>core/541/2/Org2_Gene951

MLKIQKKRMCVSVVITVGAIVGFFNSADAAPKKKKIPIQILYSFTKVSSYLKNEDASTIFCVDVDRGLLQHRY
LGSPGWQETR RRRQLFKSLENQSYGNERLGEETLAIDIFRNKECLESEIPEQMEAILANSSALVLGISSFGITGIPA
TLHSLLRQNLSFQKR SIASESFLKIDSAPSDASVFYKGVLF RGETAIVDALSQLFAQLDLSPKKIIFLGEDPEV
VQAVGSACIGWGMN FLGLVYYPAQESLFSYVHPYSTATELQEAQGLQVISDEVAQLTLNALPKMN

>core/542/2/Org2_Gene16

MSHLIPSLRNSVTSYFHKPQPIKQAAPSKSIRDICNIAYLIICVLV VVVVLVGAMLCMFIPSVGIPLCLSSLALLV
LLSIFNPCLINWISTKKTKEIAPKDASESQPTKSASRKGSPQLSPHHDHEPKNFIRTQLEKGVNYVTNKFKSGEE
SPHISDEHHS PRQSKRSSEIESSDESSPELHRKAKGKAPHTATT KESKTSTTESSKKKKKTKHSLHRTTSSIHKR
SAPKPMVPSKKRKPVLLKKT VPLPIEDLEHQSSGNESSDSSSPPPVQRKAILPWFCQPTDP

>core/543/2/Org2_Gene89

MEIKKAIQEGTAYLDYYGVPLSDCEALYILMDLLEVSSRAKLFDLVGISETMLMEYRKRLALRGQRCPTAYL
NGAVSFLGLRLRVDSRVLIPRTETELLA EYIINYLLSHSEIQTFYDICC GSGCLGLAIKKSCPHVEVVLSDVCPQ
AVAVANENAKSNGLDVKILLGDL SAPYTRPADAFVCNPPYLSFNEI IHIDPEVRCYEPWKALVGGSTGLEFYQ
RIAQELPKIVTSTGVGWLEIGSSQGESIKNIFSKHGIYGR LHQDLSGRDRIFFLEMDGRDPVSSGAYS

>core/544/2/Org2_Gene265

MAVIYWDRSKIVWSFEPWSRLTWYGVFFTVGIFLA CLSARYLALSYYGLKDHL SFSKSQLRVALENFFIYSI
LFIVPGARLAYVIFYGWSFY LQHPEEIIQIWHGGLSSHGGV L GFL LWAAIFSWIYKKKISKLTFLFLTDLC GSVF
GIAAFFIRLGNFWNQEI VGTPTSLPWGVVFS DPMQGVQGVPHVQLYEGISYLVVSGILYFLSYKRYLHLGK
GYVTSIACISVAFIRFFAEYVKSHQGVLAEDCLLTIGQILSIPLFLFGVALLIICSLKARRHRSHI

>core/545/2/Org2_Gene287

MLLRGIPAAEKILQRLKEEISQSPTSPGLAVVLIGNDPASEVYVGMKVKKATEIGIISK A HKLPSTLSSVLKL
IERLNQDPSIHGILVQLPLPKHLDSEVILQAISPDKDVDGLHPVNMGKLLLGNFDGLLPCTPAGI IELLNYYEIP
LRGRHAAIVGRSNIVGKPLAALMMQKHPQTNCTVTVLHSQSENLP EILKTADIIAALGAPLFIKETMVAPHA
VIVDVGTTRVPADNAKGYTLLGDVDFNNVVTKCAAITPVPGGVGPMTVAMLM SNTWRCYQNFS

>core/546/2/Org2_Gene601

MTEEISKDTIIEVAIDDIRVSPFQPRRVFSNEELQELIASIKAVGLIHPPV VREICTGDRVLYYELIAGERRWRAM
QLAGATTIPVILKHVIADGTAAEATLIENIQRVNLNPIEMAEAFKRLIHVFGLTQDKVAYKVGKKRSTVANYL
RLLALS KTIQESLLQGQITLGHAKVILTLEDPI LREKLNEIIIQEH LAVREAELIAKQLISEEGSSI ELKPTPLDMA
ESSKQHEELQQR LSDL CGYKVQIKTRGSKATVSFHLQNTQDLQKLEAWLSSHGTLSESLS

>core/547/2/Org2_Gene225

MPDKKAQITFSLPEVMSAIHQGKIVALPTDTVYGVFLSLYASEAEERLYALKDREPSKAFALYVNSIEDIENIS
GYPLSPTAKKLAQLFPGAITLVVKHRNPRFPKETLAFRIVDHSV VREIVDHCGTLIGTSANLSEFPSALTAQEIF
ADFADHDL CIFDGPCSHGLESTVVASDPLYIYREGLISRSVIENIAGTEAKIFHRTSHAFSKHIKIYTVKNQEQL
VSFLSGSLDFKGVVCEHPKPKNFYTRLREALKKKTPSIVFIYDINTSDYPELFPFLSPYYIE

>core/548/2/Org2_Gene212

MKNNINNNECYFKLDSTVDGDLLAANLKT FDTQAQGISSTETFSVQGNATFKDQVSATGLTSGTTYNLNAQ
NFTSSQISIDFKNNRLSNCALPKEDCDPVPANYVRSPEYFFCSKPLIGDFDFNSGESYLPLTGSEYTLYQSRNVN
SIFRFIGWKQSTRELTVGGNTAIQFLAAGTYIVSFTVGKRWGWNGWGGAIIYINNLGQVQCESTIYSGGGY
ATIGTLGTSIYRASVDVAPNPNDPNASDRYRAGIFYLSNGGSSAGIGNYSFSLLYYPDDR G

>core/549/2/Org2_Gene414

MHEVLILTFTYPLPRTLKQHPDEVHTVPISP NLSFGEGSPILIAGPCTLESYEHTVSSALT VKEAGA QVFRGSIR
KPRTSPFSFQWEKECVLWHKEAQSIHGLPTETEVL DVRDVEITAEHVDILRIGAKNMHNTPLLQEVSKSHRP
IILKRSPAATLEEWLCAA EYILASSPSCPGVILCERGIRTFEHSTRYTLDLNTVALLKEISSLPVIVDP SHAAGKR
SLVLPLASAGLSVGADGLMIEVHAHPEKALCDAKQ QITPEELHLFAKKHFCPSESRAHAIS

>core/550/2/Org2_Gene205

MKHLYLSFSPSADFFSKQGAIETQVLFGERVLVKGSTCYAYSQLFHNELLWKPYPGHSFRSTLVPCTPEFHIHP
NVSVVSVDAFLDPWGIPLPFGTLLHVNSQNTVIFPKDILNHMNTIWGSGTPQCDPRHLRRLNYNFFAELLIKD
ADLLLNFYVWGGRSVHESLEKPGVDCSGFINILYQAQGYNVPRNAADQYADCHWISSFENLPSGGLIFLYP
KEEKRISHVMLKQDSSTLIHASGGGKKVEYFILEQDGKFLDSTYLFFRNNQRGRAFFGIPRKRKAFL

>core/551/2/Org2_Gene166

MDNYLLNIKDLTITSTNPKRTLIENTSLQLKENRNLALVGESGSGKTTITKAILGFLPENCLIKTGSILFEDIDIT
KLSPKELHKIRGQKIATILQNAMGSLTPSMRIGMQIIETLRQHHKMNKEEAYNKAMQLLTDVCIPNPKYSFSQ
YPFELSGGMRQRVVIAIALASQPKLILADEPTTALDSMSQAQVLRILRNIQQQKQATILLVTHNLSLVKELCND
ICIIKDGGKLIETGTVEEIFLSPKHPYTLKLLNAVSKIPIKKTSSPILKNKFQPLMSMQGGL

>core/552/2/Org2_Gene165

MENLSSAPSRSIWKSIIQNKMLVLGLTTLIILMLGALLLPWFYQDYEQTSLKDILVSPCSRFPFGTDTLGRCMF
ARTLRGLRLSLLIATLATIDVCVGLLWATVAISGGKKIDFLMMRTTEILFSLPRIPHIILLVIFHHGLLPLILAM
TITGWIPISRIIYGQFLLLKNKPFVLSAKAMHASTFHILKKHLLPNTLAPIISTLIFTIPNAIYTEAFISFLGLGIQPP
QASLGTLVKEGINAIDYYPWLFFFPSLIMIALSISFNLIGEGAKTLCLEEGSHG

>core/553/2/Org2_Gene144

MKQPMSLIFSSVCLGLGLGSLSSCNQKPSWNYHNTSTSEEFFVHGNKSVSQLPHYPSAFRTTQIFSEEHNDPY
VVAKTDEESRKIWREIHKNLKIIGSYIPISTYGSLMHPKSAALTLKTYRPHPIWINGYERSFNIDTGKYLKNGS
RRRTSHDGPKNRAVLNLIKSSGRRCAIGLEMTEEDFVIARRREGVYSLYPVEVCSYPQGNPFVIAIYAWIADE
SACSKEVLPVKGYYSLVWESVSSDSLNAFGDSFAEDYLRSTFLANGTSILCVHESYKKVPPQP

>core/554/2/Org2_Gene562

MFKKFKPVTPGTRQLVLPADFELTTRGELRGTKSKRSLRPNKKLSFFKKSSGGRDNLGHISCRHRGGGAKQL
YRVVDFKRNDGITAKVVTVVEYDPNRSAYIALLSYEDGEKRYILAPKGIQRGDVVVSLEGSPFKPGCCMTLK
SIPLGLSVHNIEMRPSSGGKLVRSAAGLAAQVIAKSPGYVTLKMPSGEFRMLNEGCRATIGEVSADHNLNRVD
GKAGRRRWGMGVRPTVRGTAMNPVDHPHGGGEGRHNGYIPRTPWGKVTGLKTRDKNKSNKWIVKDRRK

>core/556/2/Org2_Gene568

MASIHPTAIIPEGAKIGKDVVIEPYVVIKATVTLCDNVVVKSYAYIDGNTTIGKGTIWPMSAMIGNKPQDLKYQ
GEKTYVTIGENCEIREFAIITSSTFEGTTVSIGNNCLIMPWAHVVAHNCTIGNNVVLSNHAQLAGHVQVGDYAIL
GGMVGVBHQFVRIGAHAMVGALSGIRRDVPPYTIGSGNPYQLAGINKVGLQRRQVPFATRLALIKAFKKIYRA
DGCFFESLEETLEEYGDIEVKNFIEFCQSPSKRGIERSIDKQALEEESADKEGVLES

>core/557/2/Org2_Gene612

MSDFSMETLTKTLRQQTGVGLTKCKEALEACGGNLEEAVVYLRKLGLASAGKKEHRETKEGIIAAKTDANGT
ALIEVNVETDFVANNAVREFVSNLLNDILKYKVDTVREALSQAASSQDPSLSVDELRAVTMQTVGENIRISRV
AYFPKATNSTVGIYSHGNGKTVALTMLSGSSTADSLAKDIAMHVVAAPQFLSKESVPAEIAIAKEKEVIASQI
QGKPPQEVIEKIVTGKLNTHFFQEACLLEQPFIKNADLSIQSLIDDFSKTSGSSVAIEQFILWKIGA

>core/558/2/Org2_Gene570

MLERTQRTLKREVRYSVGVIHLGKSSTLHLQPAQTNTGIVFQRQSASGNYENVPALLDHVYTTGRSTTLSRG
SAVIATVEHLMAALRSNNIDNLIQCSGEEIPIGDGSSNVFVELIDQAGICEQEDKVSIALRTRPVYYQHQDIFL
AAFPSDELKISYTLHYPQSSTIGTQYKSLVINEESFRQEIAPCRTFALYNELCFLMEKGLIGGGCLDNAVVFKD
DGIISRGQLRFADEPVRHKILDLIGDLSLVGRPFVAHVLA VSGHSSNIAFGKKILEALEL

>core/559/2/Org2_Gene665

MATAHLGRQALLHLRSWTPAIRASGNLFRQQSMSLHNNVLFAGDIVGAIKNSTAISRHALGSSHYAHAALQK
TEGFLGAADGVNTAVAGAMLWGQLLNGSMIFETDEETGELRRCNEADAEGCMTQKLQRRSALTITGKVAR
LASKTLGTATFLHEMDVVS LGANANKIGCKVTSCNLVATGCSL TESSISLYRILSTRPETISDPENRNKPSAEF
AARSKAIRNAFI AWLGDVVDLVCDALGTL SLFLPAILGVHAVLIMAILGLISCVIN FVKDYAKIG

>core/560/2/Org2_Gene217

MVLMNKRLKIILTNDGITA KGMSCLVSALLEANIGDIYIAAPQAEQSGKSMAISLNQVVCASPYAYPQPVKE
AWAVGGSPTDCVRLGLRTL FESVSPDLVISGINCGNNICKNAWYSGTIGA AKQALVDGIPSMALSQDNHISFF
QQDKAPEILKALVIYLLSQPFPCLTGLNINFPTSPGGSSWEGMRLVPPGDEFFYEEPQYLGSVNKNQYYVGKIS
GVRIGEHPSEELACMLENHISVSPIFSQNSPIGLMTLEEFQKTQENFNASLLSSELTTKIF

>core/561/2/Org2_Gene620

MELKKTAESLYSAKTDNHTVYQNSPEPRDSRDVKVFSLEGKQTRQEKT TSSKGNTRTESRKFADEEKR VDD
EIAEVGSKEEEQESQEFCLAENAFAGMSLIDIAAAGSAEAVVEVAPIAVSSIDTQWIENIILSTVESM VISEINGE
QLVELVLDASSSVPEAFVGANLTLVQSGQDLSVKFSSFVDATQMAEAADLVTNNPSQLSSLVSALKGHQLTL
KEFSVGNLLVQLPKIEEVQTPLHMIAS TIRHREEKDQRDQNQKQKQDDKEQDSYKIEEARL

>core/563/2/Org2_Gene965

MRQSFDELSQNAFKNIFNKQRFCFIFCSLCCFGFVFALFLKLCSRLAPEISLSTLGLGAFFCAFSVICASAIIVQF
LLHKESQGETSKLCCA IKNTWSSLWLSLLVSMPPFIAMVAVVTVAMLSSFLGSLPWVGKLFHTVLIFIPYLSA
TALILLFLGSFSC LFFCIPVLHNQESIDYRKLLECFRGNILRQFIGVVIALVPLALCSWLALDSFYLMTHLVEIAD
IHTWSFLAQMFVLIVPIALILTPAVSFFFNF SFSFYLA KQEEEKALVK

>core/564/2/Org2_Gene463

MHKVIVFIFLTL YSLKSYGNDVIDKPHVLVSIAPYKFLVEQIAEETCFVYAIVTNHYDPHTYELPPQ QIKELRQ
GDLWFRIGEAFEKTCERNLT CQQVDLSQNVSLIQGKPCCNQHTTNYDHTWLS PKNLKVQVETIVTTLSKKY
PQHATLYQSNGEKLLLALDQLNEEILTITSKAKQRHILVSHGAFGYFCRDYNFSQHTIEKSSHVEPSPKDVAR
VFRDIEQYKISSVILLEYSGRRSSAM LADRFHMHTVNLDPYAENVLVNLKTIATTFSSL

>core/565/2/Org2_Gene541

MYFTRDPVIETVITSREGYKLSVRNTKHFSQDPFMVEAIEVISLGNICFFRNCDH SKPFLVPAGDYEVMEVRDT
KINLKAVGLDRGVK IAGGREALIKLTKSTPLPVIDEKPLADSP EEGTEPTSPSKKEKKEARKDSFKGEKWKEK
KKLSRRRNHKEIAEVTGASQEILD TVKEELWEESQENEIVEQKKFSLPPP AKLISEVISQTVVDPVVT SADLN
ESLQALVRESSDLINALLSADDAIHFPETEEPTSASFEESSAMFFPETSSATEEE

>core/566/2/Org2_Gene941

MTRSSPAQLSRFLSEIQNKPKKSLSQNFLVDQNIVKKIVATSEVIPQDWVLEIGPGFGALTEELIAAGAQVIAIE
KDPMFAPSLEELPIRLEIIDACKYPLDQLQEYKTLGKGRVVANLPYHITTPLLTKLFLEAPDFWKTVTVMVQD
EVARRIVAQPGGRDYGSLTIFLQFFADIHYAFKVSASCFYPKPVQSAVIHMKVKETLPLSDEEIPVFFTLTRT
AFQQRKVLANTLKGLYPKEQVEQALKELGLLNVRPEVLSLNDYLALFHKMQAG

>core/567/2/Org2_Gene611

MESQSCKLTIKDLMSAGAHFGHQTRRWNPMMKLYIFEEKNGLYIINLAKTLQQLRNALPHIRKVIQDNKTVL
FVGTKKQAKCVIREAAIEAGEFFIAERWLGGMMLTNMTTIRNSIKTLDKIEKDLSRNQAYLTKKEAALLAKRH
QKLLRNLEGIRYMKKAPGLLVVVDPSYEKIAVAEAKKLGIPVLALVDTNCDPTPIDHVIPCNDDSLKSIRLIIN
VIKENIIEAKHKLGIIVSPVKSLEVPDLSAFESSQDDESEENREEDLLAKKFDGEAN

>core/569/2/Org2_Gene735

MTANTFGTLDILMKHSEDDLSRFLPKNLLVESPHPEEIPLKSLSFTMSWLPTIHPSWITIAMKEFPPEIQGQLL
AWLPEPLVQEILPLLPGISIAPHRCAPFGAFYLLDMLSKKIRPCGITEEIFLPASSANAILYYTGPKIALINCLGL
YSIAKELKHILDKVVIERVKNALSPTEKLFLTYCQSHPMKHLETTNLFSSWTTDAELRQFVHKQGLEFLGKAL
TKENASFLWYFLRRLDVGRAYIVEQTLKTWYDHPYVDYFKSRLEQCMKVLVK

>core/570/2/Org2_Gene453

MDYKLLDSGDGNKLECFGPVTLIRPSSIAVWPKSRLPELWSQAQLQYVREGERGAWKNFKRLPEEWEVAFSD
VRCLLKRTPFGLHGVFPEHMGFWPALKQAIEKHKERQVLNLFAYTGAGSIFAAKCGARVTHVDASQA AVR
WAQRNVEKNAFPERRIFWVIEDVISFLKKEIRRNKKYQVILLDPPSYGRGPDGEVFKIDKDLFPLLSLCSKLLA
DDASYFLLTSHTPGHTPEFLRAIARRSVPTLVSEAWSCGESFCGEGVGALPSGSFVQWIA

>core/571/2/Org2_Gene130

MITGVVLEKHEQRTMFSLTLLNNFTTFGLLHTPLHYNPPYPIVILLHGLASDKTGSKRSHVRLAQELTRLGIAA
LRVDLLGHGDCEGELMDFSLENYKQNIREIIEYTHSLLHIDQERLAIFGSSSLGGTLALQTLPPFNKIKALAVWA
PTISGELMAAEAQKNAPEVITMSQKGAITYAGMTLNPDFYTQFLKIDIVKELMPSARNLPPILYMQGEQDLLV
SINHRTLFTFAFANQDKPITILTYPDVDHAFPPFAESSALSDLTQWLKRELTSGE

>core/572/2/Org2_Gene639

MLLGFLCDCPCASWQCAAVANCYDSVFMSRPEHKPNIPYITKATRRGLRMKTLAYLASLKDARQLAYDFLK
DPGSLARLAKALIAPKEALQEGNLFFYGCSNIEDILEEMRRPHRILLGFSYCQPKACPEGRFNDACRYDPSH
PTCASC SIGTMMRLNARRYTTVIIPTFIDIAKHLHTLKKRYPGYQILFAVTACELSLKMFGDYASVMNLKGVG
IRLTGRICNTFKAFKLAERGVPKPGVTILEEDGFEVLARILTEYSSAPFPRDFCEIH

>core/573/2/Org2_Gene952

MRRYLFMV LALCLYRAAPLEAVVIKITDAQAVLKFAREKTLVCFNIEDTVVFPKQMVGQSAWLYNRELDLK
TTLSEEQAREQAFLEWMGISFLVDYELVSANLRNVLTGLSLKRSWVLGISQRPVHLIKNTLRILRSFNIDFTSC
PAICEDGWL SHPTKDTTFDQAMAIEKNILFVGS LKNGQPMDAALEVLLSGISSPPSQI IYVDQDAERLRSIGAF
CKKANIYFIGMLYTPAKQRVESYNPKLTAIQWSQIRKNLSDEYYESLLSYVKS KG

>core/574/2/Org2_Gene992

MKVKINDQLICIPPFISARWSQIAFIESQEGENKDQGTLLRLHLIDGKIISIPNLDQSIIDIAFQEHLLEYLETSQSGKE
DSRDDDKLGVGVLMNVLQQITKGNDIQVLPKNLISPLFSGTNPIEAILQHTPEHKDHPDAPTDVLEKMADVIR
VLSGNNATLLPRPEPHCNCMHCQIGRVMNEEDTLAVSDKDLTFRTWDIMQSGDKLYIVTNPLNPSDQFSVYL
GPPIGCTCGEPNCEHIKAVLYT

>core/575/2/Org2_Gene333

MKLLKNVLLGLFFSMSISGFSEVKVSDTFVKQDTVVEPKIRVLLSNESTTALIEAKGPYRIYGDNVLLDTAIQG
QRCVVHALYEGIRWGEFYPGLQCLKIEPVDDTASLFFNGIQYQGSLYVHRKDNHCIMVSNEVTIEDYLKSVL
SIKYLEELDKEALSACIILERTALYEKLLARNPQNFWHVKAEEEGYAGFGVTKQFYGVEEAIDWTARLVVDS
PQGLIIDAQGLLQSNVDRLAIEGFNARQILEKFYKDVDVFVIESWNEELDGEIR

>core/576/2/Org2_Gene233

MKKKLSLLVGLIFVLSSCHKEDAQNKIRIVASPTPHAELLESQEEAKDLGIKILPVDDYRIPNRLLLDKQV
DANYFQHQAFLDDECERYDCKGELVVIKVVHLEPQAIYSKKHSSLERLKSQKKLTIAIPVDRтнаQRALHLL
EECGLIVCKGPANLNMTAKDVCCKENRSINILEVSAPLLVGSLPDVDAAVIPGNFAIAANLSPKKDSLCEDL
SVSKYTNLVVIRSEDVGSPKMIKLQKLFQSPSVQHFFDTKYHGNILTMTQDNG

>core/577/2/Org2_Gene409

MVRDIQSESIGKLVFLGTGNPEGIPVPFCSCRVCQNTGIHRLRSSVLIQYQNKTLVIDAGPDFRTQMLVAGVSE
LDGVFLTHPHYDHIGGIDDLRAWYIVTQRSPLVLSASTYRFLNKAKEYLFATPNVESSLPAVLEFTILNEDCG
QEEFQGIPYTYVSYYQKSCHVTGFRFGNLAYLTDLCSYDAKIFSYPDNDVETLILSAGPSETPIPFQGHKSSHLT
VEEAKAFANHAGIKNLIITHISHCLEAERDQHPEVTFAYDGMEVLWTL

>core/578/2/Org2_Gene968

MIRFFKTLFPPGPQYSLCYASILIVLSSLVCVPTFCWLFLPELSLSKFNPSPIRNLFLVSSTLSKVPPTAIAEHLR
LSADAPTYLHEFSIKEAESSLHALGIFSSLVIEKSPDNKGITIFYTLQTPIAYVGNRSNTLCNLEGSCFLGQPYFP
SLNLPQIFFSQEDLKMQKLPKEKMLFTKILLKELAMESPKIIDLSLSDAYPGEIIVTLSSGSLRLRLPIKTLDRALD
LYKHMKKSPVIESEKQYVYDLRFPNLLLKAL

>core/579/2/Org2_Gene636

MFNNKMILIAGPCVIEGEDITLEIAGKLQSILAPYSDRIQWFFKSSYDKANRSSLNFRGPGLTEGLRILAKVKE
TFGVGILTDVHTPQDAYAAAEVCNILQVPAFLCRQTDLLVATAETGAIVNLKKGQFLSPWDMEGPINKVLST
GNNKILLTERGCSFGYNNLVSDMRSIPVLSRSGFPVIFDATHSVQLPGALSTESGGLTEFVPTLSRAALAAGAH
GLFIETHTNPKIAKSDAASMLSLEEFAALLPTWDQLFTCVSSFDMVSA

>core/580/2/Org2_Gene501

MTKVALLIAYQGTAYSGWQQQPNDLSIQEVISSLKKITKTRTPLIASGRTDAGVHAYGQVAHFRAPDHPLF
ANANLTKKALNAILPKDIVIRDVALFDDNFHARYLAIKKEYRYSLSRLAKPLPWQRHFCYTTPRHFPSTELMQE
GANLLIGTHDFASFANHGRDYNSTVRTIYTLTDIVDKGDSLSIICRGNGFLYKMVRNLVGALLDVGKGAYPPE
HLLDILEQKNRREGPSAAPAYGLSLHHVCYSSPYNNFCCEQCSVSTSNEG

>core/582/2/Org2_Gene64

MTQYYFLSSFLPTQLPESVPLFSISDLDLLYLNLSENDLCNYGLLKRFFDFENFAFFWAGKPIPFSGEVTQE
NVERMLSSQQWSDDNDFEDFFKDFLMNHKSSQDRLNHFSDLFREFLSYHQTNSSKFLQDYFRFQQQLRVVL
AGFRARVLNMDVSYVLRDEDESSDPVVLEVLQMOKDSPNYELPEEFSDLQGVLDYGLLPHTLNRALALYQFH
KLEGFCSDSYFDGNVILARCATYMFAIRNSLASVEKGREIINHIEKAIKW

>core/583/2/Org2_Gene153

MHSKFLSRRKKNSSHKEETSWDCIASSYNKIVQDKGHYYHRETILPQLPSLTLGSKSSVLDIGCGQGFLERA
LPKECRYLGIDISSRLIALAKKMRSVNSHQFKVADLSKRLEFVEPTLFSHAVAILSLQNMEFPGEAIRNTATLL
EPLGQFFIVLNHPCFRIPRASSWHYDENKKAISRHDYRLSPMKIPIMAHPGQKDSPSTLSFHFPLSYWFKELSS
HGFLVSGLEEWTSSTSTGKRAKAENLCRKEFPLFLMISCIKIK

>core/584/2/Org2_Gene765

MTLPLEPMIFWSSLSAKVMKKFLTPHCAGTFSEEDAEAKEAHLVTGKQGHRLMGNCVTFYWLVDKKNNGVI
LDAKFQYFGHPYLIPLAEAVCNLVCGKSYSEAYKMTLDDIDKSLRVHAHQPALPEDSISLYHFVIDALDTAVE
QCLEIPLEDGSLPLQNSPMNLDFEDANPYSQSDWEALTHEQKLYALRATIAEKIGPYIAMDGGEVTVESLENF
IVTIAYSGNCSGCPSSLGSTLNSIGQLLRAYIYPELVKQVDESSLNLSHP

>core/585/2/Org2_Gene782

MQGFFPLASGSKGNSAYLGTDSCKILIDLGVSKQVVTRELLSMNIDPEDIQAIFVTHEHSDHISGIKSFVKAYN
TPIVCNLETARALCHLLDSHPEFKIFSTGSSFCFQDLEVQTFNVPHDAVDPVAFIFHYREEKLGFCITDLGWVTS
WITHELYDCDYLLIESNHSPELVRQSQRPDVYKKRVLSKLGHISNQECCQLLQKIITPKLKKLYLAHLSTECNT
AELALSTVSESIAITSIAPEIALAQGITSPIYFSRLEVACPR

>core/586/2/Org2_Gene873

MAGLDLEARGKRRVVTNPAITAFGLCCGLFIIFKSVLRTSSSVELFHRLQGLSLLLISAMIADFSDGAIARIMKA
ESAFGAQFDSLSDAVTFGIAPPLIAIKSLDGIYVGNFFSSLLITSIIYSLCGVLRLVRYNLFSQKTVDVSKPYCFI
GLPIPAAAASIVSLALFLASDFFPDLPALQRLVGLLSFALLFIGGLMISPWKFPGVKHFRFNVSSFLLVVTIGLAA
CLFFSGLVDHFVEVFFLVSWLYTLVGFPIFSIIYRKKS

>core/587/2/Org2_Gene25

MKKPDNDSTFDVRSFFPFDVLCIEQLRKEMSWEVVSAKIPRLPRGWYELMGLSKEDRIDFCLDFWC SVLGIE
HKESPSICRFFSLLTIEVYIYRLEKEPYQLKMFYVFRDGRGCFQGEPPLLDFLGHHRLPPLGDRHYEKFFSIHN
GFGKWEDEGIFPMRSLAKVQKLRQQLVVMNKMQAEDNCYSLGIFPFYGYEEPFA YQSFFFDPEIRRDLPSP
NVLLNEESLEHRSLETIELLHLSKSYPSFLSWLENYLHSEEVYNE

>core/590/2/Org2_Gene452

MDCIGKHNPLVKEALALKRSRCRKSSWFLVEGAREIQKALRTGYLCQHVFCSHTLSEKEKEFLYELKRNSTK
ILYCLDSTLAQLSFKEHDSFVAVIQKRVWNKEDFLIQRKNAQPFYLIIEQVEKPGNVGAILRIADGAGVDGVI
LCNPIVDLYNPNVRRSSLGAVFSLPILSISREEGKELFKQEGWTVFVTSPRAETMYFSKNYLGPTALVFGSEKD
GLTEDWFSEDFSEIALPMLGESDSLNLATSVAAYEVVRQRWVN

>core/591/2/Org2_Gene931

MGSSMHVGVIGCSGRTGKVIVSALEQSSEYTLGPGFSRSSALTLFQVIAHNDVLVDFSHPLLTKEVVAHLLISP
KPLIIGTTGFP GKCKEAHDSLEELTHIVPVVCPNASLGAYIHKRLVMLLSQLCNPQFDIRIRETHHRYKKDSL
SGTAQDLLDTIQVKQEDWGEEYEVGQRDSSKKTIEVQSSRVGDIPGEHEVAFISSGEQILVRHTVFSRNVFG
RGILSILDWLKTLNPQPGLYSLGDTLELVLRNEHCLLKKTTDH

>core/592/2/Org2_Gene682

MEKLEFVTSLSPPDDDLITFNKQGLIAGPEEEKVAFIVRSNAMLDAGPETPASFPESLREQFDIFPEYVEVLYS
NEGLDVWEAGCTWILNNEVTIQLRKHHRKASRWLGMYSRDEVLAEAVHAVRMKFHEPVFEEVLAYQTSR
WGWRFFGPLFRSPGESYLLFFITLGLGISLWYPAGILIMLVLP MYFLMRLCMAQSYLYRAMKKIRKMLGV
PPLWVLLRLTDKEIKMFAKEPIPVLEHYARKRKLENVRWKQIYQSYFV

>core/593/2/Org2_Gene439

MSNQLQPCISLGCVSYINSFPLSLQLIKRNDIRCVLAPPADLLNLLIEGKLDVALTSSLGAISHNLGYVPGFGIA
ANQRILSVNLYAAPTFFNSPQPRIATLESRSSIGLLKVLCRHLWRIPTPHILRFITTKVLRQTPENYDGLLLIGD
AALQHPVLPGFVTYDLASGWYDLTKLPFVFALLHSTSWKEHPLPNLAMEEALQQFESSPEEVLKEAHQHTG
LPPSLQEQYALCQYRLGEEHYESFEKFREYYGTLYQQARL

>core/594/2/Org2_Gene357

MKLTKYLNTKQLRSMISRLFVRYSLPMSKQLSFFALCVLGSHPIFAQTPNPPQVRVRSEVIFIDPGHGGKDQGT
ASKELHYEEKSLTSLALTVQSYLKRMGYKPQLTRSSDVYVDLGKRVALSNRGQGDVFISIHCHSSNAAAF
GTEVYFYNGKVGSPTRNRMSEVLGKNILAAMEKNGILKSRLKTANFVVIRDTSMPAVLVETGFLSNSRERA
ALQDARYRMHVAKGIAEGVHNFLSGPSFQKPKQNI AKIRKPQIQAN

>core/597/2/Org2_Gene77

MPFDITYYTTPLEIILIWVMLNYLLKFFWGTRAMDVVFGLLAFLFLVLADKLHLPIIRRLMLHVVNIAAIVV
FIIFQPEIRLALSRI RFHGKKFFIDTQE QFVEQLAASIYQLSERQIGALVVLENKDSFDEYLSFSSVKINATFSEEL
LETIFEPSSPLHDGAVILRGDILAYARVVLP LAHDTTQLSRSMGTRHRAALGASQRSDALIITVSEENGSVSLSR
DGLLTRGVKIDRFKAVLRSILSPKEHKRKPLFSWIWKR

>core/599/2/Org2_Gene167

MTTLLSIKDLSTIRGKKILNHINLNLIKGSYLTIVGPSGSGKSSLALTILDLLKPTTGTITFHMDPKIPRARKVQ
VIWQDIDSSLNPCMSIKGIISEPLNIIGTYSKAEQNKEIYNVLDLVNLPKSVLHLKPYKLSGGQKQRIAIKALV
SKPELLICDEPLSSDLTNQSLILDLFQTIKKEYQNTLLFITHDMSAAYYIADTIAVMDQGS LVEHACREKIFST
PKHTTTQDLLDAIPFSLISTEMEPSEEYELQVASK

>core/600/2/Org2_Gene920

MKTWLFFTF LFS CSSFYASCRYAEVRSIHEVAGDILYDEENFWLILDLDLTLLQGGEALSHSIWKS KAIQGLQ
KQGTPEQEAW EAVVPFWIEIQEMGTVQPIESAIFLLIEKIQKQGKTT FVYTERPKTAKDLTLKQLHMLNVSLE
DTAPQPQAPLPKNLLYTSGILFSGDYHKGPGLDLFLEICTPLPAKIIYIDNQKENVLRIGDLCQKYGIAYFGITY
KAQELHPPIYFDNIAQVQYNYSKLLSNEAAALLLRHQMHE

>core/601/2/Org2_Gene695

MMKYLPYIAITACIHGGILLLVFASPLPKRLQPKAFQEKLVTIQPKPPVPTPSVVVDPAKTIRPSVATQPQKQ
AKCSPPQENVQKALQKPIPKVIKTEPPKPSAPTVAKKTATEKPPSTTKKNTQLSKTQLQTLSEVAQALSLH
VDKIEKSETSLKNISWPSTAQLTMHSELKATQEDELCELFRTHIALPSKGYVRIKLVLSPNGEIQECSFLSEVSA
ADKQLLTQRIQALPFQKFLEKYKVSKNISFHIKLVSNES

>core/602/2/Org2_Gene698

MDLADAHVHLSDDAFEEDINSVLQRAQDSGVSLVVNVTTTEKELNRSFAYAERFPKIRFCHVGGTPPDVDQ
DIEEDYRNFHAAAHSKKLAAIGEVLGYCFATEEGIARQKEVLQRYLALSLECELPLVVHCRGAFNDFFRML
DQYYHNDPRSRPGMLHCFTGTLEEAQELISRGWFISISGIVTFKNAQDLRDLVVELPLEHLLIETDAPFLAPVP
YRGKKNEPAHVLHTINAVANVKGMFPQELAALAYKNVLRFLHG

>core/603/2/Org2_Gene18

MFLQFFHPIVFSQSLSFLPYLGKSSGIIKCSNIVEHYLHLGGDTSVIITGVSGATFLSVDHALPISKSEKIIKILS
YILILPLILALFIKIVLRILFFKYRGLILDVKKEDLKKTLTPDQENLSLPLSPPTLKKIHALHILVRSGKTYNELI
QEGFSFTKITDLGQAPSPKQDIGFSYNSLLPNFYFHSLVSVPNISGEERALNYHKEQQEEMAVKLKTMQACSF
VFRSLHLPMSQTKDKKAGFGLLTFFPWKIYPL

>core/605/2/Org2_Gene352

MILTAAFSPCPNDIFLFRSFLKDPQFRPLLNQVTIADIETLNTLALQRRLSLMKMSAALFPLVSDYYNLMDVG
NTLGYNSGPIVLSLDPECSLDTLATPGEMTTAHALCKLYYPKAKLIPMPYDKILSAILQGKVDGGALIHEERFS
YDLQLTLRADFGELWRRKTIFPLPLGCLAIAKYVPMATVDALTAALRKSLICSLKDPITAGAKAVEYSKNKN
VTVIHRFIGTYINKETFQLSKTGKKALHMLWKANECCQYT

>core/606/2/Org2_Gene412

MIKQIGRFFRAFIIMPLSLTSCESKIDRNRIWIVGTNATYPPFEYVDAQGEVVGFIDDLAKAISEKLGKQLEVR
EFAFDALILNLKKHRIDAILAGMSITPSRQKEIALLPYYGDEVQELMVVSKRSLETPLVPLTQYSSVAVQTGT
QEHYLLSQPGICVRSFSDSTLEVIMEVRYGKSPVAVLEPSVGRVVLKDFPNLVATRLELPPECWVLGCGLGVA
KDRPEEIQTIQQAITDLKSEGVISLTKKWQLSEVAYE

>core/607/2/Org2_Gene103

MLRNQVLVYCSEGVSPYYLRHTIRFLKYYSTQEGAFDILRVDGNFLIKNPFWEETRLLVFPGGADRPYHRV
LHGLGTARIFQYVSEGGNFLGICAGAYFGSKMIYFYEPEGAPLQGARDLGFFPGTAKGPAYRGNFSYVSPSGV
RVSPQLFSDFGLYAMFNGGCFEGSEGYPGVNIESRYDDLPGKPASIVSRIVSKGLAVLSGPHIEYLPHYCR
MVKENVQKTREFLQRRERTLDRYCQNLVQRLRQPAFSKADC

>core/608/2/Org2_Gene295

MNVKDETFWSVHNLCVNYEHAADVLYHISFSLGKGS�TAILGPNGAGKSTLLKASLGLIKPSSGTVYFFNQKF
KKVRQRIAYMPQRASVDWDFPMTVLDLALMGCYSYKGMWGRISSDDRREAFHILERVGLSVADRQIGQLS
GGQQQRAFLARALMQADLYLMDELFSAIMMASFKTSVGVQLQELRDQGKTIVVVHHDLSHVRQLFDHVV
LNKRLICCGPTDECLNGDTIFQTYGCEIELLEQTLKLSRGKQFGSC

>core/609/2/Org2_Gene578

MNRRWNLVLATVALALSVASCDVRSKDKDKDQGSLVEYKDNKDTNDIELSDNQKLSRTFGHLLARQLRKS
EDMFFDIAEVAKGLQAELVCKSAPLTETEEYEEKMAEVQKLVFEKKSKENLSLAEKFLKENSKNAGVVEVQP
SKLQYKIIKEGAGKAISGKPSALLHYKGSFINGQVFSSESSEGNNEPILLPLGQTIPGFALGMQGMKEGETRVLYI
HPDLAYGTAGQLPPNSLLIFEINLIQASADEVA AVPQEGNQGE

>core/611/2/Org2_Gene1001

MENLETFILKIYRGVPGKQYWESFELPLHPGENVISALMEIEKRPVNILGEKVNPPVWEQGCLEEVCGSCSILV
NGVPRQACTALIQEYIDATQSREIVLAPLTKFPLIRDLIVDRSIMFDNLERIQGWVAADIEGETFGPQVTQEQQ
ELLYALSQCMTCCGCTEACPQIDNKSDFIGPAAISQARYFNTYPGDKRSKKRWRALMGKGGIEGCGQAHNC
VRVCPKKLPLTESISAVGREISKFSLRSLFSALFKKKK

>core/613/2/Org2_Gene343

MSKFILLLSLGVAALASKNFFIWPAPSGKTPLKLRQVLFGGALLVFSSLVALSVSSQTAELLSTMTGISLAFAP
LFYLLFLPKDITRAILFSGERPVKTSWRALGSAIRMWIIIPVTQLIGIMMSKFLTLVLPTQEIHTEVTQEVQNS
LPITGHYISMILNLGVLT PFGEEVFFRGILQTF LKNKMTRIAAVLCSSIIFSFIHIEHSLGSWVFVPVLFVFSLSAG
FLYEKDRHILSPIALHGLFNLTSLFLGIK

>core/614/2/Org2_Gene443

MAFYSPSTISKYFIYSGAGNRFLGETLPEVEDVRFLCQETRVDGFLY LKPSSCADAQLIIFNSDGSRPTMCGN
GLRCAIAHLASQKGKSDISVSTD SGLYSGYFYSWDRVLVDMTLADWRASVHRLESRPDLPKEVVCIHTGVP
HAVVILPEISTLDLSILGPFLRYHQTFSPDGVNVNFVQILGHCQLRVRTYERGVEGETAACGTGALASALVVS
NSYGWKESIQTWGGELMTVSQNRGRVYLQGSVTRDL

>core/615/2/Org2_Gene106

MFKLLKNLFLIGCCIVGYFWMRKESIVEQWLSNRLHTQVTVGRVSIRTSGIKIRHICIHNP LASERFPYAAEIEY
ADVRFSSISMLLTKQLEISELIIHGANFTIFPYDSHGTKTNWSLVWKNFHPQKETPSNLWIDRAPVLIRRCFLN
TRL YGLRANH KDIPHL SVPSLEFHSHTSSAKELPKLSEALPSLLYLAL EESLYHLNLP GDIIKPLSQQAHKHFYS
SYPQFQDRLNDINTPGTPTEEII GFIRGLFFH

>core/616/2/Org2_Gene82

MVSPLSLFHKMLLENWTPVEEPFPWPPAEKNQKIFAWALNQSKLIFVSTSGNIAQPRLVTD SMSMMIVNAAN
RTMSRDGAGTNQVL SAAVSVD SWGLSQRPLNPERQGTPLNEGECRAGMWRNADGSNHTGKQGKPHYLAQ
LLGPKAVDH HNK SQA AFD RCKNAYLNCFS LAQTLGV TFLQIPLISSGIYAPPENRKKPNSEENKVRMRWIHA
VKCALVAAMQEFGN EPGNTDRRMLIVLTDLKTPAITDPKKKSHL

>core/617/2/Org2_Gene306

MKTQQTQNIIEVWNFYWETQEIEYRDSLIEFY LPLVKS SVVHRLISGMP SHVKTEDLYASGVEGLVRAVERYN
PERSRRFEGYAVFLIKAAIIDDLRKQDWVPRSVHQKANKLSGAMDSL RQSLGKEPTDLELCEYLNISQQELSG
WFVSARPALIVSLNEEWPSQSDEGAGMALEERIPDERAETGYDVVDKQEFSLCLANAIQELEEKERKVMALY
YYEELVLKEIGKVLGVSESRSVSIH SKALLKLRAALSAFR

>core/618/2/Org2_Gene370

MWLGA YTWLNVFGILLQAAFIQNILLANFLGMCSYLACSTRVSTANGLGMSVALVLTVTGSINWVHAFITG
PKALTWISPSLASVNLGFLELIIFIVVIAAFTQILELLEKVSRLYLSLGFPLIAVNCAILGGVLFGITRSPFIP
MMIFSLGAGCGWWLAIVILATIKEKLAYS DIPKNLQGMGISFITTGLIAMAFMSLTGIDISKPSAKIQRAPLETE
VVENTTNPLKESSSKHQPSISKARTQRRSL

>core/619/2/Org2_Gene606

MLKIKHLHASCNDVKILDDFNLIQPGTMHVIMGPNGAGKSTLAKILAGDESVLVSSGEIALQEQNLLSMLPE
ERSRAGLVVGFQMPPEIPGVNNKMFLRDAYNARRRANQEGDISIDEFNTLLSTVLETYEYNATTDLFLDRNV
NEGFSGGERKRNEICQMLVLEPEMVLLDEPD SGLDVDALRLICRVLEKYRELHPTSSLCIVTHNPKLGNLIRP
DVVHLLLDGRVALSGDVSLMHELEAKSYQEVTKRVAWR

>core/621/2/Org2_Gene714

MKTIAVNSFKGGTAKTSTTLHLGAALAQYHQARVLLIDFDAQANLT SGLGLDPDCYDSLAVVLQGEKEIQE
VIRPIQDTQLDLIPADTWLERIEVSGNLAADRYSHERLK YVLGVSVDKYDYVIIDTPPSLCWLTESALIAADYA
LICATPEFYSVKGLERLAGFIQGISARHPLTILGVALSFWNCRGKNNSAFAELIHKTFPGKLLNTKIRRDITVSE
AAIHGKPVFATSPSARASEDYFNLTKE LLILLRDI

>core/622/2/Org2_Gene945

MTRQSYVLGNWKMHKTIQEAKKEYVQTLASLLQGEPLSCTIGIASPFTSLRAIHEVINTTGAFLWLGAQNVHPE
LSGFTGEISL PMLKEVGVEFVLVGHSERRHIFGESDAFIASKVK SVAQAGLVPVLCVGESLEVREEGKAHQV
IKKQLLLGL EQMDNGSEFLIAYEPVWAIGTGKVAEASDVQDIHMF CREVVAERFSEATAEEISILYGGSVKVD
NAQRFGQCSDVDGLLVGGASLEGQSFFEVAKNFNV

>core/623/2/Org2_Gene448

MHDALLSILAIQELDIKMIRLMRVKKEHQKELAKVQSLKSDIRRKVQEKELEMENLKTQIRDGENRIQEISEQI
NKLENQQA AVKKMDEFNALTQEMTTANKERRSLEHQLSDLMDKQAGGEDLIVSLKESLASTENSSSVIEKEI
FESIKKINEEGKALLEQRTELKHATNP ELLSIYERLLNKKDRVVVPIENRVCSGCHIVLTPQHENLVRKKDRL
IFCEHCSRILYWQESQVNAQENSTAKRRRRRAAV

>core/624/2/Org2_Gene196

MKPEESECLCIGVLPARWNSSRYPGKPLAKIHGKSLIQR TYENASQSSLLDKIVVATDDQHIIDHVTDFGGYA
VMTSPTCSNGTERTGEVARKYFPKAEIIVNIQGDEPCLNSEVVDALVQKLRSSPEAELVTPVALTTDREEILTE
KKVKCVFDSEGRALYFSRPIPFILKKATPVY LHIGVYAFKREALFRYLQHSSTPLSDAEDLEQLRFLEHGGKI
HVCIVDAKSPSVDYPEDIAKVEQYITCLSNAYF

>core/625/2/Org2_Gene818

MLIKLWRATYEGMYTFLVGALLKLRYRMQVEGWDTLNINPKQGCLFLANHVAEVDPIILEYLFWSRFHVRP
MAVEYLFHSRVVQWFLNSVRSIPIQLVPGKESKRS LERMNVCYEEASRALNRGESLLLYPSGRLSRTGKEEI
VNQYSAYVLLHRVMECNVVLVRVSGLWGSAFSRYKQNSTPKLGPAFKEAFRALLRRGIFFMPKR FVKITLC
QVDHLFLKQFPTKQDLNTFLASWFNQGDDNLPIEVPYA

>core/626/2/Org2_Gene510

MQICVTGVVLRSRPLGKNHTLTTLFTPEGLFTFFAKQGQTLQCDYRETLVPISLGKYTLHRNGSRLPKLTHGD
ILNAFEAIKQTYALLEASGKMIQALLASQWKEKPSHKLFSLFLNFLHRIPESSNPEFFAAIFVLKLLQYEGILDL
TPACSLCKASLPYACYRYQGHKLCKKHQHKQAISIEKEEQILQAIHAKQFSELLAIAEFPIAIAEKIFYLFDL
QEEKKSERNSSDPYHEILRLSKVVHPY

>core/627/2/Org2_Gene603

MLIVLAFRQVFFSHRSQDLRLKKNYLRLLLKQNFALTLPKERTSKGHSLMLTFDFASDFYTNIFPFLEEQKIPAV
VGVASRYIPSNAAQDLHPSHRLKPSETLAFQDEIFSNYMPFCCQNELIEMAKSPYIQLASSGFAIRNLMNPPY
LTTEILLSRHIIETITGAKPLAFLFPFGKSDPTSRKLAADHYPYSFLLGNTINRKLKTHNIYRLDIKPMQYVCPS
LFQSSRYLKNWIKESKQLYLKKQLPKR

>core/628/2/Org2_Gene169

MLMDISHILEDLAYDEGILPREAIEAAIVKQMQITPYLLHILHDATQRVPEIVNDGSYQGHLIYAMYLLAQFRE
SRALPLIIKLFAFEDDTPHAIAGDVLTEDLPRILASVCNDDSLIKELIETPKINPYVKAASISGLVTLVGAGKIPR
DKVIRYFAELLNYRLEKQPSFAWDNLIAGICTLYPGELFYPISKAFDGGGLVDTSFISMEDVENIHEETVESCIH
TLCSSTELINDTLEEMEKWLEDPIEP

>core/629/2/Org2_Gene110

MNVADLLSHLETLLSSKIFQDYGPNGLQVGDPQTPVKKIAVAVTADLETIKQAVAAEANVLIVHHGIFWKG
MPYPITGMIHKRIQLLIEHNIQLIAYHLPLDAHPTLGNNWRVALDLNWHDLKPFSSLPYLGVSFSPIDIDS
FIDLLSQYYQAPLKGSALGGPSRVSSAALISGGAYRELSSAATSQVDCFITGNFDEPAWSTALESNINFLAFGH
TATEKVGPKSLAEHLKSEFPITTFIDTANPF

>core/630/2/Org2_Gene86

MKKQGKTLFLFLSFLFSTAFSGLFASQTSSLRTIQENIFLAKTGDTVLSRGSQRTFVLVKSTTPKTVWIEIHH
FPCIAHKERPSLEQASWKTVIHQLESQSQVFVLSSEGSQFFSLNTRTKSLEPVGKSTTVPAFLQIFDLPLSPAP
ANVIKTKGKENKPWSPKVSFEGAPLTSISVNAWQGLWPKDRGPLSETGILMYFTQPDISVFPLWVSIETPKGT
SIVRAVDIGHGATSPYVYSLPDSKTQ

>core/632/2/Org2_Gene487

MSLATNNAESKFPSLQRLPNHVAIIMDGNRRWYKKHREECGHTHTSGHYYGAKVLPNILNAVLDLGIKVL
LYTFSTENFGRPKEEIQEIFNIFYTQLDKQLPYLMENEICLCIGDLKLPKGIQTKINHVSMTASFSRLELVLA
VNYGGKDELVRAFKKLHVDILNKKISSDDLSESLISSYLDTSGLTDPDLLIRTGGEMRVSNFLLWQIAYTELYI
TDTLWPDFTPQDLFEAINVYQQRSRGGK

>core/633/2/Org2_Gene713

MGNLKTLLSRFKKNTPTKMEALARKRMEGDPSPLAVRLSNPTLSSKEKEQLRHLLQHYNFREQIEEPDLTQ
LCTLSAEVKQIIHQSVLLHGERITKVRDLLKSYREGAFSSWLLLTYGNRQTPYNFLVYYELFTLLPEPLKIEM
EKMPRQAVYTLASRQGPQEKKEEIRNYRGERKSELLDRIRKEFPLVETDCRKTSPVKQALAMLTGKSQILTK
CTSLSSDEQIILEKLIKKEKVKSNLFPDTKV

>core/634/2/Org2_Gene523

MKIKFSWKVNFLICLLAVGLIFFGCSRVKREVLVGRDATWFPKQFGIYTSDTNAFLNDLVSEINYKENLNINIV
NQDWVHLFENLDDKKTQGAFTSVLPTLEMLEHYQFSDPILLTGPVLVVAQDSPYQSIEDLKGRLLGVYKFDSS
VLVAQNIPDAVISLYQHVPIALEALTSNCYDALLAPVIEVTALLETAYKGRLKIISKPLNADGLRLAILKGTNG
DLLEGFNAGLVKTRRSGKYDAIKQRYRLP

>core/635/2/Org2_Gene573

MSLLKDTVFTCLDCENTGLDVKKDRHIEIAAVRFTFDSVISSIEFLINPERVVSASQRVHHISNAMLRLDQPKIA
EVFPQIKAFFKEGDYIVGHSVGFDLQVLAQEMERIGETFLSKYTIIDTLRLAKEYGDSPNNSLES LAVHFNVPY
DGNHRAMKDVEININIFKHLCKRFRTEQLKQVLAKPIKMKYMPLGKHKGRCFSEIPLAYLQWASKMDFDS
DLLFSIRHEIKHRQKGTGFSQVNNPFMEL

>core/636/2/Org2_Gene251

MDITLVGKKVIVTGGSRGIGLGIVKLFLENGADVEIWGLNEERGQAVIESLTGLGGEVSFARVDVSHNGGVK
DCVQKFLDKHNKIDILVNNAGITRDNLLMRMSEDDWQSVISTNLTSYYTCSSVIRHMIKARSGSIINVASIVA
KIGSAGQNTYAAAKAGIIAFTKSLAKEVAARNIRVNCLAPGFIETDMTSVLNDNLKAEWLKSIPLGRAGTPED
VARVALFLASQLSSYMTAQTLLVVDGGLTY

>core/637/2/Org2_Gene772

MTQDPHDHFKSRTPEDHIKHVRDKHRVCKGEPHTTFKGFFYHLANNALSTGVFFIFRTLFFLIPTNRALQVKS
LISLGVGWTFYHGCLKARKAWAYMELSHRSMLEEKNEIEENFEQEKIELRILFENQGFKDPLLQEMVEYVCS
DSTLLD TMIREELYRKEDLPHPLIQGGSRLGGLCGLAIFLPLVLCISYTLAGVFSALMVLVLSFLKAKILKN
DKISEMVWVLGIFITSASIISSLMKLL

>core/638/2/Org2_Gene318

MTLSFHTHPLNYWTFEEFDGLPIRHGVFSKQKDAEGTVFAAKNPEIASALQSPKYCDLHQRHGTSVRCVTPT
SPTYQPADGLCTQSPLLSLHIRHSDCQAAIFYDREHHAIANVHSGWRGLLGNIYAVTVGTMKKLFHTKPQDL
FVAIGPSIGPDYAIYPDYATLFPRSFLPFMNPKNHFDLRAIARKQLTNLGISKDRIFISDLCTYTEHDAFFSSRYL
AHHPDPNLTGQHSKNRNNVTAVLLLPRD

>core/639/2/Org2_Gene613

MAKQTRRVLFKISGEALSKDSSNRIDEMRLSRLVSELRAVRNNDIEIALVIGGGNLRGLAEQKELQINRVSAD
QMGMLATLINGMAVADALKAEDIPCLLTSTLSCPQLADLYTPQKSIEALDQGKILICTTGAGSPYLTTDTGAA
LRACELNVDVLKATMHVDGVYDKDPRLFPDAVKYDFVSYKDFLSNQLGVMDASAIISLCMDSHIPRVFSFL
QHSLEKALFDPTIGTLVSEDVNHVCSPRH

>core/640/2/Org2_Gene62

MKFFFILILIVAQFPAFSAQPRTQVSASHSKQAKARRTSRIRSSAATNASVSRYKTRAAARKKIGKFEKKPSLSP
VQWVRYSGKNYSIQTPSLWQCIDDKTQLPEKLDVLLIGKGKGNLTPTINIAQEITSKSSKEYIEEILAYHKANE
MTLESGIFTQIQSPSGEFTIIKTEKNSSWGRVFCLQATTVIDHTAYIFTSTATLDDYAELSFTFLKVVSSFQIRGG
KEATSGDAILEKALEALQENENK

>core/641/2/Org2_Gene525

MHIYGLADLHLALGVPEKTMEVFGDPWIGYHQKICSEWQAVVHPEDIVLLPGDISWAMNLSEAHKDFAFIG
DLPGTKYMIRGNHDYWSSASTSKILQALPPSLYYLNQGFALLTPHLAVVGVRLWDSPTICVKKENFLTPSTQE
QSYTEQDEKIFLRELGRLLKRAFAALPKEVTEVIVMTHYPPISSDGTGPISFLEADGRVSLCLFGHIIHKVQRPI
DGFGNIRGIHYILVAADYVNFVPQEV

>core/642/2/Org2_Gene672

MKITTVKTPKIYPYDDLYSILESSLPKLNERSIVVITSKIVSLCEGAVVELEKVSDELIKQEADAYVFVEKYGI
YLTKKWGILIPSAGIDESNVEGYFVLYPRDFLLSVNTLGDWLRNFYHLEHCGIIISDSHTTPLRRGTMGLGLC
WNGFFPLYNYVGKPDGFRALKMTYSNLLDGLSAAAVLCMGEGDEQTPIAIIIEAPKITFHSSPTTLQDMSTL
AIAEDEDLYGPLLQSMWETPAPTS

>core/643/2/Org2_Gene340

MDFDYFGLSDIGRVRARNEDFWQVNLMSQVVAIADGVGGRLGGDIASQEAVTSLMELIDEQQSKLMGYGD
DQYKETLKKILLEVNGVVYEHGQMEEHLQGMGTLSFIQFRKDRAWLHVGVDSRIYRIREGELRRLTEDHSL
ENQLKNRYGLPKQSDKVYSYRHILTNVLGSRPYVMPDIRNLPCEKEDLYCLCSDGLTNMVPDIDIRDILNQPA
TLEERGNALISLANTRGGDDNATVVLVRIQ

>core/644/2/Org2_Gene464

MTIRILAEGLAFRYGSKGPNIIHDVSFSVYDGDFIGIIGPNGGGKSTLTMLILGLLTPTFGSLKTFPSHSAGKQTH
SMIGWVPQHFSYDPCFPISVKDVVLSGRLSQLSWHGKYKKKDFEAVDHALDLVGLSDHHHHCF AHLSGGQI
QRVLLARALASYEILILDEPTTNIDPDNQQRILSILKKLNRTCTILMVTHDLHHTTNYFNKV FYMKNKTLTSLA
DTSTLTDQFCCHPYKNQEFCSPH

>core/646/2/Org2_Gene905

MSYFNYQKNSVVLRLSLGLLAKFFSRLLYRVFFSFREGIYLFSSLYLKYPRLFFYDLGKYVYSLRHCPYAKLGR
LPGASLLKEGNVYGETPWSVLAKICQAFDITSQDILYDLGCGLGKVCWFVSHVVRCQVIGIDNQPHFIRFSSN
MHRKLSSGFALFDTEEFKNVLSQASYVYFYGSSFSRLLNEIILKLSEMAPGSVVISISFPLDSFSRGKECFFT
EKSCSVRFPWGKTIAYKNIRKGS

>core/647/2/Org2_Gene216

MSTLLLNPWMKAGKRIESLVRKALYTHTMLANHRKIVVALSGGKDSLTLMLKAISGRGFPDLDLHAVNI
GGKYSCGAENVKPYLTRICDQLCIPFRTIPSPYAPETPECYPCSQARRLLFQAAKEIGASAIAFGHHRDDLVQ
TALLNLLHKAFAFAGMLPVLDMVHFGVTILRPLIFTPEFWIRKFAKENG FARVTCRCPPVSLRSKAEQSLKLE
EVFPLARHNIALAIQEHGSSKSQKI

>core/648/2/Org2_Gene226

MTDYSFFRRKIGNIEAIECPGNPQDPPIILCHGYGSLADNLTFFPSICSFSKLRPTWIFPNGILPLENDFRGSRACF
PLNVLLLQELSRLYANGVGNLQEKYDELFVDVLETPKEALEELILNLNRPYNEIIIGGFSQGAILATHLVLT SQ
NPYAGALIFAGARLFNQGWEEGLKQCAQVPFLQSHGYEDEILPYHLGAHLNDLLLTKLNGQFVSFHHGGHEIP
SVVFQKMQVTVPNWIDPARG

>core/650/2/Org2_Gene638

MPILSVCNLVKKYNKKPVTNDVSFQINPGEIVGLLGPNGAGKTTAFYLTVGLIRPDSGKIIFKNVDVTKKTMD
HRARLGIGYLAQEPTIFKELTVQDNLICILEIHYKARKQQSHLLNTLVDDLQLGSCLHKKAGTSSGGERRRLEI
ACVLALNPSVLLLDEPFANVDPLVIQNVKYLIKILAGRGIGILITDHNAKELLSIADRCYLIIDGKIFFEGSSSQM
ISNPMVKQHLYLGDSFSY

>core/651/2/Org2_Gene375

MKVRIVDSGKSSAASHMAKDRDLLESQDGELILHLYEWENPCSLTYGHFMRPEKFLLSNYADLGLDAAVR
PTGGGFVFHKGDYAFSVLMSATHPSYSSSVLENYHTVNSFVAKVLEKVFRIQGMLAPEDENSSSRDSGNFCM
AKTSKYDVLFGDKKIGGAAQRKVQQGFLHQGSLFLSGSSSEFYQRFLKPEVLEEIIIEQIQIHAFPLGLEAADE
VLQEARQQVKEAFIKLFCGEGE

>core/652/2/Org2_Gene326

MTLYLLPNTLGTRAVETLPSVIGELVHRLDGLIVESDRGGRAFLSLWKIPEVHKFPLAILSKHARLPKAWDFY
LEPIVKHGENWGLISDAGLPCIADPGASLVRRARALGIPVQAFSGPCSITLALMLSGLPSSQSFITGLYLPQSPKE
RVKSIKKAATSKEVSTSVCIETSYRNVYTFESLLDTLPSYAELCVASDLSGPSELVLTRQVQSWRTTEDLGSV
KQSITKVPTIFLFHIPN

>core/653/2/Org2_Gene494

MAGHSKWANTKHKRERADHKKKGKIFSRIIKELISAVKLGGADPKSNARLRMVIQKAKENNIPNENIERNLKK
ATSAEQKNFEEVITYELYGHGGVGIIVEAMTDNKNRTASDMRIAINKRGGSLVEPGSVLYNFARKGACTVAK
SSIDEEVIFSAYAIEAGAEDLDTEDEENFLVICAPSELASVKEKLISQGATCSEDRLIYLPRLVDCDEKDGEANL
ALIDWLEQIEDVDDVYHNMS

>core/654/2/Org2_Gene575

MDISGAVKQKLLQFLGKQKKPELLATYLFYLEQALSLRPVVFVRDKIIFKTPEDAVRILEQDKKIWRETEIQIS
SEKPQVNENTKRIYICPFTGKVFADNVYANPQDAIYDWLSSCPQNMEKQGGVRIKRLVSEDPDVIKEYAVPP
KEPIIKTVFASAITGKLFHSLPPLLEDFISSYLRPMTLEEYVQNQTKFQLESSFLSLLQDALVEDKIAAFIESLADD
TAFHVIYSQWVDTEE

>core/655/2/Org2_Gene863

MGLYDRDYIQDSRVQGTAFSRVYGWMTAGLIVTSCVALGLYFSGLYRSLFSFWVWCFATLGVSFINSKI
QTLSSVAVGGLFLLYSTLEGMMFFGTLLPVYAAQYGGGVIWAAFGSAALVFGLAAYGAFTKSDLTKISKIMT
FALIGLLLVTLVFAVSMFVSMPLIYLLICYLGLVIFVGLTAADAQAIRRISSTIGDNNTLSYKLSLMFALKMY
CNVIMVFWYLLQIFSSSGNRD

>core/656/2/Org2_Gene34

MHPPIDITAIEAKLNFTFTQPKLLEIALTHPSYKNESAVQIEDSERLEFLGDAVLGLIVTEHLFLLFSPMDEGTL
TARASLVNAKACCRYTTMLGIGDYLLIGKGEKIQSERGRLSAYANLFESILGAVYLDGGLSPARKLTVPLLP
REEILPLMSGNPKNLLQQFTQKQFRVLPVYQSTAVTDAQGNVSYQIQVLVNQEVWGEKNASSKKEAEKIAA
QQALDITYGNKNQNTMDV

>core/657/2/Org2_Gene989

MEPSTNKPDCCKIFDSIASKYDRNTNITLSLGMHHFWNRSLIQILGSGYSLLDLCAGTGKVAKRYIAAHPQASV
TLVDFSSAMLDIAKQHLPQGSCSFIHSDINQLPLENHSYPLAAMAYGLRNLSDPHKALQEISRVLMPSGKLGIL
ELTPPKKTHPTYSAHKLYLRAVVPWIGKSVSKDPDAYSYLSKSIQQLPKDHDLEDLFSKSGFYIAKKKKLFLG
AATIWLLEKQ

>core/658/2/Org2_Gene980

MDVLIFYDTETTGTQIERDRIIEIAAYNSVTDESFLTYYNPEIPIPEASKIHGITDDAVLSAPKFPEAYEGFRKF
CGEDSILVAHNNDGDFDPLLGKECRRHSLEPLTNRTIDSLKWAQKYRPDLPKHNLQYLRQVYGFAENQAHR
ALDDVVILHKVFTSLIGDLPPQQVLDLLQQSYHPKVFKMPFGKYKGQPLVDIPKSYFEWLENQGALDKPENK
DIKAAIALHQP

>core/659/2/Org2_Gene685

MQNATIDQLPVSWQEQPLPCWREQLKEEWSKPYPMQQLLIFLKQEYKEHTVYPEENCVFSALRSTPFDQVRV
VILGQDPYPGKGQAHGLSFSVPEGQRLPPSLINIFRELKTDLGIEHNHGCLQSWANQGILLNTVLTVRAGEPF
SHAGKGWELFTDAIVTKLIQERTHIIFVLWGAAARKKCELLFNSKHQHAVLSSPHPSPLAAHRGFFGCSHFSKI
NYLLNKLNKPMINWKLP

>core/660/2/Org2_Gene273

MDLAVELKEGILLVDKPQGRTSFSLIRALTKLIGVKKIGHAGTLDPFATGVMVMLIGRKFTRLSDILLFEDKEY
EAIAHLGTTTDSYDCDGKVVGRSKKIPSLEEVLAAEYFQGEIQQLPPMFSAKKVQGKKLYEYARKGLSIERH
HSTVQVHLQITKYEYPLLHFVVSCKGTYIRISIAHELGTMLGCGAYLEQLRRLRSRFSIDECIDGNLLDHPDF
DISPYLRDAHGNSL

>core/661/2/Org2_Gene662

MIGDKIILFVTEDLSLSSQLKDLASQRSYQILVSPVFPTSFESVAIFCEYLLLPEQIFSPGIFPEEDLIVLFDTFQE
EAITKVLNQGATGYLLRPITAKVLDAVIRAFLRQHEVLEHSIPDTMTFGDHTFRVLNLVIESPEGSVYLTPEA
GILKKLLINRGHLCLRKNLLAEIKGNTKEIARNVDVHIASLRKKLGPYGSKIVTIRGVGYLFSDDDSIPLQNHD
NTAHPNEE

>core/662/2/Org2_Gene768

MTKVRLNKFLASAGVASRRKCDEIIFSGSVTVNGRVAEGPFVLVDPEDKVQVGGTSVHLTKKVYFMVHKAI
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KDLGKLMEGTFIDGKHVRPVSVTKIRRGTVKIVVSEGKKHEIRLFADAAGFPILELKRIRIGSLVLGGLRYGEY
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>core/663/2/Org2_Gene193

MLQAHRLCYSCDNQVILKDASFQASPGTITIILGSSGVGKTTLFRLLAGFLPLQEGELLWNGSPLNRKDVAYM
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KPILLLDEPFSSLDVLLKEQLYQDIVALAKKENKTVLLVTHDFHDVSLGDLVLYVIKNTLTPVPLDPSMRPL
NNGLCFIKDLKKHLYT

>core/664/2/Org2_Gene893

MRVIFPDKHNNFPNLSKLLKKLPSVILVTSCIAPFFSYIINKFFGIPGLLEILALS VKGIQKHFWQFLTYPLITAD
SLSLNKDQSFEITQRLLLLRNVLDFFLFYKAIQHLIRKLGAFSVLVVISGQALIIGAVLWGFMALIHSSQSFFGPE
SIICGVLT VQIFLDPEKRFTIGPTPLSVSIKWGFLFVLGFYCCILIFSGAFLLLLASMLAIVLAILFCKKEKIPNPYT
TSLRF

>core/665/2/Org2_Gene536

MPTTNCIFLDLRGHSILHQLQIEEALLRVANQNFCIINSGAKDSIVLGISRNLNQDVHISRAQADHIPIIRRYSGG
GTVFIDSNTLMVSWIMNSSEASAQPQELLAWTYGIYSPLLNTFSIRENDYVLGHKKIGGNAQYIQRHRWVH
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AQPHRKATTVLN

>core/666/2/Org2_Gene32

MLSVCYSDPCLSDFCQGKRPLRIASRNSNLAKAQVHECISLLRSWYPKLWFQLSTTETTG DREKKIPLHLVEN
SYFFTDGVDALVHKGVCDLAIHSAKDLPETPSLPVVAITRCLHPADLLVYADHYVHEPLPLSPRLGSSSLRRS
AVLKQLFPQGGQILDIRGTIEERLDQLHRGHYDAIVLAKAASRLHLHHAYSIELPPPYHALQGSLAITAKDHA
GKWKQLFTPIHCHSS

>core/667/2/Org2_Gene734

MKFFSLIFKDDDVSPNKKVLSPEAFSAFLDAKELLEKTKADSEAYVAETE QKCAQIRQEAKDQGFKEGSESW
SKQIAFLEEETKNLRIRVREALVPLAIASVRKIIGKELELHPETIVSIISQALKELTQNKHIIISVNP KDLPLVEKSR
PELKNIVEYADSLILTAKPDVTPGGCIIETEAGIINAQLDVQLDALEKAFSTILKAKNPVDEPSETSSSTDSSSL S
NDQDKKE

>core/668/2/Org2_Gene801

MNRRDMVITAVVVNAILLVALFVTSKRIGVKDYDEGFRNFASSKVTQAVVSEEKVIEKPVVAEVPSRPIAKET
LAAQFIESKPVIVTTPVPVSETPEVPTVAVPPQPVRET VKEEQAPYATVVVKKGDFLERIARANHTTVAKL
MQINDLTTTQLKIGQVIKVPTSQDVSNEKTPQTQTANPENYYIVQEGDSPWTIALRNHIRLDDLLKMNDLDEY
KARRLKPGDQLRIR

>core/669/2/Org2_Gene1019

MFFIVCFGFLIHKKHTILPPKAHIPTNAKHFP TIGNPYAPINITVFEEPPSCSACAEFTTEVFLLKKHYIDTGEISF
TLIPVCFIRGSKPAAQALLCIYHHDPRQADIDAYMEYFHRILTYPKEEGSHWATPEVLT KLAEGLKINSGRSVN
PKGLEQCIASGQYNEQIKKNLYGSQVLGGQLATPTAVVGDYLIEDPTFHEIERAIQHIRQLQAVEGDHDD

>core/670/2/Org2_Gene697

MVHFShNPiiQAYTEADFFGKSIFFCLLILSVCTWTVLHQKLAIQKNFLKAGKSLKDFLIKNRHAPLSLDIHP EL
SPFADLYFTIKRGTTLELLDKNRQSAPDRGPILSSEDIQSLETLLGAIMP KYKALLHKNSFIPATTISLAPFLGLLG
TVWGILVAFTHISSGSSGNSAIMEGLATALGTTIIGLFVAIPSLIAFNYLKAHSSSELISEIEQTAYLLLNSIEVKYR
NTNL

>core/671/2/Org2_Gene56

MTKHGKRIRGILKNYDFSYSYLREAIKQCAPPVRFQTVDVSIKLGIDPKKSDQQIRGAVFLPNGTGKTLR
ILVFASGNKVKEAVEAGADFMGSDDLVEKIKSGWLEFDVAVATPDMMREVGKLGKVLGPRNLMPTPKTGT
VTTDVAKAISELRKGKIEFKADRAGVCNVGVGKLSFESSQIKENIEALSSALIKAKPPAAKGQYLVSFTISSTM
GPGISIDTRELMA

>core/672/2/Org2_Gene113

MEKDLHLHEKKCLAHEAATQVTSGMILGLGSGSTAKEFIFALAHRIQTESLAVHAIASSQNSYALAKQLAIPL
LNPEKFSSDLTVDGADEVDPQLRMKGGGGAIFREKILLRAAKRSIILVDESKLVPLGKFRVPLEISRFRGSA
IIEIRHLGYEGEWRLQDGTDLFITDSSNYIYDIFSPNSYPNPEKDLLKLIQIHGVIEVGFVIEKVEVWSSNSQGL
ISKKYSV

>core/673/2/Org2_Gene195

MLQSCCKALLSIVVSILAFHPIPGMGVEAKSGFLGKVGWFSKKEIQEEARILPVKDSLWKRYDYTSSSGFS
VEFPGEPDHSGQIVEVPQSEITIRYDITYVTETHPDNTVYVVSWEYPEKVDISRPELNLQEGFSGMMQALPES
QVLFMQARQIQGHKALEFWIVCEDVYFRGMLISVNHTLYQVFMVYKNKNPQALDKEYEAFSQSFKITKIREP
RTIPSSVKKKVSL

>core/674/2/Org2_Gene221

MALDEINNQNPNPSQQIASSTSQTSKINQDRKTFACVTLLVVATLMILSGIVLLFTIGSLGLSVPLSGILGTFAV
TVGAVLFITGLTILVRKSLGIEQKNEDLNFLKIKTPTPPARPLMSKFSVTCSTTSIVLGMALLIGAVVSVFFLTG
YLQLGLCAGLVGLGTALFVAGLARMSPRSLADQEGSGSADSQSNIVGIGEPKAAQEQQWYKMAVVRGEDGI
PTAIRLTPEK

>core/675/2/Org2_Gene720

MSKPSPRNANQPQKPSASFNNKTRSRLAELAAQKKAKADDLEQVHPVPTEEEIKKALGNIFEGLSNGLDLQQI
LGLSDYLLLEIYTVAYTFYSQGYNEAVGLFQLLAAAQPQNYKYMLGLSSCYHQLHLYNEAAFGFFLAFDA
QPDNPIPPYYIADSLKLQQPEESNNFLDVTMDICGNNPEFKILKERCQIMKQSIEKQMAGETKKAPTKKPAG
KSKTTTNKKSGKKR

>core/676/2/Org2_Gene502

MYLEDYDVFFFDLDGLLDVTEPCFYRAFLQACAEFSLEVHWDFSTYYSHHTLGTEIFSKKFIEQYPQAEYM
AEIFAKRLQIYYKSLEHAGPALMPGVEAFIELVLSLNKTFGVVTNSPRDATHLRTMYPILNKFLFWVTRENY
ARPKPYGDSYDYAYRTFAREGMKVIGFEDSVKGLRALSKIPATLVCINSMAEITPEDYPELKGEFFSYPSFD
VLTEHCSQQKLL

>core/677/2/Org2_Gene930

MNTSHRKTIVFSYLSSTFTLLLVLNLVLSSKLIPTTFFNFIIIPGGLILYPLTFLISDVVNEIFGPKKARVMIFSFI
ANLLASSIVQIFMFFPVASPEMQTAWHCLFDLSPLRFLASLLAFIVSQQLDIVLYTFFKNRTPNSSLWLRNGS
TWISQIPDTFIVDTCILYFGMGLSFPQTLNIMFYSYIYKITFCVLTTPLFYLAVENTIRKFLGMPSTKIANTVPLIN
QP

>core/678/2/Org2_Gene151

MKKQESVLVGPSIMGADLTCLGVEAKKLEQAGSDFIHIDIMDGHFVPNLTFGPGIIAAINRSTDLFLEVHAMIIY
NPFEFIESFVRSGADRIIVHFEASEDIKELLSYIKKCGVQAGLAFSPDTSIEFLPSFLPFCDVVVLMSSVYPGFTGQ
SFLPNTIEKIAFARHAIKTLGLKDSCLEVDGGIDQQSAPLCRDAGADILVTASYLFEADSLAMEDKILLRGEN
YGVK

>core/679/2/Org2_Gene179

MKGFLSVNELIFGFQTFSSVVVLGVFFASRGKAWLTGWLSSLSSIMNVFVLKQIHLWGFEVTSADVYVIGLLT
CLNYAREHYEKNDINDAMLCSWVISIAFLVLTQLHLFLIPSPNDSSQEHFLALFSSTPRIVVASLVTLIFVQIVDI
KLFTFLQRVFSKKYFAMRSTISLLFSQLIDTIIFSFLGLYGLVSNLCDVMIFAMLVKGIVITLAIPTLTVTKAVLD
RRSS

>core/680/2/Org2_Gene508

MRPHRKHVSSKSLALKQSASTHVEITTKAFRLSMPLKQLILEKSDHLPPMETIRVVLTSHKDKLGTEVHVVAS
HGKEILQTKVHNANPYTAVINAFKKIRTMANKHSNKRKDRTKHDLGLAAKEERIAIQEEQEDRLSNEWLPVE
GLDAWDSLKTLGYVPASAKKKISKKKMSIRMLSQDEAIRQLESAAENFLIFLNEQEHKIQCIYKKHDGNYVLI
EPSLKPGFCI

>core/681/2/Org2_Gene767

MALLILLRHGQSVWNEKNLFSGWVDIPLSQQGIEEAFSAGRAIQNLPIDCIFTSTLVRSLMTALLAMTNHHSK
KIPYIVHEDPKAKEMSRIYSAEEENNMIPLYQSSALNERMYGELQGKNNKQTAEQFGEERVKLWRRSYKTAP
PQGESLYDTKQRTLPHYFEKNILPQLQNGKNVFVSAHGNSLRSLMDLEKLSEEEVLSLELPTGKPVVYQWKN
HKIEKHPEFFG

>core/682/2/Org2_Gene192

MSSQPLVTTSSSLSRVYVLTGEEKVACYKKAFNHIWHGAPAILLAAALLMFCIFGFVLGSILLGAPLEGASILY
DVILPWLLPSILVFVLLVLPLNIYAYSHHKQVLALHERITQSNYKEIYDHCEKEKKTTPNKKALSLYIESQVLVP
EYSKRFSMILGKTLKIIPKKDSPESLKHDELIQKALERAKENIYMKNQREKRDEREAKKEAKNASKTNPLW
EGLGT

>core/683/2/Org2_Gene208

MSLLIEAKNLSKTIQQNQNISILTDVSLSLHAGETISITGASGNGKTTLLHLLGTLDVPSSGSLRFFDKDLKNQ
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GEKQRVAIARALINEPAILLADEPSGNLDEETSEQIHNLLLEQASALCGILIVTHNKHLSRCSREGVLSNGKLF
FHNS

>core/684/2/Org2_Gene157

MTIRVRNLAYSVNKKKILDGVTFSLERGHITLFVGKSGSGKTMILRALAGLVQPTQGDIWIEGEAPALVFQQP
ELFSHMTVLGNCTHPQIHIGRSTEEAREKAFELLHLLDIEEVAKNYPDQLSGGQKQRVAIVRSLCMDKHTLL
FDEPTSALDPFATASFRHLLLETLRDQELTVGLTTHDMQFVHSCLDRIYLIDQGTVAGVYDKRDGELDSGHPLS
KYIHSAQ

>core/685/2/Org2_Gene41

MDLKLDEVASLLDVSEHTVLQWLKEGAIPSYSMNNEYRFSREEIENWLLHNQALMIQERGEDKEALKDLSL
KYSLYKAIHRGGVLCDVVVHSKEEALQYASKYIAQKFQLDESVLFEMLSHRENLMSTGIGEGIALPHAKDFLI
NAYYDIVVPMFLAEPIEYGALDGKPVGILFFLFACQDKSHLNLVNKIVHLGMSLNARSFFKNYPNKDQLLAY
VKEWESQTH

>core/686/2/Org2_Gene503

MILRISTVSLLTSCSFSKNSRTCFVTPERITSQKDCPVLLHPKSTTISPLYDWISPNREVITAYSFYCRGQGNSII
TPEGVLYDCDGLHHSITKEEFRIHPRLIEVVRLQLQDHPKVSIIAEFCCPKHFFHFLEASGISLSQLHLQGTAAT
FALDPPLPMEKLLATIKKLYKKNSDPSLSNFIVTEATLTNPRLTQQDLGSHTEITVEILDNLQNKALSSA

>core/687/2/Org2_Gene822

MENSQNFHDTLCQLLDYSEELYPTLASLLNVTLPNTAISASVSSIPEKAVEVPNAEPQPITPPPPTNLSQEKT
PSDWKCVPLHPDLSQNAILKEKYPALKDCSLPAPKIPCSIFVYEENNEEVLFNRLAKILTQQLFPTKLTLIHAK
TNIFVNNPNFFLALAPLNVIRYKIPTTDYHQSLTQNGCIFLPLYSSLEYEKDSQLKRNLWAILNRLPFAYTPKSS

>core/688/2/Org2_Gene876

MKPQDLSPFLWKERRPCIQDGVLYVPRHYFEHQNFSTSYHQEFFQNHTSIACELCSGNGDWVVAQAQKDP
QVLWIAVEQRFDRVRKIWSKMINHQINLRIVCGTAETFFQYYVPDQFLQRLVVNFDPWPCKMRHRKHRL
QPSFVQEISRLQDSAVFALATDDKTYLLESIEALQTHLAPRMETPYIYKMTDTYGNWFWENLWRTKGQEIFY
TEFIKKAGI

>core/689/2/Org2_Gene623

MIDPVECFPNLDGDAEAQSITQNSGTPLASELKKDISPFALGSYAAPKDTTLVQGFKPNPMAMMQDQNSNLI
DPELQEALESEELQEQINNLKGRLWDFRSTFEDSQTAAQFADEHFQAVGVIIIDLNEDLNTIAEHTQQDARKE
DKEEGSVTRKIIDWVSSGEEVLNRALLYFSDRDGNRESLANFLKVQYAVQQRATQRAELFASIVGTSVSSVKTI
MTTQLG

>core/690/2/Org2_Gene673

MTSWIELLDKQIEDQHMLKHEFYQRWSEGKLEKQQLQAYAKDYLLHIKAFPCYLSALHARCDDLQIRRQIL
ENLMDEEAGNPNHIDLWRQFALSGLVSEELANHEFSQAAQDMVATFRRLCDMPQLAVGLGALYTYEIQIP
QVCVEKIRGLKEYFGVSARGYAYFTVHQEADIKHASEEKEMLQTLVGRENPDVAVLQGSQEVLDLWNLSS
FINSTEPSCSK

>core/691/2/Org2_Gene564

MVLLSKFDFSGNKIGEEVADSLFADEGDGLQLIKDYIVAIRANKRQWSACTRNRSEVSHSTKKPFKQKGTG
NARQGCLASPQFRGGGIVFGPKPKFNQHVRINRKERKAAIRLLLAQKIQTNKLTVVDDTVFVDALTAPKTQS
ALRFLKDCNVECRSILFIDHLDHVEKNENLRSLRNLTAVKGFVYGININGYDLASAHNIVISKKALQELVERL
VSETKD

>core/692/2/Org2_Gene598

MQTLARLFGQSPFAPLQAHLEMVVSCVEYMLPIFTALRDGRYEELLEMAKLVSDKEYQADCIKNDMRNHLP
AGLFMPISRAGILEIISIQDSIADTAEDVAILLTIRRLNFYPSMETLFFRFLEKNLEAFELTMTLLHEFNQLLESSF
GGRKADKARLLVGRVAKSEHESDVLQRELMQIFFSDDFIPEKEFYLWLQVIRRTAGISDSSEKLAHRINMTLE
EK

>core/693/2/Org2_Gene925

MSTTTVKHFIHTASRWEPLKEIVASNYWHAQWINTLSFLENSGAKKISASEHPTEVKEEVLKHAAEEFRHG
HYLKTQISRISSETSLPDYTSKNLLGGLLTKYYLHLLDLRTRCVLENEYSLSGQTLKTAAYILVTYAIELRASEL
YPLYHDILKEAQSKITVKSIILEEQGHLLQEMERELKDLPHGEELLGYACQFEGELCLQFVERLEQMIFDPSSTF
TKF

>core/694/2/Org2_Gene187

MTKNAINSQTTPQPNLTDAEPIASRAQCKSIAVIISLFALGMLLLCLGIILISIPGLAAQVALGLGIVSLILGIA
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KEGAEAASSIKQAVLESTEKLIDARKQEESSRREARKKIVAEAEASRKRIQQQMAADQEALRKRKEEVAKRK

>core/695/2/Org2_Gene432

MKKYFITGLVILLPLAITIAIVTMIMNFLTQPFVGLASEFFEKFSFYTKHRALLKFVLQIILLFGLFFATVLLGFL
TRIMIFKSLLSIYDKILHRIPIKTVYKAAQQVMTTIFGSKSGSFKQVVMVPFPNANVQCIGLVAGDAPTVCCT
GEKEDDPLVTVFIPTTPNPTSGFLTFRKSDIVFLDMKIEDAFKYIISCGVLSTPMACSSPLPDELHQDQGS

>core/696/2/Org2_Gene559

MGQKGCPIGFRTGVTKRWRSWLWYGNKQEFGKFLIEDVRIRQFLRKKPSCQGAAGFVVRMSGKIEVTIQTAR
PGLVIGKKGAEVDLLKEELRALTGKEVWLEIAEIKRPELNAKLADNIARQIERRVSFRRAMKKAMQSVMD
AGAVGVKIQVSGRLAGAEIARSEWYKNGRVPLHTLRADIDYATACAETTYGIIGIKVWINLGENSSSTTPNNP
AAPSAAA

>core/697/2/Org2_Gene445

MTLYLGLNQKTARKYQAHYLPILTLFPYAKSTPQNKRALQFLPQATHVILTSPSSTHLFLSRMTSLLSKATLK
TKTYLCIGESTKERLLSFLGQVKYVVATQEIAEGIFPLLQALPSSARILYPHSSLARPVIREFLYNRFTFFSYPHY
TVKPRKLKKNILSKYKKIIFTSPSTVRAFAKIFPRFPEKTYWCQGRMTLQEFQKFSSQKQVSLLETLGKSRTSP

>core/698/2/Org2_Gene649

MLMMLMMIIGITGGSGAGKTTLTQNIKEIFGEDVSVICQDNYYKDRSHYTPEERANLIWDHPDAFDNDLLISD
IKRLKNNEIVQAPVDFVLGNRSKTEIETIYPSKVILVEGILVFENQELRDLMDIRIFVDTDADERILRRMVRDV
QEQGDSVDCIMSRYLMSVKPMHEKFIEPTRKYADIIVHGNRYRQNVVTNLSQKIKNHLENALESDETYYMVN
SK

>core/699/2/Org2_Gene234

MQSDLIQILLKETVNTLYMVSTAFFFSCAIGGMLGLGLFCTSPKSLNPKKSLYATISMILSFLT AIPFAILIVILFP
ITRWIVGTSLGPTASIVPLTIGAIPFVVTVDAFRNSALNYLESAVALGIPKRNILFGILLPESYPQLIFSLKSLV
VHLISCSTLAGFVGGGGLGQLLLQYGYRRFEWSVTTSVLVITLVLIESVRILGDFWGRRVLKYRGIL

>core/700/2/Org2_Gene781

MSTVTTEPCSSIHISLNNDWRDSQPYSLDRASELLHFRFLPSLVFSNWKVEQQIETLCHKSEKRRLISPLAKWL
GKLHKQDLLCPPAPPVSVCWINAHVGYGVFARDEIAPWTYIGEYTGILRHRQAIWMDENDYCFRYPMPLFTL
RYFTIDSGKQGNVTRFINHSEQPNAEAIGVFSEGLFHVIIRTVAPIYAGQEICYHYGPLYWKHRKKREEFIPEEE

>core/701/2/Org2_Gene565

MRSHISVMGKKEGMIHIFDKDGSLVACSVIRVEPNVVTQIKTKESDGYFSLQIGAEEMNAPAHTITKRVSKPK
LGHLRKAGGRVFRFLKEVRGSEEALNGVSLGDAFGLEVFEDVSSVDVRGISKGKGFQGVMMKKFGFRGGPGS
HGSGFHRHAGSIGMRSTPGRCFPGSKRPSHMGAEENVTVKNLEVIKVDLEKKVLLVKGAIPGARGSIIVVKHSS
RT

>core/702/2/Org2_Gene927

MQRHIVGIDTGVGKTIVSAILARALNAEYWKPIQAGNLENSDSNIVHELSGAYCHPEAYRLHKPLSPHKAQI
DNVSIEESHICAPKTTSNLIETSGGFLSPCTSKRLQGDVFSSWSCSWILVSQAYLG SINHTCLTVEAMRSRNLN
ILGMVVNGYPEDEEHWTQEIKLPIIGTLAKEKEITKTIISCYAEQWKEVWTSNHQGIQGVSGTPSLNLH

>core/703/2/Org2_Gene353

MNAVNTPKKILCIVADYREISPLIEQLDFTQINEHLYSYRCTDYHLDLYIVHVWGSTAVLNALQSYCQAYTDY
DLWINPGFVGACSP EIPLGQCYTIEKIANLTDTTPVLSEDPPYIFDALPDSLKSSLVTSPVLYHYGFHKTFKL
LDMEGYAIASQAAEHIPCSFLKITSDYTVPGDCPFSRLEEVSQKLTQTLVELPELMERAIPP KLLLPCP

>core/704/2/Org2_Gene410

MLGSLPCYPGAGNIEEYKNRYFYCQLCAEVVSPYVVPVIVVDVQGAPPTGILQVLRCKQHKFQGLPVHGPIT
SLWALEPVGKGAPQLESAMYELCSQVRNFDICSIVSWVFGGLCIFAGLIVGVMVEAPLIAGLSAWVIPCIIIGV
GAILCLFAILMAYLGRGRVREWLNLSHEYITQCHCRQIQAHSQNYSVITEYPATCALSQPITKLPNGSRRDN

>core/705/2/Org2_Gene158

MDHWLAIAARLLL RGCYTLCVSGIGILCGSILGLLIGTVTSLYFPSKLT KLLANSYVTVIRGTPLFIQILIIYFGLP
EVLPIEPTPLVAGIIALSMNSAAYLAENIRGGINSLSIGQWESAMVLGYKKYQIFVYIIPQVFKNILPSLTNEFV
SLIKESSILMVVGVP ELTKVTKDIVSRELNPME MYLICAGLYFLMTTSFSCISRLSEKRRSYDN

>core/706/2/Org2_Gene778

MKRVIYKTIFCGLTLLTSLSSCSLDPKGYNLETKN SRDLNQESVILKENRETPSLVKRLSRRSRRLFARRDQTQ
KDTLQVQANFKTYAEKISEQDERDLSFVVSAAEKSSISLALSQGEIKDALYRIREVHPLALIEALAENPALIEG
MKKMQGRDWIWNFLTQLSEVFSQAWSQGVISEEDIAAFAS TLGLDSGTVASIVQGERWP ELVDIVIT

>core/707/2/Org2_Gene602

MQKL VHNIWKKFYSFSSAIAICIVLASFLSLKIVSNTYKHSQAKRNSILLLTRA AEVAVSQGFLPSKSALSSLEQ
AYHLGGESMKPYAGFLASCFYIHNEPLRGAYYAGLAYNNSQALQLPHPIQKLLKEISEAQADQLYDVALSKS
YQLLQTANSSPEYPTLSFLTLLRVIELKELLHQDVSQDFAALKSSPLFHQFERMYSDGEWTLSKRFGKKG

>core/708/2/Org2_Gene489

MIITIDGPSGTGKSTTAKALADHLHFNYCNTGKMYRTLAYARLQSPWATLPLTKFLEEPPFSFTFATGQPLESF
FNGHLLTSELTTQEVANAASELSQLPEVRAFMQDLQRRYAQLGNCVFEGRDMGSKVFPNADLKIFLTSSPEV
RAQRRLKDLPEGTLSPEQLQAELVKRDAADAQRAHDPLVIPENGIVIDSSDLTIRQVLEKILALLFRNEL

>core/709/2/Org2_Gene342

MRKMLVLLASLGLLSPTLSSCTHLGSSGSYHPKLYTSGSKTKGVIAMLPVFHRPGKSLEPLPWNLQGEFTEEI
SKRFYASEKVFLIKHNASPQTVSQFYAPIANRLPETIIEQFLPAEFIVATELLEQKTGKEAGVDSVTASVRVRVF
DIRHHKIALIYQEII ECSQPLTTLVNDYHRYGWNSKHFDSTPMGLMHSRLFREVVARVEGYVCANYS

>core/710/2/Org2_Gene815

MSKKPLYVAHPWHSPTLTQDNYESLCCYIEITPYDSVKFELDKATGLLKVDRPQKFSNFCPCLYGLLPQTYC
GTASGNYSGEQTRREGIQGDKDPLDVCVLTEKNIHHGNILLQARPIGGLRIIDSGEADDKIIAVLEDDLVFAEIE
DISDCPGTVLDMIQHYFLTYKATPNHLIKGSPAKIEIVGIYGKKEAQKVIQLAHEDYLSYIGDTAEVN

>core/711/2/Org2_Gene595

MSVNP SGNSKNDLWITGAHDQHPDVKESGVTSANLGSHRVTASGGRQGLLARIKEAVTGFFSRMSFFRSGAP
RGSQQPSAPSADTVRSPLPGGDARATEGAGRNLIKKGYQPGMKVTIPQVPGGGAQRSSGSTTLKPTRPAPPPP
KTGGTNAKRPATHGKGPAQP PPKTGGTNAKRAATHGKGPAQP PPKGILKQPGQSGTSGKKRVSWSEDE

>core/712/2/Org2_Gene94

MNTSISEIQRFLSMIAFEKELVSEDFSVVAGIDEAGRGPLAGPVVASACILPKGKVFPGVNDSKKLSPKQRAQV
RDALMQDPEVCFGIGVISVERIDQVNILEATKEAMLQAISSLPISPDILLVDGLYLPHDIPCKKIIQGDAKSASIA
AASILAKEHRDDLMLQLHRLYPEYGFDRHKG YGTS LHVEAIRRYGPSPCHRKSFSPIKQMCAIV

>core/713/2/Org2_Gene204

MTKGSVFIIMGPPGSGKGTQSQYLANRIGLPHISTGDLLRAIIREGTPNGLKAKAYLDKGAFVPSDFVWEILKE
KLQSQACSKGCIIDGFPRTL DQAHL LDSFLMDVHSNYTVIFLEISEDEILKRVCSRFLCPSCSRIYNTSQGHTEC
PDCHVPLIRRSDDTPEI IKERLTKYQERTAPVIAYYDSL GKLCRVSSSENKEDLVFEDILKCIYK

>core/714/2/Org2_Gene369

MTSKKSYKSYFFDPLWSNNQILAILGICSALAVTTTVQTAITMGIAVSIVTGCSSFFVSLLRKFTPD SVRMITQ
LIISL FVIVIDQFLKAFFFDISKTL SVFVGLIITNCIVMGRSESLARHVTPIPAFLDGFASGLGYGWVLLVIGVIRE
LFGFGTLMGFRIIPQFVYASETHPDGYQNLSLMVLAPSAFFLLGIMIWLVNIRDSKKRKR

>core/715/2/Org2_Gene19

MYFYKYVIIDTSGYYPFLACVDNQQVLEHWSLPVGPDLGIVLEFLFKSKNLSFQGVAAVALGPGNFSATRIGIS
FAQGLAMAKNVPLLGYSSLEGYLLSKDEKKALMLPLGKRGGVLTLSSEIPEEGLNEKRRGVGPGALLSYEEA
SDYCVAHGYYHVISPNPQLFASSFSDKITVEEVAPSVEQIRRHVISQFMFVEYDKQLSPDYRSYSCIF

>core/716/2/Org2_Gene378

MATSVAPSPVPPESSPLSHATEVLNLPNAYITQPHPIPAAPWETFRSKLSTKHTLCFALTLLLTLGGTISAGYAG
YTGNWIICGIGLGIIVLTLLALLLAIPLKNKQTGTKLIDEISQDISSIGSGFVQRYGLMFSTIKSVHLPETTTQNQ
EKTRILNEIEAKKESIQNLELKITECQNKLAQKQPKRKSSQKSFMRSIKHLSKNPVILFDC

>core/717/2/Org2_Gene490

MIFRICKFFTWVAFSLFYKLKVYGVKKNFIKGPAAIAVNHNSFLDPIALHMCVHECIYHLARASLFNIPWLWK
QWGCFPVRQDEGNSAAFKIASRLFNKRKKLVIYPEGARSPDGQLQPGKVGIGMMAAKSRVPIIPVYIRGTFEA
FNRHQKIPHVWKTITCVFGTPMYFDDIIQNPEIKNKETYQIITNQTMNKIAELKAWYESGCKGDVP

>core/718/2/Org2_Gene500

MIKSSLILLSGGQGTRFGSKIPKQYLPLNGTPLVLHSLKILSSLPQIAEVIVVCDPSYQETFQEYPVSFAIPGERR
QDSVFSGLQQVSYPWVIIHDGARPFYIPDEIHDLLETAEKIGATALASPIPYTIKQRNPVRTLDRDNLAIHTPQ
CIKTEILREGLALAKEKQLTLVDDIEAAEIIGKPSQLVFNKHPQIKISYPEDLTIAQALL

>core/719/2/Org2_Gene527

MMNYEDAKLRGQAVAILYQIGAIKFGKHILASGEETPLYVDMRLVISSPEVLQTVATLIWRLRPSFNSSLLCG
VPYTALTLATSISLKYNIPMVLRRKELQNVDPSDAIKVEGLFTPGQTCLVINDMVSSGKSIETAVALEENGLV
VREALVFLDRRKEACQPLGPQGIVSSVFTVPTLIKALIAYGKLSSGDLTLANKISEILEIES

>core/720/2/Org2_Gene647

MARYCGPKNRVARRRFGANIFGRSRNPLLKKPHPPGQHGMQRKKKSDYGLQLEEKQKLKACYGMIMEKQLV
KAFKEVIHKQGNVAQMFLERFECRLDNMVYRMGFAKTIFAAQQLVAHGHILVNGRRVDRRSFFLRPGMQIS
LKEKSKRLQSVKDALESKDESSLPSYISLDKTGFKGELLVSPEQDQIEAQLPLPINISVVCEFLSHRT

>core/721/2/Org2_Gene744

MKQFILRTLNALFPNPKPSLEGWSSPFQLLIAILLSGNSTDKAVNSVTPQLFAKAPDAQSILDLP PGKLYQLIAP
CGLGERKSAYIYQLSQILVRDFHGEPPNDMALLTQLPGVGRKTASVFLGIAYGKPTFPVDTHILRLAQRWKIS
EKKSPSAAEKDLARFFGHENTPKLHLQLIYYARQYCPALHHKIDNCPICSYLAKEANSTRT

>core/722/2/Org2_Gene67

MSVQVKLTKNFRLEKQKLARLQTYLPTLKLKKALLQAEVQNAVKDAAECDKDYVQAYERIYFAELFSIP
LCTDCVEKSFEIQSIDNDFENIAGVEVPIVREVTLPASYSLLGTPIWLDTMLSASKELVVKVMAEVSKERLK
ILEEELRAVSIRVNLFEKKLIPETTKILKKIAVFLSDRSITDVGVKMAKKKIELRKARGDECV

>core/723/2/Org2_Gene63

MANLNADGKLKQICDALRLDTLKPAAEDEAAALLHNAKEQAKRIIQEAQEEARKILETAEERAHQKIKQGEVALSQAGKRALEALKQAVENKIFRESLVEWLEHVTDDPEVSTKLIQALVQALEAQGVSGNLTAYIGKHVSPRAVNELLGKAVTTKLRRKKSUVVGSFVGGVQLKVEEKNWVLDLSSSALLEIFTRYLQKDFREMIFQGS

>core/724/2/Org2_Gene661

MTYLASSIFSPEDFLYPEIISKAHYTWDILDMDQMLENHVFSGIHGTVESGVTLKNIEKIEIAEDAYVESGAYIVGPCILGSQTEVRHGAAYLRGNVITGSRCSVVGHCTEIKNSYLGHHTKAAHFAYLGDSVLSSEVNLGAGVRCANFRLDGRNIYVRSTSDKSKKIDTGRRKLGAF LGKGVAIGCNVVINPGQHILPHTRIRPGQVI

>core/726/2/Org2_Gene37

MSFVPYSLPELPYDYDALEPVISSEIMILHHQKHHQIYINNNAALKRLDAAETQQNLNELIALEPALRFNGGGHINHSLFWETLAPIDQGGGQPPKHELLSLIERFWGTMDNFLKKLIEVAAGVQGS GWAWLGFCPAKQELVLQATANQDPLEPLTGKLPLLGV DVWEHAYYLQYKNVRMDYLKAFPQIINWGH IENRFSEIIS SK

>core/727/2/Org2_Gene538

MYDYIRGTLTYVHTGAIVIECQGIGYHIAITERWAIECIRALHQDFLVFTHVIFRETEHLLYGFHSREERE CFRLISFSGIGPKLALAILNALPLKVLCSVVRSEDIRALASVSGIGKKTAEKLMVELKQKLPDLLPLDSRVETSQTH TTSSCLEEGIQALAA LGYSKIAAERMIAEAIKDLPEGSSLT DILPIALKKNFSGVNKD

>core/728/2/Org2_Gene687

MKIVIAS SHGYKIRETKTFLKRLGDFDIFSLSDFPDYKLPQE QGDSITANALTKGIHAANHLGCWVIADDTMLRVPALNGLPGPLSANFAGVGAYDKDHRKKLLDLMSSLES LVDRSAYFECCVVLVSPNQEIFKTYGICEGYISHQEKGSSGFGYDPIFVKYDYKQTF AE SEDVKNQVSHRAKALQKLAPHLQSLFEKHLLTRD

>core/729/2/Org2_Gene843

MGLPNYITFSRLFITPIFMILYLKGKWFGITPVVLPYVLLALLAISELTD AIDGYVARKFSQVTDLGKLLDPMA DSIYRISIYLTFTQPPVNLPLLLVFIFLARDSVISTLRTVCAFRGRVVAARASGKLKAILQGV SFFLILLVMIPHSLGLLSQNGLEIFASVTVSIIAVYSIASGIEYFWMNKNFLSQR AKTKDSEKNHESKD

>core/730/2/Org2_Gene228

MFIVIEGGEGSGKSSLAKALGDQLVAQDRKVLLTREPGGCLIGERLRDLILEPPHLELSRCCELFLFLGSRAQH IQEVIIPALRDGYIVICERFHDSTIVYQGIAEGLGAD FVADLCSKVVGPTPFLPNFVLLLDIPADIGLQRKHRQKVFDKFEKKPLSYHNRIREGFLSLASADPSRYLVLDARES LASLIDKVMLHTQLGLCT

>core/731/2/Org2_Gene95

MNKILVDSPFSPDHQKCCPKLFTISAPAGVGKTTLVRMLEQE FSSAFAETISVTTRKPREGEVPGKDYHFVSHEEFQRL LDRQALLEWVFLFGECYGTSMLEIERIWSLGKHAVAVIDIQGALFIRSRMP SVSIFIAPPSQEELERRLASRGSEEGSQRKERLEHSLIELAAANQFDYVIINDDLNQAYRVLKSIFIAEEHRN IL

>core/732/2/Org2_Gene692

MHAKLSFFILLSLLFSGIDCSRLHAAGRSPSLQGVLAIEIDISAKLASHEVEIVMLSERLDEQDSKCQKWTAAK
PETLAQKIRELESDQKALAKTLAVLTTSVKDLQTNLQSKLQEIQKDHRAAQLRLVRRSLLALVDSSSPGA
YADFSDPVPENIYIVREGDSLAKKYKLSVTELKKINKLSDAIYAGQRLCLQRNKQ

>core/733/2/Org2_Gene328

MIGAQQKQSGKKTASRAVRKPAKKVAAKRTVKKATVRKTAVKKPAVRKTAAKKTVAKKTTAKRTVRKTV
AKKPAVKKVAAKRVVKKTVAKKTTAKRAVRKTVAKKPVARKTTVAKGSPKAAACALACHKNHKHTSSC
KRVCSSTATRKHGSKSRVRTAHGWRHQLIKMMSR

>core/734/2/Org2_Gene247

MTSPIPFQSSGDASFLAEQPQQLPSTSESQLVTQLLTMMKHTQALSETVLQQQRDRLPTASIILQVGGAPTGG
AGAPFQPGPADDHHHPPIPPVPAQIETEITTIRSELQLMRSTLQQSTKGARTGVLVVTAILMTISLLAIIIIILAV
LGFTGVLPQVALLMQGETNLIWAMVSGSIICFIALIGTLGLILTNKNTPLPAS

>core/735/2/Org2_Gene752

MTLVPYVVEDTGRGERAMDIYSRLLKDRIVMIGQEITEPLANTVIAQLLFLMSEDPKKDIQIFINSPGGYITAG
LAIYDTIRFLGCDVNTYCIGQAASMGALLLSAGTKGKRHALPHSRMMIHQPSGGIIGTSADIQLQAAEILTLKK
HLANILSECTGQPVEKIIEDSERDFFMGAEAAISYGLIDKVVTSAKETNKDTSST

>core/736/2/Org2_Gene530

MLKLLKVSITGDLSSGKTEACQVFQELGAYVVSADIEISHSFLIPHTRIGRRVIDLLGSDVVVDGAFDAQAIAA
KVFYNSVLLQGLEAILHPEVCRIIEEQYHQSIQDGNYPFVAEVPLLYEIHAKWFDSVILVMANEDIRRERFM
KKTGRSSEDFDQRCRSLNVEEKLAQADVVENNGTKKELHQKIEEYFYALKGAL

>core/737/2/Org2_Gene899

MLILLNLSLLFYVLFDSPGSIPVFVALLKNFSRKKQQRVILRECLFALGALILFVTFGRSFFQFLDISLYAFQIIG
GFLFLTYSIKMMLAPMPEKAKDDTSKTEPIFFPLAFPVITGPAVITALLSYMEEGIYSREIIFTAMIIAWAFSLFT
LLCSSFFDRLFGNFGLLALERLFGIALLLMSVNLMLKGISIAFNIGFYIG

>core/738/2/Org2_Gene454

MFSGIIQELGEVCFFEAQGNGLSLGIKSTPLFVTPLVTGDSVAVDGVCLTLTSCNESKIFFDVIPETLACTTLGE
KRCSDQVNLEAALKMGDSIGGHLLSGHVFGTAEIFLIKENRYYFRGSKELSQYLFEEKGFIAIDGISLTLVSVDS
DTFSVGLIPETLQRTTLGKKREGERVNIEIDMSTKIQVDTVKRILASSGKD

>core/739/2/Org2_Gene877

MFAYRTLTHNVVQVSHEIFKTTVVPGDTVIDATCGNGNDSLFLARLLQGEGRLVVYDIQKEALSNAALLFE
THLSEQERSVIEMKEQSHEHILEKDVKLIHYNLGYLPKGNKEITTLARTTEISLEYALNIVRPDGLITVVCYPGH
PEGEKETHSVESLAQRLHPKEWCVSSFYVANRCRAPRLFIFQRQGSSESVDKG

>core/740/2/Org2_Gene254

MTRYPDYLSKLIFFLRKLPGIGFKTAEKLAFELISWDSEQLKILGNAFHNVASERSHCPLCFTLKESEADCHF
CREERDNQSLCIVASPKDVFFLERSKVFKGRYHVLGSSLSPITGKHIENERLSILKSRIETLCPKEIILAI DATLEG
DATAFLKQELQHFSVNISRLALGLPIGLSFDYVDSGTLARAFSGRHSY

>core/741/2/Org2_Gene511

MGFACRYLFFFIVLFASGSFGNQLLSVPCWLSEESFYTHRFDfsksypdmenmeiqaqrkkkrvefnltgefp
KLETlnyqgsfghlRAKCRGVYPVLYALNFSCSSCKMDMDFRGKWNRSSITISNQKESINLKLPKDVGIV
NTKTSLKGNVCPGSTFIKQGWGVWNKIYHNDLVGFSEVTLIFNVSSEGGTITFS

>core/742/2/Org2_Gene586

MRLFSLGTIYLFFSLALSSCCGYSILNSPYHLSSLGKSLLQERIFIPIKEDPHGQLCSALTYELSKRSFAISGRSS
CAGYTLKVELLNGIDKNIGFTYAPNKLGDKTHRHFIVSNEGRLSLSAKVQLINNDTQEVLDQCVAESVDFD
FEPDLGTANAHEFALGQFEMHSEAIKSARRILSIRLAETIAQQVYYDLF

>core/743/2/Org2_Gene134

MNWVPKTIDHVDPESEIDIRKVVSCYKLIKECQPEFRSLISELLGVIRCGLRLLKRSKYQE QARTVSD EDAPLF
CLTRSYYQDGYLTPLRAGPRDLINHYIHLRRRENPKHFFSPKHPCYYARLAFNESVCVYRELF DIERLTKMYV
EGDYSKEQEKNLQAILS FVKTLDEGKDFLIEHKD TD LIGRGFTDVFCT

>core/744/2/Org2_Gene842

MRIALSLLSLLMIFPIFGEESRPGSEDGNSNTQEIVGSQDTQVCLYHSYEQGLQASRIEGKPLVIVVLCNSGDD
GQACTIGLSETCEEVLSVLSGSIFSELANFVVLVPSGVNPLIYPPIEDPILAEIVKFKELFKDES FPTGLSIIVGV
TPEGPGDIIEVSPVSLTVEEEEETLPSEQTTEVESTSELQSEDPAIA

>core/745/2/Org2_Gene477

MSSNLHPVGGTGTGAAAPESVLNIVEEIAASGSV TAGLQAITSSPGMVNLLIGWAKTKFIQPIRESKLFQSRAC
QITLLVLGILLVVAGLACMFIFHSQLGANAFWLIIPAAIGLIKLLVTS LCFDEACTSEKLMVFQKWAGVLEDQL
DDGILNNSNKIFGHVKTEGNTSRATTPVLNDGRGTPVLSPLVSKIARV

>core/746/2/Org2_Gene12

MSLPLVLGSSSPRRKFILEKFRVPFTVIPS NFDESKVSYS GDPIAYTQELAAQKAYAVSELHSPDCIILTGD TIV
SYDGRIFTKPQDKADAIQMLKTLRNQTHDVVTSIAVLHKGKLLTGSETS QISLTMIPDHRIESYIDTVGTLNNC
GAYDVCHGGLILKKVHGCYVNVQGLPIQTLKYLLEELNIDLWDYSI

>core/747/2/Org2_Gene431

MLQEHFFLSEDVITLAQQLLGHKLITTHEGLITSGYIVETEAYRGPDDKACHAYNYRKTQRN RAMYLKGGSA
YLYRCYGMHLLNVVTGPEDIPHAVLIRAILPDQGKELMIQRRQWRDKPPHLLTNGPGKVCQALGISLENNR
QRLNTPALYISKEKISGTLTATARIGIDYAQEYRDVPWRFLSPEDSGKVLS

>core/748/2/Org2_Gene690

MTLSLVGKEAPDFVAQAVVNGETCTVSLKDYLGYVVLFFYPKDFTYVCPTELHAFQDALGEFHTRGAEVI
GCSVDDIATHQQWLATKKKQGGIEGITYPLLSDEDKVISRSYHVLKPEEELSFRGVFLIDKGGIIRHLVVNDLP
LGRSIEEELRTLDALIFFETNGLVCPANWHEGERAMAPNEEGLQNYFGTID

>core/749/2/Org2_Gene365

MFRRTGKGPFEDVQTLYEEETSSPSSYSPYSRSERPETPPSLFDNPKASEARPLNHNLT EESSLPQWSSTPRTES
LLPLEEPETTLGEGVTFKGE LAFERLLRIDGT FEGILVSKGKIIIGPKGVVKADIQLQEAIIEGVVEGNITVSGKV
ELRGGAIIKGD IQANTLCVDEGV RILGYLA IAGITDH SERERDL

>core/750/2/Org2_Gene918

MAYGTRYPTLAFHTGGIGESDDGMPPQPFETFCYDSALLQAKIENFNIVPYTSVLPKELFGNIVPVDTCVKSFK
HGAVLEVIMAGRGAALSDGTHAIATGIGICWGKDKN GELIGGWAAEYVEFFPTWINDEIAETHAKMWLKK S
LQHELDLRSIAKHSEFQFFHNYINIKQKFGFCLTALGFLNFENAEPAKVN

>core/751/2/Org2_Gene677

MKKWISILILSFLSLLSILPVLAITINHVKISQRWSDLNSQILTLKVIRDHEDQVIKH NARISKDRNNLSIESLNAS
CKQLRPLSKERERLNKLNSNSLLAQSKEVWERKRALEKSNHQLVWNCEQMHNDFAFVRLEQATEMDNEDI
ESLFSLFNPENPVAPLVFFTCWKMTKQTTP LGNEVWLTHAE AISRWI

>core/752/2/Org2_Gene693

MNIHSLWKLCTLLALLALPACSLSPNYGWEDSCNTCHHTRRKKPSSFGFVPLYTEEDFNPNFTFGEYDSKEEK
QYKSSQVAAFRNITFATDSYTIKGEENLAILTNLVHYMKKNPKATLYIEGHTDERGAASYNLALGARRANAI
KEHLRKQGISADRLSTISYGKEHPLNSGHNELAWQQNRRTEFKIHAR

>core/753/2/Org2_Gene366

MVLFSLLFPKLCYGCQAPGAYFCSNCLEKLLVEDREGRCLHCFRYLGSSETRLCSQCSPSSQLQAFSLYLPSQ
TALSVYARACEGKRPALQFFSKSIAFELASLDETPSCIA YITSTISRKIVVEVAKLEKLLRIPLWPWLPKKRQIE
KLPKGEGICFLSAYPLSQKWMQTIVGGSASPLVSISLFLSQNDQ

>core/754/2/Org2_Gene219

MKRYVVGISGASGVILAVKLIKELVNAKHQVEVIISPSGRKTLYYELGCQSFDALFSEENLEYIHTHSIQAI ESS
LASGSCPVEATIIIPCSMTTVAAISIGLADNLLRRVADV ALKERRPLILVPRETPLHTIHLNLLKLSKSGATIFPP
MPMWYFKPQSVEDLENALVGKILAYLNIPSDLTKQWSNPE

>core/755/2/Org2_Gene770

MKVIYYEIEEIPSTNTMAKSYMHLWDPYALTVISTKCQTAGTGKFGKSWKSSKGDLLNTFCFFITDLHIDVSR
LFRLGTEAVVALCKDLGITEAKIKWPNDVLVHGEKLCGVLPETLPVEGLLGVVVLGIGLNGNTTKQALKDVG
QPATSLQEILGHPIDLETTRELLIHLLGV LQENLPDSLATKSNRGN I

>core/757/2/Org2_Gene444

MADGEVHKL RDII EKELLEARRVFFSEPVTEKSASDAIKKLWYLELKDPGKPIVFVINSPPGGSVDAGFAVWDQ
IKMLTSPVTTVVVTGLAASMGSVLSLCAAPGRRFATPHSRIMIHQPSIGGPITGQATDLDIHAREILKTKARIIDV
YVEATNQPRDII EKAI DRDMWMTANEAKDFGLLDGILFSFNDL

>core/758/2/Org2_Gene47

MIKKFFIYSLIFSCSFSAPLKGICNEDVSSQSRIEEDPEVLITQLNELIETPIEEGKEIRNELQAISDGQKSSEEIEES
CGTSDSEGLSEKTDKESSNEYVLDFFD SMVQRLEGISKMCQSGQVAQIIDCFNREFDIRNRELELKNRELELRE
KDLEFKKSILDWNKEKVSRELA FQREQDIKQTLMLLKK

>core/759/2/Org2_Gene335

MSIKEDKWIREMALNADMIHPFVNGQVNVNEETGEKLISYGLSSYGYDLRLSREFKVFTNVYNSVVDPKCFT
EDIFISITDDVCIVPPNSFALARSVEYFRIPRNVLTMCIGKSTYARCGIIVNVTPFEPEWEGHVTIEISNTTPLPAK
IYANEGIAQVLFFESSTTCEVSYADRK GKYQKQQGITVPCV

>core/760/2/Org2_Gene795

MVRVSTSEFRVGLRIEIDGQPYLILQND FVKPGKGQAFNRIKVKNFLTGRVIERTYKSGESVETADIVERSMRL
LYTDQEGATFMDDETFEQEVVFW EKLENIRQWLLED TIYTLVL YNGDVVAVEPPIFMELSIAETAPGVRGDT
ASGRVLKPAVTNTGAKIMVPIFIDEGELVKVDTRTGSYESRVSK

>core/762/2/Org2_Gene988

MMKIPYARLEKGSLLVASPDINQGVFARSVILLCEHSLNGSFGLILNKTLGFEISDDIFTFEKVSNNHNRFCMGG
PLQANQMMLLHSCSEIPEQTLEICPSVYLGGDLPFLQEIASSESGPEINLCFGYSGWQAGQLEKEFLSNDWFLA
PGNKDYVFYSEPEDLWALVLKDLGGKYASLSTVPDNLLN

>core/763/2/Org2_Gene946

MIRLEYYGSPILRKKSSPIAEITDEIRNLVSDMCDTMEAHRGVGLAAPQVGKNVSLFVMCVDRETEDGELIF
SESPRVFINPVLSDPSETPIIGKEGCLSIPGLRGEVFRPQKITVTAMD LNKIFTEHLEGFTARIIMHETDHLNGV
LYIDLMEEPKDPKKFKASLEKIKRRYNTHLSKEELVS

>core/764/2/Org2_Gene880

MALNFKINRQIRAPKVRLIGSAGEQLGILAIKDALDLAREAGLDLVEVASNSEPPVCKIMDYGKYRYGLTKKE
KDSKKAQHQVRIKEVKLKPNI DENDFSTKLKQARTFVEKG NKVKITCMFRGRELAYPEHGFKVVQKMSQGL
EDIGFVEAEPKLAGRSLICVVAPGTVKTKKKQEKSHAQDENQ

>core/766/2/Org2_Gene524

MRILAGKYKGKSLKTFSNPHIRPTSGLVKEAFFSICREDIEGA AFLDLFAGMGAIGFEALS RGAASVVFVDISIK
AIQLIHTNSALLGEQLPVVIFRQDAQSAIQRLIKQKRSFDLIYIDPPYELCNCYVETLLQKIVSGNILNPEGTLFL
ENASDEEIIACEGLTLRRRRKLGKTYLAEYIVEKDP

>core/768/2/Org2_Gene845

MELVVTSRETGKKSFLKKIRQQGGIPAVVYSAGKSLANITVDALVFKKFLSNLESGALSSTVFSLSYEGRIIKA
LVKDIQYQITTYDVIHLDFEELVEDRPIKLNIPRCINAVDCIGVKLGGSLRQVIRAVRVVCKPKDIVPFLELDV
RSVGLSQTRKLSDIKIPAGIETITPLKEVAITVSRR

>core/770/2/Org2_Gene150

MVLSSQLSVGMFISTKDGLYKVTSVSKVAGPKGESFIKVALQAADSDVVIERNFKATQEVKEAQFETRITLEY
LYLEDESYLFLDLGNYEKLFIPOEIMKDNFLFLKAGVTVSAMVYDNNVFSVELPHFLELMVSKTDFPGDSL
SGGVKKALLETGIEVMVPPFVEIGDVIKIDTRTCEYIQRV

>core/771/2/Org2_Gene428

MTDTPPENEEQHESNVQNENEVEHLQQEIVTLKTELKEKNDKYLMAESENSRKRLQKERQELMQYALEN
TLIDFLNPIESMEKALGFATQMSDDVKNWALGFNMILNQFKQIFEEKGIIYSSIGQKFNPFLEAVQTEETSE
VPEGTILEEFAKGYKIGERPIRVAKVKVAKAPTPKENKE

>core/772/2/Org2_Gene712

MAAKTKTLELEDNVFLLLEGNLKRIFATPIGYTTFREFQNVVFNCAANGQQEIANFFFEMLINGKLTQELAPQQ
KQAAHSLIAEFMMPIRVAKDIHERGEFINFITSMDLTQQERCIFLNRLARVDGQEFLLMTDVQNTCHLIRHLL
ARLLEAQKNPVGEKNLQEIQEEITSLKNHFDDELTKALQ

>core/773/2/Org2_Gene495

MVETVLHNFQRYLSKYLYRVFRFPCRKKTFLLSSHRVLARPSFPVDYCPGKIYDLQEIYEELNAQLFQGALRLQ
IGWFGRKATRKGKSVVLGLFHENEQLIRIHRSLDRQEIPRFFMEYLVYHEMVHVSVPREYSLSGRSIFHGKKF
KEYEQRFPLYDRAVAWEKANAYLLRGYKKRVGGGYGRA

>core/775/2/Org2_Gene936

MNFAKIDHNHLYLTCLGDLGVACPILSTDCLPNYSEKASHEVLVYSKFRCSGEP SRLATSGNDTYYSIVSLPI
GLRYEVTSPSGRHDFNIDMHVAPKIGAVLSHGTREAKEIPGSSKDYAFFSLTARESLMISEKLAMTFQVSEVIQ
NCYSQCTKVTKTNLKEQYRHLSHNTGFELSVKSAF

>core/776/2/Org2_Gene551

MSRKAREPILLPQGVESIQDDKIIVKGPKGSLTQKSVKEVEITLKDNSIFVHAAPHVVDRPSCMQGLYWALIS
NMVQGVHLGFKEKRLEMIGVGFRASVQGAFLDLSIGVSHPTKIPISTLQVSVEKNTLISVKGLDKQLVGEFAA
SIRAKRPPEPYKGKGIRYENYVRRKAGKAAKTGKK

>core/777/2/Org2_Gene54

MYKWYVVQVFTAQEKVKKALEDFKESSGMTDFIQEIILPIENVMEVKKGEHKVVEKYIWPGYLLVKMHLT
DESWLYVKSTAGIVEFLGGGVPAVSEDEVRSILTDIEKKSGVVQKHQFEVGSRVKINDGVFVNFIGMVSEV
FHDKGRLSVMVSIFGRETRVDDLEFWQVEEVAPGQESE

>core/778/2/Org2_Gene509

MSLLNLPSSQDSASEDSTSQSQIFDPIRNRELVSTPEEKVRQRLLSFLMHKLNYPKKLIIIEKELKTLFPLLMRK
GTLIPKRRPDILIITPPTYTDAQGNTHNLGDPKPLLLIECKALAVNQNALKQLLSYNYSIGATCIAMAGKHSQV
SALFNPKTQTLDFFYPGLPEYSQLLNYFISLNL

>core/779/2/Org2_Gene362

MVEIFNYSTSIYEQHASNNRIVSDFRKEIQMEGISIRDVAKHAQILDMNPKPSALTSLLQTNQKSHWACFSPPN
NFKYQRFSTPYLAPSLGSPDQQDEIDIEKISSFLKVLTRGKFSYRSQITPFLSYKDKEEEEDPEEDDDDDPRVQ
QGKVLKALDLGVKSTNMIDYVISRIFQFVQG

>core/780/2/Org2_Gene182

MSKESIRSYSEISTPTPIFRETPSKEGVAYKLQLRSPAKDCILNRVSLKGALLRSIPFYGSFLGAKRIHSAWSA
KDAPCTTRVYHYLVGGLELLGLGVVVLACKVLATALKFLFSKASSKIKQMKWREKARNLAAKDTVQSIKEF
CSVDLTSCFTRCFRLNRVVEEGASENQTVREIIV

>core/781/2/Org2_Gene675

MTDPKIEKSALRKLFISIRRDLESEERKHEASSAVASFVRSFSKESVVLSFVSFNHEIDMQEANRILIQKCTLALP
KIDQENLYPVLIPSIDDLISVVHPKDPFSKQTPISSDKITHVLVPGLAFDQQGYRLGYGHGFYDRWLAQHPYPS
IRTIGIGYCEQKIDRLPQESHDIPLSQIYLC

>core/782/2/Org2_Gene553

MSRLKKFYTEEIRKSLFEKFGYANKMQIPVLKKIVLSMGLAEAAKDKNLFQAHLEELTMISGQKPLVTKARN
SIAGFKLREGQGIGAKVTLRGIRMYDFMDRFCNIVSPRIRDFRGFSNKGDGRGCYSVGLDDQQIFPEINLDRV
KRTQGLNITWVTTAQTDDDECTTLELMGLRFKKAQ

>core/784/2/Org2_Gene846

MAKLIVAIGNPRHGYANTRHNAGFLLADRLVEELQGPPFKPLSKCHALMTLVESSSGPLVFIKPTTFVNLSGK
AVVLAKKYFNVALSHILVLADDVNRSFGKLRLCFNGSGGHNGLKSITASLGSNEYWQLRFGVGRPLEEGV
ELSNFVLGKFSEENLQLGSIFVEASTLFTWCSKF

>core/785/2/Org2_Gene614

MSVLQDTEKKMAAALDFFHKEVKSFRGTGKAHPALVETVVVDVYGTTMRLSDIASISVADLRQLVISPYDGN
NASAIAKGIIAANLNLQPEVEGSIIRIKVPEPTADYRQEMIKQLRRKCEEAKINVRNIRREANDKLKKDSALTE
DVVKGNEKKIQELTDKFCKQLDELTKQKEAEIASI

>core/786/2/Org2_Gene763

MTTPQSPGSLSQSHLPHPHDPWDTEPTSLPEDPNDKASQELHSLVHLFRKLSIHLLSEVEKTVQQLKPDLELA
LLICEKFLYKKLENPQELALLLSTALQRHTTLRSLTPIKVFLHPEDLKTLDWISTHELPMIKHAEFFPDTSRR
SGFKIETPNGILRQEISEELDHLLSVLTA

>core/787/2/Org2_Gene482

MACEQHEGCELEEREIEIEDIKSDTKWVSITQAAKLHNVTQAIYVAIKQKKLKASKETRWEIDIKDLEEY
KRNRYSRKKSLYQGELVFDNGKGCYSINQVAQILGIPVQKVYYATRTGTIRGERKGAAWVIHVSEIERYKNE
YLSKQAAKKLKGAEPKEHQAPNFEPPTTEIFPESN

>core/789/2/Org2_Gene923

MTIILCGLPTSGKSSLGKALAKFLNLPFYDLDDLIVSNYSSALYSSSAEIKAYGDQKFSECEARILETLPPEDA
LISLGGGTLMYEASYRAIQTRGALVFLSVELPLIYERLEKRGLPERLKEAMKTKPLSEILTERIDRMKEIADYIF
PVDHVDHSSKSSLEQASQDLITLLKS

>core/790/2/Org2_Gene246

MSAPIPTPQELSDQITCLNVQYQQVSELARENKGDIEGLKTLTAALTADAGIQPSADEIYSLQTAAALILSASE
KPGSGPSGSTEGSVTVQSPCKFKKVLAVVLTHIALIAIAVLIACIIAACGGFPLLSALNLYTIGACVSLPIIASTS
VALICLCTFVANSLIKPVITVRTTR

>core/791/2/Org2_Gene469

MDRDNEVPLPKPKWIYRTGIGQDSHRFLPESSTKPCILGGIIFDHCPGFQANSDDIIFHAICNAISSVTNKIILG
KVADELLQTRGITDSGIYLEEALKSLKPNQKISHVAITIEGSRPKFLCKLSALRQNIQVMNLTPTDIGITATSG
EGLSDFGCGDGVQCFCVLTVMHEYCD

>core/793/2/Org2_Gene769

MGYVFYVIAGSIFLGISLGAYCQLYYSVKSVLFSWYLLTVYALEKRHALLALSQLVGEEDAQSQKEIDFLSQC
DKLSWRAFLKNSYEIIPTFKEMEDLLSERVQGFLIESIETIAEHDRAILCIENFWASKNLDFEIAAYEEAVEKYL
KLRQRAPRLASKLFRFLDVPSIRFSS

>core/794/2/Org2_Gene1002

MDCVDNLKLYIFRLKLPDTERISYSISPEYIREKGEEELLSPIEVEGSLGRIDSDQWILSLSLKTQLGLCCPVC
NNFFSHSVCLPDLQRVISHDEVGSGVFDCRPLIRQELLLESDFEECGQGCPCERKNILKFLEDRKKHEGNSPF
EYL

>core/795/2/Org2_Gene377

MSSTLNGVFPSSLPEESADLFITNKEIVALGEKGNVFLTHSIPMHIAAITILVIVALAGIAIICLGCYSQSILLIavg
IVLTILTLLCLQALVGFIKFIRQLPQQLHTTVQFIREKIRPESSLQLVTNAQRKTTQDTLKLyeelCDLSQKEFK
LQSTLYQKRFELSHKNEKTQN

>core/796/2/Org2_Gene894

MSIQPVSNTTTKADKVIPDSTKVISDSITINKQSAFYFCISVMLRLSESTTEYGKSILAVLEDNTIVQQQRVKELI
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>core/797/2/Org2_Gene895

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>core/798/2/Org2_Gene516

MADDTLIPKLMKNSLSQACSEGLLIAKYPPLQVIVHFDNNLVVKTHLSVAPVFSCLFLGPAAHKAMQEIVLW
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>core/799/2/Org2_Gene380

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>core/800/2/Org2_Gene908

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>core/802/2/Org2_Gene286

MSVHITPRKCFILCILSMFTLPTLFPKAHLILFSPIVLCFYCFSKDKGLVLALGCGVLSDLALGSRGVFLLLYP
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CAINSGIHKMISFFRRLVCY

>core/803/2/Org2_Gene615

MVHSPTHQCYHCQPATICYTEIDKDKVIRSYVCATCPCPSHYNNNEHLSLSKGVGVLTLECGNCKTVWHS
KQDDEQLLGCHQCYTNFKNQITSKLKSERVVSSSFTMEKGQGSLSHIGRAPGEASNTNPLLKLIALNEALQDTL
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>core/804/2/Org2_Gene496

MTAEKQNTGILGLEIRYTLPSDATYMLKWLNDPKILRGFPIQTEAEIRETVNFWVGFYRYHSSLTAVYNGNV
AGVATLVLNPYVKVSHHALISIIVGEEFRNKGIGTALLNNLIHLAKTRFKLEVLYLEVYEGNPALHLYQRFGF
VEVGRQNRFYKDEIGYLAKTTEMEKDL

>core/805/2/Org2_Gene256

MKKLLFSTFLLVLGSTSAAHANLGYVNLKRCLEESDLGKKETEELEAMKQQFVKNAEKIEEELTSIYNKLQD
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>core/806/2/Org2_Gene100

MSEVKPLFLKNDSFDLATQRFQNLINMLQEQAIEYNEYEEKNARVQNEIKEQKDFVKRCIEDFEARGLGVLK
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>core/807/2/Org2_Gene671

MCKNRGVRGIVACDPRGVIGLEGKLPWHYPEDLQFFSETIQKFPIVMGRKTTWETLPRKYFVDRAVVVFSHEK
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>core/808/2/Org2_Gene57

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>core/809/2/Org2_Gene70

MQRLGLSNLFHCLLLFLRYYYSKLVFGLTVLLAAISVICLLGCSEPSLSSFTEYVGPEYSAAAQLSIEQSCHDE
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>core/810/2/Org2_Gene849

MKQQLLLLEDVDGLGRSGDLITARPGYVRNYLIPKKKAVIAGAGTLRLQAKLKEQRLIQAAADKADSERIAQ
ALKDIVLEFQVRVDPDNNMYGSVTIADIIAEAAKKNIFLVRKNFPAHYAIKNLGKKNIPLKLKEEVTATLLV
EVTSDNEYVTVLAQGKQTEENQEG

>core/811/2/Org2_Gene232

MIINVRAPAFGITSVQQFSTNFQAAIPILNIVIGCSRISSTYAEDIEEVAQEKLEKSTHSKSSTSVNLWAHRVRGV
VEILGGGIVILALEITALVLQVIIKLIKCLIDVLCVCLFGLGVCVVAIIIGAIAFCVVVVVKYLGFCSQGEELEPIE
VKTLISPDKPYPTVVYV

>core/812/2/Org2_Gene539

MSELIIGVDPGTIVAGYAIIAVEQRYQLRPYSYGAIRLSSDMPLPMRYKTLFEQLSGVLDDTQPNAMVLETQF
VNKNPQSTMKLAMARGIVLLAAAQRDILIFEYAPNVAKKAVVGKGHASKRQVQVMVSKILNVPEVLHPSNE
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>core/813/2/Org2_Gene534

MRQFCNLLSLSRLWLALYFCQEKLHIRLLAIVGAMLSDVLDGYLARRYKATSRLGSILDPITDKVFVFCITV
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VALGFLYFLERIMDYKKQFLR

>core/814/2/Org2_Gene457

MATFRSTLLVITLFLVLDWVTKLVVLLQYKDLQILTHPTLYTHSWGRFSFSIAPVFNEGAAFGFLFSNYKYFLF
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LLLVIKFFYFPTKQTEKKR

>core/815/2/Org2_Gene621

MAKYPLEPVLAIKKDRVDRAEKVVKEKRRLLIEIEQEKLEKEAERDKVKNHYMQKIQQLRDLLDEGTTSDA
VLQIKSYIKVAVQLSEEEKVNKQKEVLAASKELEKAEVNLAKRRKEEEKTRLHKEEWMKEALKEEARA
EEKEQDEMGQLLFQLRQKKKRESGGS

>core/816/2/Org2_Gene297

MAVEQSHIKEEIEKLIGKAIKRVCNGNKENDLCRYLPGPSGGYMHFTLKKMKSAAPEQLLKMMLKTFILESETP
RTINPKPRAPRGSKKRRDFINFTKTDIERVLELARQVGDKDLLARFSPKKPLTSLKRELIRSIRNGIVSVELWNA
YVEAVKAVSSPNLEVTSPFV

>core/817/2/Org2_Gene149

MDLKQIEKLMIAMGRNGMKRFAIKREGLELELERDTRREGNRQEPVFYDSRLFSGFSQERPIPTDPKKDTIKET
TTENSETSTTTSSGDFISSPLVGTFYGGSPAPDSPSFVKPGDIVSEDTIVCIVEAMKVMNEVKAGMSGRVLEVLIT
NGDPVQFGSKLFRIAKDAS

>core/819/2/Org2_Gene215

MSKKINRNDLCPCGSNKKYKQCCLKKEEQTARYTTEGKFKFSAEVLSSASEQGEAGDNCTKLFQRLSQSLTSE
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DFIPTQEDFRISENSQKPPVEED

>core/820/2/Org2_Gene331

MSRQNAEENLKNFAKELKLPDVAFDQNNTCILFVDGEFSLHLTYEEHSDRLYVYAPLLDGLPDNTQRKLALY
EKLLEGSM LGGQMAGGGVGVATKEQLILMHCVLDMKYAETNLLKAFAQLFIETVVKWRTVCADICAGREP
SVDTMPQMPQGGGGMQPPPTGIRA

>core/821/2/Org2_Gene823

MKFWLQGCFAVVGCLLLTLPCAARRRASGENLQQTRPIAAANLQWESYAEALEHSKQDHPICLFFTGS DW
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ARMGFEPGGGAAYVSKVKSALKLR

>core/822/2/Org2_Gene473

MSRRHSAEKRDIPGDIYGSVILEKFINKVMMHGKKS VARKIVYSALERFGKKLNLE NVLEGFGEALENAKPI
LEVRSR RVGGATYQVPVEVASERRNCLAMQWIIKHARSKPGKSMEVGLATELIDCFNKQGATIKKREDTHR
MAEANKAFAHYKW

>core/823/2/Org2_Gene549

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AFKALTGLSPRKDLLRRGAIND

>core/826/2/Org2_Gene637

MTKFLYCGLFYSLGLLVLAFGTMVAIIQVDQICDVSCMNKHFQESPPFLKIKKVVNVSKQICSPEERFFHCKIDK
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SSSGGMKTLYLSLFRN

>core/827/2/Org2_Gene841

MMHRYFIPLLALLIFSPSLVRAELQPSNRKGGWPTQLSCAEGSQLFCKFEAAYNNAIEEGKPGILVFFSERPT
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AQCQAVLPLETKN

>core/828/2/Org2_Gene896

MSITTLGTLPTVNTINSSRPPEPLNTPKIGAVLFSIYELLLQAIEIRQQTVLTQSQQNLNDNTNIQQQLNQETNQI
KYAIVSAGAKEDEITRVQNQNQNYSAQRSNIQDELVTTRQNGQIILSHASTNINIIQQSSQDSSFIKTTNSIGST
VNQLNKPLG

>core/829/2/Org2_Gene351

MTTWTLNQNNLTFLKSSDEEPFLERESGLTYINIQANGNELPLFFVIRSEGEILQLICYLPYQLHESHKASTAR
LLHLLNRDIDIPGFGMDDEEQGLIFYRLVLPCLNGEIHDTLLRIYIDTIKLVCDSSHAIGLISSGNMNLDELRRQ
ALQEQQEKRNE

>core/831/2/Org2_Gene879

MATLSPEKFSGSPISISKEFPQQKMREIILQMLYALDMAPSAEDSLVLLMSQTAVSQKHVLVALNQTKSILEK
SQELDLIIGNALKNKSFDSLDELVEKNVLRRLTFEHFYSPINKAILIAEAIRLVKKFSYSEACPFQAILNDIFTDS
SLNENSLSI

>core/832/2/Org2_Gene330

MMFGHFAGYLGADPEERMTSKGKRVITLRLGVKTRVGMKDETVWCKCNIWHNRYDKMLPYLKKGSGVIV
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MYAGYGQEQQYVCEDEVFP

>core/834/2/Org2_Gene180

MSKKVVFESYEDFANVASSWPKSLRALVQGRYFVDSELKETPYRIHDFKKTPIHHRLYRSLPIISTIGGIIRLIEA
HSGPIHPRDKMKYRFEVLQAVIEILGLGVLLVFDIIGCFLAFLVAIILSLLLYCNSTFTCVQNLSFTERMLEGIG
EAVNFLA

>core/835/2/Org2_Gene350

MFFNLFSLVFKLSDELALAETIQEPISVHEMFPGSMKLEMFKMLGSLILLTTIFGFGVWAFKKFVRSRSHGFGG
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KQQTNQD

>core/837/2/Org2_Gene40

MPSYCQNQQDFSLFSLSPRLVMFLGKHSRDEILQDLTDLVDAAGLLEDKQAFFDALVRRENIMSTGIGMGV
AIPHGKLESCSNFFIAIGIHTQGILWDAIDGALVRLVFLIGGPENAEYLKLLSTLTLREESRRQQLQVNT
IEEVMNVFVGM

>core/838/2/Org2_Gene730

MADETPKENSSKESSSQFDSLKRKVKDLHSNPKVGKWKFLSHRACEAIGGCLVLVGIIADFISWAGGLFIAC
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QDTSNKPS

>core/839/2/Org2_Gene434

MTQEKIKIHVSNEQTCIPIHLVSVEKLVLTLLEHLKVTTNEIFIYFLEDKALAEHDKVFADPSLTDITLPIADP
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RKKHALLTA

>core/841/2/Org2_Gene835

MLPISILLFYVILGCLSAYIADKKKRNVIWFFAGAFFGFIGLVVLLLLPSRRNALEKPQNDPFDNSDLFDDLK
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VPSLQQALKEASK

>core/842/2/Org2_Gene283

MRIIRFDYPYGALSAQSIKDSRQNSPLVEKISEEIATNEAIRLALLAIGDREQUEKKQRHRYKLLGQKQAKVLL
SQLRHVHLDFFKKLYCDSKKKEDQEKDEKNKQKRSIKVTKKKKGISLGAAASQAIAAAAEAWVIARNKGVLE
TASTLFYQKDEEA

>core/843/2/Org2_Gene836

MEKQNLKLDVKEIEFPETVFSRDIETRVIQVIILHCLAKINGVSLGGLNLIDALFGRDIERMKGIVVEQDSKNHL
VKVRVEVNVDYGVSIPEKTEEIQGCIVSEISEYTGLHVAAVHVIIKGLTQPKDRIDEEIEEEVSVQDLSPEDFL
LENSEG

>core/844/2/Org2_Gene141

MIMTTISNSPSPALNPESLIPPTLVSSGTQTSLAYTIPAQGRRSTLRIILDIFIILGLATIISTFIVIFFLNGLNLLS
TPSISSSCLIIIVGLLFLIMGLYFMISSLDQGLVGLLQKELSQAEEEREEYIQEIEALRGAPRAESPSTWL

>core/845/2/Org2_Gene577

MRVV LHCPDIPQNTGNIGRTCVALGAELILVRPLGFSLADKFVKRAGMDYWDKLQLTVVDSIEEALHDVPED
QIFCLSTKGSASYTEFSLPSSGTYVFGSESKGLPKEILKKYYKNCLRIPMQQDIRSLNLATSVGIVLYEVVRQKT
VALQKNPTV

>core/846/2/Org2_Gene891

MEKDIFFMQQAFKEARKAYDQDEVPGCVIVKDDKIIARAHNSVEKLKDATAHAEILCIGSAAQDLDNWRL
LDTVLYCTLEPCLMCAGAIQLARIPRIVWAAPDVRLGAGGSWNIFTEHPFHTVSCCTGGVCSEEAHLMKK
FFVEKRREKSEK

>core/847/2/Org2_Gene310

MGYLPVSATDVLFESPAAPLINSANTQNQKLIELKGKQQAESSPRTITSVILEVLLVIGCCLIVLSLLAIRPALQF
TLETGHPAAIAVLAVSGTILLVAVIILFCFLAAVPFAAKKTYKYVKTVDYASWHS HQQTPTLTGTIFSGIVYAE
SQAQL

>core/848/2/Org2_Gene572

MLKKKPVSFSCIDGHIYKIFPNDLNANNTVFGGLMSLLDRLALVVAERHTESVCVTAFVDALRFYAPAYMG
ENLICKAAVNRTWRTSLEVGVK VWAENIYKQERRHITSAYFTFVAVNEDNQPIPVHQIVPETPEEKRRYNEA
DRRRQARLELK

>core/849/2/Org2_Gene776

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DAIVACGVLIQGETDHYNQIVNQVAAGIGALSLEFCLPITLSIVAAPSAEIAWQRSGIKGRHLGVSGMTTAIEM
ATLFTQI

>core/850/2/Org2_Gene742

MPFAKETEMQRTCWKCEGSVSMHVPQCPYCSAFLQDPPVASGGFSSCHISFPEGASKEEAEDLFAVSSSEDWE
AVLGDQNPTQETNKQVIPEWTWLQSWPLAALFLGIGLLAFAFLILLFSTDSGLVLTWPKNRAYFYGIIGAAVA
YRGYRKLPL

>core/851/2/Org2_Gene35

MRSALHLQHLRHFHNHGSILFENLLTIKDCFLLETKLQNFIKASKTIDTVRWRENIFRSMPEIYTVVRKRRLD
FFAAELVHRPKLSLVRDLWVFPGEEILEGEEDCMLFLLLSGDRAGSGIFFTGYPYPSDLYELEKGTTGLLLAFSS
VGIPVI

>core/852/2/Org2_Gene569

MNQPSVIKLRELLDLLPHRYPFLLVDKVL SYDIEARSITAQKNVTINEPFFMGHFPNAPIMPGVLILEALAQAA
GVLIGLVLENDNRNKRIALFLGIQKAKFRQAVRPGDVLTLQADFSLISSKGGKAWAQARVDSQLVTEAELSFA
LVDKESI

>core/853/2/Org2_Gene455

MQCPFCNHGELKVIDSRNAPEANAIKRRRECLKCSQRFTTFETVELTLQVLKRDGRYENFQESKLIHGLNAAS
SHTRIGQDQVHAIASNVKSELLGKQNREISTKEIGELVMKYLKKADMIAYIRFACVYRRFKDVGELMEVLLS
ATPDMEK

>core/854/2/Org2_Gene289

MAQKEIVSNRKALRNYEVIETLEAGIVLTGTEIKSLRDHGGNLGDAYVIVSKGEGWLLNASIAPYRFGNIYNH
EERRKRKLLLHRYELRKLEGKIAQKGMTLIPLGMFLSRGYVKVRLGCCRGKKAYDKRRTIIEREKEREVAAA
MKRRHH

>core/855/2/Org2_Gene266

MARNIKYFLILFPGILWISAGMKLLLKATAIALDPLSSFFTYCLLSMVSWGLASLKHRYLLSKTIRKQLSLSSEF
FSQKITWIAYIKQTFISRRFLIMVIMIAFSLVLRRYISNPQALFVIRATVGYALIKTAIAYFSKLQNALMENPEGN

>core/856/2/Org2_Gene198

MSKPSSCKAYLGIDYGKKRIGLAYAAEPLLLTLPIGNIEAGKNLKLSSAEALHKIILSRNITCVVLGNPLPMQKG
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LTL

>core/857/2/Org2_Gene814

MMKTKYEYSFGVPIKFFGTPDKNTLKACFICHTRGKHWGFPKGHSEDKEGPQEAERELVEETGLSVVNFF
PKVLIEQYSFNNEEQVFVRKEVTYFLAEVRGDIHADPMEICDSQWLSLQEGLRLLSFPELRDLTVEADKFINN
YLFSS

>core/858/2/Org2_Gene780

MQLLSPAFAYGAPIPKKYTCQGAGISPPLTFVDVPGAAQSLALIVEDPDVPKEIRSDGLWIHWIVYNLSTTITN
LAEGAEIFAVQGLNTSGKPVYEGPCPPDKQHRYFFTLFALDVVLPEEENVTRDQLYEAMEFHIEQAELMGTY
EKS

>core/859/2/Org2_Gene207

MEKRKDTKTIVKSSETTKSWYVVDAAGKTLGRLSSEVAKILRGKHKVTTYTPHVAMGDGVIVINAEKVRLT
GAKKGQKIYRYTGYISGMREIPFENMMARKPNYIIEHAIKGMMPRTRLGKKQLKSLRIVKGDSYETFESQK
PILLDI

>core/860/2/Org2_Gene49

MEFICPLQHARCLKKQHKIIEELFPEPFQKDHLYLKLMENSSSRDAFDKKRMLKENLVVGCQSDLYLYEVYQ
DGILFFFTYTKALMSSGIASLFTEVYSGETPSTILTCKPIFFQRLTPYLSFGRLNGGESLYMRMKQIAVQYLKPP
QT

>core/861/2/Org2_Gene624

MADLEVFQADFULLFEAGLLAIKQGDEDSARKLFQSLHILNPNHYGHDLGLALISLHKMDLFD AEERLSALIK
GNEDNWSIKAFLSLTHMLIVLHQGSSFEVRRESLESCLKFADQVIANCKIESTRALAQSVLDWHDTLVAKSA
GPLG

>core/863/2/Org2_Gene323

MKSERLKKLESELHDLTQWMQLGLVPKKEISRHQEEIRILEHKKIYEEKERLQLLKENGEEIEEYVTPRRSPAKTV
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W

>core/864/2/Org2_Gene320

MKTKMNSRKKAGQWAFNSPTPGVSSTLVLAWTPWGYDVKDVQDILERKDPMSSSLSEKDSKEFLKNLFVD
LLENGFTSVHIIHAEAEFTPLDHTGKPHFKRDNVYLP GKLLGALNEAAVQANVSADTQFTLFLTQDECNPFHD
KKRG

>core/865/2/Org2_Gene972

MGSRRKLKRSFLLIEVLMAISLVCAVLLPCIRFYIAIHRSFEEIDIFNLQLPALIDHCFLSVEEKMRQQMAEGTV
LTSGKGQTVSLAYTSQGIGYRIPYGYNVDIRQEVRGDNLKMKVCLADVVELFPDQKQAVSVQRCLCVTL

>core/866/2/Org2_Gene159

MKKKVTIDEALKEILRLEGAATQEELCAKLLAQGFATTQSSVSRWLRKIQAVKVAGERGARYSLPSSTEKTT
TRHLVLSIRHNASLIVIRTVPGSASWIAALLDQGLKDEILGTLAGDDTIFVTPIDEGRLPLLMVSIANLLQVFLD

>core/867/2/Org2_Gene278

MQNQYEQLLES LAPLLNTTLAPDKNNSCLIRFS DTHVPVQIEEDGNSGDLAVSTLLGTLPENVFRERIFKAALS
VNGSFQSSIKGILGYGEVTQQLYLS DILSMNYLNGEKLFEYLKLFSLHAKIWMESLRTGNLPDLHVLGIYYVA

>core/868/2/Org2_Gene805

MEEFVAYIVKNLVTNPEAVEIRSIEDEDNESIKLEIRVAAEDIGKII GRRGNTIHALRRTILRRVCSRLKKKVQIDL
VQPENGTDVIADQDYICDNDSSNSTEDTFGESDTCCSGHCHYDEDLNQEEQEEGNMHHSCECSNHH

>core/869/2/Org2_Gene112

MSLEKELLEETPLVLLNFYKLVSFCNYAGMILGTEKKFAIYGHVSMGQAFQGADTEGHSPQRPF AHDLLNF
VFSGFDIQVLRVVINDYKDNVIFYTRLFLEQKDREFLYVVDVDARPSDSIPLALTHKIPILCVKSVFD AVVPYEE

>core/870/2/Org2_Gene178

MNPVTFDRIQVDFIPEDTS LRINSYIVAGGLLILGVVLSILSVICLDIGLVGLSAGAAFTLGLGCLIFALFLFSFSL
ILLLSQEKRVDPVLSLYLEKEVPQYETPLYKEDLESERDMSAISERLGIIEEKLRIAEKFRYSDSVFV

>core/871/2/Org2_Gene39

MTVFCELD SGGELPEYTTPGAAGADLRANIEEPIALLPGQRALIPTGIKAEIPEGYELQVRPRSGLALKHGITVL
NSPGTIDSDYRGEIRVILINFGDSTFIIEPKMRIAQVVLSPVVQATFVVKQESLAETARGSGGFGHTGAS

>core/872/2/Org2_Gene587

MTFFEGETVFPVAVLSELHSMMLDLIKRAGKQSKCPQEKLLKLELACEELLVNIISYAYQGENSPGTIAISCISHRG
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>core/873/2/Org2_Gene537

MEQTLIIKPDSVSKAHIGEILSIFEQSGLRIAAMKMMHLSQTEAEGFYFVHRERPFFQELVDFMVS GPVVVLV
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>core/874/2/Org2_Gene548

MIKLESLFDISERKRRRKLLGRGPSSGHGKTSGRGHKGDGSRSGYKRRFGYEGGGVPLYRRVPTRGF SHKRF
DKCVEEITTGRLAELFQEGEAITLDALKAKKAIARQAVRVKILKGDLEKTFVWQDTAVVLSQGVQNLLGIT

>core/875/2/Org2_Gene203

MACSIFFRMSQGDYDDEPLSKKTACLVDTMLYPVIAVVCVVSVVLLILKVLFLLLSFPFKLCSASSALPGE
RVSLGSHFKCLYGGGLPYLLACLLIVPVIGTAIHGFIISHRTSEDARLSSAIVFMQAPILQLAGMSGLIKP

>core/876/2/Org2_Gene948

MQEHIHKELLHLGEIFRSSRESQSLSLKDVEAATSIRYSCLEAIEQGCLGKLISPVYAQGFIKKYATYLG LDGD
SILQEHPYVMKIFKEFSDHNMEMLLDLESMGGRNSPERAIHSWSNLWWAGLIIIGGIMVWWLGSLFSIF

>core/877/2/Org2_Gene588

MSLDFFEEFYHQ SILNTGTSFPEGYLNIAEILSYPHCTDANTDFLCSQSDNDFIIAESKDKLTLFNADFAIWLVP
ELVQQQAVTRGYIAVSQGEGNYEPEMAFEASGQYNQSSLILEALQLYLKDIKDTENALRSFRFNNDH

>core/878/2/Org2_Gene543

MQHARKKKFRVGRTSSHNRCLANMLKSLIHYERIETTL PKAKELRRHADKMITLAKKNSLAARRIAIGRLM
VRYNKLT SKEARQAKGGDTSVYNVDRLVVKLFDDELGNRFVERKGGYTRILKLQNRIGDNAQKCIIEFLAS

>core/879/2/Org2_Gene656

MNSKSAQKIIDS IKQILTIYNIDFDPSFGSSLSSDSDADYEYLITKTQEKIQELDKRAQEILTQTGMSKEQMEVF
ANNPDNFSPEEWLALEKVRSSCDEYRKETENLINEITLDLHPTKESKRPKQKLSSTKKNKKKNWIPL

>core/880/2/Org2_Gene363

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>core/881/2/Org2_Gene574

MGRYRRVSHSSQETLLLGT ELGQVLVPGAVLLLFGDYGAGKTEFVRGIVSGYLGDTIAEEVASPSFSILHVYG
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>core/882/2/Org2_Gene55

MSVKKVKKIIKLQIPGGKANPAPPIGPALGAAGVNIMGFCKEFNAATQDKPGDLLPVVITVYADKTFTFITKQP
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>core/883/2/Org2_Gene69

MIDMSVVGPALVLGLAMIGSAIGCGMAGVASHAVMSRIDEHGKLGMSAMPSSQSIYGFILMLLMQAAIKN
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>core/885/2/Org2_Gene831

MHPLTLPKQSRVLKRKQFLYITRSGFCCRGSQATFYVVP SRHPGTCRMGITVSKKFGKAHERNSFKRVVREV
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>core/886/2/Org2_Gene558

MLMPKRTKFRKQQKGQFAGLSKGATFVDFGEYAMQTLERGWVTSRQIEACRVAINRYLKRRGKVWIRIFPD
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>core/887/2/Org2_Gene249

MNLIDRAFLKKTIIFQSLDMDLLLTIADKTETIIFKPGSNVFSIGQPGFSFYIIVEGYITISKEKLESPLNLKPLDC
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>core/888/2/Org2_Gene183

MVNRYKSSAEFSADHYYDDNLVRMGYKRNLRGLAPVENEVCLFEENNLLSVMASIPIMGSILGLGRLHSV
WSTQDPKDSKISIFHTALGILETLGLGHIIVLLIKITITILLILFTPCLLCYFMYSAAYSDFHPI

>core/889/2/Org2_Gene189

MINFIRSYALYFAWAISCAGTLISIFYSYILNVEPCILCYYQRICLFPLTVILGISAYREDSSIKLYILPQAVLGLGI
SIYQVFLQEIPGMQLDICGRVSCSTKIFLSYVTIPMASVVAFGAIVCLLVLTCKYRG

>core/890/2/Org2_Gene696

MKYRFTEEIEEEPLVNLTPIDIVFVILMAFIVAVPLIKLDSIALAPGTQEQLSSENDSIAVIKVFADHSLTLN
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>core/891/2/Org2_Gene206

MAKSTIQESVATGRRKQAVSSVRLRPGSGKIDVNGKSFEDYFPLEIQRTTILSPLKKITEDQSQYDLIIRVSGGG
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>core/892/2/Org2_Gene669

MIAIERYQLISKFRMWLFLGCSVEERHFKQPVLSVTF SYNEVPSACLSDKLSDACCYLEVTSLIEEIAN TKPY
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>core/893/2/Org2_Gene188

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>core/894/2/Org2_Gene552

MGMTSDSIADLLTRIRNALMAEHLVVDVEHSMREAIKILKHKGFVAHYLVKEENRKRAMRVFLQYSDD
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>core/895/2/Org2_Gene545

MVKNQAQAKKSVKRKQLKNIPSGVVHVKATFNNTIVSITDPAGNVISWASAGKVGYSGRKSSAFAATVAA
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>core/896/2/Org2_Gene811

MNFVSTLTGSDFYAPVLEKLEEFADTTGQVILFSSSPDFIVHPIAQQLGISSWYASCYRDQSAEQTIYKKCLT
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>core/898/2/Org2_Gene223

MSQCQSSSTSTWEWMKSFVPNWKNPTPPLSPIPSEDEFILAYEPFVLPKTDPENANPPGTSTPNVENGIDDL
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>core/899/2/Org2_Gene628

MLEKLIKNFATYMGITSTLELDADGAYVLPISVVKVRAQQNADNEIVLSASLGALPPSADTAKLYLQMMIG
NLFGRETGGSAALGLDSEGNVVMVRRFSGDTTYDDFVRHVESFMNFSETWLSDLGLGKQ

>core/900/2/Org2_Gene344

MRDHAFSKLIGTVRAMVVEGRCPWSLQQSLVSMVEHILGECQEFHEAVLQGKTVQEVGSEAGDVLTLVLIL
CFLLEREGVLASEDVANEAMEKLRRRAPYIFAEDYKPVSIIEADRLWELAKHREKNEST

>core/901/2/Org2_Gene978

MDYKSQLVFSCPCCCKGNVCFSVFNLDVILTCNVCSSTYTFDSVIRNEIRQFVALCKRIHDANSILGNATVSVS
VEDNQMDIPFQLLFSRFPVVLNLSLDGKKIAIRFLFDALNTSILHQESDLIS

>core/902/2/Org2_Gene392

MREEGSVSFREYFRAYMCDKIVAQKNFLFTLDAVIKQAGWRSQEKLNLFFYVESQALGREIKVSLEEYIQSMV
GILGSQRTKKSFKFSVDFTPLEQALQERCSSDDDEDATATSTATGATASPTDMHEDE

>core/903/2/Org2_Gene58

MTTESLETLVEKLSNLTVLELSQLKKLLEEKWDVTASAPVVAVAAGGGGEAPVAAEPTEFAVTLEDVPADK
KIGVLKVVREVTGLALKEAKEMTEGLPKTVKEKTSKSDAEDTVKKLQDAGAKASFKGL

>core/904/2/Org2_Gene691

MKFTVALFGAEKGSYDTAYFCRSLVDLHNYLGDVSSPGITLAIKTLLSDYNVVYFRVREEGYCVDSYFFGL
HFLNTQTTLKNIIAIGLPGVGNQHIIIEASRSLCQKHNSLLLFFDHDLYDLLTFNQPF

>core/905/2/Org2_Gene132

MRAGGSLVTTPKEGQRLRSPEQLRVLDDLVSQSYPNHLHAIELDCGAIPQDLIGATYIITFADFSTYILSLRSY
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>core/906/2/Org2_Gene185

MLIGRYSSDDQFTEATKNTPTIIKLGfVRDNLEGLTNPISIVSETSSSIKDSVLRSLPILGSILGCARLYSTLSTN
DPLDETQEKIWHTIFGALETGLGLILLFKIIFVILHCIFHLVIGFCK

>core/908/2/Org2_Gene456

MPLSDDEIEQFKKRLLMKAKLSHTLEGNAQEVKKPNEATGYSQHQAQGTDTFDRITISLEVTTKEYELLRQ
INRALEKINESSYGICDVS GEEIPLARLIAIPYATMTVKAQE QFEKGLLSGN

>core/909/2/Org2_Gene550

MESSLCKKSLMKRRRALRVKVLKGSPTKPRLSVVKTNKHIYVQLIDDSIGKTLASVSTLSKLNKSQGLTKK
NQEVAKVLGTQIAELGKNLQLDRVVFDRGPFKYHGIVSMVADGAREGGLQF

>core/910/2/Org2_Gene474

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NLQEHSIVLIQGGRVKDLPGVRYHIVRGTLDCAAVKNRKQSR SRYGAKRPK

>core/911/2/Org2_Gene787

MALKDTAKMKDLLDSIQHDLAKAEKGNKAAAQVRVTD SIKLEKVAKLYRKESIKA EKSGLLKRKPSTKAP
AKVKKTA EK KAPKSSAAA KTSKAVKASKPASKKTA AKKVKKPSKARGFRK

>core/912/2/Org2_Gene727

MKRQKRKQSITLIEMMVVITLIGIIGGALAFNM RGSIHKGKVFQSEQNCAKVYDILMMEYATGGSSLKEIIAH
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>core/913/2/Org2_Gene761

MRDRLGSLSLILKV KIHKYLDTLHNQKRLALTVSRNIQATNKRIADLHLERYEHFISRDNIKHYDILLE YLKT
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>core/914/2/Org2_Gene546

MPRIIGIDIPAKKKL KISLTYIYGIGSARSDEI KKLKDPEARASEL TEEVGR LNSLLQSEYTV EGD LRRRVQS
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>core/915/2/Org2_Gene555

MIQQESQLKVADNTGAKKVKCFKVLGGSRRRYATVGDVIVCSVRDVEPNSSIKKGDVIKAVIVRTRRHITRK
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>core/917/2/Org2_Gene267

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>core/918/2/Org2_Gene93

MVNLLKELEQEQCRNDLPEFHVGDTIRLATKISEGGKERVQVFQGTVMARRGGGSGETVSLHRVAYGEGME
KSFLNNSPRIVSIEIVKRGKVARARLYYLRGKTGKAAKVKEFVGPRSSKK

>core/919/2/Org2_Gene882

MVRATGSVASRRRRKRILKQAKGFWGDRKGHIRQSRSSVMRAMAFNYMHRKDRKGDFRSLWIARLNVASR
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>core/920/2/Org2_Gene184

MRELNAFELTQPEEYRNRWVLMPCCLKRFCRTQHAKVWSYRCVHEASLYEKNCFLLTYDDKHLPQYGSL
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>core/921/2/Org2_Gene262

MATVAQTPQTTQPQPSVSHKATHRYCSWVFFKPILVSLGLLLASLTTLGLVIASGVTLISLGIGIVLAIQIVLAGI
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>core/922/2/Org2_Gene272

MTENRRIKRVNALLQEAIKVLKDVKHPKISNLWITVTRVSLSKDLHSARVYVSVMPHENTKEEAEALVKV
SAGFIAHRASKNVVLKYFPELHFYLLDDIFSPQDYIENLLWQIQEKEKS

>core/923/2/Org2_Gene719

MNKKPKKTKKAVQSKAAPVKRVPEESQEAAIQQLELAVSDLYKELPLAQTFASLTDKNQINSIIAALSGTLES
LHLEELTQGLFPSAQEDANFAKELSSVVHGLKNLTTVVNKQMVKGAE

>core/924/2/Org2_Gene459

MDNYLLGSLIFCCVLLSIGMCTIFVMTICFLRQLNKILKNIHRVTTILNFEAKILAPLMLGKKLLCGWLKKRKN
RGSLSIEDIDELLDEKKQRSWKKNLDDQGIKWCAALVLIWKVFRNKD

>core/925/2/Org2_Gene812

MDSFCFDLLKVAAKAIDDKKGNNLVVLDVRTISEFTDYFVFVEGSVNVHVKALANTIVEELKKQKVSPLHVE
GITDGNWVVIDYGFIVVHVVFVSEIRGKYRLEELWKDGFIVTSKLLAS

>core/926/2/Org2_Gene315

MPVSSAPLPTSHRPSSGNLGLMEPNKALKAKHQDKTTKTIKLLVKILVAILVIEVLGHIAAFFIPGTPPICLIILG
GLILTTVLCVLLLVIKLALVNKTEGTAEQQIKRKLSSKSI

>core/927/2/Org2_Gene91

MALKIRLRQQGRRNHVVYRLVLADVESPRDGKYIELLGWYDPHSSINYQLKSERIFYWLERGAQLSSKAEAL
VKQGAPGVYSALLSKQEARKLVVRKKRRAYRQRRSTQREEAAKDATK

>core/928/2/Org2_Gene991

MTVLFYAFLFIFLFLCVILCGLILVQESKSMGLGSSFGVDSGDSVFGVSTPDILKKVTSWCAVAFICGCLLLSFS
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>core/929/2/Org2_Gene785

MLSRIVTCFLFLLSSLPLFAEEEEAAQSKNTFVQPAVMLAIAILFFYFILWRPEQKRRKAMEKRKNDLAKGDKV
TAMGIIGTVDDIREHTVILNIASGKVEVLKGAISEILKPNDNKS

>core/930/2/Org2_Gene436

MSDIQKEEHGSTTIFHLHGKLDGISSPEVQENISQSLAAGSKNIILDCAHLDYMSSAGIRVLLQSYHQVGQHSG
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>core/932/2/Org2_Gene231

MFLKRKKRGGSQVQNKRTASPIKHAKHYLHNYLQELQKIMAARPHDAIDAWNQVFRDKYKGMSQAIGFRD
HILLVKVYNSSLYALLKQTPQNDLIMSLYQVASHVQIREIQFLLG

>core/933/2/Org2_Gene336

MSKVSVRKKNWGFRLLEEVMIKSWWVIFSILIGGFVYDRAIQELRTEELRLQSKVSSLCQDILSAQEKQRQLQ
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>core/934/2/Org2_Gene373

MWYSDYHVWILPVHERVVRLGLTEKMQKNLGAILHVDLPSVGSCKEGLVILESSKSAIEVLSPVSGEVID
INLDLVDNPQKINEAPEGEGWLAVVRLDQDWDPSNLSLMDEE

>core/936/2/Org2_Gene847

MGKKENQLYEGAYVFSVTLSEEARRKALDKVISGITNYGGEIHKIHDQGRKKLAYTIRGAREGYYYFIYFSVS
PGAITELWKEYHLNEDLLRFMTLRADSVKEVLEFASLPE

>core/937/2/Org2_Gene806

MTAVLILTSFPSEESARSLARHLITERLASCVHVFPKGTSTYLWEGKLCESSEHHIQIKSIDIRFSEICLAIQEFSG
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>core/938/2/Org2_Gene560

MFKATARYIRVQPRKARLAAGLMRNLSVQEAEQQLGFSQLKAGRCLKKVLNSAVANAELHENIKRENLSVT
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>core/939/2/Org2_Gene554

MKKQNIRVGDKVFILAGNDKGKEGKVLSLTEDKVVVEGVNVRIKNIKRSQQNPKGKRISIEAPIHISNVRLTIA
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>core/940/2/Org2_Gene371

MTTLPKYVPRSRQNPDTLTFLKRYSSVLLHSENSLSYRIFAKVLAILLTSLAVAFVTLFSCEGSQRLCALYI
GIALAICVLLTIVVYCIASKIATACKKPPSISRIV

>core/943/2/Org2_Gene563

MKDPYDVIKRHYVTEKAKMLEHLSAGTGEGKKKGSFCKDPKFVFIVSHDATKPLIAQALEAIYVDKNVKVK
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>core/945/2/Org2_Gene417

MTVFKQIIDGLIDCEKVFENENFIAIKDRFPQAPVHLLIIPKKPIPRFQDIPGDEMILMAEAGKIVQELAAEFGIA
DGYRVVINNGAEGGQAVFHLHIHLLGGRPLGAIA

>core/946/2/Org2_Gene807

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>core/947/2/Org2_Gene446

MASSATPGFDGTAPSLFPPATRPRYNFKLALFVTIAIALVWIALIATTIAIGLCIHPLCSFIFLTAIPLYFISRYICS
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>core/948/2/Org2_Gene87

MKKNTHPEYRQVLFVDSSTGYKFVCGSTYQSEKTEVFEGKEYPVCYVSVSSSSHPFFTGSKKFVDAEGRVVK
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>core/949/2/Org2_Gene26

MNEPTRTYLESEKDTQDQIEELQATCIVKNAAGIHVRPAGVIVRLFDGEPCDVHFTYAGKTINAKSIMSILML
GAPQGGEILVTIRSKEAHRILQKIQDAFSSGFGE

>core/950/2/Org2_Gene960

MSTSPIGVPSMLNAATSLNATTSKAPLPTSTLAERIKEWLPRILLIVGAIFTIAGCIVMALTKQILYGLLCVVG
GLLLALGLLLKPENCIYRNAESAARSLSNALE

>core/952/2/Org2_Gene520

MDEITPNYP LLRQDSLWNRVRVSWRADLSVSSRYEIASAIAILGLLVAFCSAAVSIIFTANPLAQVFIDGCLA
LGLLPIPLVIGLLIIGIIVLLYGIYLFPPQRE

>core/954/2/Org2_Gene468

MEPYAVIQTGSKQYQVRSQDVLDVVELLGEVASDKEVIFQDVLVFDGTKASLGSPTIANAQVKAEYLSHVKG
EKVVAYKYKKRKNYHRKHGHRQKYLRVKIREILI

>core/955/2/Org2_Gene633

MSFTYFLALPVDRLMQERFLCSPKRWAPFINSPLYTLTIADHDTPYLAKNLDKFPLPVEQWEKTVLHVSSLLK
SIFLCSDLSSLRLLACTKFEILTLNDLYCAQNI

>core/956/2/Org2_Gene504

MNERTLLLLLKKKKGLFLAILDLTQTESSLTPPELEKVLKQKKIFLSCIDRVDLQIKEFRHAFSSSELPQDIQEEL
EEIRDVIIRILDTDKRNYAQKKKEFGIYERP

>core/957/2/Org2_Gene471

MKQQKQKIRIRLKGFDQGLDRSTADIVETAKRTGARVVGGPIPLPTKREVYTVLRSPHVDKKSREQFEIRTHK
RLVDILDPTGKTIDALKMLALPAGVDIKIKAA

>core/958/2/Org2_Gene316

MSSPVVTGTSSASPVEQTKLGEFLERLSGSGRCIKIAFAASTALLLNFTVSGIVAIAMIFVATSVGAYFTVIGP
LFLLSLILLAIMLISMYKITHPSQNTPISN

>core/959/2/Org2_Gene512

MSFKRFLQQIPVRICLLIYLYQWLISPLLGSCCRFFPSCSHYAEQALKSHGFLMGCWLSIKRIGKCGPWHPPGI
DMVPKTALQEVLPEPYQEIDGGDSSHFE

>core/961/2/Org2_Gene576

MVKIISSENFDSFIASGLVLVDFFAEWCGPCRMLTPILENLAAELPHVTIGKINIDENSKPAETYEVSIIPTLILFK
DNEVARVVGLKDKEFLTNLINKHA

>core/962/2/Org2_Gene108

MSDQATTLLRIKPLGDRILVKREEEETARGGILPDTAKKKQDRAEVLVLGTGKRTDDGTLLPFEVQVGDIIIL
MDKYAGQEITIDDEEYVILQSSEIMAVLK

>core/963/2/Org2_Gene372

MDPASPVAPHVLQDHVQLSSEELSALSSGVSrvKKLTIAIMVLSLIAISLVACGLFLTGSAPLQLSIWIAASCIT
LSMLVCACWRYKISNALEKTKVAHES

>core/964/2/Org2_Gene834

MAKKSSVAREAKRRRLVEANFKKRSDLRKIVKSLSVSEEEKENARISLNKMKRDTSPTRLHNRCLLTGRPRG
YLRKFAISRICFRQMASMGEIPGVIKASW

>core/965/2/Org2_Gene2

MEQFHLDREEILLAKASALQLSEELIQEYQTSLSAVITSMKEALAIEIDDADSCESLFMHVVNVEDLREDSVT
SDFNREEFLRNVPESLGGLVKVPAVIK

>core/967/2/Org2_Gene460

MFRNNHKPKKTKCKRFRWLRGVLFGGFIATLLTCLFTPKSGVQLRKKILVKNSGAKKSRVFFKNSKQHTKS
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>core/968/2/Org2_Gene356

MATMTKKKLISTISQDHKIHPNHVRTVIQNFLDKMTDALVKGDRLEFRDFGVLQVVERKPKVGRNPKNAAV
PIHIPARRAVKFTPGKRMKRLIETPNKHS

>core/969/2/Org2_Gene666

MAPKKPNKKNVIQRRPSAEKRILTAQKRELINHSFKSKVKTIVKKFEASLKLDDTQATLSNLQSVYSVVDKA
VKRGIFKDNKAARIKSKATLKV NARAS

>core/970/2/Org2_Gene910

MKKVVTLSSIFFATYCASELSAVTVVAVPLSEAPGKIQVRPVVGLQFQEEQGSVPYSFYYPYDYGYYYPETYG
YTKNTGQESRECYTRFEDGTIFYECD

>core/971/2/Org2_Gene632

MEPRHIYIRKPETPKAPDVEKPGVPEYMTMANTPTFEGPVKTL DQLRRALIEQRGAEEGQKMYDNFIQSILIST
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>core/972/2/Org2_Gene987

MCLIDCLGRGFEEAINTVCCCSDSSESKANVATVSAGLLALTAIVSFILIILICTGVLGASGMTFGMSNVA AVL
VLVVTILLSMFLSGACFAAKREILR

>core/974/2/Org2_Gene679

MLSYLLRTAINVYSFLILAYIFASWVPDCQSARWYQLVSKCVD PFLNFFRRFVPRIGFIDPSPFVGLLCLGILPF
VILRVLRFIILNIFHSPWLLQYL

>core/975/2/Org2_Gene285

MGKPKKSRTDRALAQEIQKKSTEVLKKPARIKAKNRRKFLIAKEQKTLKHRAQEYDQLVRSLLDSQKKDTD
KVLIFNYENG FVFTDKDHFSKYSIRL

>core/976/2/Org2_Gene96

MIKKDRFTNEKLNKLFDSPLVNYAIKQAKIKIAKGDVRSSNVAIETLVLLDREGIQPEFTEEIVVTASPTVER
KRSEHTNSRKKDPSAYTWSDVK

>core/977/2/Org2_Gene476

MYEGKSRMASPTPGQLHLQQKVESKAYDYSRSLAMIATALLFFIVALILSGLSLLPQVFLPFSGAYFIIGSFLAF
IALGILLINCVCDLKQYLTSS

>core/978/2/Org2_Gene28

MSGYAKKKKEAKIMEQQFLEMEASLLEKRYEGQAGNGLVSVVINGKCDLISVKVQPTCLDPEDPEVIEDLF
RAAFKLAKEQMDQEMSLMRSTMPF

>core/979/2/Org2_Gene360

MNKSRLRLCCCLCFGSLFYFYINKQNSLTKLRLEIPCLSVRLRQLEQQNISLRFLIDKIERPDHLMEDIAALPE
YQYLEYPSEESISLLSYELP

>core/980/2/Org2_Gene732

MLAFFATSFKSVLFEYSYQSLLLILIVSAPPIILASIVGIMVAIFQAATQIQEQTFAFVAVKLVVIFGTLMISGGWL
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>core/982/2/Org2_Gene528

MLIRLFLGISLPKGFPLYLEPPLVLATFQGTQFVGTYSEATNPLYIDNLNLNYHYTQELLYKAVPCNYKSIYRE
IPLIIFPEVLIGSTPTQSTE

>core/983/2/Org2_Gene1

MLGKIIRGLSSLIVILCALNVGLIGITHNKLNIIAKLCGGVSTPATQITYIIIGIAGVICLLSFCPFCSSKSRHSHGD
SCSSGGCHSHHSDKN

>core/988/2/Org2_Gene308

MAKLVITSDDEQQEFELEDNSEIAEPCESMGIPFACTEGVCGTCVIEVLEGRENLSEFTEPEYDFLGEPEDSNER
LACQCRIKGGCVKVTF

>core/989/2/Org2_Gene423

MDDSWILEVKVTPKAKENKIVGFDGQALKVRVTEPPEKKGKANDAVISLLAKALSLPKRDVTLIAGETSRKKK
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>core/990/2/Org2_Gene479

MKKAVLIAAMFCGVVSLSSCCRIVDCCFEDPCAPSSCNPCEVIRKKERSCGGNACGSYVPSCSNPCGSTECNS
QSPQVKGCTSPDGRCKQ

>core/991/2/Org2_Gene890

MSLDKGTKEEITKKFQLHEKDTGSADVQIAILTEHIAELKEHLKRSPKDQNSRLALLKLVGQRRKLLEYLNST
DTERYKNLITRLNLRK

>core/992/2/Org2_Gene280

MSRKCP LTGKRPRRGYSYTLRGI AKKKKGIGLKVTGKTKRRFFPNMLTKRLWSTEENRFLK LKISASALRHID
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>core/993/2/Org2_Gene561

MGRSLRKGP FVDHLLKKVRAMNIEEKKTPIKTWSRRSMITPEMIGHTFEVHNGKKFLT V FVSETMVGHKL
GEFSPTRIFKSHPVKKG

>core/994/2/Org2_Gene145

MKEYLDFLVQRNVERDPQTKRHCTVSQKFGGESIDAKTTTGQLFHIAGKTEPGHGKLC LGESILKQLLALGII
TGYENRER EVVYLD

>core/996/2/Org2_Gene498

MSQKNKNSAFMHPVNISTDLAVIVGKGPMRTEIVKKVWEYIKKHNCQDQKNKRNILPDANLAKVFGSSDPI
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>core/997/2/Org2_Gene840

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>core/998/2/Org2_Gene556

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>core/999/2/Org2_Gene943

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>core/1000/2/Org2_Gene625

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>core/1001/2/Org2_Gene467

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>core/1003/2/Org2_Gene53

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>core/1004/2/Org2_Gene626

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>core/1005/2/Org2_Gene848

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>core/1009/2/Org2_Gene250

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>core/1012/2/Org2_Gene635

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>core/1013/2/Org2_Gene957

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>core/1014/2/Org2_Gene686

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>core/1015/2/Org2_Gene892

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>core/1016/2/Org2_Gene969

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>core/1018/2/Org2_Gene640

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D

>core/1019/2/Org2_Gene964

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>core/1021/2/Org2_Gene51

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>core/1023/2/Org2_Gene986

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>core/1025/2/Org2_Gene557

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>core/1027/2/Org2_Gene953

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>core/1028/2/Org2_Gene581

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>core/1031/2/Org2_Gene955

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>core/1033/2/Org2_Gene881

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>core/1034/2/Org2_Gene415

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>core/1045/2/Org2_Gene854

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>core/1046/2/Org2_Gene590

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>core/1049/2/Org2_Gene984

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>core/1050/2/Org2_Gene20

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>core/1054/2/Org2_Gene341

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>core/1056/2/Org2_Gene981

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>core/1058/2/Org2_Gene433

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>core/1067/2/Org2_Gene913

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>core/1069/2/Org2_Gene833

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>core/1070/2/Org2_Gene832

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>core/1073/2/Org2_Gene1008

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>core/0/3/Org3_Gene880

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>core/1/3/Org3_Gene918

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>core/2/3/Org3_Gene968

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WLAGLK QETGSSIVLSAGSILRIFDSQVDSSAPLPTENKEETLVSAAGVQINMSSPTPNKDKAVDTPVLADI
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>core/3/3/Org3_Gene885

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CVGLLLTQVCPLIFDRISKSKEFEKQVLETAQSLIPATKILPSEFNKDLNRLAKLQDNLNLEGFGPTWARNIV
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>core/4/3/Org3_Gene784

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>core/5/3/Org3_Gene379

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>core/6/3/Org3_Gene878

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QAFEPVLIEGKAIRIHPLVCAAFNADFDGDQMAVHVPLSVEAQLEAKVLM MAPDNIFLPSSGKPV AIPSKDM
TLGLYYLMADPTYFP EEHGGKTKIFKDEIEVLRALNNGGFID DVFGDRRDETGRGIHIHEKIKVRIDGQIIETP
GRVLFNRIVPKELGFQNY SMPSKRIS EILQCYKKVGLEATVRFLDDLKDLGFIQATKAAISMGLKDVRIPDIK
SHILKDAYDKVAIVKKQYDDGIITEGERHSKTISIWTEVSEQLSDALYVEISKQTRSKHNPLFLMIDSGARGNK
SQLKQLGALRGLMAKPNGAIIESPITSNFREGLTVLEYSISSHGARKGLADTALKTADSGYLTRRLVDVAQDV
IITEKDCGTLNHIEISAIGQGSEELLPLKDRIYGR TVAEDVYQPGDKSRLLAQSGDVLNSVQAE AID DAGIETIK
IRSTLTCE SPRGVCAKCYGLNLANGRLIGMGEAVGIIAAQSIGEPGTQLTMRTFHLGGIAATSSTPEIITNSDGIL
VYMDLRVVLGQEGHNLVLNKKGALHVVGDEGRTLNEYKLLSTKSIESLEVFPVELGVKILVADGTPVSQG
QRIAEVELHNIPICDKPGFIKYEDLVEGISTEKVVNKNTGLVELIVKQHRGELHPQIAIYDDADLSELVGTYAI
PSGAISVEEGQRVDPGM LLARLPRGAIKTKDITGGLPRVAELVEARKPEDAADI AKIDGVVDFKGIQKNKRIL
VVCDEMTGMEEHLIPLTKHLIVQRGDSVIKGQQLTDGLVVPHEILEICGVRELQKYL VNEVQEVYRLQGVD
INDKHIEIIVRQMLQKV RITDPGDTLLFGEDVNKKEFY EENRRTEEDGGKPAQAVP VLLGITKASLGTESFIS
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>core/7/3/Org3_Gene877

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LLVGRILADNIIDEACSLVYGKAGEKLSIAMLK RMLDAGIASVKIAVDADENHPIIKMLAKDPTDSYEAALKD
FYRRLRPGE PATLANARSTIMRLFFDPKRYNLGRVGRYKLN RKLGFSIDDEALSQVTLRKEDVIGALKYLIRL
KMGDEKACVDDIDHLANRRVRSVGELIQNQCRSGLARMEKIVRERMNLFDFSSDTLTPGKVVS AKGLASVL
KDDFFGRS QLSQFMDQTNPVAELTHKRRLSALGPGGLNRERAGFEVRDVHASHYGRICPIETPEGPNIGLITSLS

SFAKINEFGFIETPYRIVRDGIVTDEIEYMTADVEEECVIAQASASLDEYNMFTEPVCWVRYAGEAFEADTSTV
THMDVSPKQLVSIVTGLIPFLEHDDANRALMGSNMQRQAVPLLKTEAPVVGTGLECRAAKDSGAIVVAEED
GVVDFVDGYKVVAACHNPTIKRTYHLKKFLRSNSGTCINQQPLCAVGDVITKGDVIADGPATDRGELALG
KNVLVAFMPWYGYNFEDAIHSEKLIREDAYTSIYIEEFELTARDTKLGKEEITRDIPNVSDEVLANLGEDGIIRI
GAEVKPGDILVGKITPKSETELAPEERLLRAIFGEKAADVKDASLTVPPGTEGVVMDVKVFSRKDRLSKSDDE
LVEEAVHLKDLQKGYKNQVATLKTEYREKLGALLNEKAPAAIIHRRTAEIVVHEGLLFDQETIERIEQEDLV
DLLMPNCEMYEVKGLLSDYETALQRLEINYKTEVEHIREGDADLDHGVIRQVKVYVASKRKLQVGDKMA
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QRIWDMMIEQGLPEDGKSFLYDGKTGERFDNKVVIGYIYMLKLSHLIADKIHARSIGPYSLVTQQPLGGKAQ
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DVRPMVVDA

>core/8/3/Org3_Gene462

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LKSPEALLLELQWFQDLFKDDYFTEVQLHKMSEESIAGFKEEWLQKEYYSLIEKQIKVNTAVLEASKRLGIPT
VATNDIHYINANDWQAHEILLNVQSGETVRIAKQNTHIPNPKRKVYRSREYYFKSPAQMAELFKDIPEVISNT
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NPERLSYPDIDIDICMAGRERVINYAIERHKGKDNVAQIITFGTMKAKMAVKDVGRTLDMAKSKVNHIKHIPD
LNTTLSKALETDPDLHQLYINDAESAQVIDMALCLEGSIRNTGVHAAGVIICGDQLTNHIPICISKDSTMITTQY
SMKPVESVGMLKVDLLGLKTLTSINIAMSIAIEKKTGQSLAMATLPLDDATTFSLHQQGKTGMGIFQMESKGMQ
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SYSLGEGDVLRRAMGKKDFQQMEQEREKFCKRACNNGIDPELATVIFDKMEKFAAYGFNKSHAAAYGLITY
TTAYLKANYPKEWLAALLTCDSDDIEKIGKLIREAQSMGIPILPPHINVSSNHFVATDEGIRFAMGAIKGIGRG
LIESIVEERDHHGPHYESIRDFIQRSDLKKVSKKSIESLIDAGCFDCFDNSNRDLLASVEPLYEAIKDKKEAASG
VMTFFTLGAMDRKNEVPICLPKDIPTRSKKELLKKEKELGIYLTEHPMDTVRDHLSRSLSVVLAGEFENLPHG
SVVRTVFIIDKVTTKISSKAQKKFAVLRVSDGIDSYELPIWPDMYEEQQELLEEDRLIYAILVLDKRSDSLISC
RWMKDLSIVNENIIEYCDQAFDRIKNQVQKMSFTMSTSGKETKAKGNKPNENGHTQALAPVTLSLDLNLNR
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>core/9/3/Org3_Gene955

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TIHASEEPTVFTNKTFLKSALYRTAKKFFFLNEEGAELTIGENSQGFPSHFSLQWQGLVFKAIEILDFPTLEDIFP
KLELAHTSLENVSHDISITNVTVCAAEAKVNFTLSPVIHKKDRENHPKTRIGSVEYVAKTHEMITGPKAIALPI
YAIPLLADKFKDQLLSLLCYDSLEYRLRYDIRLLRDASFSSAYLVTPGDLDNGSLIYPNYCYSPTKGLMQVV
GMLSPKQAFIVKSEQVEDFLNERGHILQEPGFQTFINERPEGHLYTNVTEQGVLLFHVDVGDPSSTEIRFGTWT
YYTNQGGFFLEKKNDLPIQDGLIVEPQDIPAFIVKNDAAALRRLPNFFSSPPNLKDLLIEVHRQSRGKGLDLKPILV
GLGESRCWLFVFLYREDIGFSLIPTPLQGLCFLPRVIPPENVPQFLTQYAQHERILFPNPQTRPPESYELVIQSI
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TDVFKLDALAPLSVTDDTIANPEDLQFFSQLKAACLPPIQNLFSSDHQLRPYQNSGLLWMWFLYNHRLSGLL
CDEMGLGKTHQATALLDIVFQSSQPSARPKFLIVCPTSVLPHWEHILSNHLPGVSIFSFHGPKNKPSSELPPADILL
TSYGTLRQNYDKFYKIAFTIVVFDEIHMAKNKSSQIHKILCRIDAQMKLGLTGTPIENNLLFEKGLLDIILPNYL
PSDALFKKLFTKRCSSSEEEIIPSQDLLLKLTRPFILRRTKKLVLPELPDKVESIIACSLSPDQEKLYMATLQRE
KSHIQKLETPEEPATNFLHIFALLNHLKQICDHPAVFFKDPDQYKNYESGKWNFAVKLLKESLNAGYKVVVVF
SQYIHMIRIITLYLEEIGIKYASIQGKSLNRKEEIEFTTDPNCQVFVGSLLAAGTGINLTAGNVVIMYDRWWN
PAKEIQALDRVHRIGQKNTVFIYKLITEDTLEERIHYLEIEKKIRLLDKVIASQDSNILHMLNREDLLTILSYKDE
HGTSDSEESPVDAPVEDDTGVLPPEDS

>core/10/3/Org3_Gene956

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LREYVHAANALSANPFFLPLEYLEKDSAELAVLFVSVNEDTFAPANQPIEFQLVLRLLPCRSKPFYISNIRTFLEG
VLYQEPIVLNRRFFFTMQSFNASDRKLIDLLIRYVRYPNHTTEEKLLKSAYLMPPALGVILAKMFEHQLADR
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DAPGIIHHFVYHRFSPQIKRAHLRSFSRLRDIAIPEALFGSFRENALPVFQEYAEIANVHLLNSFVTL
PYVDEVRAICDMSYLDGELEAKLHFLYGSRLVPAASLALQYQDVRAFISDEGILARNLVEERKM
LEEVFSGFIYDERDGAFRVKSEKKIVEFMTETIPANQHRITFNCPENLSGQFIYDETIFELSFREGSDIN
YYEADLKVHGLLKGVPDLWD CISAKKRFLLEPKAGQQSKGTRRGKVN
SGKLPCILVLDLEKIAPVVQIFNEIGFKVLDDL
VQKCPLWSLTGISLDQFEALPVNFSMSERLIEIQKQIRGEIEFDFQDVPQQIQATLRSYQTEGVH
WLERLRKMHLNGILADDMGLGKTLQAI
IAVTQSKLEKSGCSLIVCPTSLVYNWKEEFRKFNPEFRTLVIDGVPSQRRKQLTALADR
DVAITSYNL LQKDVELYKSFRLDYVVLDEAH
HIKNRTTRNAKSVKMIQSDHRLILTGTP
IENSLEELWSLFDFLMPGLSSYDRFVGKY
IRTGNMGNKADNMVALKKKVSPFILRRMKED
VLKDLPPVSEILYHCHLTESQKELYQSYA
ASKQELSRLVKQEGFERIIHVLATLTRLKQIC
CHPAIFAKDAPEPGDSAKYDMLMDLLSSL
VDSGHKTVVFSQYTKMLGIIKKDLESRGIPFVYLDG
STKNRLDLVNQFNEDPSLLVFLISLKAGGTG
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>core/12/3/Org3_Gene935

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YIMCLSELLSQELHLDREAIEDAIHAKASVLSVPYLV
AANVSERTYKLMKLSKDWPLHVEAVVRRHYPQESV
ASDILGYVGPISLQEYKRV
TQELSQRLECVRAYEEGEDPKLPEGLASIDQVRALLES
VESNAYS
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IQEMEGAVPEAPGTKLQTL
SAELQAYADALLLEYEKTETFRSAKSLKKREKL
PPLFPWIKGGAI
ALDPNNGEILAMASSPRYRNDFVN
AKVAEDSKAVRSSIYRWLENKEHIAEIYDRKVPLIR
ERRNPLTGLCYEEILPLTFD
CFLDFLPENSVIKLQLKRNSFVGQAIEVQNLVTRLL
SLFPYEEGTCPCSAIFDAVFPNEEGHILIQE
VISLQEQQWIMECLNQHKADIEELKEALDQVFNE
LPANYDKILYTDILRLIVDPERFSPVLPSEVHRL
SLSEFTELQGRYVVLRS
AFSTILED
AFIEVHFKSWRKSEFLQYLA
AKRQEEALRKQRYPTPYVDYLEEEKTRQYKMFCQ
EHLDTFLAYLFSKTPYKEGLEPY
YDILDLWINELDNGAHRALSWNEHYLFLKERV
SHLSEHLPALFSTFREFNELQRPLLGKYPISIV
RNKRQTEQDLAASFYPVYGYGLRPHAYGQAATL
GSIFKLVSAYS
VLSQRILWGHNEEPANPLVIDKNSFGYR
SSKPHVGFFKDGTPIPTFFRGGSLPGNDFMGRG
FIDLVS
ALEMSSNPYFSLLVGEGLGDPEDLAD
AASLFGFG
EKTGLGLPGEYAGRVPHDLAYNRSGLYATAIGQHTL
VVTP
LQTAVMLASLVNGGVVYVPKLLL

GEWEGEHVSYLSSKKKRTIFMPDAVVEVLKTGMRNVIWGQYGTARAIQSQFPPQLLSRIIGKTSTAESIMRVG
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>core/13/3/Org3_Gene1019

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LCKSLGYSQVMLTSEKGEFSCRGGIVDIFPLSSPEPFRIEFWGEKIISIRSYNPSDQLSTGKVSISISPAYTEEAS
GGNYSHSLLDYFSTPPLYLFDNLEILEDFADISGTLSSLPDRFFSIGTLYDRISTSNQVYFSETPFPNVKNLKEN
RVIIIEAFHRNMEASRQAIPILYPEQIIQNDENPLLAFLQHLQEYMPPHGKPLKLAIYSTKTKSLKEARALAETV
ARGDVEIYEKGTNLTSSFALVNEAFAAISLSEFASTKVLRRQKQORTHFSVTTEEVFVPIPGETVVHIIHNGIGKFL
GIEKKPNHLNIETDYL VLEYADKARLYVPSNQAYLISRYVGTSDKAADLHHLNSSKWKRSDLTEKSLIVYA
EKLQLEAQRSTTPAFVYPPHGESVIKFAETFPYEETPDQLKTIDQIYNDMMSPKLMDRLICGDAGFGKTEVI
MRAAVKAVCDGHRQVIVMVPTTILATQHYETFKERMAGLPIEIAVLSRFSQAKVQKLICEQVASGQIDIIIIGTH
KLINKSLEFKNPGLLIIDEEQRFQVGVKVDNLKERYPMIDCLTVSATPIPRTLHMSLSGARDLSVIAMPPLDRLP
VSTFVMEHNTETLTAALRHELLRGGQAYVIHNRIESIYTLAETIRNLIPEARIGVAHGQMGAEEDLSNIFTKFKN
QKTDILVATALIENGIDIPNANTILIDHADKFGMADLYQMKGRVGRWNKKAYCYFLVPHLDRLSGPAAKRL
AALNKQEYGGGMKIALHDLEIRGAGNILGTDQSGHIGTIGFNLYCKLLKKA VSALKKHTSPLLFNDDVKIEFP
YNSRIPDTYIETGSMRIEFYQKIGNAESSEELTAIQEEMRDRFGPLPQEICWLFALAEIRLFALQHGISSIKGTAN
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>core/14/3/Org3_Gene914

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PPVRVATPMPLRPSSQGYWQCLNRMVSMVLRRAPLPLPAMQVDPILGDFNPHFVASYPNRIDNEPMYFQIKQ
FKKIAQNPDLPQQHRRLAQLSLEQALYLNNDNYL VNVPDGNCFYRAYAVGWLSALYEESSRNDIVFEQEA
TRLLDLPFASSSPANANLCAEMAELLQLCSTYCSFIDLYDGVILSQKHTATLIAFLRKLSAYAIRQQIAASSNEE
TARALFISDMQDDLLPSVLEFLAANRPYSELFQNLIDHSALPYMQSRDKLFLLLEHLPALFLTDAELQKMSPE
DQQLRKQYEREIREAFAKLSRRIADSGWDTERFNAIVKDYLPEAIRCQYSRFLATIENRRSGDLPWSPALSFFA
FLCTCPSVRFHKLCAFYKSLEDIIIASAPPQRSIQEILQISNASLSYLNEDLDSSWQREVISSNIMTILTTHESLT
ESSMPQLETLHKRIANLLKNVISTSFETPPLSNQPDLLSNLVNKLVAIHSKLELKEHFNTVCSARSLRLTRDE
GSGLSQEQLLYTQAVQLLFFILQHPQVNNRPETKDAVKELKMLLPFLQYAFKKVENEKKLQKLLRSILGS
LVLKPPARYPSTPSNKKDKETFCFKFSRHPVEMVLDPILEKNCMQFLRATFPNYQLETEAILLEKEIESTFRNG
WNVFLTRLNLFGSKLGSPSSPTALSDQFSKSFLIFCFLNNYPKLLQKKTPLAARLDAFQREASHRFTQVKDKL
LLSLKYGFPLATATINQYSRARDQLICNLLKNTVTASDGFCRSGFRQSLIGYLHSLSSNELGDILDDVKEQAEA
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>core/15/3/Org3_Gene945

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QLVLHHITNYLKQDLWKNVLFQEQQHLLAVRYNVTSKHTSSLVDKLLASYTQPISSYFSSRVERLEQISLWHQ

QIYNSLLEIPKQVFLDQLTAHISGFKKQPFSSILDDLHHFVDLLYTSETHSSLSFFKIAETFNFKHRLARYKPCA
AFTVLENMSWVERTLEFCNLDRIFNTLLVDLQEYLKQNYTPWLSPDESVALEKLLSSSEAQPVVQALREQY
QLVLIDEFQDQDKQWSIFSNNLFSKFTGSLFLIGDPKQSIYEWRSADLPTYLTAKSSFSSEDKQLQLVNNYRST
PKLMEAINQIFGKISPFLEIPGYLPIEYHALNPQSSETFENPPHAPIHFFFYETIKDQALWIFSEALRLQKEQKIPL
GNMVVLVSDSNQAFELISYATIPVSFSKNKSIFHLTETHILTTALLEAILHPENYEKISKILFSSSLFGLSLDEVTTK
KEDFTIYFQSLHSYISHHGLLATFYRVMTTQGNVLFSSPRGDLIFQEMEKLCCGYLDTISSYPYHQLLHLKNFSE
TGRWEEELAISSYSEDLTLKITTIHSSKGLEVDIVFCPGIEKSKKNKSSSELLREMYVACTRAKKQLYLPISTQ
PPSLQRSSALTNYVKLEGTQSSAYDLAIHLHQEHPDLFSYSLPKDHGHATTVLNLPLLETFALKVTPPKTIFSFS
STKFLLDTHKDSQSIPYSKLPISKQQLPLGEKTGILHKILESIFSLQDTEYLMSTIMRFIKHHTHLEGFEETILK
LLSKTFFSPLTFSSQTFSLSQVLPNKIFRETSFLFLENQELWQGVIDLFFEHEGKYIIDWKTSFLGETNSDYSSK
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H

>core/16/3/Org3_Gene690

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QINGMTPPATLSEINDLTLRIVEDVLSLHGEEAINLEEIQDIVEKQLMVAGYYDVAKNYILYREARARARANK
DQDQGEFVPQEETYVQKEDGTTYLLRKTDLKRFWSACKRFPKTTDSQLLADMAFMNLYSGIKEDEVTT
ACIMAARANIEREPDYAFIAAELLTSSLYEETLGCSSQDPNLSEIHKKHFKKEYILNGEYRLNPQLKDYLDDAL
SEVLDSLSDQQFSYMGVQNLVDRYFNLHEGRRLTAQIFWMRVSMGLALNEGEQKNFWAITFYNNLLSTFRY
TPATPTLFNSGMRHSQSSCYLSTVKDDLSHIYKVISDNALLSKWAGGIGNDWDVDRATGAVIKGTNGKSQG
VIPFIKVANDTAIAVNQGGKRKGAMCVYLENWHLDYEDFLELRKNTGDERRRTHDINTASWIPDLFFKRLEK
KGMWTLFSPDDVPGLHEAYGLEFEKLYEEYERKVESGEIRLYKKVEAEVLWRKMLSMLEYTGHPWITFKDP
SNIRSNQDHVGVVRCNLCTEILLNCSESETAVCNLGSINLVEHIRNDKLDEEKLKETISIAIRILDNVIDLNFYP
TPEAKQANLTHRAVGLGVMGFQDVLVELNISYASQEAVEFSDECSEIIAYYAILASSLLAKERGTYSYSGSK
WDRGYLPLDTIELLKETRGEHNVLDVTSSKKDWTVPVRDTIQKYGMRNSQVMAIAPTATISNIIGVTQSIEMMY
KHLFVKSNNLSGEFTIPNTYLIKLLKELGLWDAEMLDDLKYFDGSLLEIERIPNHLKKLFLTAFEIEPEWIIECTS
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>core/17/3/Org3_Gene63

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FSSTWKTMDASFMESVWWVFQSLYNQGLVYEGTKVVPFSTALGTPLSNFEASQNYKEVDDPSLVVRMPLQ
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RTYEPPFTFFQSKREEGAFRVIAASFVEESEGTVVHMAPAFGEGLVCKENHVPLVCPVDAHGSFTEEIPQ
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GKPFHRIPYVFDWFDGAMPYAQNHYFPENQKETEEAFPADFIAEGLDQTRGWFYTLTVISAILFDRPAFRN
AIVNGIILAEDGNKMSKRLNNYPSPKYVLDYTGADALRLYLLHSVVKAEDLRFSDKGIEGVLKQILLPLTNV
LSFFNTYAEYGFDPKSDIEPAYTEIDQWILSNLYSVVGKVRESMSQYHLNFAVEPFVTFIDDLTNWYIRRC

RRRFWEAEDTPDRRAAFSTLYEVLTVFCKVIAPFVPFLAEDIYQKLKLEKEPESVHLCDFPQVEMDKILPDLE
KRMHDIREIVGLGHSLRKEHKLKVRQPLANFYVVGSKDRLSLLKTFEGLIAEELNVKNVIFYEEAPSFIYTTV
KPNFRMLGKKVGSKMKEVQKALSELPNNAIDKLIQEETWVL TIDDREIALDGGDVVICRHTDPGYIARSSALF
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SDFQGENWDINGHATQIEITVSSIDS

>core/18/3/Org3_Gene944

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SHYQELFQILESHFSSYEEMFTTILNNRTQEEDCSLHIFGYAHLPKHLAEFFINLSTYFPVYFYCFSPCREYFGD
LLSDRAIDFFWNQLPDSPIKNAWEHYVLSDRQALLANLAHKSQSSQNFFLDREIDYQEMFLPSKHDSSLGVIQ
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YFTDEVDPAEDLRNKILLSSILQTQGDLHYILQLLTHPQLQQPIDQNKVPYLIKLSSEWGKISSKDRASGQ
QMKALGDLILEEYPFHQEGGRVSQVEVWETTPLYIFIQERINLYLSSSQHSYEDLFQNVFSCLEKIFVLSPEET
SFITTLRNSLFPTFATSSCSLLFFTDCLDFLLHFHKPSPLYDKPGPYIGSLSSLIPKGYVFILGANKTTSSDIFD
LLNRTTTTHEELAFSSTEDEENFHFLQILVSTKHELHISYISSAAQFNLPSPFLNHIKETLDLPVETLPTQPYLSAFF
KNKACLHTSQEYNYSLAHAFYSKKALLPSLFIPTVKQVNL PQHLSLNEIIGIFSPLDLFLKTNYNLRISYPEHL
KKQQKLFP TKHQIEDFWNECFVDKEHDLIPSISPHAEELFTYREKTILLRNGLDKDPKHSPYTVTFSSSIFEER
PYHESYLPPLSLSFQGNPVQIHGTIHGVCNEGLYLCSIDPGDSLKKTTRTLGSLPETSSEQKQLLERYVALAV
LQMSQHLSSDSALIKLTSFNTKENHHPFSDPEGYLKRVLEVYHLMSSQPIPLLSPLCWKTLDDDEEKFHQAVL
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>core/19/3/Org3_Gene841

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TYFQAIGSKPLDTISGEITYGIERIAMYLQKKTSIYDVLWNDTLTYGQITQASEKAWSEYNFDYANTEMWFKH
FEDFAEEALRTLKNGLSVPAYDFVIKASHAFNILDARGTISVTERTRYIARIRQLTRLVADSYVEWRASLNYPL
LSLSSTSEPKETSESVP MISSTEDL LLEIGSEELPATFVPIGIQQLESARQVLT DHNIVYEGLEV LGSPRRAL
LVKNVAPEVVQKA FEKKGPMLTSLFSPDGDVSPQGQQFFASQGV DISHYQDLSRHASLAIRTVNGSEYLFLL
HPEIRLRTADILMQELPLLIQRMKF PKKMVWDNSGVEYARPIRWLVALYGEHILPITLGTIIASRNSFGHRQLD
PRKISSPQDYVETLRQACVVVSQKERRMII EQGLRAHSSDTISA IPLRLIEEATFLSEHPFVSCGQFSEQFCA
LPKELLIAEMVNHQKYFPTHETSSGAISNFFIVVCDNSPNDTII EGNEKALTPRLTDGEFLFKQDLQTPLTTFIEK
LKSVTYFEALGSLYDKVERLKAHQRVFSTFSSLAASEDL DIAIQYCKADLVSAVVNEFP ELQGIMGEYYLKH
ANLPTASAVAVGEHLRHITMGQKLSTIGTLLSLDLRLDNLLACFILGLKPTSSHDPYALRRQSLEVLTLVSASR
LPIDLASLLDRLADHFPSTIEEKVWDKSKTIHEILEFIWGRLKTFMGSLEFRKDEIAAVLIDSATKNPIEILD TAE
ALQLLKEEHTEKLAVITTTNRLKKILSSLKLSMTSSPIEVLGDRESNFKQVLDAFPGFPKETS AHAFLEYFLSL
ADLSNDIQDFLNTVHIANDDGAIRNLRISLLL TAMDKFSLCHWESVAV

>core/20/3/Org3_Gene1003

MSRLDIFVFD SLIANQDQNLLEEIFCSEDTVLFKAYRTTALQSPLAAKNLNIARKVANYILADNGEIDTVKLVE
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RQAALTALFTYLRQDVGSCFATAPAILIHQEYPERFLKDLNDLISSGKLSRIVNQREIAVPINLSGCIGELFKPLR
ILDLYPDPLVKLSSSPGLKKAFSAANLIETLGDSEAQIQQLSHQYLMQKLQNVHETLTANDIHKSTLLHYYQL
QESTVRAIFFKEGLFSKEQVAFSTQHPRELSEIQRVYHYLHAYEEAKSAFIHDTQNPLLKAWEYTLATLADAS
QPTISNHIRLALGWKSEDPHSLVSLVTHFVEEEVENIRILVQQCEQTYHEARSQLEYIEGRMRNPLNNQDSQIL
TMDHMRFRQELNKALYEWDSAQEKAKKFLHLPEFLLSFYTKQIPLYFRSSYDAFIQEFALHYANAPAGFRILF
THGRTHPNTWSPISINEFIRFLSEFFTSTESSELLGKHAVINLEKETSRLVHNITAMLHTDVFQEALLTRILEAY
QLPVPPSILNHL DQLSQTPWVYVSGGTVDTL LLDYFESSEPLTLTEKHPENPHELAAFYADALKDLPTGIKSYL
EEGSHSLLSSSPHVFHSIIAGSPLFREAWDNDWYSYTWLRDVWVKQH QDFLQDTILPQLSIYAFIENFCNKYA
LQHVVHDFHDFCSDHSLTLPELYDKGSRFLSSLFTKDKTVALIYIRRLLYLMVREVVPYVSEQQLPEVLDNVSS
YLGISSRITYEKFRSLIEETIPKMTLLSSADLRHIYKGLLMQSYQKIYTEEDTYLRLLTTAMRHHNLAYPAPLLFA
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>core/21/3/Org3_Gene780

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TSATPAITTVTTGASALQPTDSLTVENISQSIKFFGNLANFGSAISSSPTAVVKFINNTATMSFSHNFTSSGGGVI
YGGSSLLFENNSGCIIFTANSCVNSLKGVTTPSSGTALGSGGAICIPTGTFELKNNQGKCTFSYNGTPNDAGAI
YAETCNIVGNQGALLLDSNTAARNNGGAICAKVLNIQGRGPIEFSRNRAEKGGAIFIGPSVGDPKQSTSTLILA
SEGNIAFQGNMLNTKPGIRNAITVEAGGEIVSLSAQGGSRLVFYDPITHSLPTTSPSNKDITINANGASGSVVFT
SKGLSSTELLLPANTTTILLGTVKIASGELKITDNAVVNVLGFATQGGGQLTLGSGGTGLLATPTGAPAAVDFT
IGKLAFDPFSFLKRDFVSASVNAGTKNVTLTGALVLDEHDVTDLYDMVSLQSPVAIPIAVFKGATVTKTGFPD
GEIATPSHYGYQGKWSYTWSRPLLIPADGGFPGGPSANTLYAVWNSDTLVRSTYILDPERYGEIVSNSLW
ISFLGNQAFSDILQDVLLIDHPGLSITAKALGAYVEHTPRQGHEGFSGRYGGYQAALSMNYTDHTTLGLSFGQ
LYGKTNANPYDSRCSEQMYLLSFFGQFPVITQKSEALISWKAAYGYSKNHLNTTYLRPDKAPKSQGGQWHNN
SYYVLISAEHPFLNWCLLTRPLAQAWDLSGFISAEFLGGWQSKFTETGDLQRSFSRGKGYNVSLPIGCSSQWF
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KNGFTNHRVSTGLKSTF

>core/22/3/Org3_Gene972

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NSENHLCYTGVPFNEMKGAMMSGEARLSEALNAAIFPSVTYGVNSGGEPREIVTLSHEDVRAFHQSQYSINR
CLFYFYGNIKPSRHLDLFLEEKLLRQATKLEKQAVSVPLQKRFKDPVRNILTYPVDHQEEDKVLFGISWLTC
EQQELLALHVLEIILMGTDASPLKSRLKSGFCKQTEMSIENDIREIPMTLVCKGCSGAGAKLEALIFASLEEII
REGISENIVEGAVHQLELSRKEITGYSLPYGLSLFFRSGLLKQHGGSAEDGLRIHSLFSELRNSLKNSDYLAKLI
RKYFLDNPHFARVILLPDTELVAKDNKDEQQLLLSVSEKLTDENKEKIQQNRELTESQE QKEDLNGILPNLA
LDKVPTSGKEFPLIKEGLSQGEVLHHECFTNDIVFIDVVDIPPLSGEELPWLRLLVFLMLQLGCGGRSYKEHL
EFLLEHTGGVDVSYDFSPHANKNSFLSPSVSIRGKALSSKSEKLCGIVSDMLTSVDFTDIPRIRELLMQHNEAL
TNSVRNSPMSYAVSMACSGNSITGAMSYLTTGLPYVKKIRELTKNFDQNIDEAVVILQRLYTKCFSGKRQIVI
SGSAHNYQQKLDKNKFYGLLDYLVIPPEPWENPSINLYVTSRGLHIPARAAFNALAFPIGDIAYDHPDAAALTV
AAEILDNVVLHTKIREQGGAYGSGAAANLSRGSFYCYSYRDPEIATTYKTFLKGVSEIASGNFTKEDIYEGAL

GVVQGLDMPVAPGSRASVAFYRLKSGRIPVLRQAFRRSVLEVTKEHICMVMDKYLESTVQETTLISFAGEEM
LRNNVLTLDKDFPIVPAI

>core/23/3/Org3_Gene305

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YATTPMLFTNNDISILFQYNRSAGFGAAIRGTSITIENTKKSLLFNGNGSISNGGALTGSAAINLINNSAPVIFSTN
ATGIYGGAIYLTGGSMILTSGNLSGVLFVNNSSRSGGAIYANGNVTFSSNNSDLTFQNNTASPQNSLPAPTPPPTP
PAVTPLLGYGGAIFCTPPATPPPTGVSLTISGENSVTFLENIASEQGGALYGKKISIDSNKSTIFLGNTAGKGGAI
AIPESGELSLSANQGDILFNKNLSITSGTPTRNSIHFGKDAKFATLGATQGYTLYFYDPITSDDLAAASAAATV
VVNPKASADGAYSGTIVFSGETLTATEAATPANATSTLNQKLEGGTLALRNGATLNVHNFTQDEKSVVIM
DAGTTLATTTNGANNTDGAITLNKLVINLDSLDGTAAVVNVQSTNGALTISGTLGLVKNSQDCCDNHGMFN
KDLQQVPILELKATSNTVTTTDFSLGTNGYQQSPYGYQGTWEFTIDTTTHTVTGNWKKTGYPHPERLAPLIP
NSLWANVIDLRAVSQASAADGEDVPGKQLSITGITNFFHANHTGDARSYRHMGGGYLINTYTRITPDAALSL
GFGQLFTKSKDYLVGHHGHSNVYFATVYSNITKSLFGSSRFFSGGTSRVTYSRNEKVKTSYTKLPKGRCSWS
NNCWLGELEGNLPITLSSRILNLKQIIPFVKAEVAYATHGGIQENTPEGRIFGHGHLNVAVPVGVRFGKNSH
NRPDFYTHIVAYAPDVYRHNPDCDTTLPIGATWTSIGNNLTRSTLLVQASSHTSVNDVLEIFGHCGCDIRRTS
RQYTLDIGSKLRF

>core/24/3/Org3_Gene595

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TVNDYLAQRDCEWVGSVLRWLGLTTGVLVSGTLLEKRKKIYQCDVVYGTASEFGFDYLRDNSIATRLEEQV
GRGYYFAIIDEVDSILIDEARTPLIISGPGEKHNPVYFELKEKVASLVYLQKELCSRIALEARRGLDSFLDVDILP
KDKKVLEGISEFCRSLWLVS KGMP LN RVLRVREHPDLRAMIDKWDVYYHAEQNKEESLERLSELYIIVDEH
NNDFELTDKGMQQWVEYAGGSTEEFVMMDMGHEYALIENDETLPADKINKKIAISEEDTLRKARAHGLRQ
LLRAQLLMERDVYIVRDDQIVIIDEHTGRPQPGRRFSEGLHQAIEAKEHV TIRKESQTLATVTLQNFFRLYEK
LAGMTGTAITESREFKEIYNLYVLQVPTFKPCLRIDHNDEFYMTEREKYHAIVNEIATIHGKGNPILVGTESVE
VSEKLSRILRQNRIEHTVLNAKNHAQEA EIIAGAGKLGAVTVATNMAGRGTDIKLDNEAVIVGGLHVIGTTR
HQSRRIDRQLRGRCARLGDPGA AKFFLSFEDRLMRLFASPKLNTLIRHFRPPEGEAMS DPMFNR LIETAQKRV
EGRNYTIRKHTLEYDDVMNKQRQAIYAFRHDVLHAESVFDLAKEILCHVSLMVASLVMSDRQFKGWTLPNL
EEWITSSFPIALNIEELRQLKDTDSIAEKIAAELIQEFQVRFDHMVEGLSKAGGEELDASAICRDVVR SVMVMH
IDEQWRIHLVDMDLLRSEVGLRTVGQKDPLLEFKHESFLLFESLIRDIRITIA RHLFRLELTV EPNPRVNNVIPT
VATSFHNNVNYGPLELTVVTDSEDQD

>core/26/3/Org3_Gene312

MSLNLERISPLLYLLDVTAKKIDTSNLIVEAMNLDEHYGYQGIWSPYWMETTTTTTSSTVPEQTNTNHRQLYV
DWTPVGYRPNPERHGEFIANTLWQSAYNALLGIRILPPQNKEHDLEASLQGLGLLINQH NREGRK GFRNHT
TGAAATSAKTAARHSFSLGFAQMF SKTRERQSPSTTSSHNYFAGLRFDSLLFRDFISTGLSLGYSYGDH HML
CHYTEILKGSSKAFFNNHTLVASLDCTFLPARITRLELQPFISAIALRCSQAS FQETGDHIRKFHPKHPLTDLSS

PIGFRSEWKTSHHIPMLWTTEISYVPTLYRKNPMEFTTLLISNGTWTTQATPVSYNSVAAKIKNTSQLFSRVTL
SLDYSAQVSSSTVGQYLKAESHCTF

>core/27/3/Org3_Gene917

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VLCQNNISYGPGGALLQGRKSKALFFRDNRGTILFLKNKAVNQDESHPGYGGAVSSISPGSPITFADNQEILF
QENEGELGGAIYNDQGAITFENNFTTSSFFSNKASFGGAVYSRYCNLYSQWGDTLFTKNAAAKVGGAIHAD
YVHIRDCKGSIVFEENSATAGGAIAVNAVCDINAQGPVRFINNSALGLNGGAIYMQATGSILRLHANQGDIEF
CGNKVRSQFHSHINSTSNFTNNAITIQGAPREFSLSANEGHRICFYDPIISATENYNSLYINHQRLLLEAGGAVIFS
GARLSPEHKKDNKNKTSIINQPVRLCSGVLSIEGGAILAVRSFYQEGLLALGPGSKLTTQGKNSEKDKIVITN
LGFNLENLDSSDPAEIRATEKASIEISGVPRVYGHTESFYENHEYASKPYTTSIILSAKKLVTAAPSREKDIQNLII
AESEYMGYGYQGSWEFSWSPNDTKEKKTHIASWTPTGEFSLDPKRRGSFIPTTLWSTFSGLNIA SNIVNNNYL
NNSEVIPLQHL CVFGGPVYQIMEQNPKQSSNNLLVQHAGHNVGARIPFSFNTILSAALTQLFSSSSQQNVADK
SHAQILIGTVSLNKSQWALSRLSSFSYTEDSQVMKHVFPYKGTSRGSRWNYGWSGSVGM SYAYPKGIRYLK
MTPFVDLQYTKLVQNPVETGYDPRYFSSSEMTNLSLPIGIALEMRFIGSRSSLFLQVSTSYIKDLRRVNPQSSA
SLVLNHYTWDIQGVPLGKEALNITLNSTIKYKIVTAYMGISSTQREGSNLSANAHAGLSLSF

>core/28/3/Org3_Gene776

MQNNRSLSKSSFFVGALILGKTTILLNATPLSDYFDNQANQLTTLFPLIDTLTNMTPYSHRATLFGVRDDTNQ
DIVLDHQNSIESWFENFSQDGGALSCKSLAITNTKNQILFLNSFAIKRAGAMYVNGNFDLSENHGSII FSGNLSF
PNASNFADTCTGGAVLCSKNVTISKNQGTAYFINNKA KSSGGAIQAAIINIKDNTGPCLFFNNAAGGTAGGAL
FANACRIENNSQPIYFLNNQSGLGGAIRVHQECILTKNTGSVIFNNNFAMEADISANHSSGGAIYCISC SIKDNP
GIAAFDNNTAARDGGAICTQSLTIQDSGPVYFTNNQGTWGGAIMLRQDGACTLFADQGDIIFYNNRHFKDTF
SNHVSVNCTRNVS LTVGASQGH SATFYDPILQRYTIQNSIQKFNPNPHEHLGTILFSSAYIPDTSTSRDDFISHFR
NHIGLYNGTLALEDRAEWKVYKFDQFGGTLRLGSRAVFSTTDEEQSSSSVGSVININNLA INLPSILGNRVAPK
LWIRPTGSSAPYSEDNNPIINLSGPLSLLDDENLDPYDTADLAQPIAEVPLLYLLDVTAKHINTDNFYPEGLNT
TQHYGYQG VWSPYWIETITTS DTSSEDTVNTLHRQLYGDWTP TGYKVN PENKGDIALSAFWQSFHNL FATL
RYQTQQGQIAPTASGEATRLFVHQNSNNDAKGFHMEATGYSLGTTSENTASNHSFGVNFSQLFSNLYESHSDN
SVASHTTTVALQINNPWLQERFSTSASLAYSYSNHHIKASGYSGKIQTEGKCYSTTLGAALSCSLSLQWRSRP
LHFTPFIQAI AVRSNQTA FQESGDKARKFSVHKPLYNLTVPLGIQSAWESKFRLPTYWNIELAYQPVL YQQNP
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>core/29/3/Org3_Gene676

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LFINPKFRQEDLDREKYAVHQEFAAHPLSDGRRVHRIQQLVAPQGHPCARFGCGNASTLTPVTTEKMAEWF
KLHYPENMCAIAYTSAPLSKAKKQFSKIFSQIPRSKNYERQEPFLPSGDTSSLKNLYINQAIQPTS NLEIYWHI
YESSHIPLGCYKALAEVLRNESKNSLVSLKNEQLITDL DVEFFRSSLNTGEFYISYELTEKGDKHYSQVIDST
FQYLR YIQEHGIPNYTLEEISTINALNYCYSSKSPLFDLLCKQIVSLGNEDLSTYPYHSLVYPKYSSSEDESALLN
LVSDPEQARFVLSSKNSEHWEEATQLHDPIFDMTYVVKALDGVQDYGKVQSLKPIALPKPNLFIPKEVTLP

VHLLKKQEFPFAPALSYQDDKLTLYHCEDHYYTAPKLSSQIRIRSPQISRSSPQFLVATELYCLAVNDQLLREY
YPATQAGLSFTSALGGDIDLRVSGYTTTVPALLNSILTSLPNLEISYETFLVYKKQLLELYQGALLNCPVRSG
LDELASQVMKETYSNTTKLSALEKLSFSEFQAFASNLFNSVHLEVMLGNLSEQQKKDYLEMLQVFTASRSS
HATKPFYYELQSQEISEIHHDYPLTANGMLLLLQDKSSPSIQGKVCAEMLFEWLHHITFEELRTQQQLGYMV
GARYREFASRPFGFLYIRSDAYSPEELLAKTSLFLNKVSASPEKFGISQEKFANIRKAYINKILEPEHSLDMMNS
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>core/30/3/Org3_Gene53

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DWDRKRFTMEPLANRAVKKAFKTLFENGYYIRGYLVNWDVPLQTALADDEVEYEEKDGWLYYIRYRMV
GSQESIVVATTRPETS LGDTGIAVSPNDERYASWIGASVEVPFVNRQIPIIGDASVDPTFGTGAVKVTPAHDKD
DYLMTGNHHLPMINILTPSGGINENGGPFAGMAKEKAREEILIALEEQGLFVRKEPYKLRVGVSYRSGAVIEP
YLSKQWFVSVSEFRGALREFVESQDIKIFPKDFVKNYLSWVNHLRDWCISRQLWWGHRIPVWYHKNDDERV
LCYDGEGIPPEVAQDPDSWYQDPDVLDTWFSSGLWPLTCLGWPDENSPDLKKFYPTALLVTGHDILFFWVT
RMVLLCSSMSGKPFSEVFLHGLIFGKSYKRYNDFGEWSYISGKEKLAYDMGEALPDGVVAKWEKLSKSKG
NVIDPLEMIATYGTDAVRLTLCSCANRGEQIDLDYRLFEEYKHFANKVWNGARFIFGHISDLQGKDLAGIDE
DSLGLEDFYILDGFNQLIHQLEEAYATYAFDKVATLAYEFFRNDLCSTYIEIHKPTLFGKQGNEASQSTKRTLL
AVLLINVLGVLHPVAPFITESLFLRIQDTLGALPEGDGDFTGHALRMLRSRACMEAPYPKAFDVKIPQDLRE
SFTLAQRLVYTIRNIRGEMQLDPRHLKAFVVCSDTTEIQSCIPILQALGGLESIQLLDKEPEKGLYSFGVVDTI
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FA

>core/31/3/Org3_Gene311

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TNNLGQGT FVDNLALNKG GALYTETNLSIKDNKGPIIHKQNRALNSDSLGGGIYSGNSLNIEGNSGAIQITSNSS
SGSGGGIFSTQTLTISSNKKLIEISENSAFANNYGSNFPNGGGGLTTTFCILNNREGVLFNNNQSQSNGGAIHAK
SIIKENGVPVYFLNNTATRGGALLNLSAGSGNGSFILSADNGDIIFNNNTASKHALNPPYRNAIHSTPNMNLQIG
ARPGYRVLFYDPIEHELPSSFILFNFETGHTGT VLFSGEHVHQNFTEMNFFSYLRNTSELRQGV LAVEDGA
GLACYKFFQRGGTLLLGQGA VITTAGTIPTPSSTPTTVGSTITLNHIAIDLPSILSFQAQAPKIWIYPTKTGSTYT
EDSNPTITISGTLTLRNSNNE DPYDSLDSLHSLKVP LLYIVDVAAQKINSSQLDLSTLNSGEHYGYQGIWSTY
WVETTTITNPTSLLGANTKHKLLYANWSPLGYRPHPERRGEFITNALWQSAYTALAGLHSLSSWDEEKGHA
ASLQGIGLLVHQKDKNGFKGFRSHMTGYSATTEATSSQSPNFSLGFAQFFSKAKEHESQNSTSSHHYFSGMCI
ENTLFKEWIRLSVSLAYMFTSEHTHTMYQGLLEGNSQGSFHNHTLAGALSCVFLPQPHGESLQIYPFITALAIR
GNLAAFQESGDHAREFSLHRPLTDVSLPVGIRASWKNHHRVPLVWLTEISYRSTLYRQDPELHSLKLLISQGTW
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>core/32/3/Org3_Gene783

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GNLSLTGNSQIIFTQNFSSDNGGVINTKNFLLSGTSQFASFSRNQAFTGKQGGVVYATGTITIENSPGIVSFSQN
LAKSGGALYSTDNCSITDNFQVIFDGNSAWEAAQAQGGGAICCTTTDKTVTLTGNKNLSFTNNTALTYGGAI
SGLKVSISAGGPTLQFQSNISGSSAGQGGGGAINIASAGELALSATSGDITFNNNQVTNGSTSTRNAINIIDTAKV
TSIRAATGQSIYFYDPITNPGTAASTDTLNLNLADANSEIEYGGAIVFSGEKLSPTEKAIAANVTSTIRQPAVLA
RGDLVLRDGVTVTFKDLTQSPGSRILMDGGTTLSAKEANLSLNLGLAVNLSSLDGTNKAALKTEAADKNISLS
GTIALIDTEGSFYENHNLSASTYPLLELT TAGANGTITLGALSTLTLQEPETHYGYQGNWQLSWANATSSKI
GSINWTRTGYIPSPERKSNLPLNSLWGNFIDIRSINQLIETKSSGEPFERELWLSGIANFFYRDSMPTRHGFRRHS
GGYALGITATTPAEDQLTFAFCQLFARDRNHITGKNHGDYTGASLYFHHTEGLFDIANFLWGKATRAPWVLS
EISQIIPLSFDAKFSYLHTDNHMKTYT DNSIIKGSWRNDAFCADLGASLPFVISVPYLLKEVEPFVKVQYIYA
HQQDFYERYAEGRAFKNKSELINVEIPIGVTFERDSKSEKGTYDLTLMYILDAYRRNPKCQTSLIASDANWMA
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>core/33/3/Org3_Gene913

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CNGDFTISQNQGTFFVNNNSVNNWGGALSTNGHCRIQSNRAPLLFFNNTAPSGGGALRSENTTISDNTRPIYF
KNNCGNNGGAIQTSVTVAIKNNSGSVIFNNNTALSGSINSNGNGSGGAIYTTNLSIDDNPGTILFNNNYCIRDGG
AICTQFLTIKNSGHVYFTNNQGNWGGALMLLQDSTCLLFAEQGNIAFQNNNEVFLTTFGRYNAIHCTPNSNLQ
LGANKGYTTAFFDPIEHQHPTTNPLIFNPANHQGTILFSSAYIPEASDYENNFISSSKNTSELRNGVLSIEDRA
GWQFYKFTQKGGILKLGHAAASIATTANSETPSTSVGSQVIINNLA INLPSILAKGKAPTLWIRPLQSSAPFTEDN
NPTITLSGPLTLLNEENRDPYDSIDLSEPLQNIHLLSLSDVTARHINTDNFHPESLNATEHYGYQGIWSPYWVE
TTTTNNASIETANTLYRALYANWTPLGYKVNPEYQGD LATTPLWQSFHTMFSLLRSYNRTGDSDIERPFLFI
QGIADGLFVHQNSIPGAPGFRIQSTGYSLQASSETS LHQKISLGFAQFFTRTKEIGSSNNVSAHNTVSSLYVELP
WFQEA FATSTVLAYGYGDHHLHSLHPSHQEAEGTCYSHTLAAAIGCSFPWQQKSYLHLSPFVQAIAIRSHQ
TAFEEIGDNPRKFVSQKPFYNLTPLPGIQGWQSKFHVPTWTELSYQPVLYQQNPQIGVTLLASGGSWDIL
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>core/34/3/Org3_Gene54

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LFSEAVILDWGA AVACGEEEDLLDIDVSKEEVLSSRMTIPGRIVGTPDYMAPERLLGHPASKSTDIYALGVVL
YQMLTLSFPYRRKKGKKIVLDGQRIPSPQEVAPYREIPPFLSAVVMRMLAVDPQERYSSVTELKEDIESHLKG
SPKWTLTTALPPKSSSWKLNEPILLSKYFPMLEVSPASWYSLAISNIESFSEMRLEYTL SKKGLNEGFGILLPT
SENALGGDFYQGYGFWLHIKERTLSVSLVKNSLEIQRC SQDLES DKETFLIALEQHNHSLSLFVDGTTWLIHM
NYLPSRSGRVAIIVRDMEDILEDIGIFESSGLRVSCLA VPDAFLAEKLYDRALVLYRRIAESFPGRKEGYEARF
RAGITVLEKASTDNNEQE FALAIEEFSKLHDGVAAPLEYLGKALVYQRLQEYN EEEKSLLLALKRYSQHPEIF
RLKDHVVYRLHESFYKRDR LALVFMILVLEIAPQAITPGQEEKILVWLKDKSRATLFCLLDPTVLELRSSKME
LFLSYWSGFIPHLNSLFHRAW DQSDVRALIEIFYVACDLHKWQFLSSCIDIFKESLEDQKATEEIVEFSFEDLGA
FLFAIQSIFNKEDA EKIFVSNDQLSPILLVYIFDLFANRALLESQGEAIFQALDLIRSKVPENFYHDYLRNHEIRA
HLWCRNEKALSTIFENYTEKQLKDEQHEL FVLYG CYLALIQQGA EAAKQHFDVCREDRIFPASLLARNYNRLG
LPKDALS YQERRLLLRQKFLYFHCLGNHDERDLCQTM YHLLTEEFQL

>core/35/3/Org3_Gene782

MKIPLHKLLISSTLVTPILLSIATYGADASLSPTDSFDGAGGSTFTPKSTADANGTNYVLSGNVYINDAGKGTA
LTGCCFTETTGDLTFTGKGYSFSFNTVDAGSNAGAAASTTADKALTFTGFSNLSFIAAPGTTVASGKSTLSSA
GALNLTDNGTILFSQNVSNNEANNNGGAIKATLSISGNTSSITFTSNSAKKLGGAIYSSAAASISGNTGQLVFM
NNKGETGGGALGFEASSSITQNSSLFFSGNTATDAAGKGGAIYCEKTGETPTLTISGNKSLTFAENSSVTQGG
AICAHGLDLAAGPTLFSNNRCGNTAAGKGGAIADSGSLSLSANQGDITFLGNTLTSTSAPTSTRNAIYLG
SAKITNLRAAQGQSIYFYDPIASNTTGASDVLINQPDNSPLDYSGTIVFSGEKLSADEAKAADNFTSILKQPL
ALASGTLALKGNVELDVNGFTQTEGSTLLMQPGTKLKADTEAISLTKLVVDLSALEGNKSVSIETAGANKTIT
LTSPLVFQDSSGNFYESHTINQAFQPLVVFTAATAASDIYIDALLTSPVQTPEPHYGYQGHWEATWADTSTA
KSGTMTWVTTGYNPNPERRASVVPDSLWASFTDIRTLQQIMTSQANSIYQQRGLWASGTANFFHKDKSGTN
QAFRHKSYGYIVGGSAAEDFSENIFSVAFQCFLFGKDKDLFIVENTSHNYLASLYLQHRAFLGGLPMPSPSGSITD
MLKDIPLILNAQLSYSYTKNDMDTRYTSYPEAQGSWTNNSGALELGGSLALYLPKEAPFFQGYFPFLKFQAV
YSRQQNFKESGAEARAFDDGDLVNCIPVGIRLEKISEDEKNNFEISLAYIGDVYRKNPRSRSTSLMVSGASWT
SLCKNLARQAFLASAGSHLTLSPHVELSGEAAAYELRGSAGHIYNVDCGLRYSF

>core/37/3/Org3_Gene301

MKSSLHWFLISSSLALPLSLNFSFAAAVVEINLGPTNSFSGPGTYTPPAQTTNADGTIYNLTGDVSITNAGSPTA
LTASCFKETTGNLSFQGHGYQFLLQNIDAGANCTFTNTAANKLLSFSGFSYLSLIQTTNATTGTGAIKSTGACS
IQSNYSCYFGQNFSNDNGGALQGSSISLSLNPNTFAKNKATQKGGALYSTGGITINNTLNSASFSENTAANN
GGAIYTEASSFISSNKAISFINNSVTATSATGGAIYCSSTSAPKPVLTLSDNCELNFIGNTAITSGGAIYTDNLVL
SSGGPTLFGKNNSAIDTAAPLGGAIADSGSLSLALGGDITFEGNTVVKGASSSQTTTRNSINIGNTNAKIVQL
RASQGNTIYFYDPITTSITAALSDALNLNGPDLAGNPAYQGTIVFSGEKLSEAEAAEADNLKSTIQQPLTLGG
QLSLKSGVTLVAKSFSQSPGSTLLMDAGTTLETADGITINNLVLNVDLSKETKKATLKATQASQTVTLGSL
LVDPSGNVYEDVSWNNPQVFSCLTLTADDPANIHITDLAADPLEKNPIHWGYQGNWALSWQEDTATKSKAA
TLTWKTGYNPNPERRGTLVANTLWGSFVDVRSIQQLVATKVRQSQETRGIWCEGISNFFHKDSTKINKGFR
HISAGYVVGATTTLASDNLITA AFCQLFGKDRDHFINKNRASAYAASLHLQHLATLSSPSSLRYLPGSESEQP
VLFDAQISYIYSKNTMKTYYTQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIKVEASYIHQDSF
KERNTTLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVADVYRKNPDCTTALLINNTSWKTTGTNLS
RQAGIGRAGIFYAFSPNLEVTSNLSMEIRGSSRSYNADLGGKFQF

>core/38/3/Org3_Gene303

MKTSIPWVLVSSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTFTPKTSATTYSLTGDVFFYEPGKGTPLSDC
FKQTTDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGQGTLSAGGVNL
ENIRKLVVAGNFSTADGGAIKGASFLLTGTSGDALFSNNSSTKGGAIATTAGARIANNTGYVRFLSNIASTSG
GAIDDEGTSILSNKFLYFEGNAAKTTGGAICNTKASGPELIISNNKTLIFASNVAETSGGAIHAKKLALSSGG
FTEFLRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTDTPKRNAINIGSNGKFTELRAAKNHT
IFFYDPITSEGTSSDVLKINNGSAGALNPYQGTILFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQKGV
LESTSFQSEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYES
HMFSDQLFSLKIVDADVDNVDISSLIPVPAEDPNSEYGFQGWVNVNWTDTATNTKEATATWTKTG
VPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFVWSSMTNFLHKTGDENRKGFRHTSGGYVI

GGSAHTPKDDLFTFAFCHLFARDKDCFIAHNSRITYGGTLFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREIP
LALDVQVSFSHSDNRMETHYTSLPESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSF
FESSDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDSWKIRGGNLSR
QAFLLRGSNNYVYNSNCELFGHYAMELRGSSRNYNVDVGTKLRF

>core/39/3/Org3_Gene796

MQRVLRLLFNLHHGEEKRAFLFLLGLVWGIGCYGTLSLAEGLFIEKLGSAELPKIYLGSSLILCVLSSLILYNL
FKKHISATALFLIPVLSILCNFYLILSSIFAIDPPRSPLFFYRIVIWSLTILSYTSFWGFDQFFNLQDGKRHFCIF
NAIIFLGDAIGSGIIASLVHTIGIQGILILFTAALVLTPIVFYVSKSLKSLSDDHDLFIDTGHPPPLSKALKLCFYD
KYTFYLLCFYFLMQLLAIAATEFNLYLKIFEIQFASKEEFELVAHIGKCSLWISLGNMCFALFAYSRIVKRLGVNNI
ILFAPLCFLSLFLFWTFKTTLSIAVLAMVVREGVTYALDDNNLQLLIYGVPNKIRNQIRIVVESFIEPIGMLVWS
LVCFLSSQQYVFCLISLIATILVCLVRSYYAKAILKNLSAQALQLTRSMQDWIKSMTVKQKRQVELFLLAHL
KHPSERHQTFQHLNLASRSVLPSSLAHMNKLSLPNKLKTIEMVKSSLWAKDFLTLELLKRWTSIFPHPAI
ASAIHLYFAEHDLLHITHIAEDLYDTVGDRLAAILTVRRQEAYGPYRDLADKRLKELLNSDQPEDIVMGLTI
LKLEKNPQNFPILLDFLNTKNEDILIVTCKALHTSVRANHKKPYCPELLKRLRQC SHNDEASQYLLKTISIALDIS
FVKDLLMTTSQKNTSRKYAEAMIGELDKEVAPAFQLVLTDEGTHNRCRILAAKALCKIDNWLLKKHAYKI
VKSKASKALFYSYHGHIYQKKYPTYNLSLLANTLNSNYAEVNFMLSLLGILGSMEHSGVLIRALTSKNQKI
KAQALESLEKNCDSHLFSLLEPFVNQPGMCYSEKYYFKCGVIPLTLKELNMMENSPSSLNKLTAQQLKEEL
SYCDPDFQSVNTIYNQEHEDFRTEESETLISFLSI

>core/40/3/Org3_Gene4

MRFSLCGFPLVFSFTLLSVFDTSLSATISLTPEDSFHGD SQNAERSYNVQAGDVYSLTGDVSI SNVDNSALNK
ACFNVTSGSVTFAGNHHGLYFNNISSGTTKEGAVLCCQDPQATARFSGFSTLSFIQSPGDIKEQGCLYSKNAL
MLLNNYVVRFEQNQSKTKGGAISGANVTIVGNYDSVSFYQNAATFGGAIHSSGPLQIAVNQAEIRFAQNTAK
NGSGGALYSDGDIDIDQNAYVLFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNHSIMGG
GAIYARKLSISSGGPTLFINNISYANSQNLGGAIAIDTGGEISLSAEKGTITFQGNRTSLPFLNGIHLLQNAKFLK
LQARNGYSIEFYDPITSEADGSTQLNINGDPKNKEYTG TILFSGEKSLANDPRDFKSTIPQNVNLSAGYLVIKE
GAEVTVSKFTQSPGSHLVLDLGTKLIASKEDIAITGLAIDIDSLSSSSTA AAVIKANTANKQISVTDSIELISPTGN
AYEDLRMRNSQTFPLLSLEPGAGGSVTVTAGDFLPVSPHYGFQGNWKLAWTGTGNKVGEFFWDKINYKPRP
EKEGNLVPNILWGNAVDVRSLMQVQETHASSLQTDRGLWIDGIGNFFHVSASEDNIRYRHNSGGYVLSVNN
EITPKHYTSMAFSQLFSRDKYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPNVNVGILSRRFLQNPLMI
FHFLCAYGHATNDMKTDYANFPMVKNSWRNNCWAIECGGSMPLL VFENGRLFQGAIPFMKLQLVYAYQG
DFKETTADGRRFSNGSLTSISVPLGIRFEKLALSQDVL YDFSFSYIPDIFRKDPSC EAAALVISGDSWLVPAAHVS
RHAFVGS GTGRYHFNDYTELLCRGSIECRPHARNYNINCGSKFRF

>core/41/3/Org3_Gene491

MKTVILNIGRKILQGIKKKKKKIGILSGLFFLDLVLLGVSSQRPTETSANVKHNL RDEKLAACPKN SAASLSAK
KSHTKKTTPGSIPSKVFSKFDATQDKTFQKTSGSAFPAKPTTLKELEERKKPRPERRTTADV KRSRFLPTQEV
EEPVPAASKEQLDSIQVWEEKQNYARRAVNAINLSIKKQLEEQTSTVTEKDVQPKTQATPHASKKNVASPST
SMPGIEKAATTVA VPQDKSEEEKVKERLTKRELTCEDLKDNGYTVNFEDISILELLQFVSKISGTNFVFD SNDL
QFNVTIVSHDPTSVDDLSTILLQVLKM HDLKVVEQGN NVLIYRNPHLSKLSTVVTDSS LKETCEAVVVTRVFR

LYSVSPSAAVNIIQPLLSDAIVSASEATRHVIISDIAGNVDKVSDLLAALDCPGTSVDMTEYEVKYANPAALV
SYCQDVLGTLAEDDAFQMFIQPGTNKIFVSSPRLANKAEQLLKSLDVPHEMAHTLDDPASTALALGGTGTTS
PKSLRFFMYKLKYQNGEVIANALQDIGYNLYVTTAMDEDFINTLNSIQWLEVNNSIVIIGNQGNVDRVIGLLN
GLDLPPKQVYIEVLILDTSEKSWDFGVQWVALGDEQSKVAYASGLLNNTGIATPTKATVPPGTPNPGSIPLP
TPGQLTGFSMDLNNSSAFGLGIIGNVLSHKGKSFLTGLGLLSALDQDGDVIVLNPRIMAQDTQQASFFVGQT
VPYQTTNTIIQETGTVTQNIDYEDIGVNLVVTSTVAPNNVVTLQIEQTISELHSASGSLTPVTDKTYAATRLQIP
DGCFLVMSGHIRDKTTKVVSQVPLLNSIPLIRGLFSRTIDQRQKRNNIMMFIKPKVISSFEEGTRVTNKEGYRYN
WEADEGSMQVAPRHAPECQGPPSLQAESDFKIIIEIAQ

>core/43/3/Org3_Gene703

MSKDKKMKPEPKKNFPTVFFLLFGVVFGVVAFQNFLAGKKARVGFSSHQIEHLVNLRLIVPEDSHKIALNDN
LVSFQGRFRDVQTQEGQLRYHYLELIDQGHRLDLQETSKSLTTLGKEVTNSILWFSASGSPICEQGYAISY
PSEVSGSVLTEPLVVTGPATPQLINLHSLQERYPTLSRSPEALRTYGSPLYELIGKYLSPVLGIGSETLKRELKD
LYQQVEVSLTQETDTEAAYTLYGQVLSTLNRISSSLVSEGGERSQLRSVRLYREEWNKYHKLVEARDLNQ
AQLEKLRGELSQTWVYFNNQELSSRSLEKQDPEVFGHWFAGAKEEWTAFFKNHSLSFKAPDQPRNLVLEKT
FKSQEPSPHYLGYLFTFLPIILVLLFVYLVFSRQMRGMSGMSAMSGKSPARMLLKQNKVTFADVAGIEEAKE
ELIEIVDFLKNPNKFTSLGGRIPKGVLLIGPPGTGKTLLIAKAVSGEADRPFFSIAGSDFVEMFVGVGASRIRDMF
EQAKRNAPCIIFIDEIDAVGRHRGAGIGGGHDEREQTLNQLLVEMDGFGTNEGVLMAATNRPDVLDKALLR
PGRFDRRVVMNLPDIKGRFEILMVHAKRIKLDPTVDLMAVARSTPGASGADLENLLNEAALLAARKDRTAV
TAVDVAEARDKVLGYKERRSLEMDAERKTTAYHESGHAHVGLCVQHGDVPDKVTIIPRGLSLGATHFLPE
KNKLSYWKKELYDQLAVLMGGRAAEEIFLGDISSGAQQDISQATKLVRSMVCEWGMSPQLGNVTDERSD
GLTGYGGYHEKSYSEETAKTIDTELRLMLDAAYQRALDIINEHKAIEELMTQMLIEFETLDSKDVKEIMDHT
WDPEKKRARLKEEGMLFKKSSDDLPPPPPKEDTLPGLGFNAT

>core/44/3/Org3_Gene253

MDSEFVGQVYSSDMDWIESMYQRFMNHETLDPSWKYFFEGYQLGQAASPSEASTKISGNETIAMLQEQKSQ
FLCTIYRYYGYLQSQISTLAPTTDSRFIQEKIAKIDLDEQVPSAGLLPKAQVSVRELIEALKKCYCGSLTLETLT
CTPELQEFVWNLMEKRQVERFAEQLLSYKDLCKATFFEEFLQIKFTGQKRFSLEGGETLVPMLEHLVHYGS
ALGISNYVLGMAHRGRLNVLTNVLGKPYRYVFMEFEDDPAARGLESVGDVKYHKGYVLKSHQKDRETTFV
MLPNASHLESVDPIVEGVVAALQHQQGHAGKEQSSLAILVHGDAAFSGQGVVYETLQLSRVPGYSTEGTLHIV
VNNYIGFTAVPRESRSTPYCTDIKMLGIPVFRVNSEDDVACIEAIEYALQVRERFSCDVIIDLCCYRKYGHNE
SDDPSVTAPLLYDQIKRKKSIREFRQYLLEGQFADISEETLASIEKEIQESLNREFQVLKGTDPPEFPKKECHH
CDRLNNGELILHDCDVSLDRETFLHMSSRLCGFPDNFHPHPKIKTLLEKRMKMAEGGVGYDWAMAEELAF
ALLIEGYNLRLSGQDSIRGTFQRHLVWSDTVTGDYSPYHLSAEQGSVEMYN SPLSEYAILGFEYGYAQA
LKTLLVWEAQFGDFANGAQIIFDQYISSGIQKWDLHSDIVLLLPHGYEGQGPEHSSSRIERYLQLAANWNFQV
VLPSTPVQYFRILREHAKRDLPLVFTPKLLRYPQCVSSIEEFTEPGGFRAILEDADPNYDASILVLCGKIY
YDYAEMLPQDRRKDFSCLRISLYPLALEDLVSLIDKYSHLKHFWWLQEEKNMGAYDYMFMALQDILPEK
LLYIGRPRSSTASGSALKSRQELVTCMETLFLSLR

>core/45/3/Org3_Gene794

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SPESTSRIRAKNRSSFSSSEESSAHIPVDTSEPAPVSIADPEPELEVVDVCDSEPEVHPVAEVLPEQPVLPET
PPQKELEPKPVKPAEPKSVVMIKSKFGPTGKHINLLAKTFKAPAKEEKVVAGSKSTKPVASDKTGKPGTSE
GGEQNNREKQFNPANRSPASGPKRDAGKKNLTDFRDRSKKSDESLKAFTGRDRYGLNEGGEEDRWRKKRV
YKPKKHYPDEASIQRPHTHIKISLPITVKDLATEMKLKASEVIQKLFHGMITYVVNDILDSETAVQFIGLEFGCTID
IDYSEQDKLCLSNLTVRDEIQSTDPSKLVIRSPIVAFMGHVDHVGKTTLIDSLRKSNAATEAGAITQHMGAF
CSTPVGDIITLTPGHEAFSAMRARGAEVCDIVVLVAGDEGIKEQTLEAIEHAKAADIAIVVAINKCDKPNF
NSETIYRQLSEINLLPEAWGGSTVTVNTSAKTGEGLSELLEMLALQAEVLELKADPSARARGLVIESELHKGL
GPVATVLIQNGSLKLGEALVFNDYCYGKVKTMHNEHNELMKEAGPSIPVLITGLSDIPKAGDPFFVVKNEKTA
RDIIARSAGQQRFALQQKKRPNFDSMLQNKTKLMIKADVQGSIEALVSSISKIKSEKVDVEILTNSVGEIS
ESDIRLAAASKAVLIGFHTGIESHAELIKSLGVRVELFTVIYHAIDAIKEIMTSLDPAAEEKDEGSAEIKEIFRS
SQVGSIIYGCIVTEGIMTRNHKVRVLRNKEILWKGTLSSLKRVKEDVKEVRKGLECGILLEGYQQAQIGDVLQ
CYEVIYHPQKL

>core/46/3/Org3_Gene630

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RIFRLTDKDNFWSMANTGPCGYCSELLFDRGPSFGNASSPLDDTDGERFLEYWNLVMEFNRTSEGSLALP
NKHVDTGAGLERLVSLIAGTHTVFEADVLELIAKTEQLSGKVYHPDDSGAAFRVIADHVRSLSFADGLLP
GNTERGYVLRKILRRSVNYGRRLGFRNPFLAEIVPSLADAMGEAYPELKNSLSQIQKVLLEEESFFKTLDRG
GNLLQQVLKSSSSSSCISGEDAFKLKDTYGMPIDEISLLAKDYDYSVDMDTFHKLEQEAKERSRKNVVSQSG
TSESIYNELHLTSEFIGYDHLSCDTFIEAIIKDHIVSSLQEKQEGAIVLKVSPFYAEKGGQVGDGSEIFCSEGT
VTHTTSPKAGLIVHHGRISQGSALTVEAAVTAQVNRYYRRKRIANNHTACHLLHKALEITLGDHIRQAGSYVDD
TKIRLDFTHPQAISPEDLLCIETLVNESIRENEPVDIREALYSVDMNSSEIKQFFGDKYSVVRVVSAGHSHEL
GGTHAEATGDIGFFRITKEHAVAMGIRRIEAVTGEKAEATVHQQSEVLEEIATLLQVPRDQIVSRLTATLDER
KQQDKRLNELENSLIQTKLDKLIHNCHQRQGITCLVHHLAEHENHRLQQYAQCLHQRIPEKLISLWTTEKNG
KYIVLSRVSDDLITQGVHAQDLLKAVLTPCGGRWGGKDQSAQGSAPALPATEVLNETLWQWISTQLI

>core/47/3/Org3_Gene942

MSTFSIQNRLRTISGESTRIIKLDHKYSGFDPRSVPAINLEELNSGIYALRHLMNALQSENTNVAALLNPNTIF
PTTSWTDYKHSRPQASSPRAPSSQTPTDIVSAAALALVLVIDGGLAELVASVTEIDLALSTISTVRQLMASYL
GLTTLTAEQEKVVFSSSYVPSEKNLLEHVKQEKAAEIQAKQEEIKAVLEAKGVSTEEIEAILKEYPDIYAADFF
KEFIEEPLHTYRAKVGAPIQEMNENAIQLLPTPPAITPDNVNEVNGMNTLSTILQAIDDAIKQAPALGGDQEIIT
ILQTLVPLVDKTTFTKAEFDLIYTATQLPNTASLKLYLTDRQIAEYRGKITKVYQNSIQNLSETKRVVENNRSM
LETQLSMFQQAQNCFTWISQANALNIAITNKYISAVLTTSMEMYGGLLCLSYMYERLADDEKAIFDKSVNE
YLPPIHVVGGSWVNGWIAKMAAYQELAEYSLGTAVTSQDQIKAYLQTRGNEFKATRHFFHNIGDQMYQFAN
ETVFGNCLTTANGAIQPDLGGFIREAMTNVGTVEADYVSNAQRILNEFNATAAHVLQLQLQIAELQKKADD
LDPGKASFTENRKFAVAAWITSESLGDALISMILNSQLPKQEAFLKPLIEEINFNNLAANALNSLLQITNEFSTT
SVYYSLSSYLVSQKTGQNLFAGDYYETLLAAAREREYIYRDTARCKQAINLVNGLLQKINSLPGATSAHKQE
MLNATTYYYQYSLSVTLNQLTVLESLLAGLKMTLQTTSNNKYDKSVFKIESFDDWIPTLAALESFLTSGFPNIS
ATGGLGPLFTQVQSDQQTYTSQGQTQQNLNQNMTTIQQEWTLVSTSMQVLNGILSQLAGAIYSN

>core/48/3/Org3_Gene542

MKKSLIIVESPAKIKTLQKLLGSEFVFASSIGHIVDLPAKEFGIDVDHDFEPQYQVLPDKQEVINHIRKLAACE
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ISPILSRKLQQRSGISAGRVQSVALKLVVDREKAIDAFVPVEYWNLRVLMQDPKTTKTFWAHLYAVQGKKW
EKEIPEGKTENDVLLINSEEKARHYAELLEKSSYTITRVEAKAKRRFAPPPFITSTLQQEASRHFRRFSASRTMSI
AQTLYEGVDLDSSTGLITYMRTDSVRVDPEALTTVREYIQQTFGKEYLPEKANVYTTKKMTQDAHEAIRP
TDINLTPDKLKNKLSDDQFKVYNLIWKRFVASQITPAIYDTLAVQITTDTEIDLRASGSLLKFKGFLAVYEEKQ
DDENDQEEDHPLPPLHAQDALIKEEVSQEQAFTKPLPRFTEASLVKELEKSGIGRPSTYATIMNKIQSREYTTK
ENQRLRPTELGKIISQFLETNFPRI MDIGFTALMEDELELIADNKKPWKLLLQEFWTTFLPVVITAEKEAVIPRI
LTNIECSKCHKGKLVKIWSKNSYFYGCSEYPECDYRTSEEELAFNKEDYAEDTPWDSPCPLCGGVMKVRHG
RYGTFLGCEKYPECRGITISHHKKGEEIEQEEPIPCPAIGCNGKIFKKRSRYNKIFYSCSEYPECSVIGNSIDAVITK
YSGTEKIPYKKKTPTKKKSSAKTTKAAKTPSKKGKAKSSVKKSSSEKKTGPLFLPSPDLAKMIGNEPVSRGEAT
KKIWDYIKEHQLQAPENKKLLVPDNNLATIIGPNPIDMFQLSKHLSQHLLTKVSNDESSASS

>core/49/3/Org3_Gene416

MKKLFVLDASGFIFRAYFALPEMKNHQQQATQAVFGFIRSLNKLIKEFSPEY MISVFDGPNNKQSRQAIYADY
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VAWNPWADQGVVGISEVIERYGIPPGNIPDYLALVGDSSDNIPGLPGCGPKKAAALLKQFGSVEGLLENLDA
VKGLSQTMLSERQETLKL SKRLALLDSNIPVPIESLTFPQHPVDEEKLIHFYIQQGFKTLVPSKQTEAATVDV
QIIKDAESLTNINLVQGGDIAFAVAYTGNHLLSLKLEGLALTQGSGVFFIALEEEGTKILPILKDFFLREDLTF
YGYNLKRDCHALLNAGIVIREISYDLALAEHLTNGGGKISFQSLLVNHGFTETAHRFAKEWGNISGLPIGRLPE
QPEQYFGEFVAYLPIIKDAILEEINRKNLNHILSDIEMPLEKVLFSMERAGVPLDVEELAILEALFETELAVLTE
EIYDLGRFPNIKSPKQLSDILYNELGLRPIDKAKSTRAEVLEALRSEHPHIEKLLAFRTIEKLLSTYVKALPKQV
DSHTQRIHPSFDQTGAVTGRLACRDPNLQNIPIRSERGILLRKAFLRSEKNSYFLSADYSQIELRFLAHLSDKS
LKFAFESGEDIHAFTASQVFHVPLEQVSKEQRMQAKT VNF GIVY GQQAFLAKVLKISIGEAQELIQAYFSRY
PEIAHFVEETIQQAADLRVTTMLGRERIIDSWNEFPGSRAASGRFAVNTRIQGSAAELIKLAMLDISQAIKQQ
QMKSRMLLQIHDELLFEVPEEEIEEMQRLVREKMESAMTLSVPIVVNIIIGKNWAEC

>core/50/3/Org3_Gene86

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EGEVDPKPSPGLQTLLRDAKQEAKTLGDEYISGDHLLAFWSSNKEPFNSWKQTTKVSFKDLKNLITKIRRG
RMDSPSAESNFQGLEKYCKNL TALAREGKLDPVIGRDEEIRRTIQVLSRRTKNNPMLIGEPGVGKTAIAEGLA
LRLIQGDVPESLKGKQLYVLDMGALIAGAKYRGFEERLKSVLKDVESGDGEHIFIDEVHTLVGAGATDGA
MDAANLLKPALARGTLHCIGATTLENYQKYIEKDAALERRFQPIFVTEPSLED AVFILRGLREKYEIFHGVRIT
EGALNAAVLLSYRYIPDRFLPDKAIDLIDEAASLIRMQIGSLPLIDEKERELAALIVKQEAIKREQSPSYQEEA
DAMQKSIDALREELASRLGWDEEKKLISGLKEKKNSLES MKFSEEEAERVADYNRVAELRYS LIPQLEEEIK
QDEASLNQRDNRLQEEVDERLIAQVVANWTGIPVQKMLEGAEKLLILEESLEERVVGQPF AVSAVSDSIR
AARVGLNDPQRPLGVFLFLGPTGVGKTELAKALADLLFNKEEAMVRFD MSEYMEKHSISK LIGSSPGYVGYE
EGGSLSEALRRRPYSVVL FDEIEKADKEVLNILLQVFDDGILTDGKKRKVNCKNALFIMTSNIGSPELADYCS

KKGSELTKEAILS VVSPVLKRYLSPEFMNRIDEILPFVPLTKEDIVKIVGIQMRRIAQRLKARRINLSWDDSVIL
FLSEQGYDSAFGARPLKRLIQKVVILLSKALLKGDIKPDTSIELTMAKEVLVFKKVETPS

>core/51/3/Org3_Gene501

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KLTKDQGSSDPITSGDQELADAFASAKAEKNQPRAKVAKKGLKESSNESLNPKEQNAKDSPKGEERTNKPQ
NAIMEDNGASPRQDPQPKSAEPSLKNTARDETPLKENKPVEEKANKKATPDSPEKKDQPEEGSKKEGSKIEA
TPLDSQKESEDKEAEEAFVQEEEEENLTEDNKEDSDSAADANDDTASDHTAEDNKETPKKVENEKS AVLSPFH
VQDLFRFDQTIFPAEIDDIAKKNISVDLTQPSRFLKVLAGANIGA EFHLD SGKTYILGTDPTTCDIVFNDLSVS
HQA KITV GNDGGILIEDLDSKNGVIVEGRKIDKTSTLSSNQVVALGTTLFLLDHHPADTIVASLSPDDYSL
FGRQQDAEALERQEAQEEEEKQKRATLPAGSFILTLFVGGLAILFGIGTASLFHTKEVVPLENIDYQEDLAQVI
NQFPTVRYTFNK TNSQLFLIGHVKNSTDKSELLYKVDALSFVKSVDNVIDDEAVWQEMNILLSKRPEFKGIS
MHSPEPGKFIITGYVKTEEQAACLVDYLNHFNYLSLLENKVVVETQMLKAIAGHLLQGGFANIHVAFVNGE
VILTYGVNND DAEKFRAVVQELSGIPGVRLVKNFAVLLPAEEGIIDLNLRYPNRYRVVTGYSRYGEISINVVVN
GRILTRGDVIDGMTVTSIQPNAIFLEKEGLKYKIDYNK

>core/52/3/Org3_Gene911

MFETFTNRAKQVIKLAKKEAQRLNHNYLGTEHILLGLLKLGQGVAVNVLRNLGIDFDTARQEVERLIGYGPE
IQVYGD PALTGRVKKS FESANEEASLLEHNYVGTEHLLL GILHQSDSVALQVLENLHIDPREVRKEILKELETF
NLQLPPSSSSSSSSSRNPSSSKSPLGHS LGSDKNEKLSALKAYGYDLTEMVRESKLDPVIGRSSEVERLILILCR
RRKNNPVLIGEAGVGKTAIVEGLAQKIILNEVPDALRKKRLITLDLALMIAGTKYRGQFEERIKAVMDEV RKH
GNILLFIDELHTIVGAGAAEGAIDASNILKPALARGEIQCIGATTIDEYRKHIEKDAALERRFQKIVVHPPSVDE
TIEILRGLKKKYEEHHNVFITEEALKAAATLSDQYVHGRFLPKAIDLLDEAGARVRVNTMGQPTDLMKLEA
EIENTKLAK EQAIGTQEYEKAAGLRDEEKKLRERLQSMKQEWENHKEEHQVPVDEEAVAQVVS LQTGIPSA
RLTEAESEKLLKLEDTLRRKVIGQND AVTSICRAIRRSRTGIKDPNRPTGSFLFLGPTGVGKSLLAQQIAIEMFG
GEDALIQVDMSEYMEKFAATKMMGSPPGYVGHEEGGHLTEQVRRRPYCVVLFDEIEKAHPDIMDLMLQILE
QGRLTDSFGRKVDFRHAIIMTSNLGADLIRKS GEIGFGLKSHMDYKVIQEKIEHAMKKHLKPEFINRLDES VI
FRPLEKESLSEIHHLEINKLDSRLKNYQMALNIPDSVISFLVTKGHSPEMGARPLRRVIEQYLEDPLAELLKES
CRQEARKLRATLVENRVAFEREEEEQE AALPSPHLES

>core/53/3/Org3_Gene868

MKIPLRFL LISLVPTLSMSNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVFKDSVVIENVPKTGET
QSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSEAANKTVTL SGFSALSFLKSPASTVTNGLGAIN
VKGNLSLLDNDKVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNSSSTRGGAIHTKNLTLSSGGETL FQGNT
APTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGATGTVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGS
TSVADALNINSPDTGDNKEYTGTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQ
DANSKLIMDLGTSLVANTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVL AISDES FYQNGFLNEDH
SYDGILELDAGKDIVISADSRSIDAVQSPYGYQGKWTINWSTDDKKATVSWAKQSFNPTAEQEAPLVPNLLW
GSFIDVRSFQNFIELGTEGAPYEKRFVWAGISNVLHRSGRENQRKFRHVSGGAVVGASTRMPGGDTLSLGFA

QLFARDKDYFMNTNFAKTYAGSLRLQHDASLYSVVSILLGEGGLREILLPYVSKTLPSCSFYGQLSYGHTDHR
MKTESLPPPPRRSRRIILLGEDMSGLESWELELLLKIPAAEDFSKSTLHL

>core/54/3/Org3_Gene799

MFNKDEIIVPKNLEEEMKESYLRYSMSVIISRALPDIRDGLKPSQRRVLYAMKQLSLSPGAKHRKCAKICGDT
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VDIVPNYDETKHEPVVFPSPKFPNLLCNGSSGIAVGMATNIPPHNLGELIEATLLLLANPQASVDEILQVMPGPD
FPTGGIICGSEGIRSTYTTGRGKIKVRARLHVEENEDKHRESIIITEMPNVNKSRLIEQIANLVNEKTLAGISDV
RDESDKDGIIRVVLEIKKGESSEIIINRLYKFTDVQVTFGANMLALDKNLPRTMSIHRMISAWIRHRKEVIRRT
RYELNKAETRAHVLEGYLKALSCLDALVKTIRESGNKEHAKERIIESFGFTEPQALAILRLYQLTGLEAEKI
QKEYEELLNKIAYYKQVLSDEGLVKDIIRNELQDLLKHHKVARRTTIEFDADDIRDIEDIITNESVIITISGDDY
VKRMPVKVFKEQRRGGHGVGTGFDMMKKGAGFLKAVYSAFTKDYLIFTNFGQCYWLKVVWLPEGERRAKG
KPIINFLEGIRPGEELAAILNIKNFDNAGFLFLATKRGVVKKVSLDAFSNPRKKGIRALEIDEGDELIAACHIVS
DEEKVMLFTHLGMVVRFPHEKVRPMGRTARGVRGVSLKNEEDKVVSQIVTENQSVLIVCDQGFGKRSLVE
DFRETNRGGVGVRISILINERNGNVLGAIPVTDHDSILLMSSQGQAIRINMQDVRVMGRSTQGVRLVHLKEGD
ALVSMEKLSSNENDDEVLSGSEEECSDTVSLR

>core/55/3/Org3_Gene941

MIYSTSISTFYKKLSLVSSMHSFAQRHRESLEHIANYEKTTAERDILKRLIEVLDQRASERYRSAVEKLHKYEV
ERATVAKSIPVAAIHEKPLSSTHASVQVTASTPAATGSGVGAYYNAVKKQWAQDLIVELNTVMTTIMASVNS
KNPANKDVFDKLNTELQALVAAGNNLTEENFQTLYNFPPEEIFTAIQRADTFTGGMKTDFTNQLAGKYGNQA
TLTQTFADGRVEGFKDILTAVQGVLTPEQFTIFAEIATELQALADHVGNFDEAGLQRIEDAGEKLA VINSSD
LTRNDKIMFCQHITDLYSDQVAALGSFDTVLDASIYVNQHQTMTFSNLSSFVGLIGTFAPIDLSSSQGDISSA
ALAGALQTARGLNSRFNELTAEQQKLINECIKSLVTFKCGEHLGAIWAYFTASTVVALNPTATMDHVKAAIL
EEAKELDNSSFQLASSIKSAMTSIVNSSGSFSVTVNSSTLQYTIYSEKNGKVEINQILLNYGSTGFLPEITKLAKT
NAESTARSYFRFKALAAVESENVQNKIEDLQSQLQQFTNMKTELFDGQLLSQASELRALPLPSAVASVLIDRY
MPKEVDYLNEIYKKLYYSNLGSSVGNSIIDAISQYVNGATYFNFASYVGQQPAVGAGGANAFPGSQESAQAK
LDQERKQAALYLQETRGA LTVIEEQRARVLKDDKITNEQRSTILDSL RNYEDNINSISGSLVLLQNYLQPLSIA
GGSVAGTFEVKEGQEQQWQARLQILEEALVSGLVGNMINGGMFPLQSTIQSDQQSFADMGQNFQLDLQMHLT
SMQQEWTVVATSLQLLNQMYLSLARSLTG

>core/56/3/Org3_Gene842

MTEKKPTPMMEQWHQCCEKAGDSVLLFRMGDFYEA FYDDAVLLSQHLELTLTQRQGIPMSGIPVSTVDITYV
DRLIGKGFKVAVAEQFGEPAKEKESKKIGPMARDIQRFTPGTLLSSTLLQEKFNNYIVAINRIGSLFGFACLD
LSTGSFFIEECENTKELVDEICRLAPSEVLSCNKFYNKETAIVMQLQQHLKLTSTYADWAFEHKFASQKLTT
HFQVASLDGFGGLKGLVPAINAAGGLLSYIQDKLLLPTKHIAIPQTRGKQQKLLIDTASQVNLELLAPLNDPQG
KNSLLRIMDHTSTPMGGRLLRQILISPFYNPKEILVRQDAVEFFLRQVTLRKNIKTYLCQVRDIERLMTKVTTG
LAGPRDIGTLRDSFSAGA QIYEQLASATLPEFFIDKCSLDTKLASLIALLSKSLNGDLPLRVSDGNIFVDEFHND
LKRLRHNQEHSQEWIWEYQERIRKETGIKKLKICFAQALGYIIEVSSEFAPQLPKDFIRQRSRLHAERFTTIEL
QQFQDDMSNISEKLQ TLETQFFKDLCSHILQLRTEILALSQSLADLDYIISLADLAHAQGYCRPRVDMSDTLCI
YRGCHPVAKTLVDTGKFIPNDTEMRGSQTRMILLTGPNMAGKSTYIRQIALLVIMAQMGSYIPAKSAHIGVID

KIFTRIGAGDNL SKGMSTFMVEMAETANILHNATDRSLVILDEVGRGTSTYDGLAIAQAVVEYLLFTDKKKA
KTLFATHYKELTTLEDHCPHVENFHAGVKDKAGQPVFLYEILKGHSQKSFGIHVARLAGFPLCVVSRAQQIL
RQLEGPESITRPAQDKMQQLTLF

>core/57/3/Org3_Gene1013

MKRAILDRLYLSVVQSPESASPRDIFTAVAKTVMEWLAKGWLKTQNGYYKNDVKRVYYLSMEFLLGRSLK
SNLLNLGILDLVRKALKTLNYDFDHLVEMESDAGLGNGGLGRLAACYLDSMATLAVPAYGYGIRYDYGIFD
QRIVNGYQEEAPDEWLRYGNPWEICRGEYLYPVRFYGRVIHYTDSRGKQVADLVDTQEVLAMAYDIPIPGY
GNDTVNSLRLWQAQSPRGFEFSYFNHGNYIQAIEDIALIENISRVLYPNDSITEGQELRLKQEYFLVSATIQDIIR
RYTKTHICLDNLADKVVVQLNDTHPALGIAEMMHILVDREELPWDKAWEMTTVIFNYTNHTILPEALERWP
LDLFSKLLPRHLEIIYEINSRWLEKVGSRYPKNDDKRRSLSIVEEGYQKRINMANLAVVGSAAKVNNGVSSFHSQ
LIKDTLFKEFYEFFPEKFINVTNGVTPRRWIALCNPRLSKLLNETIGDRYIIDLSHLSLIRSFAEDSGFRDHWKG
VKLKNKQDLTSRIYNEVGEIVDPNSLFDCHIKRIHEYKRQLMNILRVYVYNDLKENPNQDVVPTTVIFSGKA
APGYVMAKLIKLINSVADVNNQDSRVNDKLVFLPNYRVSM AEHIIPGTDLSEQISTAGMEASGTGNMKF
ALNGALTIGTMDGANIEMA EHGKENMFIFGLLEEQIVQLRREYCPQTICDKNPKIRQVLDLLEQGGFNSNDK
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PTKSCSGEGN

>core/58/3/Org3_Gene960

MKKLYHPTLFLRPLIRLSLIFALSLTISGNFPQQKSFGHCCADMHSALISGKNCEELFADFIERV LADRET LTA
RDWGTVVVLVREYLLK CIRKGD CDYGVKILQKLLALRLPKDARKDLQILWHRLNPEQAPLRDVVDQLFTIG
CHESLQDHLLFELYTVTLHSGYANRKQDMLLAKEQG DYKKAIELAKELVA ALEKGS CSPHPEIVQIEKTFLQ
KTLLALQIKVAQEAQESCDALLTPYCLSEIAYTEAMDALVLRIARGEVSRTNEVDSVLLSHALQHLPFAREKA
IPELEV LIDHGAYLESTLLYYAYFSLLELYHQNKDFASLERLLEKGD AVFVPEHPYFPEY GFFLGAYFYAKGK
YESAEKVFLQIIDPAVKLGATFARAYEYLGCIAYVQNHYEKAEEYFLRAYKSWGREESGIGLFLAYAVQKKK
TACEDMLYHPKFSFTYRHLLDSLCSLSYPHGENKGSSAIQRVHRAVPELSEIYSRCIYD MIKYRNV TYTHPIIE
LAYNQVRNLEKRNLEEICRDAQDPEYDKALAFW GALQSGASVPRSLIESSDVDEAGITIRCYEALYFHNPD AI
AML PQAFSEECNSWQTALRLVWTLVRPKGAPNHAKYWDHLVLRPHGDSL YFFGYDLQEY LIGKEDALKHL
SVFAELFPKSSLLSVYYLQGYSESSALRKVGW FVKALEEFTEISWSGEHMKTWAYIYYMVKLDLADTYISL
GNFSQAVHILEEVKEDWQVASHPKLHFLKGEDCYLAMELRWVEGLAYAYFQLHETAHLSNHLL EHV EKNLI
SPRSYRDYYGESLQRTLGLCQRFLGV

>core/59/3/Org3_Gene92

MRYDPN LIEKKWQQFWKEHRSFQANEDEDKV KYYVLDMFPYPSGAGLHVGH LIGYTATDIVARYKRARGF
SVLHPMGWDSFGLPAEQYAIRTGTHPKVTTQKNIANFKKQLSAMGFSYDEGREFATSDPDY YHWTQKLFLF
LYDQGLAYMADMAVN YCPELGTVLSNEEVENGFSIEGGYPVERKMLRQWILKITAYADK LLEGLDALDWP
ENVKQLQKNWIGKSEGALVTFHLTQEGSLEAFTTRLDTLLGV SFLVIAPEHPDLDSIVSEEQRDEV TAYVQES
LRKSERDRISSVKTKTG VFTGN YAKHPITGNLLPVWISDYVVLGYGTGVVMGVPAHDERDREFAEMFSLPIH
EVIDDNGVCIHSNYNDFCLNGLSGQEAKDYVINYLEM RSLGRAKTMYRLRDWLF SRQRYWGEPIPIIH FEDG
THRPLEDDELPLLPNIDDYRPEGFGQGPLAKAQDWVHIYDEKTGRPGCRETYTMPQWAGSCWYYLRFCDA
HNSQLPWSKEKESYWMPVDLYIGGA EHAVLHLLYSRFWHRVFYDAGLVSTPEPFKKLINQGLVLASSYRIPG

KGYSIEDVRENGTWISTCGEIVEVRQEKMSKSKLNGVDPQVLIEEYGADALRMYAMFSGPLDKNKTWSN
EGVGGCRRFLNRFYDLVTSSEVQDIEDRDGLVLAHKLVFRITEHIEKMSLNTIPSSFMEFLNDFSKLPVYSKRA
LSMAVRVLEPIAPHISEELWVILGNPPGIDQAAWPQIDESYLV AQTVTFVVQVNGKLRGRLEVAKEAPKEEVL
SLSRSVVAKYLENAQIRKEIYVPNKL VNFVL

>core/60/3/Org3_Gene13

MDSTTNSDSPILDPNPEDVEKLLDESEEESEDQSTERLLPSELFILPLNKRPFPPGMAAPILIESGPYYEVLKVLA
KSSQKYIGLVLTOKENADILKVSFNQLHKTGVAARILRIMPIEGGSAQVLLSIEERIRIIEPIKDKYLKARVSYH
ADNKELTEELKAYSISIVSVIKDLLKLNPLFKEELQIFLGHSDFTEPGKLADFSVALTTATREELQEVLETTNM
HDIRDKALILLKKELDL SRLQSSINQKIEATITKSQKEFFLKEQLKTIKKELGLEKEDRAIDIEKFSERLRKRHPV
DYAMEVIQDEIEKLQTLETSSAEYTVCRNYLDWLTIIPWGIQSKEYHDLKKAIEVLNKDHYGLDEIKQRILELI
SVGKLSKGLKGSIIICLVGPPGVGKTSIGRSIAKVLHRKFFRFSVGGMRDEAEIKGHRRTYIGAMPGKMVQALK
QSQAMNPVIMIDEVDKIGASYHGD PASALLEVLDP EQNKDFLDHYLDVRVDLSNVLFILTANVLDTIPDPLLD
RMEILRLSGYILEEKLQIAKKYLV PKARKEIGLTASEVNFQPEALKYMINNYAREAGVRTLN GNKKVLRKVA
LKIVQNQEKPKSKKITFKISSKNLQTYLGKPIFSSDRFYESTPVGVATGLAWTSLGGATLYIESVQVSSLKTDM
HLTGQAGEVMKESSQIAWTYLHSALHRYAPGYTFFPKSQVHIHIPEGATPKDGPSAGITMVTSLLSLLETPV
VNNLGMTGEITLTGRVLGVGGIREKLI AARRSRLNILIFPEDNRRDYEELPAYLKTGLKIHVSHYDDVLKVA
FPKLK

>core/61/3/Org3_Gene638

MKGTPQYHFIGIGGIGMSALAHILLDRGYEVSGSDLYESYTIESLKAKGARCFSGHDSSHVPHDAVVVYSSSI
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YSGSSKIFVAEADESDGSLKHYPRAVVITNIDNEHLN NYAGNLDNLVQVIQDFSRKVTDLNKVFYNGDCPIL
KGNVQGISYGYSPECQLHIVSYNQKAWQSHFSFTFLGQEYQDIELNLPQGHNAANAAAACGVALTFGIDINII
RKALKKFSGVHRRLERKNISESFLFLEDYAHHPVEVAHTLRSVRDAVGLRRVIAIFQPHRFSRLEECLQTFPKA
FQEADEVILTDVYSAGESPRESIILSDLAEQIRKSSYVHCCYVPHGDIVDYLRNYIRIHDVCVSLGAGNIYTIGE
ALKDFNPKKLSIGLVCGGKSCEHDISLLSAQHVS KYISPEFYDVSYFIINRQGLWRTGKDFPHLIEETQGDSPLS
SEIASALAKVDCLFPVLHGPFGEDGTIQGF FEILGKPYAGPSLSLAATAMDKLLTKRIASAVGVPPVVPYQPLNL
CFWKRNPCLCIQNLIETFSFPMIVKTAHLGSSIGIFLVRDKEELQEKISEAFLYD TDVFVEESRLGSREIEVSCIG
HSSSWYCMAGPNERCGASGFIDYQEKYGFDGIDCAKISFDLQLSQESLDCVRELAERVYRAMQGKG SARIDF
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>core/62/3/Org3_Gene625

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YFLWLSFLYFRRTPRPLFFYKAA AFLSLPFCSAILLSMLSPVGTLPALLDTRL PKFILGNNPPVS YVGGIPFYLF
YEGQSFCCLKHLIGSVGTALIFGFVMLFSVLYLCGGIALKKKKTQDGVKKAFC SFFQTCFKNLKKLINRRNYL
PKPSVPFVSKNPFSCTKSQPSRRVSETIILDG SISPLQEEIPGSKKESFFLTPHPCKRFLTKFVEPQENKAKEGK
TIALSSTPTVVRESKGKERAALPKLKS LAVPENDLPQYHLLSKNREARPESLQAELERKALILKQTLTSFGIDA
DLGNICSGPTLAAFEVLPHSGVKVQKIKSLENDIALKLQASSIRIIAPIPGKAAVGIEIPTFPQAVNFRDLLEDY
QKTNRKLQIPLLLGKKANGDNLWADLATMPHLIIAGTTGSGKSVCINTIVMSMIMTTLPSEIKLVIIDPKKVEL
TGYSQ LPHMLSPVITESREVYNALVWL VKEMESRYEILRYLGLRNIQAFNSRTRNK TIEASYDREIRETMPFM

VGIIDELSDLLLSSSQDIETPIIRLAQMARA VGIHLILATQRPSREVITGLIKANFPSRISFKVSNKVNSQIIIDEPG
AENLMGNGDMLVLLPSVFGTIRAQGAYICDEDINKVIQDLCSRFTQYVIPSFHAFDDSDSDNSGEKDPLFAQ
AKTLILQTGNASTTFLQRKLIKIGYARAASLIDQLEEARIIGPSEGA KPRQILIQNPLEG

>core/63/3/Org3_Gene176

MDPKKKNYDASAITVLEGLQAVRERPGMYIGDTGITGLHHLVYEVVDNSIDEAMAGYCSRIDVRILEDDGGIVI
VDNGRGIPIEVHERESAKQGREVSALEVVLTVLHAGGKFDKDSYKVSGGLHGVGVSCVNALSEKL VATVFK
DKKCYQMEFSRGIPVTPLQYVSVSDRQGTEIVFYDPDKIFSTCTFDRSILMKRLREL AFLNRGITIVFEDDRDVS
FDKVTFFYEGGIQSFSYLNQNKESLFSEPIYICGTRVGGDDGEIEFEAALQWNSGYSELVYSYANNIPTRQGGT
HLTGFTALTRVINTYIKAHNLA KNNKLALTGEDIREGLTAVISVKVPNPQFEGQTKQKLGNSDVSSVAQQV
VGEALTIFFEENPQIARMIVDKVFVAAQAREAAKKARELTLRKSALDSARLPGLIDCLEKDPEKCEMYIVEG
DSAGGSAKQGRDRRFQAILPIRGKILNVEKARLQKIFQNQEIGTIIAALGCGIGADNFNLSKLR YRRIIIMTDAD
VDGSHIRTLTLLTFFYRHMTALIENECVYIAQPPLYKVS KKKDFRYILSEKEMDSYLLMLGTNESSILFKSTERE
LRGEALESFINVILDVESFINTLEKKAIPFSEFLEMYKEGIGYPLYLAPATGMQGGRYLYSDEEKEEALAQEE
THKFKIIELYKVAVFVDIQNQLKEYGLDISSYLIPQKNEIVIGNEDSPSCNYSCYTLEEVINY LKNLGRKGIEIQR
YKGLGEMNADQLWDTTMNPEQRTLHVSLKDAVEADHIFTMLMGEEVPPRREFIESHALSIRINNLDI

>core/64/3/Org3_Gene795

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AVRVGDKLFL LHNGEAAQSVYSSGESWSFVDHKCGFDNIHLALYRQQGSSFNPTNTGKVFLPTNHEGLPVL
VVEFRNNKEPLVFLGEYAQGRISNKDSTIFGTALVFWRSGSDYIPLGLYDSREEKLVS LDLPITRAVIFGNDQD
SAKSSDTANH YVLFNDYMQUIVSEESGSIEGINLPFASTNNKSIVNEIGFDRDLASEKSPEALFPGLSSKLPDGQ
QAKNSIGGYYP LLRRGLLSDSKLLPLEYHALNVVSGRELATPVALRYRVLSTPHSIQLES LDRSVQKVYKL
PENPEEKPYVFETAITLTKETEDVWVTSGVPEVEIMSNASAPTIKYRVIKKNKGSLDKVKLPKVKEPLAVRRG
VYPQWILNSNGYFGIILTPLSEIASGYGSLYISGSTAPTRL SAISPKNQLYPVSKYPGYETLLPLPKDAGTHRFL
VYAGPLAEPTLKVLDKTITQEKGENPEYLD SISFRGVFAFITAPFAALLFIIMKFFKLVTGSWGISIILLTVFLKL
LLYPLNAWSIRSMRRMQILSPYIQQIQKYKNEPKRAQMEIMGLYKTNK VNPITGCLPLLIQLPFLIAMFDLLK
SSFLLRGASFIPGWIDNLTAPDVLFSWQTSIWFIGN EFHLLPILLGIVMFLQQKVTS LHKKGPVTDQQKQQQV
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>core/65/3/Org3_Gene924

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LGEDLATVLGNTSLEISLTPNLAHCASFLGLAREICHVTQANLVIPKEFSFENLPTTALDMGNDPDICPFFSYV
VITGISAQPSPIKLQESLQALKQKPINAIVDITNYIMLSLGQPLHAYDASHVALDSL RVEKLSTPESLTLLNGET
VLLPSGVPVVRDDHSLGLGGVMGAKAPSFQETTTTTVIKAAAYFLPEALRASQKLLPIPSESA YRFTRGIDPQN
VVPALQAAIHYLEIFPEATISPIYSSGEICRELKEVALRPKTLQRILGKSFSIEILSQKLQSLGFSTTPQETSLLVK
VPSYRHDINEEIDLVEEICRTESWNIETQNPVSCYTPYIKLKRETAGFLANAGLQEFTPDLLDPETVALTRKE
KEEISLQGSKH TTVLRSSLLPGLLKSAA TNLNRQAPSVQAFEIGTVYAKHGEQCQETQTLAILLTEDGESRSW
LPKPSLSFYSLKGWVERLLYHHHLSIDALTLESSALCEFHYPYQQGV LRIHKQSFATLGQVHPELAKKAQIKHP

VFFAELNLDLLCKMLKTTKLYKPYAIYPSSFRDLTLTPEDIPANLLRQKLLHEGSKWLESVTIISIYQDKSL
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>core/66/3/Org3_Gene196

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YLKRGYFASSVDYSLEHNQEKGHIDVLIKINEGPCGKIKQLTFSGISRSEKSDIQEFIQTKQHSTTTSWFTGAGL
YHPDIVEQDSLAITNYLHNNGYADAIVNSHYDLDDKGNILLYMDIDRGSRYTLGHVHIQGFEVLPKRRIEKQS
QVGPNDLYCPDKIWDGAHKIKQTYAKYGYINTNVDFLIPHATRPIYDVITYEVSEGSPYKVGLIKITGNTHTK
SDVILHETSLFPDFTFNRLKLEDTEQRLRNTGYFQSVSVYTVRSQLDPMGNADQYRDIFVEVKETTTGNLGLF
LGFSSLDNLFGGIELSESNFDFLGARNIFSKGFRCLRGGGEHLFLKANFGDKVTDYTLKWTCPHFLNTPWILGI
ELDKSINRALSKDYAVQTYGGNVSTTYILNEHLKYGLFYRGSQTSLHEKRKFLLPNIDSNGFVSAAGVNL
NYDSVDSPTPTTGIRGGVTFEVSGLGGTYHFTKLSLNSSIYRKLTRKGILKIKGEAQFIKPYSNTTAEGVPVSE
RFFLGGGETTVRGYKSFIIGPKYSATEPQGGLSSLLISEEFQYPLIRQPNISAFVFLDSGFVGLQEYKISLKDLRSS
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>core/67/3/Org3_Gene825

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AEFVELQQILCQEGRLLEFVINQTRYIGRDLFKREDSLYKLWEWLGYLPSGDVRGERLKKSAREVVDRFMRT
TCNIRKIAMTFDRHVYSVAKTAFEKAFGALETVCYYESMRESYREAFCEYEKAKLLGDEEKSAHAEQRFQDIK
NRWEDVKDAFFWVKEDGKIEIDDAIGNSCKWSERYEEHRITRARWYKVAEHQLFNATMRVKDSLREHNEA
RVAFEKERSKENQRQVQKKKEKRLRDLKELHDQELPRAQERLRELQALYPEIAVSVVEARREVASDLEKAH
ESIDKHYQSCVREQELY

>core/68/3/Org3_Gene775

MASGIGGSSGLGKIPPKDNGDRSRSPSPKGELGSHEISLPPQEHGEEGASGSSHIHSSSSFLPEDQESQSSSSAAS
SPGFFSRVRSGVDRAKLSFGNFFSAESTSQARETRQAFVRLSKTITADERRDVDSSAAATEARVAEDASVSG
ENPSQGVPELTSSGPEPQRLFSLPSVKKQSGLGRLVQTVRDRIVLPSGAPPTDSEPLSLYELNLRSSLRQELSDI
QSNDQLTPEEKAEATVTIQQLIQITEFQCGYMEATQSSVSLAEARFKGVETSDEINSLCSELTDPQLQELMSDG
DSLQNLLDETADDLEAALSHARLSFSLDDNPTPIDNNPTLISQEEPIYEEIGGAADPQRTRENWSTRLWNQIRE
ALVSLLGMILSILGSHRLRIARHAAAEAVGRCCTCRGEECTSSSEEDSMSVSGSPSEIDETERTGSPHDVPRRN
GSPREDSPLMNALVGWAHKGAKTKESSESSTPEISISAPIVRGWSQDSSVSFIVMEDDHIFYDVPRRKDGIYD
VPSSPRWSPARELEEDVFGDYEVPITSAEPSKDKNIYMTPLATPAIYDLPSRPGSSGSSSRSPSSDRVRSSSPNR
RGVPLPPVPSPAMSEEGSIYEDMSGASGAGESDYEDMSRSPSPRGDLDEPIYANTPEDNPFTQRNIDRILQERS
GGASASPVEPIYDEIPWIHGRPPATLPRPENTLTNVSLRVSPGFGPEVRAALLSESVSAMVMAESIVPPTEPGD
GESEYLEPLGGLVATTKILLQKGWPRGESNA

>core/69/3/Org3_Gene867

MLLLISGALFLTLGIPGLSAAISFGLGIGLSALGGVLMISGLLCLLVKREIPTVRPEEIPGVSLAPSEEPALQAA
QKTLAQLPKELDQLDIDIQEVFACLRLKDKSKYESRSFLNDAKKELRVFDFVVEDTLSEIFELRQIVAQEGWD

LNFLINGGRSLMMTAESLDFHVSRLGYLPSGDVRGEGLKKSACEIVARLMSLHCEIHKVAVAFDRNSY
AMAEKAFKALGALEESVYRSLTQSYRDKFLESERAKIPWNGHITWLRDDAKSGCAEKKLRDAEERWKKF
RKAVFWVEEDGGFDINNLLGDWGTVLDPYRQERMDEITFHELYEKTTFLLKRLHRKCALAKTTFEKKRSKKN
LQAVEEANARRLKYVRDWDYDQEFQKAGERLEKLHALYPEVSVSIRENKIQETRSNLEKAYEAEIENYRCCVR
EQEDYWKEEEKREAEFRERGNKILSPEELESSLEQFDHGLKNFSEKLMELEGHILKLQKEATAEVENKILSDA
ESRLEIVFEDVKEMPCRIEEEIEKTLRMAELPLLPTKKAFAEKACSQYNSCAEMLEKVKPYCKESLAYVTSKERL
VSLDEDLRRAYTECQKRFQGDSEVRACREQLRERIQEFETQGLDLVEKELLCVSSRLRNTECDCVSGV
KKEAPPGKKFYAQYYDEIYRVRVQSRWMTMSERLREGVQACNKMLKAGLSEEDKVLKEEEYWLREERK
NKEKRLVGTKIVATQQRVAAFESIEVPEIPEAPEEKPSLLDKARSLFTREDHS

>core/70/3/Org3_Gene870

MLFSKNFSTDNGGAITAKTSLTGTMSALFSENTSSKKGGAIQTSDALTITGNQGEVSFSDNTSSDSGAAIFT
EASVTISNNAKVSFIDNKVTGASSSTTGDMSSGAICAYKTSTDTKVTLTGNQMLLFSNNTSTTAGGAIYVKKL
ELASGGLTLFSRNSVNGGTAPKGGAAIAEDSGELSLSADSGDIVFLGNTVTSTTPGTNRSSIDLGTSAKMTALR
SAAGRAIYFYDPITTSSTTVTDVLKVNETPADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGGT
LSLKHGVTLQTQAFTQQADSRLEMDVGTTLPEADTSTINNVLVINISSIDGAKKAKIETKATSKNLTLSGTITLL
DPTGTIFYENHSLRNPQSYDILELKASGTVTSTAVTPDPIMGEKFHYGYQGTWGPIVWGTGASTTATFNWTKT
GYIPNPERIGSLVPNSLWNAFIDISSLHYLMETANEGLQGDRFWCAGLSNFFHKDSTKTRRGFRHLSGGYVI
GGNLHTCSDKILSAAFCQLFGRDRDYFVAKNQGTVYGGTLYYQHNETYISLPCKLRPCSLSYVPTEIPVLFSG
NLSYTHTDNDLTKYTTYPTVKGSWGNDSFALEFGGRAPICLDESALFEQYMPFMKLQFVYAHQEGFKEQG
TEAREFGSSRLVNLALPIGIRFDKESDCQDATYNLTLGYTVDLVRSNPDCCTTLRISGDSWKTFGTNLARQAL
VLRAGNHFCFNSNFEAFSQFSFELRGSSRNYNVDLGAKYQF

>core/71/3/Org3_Gene602

MTLQPSYINFTPNVTTALSGGKIDTSAIELSCSALFFQELQDKAQGLKHALGLVQELSAEALRPAQVQTSISYL
PTEESSRPGISAGIIDRTMPTFTDDEVKAILQNPNFETSKIFVEGLDKVFKSYLDSVTPPEGIDPSNPESAILNYIT
LLNNLKPKFAAGSTPTDADYNALYALPGDFVKEIEALKAADAPPKSKVHAFWQEIMTIYNNMQVLSYPVTD
YLVNQIADLSLNITAAQEVQQYLKNFYSLKIDILNPGWTDQPQATHYPADAEYNARDAGVIQSLLNLSGNYRQ
LTENMLPNTDTSLPQEIIAQIRSFQNGVNGTIIASNTLLPTTMRDLTLLGVIYTYQCCATIFGMSYGTSTPAKQN
YIDAINQEKSYWQARANGFDVTSQVFDQFATNIQSGTSYRGIDLFKNNKVNEINPIFLSQAASFLRYPNLM
SRSMYQTIEDAANRSITALDGLISGWSTQIATFQTQKNSLDPSSLKYFDTMKANKESFVTTAPLQMVYSSLML
DKYLPQQNVIASLGIQMTYSNKAAYLNLIELIKEITTFQSADIYYSLSIYLKQMNLAQAVADPIGKAVGVLNDE
KTRAMADITRCNKIKAAIDKMLVEIKADAELSKSQIRELVDTLTNFKSQSDDLIRNLSCLLGFLSGLTLKAVN
DPNATYEAFTAEIFTEPFNNWKRQLATFESFVIQGGQNGITPGGQQQLLQAMESSQQDFSTFNQNNQQLALQLE
SSAMQQEWTLVSAALALLNQMVSKIARRIKS

>core/75/3/Org3_Gene953

MVFFRNSLLHLVALSGMLCCSSGVALTIAEKMASLEHSGRGADDYEGMASFNANMREYSLQLSKLYEEARK
LRASGTEDEALWKDLIRRIGEVRGYLREIEELWAAEIREKGGNLEDYALWNHPETTIYNLVTDYGTEDSIYLI
PQEIGAIAKIATLSKFVVPKESFEDCLTQILSRLGIGVRQVNSWIKELYMMRKEGCSVAGVFSSRKDLEALPETA
YIGFVLNSNVDAHTNQHVLLKKFINPETTHVDVIAGRVWIFGSAGEVGELLKIYNFVQSESIRQEYRVIPLTAKID

PGEMISILNAAFREDLTKDVSEESLGLRVVPLQYQGRSLFLSAIAALVQQALTLIRELEEGIENPTDKTVFWYN
VKHSDPQELAALLSQVHDFVSGENKASVGAADGCGSQLNASIQIDTTVSSSAKDGSVKYGNFIADSKTGTLI
MVVEKEVLPRIQMLLKLDVPPKMVRIEVLLEFERKLAHEQKSGLNLLRLGEEVCKKGCSPSVSWAGGTGILE
FLFKGSTGSSIVPGYDLAYQFLMAQEDVRINASPSVVTMNQTPARIAVVDMSIAVSSDKDKAQYNRAQYGI
MIKMLPVINVGEEDGKSYITLETDTITFDTTGKNHDDRPDVTRRNITNKVRIADGETVIIGGLRCKQMSDSHDGI
PFLGDIPGIGKLFGMSSTSDSLTEMFVFITPKILENPVEQKERKEEALLSSRPGEREEYYQALAASEAAARAAH
KKLEMPASGVSLSQVERQEYDGC

>core/76/3/Org3_Gene650

MGYIESSTFRLYAEVIVGSNINKVLDYGVPENLEHITKGTAVTISLRGGKKVGVYQIKTTTQCKKILPILGLSD
SEIVLPQDLLDLFWISQYYFAPLGKTLKFLPAISSNVIQPKQHYRVVLKQSKAKTKEILAKLEVLHPSQGAV
LKILLQHASPPGLSSLMETAKVSQSPIHSLEKLGILDIVDAAQLELQEDLLTFFPPAPKDLHPEQQSAIDKIFSSL
KTSQFHTHLLFGITGSGKTEIYL RATSEALKQGKSTILLVPEIALTVQTVSLFKARFGKDVGVLHHKLSDSK
RTWRQASEGSLRILIGPRSALFCPMKNLGLIIVDEEHPAYKQTESPPCYHARDVAVMRGKLAHATVVLGSA
TPSLESYTNALSGKYVLSRLSSRAAAHAPAKISLINMNLEREKSKTKILFSQPVLKKIAERLEVGEQVLIFNRR
GYHTNVSCTVCKHTLKCPCPHCDMVLTFHKYANVLLCHLCNSSPKDLPQSCPKCLGTMTLQYRSGSGTEKIEKIL
QQIFPQIRTIRIDSDDTKFKGSHETLLRQFATGKADVLTQMIAGMNFSAVTLAVILNGDSGLYIPDFRASEQ
VFQLITQVAGRSGRSHLPGEILIQSFLPDHPTIHSAMRQDYSAFYSQEITGRELCEYPPFIRLIRCIFMGKCPKQT
WEEAHRVHNILKEQLESTNPLMPVTPCGHFKIKDTFRYQFLIKSAYVIPVNKKLHHALMLAKLSPKVKFMID
VDPMTTFF

>core/77/3/Org3_Gene883

MEKICGYLEQILVENKDSGDITAYIKIPNKTTPILIKGKLPQPLELGSPIQIYGVWSHSPSNTKYFQIHSYDSPLL
YEYRGVFHYLTSKLIKIGPKIAEKIIEKFQEKTCYVLDITPERLSEVSGISETRCVSICKQLCEQKILRKTLFLQ
EYNIPIHYGVRIFKKYHETSIEKICEDPFLAREMEGIGFKTADFIAMKLGVPNRNSESRLCAGIQHSLEELQEEG
HTCYPIELLIDVVAKLLNQDVFDTPITLEEIDTQILNMQKRKLLHIQDISGTLHVWTRYLHLAEKTIVSDLKRIL
FSSRRIRSIDGEKAIAWVEENLSIDLAEQQREAIKACFSEKLLIITGGPGTGKSTITQAILKIFEQVTHKIILAAPT
GKAAKRMTEITQKHSVTIHALLQYDFKTKSFRKNHDNPIDCDLIIVDESGMMDTHLLHHFLKALPDYTTLVFI
GDIHQLPVSGPGNLIKDLITSNKMTVIRLNKIFRQVHDSGIVTNAHRVNEGELPILYSETGRRDFLFFQKDDQE
EALNHHIHLVTKFVPQKYHIYPQDIQVLAPMKGTLGIYNLNKALKHALNPKKANLHGRFQSYAVGDKVMQI
RNNYNKEVFNGDIGYVSTINFEDKAVVVRMEGKHVGYSFSEDDLVLAYATSVHKEYQGSSEPCIIPIHTSHF
MMLYRNLLYTAITRGKKLVILVGTKKAIAIATRNNRVQHRCTGLAEVLKELDTKKNYADL

>core/78/3/Org3_Gene999

MLSFFYKHQKKFIGIVIAVVCVSGIGVGWGRFSRKGSAAESTSRRTVFTTASGKRYVEKDFMAMKKFFAHEAY
PFTGNPRAWNFINEGLLTDYFLTTRVGEKLFLLKVVHPGEKIFSKEKAYQPYRRFDAPFISSEEVWKSSAPQLLE
ILKVFQQIENPISKEGFLARAKLFLEERRFPHYVLRQMLEYRRQMFALPPDEALSRGKDLRLFGYQTIQDWFG
DAYLSAAVELLIRFIDEQKKVLPRPSKQEARDDFYDKAKHAYTKISKNEFSLGFEEFVNYSYFQFLEISESEFF
NMYRDILLCKRALLLLQGGVSFDFQPLTTFFVQGKDSIQVEFFRLPKEYSFKTKQELKA FEVYLKLVSLPKSD
SLDVPNEILPIATIKAKEPRLVGRRFSIDYKRVALQDLAATVPMVEVLHWQQNSEHFQEILQQFPDVETCQSY
KDFQHLKPALRDKISLFRKEILRARPERILQSLQQVQPKQSQEVLLSAGKNSALPGISDGQQLAKVLLENEVLD

LYSQDAETYYTIIVNSSFEKEEVLPYREVLKRDLASQLLTSHGHLVDMERLESALRTRYPGEEGASLWQRRRL
WKVVENHRLGRHLEGFSFSWSLDRSLKTFSRGDKELPQEFDRIFSMKVG DYSSVFMSPNEGPCYYQCLSHLLY
DRPASVDKLFLAKSQLDEELLGSYMERFIEQGVVR

>core/79/3/Org3_Gene520

MDYLEKLQVLIIEGQSANFLSLWEEYCFNDVVRGRELVEILEKVKSSSLASLFGKIVDTVVPLWEKIPEGKDK
DRVLQLILDQLTSNSQMFFDIATEYVNKKYSGEENFNEALRVVGLRDGRDFQFSLSRFDFLMHMHKGNFVFH
QGGWGVGEVMGVSFLQQKVLIEFEGIMSAKDISFETAFKSLTPLSGDHFLSRRFGDPDGFEAFKENPIEVVEI
LLRDLGPKTAKEIKDELVDLVIPEADWNRWWQSAKTKIKKGTRIISPDNPKEPYVLSDAGCSHMGQLERKLG
LSLNSAEKISLIYHFIRDLHSELKNIEIRKSLVKALQDL DVEEGNKSLLQRELLSEYLGIKDASIDKEYITSLE
DDTSRLLENMPIVALQKSFLSLVRKYSSFWQQVFMQILLYTTSPTMRDFVYKTIKNDPSSVEVLKKRLLDSA
HQPMMFPELFWFFLKLGNHEDGLFDPEDKEVLRFLFLESALNFMYQVASTPHKELGKKLHHYLVGQRYLAVR
QMIEGASLPFLKELLLLSTKCPQFSSDLNVLQSLAEVVQPTLKKHKSNVEEENVLWSTSEFSRMKAKLQSL
VGKEMVDNAKEIEDARSLGDLRENSEYKFALEKRARLQEEIRVLSEEINRARILTKDLVFTDKVGVGCKVTL
KGDAGEVVEYITILGPWDADPDSCILSLQSKLAQNMLGKKLNDVVILQGKEYKISRISQIWEEHGA

>core/80/3/Org3_Gene314

MVDKLIHPWDLDLLVSGRQKDPHKLLGILASEDSSDHIVIFRPGAHTVAIELLGELHHAVAYRSGLFFLSVPK
GIGHGDYRVYHQNGLLAHDPAFPPLWGEIDSFLFHRGTHYRIYERMGAIPMEVQGIGSVLFVLWAPHAQR
VSVVGDFNFWHGLVNPLRKISDQGIWELFVPGLGEGIRYKWEIVTQSGNVIVKTDOPYGKSFDPPPQGTARVA
DSESYSWSDHRWMERRSKQSEGPVTIYEVHLGSWQWQEGRPLSYSEMAHRLASYCKEMHYTHVELLPITEH
PLNESWGYQVTGYAPTSRYGTLQEFQYFVDYLHKENIGIILDWVPGHFPVDAFALASFDGEPLYEYTGHSQ
ALHPHWNTFTFDYSRHEVTNLLGSAFWLDKMHIDGLRVDASMLYRDYGREDEGWTPNIYGGKENLE
SIEFLKHLNSVIHKEFSGLTFAEESTAFPGVTKDVDQGGGLGFDYKWNLGWMHDTFH YFMKDPMYRKYHQ
KDLTFSWLWYAFQESFILPLSHDEVVHGKGS LVNKLPGDTWTRFAQMRVLLSYQICLP GKLLFMGGEGFY
GEWSPDRPLDWELLNHHYHKTLRNCVSALNALYIHQPYLWMQESSQECFHWVDFHDIENNVIAYYRFAGS
NRSSALLCVHHFSASTFPSYVLRCEGVKHCELLLNTDDESFSGSGKGNRAPVVCQDQGVAVGLDIELPLAT
VIYLVTF

>core/81/3/Org3_Gene861

MNKFKTYLQTALIAFFSFPA LSGSFSSIQAE EITQQVNHPGAELLSEGSYIPGLQTFRLGIKITASKGSHIYWKN
PGEIGSPLKISWQLPKGFVVEEHWPTPKVFEEEGTTFFGYEDSALIVADVRAPEGYTPGQVELRAQVEWLA
CGDSCLPGNVDLKLTLPYEEKEPSLYPDTHAEFTKTLHAQPRVLENDHSVQVAQKGKNEIILNISKKINATKA
WVNSEKADKLFAYAETSYSGGTGTAWRLKVKNLSGVQKNEKLHGILLADHTGRPVESLTIHSEVLGQTGS
AVAGLSQYITILMAFLGGVLLNIMPCVLPLVTLKVYGLIKSAGEHRSSVIANGLWFTLGVVGC FWGLAGVAF
ILKVLGHNIGWGFQLQEPMFVATLIIVFFLFALSSLGLFEMGTMFANLGGKLQSSEM KSSNNKAVGAFFNGIL
ATLVTTTPCTGPFLGSVLGLVMSLSFLQQLLIFTAIGLGMASPYLVFSVFPKMLSVLPKPGGWMSTFKQLTGFM
LLVTVTWLWVIFGSETSTTSVVVLLGGLWLAGLGAWILGRWGTPVSPKKQRVCASLLFFAFLGGAISVSGLA
SHYFAEPQQT VSVNEDSLWQPF SLEKLAQLRAQGRPVFNFTAKWCLTCQMNKPVLYGDAVQKMFETHGI
VTLEADWTRKDPGITEELARLGRASVPSYVYYPGDNSAPVVLPEKITQNLLEDVVS RFVR

>core/82/3/Org3_Gene187

MIRSPLPFISSKRALNMLGLQDEFSCPEDVVDLFLSEIELLAQQDEPSEGYLALSRSLMMTHNHPKVVKRVIF
YGVSYGLKHKSMSIFIDVLTYIDFLFEKLGISASDRLSLCSARTCINFELYSQTGEMKFLSEVVDNFRLEQLLK
MHPQLKNRLGWEHFRIGAKQEEVSLVASASVYQAVGRSFIELYHKHLESLDACGMKCLALALDLSPNNAH
IHADYAKGLVVLGTRQGKSLIERGMEHFSKAIFLSFSRDGDTLAYQNYRYSYALASVKLFDLTYKKEHFDQ
AMNILYQTVQAFPNLSGLWMVWGELLIRSGWLNSNMKYIEVGLEKLASLQKKTNDPIALSGLLATGIAILGL
YLEEPNLFKDSRHLISAMRTFPGNSALVHALGVVQLCSALYFNEDSHFASAISCFQSCLEWDL DATGMWQK
LFDAYFSWGIKKKSARLLRKAVDVASRLCSLRPEAFLFWSDRGLALKCLAEATIDEAYKEIFLSESLHYQRA
WDL SGRLEILELWGQSHYLLAELQQSLFHYDEAYTLLTKVDLTLSSSRVKLILAAVLLGKGRLQLQDTPAEE
AREILEPLVEVYLEDENFLLLLGKVYLFLFWKNKNVCLGKLARTYLEKATSLGCP EAYYTLGKFYAVIKDVN
KAWGMVIRSAQYGVRITEAKWLNDPYLANLREIHAFREVVENQKGRLWLG NKTEMKRN

>core/83/3/Org3_Gene214

MNKLLNFVSRTLGGDTALNMINKSSDLILALWMMGVVLMIIPLPPPIVDLMITINLSISVFLLMVALYIPSAHQ
LSVFPSLLLITTMFRLGINISSSRQILLKAYAGHVIQAFGDFVVGNYVVGFIIFLIITIIQFIVVTKGAERVAEVA
ARFRLDAMPGKQMAIDADLRAGMIDATQARDKRAQIQKESELYGAMDGAMKFIKGDVIAGIVISLINIVGGL
TIGVAMHGMDLAQAAHVYTLLSIGDGLVSQIPSLLIALTAGIVTTRVSSDKNTNLGKEISTQLVKEPRALLA
GAATLGVGFFKGFP LWSFSILALIFVALGILLTTKKSAAAGKKGGGSGASTTVGAAGDGAATVGDNPDDYSLT
LPVILELGKDL SKLIQHKTSGQS FVDDMIPKMRQALYQDIGIRYPGIHVRTDSPSLEGYDYMILLNEVPYVR
GKIPPHHVL TNEVEDNLSRYNLPFITYKNAAGLPSAWVSEDAKAILEKAAIKYWTPLEVIIHLHSYFFHKSSQE
FLGIQEVRS MIEFMERSFPDLVKEVTRLIPLQKLTEIFKRLVQEQISIKDLRTILES LSEWAQTEKDTVLLTEYVR
SSLKLYISFKFSQGQSAISVYLLDPEIEEMIRGAIKQTSAGSYLALDPDSVNLILKSMRNTITPTPAGGQPPVLLT
AIDVRRYVRKLIETEFPDIAVISYQEILPEIRIQPLGRIQIF

>core/84/3/Org3_Gene407

MYKRCVLDKILKGIVAGSLILLYWSSDLLERDIKSIKGNVRDIQEDIREISR VVKQQQTSQAIPAAPGVMLAPK
LVRDEAFALLFGDPSYPNLLSLDPYKQQTLP ELLGTNFHHPHGILRTAHVGKPENLSPFN GFDYVVGFDLCIPS
LASPHVGKYE EFPDLAVKIEEHLVEDGSGDKEFH IYLRPNVFWRPIDPKALPKHVQLDEVFQRPHPVTAHDI
KFFYDAVMNPYVATMRAVALRSCYEDVVS VSVENDLKL VVRWKAHTVINEEGKEERKVL YSAFSNTLSLQ
PLPRFVYQYFANGEKIHEDENIDTYRTNSIWAQNFTMHWANNYIVSCGAYYFAGMDDEKIVFSRNP DFYDPL
AALIDKRFVYFKESTDSL FQDFKTGKIDISYLPPNQ RDNFY SFMKSSAYNKQVAKGGAVRET V SADRAYTYI
GWNCFSLFFQSRQVRCAMNMAIDRERIEQCLDGQGYTISGPFASSSPSYNKQIEGWHYSPEEAARLLEE EGW
IDTDGDGIREKVIDGVIVPFRFRLCYVKS VTAHTIADYVATACKEIGIECSLLGLDMADLSQAFDEKNFDALL
MGWCLGIPPEDPRALWHSEGAMEKGSANVVG FHN EADKIIDRLSYEYDLKERNRLYHRFHEIIHEEAPYAF
LFSRHCSLLYKDYVK NIFVPTHRTDLIPEAQDET VNVTMVWLEKKEDPCLSTS

>core/85/3/Org3_Gene23

MKELRHESYNRALHKL SHQWVRYFLYTFVSCSFIVAIFTF AWLKVLYVPEYKAGEISRISLTAPMD FSLSWSA
HKFYKRTAHISEAFGKVYHLTLSPG SLLSKEGNADENTDYWFKKAADFLSTNFVDSSTQKCLKDL CIYPPLL
GKEKKTLEININSNKG NVIAQCFCCHKIFLIQENCPQCFDAIMDILKIANFEVAVDKEMSGCVKGELLGKRCI

EKITKGTPILEKYQRIDDRDAKILKQLRAQLLSVHTLFSCRSLWGAIFVLLILLWGYGALKALCPPEMLKSPQ
RFMLYIAILTLSLLWCRGTEIFCAYWVSYLSYPPILPFTAVLLGYFLGLPIAGFSCTFLALLYTLGSDLWNNWS
FLSINLLCSWRILVSLHRVSRSSVFWACMKLGGVAMGSLLMFRIFTNTISREALYADGIESFVYSLITAISVVA
LIPVFEASFGASTNFSLLTYLSPENALLKRLFKEAPGTYQHSVLVGSLAEAAAQAIGADSLYCLVAAHYHDIG
KLINPGFFSENQKILQQSGHSLSPLECAKMIMRHIPEGVNLARQAGLPESFIQVIEHHGTSVIRSAYYSHMVE
NPSTGSFDEELFRYSGNKPSSKETIIMIADSFEAASRSLKNASLPDLQRLIDQIIQGKLQDGQFSCSPITLDELA
LISKSMVQTLYGALHSRMKYPEISYQISMDSCPKPSIGGT

>core/86/3/Org3_Gene745

MPEPLYTNKLITEKSPYLLLYAHTPVNWPWGAEAFHIAAIENKPVFLSIGCKHSRWCQVMLQESYTNPEIAA
MLNEYFVNVKVDKEELPYVAKLYGDLAQMLAVSGDHQETVSWPLNVFLTPDLVPFFSVNYLGNKGKGLP
SFPQIIDKLHFMWEDAEEREALVEQAMKVLEIASFLEGCVRKEILDESSLKRTVAALYQDIDPHYGGVKAFPK
RLPGLLLQFFLRYSLEYQESRGLFFVDRSLSMVALGGVRDHIGGGVYSYTIDDKWLIPAFEKRLIDNALMALN
YLEAWACLGKEEYRGIGKQILSYILSELYSPEVGAFYSSEQAENWGAGGQNFYTWVSVEEISNALGEDAEIFCD
YYGISREGFFNGRNILHIPVHREIEELSEKYHRSIEAIEDIVDRSRDILKGIRAQRSHRSKDDLSTFNNGWMIYT
FAYAGRLLGEVEYIEIGKKCGEFVRNSLYKHHELRYRWREGEAKYRASLEDYGALILGVLALYESGCGSFWL
SFAEELMQEVVLSFRSEEGGFYSVDGRDSTLLIKQSPLSDGETISGNALICQCLLSLHLITEKKHYLTYAEDILQ
IAQACAHTHKFSSLGLLIASQNYFSRKHVKVLIALGDQEDRSPVLKCLSGLFLPYLSLIWMTQENQEHLTVL
PEYEHCLIPKGDCTATTIYVLEVDQCKRFKDLELFRRYLISL

>core/88/3/Org3_Gene7

MKRCFLFLASFVLMGSSADALTHQEAVKKKNSYLSHFKSVSGIVTIEDGVLNHNNLRIQANKVYVENTVGQ
SLKLVAHGNVMVNYRAKTLVCDYLEYYEDTDSCLLTNGRFAMYPWFLGGSMITLTPETIVIRKGYISTSEGP
KKDLCLSGDYLEYSSDSLLSIGKTTLRVCRIPILFLPPFSIMPMEIPKPPINFRGGTGGFLGSYLGMSSPISRKH
SSTFFLDSFFKHGVMGFNLHCSQKQVPENVFNMKSYYAHLRAIDMAEAHDYRLHGDFCFTHKHVNFSGE
YHLSDSWETVADIFPNNFMLKNTGPTRVDCTWNDNYFEGYLTSSVKVNSFQANQELPYLTLRQYPISIYNT
GVYLENIVECGYLNFAFSDHIVGENFSSLRLAARPKLHKTVPLPIGTLSSTLGSSLIYYSDVPEISSRHSQLSAKL
QLDYRFLHKSYYIQRRIIEPFVTFITETRPLAKNEDHYIFSIQDAFHSLNLLKAGIDTSVLSKTNPRFPRIHAKL
WTTHILSNTESKPTFPKTACELSLPFGKKNTVSLDAEWIWKKHCHWDMNIRWEWIGNDNVAMTLESLHRSK
YSLIKCDRENFILDVSRPIDQLLDSPLSDHRNLILGKLFVRPHPCWNYRLSLRYGWHRQDTPNYLEYQMILGT
KIFEHWQLYGVYERREADSRFFFFLKLDPKPKPPF

>core/89/3/Org3_Gene704

MNFQTISINLTEGKILVFETGKIARQANGAVLVRSGETCVFASACAVDLDDKVDLPLRVVDYQEKFSSTGKTL
GGFIKREGRPSEKEILVSRLIDRSLRPSFPYRLMQDVQVLSYVWSYDGQVLPDPLAICAASAALAISDIPQSNIV
AGVRIGCIDNQWVINPTKTELASSTLDLVLGATENAILMIEGHCDFFTEEQVLDAIEFGHKHIVTICKRLQLWQ
EEVGKSKNLSAVYPLPAEVLTAVKECAQDKFTELFNIKDKKVHAATAHEIEENILEKLQREDDDLFSSFNKA
ACKTLKSDTMRALIRDREIRADGRSLTTVRPITIETSYLPRTHGSCLFTRGETQTLAVCTLGSEAMAQRYEDLN
GEGLSKFYLQYFFPPFSVGEVGRIGSPGRREIGHGKLAEKALSHALPDSATFPYTIRIESNITESNGSSSMASVC
GGCLALMDAGVPISSPIAGIAMGLILDDQGAILSDISGLEDHLGDMDFKIAGSGKGITAFQMDIKVEGITPAIM
KKALSQAKQGCNDILNIMNEALSAPKADLSQYAPRIETMQIKPTKIASVIGPGGKQIRQIIETGVQIDVNDLG

VVSISASSASAINKAKEIIEGLVGEVEVGKTYRGRVTSVVAFGAFVEVLPGKEGLCHISECSRQRIENISDVVKE
GDIIDVKLLSINEKGQLKLSHKATLE

>core/90/3/Org3_Gene920

MSNQEFDLsAIRNIGIMAHIDAGKTTTTERILFYAGRTHKIGEVHEGGATMDWMAQEQRGITITSAATTVFW
LGAKINIIDTPGHVDFTIEVERSLRVLDGAVAVFDAVSGVEPQSETVWRQADKYGVPRIAFVNKMDRMGAD
YFAAVESMKEKLGANAFVHCPIGSESQFVGMVDLISQKALYFLDDTLGAKWEEKIESEDLKERCAELRANL
LEELATIDESNEAFMMKVLEDPD SITEDEIHQVMRKGVIENKINPVLCGTAFKNKG VQQLNVIVKWLPSPLD
RGNIRGINLKT DQEISLEPRRDGPLAALAFKIMTDPYVGRITFIRIYSGTLKKGSAILNSTKDKKERISR LLEMH
ANERTDRDEFTVGDIGACVGLKFSVTGDTLCDDNQEIVLERIEFPDPVIDMAIEPKSKGDREKLAQALSSLSEE
DPTFRVSTNEETGQTIISGMGELHLDILRDRMIREFKVEANVGKPQVSYKETITVSGNSETKYVKQSGGRGQY
AHVCLEIEPNPEGK GNEVVSKIVGGVIPKEYIPAVIKGIEEGLKKGVLAGYGLVDVKVSIVFGSYHEVDSSEM
AFKICGSMAVKDACRKAKPVILEPIMKVA VITPEDHLGDVIGDLNRRRGKILGQESSRGMAQVNAEVPLSEM
FGYTTSLRSLTSGRATSTMEPAFFAKVPQKIQEEIVKK

>core/92/3/Org3_Gene324

MYNLLHAHHDAASPDGRLVSHLKKLSPHIYEGEVLIENIPAYFLGFHLPQQCIQVNLKSSLAQLGVEAVLNHL
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KLEHFITLEIINDRLVVFLPILPGTICYEETIYGFLPLMSKSLTRPHLKIRKFLPLYQMVTDRPPVPEDHKILLIKT
EPLHIRTVFARVVQDLLPQGLRHTAADILEPTTQESGDIYEFYGSTSEPIERIPLEFFTLEPYKEHSFFFYRDMLQ
ETLESPQEVFRVFESIPEGEDQAAMFISKGSELLELSQDSWIIPRISPSDERHAREIQKHIEDQPCFPFLKAMET
DHITSQGVLF SRYFPSASLKG MFLSNYSRYYLQHIYFQIPSPTSGEFFSNRDRSFLLDLYFAGISVFWADLESKR
LLQYIKRRNKDVGMFVPKHQAEQFAQSYFIGIHGSLIAGDYDEFLRELLTGMHTLSQQTIFEPPQTPLAIL
TGGGSGAMELANRVATELSILSCGNLISLDTTNAYVEAKMSYAIPDLLERQADFHVDLAVFVIGGMGTD FEL
LLELISLKTGKKALVPVFLIGPVDYWWSKITALYNSNHAVGTIRGSEWVHNCFLCLSSAKAGIAIFRRYLNHTL
PIGPEHPVPEDGFVIV

>core/93/3/Org3_Gene699

MKRSRRNFEQALENLEKLKEISLATSND SYLNNPARFNQRKQTGSSVMEMKEALKNVENYLLEISCVSKSHA
DKALKESD FLIAGVQNVFSFLENQEDLYKSLLDEYSEVTKAYDEVKKNLKEVPTYDLSTDEETEEHKEPECFL
NNLVEVKRDRSYELFYMLDEQDKRFYNDALVQIIYKQNK LHETVNEG DPLTKTLLWNSEE VKNIASSLVIVN
DMPLRLFYQRALSHLDIEAVVKVHNAVMA LFFSRYEATMVFKSPKKHNIWYFND FLLFLREAWKDLNNNVI
DSQERKQTKLLASALS LGIFESKLVFEEASRYLYFNIQTKLENANGKKPLSPGQYLTDAYEELHRLISKYPNGP
LFKAMDRVLEHESRPYDPMILGILPSLEGTLKLHGKSIDIIRSPSPVTQSSILYANCNEEFLGFLNAKAHRSEVT
LVLNIQNRISRKERARSRVIEEAL EQEEHAPYVHA FSPPEPEELLQNLESIHGDIE TFADFFSILQEEFHKPLLAS
SFFLTKE LKEFVGSFLKEKLTALKDIFFAKKKILFRNDK LLLLHLLSYLIVFKLIERTNPNSIVVVS KDGLDYVS
VFIAGFAFFSREAFWDEHSLK LLLTNVLSPTLVARDRLVFVSHIELLSK FVNCLKKNRQGFSSLKSFFKDDIEG
WEFTGYLHELTEVSHKHNL

>core/94/3/Org3_Gene560

MQPCLNMSIVRNSALPLPCLSRSETFKKVRSHMKFMKVLTPWIYRKDLWVTAFLLLTAIPGSFAHTLVDIAGEP
RHAAQATGVSGDGKIVIGMKVPDDPFAITVGFQYIDGHLQPLEAVRPQCSVYPNGITPDGTVIVGTNYAIGM
GSVAVKWVNGKVSELPMLPDTLDSVASAVSADGRVIGGNRNINLGASVAVKWEDDVITQLPSLPDAMNAC
VNGISSDGSIIVGTMVDSWRNTAVQWIGDQLSVIGTLGGTTSVASAISTDGTIVVGGSENADSQTHAYAYK
NGVMSDIGTLGGFYSLAHAVSSDGSVIVGVSTNSEHRYHAFQYADGQMVDLGTLLGGPESYAQGVSGDGKVI
VGRAQVPSGDWHAFLCPFQAPSPAPVHGGSTVVT SQNPRGMVDINATYSSLKNSQQQLQRLLIQHSAKVESV
SSGAPSFTSVKGAISKQSPAVQNDVQKGTFLSYRSQVHGNVQNQQLLTGAFMDWKLASAPKCGFKVALHY
GSQDALVERAALPYTEQGLGSSVLSGFGGQVQGRYDFNLGETVVLQPFMGIQVLHLSREGYSEKNVRFPVSY
DSVAYSAAATSMGAHVFAVSLSPKMSTAATLGVERDLNSHIDEFKGSVSAMGNFVLENSTVSVLRPFASLAMY
YDVRQQQLVTL SVVMNQQLTGTL SLVSQSSYNLSF

>core/95/3/Org3_Gene18

MGVVQNQVISSIRDVLKLVWELRFAEHKMLLLSRQSGSGGTFQLSCAGHELAVLAGKSLIPGKDWSFPYY
RDQGFPIGLGCDLSEIFASFLARTTPNHSSARMMPYHYSHKKLRICQSSSVVGTQFLQAAGRAWAVKHSSAD
EVVYVSGGDGATSQGEFHEMLNFVALHQLPLITVIQNNHWAISVPFEDQCGADLASLGRCHQGLAVYEVDG
GNYTSLTETFSHAVDQARQHSVPALILIDVRLSSHNSNDNQEKYRSALDLKLSMDKDP LILLEKEAINVFGLS
PFEIEEIKAEAEQEEVRKSCEIAEALPFPSKGST SHEVFSPYTETLIDYENSESAQNLRNSEP KVMRDAISEALVEE
MTRDSGVIVFGEDVAGDKGGVFGVTRNLTEKFGPQRCFNSPLAEATIIGTAIGMALDGIHKPVVEIQFADYIW
PGINQLFSEASSIYYRSAGEWEVPLVIRAPSGGYIQGGPYHSQSIEGFLAHCPGIKVA YPSNAADAKALLKAAI
RDPNPVVFLEHKALYQRRIFSACPVFSHDYVLPFGKAAIVHPGKDLTIVSWGMPLVLSLEVAQELASRGISIEV
IDLRTMVPCDFATVLKSLEKTGRLLVIHEASEFCGFGSELVATMSEQGYAYLDAPIRRLGGLHAPVPYSKVLE
NEVLPHKESILQAAKSLAEF

>core/96/3/Org3_Gene332

MLKKPKRKPGRRTYGKSLKIFIPGTLFVHARKGFGFVSPDNPEEYPFDIFVPARDLRGALDGDH VIVSVLPYPR
DGQKLKGTISEVLARGKTTLVGTITSLVSPTSALAYTSMMSGSQLIPVELLPGR TYKIGDRILLSTPPWVDKPQE
GASPALQMLEFIGHITNAKADFQAIQAEYNLAEEFPPEVIEEASLFSQKHITQVLH SRKDLRDLLCFTIDSSTAR
DFDDAISLTYDHNNNYILGVHIADVSHYVTPHSHLDKEAAKRCNSTYFPGKVIPMLPSALSDNLCSL KPNVDR
LAVSVFMTFTKSGHLSDYQIFRSVIRSKYRM TYDEV DNIIEKKHSHPLSKILNEMATLSKKFSDIREERG CIRFV
LPSVTMSLDNLQEPVALIENHQTFSHKLIEEFMLKANEVVAYHISHQGVSLPFRSHEPPNDENLLAFQELAKN
MGFDITFTPTQEPDYQYLLQTTSAGHPLEQVLHSQFVRSMKTASYSTENKGHYGLKLDYYTHFTSPIRRYIDL
IVHRLLFNPLSIDQTHLEIIVRACSTKERVSAKAENSFENLKKTRFINKFLQE QPKTTYHAYIITANHEGLSFVV
TEFCHEGFIAAAELPKEYSLKKNALPESIPDKMKPGASIKVTIDSVNLLTQKIVWSIATTTEDKPKKIKKTPSKK
KGTKKRAS

>core/98/3/Org3_Gene961

MINKELDIGILGKIAGAIKQISIESIQKASSGHPGLPLGCAELAA YLYGYVLRQNPRDPHWINRDRFVLSAGHG
SALLYSCLHLAGFDVSLEDLQEFRQLHSRTPGHPEYGETVGV EATTGPLGQGLGNAVGMALSMKMLESRFN
RPGHEIFNGKIYCLAGDGC FMEGVCSFAGSLN LNNLVVIYDYN NVLDGYLNEISVEDTKKRFEAYG
WDVYEIDGYDFTHIHET FSSIKRGQERPVLVIAHTIIGHGSPKEGTNKAHGSPLGVEGTHETKQFWHLPEEKFF
VPPAVKNFFAHKIQEDRKAQEQLDEV RVWSKQFPELHEEFVALTSHKLPKNLESLVQSVEMPDSIAGRAAS

NKLIQVLVQHIPPYLIGGSADLSSSDGTWIANEKVIHTYDFSGRNIKYGVREFGMATIMNGLAYSQVFRPFGGT
FLVFSDYMRNAIRLAALSKLPVIYQFTHDSIFVGEDGPTHQPVEQLMSLRAIPGLYVIRPADANEVRGAWIAG
LKHTGPTVIVLSRQALPTLPAHRPFKDGVGGRGAYIVLKESGEKPDYTLFATGSEVSLALSAKELEHLDKQV
RVVSFPCWELFEAQDVDYKQSIVGGDLGIRVSIEAGSALGWYKYIGSEGLAIAMDRFGYSGASDDVSEECGF
TTEQILQRILSQ

>core/99/3/Org3_Gene261

MEKVSSYPSVPLPLGASKISPNRYRFALYASQATEVILALTDENSEVIEVPLYPDTHRTGAIWHIEIEGSDQSS
YAFRVHGPKKHGMQYSFKEYLADPYAKNIHSPQSFGSRKKQGDYAFCYLKEEPFPWDGDQPLHLPKEEMIIY
EMHVRSTQSSSRVHAPGTFLGIIKIDHLHKLGINAVELLPIFEFDETAHPFRNSKFPYLCNYWGYAPLNFFS
PCRRYAYASDPCAPSREFKTLVKTLHQEGIEVILDVVFNHTGLQGTTCSLPWIDTPSYIILDAQGHFTNYSGC
GNTLNTNRAPTTQWILDILRYWVEEMHVDGFRFDLASVFSRGPSPGSLQFAPVLEAISFDPLLASTKIIAEPWD
AGGLYQVGYFPTLSPRWSEWNGPYRDNVKAFLNGDQNLIGTFASRISGSQDIYPHGSPTNSINYVSCHDGFTL
CDTVTYNHKHNEANGEDNRDGTANYSYNFGTEGKTEDPGILEVRERQLRNFFLTLMVSQGIPMIQSGDEY
AHTAEGNNNRWALDSNANYFLWDQLTAKPTLMHFCLDLIAFRKKYKTLFNRGFLSNKEISWVDAMGNPMT
WRPGNFLAFKIKSPKAHVYVAFHVGAQDQLATLPKASSNFLPYQIVAESQQGFVPQNVATPTVSLQPHTTLIA
ISHAKEVT

>core/100/3/Org3_Gene90

MKEENSQAHYLALCRELEDHDYSYYVLHRPRISDYEYDMKLRKLLIEIERSHPEWKVLWSPSTRLGDRPSGTF
SVVSHKEPMLSIANSYSKEELSEFFSRVEKSLGTSPRYTVELKIDGIAVAIRYEDRVLVQALSRGNGKQGEDIT
SNIRTIRSLPLRLPEDAPEFIEVRGEVFFSYSTFQIINEKQQQLEKTIFANPRNAAGGTLKLLSPQEVAKRKLEISI
YNLIAPGDNDSDHYENLQRCLEWGFVSGKPRLCSTPEEVISVLKTIETERASLPMEIDGAVIKVDSLASQRVLG
ATGKHWRWALAYKYAPEEAETLLEDILVQVGRTGVLTPVAKLTPVLLSGSLVSRASLYNEDEIHRKDIRIGDT
VCVAKGGEVIPPVVRVCREKRPEGSEVWNMPEFCPVCHSHVREEDRVSVRCVNPECVAGAIEKIRFFVGR
GALNIDHLGVKVITKLFELGLVHTCADLFQLTTEDLMQIPGIRERSARNILESIEQAKHVDLDRFLVALGIPLIG
IGVATVLAGHFETLDRVISATFEELLSLEGIGEKVAHAIAEYFSDSTHLNEIKKMQDLGVCISPYHKSGSTCFG
KAFVITGTLEGMSRLDAETAIRNCGGKVGSSVSKQTDYVVMGNPNPGSKLEKARKLGVSILOQEAFTNLIHLE

>core/101/3/Org3_Gene879

MRLNIHKYLFIGNRKADFFSASRELGVVEFISKKCFITTEQGHRFVECLKVFDHLEAEYSLEALEFVKDESVSV
EDIVSEVLTLNKEIKGLLETVKALRKEIVRVKPLGAFSSSEIAELSRKTGISLRFFYRTHKDNEDEEDSPNVFY
LSTAYNFDYYLVLGVDLPRDRYTEIEAPRSVNELQVDLANLQREIRNRSRDLCDLYAYRREVLRGLCNYDN
EQRLHQAKECCEDLFDGKVFVAVAGWVIVDRIKELQSLCNRYQIYMERVPVDPDETIPTYLENKGVGVMGED
LVQIYDTPAYSDDKDPSTWVFFAFVLFSSMIVNDAGYGLLFLMSSLLFSWKFRKMKFSKHLRMLKMTAILG
LGCICWGTTTTTSFFGMSFSKTSVFREYSMTHVLALKKAEEYLLQMRPKAYKELTNEYPSLKAIRDPKAFLLAT
EIGSAGIESRYVVYDKFIDNLMELALFIGVVHLSLGMRLRYLRYRYSIGIWILFMVSAYLYVPIYLGTVSLIHY
LFHVPYELGGQIGYYGMFGGIGLAVVLAMIQRSWRGVVEIISVIQVFSVDLSYLRIYALGLAGAMMGATFNQ
MGARLPMLLGSIVILLGHSVNIILSIMGGVIHGLRLNFIEWYHYSFDGGGRPLRPLRKIVCSEDAEASGIHLDN
NSIV

>core/102/3/Org3_Gene331

MSEHKKSSKIIGIDLGTNSCVSVMEGGQAKVITSSEGTRTTPSIVAFKGNEKLVGIPAKRQAVTNPEKTLGST
KRFIGRKYSEVASEIQTVPYTVTSGSKGDAVFEVDGKQYTPEEIGAQILMKMKETA EAYLG ETVTEAVITVPA
YFNDSQRASTKDAGRIAGLDVKRIIPEPTAAALAYGIDKVGDKKIAVFDLGGGTDFDISILEIGDGVFEVLSTNG
DTLLGGDDFDEVIIKWMIEEFKKQEGIDLSKDNMALQRLKDAAEKAKIELSGVSSTEINQPFITMDAQGP KHL
ALTLTRAQFEKLAASLIERTKSPCIKALSDAKLSAKDIDDVLLVGGMSRMPAVQETVKELFGKEPNKG VNP
EVVAIGAAIQGGVLGGEVKDVL LLDVIPLSLGIETLGGVMTTLVERNTTIPTQKKQIFSTAADNQPAVTIVVLQ
GERPMAKDNKEIGRFDLTDIPPAPRGHPQIEVSFDIDANGIFHVSADVASGKEQKIRIEASSGLQEDEIQRMV
RDAEINK EEDKKRREASDAKNEADSMIFRAEKA IKDYKEQIPETLVKEIEERIENVRNALKDDAPIEKIKEVTE
DLSKHMQKIGESMQSQSASAAASSAANAKGGPNINTEDLKKHSFSTKPPSNNGSSEDHIEEADVEIIDNDDK

>core/103/3/Org3_Gene788

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NWQAISKDSETLKVSDATTYIAEHGKSTASLTSKLSKFVRNYIDVSRFRGLAIFLICVAIFKAVTLFFQRFLGQ
VVAIRVSRDLRQDYFKALQQLPMTFFHDHDIGNLSNRVMTDSASIALAVNSLMINYIQAPITFILTLGVCL SIS
WKFSILICVAFPIFILPIVVIARKIKNLAKRIQKSQDSFSSVLYDFLAGVMTVKVFRTEKFAFTKYCEHNNKISA
LEEKSAAYGLLPRLLHTIASLFFAFVVVIGIYKFAIPPEELIVFCGLLYLIYDPIKKFGDENTSIMRGCAA AERF
YEVLNHPDLHSQKEREIEFLGLSNTITFENV SFGYQEDKHILKNLSFTLHKGEALGIVGPTGSGKTTLVKLLPR
LYEVSQ GKILIDSLPITEYNKGSLRNHIACVLQNPFLFYDTVWNNLTCGKDMEEEAVLEALKRAYADEFILKL
PKG VHSVLEESGKNLSGGQQQLAIARALLKNASILILDEATSALDAISENYIKNIIGELKGQCTQHIAHKL TTL
EHVDRVLYIENGQKIAEGTKEELLQTCPEFLKMWELSGTKEYNRVFPDP HKLVANPTDMAITT

>core/104/3/Org3_Gene614

MFSRLFFTSFSAEVVNTFFESGMSEDTSPLLSKQNRKLSHNLPLKSAYLSLGT YLIALLSFWLHAKNLSNLFVV
FTFFLAGTPALIKSLDNICQKVVNIDILMTSAAFGSIFIGGALEGALLVLFAISEALGQMVSGKAKSTLVSLKQ
LAPTTGWL VLEDGNLQKVAINKIEVGNILRIKSGEVVPLDGEILHGSSSINLMHLTGEKVPK SCHPGSIVPAGA
HNMEGSFDLRVLR TGSDSTIAHIINLVIQAQNSKPRLQQR LDKYSSVYALSIFA IACGIALLVPLFTSIPL LGPQS
AFYRALAFLIAASPCALIIAIIAYLSAINACAKHGVLLKGGVILDRLVSCNSVVM DKTGTLT TTGELTCIGCDYF
GSKNETFFPSVLAL EQSSSHPIAEAIVSYLMEQKVSSLPADRYLTVPGEGVRGYFNEQEAFVGRVETGLGKVP
SEYLEDIEQKIYQAKQHGEICSLAYVGN SFALFYFRDIPRPQAKEI IQDLKDLGYPVSM LTGDHKVSAENTA EI
LGISEVFFDLTPEDKLAKIRELATQRQIMMVGDGINDAPALAQATVGIAMGEAGSATAIEAADIVLLHDSLSS
LPWIIQKAKQTKKVVSQNLALALAILLVSWPASLGIPLWLAVILHEGSTVIVGLNALRLLKS

>core/105/3/Org3_Gene563

MTFQLHAPFAPCGDQPEAIARLSAGVRNQVKSQVLLGTTGSGKTFTIANVVANVNLPTLVLAHNKTLAAQL
YQEFREFFPNNAVEYFISYYDYYQPEAYIARSDTYIEKSLLINDEIDKLRLSATRSILERRDTLIVSSVSCIYIGIS
PENYTSMALVLEV GKEYPRNILTAQLVKMHYQASPIPQRS AFRERGSVIDIFPAYESELA LRLEFLNDTLTSIE
YSDPLTMIPKESVPSATLYPGSHYV IPEAIREQAIRTIQEELEERMAFFDDRPIEKDRIFHRTTHDIEMIKEIGFCK
GIENYSRHFTGAPPGAPPTCLLDYFPEDFLLI DESHQTL PQIRAMYRGDQSRKQSLVEYGFRLPSAFDNRPLT
YEEAQKYFRKVIYVSATPGDTEVQESSGHIVQQIIRPTGIPDPMPEIRPATGQVDDLLEEIRLRLSQKHEKILVIS

ITKKLAEDMAGFLSELEIPAAYLHSGIETAERTQILTDLRSGVIDVLIGVNLLREGLDLPEVSLVAILDADKEGF
LRSTSSLIQFCGRAARNINGKVIFYADQKTRSIEETLRETERRRQIQLDYNKEHNIVPKPIIKAIFANPILQTSKDS
ESPKESQRPLSKEDLEEQIKKYEALMQRAAKEFRFNEAAKYRDAMQACKEQLLYLF

>core/106/3/Org3_Gene397

MATPAQKSPTFQDPSFVRELGSNHPVFSPLTLEERGEMAIARVQQCGWNHTIVKVSLIILALLTILGGGLLVGL
LPAVPMFIGTGLIALGAVIFALALILCLYDSQGLPEELPPVPEPQQIQIEDLRNETREVLEGTLLLEVLLKDRDAK
DPAVPQVVVDCEKRLGMLDRKLRREEEILYRSTAHLKDEERYEFLLLELLEMRS�VADRLEFNRRSYERFVQG
IMTVRSEEKEISRLQDLISLQQQTVQDLRSRIDDEQKRCWTALQRINQSQKDIQRAHDREASQRACEGTEM
DCAERQQLEKDLRRQLKSMQEWIEMRGTIHQEKAWRKQNAKLERLQEDLRLTGIAFDEQSLFYREYKEYK
LSQKLDMMQKILQEVNAEKSEKACLESVHDYEQLEQKDANLKKAAAVWEEELGKQQQEDYEQTQEIRRL
STFILEYQDSLREAEKVEKDFQELQQRYSRQEEKQVKEKILEESMNHFADLFEKAQKENMAYKKKLADLE
GAAAPTEIGEDDDWVLTDASLSQKKIRELVEENQELLKALAFKSNELTQLVADAVEAEKEISKLREHIEEQK
EGLRALDKMHAQAIKDCEAAQRKCCDLESLLSPVREDAGMRFELEVELQRLQEENAAQLRAEVERLEQEQQ
G

>core/107/3/Org3_Gene910

MSYRKIRSTLIVLGVFALYALLVLRYYKIQICEGDHWAEEALGQHEFCVRDPFRRGTFFANTTVRKGDKDLQ
QPFAYDITKFHLCADPLAIPCHRDEIIQGILQFIEGQTYDDLKSLKDKKSRYCKLYPLLDVSVHDRLSLWWK
GYATKHRLPTNALFFITDYQRSYPFGKLLGQVLHTLREIKDEKTGKAFPTGGMEAYFNHILEGDVGERKLLRS
PLNRLDTNRVIKLPKDGSDIYLTINPVIQTIAEEELERGVLEAKAQGGRLILMNSQTGEILALAQYPFFDPTNYK
EYFNNKERIEHTKVSFVSDVFEPGSIMKPLTVAIALQANEEASLKSQKKIFDPEEPIDVTRTLCPRKGSPLKDI
SRNSQLNMYMAIQKSSNVYVAQLADRIIQLSGVAWYQQKLLALGFGRKTGIELPSEASGLVSPSPHRFHINGS
EWSLSTPYSLAMGYNILATGIQMVQAYAILANGGYAVRPTLVKKIVSASGEEYHLPTKEKTRLFSEEITREVV
RAMRFTTLPGGSGFRASPKHHSSAGKTGTTEKMIHGKYDKRRHIASFIGFTPVESSEGNFPPLVMLVSIDDPEY
GLRADGTKNYMGGRCAPIFSRVADRTLTYLGILPDKKLRNCDEEAAALKRLYEEWNRSPKQGGTR

>core/108/3/Org3_Gene512

MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSVNALMSLAD
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ATDEETAIAAEWETKNADAVKVGAQITELAKYASDNQAILDSLGLTSFDLLQAALLQSVANNKAAELLK
EMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIRDAYFAGQNASGAVENAKSNNSISNIDSAKAAIAT
AKTQIAEAQKKFPDSPILQEAQMVIAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAE
NETASILMSGFRQMIHMFNTENPDSQAAQQLAAQARAACAAGDSDAAAALADAQKALEAALGKAGQQQ
GILNALGQIASAAVVSAGVPPAAASSIGSSVKQLYKTSKSTGSDYKTQISAGYDAYKSINDAYGRARNDATR
DVINNVESTPALTRSVPRARTEARGPEKTDQALARVISGNSRTLGDVYSQVSALQSVMQIISNPQANNEEIRQ
KLTSVATKPPQFGYPYVQLSNDSTQKFIKLESLEFAEGSRTAAEIKALSFETNSLFIQQVVLNIGSLYSGYLQ

>core/109/3/Org3_Gene1001

MKKLVRLCIVVLLSLLPNVLFSSDLLREEGIKKMMDKLIEYHVDAQEVSTDILSRSLSSYIQSFDPHKSYLSNQE
VAVFLQSPETKKRLLKNYKAGNFAIYRNINQLIHESILRARQWRNEWVKNPKELVLEASSYQISKQPMQWSK

SLDEVKQRQRALLLSYLSHLGASSSRYEGKEEQLAALCLRQIENHENVYLGINDHGVAMDRDEEAYQFHI
RVVKALAHSLDAHTAYFSKDEALAMRIQLEKGMCGIGVVLKEDIDGVVVREIIPGGPAAKSGDLQLGDIIYR
VDGKDIEHLSFRGVLDCLRGGHGSTVVLDIRGESDHTIALRREKILLEDRRVDVSYEPYGDGVIGKVTLHSF
YEGENQVSSEQDLRRAIQGLKEKNLLGLVLDIRENTGGFLSQAIVSGLFMTNGVVVVVSRYADGTMKCYRT
VSPKKFYDGPLAILVSKSSASAAEIVAQTLQDYGVALVVGDEQTYGKGTIQHQTITGDASQDDCFKVTVGKY
YSPSGKSTQLQGVKSDILIPSLYAEDRLGERFLEHPLPADCCDNVLHDPLTDLDTQTRPWFQKYYPNLQKQE
TLWREMLPQLTKNSEQRLSENSNFQAFLSQIKSSEKTDLSYGSNDLQLEESINILKDMILLQQCRK

>core/110/3/Org3_Gene748

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HQTYPHKLLTGRNNEGFDHIRNDNGLSGFTNPTESDHDLFFSGHAGTALSALGMAQTTPLESRTHVIPILGD
AAFSCGLTLEALNNISTDLSKFVILNDNNMSISKNVGAMSRIFSRWLHHPATNKLTKQVEKWLAIPRYGD
SLAKHSRRLSQCCKNLFCPTPLFEQFGLAYVGPIDGHNVKKLIPILQSVRNLPFPILVHVCTTKGKGLDQAQN
NPAKYHGVANFNKRESAKHLPAIKPKPSFPDIFGQTLCELGEVSSRLHVVTAMSIGSRLEGFKQKQKPERFFD
VGIAEGHAVTFSAGIAKAGNPVICSISTFLHRA LDNVFHDVCMQDLPVIFAIDRAGLAYGDGRSHHGIYDMS
FLRAMPQMIICQPRSQVVVFQQLLYSSLHWSSPSAIRYPNIPAPHGDPLTGDPNFLRSPGNAETLSQGEDVLIIL
GTLCTALSIAKHQLLAYGISATVVDPIFIKPFNDLFSLLLMSHSKVITIEEHSIRGGLASEFNNFVATFNFKVDI
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>core/111/3/Org3_Gene545

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NRLLPEDLDPNDYIDPVVSIYQEYQKKLIEANALDFDILLFLTVRLLRESPEAQELYNQLWKALLIDEYQDT
NHAQYTLMQLLSKQHRNVFAVGDPDQSIYSWRGANIHNLNFENDYPNAKVLCLEENYRSYGNILNAANALI
KNNASRLEKELRSVKGPGEKIRLFLGSTDREEADFAAEILQLHRVGNIKLRDICIFYRTNSQSRTFEDALLRR
RIPYEIIGGLSFYKRKEIQDILAFRLIFISKSDIVAFDRTVNLPKRGIGSTTIFALTQYAIAQGLPILKACQQALDT
KDVKLSKKQQEGLQEYLALFPQIEHAYNTLSLRDFIESVVRITGYLEILKEDADTFKDRKSNLEELYHKALESE
QQNPKTHLELFLDDLALKGSDDDLNLTADRVNLMTLHNGKGLEFRVSFLVGLLEEQLLPHANSLGGTYENIEE
ERRLCYVGITRAQDLLYLTAQVRSWGTVRMMKPSRFLKEIPKDYMIQVR

>core/112/3/Org3_Gene882

MKQHYSLNKSRHILRSTYKLLKSKKLAHSPADKKQLQELLEQLEEAIFEHDQETASDLAQQALAFSNRYPNS
FGRKTYELIKALLFAGVVAFLVRQFWFELYEVPTGSMRPTILEQDRILVSKTTFGLHCPFAKKPLAFNPESVTR
GGLVVFTVGDLPDADTKYFGLIPGKKRYIKRCMGRPRDFLYFYGGKIYGLDDAGKRIEFPSVHGLENLHYH
PYISFDGTTSSHTGQKTIIDFKQFNQSYGRLIFPQTSMYGQFFDHKEWHQDEPNKLKDPHLSPVSYADLFGM
GNYAMVRILTEHQARTSHLLPNPGSPTKVYLEICHTANLSYPKPLLRHYEHQLSPAIQPMKTLLPLRKEHLHLI
RNNLTTSRFIVAQGCAYKYHQFKINTSGIAKAYAILLPKVPDGCYEYSKGEAYQIGFGEIRYKLKSSHPLTQLN
DKQVIELFNCGINFSSIYNPVNPLQAPLPNRYAFFNQGNLYIMDSPVFIKNDPTLQKFVTSETEKQEGSSETQPY
IAFVDKGLPPEDFKEFVEFIHNFGIQVPKGHVLLVLDGNYPMSADSREFGFVPMENLLGSPLCTFWPIGRMGRL
TGVSAPTTLSGYLVSGIALATGLSLIGYVYYYQKRRRLFPKKEEKNHKK

>core/113/3/Org3_Gene951

MIPFTKTIGFRLWLACAVAIAPLGINIVWLNLDQYRTIVSAISTALKENAAFKANTLTQIVPLNVDVLSLFSADV
LDLDAGIPETPNVLLSNEMQKVVFQGIYNEISLIKVPNGDKIVVASSIPEHLGENYNHKIDIPKNTPFLLAALKQS
PKNQEVFSVMQANVFDAKTQELQGILYTTFSAESLLKDLLINKQSYLTVKTAILSKYGVILKASDPALHLHTV
YPMTEKEKFCQVFLNDDPCPIDSELGPLTSLPDIGENFYSFKIKDTEIWGCIENVPSIDIAVLSYAKKEESFAPL
WRRARMYTAYFFCILLGSLIAFIVARRLSLPIRKLATAMIESRKNKNCLYTDDSLGFEINRLGHIFNAMVENLH
KQQHLAKTNFEMKENAQNALHLGEQAQQRLLPNTLPSYPHIELAKAYIPAITVGGDFFDVFFVVGEGSKARLF
LIVADASGKGVNACGYSLFLKNMLRTFLSRSSSLQQAQIETSRLFYNNNTKNSGMFVTLVCVYCYHQTSTNTMEY
YSCGHPPACYLDPDGETSWLFHPGMALGFLPEVANITSKLFFHPKPGSLFVLYSDGITEAHNNNNNDMFGEERL
QAAIQGLTGKSAADAVHRLMLSVPFVGNSHQHDDITLLILKVLES

>core/114/3/Org3_Gene568

MIQVTCQKQNYEVLEGTAAELAKQLKNSHQFIGVLINERPRDLSTHLNEGDTLVFLTSEDPEGREIFLHTSA
HLLAQAVLRLWPDAIPTIGPVIDHGFYDFANLSISESDFPLIEDTVKQIVDEKLAISRFTYGDQKQALAQFPQ
NPFKTELIRELPENEEISAYSQGEFFDLCRGPHLPSTAHVKAFAKVLRTSAAYWRGDPSRESLVRIYGTSFPTSKE
LRAHLEQIEEAKKRDHRVLGAKLDLFSQQESSPGMPFFHPRGMIVWDALIRYWKQLHTAAGYKEILTPQLM
NRQLWEVSGHWDNYKANMYTLQIDDEDYAIKPMNCPGCMLYYKTRLHSYKEFPLRVAEVGHVHRQEASG
ALSGLMRVRAFHQDDAHVFLTPEQVEEETLNILQLVSTLYGTFGLEYHLELSTRPEKDTIGDDSLWELATDAL
NRALVQSGTPFIVRPGEGAFYGPKIDIHVKDAIQRTWQCGTIQLDMFLPERFELEYTTAQGTKSVPVMLHRAL
FGSIERFLGILIENFKGRFPLWLSPEQVRIITVADRHIPRAKELEEAWKRLGLVVTLDDSSSESVSKKIRNAQNM
QVNYMITLGDHEINENVLAVRTRDNRVINDVSVERFLNTILEEKNSLSLTALL

>core/117/3/Org3_Gene557

MDENRKVIVVGGGLAGLSAAMQLANLGIIVELVSLTKVKRSHSVCAQGGINAALNLKPEEEDSPYVHAYDTI
KGGDFLADQPPVLEMCLAAPRIKMLDNFGCPFNRGPSGNLDVRRFGGTLYHRTVFCGASTGQQLMYTLDE
QVRRREHAGRVIKRENHEFVRLVTDHSGRACGIILMNLFNRLLEILRGDAVIIATGGPGVIFKMSTNSTFCTGA
ANGRLFLQGMAYANPEFIQHPTAIPGRDKLRLISESVRGEGRVWVPGDSSKRIVFPDGSERPCGETGAPWY
FLEDMPAYGNLVS RDVGARAILRVCEAGLGIDGRMEAYLDVTHLPEKTRHKLEVLDIYKKFTGEDPNTV
PMRIFPAVHYSMGGAWVDWPAADDPDRDSRFRQMTNIPGCFNCGESDFQYHGANRLGANSLLSCLFAGLVS
GDEASRFIEAFGASQATSSDFDRALQQEKEENARLLSASGKENIFVLHEEIAKIMVRNVTVKRNNRDLQETM
DKLKEFRERLKNVSVLDSSPFANKSFHFVRQMGPMLELALAITKGALLRNEFRGSHYKPEFPERDDEHWLKT
TVAVYAPEEPEISYLPVDTRHVAPTLRDYTKSSTGKIELTNIPDNIRLPI

>core/118/3/Org3_Gene901

MTIIYFILAALALGILVLIHELGHLLVAKAVGMAVESFSIGFGPALFKKRIGGIEYRIGCIPFGGYVRIRGMERT
KEKGEKGKIDSVYDIPQGFFSKSPWKRLVLVAGPLANILLAVLAFSILYMNGGRSKNYSDCSKVVGWVHPV
LQAEGLLPGDEILTCNGKPYVGDKDMLTTSLLEGHLNLEIKRPGYLTVPKSKEFAIDVEFDPTKFGVPCSGASY
LLYGNQVPLTKNSPMENSELRPNDRFVWMDGTLLFSMAQISQILNESYAFVKVARNDKIFFSRQPRVLASVL
HYTPYLRNELIDTQYEAGLKGWSSLYTLPYVINSYGYIEGELTAIDPESPLPQPQERLQLGDRILAIIDGTPVSG
SVDILRLVQNHRSIIVQQMSPQELEEVSNSRDADKRFIASYHSEDLLQILNHLGESHPVEVAGPYRLLDPVQPR

PWIDVYSSES LDKQLEVAKKIKNKDKQRY YLERLDAEKQKPSLGISLKDLKVRYNPSPVVMLSNITKESLITL
KALVTGHLSPQWLSGPVGIVQVLHTGWSVGFSEVLFWIGLISMNLAVLNLLPIPVLDGGYILLCLWEIVTRRR
LNMKIVERILDPFTFLLIHFFIFLTFQDLFRFFG

>core/119/3/Org3_Gene339

MRRSVCYVNPSIARAGQISTWKFLYSLATPLPAGTKCKFDLAGSGKPTDWEAPATDLSQTRNVIYAEMPEGE
IIEATAIPVKDNPVPQFEFTLPYELQVGETLTIVMGASPNHPQVDDAGNGAQLFAQRRKPFYLYIDPTGEGNY
DEPDVFSMDIRGNVLKKIEIFTPSYVVKNRFDITVRFEDEFGNLTNFSPEETRIELSYEHLRENLNWQLFIPET
GFVILPNLYFNEPGIYRIQLKNLSTQEIFISAPIKCFADSAPNLMWGLLHGESERVDSEENIETCMRYFRDDRAL
NFYASSSFENQENLSPDIWKLINQTVSDFNEEDRFITLSGFQYSGEPHLEGVRHILHTKETKSHSKHKEYKHIPL
AKLYKSTVNHDMISIPSFTASKEHGFDFENFYPEFERVVEIYNAGWSSETTAALNNPFPIQGKDSEDPRGTVIE
GLKKNLRFGFVAGGLDDRGIYKDYFDSPQVQYSPGLTAHCNKYTRESLVEALFARHCYATTGPRIVLSFNITS
APMGSELSTGSKPGLNVNRHISGHVAGTALLKTVEIIRNGEVLHTFFPDSNNLDYEYDDMVPLSSVTLKDPNG
KAPFVFFYYLRVTQADNAMA WSSPIWVDLN

>core/120/3/Org3_Gene89

MESEKDIGAKFLGDYRILYRKQSLWSEDLLAEHRFIKKRYLIRLLL PDLGSSQPFMEAFHDVVVKLAKLNHP
GILSIENVSESEGRCLVTQE QDIPILSLTQYLKSIPRKLTELEIVDIVSQLASLLDYVHSEGLAQEEWNLD SVYI
HILNGVPKVILPDLGFASLIKERILDGFISDEENRESKIKERVLLHTSEGKQGREDTYAFGAITYYLLFGFLPQGI
FPMPSKVFSDFIYDWDFLISSCLSCFMEERAKELFPLIRKKT LGEELQNVVTNCIESSLREVDPLESSQNLPQA
VLKVGETKVSHQKESA EHLEFVLVEACSIDEAMDTAIESESSSGVEEEGYSLALQSLLVREP VVSRYVEAEK
EPPKPQILTEMVLIEGGEFSRGSVEGQRDEL PVHKVILHSFFLDVHPVTNEQFIRYLECCGSEQDKYYNELIRL
RDSRIQRRSGRLVIEPGYAKHPVVGVTWYGASGYAEWIGKRLPTEAEWEIAASGGVAALRYPCGEEIEKSRA
NFFTADTTTVM SYPPNPYGLYDMAGNVYEW CQDWYGYDFYEISAQEPESPQGAQGVYRVLRGGCWKSLK
DDLCAHRHRNNPGAVNSTYGFRC AKNIN

>core/121/3/Org3_Gene833

MKKGKLGAIVFGLLFTSSVAGFSKDLTKDNAYQDLNVIEHLISLKYAPLPWKELLFGWDLSQQTQQARLQLV
LEEKPTTNYCQKVLSNYVRS LNDYHAGITFYRTESAYIPYVLKLSEDGHVFVVDVQTSQGDIYLGDEILEVDG
MGIREAIESLRFGRGSATDYSA AVRSLTSRSAAFGDAVPSGIAM LKLRRPSGLIRSTPVRWRYTPEHIGDFSLV
APLIPEHKPQLPTQSCVLF RSGVNSQSSSSSLFSSYMVPYFWEELRVQNKQRFD SNHHIGSRNGFLPTFGPILW
EQDKGPYRSYIFKAKDSQGNPHRIGFLRISSYVWTDLEGLEEDHKDSPWELFGEIIDHLEKETDALIIDQTHNP
GGSVFYLYSLLSMLTDHPLDTPKHRMIFTQDEVSSALHWQDLLEDVFTDEQAVAVLGETMEGYCMDMHAV
ASLQNFSQS VLSWVSGDINLSKPMPLLGFAQVRPHPKHQYTKPLFMLIDEDDFSCGDLAPAILKDNGRATLI
GKPTAGAGGFVFQVTFPNRSGIKGLSLTGSLAVRKDGEFIENLGVAPHIDLGFTSRDLQTSRFTDYVEAVKTIV
LTSLSENAKKSEEQTSPQETPEVIRVSYPTTTSAL

>core/122/3/Org3_Gene821

MFGTLVSTLCCPANSERDWEDHEVNCIYIASTSDTQLEAVQGGMHITELRGEPVRVLYETGHLYAFARENTC
HSRLEVSHTVRAMTYFWDRFFSRHWNVGRRFLVFYQGN GGAYVQAALDSSMHTQDIYVLGLSPTVYIRGN
YHVQHRYVRGFWPSCLD SLAACAE NTSVLPGESSDGIFYPSLFSHTFDNAIRYGERCLLVCSEGMGMLPET

QQQTSPLTSLEGGHEVALVLNPQQNPEALSIALSRLMHEERGGRLESNYMPGRSSNPFMTSMYVLVRLNTLAQ
IYLMSPYYSFQSNDIVCLIFISSAAVETVSYIFLTVTDSTCGRRYLRVPRLVCTGLRNLALPTTLLELLILSYPRS
VEGVFPNVRFILGYMCTTRVVFFAWNLLHWPFRCLRHGIQLFVHRSIIGHTLGARITDLTLASMRYAIVFPSI
VSSCLLTALAHANTNILALDPYRLIESGDLRRPAFNDDDEMQQADNPWDAYSIGLVINTCIYMLILFANLIFMV
YSVRRYHRSRR

>core/123/3/Org3_Gene249

MTLITPAINSSRRKTHTVRIGNLYIGSDHSIKTQSMTTTLTTDIDSTVEQIYALAEHNCDIVRVTVQGIKEAQAC
EKIKERLIALGLNIPLVADIHFFPQAAMLVADFADKVRINPGNYIDKRNMFKGTKIYTEASYAQSLRLLEEKFA
PLVEKCKRLGKAMRIGVNHGSLSERIMQKYGDTIEGMVASAIEYIAVCEKLNRYRDVVFSMKSSNPKIMVTAY
RQLAKDL DARGWLYPLHLGVTEAGMGVDGIIKSAVGIGTLLAEGLGDTIRCSLTGCPTTEIPVCD SLLRHTKI
YLDLPEKKNPFSLQHSENFVSAAEKPAKTTLWGDVYGVFLKLYPHHLTDFTPEELLEHLGVNPVTKEKAFTT
PEGVVVPPELKDAPITDVLREHFLVFHHHQVPCLYEHNEEIWDSPAVHQAPFVHFHASDPFIHTSRDFFEKQG
HQGKPTKL VFSRDFDNKEEAAISIATEFGALLDGLGEAVVLDLPNLPLQDVLKIAFGTLQNAGVRLVKTEYI
SCPMCGRTLFDLEEVTTRIRKRTQHLPGLKIAIMGCIVNGPGEMADADFGFVGSKTGMIDLYVKHTCVKAHIP
MEDAEELIRLLQEHGVWKDPEETKLT V

>core/124/3/Org3_Gene420

MWTHPIAYDVIVVGAGHAGCEAAAYCSAKMGVSVLMLTSNLDTI AKLSCNPAVGGIGKGHIVREIDALGGIM
AEVTDQSGIQFRILNQTKGPAVRAPRAQVDKQLYHIHMKRLLENTPGLHIMQATVESLLDKEGVISGVTTKE
GWMFSGKTVVLSSGTFMRGLIHIGDRNFSGGRLGDPSSQGLSEDLKKGFPISRKTGTPPRL LASSINFSCME
EQPGDLGVGFVHRTEPFQPPLPQLSCFITH TMEKTKAIISANLHRSALYGGCIEGVGP RYCPSIEDKIVKFSDE
RHHVFLEPEGLHTQEIYANGLSTSMFPDVQYDMIRSVLGLENAIITRPAYAIEYDYIHGNVIHPTLESKLIEGLF
LCGQINGTTGYEEAAAQGLIAGINAVNKVFNRPPFIPSRQESYIGVMLDDLTTQILDEPYRMFTGRAEHRLLLLR
QDNACARLSHYGYELGLLSEERYELVKKQNQLLEEEKVRLQKTFRQYQGSVVS LAKALSRPEVSYDMLREA
FPNDIRDLGAVLNASLEMEIKYSGYIDRQKILIQSLEKAESLLIPEDLDYKQITALSLEAQEKLAKFTPRTL GSA
SRISGIASADIQVLMIALKKHAHH

>core/125/3/Org3_Gene81

MTTELKTEALPTRTQVDPKHCWDTTLMYANREEWKKDFDLCSSGKDRSPIWPEFSPSHYQIDNPESLLELLS
KKFSVERKLDQLYIYAHLIHDQDITNPEGESDYQSIVYLYTLFSQEISWIQPALIALSEEKVAALLSSSVLAPYR
FYLEKIFRLSPHTGTANEEKILASSFAALNVSNKAFSSLSDAEIPFGIAKDSNGEEHPLSHALASLYMQSPDQEL
RRTAYLAQFQRYDYRNTFANLLNGKVQAHLFEAKARNYPSCLEASLFQHNIPTTVYINLINETKKHTSLINR
YFNLKKEALNLKEHFHYDVYAPISQTTSKNYSYEEGVLDLVCKSLLPLGTHYVEILRNGLLSNRWVD RYENKH
KRSGAYSSGCYDSAPYILLNYTNTLYDVS VIAHEAGHSMHSYFSREAQPYHDAQYPLFLAEIASTFNEMLLM
EALSKSDQSKEDKIVIITKTLDTIFATLFRQTFFAAFEYEIHSAAEQGTPLTEEFLSATYGNLQKEFYGGVVTSD
SLSALEWARIPHFYNFYVYQYATGIIAALSFAEKILTQEPGALELYLKFLKSGRSDFPLNILKKSGLDMTTSA
PLDKAFAFITKKIDLLSSLLSED

>core/126/3/Org3_Gene947

MFRCILFGIFLLTCFSSGGVLYYLFCSHDFSIGPKEKSRSVWIEEEKEFTDSVLHHLPSQHQLHLHILCFQGFLQ
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QKLYREVIEQLAYWQEEKTRALAPLLNISIEQLLTDFLLDYISAHSLIEQKMFPEGRVILNRNINRLLKHECEW
NAKTYDRIAILLSRSYFLELVESKSADIYFDYYEMVLFYLLKKIYILEQCPYAELLPEEELVSLIMEHVFILPKDK
LYPLIQLLEMWQKHVHPNSSLVVQILVDRFSTHMEGAIRFCEALVSFSGLEELHQQIITTFEELLSNKVQQIK
TEEAKQCVALHILDPSISISEKLALSSDTLQNIVSGDDEQHTKLRNYLDLWEAIQSYDIDRQQLVHHLVYGA
KDLWKKGGNDEKALNLLQLVLRFTSYDIECESVFLFIKQAYKQALSSHAIRLLKLEKFISEANIPSIVISEAE
KANFLADAEYLF AHEDYDKCYLYSMWLTKVAPSPQSYRLAGLCLMENKRYDEALEFLCMLSPNNSINDYK
TQKALAFQCQKHQSKDRVAS

>core/127/3/Org3_Gene838

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WATHGVPTEINAHPHVDEGRSCAVVHNGIENFKELRRELTAQGIFASDTDSEIIVQLFSLYYQESQDLVFSF
CQTLAQLRGSVACALIHKDHPTILCASQESPLILGLGKEETFIASDSRAFFKYTRHSQALASGEFAIVSQGKEP
EVYNLELKKIHKDVRQITCEDASDKSGYGYMLKEIYDQPEVLEGLIQKHMDEEGHILSEFLSDVPIKSFKEI
TIVACGSSYHAGYLA KYIIESLVSPVHIEVASEFRYRRPYIGKDTLGILISQSGETADTLAALKELRNRNIAYLL
GICNVPESAIALGVDHCLFLEAGVEIGVATTKAFTSQLLLL VFLGLKLANVHGALTHAEQCSFGQGLQSLPDL
CQKLLANESLHSWAQPYSYEDKFLFLGRRLMYPVVMEEAALKKEIAYIEANAYPGGEMKHGPALISKGTPV
IAFCGDDIVYEKMIGNMMEVKARHAHVIAIAPESREDIAAVSDQQIFVPDCHFLAAPVLYTIVGQVMAYAMA
LAKGMEIDCPRNLA KSVTVE

>core/128/3/Org3_Gene680

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LIQWFYIESNNTKDFPLLFWKIGLLGGLLALVYFIRIGDPINILCYGCGLFPSIANLRLFYKEQRSTPYLDTHCFL
SAGEASGDILGGKLIQSIKSLYPNIRFWGVGGPAMRQEGQLPILNMEEFQVSGFAEVLGSLFRLYRNYRKILKT
ILKHKPATLIFIDFPDFHLLIKKLRKHGGRGKIIHYVCPISAWRPKRKRILEQHLDMLLLILPFEEGLFKNTSL
ETVYLGHPLVEEISDYKEQASWKEKFLNSDRPIVAAFPGSRRGDISRNLRIQVQAFLNSSLSQTHQFVVSSSSA
KYDEIIEDTLKAEGCQHSQIIPMNFYELMRSCDCALAKCGTIVLETALNQTPTIVMCRLRPFDFTFLAKYIFKIL
LPAYSLPNIIMNSVIFPEFIGGKKDFHP EIIATALLNQHGSKEKQKEDCRKLCKVMTTGQIASEEFLKRIFDT
LPAV

>core/129/3/Org3_Gene558

MKHTFTKRVLFFFLLVIPIPLLLNLMVVGFFSFSAAKANLVQVLHTRATNLSIEFEKKLTIHKLFLDRLANTLA
LKSYPSPAEPYAQAYNEMMALSNITDFSLCLIDPFDGSRVTKNPGDPFIRYLKQHPMKKKLSAAVGKAFL
TIPGKPLLHYLILVEDVASWDSTTTSGLLVSFYPM SFLQKDLFQSLHITKGNICLVNKYGEVLFC AQDSESSFV
FSLDLPNLPQFQARSPAIEIEKASGILGGENLITVSINKKRYLGLVLNKIPIQGTYTLSLVPVSDLIQSALKVPL
NICFFYVLAFLLMWWIFSKINTKLNKPLQELTFCMEAAWRGNHNVRFEPPQPYGYEFNELGNIFNCTLLLLLNS
IEKADIDYHSGEKLQKELGILSSLQSALLSPDFPTFPKVTFSSQHLRRRQLSGHFNGWTVQDGGDTLLGIIGLA
GDIGLPSYLYALSARSLFLAYASSDVSLQKISKDTADSFSKTTEGNEAVVAMTFIKYVEKDRSLELLSLSEGAP

TMFLQRGESFVRLPLETHQALQPGDRLICLTGGEDILKYFSQLPIEELLKDPLNPLNTENLIDSLTMMLNNETE
HSADGTLTILSFS

>core/130/3/Org3_Gene664

MRIEDFSLKLIPSSPGVYLMKDVHDQVLYIGKAKNLKNRLASYFHEKGDSRERIPFLMKKTASIEATIVVSNETE
ALLENLIKQHHPKYNVLLKDDKTFFCLAISLSHWPKEAIRTKAITSSQRQLIFGPYVSAEACHTLLEVISQ
WFPLRTCSDREFALRKRPCILYDMKRCLAPCVGYCTPEEYQGTLDKAILFLKGKIEEVVKDLEKVIQKASDNL
EFEQAANYRRTLSLIKQAMAKQQVEKFHFQONIDALGLYRHKQRTILTLLTVRSGKLLGARHFSFFENAQEDQ
DLLSSFILQYYVSQPYIPKEILTPLPLEFPTLSYVLNAESPRLRSPKTGYGKELDLAYRNAKAYAATTLPSSST
LPYQDFQNILRMSQYPYRIECYDNAHMQGAHATGVYIVFENNGFDPKQYRTFSIDSEKTQNDLALLEEVLLR
RFHSLTTALPDMIVVDGGKTHYNKTKKIIQTLNLTGIQVVZIAKEKSNHSRGLNKEKIFCETPPEGFSLPPTSNL
LQFFQILRDEAHRFAISKHRKKRGKALFEQEKIPGIGEVKRKRLQKFKSWKQVMLSSQEELEAIPGLTKKDIA
VLLARQKDFNKSD

>core/131/3/Org3_Gene237

MKEYKIENIRNFSIIAHIDHGKSTIADRLLSTSTVEEREMREQLLDSMDLERERGITIKAHPVTMTYLYEGEV
YQLNLIDTPGHVDFSYEVSRLSACEGALLIVDAAQGVQAQSLANVYLALERDLEIIPVLNKIDLPAADPVRIA
QQIEDYIGLDTTNIACSAKTGQGIPAILKAIIDLVPPPKAPAETELKALVFDSHYDPYVGIMVYVRIISGELKKG
DRITFMAAKGSSFEVLGIGAFLPKATFIEGSLRPGQVGFFIANLKKVKDKIGDVTTKTKHPAKTPLEGFKEIN
PVVFAGIYPIDSSDFDTLKDALGRLQLNDSALTIEQESSHSLGFGFRCGFLGLLHLEIIFERIIREFDLDIIATAPS
VIYKVVLKNGKVLDIDNPSGYDPDAIIEHVVEEPWVHVNIITPQEYLSNIMNLCCLKRGICVKTEMLDQHRLVL
AYELPLNEIVSDFNDKLKSVTKGYGSFDYRLGDYRKGSIIKLEVLINPEPIDAFSCLVHRDKAESRGRSICEKL
VDVIPQQLFKIPIQAAINKKVIARETIRALSKNVTAKCYGGDITRKRKLWEKQKKGKKRMKEFGKVSIPNTAFI
EVLKLD

>core/132/3/Org3_Gene1014

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DVARVEQFTFICTSTEAEAGPTNNWRDPQEMRRELHQLFRGCMQGRTRYIVPFCMGPLDSPFSIVGVELTDSP
YVVC SMKIMTRMGDDVLRSLGTSGKFLKCLHSVGKPLSPGEADVSWPCNPKSMRIVHFQDDSSVMSFGSGY
GGNALLGKKCVALARLASYMAKSQGWLAEHMLIIGITNPEGKKKYFSASFPSACGKTNLAMLMPKLPGWKIE
CIGDDIAWIRPGRDGRLYAVNPEYGFFGVAPGTSERTNPALATCRSNSIFTNVALTADGDVWWEGLTEQPP
EPLTDWL GKPKWPGGSPAHPNSRFTAPLRQCPSLDPEWNSPQGVPLDAIIFGGRRSETIPLVYEALSWEHGV
TIGAGMSSTTTAAIVGQLGKL RHDPFAMLPFCGYNMAYYFQHWLSFAENRSLKLPKIFGVNWFRKNNQGEF
LWPGFSENLRVLEWIFQRTDGLEDIAERTPIGYLPNIQKFNLNGLNLDLQTVQELFSVDAEGWLA EVENIGEY
LKIFGSDCPQQITDELLRIKSELKEK

>core/133/3/Org3_Gene504

MAAYTEASILSLASLDHIRLRAGMYIGRLGNGSQKEDGIYTLFKEVVDNGIDEFIMGHGKSLKISASDKQISIQ
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SKQGSTKDPDGT FVSFTPDPSIFPEFTFNHDFLKD KIRQYTYLHSGLEIRFNDEVFISHNGLKDLFDAEITEPLY
SPLFFQNEDLTFIFSHLEGNTERYFSFVNGQETLDGGTHLTAFKEAIVKGVNEFFGKTFVSN DIREGIVGCIAIKI

ASPIFESQTKNKLGNTQIRSSLIKDVKEAIVQALRKDKVAPELLLEKIKFNEKTRKNIQFIKQDLKSKQKKVHY
KIPKL RDCKFHYNDRSLYGEASSIFLTEGESASASILASRNPLTQAVFSLRGKPMNVFSLEETKMYKNDEL FYL
ATALGITQNEIQHLRYNKVILATDADVDGMHIRNLLITFFLKTLLPLVENNHLEFILETPLFKVRNKTTTTLYYYS
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NLITDF

>core/134/3/Org3_Gene823

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VRYERAIGGVMITASHNPPNYNGYKVYMASGGQVLPPLDQEIVAACSAVNEILSVPSIDHPNIHLIGKEYEAL
YRDTLKQLQLYPEANRISGRSLSYSPLHGTGISLVPHVLKDWGFLSVHLVEKQAIGDGDFTVQLPNPEDPE
ALTLGTEQMLANDDDLFIATDPDADRVGVVCLEDGQPYRFNGNQMASLLADHILGAWSKTRHLGEHDKLV
KSLVTTEMLSAIAKHVHVDLINVGTGFKYIGEKIESWRNSTNKFVFGAEESYGCLYGTHVEDKDAIIASALIA
EAALQQKLQGKTLCDALLSLYETYGYFANKTESVVFSAKTDEQEIRKKLSHLEEISSANFFSGKYQVEKFENY
KQGIGFNLLSKDSYAL TLPKTSMLCYFSGGGRVIIRPSGTEPKIKFYFEMSTHYPERVTDKEIQKQREAESFQ
HLDDFIFDFKEKFSNL

>core/135/3/Org3_Gene48

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LLGTVPEGRFTHKIMVPFSCFQEVTLTWVISEGTYNAHTVVAKARDAQGKECAFTMVQRWPIKQAFIEGEKI
PAHKIMDVGLRILDTQIPVLKGGTFCTPGPFGAGKTVLQHHL SKYAAVDIVILCACGERAGEVVEVLQEFPHL
IDPHTGKSLMHRTHICNTSSMPVAARESSIYLGVTIAEYYRQMGLDILLADSTSRWAQALREISGRLEEIPGE
EAFPAYLSSRIA AFYERGGAITTKDGSEGS LTICGAVSPAGGNFEETVQSTLAVVGAF CGLSKARADARRYP
SIDPLISWSKYLNQVGQILEEKVSGWGGA VKKAAQFLEKGSEIGKRMEVVGEEGVSMEDMEIYLKAELYDF
CYLQQNAFDPVDCYCPFERQIELFSLISRIFDAKFVFDSPDDARSFFLELQSKIKTNLGLKFLSEEYHESKEVIV
RLLEKTMVQMA

>core/136/3/Org3_Gene907

MTAPTESRSSPPTLLEETEPLSPNIPADIQIPRITISPPSLDVSTVASSAEDISVFIAGGPRSSSSASVASDVYELV
CLCGGDEDPEPPDSEVRTLYVNGSWQTHQEAVQELLYISEVRGEAVRLLYNDGSGMSPWPISP CRTLPTLDH
PLCQALLTVWEQFFSAPENQHREFLVIFYGDASPYIQQALTQSRHSPRIVVVGISPTVFIQGD FRVHNYRVSGD
FFSSLCDRGTRAENTTILPYSSGLEGVFLPSIRCPSFTWAVRFGEQCLVANRGEDVEDRGGLS QDAERSQLPHS
ERDLAVVIDSTDPSSMSRLVEWLNQGSPSSDMEINPYPQRCPDVALSALY AISRVSGLAQEWILASVHEGLDL
QICYSLILMHTTFAVRYFFLLFTNYPQSRERFRTARIVAQSLYLPSILVLVFD CGNVLRKLWMPQEILRAIFISA
STISGSIVFVECTRW MGRGLRHRVQQFVQQRVIGSGLPVGTVRASYRDRAGFIIGFLQTVHGGLYLPVSIMVL
NQIAIQVPRILVRPNNTAVYDLHNKSAEENWSSGDVLAVGQTLNFILCAFVLVFNLWFFVKSVLRHSRRRRR

>core/137/3/Org3_Gene714

MKKKKFIFYFVIVFSLFLWEMTSRHRPTFSFFCPPPSSIASSTLQSLPLLLTSAWHTLKAILGGFFLAITLSIVLAT
IMLSYKSAKDLLQPLFILLQCTPMFALAPLIVLWFGWGIGAVIVPTALTIFFP LTLTIYQGILSTPEELIEQFVLC

GATKFQLLIKLRIPHALPHIFSGLKIAIGSAGFAAIAGEWVASQSGLGILMLESRRNYEMELAFAGLATLSILTL
SLFQITLLIEKLIFSFRVKRMSLKHKSVAKKALSVLALIPIMLIPWKGNSKSPDKKNLTSLTLLLDWTPNPNH
IPLYAGVAKGYFKQHGLDLQLQKNTDSSSAVPHVLFEQVDMALYHALGIMKTSIKGMPIQIVGRLIDSSLQGF
LYRSQDPIYKFEDLNGKVLGFCLNNSRDLNRLLETNLRNGVVPSEVKNVSSDLISPMLLNKIDFLYGAFYNIE
GVKLQTLGMPVKCFLSDTCDLPTGPQLIVFTKKGTKASEPEIVEAFQKALQESIIFSKDHPEDAFKLYAKETKS
IPKNLYQEYLQWEETFPLLAQSQDPLSKDLVDKLLLETIIKRYPELASEVAKFSLNDLYNPSLPEEQSV

>core/138/3/Org3_Gene665

MYTEESLDNLRHSIDIVDLSEHIHLKRSGATYKACCPFHTEKTPSFIVNPAGAHYHCFGCGAHGDAIGFLMQ
HLGYSFTEAILVLSKKFQVDLVLQPKDSGYTPPQGLKEELRHINSEAEFFRYCLYHLPEARHALQYLYHRGF
SPDTIDRFHLGYGPEQSLFLQAMEERKISQEQQLHTAGFFGNKWFLFARRIIFPVHDALGHTIGFSARKFLENSQ
GGKYVNTPETPIFKKSRILFGLNFSRRRIAKEKKVILVEGQADCLQMIDSGFNCTVAAQGTAFTEEHVKELSK
LGVLKVFLLFDSDEAGNKAALRVGDLQCQTAQMSVFVCKLPQGHDPDSFLMQRGSSGLIALLEQSQDYLTFLI
SEKMSSYPKFGPREKALLVEEAIRQIKHWGSPILVYEHLKQLASLMMVPEDMVLSLANPQVTAEPQNIPIKQK
VPKIHPHIVMETDILRCMLFCGSNTKILYTAQFYFVPEDFKHPECRKLFAFMISYYEKYRKNVPFDEACQVLS
DSQILQLLTKRRLNTEALDTIFVQSLQKMADRRWREQCKPLSLNQNIQDKKLEILEDYVQLRKDRTIITLLDPE
SELIP

>core/139/3/Org3_Gene313

MSTSPISNDPRYLSLSNATEKTSLLANSRSLSPVPNSLVPSNPEDTGLRKSIFTHSVTLFAGLVVLLVAVSVVV
VALTVLAPGVPQAILLGIAISGVGIGGSIMKSLVYMVRDYMSPRMQESSRIKSALAVGTGFTVMGLVMKVG
ANFVPGGYGGLVGSLGSSAYSRRGSQTTLASFHYIYTKFFRSEKVAKGEKLTEAETIKEAKKLHYITLSIATIG
VGLAVLGILLAIAGTVLLGGAPATIAIILAPPLISIGLTTVLQTIHSSIGKWRAFLTQEKKDLFVDTSCLKDIRLE
KLPPSEVEESETSQSVIEVPDSEGIAETRISAEEDTRLSTTRQKVIFALATLLLLASIAAFIVTGFGGLTVMQVL
LVASVGSASASVTLPMVSSGFSYVAYQLKARLNISKLRWKEAKNKKRVRQFLIESGVIASDREFNQMWKTV
YKKQIQKTDAAIREEVNFEKGGEVNSALVGGILLGVGTGIMLLALVPAFAPIVPGILALGGSTLGIAGSILMR
KFVNWLYDELVKLYERRRRNRRELLYGPESKMRSIATDLVVEALAASHDHLFDLDGPVDFIDVDVDIDGAA

>core/140/3/Org3_Gene378

MTNSDNASAAGLLWAHPKEDPAFLGMIIKEFHLPPTVAQIFISRGFQTIQEIHKFLYSHLSSLYDPGLFLDMSK
AVERLLLARDRKEHVMIYGDSDDVDGMTGVALLVEFLRDIDVHVSFFLGAILKQHGETSTLIAKLKEEGITLL
ITVDCGITAGKEVSDITRQGIDVIITDHHMPTGKIPHCVATLNPCLRDTHTYPNRELTVGVVAFKLARGVLNALI
SRNLVPKSQGSLKKLLDLVTLGTITDVGVLLGENRVMVRYGIKEIARGARPGLNKLALCGVEKSEVTSTDIV
LKIAPKLNSLGRLLDDPAKGVELLLTQDDERVDALIMELDNINRERQRIEAEVFQDVQEILNSNPEILKQAAIVL
SSTAWHARVIPIISARLAKTYNKPVVIIAIQRGIGKGSARTIGSFLLGVLLKKCSSLLSYGGHDFAGVIMKED
KVEDFKKKFVHLVNSSLKKGDTLPHLEIDAYADFDAIDYDLLASMELFEPFGKGNLMPIFYSKVRQVRYPKV
LPGNHLKLYLSQKERNLEGVAFGLGRHADALKASWHYPLEIAYTPRLSQTSGSGVIHLLVRDFRISSEPRFSD

>core/141/3/Org3_Gene219

MSFLRRHISLFRSQKQLIDVFAPVSPNLELAEIHRRVIEDQGPALLFHNVISSFPVLTNLFGTKHRVDQLFSQA
PDNLIARVAHLISSTPKLSSLWKSRLDKRISSGLKKARFRFPFVSMSSVNLDHLLPLTTSWPEDGGAFLLTP

LVYTESPTLTTPNLGMYRVQRFNQNTMGLHFQIQKGGGMHLYEAEQKKQNLPVSVFLSGNPFLTLSAIAPLP
ENVSELLFATFLQGAKLLYKKTNDHPHPLLYDAEFILVGESPAKRRPEGPFQDHFQYYSQHQDFPEFHCHKI
YHRKDAIYPATVVGKPYQEDFYIGNKLQEYLSPLFPLVMPGVRRLKSYGESGFHALTAAVVKERYWRESLTT
ALRILGEGQLSLTKFLMVTQDEVPLDRFSVVLETILERLQPDRLIIFSETANDTLDYTGPSLNKGSKGIFMGIG
KAIRDLPHGYQGGKIHGVDIAPFCRGCLVLETSLEDRCIKSLLHHPDLKSWPLIILADNLRETIQSEKDFLWR
TFTRCAPANDLHALHSHFATHRPNYNFPFVIDALMKPSYPKEVEVDPSTKQKVSERWHAFFPNKETFYI

>core/142/3/Org3_Gene459

MKYRTHRCNELTSNHIGENVQLAGWVHRYRNHGGVVFIDLRDRFGITQIVCREDEQPELHQRLDAVRSEWV
LSVRGKVCPRLAGMENPNLATGHIEVEVASFEVLSKSQNLPSIADHDHINVNEELRLEYRYLDMRRGDIIEKL
LCRHQVMLACRNFMDAQGFTEIVTPVLGKSTPEGARDYLVPSRIYPGKFYALPQSPQLFKQLLMVGGLDRYF
QIATCFRDEDLRADRQPEFAQIDIEMSFQDGTQDLLPIIEQLVATLFATQGIEIPLAKMTYQEAKDSYGTDKP
DLRFDLKLKDCRDYAKRSSFSIFLDQLAHGGTIKGFVPGGATMSRKQLDGYTEFVKRYGAMGLVWIKNQE
GKVASNIAKFMDEEVFHELFAFYDAKDQDILLIAAPESVANQSLDHLRRLIAKERELYSDNQYNFVWITDFP
LFSLEDGKIVAEHHPFTAPLEEDIPLLETDPLAVRSSSYDLVLNGYEIASGSQRIHNPDLQSQIFTILKISPESIQE
KFGFFIKALSFGTTPHLGIALGLDRLVMVLTAESIREVIAFPKTQKASDLMMNAPSEIMSSQLKELSIKVAF

>core/143/3/Org3_Gene240

MSGKKDGVGRGMIFVPLSILVLIFLPLQILLDFGLCISFALSLLTVCWVFTLNSSNSAKLFPPFFLYLCLLRLGLN
LASTRWIVSSGTASSLIVSLGSFFSLGSLWAATFACLLFFVNFLMVSKGSERIAEVRSRFFLEALPAKQMALD
SDLVSGRASYKAVKKQKNALIEEGDFFSAMEGVFRFVKGDHISCILLVNVVSVTCLYYTSGYALEQMWFT
VLGDALVSQVPALLTSCAAATLISKIDKEESLLNYLFEYYKQLRQHFRVVSLIFSLCCIPSSPKFPIVLLASLL
WLAYRKEEPASEDSCIERAFSYVEGACPKESQFYQVYRAASEEVFEDLGVRPLVLTSLRIERPWLRFVGGQ
NVYLDGMTPEAVLPFLRNIAHEALNAEVVQKYLEESERVFGIAVEDIVPKKISLSSLVVLRSLLVRERSLKL
PKILEAVAVYQNSGDSLEILAELKVRKSLGYWIGRSLWDQKQTELEVITIDFHVEELINSSYSKSNPVMQENVIRR
VDSLLERSVFKDFRAIVTSCETRFEMKKMLDPHFPDLLVLSHDELPKEIPISFLGIVSDEVLP

>core/144/3/Org3_Gene208

MPKQAEYTWGSKKILDNIECLTEDVAEFKDLLYTAHRITSSEESDNEIQPGAILKGTVVDINKDFVVVDVGL
KSEGVIPMSEFIDSSEGLVLGAEEVEVYLDQAEDEEGKVLSREKATRQRQWEYILAHCEEGSIVKGQITRKVK
GGLIVDIGMEAFLPGSQIDNKKIKNLDDYVGKVCFEKILKINVERRNIVSRRELLEAERISKKAELIEQISIGEY
RKGVVKNITDFGVFLDLGDIGLLHITDMTWKRIRHPSEMVELNQELEVIILSVDKEKGRVALGLKQKEHNP
WEDIEKKYPPGKRVLGKIVKLLPYGAFIEIEEGIEGLIHISEMSWVKNIVDPSEVVNKGDEVEAIVLSIQKDEGK
ISLGLKQTERNPWDNIEEKYPIGLHVNAEIKNLNTNYGAFVELEPGIEGLIHISDMSWIKKVSHPSSELFKKGNSV
EAVILSVDKESKKITLGVKQLSSNPWNEIEAMFPAGTVISGVVTKITAFGAFVELQNGIEGLIHVSELSDKPFA
KIEDIISIGENVSAKVIKLDPDHKKVSLSVKEYLADNAYDQDSRTELDFKDSQGPKERKKKKGK

>core/145/3/Org3_Gene573

MSTRRPIQLLDPLTINQIAAGEVIENSVSVVKELIENSLDAGADEIEIETLGGGQGAIIRDNGCGFRAEDIPIALQ
RHATSKIREFSDIFSLNSFGFRGEALPSIASISKMEIQSSIEGDEGVRTVIHGGDIVSCEPCARQLGTTVIVNSLFY
NVPVRRGFQKSMQSDRLGIRKLIENRILSTANIGWSWISEGHHEIQIAKQQGFQERVAYVMGDHFMQDALTI

DKEANGVRIVGVLGSPSFHRPTRQGQKIFINDRPIESLFISKKVGDAYALLPLHRYPVFVLKLYLPSSWCDFN
VHPQKIEARILKEELVGDCIKEAIVETLACPPGILCRTHQEIEESDSVPLPMFRMLETSDVQEEESVEFDQNLFA
YSSDEVSLKQEYTSRGPKSQMDWIYSSDVRFLLTSLGRVVLAEDLEGVHIIFTAAARKHLFFLSLMQENSRM
YQSQALLIPLRLQVTPEEAFFFSHHGRTLCDLGIEISQVGPCVFSIESTPTVIGEEELKEWLLLLAARGSTDINSE
ALTALMKETLTQATFSKHQHVFDVSWLKLLWSVGKPEKGFDGARIRRLILDSDFMEG

>core/146/3/Org3_Gene222

MAVSGGGGVQPSSDPGKWNPALQGEQAEGPSPLKESIFSETKQASSAAKQESLVRSGSTGMYATESQINKAK
YRKAQDRSSTSPKSKLKGTFSKMRASVQGFMSGFGSRASRVSAKRASDSGEGTSLLPTEMMDVALKKGNRISP
EMQGGFLDASGMGGSSSDISQLSLEALKSSAFSGARSLSLSSSESSSVASFQKAIEPMSEEKVNNAWTVARL
GGEMVSSLLDPNVETSSLVRRAMATGNEG MIDLSDLGQEEVSTAMTSPRAVEGKVKVSSSDSPEANPTGIPN
SNTLERAEKEAEKQESREQLSEDQMMLARAMAGLLTGAAPQEVLSNSVWSGPSTVFPPPKFSGTLPTQRSGD
KSKHKSPGIEKSTNHTNFSPLREGTVKSAEVKSLPHPESMYRFPKDSIVSREEPEAVVKESTAFKNPENSSQNF
LPIAVESVFPKESGTGGALGSDAVSSSYHFLAQRGVSL LAPLPRATDDYKEKLEAHKGPGGPPDPLIYQYRNV
AVEPPIVLRSPQPFSGSSRLSVQGKPEAASVHDDGGGGNSGGFSGDQRRGSSGQKASRQEKKGKKLSTDI

>core/147/3/Org3_Gene406

MQKHPSFYQRFLSAYYKNLLASLSWKFFISVALIGIYAPLFASSKPLLVTWHGEIFFLLRYLFFPGYYTKPVD
LFFNVLMVTFPFILSFKLTRGWLRRWLLGLCIISQCMIFAWAYSGKVQDPALAENLKKMRAEKVRENISKV
NSEMVMLLPKDTRTWEMERRY MSTYEQLGILIKAKYRKKQEASVKKYQVAFEEKRQSPMPTLRHLEMKNE
GICLKRLQQRVDKMQRPYEMAQQA WN RATDN YRPFLMALTRIEHELRLADYNNWGQPEDLCIAYANVEKR
AEPYKKSLLAIRQVLEDYAKLRS AISFIQDKRLWIEKESEDRLILNPFSSFWEDDAGGSREM NKYVPWWQ
LSRVTRKDLLAALVFGIRIALV VAGIGITALAIGIMIGLVSGYFGGTVD MILSRFTEIWETMPVLFILMLVISIT
QQKSLLLNTVLLGCFSWTGFSRYVRIEV LKQRDRGYVLAATNLGYSHYYIMVHQILPNAIVPVISLVPFAMM
AMISCEAGLTFLGLGEESSASWGNLMREGVTGFPAESAVLWPPAILTMLLIAIALIGDGVRDALDPRLQDS

>core/148/3/Org3_Gene875

MTDFPTHFKGPKNLPIKVNPNFFERNPKVARVLQITAVVLGIIALLSGIVLIIGTPLGAPISMILGGCLLASGGAL
FVGGTIATILQARNSYKKA V NQKKLSEPLMERPEL KALDYS LDLKEVWDLHHSVVKHLKKLDLNLSETQRE
VLNQIKIDDEGPSLGECAAMISENYDACLKMLAYREELLKEQTQYQETRFNQNLT HRNKVLLSILSRITDNIS
KAGGVFSLKFSTLSSRMSRIHTTTT VILALSAVV SVMVVAALIPGGILALPILLAVAISAGVIVTGLSYLVRQIL
SNTKRN RQDFYKDFVKNVDIELLNQTVTLQRFLFEMLKGV LKEEEEVSLEGQDWYTQYITNAPIEKRLIEEIR
VTYKEIDAQTKKMKTDLEFLENEVRSGRLSVASPEDPSETPIFTQGKEFAKLRRQTSQNISTIIY GPDNENIDPE
FSLPWMPKKEEIDHSLEPVTKLEPGSREELL VEGVNPTLRELNMR IALLQQQLSSVRKWRHPRGEHYGNVI
YSDTELDRIQMLEGAFYNHLREAQEEITQSLGDLVDIQNRILGIIVEGDSDSRTEEEPQE

>core/149/3/Org3_Gene34

MANPTQSRPPSPEISIEEELQELAGSSNTETISNTPPPSCAATAEEVSLFIEGGRRNSEDEEGPLGSCEVYDVVC
ITNQGDPEVRDHEVRVMYINGSGRTQHEGILDAMNICDLRGEPVRFIHNSGYGLGSCFLGIRNRIPPRDNVISQ
AIQARWNEFFIFAENANRDYIVLFSGNGGLYLQVALDNSIYSHHILCVGIGSSYYIQGN YRVHNYRVTGDWTT
LLDRRGATAVNTTTL PYADSAEGLFLPSVRCPSYQWALRCGEQCLIMDNNQQVGFRPQDSSSEIALVVNLNQ

DHSTWTRLIEWIDRGDSQAVLELNPQPSHCRDIALTALYATTRISSLLQECLMISVTYAPEVFVITYAIVTGYSI
MTLRYFILLLTNRPGCRRHFRVLRLAALGLQSLGFLTVLDDHINVTRRVNRRPPLISVIFCTASFATGSFIYVDL
TRMFFTSLRSRLQLFVQRRLTGRGLPLRRVFNHLDSLRFSQLITFHGGFLFMPLIIGFFNQLVIQVPRVVIRP
NTTAVYDLNQTSQEAWDSDVLAIGQTINFLLCMILLVINTFFFVRSVRRNLHRRPHR

>core/150/3/Org3_Gene531

MFMNNTQNSQATEVSSEESQKKLEELVALAKEQGFITYEEINEILPMSFDTPEQIDQVLIFLTGMDIQVLNQID
VERQKEKKKEAKELEGLARRTEGTPDDPVRMYLKEMGTVPLLTRREEVEISKRIEKAQVQIERIILRFYSAK
EASIAHYLISGKERFDKIISEKEVEDKTHFLKLLPKLITLLKEEDTYLENLLLSLKQPDLSKQEA AKLND SLEK
CRIRTQAYLRFCFHC RHNVTEDFGEVVFKAYDSFLHLEQQINDLKVRAERNKFAAAKLAAAKRKLYKREVAA
GRTLEEFKKDVRMLQRWMDKSQEAKKEMVESNLRLVISIAKKYTNRGLSFLDLIQEGNMGLMKAVEKFEY
RRGYKFSTYATWWIRQAVTRAADQARTIRIPVHMIETINKVLRGAKKLMMETGKEPTPEELAEELGLTPDR
VREIYKIAQHPISLQAEVGESESSFGDFLED TAVESPAEATGYSMLKDKMKEVLKTLTDRERFVLIHRFGLL
DGKPKTLEEVGSAFNVTREIRIRQIEAKALRKM RHPISKQLRAFLDLL EEEKTGTSKVKSLKSK

>core/151/3/Org3_Gene826

MDTQSSIGNEEWRIAGTSVVSGMALGKVFFLGTSPLVRELTL PQEEVEHEIHRYYKALNRSKSDIVALEQEV
TGQQGLQEVSSILQAHLEIMKDPLLTEE VVNTIRKDRKNAEYVFSSVMGKIEESLTAVRGMPSVVD RVQDIH
DISNRVIGHLCCQH KSSLGESDQNLIFSEELTPSEVASANSAYIRGFVSLVGAATSHTAIVSRAKSIPYLANISE
ELWNI AKRYNGKLV LIDGYRGELIFNPKPATLQSCYKKELSVVAHTSQRLVRKSLHPIVSSHAGSDKDVEDLL
ENFPQTSIGLFRSEFLAVILGRPLTLREQVDLYEKLARFPGDSPSVLRLFD FGEDKPCPGIKNKKERSIRWLLDY
SVILEDQLQAIKASLQGSIKVLIPGVSDVSEIIEVKKK WETIQTRFPKGHKVSWGTMIEFPSAVWMIEEILPEC
DFLSIGTNDLVQYTLGISRESALPKHLNVTLP PAVIRMIHHVLQAAKQNQVPVSICGEAAGQLSLTPLFIGLV
QELSVAMPVINRLRNHIALLELNSCLEITEALLQAKTCSEVEELLNRNNKITS

>core/152/3/Org3_Gene1021

MVKVPWAFKNFIPKLYTSIKEGYSFNTFKKDFQAGITVGILAFPFAIAIAIGVGVSP IQGLLASIIGGLLASAMG
GSNVLISGPSSAFISILYCLSAKYGA EALFTVTLLAGVFLIAFGLTGLGTFIKYMPYPVVTGLTTGLAIIIFSSQIK
DFLGLQMGANIPADFLPKWIA YWDHLWTWDSKSF AVGLFTLLIMYFRNYKPRYPGVMIAIVTATTLVWLL
KIDIPTIGSRYGTLPTAIPLPKIPQLSITKILQLMPDAL TIAVLSGLETLLSAVVADGMTGWRHQSN CQLVAQGV
ANIGTSLFSGIPVTGSLSR TAASIKSEATTPIAGIVHSIFICIFILL LLA PLTVKIPLTCLAAVLILIAWNMSEIHHWI
HLLTAPKKDIVVLLTVFILTVMTTITAAVQVGMM LAAFLFMKQMSDLSDVISTAKYFDKDSDFLSKAEVPQN
TEIYEINGPFFFGIADRLKNLLNDIEKPPKIFILCMTRVPTIDASAMHALEEFFLECDRQGTLLLLAGVKKTPLA
DLKRYHLD ELIGVDHIFSNISALLFAQALTNLESKTSTRHLV

>core/153/3/Org3_Gene8

MGLFHLTLFGLLLCSLPISLVAKFPESVGHKILYISTQSTQQALATYLEALDAYGDHDFVLRKIGEDY LKQSI
HSSDPQTRKSTIIGAGLAGSSEALDVLSQAMETADPLQQLVLSAVSGHLGKTSDDL LFKALASPYPVIRLEA
AYRLANLKN TKVIDHLHSFIHKLPEEIQCLSAAIFLRLETEESDAYIRDLLAAKKS AIRSATALQIGEYQQKRFL
PTLRNLLTSASPQDQEAILYALGKLKDGQSY YNIKKQLQKPDVDVTLAAAQALIALGKEEDALPVIKKQALE
ERPRALYALRHLPSEIGIPIALPIFLKTKNSEAKLNVALALLELGCDTPKLLEYITERLVQPHYNETLALSFSKG

RTLQNWKRVNIIVPQDPQERERLLSTTRGLEEQILTFLFRLPKEAYLPCIIYKLLASQKTQLATTAISFLSHTSHQ
EALDLLFQAAKLPGEPPIRAYADLAIYNLTKDPEKKRSLHDYAKKLIQETLLFVDTENQRPHPSMPYLRQVT
PESRTKLMLDILETLATSKSSEDIRLLIQLMTEGDAKNFPVLAGLLIKIVE

>core/154/3/Org3_Gene916

MKTSQLFYKTSKNANKSAAVLSNELLEKAGYLFKVSKGVYTYTPLLWRVVSKMMNIIREELNAIGGQELLLP
LLHNAELWQHTGRWEAFTSEGLLYTLKDREGKSHCLAPTHEEVICSFVAQWLSSKRQLPLHLYQIATKFRDE
IRPRFGLIRSRELLMEDSYTFSDSPEQMNEQYEKLRSAYSKIFDRLGLAYVIVTADGGKIGKGKSEEFQVLCSL
GEDTICVSGSYGANIEAAVSIPPQHAYDREFLPVEEVATPGITTIEALANFFSIPLHKILKTLVVKLSYSNEEKFI
AIGMRGDRQVNLVKVASKLNADDIALASDEEIERVLGTEKGFIGPLNCPIDFFADETTSPMTNFVCAGNAKD
KHVNVNWDRLDLPQYGDFLLAEEGDTCPENPGHPYRIYQGIEVAHIFNLGTRYTDSFEVNFLDEHGQTQQ
CWMGTYGIGVGRTLAACVEQLPDDRGRIVWPKALAPFSITIAFNNGDTSQELAETIYHELQSQGYEPLDDR
DERLGFKLKDSDLIGIPYKLILGKSYQSSGIFEIESRSGEKYTVSPEAFPTWCQNHLA

>core/155/3/Org3_Gene518

MTVSVKKKSFRALVTTHFLTIINDNLYKFLLAFFLLEGKTLTENAKILSCVSFFFALPFLLLAPLAGSLADRFQ
KRNIILATRFIEILCTILGTYFFFIQSVVGGYVVLILMACHTTIFGPAKLGILPEMLPSEQLSQANGIMTAATYTG
SILGSC LAPLLVDVTHRLGVNSYVWPTLMCVIVSIISTLISFCIRPSNVKNVKQKITLVSFKDLWKVLKDTRMI
HYLTVSIFLGSFFLLIGAYTQLEIIPFVEFTLKYPKHYGAYLFPIVALGVGTGSYITGKISGKDIIKIGYVPLAAIGL
ALVFMGLYAFACSILFVLFFLLALGFLGGVYQVPLHAYVQYASPEHKRGQILAANNFLDFFGVLVAAGVIRV
LGSNLGLSPETSFFYIGWFLAVSIWTLWIWREHVYRLLLGIILRRQLGYLYLKIHQSSSPKCYFVAVQSYREIR
RVLAALTKTVRSRVIILDQKLVPGWRAWLLSWCVPTVVSVRDNDSEAQDAWAVLQANHLKTSKKFPDV
SVVCLGLPKNVERFTSILQEQQIDLHPIQLVQKEGKKRVIYTLVFPHA

>core/156/3/Org3_Gene385

MSTLLSILSVICSQAIKAFPNLEDWAPEITPSTKEHFGHYQCNDAMKLARVLKKAPRAIAEAIVAELPQEPFS
LIEIAGAGFINFTFSPVFLNQLEHFKDALKLGFQVSQPKKIIIDFSSPNIAKDMHVGHLRSTIIGDSLARIFS YVG
HDVLRNLNHIGDWGTAFGMLITYLQENPCDYSLEDLTSLYKKAYVCFTNDEEFKKRSQQNVVALQAKDPQA
IAIWEKICETSEKAFQKIYDILDIVVEKRGESFYNPFLPEIIEDLEKKGLLTVSNDAKCVFHEAFSIPFMVQKSDG
GYN YATTDLAAMRYRIEEDHADKIIIVTDLGQSLHFQLLEATAIAAGYLQPGIFSHVGFGLVLDPQGKKLKTR
SGENVKLRELLDTAIEKAEEALREHRPELTDEAIQERAPVIGINAIKYSDLSSHRTSDYVFSFEKMLRFEGNTA
MFLLYAYVRIQGIKRRLGISQLSLEGPPEIQEPAEELLALTLLRFPEALESTIKELCPHFLT DYLYNLTHKFNGFF
RDSHIQDSPYAKSRLFLCALAEQVLATGMHLLGLKTLERL

>core/157/3/Org3_Gene373

MSKLIRRVTVLALTSMASCFASGGIEAAVAESLITKIVASAETKPAPVPM TAKKVRLVRRNKQPVEQKSRG
AFCDKEFYPCEEGRCQPVEAQQESCYGRLYSVKVND DCNVEICQSVPEYATVGSPYP IELAIGKKDCVDVVI
TQQLPCEAEFVSSDPETTPTSDGKLVWKIDRLGAGDKCKITVWVKPLKEGCCFTAATVCACPELRSYTKCGQ
PAICIKQEGPDCACLRCPVCYKIEVVNTGSAIARNVTVDNPVPDGYSHASGQRVLSFNLGDMRPGDKKVFTV
EFCPQRRGQITNVATVTYCGGHKCSANVTTVVNEPCVQVNISGADWSYVCKPVEYSISVSNPGDLVLHDVVI
QDTLPSGVTVLEAPGGEICCNKVWRIKEMCPGETLQFKLVVKAQVPGRFTNQVAVTSESNCGTCTSCAETT

THWKGLAATHMCVLDTNDPICVGENTVYRICVTNRGSAEDTNVSLILKFSKELQPIASSGPTKGTISGNTVVFDALPKLGSKESVEFSVTLKGIAPGDARGEAILSSDTLTSPVSDTENTHVY

>core/158/3/Org3_Gene808

MELLSLNKSYFEIQRLRYRPEILTLETIRSKHIQETSSPPSPPELQKHIPNLCRIPEVSIYTEQETSSKPLKIGVLSGGQAPGGHNVVIGLFDALRVFNPKTRLFGFIKGPLGLTRGLYKDLDISVIYDYNNMGGFDMSSSREKIKT EEQKKNILNTVKQLKLDGLLIIGGNSNTDTAMLAEYFLAHNCKTSVIGVPKTIDGDLKNCWIETSLGFHTSC RTYSEMIGNLAKDALSAKKYHHFIRLMGQQASYTTLECGLQTLPNIALISELIATRISKSLKQLSEQLALGLVRR YKSGKNYSTVLIPEGLIEHIFDTRKLIDELNVLLANGDSSIEKILSKLSPETLKTFFHLFPKDIANQLLLARDSHGN VRVSKIAATELLAVMVKKEIEKIKPHMEFHSVSHFFGYEARAGFPSNFDNYGIALGIISALFLVRQKTGYMIT INNLAQSYTEWQGGATPLYKMMHLENRCGTETPVIKTDSVDPKSPAVQHLLQQSDSCLVEDLYRFPGPLQYF GKEELIDQRPLTLLWENQTHSPLL

>core/159/3/Org3_Gene749

MSSPPQAVASLTERIKTLLESNFCQIIVKGELSNVSLQPSGHL YFGIKDSQAFLNGAFFHFKSKYYDRKPKDGD AVIIHGKLAVYAPRGQYQIVAHALVYAGEGDLLQKFEETKRRLTAEGYFATEKKKPLPFAPQCIGVITSPTGA VIQDILRVLSRRARNYKILVYPVTVQGNSAAHEISKAIEVMNAENLADVLIARGGGSIEDLWAFNEEILVKAI HASTIPIVSAVGHETDYLTLCDFASDVRAPTPSAAAEIVCKSSEEQVQVFEGYLRHLLSHSRQLLTSKKQQLLP WRRFLDRAEFYTТАQQLDSIEIAIQKGVQGGKIHESKQRYDNISRWLQGDVSRMTCRLQSLKKMLSQALSH KALSLQVRCHQLKKSLTYPRQIQASQKLSPWRQQLDTLISRRLHYQKEEYFHKHTRLKHAHNVLEQQLRS HVQKLELLGRRLSRGCELNLQNQKIAYANVKETLATILERRYENSVARYSALKEQLHSLNPKNVLKRGYAM LDFDNENSAMISVDSLQENARVRIQLQDGEAILTVTNIEICKLIK

>core/160/3/Org3_Gene845

MDNSDNSFHTLETEQGSFLNDELAVEEVAYTESTEISDATLCFADEIQELPSPEKKVAFILNKMREALTGSSQG SDLRLFWDLRKQCLPLFNEIEDTAKRADHWRCYIELTKEGRHLKGLQDEEGSFVVGQIDLAITCLEKDILKFQ EGTEDKIFKDREDNFLESQALDKHQAFYKQHHTSLLWLSSFSSKIIDLKELINVGMRLKSKFFQRLSNLG NQVFPKRKELIEKVSQTFAEDVDAFVAKYFIGSDKETLKTTFVFLRKEIKNLQHAAKRLFVSSHVFAETRLKL SKCWDQLKGMEKEIRQEQQRLRVVSAENSKEVRQMLAEVSSLLIEGNDLSKVRKDLEGISKKIRALDLTHDD VISLKKEMQQLFDQLREKQDAAEHSYQEQLAKDKQVKKEAARSLAERITTFSTKTCSEGNITSESREEWQTLK ELLGKMSFLPPPEKISLDNQLNLALQTIVNFFEEQLLSSPDSREKLVNMRQVLKQRRERRQELKDKLEQDKKL LGSSGLDFDRAMQYSALVEEDKRALEELDASILELKQQIQQL

>core/161/3/Org3_Gene816

MPQKVLITSALPYANGPLHFGHIAGVYLPADVYARFRRLGDDVLYICGSDEFGIAITLNADREGLGYQEYV DMYHKLHKDTFEKLG FALDFFSRTTNPFHAELVQDFYSQLKASGLIENRISEQLYSEQEQRFLADRYVEGTCP RCGFDHARGDECQSCGADYEAILDIDPKSKISGVELVKKETEHSYFLLDRMKDALLSFIQGCYLPDHVRKFV VDYIEHVRRAITRDLSWGIPVPDFPGKVIFYVWFDAPIGYISGTMewaASQGNPDEWKRFWLEDGVEYVQFI GKDNLPFHSVVPAMELGQKLDYKKVDALVSEFYLLGRQFSKSEGNVYVMDKFLSSYSLDKLRVLAAT APETSDSEFTFLDFKTRCNSELVGKFGNFINRVLAFAEKNHYDKLSYHSVVLEDSDRAFLEEVRLVRDAEK

CYREYSLRKATSVIMSLAALGNVYFNQQAPWKLLKEGTRERVEAILFCACYCQKLLALISYPIIPESAVAIWE
MISPKSLENCNLDTMYARDLWKEEILDVINEEFHLKSPRLFFTVE

>core/162/3/Org3_Gene127

MHPLYVDLDTIISSYSPPLPKEFQEAASLIAVPDTSKSPVVPGVKTLFPQTYHLPYLKFBVQGENVVHTPLKVG
VMFSGGPAPGGHNVIQGLFNSLKDFHPDSSLVGVFNNGDGLTNNKSIDITEEFLSKFRNSGGFNCIGTGRKKIV
TPEAKEACLKTAEALDLDGLVIIGGDGSNTATAILAEYFAKRRPKTSIVGVPKTIDGDLQHTFLDLTFGFDTAT
KFYSSIISNISRDALSCKAHYHFILMGRSASHIALECALQTHPNIALIGEEIAEKNLPLKTIHKKICSVIADRAAM
EKYYGVILPEGIIEFIPEIINLITEIESLSEYEDKISRSPESQRLKSFPAPIIEQILNDRDAHGNVYVSKISVDKLL
IHLVSNHLQQYFPNVPFNAISHFLGYEGRSGLPTKFDNTYGYSLGYGAGILVRNHCNGYLSTIESLACPFMKW
KLRAIPVVKMFTVKQQADGTLQPKIKKYLVDIGSTAFRKFKLYRKIWALEDYSRFLGPLQIETPPMHSDNFP
PLTLLLNHNFWQRHQGCIEIPDTTY

>core/163/3/Org3_Gene513

MSRKDNEVSLARSIFNILSGTFCSRITGIFREIAMATYFGADPIVAAFWLGFRTVFFLRKILGGLILEQAFIPHFE
FLRAQSLDRAAFFRRFSRLIKGSTIIFTLLIEAVLWVVLQYVEEGTYDMILLTMILLPCGIFLMMYNVNGALL
HCENKFFGVGLAPVVVNIIWIFFVIAARHSDPRERIIGLSVALVIGFFFEWLITVPGVWKFLLEAKSPPQEHSV
RALLAPLSLGLTSSIFQLNLLSDICLARYVHEIGPLYLMYSLKIYQLPIHLFGFGVFTVLLPAISRCVQREDHER
GLKLMKFVLTLTMSVMIIIMTAGLLLLALPGVRVLYEHGLFPQSAVYAIVRVLRGYGASIIPMALAPLSVLFY
AQRQYAVPLFIGIGTALANIVLSVLGRWVLKDVSGISYATSITAWVQLYFLWYYSSKRLPMYSKLLWESIRR
SIKVMGTTMLACMITLGLNILTQTTYVIFLNPLTPLAWPLSSITAQAIAFLSESCIFLAFLFGFAKLLRVEDLINL
ASFEYWRGQRGLLQRQHVMQDTQN

>core/164/3/Org3_Gene79

MAAKNIKYNEEARKKIHKGVKTLAEAVKVTLGPKGRHVVIDKSFGSPQVTKDGVTVAKEIELEDKHENMGA
QMVKEVASKTADKAGDGTATVLAELIYSEGLRNVTAGANPMDLKRIGDKAVKVVDDELKKISKPVQHH
KEIAQVATISANNDSEIGNLIAEAMEKVGKNGSITVEEAKGFETVLDVVEGMNFNRYGLSSYFSTNPETQECV
LEDALILIYDKKISGIKDFLPVLQQVAESGRPLLIIEEIEGEALATLVNRLRAGFRVCAVKAPGFGDRRKAM
LEDIAILTGGQLVSEELGMKLENTTLAMLGKAKKVIVTKEDTTIVEGLGNKPDIQARCDNIKKQIEDSTSDYD
KEKLQERLAKLSGGVAVIRVGAATEIEMKEKKDRVDDAQHATIAAVEEGILPGGGTALVRCIPTLEAFLPML
ANEDEAIGTRIILKALTAPLKQIASNAGKEGAIIICQQVLARSANEGYDALRDAYTDMIDAGILDPTKVTRSALE
SAASIAGLLLTTEALIADIPEEKSSSAPAMPSAGMDY

>core/165/3/Org3_Gene322

MFGSESLRYQLLIQDFAKVSEEGIGLLESKEYSLLQAKLVLRALAQNSSFDDWFRSFKKQCISYPELAHDRDV
LEEFGIQVLREGIENPSVTVRVSVLAIGLARDFRLVPLLLQSCNDDSAIVRSLALQVAVNYGSESLKKAIVEL
ARNDDSIHVRIYQVVALQIEELLPLRERAENKLVDSEVERREAWKACLELSSQFLETGVAKDDIDQALFT
CEVLRNGMLPETTEIFTELLSVEHPEVQESLLLSALAWSHQLQNHKEFLSKVRHVMCTSPFAKVRFQAAALL
HLHGDPLGRDSLVEGLRSPQPLVCEAASAALCSLGIHGVPLAKEHLESLSRKAANLSILLVSRREDIERAGD
VIARYLSNPEMCWAIEYFLWDAQWNLRGDTFPLYSDMIKREIGRKLIRLLAVARYSQAKAVTATFLSGQQA

QGWSFFSGMFWEEGDVKTSEDLVTDACFAAKLEGALASLCQKKDQASLQRVSQLYNDSRWQDKLAILESV
AFSENLDVAPFLDCCHHEAPSLRSAAAGALFSIFK

>core/166/3/Org3_Gene451

MLRIFCFVISWCLIAFAQPDLSGFVSILGAACGYGFFWYSLEPLKKPSLPLRTL FVSCFFWIFTIEGIHFSWMLS
DQYIGKLIYLVWLT LITILSVLFSGFSCLLV AIVRQKRTAFLWSLPGVWVAIEMLRFYGIFSGMSFDYLGWPM
TASAYGRQFGGFLGWAGQSFAVIAVNMSFYCLLLKKPHAKMLWVLTLLLPYTFGAIHYEYLKHAFQQDKR
ALRVAVVQPAHPPIRPKLKSPIVVWEQLLQLVSPIQPIDLLIFPEVVVPFGKHRQVYPYESCAHLLSSFAPLPE
GKAFLSNSDCATALSQHFQCPVIIGLERWVKKENVLYWYN SAEVISHKGISVG YDKRILVPGGEYIPGGKFGS
LICRQLFPKYALGCKRLPGRRSGVVQVRGLPRIGITICYEETF GYRLQSYKRQGAELLVNL TNDGWYPESRLP
KVHFLHGMLRNQEFGMPCVRACQTGVTA AVDSLGRILKILPYDTRETKAPSGVLETS LPLFNYKTLYGYCGD
YPMILIAFCAVSYLGGGFLGYRLLAKKEIR

>core/167/3/Org3_Gene418

MQSSEVKPFSRLRAYLCPIYKSEFSKFVPLFLLAFFVGFNYCLLKNMKDTLVIVGSDAGAEVIPFLK VWGIVP
GAVIVTMVYGWLGSRYP RDTVFYCFMAAFLGFFFLFAVIIYPVGDSLHLNSLADKLQELLPQGLRGFIVMVR
YWSYSIYYVMSELWSSVVL SMLFWGLANQITTITEAGRFYALINTGLNLSSICAGEISYWMGKQTFVAYSFA
CDSWHSVMLNLTMLITCSGLIMIWL YRRIHHLTIDTSIPPSRRVLAEEGAATANLKEKKKPKAKARNLFLHLI
QSRYLGLAIIVLSYNLVIHLFEV VWKDVQSQIYSSHVEFNGYMSRITTLIGVVS VLA AVLTTGQCIRKWGWT
VGALVTPLVMLVSGLLFFGTIFA AKRDISIFGGVLGMTPLALAAWTGGMQNVLSRGTKFTFFDQTKEMAFIP
LSPEDKNHGKAAIDGVVSRIGKSGGSLIYQGLLVIFSSVAASLN VIALVLLIIMVVWIAVVAYIGKEYYSRAAD
AVATLKQPKPESSSIVREAQESVEQEEMAVL

>core/168/3/Org3_Gene648

MHDQRNRGHNHNHNLRLRPGSTLLEAFLILCSEHEEGIACFDEHLGSLSYREL RNAIIA VAIKVSKFSEDRVGV
MMPASIGAFIAYFGILLAGKTPVMMNWSQGLREL RACTKTVEVRRVLT SQQFIKHLTEVQGFVEYPFDLMY
MEDVRKRLSWWEKCRIGLYSKCSVPWLLRIFGVSGVESDDTAVILFTSGTEKL PKAVPLTHKNLMENQEACL
KFFDPNTQDVMLAFLPPFHAYGFNSCGLFPLLMGVHVVFASNPLNPKKLVEFIDDKKV TFFGSTPVFFDYILK
TAKKQNSCLESRLV VIGGDALKDTLYEETKKLQPQIALYQGYGATECSPVISITTKESPRKSECVGMPIEGM
DVLIISKETHIPVSSGEQGLIVVRGNSVFSGYLG NHEHQSFVSLGGDQWYLTGDLGHIGPSGDLFLEGRLSRFV
KIGGEMVSLEALESILHEHFTENQNEDAGSLV VCGIPGDKVRLCLFTTLATTIHEVNDILKSAETSSIVKISYVH
QVESIPILGIGKPDYVSLNALAVSLFG

>core/169/3/Org3_Gene801

MPFKCIFLTGGVVSSLGKGLTAASLALILERQRLNVAMLKLDPYLNVDPGTMNPFEGHEIYVTDDGVETDLD
LGHYHRFSSAALSRHSSATSGQIYARVIKREREGDYLGSTVQVIPHITNEIIQVILDAAKEHSPDVLIVEIGGTIG
DIESLPFLEAIRQFRYDHSEDCLNIHMTYVPYLQA ADEVKSKPTQHSVQTLRGIGIIPDAILCRSEKPLTQE VKS
KISLFCNVPNRAVFNVIDVKHTIYEMPLMLAQEKIANFIGEKLKLATVPENLDDWRVLVNQLSQDLPKVKIG
VVGKYVQHRDAYKSIFEALTHAALRLGHAAEIIPIDAEDENLTMELSQCDA CLVPGGFGVRGWEGKIAAAKF
CREQGIPYFGICLGMQVLVVEYARNVLNLDQANSLEMDPNTPHPIVYVMEGQDPLVATGGTMRLGAYPCLL

KPGSKAHKAYNESSLIQERHRHRYEVNPDYIQSLEDHGLRIVGTCPPQGLCEIIEVSDHPWMIGVQFHPEFVSK
LISPHPLFI AFIEAALVYSKDASHV

>core/171/3/Org3_Gene119

MRKISVGICITILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNLSG
NIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLS
IDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPH
YYNQSQVETKTITIHFI PDANTA AKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLT FNIN
KFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKLFKEALEELQ
ITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMA
FLTIFAYPSGVPPYAINHKDFLEILQ NIEQE QDHQKRSELVSQASLYLET FHIIEPIYHDAFQFAMNKKLSNLGV
SPTGVVDFRYAKEN

>core/172/3/Org3_Gene524

MLGKEEEFTCKQKQCLSHFVTNLTSDV FALKNLPEVVKGALFSKYSRSVLGLRALLLKEFLSNEEDGDVCDE
AYDFETDVQKAADFYQRVLDNFGDDSVGELGGAHLAMENVSILA AKVLEDARIGGSPLEKSTRYVYFDQKV
RGEYLYYRDPILMTSAFKDMFLGTCDFLFD TY SALIPQVRAYFEKLYPKDSKTPASAYATSLRAKVLD CIRGL
LPAATLTNLGFFGNRFRWQNLIHKLQGHNLAE LRRLGDESLTELMKVIPSFVSRAEPHHHHHQA MMQYRRA
LKEQLKGLAEQATFSEEMSSSPSVQLVYGDPDGIYKVAAGFLFPYSNRSLTDLIDYCKKMPHEDLVQILESSV
SARENRRHKSPRGLECV EFGFDILADFGAYRDLQRHRTL TQERQLLSTHHGYNFPVELLDTPMEKSYREAME
RANETYNEIVQEFPEEAQYMVP MAYNIRWFFHV NARALQWICELRSQPQGHQNYRTIATGLVREVVKFNPM
YELFFKFVDYSDIDLGR LNQEMRKEPTT

>core/173/3/Org3_Gene811

MFVGGGLVSFLLPIPDLECANNVTKTYDKKASVISRDLKLQEDCQKFWNLDPYKLESLCAYQVLYHDDYSSK
RIRELFPQIQKDEVPIFATMILTLGKVDRGFSPEEISLIQKLSYPGLSLASLRGSTEIDPNTDLARALVVSEFSGD
LGKNRADYYSNCLDILALRIHAERQRYLDQSPCVPGTSEFHKATIEAINTILFYEEAVRYPSKKEMFSDEFSFL
SSVTDRKFGVCLGVSSLYFSLSQRLDLPLEAVTPPGHIYLR YQGGEVNIETTAGGRHLPTASYCDCLDLEDLQ
VRTPEEMIGLTFMNQGSFALQKKKYKEAEEAYKKAQEYLGDEELQELLGFVQILGGKKKEGKSLIGKSPRAS
QKGSVAYDY LKGRINIPTLALLFSYPGSNYEEIASYEEELKKAMKSSMPCCEGQRR LASVAFHLGKTAEAVA
LLEKCVEDIPNDLSHLRLCKILCDRHEYTKALKYFIIAERLMEDQGFLKKDNRSFALFYEVKKIISKVAPQKA
NTLLLMESER

>core/174/3/Org3_Gene10

MSIVLDKIGKSLGTRILFDDVS VVFNPGNCYGLTGPNAGAKSTLLKIIMG MIEPTRGSISLPKKVGILRQNIDSF
HDTTVLDCVIMGNTRLWEALQRRDNLYLQEFTDAIGMELGEIEEIIIGEENGYRADSEAEELLTGIGIPNEMFD
KKMAMIPIDLQFRVLLCQALFGHPEALLLDEPTNHLDLYSINWLG NFLKDYEGTVIVVSHDRHFLNTITTHIA
DIDYDTIIIPGNYDDMVEMKTASREQEKADIKSKEKKISQLKEFVAKFGAGSRASQVQSRLREIKKLQPQEL
KKSNIQRPYIRFPLSDKSSGKVVL SLEAITKDYGDHQVIHPFSLEIYQGDKLGIIGNNGLGKTTLMKLLAGVEA
PSSGSIKLGHQ AICSYFPQNHSDVLADCGQETLFEWLRNRKTGINDQEIRSVLGKMLFGGDDAFKQIQALSGG

ETARLLMAGMMLNHNVLILDEANNHLDLESVSALSWAINDYKGTAIFVSHDRGLIQDCATKLLIFDKDKIT
FFDGTMDVDYTAGHKQLL

>core/175/3/Org3_Gene804

MKMHRLKPTLKSILPNLLFLLLTLSSCSKQKQEPLGKHLVIAMSHDLADLDPRNAYLSRDASLAKALYEGLT
RETDQGIALALAE SYTL SKDHK VYTFKLRPSVWSDGTPLTAYDFEKS IKQLYFEEFSPSIHTLLGVIKNSSAIHN
AQKSLET LGIQA KDDL TLVITL EQFPYFLT LIARPVFSPVHHTLRESYKKGTPPSTYISNGPFVLKKHEHQNYL
ILEKNPHYD HESVKLDRVTLKIIPDASTATKLFKSKSIDWIGSPWSAPISNEDQKVLSQEKILTYSVSSTLLIY
NLQKPLIQNKALRKAIAHAIDRKSILRLVPSGQEA VTLVPPNLSQLNLQKEISTEERQTKARAYFQEAKETLSE
KELAELSILYPIDSSNSSIIAQEIQRQLKDTLGLKIKIQGMEYHCFLKKRRQGDFFIATGGWIAEYVSPVAFLSIL
GNPRDLTQWRNSDY EKTLEKLYLPHAYKENLKRAEMIIEETPIIPLYHGKYIYAIHPKIQNTFGSLLGHTDLK
NIDILS

>core/176/3/Org3_Gene831

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GLGILVTRLILSTIRKVDAMGYDAAVKEEQYLSRIRELESENREIRDNRAVEDQCAHLSEENKDLRDPEYLH
GMTERLIASLEIENQALVAENILLKDOWNASLSRDFRAYKQKFPLGALEPWKEDIACIMEQNLFLKPECIAMVK
SLPLETQRLFLYPKGFQSLVNRFAPRSRFFQTPKYEYNSRNENEDGKVAAVCARLKKEFFSAVLGACSYEELG
GICERAVALKETLPLPEAVYDTLVQEFPNLLTAESLWKEWCFYSYPYLRPYLSVDYCKRLFVQLFEELCLKLF
TTGSPEDQALVRLFSYYRNHIPAVLASFGLPPPETGGSVFVLLPKQENLLWSQIEVLATRYLKDTFVRNSEWT
GSFEMMF SYNEMCKEISEGRIRFAEDYETRHSEEFPPSPLSEEGEGEEFLPPCSEEEVSVLERPDLDVDSMWV
WHPPVPKGPL

>core/177/3/Org3_Gene966

MTARAEYLDHEDFLYRSHKLQELSELGVVLYPYEFPGVFSCEDIKKT FASQELGNSEAAMSRSTPRVRFAGR
LVLFRAMGKNAFGQILDHNQTIQVMFNREFTSVHGLSEDAEITPIKFIEKKLDLGDILGIDGYLFFTHSGELTV
LVETVTLLCKSLLSLPKHAGLS DKEVRYRKRWLDLISSREVSDTFVKRSYIIKLIRNYMDAHGFLEVETPILQ
NIYGGAEAKPFTTTMEALHSETFLRISLEIALKKILVGGAPRIYELGKVFRNEGIDRTHNPEFTMIEAYAA YMD
YKEVMVFVENLVEHLVRAVNH DNTSLVYSYWKHGPQEVD FKA PWIRMTMKESIATYAGIDVDVHSDQKLK
EILKKKTTFPETAFATASRGM LIAALFDELVSDNLIAPHHITDHPVETTPLCKTLRSGDTAFVERFESFCLGKEL
CNAYSELNDPIRQRELLEQQHTKKELLPDSECHPIDEEFLEALCQGMPPAGGFGIGVDRLVMILTNAASIRDVL
YFPVMRRFDAEKTN

>core/178/3/Org3_Gene120

MLRFFAVFISTLWLITSGCSPSQSSKGIFVVMKEMPRSLDPGKTRLIADQTLMRHLYEGLVEEHSQNGEIKPA
LAESYTI SEDGTRYTFKIKNILWSNGDPLTAQDFVSSWKEILKEDASSVYLYAFLPIKNARAIFDDTESPENLG
VRALDKRHLEIQLETPCAHFLHFLTLP IFFPVHETLRNYS TSFEEMPITCGAFRPVSLEKGLRLHLEKNPMYHN
KSRVKLHKIIVQFISNANTAAILFKHKKLDWQGPPWGEPIPPEISASLHQDDQLFSLPGASTTWLLFNIQKKPW
NNAKLRLKALSLAIDK DMLTKVVYQGLAEPTDHILHPRLYPGTYPERKRQNERILEAQQLFEEALDELQMTRE
DLEKETLTFSTFSFSYGRICQMLREQWKKVLKFTIPIVGQEFTIQKNFLEGNYS LTVNQWTA AFIDPMSYLM I

FANPGGISPYHLQDSHFQTLLIKITQEHHKKHLRNQLIIEALDYLEHCHILEPLCHPNLRIALNKNIKNFNLFVRR
TSDFRFIEKL

>core/179/3/Org3_Gene217

MNVLYTKHSPSAHAWKLIGTSPKHGIYLPFSIHTKNNSCGIGEFLDLIPLISWCQKQGFSVIQLLPLNDTGEDT
SPYNSISSVALNPLFSLSSLPNIDTIPEVAKKLQDMHELCSTPSVSYTQVKEKKWAFLREYYQKCKSSLEGN
SNFSEFLESERYWLYPYGTFRAIKHHMHGEPINNWPKSLTDQENFPDLTKKFHDEVLFSSYLQFLCYQQLCEV
KAYADQHHVLLKGDLPIISKDSCDVWYFRDYFSSSRSVGAPPDLYNSEGQNWHLPIYNFSQLAKDDYIWW
KERLRYAQNFYSVYRLDHIIGFFRLWIWDSSGRGRFIPDNPKDYIKQGTEILSTMLGASSMLPIGEDLGIIPQDV
KTTLTHLGICGTRIPRWERNWESDSAFIPLKDYNPLSVTTLSTHSDTFAQWWLNSPKEAKQFAKFLHLPFQK
TLTTETQIDILKLSHESASIFHINLNDYLALCPDLVSKNLQRERINTPGTISKKNWSYRVPSLEELAIHKKFN
GYIEKILTGL

>core/180/3/Org3_Gene974

MERKRFIDCDSTKILQELALNPLDLTAPGVLSAERIKKFSLLGGGFTFSFATERLDDAILAALISLAEERGLHES
MLAMQQGQVVNYIEGFPSEMRPALHTATRAWVTDSSFTGEAEDIAVRSRVEAQRLKDFLTKVRSQFTTIVQI
GIGGSELGPKALYRALRAYCPTDKHVFISNIDPDNGAEVLDTIDCAKALVVVVSXSGTTIETAVNEAFFADY
FAKKGLSFKDHFIAVTCEGSPMDDTGKYLEVFHLWESIGGRFSSTSMVGGVVLGFAYGFEVFLQLLQGASA
MDQIALQPNARENLPMLSALISIWNRNFLGYPTAVIPYSSGLEFFPAHLQQCCMESNGKSIVQDGRRVGFST
SPVIWGEPTNGQHSFFQCLHQGTDIIPVEFIGFEKSQKGEDISFQGTSSQKLFANMIAQAIALACGSENTNPN
KNFDGMRPSSVLVSSQLNPYSLGELLSYYENKIVFQGFCWGINSFDQEGVSLGKALANRVLELLEGADASNFP
EAASLLTLFNIKFR

>core/181/3/Org3_Gene903

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AIIFMLIYAKLSNLSKQALFYAVGTPFLIFFALFPTVIYPLRDVLHPTEFADRLQAILPPGLLGLDAILRNWTF
AFYVLAELWGSVMLSMLFWGFANEITKIHEAKRFYALFGIGANISLLASGRAIVWASKLRASVSEGVPDWGI
SLRLLMAMTIVSGLVLMASYWWINKNVLTDPRFYNPEEMQKGGKAKPKMNMKDSFLYLARSPYILLAL
LVIAYGICINLIEVTWKSQKLQYPNMNDYSEFMGNFSFWTGVVSVLIMLFVGGNVIRKFGWLTGALVTPVM
VLLTGIVFFALVIFRNQASGLVAMFGTTPLMLAVVVGAIQNILSKSTKYALFDSTKEMAYIPLDQEQQVKVGK
AAIDVVAARFGKSGGALIQGGLVICGSIGAMTPYLAVILLFIIAIWLVSATKLNKLFLAQSALKEQEVAQEDS
APASS

>core/182/3/Org3_Gene863

MVWVFKSQFEGLSALKRGVHALTKAVTPAFGPRGYNVVIKKGKAPIVLTKNGIRIAKEIILQDAFESLGVKLA
KEALLKVVEQTGDGSTALLVIDALFTQGLKGIAAGLDQPQEIAGILLSVEMVYQQQLQRQAIELQSPKDV
VAMVAANHDTVLTGTVVATVISQADLKGVFSSKDSGISKTRGLGKRVKSGYLSFYFVTRPETMDVWVEEALV
LILSHSLVSLSEELIRYLELISEQNTHPLVIIAEDFDQNVLRTLILNKLNRNGLPVCVAPKAPGSRELQV
VLEDLALITGATLIGQESENCEIPVSLDVLGRVKQVMITKETFTFLEGGGDAEIIQARKQELCLAIAGSTSE
SECQELEERLAIFIGSIPQVQITADTDTEQRERQFQLESALRATKAAMKGGIVPGGGVAFLRAAHAIEV
PANLSSGMTFGFETL

LQAVRTPCLKVLAQNCGRSSEEVIIHTILSHENPRFGYNGMTDTFEDLVDAGICDPLIVTTSSLKCAVSVSCLLLT
SSFFISSRTKT

>core/183/3/Org3_Gene6

MYQENLRLLERLLYNSVQKSYADRLFSYEKTKMVHDTPLIPWEEDKEKCAEAEKAFLEQQKILLDYGKSIFW
LNENDEINLNDPWSWGLNTRVTRKVFQEVDDESERNHVKVLIQKLEDDYEKLLKESSKESTEANKKLLSDLV
DRLEDAKTKFFLKQEEVETRVKDLRARYGGTVDPKQDTEAKKKVELEASLETFLDSIESELVQCLEDQDIY
WKEQDVKDLARTQELEEQDIEAKREEAAEDLRSLNERLKKSKTMLDRAKWHIENAEDSITWWTSQIEMKD
MKARLKILKEDITSVLPEIDEIETCLSLEELPLLTRELLTKSYLKFKICSETLLKMTSVFENNIYVQEYEVQLQ
NLGFKLQGISQRFQKQDDFANLEEQVALQKKRLRELTONFEIQGFNFMKEDFKAAAKDLYIRSTAEQKMN
FDVPCMELFRRYHEEVNKPILLEMYNCADSYRDAKKKLCSLRLDEKELLQKEIKKEEFYQKKQQRHADRSR
HTTYQKLRIAEELALELKKKI

>core/184/3/Org3_Gene765

MVARGLCDPFTLVPNERLPIGPFFVPQHTSGAKGKEFAKRNFSIISGLDDILKLCILQRRPFALQWDNLSVKSD
YEEAGPAIGIRSLEPQVSQISPAHGRLCSTLVQWAPILGSEERLVWLEETMKRLKFPKSLGSKDAVIVDSEMPV
VNANPTQEIPAASETVESSPVAPGNTTDTMPAASGTTDTTSGVSEAAAAEATVDSTPGTEEEPSFSRLYALVV
QNVYPPEPPKEPEVMFTDEEKSLILEATRARMELDLNGYLADYELSKDEIQKHVPDLPENWRTNWRWSE
RLYKFFFKTKKEGLEEIFLNKELGNMILARGLAATQSQARIKVFNSLVAWLLQSFNVGRSCTAKPLPTSCLDL
FKSEFESKPKNNILTEFLVASDEEILFKGLRVLEPGIEGWYDHPDQAGEIRSVLEGLVQAGRISGYWENQPFGR
FVLRGVGERTELVELLESLVASGEIMQFFESSDEEGAFIIDNEPSKTAMLKQRFKSCVRTKLVGSAFDESLEPR
GRFTILV

>core/185/3/Org3_Gene764

MVSLHFKFLENASGKKGQSLASTAYLAALDHLLNAFPSIGERIIDEKLSQRSHLKMIASENYSSLSVQLAMGN
LLTDKYCEGSPFKRFYSCCENVDAIEWECVETAKELFAADCACVQPHSGADANLLAVMAILTHKVQGPVAVS
KLGKTVNELTEEEYTLLKAEMSSCVCLGPSLNSGGHLTHGNVRLNVMSKLMRCFPYDVNPDTECFDYAEI
SRLAKEYKPKVLIAGYSSYSRRLNFAVLKQIAEDCGSVLWVDMAHFAGLVAGGVFVDEENPIPYADIVTTTT
HKTLRGPRGGLVLATREYESTLNKACPLMMGGPLPHVIAAKTVALKEALSVDFFKKYAHQVVNNARRLAER
FLSHGLRLLTGGTDNHMMVIDLGSLGISGKIAEDILSSVGIAVNRNSLPSDAIGKWDTS GIRLGTPALTTLGMG
IDEMEEVADIIVKVLNRNIRLSCHVEGSSKKNKGELPEAIAQEARDVRNLLLRFPYPEIDLEALV

>core/186/3/Org3_Gene634

MSEQEKLSNYNADKKLFSGIDKLFQIVKGSYGPKQSLSPTSFFKERGFYAISQTELSNSYENLGVDFAKAMVN
KIHKEHSDGATTGLILLHAILQESYAALEKGISTHKLIALSKLQGEKLQEALQQQSWPIKDALKVRNIIFSSLH
MPTIADHFYNAFSVVGPEGLISITKERENDKTSMDVFQGFKIPAGYASTYFVSdTASRLTRIAHPLILITDRKIS
MIHSLPLLQEISEQNQHIIIFCEDIDPDVLATLVVNKLQGLLQVTVVTIPQLSTTNQELAEDIALFTGTHICPCQ
EASHVLAPEMVTLGSCLSIEISESQTTLIGGLHIPEVLTLKTRQLAEIIRTSCLETKKRLIKSTNRLQSSVAILPT
DEDNEPLYTLALKIMESALSRGYVPGGGVALFYASLTGTPKDDADENSIAISLLQKACCAPLKLLATNADLD
GDAVIAKLSSLGTTSLGISVFSREIEDLIAGGILDSLATTSTILAQALDTAILVLSSKILILENQYEISTL

>core/187/3/Org3_Gene967

MENEILLNIESKEIRY A HLKNGQLFDLTIERKKVRQLKGNIYRGRVTNILRNIQSAFINIDERENGFIHISDILENS
KKFEQMFDMDVDALPEEASEAPLLSSEEAPIEEFLKLDSPVLVQVVKEPIGSKGARLTSNISIPGRYL VLLPNSP
HRGVSRKIEDPHMREQLKQLIRSFEMPQDMGLICRTASTTASTEALINEAHDLLL TWKTILEKFYSTEQPCLLY
SETDILKKAVITCIDKNYKRL LIDDYATYQKCKHMLKKYSPDASIKIEYYRDSIPMFERFNIEKEIDKATRRKI
WLSSGGYLFFDKTEAMHTIDVNSGRSTQLESGVEETLVQINLEAAEEIARQLRLRNVGGLVIIDFIDMKSRKN
QRRVLERLKEHMKYDAARCTILSMSEFGLVEMTRQRNRESLMQTLFTLCRYCSGNAIKTPESVVIEIERDLK
KVINHKEHSHLCLV VHP EIASYMKQENDDNEMINLAKQLKAKLQINTSDSVHLNHYQFFSLITGESIDL

>core/188/3/Org3_Gene185

MFNLFFFTANKETTASHELIYRKNQSFSLSPVTILCLLAISVLLLLGVVFALVGCHVLAAPLGLLVWGCAASV
CSMMAIVSLMCLYKGGKPLIEPSNEEKIDPTKDLEIKDPESLKPVPVEGQSLPKERKTVSFKAKIPSIVEDDFKP
YVIQSTFYHQNKVYSKPIAERMQSLEKEITTLIVDFPRALEESSKSSGSLLRGVISEIKNLFLPRFLSRKVKYSLT
ACLRRLGSIVEEYASSDLLILLTKPEPLNMVTQQLIAHLNSLKTEKRKLTPHMQKL VLSINFWFYGWSLEEK
CIEKIVAYDPNLLTDELKAHLEAGNIVQFLSFQSSEMQRERFALFPSDAQELPSAKDGSNYVPAINSEYMY
DFKDLSVLKKSLSERLAFCEKIPSPSSWNFTSSVASHYKDFSLLFTFFSNQQSVILQNPFLLIELLHENPKCQTF
KGLLEKAMPMSNWAALFRPMLMGMLCSGIARKKELKIIAEHLGVPFKEITQAIASGKILDLLLQHLFDF

>core/189/3/Org3_Gene304

MTILRNFLTCSALFLALPAAAQVVYLHESDGYNGAINNKSLEPKITCYPEGTSYIFLDDVRISNVKHDQEDAG
VFINRSGNLFFMGNRCNFTFHNLMTEGFGA AISNRVGDTTLT LSNFSYLAFTSAPLLPQGGQAIYSLGSVM IEN
SEEVTFCGNYSSWSGAAIYTPYLLGSKASRPSVNLSGNRYLVFRDNVSQGYGGAISTHNLTLTTRGPSCFENN
HAYHDVNSNGGAIAIAPGGSISISVKS GDLIFK GNTASQDGNTIHSIHLQSGAQFKNLRAVSESGVYFYDPIS
HSESHKITDLVINAPEGKETYE GTISFSGLCDDHEVCAENLTSTILQDVTLAGGTLSLSDGVT LQLHSFKQEA
SSTLT MSPGTTLCSGDARVQNLHILIEDTDNFVPVRIRAEDKDALVSLEKLKVAFEAYWSVYDFPQFKEAFT
IPLLELLGPSFDSLLLGETTLERTQVTTENDAVRGFWLSWEEYPPSLDKDRRITPTKKT VFLTWNPEITSTP

>core/190/3/Org3_Gene150

MTNVVQETIGGLNSPRTCPCPILVIFGATGDLTARKLLPALYHLTKEGRLSDQFVCVGFARREKSNE LFRQEM
KQAVIQFSPSEL DIKVWEDFQQRLFYHRSEFDNNMGYTSLKDSLEDLDKTYGTRGNRLFYLSTPPQYFSRIEN
LNKHKLFYKNQDQGKPWSRVII EKPFGRDLDSAKQLQQCINENLNENSVYHIDHYLGKETVQNILTTRFANTI
FESCWNSQYIDHVQISLSETIGIGSRGNFFEKSGMLRDMVQNHMMQLLCLLTMEPPTTFDADEIRKEKIKILQR
ISPFSEGSSIVRGQYGP GTVQGVSVLGYREEENVDKDSRVETYVALKTVINNPRWLGVPFYLRAGKRLAKKS
TDISIIFKKSPYNLFAAECSRCP IENDLLIIRIQPDEGVALKFNCKVPGTNNIVRPVKMDFRYDSYFQTTTPEAY
ERLLCDCIIGDRTLFTGGDEV MASWKLFTPVLEEWDQDSSPSFPNYPAGSSGPKEADALIERDGRSWRPL

>core/191/3/Org3_Gene973

MSSWLSQASEVLLNQDPYIPDAPRSQESSVPKISYSITVAPQEAQKSLPKFFTQKFQSQCKSEPPITHHKTFIIAT
PRERILRFGSSFESQLHNTSQAQTSSPWNLF SQKNSTEASKALMQELTMPKSPEKTSEKALDKNLSSKQEGSC
KNFDTLHLQQHLKLFGTVDSLYSQSLDSEQQELLQSRREERSETYANQQSSEKKIETKVQIKDLCKDLFSQDQ

DSNQKQKKSPFQQDTSRKNRIAKAAQAVPVIPPPSIGVFTLSYLLTKQGILSDFSSYGCHKDSVESTQRELDAL
HEKRIETIKVSIEKEKRERLWGSLSDIIGWLAPFVSIGIGIVAILSGGGIFAFAGFFAGLISLVIKCLEKLFWDW
LEKHLPIKNEELRRKIITHIPWVVYLTPVILSICTLKVENLGFSPHIEGAIKGIQPAIESTMAALRCAILFSQAEIYKL
KGKLTKIQLDIELKSFDRDDHYERSQELLDNMESSFEALSRIILNYMRELDQVYLHSLRG

>core/192/3/Org3_Gene774

MAVGGVGGSRSPSPIPPNRRNSEDGKVSPKDNLGEHTVSSSDSSLASQGPTIEERKAQLGGTDKIPLPSVKEPG
DSPTSGRSGVLQRIWKGVKGVFKKTPQARPEVSSPRLPSHVQHGRQLPGLEGFRDRIQKRSENPEADLGKMK
RSYSDGDLDRVGHDSNEDSTEDSRSEGGEPSKSSSFLSGVRGAVSKVHGALGDIKGFQRSASEDDLTTQG
EDSAGDTVKERRSEEAEEASSKSSSFLSGVRGATSTVQGALGDAKEKVSAFGEQAAGAIRSAPGNIRTRFQRSS
SEGDLNVNKAACKHLRKALENLEKVAPEQVSPEVASRVQSLLARMEQLTHQEPTVEDLITFVESNVGSDSV
EYASIVPQDGSQAPAETAETGVEGSAQAQAWKALRDFVVSIFQAVASFFRAIASRLSSARRESAVDDL
ASESNTQWFVEQEGVSNPSAAPSLSFAEEIARRAAEMSNRNAQSLEKLESGNVTDPIQQGLGLARSFAPEGQ

>core/193/3/Org3_Gene91

MADILVIGANPTGLILANMLIQHGISVKVIDHRASPEDPSFLDCRKLVPILSCSSLELLHNSEMLGDFIQANHKI
FGARYHWKKRTLFLKFSQATDSPVPFSLSTTYQSLEQHLIDEFLKRGVIDWSTRPVTLVDNSIFIESTKVSQN
FENREIYNPKWIIACEADNNLDIRDLVKSQLRARRINREVIFINCDEGEPEEDHIIHLLPITKNFLNFVFYNPQEK
TKQLCLPQGTHSISPKLKQKLLYTYNLVISDENFHIKTSHHAFPEHGNVFLGSLSNTLLLSYLNGINNTNIIHAA
FNLAWKLLPVLKKAALKHLVITKEQEDGNILPYISPTTEKRAKKLPFSRFYTPALMYYFLKGCRCFNTTGEEY
YYPPHQALKYRSSDIKMSPDKEIHGPGPGMRAIDARLENGSFLLDPLKSSKHLLIFFKIDIPDLKEALQEEYG
EWIEICNVKEPRILNLYHANPNLSFIIRPDRYIGYRTHTFKLHELISYLLRIFASEKTS

>core/194/3/Org3_Gene376

MNWENVVRVAPSPGTDPHVGTAYMALFNEIFAKRFKGKMILRIEDTDRTRSRQDYEENIFSALRWCGIQW
DEGPDVGGPYGPYRQSERTKIYQGYVETLLKTDCAYKCFATPQELAEMRAVASTLGYRGGYDRRYRYLSPE
EVASREAAGQPYTIRLKVPLSGECVFEDYSKGRVVPWADVDDQVLVKSDGFPTYHFANVIDDHLMGITHV
LRGEEWLSSTPKHLLLYEAFGWEPVFLHMPDLLNPDGTKLSKRKNPTSIFYYRDSGYVKEAFVNFLTLMGY
SMEGDEEVYSLERIIETFNPRRIGKSGAVFDIQKLDWMNKHLYLNHEGSPECLLKELQGWLLNDEFFLKILPLC
QSRITTLAEFINLTSFFSGLLEYRVEELLQALSPEKAAILLYSYVKYLEKTDQWTKETCYLGSKWLAQAFN
VHHKKAIIPLLYVAITGKKQGLPLFDSIEILGKPRARARLVYAEKLLGGVPKKLAATVDKFMQREDFEEATFD
L

>core/195/3/Org3_Gene492

MDCRGGIPLPEPQVIGGYHVKKILSKKLRSRVVHGLHPETRHSTVIKVFSPSPSFTSRSVYNFLKEAQLHQIT
HPNIVKFHRYGKWQDCLYIAMEYIEGISLREYILAQFISLPQAIDIIFDIAQALEHLHSRNILHKDIKPENILITPQ
GKIKLIDFGLADWDTEIQRHPSVIGTPYYMSPEQRQGESHPASDIYALGLLAYELILGHLSLGRVFLSLVPE
RISKILAKALQPSNNRYSSTREFIQDIHHYRMSGDMQEDLRIKDHTVALYEQLQTQRFWLAPETLRFPDFISG
VLYHQGYPLYPHAYDTLLEGDVFNWLGYSPISNATIALSVVKSVCQQLRPLLDVCEINECLIRMKIPI
DEMGISILCLEISKENKELSWIACGKTVFWIKRQGRVVQDFESFSPGLGKITSLQIRETKVAWEIGDEAVVCTL
ELEESVASLKTLSLAELQDRRQKAIFCPIESIHGGIQSRQHGSNSPSTLISLKRIR

>core/196/3/Org3_Gene290

MLKKFINSLWKLCQQDKYQRFTPIVDAIDTFCYEPIETPSKPPFIRDSVDVKRWMLLVVIALFPATFVAIWN
GLQSIVYSSGNPVLMEQFLHISGFGSYLSFVYKEIHIVPILWEGLKIFIPLLTISYVVGGTCEVLFAVVRGHKIAE
GLLVTGILYPLTLPPTIPYWMAALGIAFGIVVSKELFGGTGMNILNPALSGRAFLFFTFPAKMSGDVWVGSNP
GVIKDSLMMKNSSTGKVLIDGFSQSTCLQTLNSTPPSVKRLHVDIAAANMLHIPHVPTQDVIHSQFSLWTETH
PGWVLDNLTLTQLQTFVTAPVAEGGLGLLPTQFDSAYAITDVIYGIGKFSAGNLFWGNIIIGSLGETSTFACLLG
AIFLIVTGIASWRTMAAFGIGAFLTGWLFKFISVLIVGQNGAWAPARFFIPAYRQLFLGGLAFGLVFMATDPVS
SPTMKLGKWIYGFFIGFMTIVIRLINPAYPEGVMLAILLGNVFAPLIDYFAVRKYRKRGV

>core/197/3/Org3_Gene156

MKFEFSVALKYLPGRGRLYSAIVSLFSVGIISLVVWLSIVFISVIHGLEQRWIEDLSQLHSPITILPSDTYYSSYY
YQIDKHSSLSNYTTKTLGEKIASPQVDPYPDES DYLLPETFPLKDCDLGGQQKDPVKMTLES LGPYLQS QH GK
VIEFEQGVGYLDIKTSLKLQKPQPRNLTHFLTYP SKLSYEDKVL PYDET DYTSAELNPFNRSPSGWQQDFHHL
EELYRGASIILPSTYKDSGYKVGDTGVFSTYSIENEKETQYTVHVIGFYNPGLSPLGGRTVFIDPDLARSIRSQS
EGLGMSNGFHLFFPNTKRIVFVKQIENILTSLGVDDYWEISSLHDYDYFQPILDQLQSDQVLFVFCILILIVA
CSNIVTMSMLLVNNKKKEIGILKAMGTSSRSLKIIFACCGAFSGACGVVIGTIFAITLKNLQFIVKALNYLQGR
ETFNTAFFGQNLPSNVHPQAIYFLGLGTLALLAAVSGALPARKVAKMHVSEILKAD

>core/198/3/Org3_Gene258

MVLFHAQASGRNRVKADAIVLPFWHFKDAKNAASFEEFEP SYLPALENFQGKTGEIELLYSSPKAKEKRIV
LLGLGKNEELTSDVVFQTYATLTRVLRKAKCSTVNILPTISELRLSAEEFLVGLSSGILSNYDYPRYNKVDR
NLETPLSKVTVIGIVPKMADAIFRKEAAIFEGVYLTRDLVNRNADEITPKKLAEVALNLGKEFPSIDTKVLGKD
AIAKEKMGLLLAVSKGSCVDPHFIVVRYQGRPKSKDHTVLIGKGVTFDSGGLDLKPGKSMLTMKEDMAGG
ATVLGILSALAVLELPINVTGIIPATENAIDGASYKMGDVYVGM SGLSVEICSTDAEGRILADAITYALKYCK
PTRIIDFATLTGAMVVSLGEEVAGFFSNNDVLAEDLLEASAETSEPLWRLPLVKKYDKTLHSDIADMKNLGS
NRAGAITAALFLQRFLEESSVAWAHLDIAGTAYHEKEEDRYPKYASGFGVRSILYYLENSLSK

>core/199/3/Org3_Gene719

MTVSYQSISTPPPEGEFDIFVDGNATEEAVVAAEVQVALPAGEQYAMLRATSEL CFGILTQSECA LTQALPPK
EKPLQEEQFLVKN GILMRSTSLPNLKP GQSQQTSLASHRNPLAQQSTSSNSTGKASTETTSSSF PFFSCKAPEG
DSSVDKTFTVSVQTPKAQEQQEASASQSQAQFHVRSYSSSTIKEHSAKEKVSQSTKSAETQKHTQTKSDATLS
PMSLYSTLHKEVPQALSSTKSQQKDEEHRDQRQQEGYEQE QE EGKKKTPWCTVESLQQTSSSNQVYESY
TPIIPDPIVEFALSESQLSVLAGKRVTNLDVLRICTELMLKMLKSRANDTMTRLEERELMERE AHELAASYSR
QAKYARWLGIATATLGILGAIAPMVGEISGDSILGFVQRISGRFKDATAKTFFKGIGKVFTSLSQLTEAASKVH
ELSESAVRVAEYRKEVFRMRQDEVTRTIEEVKDNWKSMDN FLLNILQTEHDAARSLYQ

>core/200/3/Org3_Gene575

MAASILSQELLDILPYTFLKKHCLLPIEESSEAITIAHATATS VIAQDEVKLLIKKPVRFVLKEESEILQRLQQLY
SNREGNVSDMLLTMK EEDGTTISEEEDLLETDTIPVVRLLNWILKEAIEERASDIHFEPCEDSMRIRYRIDGV
HDRHSPPSHLRSALTTRLKVLAKMDIAEHRLPQDGRIKIHIGGQEVDMRVSTVPVIYGERVVLRILDKRNIL

DIAGLHMPKGTEILFKDTITAPEGILLVTGPTGSGKTTTLYSVLQELKGPLTNIMTIEDPPEYKLPGIAQIAVKP
KIGLTFARGLRHLLRQDPDILMVGEIRDQETAETAEIAQAALTGHLVVSTLHTNDAISAIPRLLDMGIESYLLSATL
VGVVAQRLVRTICPYCKVAYTPENQEKSFLASLGKDTEMPLYRGQGCVHCFRSGYKGRQGIYEFLRPNTLFR
SEVASNRPHYHILRETAEQNGFLPILEHGIALAVSGETTLAEVLRVTKRCD

>core/201/3/Org3_Gene797

MNKKHASFSSRLGFIFSMIGIAVGAGNIWRFPVAAQNGGGAFLILWLCFLFLWSIPLIIIELSIGKLTKKAPIGA
LIKTAGKKFAWAGGFITLVTTCILAYYSTIVGWGLSYFYAYVSGKIHGNDFAKLWTSHYQSSIPLWAHLTSL
GLAYLVIRKGIVHGIEKCNKILIPAFFLCTIALLLRAVTLPGAVQGIKQLFSCDKSCFSNYKVWIEALTQNAWD
TGAGWGLLLVYAGFASKKTGVVSNAGALTAICNNLVSLIMGIIIFSTCASLDILGTTQLQDGAGASSIGITFIYLP
ELFTRLPGGIYLTTLFSSIFFLAFSMAALSSMISMLFLLSQTLAEFGIKPYISETLATIIAFVLGIPSALSLTFFSNQ
DTVWGVALIVNGLIFIYAALVYGFPKLKKEVINAAPGDLRLNKAFDYIIKYLLLLIEGILLGWYFYEGFLPENG
QWWNPISLYSLGSLVLQWSLGLIILWKFNKQLYLRFSRYNHEIL

>core/203/3/Org3_Gene925

MLKYILKRLVLIPLTLFAIVSINFVILNAAPGDVLEEKSRYSALGEAGKSDKMRSYKGRDRYLQFREAYGLNAP
HFFNTRPKITHKKIQTALQELANANNTTPSAKNAAKSLVYWGDCAKFVMPALLFEADDASRDDKYRHIAAD
LFIRGGVLQGFVGPNSPEQRAQNKEIAESNAFLVRQLNEEDLDTKVEALKGWFDHGGTEVFCYSSKQFW
KTFFLETRFARYMSRVLRLDFGTLRNDAAHKTVISEVIKRLRCSLVLSILPMIVGFVLCQIFGMIMALKRNRWID
HSLNFIFLILFSIPVFVAVPWILDNFVINKTIPFTTIPMPYSGLRSPPEVFNELSTLGRIFDLVSHGFLPFCVSYG
ALAAQSRLSRSIFLEVLSQDFICAAKARGLRWFDILYKHVGKNAAVSIVTSLASSLGTLGGALVETLNFNIDG
FGNFFYQAILNRDHNVLFSVLVGSALSLVGYLLGDICYVLLDPRVQLEGRI

>core/204/3/Org3_Gene865

MHTEFAPFLEDLVHQQVISPLDIAFASKHISDFEESFVFLAVSSALWRYGHPFLSLEENRIRPSLGGISETDLY
RGFHNLPKEVRDKLFVVVSGRLYLRSLYTIRSKLLDKLSLLCSATPNYFPPSIDSSILSEEQNFIFNKITQGCFSI
VSGGPGTGKTFLAAQLILSLVKQPKLRVIAVSPTGKATSHIRQILMKYNIFDDMVLMQTVHHFLQEYAYRRY
NSIDVLLVDEGSMVTFDLLYSLVQTLQGYEKDKKLYTSSLIILGDTNQLPPIGIGVGNPLQDLIGYFHENTFFL
KTSHRAKTGVVDQLTQSVLRGEMISFSPLPSISSAIEVLKNRFBKSLRQSEARLCVLTMRHGPWGVNLNTM
IHQRLARSDPDLRIPIMVTSRYETWGLFNGDTGLLCLKTQKLHFPQHEPIDSRALSQYVYNYVMSVHKSQGSE
YDEVIVIIPKGSEVFGVSILYTAITRAKYRVSVWGDPELTHKIIKKSNY

>core/205/3/Org3_Gene996

MNLDSKHFDINSANFLEEFKAFISFPSISADSDHLQDCENCAHFLVDHVNKIFDVELWETPGHPPIIYASYKSE
DPLSPTLMLYNHYDVQPAQLSDGWKGDPFILREENGNYARGASDNKGQCFYTLKALQHYYESQGNFPLNII
WLIEGEEESGSLALFTWLEKKKEALRADYLLIVDGGFLSEKHPYVVISGARGIVSMKISLEEGNKDMHSGVLGG
IAYNTNRALSEILSSLHHPDNSIAIEGFYDDLALPSDSRDPDLPSDTLRECEENLGFRPQGYEASYSPEESALR
PTVEINGISGGYTGPFGKTVIPYRATAYLSCRLVPNQDPDKAAHQVIHHLKQQVPSSLKFSYEILPGGSRGWRS
SANLPVVKVLQEIYSDLYNEECLRLVMPATIPIGPLLGEAAQTSPICGTSYLSDDIHAAEEHFSMDQLKKGFLSI
CQLLDKLPKIKE

>core/206/3/Org3_Gene858

MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTMESDATIAGASGKDKTSSTTKT
ETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSIEEASKSMESTLESLSLSAAQMKEV
EAVVVAALSGKSSGSAKLETPELPKPGVTPRSEVIEIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLG
LEKQAIKIDKEREYQEMKAAEQKSKDLEGTMDTVNTVMIAVSVAITVISIVAAIFTCGAGLAGLAAGAAVG
AAAAGGAAGAAAATTVATQITVQAVVQAVKQAVITAVRQAITAAIKAAVKSGIKAFIKTLVKAIKAISKGI
SKVFAKGTQMIAKNFPKLSKVISSLTSKWVTVGVGVVVAAPALGKGIMQMQQLSEMQQNVAQFQKEVGKLQ
AAADMISMFTQFWQQASKIASKQTGESNEMTQKATKLGAQILKAYAAISGAIAAGAA

>core/207/3/Org3_Gene3

MYRYSALELAKAVTLGELTATGVTQHFFHRIEEAEGQVGAFISLCKEQALEQAELIDKKRSRGEPLGKLAGV
PVGIKDNIHVTGLKTTCASRVLENYQPPFDATVVERIKKEDGILGKLNMDDEFAMGSTTLYSAFHPTHNPWDL
SRVPGSSGSSGSAAAVSARFCPVALGSDTGGSIRQPAAFCGVVGFKPSYGAVSRYGLVAFASSLDQIGPLANT
VEDVALMMDVFSGRDPKDATSREFFRDSFMSKLSDEVKPVIGVPRTFLEGLRDDIRENFFSSLAIFEGEGTHLV
DVELDILSHAVSIYYILASAEAAATNLARFDGVRYGYRSPQAHTISQLYDLSRGEGFGKEVMRRILLGNYVLSA
ERQNVYYKKATAVRAKIVKAFRTAFEKCEILAMPVCSSPAFEIGEILDVPTLYLQDIYTVAMNLAYLPAIAVP
SGFSKEGLPLGLQIIGQQGQDQVCQVGYSFQEHAQIKQLFSKRYAKSVVLGGQS

>core/208/3/Org3_Gene1005

MNGCWEDLKQTIFWVGEHDCTDIETVRKSCMWLDTRYADKFILREKEEKMERHELPHATMVRKASGHAYA
KAKAAFEKERSNENQRKVVDVEKWLSKGLAEFRNQESRRARERLRELQTLYPEVSVEERVLERQRTKKVNL
ENLYADIEKKYHHCVREQEYHWEVENKEAEYRENGEKVLSAEVSECLQRLEDCLTWSKKLTKAEESVF
EMKFDATEKLGKVLSDVTNRLEILCEDAEEMIFRIEIEIEMTLRMVELPLLFMKNTFEKASLQYNSCKEMLA
KVEPQCKESPTYRSSQERLERLNQDLQTAYTNCQERLQGFSDLESKVRTCRDHLREQMKHFEVQGLNFINEE
LLWVGAEFLTQARLDLVATVPYMEFYLYHNIKREKVRSQWMAKTERYREIRQAFQGVMMKEDLLAEDTIL
KEEDYWLLRDDWLLRDERKNRQRRLLCNKIAAAQQRVKGF

>core/209/3/Org3_Gene815

MLGILLIASGHIIFLAVAIPGLSSAVALGLGCGMTALGTVLLITGLVLLIRSEKLALQVEIKQARTRVNNELDQL
SQYVFYTENVLDNLKRWSYRDLGFVRQAQEEVTNLEQDIEEIFLTRDIRNALDNEEFFMTHAKQCLAQVGE
SLFQDASIDEFINLAHLSEIRQHLDINDPRWSMITKKVKGTVVRFIYVSTMYKQIKSNFEKSDFGQLRKMLLN
NYKTIEEVLYQSFRQGYNRAALLSEKTRIIHTSSLLHWEKDEDDKHLNIKNECASRLNFKKFRTLFLGLSEEDV
IDFTGASGWDCSKLPRKEVPLDGGKKKLRFKRTFADEQVGDWDRTTSLEHMTPEEDPLDRLMDQVEQEAT
SVLKDQDRYWKEIETSEAKFRSLPREDDFEKQSQIDSYIRDLDHLSVWANQLSAAEDALIEVTDVQEHGNR
EMLKNIQQGLELIEDAVKATLPRVDFIQELLEKEELPLVAARMSLENS

>core/210/3/Org3_Gene753

MTFPCGNCNCYYRETPPPNPGGEDIPLQEGGQSGSQGGRVITQQPGTGGREMGISLGSDNVLGMVEQAGSL
NNLLDSARMQRLGHYCYRTGTPWCREHCPGFLQWIWGGCCACCLETVDDPDNPSAQFLQQLIQQYGPICVG
MSFQQLPHCTQKIEQGEPLGDGDKQEVENGCKLHRELLKAAQPRCMGESLVKLLQNNGLGEDMQQTTPWS

LILQAVSEGALSFVTSSDNPPTCWILQPEQQPCPPPPTDEEQQLQGAVGGAPAPQQKKHPAQECRVTCCLNFRT
LLQKLSRLEVLSLESGYKGPLGQAAKQIVDLIKKSLKRLVASDLATFLGPGIGLSLESQVFEVLVLLCLLSKGY
LPLDPLHPEQTVLDPRVQGPWQRILRKVLVTTTAGENIWRQTQGEAPRQAPPPDPWDDDEIERDGIVTGGG
FGIPCQCLRCWRKLPTEKRPNRWL

>core/211/3/Org3_Gene969

MHMSNPISLFSPAELIAKYNLIPKTSPIYPRRTELIILEENACQTRLTNVAQVLHPSSLFMSKILNPGCGSGGP
LCWVILNILAFIITSVLFIILLPVNLIVAGLRLFMPLPPKKIVEDLSEPTTEETNEVIQPFIFALQALLFEDNKLRSF
KIVEQSVGKAPLPNPFLKRLVAISPQESQEAMRKIPDLCSQLKKVLKSLGVLTPEWKHMLKYFEGLKNEHDS
NPDKKTFPILIKLLIEALTGKSSLPKTPSTKEKMQAALFIASSCKTCKPTWGEVITRSLNRLYSIANEGDNQLLI
WVQEFKERELMSIQDGDDAEEYRFAAQQHGERYTEAIEQVLRNESAAKLQWHVINTMKFFHGKNLGLVTE
HLQDTLGALTLRQTTVDTHQGREDADLSAALFLNKYLNsgnQLVNSVFKSMQKADPETKALIREFALDILYA
SLRLPQTSaHTEVFSTLLMDPETYEPNKACIAYLlyVLKIIEL

>core/212/3/Org3_Gene866

MSAVYADWESVIGLEVHVELNTASKLFSSALNRFGDEPNTNISTVCTGLPGSLPVLNQSAVEKAVLFGCAVE
GEISLLSRFDRKSYFYPDSPRNFQITQFEHPIIRGGRIKAIVQGEERYFELAQTHIEDDAGMLKHFGEFAGVDYN
RAGVPLIEIVSKPCMFCPEDAVAYATSLVSLLDYIGISDCNMEEGSIRFDVNVSVRPKGSPELRNKVEIKNMNS
FAFMAQALEAEKQRQIDEYLNQPNKDPKLVIPAATYRWDPEKKKTVLMRLKESAEDYKYFPEPDLPTLQLTE
SYIERIRKTLPELPYDKYHRYIQEYGLSEDIASILISDKNIATFFEVACKDCKNFRSLSNWVSVEFGGRCKTLGV
KLPSGIFPEGVAQLVNAIDQGVTGKIAKEIADLMMESPGKNPEEILKEKPELLPMSDEGELQKIIAEVVLANP
ESIVDYKNGKTKALGFLVGQIMKRTAGKAPPKRVNELLLLLLELDKG

>core/213/3/Org3_Gene687

MITKQLRSWLAVLVGSSLLALPLSGQAVGKKESRVSELPQDVLLKEISGGFSKVATKATPAVVYIESFPKSQA
VTHPSPGRRGPYENPFDYFNDEFFNRFFGLPSQREKPSKEAVRGTGFLVSPDGYIVTNNHVVEDTGKIHVTL
HDGQKYPATVIGLDPKTDLAVIKISQNLPLYLSFGNSDHLKVGDWAIAGNPFGQLATVTVGVISAKGRNQL
HIADFEDFIQTDAAINPGNSGGPLLNIDGQVIGVNTAIVSGSGGYIGIGFAIPSLMANRIIDQLIRDGQVTRGFLG
VTLQPIDAELAACYKLEKVYGALVTDVVKGSPADKAGLKQEDVIIAYNGKEVDSLSMFRNAVSLMNPDTRI
VLKVVREGKVIEIPVTVSQAPKEDGMSALQRVGIRVQNLTPETAKKLGIAPETKGILIISVEPGSVAASSGIAPG
QLILAVNRQKVSSIEDLNRTLKDSNNENILLMVSQGDVIRFIALKPEE

>core/214/3/Org3_Gene827

MWNRCQVFSSFFFRYPISSWLIRLRASCECFQQRHPIFLCGLYWLAGITSRGYPECSALILIFLGMFLPRNPKQ
WLPLASAWIISLMLTPAPFLHDGPISGTFVIHHAGGQGTYTGEALCIQTPCGKRAHHLSCQILSESRLKLVY
ELEGTLHHTSQIVFKSNACYKEIPRSRFYIMKEKCRESSCHFLNHRFPSSEVGPFASSLLLGTPLPQNLRDLFRQ
KGLSHLFAISGWHFSLCATTWMLCALLPLKIKILSFIVLTSACIFPMSLSVWRSWISVTLLCFSWCFSGSCS
GLNRLGAGFILCSIFFSPFSPTFVLSFLATLGILLFFPKIFSFLYTPWTQFLSPFWLYPIRYLAMTLAISLSAQLFIV
LPIMQYFGSLPLEGLLYNLIVPFTILPIIVFLIATIILPCCSPITEALIQGFLSHPWLHNPNIKLTLSFAPVPPWMLTL
ASLILFFIGILRTNVSPYASTSATSRYFIETL

>core/215/3/Org3_Gene596

MLKIAILGRPNVGKSSLFNRLCKRSLAIVNSQEGTTRDRLYGELHAFGVPAQVIDTGGVDHNSDYFQKHIYN
QALTGAKEADVLLLVIDIRCGITEEDAHLAKLLLPLKKPLILVANKADSRQEELQIHETYKLGIRDIVVTSTAH
DKHIDTLLQRIKLVANLPEPREEEEEGLEELSVDEHEESEAAALPSNTFPDFSEVFTEGFSPEEPCTIPESPQQAPK
TLKIALIGRPNVGKSSIINGLLNEERCIIDNTPGTTRDNIDILYSHKDRQYLFIDTAGLRKMKSVKNSIEWISSR
TEKAISRADICLLVIDATQKLSSYEKRILSLISKRKKPHIILINKWDLLEEVRMEHYCKDLRATDPYLGQAKML
CISATTKRNLKKIFSAIDELHHVVSNNKVPTPIVNKTLASALHRNHPQVIQGRRLRIYYAIQKTTTPLQFLLFINA
KSLTCKHYEYYLKNTLKSSFNLYGIPFDLEFKEKPKRHN

>core/216/3/Org3_Gene832

MNMPVPSAVPSANITLKEDSSTVSTASGILKTATGEVLVSCTALEGSSSTDALISLALGQIILATQQELLQSTN
VHQLLFLPPEVVELEIQVVDLLVQLEHAETITSEPQETQTQSRSEQTLPQQSSSKQSALSPRSLKPEISDSKQQQ
ALQTPKGSAVRKHSEAPSPETQARASLSQASSSSQSRSLPPQESAPERTLLEQQKASSFSPLSQFSAEKQKEALT
TSKSHELKRDQDRQQREQHDRKHDQEEDAESKKKKKKRGLGVEAVAEEPGENLDIAALIFSDQMRPPAE
ETSKKETTFKKKLSPMSVFSRFPKSNPLSVGSSIHGPIQTPKVENVFLRFMKLMARILGQAEAEANELYMRV
KQRTDDVDTLTVLISKINNEKKDIDWSENEEMKALLNRAKEIGVTIDKEKYTWTEEEKRLLKENVQMRKEN
MEKITQMERTDMQRHLQEISQCHQARSNVLKLLKELMDTFIYNLRP

>core/217/3/Org3_Gene975

MTSRTKSSKNLGTIALAGMVVSSIIGGGIFSLPQNMAATAGAGAVILSWILTGFGMFFIANTFRILSTIRPDLKE
GIYMSYREGFGPYIGFTIGWGYWLCQIFGNVGYAVITMDALNYFFPPYFQGGNTLPAILGGSILIWVFNFIVLK
GIRQASIINVIGTIFKIIPLIIFIILTAFKKLAVFKTDFWGHAVTKAQPSLGSVSSQLKGTMLVTLWAFIGIEGAV
VMSGRAKNPLSVGQATVLGFLGCLTIYILFSLPFGSLFQHQLANIPNPSTAGVLDILVGKWGEVLMNVGLIIA
VLSSWLSWTIIVAEIPFSAAKNGTFPEIFTIENKEKSPSVSLYITSSVMQLAMLLVYFSSNAWNTMLSITGVMV
LPAYLASAAFLFKLSKSKTYPKKGSIKAPLAMITGILGVVYSLWLIYAGGLKYLFMALVLLALGIPFYIDAGK
KKKNAKTFFAKKEIVGMTFIGLLALTAIFLFSTG

>core/218/3/Org3_Gene881

MITRTKIICTIGPATNSPEMLAKLLDAGMNVARLNFSHGSHETHGQAIGFLKELREQKRVPLAIMLDTKGPEIR
LGNIPQPISVSQGQKLRLVSSDIDGSAEGGVSLYPKGIFPFVPEGADVLIDDGYIHAVVVSSEADSLELEFMNS
GLLKSHKSLSIRGVDVALPFMTEKDIALDKFGVEQNMDVNAASFVRYGEDIMRKCLADLGNPKMPIIAKI
ENRLGVENFSKIAKLADGIMIARGDLGIELSVVEVPNLQKMMAKVSRETGHFCVTATQMLES MIRNVLPTRA
EVSDIANAIYDGSSAVMLSGETASGAHPVA AVKIMRSVILETEKNLSHDSFLKLDDSNSALQVSPYLSAIGLA
GIQIAERADAKALIVYTESGSSPMFLSKYRPFPIIAVTPSTSVYYRLALEWGVYPMLTQESDRAVWRHQACI
YGIEQGILSNYDRILVLSRGACMEETNNLTITIVNDILTGSEFPET

>core/219/3/Org3_Gene484

MGESVKVFLEEREDYPYGFVTPIESQGLTRGLSEETIEEIAALRNEPQFIIDFRLQAYRYWKQLHEPAWARLH
YGPIAYDDIVYFSSPKQKKPLGRLEDADPEILDTFKKLGIPLDEQKRLNVENVAVDLVFDSVSIGTTTFKEALE
KAGVIFCSLGEAIQEHPNLVKKYLGSVVSHRDNFFAALNAAVFSDGSFVYVPKGVKCPMDISTYFRINNKEA

GQFERTLIVVEDGGYASYLEGCTAPAYSSNQLHAAVVELVAHEHAVIRYSTVQNWYAGDKKTGKGGIYNFV
TKRGLCAGYRSKISWSQVEVGAAITWKYPSCILKGDESVGEFYSVALTSGKMQADTGTKMLHVGKRTTSTV
ISKGISSESKNTFRSLVSLGKKAHSSNYTQCDSMLIGKASGAYTDPKIVVENSTSSIEHEATTSKLREDQLLY
LRSRGLSPEEAVSLVIHGFCREIIEQLPLEFAQEASKLLLIKLENSVG

>core/220/3/Org3_Gene282

MDLKELLHGVQAKIYGKVRPLEVRNLTRDSRCVSVGDIFIAHKGQRYDGNDFAVDALANGAIAIASSLYNPF
LSVVQIITPNLEELEAELSAKYEYEPSSKLHTIGVTGTNGKTTVTCLIKALLDSYQKPSGLLGITIEHILGEGVIK
DGFTTPTPALLQKYLATMVRQNRDAVVMEVSSIGLASGRVAYTNFDTAVLTNITLDHLDHFHGTFTFYVAAK
AKLFSLVPPSGMVMVINTDSPYASQCIESAKAPVITYGIESAADYRATDIQLSSSGTKYTLVYGDQKIACSSSFIG
KYNVYNLLAAISTVHASLRCDLEDLLEKIGLCQPPPGRLDPVLMGPCPVYIDYAHTPDALDNVLTGLHELLPE
GGRLIVVFGCGGDRDRSKRKLMAQVVERYGFAVVTSDNPRSEPPEDIVNEICDGFYSKNYFIEIDRKQAITYA
LSIASDRDIVLIAGKGHEAYQIFKHQTVAFDDKQTVCEVLASYV

>core/222/3/Org3_Gene238

MQTNIGLIGLAVMGKNLVLNMIDHGFSVSVYNRTPEKTRDFLKEYPNHRELVGFESEDFVNSLERPRKIML
MIQAGKPVDQSIHALLPFLEPGDVIIDGGNSYFKDSERRCKELQEKGILFLGVGISGGEEGARHGPSIMPGGNP
EAWPLVAPIFQSIAAKVQGRPCCSWVGTGGAGHYVKAVHNGIEYGDILICEAYGILRDFLKL SATAVATILK
EWNTLELESYLIRIASEVLALKDPEGIPVIDTILDVVGQKGTGKWTALNSGVPLSLIIGAVLARFLSSWKEI
REQAARNYPGTPLIFEMPHDPSVFIQDVFHALYASKIISYAQGFMLLGEASKEYNWGLDLGEI ALMWRRGGCII
QSAFLDVIHKGFAANPENTSLIFQEYFRGALRHAEMGWRRTVVTAIGAGLPIPCLA AAITFYDGYRTASSSMS
LAQGLRDYFGAHTYERNDRPRGEFYHTDWVHTKTTERVK

>core/223/3/Org3_Gene938

MRDVSELFRTHFMHYASYVILERAIPHILDGLKPVQRRLLWTLFLMDDGKMHKVANIAGR TMALHPHGDAP
IVEALVVLANKGYLIDTQGNFGNPLTGDPHAAARYIEARLSPLARETLFNTDLIAFHDSYDGREKEPDILPAKL
PVLLLHGVDGIAVGM TTKIFPHNFAELLKAQIAILNDKKFTVFPDFPSGGLMDPSEYQDGLGSITLRASIDIIND
KTLVVKQICPQSTTETLIRSIENAAKRGTIKIDTIQDFSTDVPHIEIKLPKGSRAKEMPLLLFEHTECQVILYSKPT
VIYENKPVECSISEILKLHTTALQGYLEKELLLLQEQLTLDHYHKTLEYIFIKHKLYDSVREVLAINKKISADDL
HQA V LHALEPWLHELATPVTKQDTSQLASLTIKKILCFNEEACTKELLAIEKKQAAIQKDLGRLKEVTVKYL
KGLLERHGH LGERKTQITNFKTAKTSILKQQT LI

>core/224/3/Org3_Gene729

MLCATVSGPSFCEAKQQILKSLHLVDIIELRDLINELDDQELHTLITTAQNPILTFRQHKEMSTALWIQKLYSL
AKLEPKWMDIDVSLPKTALQTIRKSHPKIKLILSYHTDKNEDLDAIYNEMLATPAEIIYKIVLSPENSSEALNYI
KKARLLPKPSTVLCMGTHGLPSRVLSP LISNAMNYAAGISAPQVAPGQPKLEELLSYNYSKLSEKSHIYGLIG
DPVDRSISHL SHNFLLSKLSLNATYIKFPVTIGEVVTF FSAIRDLPFSGLSVTMPLKTAIFDHVDALDASAQLCE
SINTLVFRNQKILGYNTDGEGVAKLLKQKNISVNNKHIAIVGAGGAAKAIAATLAMQGANLHIFNRTLSSAA
ALATCCKGKAYPLGSL ENFKTIDIINCLPPEVTFPWRFPPIVMDINTKPHPSPYLERAQKHGSLIIHGYEMFIEQ
ALLQFALWFPDFLTPESCDSFRNYVKNFMAKV

>core/225/3/Org3_Gene297

MMSRLRFRLAALGIFILLVPNSVSAKTIVASDKEKVGVLVYDNSVEAFQQILDCIDHANFYVELCPCMTGGR
TLKEMVDHLEARMMDLVPELCSYIIIQPTFTDAEDQKLLKALKERHPNRFFYVFTGCPPSTSILAPNVIEMHIKLS
IIDGKYCILGGTNFEEFMCTPGDEVPEKVDNPRFLVSGVRRPLAFRDQDIMLRSTAFGLQLREEYHKQFAMW
DYAAHHMWFIDNPEQFAGACPPLTLEQAEETVFPGFDKHEDLVLDSSKIRIVLGGPHDKQPNPVTQEYLKLI
QGARSSVKLAHMYFIPKDELLNALVDVSHNHGVHLSLITNGCHELSPAITGPYAWGNRINYFALLYGKRYPL
WKKWFCEKLPYERVSIYEFAIWETQLHKKCMIIDDEIFVIGSYNFGKKSDAFDYESIVVIESPEVAAKANKV
FNKDIGLSIPVSHGDIFSWSYFHSVHHTLGHLLQLTYMPA

>core/226/3/Org3_Gene670

MRIVQVAVEFTPIVKVGGLGDAVASLSKELAKQNDVEVLLPHYPLISKFSSSQVLSERSFYEFGLGKQQASAI
YSYEGTLTLTIITLDSQIELFSTTSVYSENNVVRFSFAAAAAAYLQEADPADIVHLHDWHVGLLAGLLKNPLN
PVHISKIVFTIHNFGYRGYCSTQLLAASQIDDFHLSHYQLFRDPQTSVLMKGALYCSDYITTVSLTYVQEINDY
SDYELHDAILARNSVFSGIINGIDEDVWNPKTDPALAVQYDASLLSEPDLFTKKEENRAVLYEKLGISSDYFP
LICVISRIVEEKGPFEFMKEIILHAMEHSYAFILIGTSQNEVLLNEFRNLQDCLASSPNIRLILDFNDPLARLTYAA
ADMICIPSHREACGLTQLIAMRYGTVPVLRKTGGLADTVIPGVNGFTFFDTNNFNEFRAMLSNAVTTRYQEP
DVWLNLIESGMLRASGLDAMAKHYVNLYQSLLS

>core/227/3/Org3_Gene656

MAFSHIEGLYFYNTASQKKELFFPNHTPVRLYTCGPTVYDYAHIGNFRITYVFEDILKRTL VFFGYSVTHVMNI
TDVEDKTIAGASKKNIPLQEYTPYTEAFFEDLDTLNIARADFYPHATHYIPQMIQAITKLLEQGIAYIGQDAS
VYFSLNRFPNYGKLSHLDLSSLRCCSRISADEYDKENPSDFVLWKAYNPERDGVIIYWESPFKGKRPGWHL
SIMAMELLGDSLDIHAGGVDNIFPHHENEIAQSEALSGKPFARYWLHSEHLLIDGKKMSKSLGNFLTLDLLH
QEFTGQEVRYMLLQSHYRTQLNFTEEALLACRHALRRLKDFVSRLEGVDLPGESPLPRTLDSQQFIEAFSRA
LANDLNVSTGFASLDFVHEINTLIDQGHFSKADSLYILDTLKKVDTVLGVLPLTTSCIPETVMQLVAEREEA
RKTKNWAMADTLRDEILAAGFLVEDSKSGPKVKPL

>core/228/3/Org3_Gene316

MDTIDTPGEQGSQSFGNSLGARFDLPRKEQDPSQALAVASYQNKTDSQVVEEHLDELISLADSCGISVLETRS
WILKTPSASTYINVGKLEEIEILKEFPSIGTLIIDEIITPSQQRNLEKRLGLVVLDRTELILEIFSSRALTAENIQ
VQLAQARYLLPRLKRLWGHLNRQKSGGGSGGFVKGEKQIELDRRMVRRERIKLSAQLKAVIKQRAERRK
VKSRRGIPTFALIGYTNSGKSTLLNLLTAADTYVEDKLFATLDPKTRKCVLPGGRHVLLTDTVGFIRKLPHL
VAAFSTLEAAFHEDVLLHVVDASHPLALEHVQTTYDLFQELKIEKPRIITVLNKKVDRLPQGSIPMKLRLLSPL
PVLISAKTGEGIQNLLSLMTEIIQEKS LHVTLNFPYTEYGKFTL CDAGVVASSRYQEDFLVVEAYLPKELQKK
FRPFISYVFPEDCGDDEGRGPVLESSFGD

>core/229/3/Org3_Gene186

MDSRTSHLDDELSFKLEKAFTCLSTDIHSHDLSKIVIEYNPIDLAYAVSCLPSESRAILYKNLSCITAKVAFIINT
DSASRWAIFRRLSDSEVCALIEQMPPDEAVWVLDDIPDRRYRRILELIDSKKALKIRD LQKHGRNTAGRLMTN
EFAFLMETTVKDVSA CIRS NPGIDLTRLVFLDFK GELQGVVTDRSLIINPPEMSLKQIMNQIEHKVLPDATR

EEVVDLVERYKIAALPVVDEENFLIGAITYEDVVEAIEDIADETIARMAGTTEDVGYQTCHVVQRFLLRAPWL
LVTLFAGLISASVMAYFQKISPALLALIIFFIPLINGMSGNVGVQCSTILVRSMATGTLSFGRRRETIFKEMSIGL
LTGVVLGILCGLVVYLMGFLGLNIFSGGGIQLGVTVAATGVLGASLTATTLGVLSPPFFAKLGVDPALASGPV
TALNDIMSMIIFFLIAGGINFLFFN

>core/230/3/Org3_Gene803

MNKKKRFLSLLFLTAVLLGIWFSPHPASINSNAWQLFAIFTTTIMGIIFQPVPMGAIAIIGISTLLLTQTLTLEQG
LSGFHNPIAWLVFLSFSIAKGIIKTGLGERIAYFFVSALGKSPLGLSYGLVITDFFLAPAIPSVTARAGGILYPVV
TSLSDSFGSSAEKGTQDLIGSFLIKVAYQSSVITSAMFLTAMAGNPLVAALAGHVGVSLSWVLWAKAAIIPGL
LSLFLMPIILYKLYPPKITSCEEAIRSAKLRLKEMGPLKKEEKTILMIFLLVVLWTFGDLLGISATTAALIGLSL
LILTNIWDWQKDVIANTTAWETFIWFGALIMMASFLNQLGFIPLVGDSAAAALVSGLSWKIGFPLLFLIYFYSHY
LFASNTAHIGAMYPIFLAVSISLGTNPIFAALTLAFASNLFGGALTHYGSGPAPLYFGSHLVTVQEWWRSGFALS
IVNIVIWIGIGSLWWKALGLI

>core/231/3/Org3_Gene997

MTTKSLDSFNSVISKNKIHFIISLGCSRNLVDSEVMLGILLKAGYESTNEIEDADYLILNTCAFLKSARDEAKDY
LDHLIDVKKENAKIIVTGCMTSNHKDELKPWMSHIHYLLGSGDVENILSAIESRESGEKISAKSYIEMGEVPRQ
LSTPKHYAYLKVAEGCRKRCAFCIIPSIK GKLRSKPLDQILKEFRILVNKSVKEIILIAQDLGDY GKDLDSTRSS
QLESLLHELLKEPGDYWLRLMYLYPDEVSDGIIDLMQSNPKLLPYVDIPLQHINDRILKQMRRTTSREQILGFL
EKLRAKVPQVYIRSSVIVGFPGETQEEFQELADFIGEGWIDNLGIFLYSQEANTPAAELPDQIPEKVKESRLKIL
SQIQKRNVDKHNQKLIGEKIEAVIDNYHPETNLLL TARFYGQAPEVDPCIIVNEAKLVSHFGERCFIEITGTAG
YDLVGRVVKKSQNQALLKTSKA

>core/232/3/Org3_Gene183

MHSHSKPTKPLGTFTVGMLSLAVVISLRNLPLTAKHGLSTLFFYGLAVICFMIPYALISAELASFKPQGGIYIWA
RDALGKWWGFFAIWMQWFHNMTWYPVLAFAIASTIVYKINPELAHNKVYIATVILAGFWILTFNFLGITSS
ALFSSICVII GTLIPGVILVSLALFWIFSGNP IASLSWGNLLPNFSNVSSLVLLAGMLLALCGLEANANLASDM
VNPRKNYPKAVFIGAIATLTILVLGSLSIAIVIPKEEISLVGLVKTFTLFFDKYNLSWMTGIVVMTIAGSLGE
LNAWMFAGTKGLFISTQNDCLPRLFKKVNSKNVPTNMLFQGIVVTIFTLLFLCLDSADLVYWILTALSVQM
YLAMYICLFLAGPILRIKEPRAQRLYSVPGKFLGICTMSILGILSCAFALWVSFLPPRELAQISEGSKIGYTTFLL
LAFSLNCLIPFGIYFTHKRLSKKS

>core/233/3/Org3_Gene760

MDKSTGVPLPSPPHSKESEMIVLGCMLTGVHYLNLAANQLYEEDFYYLEHKIIFRVLQDAFKQDKPIDVHLA
GEELKRHNQITVIGGPSYLITLAEFAGTAAYLEEYVDIIRSKSILRKMISTAKEIEKRALEQPKNVAEALDEAQN
SFFKISQSTSVSQYTLVADKLRLGLTTTTDKPYLVQLQERQELFLQNAQGDNKSFFTGIPTHFIDLDQLIHGFS
NLMILAAPAMGKTALALNIAENLCFQNRPLIGIFSLEMTVDQLIHRMICSRSSEVDSKKISIGDLSGHDFQRIVS
VINEMQEHTLLIDDQPGLKVSDLRARARRMKESYDIQFLIIDYLQLLSGSGTLRATESRQTEISEISRMLKTLAR
ELNIPILCLSLSRKVEDRANHRPMMSDLRESGSIEQSDSLVMFLLRREYYDPNDKPGTAELIIAKNRHGSIGS
VPLVFEKELARFRNYSAFECIS

>core/234/3/Org3_Gene522

MKITVNRGLDLSLQGSPKESGFYNKIDPEFVSIDLRPFQPLSLKLKVEQGDVCSGAPIAEYKHFPNTYITSHV
SGVVTAIRRGNKRSLLDVIKKKTPGPTSTEYTYDLQTLRSDDLSEIFKENGLFALIKQRPFDIPAIPQTQTPRDVFIN
LADNRPFTPSPEKHLALFSSREEGFYVFVVGVRAlAKLFGRLPHIVFRDRLTLPTQELKTIAHLHTVSGPFPSGS
PSIIHSVAPITNEKEVVFTLSFQDVLTIHGLFLKGRILHEQVTALAGTALKSSLRRYVITTKGASFSSLINLNDI
SDNDTLISGDPLTGRLCKKEEPPFLGFRDHSISVLHNPTKRELFSFLRIGFNKPTFTKTYLSGFFKKKRTYTNP
TNLHGETRPIIDTDIYDKVMPMRIPVVPLIKAVITKNFDLANELGFLEVCGEDFALPTLIDPSKTEMLTIVKESLI
EYAKESGILTPHQD

>core/236/3/Org3_Gene415

MKEERSSEILPRVKETKKHAYVSMQEKSVCGECAVVASESEEAESVTVTKIACLQRMGIEELNILARQYGVK
NIGSLTKSQVVFEIVKAKSERPDELLIGEGVLEVLDPDGFGLRSPTYNYLPSAEDIYVSPAQIRRFDLKKGDTIIG
TIRSPKEKEKYFALLKVDKINGSTPDKAKERVLFENLTPLYPNQRIVMEMGKDHLAERVLDLTAPIGKGQRG
LIVAPPRSGKTVILQSIHAHAIVNNPDIVLIVLLIDERPEEVTDMIRQVRGEVVASTFDEQPERHIQVAEMVIEK
ARRLVEHGNDVVILLDSITRLARAYNTVQPHSGKILTTGGVDASALHKPKRFFGAARNIEGGGSLTILATALIDT
GSRMDEVIFEEFKGTGNMELVLDRLSDRRTYPAIDLIKSGTRKEELLYHPSELERVYLFRQAIADLTIDAM
HLLGLRLKKTNSNAEFLLSLKE

>core/237/3/Org3_Gene539

MNFKLPVYHIGLTKAENNTIKIAILQKTCKGWIVCHCEQIPEGKTWSLPPKKYFAAPTTFSLQGS DILVKSSSSS
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ADIFFLAEQSPKSLPAYLLIYGGSEEVTCIFVKNHAI AVARSFSNHSTKKSCDDIHATLQYIQETFPQTVLP AIH
VAQISPNLQKILEQKLSLPLVVCQSM TYGVEDEDWEIYGDTIAAAHHGASRRPLTFPYDATSVSPAAQKHWL
LRSSLLIGKYALMATVVVSLGSLV LKLKSLSSSASNHFACPEEGVLPRSLKAAEKT VKAIGKKNSASNYPL L
PTIPTSEQTLKFLALGKSSPSIKFSYFSYTM TSYP SKDNPSLPYSALVEVKGGQGPEDIPQFLKKISSHPKLQH V
SESLEDQRSFKLQFTLSS

>core/238/3/Org3_Gene606

MTESVYSPSAMHVNSLADKLKAINQEHI LDIWPSLSPKQQQRLFQQLT SVDIDFFRKQQQLLSSPTAILKDFHP
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AGQPLPLAFMTSPLNTRQTRSFFESNDYFHLDPNQVDFFCQPLWPLLTLSGDLFLEDMDTLALGPNGNGCIAT
LLYTSGVWEKWKNAGIEMVSVIPIDNPLALPFDVELCGFHAMSNN EVTIKAALRQTAIEDVGILVKSHDSGK
TSVIEYSEIPQNERFALNEDGKLKYCLANIGLYCLSMDFIRHAAYQQLPLYKVH KHAKQLGHTSLNEKNAWK
FEEFIFDLFCYSDHCQTLVYPRQECFAPLKNLEGNHSPD TVRQALSDRERQLFHKVTGKKLS PNTTTFE LEADF
YYPSTSTSLHWENKAFFEEPFFEAS

>core/239/3/Org3_Gene589

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PGVPFSSRILSSTGILELEVLPKKLAIIGGGVIGCEFASL FHTLGVEITVIEALDHILAVNNKEVSQTVTNKFTKQ

GIRILTKASISAIEESQNQVRITVNDQVEEFDYVLVAIGRQFNTASIGLDNAGVIRDDRGVIPVDETMRTNVPNI
YAIGDITGKWLLAHVASHQGVIAAKNISGHHEVMDYSAIPSVIFTHPEIAMVGLSLQEAEQQNLPAKLTKFPF
KAIGKAVALGASDGFAAIVSHEITQQILGAYVIGPHASSLIGEMTLAIRNELTLPCIYETVHAHPTLSEVWAE
GALLATNHPLHFPPKS

>core/240/3/Org3_Gene32

MMSSKRTSKIAVLSILLTFTHSIGFANANSSVGLGTVYITSEVVKKPQKGSERKQAKKEPRARKGYLVPSSRT
LSARAQKMKNSSRKESGGCNEISANSTPRSVKLRRNKRAEQKAAKQGFSAFSNLTKSLLPKLPSKQKTSIH
EREKATSRFVNESQLSSARKRYCTPSSAAPSLFLETEIVRAPVERTKELQDNEIHIPVVQVQTNPK EQNTKTTK
QLASQASIQQSEGTEQSLRELAQGASLPVLVRSNPEVSVQRQKEELLKELVAERRQCKRKSVRQALEARSLT
KKVARGGSVTSTLRYDPEKAAEIKSRRNCKVSPEAREQKYSSCKRDARANGKQDKTTPSEDASQEEQQTGA
GLVRKTPKSQVASNAQNFYRNSKNTNIDSYLTANQYSCSSEETDWPCSSCVSKRRTHNSISVCTMVVTVIAMI
VGALIINANATESQTTSDPTPTPTP

>core/241/3/Org3_Gene899

MRAWEEFLLLQEKEIGTNTVDKWLRSLKVLCFDACNLYLEAQDSFQITWFEEHIRHKVKSGLVNNNNKPIRV
HVTSDKAAPFYKEKMQMQEKTAYFTMHYGSVNPEMTFSNFLVTPENDLPFRVLQEFTKSPDENGGVTFNPI
YLFGEPSGSKTHLMQSAISVLRSEGGKILYVSSDLFTEHLVSAIRSGEMQKFRSFYRNIDALFIEDIEVFSGKSA
TQEEFFHTFNSLHSEGKLIVVSSSYAPVDLVAVEDRLISRFEWGVAIPIHPLVQEGLRSFLMRQVERLSIRIQET
ALDFLIYALSSNVKTLLHALNLLAKRVMYKKLSHQLLYEDDVKTLLKDVLEAAGSVRLTPLKIIRNVAQYYG
VSQESILGRSQSREYVLPRQVAMYFCRQKLSLSYVRIGDVFSRDHSTVISSIRLIEQKIEENSHDIHMAIQDISKN
LNSLHKSLEFFXSEEMII

>core/242/3/Org3_Gene715

MRQEKDSL GIVEVPEDKLYGAQTMRSRNFFSWGPELMPYEVIRALVWIKKCAAQANQDLGFLDSKHCDMIV
AAADEILEGGFEEHFPLKVWQTGSGTQSNMNVNEVIANLAIRHHGGVLGSKDPIHPNDHVNKSQSSNDVFPT
AMHIAAVISLKNKLIPALDHMIRVLDKVEEFRHDVKIGRTHLMDAVPMTLGQEFSGYSSQLRHCLIESIAFSL
AHLYELAIGATAVGTGLNVPEGFVEKIIHYLRKETDEPFIPASNYFSALSCHDALVDAHGSLATLACALTKIAT
DLSFLGSGPRCGLGELFFPENEPGSSIMPGKVNPTQCEALQMVCAQVLGNNQTVIIGGSRGNFELNVMKPVII
YNFLQSVDLLSEGMRASFSEFFVKGLKVNKARLQDNINNSLMLVTALAPVLGYDKCSKAALKAFHESISLKEA
CLALGYLSEKEFDRLVVPENMVGNH

>core/243/3/Org3_Gene771

MNFSLFLFFLIAIQGICLYVGRRGSKKVEDRESYFLAGRSLKIFPLMMTFIATQIGGGVLLGAAEEAF CYGYGG
ILYPLGVALGLIFLGMGPGKRLAEGSLTTVVSIFEVFYGSKKLRKIAFLLSAGSLFFILVAQVIALDRLFSSFPFG
KYVTVAFWIVLASYTSTGGFRGVVRTDVIQAGFLLI AVL VCGVSVWLSVPKSLSVLDPFQSLPCA KLSNWIF
MPMLFMLVEQDMVQRCVAASSPKRLQWAAVGAGLVLLL FNFIFLFLGSLGAKAGLKAGCPLIDTIAYFCNPS
LAAVMAAAIGVAILSTADSLMNAVSQLIAEEYPTLKAPYYRYLVGLAVAAPLVAIGFTNIVDVLISYSLSV
CCLSVPGFYLLAPKGRRVSGAAAWAGVLVGALGYGWVQIVSLGMFGELLA WVGSLVAFSFGFIEITWK
NKVKTQT

>core/244/3/Org3_Gene681

MQQSVRKLFGTGVRGRANFEPMTVETTVLLGKAVARVLRREGSRGKHRVVVGKDTRLSGYMFENALIAGL
NSMGIETLVLGPIPTPGVAFITRAYRADAGIMISASHNPYRDNGIKIFSLEGFKISDVLEQRIETMVSEADFGPLP
EDHAVGKNKRVIDAMGRYVEFVKATFPKGRTLKGLKIVLDCAHGASYKVAPSVFEELDAEVICYGCEPTGIN
INEHCGALFPQVIQKAVIEHQAHLGIALDGDGDRIIMVDEKGHIVDGDMLISICAGDLKKRSALPHNRVVATI
MTNFGVLKYLEGLGLQVFTSPVGDRHVLHAMLEHEVTLGGEQSGHMIFLDYNTTGDGIVSALQVLRIMIESE
SMLSDLTAPIVKSPQTLINAVREKIPIETIPLIERTLRDVQDALGPSGRILLRYSGTENICRVMVEGHKKHQV
DCLAKALADVIDAELGTGSRE

>core/245/3/Org3_Gene386

MQIAQVFGCGRLNGEVKVSGAKNAATKLLVASLLSDQKCTLRNVPDIGDVSLTVELCKSLGAHVSWDKETE
VLEIYTPEIQCTRVPPTFSNVNRIPIILLGALLGRCPEGVYVPTVGGDAIGERTLNFHFEGLKQLGVQISSDSSG
YYAKAPRGLKGNYIHLPPYPSVGATENLILAAIHAKGRTVIKNVALEAEILDVLFLQKAGADITTDNDRTIDIF
GTGGLGSVDHTILPDKIEAASFGMAAVVSGGRVFVRNAKQELLIPFLKMLRSIGGGFLVSESGIEFFQERPLVG
GVVLETDVHPGFLTDWQQPFVLLSQAQGSIVIHETVHENRLGYLHGLQHMGAECQLFHQCLSTKACRYAI
GNFPHSAVIHGATPLWASHLVIPDLRAGFAYVMAALIAEGGGSIIENTHLLDRGYTNWVGKLRLSLGAKIQIFD
MEQEELTTSPKSLALRDASL

>core/246/3/Org3_Gene622

MLYFIEQLNKLSTSFVFPMILLGGFLTWKLRGLQFHGLKLGFNLMLQNKLDDSSSKANEVSSYEAVAGIL
AGNFGTGNIAGMAVALACGGPGALVWWLAALLGAIVQYAGSYLGSKYRKPEGNTGEFIGGPIACLAFGM
RKKILAGFFALFTIMTAFCAAGNCVQVSCIVPLCAEGTPGKLLVGILLALVIPVLAGGNNRILRFSARVIPFIAG
FYCISCGIILFQHASAILPAIKLICSSAFGIKAGLAGIGGYTLSQVISTGINRAVMATDCGSGMVSIQANTKSKN
PVVDGLVTLVPPVIVMVVCSITMLVLIVSGAYSSGAQGTLMVMSAFKNSLGSLSVIVILAMALFGYTTILTW
FACAEKSLQYMIPGRRANLWLKAIYVLIIPLGGVIDMRMIWALSDTGFSGMVILNCIALIALLKDVLSTNRDV
ALLKERECSVADPVRNLDA

>core/247/3/Org3_Gene628

MFNVNFKFLEGLHQAPRYTSYPTALEWEPDAAPALLAFQRIRENPPQLSLYFHIPFCQSMCLYCGCSVVLN
RREDIVEAYINTLIQEMKL VVETIGFRPQVSRIHFGGGTPSRLSRELFTLLFDHIHKLFDLSHAEEIAIEVDPRSL
RNDMEKADFFQNVGFNRVSLGVQDTQADVQEAVRRRQSHEESLKAYEKFELAFQSINIDLIYGLPKQTKES
FSKTIQDILAMYPDRLALFSFASVPWIKPHQKAMKASDMPSMEEKFAIYSQSRHLLTKAGYQAIGMDHFSLP
HDPLTLAFKNKTLIRNFQGYSLPPEEDLLGLGMTSTSFIRGIYLNQAKTLEEYHNTVLRGTFATVSKILTDD
RIRKWAHKLMTFTINKEEFFNLFGYEFDTYFIESRDRLLISMETTGLIHNSPGSLKVTPLGELFVRVIATAFDH
YFLNKVSKKECFASI

>core/248/3/Org3_Gene431

MTTLRQFFLITELRQKLFYTFALLTACRVGVFIPVPGINGELAVAYFKQLLGSGQNLFQLADIFSGGAFAQMT
VIALGVVPYISASIIVQLFLVFMPALQREMRESSDQGKRRIGRLTRLFTVALAVIQSLLFAKFALRMNLTIPGIV
LPTLLSSKLFVGPWIFYITTVVVMTTGTLLLMWIGEQISDKGIGNGISLIIALGILSSFPSVLGSIVNKNLNGSQD

SSDLGLISILILALVFVFLITLIIIEGVRKIPVQYARRVIGRREVPGGGSYLPLKVNYAGVIPVIFASSLLMFPA
TIGQFIASESSWMKRIAALLAPGSLVYSICYVLLIIFFTYFWTATQFHPEQIASSEMKKNNAFIPGIRQGKPTQHY
LEYTMNRVTLLGALFLAAIAILPSLLGCLLRVDSNVSYFLGGTAMLIVVGVVLDTMKQVDAFLLMRRYDSVL
KTDRTKGRH

>core/250/3/Org3_Gene461

MNVWTKFFQPPKHIKEIEDQEVVKKKYKYWRIRIFYSMFIGYIFYFYFTRKSFTFAMPTLIADLGFDKAQLGIIG
STLYFSYGISKFVSGVMSDQSNPRYFMAIGLMITGLTNIFFGMSSSIVLFALWWGLNGWFQGWGWPPCARLL
THWYAKSERGTWWSVWSTSHNIGGALIPILTGFIIDYSGWRGAMYVPGILCIGMGLVLINRLRDTPQSLGLPPI
EKYKRDPHHAHHEGKSASEGTEEIERELSTREILFTYVLTNQWLWFLAAASFFIYVRMAVNDWSALFLIETK
HYAAVKANFCVSLFEIGGLFGMLVAGWLSDKISKGNRGP MNVLFSLGLLFAILGMWFSRSHNQWWVDGTL
LFVIGFFLYGPQMMIGLAAAELSHKKAAGTASGFTGWFAYFGATFAGYPLGKVTDVWGWKGFFIALLACAS
IALLLFLPTWNATEKNTRSKA

>core/251/3/Org3_Gene806

MKKVLIANRGEIAVRIIRACHDLGLSTVAVYSLADQEALHVLLADEAICIGEPQAAKSYLKISNILAACEITGA
DAVHPGYGFLSENANFASICESCGLTFIGPSSESIAMMGDKIAAKSLAKKIKCPVIPGSEGIIEDESEGLKIAEKI
GFPIVIKAVAGGGGRGIRIVKEKDEFYRAFSAARAEAEAGFNPNVYIEKFIENPRHLEIQVIGDTHGNYVHLG
ERDCTIQRRRQKLIEETPSPILNAEIRVKVGKIAVDLARSAGYFSVGTVEFLLDKDKKFFYFMEMNTRIQVEHTI
TEEVTGIDL VKEQIHVAMGNKLPWKQKNIEFSGHIIQCRINAEDPTNNFSPSPGRLDYYLPPAGPSIRVDGACY
SGYAIPPPYYDSMIAKVIKGNREEAIAIMKRALKEFHIGGVQSTIPFHQFMLDNP KFLESNYDINYIDNLLAQ
GNSFFKEF

>core/252/3/Org3_Gene25

MATKTKTQWTCNQC GATAPKWLGCPCGCHNWNSLVEEYVPQARSGTSSRSSTSAIALSSIELENESRIFIDHA
GWDRILGGGVVRGSLTLLGGDPGIGKSTLLLQTAERLASQKYKVLYVCGEESVTQTSRAKRLNISSPLIYLF
PETNLDNIKQQIATLEPDILIISIQIIFNPTLNSAPGSVAQVREVTYELMQIAKSAQITTFIIGHVTKSGEIAGPRV
LEHLVDTVLYFEGNSHANYRMIRSVKNRFGPTNELLILSMHADGLKEVSNPSGLFLQEKTGPTTGSMIPIIEG
SGALLIELQALVSSSPFANPVRKTAGFDPNRFSLLAVLEKRAQVKLFTMDVFLSITGGLKIIIEPAADLGALLA
VASSLYNRLLPNNSIVIGEVLGGEIRHVAHLERRIKEGKLMGFEGAILPEGQISSLPKEIRENFRLQG VKTIKD
AIRLLL

>core/253/3/Org3_Gene620

MLKILKIKVLVFPLALLMGCNSIGYAGPQGS LQTNSQTKVKIGSEVWIEQKLRQYPELLWLTESGGAPLLTST
PIDMAYSEKLFNKKVPALDIAIRSMIHLHLLIQGSRQSYMQLSQILPSEEGGMTEFKQFQTAHKQLLFFLNPKS
FDNTRLILETAIVLRHVGC SAKAVTTFKPYFTDSCPQS FYAKALHVLRTFPELCPSYARLSPEQQEVLLSLRRL
GNYDSLLNLTEVP SAQLLSAWRTRRSLAILDLYLYCLDTCGDKNCSQEFYINFAPLLSMLQQHATIEEAFSRY
FTYRANRLGFEGTSRTD MTLVRLATLMNLSPEASTLAWSFKNLPSDEAENLVNSFYTVQGEHIPLTFRGLPS
LVAGLSVATHGSTVSPENRLRQLYSTMLSLLVKSLSHREMLNKQLLPQGTVLDFSETTLSSGGLDVFAESIA
VRIHLNGAVSINL

>core/254/3/Org3_Gene805

MRKRHSFDSTSTKKEAVSKAIQKIIKIMETTDPSLNVETPNAEIESILQEIKEIKQKLSKQAEDLGLLEKYCSQE
TLNLENTNASLKL SIGSVIEELASLKQLVEESIEESLGQQDQLIQSVLIEISDKFLSSIGETLSGNLDMNQNVIQ
GLLIKENPEKSEAASVGYYVQTLLEPLSKRIGETHKKVATHDVNISSLQFHMMSVAGGRFRGHIDMNGYRVLG
LGEPKNGEDAVSKDYLERIVSSQLTIDKVEDKPITKPNKGKLLYSQGTSPKLEGPLPLGLLTSGISGFTWKSAS
KSNDGSFPFSALRHKETESD TDCFQITSTTLSGNQAGTYTWSLSLKVLVPSIFQIEKPEVQLSLVYSYEDWLPID
NIFNMSQPRTIPLALLGQTMLAGQKYDILELAAHQTNQTLMISPNC SRFSLQLKQTNQFENSPVDFYIVHAAH
SCHWSGF

>core/255/3/Org3_Gene287

MLTCNECTTWEQFLNYVKTRCSKTAFENWISPIQVLEETQEKIRLEV PNIFVQNYLLDNYKRDLC SFVPLDVH
GEPALEFVVAEHKKPSAPVASQKESNEGISEVFEETKDFELKLNLSYRFDNFIEGPSNQFVKSAAVGIAGKPGR
SYNPLFIHGGVGLGKTHLLHAVGHYVREHHKNLRIHCITTEAFINDLVYHLKSKSVDKMKNFYRSLDLLLVD
DIQFLQNRQNFEEEF CNTFETLINLSKQIVITSDKPPSQLKL SERI IARMEWGLVAHV GIPDLETRVAILQHKAE
QKGLLIPNEMAFYIADHIYGNVRQLEGAINKLTAYCRLFGKSLTETT VRET LKELFRSPTKQKISVETILK SVA
TVFQVKLNDLKGNSRSKDLVLARQIAMYLAKTLITDSLVAIGA AFGKTHSTVLYACKTIEHKLQNDETLKRQ
VNLCKNHIVG

>core/256/3/Org3_Gene675

MILPPYSYSLKIGAAVLFFCSILHTFLTPWLYTLCQSYEHKKLVFPECWKRYARLSELFRILSRVEIVFFLWAVP
LFFWFLYTEGYRISMAYFNSRNYGFAVFIMVILILLESRPVYFAELVLSSIAKLGKTSPKSWWWTLM IAPLL
SCLLKETGAMII GATLLMRHFYVFSPSRRFAYATMGLLFSNISIGGLTSYVSSRALFLIFPALKWEHSFFLSHFA
WKAI VAILISTTIYYFIFRKEFKKFPDIPSDKDPSVEKVPWWIICVNIIFVGSII LSRSTPLFMGALLLFYLG FQKFT
IFYQDPINLSKVCYVGLFYAGLVVFGDLQEWVVLNMQGLSDFGYMTVSYTLSIFLDNALVNYLVHNL SVA
TDCYHYLVVAGCMAAGGLTLVSNIPNIVGYLILRSAPFSSTIHMGWFLFGALGPSIISLG VFWLLKNVPEFLYC
FFR

>core/257/3/Org3_Gene533

MSEPRFVCLSLGSNLGNRFKNLQIARTLLGEQAVLGLRSSVILETEALLPGSPPEWDLPYFNSVLVGETTSL
RELLVTIKQIEKVVGRAEESPPWSPRTIDVDILLYGDES FCCDHTEITIPLSNLLSRPFLIALIASLCPYRRFCTQG
SPYHNFTFGELAHHLPSPPGMIRRSLSPTDMLMGVVNVNTNDSMSDGGMFLDPEKAVAQA EKLFTEGA AVIDF
GAQATNPVKVKQFLSVDQEWERLEPVLRL LKETWSNRKQYPIISLDTFYPEILRAMDIYPIQWINDVSGGSQS
MAEVARDCELSLVMNHSSSLPVDPKNILSFSVPIGEQLLSWGEKQLKMFSDVGLNANQVIFDPGIGFGKGAA
QSLATLYEIAKFKRLGCPILIGHSRKSFLSLFGNHDPKDRDWETVGLSILLQQQGV DYL RVHNVA AHQKALS
VAACEACAPI

>core/258/3/Org3_Gene358

MNRLLSLLSVFDDFFWSYVAFILIIVLGVSFWSKSRFFQFTKFSQFCKLFRYYSQNPQERETKQGVHPLKVFFA
SAGGNIGIGNVVGIVTAACIGGPGALFWVWIAGIFGSIVKYSEVYLG IFRKLDRDGVYQGGPMYFLIKAFKT
PVVSVIVAILLCIYGVEIYQFSVITDSL AHCWNL PKVYPMLGLLFLVFYAIRGGLQRIGKICSIVLPFFM LLYCA

LSLYILVKEFHTLPHLLSTVFSSAFKQGSALGGFAGCTVATTIHQGISRAAYSGDIGIGFDSIIQSESSAKDPSTQ
AQLSIVGIAIDNLICTLSLLMVLASGSWSLGLLENASQVVEHTLASYPFMVKFFLPTFFFVTGYTTIISYFLVGKK
CAKFLYGNTGAKIYTLYGLLILPLFCFLSQNTALLIMSVSGALLLCFNLLGVFILRKEVIFPARAASLTETSLST
E

>core/259/3/Org3_Gene229

MLSCVFSDTIFLSSFLAVTLICMTTALWGTILLISKQPLLSESLSHASYPGLLVGALMAQYVFSLQASIFWIVLF
GCAASVFGYGIIVFLGKVCKLHKDSALCFVLVFFFAIGVILASYVKESSPTLYNRINAYLYGQAATLGFLEAT
LAAIVFCASLFALWWYRQIVVTTFDKDFAVTCGLKTVLYEALSLIFISLVIVSGVRSVGIVLISAMFVAPSLG
ARQLSDRLSTILISAFFGGISGALGSYISVAFTCRAIIGQQAVPVTLPGLVVICAGLLAGLCLLFSPKSGWVI
RFVRRKHFSFSKDQEHLKVFVWHISHNRLLENISVRDFVCSYKQYQYFGPKPFPRWRVQILEWRGYVKKEQDY
YRLTKKGRSEALRLVRAHRLWESYLVNSLDFSKEVHELAEIEHVLTEELDHTLTEILNDPCYDPHRQIIPNK
KKEV

>core/260/3/Org3_Gene817

MINSLSQKLSSIFSFLVSSRRINEENISESIREVRLALLDADVNYHVVKDFISKVKEKILGEEIWKHVSPGQQFIR
CLHEELVAFLSDGREEFTIQKTPSIILLCGLQGAGKTTTAAKLADYVIKNKKAKKVLVVPCLDKRFAAVDQL
KILVAQTKAEFYQSQENKPIDVVVKALAYAKENGHDFVILDTAGRLNIDNELMEELTAIQKVSQANERLFVM
NVAMGQDVLATVQAFDQSLDLTGVLISMTDGDARAGAVFSIKHVLGKPIKFEGCGERIQDLRSFDPQSMAER
ILGMDTINFKEMREYISEEEDAELGKKLVTAFTYEDYYKQMKAFRRMGPLRKLLGMMPGFNNAKPSQ
KEIEDSEQMKRTEAIIISMTPEERKELVELDMSRMKRIASGCGLTLGDVNQFRKQMSQSKKFFKGMSKGK
MEQVRKKMSGGNQWR

>core/261/3/Org3_Gene57

MDALILSRIQFGLFITFHLYFVPLSMGLSMMLVIMEGLYLVTKKQIYKQMTWFWVGIFALTFLVGVVTGIMQI
FSFGSNWANFSEYTGNI FGTLGSEGVF AFFLESGFLGILLFGRHKVSKKMHFFSTCMVALGAHMSAFWIICA
NSWMQTPSGYEMVMHKGKLI PALTSFWGVVFSPTTIDRFIHAVLGTWLSGVFLVISVSAYYLWKKRHHEFA
KQGMKIGTICAVIVLVQLWSADVTARGVAKNQPAKLAAFEGIFKTEEYTPIWAFGYVDMEKERVIGLPIPG
ALSFLVHRNIKTPVTGLDQIPRDEWPNVQAVFQLYHLMIMLWGVMVALTLISWSAYKGWRWALKPFFLVIL
TFSVLLPEICNECGWCAAEMGRQPWVVQGLLTKKDAVSPIVQANQIVQSLVIFSLVFIALLTLFITVLCKKIKH
GPEEENDLTEFEVK

>core/262/3/Org3_Gene848

MRAMLLEDWVSLMLSDVSCPKCDKKITGFAIDSQKVQPGDLFFALPGNATDGHQFLKHAATAGAVAAVVS
HDYQGDSFGLELIRVDDTKSALQEAGSNQCNLFQGTLVGITGSVGKTTTKEFSKITLSSYKTHASPKSYNSQL
TVPLSLLMAEGDEDVMILEMGVSEPGNMQDLLRIVQPEIAVITHINDQHAMHFPQGIQEILKEKSYILQKSKL
QLLPKDSPPYYDLRSCSPTAEKFSFSFNDPLADFCYKAISGDSVVIQTPEENYCLPIAFSYKPAYTNLLIAVALS
WILEVPEEGVIRSLPELKLPPMRFEHSMRNGMQVINDAYNACPEAMIAALDALPLPSDGGKIILILGHMAELG
RYSEEGHALVAEKAASRGDMIFFIGEKWIPVQSVLKSYSCEVSFFSSAQDVKDILKQVARYGDVILLKGSRAL
ALESLLACF

>core/263/3/Org3_Gene234

MSNITSPVIQNNRSCNYYFELKNSTTIHIVISAILLCGALIAFLCVAAPVSYILSGALLGLGLLIALIGVILGIKKIT
PMISSKEQVFPQELVNRIRAHYPKFVSDVFSEAKPNLKDLSIFIDLLNQLHSEVGSSTNYNVSEELQQKIDTFEG
IARLKNEVRTASLKRLESAASSRPLFPSLPKILQKVFPFFWLGEFISAGSKVVELHRVKKIGGSLEEDLSDYIKP
EMLPTYWLIPLDFRPTNSSILNLHTLVLARVLTRDVFQHLKYAALNGEWNLNHSDLNTMKQQQLFAKYHAAY
QSYKHLSQLQEQDEFYNLLLCIFKHRYSWKQMSLIKTVPADLWENLCCLTLDHTGRPQDMEFASLIGTLYT
QGLIHKESEAFSSLTLLSLDQFKTIRRQSTNIAMFLENLATHNSTFRSLPPITVHPLKRSVFSQPEEDESSLIG

>core/264/3/Org3_Gene872

MVITNLSINADTIYGKNPINIVASAANKNITLTGTLALVNADGAFYENHTLQDSQDYSFVKLSPGAGGTIITQD
ASQKPLEVAPSRPHYGYQGHWNVQVIPGTGTQPSQANLEWVRTGYLPNPERQGSLVPNSLWGSFVDQRAIQ
EIMVNSSQILCQERGVWGAGIANFLHRDKINEHGYRHSGVGYLVGVGTHAFSDATINAAFCQLFSRDKDYY
VSKNHGTSYSGVVFLEDTFEFRSPQGFYTDSSSEACCNQVVTIDMQLSYSHRNNDMKTKYTTYPEAQGSWA
NDVFGLEFGATTYYYPNSTFLFDYYSPFLRLQCTYAHQEDFKETGGEVRHFTSGDLFNLAVPIGVKFERFSDC
KRGSYELTFAYVPDVIRKDPKSTATLASGATWSTHGNNLSRQGLQLRLGNHCLINPGIEVFSGHAIELRGSSR
NYNINLGGKYRF

>core/265/3/Org3_Gene731

MLTYKVSPSSVYGNAPFSSKSHTLRAILWASVAEGKSIINYLDSPDTEAMICACKQMGASIKKFPQILEIVG
NPLAIFPKYTLIDAGNSGIVLRFMTALACVFSKEITVTGSSQLQRRPMAPLLQALRNFGASFHFSSDKSVLPFT
MSGPLRSAYSDEGSDSQFASALAVACSLAEGPCSFTIIEPKERPWFDSLWWLEKLHLPYSCSDTTYSFPGSS
HPQGFSYHVTGDFSSAAFIAAAALLSKSLQPIRLRLNDILDIQGDKIFFSLMQNLGASIQYDNEEILVFPSSFSGG
SIDMDGCIDALPILTVLCCFADSPSHLYNARSADKESDRILAITEELQKMGACIQPTHDGLLVNPSPLYGAVL
DSHDDHRIAMALTIAALYASGDSRIHNTACVRKTFPNFVQTLNIMEARIEECHDNYSMWSTHKKRVFARESF
G

>core/266/3/Org3_Gene570

MTSGVSGSSSQDPTLAAQLAQSSQKAGNAQSGHDTKNVTKQGAQAEVAAGGFEDLIQDASAQSTGKKEATS
STTKSSKGEKSEKSGKSKSSTSVASASETATAQAVQGPGLRQNNYDSPSLPTPEAQTINGIVLKKGMGTAL
LGLVMTLMANAAGESWKASFQSQNQAIRSQVESAPAIGEAIKRQANHQASATEAQAKQSLISGIVNIVGFTV
SVGAGIFSAAKGATSALKSASFAGETGASAAGGAASKALTSASSSVQQTMASTAKAATTAASSAGSAATKA
AANLTDDMAAAASKMASDGASKASGGLFGEVLNKNPWSEKVS RGMNVVKTQGARVASFAGNALSSSMQ
MSQLMHGLTAAVEGLSAGQTGIEVAHHQRLAGQAEQAQAEVLKQMSSVYGQQAGQAGQLQEQAMQSFNTA
LQTLQNIADSQTQTTS AIFN

>core/267/3/Org3_Gene873

MTLQPYQASSRKYRPQIFREILGQSSVAVLKNALVFNRAAHAYLFSGIRGTGKTTLARILAKALNCVHLS
GEPCNQCFSCKEIASGSSLDVLEIDGASHRGIEDIRQINETVLFTPVKAKFKIYIIDEVHMLTKEAFNALLKTLE
EPPQHVKFFFATTEIHRIPGTILSRCQKMHLQRIPEKTILEKLSLMAQDDHIEASQEALAPIARAAQGSLRDAES
LYDYYISLFPKSLSPDTVAQALGFASQDSLRTLDNAILQRDYATALGIVTDFLNSGVAPVTFLHDLTLFYRNLL

LTNSTTSKFSSQYKTEQLLEIIDFLGESAKHLQNTIFEQTFLETVIIIIRIYQRPVLSELISSIKSRQFEGLRNIKEP
TLTQQVSAPQPQPTYKEQSFLEKKNQPAAEGKIISVEVKSSASIKSAAVDTLLQFAVVEFSGILRQ

>core/268/3/Org3_Gene592

MLKHDTIAAIATPPGEGSIAVVRLSGPQAIVIADRIFSGSVASFASHTIHLGQVIFEETLIDQALLLLMRSRPSFT
GEDVVEFQCHGGFFACSQLDALIALGARPALPGEFSQRAFLNGKIDLVQAEAIQNLIVAENIDAFRIAQTHFQ
GNFSKKIQEIHTLIIEALAFLEVLADFPPEEQPDLLVPQEKIQNALHIVEDFISSFDEGQRLAQGTSLILAGKPNV
GKSSLLNALLQKNRAIVTHIPGTTRDILEEQWLLQGKRIRLLDTAGQRTTDNDIEKEGIERALSAMEEADGIL
WVIDATQPLEDLPKILFTKPSFLLWNKADLTPPPFLDTSLPQFAISAKTGEGLTQVKQALIQWMQKQEAGKTS
KVFLVSSRHHMILQEVARCLKEAQQNLYLQPPEIIALELREALHSIGMLSGKEVTESILGEIFSKFCIGK

>core/269/3/Org3_Gene600

MPRSLSNEQFSVDLEESPGCIVSALVKVSPEVLNKLNKQALKKKIKEITLPGFRKGKAPDDVIASRYPTNVRK
ELGELVTQDAYHALSTVGDRRPLSPKAVRSNSITQFDLQEGAKVEFSYEAFPAISDLPWENLSLPQEEAASEIS
DSDIEKGLTNIGMFFATKTPVERPSQEGDFISISLHVSKSNDENASSAAIFENKYFKLSEEEMTDAFKEKFLGIS
TGHRVVETITSPEIQSFLRGDTLTFTVNAVIEVSIPEIDDEKARQLQAESLDDLKAKLRIQLEKQAKDKQLQKR
FSEAEDALAMLVDFELPTSLLEERISLITREKLLNARLIQYCSDEELEKRKSELIKEAEEDATKALKLLFLTHKI
FSDEKLTISREELQYMMDVCSRERFGQQPPKDISNDTLQELVMSARDRLTYSKAIEHVLRKAELLASTPSA

>core/270/3/Org3_Gene496

MDQLTTDFDTLMSQLGDVNLTTVVGRITEVVGMLIKAVVPNVRVGEVCLVKRNGMEPLVTEVVGFTQSFAF
LSPLGELSGVSPSSEVIPTGLPLHIRAGNGLLGRVLNGLGEPIDVETKGPLQNVDDQTFPIFRAPPDPLHRAKL RQ
ILSTGVRCIDGMLTVARGQRIGIFAGAGVGKSSLLGMIARNAEEADVNVIALIGERGREFIEGDLGEEGM
KRSVIVVSTSDQSSQLRLNAAYVGTAIAEYFRDQGKT VVLMMDSVTRFARALREVGLAAGEPPARAGYTPS
VFSTLPRLLERSGASDKGTITAFYTVLVAGDDMNEPVADEVKSILDGHIVLSNALAQAYHYPAIDVLASISRL
LTAIVPEEQRRRIIGKAREVLAKYKANEMLIRIGEYRRGSDREIDFAIDHIDKLN RFLKQDIHEKTNYEEAAQQL
RAIFR

>core/271/3/Org3_Gene594

MWLVLWALAASLAIALVAKGYRFRVYFRRYAVQVIREVRLSMELKEWALAEQQLLPILKKRSYRRQCLFE
YMRILRKMQRFESEKLLAEAKKLGLRGPYFFLEIAYKAYRFGAFKECAQAFASVPQDLFEEEDA AKYASAL
VRLGDLDAACSLIEPWISPLSHQETFVTMGHIYFTSKRYKDAIDFYNRANALGVC PVEVTYNLAQAYRITSSY
AKAGKLFRKLLSNPVYKEEALFNIGLCEQKLGRPGKALLIYQSSDLWSRGDALLMKYAAMAAMDQRDYVL
AEP CWELALRCSTFAKDYKCGLGYGFSLCRLRKYGDAERVYCNLIQNFPECLTACKALAWLCGVGYATLLG
SEGLMYAKKAVELDHSCETLELLSACEARCGNFDAAYEIQSFLSSRDTSLQEKQRRSQILRILRKKLPLNDH
HIVEVDALLAA

>core/272/3/Org3_Gene413

MIENDFPEASNFESSHFYRDKVGVILCGGEGKRLSPLTNCRCCKPTVSFGGRYKLIDIPISHAISAGFSKIFVIGQ
YLYTYTLQQHLFKTYFYHGV LQDQIHLLAPEARQGDQIWYQGTADAIKNNLLYFEDTEIEYFLILSGDQLYNM
DFRSIVDTAIRTHVDMVLVAQPIPEKDAYRMGVLDIDSEGKLIDFYEKPQEKEVLKRFQLSSDDRRIHKL TEDS

GDFLGSMGIYLFRRDSLFSLLREEEGNDFGKHLIQAQMKRGQVQTLLYNGYWADIGTIESYYEANIALTQKP
HAEKRGLNCYDDNGMIYSKNHHLPGAIITDSMISSLLCEGCVINTSHVSRSVLGIRSKIGENSVVDQSIIMGN
ARYGSPSPSLGIGKDCEIRKAIIDENCCIGNGVKLQNLKGYIKYDSPDKKLFVRDNIIVPQGTHIPDNYIF

>core/273/3/Org3_Gene812

MLNCSNQKHTVTFEEACQVFPGGVNSPVRACRSVGVTPPIVSSAQGDIFLDTHGREFIDFCGGWGALIHGHSH
PKIVKAIQKTALKGTSYGLTSEEEILFATMLLSSLKLKEHKIRFVSSGTEATMTAVRLARGITNRSIIKFIGGYH
GHADTLLGGISTTEETIDNLTSLIHTSPHSLISLPYNNNSQILHHVMEALGPQVAGIIFEPICANMGIVLPKAEF
LDDIIELCKRFGSLSIMDEVVTGFRVAFQGAKDIFNLSPDITIYGKILGGGLPAAALVGHRSLDHLMPGTFIQ
AGTMSGNFLAMATGHAAIQLCQSEGFYDHLSQLALFYSPIEEEIRSQGFPVSLVHQGTMFSLFFTESAPTDF
EAKNSDVEKFQTFYSEVFDNGVYLSPSPLEANFISSAHTENLTYAQNIIDSLIKIFDSSAQRFF

>core/274/3/Org3_Gene544

MFQQKQKLSLKYLPRLMQQGLQMLQSPLTELSSYVVQEIIDNPFFDLSSLEEEEWSPCYRPTNSTFSYLNQTP
GPQESLYTRLLPQIEEAFSTAEERFIAHQIAGNLSDEGLFLRNPEDFAQELELPLEKIHKVVWDTIQNLSPEGIASP
SLQSYWMKLLRNSSHQQAYSIVRDCYPLMTNCEFAPIMKKFSLSLSELRNILKKALGSIPWCPAAACTVKPM
VSTPLPDIYLFYSSGSWKIEVSTRGLPSIKLNKETFFHYEHLPKKEEQKNLSQQILSAKWLIKNLKREQTLLQV
METLLPKQEDFLLGKIPAPYPLGIKDLAEDLSFHSTIFRAIENKAVAAPIGIFPLKHLFPRGIHQDSSHSKENVL
QWIRQWIAEQTPLSDSVISDRITAKGIPCARRTVAKYRAQLKILPANKRKKLFYIRSSNSHFRDRQF

>core/275/3/Org3_Gene739

MSKIVYKFGGTSLATAENICLVCDIICKDKPSFVVVSAIAGVTDLLVDFCSSSLREREEVLRKIEGKHHEIVKNL
AIPFPVSTWTSRLLPYLQHLEISDLDFARILSLGEDISASLVRAVCSTRGWDLGFLEARSVILTDDSYRRASP
DLMKAHWHQLELNQPSYIIQGFISNGLGETVLLGRGGSDYSATLIAELARATEVRIYTDVNGIYTMDPKVIS
DAQRIPELSFEEMQNLA SFGAKVLYPPMLFPCMRAGIPIFVTSTFDPEKGGTWVYAVDKSVSYEPRIKALSLS
QYQSFCSDYTVLGCGLLEEILGILESHGIDPELMIAQNNVVGFMDDDIISQEAQEHLDVLSLSSVTRLHHS
VALITMIGDNLSSPKVSTITEKLRGFQGPVFCFCQSSMALSFVASELAEGHIEELHNDYVKQKAIIVAT

>core/276/3/Org3_Gene49

MQTIYTKITDIKGNLITVEAEGARLGELATITRSDGRSSYASVLRFDLKKVTLQVFGGTSGLSTGDHVTFLGRP
MEVTFGSSLLGRRLNGIGKPIDNEGECFGEPIEIAPTFPNVCRIVPRSMVRTNIPMIDVFNCVLKSQKIPIFSSSG
EHHNALLMRIAQAQTDADIVVIGGMGLTFVDYSFFVEESKKLGFADKCVMFHKAVDAPVECVLVPDMALAC
AEKFAVEEKKNVLVLLTDMTAFADALKEISITMDQIPANRGYPGSLYSDLALRYEKA VEIADGGSITLITVTT
MPSDDITHPVPDNTGYITEGQFYLRNNRIDPFGSLSRLKQLVIGKVTRREDHGDLANALIRLYADSRKATERMA
MGFKLSNWDKKLLAFSELFETRLLMSLEVNIPLLEALDIGWKILAQSFTSEEVGIIKAQLINKYWPKAACLSK

>core/277/3/Org3_Gene727

MISFRLLLLSGLCALGISSYAETPKETTGHYHRYKARIQKKHPESIKESAPSETPHHNSLLSPVTNIFCSHPWKD
GISVSNLLTSVEKATNTQISLDFSILPQWFYPHKALGQTQALEIPSWQFYFSPSTTWTLYDSPTAGQGIVDFS
LIHYWQTNGVDANQAAGTASSMNDYSNRENNLAQLTFSQTFPGDFLTLAIGQYSLYAIDGTLYDNDQYSGFI
SYALSQNASATYSLGSTGAYLQFTPNSEIKVQLGFQDSYNIDGTNFSIYNLTKSKYNYFYGYASWTPKPCSGDG

QYSVLLYSTRKVPEQNSQVTGWSLNAAQHIHEKLYLFGRINGATGTALPINRSYVLGLVSENPLNRHSQDLL
GIGFATNKVNKAISNVNKLRRYESVMEAFATIGFGPYISLTPDFQLYIHPALRPERRTSQVYGLRANLSL

>core/278/3/Org3_Gene809

MMLRGVHRIFKCFYDVVLVCAFVIALPKLLYKMLVYGKYKKS LAVRFGLKKPHVPGEGLPVWFHGASVGE
VRLLLPVLEKFCEEFPGWRC LVTSC TELGVQVASQVFIPMGATVSILPLDFSIIKS VVAKLRPSLAVFSEGDC
WLN FIEEAKRIGATT LVINGRISIDSSKRFKFLKRLGKNYFSPVDGFL LQDEVQKQRFLSLGIPEHKLQVTGNIK
TYVAAQTALHLERETWRDRLRLPTDSKL VILGSMHRSDAGK WLPVVQKLIKEGSVSVLWVPRHVEKTKDVE
ESLHRLHIPYGLWSRGANFSYVPVVVVDEIGLLKQLYVAGDLAFVGGTFDPKIGGHN LLEPLQCEVPLIFGPH
ITSQSELAQRLLLSGAGLCLDEIEPIIDTVSFL LNNQEVREAYVQKGKVFVKAETASFDRTWRALKSYIPLYKN
S

>core/279/3/Org3_Gene468

MKRPFPTYLCIIFYGSCASLSLHAGLSFPEVRGATAAVVHADSGKV FYDKDIDAVIYPASMTKIAT ALFILKHY
PTVLDTLIKVKQDAIASITPQAKKQSGYRSPPHWLETDGSTIQLHLREELLGWDLFHALLVCSANDAA NVLA
MACCGSVEKFMDKLNFFLKEEIGCTHTHFNNPHGLHHPNHYYTTTRDLISIMRCALKEPPFRGVISTTSYKIGAT
NLHGERILSPTNKLLLPGSTYHYPPALGGKTGTTKTAGKNLIMAAEKNRLLVTIATGYSGPVSDLYQDVIAL
CETVFNEPLL RKELVPPSDCLQLEIANLGKLS CPLPEGLYYDFYASEDREPLSVSFIAHADAFPIEQGDLLGHW
VFYDDEGKKISSQPFYAPCRFERTIKPWKLYMKRVFTSYRTYMSITMLLMYFRIRKHRKYKNLKHYSKI

>core/280/3/Org3_Gene850

MKRAIIIGAGISGLAAGWWLHKKFPQAEILVLDKEAYAGGFVRTE SPQGFSFDLGPKGFLTRGDGEYTLKLIH
ELGLQNSLIFSDRAAKNRFVYYRGKARKISTWTLRLKGLLPSLIKDFRAPCYTQDSSVQDFLKRHSSQNFTSYI
LDPLITAIRAGHSSILSTHMAFPELAKREASSGSLLRSYLKNRSPKSKTDRYLASLSPSMGTLITTIQEKL PAT
WKFSTSVTHIDCSPKEACVTTTPSETFFADMVIYTGPLQQLPVLLPNYGIENLSKRVL PWNLSSISLGWHHANFS
LPKGYGMLFADELPLL GIVWNSQIFPQATPGKTVLSLLIEGKWRESEAHAF AIAALSEYLNINQKPD AFALFSS
QDGMPQH AVGFLERKERILPHLPGNLKIVGQNIAGPGLNRCIASAYHAICDLHTEETLAQPQSSL

>core/281/3/Org3_Gene121

MFSRWITLFLLFISLTGCSSYSSKHKQSLIPIHDDPVAFSPEQAKRAMDLSIAQL LFDGLTRETHRESNDLELAI
ASRYTVSEDFCSYTFFIKDSALWSDGTPITSEDIRNAWEYAQENSPHIQIFQGLNFSTPSSNAITIHLDSPNPDPF
KLLAFPAFAIFKPENPKLFSGPYTLVEYFPGHNIHLKKNPNYYDYHCVSINSIKLLIIPDIYTAIHL LN RGKVDW
VGQPWHQGIPWELHKQSQYHYTYTPVEGAFWLCLNTKSPHLNDLQNRHRLATCIDKRSIIEEALQGTQQPAE
TL SRGAPQPNQYKKQKPLTPQEKLVL TYPSDILRCQRIAEILKEQWKAAGIDLILEGLE YHLFVNKRKVQDYA
IATQTGVAYYPGANLISEEDKLLQNF EIPIYYLSYDYLTQDFIEGVIYNASGAVDLKYTYFP

>core/282/3/Org3_Gene209

MNKNLVAIFDYMEKEKGIQRSTIIGAIESALKIAAKKTLRDDANISVNINSRTGDIEVFCEKEIVEICQNPSKEIP
LDKAREYDPDCQIGQYMDVPFVSDNFGRIA AHAARQIIGQKL RHAERDVIYEEYRHRVNETLSGVVKRFAKG
SNLIIDL GKVEAILPTRFY PKTEKHKIGDKIYALLYEVQESENGGAEVILSRSHA EFVKQLFIQEVPELEEGSVEI
VKIAREAGYRTKLAVRSSDPKTD PVGAFVGMGRSRVKNIIRELNDEKIDIVNYS PVSTELLQNLLYPIEIQKIAI

LEDDKVIAIVVNDADYATVIGKRGINARLISHILDYELEVQRMSEYNKLLLEIQRLQLAEFDSPHLDQPLEMEGI
SKLVIQNLEHAGYDTIRRVLLASANDLASVPGISLELAYKILEQVSKYGESKVVDEKPEIED

>core/283/3/Org3_Gene904

MSMTIVPHALFKNHCECHSTFPLSSRTIVRIASLFCIGALAALGCLAPPVSYIVGSLAFIAFVILSLVILALIF
GEKKLPPTPRIIPDRFTHVIDEAYGLSISAFVREQQVTLAEFRQFSTALLCNISPEEKIKQLPSELRSKVESFGISR
LAGDLEKNNWPIFEDLLSQTCPYWLQTFISAGDPQVCRDLGVPRECYGYWLGPLGYSTAKATIFCKETHH
ILQQLTKEDVLLLNKALQEKWDTDEVKAIVERIYTTYTARGTLKTEAGGLTKETISKELLLSLHGYSFDQL
QLITQLPRDAWDWLCFVDNSTAYNLQLCALVGALSSQNLLDESSIDFDVNLGLYVIQDLKEAVQAFSASDEP
KKELGKFLLRHLSSVSKRLESVLRQGLHRIALEHGNARARVYDVNFVTGARIHRKTSIFFKD

>core/284/3/Org3_Gene957

MNHLNKEKLHIHNWQPYRACGLLSKVSGNLIQVDGLSACLGECKISSTKDPNLLAEVIGFHNHTTLLMSLSP
LHSVALGTEVLPLRRPPSLHLSHDLLGRVLDAFGNPIDKKEDLPKTHRKPLLSLPPSPMMRQPIDQIFPTGIKAI
DAFLT LGKGQRIGVFSEPGSGKSSLLSAIALGSKSTINVIALIGERRREVREHIEKHSNALKQQRTHIAAPAHET
APTKVIAGRAAMTIAEYFREQGHEVLFIMDSLRSWIAALQEVALARGETLSAHQYAASVFHHVSEFTERAGN
NDKGSITALYAILYYPKHPDIFTDYLSLLDGHFFLTSQGKALASPPIDILSSLSRSAQALALPHHYAAAERLRS
LLKVYNEALDIIHLGAYTPGQDEELDKAVKLLPSIKAFLAQLSSYCYLDNTLTKQLEALADS

>core/285/3/Org3_Gene712

MLKPMYVLSKRLYRWVNQLIKLGDLVKNSRFSFVWVFISALLLIFGCLGCASVVKVSLVPFLLLSFLAFPLI
LCFRGKGYALLLGVFVTLYVAKYVVGETLYVSFWLSGLGVSFLLAFGLFLQGVWLAQEEEMVKGKEQLRL
SEDLDAQRSAYEDLLLTQSKEKEFLDARAQGLDRELTECQELLKAAYQKQEYLTIDLKILADQKNSWLEDY
AELHNKYIELVSKNGDVVFPWVAEPSVGESQGSERVDVSRWVSALQEKEESLERLRNEILVEKQRCSDYEHR
CQELGLLLQNFTALERRCEELQNLLNQKETQINELHQLVCKSEEKVSVEPSAHAETSCVEEKQYKGLYSQLQ
EQFLEKSETLSLVRKKLFAVQEKYLTLLKKKEELTKQDISFDDISMIQGLLERIEILEEEVSHLEELVSRSLSL

>core/286/3/Org3_Gene552

MLRQLCFQVFFFCFASLVYAEELVVVRSEHITLPIEVSCQTDTKDPKIQKYLSSLTEIFCKDIALGDCLQPTAA
SKESSSPLAISRLHVPQLSVVLLQSSKTPQTLCSTISQNLSDVRQKIHHAADTVHYALTGIPGISAGKIVFALS
SLGKDQKLKQGELWTTDYDGKNLAPLTTECSLSITPKWVGVS NF PYLYVSYKYGVPKIFLGSLENTEGKKV
LPLKGNQLMPTFSRKKLLAFVADTYGNPDLFIQPFSLTSGPMGRPRRLNENFGTQGNPSFNPEGSQLVFISN
KDGRPRLYIMSLDPEPQAPRLTCKYRNSSCPAWS PDGKKIAFCSVIKGVRQICIYDLSSGEDYQLTTSPTNKE
SPSWAIDSRHLVFSAGNAEESELYLISLVTKKTNKIAIGVGEKRFPSWGAFPPQPIKRTL

>core/287/3/Org3_Gene959

MTWPSGLYFICIASLIFCAIGVILAGVILLSRKLFIKVHPCKLKINDNEELTKTVESGQTLLVSLSSGIPIPCG
GKATCKQCKVRVVKNADEPLETDRSTFSKRQLEEGWRLSCQCKVQHDMSEIEERYLNASSWEGTVISNDN
VATFIKELVVAVDPNKPIPFKPGGYLQITVPSYKTNSSDWKQTMapeyySDWEHFHFLFDQVIDNSQLPADSA
NKAYSLASYPaelptikfniriATPPFINGKPNSEIPWGVCSYVFSLKPGDKITVSGPYGESFMKDDDRPLIFLI

GGAGSSFGRRSHILDLLLNKHSKREIDLWYGARSLKENIYQEEYENLERQFPNFHYHLVLSEPLPEDIAAGWDK
DDPTKTNFLFRAFNLGQLSRLDNPEDYLYYVCGPPLHNSSILKLLGDYGVERSIILDDFGS

>core/288/3/Org3_Gene932

MTVTLPKGVFDIFPYLADAKQLWRHTSLWHSVEKAIHTVCMLYGFCEIRTPIFEKSEVFLHVGEESDVVKKE
VYSVLDRKGRSMTLRPERTAAVVSFAFLEHGASHRSDIKFYIILPMFRYERQQAGRYRQHHQFGVEAIGVRHP
LRDAEVLALLWDFYSRVGLQHMQIQLNFLGGSETRFRYDKVLRAYLKESMGELSALSQQRFSTNVLRILDSK
EPEDQEIRQAPPILDYVSDDELKYFNEILDALRVLEIPYAINPRLVRGLDYSDLVFEATTTTFQEVSYALGGGG
RYDGLISAFGGASLPACGFGVGLERAIQTLLAQKRIEPQFPHKLRLIPMEPDADQFCLEWSQHLLRRLGIPTDVD
WSHKKVKGALKAASTEQVSFVCLIGERELISQQLVIKNMSLRKEFFGTKEEVEQRLLYEIQNTPL

>core/289/3/Org3_Gene889

MFRKLFPPFSKKKTGQKQRLRNNGLLQAIQSIKVLLHNEASKEACVLSYYGLLTCVPILVFFLRLSQHLFTNLN
WKEWLIKFPDYKKPIVAIVEAAYHATESNIGLVLVGSFYVFCWAGILMLLSLEDGLNKIFRDSWTPISLKRLV
SYFVITLVSPMIFIIVCGSWIYITQIMPIQYAKLFSLSHSMTALYFISRFVPYLLLYLALFCCYAFLPRVAIQKTS
LISTLIIGSVWVIFQKAFFSLQVSIFNYSFTYGALVALPSFLLLLYIYTMILYFGGALTFIIQNRGCTFIFLGDKILP
SCYLQLITSTYILALTTRQFNEGLSPLTAQFIAKQSKVPIGEVSQCLDVLEKEGFLFPYNNGYQPVFNFSELITK
DIADKLLHREIFKKFNPDLGITFIENSFQNFQASKNKENLTLSEIARRIK

>core/290/3/Org3_Gene839

MVCENNILSGRGLELLKKKSNITLTPTIYSVSNHNIKLDKDFSPHALSVIKTLRKAGYIAYIVGGCIRDLLLNTTP
KDFDISTSAKPEEIKAIKNCILVGKRFRLAHIRFSKQIIEVSTFRSGSTDEDVLITKDNLWGTPEEDVLRRDFTI
NGLFYDPEHEEHIDYTGGVNDLNRNRYLRTIGDPFTRFKQDPVRMLRLLKILSRSPFTVETQTQEALIAQRQELIK
SSRARVFEELIKMLNSGAANKNFFQLLIENHLLLEILFPYMDKALRLNRALEEQTATYALKALDDKILKKEAEYDR
HQLMAIFLPLVNFNVRYPKHQKHPYLSLTSVFDYIKNFLEQFFADSFTSCSKNFILTALILQMQRRLTPLIPTK
KALFFNKLLHHTRFLEALSLEIRSIVYPKLDKVYVAWIRHHQTLKCKKDSHSQK

>core/291/3/Org3_Gene202

MISLLKMPKLSPTMEVGTIVKWHKKSNDQVSFGDVIVEISTDKAILEHTANEDGWIREILRHEGEKIVIGTPIA
VLSTEANEPFNLEELLPKTEPSNLEASPKGSSEEVSPATTPQAASATFTAVTFKPEPPLSSPLVFKHVGTNNLS
PLARQLAKEKNIDVSSIQSGPGGRIVKKDLEKAPPKSIAGFGYPESPEVPPGSYHEENLSPIREVIAARLQAAK
ISIPHFYVRQQVYASPLLNLLKELQAQGIKLSINDCIVRACALALKEFPSINSGFNSVDNKIVRFDTIDISIAVAIP
DGIITPIIRCADRKNLGMISAEIKSLALKARNQSLQDTEYKGGSFVSNLGMTGITEFTAIVNPPQAAILAVGSV
TEQALVLDGEITIGSTCNLTLSVDHRVIDGYPAAMFMKRLQKILEAPAVLLN

>core/293/3/Org3_Gene859

MFEAVIADIQAREILDSRGYPTLHVKVTTSTGSGVEARVPSGASTGKKEALEFRDSTDSPRYQGKGVLQAVKN
VKEILFPLVKGCSVYEQSLIDSLMMDSDGSPNKETLGANAILGVSLATAHAAAATLRRPLYRYLGGCFACSLP
CPMMNLINGMHADNGLGFQEFMIRPIGASSIKEAVNMGADVFTLTKLLHERGLSTGVGDEGGFAPNLAS
NEEALELLLLAIEKAGFTPCKDISLALDCAASSFYNVKTGTYDGRHYEEQIAILSNLCDRYPIDSIDGLAEED

YDGWALLTEVLGEKVQIVGDDLFVTNPILILEGISNGLANSVLIKPNQIGTLTETVYAIKLAQMAGYTTIISHR
SGETTDTTIADLAVAFNAGQIKTGSLRSERVAKYNRLMEIEEELGSEAIFTDSNVFSYEDSEE

>core/294/3/Org3_Gene949

MDIKKLFCLFLCSSLIAMSPIYGKTGDYEKLTLTGINIIDRNGLSETICSKEKLKKYTKVDFLAPQPYQKVMRM
YKNKRGDNVSCLTAYHTNGQIKQYLECLNNRAYGRYREWHVNGNIKIQAIEVIGGIADLHPSAESGWLFDDQT
TFAYNDEGILEAAIVYEKGLLEGSSVYYHTNGNIWKECPYHKGVPPQGGKFLTYTSSGKLLKEQNYQQGKRHG
LSIRYSEDSEEDVLAWEEYHEGRLLKAEYLDPQTHEIYATIHEGNIGIQAIFYGKYAVIETRAFYRGEPYGVTR
FDNSGTQIVQTYNLLQGAKHGEEFFYPETGKPKLLLNWHEGILNGIVKTWYPGGTLESCKELVNNKKSGLL
TIYYPEGQIMANEEYDNDLLIKGEYFRPGDRHPYSKIDRGCCTAVFFSSAGTITKKIPYQDGKPLLN

>core/295/3/Org3_Gene60

MKKTMMVIDTSVFIYDPEALFSFENTRIIPFPVIEELEAFGKFRDESAKNASRALSNIRLLLLENAKTKVTDGVLLP
SGSELRIEVAPLSNDDRRGKLLTLELLKIIAKREPMVFVTKSLGRRVRAEALQIESRDYESKRFSFRSLYRGFRE
LQVSQEDIENFYKNGYLDLPLDVSSPNEYFFMSAGENHFALGRYYVSEGKIIALKAMDKSVWGIKPLNTEQ
RCALDLLLRDDVKLVTLIGQAGSGKTILALAAAMHKVFDKETYNKVLVSRPIVPMGRDIGFLPGLKEDKLM
HWMQPIYDNMEVLFSINQMGNSSSEALQALMDAKKLEMEALTYIRGRSLPKAFIIDEAQNLTPHEIKTIISRAG
KGTKIVLTGDPTQIDSLYFDENSNGLTYLVGKFHHLALYGHMFMTRTERSELAAAAATIL

>core/296/3/Org3_Gene616

MLDIKIIRKTPEECETRLRKKDPKISLEPVLSLDKEVRQLKTDSETLQAQRRLLSQDIHKAKTQGV DATNLIQE
VETLAADLEKIEQHLDQKNAQLHELLSHLPNYPADDIPVSEDKAGNQVIKSVGDLPIFSFPPKHHLELNQELDI
LDFQAAAKTTGSGWPAYKNRGVLEWALLTYMLQKQAAHGFQLWLPPLLVKKEILFGSGQIPKFDGQYYR
VEDGEQYLYLIPTAEVVLNGFRSQDILTEKELPLYAACTPCFRREAGAAGAQERGLVRVHQFHKVEMFAFT
TPNQDDIAYEKMLSIVEEMLTELKLPYRLSLLSTGDMSFTASKTIDAEVWLPGQKAFYEVSSISQCTDFQSRRS
GTRYKDSQGKLQFVHTLNGSGLATPRLLVAILENNQQADGSVVIPEVLRPYLGGLEILLPKDQ

>core/297/3/Org3_Gene933

MLPLIIFVLLCGFYTSWNIGANDVANAVGPSVSGSVLTLRQAVVIAAIFEFFGALLLGDRVAGTIESSIVSVTN
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GGCVAYLIFSFIIRRHIFYKNDPVLAMVRVAPFLAALVIMTLGTVMISGGVILKVSSTPWAVSGVLVCGLLSYII
TFYYVHTKHCSYISDTPKKGSLTYRLKERGGNYGRKYLVERIFAYLQIIVACFMAFAHGSNDVANAIAPVA
GVLRQAYPASYSYTLIRLMAFGGIGSVIGLAIWGW RVIETVGCKITELTPSRGFSVGMGSALTIALASILGLPI
STTHVVVGAVLGIGLARGIRAINLNIIKDIVLSWFITLPAGALLSILFFFALRALFH

>core/298/3/Org3_Gene1017

MIMGLQSRLQHCIEVSQNSNFDSQVKQFIYACQDKTLRQSVLKIFRYHPLLKIHDIARAVYLLMALEEGEDLG
LSFLNVQQYPSGAVELFSCGGFPWKGLPYPAEHAIEFGLLLLQIAEFYEESSQAYVSKMSHFQQALFDHQGSVF
PSLWSQENSRLKKEKTTLSQSFLFQLGMQIHPEYSLEDPALGFWMQRTRSSSAFVAASGCQSSLGAYSSGDV
GVIAYGPCSGDISDCYYFGCCGIAKEFVCQKSHQTTEISFLTSTGKPHPRNTGFSYLRDSYVHLPIRCKITISDK

QYRVHAALAEATSAMTFSIFCKGKNCQVVDGPRLRSCSLDSYKGP GNDIMILGENDAINIVSASP YMEIFALQ
GKEKFWNADFLINIPYKEEGVMLIFEKKVTSEKGRFFTKMN

>core/299/3/Org3_Gene733

MDKQSSGNSGCIWHPFTQSALDSTPIKIVRGEGAYLYAESGTRYLDAISSWWCNLHGHGHPYITKKLCEQAQ
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DTFGAMSIAGTSPTTVPFHDLFLPSSTIAAPYYGKEELAIAQA KTVFSESNIAAFIYEPLLQGAGGMLMYNPEG
LKEILKLAKHYGVLCIADEILTGFGRTGPLFASEFTDIPPDII CLSKGLTGGYLPLALT VTTKEIHDAFVSQDRM
KALLHGHTFTGNPLGCSAALASLDLTLSPECLQQRQMIERCHQEFQEAHGSLWQRCEVLGTVLALDYP AEAT
GYFSQYRDHLNRFFLERGVLLRPLGNTLYVLP PYCIQEEDLRIIYSHLQDALCLQPQ

>core/300/3/Org3_Gene19

MAEISTPSLPDSSIVSQKTPPVPDPDSSPDHIPTIPTQAPFKPQRKKETPSSIVNAIAFAILAFLSCLGGVFAICLGC
SLEITMPLFILTA VFIAFTLLYFIHYLEKPKIPEPLTPPPSP TLRAPTLTPEIPAPAPGIPLPPTLPKVDRTKLTCNP
DIHYPSTYDPKACFSLLKQLFSLDPETRPEDRKYSNKLASILLRSKEKSGFRFHCFCG HGFSDKILNKKSGAVV
ISSHSSMDFSTTLGRAFAVTTCLQRSCWEKIKNNIPTPEKHLPIGSCVSGP WDVEEGAQLYTSHLIVINPPTLET
LIKEKMRRAITLKDFSMKEAFTNLVLA YLQCFDICIEHNLESVQLEVFGLNNLSADQEEFTTWESCCHLALLE
SVRILLASKEEYALS NVSVNSISQVPLQTACRALFN

>core/301/3/Org3_Gene943

MKKQVYQWLASVVLLALTISGYAELPLSEQKVKSHTYTTLDEVKDYL SKRGFVKTRKQDGVLRIAGDVRRAR
WLYFREDIKNPSDKDKYNPLPVNRYRSEFYLYIDYRAERNWLSSKM NWTAIAGGENTAAGVDINRAFLGYR
FYKNPETRTDFFMEIGRSGLDLFESEVQFQSNFDGLHIYWTRELSKDYPYQVIVHGGPFVVM TTKKHYAW
VVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWL VGKHSQVPWINGQKKPLYL
YGAFLMNPLAKATKTTLNGKENLAWFIGGT LGGLRKAGDWSATVRYEYVEALS VPEIDVSGIGRGNLLKFW
FAQAIAANYDPKEANGFTNYKGFSALYMYGITDSLFRAYGAYSKPANDKLGSDFTFRKFDLG IISAF

>core/302/3/Org3_Gene998

MQSWLQSLQERNILENFTAGLESVEGPAAAYLGFDPTAPALHIGHWIGICFLKRLAALGITPIALVGGATGMV
GDPSGKQSERSLLQTSEVFDNSQKITACLQRYLPGVTLVNNADWLQEISLIDFLRDIGKH FRLGQMLVKDTIK
QRVHSDEGISYTEFSYLILQSYDFYHLFKNYGTILQCGGSDQWGNITSGIDFIRRKGLGQAYGLTY PLLTNAQ
GKKIGKTESGTVWLDSDLTSPFELYQYLLRLPDDTIPKIARTLTLLSNEEIQDIDRRVQTD PVAVKEFVAQDILS
AIHGDLGLEEALSVTRSMHPGNLSSLSEKDFHEL FAGGMGASLDKSEVLGKRWLGLFLVLGLCKSKGEIRRLI
EQKGVYINNVPIANEHSVCEEQDICYGHYVLLAQGKKRKLVL YLN

>core/303/3/Org3_Gene773

MTVAEVKGTFLVCLGCRVNQYEVQAYRDQLTILGYQEVL DSEIPADLCIINTCAVTASAESSGRH A VRQLC
RQNPTAHIVVTGCLGESDKEFFASLDRQCTLVSNKEKSRLIEKIFS YDTTFPEFKIHSFEGKSRAFIKVQDGCNS
FCSYCIIPYLRGRSVSRPAEKILAEIAGVVDQGYREVVIAGINVG DYCDGERSLASLIEQVDQIPGIERIRISSIDP
DDITEDLHRAITSSRHTCPSSHLVLQSGSNSILKRMNRKYSRGDFLDCVEKFRASDP RYAFTTDVIVGFPGESD

QDFEDTLRIIEDVGFIKVHSFPFSARRRTKAYTFDNQIPNQVIYERKKYLAEVAKRVGQKEMMKRLGETTEVL
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>core/304/3/Org3_Gene598

MNKKNLTICSFCGRSEKDVEKLIAGPSVYICDYCIKLCSGILDKKPSSTISSAPVSETPSQPSDLRVLTPKEIKKH
IDEYVIGQERAKKTIAVAVYNHYKRIRALLHNKQVSYGKSNVLLLGP TGSGKTIAKTLAKILDVPFTIADAT
TLTEAGYVGEDVENIVLRLLQAADYDVARAERGIIYIDEIDKIGRTTANVSITRDVSGEGVQQALLKIVEGTTA
NVPPKGGRKHPNQEYIRVNTENILFIVGGAFVNLDKIIAKRLGKTTIGFSDDQADLSQKTRDHLAKVETEDLI
AFGMIPEFVGRFNCIVNCEELSLDELVAILTEPTNAIVKQYMELFAEENVKL VFKKEALYAIKKAKQAKTGA
RALGMILENLLRDL MFEIPSDPTVEAIIHQEDTIAENKAPIIIIRRTPEAIA

>core/305/3/Org3_Gene55

MIKFLSQLFIRHWPRKVVS LGFAIIWILVGQSVTITRTL TNVPVRIVDLHPDQTVLGLQKSGFLNKKVSLTITG
NKNTVQDLRPSNLEVVISAA NHTESWIATIDKHNLSVDHEINIRKDIHSVDANDIFVRLTQYVTE DILLTITKP
IGSPPKG YEYLDVWP KYLNQKVSGPKEYINALKEQGLELTFNLNKISFEELERNRIAQGS HDEIIFPIPK EWKKI
LIPFENTFMDLNDPQADFLRL LFLKRECIPLNLNLPVLF FFPVTFIQTMNPLEYSLDPVPPIILNHGIHQINIPLYV
KDVS RQFLDVVKNNMVL TIVMPSPQDPSSINWAEFLDEKTLENTFLQTIIAQEHGILHDIALIDEAGIRHRFRE
YLRKLALFTADGEPLNLIAEIKNNKVVIQTKTKETTKLYKKEW

>core/306/3/Org3_Gene716

MLKLQLCALFLFGYLAIVFEHIVRVNKS AIALAMGGLMWLVCFSHIPMADHMILVEEIADMSQVIFFLFSAM
AIVELIDAHKGFSVIVKFCRIQSRTL L LWALIGLSFFLSAALDNLT SIIIIISILKRLVKAREDRLLLGAICVIAVNA
GGAWTPLGDVTTTMLWINNKITSWGIIRALFVPSLVCVLVAGFCGQFFLRKR GSTLIAKDVELQSAPPKSLWII
FIGLGSLLMVPVWKACLG LPPFMGALLGLGLVWLTSDWIHSPHGEDRYHLRVPHILTKIDISSITFFIGILLAVN
ALS FANLLTDFSLWMDKIFSRNVVAIVIGLLSSVLDNVPLVAATMGMYTLPLDDTLWKLIAYAAGTGGSILII
GSAAGVAFMGLEKVDFLWYFKRISWIALASYFGGLFSYFVLES LNFFI

>core/307/3/Org3_Gene893

MSSAIARDCFPSPSPQPSSTLGVHPPKYKSLILSVSLIVLGVLLLCVGM LLLVN AIFSFSVLTVGLGGAGVFLGS
LLLILGLIFFVSYHRKLSEATRSLEQKITLEYHPWADLRKELNEVQEWSN FLLDEWEDFKEVVAQHKSQFATF
EGDLLLFGREVEKEYETIWKELDGRDVALLTELKNIWGPLEFLRKKGDRLQCEIDKLRKEVMKV GKSGLKLA
CELTKFKSALKDVKIEQECYRDKRKVEKLEVFPEGYRRELLEVLKTRLSVEKEIQLFEEVVS AFEEKLASLHR
TVFSEEELQEALDKAKAELLDIQVRKSVVEDLSCEPTLIQYHLLRLYE VQCRIVEQFLTQTFSSSEQEKVLEEYE
ALKARIRKTLRVKLDQVRANVAFVASTTDLLSESES LDGNDSVFEDAHD DFLD

>core/309/3/Org3_Gene618

MIETREEVGSANFVSLERAIEDLRAGKFVIVVDEASREDEGDLIIAGEKITVEKMTFLLQHTTG VVCAALSQER
LLSLDLPPMVKDNRCRFTPFTVSVDAAHGVTTGVSAADR TKVVQLLADPKSKPEDFISPGHFFPLASSPGGV
LKRA GHTTESTVDLMELAGLQPCGVLAELVNEDYSMMRLPQILEFARKHNIAVIPVTSIIAHRMLSDRLVSKIS
SARLP TIYGDFTIHVYESLLEGMQHLALVKGNVAGKSNVLVRVHSECVTGDILGSKRCD CGEQLSSAMS YIA

EKGTGVLVYLRGQEGRGIGLGHKVRAYALQDNGYD TVDANLAMGFPVDSREYGIGA QILVDLKLTTIKLIT
HNPQKYFGLQGFGLSITERVPLPVRISEDNEQYLRTKQERMGHWLDLPCCNNRVQ

>core/310/3/Org3_Gene857

MLCYSPNYVTDLYRISLSAEESLGGIRAFPAESLLGGACALNFPDLEERLPDLRKELLFLGSNDRPDACGGK
FSLQLASSKECYIAALKERVYLVNTNSSRGPVYSFSPKGVPTELWIECFSVSDGRVEVKVRLQGLHKELISKP
RDCETLFLNPPANKLDCWEIAGFRVDASFPVKQKIRRIGVDKFLMHGGA EYADKATKERVDFVSSDEENYS
RYLAVGDVLLWDGNCWQTCGEFQGASSRAPLFEVKRIDDKVM IADLWNVGGTQRQTISLVKGVPSPIEINE
VIREIEFTGMRSWSKPIVLVGGQRLILSPDDWILRTAKGWEKLSRADQIQDYVTGKVTGPLL VFEKLEKDLRG
FVLRGHMFNAQRTL VETISLPLKQGFEPAVASQEVSSNTRSAAAHPGATNRGGS

>core/311/3/Org3_Gene785

MSQPPINPLGQPQVPAAASPSGQPSVVKRLKTSSTGLFKRFITVPDKYPKMRYVYDTGIIALAAIAILSILLTAS
GNSLMLYALAPALALGALGVTL LISDILDSPKAKKIGEAITAIVVPIIVLAIAGLIAGAFVASSGTMLVFANPM
FVMGLITVGLYFMSLNKLTLDYFRREHLLRMEKKTQETAEPILVTPSADDAKKIAVEKKKDL SASARMEEHE
ASQRQDARHRRIGREAQGSFFYSSRNPEHRRSFGSLSRFKTKPSDAASTRPASISPPFKDDFQPYHFKDLRSSSF
GSGASSAFTPIMPASSRSPNFSTGTVLHPEPVYPKGGKEPSIPRVSSSSRRSPRDRQDKQQQQQNQDEEQKQQS
KKKSGKSNQSLKTPPPDGKSTANLSPSNPFS DGYDEREKRKHRKNK

>core/312/3/Org3_Gene962

MCQRILILGTGITGKSVARFLYQQGHYLGADNSLES LISVDHLHDLRLMGASEFPENIDL VIRSPGIKPYHPW
VEQAVSLKIPVVTDIQVALKTPEFQRYPSFGITGSNGKTTTTLFLTHLLNTLGIPAIAMGNIGLPILDHMGQPGV
RVVEISSFQLATQEEHVPALSGSVFLNFSRNHLDYHRNLDAYFDAKLRIQKCLRQDKTFWVWEECSLGNSYQ
IYSEEIEEILDKGDALKPIYLHDRDNYCAAYALANEVGWVSPEGFLKAIRTFEKPAHRLEYLGKKDGVHYIND
SKATTVTAVEKALMAVGKDVIVILGGKDKGGDFPALASVLSQTTKHVIAMGECRQTIADALSEKIPLTLSKD
LQEAVSIAQTIAQEGDTVLLSPGCASFDQFQSFKERGAYFKLLIREMQAVR

>core/313/3/Org3_Gene644

MSKKRVVVTGFGVVSCLGNEVDTFYDNLLAGVSGVRPITSFPCEDYATRFAGWIPEFNPEPYVDKKQARRV
DPFITYAMVAAKKAIAMSRWDKDHLPSPDPVRCGVIVGSGMGGLSTLDQGMERLLVIHKKLS PFFIPYIITNMA
PALIAMDFGLMGPNYSISTACATGNYCIDAAYQHLVSGRADMIICGGTEAAVN RIGLEGFIANRALSERNDAP
DQASRPWDRDRDGFVLGEGAGILVLETLESALRRDAPIFAEMLGSYVTCDAFHITAPRDDGEGITACVLGAL
NSAGIPKERVNYVNAHGTSTPLGDLSEVLAVKKAFGSHVRNLRMNSTKSLIGHCLGAAGGVEAVVAIQAILT
GKLHPTINLDNPIAEIEDFDVVANKAQDWDIDVAMSNSFGFGGHNSTILFSRYVP

>core/314/3/Org3_Gene482

MLVSIETFSSIASGSPVQKAAEACYTQYSKQPSSKEVLSSFSWIQELSLFPDRYNLATGASELIKQHWLHNNHS
LAFECILINGKYEPSLSQLPEGVIVCGIDEARGSLSSFMQGFVDNKHPLAFLNAVCS EDRGVVIYIPEEMQTSDP
IFVRHISFPTVSDHDVIFSPRIVVILGQRASAQIQISHDVDLEMVGSSKTIVNGVT ELFVGE GADLTVFMVPGYS
EEDTLWSSTIATVEKDAICRMTQNLLESCQGFGWFDNTSYIVGKKGHAESLVLVQSPRK TWVNNLMSHDAE

ETVSRQNIKSILYSGHFLFEGTISISSQGDLS DANQKHDTLLLSSEARVSTFPRLEIETDEVKASHGATVGPLDP
QQIFYMRSRGMTEAEAQEKLIHGFLKQGLVSDTFLGSSFQLNQTS

>core/315/3/Org3_Gene853

MRYHKYFRYVNSWVFLVVLTLMLLSVVVISMDPTAMLVTSSKGLLTNKSIMQLRHFALGWVVFICAYFD
YHLFKRWAWVLYFFMICALVGLFFVPSVQNVHRWYRIPFIHMSVQPSEYGKL VIVIMLSYILES RKADITSKT
TAFLACL VVALPFFLILKEPD LGTALVLC PVTLTIFYLSNVHSLLVKFCTVVATIGIIGSLLIFSGIVSHQKV KPY
ALKVIKEYQYERLSPSNHHQRASLISIGLGGIRGRGWKTGEFAGRGWLPYGYTDSVFSALGEEFGLLGLLFTL
GLFYCLICFGCRTVAVATDDDFGKLLAAGITVYLAMHV LINISMMCGLLPITGVPLILISYGGSSVISTMASLGV
LQSIYSHRFAKY

>core/316/3/Org3_Gene350

MKLWMKIFIGL FVGVT LGLVLEDKAIFFKPIGDIFLNLLSMV VYPLVFCSMVLG IASISDMKKLGRIGIKSVGL
YLGTTALAIVIGLCFAWIFSPGN GCDFAQAQSMDSAVTVIDSNKTAAYFLSIIAQVFSPNPVRSFAEGNILQIIF
AIFLGIALRLSGERGRPVERFIDGFSEIMLRMVNMIMSFAPYGVGASMAWISGNHGLGV LWQLGKFIIAYYLA
CLFHATLVFGGLVRF GCKMSFSKFLSSMMDAISCAVSTASSSATLPVTMRCVSKNLGVSAEVS GFVLPLGAT
VNMNGTAIFQGMAAVFIAQAYNCPLSLSSLLLLVVTATFSAVGSAGVPGGGMITLGSVLASVGLPIQGIAILA
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>core/317/3/Org3_Gene548

MKKIFYSFVLLSCIFPYVGCAQVFVGLDRIFSEGEYTRCIQGKKIALISHSAAINSRGQDALSVFYSRKHDCTVE
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KASERYGKQLIVLDRPNPMGGRIVDGPLPNPTTSGSLAIPYCYGMTPGELALFFKKTYAPNANVVVIPMKGW
NRSMTFDETGLIWMPTSPQMPDPQSPFFYAATGILGALSVASIGVGYTL PFKVLGAPWMDGEKVADELNRM
KLPGVLF LPFFYEPFFGKYKMEMCSGVLLVLQDPKIFYPVETQCTIWGV LKALYPKQVEQTLKSIERIPARRSS
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>core/318/3/Org3_Gene855

MKKNASHKTNDKKSLSIWSIGGSIFAMFFGAGNIVFPLALGYHYNAHPWSAYFGMMLTAVCVPLLGLV SML
FYSGDYQKFFFSIGRIPGMIFITAIILLIGPFGGIPRAIAVSHATLISLSEHKSAFIPSLPIFSAICCVLIYIF SCKLSRL
IQWLGSVFFPIMLV TLLWVIIRSFMIPTHPMVQEFIPNARQAWLAGFIEGFNTMDLLAAFFFC SIVLISLRQLVA
EEKHPTEEEIPLSFQGISKKNKRS LALGFFLAAILLGMTYLG FVL SAARHAGLLVNVSKGHILGRISAIALGPNS
ILAGVSVFIACLTTEIALVGIVADFLARVVSFKKLNYASAVICTLIPTYLISILNFETISHLLLPLLQLSYPALIVLA
CGNIAYKLWNFRYSPVLFYLTLSLTIVLKL VN

>core/319/3/Org3_Gene144

MDKETLENIYRHFYRFLKLNILPAFLG LLLL CSPNTLN YTQVDVIFSDRLCSCLLIFLAIASLTKRSLLWLGAP
LGIWVTLFACVAGRSPTIFANDTLIGFAILAVVCISPTRPEALEVGPTLPEGFSYNPSAGGRRAAVLFLSLLGWL
EARYLTASSLGITSSQSSNFLLLYSSIMTVYSLLVVL SLAGSERRWHTRPKIVIATALALTGVII LTLLPIILHQLR
YDCWLCLCLTIEPALAVVFAYDETRATLRYISQFLGDKRALTRASFFGSEYYKHTLSWEERTV LPLRKAYKQ

AFEGISFPINQLLAILVATVFKVNSSMGLPTFPRNFLNICCWFIIVLFILAFaesLRHLRWMNLIFSAAILFSPVL
FHIPVESPMFLPIIVTGLLILSIGKRRRTKRKL

>core/320/3/Org3_Gene908

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KQQIDIIQPQELKEVLQSCKDFGVVNQEEsRLLYGYLSLSDCSVKERMQPRQDILFYDIQTPLENLYLLFSKQH
CSRVPICNDNLQNLLGICTARSLLLHDKPLQSSDDLPLKKPYMPETISAKMALCQMAAEDETlGMIIDEY
GSIEGLITQEDLFEIVAGEIVDQRDNKILYTTSGADVIIASGTLELREFSEIFDINLPTNNNIATIGGWLIEQIGTIP
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>core/321/3/Org3_Gene807

MDESDGEEASKDSAFSASFsyEFVKsSTRESKNTVTHSTASRTLYILRQDCSYDPRALKVDDEFryWVEKRL
DAKNPDSLNAFVKEVGTHYVASVTYGGIGFQVLKMSYLQVEELEKEKISISVAAASSLLKSKTSNATEKGYS
SYQSESSAQTVFLGGTVLPDLQQDKLDFKDWSESIPNEPILAISVSSITDLIPELFPSEDAQVLSQKKSALGQV
ILNYLESHKPKKEEGPKPVQITSGFNSSSSVFTLQAAKAPKTVSFPYIDYwSTIPYLFPTLKETSGAQPLSFYLRf
DDIFEQQNLVHNTSYILASTSVRLGYFGDSYRDYDALSFYGSWPQAYFDWAGYKDRCTWTLEKLNTTGDLf
IRSGDEIRLKHNTSGKYLATTSMsDGYQTLTCTTQTSDSVFIITV

>core/322/3/Org3_Gene688

MNLPVSLACLLLsgCVFFLGvFVSSsLYARKKRAFLEKIQKLEHENQLLQTSLNLSRHQEQLIEDFSNRLALSS
HKLIKDMKEEAQNYFGDTSKSFQSILSPIQTTLTTFKQSLETfETKHAEDRGRlKEQISQLLAVEKKLEHETHV
LTDILKHPSRGRWGEIQLERILELAGMLKYCDYDSQTtsAQGAfRADIIIRLPQDRCLIIDAKAPISDSYfSVE
EIDKGDLVDKIKEHIKTLKSKSYWEKFHQsPEYVILFLPGESLFNDAIRLAPELMEIGASSNVILSSPLTLLALLK
TIAYMWKQENLQKQIQEVsLLGKELHRRlQVVfTHFQKIGKLNlNQTVQSYNDMTSSfQYRVLPtLRKFEGLE
TSSSHQIEEPTPIESLATSFPHTCDIDTNLAVIESLEKQD

>core/323/3/Org3_Gene770

MKTAFHSCYSWFCWLFsFLVLFVGGIAGGEPLCPDCKYETKSVLRSDQLPDHLWNYENDCYLTGYVQsLLD
MHFLDSRTQVVIEKNRAYLFSLPVDSSLSEAITNFVRDLPFICAVEICERPYGECITRSSAERPLLpKEKTLGMPI
FCGKEGVWLPQNTILFSPLIADPRQVTNSAGIRfNEKVVGNRVGATIFGGDFILLRLFDVSRFHVDCDFGIQGG
VFSVFDLDHPESCMVNSDFFVAGLWSGAIDKWSFRFRLWHLSSHLGDEFILThPNfPRFNLSDEGVDLfISFR
YTPQIRLYGGCGYIVSRDLTFPERPFYCEWGAELRPFGlREGNLHAQPIFAMHFRCWEEQKFGLDQSYILGME
WAKFQEIGRKIRAVLEYHQGFsKEGQfIREPCNYYGfRLTYGF

>core/324/3/Org3_Gene597

MTTIAIEAAKKVLIKLrNAGYQAYfVGGCVRDMLMNRPLEDIDIATNASPTIVSTIFPDVISIGVAfGIIVVKQD
GRLFEVATFRSDGEYKDGRHPDRIIFSSMREDALRRDFTVNGMYYPfEDKVFDfVEGTRDIEKKVIRAIGHp
RLRFSEDKLRILRAIRfSSSLGFTLDPTTERAIKEAPALVNSVSPERIWQELKKMLKRQPYGALSLLLKLKVLI
fPELRDIPYsLLRTTIEFARKFNpTHfPEILFLLPLFQGVSEEAATVAFGRLRISNKELKLIESWYEALPHfQNQS

GNRVFWAHFLASPTAPLFLELFSALQKDPSRQQHFISRVQELESRLQFILRIKTSSPVVSAPDLIAKGISPGRLL
GDLLREAEILSIENECLDKEKILLLLQEKGFWK

>core/325/3/Org3_Gene481

MKNLKEDFPIFAAKAKENEPFIYLD SAATTQKPQQVIDAVANFYTSSYATVNRAIYSSSRNVTEAYAAVREK
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DSGLIDLDDLEKLLNEGAQFVSIPHVSNTGCVQPLQQVAELVHRYDAYLAVDGAQGAPHLPIDVQLWDVD
FYVFSSHKIYGPTGIGVLYGKKDLLDQLPPVEGGGDMVAIYDHQNPEYLPAPMKFEAGTPNIAGVLGLGAAL
DYLDGLSAKFIYDKEIALTTYLHKELLEIPGVEILGPSIEEPRGALIGMTIDGAHPLDLGFLDLRGIAVRTGHQ
CAQPAMERWNVGHVLRVSLGIYNDEDDIDQFILVLQDSLDKIRR

>core/326/3/Org3_Gene131

MVVVALFILGIFFLSGSLAFLVHTSCGVLLGAALPILCIGLVLLAVALIVFLCHKHKTRQDLDDYDQDLDSLVI
HKKEIPNDISELRVTFEKLQNLQFHTKDFSDLSQELQGKFINCMEKWLTLEDEVTKFLIVRDRFLETRRNFTT
FGEQVKGIQSNIFDLHEEKSSLYLELYRLRKDLQVLLNFFLLPPGILKVDYDEIEAIKGLFIRLTSRLDKLDVKA
QERKKFINEMSREFKEVEKAFDIVDRATKKLMDRAKKESPARLFMGRTESLLEMKKNEEALKNQGLDPENL
SHPELFSPYQQLLILNYLNSEIVLHHYEFLISGTVTSGLTLEECENRMRAASTGLNALLVRKLQFRGAIKSAYF
EKLTEIEKELRSLQDVIKSLELELIHKIKDIVTEET

>core/327/3/Org3_Gene245

MTDSNPLPSYTDASLYRTPAKHSYPIRLPLNRTDRIEKILKIVTLTLALACALGFSIAAGILAMPIFS AVVVITLA
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GYEALLEQNWDLLPSLAAVDPSFTTETPQQPCFIWKLKDSKLIFISTSGDIAVPRIKTQGRVMIVNAANENISR
EGGGTNKALSLATSLQCWNASRLPRAHSRSGSQLQPGECRSAKWENS DHTSNDHVP GKAHFLAQLLGPEAA
KCNNDPKQAFEVSKKAFHNLFQEA EIIGVDVIQLPLIGCNLFA PSRLLNLGKTRA EWIEAIKLALITSLQDFGW
EQDNQEEQKIILTDKDQPPIPPRFDLTTP

>core/328/3/Org3_Gene798

MKKQRSHYTKNNLLLLLSILVGLGLGSVQSPWIVYSAECIANTFLKFLRLLSIPLVFCALGSTITSIQNFNTMVT
LGKRILYYTLLTTVIAASIGLLLFFLLRPQMITQDALATTTKCNPLGYLDVLSDTLPENIFKPFLQGNVISAACL
AVLLGTASLFLQEKEKHFNQFFNSFFSIFLN LARGGLKLLPIAMLGFSVILFKELKDQSNLTMFAEYLLCVIG
ANLAQG FIVLPILLKINKVSPLKVAKAMSPALVTAFFSKSSAATLPLTMELAEDDLKINKNLSRFSFPLCSVIN
MNGCAAFILITVLFVATSNGMIISPLMSLGWIFIATLAAIGNAGVPMGCYFLTLSLLTSMNVPLSILGLILPFYT
VIDMIETSLNVWSDCCVVSLAN

>core/329/3/Org3_Gene265

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LQVGSESSRNCYRALGITPDYAPFTQIFIVVIFAELLPLTISRKIPEKLALWGAPILYYSHYIFYPLIQLIGSLTEGL
YYLLNIRKEKLNSTLSRDEFQKALETHHEEQDFNTIATNIFLSATCADQVCQPLEQVTMLPSSANVKDFCRTI
KNTDINFIPVYHKARKNVIGIAHPKDFVNKALDEPLINNLHSPWFITAKSKLIRILKEFRDNRSSVAVVLNASG

EPIGILSLNAIFKILFNTTNI AHLKPKTISVIERTFPGNSRIKDLQKELDIQFPQYPVETLAQLVLQLLDSPA EVGT
SVIINNLLLEVKEMSLSGIKTVSIKNLLS

>core/330/3/Org3_Gene475

MDKLT VQDLSPEEK KVLVRVDFNVPMQDGKILDDIRIR SAMPTINYLLKKHAAVILMSHLGRPKGQGFQEEY
SLQPVVDVLEGYLGHHVPLAPDCVGEVARQAVAQLSPGRVLLLENLRFHIGEEHPEKDPTFAAELSSYGDFY
VNDAFGTSHRKHASVYVVPQAFPGRAAAGLLMEKELEFLGRHLLTSPKRPFTAILGGAKISSKIGVIEALLNQ
VDYLLLAGGMGFTFLQALGKSLGNSLVEKSALDLARNVLKIAKSRNVTIVLPSDVKAAENLQSKEYSVISIDQ
GIPPHLQGF DIGPRTTEEFIRIINQSATVFWNGPVG VYEVPPFDSGSIAIANALGNHPSAVTVVGGGDAAAVVA
LAGCSTKVSHVSTGGGASLEFLEQGFLPGTEVLSPSKS

>core/331/3/Org3_Gene851

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LTTSGTPEYRVNEACIDEWKEILLSSSLNIASIY WEEKVAARGISTYYETKLLYGAPSIQQKLSLPSDGNSASFS
LRPRSFFQPQITQAAKIIETAKEFINPEGSETLLDLYCGAGTIGIMLSPYVKNVIGVEIIPDAVASAQENIKANNK
EDCVEVYLEDAKAFCKRNENCKAPDVIIIDPPRCGMQSKVLKYILRIGSPKIVYISCNPKTQFQECADLISGGY
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>core/332/3/Org3_Gene530

MLLVRKWLHTCFKYWIYFLPVV TLLLPLVCYPFLSISQKIYGYFVFTTISSLGWFFALRRRENQLKTA AVQLL
QTKIRKL TENNEGLRQIRESLKEHQQESAQLQIQSQKLKNSLFHLQGLLVKTKGEGQKLETLLLHRTEENRCL
KMQVDSL IQECGEKTEEVQTLNRELAETLAYQQALNDEYQATFSEQRNMLDKRQIYIGKLENKVQDL MYEI
RNLLQLES DIAENIPSQESNAVTGNISLQLSSELKKIAFKAENIEAASSLTASRYLHTDTSVHNYSLECRQLFDS
LREENLGMLFVYARQSQR AVFANALFKTWTGYCAEDFLKFGSDIVISGGKQWMEDLHSSREECSGRLVIKT
KSRGHL PFRYCLMALNKGPLCYHVLGVLYPLHKEVLQS

>core/333/3/Org3_Gene59

MRMLQISM LLLALGTAINSPA IYAADSQSVSFPEQLPSSFTGEIKGNHVRMRLAPHTDGTHREFSKGDLVAVI
GESKDYYVISAPPGITGYVFRSFVLDNVVEGEQVNVRLEPSTSAPVLVRLSRGTQIQPASQEPHGKWLEV VLP
SQC VFYVAKNFVANKGPIELYTQREGQKKIAMDLINSALNFAHIELEKSLNEIDLEAIYKKINLVQSEEFKDVP
GIQGLIQKALEEIQDAYLSKSLESQNTSIASSQCSTPKVSSEVTTSLLSRHIRKQTALKTAPLTQGRENLEYSLF
RIWASMQQGNDHSEALTQEAFYRAEQKKKQVLAGVLEVYPHVVKNNPGDYLLKAQENTIAFLYGTSINLEQ
WLGKRVTVECLPRPNNHFAFPAYYVVGIKEAS

>core/334/3/Org3_Gene215

MAASGGTGGLGGTQGVNLA AVEAAAAKADAAEVVASQEGSEMNM IQQSQDLTNPAAATR TKKKEEFQT
LESRKKGEAGKAEKKSESTE EKPDTDLADKYASGNSEISGQELRGLRDAIGDDASPEDILALVQE KIKDPALQ
STALDYL VQTTPPSQGKLKEALIQARNTHTEQFGRTAIGAKNILFASQEYADQLNVSPSGRLSLYLEVTGDTH
TCDQLLSMLQDRYTYQDMAIVSSFLMKGMATELKRQGPYVPSAQLQVLMTETRNLQAVLTSYDYFESRVPI

LLDSLKAEGIQTPSDLNFVKVAESYHKIINDKFPTASKVEREVRNLIGDDVDSDVTGVLNLFFSALRQTSSRLFS
SADKRQQLGAMIANALDAVNINNEDYPKASDFPKPYPWS

>core/335/3/Org3_Gene800

MVYFMVVFSPSESVVKANSVVRSNFCYFLENKFVSPSESTEVMFSEIMKGRVPDIESLFDRPTDMMMTGFKA
AQNLGNLFNSFGILIMCFSQCKSCQTPEKETS AIVLGATLLFFVIALILGPTLGALVYCAYKVYTLGKMIYSLN
KAKAKVLRHPAQNVFHRAAGVATIRSSEEAVKACKLYKSAMIGSLVVS LIASLALIALTAGIVLVLFFVAPGA
APVITAAMMGCCAAGGGALLISLLGLWIAIVRKAKHQEACVGHLTNVVLHTAVSEALLHDPSHFQTNALAR
DLFLTDCLSHYGHLFSNEEVAQLVQGGAPGGGSRPSQHYGGSSDYQNR RGNGNFGGSHFGGGGGFAGSHF
GAGYPTAPT MPSAPPPFPPPAYDTIYG

>core/336/3/Org3_Gene329

MLSVTIVLVGLEMARSKVSKRDSKILDILFATTELYLKTGQPVGSKTLKESFCSDLSTATIRNYFAELEAEGFL
KKNHTSGGRIPTDLALRHYVDHQEECPAEISAPIFDKISQLPSESRNIIKDLQKATELLGEILDLP TFFSSPRFEN
DSVTNIQITQVDKQRAV TILSTEFQGIFTDTLWLPEACDTLSIKRIEKFLQNYIRKLPTNEELSKKEEHL SMSLY
NEVVVRYLTRYCNFSEEDLYQTGMSKLLKYEAFKDPEVLALGLSLFENRRQMCELLNIGMHKGRATAFIGK
ELSDILGTSNPGCSVITIPYYMNR SPLGALGILGPINLPYKEALPLLKLFANKINETLTQSFYKFKLSFRRPLTSN
CKLSNEPILRTEYSSIKLLPSKETL

>core/337/3/Org3_Gene326

MRRNPHFSL LKPQYLFSEISKKLAQFRKENPEISVIDLSIGDTTQPLCRSITQAIKEFCVSQEKQETYRGYGPET
GLEKLRTKIAS E VYENRISPEEIFISDGAKPDIFRLFSFFGSEKTLGLQDPVYPAYRDIAHITGIRDIIP LACRKET
GFIPELPNQ QSLDILCLCYPNNPTGTVLTFQQQLQALVNYANQHGTVLIFDAAYS AFVSDPSLPKSIFEIPEAKYC
AIEINSFSKSLGFTGMRLAWNVIPKELTYDNNEPMINDWKRLFATTENGASLLMQEAGYYGLDLFPTPPAISL
YLTNAQKLKKSLETAGFSVHGGDHAPYLWVELPEGISDEEAFDFFLHQYHIAVTPGHGFGSCGQGFVRFSAL
TQPQNIALACDRLCTASLKETMVLA

>core/338/3/Org3_Gene682

MSNKVLGGSL LIAGSAIGAGVLAVPVLTA KGGFFPATFLYIVSWLFSMASGLCLLEVMTWMKESKNPVNML
SMAESILGHVGKISICLVYLFLFYSL LIAYFCEGGNLCRVFN CQNLGISWIRHLGPLGFAILMGPIIMAGTKVID
YCNRRFFMFGLTVAFGIFC ALGFLKIQPSFLVRSSWLT TINAFPVFFLAFGFQSIPTLYYYMDKKVGDVKKAILI
GTLIPLVLYVLWEVVVLGAVSLPILSQAKIGGYTAVEALKQAHR SWAFYIAGELFGFFALVSSFVGV ALGVM
DFLADGLKWNKKSHPF SIFFLTFIIP LAWAVCYPEIVLTCLKYAGGF GA AVIIGVFPTLIVWKGRY GKQHHRE
KQLVPGGKFALFLMFL LIVINVVS IYHEL

>core/339/3/Org3_Gene236

MVNIQPVYRNTQVNYSQATQFSVCQPALSLIIVSVVA AVLAI VALVCSQSLLSIELGTALVLVSLILFASAMFM
IYKMRQEPKELLIPKKIMELIQEHYPSIVVDFIRDQEV SIYEIHHLISILNKTNVFDKAPVYLQEKLLQFGIEKFK
DVHPSKLPNFEEILLQHCPLHWLGRLVYPMVSDVTPGT YGYWCGPLGLYENAPSLFERRSLLLLKKISFGEF
ALLEDGLKKNTWSSSELVQIRQNL FTRY YADKEEVDEAELNADYEQFDSL LHLIFSHKLS

>core/340/3/Org3_Gene519

MSFFNHIPTFSPDAILGLQNVFFADKRPEKVNLVIGVYEHPQKRYGGLSCIRKAQTVILEEEQNKSYLPISGLQI
FLDEMRELVFGAVDPSAIVGFQSLGGTGALHLGARLLSVAKGSGKVYVPEQTWSNHIRIFSQEGLEVIRYPY
SKEQKQLLFEPLIAFLKEVEKNSVILLHGCCHNPTGVDFTEDMWKELAILMKERELIPFFDTAYQGFAHGIEL
DRKPIEIFISEGNTVLVAASSSKNFALYGERVGYFAVHSTFTDELVKIHSFLEEKIRGEYSSPQRWGVEIVSTILS
NPYLKEEWQSELNFIRESLGKMRTFRVQALRKVAGHTFDFLLSQHGFFAYPGFSDKQVFLFLREQHAVYTTAG
GRMNLNGITEKNIDHVVSFIQAYEL

>core/341/3/Org3_Gene130

MVVSIIYSEILSFSELTSCKHSLFPFGPIETASIRIHHVFNVVIVCLIIILGTLFVCLGMVFLGVFSTYLLGMSSMILG
LLISIGLALLKFKERYGLEPKELFGVEGGFDKKLPSEIIQMMDQIADLARELDLEQKKDTLIRGFSARLDVLE
GSKTEKKQILKIGVPRNLSEIQERAQEQNSILEQCKEALLFRRKSAQEIFKKLYDRKAAFWRSYREDLWCYSEI
HVSKKALSPLYIGDVFEGTAPHFLMEAYAMCRTAKNLRNYVKVCVEDMRVNEEKKRAKQLSVSELLCCCT
EIETDLENETNLFTSDSEDLVEEYQIHCIQRTMLHALWAIYNDEVVSRKPIDTLDRVRARMAVEDCIETFEELQ
MCVVHTKTLELEIAQLYVDILLEA

>core/343/3/Org3_Gene39

MSKETFQRNKPINIGTIGHVDHGKTTLTAAITRALSGDGLASFRDYSSIDNTPEEKARGITINASHVEYETPN
RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSATDGAMPQTKEHILLARQVGVPYIVVFLNKVDMISQE
DAELIDL VEMELSELEEKGKGCPIIRGSALKALEGDANYIEKVRELMQAVDDNIPTPEREIDKPFLMPIEDV
FSISGRGTVVGTGRIERGIVKVSDKVQLVGLGETKETIVTGVMFRKELPEGRAGENVGLLLRGIGKNDVERG
MVVCQPNSVKPHTKFKSAVYVLQKEEGGRHKPFFSGYRPQFFFRITDVTGVVTLPEGTEMVMPGDNVELDV
ELIGTVALEEGMRFAIREGGRTIGAGTISKINA

>core/344/3/Org3_Gene1004

MFEFRFPKIGETSSGGSIVRWLKNLGDHVARDEPLIEVSTDKIATELPSPKAGRLVRFCVNEGDEVASGDVLG
LIELEEISEADDESTSCPLTSCETKSEAGSSSSSVWFSPA VLSLAQREGIGLDNLQKIAGTGKGGRVTRQDLEA
YISESQQVSIPEIFQGEVNRIPMSPLRRRAIASSLSKSSDEVPHASLVVDVDVTDLMNLISGERQRFLDTHGVKLT
ITSFIVQCLAQTLRQFPLLNGSLDGTTIVMKKSVNVGVAVNLNKEGVVVPVIHNCQDRGLVSIKALADLSSR
ARLNKLDPSEVQDGSVTVTNFGMTGALIGMPIIRYPEVAILGIGTIQKR VVVRDDDSLAIKRMVYVTLTFDHR
VLDGIYGSEFLTSLKNRLESVTMG

>core/345/3/Org3_Gene17

MDYYSILGISKTASAEI KAYRKLAVKYHPDKNPGDAAA EKRFKEVSEAYEVLSDPQKRDSYDRFGKDGPF
AGAGGFGGAGGMGNMEDALRTFMGAFGGEFGGGSFFDGLFGGLGEAFGMRS DPAGARQGASKKVHINLTF
EEAAHGVEKELVVSGYKSCETCSGQGAVNPQGIKSCERCKGSGQVVQSRGFFSMAS TCPECGGEGRIITDPCS
SCRGQGRVKDKRSVHVHIPAGVDSGMRLKMEGYGDAGQNGAPSGDLYVFIDVESHPVFERRGDDLILELPIG
FVDAALGMKKEIPTLLKTEGSCRLTVPEGIQSGTILKVRNQGFNPVHGKGRGDLLVRISVETPQNLSEEQKEL
LRTFASTEKAENFPKKRSFLDKIKGFFSDFTV

>core/346/3/Org3_Gene115

MSSPVNNTPSAPNIPIAPTTPGIPTTKPRSSFIEKVIIIVAKYILFAIAATSGALGTILGLSGALTPGIGIALLVIFFV
SMVLLGLILKDSISGGEERRLREEVSRFTSENQRLTVITTTLETEVKDLKAAKDQLTLEIEAFRNENGNLKT
EDLEEQVSKLSEQLEALERINQLIQANAGDAQEISSELKKLISGWDSKVVEQINTSIQALKVLLGQEWVQEAQ
THVKAMQEQIQALQAEILGMHNQSTALQKSVENLLVQDQALTRVVGELLESENKLSQACCSALRQEIEKLAQ
HETSLQQRIDAMLAQEQNLAEQVTALEKMKQEAQKAESEFIACVRDRTFGRRETTPPTTPVVEGDESQEED
GGTPPVSQPSSPVDRATGDGQ

>core/347/3/Org3_Gene576

MPRYRYTYLDPKERRKRGYLEALHIQEAREKLAQENIQVLDIREVALRRMSIKSTELIVFTKQLLLLLRSGPL
YESLVSLRDQYHEQKMGLLLTSFMETLRSGGSLSQAMAAHPNIFDHFYCSGVAAGESVGNLEGCLQNIIVL
EERAQITKKMVGALSYPVLLVFSFAVMLFFLLGVIPSLKETFENMEVKGLTKIVFGVSDCLSAYRYLFLGFA
SALITVGILMRHRIPWKKILEKLLFALPGTKKFVVKVAVNRFCSSVASAILKGGGTLLIEGLDLGCDAIPYDRLKT
DMRDIVQAVIGGGSLSQELAQRSWVPKLAIGMIALGEESGDLADVLGYVAHIYNEDTQKTLASITSWCQPVI
LIFLGGLIGVIMLAILIPLTSNIQTL

>core/348/3/Org3_Gene603

MHPKIEKRNSLPLTAVAPVFEEASYHPSVATTVDYVDATTLRHLTVLKDVKEARNLDLGKAFLTSMKQGFI
NTGTELAIIQASLADQSSRESRKKEEKIFHQHLGKAAPQAATATSGVQPTADPVADKMPLQSAFAYVLLDKYI
PAQEEALYALGRELNLSGYAQNLFSPLLDMSFNSAPINYNLGSYISQTSGTANFAYGYEMILSRYNNEVSQ
CRLDIASITVKAKAALANMSASVKANVSLTDAQKKQIEDIIASYTKSLDVIHTQLTDVMTNLSITFVPGLNKY
DPSYRIVGGDLIIALQNDEKVLVDGKVDITTAVNEGGLLNFFTTVLTDVQNYGDLAQTQQMLDLELKAM
QQQWSLVSASLKLNGMYTTVISGFKN

>core/349/3/Org3_Gene486

MKKLLKSALLSAAFAGSVGSLQALPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDASLRAGFYGDYVFD
RILKVDAPKTFMSGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG
YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGCATLGAEFQYAAQ
SKPKVEELNVICNVSQFSVNPKPKGYKGVAFFPLPTDAGVATATGTKSATINYHEWQVGASLSYRLNSLVPYIG
VQWSRATFDADNIRIAQPKLPATVLNLTAWNPSLLGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVG
ATLVDADKWSLTAEARLINERAAHVSGQFRF

>core/350/3/Org3_Gene309

MMKQGVGQDAKELYTFLSRGNEHYQPCLWFSLEEELGFLFDEKMLCAPLSEDHYCHSYLVDLVDQHLKDLI
LSMFLDPQNISAGELLKVSINVGDSFSPLQKDFLSMVLREDETGKNVVVVFKGVLSLPATQVCKLVEELNSK
DYSYLNIFSCHGDSSPQLLFRKELEGTSGRYFTVICALYLGDTDMRSLQLASERIMVSREFDLVDAYAARCKL
LKIDHTNWRPGTFSRHADFADAVDVSAGFNSREFKLITQANQGILESSELPLPSKTFWEGFLAFCDRVTVTRH
FIPMLDAAIKQAVWTHKHPSLIDKECEALDLKTQCLPSIVSYLEYVTNSHEKTSKGPFIQKEIADCSPLEALF
PGSDEDVPSTSEDPSDDHPSDLEDS

>core/351/3/Org3_Gene472

MGTPISGNDGDRNTISDPLEESAAEEGDSLEDRVSESATQVIETIADTGIPEATPSEGNSDLNSDLVDRVEY
EARGSLTTMLARIRKAVSQIWMHVKTKRHPKEQGVRSLGDIPCDLLKATRLPKETAEPYFYALETALASC
RSFFFHVFLRLFTLLRRQHPEAPLDLCGTDPISEAAVAFALILRSCCKWVATDAVQEGLPLEVIEEAGMYNA
FSLEATTTVEEVSKRLSELLYSKRIDGLANVRGITKIITSPYLGAGQCVSVVDNLKTYDLGRNYTQVLACAS
QIDEFADKGENEALVMKDILYLVRQDRSKELGDFLMMWSEEHASEVNYDVVLAILEVNLPILEEDYRSHPLA
YQKKLNYVICQFFCSERLTSIEPKD

>core/352/3/Org3_Gene337

MLHILLAIFCILLFLAFGLTQPSCHGSSKFLKTLNQRFFKDKGREYPPFPSAPTILATLLCILYGALGTKLYTLLP
PKTAHKDLLFWPLYSLSALIAYGFLPPWISTKVPKETTAAHLRFLASVFQLGLFPLQLLFYRRRPNQQVRSSTSF
QSQLSEALSAFDNLIVREVMIPKVDIFALPEETTLQEALVLVSEEGYSRVPVYKKNLDNITGILLVKDLLLLYT
SSHDLSQPISSVAKPPFYAPEIKKASSLLQEFRQKHRHLAIIVNEYGFTEGIATMEDIIEEIIIGEIADEHDVQENTP
YKKIGSSWIVDGRMNISDAEEYFNLKIDHENSYDTLGGHV FHKVGAVPQKGMRIHHENFDIEIITCTERNVGK
LKITPRKRKFNIS

>core/353/3/Org3_Gene398

MAIKNILVVDDEPLLRLDFLSELLTSQGFIPDTAENLRNALQMIRSRDYDLVISDMSMPDGSGLDLIKIKQSSPH
TPVLVVTAYGSIENAVEAMHQGAFNYLTKPFSSEALFAFISKAEEELKNLVHENLFLHSQTPDSSHPLIAESKA
MKDLLAIAKKAASSSANIFIHGSGCGKEVLSFFIHHNSPRANHPYIKVNCAAIPETLLESELFGEKGAFTGA
TTKKAGRFELAHKGTLLLDEITEVPVNLQAKLLRAIQEKEIEHLGGTKTLSVDVRILATSNRKLKEAIDDKSFR
QDLYYRLNVIPLHLPPLRDRQDDILPLANYFLNKFCRMNNTPLKTLSPKAQELLNYPWPGNIRELSNVLERV
VILENTSLLTEDMLALA

>core/354/3/Org3_Gene685

MHLHEYQAKDLLASYDVPPIPPYWVVSSEEEGELLITKSGLDSAVVKVQVHAGGRGKHGGVIVAKSSAGILQ
AVAKLLGMHFTSNQTADGFLPVEKVLISPLVAIQREYYVAVIMDRKHRCPVLMLSKAGGMDIEEVAHSSPEQ
ILTLPLTSYGHIYSYQLRQATKFMeweGEVMHQGVQLIKKLAKCFYENDVSLLEINPLVLTLEGELLVLDSKI
TIDDNALYRHPNLEVLYDPSQENVRDVLAKQIGLSYIALSGNIGCIVNGAGLAMSTLDILKLHGGNAANFLDV
GGGASQKQIQEAVSLVLSDES VKVLFINIFGGIMDCSVVASGLVAVMETRDQVVPTVIRLEGTNVELGKEIVQ
QSGIPCQFVSSMEEGARRAVELSM

>core/355/3/Org3_Gene636

MKWFVISCLLGIFSLGLIMVFDTSsAEVLDRSLECSTHKALIRQVTYLILGLGVASLLYMMEWDRFLKISPVLL
SGAALALICVFIPGLGICRNGARRWLGFQGLTIQPSEFVKYLVPIVALYFLTSSLYQKQLKMFLKLTAILFIPIL
LIAIEPDNGSAAVISASLIPVFIMTSVRLRYWLLPLLCVLIAGGALAYRMPYVRYRLNVYLHPELDIKGRGHQP
YQAKIAAGSGKLLGKPGASLQKLTYLPEAQNDYIAAIYAEFGFLGMLVLILLYMCFVYGGYAIKASSLE
GAALAMVITLIISMQAfMNLGVVSGLLPSKGVNLPFFSQGGSSLIANMCGVTLLLKVYDEENSKSSLGCRRFR
RPHCPSSLGKGSFFS

>core/356/3/Org3_Gene768

MSSVQNQSSGTPNPEEVTSPESTEENKNVVSDEAQATHAVALPIVTQLSLPEGVGTSSSEETASNPKVDEIVA
EVSSRAVADQISSLVERVGELLDDLKGAQSLFTSFQSELKNCLPAWKSSTRRLETRGAGDNADIARLELFRSDY
EAVLGHANQFHGKAHLILSKLTDVHHKLQGLSREDLSLAFDNNDRVLEHLGSLGLDVEDAEGNWSLSCERGI
PRLVLTADSMVLVQIKKVNLPTEELRTLQGTTESSDPRVEESLSCERLLNELRRLWANFVGVFISSCYDNIVF
VLMWIVRRINLLPGLGCLPFHNPDASQEDQRSSSGERSTRRERLSRRSDLSEEEMIVRAEGESIHPESPHGDGR
NQPSRGDKQDSDSEEEETEL

>core/357/3/Org3_Gene611

MEKPQNRKAPRIFWLNNQVAIPPSERVKESYALHSDIFSLPPGSALKLAEKTEESIRQLVGLKDSHIFRFVPHFP
HVVHIVLAALVENLSMFQGRNHIILPAHDQQLINSLCRHQGLGTTYDWVTVNHEGRIVEEQLIETLSPRSLLF
SLSAAHGLTGVIQPLDPLLSLCKDRRILLHLDISDILGRAPLTPEILNADIITFSSAALGGMGSIGGIFIRKSLERV
FSSWFPPHTSASLCFSAVAAMQTACEERISALPLFTFHTSNLCKKLIQELQSVLPSIQLAFSEVQNRLPNIVVAA
IPDIPAESLAFHLHQGGIYPSLGYERFQPLAQVLQNCGISPFLCHSALHFSLTERSKDLEFSKLARAMHDAIKHL
TPLLGSSS

>core/358/3/Org3_Gene471

MILDFQFSIGYYLRVLELAIRDGTRILAYDRKRLLLDAWPVNDPLPTNYDTSVSTIRQVIHELFSWSAISYSISS
RLLAIIELRLHEEKPQTGWLYRLFFPSKYHIKKAIVDKLCMFKSLILFESKRPVDKIVQAANKVFSKKGKSNFSS
WEDFTHEVTVSEVQTPLAGEVQRRLAADASLQMIIEALTTLEGHTAYLPLSLELLNQFIGEKAQPLKTLSEK
SYVLLRELIQLFSLSAEDFQTIIMSIISDSLSEVLANSIGNQPLTFHGKTFVGLWQETALASPEDSKLALGFLAE
VLRKVIVEKKLHVSKSDNTTPEEVGNIYSIRDQNPALWDKMITMLLMRWLLDYDRDIGIALRKAAEYYNPHP
SFWRQFLRLWQRRP

>core/360/3/Org3_Gene895

MSAMISLSSSHEASIASNTQVRDVLVSLAMDEFVEHNTEILPIKVFLARGTSSSTAIDDLKDVVETEGETHHFQ
VYSNISLKMIIYQRFEEKIFGIGCCPLLLVTDSHHTDPCGALITGIFAAVLFTVLAIVFGPTLGILCYSAYKIYQLT
KKISSLSRTHTEVINSVQKSDPFIHRSGAVAAAAASQSTIKACKVFRQSTLIFFVLGLIITISLAALIVGLVFALFF
LDPGAPAVMTAAMIGCCAAGGTGILLSVIGFLLASVYSVQKSQEGVHHMHTALLRCIVSNTIIQMPYLPITPG
TKKVLTSIRRYQQFFSDDEYRDIESEVPLNRQTTPPSYETLFHEEGSDGSSNVIPRESPPAYSTIDSSNSPFPSS
SPAPYYR

>core/361/3/Org3_Gene1020

MSETIITTPHVVKLISNFFQKKLFSSISTAYPLVIITDVSQVQHLLGPILDHIKMLGYQVIVLTFPPGEPNKTWET
FISLQYQLVDQNISPKSSIIIGGGTVLDMTGFLAATYCRGLPLYLIPTTITAMVDTSIGGKNGINLRGIKNRLGT
FYLPKEVWMCPQFLSTLPREEWYHGIAEAIKHGFIADAYLWEFLNSHSMKMLFSSSQILHEFIKRNCQIKAAIVA
EDPYDRSLRKILNFGHSIAHAETLAKGTVNHGQAVSVGMMIETRISLAEGVMKTPQLIDQLERLLKRFPNPST
LKDLQSIVPEHLHNSLYSPENIIYTLGYDKKNLSQHELMIMIEHLGRAAPFNGTYCASPMEILYDILWSECH
VMRHC

>core/362/3/Org3_Gene735

MLCQQFLIEALARRKSKHTYRSLNSHLIDFTSNDYLGFASSPELRKEYITKLHAIESLGATGSRLLTGHSQ
CQRIEEQLAAYHNFESCLIFNTGYTANLGLLYALATDQDRILHDLYIHASIYDGIKLSKAQSFPFNHNDLNHLE
KRLASSHLGRTFVCVESVYSLHGSVAPLQAISEL CERY SAYLIVDEAHAVGVFGDQGEGLVSALGLQDKVLA
TVYTFGKALGTHGAAIAGSSILKDYLINFCRPFIYT TAQPPHALTAIELAYEHNQRAFNQREHLSALIHFFREK
AQNLGLQLMKDNTTTPIQSICVSGSHRARQAALQIQNSGYDVRPIVSPTVKQREELLRICLHAFNTKNEIDHLL
HTLEQIFLCNVSSL

>core/363/3/Org3_Gene188

MSCFNLTSTNESLRPISPKASFPKQGWQSYFRSALRKHRSDTLSVSVCKVNKYDANL FVRLTVIALAVVGVLI
LFSIMLASIQGTLVITSWPLVTAAILIPTILLTGGMYLHRLGKKVDVISGVCIPPF SRRCWVPISSHTLEKFDEK
HVSACSYLDISTLSADGSGIAAVYQCPPLL FRAFPFCGIPCAMPFVALLRMIYNLIRFLVVPFYIIFRMIYEHFFC
KHLPEDDRFIYKDVAREMGRSLAAFLKAPFYASACMIGAFYSLLDPLAGRVLMG SVERDWN DN VILARSVS
LANEAHSLFRFEGGGGRKGLGQHAFYMLCCQPQSVFLFDKGEIVSGAHPSIQLPERRGLDTSGRYPHISVIPD
SGNDSAKNFIV

>core/364/3/Org3_Gene473

MGINPSGNRSPDDVWVRGAQGDSSSTQGTGATNSNLGAHNVTSTSQPQVASKAKQLWQTVREFFLGKKSP
DSSQGASGPAMQSPSGPTIRPTRPAPPPPTTGGANAKRPATHGKGRAPQPPTAGSSSGSEQPTAMSSEVAKLV
SELKDAVHSHAESQKVLKKVSQELQTKWTDWENNRGPDYLLHGYRVIARALQQTYTEQSMLIEGTSSTGPV
PQAVTVAKDAVTQTVRGAIKNLENPKPGNDPDGVLMQVVISLGIEGPTLDPGESIQNFLETRVSDFGGDDSDI
DYTSDIARLGSALDRVRENHPNEMPRIWIALARELGAAVHSHATSVRIANAGKNHTRDVVRMANESSRLLQ
GMKVLSVGAWANTMTVLIGDLFE

>core/365/3/Org3_Gene653

MIPSPTPINFRDDTILETDPKPSLIMFSSKKTEIASERRKAHPTL FKVLTGIWNIVKFIISIILFLPLALLWVLKKTC
QFFILPSSIISQSMSTAVAIRRM TFLSHIKQLLSLKEISAADRVVIQYDDL VVDSLAIKIPHALPHRWILYSQGN
SGLMENLFDRGDSSLHQLAKATGSNLLVFNYPGIMSSKGEAKRENLVKSYQACVRYLRDEETGPKANQIIAF
GYSLGTSVQAAAALDREVTDGSDGT SWIVVKDRGPRSLADV ANQICKPIASAIKLVGWNIDSVKP SERLRCPEI
FIYNSNHDQELISDGLFERENC VATPFLELPEVKTS GTKIPIPERDLLHLNPLSPNVVDRLAAVISNYLDSEN RK
SQQPD

>core/366/3/Org3_Gene902

MKHLAVLGSTGSIGRQTLEIVRRYPSEFKIISMASYGNNLRLFFQHLEEFAPLAAAVYNEEVYNEACQRFPHM
QFFLGQEGLTQLCIMDTVTTVVAASSGIEALPAILESMKKGKALALANKEILVCAGELVSKTAKENGIVLPI
DSEHNALYQCLEGR TIEGIKKLILTASGGPLL NKSLEELSCVT KQDVLNHPIWNMGSKVTVDSSSTLVNKGLEII
EAYWLFGL ENVEILAVIHPQSLIHGMVEFLDGSVISIMNPPDMLFPIQYALTAPERFASPRDGMDFSKKQTLEF
FPVDEERFPSIRLAQQVLEKQGSSGSFFNAANEVLVRRFLCEEISWCDILRKLTTLMECHKVYACHSLEDILEV
DGEARALAEI

>core/367/3/Org3_Gene952

MKDLGTLGGTSSTAKTVSPDGKVMGRSQUIADGSWHAFMCHTDFSSNNVLFDL DNTYKTLRENGRQLNSIF
NLQNMMLQRASDHEFTEFGRSNIALGAGLYVNALQNLPSNLAAQYFGIAYKIRPKYRLVVFLDHNFS SHVPN
NFNVSHNRLWMGAFIGWQSDALGSSVKVSFGYGKQKATITREQLENTEAGSGESHFEGVAAQIEGRYGKS
LGGHVRVQPFLGLQFVHITRKEYTENAVQFPVHYDPIDYSTGVVYLGIGSHIALVDSLHV GTRMGMEQNFAA
HTDRFSGSIASIGNFVFEKLDVTHTRAFAEMRVNYELPYLQSLNLILRVNQQLQGVMGFSSDLRYALGF

>core/368/3/Org3_Gene617

MEDFSEQQLFFMRRAIEIGEKGGRITAPPNPWVGCVVVQENRIIGEGFHAYAGGPHAEELAIQNASMPISGSDV
YVSLEPCSHFGSCPPCANLLIKHKVSRVFVALVDPDPKVAGQGIAMLRQAGIQVYVGIGESEAQASLQPYLY
QORTHNFPWTILKSAASVDGQVADSQGKSQWITCPEARHVDVGKLRAESQAILVGSRTVLSDDPWLTARQPQG
MLYPKQPLRVVLDSRGSVPPTSKVFDKTSPTLYVTTERCPENYIKVLDSLDVPVLLTESTPSGVDLHKVYEYL
AQKKILQVLVEGGTTLHTSLLKERFVNSLVLYSGPMILGDQKRPLVGV LGNLLESASPLTLKSSQILGNSLKV
VWEISPQVFEPIN

>core/369/3/Org3_Gene654

MNLSNRSDILSGIFSNPHVSYFSSTHAKQLSDFSKKHPILTKIVTIIVKIFKLLIGLIIPPLGIYWLCQLVCSLALF
PRSSMLYSVLKTCFKKYRLEQEIQDYFVKNLDPSFKDPAVSESKRITIQDHLTIDTLAIHFSTARPKRWLLISL
GSGDFLEDMIGLKDSLFLSWKELAKLLGANILIYNYPGVKSSTGKLNLENLATAHNLCAYLQDKIQGPGAN
EIITYGYSLGGVVQSAALQKNPFTNSETSWVAVKDRAPHSLPAAANSFFGPIGKLI AVLARWKMDAEKNSRE
LPCPEILVYSADRF RPSEVGDDTALLPEFTLAHAIKRTPFARSKKFIGE VNLLHSSPLKHPTIQKLAE AILESLSR
KN

>core/370/3/Org3_Gene85

MNTSLKRPLKSHFDVVGSFLRPEHLKKTRESLKEGSISLDQLMQIEDIAIQDLIKKQKAAGLSFITDGEFRRAT
WHYDFMWGFFHGVGHHRATEGVFFDGERAMIDDTYLTDKISVSHHPFVDHFKFVKALEDEFTTAKQTL PAPA
QFLKQMIFPNNIEVTRKFYPTNQELIEDIVAGYRKVIRDLYDAGCRYLQLDDCTRGG LVDPRVCSWYGIDEK
GLQDLIQQYLLINN LVIADRPDDL VVNLHVCRGNYHSKFFASGSYDFIAKPLFEQTNVDGYYLEFDHERSGDF
SPLTFISGEKTVCGLVTSKTPTLENKDEVIARIHQAADYLPLERLSLSPQCGFASCEIGNKL TEEEQWAKVAL
VKEISEEVWK

>core/371/3/Org3_Gene929

MSDNAHNLLYDKFELPEAVKMLPVEGLPIDKHARFIAEPLERGMGHTLGNALRRALLIGLEAPAIISFAMTGV
LHEYMAIEGVIEDVTNIILNLKGALLKKYPMQDSSLGRTTQVLKASISIDASDLAAANGQKEVTLQDLLQEGD
FEAVNPDQVIFTVTQPIQLEVVLR IAFGRGYTPSERIVLEDKGVYEIVLDAAFPVTLVNYFVEDTRVGQD TDF
DRLVLIVETDGRVTPKEALAFSTQILTKHFSIFENMDEKKIVFEEAISIEKENKDDILHKLILGINEIELSVRSTNC
LSNANIETIGELVIMPEPRLLQFRNFGKKSLCEIKNKLKEMKLELGMDLTQFGVGLDNVKEKMKWYAEKIRA
KNIKG

>core/372/3/Org3_Gene255

MNGKAPLALYIHIPFCTKKCRYCSFYTIPYKSESVSLYCNAV IQEGLRKLAPIQETHFIETVFFGGGTPSLVSPL
DLKRILKELAPHAREITLEANPENLTVSYLRQLQETPINRISVGVQTFDD SILQLLGRTHSSSAITALQECQNH

GFSNLSIDLIYGLPTQSLEIFLSDLHQALTLPITHISLYNLTIDPHTSFYKHKILVPTIAQEEILAEMSLLAENLLL
SQGFQRYELASYAKPDYPAKHNLYYWTD RPFLGLGV SASQYLHGERSKNYSHISHYLRAVRKNLPTQETSEI
LPKKERIKEALALRLRLLEGADLAEFPSTLISMLTQDVKLQNLFSVHGQCLALNRQGRLFHDTIAEEIMGYSF

>core/373/3/Org3_Gene763

MSIAIAREQHAAILDMHPKPSIAMFSSEQARTSWEKRQAHPYLYRLLEIHWGVVKFLLGLIFFIPLGLFWVLQK
ICQNFILLGAGGWIFRPICRDSNLLRQAYAARLFSASFQDHVSSVRRVCLQYDEVFIDGLELRPNAPDRWM
LISNGNSDCLEYRTVLQGEKDWIFRIAEESQSNILIFNYPGVMKSQGNITRNNVKSQYQACVRYLRDEPAGPQ
ARQIVAYGYSLGASVQAEALSKEIADGSDSVRWFVVKDRGARSTGAVAKQFIGSLGVWLANLTHWNINSEK
RSKDLHCPELFIYGKDSQGNLIGDGLFKKETCFAAPFLDPKNLEECSGKKIPVAQTGLRHDHILSDDVIKEVAG
HIRRHFDN

>core/374/3/Org3_Gene135

MALKFHLLHQSKKSQARVGGIETSHGVIDTPAFVPVATHGALKGVIDHSDIPLLFCNTYHLLLHPGPEAVAKL
GGLHQFMGRQAPIITDSGGFQIFSLAYGSVAEEIKSCGKKKGMSLVKITDEGAWFKSYRDGRKLFLSPELSV
QAQKDLGADIIPLELLPFHTDQEYFLTSCSRITYVWEKRSLEYHRKDPRHQSMYGVHGGLDPEQRRIGVRF
VEDEPFDGSAIGGSLGRNLQEMSEVVKITTSFLSKERPVHLLGIGDLP SIYAMVGFIDSFDSSYPTKAARHGLI
LSKAGPIKIGQQKYSQDSSTIDPSCSCLTCLSGISRAYLRHLFKVREPNAAIWASIHNLHMQVMKEIREAIL
KDEI

>core/375/3/Org3_Gene843

MAPIHGSNAFVEDILHSHPSQATYFSSTRAQKLHEFKDRHPVLTRIASVIIKIFKVLIGLIILPLGIYWLCQTLCT
NSILPSKNLLKIFKKQPNKTKLKTNYLRALQDYSSKNRVASMRRVPILQDNVLIDTLEICLSQAPTNRWMLISL
GSDCSLEEIACKEIFDSWQRF AKLIGANILVYNYPGVMSSTGSSSLKDLASAHNICTRYLKDKEQGP GAKEIIT
YGYSLGGLIQAEALRDQKIVANDDTTWIAVKDRCP LFISPEGFHSCRRIGKLVARLFGWGTKAVERSQDLPC L
EIFLYPTDSLRRSTVRQNKLLAPELTLAHAIKNSPYVQNKEFIEVRLSSDIDPIDSKTRVALATPILKKLS

>core/376/3/Org3_Gene246

MSTTEPNLTNVNLTMLISSESMPTQLASHKLKGLDLVAFILIIGIAVSSGTAAIILGIPLL FILTALAVLA FSILLY
FLLREPKSPISVTHQPTPIIKD TDLPVPPLALTPVPTEAVLEEPP LPSRTHQTLLQENWDRIPDLQANTDMPFI
AADNQ TGYAWHLKNSNLTLISTLGPIEKPRYKTQGIVMIVNAATPNMANNVKGTSLALAKATSVRCWENSK
KSPDPLRSKQPLQLGECRS AKWENLNGTTNAGKAGLPQFLGQLLGPKASDYNYNPND AFTFCRQAYLNC LN
EAKRRKTTVVQLPLLSSHFP GSPKDEETSLRLQWIDGVKLALIDALQTFGSEAENQNQPWV IILTTLARHPLI
TP

>core/377/3/Org3_Gene493

MAVAADSSASWLKSRNNFLSSLGKTEEQVA APEFPKELCQHKIREKFRLEDVQVSIKFRGSITAVEATKEFGV
HLLIQPMVVQPWEVENLLFLTSEEDLQELMVA VFDDASLASFYFEKDKLLGFHYFVAEACKLFEELQWVP
SLSAKVGGDAIFTATSLQGSFQVVDISRLD GKNVRCRLLLPEDTFQSCQKFFSGLHDESDLHNIDQTQQISLS
VEVGYSQLTQEEWHQVVPGSFIMLDSCLYDPETEESGALLTVQKHQFFGGRFLTPSSGEFKITSYPNLTHEDP

PLPENPQASAAPLPGYSRLVVEVARYSLAVSEFIKLNLSILSLGNHPAYGVDIILDGAKVGRGEIHALGDVLGI
RVLEV

>core/378/3/Org3_Gene266

MIYLDNNAMTPPERGLLEFLQKTFLIEGTYANPSSVHQLGKKSRQLVLEASHWMQKVLSFQGRVLYTSGATE
SLNLAIASLPKDSHVITSGSEHPAILEPLKHSSLSVSYLNPEEGRCVLTIEQIERAVTPKTSAILLGWVNSETGAK
ADIAAIAHFAQERQLQFIVDATANVGKERIVLPSGVTMAAFSGHKFHALSGIGALLVSPGVKLHPQLWGGGQ
QGGLRAGTENLWGIASLLYIFKYLDLHQERISQEILTHRNGFEKAIAKARIPDVHIHCADQPRANNVSAIAFPPL
EGEVLQIALDIEGVACGYGSACSSGATAPFKSLVSMGVDEELTLATLRFSSFHLLLQEDVERAVGIIKVVVERL
KNS

>core/379/3/Org3_Gene649

MTTSDVIDFVTNDFLGFARSPTIYCEVSKRFQIHCQQFPHEKLGIRGSRLMVGPPSSVIDDLESKIASYHGAPNA
FIVNSGYMANLGLCHHVSRSTDVLLWDEEVHMSVVHLSLSAISGQHHTFHNNLEHLESLLQCYRISSKGRIFI
FVSSVYSFRGTLAPLEQIIALSKKYHAHLIVDEAHAMGIFGDDGKGLCHALGYENFYAVLVITYGKALGTMG
ASLLTSSEVKYDLMQNSPPLRYSTSLSPHTLISIGTAYDFLASEGEIARKQVFKLKEHFHECFDSHAPGCVQPIF
LPHTCLEEAISVLETTGIHVGVAFAKHPFLRVNLHAYNTVDEVNLLAQVMKPYLEKSSHRVHINHEFHLWR
ELCQH

>core/380/3/Org3_Gene970

MMLVYCFDPSVPTSPEHRLMAALDRWFFLGGHRVRILTLEGNHYRAFQENMSISTVEKILKLISYLLIPIVLIA
LLIRCFLHSRFGKCNWKCDLSLDARVPHDVQPFNDFQLFNNQERLNIWKNRRYVSGIDVLMVPVDYLRSQFPG
FKEIPEAIRCENYVSDGQFSEESKTSYLRAMLTDIVGYILSLDETYWTNVILKIRAMCITFESFPGKEADPNYSP
RVTHHYFDESWKALARHVLGEGNMVNRLDEALIRTEKPGKEGECITKQFLKDYCKKHLEVMSCPDFIESLV
DEKIREFRCP SILNSAVCDVIDRKCQEHLKAIINEANRRLPGMKNSSFTMRGNQVLFYTIFSPPKLPPAASSVY
F

>core/381/3/Org3_Gene340

MTTCLPQPPKTSPLYSIFEKLDAQERLSSDALHLLLLTNKEDQRTLWNFADQVRKQRVGDTVYYSSSTLYLY
PTNFCDFSCKFCSFYAKPGDPKGWLYSPDDLQIQNIKTPITEVHIVGGCFPSCNLQYYSDLFTKIKEYDPQIH
IKALTAIEYAYLSDLNLSIRDVLLTLKDAGLDSIPGGGAEILVDKIRNFLAPKRLSSSDFLNIHKMAHQLGIHS
NITMLCYHKEGPEDLVTHMVKVRDLQDETQGFKNFILLKFAQENNVLGKRLRKSGQGHAIPKSLMAVARIF
LDNFSNMKALWNYLGIEAALDLLSCGANDLSSTHMGEKVFMMASSKEPIKMDAEGMAALITQQGRTPCLTN
SSHV

>core/382/3/Org3_Gene1007

MRRQVREIMQQTIVIVAMSGGVDSSVVAYLFKKFTNYKVIGLFMKNWEEDSEGGLCSSTKDYEDVERVCLQ
LDIPYYTVSFAKEYRERVFARFLKEYSLGYTPNPDILCNREIKFDLLQKKVQELGGDYLATGHYCRLNTELQE
TQLLRGCDPQKDQSYFLSGTPKSALHNVLFP LGEMNKTEVRAIAAQAALPTAEKKDSTGICFIGKRPFKEFLE
KFLPNKTGNVIDWDTKEIVGQHQAHHYYTIGQRRGLDLGGSEKPCYVVGKNIEENSIYIVRGEDHPQLYLRE

LTARELNWFTPPKSGCHCSAKVRYRSPDEACTIDYSSGDEVKVRFSQPVKAVTPGQTIAFYQGDTCLGSGVID
VPMIPSEG

>core/383/3/Org3_Gene271

MTKIAFSEKAKNFPVEALKKWFENKRSRSLPWRDNPTPYSVVWSEVMLQQTRAEVVIDYFNQWMERFPTIES
LAAAKEEDVIKLWEGLGYYSRARHLLLEGARMVMEEFHGKIPDDAISLAQIRGVGPYTVHAILAFAFKRRAAA
VDGNVLRVLSRIFLIETSIDLESTRTWVSRIAQALLPHKSPEVIAEALIELGACICKKVPQCHRCPPVRQACGAW
RENKQFVLPVRHARKKVIFLHRLVAIVLYDGSLVVEKRRPKEMMAGLYEFPYIEVEPEEGLQDIEGFTKKME
LSLESPLEFLGNLKEQRHAFTNHKVHLCPIIFKATSLPQFGELHLLSDIDHLAFSSGHKKIKDALLIYLGDVRSR
ESIGV

>core/384/3/Org3_Gene390

MQENLDKRLEALRTEISLAARSLFDLDDKKQKELQVLEESSEENFWQDSVHAGKISEQIVSLRRQIQEYQELK
SKIDAIEFFLEDADALEDPAICEDLEKEFLFCEKKLAVWETQRLLSGEADKNSCFLTINAGAGGTESCDWVEM
LFRMYSRWATKHQWALEVVDRLDGEVVGIKHVTVKFSGMYAYGYAKAERGVRHLVRISPFDSNGKRHTSF
ASVDVFPEIDDQIKIEIRPNDLRIDTFRSSGAGGQHVNVTESAVRITHLPSGVVVSCQNERSQIQNRESCMKML
QAKLYQQVLQERLEKQSLDRKDKKEIAWGSQIRNYVFQPYTLVKDVRTGHETGNVQAMLDGELLDEFIKAY
LAEFGEVS

>core/385/3/Org3_Gene35

MAVEGRVNSSQALNQDCQEVLANQSKGLLRCRILSIVVAVITFIAGVVLIALTASILTSVPYLALGVFLIV
TLGCIIFALCSEKIKKVPPTPISHKEEIIAWFEERKNIDMEKEKEDPEHFGRTATDIPMRSALDQFNHSCHHIHES
PALTETYRSHQDVLLFKDWCPVTLPDVTSEEEVLIRSVVGSYLLMEACVPKVSMLIDELHNKCLKSPSERECLF
IDKKTQQRKASFLFTQKDLATFFLAYTRVNDGHLAPFRAGAKWILIHVRLRRQHNQNDFFTPGHSCYYARL
AFNQTQRLYHQLFNVEKLRSIYANMDKDPLCHPWAFIPIYDLLKTEDHGDGFLEQQEDREYPSRAAQDQFW
G

>core/386/3/Org3_Gene601

MSPHRNLFKLKNFSNRLYNRALGRFDKVFNFSSGNVGIDLGTANTLVYVRGRGIVLSEPSVVAQTHAVL
AVGHKAKAMLGKTPRKIMAVRPMKDGVIADFEIAEGMLKALIKRVTPSRSVFRPRILIAVPSGITGVEKRAVE
DSALHAGAQEVLIEEPMAAAIGVDLPVHEPAASMIIDIGGGTTEIAIISLGGIVESRSLRIAGDEFDECIINYMR
RTYNLMIGPRTAEEIKITIGSAYPLGDQELEMEVRGRDQVAGLPITKRINSVEIRECLAETPIQQIIECVRLTLEKC
PPELSADLVERGMVLAGGGALIKGLDKALSKNTGLSVITAPHLLAVCLGTGKALEHLDQFKKRKGNLV

>core/387/3/Org3_Gene900

MKFVVSRLNELGNLIKKIQSVVPQNTPIPVLTHTVLIETYNDELVFTATDLTVSTRCVTKAKVYEKGAISIPSKRF
FQLVKELTEANLEISSAGEMAQITSGSSCFRLLSMEKEDFPMLPDIQNALRFSPLAEQLKTMQLQRTSFVAVSRE
ESRYVLTGVLLAIANGVATIVGTDGKRLAKIDAEVTLDKSFSGEYIPIKAVEEIIKMCSDEGEATIFLDQDKIA
VECDNTLLITKLLSGEFPDFSPVISTESNVKLDLHREELITLLKQVALFTNESSHSVKFSFLPGELTLTANCTKV
GEGKVSMVAVNYSSELLEIAFNPFFFLDILKHSKDELVSLGISDSYNPGIITDSASGLFVIMPMRLHDD

>core/388/3/Org3_Gene700

MLIWKRHLLTRFWFALTSLVLALIFYASIHHSHTLKGASTAASGASVKLSILYYLAQISLKAEFLMPQLVA
VATTSTLFAMQNKREIILLQASGLSLKSLMHPLLLSGAVIMMVLYANFQWLHPICEKISITKENMDRGTDDKE
QGKIPALYLKDQTVLLYSSIEPKTLTLNNVFWIKDPKTIYTMEKLAFTTSLPIGLNVTQFFANDSENLELKEFF
DMKEFPEIEFNFYENPFSLKFSAGNKNRLSEFFKAIPWNATGLGLSTQVPQRILSLLAQFYVVLISPLACMAAII
LSAYLCLRFSRTPTVTLAYLIPLGTVNIFFVFLKAGIVLASSSVLPTLPVMAFPLIVLFLLTNYAYAKLQ

>core/389/3/Org3_Gene380

MKFPRISISDLIPTQMVIWWRGGGNVHYVPNAQNLPKKILGGVLACFGLALLGCAAFAGVCQTIFPCIGLMI
LGLVLLGFAYLQYSKGWSRFRPLFRETKVFEKPINWLGCLSLLQSWKKIRPGCYHHPGCPQVEICEGSQEIV
TKIFQKKSDRNTSIFLIQEMDQIALRQGIEKSSLSRKTFIDPSVVSSLLSEIQREEQQYLDPKVISWSSEDQASD
RTHPKSAIYVNISDAAQEPQGRCYIDAYTKAFFTVLDQIGDPNIVKKHTIYVLTPILGVPDALPKEEQENLKL
SQAFLYSAEQVAKRMREEKQDSIRIKFIFTDPTSPTSIFYSPHSSSTPHSVTPISLSGFVGEQESYTFA

>core/390/3/Org3_Gene860

MSKKIKVLGHLLCTLFRGVLCAAALSNIGYASTSQESPYQKSIEDWKGYTFTDLELLSKEGWSEAHASNG
SRIVGASGAGQGSVTAVIWESHLLIKHLGTLGGEASSAEGISKDGEVVGWSDTREGYTHAFVFDGRDMKDL
GTLGATYSVARGVSGDGSIIVGVSATARGEDYGWQVGKWEKGKIKQLKLLPQGLWSEANAISEDGTVIVG
RGEISRNHIVAVKWNKNAVYSLGTLGGSVASAEAISANGKVIVGWSTTNNGETHAFMHKDETMHDLGTLG
GGFSVATGVSADGRAIVGFSVKTGEIHAFYYAEGEMEDLTTLGGEEARVFDISSEGNDIIGSIKTDAGAERA
YLFHIIHK

>core/391/3/Org3_Gene351

MKKRFPSTLFLFYRRVTIAISLEGILGWGWLGSLLSKVFAFLVACWNRFSWSTPYRARSTVISVGNIVVGGAG
KTPTVLWLAELRLRGYSCGVLSRGYKSQSSRQKCLTVVDSKVHSASYVGDEPLLMAEKLPEGSVWVHKD
RRISAARAAEKFGILLDDGLQYRKLHKDVEIAVVNGQDPLGGRAFFPKGRLRDFPLRLKTVDAIIVNGGGKE
AGTVVKRVSNAPOIFVKPTIASVVWTHNGERIPKEALRELRVGVFCGLGFPQGFLNMLREEGIHILGKYLLPD
HAAITKKELNYFCQQMAMRQGQGLLCTEKDSVKLPRLSGEVSLPIAKVEMRLSVNQDDTLNLMIEQIHK
NRGN

>core/392/3/Org3_Gene922

MNVPDSKNLHPPAYELLEIKARITQSYKEASAILTAIPDGILLSETGHFLICNSQAREILGIDENLEILNRSFTD
VLPDTCLGFSIQEALESKVPKTLRLSLCKESKEKEVELFIRKNEISGYLFIQIRDRSDYKQLENAIERYRNIAEL
GKMTATLAHEIRNPLSGIVGFASILKKEISSPRHQRMLSSIISGTRSLNNLVSSMLEYTKSQPLNLKIINLQDFFS
SLIPLLSVSFPNCKFVREGAQPLFRSIDPDRMNSVWNLVKNVETGNSPITLTLHTSGDISVTNPGTIPSEIMD
KLFTPFFTCKREGNGLGLAEAQKIIRLHGGDIQLKTSDSAVSFFIIPELLAALPKERAAS

>core/393/3/Org3_Gene212

MSHTECGIVGLPNVGKSGLFNALTGAQVASCNYPFCTIDPNVGIVPVIDERLEALAKISNSQKIIYADMKFVDI
AGLVKGASDGAGLGNRFLSHIRETHAIAHVVRCFDDPDVTHVSGKVNVPVEDIEVINLELIFSDFSSAKNIHSLK

EKLA KGKREVGALLPLFDTHIAHLEKGLPLRTLELTPEQIVALKPYPFLTMKPMFYIANVDESSLPDMDNDYV
AAVREVA AKENSKVVPICVRIEEEEIVSLPIEERLEFLMSLGLEKSGLHRLVRAAYDTLGLISYFTTG PQESRAW
TVVRGSSAWEAAGEIHTDIQKGFIRA EVITFEDMIECQGRAAARELGKLHIEGRDYIVQDGD TMLFLHN

>core/394/3/Org3_Gene252

MTTEVRIPNIAESISEVTVASLLVTEGALIQENQGLLEIESDKVNQLIYAPVSGRIFWEVSEGDVVPVGGVVGKI
EPAGEGEELGDSQSKETIEAEIICFPQSGVRQSPPENKTFIPLRDQMDQGSQGLSAGDRGETRERMTSIRKTISR
RLLSALHESAMLTTFNEVYMTPLFHLRKEKQEEFLSRYG VKLGFM SFFVKAVLEALKAYPRVNAYIDGEEIV
YRHY YDISIAVGIDRGLVVPVIRDCDKLSNGEIEQKLADLALRAREGLLAIAELEGGGFTITNGG VYGSLSTPI
INPPQVGILGMHKIEKRPVVDNEIVIADMMYVALSYDHRLIDGKEAVGFLVKVKEGLENPASLLDL

>core/395/3/Org3_Gene470

MVPFRQHHAYQLLKQLHTSAISEADRVSYFQKQNRSLGSKDRQWIQNIIFNILRHRRLLETILDSGEQVTPEA
LVAKVNEGVLNLDSSAIPWPVRY SISDDL AHFLVQDYGEEQAEEIAKIWLTEAPITIRVNTDKISVKELQEK
LEY PSSPGELPEALHFSKRHPLQSTEAFRRGFFEIQDENSQRISQGISLTDKDIVLDFCAGAGGKSLIFAQKAKH
VVINDSRKAILQTAKHRLLRAGARNFSLADQLRLGSFSVVIVDAPCSGTGVFRRHPEHKWQFSKKLLLNYVR
VQKSILKQASAYVGPRGRLVYITCSLLKEENEAHVAYMHSLGWKEVHRKTLPLQVGKGDAFFTSHFQKI

>core/396/3/Org3_Gene746

MKLYQTLRGIVLVSTGCIFLGMHGGYAAEVPVTSSGYENLLESKEQDPSGLAIHDRILFKVDEENVVTALDVI
HKLNLLFYNSYPHLIDSFPARSQYYTAMWPVVLESVIDEFLMVADAKAKRIATDPTAVNQEIEEMFGRDLS
LYAHFEMSPNDIFNVIDRTLTAQRVMGMMVRSKVMLKVTPGKIREYYRKLEEEASRKVIWKYRVLTIKANT
ESLASQIADKVRARLNEAKTWDKDRLTALVISQGGQLVCSEEF SRENSELSQSHKQELDLIGYPKELCGLPKA
HKSGYKLYMLLDKTS GSIEPLDV MESKIKQH LFALEAESVEKQYKDRLRKRYGYDASMIAKLLSEEAPPLFS
LL

>core/397/3/Org3_Gene923

MAFKRKTRWLWQVLILSVGLNMLFLLFYSAIFRKDIYKHLHLSGPLIAKSSRKVYLSEDFLNEISQASLDDLI
SLFKDERYMYGRPIKLWALSVAIASHHIDITPVLSKPLTYTELKGSSVRWLLPNIDLKDFPVILDYLRCHKYPY
TSKGLFLLIEKMVQEGWVDEDCLYHFCSTPEFLYLRTLLVGADVQASSVASLARMVIRCGSERFFHFCNEESR
TSMISATQRQKVLKSYLDCEESLAALLLVHDSDVVLHEFCDEDLEKVIRLMPQESPYSQNFFSRLQHSPRRE
LACMSTRRVEAPRVQEDQDEEYVVQDGD SLWLI AKRFGIPMDKIIQKNGLNHHRLFP GKVLKLP AKQS

>core/398/3/Org3_Gene1015

MAVVSTPFFNRNLWYRLLSSRFS LWKSYCPRFFLDYLEAFGLLSDFLDHQA VIKFFELETHFSYYPVSGFVAP
HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ
RIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQET
LFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFVLCQ

>core/400/3/Org3_Gene69

MKIDILSLFPGYFDGPLQTSILGRAIKQRLLDVQLTNLRDFGLGKWQVDDTPFSGGGMLLMAEPVTSAIRSV
RKENSKVIYLS PQGALLTAEKSRELA AASHLILLCGHYEGIDERAIESEVDEEISIGDYVLTNGGIAALVLIDAV
SRFIPGVLGNQESAERDSL ENGLLEG PQYTRPREFEGKEVPEVLLQGDHKAISQWRLEQSERRTYERRPDLYL
NYLYKRSIDHKFDEETTTNRDHF KCDKISVVLEV NKLKRAKNFYCKVFGLDAMSCENKFCLPHEGKTIFWLR
EVQAEKKNIVTLSLSLDCACEEDFCYLLRRWELFGGKLL EKQADEHAVWALA QDLDGHAWIFSWHRMK

>core/401/3/Org3_Gene213

MGEKTEKATPKRLRDARKKGVAKSQDFPSAVTFIVSMFTA FSLSTFFFKHLGGFLVSMLSQAPTRHDPVITL
FYLKNCLMLILTASLPLLGAVAVVG VIVGFLIVGPTFSTEVFKPDIKKFNPIENIKQKF KIKTLIELIKSILKIFGA
ALILYITLKS KVS LIIETAGVSP IITAQIFKEIFYKAVTSIGIFFLIVAILDLVYQRHNF AKELKMEKF EVKQEFKD
TEGNPEIKGRRRQIAQEIA YEDSSSQVKHASTVVS NPKDIAVAIGYMPEKYKAPWIIAMGINLRAKRILDEAEK
YGIPIMRNVPLAHQLLDEGKELKFIPESTYEAIGEILLYITSLNAQNPNKNTNQP DHL

>core/402/3/Org3_Gene198

MSEAPVYTLKQLAELLQVEVQGN IETPISGVEDISQAQPHHIAFLDNEKYSSFLKNTKAGAILSRSQAMQHA
HLKKNFLITNESPSLTFQKCIELFIEPVTSGFPGIHPTAVIHPTARIEKNVTIEPYVVISQHAHIGSDTYIGAGSVIG
AHSV LGANCLIH PKVVIRERVLMGNRVVVQPGAVLGSCGFGYITNAFGHHKPLKHLGYVIVGDDVEIGANTT
IDRGRFKNTV IHEGTKIDNQVQVAHHVEIGKHSIIVAQA GAGSTKIGE HVIIGGQTGITGHIS IADHVIMIAQTG
VTKSITSPGIYGGAPARPYQETHRLIAKIRNLPKTEERLSKLEKQVRDLSTPSLAEIPSEI

>core/403/3/Org3_Gene347

MSGPSRTESSQVSVLSYVPRDKEIAPKKQFTIAKISTLAILASLALGALVAGISLTIVLGNPVFLALLITTALFSV
VTFLVYHQMTSKVSSNWQKVLEQNFKPLGKA WQEK NVDCYSNEMQFYNNHLNPKFKVAIQTDASQPFQPT
FLTGLRVIEKNQSTGIIFNPVGPTNLIDNTATNLSTILYSTLKDKSVWDTCKQREGGPAKGEDPFSPT EVRVVK
LPNEALDQTFNLNLSSAEKKSILPTFLGHVCGPKSEELPNQQEYYRQALLAYENCLKAAIESHAAI VALPLFTS
VYEVPP EEILPKEGTFYWDNQTQAFCKRALLDAIQNTALRYPQRSLLVILQDPFNTIESQSRSEE

>core/404/3/Org3_Gene730

MKNSFGSLFSFTTWGESHGPSIGVVIDGCPAGLELHESDFVPAMKRRRPGNPGTSSRKENDIVQILSGVYK GK
TTGTPLSLQILNTDVDSSPYENSERLYRPGHSQYTYEKKFGIVDPNGGGRSSARETACRVAAGVVAEKFLAN
QNIFTLAYLSSLGSLTLPHYLKISP ELIHKIHTSPFYSPLPNEKIQEILTSLHDDSDSLGGVISFITSPIHDFLGEPLF
GKVHALLASALMSIPAAKGFEIGKGFAS AQMRGSQYTDPFVMEGENITLKSNNCGGTLGGITIGVPIEGRIAF
KPTSSIKRPCATVTKTKKETTYRTPQTGRHDPCVAIRAVPVVEAMINLVLADLVLYQRCSKL

>core/405/3/Org3_Gene937

MTLPNDLLET LVKRKESPQANKVWPVTTFSLARNLSVSKFLPCLSKEQKLEILQFITSHFNHIEGFGEFIVLPLK
DTPLWQKEFLLEHFLLPYDLVGNPEGEALVVS RSGDFLAAINFQDHLVLHGIDFQGNVEKTL DQLVQLDSYL
HSKLSFAFSSEFGFLTTPNPKNCGTGLKSQCFLHIPALLYSKEFTNLIDEEVEIITSSLLLGVTFPGNIVVLSNRC
SLGLTEELLSSLRITASKLSVAEVA AKKRLSEENSGDLKNLILRSGLLTHSCQLELKETLDALSWIQLGIDL
LIKVTENHPLWNPLFWQIRRAHLALQKQAENSRDLQKDTISHLRASVLKELTKGLSPESF

>core/406/3/Org3_Gene637

MMKKIRKVALAVGGSGGHIVPALSVKEAFSREGIDVLLLGKGLKNHPSLQQGISYREIPSGLPTVLNPIKIMSR
TSLCSGYLKARKELKIFDPDLVIGFGSYHSLPVLLAGLSHKIPLFLHEQNLVPGKVNQLFSRYARGIGVNFSP
VTKHFRCPAEEVFLPKRSFSLGSPMMKRCTNHTPTICVVGGSQGAQILNTCVPQALVKLVNKYPNMYVHHIV
GPKSDVMKVQHVYNRGEVLCCVKPFEEQLLDVLLAADLVISRAGATILEEILWAKVPGILIPYPGAYGHQEV
NAKFFVDVLEGGTMILEKELTEKLLVEKVTFALDSHNREKQRNSLAAYSQQRSTKTFHAFICECL

>core/407/3/Org3_Gene66

MKKKVAEYLNRLAEVEIKISNPEIFSNSKEYSALSKEHSYLLELKNAAYDKILNLEKVLADDKQALAIEKDP
VVMLEEGINENKVELEKLNKILESLLVPPDPDDDLNVIMELRAGTGGEAAALFVGDCVRMYHLYASSKGWK
YEVLSASESDLKGYKEYVMGISGTGVKRLLQYEAGTHRVRVPETETQGRVHTSAITIAVLPEPSEEDTELLI
NEKDLKIDTFRASGAGGQHVNVTDASVRITHLPTGVVVTCQDERSQHKNKDKAMRILKARIRDAEMQKRHN
EASAMRSAQVGSGDRSERIRTYNFSQNRVTDHRIGLTLYNLDKVMEGDLDPITTAMVSHAYHQLLEHGN

>core/408/3/Org3_Gene701

MPILWKVLIFRYLKTAAFCTLSLICISIISSLQEIVAYIAKDVPYDTVLRLMAYQIPYLLPFILPGSCFVSAFSLFR
KLSDNNHMTFLRASGASQSIIMFPVLMVSGAICCLNFYTCSELASICRYQTCKEIANMAMTSPALLLQTLQKK
ENNRIFIAVDHCAKSKFDNVIVALKGNNEISHVGIKSIIPDTTKDTVAKDVFISKLPDSLTESSSPSSQRFYIE
TLDELLIPKITSTLFAGKSYLKTRTDYLPWKQLVKQSLKHSHPETLRRVAIGFLCITLTYAGMILGIHKPRFRK
SIALYFIFPILDILLIVGKNTKNLPLAFMLFVFPQLVSWVVF AARAYRESRGYA

>core/409/3/Org3_Gene272

MSLLSGHRLEGFPPIAEVMAACDRCSMDFCEILKSQSMDLWADAASCVDGLLQDPFWSTAIASGIAKSSLQE
TEFECESKVMVLSSWGEQGAQVCSPFNLERICMSFPSLKVFSLKKNGCENMGIQLSASCMNLLMSIFFVATN
GGSTPIWITKENLMALVALVLSHYQCYFVPATGDPQRGNILGNPEVNAILARGMGMRVDLERKRGGESSSR
YLELAARCFENSLTKTSLSDANNVQERDKCLLQMSTSLMHTAGLNLQRPPVPTPSGVT AHPQPQDPVPTS
QPSLLGARERSPVSSRGRFPVVLPLSVISPRSHPGRVERRDLEDEEEVVMF

>core/410/3/Org3_Gene574

MSHDRILRAQRALSEHNLDAILVEKSEDLAYFLHDEAIAIGILLIGQQEVMFFVYRMDKDLYSHIQRVPLTFLT
QDVVADLSLYVQKQRYQKIGFDSASTVYHKFAQRQVLPCLWEPLECFTEKIRSIKSEEEIRRMQEAALGSA
GYDYVL TLLREGITEKEVVRQLRAFWAEAGAEGPSFPPIAFGEHSAPHSIPTDRPLKKGDIVLIDIGVLLNGY
CSDMTRMTALGTPHPKLLESYPVVVEAQKRAMALCKEGLWGDIDAEAVRVLREHHLDTYFIHGIGHGVG
RHIHEYPCSPRGSQVKLESGMTITVEPGVYFPGIGGIRIEDTLCIDKNKNFSLTARPVISELVCL

>core/411/3/Org3_Gene220

MNKRQKDCLKICVIISTLILVGIFARAPRGDTFKTFLKSEEAIYSNQCNE DMRKILCDAIEHADEEIFLRIYNLS
EPKIQQSLTRQAQAKNKVTIYYQKFKIPQILKQASNVTLVEQPPAGRKL MHQKALSIDKKDAWLGSANYTNL
SLRLDNNLILGMHSSELCDLIITNTSGDFS IKDQTGKYFVLPQDRKIAIQAVLEKIQTAQKTIQVAMFALTHSEII

QALHQAQQRGIHVDIIDRSHSKLTFKQLRQLNINKDFVSINTAPCTLHHKFAVIDNKTLLAGSINWSKGRFSL
NDESLIILENLTKQQNQKLRLMIWKDLAKHSEHPTVDDEEKEIIEKSLPVEEQAAA

>core/412/3/Org3_Gene536

MNLDPDRKKALEAAVAYIEKQFGAGSIMSLGRHSATHEISTIKTGALSDDLALGIHGVPKGRVIEIFGPESGKT
TLATHIVANAQKMGGVAAYIDAEHALDPSYASLIGVNIDDLNISQPDCEGALSIAELLARSGAVDVVIDSV
AALVPKSELEGDIGDVHVGLQARMMSQALRKLATLSRSQTCVFINQIREKIGVSFGNPETTTGGRALKFYSS
SIRLDIRRIGSIKGSNDSDIGNRIKVKVAKNKLAPPFRIAEFDILFNEGISSAGCILDALAVEYNIEKKGSWFNYQE
KKLGQGREFVREELKRNRLFEIEKRIYDVIAANKTPSVHANETPQEVPAQTVEA

>core/413/3/Org3_Gene642

MNLCKRISFEEGLELTVSSPIERLQERADAIKERYPSNEVTYVLDANPNYTNICKIDCTFCAFYRKPKSPDAY
LLSFDEVRSLLQRYVSSGVKTVLLQGGVHPGLGIDYLEELVRITVQEFPSIHPHFFSAVEIEHACRVSGISIEQG
LQRLWDAGQRTIPGGGAELSERVRKIISPKKMQPGGWINLHKLALHLMGFRRTATMMFGHVENPEDILHLQ
TLRDAQDSCPGFYSPFWSYKPGNTALRRNVPQQASIETYRILALGRIFLDNFDHVAASWFGEGKSLGAKAL
HYGADDFGGVILDESVMKATGWSIQSSEEEICNIIRSEGFIPVERNTFYQHISCTVSSL

>core/414/3/Org3_Gene647

MKYSLNFKEIKIDDYERVIEVTCSEKVRHLHAIHQTAVGPALGGVRASLYSSFEDACTDALRLARGMTYKAI
SNTGTGGGKSVIILPQDAPSLTEDMLRAFGQAVNALEGTYICAEDLGVSINDISIVAEETPYVCGIADVSGDPSI
YTAHGGFLCIKETAKYLWGSSSLRGKKIAIQGIGSVGRRLQLSLFFEGAELYVADVLERAVQDAARLYGATIV
PTEEIHAECDIFSPCARGNVIRKDNLADLNCKAIVGVANNQLEDSSAGMMLHERGILYGPDYLVNAGGLLN
VAAAIEGRVYAPKEVLLKVEELPIVLSKLYNQSKTTGKDLVALSDSFVEDKLLAYTS

>core/417/3/Org3_Gene182

MLNIHDILGNDDENLLSYQCKHITKDKLTLPSHDFVDKVFGLSDRNNRVLRSLQTMFSHGRLANSGLYSILPV
DQGIEHSAGASFAINPIYFDPENIVKLAIESGCSAVASTYGTLSLLSRKYAHKIPFMLKLNHNELLSYPTKYHQI
FFTQVEAAYSMGAVAVGATVYFGSETSNEEIVAVSNAFAKARSLGLATVLWCYLRNPAFVANGVDYHTAA
DLTGQADHLGATLGADIVKQKLPTCQGGFKAINFGKTDERVYSELSSNHPIDLCRYQVLNSYCGKVGLINS
GPSGKNDFTEAARTAVINKRAGGMGLILGRKAFQRPLSEGIQLNLVQDIYLDPNITIA

>core/418/3/Org3_Gene847

MIPLIPMFLKQSLFFSLALTGMTTLVLTVSLGVPVMKWLKRKNYRDYIHKEYCEKLEMLHKDKAEVPTGGG
VLLFISLIASLLVWLPWGKFSTWFFIILLTCYAGLGWYDDRIKIKRKQGHGLKAKHKFMVQIAIAAFTLIALPY
IYGSTEPLWTLKIPFMEGMLSPLFWLGKVFCLGLALVAIIGTSNAVNLTGDLGLAAGTMSFAALGFIFVALR
SSTIPIAQDVAYVLAALVGACIGFLWYNGFPAQLFMGDTGSLLLGGLLGSCAVMLRAECILVIGGVFVAEA
GSVILQVLSCRLRKKRLFLCSPLHHHYEYQGLPETKIVMRFWIFSVCAGLGIAAVLWR

>core/419/3/Org3_Gene725

MRIAVLGAGYAGLSVTWHLHLSQGTATIDLFDPILGEGASGMSSGLLHAFTGKKALKPPLADQGINATHA
LITEASKALNPVIVISQGILRPAIDEDQAQLFTERVEEFPEVEWWEKARCEISIPSMVIPPNLALFIKSGVTLN

NDLYIQGLADACMKLGTQFYDELIEDLADIEEFYDHIIVTPGANASILPELKDMPVNKVKGQLEISWPKDLA
MLSFSINAHKYMVANTQKNTCILGATFEHNQPEETPDPAIAYQEIMPPVLSLFPGLKDAQVLHCYAGMRSSS
KSRLPVISRIREKLWFLGGLGSKGLLYHGITGDMLAQAVLRKSTAYIAKEFLFTI

>core/420/3/Org3_Gene657

MILLQNIKRCSLKQLKVLATLLLSLSLPTLEAAENRDSDSIVWHLDYQEALQKSKEAELPLLVIFSGSDWNGP
CMKIRKEVLESPEFIKRVQGKFVCVEVEYLKHRPQVENIRQQNLALKSKFKINELPCMILLSHEEREIYRIGSFG
NETGSNLGDSLCHIVESDSLLRRAFPMMTSLSELQRYRRLAEELSHKEFLKHALELGVRSDDYFFLSEKFR
LLVEVGKMDSEECQRIKKRLLNKDPKNEKQTHFTVALIEFQELAKRSRAGVRQDASQVIAPLESYISQFGQQD
KDNLWRVEMMIAQFYLDSDQWHHALQHA EVAFEAAPNEVRSHISRSL EYIRHQS

>core/421/3/Org3_Gene367

MYLQEKFKAQQVPLVLRELLSCSDSINDSDPIYRMVFDSNDTTISYKVGDALGVLPENSKEVSEHVLQLLGYS
PTTLVNVKKTSEKVSQAQKFIQGYVDLDKIPAKLNSFFPDKDPKITLYDAIQEYRPQIPIELFAESVFLLPRFYSI
ASSPDLHPKSIELLVKHVSYPGKYQKRFGVCSSFLCSELQVNDSAYIFVQPTKHFTLSTQTEGKPLVMIGAGT
GIAPYKAFLEERLFNKDPGNNLLFFGERKEKVNFFYYREFWNHAE EEGKLKLF LAFSRERDQKVYVQDLLRIQ
KDEVRKAYEEGGFFFVCGRKVLGIEVKHALEEILGKDTLASLRKEHRYVVDVY

>core/422/3/Org3_Gene199

MDVSRKINRHTQFYVDSIDGVIKNFDHKPSEDKSRDHEELEEKLLTITKRIVASAQEFQNRKTDSKNYYLKKT
QWLPFKNEELEQTKELFAMLTSMDDKIAQLFFYSPGCSSDWVEFTEVICHNLDSIGLGGVLLCCGLFEQQCEH
VVTVNKKLDLPLLLGTTVVNSLRYYLTYRNLNLCQSMSELGKELGDVLKQHGVAFTLIFKEIVDIDLLNYV
KLIQGLKRSQNIQARIYDNDVPTLPSVSSSIALRYS LANTIRGLALHVD FSSLKFISPSILSNTEHTAKALNSGG
ECFIFSNLDEFNLGMKIVMQLLRTGKISPEILNKNIMKILMIKRRVRSLYI

>core/423/3/Org3_Gene691

MEADILDGKLKRVEVSKKGLVNCNQVDVNQLVPIKYKWAWEHYLNGCANNWLPTEVPMARDIELWKSDE
LSEDERRVILLNLGFFSTAESLVGNINVLAIKFHITNPEARQYLLRQAFEEAVHTHTFLYICESLGLDEGEVFNA
YNERASIRAKDDFQMTLTVDVLDPNFSVQSSEGLGQFIKNLVGYYIIMEGIFFYSGFVMILSFHRQNKMTGIGE
QYQYILRDETIHLNFGIDLINGIKEENPEVWTTTELQEEIVALIEKAVELEIEYAKDCLPRGILGLRSSMFIDYVRH
IADRRLERIGLKPIYHSRNPFPWMSETMDLNKEKNFFETRVT EYQTAGNLSW

>core/426/3/Org3_Gene58

MELSLTSLPLAWYVILGVAVFAYSFGDGF DLGLGAVY LKAKEDKERRILLNSIGPVWDGNEVWLVIIVGGL
FAGFPACYATLLSIFYMPIWTLVLLYIFRGCSLEFRSKSES VSWKIFWDIIFICSGTAISFFLG TIVGNLILGLPLSP
DTSYASLSWILFFRPYAALCGAVVASAFAIHGSCFALMKTSDSLNARIAQQFPYILSSFLVFYVFLGASLISIP
KRFD APTYPLILLIALTSCCCVAAKTSVSKKRYGYAFIYSTLNLLSLILSAATLT FPNILLSTVDPQYSYTIYN
SAVETKTLKSLLIIVLIGLPFIITYTCYIYRVFRGKT NFPSIY

>core/427/3/Org3_Gene604

MNSKMLKHLRLATLSFSMFFGIVSSPAVYALGAGNPAAVPLPGVNPEQTGWCAFQLCNSYDLFAALAGSLK
FGFYGDYVFSESAHITNVPVITSVTTS GTGTTP TITSTTKNVDFDLNNSISSSCVFATIALQETSPAAIPLLDIAF
TARVGGLKQYYRLPLNAYRDFTSNPLNAESEVTDGLIEVQSDYGIVWGLSLQKVLWKDGVSVFVGVSADYRH
GSSPINYIIVYNKANPEIYFDATDGNLSYKEWSASIGISTYLNDYVLPYASV SIGNTSRKAPSDSFTELEKQFTN
FKFKIRKITNFDRVNF CFGTTCCISN NFYYSVEGRWGYQRAINITSGLQF

>core/428/3/Org3_Gene971

MMEVYSFSPSVRTSFQHRVMAALDNWFFLGGRRLKVVS LDSCNSGQACEEYVPISTTEKVLKILSYLLIPIV
ALLIRYLLHSNFTAKVSQKPWLKTLQLGIDIKSFILPGSHVNTMDSATLFKAIRLEGKRVDVEYHRLHSSDKV
VFYIPAQKLPDDLRLTHWLPEKETRKTEYVRHMLAHVMGYLTSQGKERLQQVVQDSRSSTSLGAEKVLQYR
FIDHPQSQGEFQRLLENITTKGSEDKEVVQSDLFDMAFQCWWPQFISVIQSPTFSEELVHEMSQKLDLDCIYP
EDDEFEQKFLNTLLKAVLLHGFEGISVASMGVIFLICPDSLALQIPFLRNQK

>core/429/3/Org3_Gene564

MNKKKRVL TGDRPTGKLHLGHWVGSIKNRLELQNSPEYDCFFIADLHTLTTKIRKEEVLDVDNHIYEV
WLSVGIDPTKSIHYLQSAIPEIYELHLLFSMLISINRVMGIPSLKDMARNASIEEGSLSYGLIGYPILQSADILLAK
AQFVPVGKDNEAHVELTRDIARNFNRLYGQVFPEPEVLQGELTSLVGIDGQGKMSKSANNAYLSDS DATITE
KVRKMYTDPNRIRATTPGRVEGNPLFIYHDIFNPHKDEV EEFKARYRQGC IKDIEVKARLAEELIHF LKPIKER
RSEFLSKPLALQNVLEDGTHKMREVAKV TMEEVHDKFGF SHKWRSLLK

>core/430/3/Org3_Gene118

MLTLGLESSCDE TACAIVNEDKQILANIIASQDIHAS YGGVPELASRAHLHIFPQVINKALQQANLLIEDMDL
IAVTQTPGLIGSLSVGVHFGKGIAIGAKKSLIGVNHVEAHL YAA YMAAQNVQFPALGLVVSGAHTAAFFIENP
TSYKLIGKTRDDAIGETFDKVG RFLGLPYAGPLIEKLAL EGS EDSYPFSPAKVPNYDFSFSGLKTAVLYAIKG
NNSSPRSPAPEISLEKQRDIAASFQKA ACTTIAQKLPTIIKEFSCRSILIGGGVAINEYFRSAIQ TACNLPVYFPPA
KLCSDNAAMIAGLGGENFQKNSSIPEIRICARYQWESVSPFSLASP

>core/431/3/Org3_Gene77

MENAMSSSFVYNGPSWILKTSVAQEVFKKHGKG IQVLLSTSVMLFIGLGVCAFIFPQYLIVFVLTIALLM LAIS
LVLFLLIRSVRSSMVDRLWCSEKGYALHQHENGPF LDV KRVQQILLRSPYIKVRALWPSGDIPEDPSQA AVLL
LSPWTFSSVDVEALLPSPQEKEGKYIDPVL PKLSRIERV SLLVFLSAFTLDDLNEQGVNPLMNNEEFLFFINK
KAREHGIQDLKHEIMSSLEKTGVPLDPSMSFQVSQAMFSVYRYLRQRDLT TSELRCFHLLSCFKGDVVHCLA
SFENPKDLADSDFLEACKNVEWGEFISACEKALLKNPQG ISIKDLKQFLVR

>core/432/3/Org3_Gene200

MDSSAPYNIASQGTEKSTVERILDLYGPASCIKFLKQMV LIREFEARGE EAYLEGLVGGFYHSYAGQEAVATA
AIANTGLDPWVFSSYRCHALAILLNIP LQEIAAELLGKETGCALGRG GSMHMC GPNFPGGFGIVGGQIPLAAG
AAFTIKYQE QKNRVSLCFIGDGAVAQGVF HETLNFVSLHQLPLMLIENNGWSMG TSLNRAVAKQPIAESQG
SSYDIRAVTVNGFDLFNSLLGFREAYRYMVDTESPVLVECLSRFRGHSISDPNLYRSKEEMQCLFKKDPIVL
AKDWLIRLEVLTEEFQNI RQECKTAVLEAFSNAKLSSDPSVT TLEEGVYA

>core/433/3/Org3_Gene98

MKLYSISSDVPDPWIFQLMSKVDSYFLGGNRIKVVSIVMQEPNLIIGKVENVRISTIVKILKILSFLIFPLILIAL
ALHYFLHAKYANHLLVSKILERAPQYVPIPGRSGDTASHYKLTTLVPSQKNLQAMGSNPLEVEAALRTTKP
SFFCVPKAYRQIISSHGIRFSLDLEQLADDINLDSVSWPTEYLNSTMDFCADKRVIQNVQNLRTGTYINSV
GKRSLLKFMLQHLFIDGITQENPEALPNNTSGRLTLFPSVRYIYSHFTPNQNTIWPQVFFRQGPLDEDRGGGFEL
LEQLQELGVRFPICPSQGPDPNPNFQGFQGIRIYWEDSYQPNKEV

>core/434/3/Org3_Gene641

MLPFEFEFNTTSSPECDVCLDPQKLFVKLFKRTIVLLSGPTGSGKTDVSLALAPMIDGEIVSVDSMQVYQGMD
IGTAKVSLKARQEIPHHLLDIRHVQEPFNVVDFYYEAIQACQNILSRNKVPILVGGSGFYFHAFLSGPPKGPAA
DPQIREQLEAIAEEHGVSALYEDLLLKDPEYAQTITKNDKNKIIRGLEIIQLTGKKVSDHEWDIVPKASREYCC
RAWFLSPETEFLKNNIQMRCEAMLQEGLLVEVRGLLNQGIENPSAFKAIGYREWIEFLDNGEKLEEYEETKR
KFVSNNSWHYTKKQKTWFKRYSIFRELPTLGLSSDAIAQKIAKDYLLYS

>core/435/3/Org3_Gene609

MFFQNLAKKLTALGISPLGCLLIGGVVSCAILFGRSSNPSLAPTQVKTEKTSGNWLKLTQMGNPKLIESLTKK
EQLEKDLTSFHPIASAKVAIALSTEDDVMSPLHLSVILTLRKEESLTPSLLFSITDYLCSSLPGLKREHISLSDNL
GNLYIPESITVNSLFIHTLENYLGKIFPKEHFALAYHAKAEKPTLQLTLNENYIAHLTKEESEKIVAHTKHLY
QNYDDSYDIVIETLPFARLQNKKSFPKVLIGSMILVISLMIVALASFYLARHAYERVSPEPRKIKRGINISKLE
IIQKESPEKIALILSYLDPKKAELNRLPEDLKHQVLKYKL

>core/436/3/Org3_Gene181

MSEQHSPIISVQDVSKKLGDHILLSKVSFSVYPGEVFGIVGHSGSGKTTLLRCLDFLDMPSTSGSISVAGFDNSLP
TQKFSRRNFSKKVAYISQNYGLFSSKTVFENIAYPLRIHHEMSKSEVEEQVYDTLNLNLYHRHDAYPGNLS
GGQKQKVAIARAIVCQPEVVLCDEITSALDPKSTENIERLLQLNQERGITLVLSHEIDVVKKICSHVLVMHQ
GAVEELGTTEELFLNSENSITNELFHEDINIAALSSCYFAEDREEVLRNLNFSKELAIQGIISKVIQTGLVSINILSG
NINLFRKSPMGFLIIVLEGEVEQRKKAKELLIELGVVIKEFY

>core/437/3/Org3_Gene769

MTILRKLSQYLFFFSLFCSEFIYVATCGSQPDSVSSPKIAIFLSFPHPLEDCSKSCIETLKDFENLPEIVVLNAEDSI
VKARKIARSLHTDKNVVAIVTLGTIATKVMCHIETQKPVIIYAAVPDRESLTPPKNTMNIYGVNDTLNINQYCF
AIQAVATNAQSIVYLPSEPFPSDLQKEIVKKLHASGIEVIEISITSSTFKTRIRQAIDKRPSAIFIPLSPLSHKEGT
AFLQEILKEKIPIITDDTSLISEGACIACSVDYKKSGKQIAKIVHHLLYNNHDVDSLKIIAQRLSPTTTFNEDIK
YLGIKLHKTERNQFLSFKSKKLEKSEKGNVAVS

>core/438/3/Org3_Gene698

MEMKEEIEAVKQQFHSELDQVNSSQALADLKVRYLGKKGIFRSFSEKLKQCTDKAKLGSINDFKTYVEDLL
QEKSLVLLASEQAEAFSKEKIDSSLPGDSQPSGGRHILKSILDDVVDIFVHLGFCVREAPNIESEANNFTLLNFT
EDHPARQMHDFTFYLNATTVLRTHTSNVQARELKKQPPKVVAPGLCFRNEDISARSHVLHFHQVEAFYVDH

NVTFSDLTAILSAFYHSFFQRKTELFRHSYFPFVEPGIEVDVSCECCGKGCALCKHTGWLEVAGAGMIHPQV
LRNGNVDPEIYSGYAVGMGIERLAMLYGVSDIRLSENDLRFLQQFS

>core/439/3/Org3_Gene242

MATISPISLTVDHPLVDTKKKSCSNFDKIQSRILLITAIFAVLVTIGTLLIGLLLNIPIYFALTGISFIAVVLNSFILY
KRATTLLKPRACGKHKEIKPKRVSTNLQYSSISIAINRSKENWEHQPKDLQNLPAAPSALLTDNPYEIWKAKHS
LFSLVSLLPGGNPEHLLISASENLGKTLLEETSQNAPISSYVDTTPSPKSLLEAIQETRVEINTELPAGDSGER
LYWQPDFRGRVFLPQIPTTPEAIYQYYALYVTYIQTAINNTQIIQIPLYSLREHLYSRELPPQSRMQQSLAMI
TAVKYMAELHPEYPLTIACVERSLAQLPQESIEDLS

>core/440/3/Org3_Gene485

MEEAAKHLAKEFLCSGINLFLSGEYEQAEKRLKETLELDSTAALAYCYLGIIALETGRVSEALNWCSKGLASE
PGDSYLRICYGVALDRGNQYEAIEQYSAYVALHPDDVECWFSLGSVYHRLKRLQEALDCFDKILALDPW
NPQSLYNKAVILSEMDDEAESIRLLEVAVAKNPLYWKAWVKLGFLSRSKRWDKATEAYERVVQLRPDLSD
GHYNLGLCYLTLDKTRLALKAFQEALFLNAEDADAHFYVGLAHLDLKQMREAYEAFNSALSINLEHERAHY
LLGYLHHMQGETDKATKELLFLQKKDSTFAPLLQKTVVSDPSSMQFERRLDTIS

>core/441/3/Org3_Gene503

MVLGVVGISYREAALKERERAIQYLQSFEKNLFLAQRFLGKGGAFIPLLTCHRAELYYYSESPEIAQAALLSEL
TSQGIRPYRHRGLSCFTHLFQVTSIGDSLIFGETEIQGQVKRAYLKGSKERELPFDLHFLFQKALKEGKEYRSRI
GFPDHQVTIESVVQEILLSYDKSIYTNFLFVGYSINRKAAYLYQHGYHRITFCSRQQVTAPYRTLSRETLSF
RQPYDVIFFGSSESASQFSDLSCESLASIPKRIVDFNVPRTFLWKETPTGFVYLDIDFISECVQKRLQCTKEGV
NKAALLTCAAKKQWEIYEKKSSHITQRQISSPRIPSVLSY

>core/442/3/Org3_Gene75

MFPSANQESRTRNVPLGIFHGLVACLYWGIVFVIPNFLGSFGDLDIVLTRYTIFGIFSLIACAINKPSVIKKTPLYI
WRKSLWTLINPVYYFGITLGIRYVGSAITVVIASLAPTAVLYHSNTKQKELPYSLLEFAISSVIITGVILTHLSA
LNLPTAASPLYSILGVIAVILSTSLWVIYVIRNQSLLEKHPNLTPDTWSYLGISALIIICLPMIIILDLCGITHVTHN
LISHTPGSERLLFLLCSAMGIFSSAKALIAWNKASLNLSPALLGAILIFEPIFGLVLTLYLSQSLPSLQEGIGIFL
MLGGSLLCLVLFGRKVQKSLENSQVSSSNE

>core/443/3/Org3_Gene561

MKKTCCQNYRSIGVVSFVFLVLTQTFLAGHFIDIGTSGLYSWARGVSGDGRVVVGYEAGNAFKYVDGEK
FLLEGLVPRSEALVFKASYDGSVIIIGISDQDPSCRAVKWVNGALVDLGIFSEGMQSFAEGVSSDGKTIVGCY
SDDTETNFAVKWDETGMVVLNLPEDRHSCAWDASEDGSVIVGDAMGSEEIAKAVYWKDGEQHLLSNIPG
AKRSSAHAVSKDGSFIVGEFISEENEVHAFVYHNGVIKDITLGGDYSVATGVS RDGKVIVGHSTRTDGEYR
AFKYVDGRMIDLGTLLGGSASFAFGVSDDGKTIVGKFETELGECHAFIYLD

>core/444/3/Org3_Gene790

MTHQVAVLHQDKKFDVSLRPKGLEEFYQHHLLKERLDLFLCAALQRGEVPGHCLFFGPPGLGKTSLAHIVA
YTVGKGLVLASGPQLIKPSDLLGLLTSLQEGDVFFIDEIHRMGKVAEEYLYSAMEDFKVDITIDSGPGARSVR

VDLAPFTLVGATTRSGMLSEPLRTRFAFSARLSYYSQDLKEILVRSSHLLGIEADSSALLEIAKRSRGTPRLA
NHLLRWVRDFAQIREGNCINGDVAEKALAMLLIDDWGLNEIDIKLLTTIIDYYQGGPVGIKTLSVAVGEDIKT
LEDVYEPFLILKGFIIKTPRGRMVTQLAYDHLKRHAKNLLSLGEGQ

>core/445/3/Org3_Gene946

MSYSLRNKKTICVYIIIALGILSFRSIPQEVYDKIRSSFVSLHVKFFPKIRQAPSSHLANLELENLVLKERVASL
EEKLKL YEVS NHTPPLFPEILTPYFHKLVEGKVYRDTYTHWSSSCWVNVGKTHGIKKNSPVLSGNVLVGLVD
YVGEHQSRIRLITDVGMKPSVVMAMRGDIQSWWIKHSLRELIRQVEQISHAYILEKDKYEKISQLQELDSLIQGE
GENQALLRGILSGVGGALWKEGSLCLEGEGFYFSEGKTLLPGDILVTTGLDGVFP PGLLVARVTKVKAPRDG
ACTFKIEAQSLEEKLMELDQLFILPPLEFNPNDRPDIFGLLWD

>core/446/3/Org3_Gene427

MKVVINGFGRIGRLVLRQILKRNSSVEVLAINDLVPGDALTYLFKFDSTHGRFPEDVRCEADHLIVGKRKIQF
LSERNVQNLPWKDLGVDLVIECTGLFTKKEDA EKHIQAGAKRVLISAPGKGDIPTFVMGVNHKTFNPEKDFV
ISNASCTTNCLAPIAKVLLDNFGITEGLMTTVHAATATQLVVDGPSKKDWRGGRGCLQNIIPASTGAAKAVT
LCLPELK GKLTGMAFRVPIEDVSVVDLTVRLDKSTTYDDICKAMKQASETDLKGILDYTD EQVVSSDFIGSEY
SSIFDALAGIALNDRFFKLVAWYDNETGYATRIVDLLEYVEKNSK

>core/447/3/Org3_Gene363

MFVDQITLELRAGKGGNGVVAWRKEKYLPGGPGYGGNGGNGG SVIIEATTSVYSFEAYRNIRFLKAPDGQS
GATNNRTGRSGKDLIVSVPTGTLLRDAETGEILHDFTVDGERLLVSQGGKGGKGNTFFKTSVNRAPTKATPG
KPGEIRQVELELKLIADIGLVGFNPAGKSTLFNTLAHTEVKVGAYPFTTLAPSLGLVLCKDRLYQKPWIIADIP
GIIEGA HQNKGLGLDFLRHIERTLLLLFVIDVSKRERNSPEEDLET LIHELHSHQPDFEKKDMLVALNKIDDLL
PDEQEECLQSFQKRFPSTYTFVLISGLTGEGVDGLYRFFTQRLAV

>core/448/3/Org3_Gene194

MWFSVNKNKKAIIWATGSYLPEKVLSNADLEKMVDTSDEWIVTRTGIKERRIAGPQEYTS LMGAIAAEKAI
ANAGLSKDQIDCIIFSTAAPDYIFPSSGALAQAHLGIEDVPTFDCQAACTGYLYGLSVAKAYVESGTYNHLLI
AADKLSSFVDYTDNRNTCVLFGDGGAACVIGESRPGSLEINRLSLGADGKLGELLSLPAGGSRCPASKETLQSG
KHFIAMEGKEVFKHAVRRMETA AKHSIALAGIQEEDIDWFVPHQANERIIDALAKRFEIDESRVFKSVHKYGN
TAASSVGIALDELVHTESIKLDDYLLLVAFGGGLSWGAVVLKQV

>core/449/3/Org3_Gene541

MAAPIFIKNILLRSSIVYAPLAGFS DYPYRCMSALYQPGLMFCEMVKVEGILYAPERTSKLLDYNENMRPIGA
QLCGSNPETSGEAAKILEGLGFDLIDLNCGCPTDKITKDGS GSGLLKTPELIGRILDKIINSVSIPVTVKIRSGWD
MEHINVEDTVRIIRDAGASAVFVHGRTRAQGYHGPSKQEYISRAKAAAGKEFPVFGNGDIFSPEAAQAMLTT
GCDGVLVARGTLGAPWIGKQIQDYLT TGSYEKIPFIKRKA AFLEHMRLVEDYYYQSETKFLSETRKLCGHYLIS
AAKVRFLRSSLA KATSYQEVYQLVNDYEEADDSLET FVKC

>core/450/3/Org3_Gene37

MSTPLSSGGISPSDQYVPQELFCDRLLLLSSSRNSPDSNASGDSPIVSPPIALVALTDLKLVPYNQNSFSWTTRLK
NAVEKIGLFLQRNWKYILLYILAWALILVCHHTVALTLTIWLGVLGIGVVFGIFTATCLDKENKHRHVNSL
WNLINHGILQLDPNGTRQILLATMIASISALIYAVPQAVGLVIGFSIGNQLSINTVYGARLGDEATY AIDRKAH
KKRIENIEQAINQHQQIHKHQMINKQLNALIEINRNNQTDPATANLLASLKLNLNQPMPCFSMPECGVTSSYL
DLNNNSPDDIARADQCIMTSLSQTLLQKKEPDRIIESNH

>core/451/3/Org3_Gene585

MVRRSISFCLFFLMTLLCCTSCNSRSLIVHGLPGREANEIVLLVSKGVAAQKL PQAAAAATAGAATEQMWDI
AVPSAQITEALAILNQAGLPRMKGTSLLDLFAKQGLVPSELQEKIRYQEG LSEQMASTIRKMDGVVDASVQIS
FTTENEDNLPLTASVYIKHRGVLDNPNSIMVSKIKRLIASAVPGLVPENVSVVSDRAAYS DITINGPWGLTEEI
DYVSVWGIILAKSSLTKFRLIFYVLILILFVISCGLLWVIWKTHTLIMTMGGTKGFFNPTPYTKNALEAKKAEG
AAADKEKKEDADSQGESKNAETSDKDSSDKDAPEGSNEIEGA

>core/452/3/Org3_Gene605

MKQHIGYLGMGIWGFCLASLLANKGYPVVAWSRNPDLIKQLQEERRHPLAPNVVISPNLSFTTDMKEAIHNA
FMIVEGVTSAGIRPVAEQLKQITDLSVPFVITSKGIEQNTGLLLSEIMLEVLGDSVTPYLG YLSGPSIAKEVLNG
SPCSVVVSAYDSQTLKQIHEAFSLPTFRVYPNTDIKGAALGGALKNVIAIACGIAEGLSFGNNAKAGLVTRGL
HEMRKLAAIMDCKPETLNGLAGLDLCVTCFSESSRNLRFGHLLAQGLTFEQAKAKIGMVVEGAYTALSAY
QVAKHHKIDMPITGTIYRVLYENLDLKEGIALLLQRNTKEEFL

>core/453/3/Org3_Gene409

MKPLGFQENLEALCNKTSRQLLKYLIKQILFVCGASLLIALEFSFFLYFFLFSGKTVIPAFCLACFFLTLFVCLV
TRLYLLSGKGDFFDLASEYLQGA VPPNKR SQNIVEEQSHLAAAATKLSINLQ NQEYSLLSEIFKFLPKHDLIR
KFSCFCFWKDYFLFRECLLQKAIEAYIKVVQAIPVDLSAHVSLADAYVALSGLYADPRKYPEFDANYWIPSG
RYS AEIQEKFFATARRAIEEFQILNEYAPGNAWVHAQLAYSYHDLQMPMEEIQEYEIVLKLKPNDVETMSKL
GILYFQQGMNAKGLRIYEEIKKRDYKKSQKLIKFYGVEYKY

>core/455/3/Org3_Gene578

MQPFIFTLLCLTSLVSLVAFDAANARKRCACAQTIERGENFFSIKRSACAEIEYQEKS RHASAIERISKDKGKV
TPKQIAKVATKKKQRYRLLQVPFSRPPNNSRYNLYALLSEPPECYS DTASWYAIFIRLLRRAYVDTGNVPPGS
EYAIANALISNKQEILERGAQLGPDVIETLTLPEEQAEIFYKMLKGSSNSQSLLNFLHYEEKSLGHCKLNLIFM
DPLLLEAVLDHPDAYRETSLLRDGIWEAVKRQEHAIQEHGQAAALELFKTRTDFRLELRDKMQLLLSRYDLL
PLLNKKMFDYTLGSAGDYFLVDPDTKAISRCRCPSKSIKL

>core/456/3/Org3_Gene446

MATNAIRSAGSAASKMLLPVAKEPAAVSSFAQKGIYCIQQFFTNPGNKLAKFVGATKSLDKCFKLSKAVSDC
VVGSL EEAGCTGDALTSARNAQGMLKTTREVVALANVLNGAVPSIVNSTQR CYQYTRQAFELGSKTKERKT
PGEYSKMLLTRGDYLLAASREACTAVGATTYSATFGVLRPLMLINKLTAKPFLDKATVGNFGTAVAGIMTIN
HMAGVAGAVGGIALEQKLFKRAKESLYNERCALENQSQSLSGDVILSAERALRKEHVATLK RNVLTLLLEKA
LELVVDGVKLIPLPITVACSAAISGALTAASAGIGLYSIWQKTKSGK

>core/457/3/Org3_Gene977

MRIAVLGVTGLVGQKFVALLHKWYRDWVIAEVVASNSKYGQSYGDACIWQEPIGMPPEMVRLPIRKIEEV
QSDIVDSFLPSSAESMEAYCLSQGKVVFNSASTYRMHSSVPIIPEVNSDHFQLLEEQPYPGKIITSPNCCVSGIT
LALAPLRKFSLDHVHIVTLQSASGAGYPGVPSLDLLANTVPHIVGEEKILRETVKILGSSKQPLPCKLSVTVH
RVPVAYGHTLSLHVTFSKDVDLDEILYSYQEKNEFPNTYQLYDNPWSPQARKHLSHDDMRVHLGPITYGG
DFRTIKMNVLIHNLVRGAAGTLLASMENYFFDYLKREMCLR

>core/458/3/Org3_Gene417

MKTLWHFVSKAFLSIVGLCCGVVLAFFVIFALIASSLGNGDATFVSLPDAQGEVKDLGKTAPIIAVIEMKDVI
ASSKNTAKTIQNILEGFEKAPLKDRVKGIVIDMDCPGGEVFEIDRIYSMLRFWKERKGFPIYIYVNGLCASGGY
YVSCAATKIYATSSSLIGSIGVRSGPFFNVKEGLNRYGVESDLLTAGKDKAPMNPYTPWTSHDREERQATLDF
LYGQFVDIVTQNRPLLTKEKLVHTLGARIFSPEKAKQEGYIDVVGATKEQVLQDIVAVCKIEDNYRVIGSGGD
GWWKRVASAAASSPLVTGMIKHDILPLSHDAAIIPPYLAL

>core/460/3/Org3_Gene523

MSSLTLSRRPRRNRKTAAIRDLLAETHLSPKDLIAPFFVKYGNNIKEEIPSLPGVFRWSLDLLLKEIERLCTYGL
RAVMLFPIIPDDLKDAYGSYSSNPKNILCHSIHEIKNAFPHLCLISDIALDPYTTHGHGDGIFLNGEVLNDESVRIF
GNIATLHAEMGADIVAPSDMMDGRIGYIRSKLDQSGYSKTSIMSYSVKYASCLYSPFRDALSSHVTSGDKKQ
YQMNPKNVLEALLESSLDEEEGADILMVKPAGLYLDVIYRIRQNTCLPLAAYQVSGEYAMILSAFQQGWLD
KETLFHESLIAIKRAGADMIISYSAPFILELLHQGFEF

>core/461/3/Org3_Gene94

MNIYQFSPGASPNWQASLMAQLNSYFCLGGETVTRIISLRPSGLILAKKEKAVVSTAEEKILKILSFILFPLVLIAL
AIRYLLYNKFNKDLDRVFFIPTTEITKAELIIAKNPALVKEAALTVSPLFYSLPKKYQLMKVETP

>core/462/3/Org3_Gene95

MLLEDLDTDSIPWPKLYLSEDFDFAYYPESKAIIDTVAKLEKNNPGEEFCLESKKILARYLLEQLFKLETGLNF
PTSTIDGGRESFLIEFSHETKKPTVWAFIYFYYYHSNGPKLEKDFKQAGCEVHNRLNLGLKYRPQAGAQN
GRNGGPYPGPIGFLIVWEENYGSVLKDHGFIKDN

>core/463/3/Org3_Gene677

MQFSRYLRYAFDNQYLPEPLYQKFSVFHQNYIDAATKKAAADQAEVLCCLQWVKVIIEDLKNPFIFPPYHKKI
RAPIDLFRLSIDFFSLVIDDKNSRILNLHRLKEIEEYIARGDNVLLANHQTECDPQLMYALGKTHPELMEN
MIFVAGDRVTSPLARPFSMGCDLLCIYSKRHIATPPELREEKLLHNQKSMQILKTLLNEGKFIYVAPAGGR
DRKNAEGRLYPSEFSPESIEVFRLLAKASNQTTHFYPFALKTYDILPPPKIENAIQEQRRAIFFAPVFFNFGAELF
FDALCSKEELIHCDKHAQRTLRAEKVFSIVKNLYEEL

>core/464/3/Org3_Gene736

MREETVSWSLIEDIREIYHTPVFELIHKANAILRSNFLHSELQTCYLISIKTGGCVEDCAYCAQSSRYHTHTVPEP
MMKIVDVVERAKRAVELGATRVCLGAAWRNAKDDRYFDRVLAMVKSITDLGAEVCCALGMLSEEQAKKL
YDAGLYAYNHNLDSSPEFYETIITRSYEDRLNTLDVVNKSISTCCGGIVGMGESEEDRIKLLHVLATRDHIP

ESVPVNLLWPIDGTPLQDQPPISFWEVLRTIATARVVFPRSMVRLAAGRAFLTVEQQTLCFLAGANSIFYGDK
LLTVENNDIDEDAEMIKLLGLIPRPSFGIERGNPCYANNS

>core/465/3/Org3_Gene315

MIDIMQHFKPYTMVPGQKLPIPGSLLYAQVFPTLWRLFSSKHEILNEQTLQVQGPKRFAVFQDLHRGGLAV
TSERYKYYLLPSGECTQSIK GKLP SAAQAGPLLSLGVH KHADWQKVRCRRDLKEILPLWFRFAAMAPKGSY
RDLETTAIGSLVKTAHQ RVLHRETTEIAPALLSIALAGFSECFLPRS YDEEFQGILPQDGDPEGGVPFELLSYSF
GMIQDIFLRHQGQLVEILPALPPEFPCGRLIHVALPNLGTLSIVWTKKTIRQVELHAEYSGEVFLKFCSSLCSAR
LREWSERRLSGSKRLSLGETLEIKAGTTYLWDCFHK

>core/466/3/Org3_Gene629

MSAFFDLLKSQTASHPPIWLLRQVGRYMPPYQELKGSQSLKTFFHNTEAIVEATLLGPSLLHVDAAILFADILS
ILDGFAVTYDFAPGPRIQFSPEQPFTFTSDPQTIFS YLLDAIRTLKQKLPVPLIVFAASPFTLACYLIDGGASKDF
SKTMSFLYVYPEKFDQLISTIIEGTAIYLKTQMDAGAAAVQLFESSRLRLPSALFTRYVTEPNRRLIAKLKEQAI
PVSLFCRCFEENFYTLQATQADTLHPDYHVDLHRIQKNLMLSLQGNLDP AIFLLPQEKLLHYVEAFLVPLRTY
PNFIFNSGHGILPETPLENVQLVVS YVQRQL

>core/467/3/Org3_Gene349

MPSPMISTDVCQDILGKQKEAVDFFFQAFQPK EAMQLAEKILGHSGWVFFSGVGKSGCVARKLVATLQSLSE
RALFFSPVDLLHGD LGLVSPGDIVCLFSKSGETQELLDTVPHLKSRRAILVAITSM PYSNLAALSDLVVILPSV
AELDPFNLIPTNSTTCQMIFGDFLAML LFHSRGVSLSTYGKNHPSGQVGMKANGKVKDFMFPKTEVPFCHLG
DKVSFSLEVFSAYGCGCVCIVDPQFRLMGIFTDGD LRRSLASYGGEVLSLSLEKVM TANPRCITEDSDIAIALQ
LMESSSPVAVLPVLDNEENRHVTGLLHMHTLAKAGLL

>core/468/3/Org3_Gene724

MAFKEVVRVAVTGGKGQIAYNFLFALAHGDVFGVDRGVDLRIYDVPGTERALSGVRMELDDGAYPLLHRL
RVTTSLNDAFDGIDAAFLIGAVPRGPGMERGDLLKQNGQIFSLQGAALNTAAKRDAKIFVVGNPVNTNCWIA
MKHAPRLHRKNFHAMLR LDQNRMHSM LAHRAEVPLEEVS RVVIWGNHSAKQVPDFTQARISGKPAAEVIG
DRDWLENILVHSVQNRGSAVIEARGKSSAASASRALAEAARSIFCPKSDEWFSSGVCSDHNPYGIPEDLIFGFP
CRMLPSGDYEIIPGLPWE PFIRNKIQISLDEIAQEKASVSSL

>core/469/3/Org3_Gene201

MPKHKLTLEIREALREAIDEEMSRDPNVCILGEEVGDYNGAYKVTKGLLDKWGPKRVIDAPISEAAFSGIGIGA
ALSGLRPIIEFM SWNFSFVALDQIISHAAKM HFMTGGKFSVPIVFRGPNGAAAQVSCQHS HCVESLYANIPGLI
IIAPSNPYDAKGLLKS AIRNNNPVLFLENELEYNLKGEVPTEEYLVPIGKAHRVQEGNDLTIITYSRMVSITKEA
CSLAKKRWGLSIEIIDLRTIKPLDISTILSSVRKTSRCIVIEEGHYFAGISSEIIALITEHVFDSLDAPPLRVCQKETP
MPYSKILEQATLPNVNRILDTIEKVMR

>core/470/3/Org3_Gene45

MSNQFDQLKKLSTIVCDSGDPELVKASGSQDATTNPSLILKVAQEPKFQELLNEAVVWGIRQNGDDLQTLFSFI
LDKIQVNFAL EIIKNIPGRISLEIDARLSFNVEAMVQRAVFLSQLFEAMGGDKRLLVKIPGTWEGIRAVEFLE

AKGIACNVTLIFNLVQAIAAAKAKATLISPFVGRIDWWIAAYGDEGYSIDADPGVASVSNIYAYYKKFGIPT
QIMAASFRTKEQVLALAGCDLLTISPKLLDELKKSQHPVKKELDPAEAKKLDVQPIELTESFFRFLMNEDAMA
TEKLAEGIRIFAGDTQILETAITEFIKQIAAEGA

>core/471/3/Org3_Gene926

MTTPAYLLANFGGPRHAKDLQEFLISLLTDRDVTGTFLPRVLHRHLFTFIAKKRVPKVLPQYQSLQNWSPYIF
DTETLAKTLSEILRAPVIPFHRYLPSTHEKTLLALRTLHTRHVIGIPLFPHTYSVTGSIVRFFMKHVPEIPISWIP
QFGSDSKFVSLITCHIRDFLQKLGILEKECCFLFSVHGLPVRYISQGDPYSKQCYESFSAITTNFKQSENFLCFQS
KFGPGKWLSPTAQLCQNIDTDKPNVIAVPFGFISDHLETLYEIERDYLPLLSRGYRALRIPAIYSSPLWVSTL
VDIVKENSTVVAEELIKSGKKHTGIR

>core/472/3/Org3_Gene231

MDAKMGYIFKVMRWIFCFVACGITFGCTNSGFQNANSRPCILSMNRMIHDCVERVVGNRLATAVLIKGSLDP
HAYEMVKGDKDKIAGSAVIFCNGLGLEHTLSLRKHLENNPNNSVKLGERLIARGAFVPLEEDGICDPHIWMDL
SIWKEAVIEITEVLIEKFPEWSAEFKANSEELVCEMSILDSWAKQCLSTIPENLRYLVSGHNAFSYFTRRYLATP
EEVASGAWRSRCISPEGLSPEAQISVRDIMAVVDYINEHDVSVVFPEDTLNQDALKKIVSSLKKSHLVRLAQK
PLYSDNVDDNYFSTFKHNVCCLITEELGGVALECQR

>core/473/3/Org3_Gene342

MMTYPVPQNPLLLRILRLMDAFSKSDDERDFYLD RVEGFILYIDLDKDQEDLNKIYQELEENAERYCLIPKLT
FYEVKKIMETFINEKIYDIDTKEKFLEILQSKNAREQFLEFIYDHEAELEKWQQFYVERSRIIIEWLRNNKFHF
VFEEDLDFTKNVLEQLKIHLDKVGKEITQARQLLSNKAKIYYSNEALNPRPKRGRPPKQSAKVETETTISD
IYTKVPQAARRFLFLPEITSPSSITFSEKFDTEEEFLANLRGSTRVEDQLNLNLSERFASLKELSAKLGYSLSLST
GDFFGDDDEKVVTCTKGSKRGRKKSS

>core/474/3/Org3_Gene964

MHSELPNYQNIVESVVTEITTQLLNYSRSEHRLVPFWEKSDGSFITAADYGSQYYLKQQLAKAFNPFIGEETL
YPDQDNEKIPEILKFTRLLTSSVSRDDLSTLVPPPSPTSLFWLVDPIDGTAGFIRHRAFAVAISLIYEYRPILSVM
ACPAYNQTFKLYSAAKGHGLSIVHSQNLDRRFVYADRKQTKQFCEASLAALNQHHATRKLSTGLTNTSPSP
RRVESQYKYALVAEGAVDFFIRYPFIDSPARAWDHVPGAFVVEEAGGRVTDALGAPLEYRKESLVLNHNAVI
LASGDQETHETTLAALQNQLNVVPTDKLIAL

>core/475/3/Org3_Gene507

MKTVTSFTVCKENSGRLDKYLTEVHPKYSRAFYQEHILSGLVQINGQINTRVATRLNCGDIVTIDIQEKEELLE
LLPEAIPLDKVYEDGMILVINKPRDMVVHPAPGHFHGTLVHALLHEIGERLKEEFPEEPWRPGIVHRLDKDTS
GLIITAKTRQAKKVSELFSTKRLKKSYLAVCIGKPRSTTIHTHISRHQNKREMTVSSQGKEAVTHCQVLAF
NGKLSFVALSPETGRTHQLRVHMKHLGTPILGDPVYGIPSMNSSYGLDKQQLHAYSVDFTHPETRQFCSLKA
GLPEDMRSLLIKEFRNETTILNKNLLESILKEQ

>core/476/3/Org3_Gene171

MTIDMHCDLLSHPHFCRKDPAVRCSPEQLLSGGVRQQVCAIFVPHSRGEPNCDKQNSLFFSLPNQYPDIGLLS
YEEEENGSSSQKKSLSLIRSIENASALGDDTAPLGTLLAKLIHLTKQGPLAYLGIVWKGDNRFGGGTEAPKRL
SNDGKVLLDIMYELGVPIDLSHCSDKLAEDILDYTADKLPNLAVIASHSNFRSVLDHRRNLVDAHAKIVRRK
GVIGLNLVRSYVGDSLGDLEKHVLHAENLGILSSIVLGSDDFFYANEDENFFFNECSSAEAHVPLNQLIHRIFSK
GKAESILSSRAEKFLKQVIVEQVNPKITDVKL

>core/478/3/Org3_Gene813

MIEFAFVPHTSVTADRIEDRMACRMNKLSTLAITSCLVLISSVCIMIGILCISGTVGTYAFVVGIIFSVLALVACV
FFLYFFYFSSEEFKASSQEFRFLPIPAVVVSALRSYEYISQDAINDVIKDTMQLSTLSSLLDPEAFFLEFPYFNSLI
VNHSMEADRLSREAFLLILLGEITWKDCETKILPWLKDPNITPDDFWKLLKDHFDLKDFFKKRIATWIRKAYPE
IRLPKKHCLDKSIYKGCCKFLLLAENDVQYQRLHVKCYFSGEFPAMVLGLGSEVPMVLGLPKVPKDLTWE
MFMENMPVLLQSKREGHWKISLEDVASL

>core/479/3/Org3_Gene280

MELLPHEKQVVEYEKAIAEFKEKNKNSLLSSSEIQKLEKRLDKLKEKIYSDLTPWERVQICRHPSRPRTVNYI
EGMCEEFFVELCGDRTFRDDPAVVGGFVKIQGQRFVLIGQEKGCDTASRLHRNFGMLCPEGFRKALRLGKLA
EKFGLPVVFLVDTPGAYPGLTAEERGQGWAIKCNLFELSRLATPVIIIVIGEGCSGGALGMAVGDSVAMLEH
SYYSVISPEGCASILWKDPKKNSEAAASMLKMHGENLKQFGIIDTVIKEPIGGAHHPALVYSNVREFIIQEWLR
LKDLAIEELLEKRYEKFRSIGLYETTSSESGPEA

>core/480/3/Org3_Gene477

MASNPILQIEDLSITLAKQRQQYPIVQSLSFTINEGQTLAIIGESGSGKSVSAHAILRLLPCPPFSVSGQVNFQGH
NLLTASRSIQKKIIGTEISMIFQNPQASLNPVFTIEQQFREIIHTHLALTAEVAKKMLYALEETGFHDPRLCLNL
YPHQLSGGMLQRICIAMALLCSPKLLIADEPTTALDVSQYQILQLLKTQKKTGMSLLIITHNMGVVAETAD
DVLVLYAGRMVECAPAVQMFHNPSHPYTRDLLASRPSLQPQQLGSFNPIPGQPPHYTAFPSGCRYHPRCSKIL
NRCSAEAPEIYPVREGHKVRCWLYDD

>core/481/3/Org3_Gene228

MALGPSPYYGVSFQFFSVFFSRLFSGSLFTGSLYIDDIQIIVFLAISCSGAFAGTFLVLRKMAMYANAVSHTVL
FGLVCVCLFTHQLTTLSTLGTTLAAMATAMLTGFLIYFIRNTFKVSEESSTALVFSLLFSLSLVLLVFMTKNAH
IGTELVLGNADSLTKEDIFPVTIVILANAVITIFAFRSLVCSSFDSVFASSLGIPIRLVDYLIIFQLSACLVGAFKA
VGVLMAFLIIPSLIAKVIKSIKSLMAWSLVFSIGTAFLAPASSRAILSAYDLGLSTSGISVVFLTMMYIVVK
FISYFRGYFSKNFEKISEKSSQY

>core/482/3/Org3_Gene478

MTTNFPQPLIQATSLTKHYKRSFWFQGKTIASRPVDDVSFSLYSRRVGLIGESGSGKSTLALALAGLLPLTS
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LSEEFYRYPHQLSGGQQQRVSIARALLGVPQLIICDEIVSALDLSIQAQILNMLAELQKKLSLTYLFISHDLAV
VRSFCTEVFIMYKGQIVEKGNTKRIFSDPQHPYTRMLLNAQLPETPDQRQSKPIFQYHKDSEESCSTGCYFY
NRC PQKQEACKSEIIPNQGDAAHHTYRCIH

>core/483/3/Org3_Gene516

MEKKYYALAYYYITRVDNPHEEIALHKKFLEDLDVSCRIYISEQGINGQFSGYEPHAELYMQWLKERPNFSKI
KFKIHNIKENIFPRITVKYRKELAAALGCEVDLSKQAKHISPQEWHEKLQENRCLILDVRNNEYWKIGHFDNAT
LPDIQTFREFPEYAEKLAQECDPETTPVMMYCTGGIRCELYSPVLLEKGFKEVYQLDGGVIAYGQQVGTGKW
LGKLFVFDDRLAIPIDESDPDVAPIAECCHCQTPSDAYYNCANTDCNALFLCCDECIHQHQGCCGEECSQSPR
VRKFDSSRGNKPFRAHLCEISENSESASCCLI

>core/484/3/Org3_Gene404

MKQLLFCVCFAMSCSAYASPRRQDPSVMKETFRNNYGIIVSGQEWVKRGSDGTITKVLKNGATLHEVYSG
GLLHGEITLTFPHTTALDVVQIYDQGRLVSRKTTFFVNGLPSEQELFNEDGTFVLTRWPDNNDSDTITKPYFIET
TYQGHVIEGSYTSFNGKYSSSIHNGEGVRSVFSSNNILLSEETFNEGVMVKYTTFYPNRDPESITHYQNGQPHG
LRLTYLQGGIPNTIEEWRYGFQDGTTFVFKNGCKTSEIAYVKGVKEGLELRYNEQEIVAAEEVSWRNDFLHGER
KIYAGGIQKHEWYYRGRSVSKAKFERLNAAG

>core/486/3/Org3_Gene447

MNLKVVYFGTPTFAATVLQDLLHHKIQITAVVTRVDKPQKRSAQLIPSPVKTIALTHGLPLLQPSKASDPQFIE
ELRAFNAADVFIWVAYGAILRQIVLDIPRYGCYNLHAGLLPAYRGAAPQRCIMEGATESGNTVIRMDAGMDT
GDMANITRVPIGPDMTSGELADALASQGAEVLIKTLQQIESGQLQLVSQDAALATIAPKLSKEEGQVPWDKP
AKEAYAHIRGVTPAPGAWTLFSFSEKAPKRLMIRKASLLAEAGRYGAPGTVVVTDRQELAIACSEGAICLHE
VQVEGKGSTNSKSFLNGYPAKKLKIVFTLNN

>core/488/3/Org3_Gene291

MSKGSSKHTVRINQTWYIVSFILGLSLFAGVLLSTIYYVLSPIQEQAATFDRNKQMLLAHILDFKGRFQIQEK
KEWVPATFDKKTQLLEVATKKVSEVSYPELELYAERFVRPLLTAQGKVFSFEEKNLNPIEFFEKYQESPPCQ
QSPLPFYVILENSTRTENMSGADVAKDLSTVQALIFPISGFGLWGPIHGYLGVKNDGDTVLTAWYQQGETP
GLGANITNPEWQEQQFYGKKIFLQDSSGTTNFATTDLGLEVVKGSVRTTLGDSPKALSAIDGISGATLTCNGVT
EAYVQSLACYRQLLINFSNLTHEKKTGE

>core/489/3/Org3_Gene425

MRLLSILKLHLFSLRSSSSLSPHYHSCSRSMHLHLLCRWKDADIMEWQQICNILSGVCSRMSGKLVSLQKETQ
DSCHQEHERIHLQYREQLSALEEEYRRREEAKNQDLEKLQQENTWLQNRLAEKLQQIRHQSDIIDEIKKELLQ
SVQRTEISEGRRLCYEHKIKQLEEQLQRYVSQHGAPSIIEEDKSSAAYAEINRLKKSLIDLQQEKDIYIKTYHS
EIAKLREKLQRQEGAQTSSEVCSIEKLTQVQTDLAEEKKAIALLDIVIDQYCQLRDLHKEKGMAMPSNTKL
DHLKGLLGKEPESEVDVVFSESKSLGS

>core/490/3/Org3_Gene679

MEVQIGIDLMGGDHSPLVVWQVLVDVLKSQSSTIPFAFTLFASEEIRKQIQEEFISDLPQEKFPKIISAENFVAM
EDSPLAAIRKKSSSMALGLDYLQEDKLDAFISTGNTGALVTLARAKIPLFPAVSRPALLVCVPTMRGHAVILD
VGANISVKPEEMVGFARMGLAYRQCLGDSKIPTIGLLNIGSEERKGTEAHRQTFRMLRETFGAFLGNIESGA

VFDGAADIVVTDGFTGNIFLKTAEGVFEFLQRILGDKLEADIQRRLDYTFYPGSVVCGLSKLVIKCHGKACGS
SLFHGILGSINLAQARLCKRILSNLI

>core/491/3/Org3_Gene392

MLISISLATLPILAFSWASFIEPNWLRTTAIPWRLPKKHAHLHGLRIAQISDLHFHKRVPEKFLNKVSKSIKNFSP
DLIVFCGDLLCRARLEDKERLETFLNTLEAPLGVFMAILGNHDYSSYISRNTKGEITCIPEEKSRIQRAIIAVMQG
LFSSPSYRYDPNLTPQEPHPDLLKLLKNTPLTLLHNTTHVIPNTLNIVGLGDLFARQFHPEQAFKNYDPSLPGL
LLSHNPDGITRLQQYPGDFVLSGSHGHPQVTLSPKFKARKFFERLSGLENPYLARGYFVTKEGKQLYVNRGL
GGLKRIRFCSPPEICYITCSYD

>core/492/3/Org3_Gene702

MVLSSDLLRDDKQLDLFFASLDVKKRYLLALSGGSDSLFLFYLLKERGVSTAVHIDHGWIRSTSAQEAKELE
ELCAREGVPPVLYTLTAEQGDKDLENQARKKRYAFLYESYRQLDAGGIFLAHHANDQAETVLKRLLESAAH
LTNLKAMAERSYVEDVLLLRPLLHIPKSSLKEALDARGISYLQDPSNEDERYLRARMRKKLFPWLEEVFGKNI
TFPLLTLGEESAELSEYLEKQAQPFFSAATHQDSQGELPCPDCLIQQAFLCKWVMKKFFNNAGIAVSRHFLQ
MVYDHLSSCATLRMRNKIIVKPGVVVID

>core/493/3/Org3_Gene464

MKFLLYVPLLLVLVSTGCDAPVSFEPFSGKLSTQRFEPQHSAAEYFSQGQEFLLKGNFRKALLCFGIITHHFP
RDILRNQAQYLIGVCYFTQDHPDLADKAFASYLQLPDAEYSEELFQMKYAIAQRFAQGKRKRICRLEGFPKL
MNADEDALRIYDEILTAFPSKDLGAQALYSKAALLIVKNDLTEATKTLKKLTLQFPLHLSSEAFVRLSEIYLQ
QAKKEPHNLQYLHFAKLNEEAMKKQHPNHPLNEVVSANVGAMREHYARGLYATGRFYEKKKKAEAAANIY
YRTAITNYPDTLLVAKCQKRLDRISKHTS

>core/494/3/Org3_Gene328

MNRRKARWVVALFAMTALISVGCCPWSQAKSRCIDKYIPVVRNLLEVCGLPEAENVEDLIESSSAWVLTPE
ERFSGELVSICQVKDEHAFYNDLSLLHMTQAVPSYSATYDCAVVFGGPLPALRQRLDFLVREWQRGVRFKKI
VFLCGERGRYQSIEEQEHFFDSRYNPFPTENWESGNRVTPSSEEEIAKFVWMQMLLPRAWRDSTSGVRVTF
LLAKPEENRVVANRKDTLLLFRSYQEAFGRVLFVSSQPFIGLDACRVGQFFKGESYDLAGPGFAQGVLKYH
WAPRICLHTLAEWLKETNGCLNISEGCFG

>core/495/3/Org3_Gene810

MRKVAFLVSCFLSVAIGASAAPVRVPGFPQIPEDLVQIKTEVCPKQEVCLAVTIKCDDHNLIGVLHLPNTPTPE
GGFPTVVLFHGFRTKFGGLTGAYRKLGRKFAAAGIATLRVDMAGCGDSEGVAEEVPIETYLRDAQTILETV
QEHPDLNAYRLGISGFSLGCHIAFELAKIYNPRDLNIKALSVWAPIADGGILLKELYENFSKHGEGDIISVGKDF
GFGPPPIIVCSGDVDLLIRIQDHVTANSLPTKPYILHQQGIDDTLVSRTQQTLFKNTAPGRMTFISYPNTGHNLA
TAPDLDMILDQIVSHFQRTL

>core/496/3/Org3_Gene787

MFKLLFHIAAFAGHVLSTPIFIVQDACGIDEEACKNPPPRPFSQVQYLKVNDKFKKLPHQTIGYRQYDGTG
LCTLPITEHSGLLFSTGYIGADIQWKSSLPISETDPNGLGWATFQDTSFYNYVLLSLGAYTSLKNWQWSIILS

GLVDPKNIEMGYGLYQGVLSGKYQATEKLSAIFGVINETGLHQEKAWPLVGVSYKATDQLTLNCIYPVNFSI
DYRSTSVCNLGLAYRLTRFRKKLYKNHLISSRGIFEYQGREIEANVKLTPWPGSFIKGFYGWSIGNDISIADDH
NNNKTSHTFKTSAFFGGSAVMNF

>core/497/3/Org3_Gene128

MLVELEALKREFAHLKDQKPTSDQEITSLYQCLDHLEFVLLGLGQDKFLKATEDEDVLFESQKAIDAWNALL
TKARDVLGLGDIGAIYQTIEFLGAYLSKVNRRAFCIASEIHFLKTAIRDLNAYYLLDFRWPLCKIEEFVDWGN
DCVEIAKRKLCTFEKETKELNESLLREEHAMEKCSIQDLQRKLSDIIEHLDVSLFCFSKTPSQEEYQKDCLYQS
RLRYLLLLYEYTLCKTSTDFQEQAARAKEEFIREKFSLLELEKGIKQTKELEFAIAKSKLERGCLVMRKYEAA
AKHSLDSMFEEETVKSPRKDTE

>core/498/3/Org3_Gene256

MTLPMQKSLTSFDDFSQAYAELKVPALIGSALEDDKDALIELLVSESFKELGGQGLMPATLMSWTETFALFQ
EHETLGIIHAELKPLATKEFLSRYPARNPQPHLTILIFTTKQECFRELSKALPSALSLSLFGWPAADRQKRIIRLLL
QRAERVGISCSQSLASFLRALASTSLPDILSEFDKLLCSVGKKTSLDHSDIKELVVKKEKASLWKFRDSLLKR
DPVEGHQQHLFLEDGEDPLGIITFLRTQCLYGLRSIEEGSKENKHRMFVLYGKERLHQALNSLFYAETLIKN
NVQDPIVAVETLVIRMVNL

>core/499/3/Org3_Gene122

MFSYIKNRILFNLLSLWIVLTLTFLVMKTIPGDPFNDEGCNVLSEEVLQTLKSRYGDKPLYQQYTQYLHSIAK
LDFGNSLVYKDRKVNTIISTAFPIAAILGLQSLFLSIGGGIALGTIAALKKKKQRRYILGASILQISIPAFIFATLLQ
YVFAVKIPLLPIACWGSFTHLTILPTLALAVTPMAFIIQLTYSSVSAALNKDYVLLAYAKGLSPLKVVVILHILPYA
IFPTISYSAFLTTHVTITGTFAIENIFCIPGLGKWFICSIKQRDYPVALGLSVFYGTFLMLSSLLSDLIQSIIDPQIRYA
HGKEKKRK

>core/500/3/Org3_Gene226

MAMLPKFFLVLLCLGLCSCSQKTTTIEGEQMTIFYRIVLGTSLSAKEKASLSQQIDRCFHKIDSIYNNWNPNPYSE
LSIINRAPADVPIITLSVELSEFLDQVDTLYKLSEGRFDPTVGPLKTLWLLHLKSQTLPPKDVWEQHYKDMGW
QHLEFQSNTKTLIKKNPHVQIDLCGVVKGYYAVDCLNEICNTFCPNNYVEWGGEIKTSGHHPSGRPWRIFSEA
AGTILDIDDMAIATSGNHIQKWCVEGKIYTHILDTRTGKPLELSSYPIQSVSVVHPSCAYADAIATVLMTFDSK
IEAKQWAEHHILTYINDGASS

>core/501/3/Org3_Gene370

MWRVVLRLIIFILGRAVFPLRASESFSWETSTCLTVLGIPFIDIILTNEDEFVAQCGLQIGTISSTNNAKIKEIFLI
YKEKFPEASISFKRKEPLNLSQSHLSDLGILCMRNGETYAEGMANKENGPAKQPKDLRLVLRCPNQPDLL
YSEKEAEKGIETNTCLCNQGYTLLDGQLILYGDSIEKFLKETKRKNHNTLVLDLCSQVVTFLGRFWSLLNY
VQVFLSEDSAKILAGIPDLAQATQLLSHTVPLLFIYTNDHSIHIEQKGESSFTYNQDLTEPILGFLFGYINRGSM
EYCFNCAQSSLGET

>core/502/3/Org3_Gene11

MIASIYSFLDYLMVKASPHLTRNYCLDLNGLKIFLEERGNLAPSSPLQLATEKRKVSELPFSLFTKEHVRM
YIAKLIENGKAKRTIKRCLSSIKSFAHYCVIQKILLENPAETIHGPRLPKELPSPMTYAQVEVLMATPDISKYHG
LRDRCLMELFYSSGLRISEIVAVNKQDFDLSTHLIRIRGKGKKERIIPVTSNAIQWIIQIYLNHPDRKRLEKDPQA
IFLNRFGRRISTRSIDRSFQEYLRRSGLSGHITPHTIRHTIATHWLESMDLKTIQALLGHSSLETTTVYTQVSV
KLKKQTHQEAPHA

>core/503/3/Org3_Gene207

MIHSRLIIIGSGPSGYTAAIYASRALLHPLLFEFFSGISGGQLMTTTEVENFPGFPEGILGPKLMNNMKEQAVR
FGTKTLAQDIISVDFSVRPFILKSKEETYSCDACIIATGASAKRLEIPGAGNDEFWQKGVTACAVCDGASPIFK
NKDLYVIGGGDSALEEALYLTRYGSHVYVHRRDKLRASKAMEARAQNNEKITFLWNSEIVKISGDSIVRSV
DIKNVQTQEITTREAAGVFFAIGHKPNTDFLGGQLTLDESGYIVTEKGTSTSVPGVFAAGDVQDKYYRQAV
TSAGSGCIAALDAERFLG

>core/504/3/Org3_Gene717

MRKLILCNPRGFCSGVVRAIQVVEVALEKWGAPIYVKHEIVHNRHVVNALRAKGAIFVEELVDVPEGERVYI
SAHGIPPSVRAEAKARKLIDIDATCGLVTKVHSAAKLYASKGYKIILIGHKKHVEVIGIVGEVPEHITVVEKVA
DVEALPFSSDTPLFYITQTTLSDDDVQEISSALLKRYPSIITLPSSSICYATTNRQKALRSVLSRVNYVYVVGDV
NSSNSNRLREVALRRGVPADLINNPEDIDTNIVNHSGDIAMTAGASTPEDVVQACIRKLSSLIPGLQVENDIFA
VEDVVFQLPKELRCS

>core/505/3/Org3_Gene588

MKCRPTLNTDQPRVRKKLPERFPKWLRPLPQGSFAHATDATIKRSGMPTVCEEALCPNRAECWSRKTATY
LALGDVCTRSCGFCNIGHSKTPPALDPTEPERIALSAKELGLKHVVITMVARDDLEDGGAQGLVDIIQKLREE
LPQATTEVLASDFQGNVSALHTLLDSGITYNHNHNVETVARLSPLVRHKATYARSMFMLEQAANYLPDLKIKS
GIMVGLGEMEGEVKQTLQDLASIGVRIVTIGQYLRPSRKHLQVKSYVTPETFDYYRRVGEAMGLFVYAGPFV
RSSFNADMILASVQDKASA

>core/507/3/Org3_Gene898

MKKRYAFLFPGQGSQYVGMGQDLYMEYPEVRELVDFAERLGFSLTSIMFEGPEDLLMETVHSQLAIYLHS
MAVVKVLSQRSSIQPSLVSGLSLGEYTALVASDRISVLDGLELVRKRGQLMNEACNQSPGAMAALLGLPSEV
IEENITSLGQGIWIANYNAPKQLVVAGIAEKVDQAIELFRDLGCKKAVRLKVSGAFHTPLMQVAQDGLAPDI
YALCMKDSSLPLVSHVVGKSLVNTEEMRECLARQMTSPTLWYQSCYHIESEVDEFLELGPVKVLAGLNRSIG
ISKPITSLGTFAQIEKFLSEV

>core/508/3/Org3_Gene382

MLNSNKFKSKTGAYGDLFQRVVVHSLVLTFLVLLLYSSLFPLTSFALGFITATCGAVGTYEYSSMAKAKMHY
PLSTFSAIGSFLFLALSFLSIRWGHSLPGFFDALPWTLIVVWVWSIFRVRKSTIGALQLSGVTLSILYVGPIRL
FLHVLYSFIHTQEPYLGIIWWASFLIATTKGADIFGYFFGKAFGNKKIAPQISPNTVVGVFVAGCLGATLISFIFF
LQIPTRFASYFPMPAILPLGLALGITGFFGDIIESIFKRDAHLKNSNKLKAVGGMLDTLDSLLLSTPIAYLFLIT
QSKEFIG

>core/509/3/Org3_Gene29

MRLFSYDKPKIKVQKIKADGFSGWLKC�HCHEMIHANELGQNYNCCPKCSYHYRITAIERVKLLADKDSWR
PLYTDLKSQDPLEFIDTDTYANRLEKARKNTTESEGVIVGICTIGLHPVALAVMDFNFMAGSMGAVVGEKLT
RLIEEAIETRLPPVIVSASGGARMQESVFSLMQMVKTSAAALAKLHEAGLPYISVLTNPTSGGVTASFAALGDIII
AEPKALICFAGPRVVAQVIGEDLPEGAQKSEFLLEHGMIDKIVERKELKTTLQTLDDYFLAQEYTTGGKSKAPR
DLSKRLKEIFLLTDDSE

>core/510/3/Org3_Gene983

MEIAYSLTSSFSVDSVTVGFFDGGCHLGHSNLLSILTSYSGSSGVITFDSHPQTVLSLNHTKLINTKEERLQLLQT
FPIDWLGVLTFDLNFANQSAEEFLTLLHRNLKCKRLILGYDSCIGKEQQSNTEALDTIGKPLGIEVIKIPPYRMD
NIVVSSKAIRQFLSAGNLECAHRFLGHPY AISGKITEGSGIGGSLGFATINLPREESLIPLGVYACEIRYDSTTCQ
GVMNLGTAPTFGRESLYAEAHIFSFAENLYGKEVSIIPRKFLREEKKFQSKETLIRAIEKDILDADAQDWFAKGSF
NYEGTA

>core/511/3/Org3_Gene12

MSSRELIILGCSSQQPTRTRNQGAYLFRWNGEGLLFDPGEGTQRQFIFANIAPTTVNRIFVSHFHGDHCLGLGS
MLMRLNLDKVSHPIHCYYPASGKKYFDRLRYGTIYHETIQVVEHPISEEGIVEDFGSFRIEAQRLQHQVDTLG
WRITEPDTIKFLPKELSRGIRGLIIQDLIRDQEISIGGSTVYLSDVSYVRKGDSIAIADTLPCQAAIDLAKNSCM
MLCESTYLEQHRHLAESHFHMTAKQAATLAKRAATQKLILTHFSARYLNLDIFYKEASAVFPNVSVAQEYR
SYPFPKNPLLK

>core/512/3/Org3_Gene582

MRSIFRFSLCFFTLVSCCFADASLYENSCPSRCQPTPPPSNSNPLNVVQQPVAASSVPSYMPPLNADDVLPRD
HLSDGFSFSDTYPDITTQAILIFLALSPFLVMLLTSYLKIIITLVLLRNALGVQQTTPPSQVLNGIALILSIYVMFPT
GVAMYKDARKEIEANTIPQSLFTAEGAETVFVALNKSKEPLRSFLIRNTPKAQIQSFYKISQKTFPSEIRAHLLTA
SDFVIIIIPAFIMGQIKNAFEIGVLIYLPFFVIDLVTANVLVAMQMMMLSPLSISLPLKLLLIVMVDGWTLLLQGL
MISFK

>core/513/3/Org3_Gene836

MKEAAPMHFPFPVRRSVWLNRYSTFRIGGPANYFKAIHTIEEAREVIRFLHSINYPFLIIGKGSNCLFDDRQFD
GFVLYNAIYGKQFLEDARIKAYSGLSFAALGKATAYNGYSGLEFAAGIPGSVGGAI FMNAGTNESDISSVVRN
VETINSEGELCSYSVEEELS YRSSRFHRQQEFILSATLQLSKKQVSADHSKSILQHRLMTQPYTQPSAGCIFRN
PEGTSAGKLIDAAGLKGLAIGGAQISPLHANFIINTGKATSDEVKQLIAIIQSTLKTQGIDLEHEIRIIPYQPKIHS
PVSEK

>core/514/3/Org3_Gene569

MSLFLVFLTAFIWSSSFALSKLVMNASAPIFATGARMVIAGAILALAAWFRGGFVGISKKIFLYIVLLALTGFY
LTNIFEFIGLQSLSSSKTCFIYGLSPLMSALFSYIQLKEKVTLKKVLGLSLGLVSYICYLTFGGGGDDSQPWTW
QIGLPELLILGAASLASFGWTLLRQIEKQSTLSVTAINAYAMLIAGMLSIMHSAVVEPWRLPVQDISQFLYAT

LALVVISNLICYNLYAKLLRKYSSTFLSFCNLVMPLYSGFYGWILLGEKGVSLGLVLAVAFMVAGCRLIYHEE
FRQGYIVS

>core/515/3/Org3_Gene593

MQKPQYIDRITKKKVIEPIFYEKTMLFLYNSKLGKKLSVFLSTHPIFSRIYGWLQRCSWTRRQIRPFMNRYKIS
EKELTKPVADFTSFNDFTRKLKPEARPIVGGKEVFITPVDGRYLVYPNVSEFDKFIVKSKAFSLPKLLGDHEL
TKLYAHGSIVFARLAPFDYHRFHPCDCLPQKTRCVNGALFSVHPLAVKDNFILFCENKRTVTVLETEQFGNV
LYLEV GAMNVGSIVQTFSPNQTYAKGDEKGFFAFGGSTVILLFLPNAIRFDNDLLKNSRMGFETRCLMGQSL
GRSQREEI

>core/516/3/Org3_Gene722

MTMPSTQFHTTILEQFSLFLSVDRGLCQQSIAAYRQDISSFLTISAISSPQDISQNSVYIFAEELYRRKEAETTLA
RRLIALKVFFLFLKDQQLLPYPPIIEHPKIWKRLPSVLTPQEV DALLAVPLQMEKNPRHLAFRDTAILHTLYST
GVRVSELCDLRLGHVSDDCIRVTGKGSKTRLVPLGSRAREAIDAYLCPFRDQYQKKNPHEDHLFLSTRGHKL
ERSCVWRRIHNYAKQVTSKPVSPHSLRHAFATHLLDNKADLRVIQEMLGHARIASTE VYTHVAADSLIEKFL
AHHPRNL

>core/517/3/Org3_Gene274

MLKIDLTGKVAFVAGIGDDQGYGWGIAKLLAEAGATHIVGTWVPIYKIFSQSWELGKFNESRKLSNGTLLEIA
KIYPMDASFDSPEDVPEDIAENKRYKGITGFTISEVAEQVKKDFGHIDILVHSLANSPEISKSLLET SRKGYLAA
LSASSYSFVSLLSHFGSIMNRGGSTISLTYLASMRAVPGYGGGMSSAKAALES DTKTLAWEAGRRWGIRVNT
ISAGPLASRAGKAIGFIERMVDYYQEWAPIPEAMNAEQVGAVAAFLASPLASAITGETLYVDHGANVMGIGP
EMFPKDS

>core/518/3/Org3_Gene751

MPPPFVVTLT TSAQNLRDQLKEKNFISQPQNTVFQARSNTVTCTLYPSGKLVIQGKGSEEFIEFFLEPEILHT
FTHARVEQDLRPLRGVDESGKGDFFGPLCIAAVYASNAEILKKLYENKVQDSKNLKDTKIASLARIIRSLCVC
DVIIYPEKYNELYGKFQNLNTLLAWAHATVINNLAPKPAGDVFAISDQFAASEYTLLKALQKKETDITLIQK
PRAEQDVVVAAASILARDAFVQSIQKLEEQYQVQLPKGAGFNVKAAGREIAKQRGKELLAKISKTHFKTFDE
ICSGK

>core/519/3/Org3_Gene174

MHLEENQGW EALLRKVYHQEVPPAILLHGFTLPVLQDKAEQLASEILLSSSPGSEHKVSQKIHPDIYQFFPEG
KGRLHSIDLPRGIKKQIYISPFEANYKIYIIHEADRMTLAAISAF LKVFEPPKHAVIILTTAKVQRLPKTIISRSL
IFIERGEKILCSKETFSYLFY AQCEIPVTEVSQIIKESSETDKQVLRDKVQRFMEV LLELYRDRYTLNLGLKAS
ALNYPEHVKEILQLPLLPLDKVLLIVESACRSLNNSSSAASVLEWVAIQLVSLQYKEKELVSVSPGQDLSN

>core/520/3/Org3_Gene167

MRLNYFLNLVNFKY SIFSILFLSASTVFALSINEISQNL SFKEGFKISVFGAIAFVFARTTGIVVNQCIDRFIDKKN
TRTSKRVL PANLVSLNFAWVLSLFC SFLFLCKILRIFSLGIASLTLMIVYPYMKRV TFFCHWGLGLVYTVAI

LMNFCAFAESGLSMRLCFLALLWGGSVGMVIAANDIYAIEDTEFDREEGLRSVPAHYGEKKAVEIAKVN LW
VSYLAYIFSGFVGSLDKEFYFTAIIPLVVILKVVRMYSNYSKKDQEGESKFFLANIAIALSFLVSMTLFWSLSR

>core/521/3/Org3_Gene284

MSERAHIPVLVEECLALFAQRPPQTFRDVTLGAGGHAYAFLEAYPSLTCYDGSDRDLQALAI AEKRLET FQD
RVSFSHASFEDLANQPTPRLYDGV LADLG VSSMQLD T LSRGFSFQGEKEELDMRMDQTQELSASDVLNSLKE
EELGRIFREYGEEPQWKSAAKAVVHFRKHKKILSIQDVKEALLGVFPHYRFHRKIHPLTLIFQALRVYVNGED
RQLKSLTSAISWLAPQGRLVIISFCSSDRPVKWFFKEAEASGLGKVITKKVIQPTYQEVRRNPRSRSAKLRC
FEKASQ

>core/522/3/Org3_Gene556

MSRHEICPEVSHKKGKYYSTFIFRCIHSLAGIAFTFFLCEHLFTNMLASSYFSQGKGFVAMVNGFHKIPGLKII E
VAGLVLPFLCHAIIGIVYLFQGKSNCYSGDGRPHLRYAKNYSYTWQRWTAWILLFGIAFHVVHLRFIRYPVH
VDIHGTTYAYAVDIQPSRYDVIVRGTKGFLTLNLPNTEASSIEVSRHDLGGADAALLSERNSYLLTPSAGTAFLY
VVRDALGSLFIALLYTILVIAAAFHGFNGLWTFCCRWGVVVS LRMQGVLRIVCYLAMIVVTFMGVSAVWNL
YSVA

>core/524/3/Org3_Gene802

MRRFLFLILSSLPLVAFSADNFTILEEKQSPLSRVSIIFALPGVTPV SFDGNCSIPWF SHSKKTLEGQRIYYSGDSF
GKYFVVSALWPNKVSSAVVACNMILKHRVDLILIIGSCYSRSQDSRFGSVLVSKGYINYDADVRPFFERFEIPD
IKKSVFATSEVHREAILRGGEFISTHKQEIEELLKTHGYLKSTTKTEHTLMEGLVATGESFAMSRNYFLSLQK
LYPEIHGFDSVSGAVSQVCYEYSIPCLGVNILLPHPLESRSNEDWKHLQSEASKIYMDTLLKSVLKELCSSH

>core/525/3/Org3_Gene165

MSHGPRPTKFSFPLYFSKTL SWFILGGFLAACGVQMVLVPNELIDGGIVGLSIIASHFLGHKALPFCLVLFNL PF
VFLAFKQIGKYFVIQMLTAVIIFSCSLWLIDQLPSWLGMSPFVFKGSEMETVVLGGAIIGVGCGLIIRHGGSTD
GTEILGIIINKKKGYTVGQIILFVNFFIFALSGIVYKNWHTAFVSFLT YGIATKVM DMVILGLEDTKSVTIITSSP
RKLGHILMETLGIGLTYIHAEGGYSGEPRNLLYVVVERLQLSQLKEIVHREDPSAFIAIENLHEVINGRRT

>core/526/3/Org3_Gene633

MQEKPRHVHRIIHISDVHFHVLVPNPVHCFNKRLKGLLRKVFGLVHFQATTIGQRF PKVVRSLGADSV CITGD
FSLTAMDGEFLLAKHFVETLAKHSSVYLLPGNHDVYTLKSLAQQT FYTHFPNDQLQQNKVS FHKITDHWL
ILLDCSCLNGWFSANGVVHLAQISAIETFLLSLSPEENVIIANHYPLLSSQNPSHDLINNTHLQNVLKKYPKVRL
YLHGHEHQAAVYNCA DTSPSYILNSGSISLPTNSRFHVIDLYPEKYQVHTMILKNLLDFDAPLEIANEATWDC
QKL

>core/527/3/Org3_Gene275

MEKLLVTDIDGTITHQSHHLDDKKVYERLYALHQAGWKLFFLTGRYYKYAARLFSDFDAPYLLGCQNGASV
WSSTSSNLLYSKSLPSDLLCILQDCMEGATALFSVESGAPYGDHYYRFSPTPIAQDLHEYVDPRYFPNAKEREI
LFETRSLKDDYAFPSFAAAKVFGLRDEVIRIQKELERQEALTSVATMTLMRWPFDFRYAILFLTDKSVSKGKA

LDRVVNILYDGKKPFVVMASGDDANDLDLIERGDFKIVMSSAPEEMHVVHADFLAPPADKNGILSAWEAGVRY
YDDLMSL

>core/528/3/Org3_Gene463

MKKLILYFAAFVASLFCGVFLWDRVPCAQKIMRLAADHSSEVFSKSCRFVRKISGFEELQVFERHVSPEQALA
LFPEYRDGKSFVELAFIPHTLMHVRFSKEEPVKKHIISQEGEILWSLVNGEMVLHTGTWTCCKGFRECLLLHA
GKQDMRVIQTLATLGGTTSRESLAQALALKNIRAERVIKECQKKKLIFASGNQIGTHFQQFQPIRGCTTTLNN
NPVWLQKPRHAAVFPAQYSEDRVRHLVKMIFGDNFLIVRSSMVYVPVYKISLVSADNSVRVEYINAVTGKSF
QDL

>core/529/3/Org3_Gene686

MFHSLSKNTPIITQGITGKAGSFHTEQCLAYGTNFVGGVTPGKGGTLWLDLPVYDSVLEAKQATGCRATMIF
VPPPYAAEAILEAEEAGIELIVCITEGIPVRDMLEVARVMDNSTSQLIGPNCPGIIKPGECKIGIMPGYIHLPGNI
GVVSRSGTLTYEAVWQLTQLKIGQSICVGIGGDPLNGTSFIDVLQALEEDPYTELILMIGEIGGSAEEEEAAWI
QAHCTKPVVAFIAGVTAPKGKRMGHAGAIISGNSGDAKSKIQVLRESGVTTVVESPAHIGKTVDAVLRAKEL

>core/530/3/Org3_Gene631

MSKHTSESRIAQDMLERYSGSSVKQFCPYLLL TNFSYYIQTFAKLHGVPVFEGSMFSAAHAPHLKTSILDFKL
GSPGAALTIDLCNFLPDLKAALMLGMCGLRSHYQVGDYFVPVASIRGEGTSDAYFPPEVPALANFVVQKAT
TEVLEDKKANYHIGITHHTNIRFWFNKKFRKKLYETKAQSAEMECATLFAAGYRRNLPIGALLLISDLPLRK
EGIKTKSSGNFIFNTYTEDHILTGQEVIENTLEKVMLKRAASDHKKDQQYRGLPHMEVGEADDTMASGSETSD
SDY

>core/531/3/Org3_Gene514

MKVLPPPSIPLLGAHTSTAGGLKNAIYEGRDIGASTVQIFTANQRQWQRRALKEEVIEDFKAALKETDLSYIM
SHAGYLINPGAPDPVILEKSRIGIYQEILDCITLGISFVNHPGAALKSSKEDCMNKIVSSFSQSAPLFDSSPLV
VLLETTAGQGTLIGSNFEELGYLVQNLKNQIPIGVCVDTCHIFAAGYDITSPQGWEDVLNEFDEYVGLSYLRA
FHLNDSMFPLGANKDRHAPLGEGYIGKESFKFLMTDERTRKIPKYLETPGGPENWQKEIGELLKFSKNRDS

>core/532/3/Org3_Gene362

MLSSLIRDSFPLLILLPTFLAALGASVAGGVMGTIYVVKRIVSISGSISHAILGGIGLTLWIQYKLHLSFFPMYGA
IVGAIFLALCIGKIHLKYQEREDSLIAMIWSVGMAIGIIFISRLPTFNGELINFLFGNILWVTPSDLYSLGIFDLLV
LGIVVLCHTRFLALCFDERYTALNHCSVQLWYFLLLVLTAITIVMLIYVMGTILMSMLVLPVAIACRFSYKM
TRIMFISVLLNILCSFSGICIA YCLDFPVGPTISLLMGLGYTASLCVKKRYNPSTPSPVSPEINTNV

>core/533/3/Org3_Gene713

MKRNDPCWCGSGRKWKQCHYPQPPKMSPEALKQHYASQYNILLKTPEQKAKIYNACQITARILDELCKASQ
KGVTTNELDELSQELHKKYDAIAAPFHYGSPPFPKTICTSLNEVICHGIPNDIPLKDGDIMNIDVSCIVDGYYG
DCSRMVMIGEVP EIKKKICQAACLELND SIAILKPGIPLCEIGEAEARADTYGFSVVDQFVGHGVGIEFHENPY
VPHYRNRSMIPLAPGMIFTIEPMINVGKKEGVVDPKNQWEARTCDNQPSAQWEHTIAITETGYEILTLLND

>core/534/3/Org3_Gene740

MHLLTATVTPFFPNGTIDFASLERLLSFQDAVGNGVVLLGSTGEGLSLTKKEKQALICFACDLQLKVPLFVGT
SGTLLEEVLDWIHFCDNLPISGFLMTTPYTKPKLCGQILWFEAVLNAAKHPAILYNIPSRAATPLYLDTVKAL
AHHPQFLGIKDSGGSVEEFQSYKSIAPHIQLYCGDDVFWSEMAACGAHGLISVLSNAWPEEAREYVLNPQEQ
DYRSLWMETCRWVYTTTNPIGIKAILAYKKAITHAQLRLPLSIEDFDLENVSPAVESMLAWPKLRTSVFSYS

>core/535/3/Org3_Gene684

MFKFFRNKLQSLFKKNISLDLIEDAESLFYEADFGTELTEELCARLRRTKKADASTIKDLITVLLRESLEGLPSQ
ASQSSQTRPIVSLLLGTNGSGKTTTAAKLAHYKERSVMLVATDTFRAAGMDQARLWANELGCGFVSGQ
PGGDAAAIAFDGIQSAIARGYSRVIIDTSGRLHVHGNLMKELSKIVSVCCKALEGAPHEIFMTVDSTLGNNNAIE
QVRVFHDVVPLSGLIFTKVDGSAKGGTLFQIAKRLKIPTKFIGYGESLKDLNEFDLDFLNKLFPEVEKI

>core/536/3/Org3_Gene161

MKRRNLQKILPNASTPSTNVAENTGIKDQNLFLDQATLNV DGNVDIENFLETRDLKVADTITSPCEFTVGGGL
SAESSQFKATTLSKGLEITSEDQDGRVPKFTNVSDPQSPRDALTYNYYRNTGCQALNLYTYYSSSQPTTVGKP
IETVCQNPNPETYRISASAKIYDAVTRFPYIQFKAPGIYQVTIQIRRESGQHSGLDNPNLYLNL MIGNNKTLLCA
SDTRGYSGGHRTSIAVTGTFTLTEIVATPPHDYPWLFLETTIGLDIKSMSTCVIWFPPQANFAEVD

>core/537/3/Org3_Gene915

MQIPRSIGTHDGSFHADEV TACALLIIFDLVDENKIIRS RDPVVL SKCEYVCDVGGVYSIENKRFDHHQVSYDG
SWSSAGMILHYLKEFGYMDCEEYHFLNNTLVHGVDEQDNGRFFSKEGFCFSFSIIKIYNPREEEETNSDADFS
CALHFTIDFLCRLRKKFYDRVCRGIVREAMETEDMCLYFDRPLAWQENFFFLGGEKHPAAFVCFPSCDQWI
LRGIPPNLDRRMEVRVPF PENWAGLLGKELSKVSGIPGAVFCHKGLFLSVWTNRESCQRALRLTLQDRGII

>core/538/3/Org3_Gene580

MGISLPELFSNLGSAYLDYIFQHPPAYVWSVFLLLLARLLPIFAVAPFLGAKLFPSPIKIGISLSWLAIIFPKVLA
DTQITNYMDNNLFYVLLVKEMIIGIVIGFVLAPFYAAQSAGSFITNQQGIQGLEGATSLISIEQTSPHGILYHYI
VTIIFWLVGHRIVISLLLQTLEVIPIHSFFPAEMMSLSAPIWITMIKMCQLCLVMTIQLSAPAALAMLMSDLFL
GIINRMAPQVQVIYLLSALKAFMGLLFLTLAWWFIKQIDYFTLAWFKEVPIMLLGSNPQVL

>core/539/3/Org3_Gene525

MLHALDTYRPSIESAIEKALEGFGPIGHPIRSPVEYALQGGGKRLRPGLVCMMAQGLGLNHDVMDSALAVEF
VHTSTLIADDLPMDND DERRGRPTVHKAFDEATALLASYALIPAAYSHLRLNAKKLKEQGCDPREIDIA YNI
IGDITDKNIGCSGVLGGQYDDMFFSNRGQEHVQSIMIKKTGSLFEIACISGWLFGGGDPQFAPIITSFSNNFGLL
FQIKDDFSDLQKDSQQIGLNYALLFGEKAALELLARSQNNCLELLDRLSAGGLKNSSEFETIISLSGSF

>core/540/3/Org3_Gene160

MSNPTPKTKISIPTFVRFN IQSINLTEDQKKTTFTVGGKVTTENTVVRGDLTCTDGGGLTCQSDLTIQKDINIRPT
STNSMVF DGRNLNSNSPLSYKNSQGQDITDY EKMSSGKPQEYVPFGYYKRTQIMMAQRAAHSSGYVGGGSV
PSGSYVPWNKFDQTSTQKTSGTEIYIDPNDSTKL VFEVNNKVPKLF RISVIMAKHGSWLDNGTGADILLAANE
YEQGGGRINVTDLAMTTSRGSSYYETRPLQVVCVTTYAQNNGYFTFQNRAGGGLRVSFFSWNIVALPYVE

>core/541/3/Org3_Gene755

MLKIQKKRMCVSVVITVGAIVGFFNSADAAPKKKKIPIQILYSFTKVSSYLKNEDASTIFCVDVDRGLLQHRY
LGSPGWQETRRRQLFKSLENQSYGNERLGEETLAIDIFRNKECLESEIPEQMEAILANSSALVLGISSFGITGIPA
TLHSLLRQNLSFQKRSIASESFLKIDSAPSDASVFYKGVLFRRGETAIVDALSQLFAQLDLSPKKIIFLGEDPEV
VQAVGSACIGWGMNFLGLVYYPAQESLFSYVHPYSTATELQEAQGLQVISDEVAQLTLNALPKMN

>core/542/3/Org3_Gene828

MSHLIPSLRNSVTSYFHKPQPIKQAAPSKSIRDICNIAYLIIICVLVVVVVLVGAMLCMFIPSVGIPLCLSSLALLV
LLSIFNPCLINWISTKKTKEIAPKDASESQPTKSASRKGSPQLSPHHDHEPKNFIRTQLEKGVNYVTNKFSGEE
SPHISDEHHSPRQSKRSSEIESSDESSPELHRKAKGKAPHTATTKGSKTSTTESSKKKKKTKHSLHRTTSSIHKR
SAPKPMVPSKKRKPVLLKKTVPPLIEDLEHQSSGNESSDSSSPPPVQRKAILPWFCCKQPTDP

>core/543/3/Org3_Gene67

MEIKKAIQEGTAYLDYYGVPLSDCEALYILMDLLEVSSRAKLFDLVGISETMLMEYRKRLALRGQRCPTAYL
NGAVSFLGLRLRVDSRVLIPRTETELLA EYIINYLLSHSEIQTFYDICC GSGCLGLAIKKSCPHVEVVLSDVCPQ
AVAVANENAKSNGLDVKILLGDLSAPYTRPADAFVCNPPYLSFNEIIHIDPEVRCYEPWKALVGGSTGLEFYQ
RIAQELPKIVTSTGVGWLEIGSSQGSEIKNIFSKHGIYGR LHQDLSGRDRIFFLEMDGRDPVSSGAYS

>core/544/3/Org3_Gene204

MAVIYWDRSKIVWSFEPWSRLTWYGVFFTVGIFLACLSARYLALSYYGLKDHLFSFSKSQLRVALENFFIYSI
LFIVPGARLAYVIFYGWSFYLQHPEEIIQIWHGGLSSHGGVLGFLWAAIFSWIYKKKISKLTFLFLTDLCGSVF
GIAAFFIRLGNFWNQEIVGTPTSLPWGVVFS DPMQGVQGVVHPVQLYEGISYLVVSGILYFLSYKRYLHLGK
GYVTSIACISVAFIRFFAEYVKSHQGKVLAE DCLLTIGQILSIPLFLFGVALLIICSLKARRHRSHI

>core/545/3/Org3_Gene225

MLLRGIPAAEKILQRLKEEISQSPTSPGLAVVLIGNDPASEVYVGMKVKKATEIGIISKAHKLPSDSTLSSVLKL
IERLNQDPSIHGILVQLPLPKHLDSEVILQAISPDKDVDGLHPVNMGKLLLGNFDGLLPCTPAGIHELLNYYEIP
LRGRHAAIVGRSNIVGKPLAALMMQKHPQTNCTVTVLHSQSENLP EILKTADIIAALGAPLFIKETMVAPHA
VIVDVGTTTRVPADNAKGYTLLGDVD FNNVVTKCAAITPVPGGVGPMTVAMLSNTWRCYQNFS

>core/546/3/Org3_Gene479

MTEEISKDTIIEVAIDDIRVSPFQPRRVFSNEELQELIASIKAVGLIHPPVREICTGDRVLYYELIAGERRWRAM
QLAGATTIPVILKHVIADGTAAEATLIENIQRVNLNPIEMAEAFKRLIHVFGLTQDKVAYKVGKKRSTVANYL
RLLALSKTIQESLLQGQITLGHAKVILTLEDPILREKLNEIIIQEHLAVREAELIAKQLISEEGSSIELKPTPLDMA
ESSKQHEELQQRLSDLCGYKVQIKTRGSKATVSFHLQNTQDLQKLEAWLSSHGTLSESLS

>core/547/3/Org3_Gene172

MPDKKAQITFSLPEVMSAIHQGKIVALPTDTVYGVFVLSLYASEAEERLYALKDREPSKAFALYVNSIEDIENIS
GYPLSPTAKKLAQLFPGAITLVVKHRNPRFPKETLAFRIVDHSV VREIVDHC GTLIGTSANLSEFP SALT AQEIF
ADFADHDL CIFDGPCSHGLESTVVASDPLYIYREGLISRSVIENIAGTEAKIFHRTSHAFSKHIKIYTVKNQEQL
VSFLSGSLDFKGVVCEHPKPKNFYTRLREALKKKTPSIVFIYDINTSDYPELFPFLSPYYIE

>core/548/3/Org3_Gene159

MKNNINNNECYFKLDSTVDGDLLAANLKTFTDTQAQGISSTETFSVQGNATFKDQVSATGLTSGTTYNLNAQ
NFTSSQISIDFKNNRLSNCALPKEDCDPVPANYVRSPEYFFCSKPLIGDFDFNSGESYLPLTGSEYTLYQSRNVN
SIFRFIGWKQSTRELTVGNTAIQFLAAGTYIVSFTVGKRWGWNNGWGGAIYINNGLGQVQCESTIYSGGGY
ATIGTLGTSIYRASVDVAPNPNDPNASDRYRAGIFYLSNGGSSAGIGNYSFSLLYYPPDDR

>core/549/3/Org3_Gene320

MHEVLILTFTYPLPRTLKQHPDEVHTVPISPNSFGEGSPILIAGPCTLESYEHTVSSALTVKEAGAQVFRGSIR
KPRTSPFSFQWEKECVLWHKEAQSIHGLPTETEVLDVRDVEITAETHVDILRIGAKNMHNTPLLQEVSKSHRP
IILKRSPAATLEEWLCAAHEYILASSPCPGVILCERGIRTFEHSTRYTLDLNNTVALLKEISSLPVIVDP SHAAGKR
SLVLPLASAGLSVGADGLMIEVHAHPEKALCDAKQKITPEELHLFAKKHFCPSESRAHAIS

>core/550/3/Org3_Gene896

MKHYSFSPSADFFSKQGAJETQVLFGERVLVKGSTCYAYSQLFHNELLWKPYPGHSFRSTLVPCTPEFHIHP
NVSVVSVDAFLDPWGIPLPFGTLLHVNSQNTVIFPKDILNHMNTIWGSGTPQCDPRHLRRLNYNFLAELLIKD
ADLLLNFYVWGGRSVHESLEKPGVDCSGFINILYQAQGYNVPRNAADQYADCHWISSFENLPSGGLIFLYP
KEEKRISHVMLKQDSSTLIHASGGGKKVEYFILEQDGKFLDSTYLFFRNNQRGRAFFGIPRKRKAFL

>core/551/3/Org3_Gene123

MDNYLLNIKDLTITSTNPKRTLIENTLSLQKENRNLALVGESGSGKTTITKAILGFLPENCLIKTGSILFEDIDIT
KLSPKELHKIRGQKIATILQNAMGSLTPSMRIGMQIETLRQHHKMNKEEA YNKAMQLLTDVCIPNPKYSFSQ
YPFELSGGMRQRVVIAIALASQPKLILADEPTALDSMSQAQVLRILRNIQQKQATILLVTHNLSLVKELCND
ICIIKDGLIETGTVEEIFLSPKHPYTLKLLNAVSKIPIKKTSSPILKNKFQPLMSMQGGL

>core/552/3/Org3_Gene891

MENLSSAPSRSIWKSIIQNKMLVLGLTTLIILMLGALLPWFYQDYEQTSLKDILVSPCSRFPFGTDTLGRCMF
ARTLRGLRLSLLIATIALIDVCVGLLWATVAISGGKKIDFLMMRTTEILFSLPRIPHIILLVIFHHGLLALILAM
TITGWIPISRIIYGQFLLLKNKPFVLSAKAMHASTFHILKKHLLPNTLAPIISTLIFTIPNAIYTEAFISFLGLGIQPP
QASLGTLVKEGINAIDYYPWLFFFPSLIMIALSISFNLIGEGAKTLCLEEGSHG

>core/553/3/Org3_Gene110

MKQPMSLIFSSVCLGLGLGSLSSCNQKPSWNYHNTSTSEEFFVHGNKSVSQLPHYPSAFRTTQIFSEEHNDPY
VVAKTDEESRKIWREIHKNLKI KGSYIPITYGSLMHPKSAALTLKTYRPHPIWINGYERSFNIDTGKYLKNGS
RRRTSHDGPKNRAVLNLIKSSGRRCAIGLEMTEEDFVIARRREGVYSLYPVEVCSYPQGNPFVIAAWIADE
SACSKEVLPVKGYYSLVWESVSSDSLNAFGDSFAEDYLRSTFLANGTSILCVHESYKKVPPQP

>core/554/3/Org3_Gene442

MFKKFKPVTGTRQLVLPADFELTTRGELRGTKSKRSLRPNKKLSFFKKSSGGRDNLGHISCRHRGGGAKQL
YRVVDFKRNDGITAKVVTV EYDPNRSAYIALLSYEDGEKRYILAPKGIQRGDVVVSGEGSPFKPGCCMTLK
SIPLGLSVHNIEMRPSSGGKL VRSAGLAAQVIAKSPGYVTLKMPSGEFRMLNEGCRATIGEVS NADHNL RVD
GKAGRRRRWMGVRPTVRGTAMNPVDHPHGGGEGRHNGYIPRTPWGKVTGLKTRDKNKSNKWIVKDRRK

>core/556/3/Org3_Gene448

MASIHPTAIIPEGAKIGKDVVIEPYVVIKATVTLCDNVVVKSAYAYIDGNTTIGKGTTIWPSAMIGNKPQDLKYQ
GEKTYVTIGENCEIREFAIITSSTFEGTTVSIGNNCLIMPWAHVVAHNCTIGNNVVLSNHAQLAGHVQVGDYAIL
GGMVGVHQFVRIGAHAMVVGALSIGRRDVPPTYIGSGNPYQLAGINKVGLQRRQVPFATRLALIKAFKKIYRA
DGCFFESLEETLEEYGDIPVKNFIEFCQSPSKRGIERSIDKQALEEESADKEGV LIES

>core/557/3/Org3_Gene936

MSDFSMETLKT LRQQTGVGLTKCKEAL EACGGNLEEAVVYLRKLGLASAGKKEHRETKEGIIAAKTDANGA
ALIEVNVETDFVANNAVREFVSNLLNDILKYKVDTVEALSQAASSQDPSLSVDELRAVTMQTVGENIRISRV
AYFPKATNSTVGIYSHGNGKTVALTMLSGSSTADSLAKDIAMHVVAAPQFLSKESVP AE AIAKEKEVIASQI
QGKPPQEVIEKIVTGKLN TFFQEAC LLEQPF IKNADLSIQSLIDDFS KTS GSSVAIEQFILWKIGA

>core/558/3/Org3_Gene450

MLERTQRTLKREVRYS GVG IHLGKSSTLHLQPAQTNTGIVFQRQSASGNYENVPALLDHVYTTGRSTTL SRG
SAVIATVEHLMAALRSNNIDNLI IQCSGEEIPIGDGSSNVFVELIDQAGICEQEDKVS IARLTRPVYYQH QDIFL
AAFPSDELKISYTLHYPQSSTIGTQYKSLVINEESFRQEIAPCRTFALYNELCFLMEKGLIGGGCLDN AVVFKD
DGIISRGQLRFADEPV RHKILD LIGDLSLVGRPFVAHVLA VSGHSSNIAFGKKILEALEL

>core/559/3/Org3_Gene528

MATAHLGRQALLHLRSWTPAIRASGNLFRQQMSLHNNVLFAGDIVGA IKNSTAISRHALGSSHYAHAALQK
TEGFLGAADGVNTAVAGAMLWGQLLNGSMIFETDEETGELRR CNEADAEGCMTQKLQRRSALTITGKVAR
LASKTLGTATFLHEMDVVS LGANANKIGCKVTSCNLVATGCSL TESSISLYRILSTRPETISDPENRNKPSAEF
AARSKAIRNAFI AWLGDVVDLVC DALGTLSLFLPAILGVH AVLIMAILGLISCVIN FVKDYAKIG

>core/560/3/Org3_Gene164

MVLMNKRLKIILTND DGITAKGMSCLVSALLEANIGDIYIAAPQAEQSGKSMAISLNQVVCASPYAYPQPVKE
AWAVGGSP TDCVRLGLRTL FESVSPDLVISGINCGNNICKNAWYSGTIGA AKQALVDGIPSMALSQDNHISFF
QQDKAPEILKALVIYLLSQPF PCLTGLNINFPTSPGGSSWEGMRLVPPGDEFFYE EPQYLGSVNKNQYYVGKIS
GVRIGEHPSEELACMLENHISVSPIFSQNSPIGLMTLEEFQKTQENFNASLLSSEL TTKIF

>core/561/3/Org3_Gene494

MELKKTAESLYSAKTDNHTVYQNSPEPRDSRDVKVFSLEGKQTRQEKT TSSKGNTRTESRKFADEEKR VDD
EIAEVGSKEEEQESQEFCLAENAFAGMSLIDIAAAGSAEAVVEVAPIAVSSIDTQWIENIILSTVESMVISEINGE
QLVELVLDASSSVPEAFVGANLTLVQSGQDLSVKFSSFVDATQMAEAADLV TNNPSQLSSLVSALKGHQLTL
KEFSVGNLLVQLPKIEEVQ TPLHMIAS TIRHREEKDQRDQNQKQKQDDKEQDSYKIEEARL

>core/563/3/Org3_Gene830

MRQSFDELSQN AFKNIFNKQRFCFIFCSLCCFGFVFALFLKLCSRLAPEISLSTLGLGAFFCAFSVICASAIIVQF
LLHKESQGETSKLCCA IKN TWSSLWLSLLVSM PFFIAMVAVVTVAMLSSFLGSLPWVGKLFHTVLIFIPYLSA
TALILLFLGSFSC LFFCIPVLHNQESIDYRKLL ECFRGNILRQFIGVVIALVPLALCSWLALDSFYLMTHLVEIAD
IHTWSFLAQMFVLIVPIALILTPAVSFFFNF SFSFYLA KQEE EKALVK

>core/564/3/Org3_Gene919

MHKVIVFIFLTLYSLKSYGNDVIDKPHVLVSIAPYKFLVEQIAEETCFVYAIVTNHYDPHTYELPPQQIKELRQ
GDLWFRIGEAFEKTCERNLTCQQVDLSQNVSLIQGKPCCNQHTTNYDTHTWLSPKNLKVQVETIVTTLSKKY
PQHATLYQSNGEKLLLALDQLNEEILTITSKAKQRHILVSHGAFGYFCRDYNFSQHTIEKSSHVEPSPKDVAR
VFRDIEQYKISSVILLEYSGRRSSAMLADRFHMHTVNLDPYAENILVNLKTIATTFSSL

>core/565/3/Org3_Gene426

MYFTRDPVIETVITSREGYKLSVRNTKHFSQDPFMVEAIEVISLGNICFFRNCDHSPFLVPAGDYEVMVRDT
KINLKA VGLDRGVK IAGGREALIKLTKSTPLPVIDEKPLADSP EEGTEPTSPSKKEKKEARKDSFKGEKWKEK
KKLSRRRNHKEIAEVTGASQEILD TVKEELWEESQENEIVEQKKFSLPPPAKLISEVISQTVVDPV VTSADLN
ESLQALVRESSDLINALLSADDAIHFPETEEETPSASFEESSAMFFPETSSATEEE

>core/566/3/Org3_Gene747

MTRSSPAQLSRFLSEIQNKPKKSLSQNFLVDQNVKKIVATSEVIPQDWVLEIGPGFGALTEELIAAGAQVIAIE
KDPMFAPSLEELPIRLEIIDACKYPLDQLQEYKTLGKGRVVANLPYHITTPLLTKLFLEAPDFWKTVTVMVQD
EVARRIVAQPGGRDYGSLTIFLQFFADIHYAFKVSASCFYPKPQVQSAVIHMKVKETLPLSDEEIPVFFTLTRT
AFQQRRKVLANTLKG LYPKEQVEQALKEGLLLNVRPEVLSLNDYLALFHKMQAG

>core/567/3/Org3_Gene487

MESQSCKLTIKDLMSAGAHFGHQTRRWNP KMKLYIFEEKNGLYIINLAKTLQQLRNALPHIRKVIQDNKTVL
FVGTKKQAKCVIREAAIEAGEFFIAERWLGGMLTNMTTIRNSIKTLDKIEKDL SRNQAYLTKKEAALLAKRH
QKLLRNLEGIRYMKKAPGLLVVVDPSYEKIAVAEAKKLGIPVLALVDTNCDPTPIDHVIPCNDDSLKSIRLIIN
VIKENIIEAKHKLGI EIVSPVKSLEVPDLSAFESSQDDESDEENREEDLLAKKFDGEAN

>core/569/3/Org3_Gene584

MTANTFGTLDILMKH SKEDDL SRFLPKNLLVESPHPEEIPLKSLSFTMSWLPTIHP SWITIAMKEFPPEIQGQLL
AWLPEPLVQEILPLLPGISIAPHRCAPFGAFYLLDMLSKKIRPCGITEEIFLPASSANAILYYTGPKIALINCLGL
YSIAKELKHILDKVVIERVKNALSPTEKLFLTYCQSHPMKHLETTNFLSSWTTDAELRQFVHKQGLEFLGKAL
TKENASFLWYFLRRLDVGRAYIVEQTLK TWYDHPYVDYFKSRLEQCMKVLVK

>core/570/3/Org3_Gene353

MDYKLLDSGDGNKLECFGPVTLIRPSSIAVWP KSRPELWSQAQLQYVREGERGAWKNFKRLPEEWEVAFSD
VRCLLKRTPFGLHGVFPEHMGFWPALKQAIEKHKERQVLNLFAYTGAGSIFAAKCGARVTHVDASQA AVR
WAQRNVEKNAFPERRIFWVIEDVISFLKKEIRRNKKYQVILLDPPSYGRGPDGEVFKIDKDLFPLLSLCSKLLA
DDASYFLLTSHTPGHTPEFLRAIARRSVPTLVSEAWSCGESFCGEGVGALPSGSFVQWIA

>core/571/3/Org3_Gene97

MITGVVLEKHEQRTMFSLTLLNNFTTFGLLHTPLHYNPPYPIVILLHGLASDKTGSKRSHVRLAQELTRLGIAA
LRVDLLGHGDCEGELMDFSLENYKQNIREIIEYTHSLLHIDQERLAIFGSSLGGTLALQTL PFFN KIKALAVWA
PTISGELMAAEAAQKNAPEVITMSQKGAITYAGMTLNPDFYTQFLKIDIVKELMP SARNLPILYMQGEQDLLV
SINHRTLFT EAFANQDKPITILTYPDVDHAFPPFAESSALSDLTQWLKRELTSGE

>core/572/3/Org3_Gene510

MLLGFLCDCPCASWQCAAVANCYDSVFMSRPEHKPNIPYITKATRRGLRMKTLAYLASLKDARQLAYDFLK
DPGSLARLAKALIAPKEALQEGNLFFYGCSNIEDILEEMRRPHRILLGFSYCQKPKACPEGRFNDACRYDPSH
PTCASCISIGTMMRLNARRYTTVIIPTFIDIAKHLHTLKKRYPGYQILFAVTACELSLKMGFDYASVMNLKGVG
IRLTGRICNTFKAFKLAERGVKPGVTILEEDGFEVLARILTEYSSAPFPRDFCEIH

>core/573/3/Org3_Gene756

MRRYLFMVLALCLYRAAPLEAVVIKITDAQAVLKFAREKTLVCFNIEDTVVFPKQMVGQSAWLYNRELDLK
TTLSEEQAREQAFLEWMGISFLVDYELVSANLRNVLTGLSLKRSWVLGISQRPVHLIKNTRLILRSFNIDFTSC
PAICEDGWLSHPTKDTTFDQAMAIEKNILFVGSLKNGQPMDAALEVLLSGISSPPSQIHYVDQDAERLRSIGAF
CKKANIYFIGMLYTPAKQRVESYNPKLTAIQWSQIRKNLSDEYYESLLSYVKSKG

>core/574/3/Org3_Gene995

MKVKINDQLICIPPFISARWSQIAFIESQEGENKDQGTLRHLIDGKIISIPNLDQSIIDIAFQEHLLEYLETSSQSGKE
DSRDDDGLGVGVLNMVNLQQITKGNDIQVLPKNLISPLFSGTNPIEAILQHTPEHKDHPDAPTDVLEKMADVIR
VLSGNNATLLPRPEPHCNCMHQCIGRVMNEEDTLAVSDKDLTFRTWDIMQSGDKLYIVTNPLNPSDQFSVYL
GPPIGCTCGEPNCEHIKAVLYT

>core/575/3/Org3_Gene262

MKLLKNVLLGLFFSMSISGFSEVKVSDTFVKQDTVVEPKIRVLLSNESTTALIEAKGPYRIYGDNVLLDTAIQG
QRCVVHALYEGIRWGEFYPLQCLKIEPVDDTASLFFNGIQYQGSLYVHRKDNHCIMVSNEVTIEDYLKSVL
SIKYLEELDKEALSACIILERTALYEKLLARNPQNFWHVKAEEEGYAGFGVTKQFYGVEEAIDWTARLVDS
PQGLIIDAQGLLQSNVDRLAIEGFNARQILEKFYKDVDVFFVIESWNEELDGEIR

>core/576/3/Org3_Gene179

MKKKLSLLVGLIFVLSSCHKEDAQNKIRIVASPTPHAELLESQEEAKDLGIKILPVDDYRIPNRLLLDKQV
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EECGLIVCKGPANLNMTAKDVCCKENRSINILEVSAPLLVGSLPDVDAAVIPGNFAIAANLSPKKDSLCEDL
SVSKYTNLVVIRSEDVGSPKMIKLQKLFQSPSVQHFFDTKYHGNILTMTQDNG

>core/577/3/Org3_Gene317

MVRDIQSESIGKLVFLGTGNPEGIPVPFCSCRVCQNTGIHRLRSSVLIQYQNKTLVIDAGPDFRTQMLVAGVSE
LDGVFLTHPHYDHIGGIDDLRAWYIVTQRSPLVLVSASTYRFLNKAKEYLFATPNVESSLPAVLEFTILNEDCG
QEEFQGIPYTYVSYQKSCHVTFGRFGNLAYLTDLCSYDAKIFSYPDNDVETLILSAGPSETPIPFQGHKSSHLT
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>core/578/3/Org3_Gene846

MIRFFKTLFPPGPQYSLCYASILIVLSSLVCVPTFCWLFLPELSLSKFNPSPIRNFLVSSTLSKVPPTAIAEHLR
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SLNLPQIFFSQEDLKMQKLPKEKMLFTKILLKELAMESPKIIDLSLSDAYPGEIIVTLSSGSLLRLPIKTLDRALD
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>core/579/3/Org3_Gene940

MFNNKMILIAGPCVIEGEDITLEIAGKLQSILAPYSDRIQWFFKSSYDKANRSSLNSFRGPGLTEGLRILAKVKE
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GNNKILLTERGCSFGYNLVSMDRSIPVLSRSGFPVIFDATHSVQLPGALSTESGGLTEFVPTLSRAALAAGAH
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>core/580/3/Org3_Gene762

MTKVALLIAYQGTAYSGWQQQPNDLSIQEVISSLKKITKTRTPLIASGRTDAGVHAYGQVAHFRAPDHPLF
ANANLTKKALNAILPKDIVIRDVALFDDNFHARYLTIAKEYRYSLSRLAKPLPWQRHFCYTPRHPFSTELMQE
GANLLIGTHDFASFANHGRDYNSTVRTIYTLDIVDKGDSLSIICRGNGFLYKMMVRNLVGALLDVGKGAYPPE
HLLDILEQKNRREGPSAAPAYGLSLHHVCYSSPYNNFCCEQCSVSTSNEG

>core/582/3/Org3_Gene819

MTQYYFLSSFLPTQLPESVPLFSISDLDDLLYLNLSENDLCNYGLLKRFFDFENFAFFWAGKPIPFSGEVTQE
NVERMLSSQQWSDDNDFEDFFKDFLMNHKSSQDRLNHFSDLFREFLSYHQTNSSKFLRDYFRFQQQLRVVL
AGFRARVLNMDVSYVLRDEDSSDPVVLEVLMQKDSPNYELPEEFSDLQGVLDYGLLPHTLNRALALYQFH
KLEGFCSDSYFDGNVILARCATYMFAIRNSLASVEKGREIINHIEKAIKW

>core/583/3/Org3_Gene888

MHSKFLSRRKKNSSHKEETSWDCIASSYNKIVQDKGHYYHRETILPQLPSLTLGSKSSVLDIGCGQGFLERA
LPKECRYLGIDISSRLIALAKKMRSVNSHQFKVADLSKRLEFVEPTLFSHAVAILSLQNMEFPGEAIRNTATLL
DPLGQFFIVLSHPCFRIPRASSWHYDENKKAISRHDYRLSPMKIPIMAHPGQKDSPSTLSFHFPLSYWFKELSS
HGFLVSGLEEWTSSTKTSTGKRAKAENLCRKEFPLFLMISCIKIK

>core/584/3/Org3_Gene610

MTLPLEPMIFWSSLSAKVMKKFLTPHCAGTFSEEDAEAKEAHLVTGKQGHRLMGNCVTFYWLVDKKNQVI
LDAKFQYFGHPYLIPLAEAVCNLVCCKSYSEAYKMTLDDIDKSLRVHAHQPALPEDSISLYHFVIDALDTAVE
QCLEIPLEDGSLPLQNSPMNLD FEDANPYSQSDWEALTHEQKLYALRATIAEKIGPYIAMDGGEVTVESLENF
IVTIAYSGNCSGCPSSLGSTLNSIGQLLRAYIYPELQVKVDESSLNLSHP

>core/585/3/Org3_Gene624

MQGFFPLASGSKGNSAYLGTDSCKILIDLGVSKQVVTRELLSMNIDPEDIQAIFVTHEHSDHISGIKSFVKAYN
TPIVCNLETARALCHLLDSHPEFKIFSTGSSFCFQDLEVQTFNVPHDAVDPVAFIFHYREEKLGFCITDLGWVTS
WITHELYDCDYLLIESNHSPELVRQSQRPDVYKKRVLSKLGHISNQEKGQLLQKIITPKLKKLYLAHLSTECNT
AELALSTVSESIASITIAPEIALAQGITSPIYFSRLEVACPR

>core/586/3/Org3_Gene689

MAGLDLEARGKRRVVTNPAITAFGLCCGLFIIFKSVLRTSSSVELFHRLQGLSLLLISAMIADFS DGAIARIMKA
ESAFGAQFDSLSDAVTFGIAPPLIAIKSLDGIYVGNFFSSLLLITSIIYSLCGVLRLVRYNLF SQKTVDVSKPYCFI
GLPIPAAAASIVSLALFLASDFFPDLP AQLRVGLLSFALLFIGGLMISPWKFPGVKHFRFNVSSFLLVVTIGLAA
CLFFSGLVDHFVEVFFLVSWLYTLVGFPIFSIIYRKKS

>core/587/3/Org3_Gene20

MKKPDNDSTFDVRSFFPFDVLCIEQLRKEMSWEVVSAKIPRLPRGWYELMGLSKEDRIDFCLDFWC SVLGIE
HKESPSICRFFS LLETIEVYIYRLEKEPYQLKMFYVFRDGRCGFQGEPPLLDFLGHHRLPPLGDRHYEKFFSIHN
GFGKWEDEGIFPMRSLAKVQKLRQQLVVMNKMQAEDNCYSLGIFPFYGYEPPFAYQSFFFDPEIRRDLPSP
NVLLNEESLEHRSLETIELLHLSKSYYP SFLSWLENYLHSEEVYNE

>core/590/3/Org3_Gene352

MDCIGKHNPLVKEALALKRSRCRKSSWFLVEGAREIQKALRTGYLCQHVF CSTHLSEKEKEFLYELKRNSTK
ILYCLDSTLAQLSFKEHHSFVAVIQKRVWNKEDFLIQRKNAQPFYLIIEQVEKPGNVGAILRIADGAGVDGVI
LCNPIVDLYNPVVRSSLGAVFSLPILSISREEGKELFKQEGWTVFVTSPRAETMYFSKNYLGPTALVFGSEKD
GLTEDWFSEDFSEIALPMLGESDSLNLATSVA AVAYEVVRQRWVN

>core/591/3/Org3_Gene738

MGSSMHVGVIGCSGRTGKVIVSALEQSSEYTLGPGFSRSSALTLFQVIAHNDVLVDFSHPLLTKEVVAHLLISP
KPLIIGTTGFP GKCKEAHDSLEELTHIVPVVCPNASLGAYIHKRLVMLLSQLCNPQFDIRIRETHHRYKKDSL
SGTAQDLLDTIQQVKQEDWGEEYEVGQRDSSKKTIEVQSSRVGDIPGEHEVAFISSGEQILVRHTVFSRNVFG
RGILSILDWLKTLNPQGLYSLGDTLELVLRNEHCLLKKTDDH

>core/592/3/Org3_Gene543

MEKLEFVTSLSPPDDDLITFNKQGLIAGPEEEKVAFLVRSNAMLDAGPETPASFPESLREQFDIFPEYVEVLYS
NEGLDVWEAGCTWILNNEVTIQLRKHHRKASRWLGMYSRDEVLAHEAVHAVRMKFHEPVFEEVLAYQTSR
WGWRRFFGPLFRSPGESYLLFF TILGLGISLWYPAGILIMLVLP MYFLMRLCMAQSYLYRAMKKIRKMLGV
PPLWVLLRLTDKEIKMFAKEPIPVLEHYARKRKLENVRWKQIYQSYFV

>core/593/3/Org3_Gene766

MSNQLQPCISLGC VSYINSFPLSLQLIKRNDIRCVLAPPADLLNLLIEGKLDVALTSSLGAISHNLGYVPGFGIA
ANQRILSANLYAAP TFFNSPQPRIATLESRSSIGLLKVL CRHLWRIPTPHILRFITTKVLRQTPENYDGLLLIGD
AALQHPVLPGFV TYDLASGWYDLTKLPFVFALLHSTSWKEHPLPNLAMEEALQQFESSPEEVLKEAHQHTG
LPPSLLQEYYALCQYRLGEEHYESFEKFREYYGTLYQQARL

>core/594/3/Org3_Gene909

MKLT KYLNTKQLRSMISRLFVRYSLPMSKQLSFFALCVLGSHPIFAQTPNPPQRRVRSEVIFIDPGHGGKDQGT
ASKELHYEEKSLTSLALT VQSYLKRMGYKPQLTRSSDVYVDLGKRVALSNRGQGDVFISIHCHNHSSNAAAF
GTEVYFYNGKVGSPTRNRMSEVLGKNILAAMEKNGILKSRGLKTANFVVIRDTSM PAVLVETGFLSNSRERA
DLQDARYRMHVAKGIAEGVHNFLSGPSFQKPKQNI AKIRKPKIQAN

>core/597/3/Org3_Gene56

MPFDITYYTTP LLEIILIWVMLNYLLKFFWGTRAMDVVFGLLAFLFLVLADKHLHP IIRRLMLHVVNIAAIVV
FIIFQPEIRLALSRI RFHGKKFFIDTQE QFVEQLAASIYQLSERQIGALVVLENKDSFDEYLSFSSVKINATFSEEL
LETIFEPSSPLHDGAVILRGDILAYARVVLPLAHD TTQLSRSMGTRHRAALGASQRSDALIITVSEENGSVSLSR
DGLLTRGVKIDRFKAVLRSILSPKEHKRKPLFSWIWKR

>core/599/3/Org3_Gene124

MTTLLSIKDLSTIRGKKILNHINLNLIKGSYLTIVGPSGSGKSSLALTILDLLKPTTGTITFHMDPKIPRARKVQ
VIWQDIDSSLNPCMSIKGIISEPLNIIGTYSKAEQNKEIYNVLDLVNLPKSVLHLKPYKLSGGQKQRIAIKALV
SKPELLICDEPLSSLDTLNQSILDLFQTIKKEYQNTLLFITHDMSAAYYIADTIAVMDQGSLVEHACREKIFST
PKHTTTQDLLDAIPFSLISTEMEPSEEYELQVASK

>core/600/3/Org3_Gene728

MKTWLFFFTFLFSCSSFYASCRYAEVRSIHEVAGDILYDEENFWLILDLDLDDTLLQGGEALSHSIWWSKAIQGLQ
KQGTPEQEAWEAVVPFWIEIQEMGTVPQIESAIFLLIEKIQKQGKTTFFVYTERPKTAKDLTLKQLHMLNVSLE
DTAPQPQAPLPKNLLYTSGILFSGDYHKGPGLDLFLEICTPLPAKIIYIDNQKENVLRIGDLCQKYGIAYFGITY
KAQELHPPIYFDNIAQVQYNYSKLLSNEAAALLLRHQMHE

>core/601/3/Org3_Gene862

MMKYLPYIAITACIHGGILLLVFASPLPKKRLQPKAFQEKLVTIQPKPPVPTPSVVVDPAKTIRPSVATQPQKQ
AKCSPPQENVQKALQKPIPKVIKTEPPKPSAPTVAKKTTATEKPPPSTTKKNTQLSKTQLQTLSEVAQALSLH
VDKIEKSETSLKNISWPSTAQLTMHSELKATQEDELCELFRTHIALPSKGYVRIKLVLSPNGEIQECSFLSEVSA
ADKQLLTQRIHALPFQKFLEKYKVSKNISFHIKLVSNES

>core/602/3/Org3_Gene555

MDLADAHVHLSDDAFEEDINSVLQRAQDSGVSLVVNVTTTEKELNRSFAYAERFPKIRFCHVGGTPPQDQDQ
DIEEDYRNFHAAAHSKKLAAIGEVLGYCFATEEGIARQKEVLQRYLALSLECELPLVVHCRGAFNDFFRML
DQYYHNDPRSRPGMLHCFGTGLEEAQELISRGWFSISGIVTFKNAQDLRDLVVELPLEHLLIETDAPFLAPVP
YRGKKNEPAHVLHTINAVANVKGMFPQELAALAYKNVLRFLHG

>core/603/3/Org3_Gene14

MFLQFFHPIVFSQSLSFLPYLGKSSGIIKCSNIVEHYLHLGGDTSVIITGVSGATFLSVDHALPISKSEKIIKILS
YILILPLILALFIKIVLRILFFKYRGLILDVKKEDLKKTLTPDQENLSLPLSPPTLKKIHALHILVRSGKTYNELI
QEGFSFTKITDLGQAPSPKQDIGFSYNSLLPNFYFHSLVSVPNISGEERALNYHKEQQEEMAVKLKTMQACSF
VFRSLHLPMSMQTKDKKAGFGLLTFFPWKIYPL

>core/605/3/Org3_Gene278

MILTAAFSPCPNDIFLFRSFLKDPQFRPLLNQVTIADIETLNTLALQRRLSLMKMSAALFPLVSDYYNLMDVG
NTLGYNSGPVLSLDPECSLDLATPGEMTTAHALCKLYYPKAKLIPMPYDKILSAILQGKVDGGALIHEERFS
YDLQLTLRADFGELWRRKTIFPLPLGCLAIAKYVPMATVDALTAALRKSLICSLKDPITAGAKAVEYSKNKN
VTVIHRFIGTYINKETFQLSKTGKKALHMLWKANECQYT

>core/606/3/Org3_Gene772

MIKQIGRFFRAFIIMPLSLTSCESKIDRNRIWIVGTNATYPPFEYVDAQGEVVGFIDIDLAKAISEKLGKQLEVR
EFAFDALILNLKKHRIDAILAGMSITPSRQKEIALLPYYGDEVQELMVVSKRSLETPLVPLTQHSSVAVQTGTG
QEHYLLSQPGICVRSFDSTLEVIMEVRYGKSPVAVLEPSVGRVVLKDFPNLVATRLELPPECWVLGCGLGVA
KDRPEEIQTIQQAITDLKSEGVIQSLTKKWQLSEVAYE

>core/607/3/Org3_Gene76

MLRNQVLVYCSEGVSPYYLRHTIRFLKYYSTQEGAFDILRVDGNFLIKNPFWREETRLLVFPGGADRPYHRV
LHGLGTARIFQYVSEGGNFLGICAGAYFGSKMIYFYEPAGAPLQGARDLGFFPGTAKGPAYRGNFSYVSPSGV
RVSPQLFSDFLGYAMFNGGCFEGEGSEGYPGVNIESRYDDLPGKPASIVSRIVSKGLAVLSGPHIEYLPHYCR
MVKENVQKTREFLQRETTLDRYCQNLVQRLRQPAFSKADC

>core/608/3/Org3_Gene230

MNVKDETFWSVHNLVCVNYEHA AVL YHISFSLGKGSLTAILGPNGAGKSTLLKASLGLIKPSSGT VYFFNQKF
KKVRQRIAYMPQRASVDWDFPMTVLDLALMGCSYKGMWGRISSDDRREAFHILERVGLSVADRQIGQLS
GGQQQRAFLARALMQKADLYLMDELFS AIDMASFKTSVGV LQELRDQGKTIVVVHHDLSHVRQLFDHVVL
LNKRLICCGPTDECLNGDTIFQTYGCEIELLEQTLKLSRGKQFGSC

>core/609/3/Org3_Gene458

MNRRWNLVLATVALASVASC DVRSKDKDKDQGS LVEYKDNKDTNDIELSDNQKLSRTFGHLLARQLRKS
EDMFFDIAEVA KGLQAELVCKSAPLTET EYEEKMAEVQKL VFEKKSKENLSLA EKFLKENS KNAGVVEVQP
SKLQYKIIKEGAGKAISGKPSALLHYKGSFINGQVFS SSEGNNEPILLPLGQTIPGFALGMQGMKEGETRVLYI
HPDLAYGTAGQLPPNSLLIFEINLIQASADEVA AAVPQEGNQGE

>core/611/3/Org3_Gene1002

MENLETFILKIYRGVPGKQYWESFELPLHPGENVISALMEIEKRPVNILGEK VNPVVWEQGCLEEVCGSCSILV
NGVPRQACTALIQEYIDATQSREIVLAPLTKFPLIRDLIVDRSIMFDNLERIQGWVAADIEGETFGPQVTQEQQ
ELLYALSQCMT CGCCTEACPQIDNKSDFIGPAAISQARYFNTYPGDKQSKKRWRALMGKGGIEGCGQAHNC
VRVCPKKLPLTESISAVGREISKFSLSLFSALFKKKK

>core/613/3/Org3_Gene269

MSKFILLLSLGVAALASKNFFIWPAPSGKTPLKLRQVLFGGALLVFSSLVALSVSSQTAELLSTMTGISLAF AF
LFYLLFLPKDITRAILFSGERP VKTSWRALGSAIRMWIIIPVTQLIGIMMSKFLTLVLPTQEIH TQEVTQEVQNS
LPITGHYISMILNLGVLT PFGEEVFFRGILQTF LKNKMTRIAAVLCSSII FSIHIEHSLG SWVFVPVLFVFSLSAG
FLYEKDRHILSPIALHGLFNLT SLLFLGIK

>core/614/3/Org3_Gene343

MAFYSPSTISKYFIYSGAGNRFL LGETLPEVEDVRFLCQETRVDGFLYLKPSSCADAQLIIFNSDGS RPTMCGN
GLRCAIAHLASQKGKSDISVSTDSGLYSGYFYSWDRVLVDMTLADWRASVHRLESRPDLPKEVVC IHTGVP
HAVVILPEISTLDLSILGPFLRYHQT FSPDGVNVNFVQILGHCQLRVRTYER GVEGETAACGTGALASALVVS
NSYGWKESIQTWGGELMTVSQNRGRVYLQGSVTRDL

>core/615/3/Org3_Gene78

MFKLLKNLFLIGCCIVGYFWMRKESIVEQWLSNRLHTQVTVGRVSIRTSGIKIRHICIHNP LASERFPYAAEIEY
ADVRFSSISMLLTKQLEISELIIHGANFTIFPYDSHGTKTNWSLVWKNFHPQKETPSNLWIDRAPVLIRRCLFLN
TRLYGLRANH KDIPHLSPSLEFHSHTSSAKELPKLSEALPSLLYLAL EESLYHLNLP GDIIKPLSQQA HKHFYS
SYPQFQDRLNDINTPGTPT EEIIGFIRGLFFH

>core/616/3/Org3_Gene61

MVSPLSLFHKMLLENWTPVEEPPWPPEAKNQKIFAWALNQSKLIFVSTSGNIAQPRLVTDSMSMMIVNAAN
RTMSRDGAGTNQVLAAVSVDWGLSQRPLNPERQGTPLNEGECRAGMWRNADGSNHTGKQGKPHYLAQ
LLGPKAVDHHNKSQAAFDRCKNAYLNCFSLAQTLGVTFQLQIPLISSGIYAPPENRKKPNSEENKVRMRWIHA
VKCALVAAMQEFGNPGNTDRRMLIVLTDLKTPAITDPKKKSHL

>core/617/3/Org3_Gene239

MKTQQTQNIIEVWNFYWETQEIEYRDSLIEFYLPVKSVVHRLISGMPSHVKTEDLYASGVEGLVRAVERYN
PERSRRFEGYAVFLIKAAIIDDLRKQDWVPRSVHQKANKLSGAMDSLRLQSLGKEPTDLELCEYLNISQQELSG
WVFSARPALIVSLNEEWPSQSDEGAGMALEERIPDERAETGYDVVDKQEFSLCLANAIQELEEKERKVMALY
YYEELVLKEIGKVLGVSESRSVSIHASKALLKLRAALSAFR

>core/618/3/Org3_Gene293

MWLGAYTWLNVFGILLQAAFIQNILLANFLGMCSYLACSTRVSTANGLGMSVALVLTVTGSINWVHAFITG
PKALTWISPSLASVNLGFLELIIFIVVIAAFTQILELLEKVSRLYLSLGIFLPLIAVNCAILGGVLFGITRSPFIP
MMIFSLGAGCGWWLAIVILATIKEKLAYS DIPKNLQGMGISFITTGLIAMAFMSLTGIDISKPSAKIQRAPLETE
VVENTTNPLKESSSKHQPSISKARTQRRSL

>core/619/3/Org3_Gene483

MLKIKHLHASCNDVKILDDFNLNIPGTMHVIMGPNGAGKSTLAKILAGDESVLVSSGEIALQEQNLLSMLPE
ERSRAGLFVGFQMPPEIPGVNNKMFLRDAYNARRRANQEGDISIDEFNTLLSTVLETYEYNATTDLFLDRNV
NEGFSGGERKRNEICQMLVLEPEMVLLDEPDSDLVDALRLICRVLEKYRELHPTSSLCIVTHNPKLGNLIRP
DVVHLLLDGRVALSGDVSLMHELEAKSYQEVTKRVAWR

>core/621/3/Org3_Gene567

MKTIAVNSFKGGTAKTSTTLHLGAALAQYHQARVLLIDFDAQANLTSGLGDPDCYDSLAVVLQGEKEIQE
VIRPIQDTQLDLIPADTWLERIEVSGNLAADRYSHERLK YVLGSVQDKYDYVIIDTPPSLCWLTESALIAADYA
LICATPEFYSVKGLERLAGFIQGISARHPLTILGVALSFWNCRGKNNSAFAELIHKTFPGKLLNTKIRRDITVSE
AAIHGKPVFATSPSARASEDYFNLTKEILLILLRDI

>core/622/3/Org3_Gene979

MTRQSYVLGNWKMHKTIQEAEKEYVQTLASLLQGEPLSCTIGIASPFTSLRAIHEMINTTGAFWLGAQNVHP
ELSGAFTGEISLPMLKEVGVEFVLVGHSERRHIFGESDALIASKVKSVAQAGLVPVLCVGESLEVREEGKAHQ
VIKKQLLLGLEQMDNGSEFLIAYEPVWAIGTGKVAEASDVQDIHMF CREVVAERFSEATAEEISILYGGSVKV
DNAQRFGQCSDVDGLLVGGASLEGQSFFEVAKNFNV

>core/623/3/Org3_Gene348

MHDALLSILAIQELDIKMIRLMRVKKEHQKELAKVQSLKSDIRRKVQEKELEMENLKTQIRDGENRIQEISEQI
NKLENQQA AVKKMDEFNALTQEMTTANKERRSLEHQLSDLMDKQAGGEDLIVSLKESLASTENSSSVIEKEI
FESIKKINEEGKALLEQRTELKHATNPPELLSIYERLLNNKKDRVVVPIENRVCSGCHIVLTPQHENLVRKKDRL
IFCEHCSRILYWQESQVNAQENSTAKRRRRRAAV

>core/624/3/Org3_Gene148

MKPEESECLCIGVLPARWNSSRYPGKPLAKIHGKSLIQRTYENASQSSLLDKIVVATDDQHIIDHVTDFGGYA
VMTSPTCSNGTERTGEVARKYFPKAEIIVNIQGDEPCLNSEVVDALVQKLRSSPEAELVTPVALTTDREEILTE
KKVKCVFDSEGRALYFSRSPFILKKATPVYLHIGVYAFKREALFRYLQHSSTPLSDAEDLEQLRFLEHGGKI
HVCIVDAKSPSVDYPEDIAKVEQYITCLSNAFY

>core/625/3/Org3_Gene965

MLIKLWRATYEGMYTFLVGALLKLRYRMQVEGWDTLNINPKQGCLFHANHVAEVDPIILEYLFWSRFHVRP
MAAEYLFHSRVVQWFLNSVRSIPIQLVPGKESKRSLERMNVCYEEASRALNRGESLLYPSGRLSRTGKEEI
VNQYSAYVLLHRVMECNVVLVRVSGLWGSAFSRYKQNSTPKLGPAFKEAFRALLRRGIFFMPKRFBKITLC
QVDHLFLKQFPTKQDLNTFLASWFNQGDDNLPIEVPYA

>core/626/3/Org3_Gene401

MQICVTGVVLRSRPLGKNHTLTTLFTPEGLFTFFAKQGQTLQCDYRETLVPISLGKYTLHRNGSRLPKLTHGD
ILNAFEAIKQTYALLEASGKMIQALLASQWKEKPSHKLFSLFLNFLHRIPESSNPEFFAAIFVLKLLQYEGILDL
TPACSLCKASLPYACYRYQGHKLCKKHQHKQAISIEKEEQILQAIHAKQFSELLAIAEFPIAIAEKIFYLFDSL
QEEKKSERNSSSEDYPYHEILRLSKVVHPY

>core/627/3/Org3_Gene480

MLIVLAFRQVFFSHSRSQLDRLKKNYLRLLLKQNFALTLPKERTSKGHSLMLTFDFASFDFYTNIFPFLEEQKIPAV
VGVASRYIPSNAAQDLHPSHRLKPSETLAFQDEIFSNYMPFCCQNELIEMAKSPYIQLASSGFAIRNLMNPNPY
LTTEILLSRHHIETITGAKPLAFLFPFGKSDPTSRKLAADHYPYSFLLGNTINRKLKTHNIYRLDIKPMQYVCPS
LFQSSRYLKNWIKESKQLYLKKQLPKR

>core/628/3/Org3_Gene126

MLMDISHILEDLAYDEGILPREAIEAAIVKQMQITPYLLHILHDATQRVPEIVNDGSYQGHLIYAMYLLAQFRE
SRALPLIIKLFAFEDDTPHAIAGDVLTEDLPRILASVCNDDSLIKELIETPKINPYVKAAAISGLVTLVGAGKIPR
DKVIRYFAELLNYRLEKQPSFAWDNLIAGICTLYPGELFYPISKAFDGGGLVDTSFISMEDVENIHEETVESCIIH
TLCSSTELINDTLEEMEKWLEDFPIEP

>core/629/3/Org3_Gene82

MNVADLLSHLETLLSSKIFQDYGPNGLQVGDPQTPVKKIAVAVTADLETIKQAVAAEANVLIVHHGIFWKG
MPYPITGMIHKRIQLLIEHNIQLIAYHLPLDAHPTLGNNWRVALDLNWHDLKPFSSLPYLGVQGSFSPIDIDS
FIDLLSQYYQAPLKGSALGGPSRVSSAALISGGAYRELSSAATSQVDCFITGNFDEPAWSTALESNINFLAFGH
TATEKVGPKSLAEHLKSEFPITTFIDTANPF

>core/630/3/Org3_Gene64

MKKQGKTLFLFLSFLSTAFSGLFASQTSSLRTIQENIFLAKTGDYTVLSRGSQRTFVLVKSTTPKTVWIEIIH
FPCIAHKERPSLEQASWKTVIHQLESQSQVFVVSLSSEGSQFFSLNTRTKSLEPVGKSTTVPAFLQIFDLPLSPAP
ANVIKTKGKENKPWSPKVSFEGAPLTSISVNAWQGLWPKDRGPLSETGILMYFTQPDISVFPLWVSIETPKGT
SIVRAVDIGHGATSPYVYSLPDSKTQ

>core/632/3/Org3_Gene381

MSLATNNAESKFPSLQRLPNHVAIIMDGNRRWYKKHREECGHTHTSGHYYGAKVLPNILNAVLDLGIKVLTL
LYTFSTENFGRPKEEIQEIFNIFYTQLDKQLPYLMENEICLRCIGDLSKLPKGIQTKINHVSMTASF SRLELVLA
VNYGGKDELVRAFKKLHVDILNKKISSDDLSESLISSYLDTSGLTDPDLLIRTGGEMRVSNFLLWQIAYTELYI
TDTLWPDFTPQDLFEAINVYQQRSRRGK

>core/633/3/Org3_Gene566

MGNLKTLLSRFKKNTPTKMEALARKRMEGDPSPLAVRLSNPTLSSKEKEQLRHLLQHYNFREQIEEPDLTQ
LCTLSAEVKQIHHSVLLHGERITKVRDLLKSYREGAFSSWLLLTYGNRQTPYNFLVYYELFTLLPEPLKIEM
EKMPRQAVYTLASRQGPQEKKEEIRNYRGERKSELLDRIRKEFPLVETDCRKTSPVKQALAMLTGKSQILTK
CTSLSSDEQIILEKLIKKEKVKSNLFPDTKV

>core/634/3/Org3_Gene410

MKIKFSWKVNFLICLLAVGLIFFGCSRVKREVLVGRDATWFPKQFGIYTSDTNAFLNDLVSEINYKENLNINIV
NQDWVHLFENLDDKKTQGAFTSVLPTLEMLEHYQFSDPILLTGPVLVVAQDSPYQSIEDLKGRIGVYKFDSS
VLVAQNIPDAVISLYQHVPIALEALTSNCYDALLAPVIEVTALIETAYKGRLKIISKPLNADGLRLAILKGTNG
DLLEGFNAGLVKTRRSGKYDAIKQRYRLP

>core/635/3/Org3_Gene453

MSLLKDTVFTCLDCEMTGLDVKKDRIIEIAAVRFTFDSVISSIEFLINPERVVSAESQRVHHISNAML RDQPKIA
EVFPQIKAFFKEGDYIVGHSVGFDLQVLAQEMERIGETFLSKYTIIDTLRLAKEYGDSPNNSLES LAVHFNV
DGNHRAMKDVEININIFKHLCKRFR TLEQLKQVLAKPIKMKYMPLGKHKGRCFSEIPLAYLQWASKMDFDS
DLLFSIRHEIKHRQKGTGFSQVNNPFMEL

>core/636/3/Org3_Gene193

MDITLVGKKVIVTGGSRGIGLGIVKLFLENGADVEIWGLNEERGQAVIESLTGLGGEVSFARVDVSHNGGVK
DCVQKFLDKHNKIDILVNNAGITRDNLLMRMSEDDWQSVISTNLTSLYYTCSSVIRHMIKARSGSIINVASIVA
KIGSAGQTNAAAAGIIAFTKSLAKEVAARNIRVNC LAPGFIETDMTSVLNDNLKAEWLKS IPLGRAGTPED
VARVALFLASQLSSYMTAQTLVVDGGLTY

>core/637/3/Org3_Gene615

MTQDPHDHFKSRTPEDHIKHVRDKHRVCKGEPHTTFKGFFYHLANNALSTGVFIFFIRTLFFLIPTNRALQVKS
LISLGVGWTFYHGCLKARKAWAYMELSHRSMLEEKNEIEENFEQEKIELRILFENQGFKDPLLQEMVEYVCS
DSTLLLDTMIREELYIRKEDLPHPLIQGGSRLGGLCGLAIFLPLVLCISYTLAGVFSALMVLVLSFLKAKILKN
DKISEMVWVLGIFITSASIISSLMKLL

>core/638/3/Org3_Gene250

MTLSFHTHPLNYWTFEEFDGLPIRHGVFSKQKDAEGTVFAAKNPEIASALQSPKYCDLHQRHGTSVRCVTPT
SPTYQPADGLCTQSPLLSLHIRHSDCQAAIFYDREHHAIANVHSGWRGLLGNIYAVTVGTMMKKLFHTKPQDL
FVAIGPSIGPDYAIYPDYATLFPRSFLPFMNPKNHFDLRAIARKQLTNLGISKDRIFISDLCTYTEHDAFFSSRYL
AHHPDPNLTGQHSKNRNNVTAVLLLP RD

>core/639/3/Org3_Gene488

MAKQTRRVLFKISGEALSKDSSNRIDEMRLSRLVSELRAVRNNDIEIALVIGGGNILRGLAEQKELQINRVSAD
QMGMLATLINGMAVADALKAEDIPCLLTSTLSCPQLADLYTPQKSIEALDQGKILICTTGAGSPYLTTDTGAA
LRACELNVDVLIKATMHVDGVYDKDPRLFPDAVKYDFVSYKDFLSNQLGVMDAS AISLCMDSHIPRVFSFL
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>core/640/3/Org3_Gene46

MKFFILFILIVAQFPAFSAQPRTQVSASHSKQAKARRTSRIRSSAATNASVSRYKTRAAARKKIGKFEKKPSLSP
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MTLESGIFTQIQSPSGEFTIIKTEKNSSWGRVFCQLQATTVIDHTAYIFTSTATLDDYAELSFTFLKVVSSFQIRGG
KEATSGDAILEKALEALQENK

>core/641/3/Org3_Gene412

MHIYGLADLHLALGVPEKTMEVFGDPWIGYHQKICSEWQAVVHPEDIVLLPGDISWAMNLSEAHKDFAFIG
DLPGTKYMIRGNHDYWSSASTSKILQALPPSLYLNQGFALLTPHLAVVGVRLWDSPTICVKKENFLTPSTQE
QSYTEQDEKIFLRELGRLLKRAFAALPKEVTEVIVMTHYPPISSDGTGPGPISEFLEADGRVSLCLFGHIHKVQRPI
DGFGNIRGIHYILVAADYVNFVPQEV

>core/642/3/Org3_Gene948

MKITTVKTPKIYPYDDLYSILESSLPKLNERSIVVITSKIVSLCEGAVVELEKVSDELKQEADAYVFVEKYGI
YLTKKWGILIPSAGIDESNVEGYFVLYPRDVLLSVNTLGDWLRNFYHLEHCGIIISDSHTTPLRRGTMGLGLC
WNGFFPLYNYVGKPDGCFGRALKMTYSNLLDGLSAAAVLCMGEGDEQTPIAIIIEAPKITFHSSPTTLQDMSTL
AIAEDEDLYGPLLQSMWETPAPTS

>core/643/3/Org3_Gene789

MDFDYFGLSDIGRVRARNEDFWQVNLMSQVVAIADGVGGRLGGDIASQEAVTSLMELIDEQQSKLMGYED
DQYKETLKKILLEVNGVVYEHGQMEEHLQGMGTTLSEFIQFRKDRAWLFHVGDRIYRIRREGELRRLTEDHSL
ENQLKNRYGLPKQSDKVYSYRHILT NVLGSRPYVMPDIRNLPCEKEDLYCLCSDGLTNMVPDIDIRDILNQPA
TLEERGNALISLANTRGGDDNATVVLVRIQ

>core/644/3/Org3_Gene361

MTIRILAEGLAFRYGSKGPNIIHDVSFSVYDGDFIGIIGPNGGGKSTLTMLILGLLTPTFGSLKTFPSHSAGKQTH
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QRVLLARALASYEILILDEPTTNIDPDNQQRILSILKKNRTCTILMVTHDLHHTTNYFNKV FYMKNKTLTSLA
DTSTLTDQFCCHPYKNQEFSCSPH

>core/646/3/Org3_Gene718

MSYFNYQKNSVVLRLSLGLLAKFFSRLLYRVFFSFREGIYLFSSLYLKYPRLFFYDLGKYVYSLRHCPYAKLGR
LPGASLLKEGNVYGETPWSVLAKICQAFDITSQDILYDLGCGLGKVCFWFSHVVRQCQVIGIDNQPHFIRFSSN
MHRKLSSGFALFDTEEFKNVLSQASYVYFYGSSFSRLLNEIILKLEMAPGSVVISISFPLDSFSRGKECFFT
EKSCSVRFPWGKTIAYKNIRKGS

>core/647/3/Org3_Gene163

MSTLLLNPPWMKAGKRIESLVRKALYTHTMLANHRKIVVALSGGKDSL TLLMLKAISGRGFPDLDLHAVNI
GGKYSCGAENVNKPYLTRICDQLCIPFRTIPSPYAPETPECYPCSQARRLLFQAAKEIGASAIAFGHHRDDL VQ
TALLNLLHKA EFAGMLPVLD MVHFGVTILRPLIFTPEFWIRKFAKENG FARVTCRCPPVSLRSKAEQSLKLE
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>core/648/3/Org3_Gene173

MTDYSFFRRKIGNIEAIECPGNPQDPPIILCHGYGSLADNL TFFPSICSFSKLRPTWIFPNGILPLENDFRGS RACF
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NPYAGALIFAGARLFNQGWEEGLKQCAQVPFLQSHGYEDEILPYHLGAHLNDLLLTKLNGQFV SFHGGHEIP
SVVFQKMQVTVPNWIDPARG

>core/650/3/Org3_Gene509

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ACVLALNPSVLLLDEPFANVDPLVIQNVKYLIKILAGRGIGILITDHNAKELLSIADRCYLIIDGKIFFEGSSSQM
ISNPMVKQHLYLGDSFSY

>core/651/3/Org3_Gene298

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AKTSKYDVLFGDKKIGGAAQRKVQQGFLHQGSLFSLGSSEFYQRFLKPEVLEEIIIEQIQIHAF FPLGLEAADE
VLQEARQQVKEAFIKLFCGEG L

>core/652/3/Org3_Gene791

MTLYLLPNTLGTRAVETLPSVIGELVHRLDGLIVESDRGGRAFLSLWKIPEVHKFPLAILSKHARLPKAWDFY
LEPIVKHGENWGLISDAGLPCIADPGASL VRRARALGIPVQAFSGPCSITLALMLSG LPSQSFTFLGYLPQSPKE
RVKSIKKAATSKEVSTSVCIETPYRNVYTFESLLDTLPSYAE LCVASDLSGPSELVLTRQVQSWRTTEDLGSV
KQSITKVPTIFLFHIPN

>core/653/3/Org3_Gene388

MAGHSKWANTKHKERADHKKGKIFSRIIKELISAVKLGGADPKSNARLRMVIQKAKENNIPNENIERNLKK
ATSAEQKNFEEV TYELYGHGGVGIIVEAMTDNKNRTASDMRIAINKRGGSLVEPGSVLYNFARKGACTVAK
SSIDEEVIFS YAIEAGAEDLDTEDEENFLVICAPSELASVKEKLISQGATCSEDRLIYLPRLVDCDEKDGEANL
ALIDWLEQIEDVDDVYHNMS

>core/654/3/Org3_Gene455

MDISGAVKQKLLQFLGKQKKPELLATYLFYLEQALSLRPVVFVRDKIIFKTPEDAVRILEQDKKIWRETEIQIS
SEKPQVNENTKRIYICPFTGKVFADNVYANPQDAIYDWLSSCPQNMEKQGGVRIKRFLVSED PDVIKEYAVPP
KEPIIKTVFASAITGKLFHSLPPLLEDFISSYLRPMTLEE VQNQTKFQLESSFLSLLQDALVEDKIAAFIESLADD
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>core/655/3/Org3_Gene683

MGLYDRDYIQDSRVQGTFA SRVYGWMTAGLIVTSCVALGLYFSGLYRSLFSFWVWCFATLGV SFFINSKI
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FALIGLLLVTLVFAVVS MFVSMPLIYLLICYLGLVIFVGLTAADAQAIRRISS TIGDNNTLSYKLSLMFALKMY
CNVIMVFWYLLQIFSSSGNRD

>core/656/3/Org3_Gene26

MHPPIDITAIEAKLNFTFTQPKLLEIALTHPSYKNESAVQIEDSERLEFLGDAVLGLIVTEHLFLLFPSMDEGTLS
TARASLVNAKACCRYTTMLGIGDYLLIGKGEKIQSERGRLSAYANLFESILGAVYLDGGLSPARKLTVPLLPP
REEILPLMSGNPKNLLQQFTQKQFRVLPVYQSTAVTDAQGNVSYQIQVLVNQEVWGEGNASSKKEAEKIAA
QQALD TYGNKNQNTMDV

>core/657/3/Org3_Gene993

MEPSTNKPDCCKIFDSIASKYDRNTILSLGMHHFWNRSLIQILGSGYSLLDLCAGTGKVA KRYIAAHPQASV
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ELTPPKKTHPTYSAHKLYLRAVVPWIGKSVSKDPDAYSYLSKSIQQLPKDHDLEDLFSKSGFYIAKKKKLFLG
AATIWLLEKQ

>core/658/3/Org3_Gene984

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ALDDVVILHKVFTSLIGDLPPQQVLDLLQQSYHPKVFKMPFGKYKGQPLVDIPKSYFEWLENQGALDKPENK
DIKAAIAL LHQPT

>core/659/3/Org3_Gene546

MQNATIDQLPVSWQEQLPLCWREQLKEEWSKP YMQQLLIFLKQEYKEHTVYPEENCVFSALRSTPFDQVRV
VILGQDPYPGKGQAHGLSFSVPEGQRLPPSLINIFRELKTDLGIENHKGC LQSWANQGILLNNTVLTVRAGEPF
SHAGKGWELFTDAIVTKLIQERTHIIFVLWGAAARKKCELLFNSKHQHAVLSSPHPSPLAAHRGFFGCSHFSKI
NYLLNKL NKPMINWKLP

>core/660/3/Org3_Gene211

MDLAVELKEGILLVDKPQGRTS FSLIRALTKLIGVKKIGHAGTLDPFATGVMVMLIGRK FTRLSDILLFEDKEY
EAIAHLGTTTDSYDCDGKVVG RSKKIPSL EEVLSAAEYFQGEIQQLPPMFSAKKVQGKKLYEYARKGLS IERH
HSTVQVHLQITKYEYPLLHFVVSCSKGTYIR SIAHELGTMLGCGAYLEQLRRLRSGRFSIDECIDGNLLDHPDF
DISPYLRDAHGNSL

>core/661/3/Org3_Gene527

MIGDKIILFVTEDLSLSSQLKDLASQRS DYQILVSPVFPTSFESVAIFCEYLLLPEQIFSPGIFPEEDLIVLFDTFQE
EAITKVLNQGATGYLLRPITAKVLD AVIRAFLRQHEVLEHSIPDTMTFGDHTFRVLNLVIESPEG SVYLT PSEA
GILKKLLINRGHLCLRKNLLAEIKGNTKEI IARNVDVHIASLRKKLGPYGSKIVTIRGVGYLFSDDDSIPLQNHD
NTAHPNEE

>core/662/3/Org3_Gene854

MTKVRLNKFLASAGVASRRKCDEIIFSGSVTVNGRVAEGPFVLVDPEDKVQVGGTSVHLTKKVYFMVHKAI
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KDLGKLMEGTFIDGKHVRPVSVTKIRRGTVKIVVSEGKKHEIRLFADAAGLPILELKRIRIGSLVLGGLRYGEY
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>core/663/3/Org3_Gene146

MLQAHRLCYSCDNQVILKDASFQASPGTITIILGSSGVGKTTLFRLLAGFLPLQEGELLWNGSPLNRKDVAYM
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KPILLLDEPFSSLDVLLKEQLYQDIVALAKKENKTVLLVTHDFHDVSCLGDVLYVIKNKTLTPVPLDPSMRPL
NNGLCFIKDLKKHLYT

>core/664/3/Org3_Gene708

MRVIFPDKHNNFPNLSKLLKKLPSVILVTSCIAPFFSYIINKFFGIPGLLEILALSVKGIQKHFWQFLTYPLITAD
SLSLNKDQSFEITQRLLLLRNVLDFFLFYKAIQHLIRKLGAFSVLVVISGQALIIGAVLWGFMALIHSSQSFFGPE
SIICGVLTQIFLDPEKRFTIGPTPLSVSIKWGFLFVLGFYCCILIFSGAFLLLLASMLAIVLAILFCKKEKIPNPYT
TSLRF

>core/665/3/Org3_Gene421

MPTTNCIFDLRGHSILHQLQIEEALLRVANQNFCIINSGAKDSIVLGISRNLNQDVHISRAQADHIPIIRRYSGG
GTVFIDSNTLMVSWIMNSSEASAQPQELLAWTYGIYSPLLNTFSIRENDYVLGHKKIGGNAQYIQRHRWVH
HTTFLWDIDLDKLSYYLPIPQQQPTYRNQRSHEEFLLTLRPWFPSRDDFLERIKASGSLLFTWEEFLDNELEEIL
AQPHRKATTVLN

>core/666/3/Org3_Gene24

MLSVCYSDPCLSDFCQGKRPLRIASRNSNLAKAQVHECISLLRSWYPKLWFQLSTTETTGDREKKIPLHLVEN
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AVLKQLFPQGQILDIRGTIEERLDQLHRGHYDAIVLAKAASRLHLHHAYSIELPPPYHALQGSLAITAKDHA
GKWKQLFTPIHCHSS

>core/667/3/Org3_Gene583

MKFFSLIFKDDDVSPNKKVLSPEAFSAFLDAKELLEKTKADSEAYVAETEQKCAQIRQEAKDQGFKEGSESW
SKQIAFLEEETKNLRIRVREALVPLAIASVRKIIGKELELHPETIVSIISQALKELTQNKHIIISVNPKDLPLVEKSR
PELKNIVEYADSLILTAKPDVTPGGCHETEAGIINAQLDVQLDALEKAFSTILKAKNPVDEPSETSSSTDSSSL
NDQDKKE

>core/668/3/Org3_Gene635

MNRRDMVITAVVVNAILLVALFVTSKRIGVKDYDEGFRNFASSKVTQAVVSEEKVIEKPVVAEVPSRPIAKET
LAAQFIESKPVIVTTPVPVSETPEVPTVAVPPQPVRET VKEEQAPYATVVVKKGDFLERIARANHTTVAKL
MQINDLT TTTQLKIGQVIKVPTSQDVSNEKTPQTQTANPENYYIVQEGDSPWTIALRNHIRLDDLLKMNDLDEY
KARRLKPGDQLRIR

>core/669/3/Org3_Gene1018

MFFIVCFGFLIHKKHTILPPKAHIPTNAKHFTIGNPYAPINITVFEEPPSCSACAEFTTEVFPLLKKHYIDTGEISF
TLIPVCFIRGSKPAAQALLCIYHHDPRQADIDAYMEYFHRILTYPKEEGSHWATPEVLTklaEGLKINSGRSVN
PKGLEQCIASGQYNEQIKKNNLYGSQVLGGQLATPTAVVGDYLIEDPTFHEIERAIQHIRQLQAVEGDHDD

>core/670/3/Org3_Gene554

MVHFSHNPIIQAYTEADFFGKSIFFCLLILSVCTWTVLHQKLAIQKNFLKAGKSLKDFLIKNRHAPLSLDIHPEL
SPFADLYFTIKRGTTLELLDKNRQSAPDRGPILSSEDIQSLETLLGAIMPKYKALLHKNSFIPATTISLAPFLGLLG
TVWGILVAFTHISSGSSGNSAIMEGLATALGTTIIGLFVAIPSLIAFNYLKAHSSSELISEIEQTAYLLLNSIEVKYR
NTNL

>core/671/3/Org3_Gene42

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ILVFASGNKVKEAVEAGADFMGSDDLVEKIKSGWLEFDVAVATPDMMREVGKLGKVLGPRNLMPTPKTGT
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>core/672/3/Org3_Gene84

MEKDLHLHEKKCLAHEAATQVTSGMILGLGSGSTAKEFIFALAHRIQTESLAVHAIASSQNSYALAKQLAIPL
LNPEKFSSDLTVDGADEVDPQLRMKGGGGAIFREKILLRAAKRSIILVDESKLVPVLGKFRVPLEISRFRGSA
HIEIRHLGYEGEWRLQDTGDLFITDSSNYIYDIFSPNSYPNPEKDLLKLIQIHGVIEVGFVIEKVEVWSSNSQGL
ISKKYSV

>core/673/3/Org3_Gene147

MLQSCKKALLSIVVSILAFHPIPGMGVEAKSGFLGKVKGWFSKKEIQEEARILPVKDSLWKRYDYTSSSGFS
VEFPGEPDHSGQIVEVPQSEITIRYDTYVTETHPDNTVYVVSVWEYPEKVDISRPELNLQEGFSGMMQALPES
QVLFMQARQIQGHKALEFWIVCEDVYFRGMLISVNHTLYQVFMVYKNKNPQALDKEYEAFSQSFKITKIREP
RTIPSSVKKKVSL

>core/674/3/Org3_Gene168

MALDEINNQNPNPSQQIASSTSQTSKINQDRKTFACVTLLVVATLMILSGIVLLFTIGSLGLSVPLSGILGTFV
TVGAVLFITGLTILVRKSLGIEQKNEDLNFLKIKTPTPPARPLMSKFSVTCSTTSIVLGMALLIGAVVSVFFLTG
YLQLGLCAGLVGLGTALFVAGLARMSPRSLADQEGSGSADSQSNIVGIGEPKAAQEQKWKMAVVRGEDGI
PTAIRLTPEK

>core/675/3/Org3_Gene572

MSKPSPRNANQPQKPSASFNNKTRSRLAELAAQKKAKADDLEQVHPVPTEEEIKKALGNIFEGLSNGLDLQQI
LGLSDYLLEEIYTVAYTFYSQGKYNEAVGLFQLLAAAQPQNYKYMLGLSSCYHQLHLYNEAAFGLFLAFDA
QPDNPIPPYYIADSLKLQQPEESNNFLDVTMDICGNNPEFKILKERQCQIMKQSIEKQMAGETKKAPTCKPAG
KSKTTTNKKSGKKR

>core/676/3/Org3_Gene394

MYLEDYDVFFFDLDGLLVDTEPCFYRAFLQACAEFSLEVHWDFSTYYSHTTLGTEIFSKKFIEQYPQAEYM
AEIFAKRLQIYYKSLEHAGPALMPGVEAFIELVLSLNKTFGVVTNSPRDATHLRTMYPILNKFLFWVTRENY
ARPKPYGDSYDYAYRTFAREGMKVIGFEDSVKGLRALSKIPATLVCINSMAEITPEDYPELKGKEFFSYPSFD
VLTEHCSQQKLL

>core/677/3/Org3_Gene737

MNTSHRKTIVFSYLSSTFTLLLVLNLVLSSKLIPTTFNFIIPGGLILYPLTFLISDVVNEIFGPKKARVMIFSFI
ANLLASSIVQIFMFFPVASPEMQTAWHCLFDLSPLRFLASLLAFIVSQQLDIVLYTFFKNRTPNSSLWLRNGS
TWISQIPDTFIVDTCILYFGMGLSFPQTLNIMFYSYIYKITFCVLTTPLFYLAVENTIRKFLGMPSTKIANVTPLIN
QP

>core/678/3/Org3_Gene887

MKKQESVLVGPSIMGADLTCLGVEAKKLEQAGSDFIHIDIMDGHFVPNLTFGPGIIAAINRSTDLFLEVHAMII
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SFLPHTIEKIAFARHAIKTLGLKDSCLIEVDGGIDQQSAPLCRDAGADILVTASYLFEADSLAMEDKILLRGEN
YGVK

>core/679/3/Org3_Gene133

MKGFLSVNELIFGFQTFSSVVVLGVFFASRGKAWLTGWLSSLSSIMNVFVLKQIHLWGFEVTSADVYVIGLLT
CLNYAREHYEKNDINDAMLCSWVISIAFLVLTQLHLFLIPSPNDSSQEHFLALFSSTPRIVVASLVTLIFVQIVDI
KLFTFLQRVFSKKYFAMRSTISLLFSQLIDTIIFSFLGLYGLVSNLCDVMIFAMLVKGIVITLAIPTLTVTKAVLD
RRSS

>core/680/3/Org3_Gene399

MRPHRKHVSSKSLALKQSASTHVEITTKAFRLSMPLKQLILEKSDHLPPMETIRVVLTSHKDKLGTVEHVVAS
HGKEILQTKVHNANPYTAVINAFKKIRTMANKHSNKRKDRTKHDLGLAAKEERIAIQEEQEDRLSNEWLPVE
GLDAWDSLKTLGYVPASAKKKISKKKMSIRMLSQDEAIRQLESAAENFLIFLNEQEHKIQCIYKKHGDGNYVLI
EPSLKPGFCI

>core/681/3/Org3_Gene958

MALLILLRHGQSVWNEKNLFSGWVDIPLSQQGIEEAFSAGRAIQNLPIDCIFTSTLVRSLMTALLAMTNHHSK
KIPYIVHEDPKAKEMSRIYSAEEENNMIPLYQSSALNERMYGELQGKNKKQTAEQFGEERVKLWRRSYKTAP
PQGESLYDTKQRTLPHYFEKNILPQLQHGNVVFVSAHGNSLRSLIMDLEKLSEEEVLSLELPTGKPVVYQWKN
HKIEKHPEFFG

>core/682/3/Org3_Gene145

MSSQPLVTTSSSLSRVYVLTGEEKVACYKKAFNHIWHGAPAIILAAALLMFCIFGFVLGSILLGAPLEGASILY
DVILPWLLPSILVFVLLVLPLNIYAYSHHKQVLALHERITQSNYKEIYDHCEKEKKTTPNKKALSLYIESQVLVP
EYSKRFFSSMILGKTLKIIPKKDSPESLKHDELIQKALERAKENIYMKNQREKRDEREAKKEAKNASKTNPLW
EGLGT

>core/683/3/Org3_Gene155

MSLLIEAKNLSKTIQQNQNNISILTDVSLSLHAGETISITGASGNGKTTLLHLLGTLDVPSSGSLRFFDKDLKNQ
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GEKQRVAIARALINEPAILLADEPSGNLDEETSEQIHNLLLEQASALCGILIVTHNKHLSRCSREGVLSNGKLF
FHNS

>core/684/3/Org3_Gene116

MTIRVRNLAYSVNKKKILDGVTFSLERGHITLFVGKSGSGKTMILRALAGLVQPTQGDIWIEGEAPALVFQQP
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FDEPTSALDPFATASFRHLLLETLRDQELTVGLTTHDMQFVHSCLDRIYLIDQGTVAGVYDKRDGELDSGHPLS
KYIHSAQ

>core/685/3/Org3_Gene822

MDLKLDEVASLLDVSEHTVLQWLKEGAIPSYSMNNEYRFSREEIEDWLLHNQALMIQERGEDKEALKDLSL
KYSLYKAIHRGGVLCDVVVHSKEEALQYASKYIAQKFQLDESVLFEMLSHRENLMSTGIGEGIALPHAKDFLI
NAYYDIVVPMFLAEPIEYGALDGKPVGILFFLFACQDKSHLNLVNKIVHLGMSLNARSFFKNYPNKDQLLAY
VKEWESQTH

>core/686/3/Org3_Gene395

MILRISTVSLLTSCSFSKNSRTCFVTPERITSQKDCPVLLHPKSTTISPPLYDWISPNEVITAYSFYCRGQGNSII
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>core/687/3/Org3_Gene651

MENSQNFHDTLCQLLDYSEELYPTLASLLNVTLNPNTAISASVSSIPEKAVEVPNAEPQPITPPPPTNLSQEKT
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TNIFVNNPNFFLALAPLNVIRYKIPTTDYHQSLTQNGCIFLPLYSSLEYEKDSQLKRNLWAILNRLPFAYTPKSS

>core/688/3/Org3_Gene692

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QPSFVQEISRLQDSAVFALATDDKTYLLESIEALQTHLAPRMETPYIYKMTDTYGNSWFENLWRTKGQEIFY
TEFIKKAGI

>core/689/3/Org3_Gene497

MIDPVECFPNLDGDAEAQSITQNSGTPLASELKKDISPFALGSYAAPKDTTLVQGFKPNPMAMMQDQNSNLI
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DKEEGSVTRKIHDWVSSGEEVLNRALLYFSDRDGNRESLANFLKVQYAVQRATQRAELFASIVGTSVSSVKTI
MTTQLG

>core/690/3/Org3_Gene535

MTSWIELLDKQIEDQHMLKHEFYQRWSEGKLEKQQQLQAYAKDYYLHIKAFPCYLSALHARCDDLQIRRQIL
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QVCVEKIRGLKEYFGVSARGYAYFTVHQEADIKHASEEKEMLQTLVGRENPD AVLQGSQEVLDLWNFLSS
FINSTEP CSCK

>core/691/3/Org3_Gene444

MVLLSKFDFSGNKIGEEVADSLFADEGDGLQLIKDYIVAIRANKRQWSACTRNRSEVSHSTKKPFKQKGTG
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ALRFLKDCNVECRSILFIDHLDHVEKNENLRSLRNLTAVKGFVYGININGYDLASAHNIVISKKALQELVERL
VSETKD

>core/692/3/Org3_Gene476

MQTLARLFGQSPFAPLQAHLEMVVSCVEYMLPIFTALRDGRYEELLEMAKLVS DKEYQADCIKNDMRNHLP
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GGRKADKARLLVGRVAKSEHESDVLQRELMQIFFSDDFIPEKEFYLWLQVIRRTAGISDSSEKLAHRINMTLE
EK

>core/693/3/Org3_Gene732

MSTTTVKHFIHTASRWEVLKEIVASNYWHAQWINTLSFLENSGAKKISASEHPTEVKEEVLKHAAEEFRHG
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YPLYHDILKEAQSKITVKSIILEEQGHLQEMERELKDLPHG EELLGYACQFEGELCLQFVERLEQMIFDPSSTF
TKF

>core/694/3/Org3_Gene140

MTKNAINSQTTPQPNLTDAEPIASRAQCKSIAVIISLFALGMLLLCLGIILISIPGLAAQVALGLGIVSLILGIA
LANIGFLCLLLRCKQVPQKPD TLPSESSKQPSEGSTPTALPWQAGEFLEKVQVSATPILLPKNKDEELSAKVM
KEGAEAASSIKQAVLESTEKLIDARKQEESRREARKKIVAEAEASRKRIQQQMAADQEALRKRKEEVAKRK

>core/695/3/Org3_Gene334

MKKYFITGLVILLPLAITIAIVTMIMNFLTQPFVGLASEFFEKFSFYTKHRALLKFVLQIILLFGLFFATVLLGFL
TRIMIFKSLLSIYDKILHRIPKTVYKAAQQVMTTIFGSKSGSFKQVVMVPFPNANVQCIGLVAGDAPTVCCT
GEKEDDPLVTVFIPTTPNPTSGFLTFRKSDIVFLDMKIEDAFKYIISCGVLSTPMACSSPLPDELHQDQGS

>core/696/3/Org3_Gene759

MGQKGCPIGFRTGVTKKWRSLWYG NKQEF GKFLIEDVRIRQFLRKKPSCQGAAGFVVRMSGKIEVTIQTAR
PGLVIGKKGA EVDLLKEELRALTGKEVWLEIAEIKRPELNAKL VADNIARQIERRVSFRAMKKAMQSVMD
AGAVGVKIQVSGRLAGAEIARSEWYKNGRVPLHTLRADIDYATACAETTYGIIGIKVWINLGENSSSTTPNNP
AAPSAAA

>core/697/3/Org3_Gene345

MTLYLGLNQKTARKYQAHYLPILTLFPYAKSTPQNKRALQFLPQATHVILTSPSSTHLFLSRMTSLLSKATLK
TKTYLCIGESTKERLLSFLGQVKYVVATQEIAEGIFLLQALPSSARILYPHSSLARPVIREFLYNRFTFFSYPHY
TVKPRKLKKNILSKYKKIIFTSPSTVRAFAKIFPRFPEKTYWCQGRMTLQEFQKFSSQKQVSLLETLGKSRTSP

>core/698/3/Org3_Gene517

MLMMLMMIIGITGGSGAGKTTLTQNIKEIFGEDVSVICQDNYYKDRSHYTPEERANLIWDHPDAFDNDLLISD
IKRLKNNEIVQAPVDFVLGNRSKTEIETIYPSKVILVEGILVFENQELRDLMDIRIFVDTDADERILRRMVRDV
QEQGDSVDCIMSRYLMSVKPMHEKFIEPTRKYADIIVHGNRYRQNVVTNILSQIKKNHLENALESDETYVMVN
SK

>core/699/3/Org3_Gene180

MQSDLIQILLKETVNTLYMVSTAFFFSICAIGGMLGLGLFCTSPKSLNPKKSLYATISMILSFLTAIPFAILIVILFP
ITRWIVGTSLGPTASIVPLTIGAIPFVVITIVVDAFRNSALNYLESAVALGIPKRNILFGILLPESYPQLIFSLKSLV
VHLISCSTLAGFVGGGGLGQLLLQYGYRFEWSVTTSVLVITLVLIESVRILGDFWGRRVLKYRGIL

>core/700/3/Org3_Gene852

MSTVTTEPCSSIHISLNDWRDSQPYSLDRASELLHFRFLPSLVFSNWKVEQQIETLCHKSEKRRLISPLAKWL
GKLHKQDLLCPPAPPVSVCWINAHVGYGVFARDEIAPWTYIGEYTGILRHRQAIWMDENDYCFRYPMPLFTL
RYFTIDSGKQGNVTRFINHSEQPNAEAIGVFSEGLFHVIIRTIAPIYAGQEICYHYGPLYWKHRKKREEFIPEEE

>core/701/3/Org3_Gene445

MRSHISVMGKKEGMIHIFDKDGSLVACSVIRVEPNVVTQIKTKESDGYFSLQIGAEEMNAPAHTITKRVSKPK
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HGSGFHRHAGSIGMRSTPGRCFPGSKRPSHMGAEENVTVKNLEVIKVDLEKKVLLVKGAIPGARGSIVIVKHSS
RT

>core/702/3/Org3_Gene734

MQRHIVGIDTGVGKTIVSAILARALNAEYWKPIQAGNLENSDSNIVHELSGAYCHPEAYRLHKPLSPHAAQI
DNVSIEESHICAPKTTSNLIETSGGFLSPCTSKRLQGDVFSSWSCSWILVSQAYLG SINHTCLTVEAMRSRNLN
ILGMVVNGYPEDEEHWTQEIKLPIIGTLAKEKEITKTIISCYAEQWKEVWTSNHQGIQGVSGTPSLNLH

>core/703/3/Org3_Gene279

MNAVNTPKKILCIVADYREISPLIEQLDFTQINEHLYSYRCTDYHLDLYIVHVWGSTAVLNALQSYCQAYTDY
DLWINPGFVGACSPCIPLGQCYTIEKIANLTTDTPPVLSIEDPPYIFDALPDSLKSSLVTSPVLYHYGFHKTFKL
LDMEGYAIASQAAEHHPSCFLKITSDYTVPGDCPFSRLEEVSQKLQTQLVELLPELMERAIPPKLLPCP

>core/704/3/Org3_Gene318

MLGSLPCYPGAGNIEEYKNRYFYCQLCAEVVSPYVVPVIVVDVQGAPPTGILQVLRCKQHKFQGLPVHGPIT
SLWALEPVGKGAPQLESAMYELCSQVRNFDICSIVSWVFGGLCIFAGLIVGVMVEAPLIAGLSAWVIPCIIIGV
GAILCLFAILMAYLGRGRVREWLNLSHEYITQCHCRQIQAHSQNYSVITEYPATCALSQPITKLPNGSRRDN

>core/705/3/Org3_Gene890

MDHWLAIARLLLRCGYTLCVSGIGILCGSILGLLIGTVTSLYFPSKLTKLLANSYVTVIRGTPLFIQILIIYFGLP
EVLPIEPTPLVAGIIALSMNSAAYLAENIRGGINSLSIGQWESAMVLGYKKYQIFVYIIPQVFKNILPSLTNEFV
SLIKESSILMVVGVP ELTKVTKDIVSRELNPME MYLICAGLYFLMTSSFSCISRLSEKRRSYDN

>core/706/3/Org3_Gene621

MKRVIYKTIFCGLTLLTSLSSCSLDPKGYNLETKNRDLNQESVILKENRETPSLVKRLSRRSRRLFARRDQTQ
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MKKMQGRDWIWNFLTQLSEVFSQAWSQGVISEEDIAAFASLTGLDSGTVASIVQGERWP ELVDIVIT

>core/707/3/Org3_Gene934

MQKL VHNIWKKFY SFSSAIAICIVLASFLSLKIVSNTYKHSQAKRNSILLLTRA AEVAVSQGFLPSKSALSSLEQ
AYHLGGESMKPYAGYLASC FYIHNEPLRGAYYAGLAYNNSQALQLPHPIQKLLKEISEAQADQLYDVALSKS
YQLLQTANSSPEYPTLSFLTLLRVIELKELLHQDVSQDFAALKSSPLFHQFERMYSDGEWTLSKRFGKKG

>core/708/3/Org3_Gene383

MIITIDGPSGTGKSTTAKALADHLHFNYCNTGKMYRTLAYARLQSPWATLPLTKFLEPPFSFTFATGQPLESF
FNGHLLTSELTTQEVANAASELSQLPEVRAFMQDLQRRYAQLGNCVFEGRDMGSKVFPNADLKIFLTSSPEV
RAQRRLKDLPEGTLSPEQLQAE LVKRDAADAQRAHDPLVIPENGIVIDSSDLTIRQVLEKILALLFRNEL

>core/709/3/Org3_Gene268

MRKMLVLLASLGLLSPTLSSCTHLGSSGSYHPKLYTSGSKTKGVIAMLPVFHRPGKSLEPLPWNLQGEFTEEI
SKRFYASEKVFLIKHNASPQTVSQFYAPIANRLPETIIEQFLPAEFIVATELLEQKTGKEAGVDSVTASVRVRVF
DIRHHKIALIYQEII ECSQPLTTLVNDYHRYGWN SKHFDSTPMGLMHSRLFREVVARVEGYVCANYS

>core/710/3/Org3_Gene646

MSKKPLYVAHPWHSPTLTQDNYESLCCYIEITPYDSVKFELDKATGLLKVDRPQKFSNFCPCLYGLLPQTYC
GTASGNYSGEQTRREGIQGDKDPLDVCVLTEKNIHHGNILLQARPIGGLRIIDSGEADDKIIAVLEDDL VF AEIE
DISDCPGTVLDMIQH YFLTYKATPNHLIKGSPAKIEIVGIYGKKEAQKVIQLAHEDYLSYIGDTAEVN

>core/711/3/Org3_Gene474

MSVNP SGNSKNDLWITGAHDQHPDVKESGVTSANLGSHRVTASGGRQGLLARIKEAVTGFFSRMSFFRSGAP
RGSQQPSAPSADTVRSPLPGGDARATEGAGRNLIKKGYQPGMKVTIPQVPGGGAQRSSGSTTLKPTRPAPPPP
KTGGTNAKRPATHGKG PAPQPPKTGGTNAKRAATHGKG PAPQPPKGILKQPGQSGTSGKKRVSWSD ED

>core/712/3/Org3_Gene71

MNTSISEIQRFLSMIAFEKELVSEDFSVVAGIDEAGRGPLAGPVVASACILPKGKVFPGVNDSKKLSPKQRAQV
RDALMQDPEVCFGIGVISVERIDQVNILEATKEAMLQAISSLPISPDILLVDGLYLPHDIPCKKIIQGD AKSASIA
AASILAKEHRDDLMLQLHRLYPEYGFDRHKGYGTS LHVEAIRRYGPSPCHRKSFSPIKQMCAIV

>core/713/3/Org3_Gene152

MTKGSVFIIMGPPGSGKGTQSQYLANRIGLPHISTGDLLRAIIREGTPNGLKAKAYLDKGAFVPSDFVWEILKE
KLQSQACSKGCIIDGFPRTLDDQAHLLDSFLMDVHSNYTVIFLEISEDEILKRVCSRFLCPSCSRIYNTSQGHTEC
PDCHVPLIRRSDDTPEIIKERLTKYQERTAPVIAYYDSLGLKCRVSSSENKEDLVFEDILKCIYK

>core/714/3/Org3_Gene292

MTSKKSYKSYFFDPLWSNNQILAILGICSALAVTTTVQTAITMGIAVSIVTGCSSFFVSLLRKFTPDSVRMITQ
LIIISLFVIVIDQFLKAFFFDISKTLVSFVGLIITNCIVMGRSESLARHVTPIPAFLDGFASGLGYGWVLLVIGVIRE
LFGFGTLMGFRIIPQFVYASETHPDGYQNLSLMVLAPSAFFLLGIMIWLVNIRDSKKRKR

>core/715/3/Org3_Gene15

MYFYKYVIIIDTSGYYPFLACVDNQQVLEHWSLPVGPDLGIVLEFLFKSKNLSFQGVAVALGPGNFSATRIGIS
FAQGLAMAKNVPLLGYSSLEGYLLSKDEKKALMLPLGKRGGVLTLSSEIPEEGLNEKRRGVGPGALLSYEEA
SDYCVAHGYYHVISPNPQLFASSFSDKITVEEVAPSVEQIRRHVISQFMFVEYDKQLSPDYRSYSCIF

>core/716/3/Org3_Gene300

MATSVAPSPVPESSPLSHATEVLNLPNAYITQPHPIPAAPWETFRSKLSTKHTLCFALTLLLTLGGTISAGYAG
YTGNWIICGIGLGIIVLTLILALLLAIPKKNKQTGTKLIDEISQDISSIGSGFVQRYGLMFSTIKSVHLPCLTTQNG
EKTRILNEIEAKKESIQNLELKITECQNKLAQKQPKRKSSQKSFMRSIKHLKSNPVILFDC

>core/717/3/Org3_Gene384

MIFRICKFFTWVAFSLFYKLVYGVKKNFIFKGPAAIAVNHNFLDPIALHMCVHECIYHLARASLFNIPWLWK
QWGCFFVRQDEGNSAAFKIASRLFNKRKKLVIYPEGARSPDQQLQPGKVGIGMMAAKSRVPIIPVYIRGTFEA
FNRHQKIPHVWKTITCVFGTPMYFDDIIQNPEIKNKETYQIITNQTMNKIAELKAWYESGCKGDVP

>core/718/3/Org3_Gene393

MIKSSLILLSGGQGTRFGSKIPKQYLPLNGTPLVLHSLKILSSLPQIAEVIVVCDPSYQETFQEYPVSFAIPGERR
QDSVFSGLQQVSYPWVIIHDGARPFYIYDEIHDLETAEKIGATALASPIPYTIKQRNPVRTLDRDNLAIIHTPQ
CIKTEILREGLALAKEKQLTLVDDIEAAEIIIGKPSQLVFNKHPQIKISYPEDLTIAQALL

>core/719/3/Org3_Gene927

MMNYEDAKLRGQAVAILYQIGAIFGKHILASGEETPLYVDMRLVISSPEVLQTVATLIWQLRPSFNSSLLCG
VPYTALTLATSISLKYINIPMVLRRKELQNVDPSSDAIKVEGLFTPGQTCLVINDMVSSGKSIETAVALEENGLV
VREALVFLDRRKEACQPLGPQGIKVSSVFTVPTLIKALIAYGKLSSGDLTLANKISEILEIES

>core/720/3/Org3_Gene515

MARYCGPKNRVARRFGANIFGRSRNPLLKKPHPPGQHGMQRKKKSDYGLQLEEKQKLKACYGMIMEKQLV
KAFKEVIHKQGNVAQMFLERFECRLDNMVYRMGFAKTIFAAQQLVAHGHLVNGRRVDRRSFFLRPGMQIS
LKEKSKRLQSVKDALESKDESSLPSYISLDKTGFKGELLVSPEQDQIEAQLPLPINISVVCEFLSHRT

>core/721/3/Org3_Gene591

MKQFILRTLNALFPNPKPSLEGWSSPFQLLIAILLSGNSTDKAVNSVTPQLFAKAPDAQSILDLPPGKLYQLIAP
CGLGERKSAYIYQLSQILVRDFHGEPPNDMALLTQLPGVGRKTASVFLGIAYGKPTFPVDTHILRLAQRWKIS
EKKSPSAAEKDLARFFGHENTPKLHLQLIYYARQYCPALHHKIDNCPICSYLAKEANSTR

>core/722/3/Org3_Gene50

MSVQVKLTKNFRLEKQKLARLQTYLPTLKLKKALLQAEVQNAVKDAAECDKDYVQAYERIYAFaelFSIP
LCTDCVEKSFEIQSIDNDFENIAGVEVPIVREVTLPASYSLLGTPIWLDTMLSASKELVVKVMAEVSKERLK
ILEEELRAVSIRVNLFEKKLIPETTKILKKIAVFLSDRSITDVGGQVKMAKKKIELRKARGDEC

>core/723/3/Org3_Gene47

MANLNADGKLKQICDALRLDTLKPAAEDAAAALLHNAKEQAKRIIQEAQEEARKILETAEERAHQKIKQGEVA
LSQAGKRALEALKQAVENKIFRESLVEWLEHVTTDPEVSTKLIQALVQALEAQGVSGNLTAYIGKHVSPRAV
NELLGKAVTTKLRRKKSvvvGSFVGGVQLKVEEKNWVLDLSSSALLEIFTRYLQKDFREMIFQGS

>core/724/3/Org3_Gene526

MTYLASSIFSPEDFLYPEIISKAHYTWDILDLMDQMLENHVFSGIHGTVESGVTLKNIEKIEIAEDAYVESGAYI
VGPCILGSQTEVRHGAYLRGNVITGSRVVGHCTEIKNSYLGHHTKAAHFAYLGDSVLSSEVNLGAGVRCA
NFRLDGRNIYVRSTSDKSKKIDTGRRKLGAFLGKGVAIGCNVVINPGQHILPHTRIRPGQVI

>core/726/3/Org3_Gene28

MSFVPYSLPELPYDYDALEPVISSEIMILHHQKHQIYINNNAALKRLDAAETQQNLNELIALEPALRFNGGG
HINHSLFWETLAPIDQGGGQPPKHELLSLIERFWGTMDNFLKKLIEVAAGVQGSWAWLGFCPAKQELVLQ
ATANQDPLEPLTGKLPLLGVDVWEHAYYLQYKNVRMDYLKAFPQIINWGHENRFSEIISK

>core/727/3/Org3_Gene423

MYDYIRGTLTYVHTGAIVIECQGIGYHIAITERWAIECIRALHQDFLVFTHVIFRETEHLLYGFHSREERECFRI
LISFSGIGPKLALAILNALPLKVLCSVVRSEDIRALASVSGIGKKTAEKLMVELKQKLPDLLPLDSRVETSQTH
TSSCLEEGIQALAAALGYSKIAAERMIAEAIKDLPEGSSLTDLPIALKKNFSGVNKD

>core/728/3/Org3_Gene864

MKIVIASHHGYKIRETKTFLKRLGDFDIFSLSDFPDYKLPQEQEDSITANALTKGIHAANHLGCWVIADDTMLR
VPALNGLPGPLSANFAGVGAYDKDHRKKLLDLMSSLESVDRSAYFECCVVLVSPNQEIFKTYGICEGYISHQ
EKGSSGFGYDPIFVKYDYKQTFaelSEDVKNQVSHRAKALQKLAPHLQSLFEKHLLTRD

>core/729/3/Org3_Gene669

MGLPNYITFSRLFITPIFMILYLKGKWFGITPVVLPYVLLALLAISELTDaidGYVARKFSQVTDLGKLLDPMA
DSIYRISIYLTFTQPPVNLPLLLVFIFLARDSVISTLRTVCAFRGRVVAARASGKLKAILQGVSFLLVMIPHSL
GLLSQNGLEIFASVTVSIIAVYSIASGIEYFWMNKNFLSQRAKTKDSEKNHESKD

>core/730/3/Org3_Gene175

MFIVIEGGEGSGKSSLAKALGDQLVAQDRKVLLTREPGGCLIGERLRDLILEPPHLELSRCCELFLFLGSRAQH
IQEVIIPALRDGYIVICERFHDSTIVYQGIAEGLGADFVADLCSKVVGPTPFLPNFVLLLDIPADIGLQRKHRQK
VFDKFEKKPLSYHNRIREGFLSLASADPSRYLVLDARESLSLIDKVMLHTQLGLCT

>core/731/3/Org3_Gene72

MNKILVDSPFSPDHQKCCPKLFTISAPAGVGKTTLVRMLEQEFSFAETISVTTRKPREGEVPGKDYHFVSHE
EFQRLLEDQALLEVWVFLFGECYGTSMLEIERIWSLGKHAVAVIDIQGALFIRSRMPSPVSIFIAPPSQEELERRLA
SRGSEEGSQRKERLEHSLIELAAANQFDYVIINDDLNQAYRVLKSIFIAEEHRNIL

>core/732/3/Org3_Gene550

MHAKLSFFILLSLLFSGIDCSRLHAAGRSPSLQGVLAIEIDISAKLASHEVEIVMLSERLDEQDSKCQKWTA
AKPETLAQKIRELESDQKALAKTLAVLTTSVKDLQTNLQSKLQEIQKDHRAQAQDLRLVRRSLLALVDSSSPGA
YADFSDPVPENIYIVREGDSLAKKYSKLSVTELKKINKLDSDAIYAGQRLCLQRNKQ

>core/733/3/Org3_Gene257

MIGAQQKQSGKKTASRAVRKPAKKVAAKRTVKKATVRKTAVKKPAVRKTAAKKTVAKKTTAKRTVRKTV
AKKPAVKKVAAKRVVKKTVAKKTTAKRAVRKTVAKKPVARKTTVAKGSPKAAACALACHKNHKHTSSC
KRVCSSTATRKHGSKSRVRTAHGWRHQLIKMMSR

>core/734/3/Org3_Gene190

MTSIPFQSSGDASFLAEQPQQLPSTSESQLVTQLLTMMKHTQALSETVLQQQRDRLPTASIILQVGGAPTGG
AGAPFQPGPADDHHHPPIPPVPAQIETEITTIRSELQLMRSTLQQSTKGARTGVLVVTAILMTISLLAIHILAV
LGFTGVLPQVALLMQGETNLIWAMVSGSIICFIALIGTLGLILTNKNTPLPAS

>core/735/3/Org3_Gene599

MTLVPPYVVEDTGRGERAMDIYSRLLKDRIVMIGQEITEPLANTVIAQLLFLMSEDPKKDIQIFINSPGGYITAG
LAIYDTIRFLGCDVNTYCIGQAASMGALLSAGTKGKRHALPHSRMMIHQPSGGIIGTSADIQLQAAEILTLKK
HLANILSECTGQPVEKIIEDSERDFFMGAEAAISYGLIDKVVTSAKETNKDTSST

>core/736/3/Org3_Gene928

MLKLLKVSITGDLSSGKTEACQVFQELGAYVVSADDEISNSFLIPHTRIGRVIDLLGSDVVVDGAYDAQAIAA
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>core/737/3/Org3_Gene834

MLILLNLSLLFYVLFDSPGSIPVFVALLKNFSRKKQQRVILRECLFALGALILFVTFGRSFFQFLDISLYAFQIIG
GFLIFTVSIKMMLAPMPEKAKDDTSKTEPIFFPLAFPVITGPAVITALLSYMEEGIYSREIIFTAMIIAWAFSLFT
LLCSSFFDRLSGNFGLLALERLFGIALLLMSVNLMLKGISIAFNIGFYIG

>core/738/3/Org3_Gene354

MFSGIIQELGEVCFEFAQGNGLSLGIKSTPLFVTPLVTGDSVAVDGVCLTLTSCNESKIFFDVIPETLACTTLGE
KRCSDQVNLEAALKMGDSIGGHLLSGHVFGTAEIFLIKENRYYFRGSKELSQYLFEEKGFIAIDGISLTLVSVDS
DTFSVGLIPETLQRTTLGKKREGERVNIEIDMSTKIQVDTVKRILASSGKD

>core/739/3/Org3_Gene693

MFAYRTLTHNVVQVSHEIFKTTVVPGDTVIDATCGNGNDSLFLARLLQGEGRLVVYDIQKEALSNALLFE
THLSEQERSVIEMKEQSHEHILEKDVKLIHYNLGYLPKGNKEITTLARTTEISLEYALNIVRPDGLITVVCYPGH
PEGEKETHSVESLAQRLHPKEWCVSSFYVANRCRAPRLFIFQRQGSSESSVDKG

>core/740/3/Org3_Gene195

MTRYPDYLSKLIFFLRKLPGIGFKTAEKLAFELISWDSEQLKILGNAFHNVASERSHCPLCFTLKEADCHF
CREERDNQSLCIVASPKDVFFLERSKVFKGRYHVLGSLSPITGKHIENERLSILKSRIETLCPKEIILAI DATLEG
DATAFLKQELQHFSVNISRLALGLPIGLSFDYVDSGTLARAFSGRHSY

>core/741/3/Org3_Gene402

MGFACRYLFFFIVLFASGSFGNQLLSVPCWLSEEEESFYTHRFDFSKSYPD MENMEIQAQRKKRVEFNLTGEFP
KLETLN YQGSFGHLRAKCRGVYPVLYALNFSCSSCKMDMDFRGKWNRSSTITISNQKESINLKL PKDVGIV
NTKTSLKGNVCPGSTFIKQGWGVWNKIYHNDLVGFSEVTLIFNVSSEGGTITFS

>core/742/3/Org3_Gene465

MRLFSLGTIYLFFSLALSSCCGY SILNSPYHLSSLGKSLLQERIFI APIKEDPHGQLCSALTYELSKRSFAISGRSS
CAGYTLKV ELLNGIDKNIGFTYAPNKLGDKTHRHFIVSNEGRLSLSAKVQLINNDTQEVLIDQCVARESVD FD
FEPDLGTANAHEFALGQFEMHSEAIKSARRILSIRLAETIAQQVYYDLF

>core/743/3/Org3_Gene101

MNWVPKTIDHVDPESEIDIRKV VSCYKLIKECQPEFRSLISELLGVIRCGLRLLKRSKYQE QARTVSD EDAPLF
CLTRSYYQDGYLTPLRAGPRDLINHYIHLRRRENPKHFFSPKHPCYYARLAFNESVCVYRELFDIERLTKMYV
EGDYSKEQEKNLQAILS FVKTLDEGKDFLIEHKD TDLIGRGFTDVFCT

>core/744/3/Org3_Gene668

MRIALSLLSLLMIFPIFGESRPGSEDGNSNTQEIVGSQDTQVCLYHSYEQGLQASRIEGKPLVIVVLCNSGDD
GQACTIGLSETCEEVLSVLSGSIFSELANFVVLVPSGVNPLIYPPIEDPILAEIVKF KELFKDESFP TGLSIIVGV
TPEGPGDII EVSPVSLTVEEEEETLPSEQTTEVESTSELQSEDPAIA

>core/745/3/Org3_Gene372

MSSNLHPVGGTGTGAAAPESVLNIVEEIAASGSV TAGLQAITSSPGMVNLLIGWAKTKFIQPIRESKLFQSRAC
QITLLVLGILLV VAGLACMFIFHSQLGANAFWLII PAAIGLIKLLVTS LCFDEACTSEKLMVFQKWAGVLEDQL
DDGILNNSNKIFGHVKTEGNTSRATTPVLNDGRGTPVLSPLVSKIARV

>core/746/3/Org3_Gene9

MSLPLVLGSSSPRRKFILEKFRVPFTVIPSNFDESKVSYSGDPIAYTQELAAQKAYAVSELHSPDCIILTGDITV
SYDGRIFTKPQDKADAIQMLKTLRNQTHDVVTSIAVLHKGKLLTGSETSQISLTMIPDHRIESYIDTVGTLNNC
GAYDVCHGGLILKKVHGCVYNVQGLPIQTLKYLLEELNIDLWDYSI

>core/747/3/Org3_Gene333

MLQEHFFLSEDEVITLAQQLGHKLITTHEGLITSGYIVETEAYRGPDDKACHAYNYRKTQRNRAMYLGKSSA
YLYRCYGMHLLNVVTGPEDIPHAVLIRAILPDQGKELMIQRRQWRDKPPHLLTNGPGKVCQALGISLENNR
QRLNTPALYISKEKISGTLTATARIGIDYAEYRDVPWRFLSPEDSGKVLS

>core/748/3/Org3_Gene549

MTLSLVGKEAPDFVAQAVVNGETCTVSLKDYLGYVVLFFYPKDFTYVCPTELHAFQDALGEFHTRGAEVI
GCSVDDIATHQQWLATKKKQGGIEGITYPLLSDEDKVISRSYHVLKPEEELSFRGVFLIDKGGIIRHLVVNDLP
LGRSIEEELRTLDAIFFETNGLVCPANWHEGERAMAPNEEGLQNYFGTID

>core/749/3/Org3_Gene288

MFRRTGKGPFEDEVQTLYEEETSSPSSYSPYSRSERPETPPSLFDNPKASEARPLNHNLTEESSLPQWSSTPRTES
LLPLEEPETTLGEGVTFKGEAFERLLRIDGTFEGILVSKGKIIGPKGVVKADIQLQEAIIEGVVEGNITVSGKV
ELRGGAIIKGDIAQANTLCVDEGVRILGYLAIAGITDHSEERERDL

>core/750/3/Org3_Gene726

MAYGTRYPTLAFHTGGIGESDDGMPPQPFETFCYDSALLQAKIENFNIVPYTSVLPKELFGNIVPVDTCVKSEK
HGAVLEVIMAGRGAALSDGTHAIATGIGICWGKDKNGELIGGWAAEYVEFFPTWINDEIAETHAKMWLKK
LQHEDLRSIAKHSEFQFFHNYINIKQKFGFCLTALGFLNFENAEPKVN

>core/751/3/Org3_Gene538

MKKWISILSFLSLLSILPVLAITINHVKISQRWSDLNSQILTLKVIRDHEDQVIKHNRISKDRNNLSIESLNAS
CKQLRPLSKERERLNKLNSNSLLAQSKEVWERKRALEKSNHQLVWNCEQMHNDFAFVRLEQATEMDNEDI
ESLFSLFNPENPVAPLVFFTCWKMTKQTTPLGNEVWLTHAEAISRWI

>core/752/3/Org3_Gene551

MNIHSLWKLCTLLALLALPACSLSPNYGWEDSCNTCHHTRRKKPSSFGFVPLYTEEDFNPNFTFGEYDSKEEK
QYKSSQVAAFRNITFATDSYTIKGEENLAILTNLVHYMKKNPKATLYIEGHTDERGAASYNLALGARRANAI
KEHLRKQGISADRLSTISYGKEHPLNSGHNELAWQQNRRTEFKIHAR

>core/753/3/Org3_Gene289

MVLFSLLPKLCYGCQAPGAYFCSNCLEKLLVEDREGRCLHCFRYLGSSETRLCSQCSPSSQLQAFSLYLPSQ
TALSVYARACEGKRPALQFFFSKIAFELASLDETSPSCIAIYTSTISRKIVVEVAKLEKLLRIPLWPWLPKKRQIE
KLPKGEGICFLSAYPLSQKWMQTIVGGSASPLVSISLFLSQNDQ

>core/754/3/Org3_Gene166

MKRYVVGISGASGVILAVKLIKELVNAKHQVEVIISPSGRKTLYYELGCQSFDAKFSEENLEYIHTHSIQAISS
LASGSCPVEATIIIPCSMTTVAAISIGLADNLLRRVADVALKERRPLILVPRETPLHTIHLENLLKLSKSGATIFPP
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>core/755/3/Org3_Gene613

MKVIYYEIEEIPSTNTMAKSYMHLWDPYALTVISTKCQTAGTGKFGKSWKSSKGDLLNTFCFFITDLHIDVSR
LFRLGTEAVVALCKDLGITEAKIKWPNDVLVHGEKLCGVLPETLPVEGLLGVVVLGIGLNGNTTKQALKDVG
QPATSLQEILGHPIDLETTRELLIHLLGVLQENLPDSLATKSNRGN

>core/757/3/Org3_Gene344

MADGEVHKLRDIIKEKELLEARRVFFSEPVTEKSASDAIKKLWYLELKDPGKPIVFVINSPGGSVDAGFAVWDQ
IKMLTSPVTTVVVTGLAASMGSVLSLCAAPGRRFATPHSRIMIHQPSIGGPITGQATDLDIHAREILKTKARIIDV
YVEATNQPRDIIKAIDRDMWMTANEAKDFGLLDGILFSFNDL

>core/758/3/Org3_Gene36

MIKKFFIYSLIFSCSFSAPLKGICNEDVSSQSRIEEDPEVLITQLNELIETPIEEGKEIRNELQAISDGQKSSEEIEES
CGTSDSEGLSEKTDKESNEYVLDFDSMVQRLEGISKMCQSGQVAQIIDCFNREFDIRNRELELKNRELELRE
KDLEFKKSILDWNKEKVSRELAHQREQDIKQTLMLLKK

>core/759/3/Org3_Gene263

MSIKEDKWIREMALNADMIHPFVNGQVNVNEETGEKLISYGLSSYGYDLRLSREFKVFTNVYNSVVDPKCFT
EDIFISITDDVCIVPPNSFALARSVEYFRIPRNVLTMCIGKSTYARCGIIVNVTPFEPEWEGHVTIEISNTTPLPAK
IYANEGIAQVLFFESSTTCEVSYADRKGGKYKQKQGKITVPCV

>core/760/3/Org3_Gene632

MVRVSTSEFRVGLRIEIDGQPYLILQNDFVKPGKGQAFNRIKVKNFLTGRVIERTYKSGESVETADIVERSMRL
LYTDQEGATFMDDETFEQEVVFWEKLENIRQWLLEDTIYTLVLYNGDVVAVEPPIFMELSIAETAPGVRGDT
ASGRVLKPAVTNTGAKIMVPIFIDEGELVKVDTRTGSYESRVSK

>core/762/3/Org3_Gene992

MMKIPYARLEKGSLLVASPDINQGVFARSVILLCEHSLNGSFGLILNKTLGFEISDDIFTFEKVSNNHNRFCMGG
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PGNKDYVFYSEPEDLWALVLKDLGGKYASLSTVPDNLLN

>core/763/3/Org3_Gene750

MIRRLEYYGSPILRKKSSPIAEITDEIRNLVSDMCDTMEAHRGVGLAAPQVGKNVSLFVMCVDRETEDGELIF
SESPRVFINPVLSDPSETPIIGKEGCLSIPGLRGEVFRPQKITVTAMDNLGKIFTEHLEGFTARIIMHETDHLNGV
LYIDLMEEPKDPKKFKASLEKIKRRYNTHLSKEELVS

>core/764/3/Org3_Gene695

MALNFKINRQIRAPKVRLIGSAGEQLGILAIKDALDLAREAGLDLVEVASNSEPPVCKIMDYGKYRYGLTKKE
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EDIGFVEAEPKLAGRSLICVVAPGTVKTKKKQEKSHAQDENQ

>core/766/3/Org3_Gene411

MRILAGKYKGKSLKTFSNPHIRPTSGLVKEAFFSICREDIEGAFLDLFAGMGAIGFEALSARGAASVVFDISIK
AIQLIHTNSALLGEQLPVVIFRQDAQSAIQRLIKQKRSFDLIYIDPPYELCNCYVETLLQKIVSGNILNPEGTLFL
ENASDEEIACEGLTLRRRRKLGKTYLAEYIVEKDP

>core/768/3/Org3_Gene840

MELVVTSRETGKKSFLKKIRQQGGIPAVVYSAGKSLANITVDALVFKKFLSNLESGALSSTVFSLSYEGRIIKA
LVKDIQYQITTYDVIHLDFEELVEDRPVKLNIPRCINAVDCIGVKLGGSRLRQVIRAVRVVCKPKDIVPFLELDV
RSVGLSQTRKLSDIKIPAGIETITPLKEVAITVSRR

>core/770/3/Org3_Gene114

MVLSSQLSVGMFISTKDGLYKVTSSVKVAGPKGESFIKVALQAADSDVVIERNFKATQEVKEAQFETRTLEY
LYLEDESYLFLDLGNYEKLFIPQEIMKDNFLFLKAGVTVSAMVYDNNVFSVELPHFLELMVSKTDFPGDSL
SGGVKKALLETGIEVMVPPFVEIGDVIKIDTRTCEYIQRV

>core/771/3/Org3_Gene330

MTDTPPENEEQHESNVQNENEVEHLQQEIVTLKTELKEKNDKYLMALAESENSRKRLQKERQELMQYALEN
TLIDFLNPIESMEKALGFATQMSDDVKNWALGFNMILNQFKQIFEEKGIIYSSIGQKFNPFLEAVQTEETSE
VPEGTILEEFAKGYKIGERPIRVAKVKVAKAPTPKENKE

>core/772/3/Org3_Gene565

MAAKTKTLEEDNVFLLLEGNLKRIFATPIGYTTTFREFQNVVFNCAANGQQEIANFFFEMLINGKLTQELAPQQ
KQAAHSLIAEFMMPIRVAKDIHERGEFINFITS DMLTQQERCIFLNRLARVDGQEFLM TDVQNTCHLIRHLL
ARLLEAQKNPVGEKNLQEIQEEITSLKNHFDELTKALQ

>core/773/3/Org3_Gene389

MVETVLHNFQRYLSKYLYRVFRFPCRKKTFLSSHRVLARPSFPVDYCPGKIYDLQEIYEELNAQLFQGALRLQ
IGWFGRKATRKGKSVVLGLFHENEQLIRIHRSLDRQEIPRFFMEYLVYHEMVHSSVVPREYSLSGRSIFHGKKF
KEYEQRFPDYDRAVAWEKANAYLLRGYKKRVGGGYGRA

>core/775/3/Org3_Gene742

MNFAKIDHNHLYLTCLGDLGVACPILSTDCLPNYSEKASHEVLVYSKFRCSGEP SRLATSGNDTYYSIVSLPI
GLRYEVTSPSGRHDFNIDMHVAPKIGAVLSHGTTREAKEIPGSSKDYAFFSLTARESLMISEKLAMTFQVSEVIQ
NCYSQCTKVTKTNLKEQYRHLSHNTGFELSVKSAF

>core/776/3/Org3_Gene434

MSRKAREPILLPQGVEVSIQDDKIIVKGPKGSLTQKSVKEVEITLKDNSIFVHAAPHVVDPRSCMQGLYWALIS
NMVQGVHLGF EKRL EMIGVGFRASVQGAFLDLSIGVSHPTKIPISTLQVSVEKNTLISVKGLDKQLVGEFAA
SIRAKRPPEPYKGKGIRYENEYVRRKAGKAAKTGKK

>core/777/3/Org3_Gene820

MYKWYVVQVFTAQEKKVKKALEDFKESGMTDFIQEIILPIENVMEVKKGEHKVVEKYIWPGYLLVKMHLT
DESWLYVKSTAGIVEFLGGGV PVALSEDEVRSILTDIEKKSGVVQKHQFEVGSRVKINDGVFVNFIGTVSEV
FHDKGRLSVMVSIFGRETRVDDLEFWQVEEVAPGQESE

>core/778/3/Org3_Gene400

MSLLNLPSSQDSASEDSTSQSQIFDPIRNRELVSTPEEKVRQRLLSFLMHKLNYPKKLIIEKELKTLFPLLMRK
GTLPKRRPDILITPPTYTDAQGNTHNLGDPKPLLLIECKALAVNQNALKQLLSYNYSIGATCIAMAGKHSQV
SALFNPKTQTLDFYPGLPEYSQLLNYFISLNL

>core/779/3/Org3_Gene285

MVEIFNYSTSIYEQHASNNRIVSDFRKEIQMEGISIRDVAKHAQILDMNPKPSALTSLLQTNQKSHWACFSPPN
NFKYQRFSTPYLAPSLGSPDQQDEIDIEKISSFLKVLTRGKFSYRSQITPFLSYKDKEEEEEDEDPEEDDDDDPRVQ
QGKVLKALDLGVKSTNVMIDYVISRIFQFVQG

>core/780/3/Org3_Gene136

MSKESIRSYSEISTPTPIFRETPSKEGVAYKLQLRSPAKDCILRN RVSLKGALLRSIPFYGSFLGAKRIHSAWSA
KDAPCTTRVYHYLVGGLELLGLGVVVLACKVLATALKFLFSKASSKIKQMKWREKARNLAAKDTVQSIKEF
CSVDLTSCFTRCFRLRN RVVEEGASENQTVREIIV

>core/781/3/Org3_Gene537

MTDPKIEKSALRKLFISIRDLSEERKHEASSAVASFVRSFSKESVVL SFVSFNHEIDMQEANRILIQKCTLALP
KIDQENLYPVLIPSIDDLISVVHPKDPFSKQTPISSDKITHVLVPGLAFDQQGYRLGYGHGFYDRWLAQHPYPS
IRTIGIGYCEQKIDRLPQESHDIPLSQIYLC

>core/782/3/Org3_Gene436

MSRLKKFYTEEIRKSLFEKFGYANKMQIPVLKKIVLSMGLAEAAKDKNLFQAHLEELTMISGQKPLVTKARN
SIAGFKLREGQGIGAKVTLRGIRMYDFMDRFCNIVSPRIRDFRGFSNKGDGRGCYSVGLDDQQIFPEINLDRV
KRTQGLNITWVTTAQTDDDECTTLELMGLRFKKAQ

>core/784/3/Org3_Gene671

MAKLIVAIGNPRHGYANTRHNAGFLLADRLVEELQGPPFKPLSKCHALMTLVESSSGPLVFIKPTTFVNLSGK
AVVLAKKYFNVALSHILVLADDVNRSFGKLRLCFNGSGGHNGLKSITASLSGNEYWQLRFGVGRPLEEGV
ELSNFVLGKFSEENLQLGSIFVEASTLFTWCSKF

>core/785/3/Org3_Gene489

MSVLQDTEKKMAAALDFFHKEVKSFRGTGKAHPALVETVVVDVYGTMMRLSDIASISVADLRQLVISPYDGN
NASAIAKGIIAANLNLQPEVEGSIIRIKVPEPTADYRQEMIKQLRRKCEEAKINVRNIRREANDKLKKDSALTE
DVVKGNEKKIQELTDKFCKQLDELTKQKEAEIASI

>core/786/3/Org3_Gene608

MTPQSPGSLSQSHLPHPHDPWDTEPTSLPEDPNDKASQELHSLVHLFRKLSIHLLSEVEKTVQQLKPDILLELA
LLICEKFLYKKLENPQELALLLSTALQRHTTLRSLTPIKVFLHPEDLKTLDWISTHELPMIKHAEFFPDTSCRR
SGFKIETPNGILRQEISEELDHLSSVLTA

>core/787/3/Org3_Gene377

MACEQHEGCEYELEEREIEIDIKSDTKWVSITQAAKLHNVTRQAIYVAIKQKKLKASKETRWEIDIKDLEEY
KRNRYSRKKSLYQGELVFDNGKGCYSINQVAQILGIPVQKVYYATRGTIRGERKGAAWVIHVSEIERYKNE
YLSKQAAKKLKGAEPKEHQAPNFEPPTTEIFPESN

>core/789/3/Org3_Gene976

MTIILCGLPTSGKSSLGKALAKFLNLPFYDLDDLIVSNYSSALYSSSAEIYKAYGDQKFSECEARILETLPPEDA
LISLGGGTLMYEASYRAIQTRGALVFLSVELPLIYERLEKRGGLPERLKEAMKTKPLSEILTERIDRMKEIADYIF
PVDHVDHSSKSSLDQASQDLITLLKS

>core/790/3/Org3_Gene189

MSAPIPTQELSDQITCLNVQYQQVSELARENKGDIEGLKTLTAALTADAGIQPSADEIYSLQTAAALILSASE
KPGSGPSGSTEGSVTVQSPCKFKKVLAVVLTIIALIAIAVLIACIIAACGGFPLLSALNLYTIGACVSLPIASTS
VALICLCTFVANSLIKPVITVRTR

>core/791/3/Org3_Gene366

MDRDNEVPLPKPKWIYRTGIGQDSHRFLPESSTKPCILGGIIFDHCPGFQANSDDIIFHAICNAISSVTNKIILG
KVADELLQTRGITDSGIYLEEALKSLKPNQKISHVAITIEGSRPKFLCKLSALRQNIQVMNLTPTDIGITATSG
EGLSDFGCGDGVQCFCVLTVMYCD

>core/793/3/Org3_Gene612

MGYVFYVIAGSIFLGISLGAYCQLYYSVKSVLFSWYLLTVYALEKRHALLALSQLVGEEDAQSQKEIDFLSQC
DKLSWRAFLKNSYEIIPTFKEMEDLLSERVQGFLESJETIAEHDRAILCIENFWASKNLDFEIAAYEEAVEKYL
KLRQRAPLRLASKLFRFLDVPSIRFSS

>core/794/3/Org3_Gene988

MDCVDNLKLYIFRLKLPGDTERISYSISPEYIREKGEEELLSPIEVEGSLGRIDSDQWILSLSLKTQLGLCCPVC
NNFFSHSVCLPDLQRVISHDEVGSGVFDCRPLIRQELLLESDFEECGSGQGCPPERKNILKFLEDRKKHEGNPF
EYL

>core/795/3/Org3_Gene299

MSSTLNGVFPSSLPEESADLFITNKEIVALGEKGNVFLTHSIPMHIAAITILVIVALAGIAIICLCGCYSQSILLIAVG
IVLTILTLLCLQALVGFIKFIRQLPQQLHTTVQFIREKIRPESSLQLVTNAQRKTTQDTLKL YEELCDLSQKEFK
LQSTLYQKRFELSHKNEKTQN

>core/796/3/Org3_Gene709

MSIQPVSNTTTKADKVIPDSTKVISDSITINKQSAFYFCISVMLRLSESTTEYGKSILAVLEDNTIVQQQRVKELI
NLPLLKVPDLQKKDGSDDKEYKNQNEIQAYQSSNQQISANRQMIQQELSSAQQRAQANQKSVNSTTIESMQIL
QATSSMLSTLKELTIKANLTNSPSD

>core/797/3/Org3_Gene710

MWIIDPLSAKKPLQAAINVPGTPTGGPNTATADDIIAKFSKDSNPLIVTVYYVYQSVLVAQDNLSIIAQELQA
NSSAQTYLNNQEALYQYVSIPKNKLNDNSSSYLQNIQSDNQAIGASRQAIQNQISSLGNAAQVISSNLNTNNNI
IQQSLQVGQALIQTFSQIVSLIANI

>core/798/3/Org3_Gene405

MADDTLIPKLMKNSLSQACSEGLLIAKYPPQLQVIVHFDNNLVVKTHLSVAPVFSCFLGPAAHKAMQEIVLW
CSRYANKEHPPFSSHFAKDLIPSQYLEILNCVAEIPFGEQQTYAEIAKKTDTHPRTVGAACKQNPFLFFPCHR
VVGSHGERNYVLGPVIHEILLKFENSY

>core/799/3/Org3_Gene786

MGFKNICKQGSQLYLNGIFPERILARKLKNCASYPRTALTIEVLVSSVLGALKVILIPCASTYAALTPLPLRALF
NAIKTKSCQHLASYAMAWLLNILTIAVIIGLVFSLVFIPPPVVFISLGLMSVTTSVTLFQVHKNLFPPYEPPPSR
PHTPPFADEYVPLISESYFD

>core/800/3/Org3_Gene720

MSHLNYLLEKIAASSKEDFPFPDDLESYLEGYVPDKNIALDTYQKIFKISSEDLEKVYKEGYHAYLDKDYAKS
ITVFRWL VFFNPVSKFWFSLGASLHMSEQYSQALHAYGVTAVLRDKDPYPHYAYICYTLTNEHEEA EKAL
EMAWVRAQHKPLYNELKEEILDIRKHK

>core/802/3/Org3_Gene224

MSVHITPRKCFILCILSMFTLPTLFPKAHLILFSPIVLCFYCFSKDKGLVLALGCGVLSDLALGSRGVFLLLYP
LTALITHKAHLIFSKEKAALVIVNMIFYGVFLLLTIPMCALFGHEVRWSIDVLMIPLKCSFLDNLIFTSVIYILP
CAINSGIHKMISFFRRLVCY

>core/803/3/Org3_Gene490

MVHSPTHQCYHCQQPATICYTEIDKDKVIRSYVCATCPCPSHYYNNEHLSLSKGVGVLTLECGNCKTVWHS
KQDDEQLLGCHQCYTNFNQITSKLKSERVSSSFTMEKGQGSLSHIGRAPGEASNTNPLLKLIALNEALQDTL
EREDYEQA AVIRDQINHLKTKNPDDPS

>core/804/3/Org3_Gene921

MTAEKQNTGILGLEIRYTLPSDATYMLKWLNDPKILRGFPIQTEAEIRETVNFWVGFYRYHSSLTAVYNGNV
AGVATLVLNPYVKVSHHALISIIIVGEEFRNKGIGTALLNNLIHLAKTRFKLEVLYLEVYEGHPALHLYQRFGF
VEVGRQNRFYKDEIGYLAKTTEKDL

>core/805/3/Org3_Gene197

MKKLLFSTFLLVLGSTSAAHANLGYVNLKRCLEESDLGKKETEELEAMKQQFVKNAEKIEEELTSIYNKLQD
EDYMESLSDSASEELRKKFEDLSGEYNAYQSQYYQSINQSNVKRIQKLIQEVKIAAESVRSKEKLEAILNEEA
VLAIAPGTDKTTEIIAILNESFKKQN

>core/806/3/Org3_Gene884

MSEVKPLFLKNSFDLATQRFQNLINMLQEQAIEYNEYEEKNARVQNEIKEQKDFVKRCIEDFEARGLGVLK
EELASLTRDFHDKAKAETSMLIECPCIGFYYSIHQEEQRQRQERLQKMAERYRDCKQVLEAVQVEQKDMISS
RVVVDDSYFEEEEKEDQKVDNRKKEQD

>core/807/3/Org3_Gene534

MCKNRGVRGIVACDPRGVIGLEGKLPWHYPEDLQFFSETIQKFPIVMGRKWTWETLPRKYFVDRAVVVFSHEK
RQGVHGEIWVTSLEEFLLLDLSSPTFLIGGGELYSLFLENQIVRDFFISHIKKEYAGDTFFPLSLLETWTKTVLR
DTQKITTCYYENHHSQNTKNISL

>core/808/3/Org3_Gene43

MKQEKTLLLQEVEDKISAAQGFILLRYLRFTAAYSREFRNSLSGVSAEFEVLKKRIFFAIEAAGLEVDCSDTD
GHLGVVFSCGDPVSAAKQVLDFNKQHKDSLVLFLAGRMDNASLSGAEVEAVAKLPSLKELRQQVVGLFAAP
MSQVVGIMNSVLSGVISCVDQKAGKN

>core/809/3/Org3_Gene52

MQRLGLSNLFHCLLLFLRYYYSKLVFGLTVLLAAISVICLLGCSEPSLSSFTEYVGPEYSAAAQLSIEQSCHDE
VYGQQVVVTWSLPSRMRKCLPVTLYLWVYYGNGKVEKLTYEVNQSAGYRVYCLKGLEYKELQGIISYRVA
LCSGNQEIVSRRHHLWMEVISLDSF

>core/810/3/Org3_Gene674

MKQQLLLLEDVDGLGRSGDLITARPGYVRNYLIPKKKAVIAGAGTLRLQAKLKEQRLIQAAADKADSERIAQ
ALKDIVLEFQVRVDPDNNMYGSVTIADIIAEAAKKNIFLVRKNFPAHYAIKNLGKKNIPLKLKEEVTATLLV
EVTSDNEYVTVLAQGKQTEENQEG

>core/811/3/Org3_Gene178

MIINVRAPAFGITSVQQFSTNFQAAIPILNIVIGCSRISSTYAEDIEEVAQEKLEKSTHSKSSTSVNLWAHRVRGV
VEILGGGIVILALEITALVLQVIIKLIKCLIDVLCVCLFGLGVCVVAIIIGAIACVVVVVVKYLGFCSQGEELEPIE
VKTLISPDKPYPTVVYV

>core/812/3/Org3_Gene424

MSELIIGVDPGTIVAGYAIIAVEQRYQLRPYSYGAIRLSSDMPLPMRYKTLFEQLSGVLDDTQPNAMVLETQF
VNKNPQSTMKLAMARGIVLLAAAQRDILIFEYAPNVAKKAVVGKGHASKRQVQVMVSKILNVPEVLHPSNE
DIADAFALAICHTHVARSPLCGVR

>core/813/3/Org3_Gene419

MRQFCNLLSLSRLWLALYFCQEKLHIRLLAIVGAMLSDVLDGYLARRYKATSRLGSILDPITDKVVFVFCITV
LYMEGSLSIAHLFFICARDLFLIIFVCYLSLVKGWKGYDYGSLFWGKIFTVVQFIILLGVTAGGEIPWTGLVPL
VALGFLYFLERIMDYKKQFLR

>core/814/3/Org3_Gene357

MATRFRSTLLVITLFLIDWVTKLVVLLQYKDLQILTHPTLYTHSWGRFSFSIAPVFNEGAAGLFSNYKYFLF
LLRIFVILGLLAYLFFKKKSIQSTTQTALVLLCAGAIGNVGDIIFYGHIVDFISFNYKQWAFPTFNVADVLISLGT
LLLVIKFFYFPTKQTEKKR

>core/815/3/Org3_Gene495

MAKYPLEPVLAIKKDRVDRAEKVVKEKRRLLEIEQEKLREKEAERDKVKNHYMQKIQQLRDLLDEGTTSDA
VLQIKSYIKVVAVQLSEEEKVNKQKEVVLAASKELEKAEVNLAKRRKEEEKTRLHKEEWMKEALKEEARA
EEKEQDEMGOQLLQRLRQKKKRESGGS

>core/816/3/Org3_Gene232

MAVEQSHIKEEIEKLIGKAIKRVCNGKENDLCRYLPGPSGGYMHFTLKKMKSAAPEQLLMLKTFILESETP
RTINPKPRAPRGSKKRRDFINFTKTDIERVLELARQVGDKDLLARFSPKKPLTSLKRELIRSIRNGIVSVELWNA
YVEAVKAVSSPNLEVTSPFV

>core/817/3/Org3_Gene113

MDLKQIEKLMIAMGRNGMKRFAIKREGLELELERDTRREGNRQEPVFYDSRLFSGFSQERPIPTDPKKDTIKET
TTENSETSTTTSSGDFISSPLVGTFYGGSPAPDSPSFVKPGDIVSEDIVCIVEAMKVMNEVKAGMSGRVLEVLIT
NGDPVQFGSKLFRIAKDAS

>core/819/3/Org3_Gene162

MSKKINRNDLPCGSNNKKYQCCLKKEEQTARYTTTEGKFKFSAEVLSSASEQGEAGDNCTKLFQRLSQSLTSE
QKAAVGKFHQITKNKEVMSKKALKKAQAKEEKLVTEKLQQHNFEILNTGENLAPPMESTATLNQDTNMFVCE
DFIPTQEDFRISENSQKPPVEED

>core/820/3/Org3_Gene260

MSRQNAEENLKNFAKELKLPDVAFDQNNTCILFVDGEFSLHLTYEEHSDRLYVYAPLLDGLPDNTQRKLALY
EKLLEGSM LGGMAGGGVG VATKEQLILMHCVLDMKYAETNLLKAFQAFIETVVKWRTVCADICAGREP
SVDTMPQMPQGGGGMQPPPTGIRA

>core/821/3/Org3_Gene652

MKFWLQGCAFGVGLLLTLPCCAARRRASGENLQQTRPIAAANLQWESYAEALEHSKQDHKPICLFFTGSDW
CMWCIKMQDQILQSSEFKHFAGVHLHMVEVDFFQKNHQPEEQRQKNQELKAQYKVTGFPELVFIDAEGKQL
ARMGFEPGGGAAYVSKVKSALKLR

>core/822/3/Org3_Gene1000

MSRRHSAEKRDIPGDIYGSVILEKFINKVMMHGGKKSARKIVYSALERFGKKLNLENVLEGFGEALENAKPI
LEVRSRRVGGATYQVPVEVASERRNCLAMQWIIKHARSKPGKSMEVGLATELIDCFNKQGATIKKREDTHR
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>core/823/3/Org3_Gene433

MSLSKNSHKEDQLEEKVLVNNRCSKVVKGGRKFSFSALILVGDGKGRLGYGFAKANELTDAIRKGGEAAKK
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KALTGLSPRKDLLRRGAIND

>core/826/3/Org3_Gene508

MTKFLYCGLFYSLGLLVLAFGTMVAIIQVDQICDVSCMNKHFQESPPFLKIKKVNVSQICSPEERFFHCKIDK
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SSSGGMKTLYLSLFRN

>core/827/3/Org3_Gene667

MMHRYFIPLLALLIFSPSLVRAELQPSNRKGGWPTQLSCAEGSQLFCKFEAAYNNAIEEGKPGILVFFSERPT
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AQCQAVLPLETKN

>core/828/3/Org3_Gene711

MSITTLGTLPTVNTINSSRPPEPLNTPKIGAVLFSIYELLLQAIEIRQQTIVLTQSQQNLNDNTNIQQQLNQETNQI
KYAIVSAGAKEDETRQVQNNQNYSAQRSNIQDELVTTRQNGQIILSHASTNINIIQQQSSQDSSFIKTTNSIGST
VNQLNKPLG

>core/829/3/Org3_Gene277

MTTWTLNQNNLTKFLKSSDEEPFLERESGLTYINIQANGNELPLFFVIRSEGEILQLICYLPYQLHESHKASTAR
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ALQEQQEKRNE

>core/831/3/Org3_Gene694

MATLSPEKFSGSPISISKEFPQQKMREIILQMLYALDMAPSAEDSLVPLLMSQTAVSQKHVLVALNQTKSILEK
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SLNENSLSI

>core/832/3/Org3_Gene259

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MYAGYGQEQQYVCEDEVPF

>core/834/3/Org3_Gene134

MSKKVFFESYEDFANVASSWPKSLRALVQGRYFVDSELKETPYRIHDFKKTPIHHRLYRSLPIISTIGGIIRLIEA
HSGPIHPRDKMKYRFEVLQAVIEILGLGVLLVFDIIGCFLAFLVAIILSLLLYCNSTFTCVQNLSFTERMLEGIG
EAVNFLA

>core/835/3/Org3_Gene276

MFFNLFSLVFKLSDELALAETIQEPISVHEMFPGSMKLEMFKMLGSLILLTTIFGFGVWAFKKFVRSRSHGFGG
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KQQTNQD

>core/837/3/Org3_Gene31

MPSYCQNQQDFSLFSLSPRLVMFLGKHSRDEILQDLTDLVDAAGLLEDKQAFFDALVRRENIMSTGIGMGV
AIPHGKLESCSNFFIAIGIHTQGILWDAIDGALVRLVFLIGGPENAEYLKLLSTLTLSLREESRRQQLLQVNT
IEEVMNVFVGM

>core/838/3/Org3_Gene579

MADETPKENSSKESSSQFDSLKRKVKDLHSNPKVGKWKFLSHRACEAIGGCLVLVGIIADFISWAGGLFIAC
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QDTSNKPS

>core/839/3/Org3_Gene336

MTQEKIKIHVSNEQTCIPIHLVSVEKLVLTLLEHLKVTTNEIFIYFLEDKALAEHDKVFADPSLTDITLPIDAP
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RKKHALLTA

>core/841/3/Org3_Gene662

MLPISILLFYVILGCLSAYIADKKKRNKRVIGWFFAGAFFGFIGLVVLLLLPSRRNALEKPQNDFDNDLFDDDLK
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VPSLQQALKEASK

>core/842/3/Org3_Gene221

MRIIRFDPYGALSAQSIKDSRQNSPLVEKISEEIATNEAIRLALLAIGDREQEEKQRRHYKLLGQKQAKVLL
SQLRHVHLDFFKLYCDSKKKEDQEKDEKNKQKRSIKVTKKKKGISLGAAASQAIAAAAEAWVIARNKGVLE
TASTLFYQKDEEA

>core/843/3/Org3_Gene663

MEKQNLKLDVKEIEFPETVFSRDIETRVIQVILHCLAKINGVSLGGNLIDALFGRDIERMKGIIYVEQDSKNHL
VKVRVEVNVDYGVSIPEKTEEIQGCIVSEISEYTGLHVAAVHVIIKGLTQPKDRIDEEIEEEVSVQDLSPEDFL
LENSEG

>core/844/3/Org3_Gene108

MIMTTISNSPSPALNPELSLIPPTLVSSGTQTSLAYTIPAQGRRSTLRILDFIILGLATIISTFIVIFFLNGLNLLS
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>core/845/3/Org3_Gene457

MRVV LHCPDIPQNTGNIGRTCVALGAELILVRPLGFSLADKFVKRAGMDYWDKLQLTVVDSIEEALHDVPED
QIFCLSTKGSASYTEFSLPSSGTYVFGSESKGLPKEILKKYYKNCLRIPMQQDIRSLNLATSVGIVLYEVVRQKT
VALQKNPTV

>core/846/3/Org3_Gene706

MEKDIFFMQQAFFKEARKAYDQDEVPGCVIVKDDKIIARAHNSVEKLKDATAHAIEILCIGSAAQDLDNWRL
LDTVLYCTLEPCLMCAGAIQLARIPRIWAAAPDVRLGAGGSWNIFTEEHPFHTVSCTGGVCSEEAHLMKK
FFVEKRREKSEK

>core/847/3/Org3_Gene905

MGYLPVSATDVLFEAPLINSAYTQNQKLIELKGKQQAESSPRITITSVILEVLLVIGCCLIVLSLLAIRPALQF
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SQAQL

>core/848/3/Org3_Gene452

MLKKKPVSFSCIDGHIYKIFPNDLNANNTVFGGLMSLLDRLALVVAERHTESVCVTA FVDALRFYAPAYMG
ENLICKAAVNRTWRTSLEVGVKVAENIYKQERRHITSAYFTFVAVNEDNQPIPVHQIVPETPEEKRRYNEA
DRRRQARLELK

>core/849/3/Org3_Gene619

MKTLKGHLSAKNLR IAVGSCFNQAMADALVSGTQETFLKFGGSEDGLMTIRVPGA FEPCTIKKLLSSERKF
DAIVACGVLIQGETDHYNQIVNQVAAGIGALSLEFCLPITLSIVAAPS AEIAWQRSGIKGRHLGVSGMTTAIEM
ATLFTQI

>core/850/3/Org3_Gene590

MPFAKETEMQRTCWKCEGSVSMHVPQCPYCSAFLQDPPVASGGFSSCHISFPEGASKEEAEDLFAVSSSEDWE
AVLGDQNPTQETNKQVIPEWTWLQSWPLAALFLGIGLLAFAFLILLFSTDSGLVLTWPKNRAYFYGIIGAABA
YRGYRKLPL

>core/851/3/Org3_Gene27

MRSALHLQHLRHFHNHGSILFENLLTIKDCFLLETKLQNFIKASKTIDTVRWRENIFRSMPEIYTVVRKRRLD
FFAAELVHRPKLSLVRDLWVFPGEEILEGEEDCMLFLLLSGDRAGSGIFFTGYPYPSDLYELEKGTTGLLLAFSS
VGIPVI

>core/852/3/Org3_Gene449

MNQPSVIKLRELLDLLPHRYPFLLVDKVLSYDIEARSITAQKNVTINEPFFMGHFPNAPIMPGVLILEALAAQAA
GVLIGLVLENDRNKRIALFLGIQKAKFRQAVRPGDVLTLQADFSLISSKGGKAWAQARVDSQLVTEAELSFA
LVDKESI

>core/853/3/Org3_Gene355

MQCPFCNHGELKVIDSRNAPEANAIKRRRECLKCSQRFTTFETVELTLQVLKRDGRYENFQESKLIHGLNAAS
SHTRIGQDQVHAIASNVKSELLGKQNREISTKEIGELVMKYLKKADMIAYIRFACVYRRFKDVGELMEVLLS
ATPDMEK

>core/854/3/Org3_Gene227

MAQKEIVSNRKALRNYEVIETLEAGIVLTGTEIKSLRDHGGNLGDAYVIVSKGEGWLLNASIAPYRFGNIYNH
EERRKRKLLLHRYELRKLEGKIAQKGMTLIPLGMFLSRGYVKVRLGCCRGKKAYDKRRTIHEREKEREVAAA
MKRRHH

>core/855/3/Org3_Gene205

MARNIKYFLILFPGILWISAGMKLLLKATAIALDPLSSFFTYCLLSMVSWGLASLKHRYLLSKTIRKQLSLSSEF
FSQKITWIAYIKQTFISRRFLIMVIMIAFSLVLRYSNPQALFVIRATVGYALIKTAIAYFSKLQNALMENPEGN

>core/856/3/Org3_Gene149

MSKPSSCKAYLGIDYGKKRIGLAYAAEPLLLTLPIGNIEAGKNLKLSAEALHKIILSRNITCVVLGNPLPMQKG
LYSSLQEEVSLLAEELKKLSTVEIILWDERLSSVQAERMLKQDCGLSRKDRKGKTDSLAA TLILTSFLDSLPPK
LTL

>core/857/3/Org3_Gene645

MMKTKYEYSFGVPIKFFGTPDKNTLKACFICHTRGKHWGFPKGHSEDKEGPQEAERELVEETGLSVVNFF
PKVLIEQYSFNNEEQVFVRKEVTYFLAEVRGDIHADPMEICDSQWLSLQEGLRLLSFPELRDLTVEADKFINN
YLFSS

>core/858/3/Org3_Gene623

MQLLSPAFAYGAPIPKKYTCQGAGISPPLTFVDVPGAAQSLALIVEDPDVPKEIRSDGLWIHWIVYNLSTTITN
LAEGAEIFAVQGLNTSGKPVYEGPCPPDKQHRYFFTLFALDVVLPEEENVTRDQLYEAMEFHIEQAELMGTY
EKS

>core/859/3/Org3_Gene154

MEKRKDTKTTIVKSSETTKSWYVVDAAGKTLGRLSSEVAKILRGKHKVTTYTPHVAMGDGVIVINAEKVRLT
GAKKGQKIYRYTGYISGMREIPFENMMARKPNYIIEHAIKGMMPRTRLGKKQLKSLRIVKGDSYETFESQK
PILLDI

>core/860/3/Org3_Gene876

MEFICPLQHARCLKKQHKIIEELFPEPFQKDHLYLKLMENSSSRDAFDKKRVLKENLVVGCQSDLYLYEVYQ
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QT

>core/861/3/Org3_Gene498

MADLEVFQADFALLFEAGLLAIKQGDEDSARKLFQSLHILNPNHYGHDLGLALISLHKMDLFD AEERLSALIK
GNEDNWSIKAFLSLTHMLIVLHQSSFEVRRESLESCLKFADQVIANCKIESTRALAQSVLDWHDTLVAKSA
GPLG

>core/863/3/Org3_Gene254

MKSERLKKLESELHDLTQWMQLGLVPKKEISRHQEEIRILEHKKIYEEKERLQLLKENGEIEEYVTPRRSPAKTV
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W

>core/864/3/Org3_Gene251

MKTKMNSRKKAGQWAFNSPTPGVSSTLVLAWTPWGYDYDKDVQDILERKDPMSSSLSEKDSKEFLKNLFVD
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KRG

>core/865/3/Org3_Gene856

MGSRRKLKRSFLLIEVLMAISLVCAVLLPCIRFYIAIHRSFEEIDIFNLQLPALIDHCFLSVEEKMRQQMAEGTV
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>core/866/3/Org3_Gene117

MKKKVTIDEALKEILRLEGAATQEELCAKLLAQGFATTQSSVSRWLRKIQAVKVAGERGARYSLPSSTEKTT
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>core/867/3/Org3_Gene216

MQNQYEQLLES LAPLLNTTLAPDKNNSCLIRFS DTHVPVQIEEDGNSGDLAVSTLLGTLPENVFRERIFKAALS
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>core/868/3/Org3_Gene639

MEEFVAYIVKNLV TNPEAVEIRSIEDDNESIKLEIRVAAEDIGKII GRRGNTIHALRRTILRRVCSRLKKKVQIDL
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>core/869/3/Org3_Gene83

MSLEKELLEETPLVLLNFYKLVSFNCYAGMILGTEKKFAIYGHVSMGQAFQGADTEGHSPQRPF AHDLLNF
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>core/870/3/Org3_Gene132

MNPVTFDRIQVDFIPEDTSLRINSYIVAGGLLILGVVLSILSVICLDIGLVGLSAGAAFTLGLGCLIFALFLFSFSL
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>core/871/3/Org3_Gene30

MTVFCELDSGGELPEYTTPGAAGADLRANIEEPIALLPGQRALIPTGIKAEIPEGYELQVRPRSGLALKHGITVL
NSPGTIDSDYRGEIRVILINFGDSTFII EPKMRIAQVVLSPVVQATFVVKQESLAETARGSGGF GHTGAS

>core/872/3/Org3_Gene466

MTFFEGETVFP AVLSELHSM LDIKRAGKQSKCPQEKLLKLELACEELLVNIISYAYQGENSPGTIAISCISHRG
DLEVVIKDHGPSFNPLAVSINI QEDLPLEQRKLGGLGIFLAKSSVDEFLYAREDHCNIVHLKMLNGQHS

>core/873/3/Org3_Gene422

MEQTLSIIKPDSVSKAHIGEILSIFEQSGLRIAAMKMMHLSQTEAEGFYFVHRERPFFQELVDFMVS GPVVVLV
LEGANAVSRNRELMGATNPAAEASGTIRAKFGESIGVNAVHGSDTLENA AVEIAYFFSKIEVVNASKPLV

>core/874/3/Org3_Gene432

MIKLESLFDISERKRRKLLGRGPSSGHGKTSGRGHKGDGSRSGYKRRFGYEGGGVPLYRRVPTRGF SHKRF
DKCVEEITTGRLAELFQEGEAITLDALKAKKAIARQAVRVK VILKGDLEKTFVWQDTAVVLSQGVQNLLGIT

>core/875/3/Org3_Gene151

MACSIFFRMSQGDYDDEPLSKKTACL VVDTMLYPVIAVVC AVVS VVLLILKVLFLLLSFPFKLCSASSALPGE
RVSLGSHFKCLYGGGLPYLLACLLIVPVIGTAIHGFIISHRTSEDARLSSAIVFMQAPILQLAGMSGLIKP

>core/876/3/Org3_Gene752

MQEHIHKELLHLGEIFRSSRESQSLSLKDVEAATSIRYSCLEAIEQGCLGKLISPVYAQGFIKKYATYLG LDGD
SILQEHPYVMKIFKEFS DHNMEMLLDLESMGGRNSPERAIHSWSNLWWAGLIIGGIMVWWLGSLFSIF

>core/877/3/Org3_Gene467

MSLDFFEEFYHQ SILNTGT SFPEGYLNIAEILSYPHCTDANTDFLCSQSDNDFIIAESKDKLTLFNADFAIWLVP
ELVQGGQAVTRGYIAVSQGE GNYEPEMAFEASGQYNQSSLILEALQLYLKDIKDTENALRSFRFNNDH

>core/878/3/Org3_Gene428

MQHARKKKFRVGR TSSHNR CMLANMLKSLIHYERIETTL PKAKELRRHADKMITLAKKNSLAARRIAIGRLM
VRYNKLT SKEARQAKGGDTSVYNVDRLV VNKLFDELGNRFVERKGGYTRILKLQNRIGDNAQKCIIEFLAS

>core/879/3/Org3_Gene521

MNSKSAQKIIDSIIKQILTIYNIDFDPSFGSSLSSDSDADYEYLITKTQEKIQELDKRAQEILTQTGMSKEQMEVF
ANNPDNFSPEEWLALEKVRSSCDEYRKETENLINEITLDLHPTKESKRPKQKLSSTKKNKKKNWIPL

>core/880/3/Org3_Gene286

MLDNEWKAILGWGDDELEELRISGYSFLRQGHYSKAILFFEALVILDPLSIYDHQTLGGLYLQIGENSQALAV
LDQALRMQGDHLPTLLNKTKALFCLGRIEEATAIATYLSSCPIPAIANDAEALLMSYSKATKKNAALVR

>core/881/3/Org3_Gene454

MGRYRRVSHSSQETLLLGTGELGQVLVPGAVLLLFGDYGAGKTEFVRGIVSGYLGDTIAEEVASPSFSILHVG
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>core/882/3/Org3_Gene41

MSVKKVIKIILQIPGGKANPAPPIGPALGAAGVNMIGFCKEFNAATQDKPGDLLPVVITVYADKTFTFITKQP
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>core/883/3/Org3_Gene51

MIDMSVVGPAVLGLAMIGSAIGCGMAGVASHAVMSRIDEHGKLGMSAMPSSQSIYGFILMLLMQAAIKN
GTLSPVGGIAIGLSVGAALLVSSVMQKGCCVSGIQAYARSSSIYGKCYAAIGIVESFSLFAVVFALLLL

>core/885/3/Org3_Gene658

MHPLTLPKQSRVLKRKQFLYITRSGFCCRGSQATFYVVP SRHPGTCRMGITVSKKFGKAHERNSFKRVVREV
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>core/886/3/Org3_Gene440

MLMPKRTKFRKQQKGQFAGLSKGATFVDFGEYAMQTLERGWWTSRQIEACRVAINRYLKRRGKVWIRIFPD
KSVTKKPAETRMGKGKGAPDHWVAVVRPGRILFEVANVSKEDAQDALRRAAAKLGIKTRFVKRVERV

>core/887/3/Org3_Gene191

MNLIDRAFLKKTIIFQSLDMDLLLTIADKTETIIFKPGSNVFSIGQPGFSFYIIVEGYITISKEKLESPLNLKPLDC
FGEESLFNKNPREYNASANTQVRMLVLSKGQILNIVEECPSVALSFLELYAKQIKFREP

>core/888/3/Org3_Gene137

MVNRYKSSAEFSADHYYDDNLVRMGYKRNLRLGLAPVENEVCLFEENNLLSVMASIPIMGSILGLGRLHSV
WSTQDPKDSKISIIFHTALGILETLGLGIIVLLIKITITILLILFTPCLLCYFMYSAAYSDFHPI

>core/889/3/Org3_Gene142

MINFIRSYALYFAWAISCAGTLISIFYSYILNVEPCILCYYQRICLFPLTVILGISAYREDSSIKLYILPQAVLGLGI
SIYQVFLQEIPGMQLDICGRVSCSTKIFLSYVTIPMASVVAFGAIVCLLVLTCKKYRG

>core/890/3/Org3_Gene553

MKYRFTEEIEEEPLVNLTPIDIVFVILMAFIVAVPLIKLDSIALAPGTQEQEVLSSENDSIAVIKVFADHSLTLN
EHPITLQELTVRLTLLHKAYPEKTPLLLQDGETSFRTYQNVKNAIEAAGFHELHVALQN

>core/891/3/Org3_Gene153

MAKSTIQESVATGRRKQAVSSVRLRPGSGKIDVNGKSFEDYFPLEIQRTTILSPLKKITEDQSQYDLIRVSGGG
IQGQVIATRLGLARALLKENEENRQDLKSCGFLTRDPRKKERKKYGHKKARKSFQFSKR

>core/892/3/Org3_Gene532

MIAIERYQLISKFRMWLFLGCSVEERHFKQPVLISVTFSYNEVPSACLSDKLSDACCYLEVTSLEEIIANTKPY
ALIEHLANELFDSLVISFGDKASKIDLEVEKERPPVPNLLNPIKFTISKELCPSPVLSA

>core/893/3/Org3_Gene141

MPYYANTLEFIQGTQSLCPLFKYGFVRHHYKGQLEIEDASHDWDFFLEPPSTWKRTLLAAIPILGSGVIGLGRIFS
IWSIREPQDSQEYKSIFWHTLCAVLEILGLGIVALILKILATFIMAMPGLKRVATFLFYS

>core/894/3/Org3_Gene435

MGMTSDSIADLLTRIRNALMAEHLYVDVEHMKMREAIVKILKHKGFVAHYLVKEENRKRMRVFLQYSDD
RKPVIHQLKRVSKPSRRVYVSAAKIPYVFGNMGISVLSTSQGVMEGSLARSKNIGGELLCLVW

>core/895/3/Org3_Gene429

MVKNQAQAKKSVKRKQLKNIPSGVVHVKATFNNTIVSITDPAGNVISWASAGKVGYSGRKSSAFAATVAA
QDAAKTAMNSGLKEVEVCLKGTGAGRESAVRALISAGLVVSVIRDETPVPHNGCRPRKRRRV

>core/896/3/Org3_Gene844

MNFVSTLTGSDFYAPVLEKLEEAFADTTGQAILFSSSPDFIVHPIAQQLGISSWYASCYRDQSAEQTIYKKCLT
GDKKAQILSYIKKINQARSHTFSDHILDLPFLMLGEEKTVVRPQGRLLKMAKKYYWNIV

>core/898/3/Org3_Gene170

MSQCQSSSTSTWEWMKSFVPNWKNPTPPLSPIPSEDEFILAYEPFVLPKTDPENANPPGTSTPNVENGIDDL
NPLLGQPNEQNNANPNPGTSGSNPTSLPAPERLPETEENSQEEEQGSQNNEDLIG

>core/899/3/Org3_Gene502

MLEKLIKNFATYMGITSTLELDADGAYVLPISVVKVRAQQNADNEIVLSASLGALPPSADTAKLYLQMMIG
NLFGRETGGSALGLDSEGNVVMVRRFSGDTTYDDFVRHVESFMNFSETWLSDLGLGKQ

>core/900/3/Org3_Gene270

MRDHAFSKLIGTVRAMVVEGRCPWSLQQSLVSMVEHILGECQEFHEAVLQGKTVQEVGSEAGDVLTLVLIL
CFLLEREGVLASEDVANEAMEKLRRRAPYIFAEDYKPVSIIEADRLWELAKHREKNEST

>core/901/3/Org3_Gene982

MDYKSQLVFSCPCCCKGNVCFVFNLDVILTCNVCSSTYTFDSVIRNEIRQFVALCKRIHDANSILGNATVSVS
VEDNQMDIPFQLLFSRFPVVLNLSLDGKKIAIRFLFDALNTSILHQESDLIS

>core/902/3/Org3_Gene306

MREEGSVSFREYFRAYMCDKIVAQKNFLFTLDAVIKQAGWRSQEKLNLFFYVESQALGREIKVSLEEYIQSMV
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>core/903/3/Org3_Gene44

MTTESLETLVEKLSNLTVLELSQLKKLLEEKWDVTASAPVVAAGGGGEAPVAAEPTEFAVTLEDVPADK
KIGVLKVVREVTGLALKEAKEMTEGLPKTVKEKTSKSDAEDTVKKLQDAGAKASFKGL

>core/904/3/Org3_Gene950

MKFTVALFGAEKGSYDTAYFCRSLVDLHNYLGDVSSPGITLAIKTLTLLSDYNVVYFRVREEGYCVDSYFFGL
HFLNTQATLKNIIAIGLPGVGNQHIIEASRSLCQKHNSLLLFFDHDLYDLLTFNQPF

>core/905/3/Org3_Gene99

MRAGGSLVTTYPKQGRLRSPEQLRVLDDL VQSYPNHLHAIELDCGAIPQDLIGATYIITFADFSTYILSLRSY
QANSPSDDTWGIWFGSIDDPVQAVISFLKDHGFALPSTLAQDPLLCTNK

>core/906/3/Org3_Gene894

MLIGRYSSDDQFTEATKNTPTIIKLG FARDNLEGLTNPISIVSETSSSIKDSVLRSLPILGSILGCARLYSTLSTN
DPLDETQEKIWHITIFGALETGLGLILLFKIIFVILHCIFHLVIGFCK

>core/908/3/Org3_Gene356

MPLSDDEIEQFKKRLLMKAKLSHTLEGNAQEVKKPNEATGYSQHQADQGTDTFDRTISLEVTTKEYELLRQ
INRALEKINESSYGICDVS GEEIPLARLIAIPYATMTVKAQEQFEKGLLSGN

>core/909/3/Org3_Gene930

MESSLCKKSLMKRRRALRVKVLKGSPTKPRLSVVKTNKHIYVQLIDDSIGKTLASVSTLSKLNKSQGLTKK
NQEVAKVLGTQIAELGKNLQLDRVVFDRGTFKYHGIVSMVADGAREGGLQF

>core/910/3/Org3_Gene369

MPTINQLIRKRRKSSLARKKSPALQKCPQKRGVCLQVKTTPKKPNSALRKVAWVRLSNGQEVIAIYGGEH
NLQEHSIVLIQGGRVKDLPGVRYHIVRGTLDCAAVKNRKQSRSTRYGAKRPK

>core/911/3/Org3_Gene627

MALKDTAKKMKDLLDSIQHDLAKAEKGNKAAAQVRVTDSEKLEKVAKLYRKESIKAESGLLKRKPSTKAP
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>core/912/3/Org3_Gene577

MKRQKRKQSITLIEMMVVITLIGIIGGALAFNMRGSIHKGKVFQSEQNCAKVYDILMMEYATGGSSLKEIIAH
KETVVEEASWCKEGRKLLKDAWGEDLIVQLNDKGDDLVIKSRVQSSNKK

>core/913/3/Org3_Gene607

MRDRLGSLSLILKVKIHKYLDTLHNQKRLALTVSRNIQATNKRIADLHLERYEHFISRDNIKHYDILLEYLKTL
QSSLYKQQSESLRFLEIHHQQLQELINRRKIIEKIKNNKYSKDQEIGT

>core/914/3/Org3_Gene430

MPRIIGIDIPAKKKLKISLTYIYGIGSARSDEIHKKLKDPEARASELTEEEVGRLNSLLQSEYTVEGDLRRRVQS
DIKRLIAIHSYRGQRHRLSLPVRGQRTKTNSRTRKGKRKTVAGKKK

>core/915/3/Org3_Gene931

MIQQESQLKVADNTGAKKVKCFKVLGGSRRRYATVGDVIVCSVRDVEPNSSIKKGDVIKAEIVRTRRHITRK
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>core/917/3/Org3_Gene206

MEIIHIGTDIIEISRIREAIATHGNRLNLRIFTEAEQKYCLEKTDPIPSFAGRFAGKEAVAKALGTGIGSVVAWKD
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>core/918/3/Org3_Gene70

MVNLLKELEQEQCRNDLPEFHVGDTIRLATKISEGGKERVQVFQGTVMARRGGGSGETVSLHRVAYGEGME
KSFLNNSPRIVSIEIVKRGKVARARLYYLRGKTGKAAKVKEFVGPRSSKK

>core/919/3/Org3_Gene697

MVRATGSVASRRRRKRILKQAKGFWGDRKGHIRQSRSSVMRAMAFNYMHRKDRKGDFRSLWIARLNVASR
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>core/920/3/Org3_Gene138

MRELNAFELTQPEEYRNRWVLMPCCLKRFCRTQHAKVWSYRCVHEASLYEKNCFLLTYDDKHLPQYGSL
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>core/921/3/Org3_Gene203

MATVAQTPQTTQPQPSVSHKATHRYCSWVFFKPILVSLGLLLASLTTLGLVIASGVTLISLGIGIVLAIQIVLAGI
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>core/922/3/Org3_Gene210

MTENRRIKRVNALLQEAIKVKDKVHPKISNLWITVTRVSLSKDLHSARVYVSVMPHENTKEEAEALKV
SAGFIAHRASKNVVLKYFPELHFYLDIFSPQDYIENLLWQIQEKEKS

>core/923/3/Org3_Gene571

MNKKPKKTKKAVQSKAAPVKRVPEESQEAAIQQLELAVSDLYKELPLAQTFASLTDKNQINSIIAALSGTLES
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>core/924/3/Org3_Gene359

MDNYLLGSLIFCCVLLSIGMCTIFVMTICFLRQLNKILKNIHRVTTILNFEAKILAPLMLGKKLLCGWLKKRKN
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>core/925/3/Org3_Gene643

MDSFCFDLLKVAAKAIDDKKGNNLVVLDVRTISEFTDYFVFVEGSVNVHVKALANTIVEELKKQKVSPLHVE
GITDGNWVVIDYGFIVVHVVFVSEIRGKYRLEELWKDGFIVTSKLLAS

>core/926/3/Org3_Gene247

MPVSSAPLPTSHRPSSGNLGLMEPNKALKAKHQDKTTKTIKLLVKILVAILVIEVLGIIAAFFIPGTPPICLIILG
GLILTTVLCVLLLVIKLALVNKTEGTAEQQIKRKLSSKXIS

>core/927/3/Org3_Gene68

MALKIRLRQQGRRNHVYRLVLADVESPRDGKYIELLGWYDPHSSINYQLKSERIFYWLERGAQLSSKAEAL
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>core/928/3/Org3_Gene994

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>core/929/3/Org3_Gene626

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>core/930/3/Org3_Gene338

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>core/932/3/Org3_Gene177

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>core/933/3/Org3_Gene264

MSKVSVRKKNWGFRLLEEVMIKSWWVIFSILIGGFVYDRAIQELRTEELRLQSKVSSLCQDILSAQEKQRQLQ
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>core/934/3/Org3_Gene296

MWYS DYHVWILPVHERV VRLGLTEKMQKNLGAILHVDLPSVGS LCKEGEVLVILESSKSAIEVLSPVSGEVID
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>core/936/3/Org3_Gene672

MGKKENQLYEGAYVFSVTLSEEARRKALDKVISGITNYGGEIHKIHDQGRKKLAYTIRGAREGYYYFIYFSVS
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>core/937/3/Org3_Gene640

MTAVLILTSFPSEESARSLARHLITERLASCVHVFPKGTSTYLWEGKLCES EHHIQKSIDIRFSEICLAIQEFSG
YEVPEVLLFPIENGDPRYLNWL TILSYPEKPPLSD

>core/938/3/Org3_Gene441

MFKATARYIRVQPRKARLAAGLMRNLSVQEAEQ LGFSQLKAGRCLKKVLNSAVANAELHENIKRENLSVT
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>core/939/3/Org3_Gene437

MKKQNIRVGDKVFILAGNDKGKEGKVLSLTEDKV VVEGVNVRIKNIKRSQQNPKGKRISIEAPIHISNVRLTIA
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>core/940/3/Org3_Gene294

MTTLPKYVPRSRQNPDTLTFLKRYSSVLLHSENSLSYRIFAKVLAILLTSLAVAFVTLFSCEGSQ LRLCALYI
GIALAICVLLTIVVYCIASKIATACKKPPSISR IEIV

>core/943/3/Org3_Gene443

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>core/945/3/Org3_Gene323

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>core/946/3/Org3_Gene963

MNLSAKEYGDIIVIYLQGS LDAVSVPSVQEYLEQFIQKKHLKIALNVTDVSYISSAGIRLLLLSNFKLVQSLGGK
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>core/947/3/Org3_Gene346

MASSATPGFDGTAPSLFPPATRP RYNFKLALFVTIAIALVWIALIATTIAIGLCIHPLCSFIFLTAIPLYFISRYICS
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>core/948/3/Org3_Gene65

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>core/949/3/Org3_Gene21

MNEPTRTYLESEKDTQDQIEELQATCIVKNAAGIHVRPAGVIVRLFDGEPCDVHFTYAGKTINAKSIMSILML
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>core/950/3/Org3_Gene792

MSTSPIGVPSMLNAATSLNATTSKAPLPTSTLAERIKEWLPRILLIVGAIFTIAGCIVMALTKQILYGLLCVVG
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>core/952/3/Org3_Gene408

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>core/954/3/Org3_Gene365

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>core/955/3/Org3_Gene506

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>core/956/3/Org3_Gene396

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>core/957/3/Org3_Gene368

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>core/958/3/Org3_Gene248

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>core/959/3/Org3_Gene403

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>core/961/3/Org3_Gene456

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>core/962/3/Org3_Gene80

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>core/963/3/Org3_Gene295

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>core/964/3/Org3_Gene661

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>core/965/3/Org3_Gene2

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>core/967/3/Org3_Gene360

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>core/968/3/Org3_Gene281

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>core/969/3/Org3_Gene529

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>core/970/3/Org3_Gene721

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>core/971/3/Org3_Gene505

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>core/972/3/Org3_Gene818

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>core/974/3/Org3_Gene540

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>core/975/3/Org3_Gene223

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>core/976/3/Org3_Gene73

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>core/977/3/Org3_Gene371

MYEGKSRMASPTPGQLHLQQKVESKAYDYSRSLAMIATALLFFIVALILSGLSLLPQVFLPFSGAYFIIGSFLAF
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>core/978/3/Org3_Gene22

MGSGYAKKKKEAKIMEQQFLEMEASLLEKRYEGQAGNGLVSVVINGKCDLISVKVQPTCLDPEDPEVIEDLF
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>core/979/3/Org3_Gene283

MNKS RFLRLCCCLCFGSLFYFYINKQNSLTKLRLEIPCLSVRLRQLEQQNISLRFLIDKIERPDHLMEIAALPE
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>core/980/3/Org3_Gene581

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>core/982/3/Org3_Gene414

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>core/983/3/Org3_Gene1

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>core/988/3/Org3_Gene241

MAKLVITSDDEQQEFELEDNSEIAEPCESMGIPFACTEGVCGTCVIEVLEGRENLSEFTEPEYDFLGEPEDSNER
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>core/989/3/Org3_Gene327

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>core/990/3/Org3_Gene374

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>core/991/3/Org3_Gene705

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>core/992/3/Org3_Gene218

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>core/993/3/Org3_Gene758

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>core/994/3/Org3_Gene111

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>core/996/3/Org3_Gene391

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>core/997/3/Org3_Gene666

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>core/998/3/Org3_Gene438

MASEPRGSRKVKIGVVVS AKMEKTVVVRVERIFSH PQYLKVVRSSKKYYAHTELKVSEGDKVKIQETRPLSK
LKRWRVIEHVG VVS

>core/999/3/Org3_Gene978

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>core/1001/3/Org3_Gene364

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>core/1005/3/Org3_Gene673

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>core/1014/3/Org3_Gene547

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>core/1016/3/Org3_Gene849

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>core/1018/3/Org3_Gene511

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>core/1019/3/Org3_Gene829

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>core/1023/3/Org3_Gene991

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>core/1025/3/Org3_Gene439

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>core/1028/3/Org3_Gene460

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>core/1031/3/Org3_Gene761

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>core/1033/3/Org3_Gene696

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>core/1034/3/Org3_Gene321

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>core/1037/3/Org3_Gene375

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>core/1045/3/Org3_Gene678

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>core/1046/3/Org3_Gene469

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>core/1049/3/Org3_Gene989

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>core/1050/3/Org3_Gene16

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>core/1054/3/Org3_Gene267

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>core/1056/3/Org3_Gene985

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>core/1058/3/Org3_Gene335

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>core/1067/3/Org3_Gene723

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>core/1068/3/Org3_Gene990

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>core/1070/3/Org3_Gene659

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>core/2/4/Org4_Gene773

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QRMELDFSTNVWGSGLGVEDCQNIGEFDGFKHHLTGYSGLD TQLVEDFLIGGCFSQFFGKTESQSYKAKN
DVKSYMGAAYAGILAGPWLIKGA FVYGNINNDLTTDYGTLGISTG SWIGKGFIAGTSIDYRYIVNPRRFISAIV
STVVPFVEAEYVRIDLPEISEQGKEVRTFQKTRFENVAIPFGFALEHAYS RGSRAEVNSVQLAYVFDVYRKR P
VSLITLKDAAYSWSKSYGVDIPCKAWKARLSNNT E WNSYLS TYLAFNYEWREDLIA YDFNGGIRIIF

>core/3/4/Org4_Gene620

MASSSNNSTKQDGIPSWVNPVQWNRASQVGDQEAKSLTPEAQTSSRSWFSRKHFLFVLDVSLEEMENNDL
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LSQYPDLRKSTLYKYSITHVKPKKGFVVKLVENLRPDLHKNKDDGGAAADSRLDFAGYGVKHYQTDALLG
VSGVNSVEWQRLASLIMSVKNDILNDVGSREPIDKAQRSALVVS GDKDIGGEIQPGGILDISRDILAICGYGMNV
GVEAKKAIDQYKKWYLNSSTFIAWNPQLPAIAQSYLLEQQQHLDYAAKIFQDLSALTAYGTGQALEDLDSL
LCYYDQLIESKGVGEKIIASIHQKHLDLAMQDSCDQEHLKKWSNLYHVFSLTIKEFTEGKLEQNEVVSRIQRL
RGKLEKSKCSILGNCRNTAEYATKSEKKLADYLLQIGDREPFLTGMHKAIAATGKAIQKGVEGVISQHPKQIM
MLRCSIERLEGMLRREDWGAILQKNEDEV LALKSTMEAQLQGFKDLVGAWEGKYQEFKKNKLSKVLVYDF
TKSYSNLLNRLEVLHAESSTDDLVLHVDRMSED LKKTIEEIDGNLFQVTPEELSLAREYQGLMNELPLIVQE
GNRLQEVISSEGVVSQGLMMLNSLLNRDEKINKNIESSRKNLVAIAKQARSDARNIDSQGLAPLIQRNRASLDNI
LQNMHLFNGSIRNIHALDTETLVATSSNMFSAMHTFDWNIYTNLLDVLEIQSKPAPAPMENPDLPGALPEEVQ
DAVAEDVSGTHRLHHQVLKRRCADLKNMISQLQKSINKWGMAKAIVLGIVAVLFCVLSTIFIGQNILSLLILS
CVGLLLTQVCPLIFDRISKSKEFEKQVLETAQSLIPATKILPSEFNKDLNRLAKLQDNLNLEGFGPTWARNIV
SDLEGIPTKEKSLKDLTKEFRKDSKNLNKRIKRRFKEGLGQEAPVVRPTIPQDIRGAEVFAELHRELEHLQKQ
KEEISIRGDALVQERMGLCLEKSKYDNEKAHAAAMTKKVVKLQNI DRLQKNNETYVRIQNFFRTLIQEKLGR
DTVQEIDVVKEAKELHELAAIIYGNTSGKSQKQRAKKQFKENVLHIAGKGQLELLEAYLNV TASQGLCRHQ
MQASFRERILLNPDGAKHGEAERTLASREEM LKTLGLSYLTPFVRFSSPESTQSGYNQILKVREQLFDIEQRLQ
NQETVSPEDYAAVQAALAAAYVRKHESLIVSTYGLGAQEGQTSSKVTTLMRDLHAVEELVEMGVETYRLNRS
DQILHRVHSLVHSHLRDSNSSGNGIIDVVKKLFELLNNGNPNPSDPECQKYMQILLDAPVSLLYGAFKSFKNE
FLLNFTELNIANSTKAAEEEEAKRYVEEKGRGFETYWEEAKQRLEAIAAELDDLKNQETLLEQEIRLANLKISIF
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LGLLGREEAA

>core/4/4/Org4_Gene449

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NTATDKGGAIYSKEKDSTLDANTGVVTFKSNTAKTGGAWSSDDNLALTSNTQVLFQENKTTGSAGQANNPE
GCGGAICCYLATATDKTGLAISQNQEMSFTSNTATANGGAIYATKCTLDGNTTLTFDQNTATAGCGGAIYTE
TEDFALTGSTGTVTFSTNTAKTGGALYSKGNSSLTGNTNLLFSGNKATDSASSPANQDGC GGAILAFIDSGSV
SDKTGLSIANNQEVSLTSNTATVSGGAIYATKCILTGNGSLTFDGNTAGTSGGAIYTETEDFTLTGSTGTVTFN
ANTAKTGGALYSKGNNSLSGNTNLI FSGNKSTDSSGSSANQDGC GGAILSFLSASASAKKGLVIEDNENVSL
SGNTATVSGGAIYATKCALHGNTTLTFDGNTAGTSGGAIYTEDQDFTLTGSTGTVTFSTNTAKTAGALHTKG
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SGSESINFDGNTAETSGGAIYSKNLSITANGPV SFTNNSGGKGGAIIYIADRGELSLEAIDGDITFSGNRATEGTS
TPNSIHLGAGAKITKLAAAPGHTIYFYDPITMEAPASGGTIEELVINPVVKAIVPPPQPKNGPIASVPVVPVAPA
NPNTGTIVFSSGKLSSQDASIPANTTTILNQKINLAGGNVVLKEGATLQVYSFTQQPDSTV FMDAGTTLETTTT
NNTDGSIDLKNLSVNLDALDGKRMITIAVNSTSGGLKISGDLKFHNNEGSFYDN PGLKANLNL PFLDLSSTSG
TVNLDDFNPISSMAAPDYGYQGSWTLVPKVGAGGKVTLVAEWQALGYTPKPELRATLVPNSLWNA YVNI

HSIQQEIATAMSDAPSHPGIWIGGIGNAFHQDKQKENAGFRLISGGYIVGGSMTPQEYTFAVAFAFSQLFGKSK
DYVVSDIKSQVYAGSLYAQSSYVIPLHSSLRHVLSKVLPELPGETPLVLHGQVSYGRNHHNMTTKLANNTQ
GKSDWDSHSFAVEVGGSLPVDLNYRYLTSYSPYVKLQVVSVNQKGFQEVAAADPRIFDASHLVNVSIPMGLTF
KHESAKLPSALLLTGYAVDAYRDHPHCLTSLTNGTSWSTFATNLSRQAFFAEASGHLKLLHGLDCFASGSC
ELRSSRSYNANCGTRYSF

>core/5/4/Org4_Gene372

MKQKVKRNFIIICVFALALYYVLPTCLYYAKPLDKKIDGNEAEHIIKSFTKQAQQVRKDVIPRVSAISSLHL
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FVSYSFENEQEIASSILQRVYSACTFPKQKDCSCSYPSIWETAPKEQLLQYTKNLSSGFEVFSSRLSAFCQQSFS
SNQDRLTFLSRLSSLSNDAAIDVEDQKLLKSVYETLSQTACIRSLDCPYIEGLRLDCSESSLFFSSIEYCPKERKI
FLTLHSDLLAQRSLKEQRLDFDSRLAVAKQKLSKNLTVQVEDYNDGFSFQWMDKDTQGKIILQGERLLQ
GIAEHLTALTLHRPAAESCDLIPENFPVFCRQPRESEAFGCYIFSPNTDCKHFSKGSVYILLKGLRSIVAKYQQG
GGKELQSFEKDLQNLNCFSSHTEAISWTLGEDQVLEIRHPLQQFLDVWGEFVIGKEGCAFLEVKDIDKDLA
TVNQIEKNRQSDLVRWHEQYRHAKCSMDLQERLSAPIPYQNLFLENMMLNMRKFSRGENILRLGIDFVGGR
QLLLSFKDHQGKQLTDKEDILKVSELYARLNKLGVSEIELRREGDYIHLSVPGSSTISSSEILRTSKMSFHVV
NERFSSYSASRYEVQRFLDYLWFTSQAQGKTSPEEINTFASALFNKEVDVPPSVHEAITKLKSEGLAFSPSGCE
TPSTDLDTTFSMIAIGKDAEQKANPLVIVFRNYALDGASLKDIRPEFAAGEGYVLNFSVKDTSPKKMAEKLSP
TESFHTWTSAYCQEGISGTANGQYSANRGWRMAVVIDGYMVSSPILNVPLKNHASVSGKFTHREVSKLASD
LKSGAMSFVPEVLSEETISSDLGKKQCTQGIISACGLAMLIVLMSVYYRFGGVIAAGAVLLNLLLIWAALQY
LDAPLTLSGLAGIVLAMGMAVDANVLVFERIREEFLLSQSLKKSVEKGYTKAFGAIFDSNLTTVLASALLFFL
DTGPIKGFALTILGIFSSMFTALFMTKFFFMLWMNKTQHTQLHMMNKFVGIKHDFLGGCKKLWAVSGSVF
LLGCVALGFGAWNSVLGMDFKGGYAFTFNPKEHGISDVAQMRGKVVHKLQEAGLSSRDFRIQTFGSSEKIKI
YFSDKALSYTKADTSLSPKINDHELALAVGLLSETGLDFSTETLNETQNFWSKVSSKLSKKMRYQATIGLLGA
LAIILLYVSLRFEWQYAFSAVCALIHDLATCAVLFIHFFLKKIQIDLQAIGALMTVLGYSLNNTLIIFDRIRED
RQANLFTPMHVLVNDALQKTFSRTVMTTATTLVLLMLLFIGGSSVFNF AFIMTIGILLGTLSSLYIAPPLLLF
MVRKENRSK

>core/6/4/Org4_Gene663

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KLAKRLKIIIEGFVSSSNHPEWMVLKNIPVPPDLRPLVPLDGGRFATSDLNDLYRRVINRNNRLKAILRLKTPE
VIVRNEKRMLQEAVDALFDNGRHGHVPMGAGNRPLKSLSEMLKGKNGRFRQNLLGKRVDYSGRSVIIVGPE
LKFNQCGLPKEMALELFEPFIIKRLKDQGSVYTIRSAKKMIQRGAPEVWDVLEEIIKGHPVLLNRAPTLHRLGI
QAFEPVLIEGKAIRVHPLVCAAFNADFDGDQMAVHVPLSVEAQLEAKVLMMAPDNIFLPSSGKPVAIPSKDM
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SHILKDAYDKVAIVKKQYDDGIITEGERHSKTISIWTEVSEQLSDALYVEISKQTRSKHNPLFLMIDSGARGNK
SQLKQLGALRGLMAKPNGAIIESPITSNFREGLTVLEYSISSHGARKGLADTALKTADSGYLTRRLVDVAQDV
IITEKDCGTLNHIEISAICQGSEELLPLKDRIYGR TVAEDVYQPGDKSRLLAQSGDVLNSVQAE AIDDAGIETIKI

RSTLTCESPRGVCAKCYGLNLANGRLIGMGEAVGIIAAQSIGEPGTQLTMRTFHLGGIAATSSTPEIITNSDGIL
VYMDLRVVLGQEGHNLVLNKKGALHVVRDEGRTLNEYKKLLSTKSIESLEVFPVELGVKILVADGTPVSQG
QRIAEVELHNIPIICDKPGFIKYEDLVEGISTEKVVNKNNTGLVELIVKQHRGELHPQIAIYDDADLSELVGTYAI
PSGAISVEEGQRVDPGMLLARLPRGAIKTKDITGGLPRVAELVEARKPEDAADIAKIDGVVDFKGIQKNKRIL
VVCDEITGMEEEHLIPLTKHLIVQRGDSVIKGGQLTDGLVVPHEILEICGVRELQKYL VNEVQEVYRLQGVDI
NDKHIEIIVRQMLQKVRITDPGDTTLLFGEDVNKKEFYEENRRTEEDGGKPAQAVPVLLGITKASLGTESFISA
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>core/7/4/Org4_Gene664

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ALLVGRILADNIIDEASSLVYGKAGEKLSTAMLRMLDAGIASVKIAVDADENHPIIKMLAKDPTDSYEAALK
DFYRRLRPGEATLANARSTIMRLFFDPKRYNLGRVGRYKLNRLGFSMDDEALSQVTLRKEDVIGALKYLI
RLKMGDEKACVDDIDHLANRRVRSVGELIQNQCRSGLARMEKIVRERMNLFDFSSDTLTPGKVVSAGGLAS
VLKDFFGRSQLSQFMDQTNPVAELTHKRRLSALGPGGLNRERAGFEVRDVHASHYGRICPIETPEGPNIGLITS
LSSFAKINEFGFIETPYRIVRDGIVTDEIEYMTADVEEECVIAQASASLDEYNMFTEPVCWVRYAGEAFEADTS
TVTHMDVSPKQLVSVITGLIPFLEHDDANRALMGSNMQRQAVPLLKTEAPVVGTTGLECRAAKDSGAIVVAE
EDGVVDFVDGYKVVAACHNPTIKRTYHLKKFLRSNSGTCINQQPLCAVGDVITKGDVIADGPATDRGELA
LGKNVLVAFMPWYGYNFEDAIHSEKLIREDAYTSIYIEEFELTARDTKLGKEEITRDIPNVSDEVLANLGEDGII
RIGAEVKPGDILVGKITPKSETELAPEERLLRAIFGEKAADVKDASLTVPPGTEGVMDVKVFSRKDRLSKSD
DELVEEAVHLKDLQKGYKNQVATLTKTEYREKL GALLLNEKAPAAIIHRRTAEIVVHEGLLFQETIERIEQED
LVDLLMPNCEMYEVLKGLLSDYETALQRLEINYKTEVEHIREGDADLDHGVIRQVKVYVASKRKLQVGDK
MAGRHHGNGGVVSKIVPEADMPYLSNGETVQMILNPLGVPSRMNLGQVLETHLGAAKTAGIYVKTPVFEGF
PEQRIWDMMIEQGLPEDGKSFLYDGKTGERFDNKVVIGYIYMLKLSHLIADKIHARSIGPYSLVTQQPLGGKA
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LDVRPMVVDA

>core/8/4/Org4_Gene312

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LKSPEALLLELQWFQDLFKDDYFTEVQLHKMSEESIAGFKEEWLQGEYYSLEIKQIKVNTAVLEASKRLGIPT
VATNDIHYINANDWQAHEILLNVQSGETVRIAKQNTHIPNPKRKVYRSREYYFKSPAQMAELFKDIPEVISNT
LEVAKRCDFTFDFSKKHYPYVPESLKTLSYTEEDRYQASAVFLKQLAEALPKKYSSEVLAHIAKKFPHRD
PIDIVKERMDMEMAIIIPKGMCDYLLIVWDIIHWAKANGIPVGPGRGSGAGSVLLFLLGITEIEPIRFDLFFERFI
NPERLSYPDIDIDICMAGRERVINYAIERHKGDNVAQIITFGTMKAKMAVKDVGRTLDMALSKVNHIKHIPD
LNTTLSKALETDPDLHQLYINDAESAQVIDMALCLEGSIRNTGVHAAGVIICGDQLTNHIPICISKDSTMITTQY
SMKPVESVGMKLVDLLGLKTLTSINIAMS AIEKKTGQSLAMATLPLDDATTFSL LHQGKTMGIFQMESKGMQ
ELAKNLRPDLFEEIIMGALYRPGPMDMIPSFINRKHGKEIIEYDHPLMESILKETYGIMVYQE QVMQIAGALA
SYSLGEGDVLRRAMGKKDFQQMEQEREKFCKRACNNGIDPELATVIFDKMEKFAAYGFNKSHAAAYGLITY
TTAYLKANYPKEWLAALLTCDSDDIEKV GKLIREAQSMGIPILPPHINVSSNHFVATDEGIRFAMGAIKGIGHG

LIESIVEERDHHGPYESIRDFIQRSDLKKVSKKSIESLIDAGCFDCFDSNRDLLLASVEPLYEAIKDKKEAASG
VMTFFTLGAMDRKNEVPICLPKDIPTRSKKELLKKEKELLGIYLTEHPMDTVRDHLSRLSVVLSGEFENLPHG
SVVRTVFIIDKVTTKISSKAQKKFAVLRVSDGIDSYELPIWPDMYEEQQELLEEDRLIYAILVLDKRSDSLISC
RWMKDL SIVNENIIYECDQAFDRIKNQVQKMSFTMSTSGKETKTKGNKPNENGHTQALAPVTLSLDLNELRH
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>core/9/4/Org4_Gene860

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TIHASEEPTVFTNKTFLKSALYRAAKKFFFLNEEGAELTIGENSQGFP SDFSLQWQGLVFKAEILD FPTLEDIFP
KLELAHTSLKNVSHDISITNVTVC AEEAKVNFTLSPVIHKKDRENHPKTKIGSVEYVAKTHEMITGPKAIALPI
YAIPLLADKFKDQLLSLLCYDSLEYRLRYDIRLLRDASF SFSAYLVTPGDLDNGSLIYPNYCYSPTKGLMQVV
GMLSPKQAFIVKSEQVEDFLNERGH LIQEPGFQTFINERPEGHLYTNVTEQGVLLFHYDVGDPSSTEIRFGTWT
YYTNQGFFLEKKNDLPIQDGLIVEPQDIPAFIVKNDAA LRRLPNFFSSPPNLKDLLIEVHRQSRGKGLDLKPILV
GLGESRCRLFGVFLYREDIGFSLIPTPLQGLCSLPRVIPPENVPQFLTQY AQHERILFPDPQTRPPESYELVIQSIH
RPHPASPLHLQLELKTNLG SVPIGIALQGLKSKHTFLTQAGFLDLKQNL FQFLQQLSTQKC VIAENTVIANIT
DVFKLDALAPLSVTDDTIANPEDLQFFSQLKAACLPPIPNL FSSDHQLRPYQNSGLLWMWFLYNHRLSGLL
CDEMGLGKTHQATALLDIVFQSSQPSARPKFLIVCPTSVLPHWEHILSNHLP GVSIFSFGPNKPSSELPTADILL
TSYGTLRQNYDKFYKIAFTIVVFDEIHMAKNKSSQIHKILCRIDAQM KLGLTGTPIENNLLFEKGLLDIILPNYL
PSDALFKKLFTKRCSS EEEIIPSQDLLLKLTRPFILRRTKKLVLP ELPDKVESIIACSLSPDQEKLYMATLQRE
KSHIQKLETPEEPATNFLHIFALLNHLKQICDHPAVFFKDPDQYKNYESGK WNAFVKLLKESLNAGYKVVVF
SQYIHMIRIITLYLEEIGIKYASIQGKSLNRKEE IETFTTDPNCQVFVGSLLAAGTGINLTAGNVVIMYDRWWN
PAKENQALDRVHRIGQKNTVFIYKLITEDTLEERIH YLIEKKIRLLDKVIASQDSNILHMLNREDLLTILSYKDE
HGTSDSEESPVDTPVEDDTGVLPPEDS

>core/10/4/Org4_Gene849

MLNFRKLRRDFSANILQDGKELFEQGAVIDAKILSMNGETVCISAQIRGLYDNIYECEIEVDRSESDTVDSNCD
CSYNYDCQHIVALLFYLEQYFNEMVVA YARSADLET DHEINEEVKKELKETFVAAATKEEERKDREHQKEIL
REYVHAANALSANPFFLPLEYLEKDSAELAVLFVSVNEDTFAPANQPIEFQLVLR LPCRSPFYISNIRTFLEG
VLYQEPIVLNGRRFFFTMQSFNASDRKLIDLLIRYVRYPNHTTEEKLLKSAYLMPPALGVILAKMFEHQLADR
GGGSLGEKESFSGLFCGNLEEPLCWSLTPAKMKFNLDFFDMPYKALLMTPVILVDDDEVQPEQTMLLESDAP
GIIHHFVYHRFSPQIKRAHLRSFSRLRDIAIPEALFGSFRENALPVFQEYAEIANVHLLNSFVTLPYVDEVRAIC
DMSYLDGELEAKLHFLYGSLRVPAASLALQYQDVRAFISDEGILARNLVEERKM LEEVFSGFIYDERDGA FH
VKSEKKIVEFMTETIPANQHRITFNCPENLS DQFIYDETIFELSFREGSDINYYEADLKVHG LLKGVPLDLLWD
CISAKKRFLLELPKAGQQSKGTRRGKVN SGKLP CILVLDLEKIAPVVQIFNEIGFKVLDDL VQKCPLWSLTGISL
DQFEALPVNFSMSERLIEIQKQIRGEIEFDFQDVPQQIQATLSYQTEGVHWLERLRKMHLNGILADDMGLGK
TLQAIIAVTQSKLEKSGCSLIVCPTSLVYNWKEEFRKF NPEFRTLVIDGVPSQRRKQLTALADHDVAITSYNL
LQKDVELYKSFRFDYVVLDEAHHIKNRTTRNAKSVKMIQSDHRLILTGTPIENSLEELWSLFDFLMPGLSSY
DRFVGKYIRTGNMGNKADNMVALKKKVSPFILRRMKEDVLKDLPPVSEILYHCHLTESQKELYQSYAASA
KQELSRLVKQEGFERIHHV LATLTRLKQICCHPAIFAKDAPEPGDS AKYDMLMDLLSSSLVDSGHKTAVFSQY

TKMLGIIKKDLESRGIPFVYLDGSTKNRLDLVNQFNEDPSLLVFLISLKAGGTGLNLVGADTVIHYDMWWNP
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>core/12/4/Org4_Gene292

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GSVPYLVAANVSERTYK LKMLSKDW PGLHVEAVRRRHYPQESVASDILGYVGPISPQEYKRV TQELS QLRE
CVRAYEEGEDPKLPEGLASIDQVRALLES MESNAYS LNALVGKMGVEACWDSKLRGKIGKKPILVDRRGNFI
QEMEGAVPEAPGTKLQLTSLAELQAYADALLLEYEKTETFRSAKSLKKREKL PPLFPWIKGGAIHALDPNNGE
ILAMASSPRYRNND FVNAKVAEDSKAVRSSIYRWLENKEHIAEIYDRKVPLIRERNPLTGLCYEEILPLTFDC
FLDFLFPENSVIKLQLKRNSFVGQAIEVQNLVTRLLSLFPYEEGTCPCSAIFDAVFPNEEGHILIQEVISLQE QK
WIMECLNQHKADIEELKEGLDQVFNELPANYDKILYTDILRLIVDPERFSPVLPSEVHRLSLSEFTELQGRYVV
LRS AFSTILED AFIEVHF KSWRKSEFPQYLA AKRQEEALRKQRYPTPYVDYLEEEKTRQYKMFCQEHLDTFLA
YLFSKTPYKEGLEPYDILDLWINELDN GAHRALS WHEHYLFLKERVSHLSQHLPALFSTFREFNELQRPLLG
KYPISIVRNKRQTEQDLAASFYPVYGYGYLRPHAYGQAATLGSIFKLVSAYSVLSQRILWGHNEEPANPLVII
DKNSFGYRSSKPHVGF FKGDTPIPTFFRGGSLPGNDFMGRGFIDLVS ALEMSSNPYFSLLVGEGLGDPEDLAD
AASLFGFG EKTGLGLPGEYAGRVPHDLAYNRSGLYATAIGQHTLVVTP LQTAVMLASLVNGGVVYVPKLLL
GEWEGEHVSYLSSKKKRTIFMPDAVVEVLKTGMRNVIWGQYGTARAIQS QFPPQLLSRIIGKTSTAESIMRVG
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>core/13/4/Org4_Gene819

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LCKSLGYSQVMLTSEKGEFSCRGGIVDIFPLSSPEPFRIEFWGEKIISIRSYNPSDQLSTGKVSKISISPAYTEEAS
GGNYSHSLLDYFSTPPLYLFDNLEILED FADISGTLSSLPDRFFSIGTLYDRISTSNQVYFSETPFPNVKNLKEN
RVII EAFHRNIEASRQAIPILYPEQII QNDENPLLAFLQHLQEYMPPHGKPLKLAISTKTKSLKEARALAETVA
RGDVEIYEKTGNLTSSFALVNEAFAAISLSEFASTKVLRRQKQRTHFSVTTEE VFVPIGETVVHIHNGIGKFLG
IEKKPNHLNIETDYL VLEYADKARLYVPSNQAYLISRYVGTSDKAADLHHLNSSKWKRSDLTEKSLIVYAE
KLLQLEAQRSTTPAFVYPPHGESVIKFAETFPYEETPDQLKTIDQIYNDMMSPKLMDRLICGDAGFGKTEVIM
RAAVKAVCDGHRQVIVMVPTTILATQHYETFKERMAGLP IEI AVL SRFSQAKVQKLIYEQVASGQIDIIGTHK
LINKSLEFKNPGLLIIDEEQRFGVKVKDNLKERYPMIDCLTVSATPIPRTLHMSLSGARDLSVIAMPPLDRLPVS
TFVMEHNTETLTAALRHELLRGGQAYVIHNRIESIYTLAETIRNLIPEARIGVAHGQMGAEDLSNIFTKFKNQK
TNILVATALIENGIDIPNANTILIDHADKFGMADLYQMKGRVGRWNKKAYCYFLVPHLDRLSGPAAKRLAAL
NKQEYGGGMKIALHDLEIRGAGNILGTDQSGHIGTIGFNLYCKLLKKAVSALKKHTSPLLFNDDVKIEFPYNS
RIPDTYIETASMRIEFYQKIGNAESSEELTAIQEEMRDRFGPLPQEICWLFALAEVRLFALQHGISSIKGTANAL
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>core/14/4/Org4_Gene955

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PVKKPTPPPKAPPPVRVATPMPLRPSSQGYWQCLNRMVSMVLRRAPLPLPAMQIDPILGDFNPHFVASYPNRI

DNEPMCFQIEQFKKIAQNPDLPQQHRRLAQLSLEQALYLNDNYYLVNVPDGNCFYRAYAVGWLSALYEEES
SRNDIVFEQEATRLLDLPFAASSPANANLCAEMAELLQLCSTYCSFIDLYDGVILSQKHTATLIAFLRKLSAYA
IRQQAASSNEETARALFISDMQDDLLPSVLEFLAANRPYSELFQNLIDHSALPDMQSRDKLFLLEHLPALFL
TDAELQKMSPEDQQLRKQYEREIREAFAKLSRRIADSGWDTDRFNAIVKDHLPEAIRCQYSRFLATIENRRSG
DLPWSPALSFFAFLCTCPSVRFHKLCAIFYKSLEDIIIASAPPQRSIQEILQISNASLSYLNEDLDSSWQREVISSN
IMTILTTHESLTLESSMPQLETLHKRIANLLKNVISTSFETPPLSNQPDLLPNLVNKLVAIHSKHELKEHFNTV
CSARSLRLTRDEGSGLSQEQDLLYTQAVQLLFFILQHPQVNNRPETKDAVKELKMLLLPLQYAFKKVENEK
KFQKLLRSILGSLVLKPPARYPSTPSNKKETFCFKFSRHPEVMVLDPILEKNCMQFLRATFPNYQLETEAILL
EKEIESTFRNGWNVFLTRLNLFSGSKLGSPSSPTALSDQFSKSFLIFCFLNNYPKLLQKETPLAARLDAFQREAS
HRFTQVKDKLLLSLKYGFPLATATINQYSRARDQLICNLLKNTVTASDGFCRSGFRQSLIGYLHSLSSNELGDI
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LLPRNPRTEDQNSKPDSSNP

>core/15/4/Org4_Gene261

MKPFNIFDSNSSIQGKFFLEASAGTGKFTTIEQIVLRALIEGSLTHVEHALAITFTNASTNELKVRIKDNLAQTL
RELKAVLNSQPASLPTYLDINCNVKQIYMQVRNALATLDQMSLFTIHGFCNFVLEQYFPKTRLIHKNPALTHS
QLVLHHITNYLKQDLWKNVLFQEQLHLLAVRYNVTSKHTSSLVDKLLASYTQPISSYFSSRVERLEQISLWHQ
QIYNLSLEIPKQVFLDQLTAHISGFKKQPFFILDDLHHFVDLLYTSETHSSLSFFFKIAETFNFKHRLARYKPCA
AFTVLENMSWVERTLEFCNLDRIENTLLVDLQEYLKQNYTPWLSPDESVFALEKLLSSSEAQPVVQALREQY
QLVLIDEFQDQDQKQWSIFSINLFIKFTGSLFLIGDPKQSIYEWARNADLPTYLKAKSSSFEDKQLQLVNNYRS
TPKLMEAINQIFGKISPFLEIPGYLPIEYHALNPQSSETFENPPHAPIHFFFYETIKDQALWIFSEALRLQKEQKIP
LGNMVVLVSDSNQAFELISYATIPVSFSKNKSIFHLTETHILTALLEAILHPENYEKISKILFSSFLGLSLDEVTT
KKEDFTIYFQSLHSYILHHGLLATFYRVMTTQGNVLFSSPRGDLIFQEMEKLKCGYLDTISSYPYHQLLHLKNFS
ETGRWEEELAISSYSEDLETALKITTIHSSKGLLEYDIVFCPGIEKSKKNKSSSELLREMYVACTRAKKQLYLPST
QPPSLQRSSALTNYVKLEGTQSSAYDLAIHLHQEHPDLFSYSLPKDHGHATTVLNLPLLETFALKVTPPKTIFS
FSSTKFLDTHKDSQSIPYSKLPISKQQLPLGEKTGILHKILESIFSLQDTEYLMSTIMRFIKHHTHLEGFEETIL
KLLSKTFFSPLTFSSQTFSLSQVLPNKIFRETSFLFLENQELWQGVLDLFFEHEGKYYIIDWKTSFLGETNSEYSK
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YH

>core/16/4/Org4_Gene757

MVEVEEKHYTIVKRNGMFVPFNQDRIFQALEAAFRDTRSLETSSPLPKDLEESIAQITHKVVEVLAKISEGQ
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QINGMTPPATLSEINDLTRIVEDVLSLHGEGAINLEEIQDIVEKQLMVAGYYDVAKNYILYREARARARANK
DQDGQEEFVPQEETYVVQKEDGTTYLLRKTDLERFSWACKRFPKTTDSQLLADMAFMNLYSGIKEEEVTT
ACIMAARANIEREPDYAFIAAELLTSSLYEETLGCNSQDPNLSEIHKHFKKEYILNGEEYRLNPQLKDYDLDAL
SEVLDLSRDQQFSYMGVQNLVDRYFNLHEGRRLETAQIFWMRVSMGLALNEGEQKNFWAITFYNNLLSTFRY
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VIPFIKVANDTAIAVNQGGKRKGAMCVYLENWHLDYEDFLELRKNTGDERRRTHDINTASWIPDLFFKRLEK
KGMWTLFSPDDVPGLHEAYGLEFEKLYEYERKVESGEIRLYKKVEAEVLWRKMLSMLEYETGHPWITFKDP
SNIRSNQDHVGVVRCSNLCTEILLNCSESETAVCNLGSINLVEHIRNGKLDEEKLKETISIAIRILDNVIDLNFYP

TPEAKQANLTHRAVGLGVMGFQDVLVELNISYASQEAVEFSDECSEIIAYYAILASSLLAKERGTYASYSGSK
WDRGYLPLDTIELLKETRGEHNVLDVTSSKKDWTVPVRDTIQKYGMRNSQVMAIAPTATISNIIGVTQSIEMMY
KHLFVKSNSLSGFTIPNTYLIKKLKELGLWDAEMLDDLKYFDGSLLEIERIPNHLKKLFLTAFEIEPEWIIECTS
RRQKWIDMGVSLNLYLAEPDGKKLSNMYLMAWKKGLKTTYLRSQAATSVEKSFIDINKRGIQPRWMKNK
SASTSIVVERKTPVCSMEEGCESCQ

>core/17/4/Org4_Gene644

MTADEVGKNSFAKKEEQVLKFWKDNQIFEKSLQNRQGKTLYSFYDGPPFATGLPHYGHLLASTIKDVVGRY
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FSSTWKTMDASFMESVWWVFQSLYNQGLVYEGTKVVPFSTALGTPLSNFEASQNYKEVDDPSLVVRMPLQ
NDSASLLVWTTTPWTLPSNMAIAVGEALVYVRIQDKKSGEQWILSQGCVSRWFSNPEEFVILESFSGKDLVG
RTYEPPTFFQSKREEGAFRVIAASFVEESEGTVVHMAPAFGEGDFLVCKENHVPLVCPVDAHGSFTEEIPQ
YQGQYIKHADKEIIFLKKKEGRIFYHGTVKHRYPCWRTDTPLIYKAVNSWFVAVEKIKDKMLRANSSIHVW
PEHIQEFRFGKWLEGARDWAISRNRWGTPIPIWKSADGEILVVGSIREEELTGTQITDIHRHFIDDLNIVKD
GKPFHRIPYVFDWFDGAMPYAQNHYPFENQKETEEAFPADFIAEGLDQTRGWFYTLTVISAILFDRPAFRN
AIVNGIILAEDGNKMSKRLNNYPSPKYVLDTYGADALRLYLLHSVVVKAEDLRFSDKGIEGVKQILLPLTSV
LSFFNTYAELYGFDPKSQDIEPAYTEIDQWILSNLYSVVGKVRESMSQYHLNFAVEPFVTFIDDLTNWYIRRC
RRRFWEAENTPDRRAAFSTLYEVLTVFCKVIAPFVFLAEDIYQKLKLEKEPESVHLCDFPQVEMDKILPDLE
KRMHDIREIVGLGHSLRKEHKLKVRQPLANFYVVGSKDRLSLLKTFEGLIAEELNVKNVIFYEEAPSFIYTTV
KPNFRMLGKKVGSKMKEVQKALSELPNNAIDKLIQGETWVLTIDDREIALDGGDVVICRHTDPGYIARSSAL
FSVILDCQLTEPLIVEGIARELVNKINTMRRNQQLHVS DRIALRIKTTEAVHRAFLDYENYICEETLIIAYDFTQ
NSDFQGEDWDINGHATQIEITVSSIDS

>core/18/4/Org4_Gene262

MNATKHCRASFNSPRHLLAQLAEDITSTHQKPFTKRWILVANATTGHWIKNQLVHALSDHIFMGSTIFTASD
SIVKHLFLGSGCSQPNIPDYLTLPLINNILEEISKASKFENGREFLSPTYETTKKLAAAFKQFHTFSQRPTKNA
SHYQELFQILESHFSSYEEMFTTILNNRTQEEDCSLHIFGYAHLPKHLAEFFINLSTYFPVYFYCFSPCREYFGD
LLSDRAIDFFWNQLPDSPKNAWEHYVLSDRQALLANLAHKSQSSQNFFLDREIDYQEMFLPSKHDSSLGVIQ
NSILDLKPTSPQDFSQTKQTICIYRALNIPREVQEVFCKVTELLHRGVSPEEIFILSSHIESYKVHLNAIFNPHVPI
YFTDEVDPQAEDLRNKILLSSILQTQGDLYILQLLTHPQLQQPIDQNKVPYLIKLSLEWKGISSKDRASGQ
QMKALGDLILEEYPFHQEGGRVSQVEVWETTVPLIYFIQERINLYLSSSQHSYEDLFQNVFSCLEKIFVLSPEET
SFITTLRNSLFPTFATSSCSLLFFTDCLDFLLHFHKPSPLYDKPGPYIGSLSSLIPKGYVFILGANKTTSSDIFD
LLNRTTTHEELAFSSSTEDEENFHFLQILVSTKHELHISYISSAAQFNLPSPFLNHIKETLDLPVETLPTQPYLSAFF
KNKACLHASQEYNYSLAHAFYSSKALLPSLFIPNVKQVNLPQHLSLNEIIGIFSPLDLFLKTNYNLRISPEHL
KKQQKLFPKTHQIEDFWNECFVDKEHDLIPSISPHAEELFTYYREKTILLHNGLDKDPKHSPYTVTFSSSIFEER
PYHESYLFPPSLSFQGNPVQIHGTIHGVCNEGLYLC SIDPRDSLKKTTRTLGSLPETSSEQKQLLERYVALAV
LQMSQHLSSDSALIKLTSFNTKENHHPPFSDEGYLRKVLEVYHLMSSQPIPLLSPLCWKTLDDDEEKFHQAVL
SAISEEAKNPSLPFWQFHNRIEETLNHVGASERLKILSLFRGPCEAV

>core/19/4/Org4_Gene786

MSEHPLTLQSMIATILRFWSEQGCVIHQGYDLEVAGAGTFNPATFLRALGPEPYKAAYVEPSRRPQDGRYGMH
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TYFQAIGSKPLDTISGEITYGIERIAMYLQKKTSIYDVLWNDTLTYGQITQASEKAWSEYNFDYANTEMWFKH
FEDFAEEALRTLKNGLSVPAYDFVIKASHAFNILDARGTISVTERTRYIARIRQLARLVADSYVEWRASLNYPL
LSLSSTSEPKETSESVVPMISSTEDLLEIGSEELPATFVPIGIQQLESLARQVLT DHNIVYEGLEVLGSPRRLAL
LVKNIAPEVVQKA FEKKGPMLTSLFSPNGDVSPQGQQFFASQGV DISHYQDLSR HASLAIRTVNGSEYL FLLH
PEVRLRTADILMQELPLLIQRMKFPKKMVWDNSGVEYARPIRWLVALYGEHILPITLGTIIASRNSFGHRQLDP
REISSPQD YVETLRQACVVVSQKERRMIEQGLRAHSSDTISA IPLPRLIEEATFLSEHPFVSCGQFSEQFCALP
KELLIAEMVNHQKYFP THETSSGAISNFFIVVCDNSPNDTIIEGNEKALTPRLTDGEFLFKQDLQTPLTTFIEKL
KSVTYFEALGSLYDKVERLKAHQRVFSTFSSLAASKDLDAIQYCKADLVSAVVNEFP ELQGIMGEYYLKHA
NLPTASAVAVGEHLRHITMGQKLSTIGTLLSLLDRLDNLACFILGLKPTSSHDPYALRRQSLEVLTLVSASRL
PIDLASLLDRLADHFPSTIEEKVWDKSKTIHEILEFIWGRLKTFMGSLEFRKDEIAAVLIDSATKNPIEILDTAEA
LQLLKEEHTEKLAVITTTNRLKKILSSLKLSMTSSPIEVLGDRESNFKQVLD AFPEFPKETS AHAFLEYFLSLA
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>core/20/4/Org4_Gene980

MYSCYSKGISHNYLLHPMSRLDIFVFDSLIANQDQNLLEEIFCSEDTVLFKAYRTTALQSPLAAKNLNIARKV
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NLIRHTLALNPQTILSTIHVRQAALTALFTYLRQDVGSCFATAPAILHQEYPERFLKDLNDLISSGKLSRIVNQ
REIAVPINLSGCIGELFKPLRILDLYPDPVVKLSSSPGLKKA FSAANLIETLGDSEA QIQQLLSHQYLMQKLQNV
HETLTANDIIKSTLLHYYQLQESTVRAIFFKEGLFSKEQVAFSTQHPRELSEIQRVYHYLHAYEEAKSAFIHDT
QNPLLKAWEYTLATLADASQPTISNHRLALGWKSEDPHSLVSLVTHFVEEEVENIRILVQQCEQTYHEARSQ
LEYIEGRMRNPLNNQDSQILTMDHMRFRQELNKALYEWDSAQEKAKKFLHLPEFLLSFYTKQIPLYRSSYD
AFIQEFAHLYADAPAGFRILFTHGRTHPNTWSP IYSINEFIRFLSEFFTSTESELLGKHAVINLEKETSRLVHNIT
AMLHTDVFQEALLTRILEAYQLPVPPSILNHL DQLSQTPWVYVSGGTVDTL LLDYFESSEPLTLTEKHPENPH
ELAAFYADALKDLPTGIKSYLEEGSHSLLSSSPTHVFSIIAGSPLFREAWDNDWYSYTWLRDVWVKQH QDFL
QDTILPQPSIYAFIENFCNKYALQHVVHDFHDFCSDHSLTPELYDKGSRFLSSLFTKDKTVALIYIRRLLYLM
VREV P YVSEQQLPEVL DNVSSYLGISSRITYEKFRSLIEETIPKMTLLSSADLRHIYKGLLMQSYQKIYTEEDM
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>core/21/4/Org4_Gene440

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TTANPAVTTVTTGASALQPTDSLTVENISQSIKFFGNLANFGSAISSSPTAVVKFINNTATMNF SHNFTSSGGG
VIYGGSSLLFENNSGCIIFTANSCVNSLKGLTPSSGTYALGSGGAICIPTGT FELKNNQGKCTFSYNGTPNDAG
AIYAETCNIIGNQGALVLD SNTAAKNNGGAICAKVLNIQGRGPIEFAKNRAEKGG AIFVGPSVGDP AKKTSTLTI
LASEGDITFQGNMLNTKPGIRNAITVEAGGEIVSLSAQGGSR LVFYDPITHSLPTTSPSNKDITINANGASGSVV
FTSQGLSSTELL LPANTTTTLLGTVKIASGELKITDN AVVNVLGFATQNSGQLTLGSGGTLGLATTSGTPAAV
NFTIGKLA FDFPFSFLKRDFVSASVNAGTKDITLTGALVLDEHDVTDLYDMVSLQSPVAIPIAVFKGANVTKTG
FPDGEIATPSHYGYQGKWSYTW SRPLLIPAPDGGFP GGLSPSANTLYAVWNSDTLMRSTYILDPERYGEIVSN

SLWISFLGNQAFSDILQDVLLIDHPGLSITAKALGAYVEHTPRQGHEGFSGRYGGYQAALSMNYTDHTTLGLS
FGQLYGKTNANPYDSRCSEQMYLLSFFGRFPIVTQKSEAFISWEAAYGYSKNHLNTTYLRPDKAPKSQGQW
HNNSYYVLISAEHPFLNWCLLTRPLAQAWDLSGFISAEFLGGWQSKFTETGDLQRSFSRKGKGYNVSLPIGCSS
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>core/22/4/Org4_Gene760

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NSENQLCYTGVVFNEMKGAMMSGEARLSEALNAAIFPSVTYGVNSGGEPREIVTLSHEDVRAFHQSQYSINR
CLFYFYGNIKPSRHLDLFLEEKLLRQATKLEKQAVSVPLQKRKFKEPVRNILTYPVDHQEEDKVLFGISWLTCSIL
EQQELLALHVLEIILMGTDASPLKSRLKSGFCKQTEMSIENDIREIPMTLVCKGCGSPAGAQLKLEALIFASLEEI
REGISENIVEGAVHQLELSRKEITGYSLPYGLSLFFRSGLLKQHGGSAEDGLRIHSLFSELRNSLKNSDYLAKLI
RKYFLDNPHFARVILLPDTELVAKENKDEQQLLLSVSEKLTDENKEKIQQNVRELTESQEQLKEDLNGILPNLA
LDKVPTSGKEFPLIKEGLSQGEVLHHECFTNDIVFIDVVDIPPLSGEELPWLRLLVFLMLQLGCGGRSYKEHL
EFLLEHTGGVDVSYDFSPHANKNSFLSPSVSIRGKALSSKSEKLCGIISDMLTSVDFTDIPRIRELLMQHNEALT
NSVRNSPMSYAVSMACSGNSITGAMSYLTTGLPYVKKIRELTKNFDQNIDEAVVILQRLYTKCFSGKRQIVIS
GSAHNYQQLKYNKFYGLLDYLIVPEPWFENPSINLYVTSQGLHIPARAAFNALAFPIGDIAYDHPDAAALTV
AEILDNVVLHTKIREQGGAYGSGAAANLSRGSFYCYSYRDPEIATTYKTFLKGVSEIASGNFTKEDIYEGALG
VIQGLDMPVAPGSRASVAFYRLKSGRIPVLRQAFRRSVLEVTKHEICMVMKYLESTVQETTLISFAGEEMLR
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>core/23/4/Org4_Gene441

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YATTPMLFTNNDLSILFQYNRSAGFGAAIRGTSITIENTTKSLLFNGNGSISNGGALTGSAAINLINNSAPVIFSTN
ATGIYGGAIYLTGGSMILTSGNLGVSFVNNSARSGGAIYANGNVTFSNNSDLTFQNNTAS PQNSLPAPT PPPT
PPAVTPLLGYGGAI FCTPPATPPPTGVSLTISGENTVTFLENIASEQGGALYGKKISIDSNKSTIFLGNTAGKGG
AIAIPESGELSLSANQGDILFNKNLSITSGASTRNSIHFGKDAKFATLGATQGYTLYFYDPITSDDL SAASAAAT
VVVNP KASADGAYSGTIVFSGETLTATEAATPANATSTLNQKLELEGGTLALRNGATLNVHSFTQDERSVVI
MDAGTTLAT TNGAANNTDGAITLNNLVINLDSL DGTAAVNVQSTNGALSISGTLGLVKNSQDCCDNHG
MFNKDLQQVPILELNATSTTVTTTDFSVGTNGYQQSPYGYQGTWEFTIDTTNHKVTGDWKKTG YIPHPERLA
PLIPNSLWANVIDLRAVSQASAAGGEDIPGKQLSITGITNFFHANHTNDARSYRHMGGGYLINTYTRITPDAA
LSLGFGQLFTKSKDYLVGHGHSNVYFATVYSNITKSLFGSSRFFSGGTSRV TYSRNEKVKTSYTKLPKGRCS
WSNNCWLGELEGNLPITLSSRILNLKQIIPFVKA EVAYATHGGIQENTPEGRIFGHGHLLNVAVPVGVRF DKN
SHNRPDFYTIIVAYAPDVYRHNPNCDTTL PINGATWTSIGNNLTRSTLLVQASSHTSVNDVLEIFGHGCGDIRR
TSRQYTL DIGSKLRF

>core/24/4/Org4_Gene183

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TVNDYLAQRDCEWVGSVLRWLGLTTGVLVSGTLLEKRKKIYQCDVVYGTASEFGFDYLRDNSIATRLEEQV
GRGYYFAIIDEVDSILIDEARTPLIISGPGEKHNPVYFELKEKVASLVYLQKELCSRIALEARRGLDSFLDVDILP
KDKKVLEGISEFCRSLWLVS KGMP LNRVLRVREHPDLRAMIDKWDVYYHAEQNKEESLERLSELYIIVDEH
NNDFELTDKGMQQWVEYAGGSTEEFVMMDMGHEYALIENDETLPADKINKKIAISEEDTLRKARAHGLRQ
LLRAQLLMERDVDYIVRDDQIVIIDEHTGRPQPGRRFSEGLHQAIEAKEHV TIRKESQTLATVTLQNFFRLYEK
LAGMTGTAITESREFKEIYNLYVLQVPTFKPCLRIDHNDEFYMTEREKYHAIVNEIATIHGKGNPILVGTESVE
VSEKLSRILRQNRIEHTVLNAKNHAQEA EIIAGAGKLGAVTVATNMAGRGTDIKLDNEAVIVGGLHVIGTTR
HQSRRIDRQLRGRCARLGDPGA AKFFLSFEDRLMRLFASPKLNTLIRHFRPPEGEAMSDPMPFNRLIETAQKRV
EGRNYTIRKHTLEYDDVMNKQRQAIYAFRHDVLHAESVFDLAKEILCHVSLMVASLVMSDRQFKGWTLPNL
EEWITSSFPIALNIEELRQLKDTDSIAEKIAAELIQEFQVRFDHMVEGLSKAGGEELDASAICRDVVRSVMVMH
IDEQWRIHLVDMDLLRSEVGLRTVGQKDPLLEFKHESFLLFESLIRDITIRHLFRLELTVEPNPRVNNVIPT
VATSFHNNVNYGPLELTVVTDSEDQD

>core/26/4/Org4_Gene437

MRPICLSILSTALCCSLSGNEVPNLASCQMSRKDISAFHTSPSFRLNVTPEPLVSSFRPSNLLNGFGHDITQDITI
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TTTSGFGGALHALDGYITNNLGEGKFLDNVSKNRGGAIYVGVSLSITDNLGPIVIKKNQTLEDSSFGGGIFGRA
INIEGNYQNIQINDNASGQGGGIFSALGISISSNKEIIEISNNSASSVNTASGKLYPGGGGIMCTSLIVENNPGLI
FNNNTAALSGGAIHTRSFIQNGGPTAFINNSATSGGALINLSGIGSTPQNFFLSADYGDILFNNNTITSSSPQPG
YRNALYAAPGINLKLGARQGYKILFYDPIDHDQTTTDPIVFNYPHHLGTVLFSGINVDSNATNPLNFLSKLSN
SSRLERGVLAIEDRAAISCKTLSQTGGTLRLGNAALIRTKGPGSSINFNAVAINLPSILQSEASAPKFWIYPTLTG
SAYSEDTSSTITLSGPLTFLNDENENPYDSL DLSEPRKDIPLLYLLDVTAKKIDTSNLIVEAMNLDEHYGYQGI
WSPYWMETTTTTTSSSTVPEQTNTNHRQLYVDWTP LGYRPNPERQGEFVANTLWQSAYNALLGIDTLSPQNLT
EHSLEASLQGLGLLINQH NREGRKGFRNHTTGYAATTSAKTTASHKFSLGFAQMFSKTRERQSHNKISSHNY
FAGLRFD SLLFKDFLSTALSIAYSYGDHHLHCHYTKTLKGSSEAFFNNHTLAASLDCTFLSARITRTLQLQPMFI
KAIALHSSHASFQETGSHARKFNTEHPLIDLSSPIGFRSEWKTSHQAMLWTTEISYIPTLYRK NPELLTTLIVSN
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>core/27/4/Org4_Gene390

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VLCQNNISYGP GGALLLQGRKSKALFFRDNRGTILFLKNKAVNQDESHPGYGGAVSSISPGSPITFADNQEILF
QENEGELGGAIYNDQGAITFENNFQTTSFFSNKASFGGAVYSRYCNLYSQWGDTLFTKNAAVKVGGAIHAD
YVHIRDCKGSIVFEENSATAGGAIAVNAVCDINAQGPVRFINNSALGLNGGAIYMQATGSILRLHANQGDI EF
CGNKVRSQFHSHINSTSNFTNNAITIQGAPREFSLSANEGHRICFYDPIISATENYNSLYINHQRLL EAGGAVIFS
GARLSPEHKKENKNKTSIINQPVR LSCGVLSIEGGAILAVRSFYQEGGLLALGPGSKLTTQGKNSEKDKIVITN
LGFNLNL DSSDPAEIRATEKASIEISGVPRVYGHTE SFYENHEYASKPYTTSIILSAKKLV TAPSRPEKDIQNLI
AESEYMGYGYQGSWEFSWSPNDTKEKKTIASWTP TGEFSLDPKHRGSFIPTTLWSTFSGLN IASNIVNNNYL
NNSEVIPLQHLCVFGGPVYQIMEQNPKQSSNNLLVQHAGHNVGARIPFSFNTILSAALTQLFSSSSQQNVADK
SHAQMLIGTVSLNKS WQALSRLSSFSYTEDS QVMKHVFPYKGT SRGSRWNYGWSGSGVMSYAYPKGIRYL

KMTPFVDLQYTKLVQNPVETGYDPRYFSSSEMTNLSLPIGIALEMRFIGSRSSLFLQVSTSYIKDLRRVNPQSS
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>core/28/4/Org4_Gene990

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WRSRPLHFTPFQIAIAVRSNQTAFAQESGDKSRKFAVHKPLYNLTVPLGIQSAWESKFRLPTYWNIELAYQPVL
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>core/29/4/Org4_Gene777

MFWKLLCPILICTSLSITSCQQFKVVPNQCPLQVSTPAAADQKIEKIICSNGLPLLIISDPNLPTSGAALLVKTG
NNADPEEYPGMAHFTEHCVFLGNEKYPEVSGFPGFLENNGVHNAFTYPNKTVPFVSVEHSAFSDALDQFVH
LFINPKFRQEDLDREKYAVHQEFAAHPLSDGRRVHRIQQLVAPQGHPCARFGCGNASTLTPVTTEKMAEWF
KLHYPENMCAIAYTSAPLSKAKKQFSKIFSQIPRSKNYERQEPFLPSGDTSSLKKLYINQAIQPTSNLEIYWHI
YESSHIPPLGCYKALAEVLRNESKNSLVSLKNEQLITDL DVEFFRSSLNTGEFYISYELTEKGDKHYSQVIDST
FQYLR YIQEHGIPNYTLEEISTINALNYCYSSKSPLFDLLCKQIVSLGNEDLSTYPYHSLVYPKYSSSEDESALLN
LVSDPEQARFVLSSKNSEHWEEATQLYDPIFDMTYVVKALDGVQDYGKVQSLKPIALPKPNLFIPKEVTLP
VHLLKKQEFPPAPALSYQDDKLTLYHCEDEHYTAPKLSSQIRIRSPQISRSSPQFLVATELYCLAVNDQLLREY
YPATQAGLSFTSALGGDGIDLRVSGYTTTVPTLLNSILTSLPNLEISYETFLVYKKQLELYQGALLNCPVRSG
LDELASQVMKETYSNTTKLSALEKLSFSEFQAFASNLFSNVHLEVMVLGNLSEQQKKDYLEMLQAFTASRSS
HATKPFYYELQSQEISEIHHDYPLTANGMLLLLQDKSSPSIQGKVCAEMLFEWLHHITFEELRTQQQLGYMV
GARYREFASRPFGFLYIRSDAYSPEELLAKTSLFLNKVSASPEKFGMSQEKFANIRKAYINKILEPEHSLDMMN
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>core/30/4/Org4_Gene654

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DWDRKRFTMEPLANRAVKKAFKTLFENGYYIRGYLVNWD PVLQTALADDEVEYEEKDGWLYYIRYRMV
GSQESIVVATTRPETLLGDTAIAVSPNDERYASWIGASVEVPFVNRQIPIIGDASVDPTFGTGAVKVTPAHDKD
DYLMTGNHHLPMINILTPSGGINENGGLFAGMAKEKAREEILIALEEQGLFVRKEPYKLRVGVSYRSGAVIEP
YLSKQWFVSVSEFRGALREFVESQDIKIFPKDFVKNYLSWVNHLRDWCISRQLWWGHRIPVWYHKNDDERV
LCYDGEGIPEEVAQDPDSWYQDPDVLDTWFSSGLWPLTCLGWPDENSPDLKKFYPTALLVTGHDILFFWVT
RMVLLCSSMSGKPFSEVFLHGLIFGKSYKRYNDFGEWSYISGKEKLAYDMGEALPDGVVAKWEKLSKSKG
NVIDPLEMIATYGTDAVRLTLCSCANRGEQIDLDYRLFEEYKHFANKVWNGARFIFGHISDLQGKDLAGIDE
DSLGLEDFYILDGFNELIHQLEEAYATYAFDKVATLAYEFFRNDLCSTYIEIHKPTLFGKQGNEASQSTKRTLL
AVLLINVLGVLHPVAPFITESLFLRIQDTL GALPEGDGDAFTGHALRMLRSRACMEAPYPKAFDVKMPQDLR
ESFTLAQRLVYTIRNIRGEMQLDPRLHLKAFVVCSDTTEIQSCIPILQALGGLESIQLLDKEPEKGLYSFGVVD
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SFA

>core/31/4/Org4_Gene438

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SITNNLGQGTVDNLALNKGALYTETNLSIKDNKGPIIHKQNRNLNSES LGGGIYSGNSLNIEGNSGAIQISSNS
SGAGAGIFSTQTLTISSNKKLIEISENSAFANNYGSNFPNPGGGGLSTNFCTISNNREGVLFNNNQSQRNNGGAIH
AKSIIKENGVPVYFLNNTATWGGALLNLSGGSGNGSFVLSADNGDIIFNNNTASKNAPNPPYRNAIHSTPNMN
LQVGARPGYRVLFYDPIEHEHPSSFPLLFNFETGHTGTVLFSGKYVHQNFTEEMNFFSYLRNTSELRQGV LAV
EDGAGLACYKFFQRGGTLLLKGKAVITTAGTIPTSPSTRTTVGSTITLNHIAIDLPSILSFAQAPKIWIYPTKTG
STYTEDSNPTITISGTLNLLNSNEDPYDSLDSLHSEKVP LLYIVDVAAQKINSSQLDLSTLNSSEHYGYQGI
WSTYWVETTTITNPTSLLGANTKHKLLYANWTPLGYRPHPERRGEFITNALWQSAYTALAGLHSLSSWDEE
KGHAASLQGIGLLVHQDKNGFKGFRSHTTGYSATTEATSSQSPNFSLGFAQFFSKAKEHESQNSTSSHHYFS
GMCIENTLLKEWIRLSMSLAYMFSSEHTHTMYQGLLGSSQGSFHNHTLAGALSCVFLPQPQGHSLQIYPFIT
ALAIRGKLA AFQESGDHAREFSLHHPLTNVSLPVGIRASWKNHHRVPLVWLTEISYRSTLYRQDPELHSKLLI
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>core/32/4/Org4_Gene447

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NLSLTGNSQIIFTQNFSSDNGGVINTKNFLLSGTSQFASF SRNQAFTGKQGGVVYATGTVTIENNP GIVSFSQN
LAKGSGGALYSTDNCSITDNFQVIFDGNSAWEAAQAQGAICCTTTDKTVTLTG NKNLSFTNNTALTYGGAI
SGLKVSISAGGPTLFQSNISGSSAGQGGGGAINIASAGELALSATSGDITFNNNQVTNGSTSTRNAINIIDTAKV
TSIRAATGQSIYFYDPITNPGTTASTDTLNLNLADANSEIEYGGAIVFSGEKLSPT EKAIAANVTSTIRQPAVLA
RGDLVLRDGVTVTFKDLTQSPGSRILMDGGTTLSAKEANLSLNLGLAVNLSSLDGTNKAALKTEAADKNISLS
GTIALIDTEGSFYENHNLKSASTYPLLELT TAGANGTITLGALSTLTLQEPETHYGYQGNWQLSWANATSSKI
GSINWTRTGYIPSPERRSNLPLNSLWGNFIDIRSINQLIETKSNGEPFERELWLSGIANFFYRDSMPTRHGFRHIS
GGYALGITATTPAEDQLTFAFCQLFARDNRN HITGKNHGD TYGASLYFHHTEGLFDIANFLWGKATRAPWVLS
EISQIPLSFD AKFSYLHTDNHMKTY YTDNSI IKG SWRND AFCADLGASLPFVISVPYLLKEVEPFVKVQYIYA
HQQDFYERHAEGRAF NKSELINVEIPIGVTFERDSKSEKGT YDLTLMYILDAYRRNP KCQTS LIASDANWMA
YGTNLARQGFSVRAANH FQVNP HMEIFGQFAFEVRSSSRNYNTNLGSKFCF

>core/33/4/Org4_Gene967

MFGMTPAVYSVQTN SLEKSALERDEEFRTSFPLDSLSTLTGFSPITTFVGNRHNSPQDIVLSNYKSIDNILLW
TSAGGALSCNNFLLSNVEDHAFFSKNLAIGTGGA IACQGACTITKNKGPLIFFSNRGLNNASTGGETRGGAI A
CNGDFMISQNQGTFYFVNNSVNNWGGALSTNGHCRIQSNTGPLLFFNNTAPSAGGALRSENTTISDNTRPIYF
KNNCANNGGAIQTNSTITIKNNSG SVIFNNNTALSASIDSGNGSGGAIYTTSLSIDDNPGTIIFNNNYCSR DGA
ICIQSLTIKNSGHVYFTNNQGNWGGALMLRRDSTCLLFAEQGNIAFQNN EVFLTAFGRYNAIHCTPNSNLQLG
ANKGYTTAFFDPIEHQHPTTNPLIFNP NANHQGTILFSSAYIPEASDYENNFISSSKNTSEL RNVLSIEDRAGW
QFYKFTQKGGILKLGHAA SIATTANSETPSTSVGSQVIINN LAINLPSILAKGKAPTLWIRPLQSSAPFTEDNNP
TITLSGPLTLLNEENRDPYDSMDLSEPLQNIHLLSLSDVTARHINTDNFHPESLNTTEHYGYQGIWSPYWVETI
TTTNNAS IETANTLYRALYANWTPLGYKVNPEYQGD LATTPLWQSFHTMF SLLRSYNRTGDS DIERPFLEIQG
IADGLFVHQNSIPGTPGFRIQSTGYSLQASSETSLHQKISLGFAQFFTRTKEIGSSNNVSAHNTVSSSLYVELPWF
QEAFATSTVLAYGYGDHHLHSLHPSHQEQAE GTCYSHTLAAAIGCSFPWQQKSYLHLSPFVQAIAIRSHQTAF

EEIGDNPRKFVSQKPFYNLTPLGIQGWQSKFHVPTWTLSESYQPVLYQQNPQIGVTLLASGGSWDILGPN
YVRNALGYKVHNQTALFRSLDLFLDYQGSVSSSTSTHHLQAGSTLKF

>core/34/4/Org4_Gene653

MERYDIVRIIGKGGMGEVYLAYDPVCSRKVALKKIREDLAENPLLKRRFLREARIAADLIHPGVVPVYTIYSE
KDPVYYTMPYIEGYTLKTLLKSVWQKESLSKELAEKTSVGAFLSIFHKICCTIEYVHSRGILHRDLKPDNILLG
LFSEAVILDWGAACVACGEEEDLLDIDVSKEEVLSSRMTIPGRIVGTPDYMAPERLLGHPASKSTDIYALGVVL
YQMLTSLFPYRRKKGKKIVLDGQRIPSPQEVAPYREIPPFLSAVVMRTLAVDPQERYSSVTELKEDIESHLKGS
PKWTLTTALPPKKSSSWKLNELLKSKYFPMLEVSPASWYSLAISNIESFSEMRLEYTLSSKKGLNEGFGILLPTS
ENALGGDFYQGYGFWLHIKERTLSVSLVKNLSLEIQRCSQDLESDEKTFLLIALEQHNHSLSLFVDGTTWLIHMN
YLPSRSGRVAIIVRDMEDILEDIGIFESSGSLRVSLAVPDAFLAEKLYDRALVLYRRIAESFPGRKEGYEARFR
AGITVLEKASTDNNEQEFSLAIEEFSKLHDGVAAPLEYLGKALVYQRLQEYNEEIKSLLLALKRYSQHPEIFRL
KDHVVYRLHESFYKRDRLALVFMILVLEIAPQAITPGQEEKILVWLKDKSRATLFCLLDPTVLELRSSKMELF
LSYWSGFIPHLNSLFHRAWQSDVRLAIEIFYVACDLHKWQFLSSCIDIFKESLEDQKAKEEIVEFSFEDLRAF
LFAIQSIFNKEDAEEKIFVSNDQLSPILLVYIFDLFANRALLESQGEAIFQALDLIRSKVPENFYHDYLRNHEIRAH
LWCRNEKALSTIFENYTEKQLKDEQHELFLVLYGCYLALIQGAEEAAKQHFDVCREDRIFPASLLARNYNRLGL
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>core/35/4/Org4_Gene446

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ALNLTDNLTILFSQNVSNNEANNNGGAITAKTLLSISGNTSSITFTSNSAKKLGGAIYSSDGASISGNTGQLVFMN
NKGETGGGALGFEASSITQNSSLFFSGNTATDTAGKGGAIKCEKTSQTPTLTISGNKSLTFTENSSVAEGGAIC
AHGLDLAAGPTLFSNNRCGNTAAGKGGAIADSGSLSLSANQGDITFLGNTLTSTSAPTSTRNAIYLGSSAK
ITNLRAAQGQSIYFYDPIASNTTGASDVLTTINQPDNSPLDYSGTIVFSGEKLSADEAKAADNFTSTLKQPLAL
ASGTLALKGNVELDVNGFTQTEGSTLLMQPGTKLKADTEAISLTKLVVDLSALEGNKSVSIETAGANKTITLT
SPLVFQDSSGNFYESHTINQAFTQPLVVFTAATAASDIHIDALLTSPVQTPESHYGYQGHWEATWADTSTAKS
GTMTWVTTGYNPNPERRASVVPDSLWASFTDIRTLQQIMTSQANSIYQQRGLWASGTANFFHKDKSGTNQA
FRHKSYGYIVGGSAAEDFSENIFSVAFQCLFGKDKDLFIVENTSHNYLASLYLQHRAFLGGLPMPSPFGSITDML
KDIPLILNAQLSYSYTKNDMDTRYTSYPEAQGSWTNNSGALELGGSLALYLPKEAPFFQGYFPFLKFQAVYS
RQQNFKESGAEARAFDDGDLVNCISIPVGIRLEKISEDEKNNFEISLAYIGDVYRKNPRSRSTSLMVSGASWTSL
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>core/37/4/Org4_Gene445

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IQSNYSCYFGQNFSNDNGGALQGSSISLSLNPNTFAKNKATQKGGALYSTGGITINNTLNSASFSENTAATN
GGAIYTEASSFISSNKAISFLNNSTTAASATGGAIYCSSTSAPKPVLTLSDNELNFIGNTAITSGGAIYTDNLVL
SSGGPTLTKNNSAIDTAAPLGGAIAIADSGSLSLSALGGDITFEGNTVVKGASSSQTTTRNSINIGNTNAKIVQL
RASQGNTIYFYDPITTSITAALSDALNLNGPDLAGNPAYQGTIVFSGEKLSEAEAAEADNLKSTIQQPLTLAGG
QLSLKSGVTLVAKSFSQSPGSTLLMDAGTTLETADGITINNLVLNVASLKETKKATLKATQASQTVTLSGSLS

LVDPSGNVYEDVSWNNPQVFSCSLTLTADDPANIHITDLAADPLEKNPIHWGYQGNWALSWQEDTATKSKAA
TLTWTKTGYNPNPERRGTLVANTLWGSFVDVRSIQQLVATKVRQSQETRGIWCEGISNFFHKDSTKINKGFR
HISAGYVVGATTTLASDNLITAAFCQLFGKDRDHFINKNRASAYAASLHLQHLATLSSPSLLRYLPGSESEQP
VLFDAQISYIYSKNTMKTYYTQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYSPFIKVEASYIHQDSF
KERDTTLVRSFDSGDLINVSVPIGITFERFSRNERASYEATVIYVADVYRKNPDCTTALLINNTSWKTTGTNLS
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>core/38/4/Org4_Gene443

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ENIRKLVVAGNFSTADGGAIKGASFLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIASSTG
GAIDDEGTSILSNKFLYFEGNAAKTTGGAICNTKASGSPELIISNNETLIFASNVAETSGGAIHAKKLALSSGG
FTEFLRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGSTDTPKRNAINIGSNGKFTELRAAKNHT
IFFYDPITSEGTSSDVLKINNGSAGAPNPYQGTILFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQKGVTL
ESTSFSQEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKIVVSGKLNLIIDIEGNIYES
HMFSDHQLFSLLKITVDADVDTNVDISSLPVPAEDPNSEYGFQGKWNVNWTDTTTNTKEATATWTKTGTV
PSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFVWSSMTNFLHKTGDENRKGFRHTSGGYVIG
GSAHTPKDDLFTFAFCHLFARDKDCFAHNNRSRTYGGTLFFKHSHTLQPQSYLRLGRAKFSESAIEKFPREIPL
ALDVQVSFSHSDNRMETHYTSLPESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSFF
ESSSDGRGFSSGRLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDSWKIRGGNLSR
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>core/39/4/Org4_Gene534

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NAIIFLGDAIGSGIIASLVHTIGIQGILILFTAALVLTPIVFYVSKSLKSLSDDHDLFIDTGHPPPLSKALKLCFYD
KYTFYLLCFYFLMQLLAIAATEFNLYLKIFEIQFASKEEFELVAHIGKCSLWISLGNMCFALFAYSRIKRLGVNNI
ILFAPLCFLSLFLFWTFKTTLSIAVLAMVVREGVTYALDDNNLQLLIYGVPNKIRNQIRIVVESFIEPIGMLVWS
LVCFLSSQYVFCLISLIATILVCLVRSYYAKAILKNLSAQALQLTRSMQDWIKSMTVKQKRQVELFLLAHL
KHPSERHQTFQHLNLASRSVLPSSLAHMNKLSPNKLKTIEMVKSSLWAKDFLTLELLKRWTSIFPHPAI
ASAIHLYFAEHDLLHITHIAEDLYDTVGDRLLAAILTVRRQEAYGPYRDLADKRLKELLNSDQPEDIVMGLTI
LKLEKNPQNFPILLDFLNTKNEDILIVTCKALHTSVRANHKKPYCPELLKRLRQCSDHNDASQYLLKTISNALDI
SFVKDLLMTTSQLKNTSRKYAEAMIGELDKEVAPAFLQVLTDEGTHNRCRILAAKALCKIDNWLKKHAYK
IVKSKASKALFYSYHGHYIQKKYPTYNLSLLVNTLNSNYAEVNFMLSLLGILGSMEHSDVLIRALTSKNQKI
KAQALESLEKNCDSHLFSLEPFVNQPGMCYSEKYYFKCGVIPLTLKELNNMMENSPSSLNKLTAQQLKEEL
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>core/40/4/Org4_Gene700

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MLLNNYVVRFEQNQSKTKGGAISGANVTIVGNYDSVSFYQNAATFGGAIHSSGPLQIAVNQAEIRFAQNTAK

NGSGGALYSDGDIDIDQNAAYVLFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNHSIMGG
GAIYARKLSISSGGPTLFINNISYANSQNLGGAIAIDTGGEISLSAEKGTITFQGNRTSLPFLNGIHLLQNAKFLK
LQARNGYSIEFYDPITSEADGSTQLNINGDPKNKEYTGTLFSGEKSLANDPRDFKSTIPQNVNLSAGYLVIKE
GAEVTVSKFTQSPGSHLVLDLGTKLIASKEDIAITGLAIDIDSLSSSSTAATAVIKANTANKQISVTDSELISPTGN
AYEDLRMRNSQTFPLLSLEPGAGGSVTVTSGDFLPVSPHYGFQGNWKLAWTGTGNKVGEFFWDKINYKPRP
EKEGNLVPNILWGNAVDVRSLMQVQETHASSLQTDRLWIDGIGNFFHVSASEDNIRYRHNSGGYVLSVNN
EITPKHYTSMAFSQLFSRDKDYAVSKNEYRMYLGSYLYQYTTSLGNIFRYASRNPNVNVGILSRRFLQNPLMI
FHFLCAYGHATNDMKT DYANFPMVKNSWRNNCWAIECGGSMPLLVFENGRLFQGAIPFMKLQLVYAYQG
DFKETTADGRRFSNGSLTSISVPLGIRFEKLALSQDVL YDFSFSYIPDIFRKDPSCEAALVISGDSWLVPAAHVS
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>core/41/4/Org4_Gene286

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VEEPVPAASKEKLDSIQVWEEKQNYARRAVNAINLSIKKQLEEQTSTVTEKDVQPKTQATPHA AKKNVASPS
TSMPIEKAATTVAVPQDKSEEEKVKERLTKRELTCEDLKDNGYTVNFEDISILELLQFVSKISGTNFV FDSND
LQFNVTIVSHDPTSVDDLSTILLQVLKM HDLKVVEQGNNVLIYRNPHLSKLSTVVTDSSLKETCEAVV VTRVF
RLYSVSPSAAVNIIQPLLSHDAIVSASEATRHVIISDIAGNVDKVSDLLAALDCPGTSVDMTEYEVKYANPAAL
VSYCQDVLGTMAEDDAFQMFIQPGTNKIFVSSPRLANKAEQLLKS LDVPEMAHTLDDPASTALALGGTGT
TSPKSLRFFMYKLKYQNGEVIANALQDIGYNLYVTTAMDEDFINTLNSIQWLEVNN SIVIIGNQGNVDRVVS L
LNGLDLPPKQVYIEVLILDT SLEKSWDFGVQWVALGDEQSKVAYASGLLNNTGIATPTKATVPPGTPNPGSIP
LPTPGQLTGFS DMLNSSSAFGLGIIGNVL SHKGKSFLT LGGLLSALDQDGD TVIVLNPRI MAQDTQQASFFVG
QTPYQTTNTIIQETGTVTQNI DYEDIGVNLVVTSTVAPNNVVTLQIEQTISELHSASGSLTPVTDKTYAATRL
QIPDGCFLVMSGHIRDKTTKV VSGVPLLNSIPLIRGLFSRTIDQRQQRNIMMFIKPKVISSFE EGTRVTNKEGYR
YNWEADEGSMQVAPRHAPECQGPPSLQAESDFKIIIEIAQ

>core/43/4/Org4_Gene223

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PSEVSGSVLTEPLVVTGPATPQLINLHSLQERYPTLSRSPEALRTYGS DLYELIGKYLSPVLGIGSETLKRELKD
LYQQVEVSLTQETDTEAAYTLYGQVLSTLNRISSSLV VSEGGERFSQLRSVRLYREEWNKYHKLVEARDLNQ
AQLEKLRGELSQT VWFYFNNQELSSRSLEKQDPEVFGHWFAGAKEEWTA FKFNHLSL SFKAPDQPRNLVLEKT
FKSQEPSPHYLG YLFTFLPIILVLLFVYLVFSRQMRGMSG SAMSFGKSPARMLLKGNKVTFADVAGIEEAKE
ELIEIVDFLKNPNKFTSLGGRI PKGVLLIGPPGTGKT LIAKAVSGEADRPFFSIAGSDFVEMFVG VGASRIRDMF
EQAKRNAPCII FIDEIDAVGRHRGAGIGGGHDEREQTLNQLL VEMDGFGTNEG VILMAATNRPDVL DKALLR
PGRFDRRVVMNLPDIKGRFEILMVHAKRIKLDPTVDLMAVARSTPGASGADLENLLNEAALLAARKDRTAV
TAVDVAEARDKVLYG KERRSLEMDAEERKTTAYHESGHAVVGLCVQHGD PVDKVTIIPRGLSLGATHFLPE
KNKLSYWK KELYDQLAVLMGGRAAE EIFLGDISSGAQQDISQATKLVRSMVCEWGMSPQLGNV TYDERSD
GLTGYGGYHEKSYSEETA KTIDTELRMLLDAAYQRALDIINEHKAEIELMTQMLIEFETLDSKDVKEIMDHT
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>core/44/4/Org4_Gene486

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CTPELQEFVWNLMEKRQVERSAEQLLRSYKDLCKATFFEEFLQIKFTGQKRFSLEGGETLVPMLEHLVHYGS
ALGISNYVLGMAHRGRLNVLTNVLGKPYRYVFMEFEDDPAARGLESVGDVKYHKGYVLKSHQKDRETTFV
MLPNASHLESVDPIVEGVVAALQHGHAGKEQSSLAILVHGDAAFSGQGQVYETLQLSRVPGYSTEGTLHIV
VNNYIGFTAVPRESRSTPYCTDIKMLGIPVFRVNSEDDVACIEAIEYALQVRERFSCDVIIDLCCYRKYGHNE
SDDPSVTAPLLYDQIKRKKSIREFRQHLLLEGQFADISEETLASIEKEIQESLNCEFQVLKGTGPEPFPKKECHH
CDRLNNGELILRDCDVSLDRETLFHMSSRLCGFPENFHPHPKIKTLLEKRMKMAEGGVGYDWAMAEELAFA
SLLIEGYNLRLSGQDSIRGTFSQRHLVWSDTVTGDYSPLYHLSAEQGSVEMYNSPLSEYAILGFEYGYAQQA
LKTLLVLEAQFGDFANGAQIIFDQYISSGIQKWDLHSDIVLLLPHGYEGQGPEHSSSRIERYLQLAANWNFQV
VLPSTPVQYFRILREHAKRDLPLVIFTPKLLLRYPQCVSSIEEFTEPGGFRAILEDADPNYDASILVLCSGKIY
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>core/45/4/Org4_Gene928

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PPQEKELEPKPVKPAEPKSVVMIKSKFGPTGKHINHLLAKTFKAPAKEEKVVAGSKSTKPVASDKTGKPGTSE
GGEQNNREKQFNPNRSPASGPKRDAGKKNLTDFRDRSKKSDESLKRAFTGRDRYGLNEGGEEDRWKRRV
YKPKKHIDEASIQRPHTHIKISLPITVKDLAAEMKLKASEVIQKLFHIGMTYVVNDILDSETAVQFIGLEFGCTID
IDYSEQDKLCLSNLTVRDEIQSTDPSKLVIRSPIVAFMGHVDHGKTTLIDSLRKSNAATEAGAITQHMGAFC
CSTPVGDTILTDPGHEAFSAMRARGAEVCDIVVLVAGDEGIKEQTLEAIEHAKAADIAIVVAINKCDKPNF
NSETIYRQLSEINLLPEAWGGSTVTVNTSAKTGEGLSELLEMLALQAEVLELKADPSARARGLVIESELHKGL
GPVATVLIQNGSLKLGEALVFNDYCYGKVKTMHNEHNEMLMKEAGPSIPVLITGLSDIPKAGDPFFVVKNEKTA
RDIIEARSAGQQRFALQQKKRPNFDSMLQNKTKLKMVKADVQGSIEALVSSISKIKSEKVDVEILTNSVGEIS
ESDIRLAAASKAVLIGFHTGIESHAELIKSLGVRVELFTVIYHAIDAIKEIMTSLLDPIAEEKDEGSAEIKEIFRS
SQVGSYGCIVTEGIMTRNHKVRVLRNKEILWKGTLSSLKRVKEDVKEVRKGLECGILLEGYQQAQIGDVLQ
CYEVIYHPQKL

>core/46/4/Org4_Gene195

MLSNTIRSNFLKFYANRHHTILPSSPVFPHNDPSILFTNAGMNQFKDIFLNKEKVSYSRATTSQKCIRAGGKH
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RIFRLTDKDNFWSMANTGPCGYCSELLFDRGPSFGNASSPLDDTDGERFLEYWNLVFMENRTSEGSLALP
NKHVDGTGAGLERLVSLIAGTHTVFEADVLELIAKTEQLSGKVYHPDDSGAAFRVIADHVRSLSFAIADGLLP
GNTERGYVLRKILRRSVNYGRRLGFRNPFLAEIVPSLADAMGEAYPELKNSLSQIQKVLTLLEESFFKTLDRG
GNLLQQVLKSSSSSSCISGEDAFKLKDTYGMPIDEISLLAKDYDYSVDMDTFHKLEQEAKERSRKNVVSQSQG
TSESIYNELHLTSEFIGYDHLSCDTFIEAIIKDHIVSSLQEKQEGAIVLKVSPFYAEKGGQVGDSEIFCSEGTFI
VTHTTSPKAGLIVHHGRISQGSALTVEAAVTAQVNRYYRRKRIANNHTACHLLHKALEITLGDHIRQAGSYVDD
TKIRLDFTHPQAISPEDLLCIETLVNESIRENEPVDIREALYSVDMNSSEIKQFFGDKYSDVVRVVSAGHSHEL

GGTHAEATGDIGFFRITKEHAVAMGIRRIEAVTGEKAEATVHQQSEVLEEIATLLQVPRDQIVSRLTATLDER
KQQDKRLNELENSLIQTKLDKLIHNCHQRQGITCLVHHLAEHENHRLQQYAQCLHQRIPEKLISLWTTEKNG
KYIVLSRVSDDLITQGVHAQDLLKAVLTPCGGRWGGKDQSAQGSAPALPATEVLNETLWQWISTQLI

>core/47/4/Org4_Gene270

MSTFSIQNRPRTISGESTRIIKLDHKYSGFDPRSVPAINLEELNSGIYALRHLMNALQSENTNVAALLNPNTIF
PTTSWTDYNHSRPQASSPRAPSSQTPTDIVSAAALALVPVIDGGLAELVASVTEIDL GALSTISTVRQLMASYL
GLTTLTAEQEKVVFSSSYVPSEKNLLEHV KQEKA AEIQA KQEEIKA ELEAKGVSTEEIEAILKEYPDIYAADFF
KEFIEEPLHTYRAKVGAPIQEMNENAIQLLPTPPAITPDNVNEVNGMNTLSTILQAIDDAIKQAPALGGDQEIT
ILQTLVPLVDKTTFTKA EFDLIYTATQLPNTASLKLYLTDRQIAEYRGKITKVYQNSVQNLSETKRVENNRS
MLETQLSMFQQAQNC FVTWISQANALNIAITNKYISAVLTTSMEMYGGLLCLSYMYERLADDEKAIFDKSVN
EYLP IHIVVGGSWVNGWIAKMAAYQELAEYSLGTAVTSQDQIKAYLQTRGNEFKATRHHFFHDIGDQMYQFA
NETVFGNCLTTANGAIQPNLGGFIREAMTNVGTVEADYVSNAQRILNEFN TAATAHVLQLQLQIAELQKKAD
DLDPGKASFTENRKF A VAAWITSESLGDALISMILNSQLPKQEAFLKPLIEEINFNNLAANALNSLLQITNEFST
TSVYYSLSSYL VQSKTGQNLFAGDYYETLLAAAREREYIYRDTARCKQAINLVNGLLQKINSLPGATSAQKQ
EMLNATYYQYSLSVTLNQLTVLESLLAGLKMTLQTTSNNKYNKSVFKIESFDDWIPTLA ALESFLTSGFPNIS
ATGGLGPLFTQVQSDQQTYTSQGQTQQLNLQNQMTTIQQEWTLVSTSMQVLNGILSQLAGAIYSN

>core/48/4/Org4_Gene894

MKKSLIIVESPAKIKTLQKLLGSEVFVASSIGHIVDLPakeFGIDVDHDFEPQYQVLPDKQEVINHIRKLAACE
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ISPILSRKLQQRSGISAGRVQSVALKL VVDREKAIDAFVPVEYWNLRVLMQDPKTTKTFWAHLYAVQGKKW
EKEIPEGKTENDVLLINSEEKARHYAELLEKSSYTITRVEAKAKRRFAPPPFITSTLQQEASRHRFSASRTMSI
AQTLYEGVDL DSEDSTGLITYMRTDSVRVDPEALTTVREYIQQTFGKEYLPEKANVYTTKKMTQDAHEAIRP
TDINLTPDKLKNKLSDDQFKVYNLIWKRFVASQITPAIYDTLAVQITTDTEIDLRASGSLKFKGFLAVYEEKQ
DDENDQEEDHPLPPLHAQDV LIKEEVSQEQAFTKPLPRFTEASLVKELEKSGIGRPSTYATIMNKIQSREYTTK
ENQRLRPTELGKIISQFLETNFRIMDIGFTALMEDELELIADNKKPWKLLLQEFWTTFLPVVITAEKEAVIPRI
LTNIECSKCHKGKLVKIWSKNSYFYGCSEYPECDYRTSEEELAFNKEDYAEDTPWDSPCPLCGGVMKVRHG
RYGTFLGCEKYPECRTISIHKKGEEIEQEEPIPCPAIGCNGKIFKKRSRYNKIFYSCSEYPECSVIGNSIDAVITK
YSGTEKIPYKKKTPIKKKSSAKTTKAAKAPSKKGKAKSSVKSSEKKTGPLFLPSPDLAKMIGNEPVSRGEAT
KKIWDYIKEHQLQAPENKKLLVPDNNLATIIGPNPIDMFQLSKHLSQHLLTKVSNDESSASS

>core/49/4/Org4_Gene340

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K S N R Q K K F E D I P P Q I A L V K E Y C S L I G L A Y L E K E S V E A D D V I A S I A K K A R E E N Y K V Y V C T A D K D L L Q L V N D H V
V A W N P W A D Q G V V G I S E V I E R Y G I P P G N I P D Y L A L V G D S S D N I P G V P G C G P K K A A A L L K Q F G S V E G L L E N L D A
V K G L S Q T M L S E R Q E T L K L S K R L A L L D S N I P I P V P I E S L T F P Q H P V D E E K L I H F Y I Q Q G F K T L V P S K Q T E A A T V D V
Q I I K D A E S L T N I L N L V Q G G D I A F A A A Y T G N H L L S L K L E G L A L T Q G S G V F F I A L E E E G T K I L P I L K D F F L R E D L T F
Y G Y N L K R D C H A L L N A G I V I R E I S Y D L A L A E H L T N G G G K I S F Q S L L V N H G F T E T A H R F A K E W G N L G L P I G R L P E
Q P E Q Y F G E L V A Y L P I I K D A I L E E I N R K N L N H I L S D I E M P L E K V L V S M E R A G V P L D V E E L A I L E A L F E T E L A V L T E
E I Y D L S G R P F N I K S P K Q L S D I L Y N E L G L R P I D K A K S T R A E V L E A L R S E H P I I E K L L A F R T I E K L L S T Y V K A L P K Q V

DSHTQRIHPSFDQTGTVTGRLACRDPNLQNIPIRSERGILLRKAFLRSEKNSYFLSADYSQIELRFLAHLSDQKS
LKFAFESGEDIHAFSTASQVFHVPLEQVSKEQRMQAKTVNFGIVYGQAFGLAKVLKISVGAEQELIQAYFSR
YPEIAHFVEETIQQAAKDLRVTTMLGRERIIDSWNEFPGSRAASGRFAVNTRIQGSAAELIKLAMLDISQAIKQ
QQMKSRMLLQIHDELLFEVPEEEIEEMQRLVREKMESAMTSLVPIAVNILIGKNWAEC

>core/50/4/Org4_Gene34

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EGEVDPKPSPGLQTLLRDAKQEAKTLGDEYISGDHLLLAFWSSNKEPFNSWKQTTKVSFKDLKNLITKIRRG
RMDSPAESNFQGLEKYCKNLTAAREGKLDPVIGRDEEIRRTIQVLSRRTKNNPMLIGEPGVGKTAIAEGLA
LRLIQGDVPESLKGKQLYVLDMGALIAGAKYRGEFEERLKSVLKDVESGDGEHIFIDEVHTLVGAGATDGA
MDAANLLKPALARGTLHCIGATTLENYQKYIEKDAALERRFQPIFVTEPSLEDAVFILRGLREKYEIFHGVRIT
EGALNAAVLLSYRYIPDRFLPDKAIDLIDEAASLIRMQIGSLPLPIDEKERELAALIVKQEAIKREQSPSYQEEA
DAMQKSIDALREELASRLGWDEEKKLISGLKEKKNSLESMTKFSEEEAERVADYNRVAELRYSPLIPQLEEEIK
QDEASLNQRDNRLQEEVDERLIAQVVANWTGIPVQKMLEGEAEKLLILEESLEERVVGQPFVSAVSDSIR
AARVGLNDPQRPLGVFLFLGPTGVGKTELAKALADLLFNKEEAMVRFDMSSEYMEKHSISKLIGSSPGYVGYE
EGGSLSEALRRRPYSVVLFDIEKADKEVLNILLQVFDDGILTDGKKRKVNCKNALFIMTSNIGSPELADYCS
KKGSELTKEAILSVVSPVLKRYLSPEFMNRIDEILPFVPLTKEDIVKIVGIQMRRIAQRLKARRINLSWDDSVIL
FLSEQGYDSAFGARPLKRLIQQKVILLSKALLKGDIPDTSIELTMAKEVLVFKKVETPS

>core/51/4/Org4_Gene280

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ETTQLKNEDTILLGSNQYSFLSDEFDPQDLVYDFDIPEENFSNDSGDLSDSNEQGKDLEPRQTSETNHSPKPKE
KLTKDQGSSDPITSRDQELADAFASAKAEKNQPRAKVAKKGLKESSNESLNPKEQNAKDSPKGEERTNKPQ
NAIMEDNGASPSQDPQPKSAEPSLENTARDETPLKENKPVEEKANKKATPDSPEKKDQPEEGSKKEGSKIEAT
PADSQKESEDKEAEEAFVQEEEEENLTEDNKEDSDSAADANDDTASDHTAEDNKETPKKVENEKSAVLSPFH
VQDLFRFDQTIFPAEIDDIKKNISVDLTQPSRFLKVLGAGANIGAIEFHLDGKTYILGTDPTTCDIVFNDLSVS
HQAKITVGNDDGILIEDLDSKNGVIVEGRKIDKTSTLSSNQVVALGTTFLFLIDHHAPADTIVASLSPDDYSL
FGRQQDAEALERQEAQEEEEKQKRATLPAGSFILTLFVGGLAILFGIGTASLFHTKEVVPLENIDYQEDLAQVI
NQFPTVRYTFNKTNSQLFLIGHVKNSTDKSELLKYVDALSFKSVDDNVIDDEAVWQEMNILLSKRPEFKGIS
MHSPEPGKFIITGYVKTEEQAACLDYLNHFNYLSLENKVVVETQMLKAIAGHLLQGGFANIHVAFVNGE
VILTYGVNDDAEKFRAVVQELSGIPGVRLVKNFAVLLPAEEGIIDLNLRYPNRYRVGTGYSRYGEISINVVN
GRILTRGDVIDGMTVTSIQPNAIFLEKEGLKYKIDYNK

>core/52/4/Org4_Gene455

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NLQLPPSSSSSSSSSRNPSSSKSPLGHSLGSDKNEKLSALKAYGYDLTEMFRESKLDPVIGRSSEVERLILILCR
RRKNNPVLIGEAGVGKTAIVEGLAQKIILNEVPDALRKKRLITLDLALMIAGTKYRGQFEERIKAVMDEVKHH
GNILLFIDELHTIVGAGAAEGAIASNILKPALARGEIQCIGATTIDEYRKHIEKDAALERRFQKIVVHPPSVDE
TIEILRGLKKKYEEHNVFITEEALKAAATLSDQYVHGRFLPDKAIDLLDEAGARVRVNTMGQPTDLMKLEA
EIENTKLAKEQAIGTQEYEKAAGLRDEEKKLRERLQSMKQEWENHKEEHQVPVDEEAVAQVVSLQTGIPSA

RLTEAESEKLLKLEDTLRRKVIGQNDAVTSICRAIRRSRTGIKDPNRPTGSFLFLGPTGVGKSLLAQQIAIEMFG
GEDALIQVDMSEYMEKFAATKMMGSPPGYVGHEEGGHLTEQVRRRPYCVVLFDEIEKAHPDIMDMLQILE
QGRLTDSFGRKVDFRHAIIMTSNLGADLIRKSGEIGFGLKSHMDYKVIQEKIEHAMKKHLKPEFINRLDESVI
FRPLEKESLSEIIHLEINKLDSRLKNYQMALNIPDSVISFLVTKGHSPEMGARPLRRVIEQYLEDPLAELLKES
CRQEARKLRATLVENRVAFEREEEEQEAAALPSPHLES

>core/53/4/Org4_Gene699

MKIPLRFLLLISLVPTLSMSNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVFKDSVVIENVPKTGET
QSTSCFKNEAAAGDLNFIGGGFSFTFSNIDATTASGAAIGSEAANKTVTLSGFSALSFLKSPASTVTNGLGAIN
VKGNLSLLDNDKVLIQDNFSTGDGGAINCADSLKIANNKSLSFIGNSSSTSGGAIHTKNLTLSSGGETLFGQNT
APTAAGKGGAIADSGTLSISGDSGDIIFEGNTIGATGTVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGS
TSVADALNINSPDTGDNKEYTGTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQ
DANSKLIMDLGTSLVANTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAIKDESFYQNGFLNEDH
SYDGILELDAGKDIVISADSRSIDAVQSPYGYQGKWTINWSTDDKKATVSWAKQSFNPTAEQEAPLVPNLLW
GSFIDVRSFQNFMELGTEGAPYEKRFVWAGISNVLHRSGRENQRKFRHVSGGAVVGASTRMPGGDTLSLGF
AQLFARDKDYFMNTNFAKTYAGSLRLQHDASLYSVVSILLGEGGLREILLPYVSKTQPCSFYQGQLSYGHTDH
RMKTESLPPPPPTLSTDHTSWGGYVWAGELGTRVAVENTSGRGFFQEYTPFVKVQAVYARQDSFVELGAISR
DFSDSHLYNLAIPGLIKLEKRFQAEQYYHVAMYSPPDVCRSNPKCTTTLLSNQGSWKTGKSNLARQAGIVQAS
GFRSLGAAAELFGNFGFEWRGSSRSYNVDAGSKIKF

>core/54/4/Org4_Gene545

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GDYHPHGSESVIYPTLVRMAQNWAMRYPLVDGQGNFGSIDGDPAAAMRYTEARLTHSAMYLMEDLDKDTV
DIVPNYDETKHEPVVFPSPKFPNLLCNGSSGIAVGMAATNIPPHNLGELIEATLLLLANPQASVDEILQVMPGPDF
PTGGIICGSEGIRSTYTTGRGKIKVRARLHVEENEDKHRESIIITEMPYNVNKSRLIEQIANLVNEKTLAGISDVR
DESDKDGIRVVLEIKKGESSEIINRLYKFTDVQVTFGANMLALDKNLPRTMSIHRMISAWIRHRKEVIRRRTR
YELNKAETRAHVLEGYLKALSCLDALVKTIRESGNKEHAKERIIESFGFTEPQALAILERLRYQLTGLEAEKIQ
KEYEELLNKIAYYKQVLSDEGLVKDIIRNELQDLLKHHKVARRTTIEFDADDIRDIEDIITNESVIITISGDDYV
KRMPVKVFKEQRRGGHGVGTGFDMMKKGAGFLKAVYSAFTKDYLIFTNFGQCYWLKVWQLPEGERRAKGK
PIINFLEGIRPGEELAILNIKNFDNAGFLFLATKRGVVKVSLDAFSNPRKKGIRALEIDEGDELIAACHIVSDE
EKVMLFTHLGMAVRFPHEKVRPMGRTARGVRGVSLKNEEDKVVSCQIVTENQSVLIVCDQGFGRSLVEDF
RETRNGGVGVRSILINERNGNVLGAIPVTDHDSILLMSSQGQAIRINMQDVRVMGRSTQGVRLVHLKEGDAL
VSMEKLSSNENDDEVLSGSEEECSDTVSLR

>core/55/4/Org4_Gene271

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ERATVAKSIPVAAIHEKPLSSTHASVQVTASTPAATGSGVGAYYNAVKKQKWAQDLIVELNTVMTTIMASVNS
KNPANKDVFDKLNTELQALVAAGNNLTEENFQTLYNFP EEIFTAIQRADTFTGGMKTDFTNQLAGKYGNQA
TLTQTFADGRVEGFKDILTAVQGVLTPAQFTIFAEIATELQALADHVGNFDEAGLPRIEDAGEKLA VINSSDL
TRNDKIMFCQHITDLYSDQVAALGSFDTVLDA SIYVNQH QGTMFSNLSSFVGS LIGTFAPIDLSSSQGDISSAA
LAGALQTARGLNSRFNELTAEQQKLINECVKSLDTFKCGEHLGAIWAYFTASTVVALNPTATMDHVKA AILE

EAKELDNSSFQLASSMKSAMTSIVSSNGSFSVTVNSNTLQYTIYSEKSGKVEINQILLNYGSTGFLPEITKLAKT
NAESTARSYFRFKALAAVESENVQNKIEDLQSQLQQFTNMKTELFQDGLSQASELRALPLPSAVASVLIDRY
MPKEVDYLNEIYKKLYYSNLGSSVGNISIIDAISQYVNGATYFNFASYVGGQPAVGAGGANAFPGSQESAQAK
LDQERKQAALYLQETRGAFTVIEEQRARVLKDDKITNEQRSTILDSLRYEDNINSISGSLVLLQNYLQPLSIA
GGSVAGTFEVKGGQEQWQARLQILEEALVSLVGNMNGGMFPLQSTIQSDQQSFADMGQNFQLDLQMHL
TSMQQEWTVVATSLQLLNQMYLSLARSLTG

>core/56/4/Org4_Gene789

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LSTGSFFIEECENTKELVDEICRLAPSEVLSCNKFYNKETAIVMQLQQHLKLTSTYADWAFEHKFASQKLTT
HFQVASLDGFGKGLVPAINAAGGLLSYIQDKLLLPTKHIAIPQTRGKQQKLLIDTASQVNLELLAPLNDPQG
KNSLLRIMDHTSTPMGGRLLRQILISPFYNPKEILVRQDAVEFFLRQVTLRKNIKTYLCQVRDIERLMTKVTTG
LAGPRDIGTLRDSFSAGA QIYEQLASATLPEFFIDKCSLDTKLASLIALLSKSLNGDLPLRVSDGNIFVDEFHND
LKRLRHNQEHSQEWIWEYQERIRKETGIKKLKICFAQALGYIIEVSSEFAPQLPKDFIRRQSRLLHAERFTTIEL
QQFQDDMSNISEKLQTLTETQFFKDLCSHILQLRTEILALSQSLADLDYIISLADLAHAQGYCRPRVDMSDTLCI
YRGCHPVAKTLVDTGKFIPNDTEMRGSQTRMILLTGPNMAGKSTYIRQIALLVIMAQMGSYIPAKSAHIGVID
KIFTRIGAGDNLSKGMSTFMVEMAETANILHNATDRSLVILDEVGRGTSTYDGLAIAQAVVEYLLFTDKKKA
KTLFATHYKELTTLEDHCPHVENFHAGVKDKAGQPVFLYEILKGHSQKSFGIHVARLAGFPLCVVSRAQQIL
RQLEGPESITRPAQDKMQQLTLF

>core/57/4/Org4_Gene993

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SNLLNLGILDLVRKALKTLNYDFDHLVEMESDAGLGNGGLGRLAACYLDSMATLAVPAYGYGIRYDYGIFD
QRIVNGYQEEAPDEWLR YGNPWEICRGEYLYPVRFYGRVIHYTDSRGKQVADLVDLTQEVLAMAYDIPIPGY
GNDTVNSLRLWQAQSPRGFEFSYFNHGNYIQAIEDIALIENISRVLYPNDSITEGQELRLKQEYFLVSATIQDIIR
RYTKTHICLDNLADKV VVQLNDTHPALGIAEMMHILVDREELPWDKAWEMTTVIFNYTNHTILPEALERWP
LDLFSKLLPRHLEIIYEINSRWLEKVGSRYPKNDDKRRSLSIVEEGCQKRINMANLAVVGS AKVNGVSSFHSQ
LIKDTLFKEFYEFFPEKFINVTNGVTPRRWIALCNPRLSKLLNETIGDRYIVDLSHLSLIRSAEDSGFRDHWKE
VKLKNKQDLTSRIYNEVGEIVDPNSLFDCHIKRIHEYKRQLMNILRVYVYNDLKENPNQDVVPTTVIFSGKA
APGYVMAKLIK LINSVADV VNQDSRVNDKLKVLFLPNYRVSM AEHIIPGTDLSEQISTAGMEASGTGNMKF
ALNGALTIGTMDGANIEMA EHIGKENMFIFGLLEEQIVQLRREYCPQTICDKNPKIRQVLDLLEQGGFFNSNDK
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PTKSCSGEGN

>core/58/4/Org4_Gene823

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GCHESLQDHLLFELYTMTLHSGYENRKQDMLLAKEQG DYKKAIELAKELVA ALEKGSCSPHPEIVQIEKTFL
QKTLALQIKVAQEAQESCDALLTPYCLSEIAYTEAMDALVLRARGEVSRTNEVDSVLLSHALQHLPFAREK
AILELEV LIDHGAYLESTLLYYAYFSLLELYHQNKDFASLERLLEKGDAVFVPEHPYFPEYGGFLGAYFYAKG

KYESAEKVFLQIIDPAVKLGATFARAYEYLGCIAYVQNHYEKAE EYFLRAYKSWG REESGIGLFLAYAVQKK
KTACEDMLYHPKFSFTYRHL LDSLCSLSYPHGENKGSSAIQRVHRAVPELSEIYSRCIYDMIKYRNV TYTHPII
ELAYNQVRNLEKRNLEEICRDAQDPEYDKALAFWGALQSGASVPRSLIESSDVDEARITIRCYEALYFHNPD A
IAMPLQAFSEECNSWQTALRLVWTLVRPKGAPNHAKYWDHLVLRPHGDSL YFFGYDLQEYLIGKEDALKHL
SVFAELFPKSSLLSLVYYLQGYSESSALRKVGWVFKALEEFNEISWSGHEMKTWAYIYYMVKLDLADTYISL
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>core/59/4/Org4_Gene617

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LYDQGLAYMADMAVN YCPELGTVLSNEEVENGFSIEGGYPVERKMLRQWILKITAYADKLLEGLDALDWP
ENVKQLQKNWIGKSEGALVTFH LTQEGSLEAFTTRLDTLLGVSFLVIAPEHPDLDSIVSEEQRDEVTAYVQES
LRKSERDRISSVKTKTG VFTGN YAKHPITGNLLPVWISDYVVLGYGTGVVMGVP AHDERDREFAEKFSLPIH
EVIDDDGVCIHSTYND FCLNGLSGQEAKDYVINYLEM RSLGRAKTMYRLRDWLF SRQRYWG EPIPIIH FEDG
THRPLEHDELPLLP NIDYRPEGFGQGPLAKAQDWVHIYDEKTGRPGCRETYTMPQWAGSCWYYLRFCDA
HNSQLPWSKEKET YWMPVDLYIGGAEHAVLHLLYSRFWHRVFYDAGLVSTPEPFKKLINQGLVLAFSYRIPG
KGYVSIEDVREENG TWISTCGEIVEVRQEKMSKSKLNGVDPQV LIEEYGADALRMYAMFSGPLDKNKTWSN
EGVGGCRRFLNRFYDL VTSSEVQDIEDRDGLVLAHKL VFRITEHIEKMSLNTIPSSFMEFLNDFS KL PVYSKHA
LSMAVRVLEPIAPHISEELWVILGNPPGIDQAAWPQIDESYLVAQTVTFV VQVNGKLRGRIEVAKEAPKEEVL
SLSRSVVAKYLENAQIRKEIYVPNKL VNFVL

>core/60/4/Org4_Gene5

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ADNKELTEELKAYSISIVSVIKDLLKLNPLFKEELQIFLGHSDFTEPGKLADFSVALTTATREELQEVLETTNM
HDRIDKALILLK KELDLSRLQSSINQKIEATITKSQKEFFLKEQLKTIKKELGLEKEDRAIDIEKF SERLRKRHPV
DYAMEVIQDEIEKLQTLETSSAEYTVCRNYLDWLTIIPWGIQSKEYHDLKKA EIVLNKDHYGLDEIKQRILELI
SVGKLSKGLKGSII CLVGP PGVGKTSIGRSIAKVLHRKFFRFSVGGMRDEAEIKGHRRTYIGAMP GK MVQALK
QSQAMNPVIMIDEVDKIGASYHGDPASALLEVLDP EQNKDFLDHYLDVRVDLSNVLFILTANVLD TIPDPLLD
RMEILRLSGYILEEKLQIAKKYLVPKARKEIGLTASEVNFQPEALKYMINNYAREAGVRTLN GN IKKVL RKVA
LKIVQNQEKP KSKKITFKISSKNLQTYLGKPIFSSDRFYESTPVGVATGLAWTSLGGATLYIESVQVSSLKTDM
HLTGQAGEVMKESSQIAW TYLHSA LHRYAPGYTFFPKSQVHIHIPEGATPKDGPSAGITMVT SLLSLLLETPV
VNNLGMTGEITLTGRVLGVGGIREKLI AARRSRLNILIFPEDNRRDYEELPAYLKTGLKIH FVSHYDDVLKVA
FPKLLK

>core/61/4/Org4_Gene810

MKGTPQYHF IGIGGIGMSALAHILLDRGYEVSGSDLYESYTIESLKAKGARCFSGH DSSHVPHDAVVVYSSSI
APDNVEYLTAIQRSSRL LHRAELLSQLMEGYESILVSGSHGKTGTSSLIRAI FQEAQKDPSYAIGGLAANCLNG
YSGSSKIFVAEADESDGSLKH YTPH AVVITNIDNEHLN NYAGNLDNLVQVIQDFSRKVTDLNKVFYNGDCPIL
KGNVQGISYGY SPECQLHIVSYNQKAWQSHFSFTFLGQEYQDIELNLP GQHNAANAAAACGVALTFGIDINII

RKALKKFSGVHRRLERKNISESFLFLEDYAHHPVEVAHTLSVRDAVGLRRVIAIFQPHRFSRLEECLQTFPKA
FQEADEVILTDVYSAGESPRESIILSDLAEQIRKSSYVHCCYVPHGDIVDYLRNYIRIHDVCVSLGAGNIYTIGE
ALKDFNPKKLSIGLVCGGKSCEHDISLLSAQHVSKEYISPEFYDVSYFIINRQGLWRTGKDFPHLIEETQGDSPLS
SEIASALAKVDCLFPVLHGPFGEDGTIQGFFEILGKPYAGPSLSLAATAMDKLLTKRIASAVGVPVVPYQPLNL
CFWKRNPCLCIQNLIETFSFPMIVKTAHLGSSIGIFLVRDKEELQEKISEAFLYD TDVFVEESRLGSREIEVSCIG
HSSSWYCMAGPNERCGASGFIDYQEKYGF DGIDCAKISFDLQLSQESLDCVRELAERVYRAMQGKGSARIDF
FLDEEGNYWLSEVNPIPGMTAASPFLQAFVHAGWTQEQVVDHFIIDALHKFDKQQTIEQAFTKEQDLVKR

>core/62/4/Org4_Gene828

MIRERKKSRRHPRPLTPLAAKASLYLFFACFSGLSLWSFHRDQPCTQNWIGLLGWSFSSFLLYFFGAAAFFIPL
YFLWLSFLYFRRTPRPLFFYKAAAFSLSPFCSAILLSMLSPVGTLPGLLDTRLPKFILGNNPPVS YVGGIPFYLF
YEGQSFCLKHLIGSVGTALIFGFVMLFSVLYLCGGIALKKKTFQDGVKKAFC SFFQTCFKNLKKLINRRNYL
PKPSVPFVSKNPFSCTKSQPSRRVSETHLDGSISPLQEEIPGSKKESFFLTPHPCKRFLT K FVEPQENKAKEGK
TIALPSTPTVVRESKGKERAALPKLKS LAVPENDLPQYHLLSKNREARPESLQAELERKALILKQTLTSFGIDA
DLGNICSGPTLAAFEVLPHSGVKVQKIKSLENDIALKLQASSIRIIAPIPGKAAV GIEIPTFPFQAVNFRDLLEDY
QKTNRKLQIPLLLGKKANGDNLWADLATMPHLIIAGTTGSGKSVCINTIVMSMIMTTLPSEIKLVIIDPKKVEL
TGYSQLPHMLSPVITESREVYNALVWLVKEMESRYEILRYLGLRNIQAFNSRTRNK TIEASYDREIPETMPFM
VGIIDELSDLLLSSSQDIETPIIRLAQMARAVGIHLILATQRPSREVITGLIKANFPSRISFKVSNKVNSQIIIDEPG
AENLMGNGDMLVLLPSVFGTIRAQGAYICDEDINKVIQDLCSRFTQYVIPSFHAFDDSDSDNSGEKDPLFAQ
AKTLILQTGNASTTFLQRKCLKIGYARAASLIDQLEEARIIGPSEGAKPRQILIQNPLEG

>core/63/4/Org4_Gene544

MDPKEKNYDASAITVLEGLQAVRERPGMYIGDTGITGLHHLVYEVVDNSIDEAMAGYCSRIDVRILEDGGIVI
VDNGRGIPIEVHERESAKQGREVSALEVLTVLHAGGKFDKDSYKVSGGLHGVGVSCVNALSEKLVATVFK
DKKCYQMEFSRGIPVTPLEYVSASDRQGTEIVFYDPDKIFSTCTFDRSILMKRLREL AFLNRGITIVFEDDRDVS
FDKVTFFYEGGIQSFSVSYLNQNKESLFSEPIYICGTRVGDDGEIEFEAALQWNSGYSELVYSYANNIPTRQGGT
HLTG FATALTRVINTYIKAHNLA KNNKLALTGEDIREGLTAVISVKVPNPQFEGQTKQKLGNSDVSSVAQQV
VGEALTIFFEENPQIARMIVDKVFVAAQAREAAKKARELTLRKSALDSARLPGLIDCLEKDPEKCEMYIVEG
DSAGGSAKQGRDRRFQAILPIRGKILNVEKARLQKIFQNQEIGTIIAALGCGIGADNFNLSKLR YRRIIIMTDAD
VDGSHIRTLTLLTFFYRHMTALIENECVYIAQPPLYKVS KKKDFRYILSEKEMDSYLLMLGTNESSILFKSTERE
LRGEALESFINVILDVESFINALEKKAIPFSEFLEMYKEGIGYPLYLAPATGMQGGRYLYSDEEKEEALAQEE
THKFKIIELYKVAVFVDIQNLKEYGLDISSYLIPQKNEIVIGNEDSPSCNYSCYTLEEVINY LKNLGRKGIEIQR
YKGLGEMNADQLWDTTMNPEQRTLIRVSLKDAVEADHIFTMLMGEEVPPRREFIESHALSIRMNNLDI

>core/64/4/Org4_Gene526

MNKRTLLFVSLIGIAFVGCQIFFGYNEFRSCKNLA EKQRKISEQTLAAVESVGLSVASWDTDVNGEEHKNNY
AVRVGDKLFL LHNGEAAQS VYSSGESWSFVDHKCGFDNIHLALYRQQGSSFNPTNTGKVFLPTNHEGLPVL
VVEFRNNKEPLVFLGEYAQGRISNKDSTIFGTALVFWRSGSDYIPLGLYDSREEKLVS LDDLPI TRAVIFGNDQD
SAKSSDTANH YVLFNDYMQUIVSEESGSIEGINLPFASTNNKSIVNEIGFDRDLASEKSPEALFPGLSSKL PDGQ
QAKNSIGGYYP LLRRGLLSDSKLLPLEYHALNVVSGRELATPVALRYRVLSYTPHSIQLES LDRSVQKVYKL
PENPEEKPYVFETAITLTKETEDVWVTSGVPEVEIMSNASVPTIKYRVIKKNKGSLDKVKLPKVKEPLAVRRG

VYPQWILNSNGYFGIILTPLSEIASGYGSLYISGSTAPTRLSAISPKNQLYPASKYPGYETLLPLPKDAGTHRFL
VYAGPLAEPTLKVLDKTITQEKGGENPEYLDSISFRGVFAFITAPFAALLFIIMKFFKLVTGSWGISIILLTVFLKL
LLYPLNAWSIRSMRRMQILSPYIQQIQQKYKNEPKRAQMEIMGLYKTNKVN PITGCLPLLIQLPFLIAMFDLLK
SSFLLRGASFIPGWIDNLTAPDVLFSWQTSIWFIGNEFHLLPILLGIVMFLQQKVTSLHKKGPVTDQQKQQQV
MGNMMAILFTAMFYNFPSGLNIYWLSSMILGVVQQWITNKILDSKHLKNEVVLNNKKHR

>core/65/4/Org4_Gene354

MRIPITLLQTYFSEPLSTKEILEACDHIGIEAEIENTTLYSFTSVITAKILHTIPHPNADKLRVATLTDGAKEHQV
VCGAPNCEAGLIVALALPGAKLFDSEGKAYTIKKSKLRGVESQGMCCGADELGLDELQIQERALLELPEATP
LGEDLATVLGNTSLEISLTPNLGHCASLLGLAREICHVTQANLVIPKEFSFENLPTTALDMGNDPDICPFFSYV
VITGISAQPSPIKLQESLQALKQKPINAIVDITNYIMLSLGGQPLHAYDASHVALDSL RVEKLSTPESLTLLNGET
VLLPSGVPVVRDDHSLGLGGVMGAKAPSFQETTTTTTVEAAAYFLPEALRASQKLLPIPSESAYRFTRGIDPQN
VVPALQAAIHYLEIFPEATISPIYSSGEICRELKEVALRPKTLQRILGKSFSIEILSQKLQSLGFSTTPQETSLLVK
VPSYRHDINEEIDLVEEICRTESWNIETQNPVSCYTPYKLRKRETARFLANAGLQEFFTPDLLDPETAALTRKEK
EEISLQGSKHTTVLRSSLLPGLLKSAAATNLNRQAPSVQAFEIGTVYAKHGEQYQETQTLAILLTEDGESRSWLP
KPSLSFYSLKGWVEKLLYHHHLSIDALTESSALCEFHPYQQGVLRHKQSFATLGQVHPELAKKAQIKHPVF
FAELNLDLLCKMLKKTTKLYKPYAIYPSSFRDLTLTPEDMPANLLRQKLLHEGSKWLESVTIISIYQDKSLET
RNKNVSLRLVFQDYERTLSNQDIEEYCYRLVALLNELLTDTKGTINS

>core/66/4/Org4_Gene532

MLIMRNKVILQISILALIQTPLTLFSTEKVKEGHVVVDSITIITEGENASNKHPLPKLKTRSGALFSQLDFDEDLR
ILAKEYDSVEPKVEFSEGKTNIALHIAKPSIRNIHISGNQVVPEHKILKTLQIYRNDL FEREKFLKGLDDLRTY
YLKRGYFASSVDYSLEHNQEKGHIDVLIKINEGPCGKIKQLTFSGISRSEKSDIQEFIQTKQHSTTTSWFTGAGL
YHPDIVEQDSLAITNYLHNNGYADAIVNSHYDLDDKGNILLYMDIDRGSRYTLGHVHIQGFVLPKR LIEKQS
QVGPNDLYCPDKIWDGAHKIKQTYAKYGYINTNVDFLIPHATRPIYDVTYEVSEGSPYKVGLIKITGNTHTK
SDVILHETSLFPGDTFNRLKLEDTEQRLRNTGYFQSVSVYTVRSQLDPMGNADQYRDIFVEVKETTTGNLGLF
LGFSSLDNLFGGIELSES NFDFLGARNIFSKGFRC LRGGGEHLFLKANFGDKVTDYTLKWKPHFLNTPWILGI
ELDKSINRALSKDYAVQTYGGNVSTTYILNEHLKYGLFYRGSQTSLHEKRKFLLGPNIDS NKG FVSAAGVNL
NYDSVDSRPTPTTGIRGGVTFEVSGLG GTYHFTKLSLNSSIYRKLTRKGVLKIKGEAQFIKPYSNTTAEGVPVS
ERFFLGGETTVRGYKSFIIGPKYSATEPQGGLSSLLISEEFQYPLIRQPNISAFVFLDSGFVGLQEYKISLKD LRSS
AGFGLRFDVMNNVPVMLGFGWPFRPTETLNGEKIDVSQRFF FALGGMF

>core/67/4/Org4_Gene970

MLLLISGALFLTLGISGLSAAISFGLGIGFSALGGVLVVSGLLCLLVKQEVSEERPEEIPAVQPEEIEGVPVTPF
EKPALDEAQKEQKAQKILEQLPKELDQLDRYIQEVVSCFRKLKDLKCEDQGLLKDAKEKLQVFD FVWKDM
MTEFVELQQIIVQEGWYKELHIQNLDDLGP NLFNDSRLSEHCVSLCYLEELCGYLP SGDARASRLKRS LREV V
ARFMKVVDTRKVAITFERNNYGVAKKTFEETFRALED CVCRSLSKSYRDAFYEYEKAKILRS GHIEWLRDD
RNSVLAEQRFQDARDRWEYLKETVFWVKEDGSIDIEDVANPSAWNDRFPVRMFFQDRQDKILGDESWEWW
GGCRKAYHTSHAVLQAAFEKDKSKDNLQKVKKHDERMFTFFQKNCDREYQKALERLRELQALYPEVSVSL
VEAGREENLGSNLERAYENLEEKYQRCVRDQEDYWRKVEKEEAEFRANGTKIRSMEEVLGYIQILED LIESW
SLKINKFEQSVLGFNF EVTQELDNKILFHATNRLNVLGEDIKDMLSRVEEIE MMLRVIELPLLPIKQALEKAFV

QYNSCKAKLTKVEPCFRESPAYITSEERLQSLDQTLERAYKEYQKRFQEPSRLESEVSGCREHLREQVKQFET
QGLDLIKEELIFVSDVLFRKMVSRLVSTVHVPFMEFYEYFELHRLRLRAQWMANAEIYSKVRKAFFPEMLKE
TLEKAKAPREEEYWLLCEERKSKEKRLILNKIEAAQQRVKDLEPPPIKETGKQKRK

>core/68/4/Org4_Gene436

MASGIGGSSGLGKIPPKDNGDRSRSPSPKGELGSHEISLPPQEHGEEGASGSSHIHSSSSFLPEDQESQSSSSAAS
SPGFFSRVRSGVDRAKLSFGNFFSAESTSQARETRQAFVRLSKTITADERQDVSAAATEARVAEDASVSG
ENPSQGVPEPSSGPEPQRLFSLPSVKKQSGLGRLVQTVRDRIVLPSGAPPDSEPLSLYELNLRLSSLRQELSDI
QSNDQLTPEEKAEATVTIQQLIQITEFQCGYMEATQSSVSLAEARFEGVETSDEINSLCSELTDPQLQELMSDG
DSLQNLDETADDLEAALSHVRVSFSLDDNPTPIDNNPTPISQEEPIYEEIGGAADPQRTRENWSTRLWNQIRE
ALVSLGMLSILGSILHRLRIARHAAAEAVGRCCTCRGEECTSSSEGDSMSVSGSPSEIDETERTGSPHDVPRRD
GSPREDSPLMNALVGWARKHGAKTKESSESSTPEISISAPIVRGWSQDSSVSFIVMEDDHIIYDVPRRKDGIYD
VPSSPRWSPARELEEDVFGDDEVPTTSVEPSKDENIYMTPLATPAIYDLPSRPGSSGSSRSPSSDRVRSSSPNR
RGVPLPPVPSPAMSEEGSIYEDMSGASGAGESDYEDMSRSPSPRGDLDEPIYANTPEDNPFTQRNIDRILQERS
GGASASPVEPIYDEIPWIHGRPPATLPRPEHTLTNVSLRVSPGFGPEVRAALLSESVSATMVGAENAVAPTEPG
HGESEYLEPLGELVATTKILLQKGWPSGESNA

>core/69/4/Org4_Gene683

MLLLISGALFLTGLIPGLSGAISFSLGIGLSALGGVLMISGLLCLLVKREVSEERPEEIPTVQPEGVPLAPSEEP
LQAAQKTLAQLPKELDQLDQTDIQEVFACLRKLKDSKYESRSFLQDAKEKLRIQDFVVEDALSEIFELRQIVDQ
EGWDLNFLINGGRSLMVTAEPESLDLFHVWKRLGYLPSGDVRGEELKKSVEIVARLMRLYCEIHKVAVAF
DRNSYAMA EKAFKALGALEESVYRSLTQSYRDKFLESERAKILWNGHITWLRDDAKSGCAEKKLRDAEER
WKKFRKAVFWVEEDGRIEITYVIGDRGEVLEPYRQERMNEITFHELYDKITSVKDTHRKYALAKTTFEKKRS
RRNLQAVEEANACRLKYVRDWDYDQEFQKAGERLEKLHALYPEVSVSIRENRIQATRSNLEKAYEAEENYR
CCVREQEDYWKEEEKREAEFREKGTKVYSPEEVSEHLQILEDLLEVCSSTLTIAEVVVLGVGLEATEEIEYIL
SDAANRLKVLCEDADDMTFRIKEIEMMLRMAELPLLPIKQAFNAFVQYNSCKENLAKVEPYCQESPAYVNS
NKRLES LDQALQNVYQEYQKRFQGGASGLESEVSAYREYLREQITEFETQGLDVIKEELLFVSSTLKS KSSYDP
LIAKVPCMKFYYQYYDGIDKARVQSRWLEKSERYRKAKKGFQEMLKEGLFKEDQALKEEDYRLYREERMN
KESHLICNKIAAARRRVQEFESMEISEIPEEKAGFMDKARS LFTREDRS

>core/70/4/Org4_Gene969

MLFSKNFSTDNGGAITAKTSLTGTTSALFSENTSSKKGGAIQTS DALTITGNQGEVSFSDNTSSDSGAAIFTE
ASVTISNNAKVVSFIGNKVTGASSTTTGDMSSGAICAYKTSTD TKVALTGNQMLLSNNTSTTAGGAIYVKKL
ELASGGLTLFSGNSVNGGTAPKGGAI AIEDSGELSLSADSGDIVFLGNTVTSTTPGTNRSSIDLGTS AKMTALR
SAAGRAIYFYDPITTAATTTVADV LKVN ET PADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGGT
LSLKHGVT LQTQAFTQQADSRLEMDVGTTL EPADTSTINNLVINISSIDGAKKAKIETKDTAKNLTLSGTITLL
DPTGTIFYENHSLRNPQSYDILELKASGTVTSTAVTPDPIMGEKFHYGYQGTWGPIVWGTGASTTATFNWTKT
GYIPNPERIGSLVPNSLWNAFIDISSLHHLMETANEGLQGDRALWCAGLSNFFHKDSTKTRRGFRHLSGGYVI
GGNLHTCSDKILSAAFCQLFGRDRDYFVAKNQGT VYGGTLYYQHNETYISLPCKLRPCSLSYVPTEIPVLFSG
NLSYTHTDNDLKT KYTTYPTVKGSWGNDSFALEFGGRAPICLDESALFEQYMPFMKLQFVYAHQEGFKEQG

TEAREFGSSRLVNLALPIGIRFDKESDCQDATYNLTLGYTVDLVRSNPDCTTTLRISGDSWKTFGTNLARQAL
VLRAGNHFCFNSNFEAFSQFSFELRGSSRNYNVDLGAKYQF

>core/71/4/Org4_Gene848

MTLQPSYIHFTRNVTTALSGGKIDTSAIELSCSALFFQELQDKAQGLKHALGLVQELSAEALPPAQVQTSISYP
PTEEFSRPGISAGIIDRTMPTFTDDEVKAILQNPNFETSKIFVEGLDKVFKSYLDSVTPPEGIDPSNPESAILNYIT
LLNNLKPKFAAGATPTDADYNALYALPGDFVKEIEALKAPDAPPKSKVHAFWQEIMTIYNNMQVLSYPVTD
YLVNQIADLSLNITAAQEVQQYLKNFYLSILKDILNPGWTDQPQATHYPADAEYNARDAGVIQSLLNLSGNYRQ
LTENMLPNTDTSLPQEIIAQIRNFQNGVNGTIISTQTTPSATMRLDTLLGVIYTYQCCATIFGTSYGTSTPAKQN
YIDAINQEKSYPWQARANGFDVTSQVFEQFVTNIQSGTQYRGMDFKNNKVNEINPIFLSQAASFLRYPYNL
MSRSMYQTIEDAANRSITALDGLISGWSTQIATFQTQKNSLDPSLLKYFDTMKANKESFVTTAPLQMVYSSL
MLDKYLPQTQQNVIASLGIQMTYSNKAAYLNELIKEITTFQSADIYYSLSIYLLKQMNLLQAVADPIGKAVGVNL
DEKTRAMADITRCNKIKAAIDKMLVEIKADAELSKSQIRELVDTLTNFKSQSDDLIRNLSCLLGFLSGLTLKAV
NDPNATYEAFTAEIFTEPFNNWKRQLATFESFVIQGGQNGITPGGQQQLQAMESSQQDFSTFNQNNQQLALQ
LESSAMQQEWTLVSAALALLNQMVSKIARRIKS

>core/75/4/Org4_Gene871

MVFFRNSLLHLVALSGMLCCSSGVALTIAEKMASLEHSGSGADDYEGMASFNANMREYSLQLSKLYEEARK
LRASGTEDEALWKDLIRRIGEVRGYLREIEELWAAEIREKGGNLEDYALWNHPETTIYNLVTDYGTEDSIYLI
PQEIGAIIKIATLSKFVVPKESFEDCLTQILSRLGIGVRQVNSWIKELYMMRKEGCSVAGVFSSRKDLEALPETA
YIGFVLNSNVDAHTNQHVLLKKFINPETTHVDVIAGRVWIFGSAGEVGELLKIYNFVQSESIRQEYRVIPLTKID
AGEMISILNAAFREDLTKDVSEESLGLRVVPLQYQGRSLFLSGTSALVQQALTLIRELEEGIENPTDKTVFWYN
VKHSDPQELAALLSQVHDFVSGENKASVGAADGCGSQLNASIQIDTTVSSSAKDGSVKYGNFIADSKTGTLI
MVVEKEVLPRIQMLLKKLDVPPKMMVRIEVLLFERKLAHEQKSGLNLLRLGEEVCKKGCSPSVSWAGGTGILE
FLFKGSTGSSIVPGYDLAYQFLMAQEDVRINASPSVVTMNQTPARIAVVDEMSIAVSSDKDKAQYNRAQYGI
MIKMLPVINVGEEDGKSYITLETDTITFDTTGKNHDDRDPDVTRRNITNKVRIADGETVIIGGLRCKQMSDSHDGI
PFLGDIPGIGKLFMGMSSTSDSLTEMFVFITPKILENPVEQQERKEEALLSSRPGEREEYYQALAASEAAARAAH
KKLEVFPASGVSLSQVEGQEYDGC

>core/76/4/Org4_Gene799

MGYIESSTFRLYAEVIVGSNINKVLDYGVPENLEHITKGTAVTISLRGGKKVGVYIYQIKTTTQCKKILPILGLSD
SEIVLPQDLLDLFWISQYYFAPLGKTLKFLPAISSNVIQPKQHYRVVLKQSKAKTKEILAKLEVLHPSQGAV
LKILLQHASPPGLSSLMETAKVSQSPIHSLEKLGLDIVDAAQLELQEDRLTFFPPAPKDLHPEQQSAIDKIFSSL
KTSQFHTHLLFGITGSGKTEIYLRATSEALKQGKSTILLVPEIALTVQTVSLFKARFGKDVGVLLHHKLSDSK
RTWRQASEGSLRILIGPRSAFCPMKNLGLIIVDEEHDPAYKQTESPPCYHARDVAVMRGKLAHATVVLGSA
TPSLESYTNALSGKYVLSRLSSRAAAAHAPAKISLINMNLEREKSKTKILFSQPVLKKIAERLEVGEQVLMFFNR
RGYHTNVSCTVCKHTLKCPHCDMVLTFFHKYANVLLCHLCNSSPKDLPQSCPCLGTMTLQYRGSGETEKIEKI
LQQIFPQIRTIRIDSDTTKFKGSHETLLRQFATGKADVLIGTQMIAGMNFSAVTLAVILNGDSGLYIPDFRASE
QVFQLITQVAGRSGRSHLPGEILIQSFLPDHPTIHSAMRQDYSAFYQSQEITGRELCEYPPFIRLIRCIFMGKCPKQ
TWEEAHRVHNILKEQLESTNPLMPVTPCGHFKIKDTFRYQFLIKSAYVIPVNNKKLHMLAKLSPKVKFMID
VDPMTTFF

>core/77/4/Org4_Gene30

MEKICGYLEQILVENKDSGDITAYIKIPNKTTPILIKGKLPQPLELGSPIQIYGVWSHSPSNTKYFQIHSYDSPLL
YEYRGVFHYLTSLIKGIGPKIAEKIIEKFQEKTCYVLDITPERLSEVSGISETRCVSICKQLCEQKILRKTLFLQ
EYNIPIHYGVRIFFKYQEKSIEKICEDPFLAREMEGIGFKTADFIAMKLGVPNRSESRLCAGIQHSLEELQEEG
HTCYPIELLIDVVAKLLNQDVFDTPITLEEIDTQILNMQKRKLLHIQDISGTLHVWTRYLHLAEKTIVSDLKRIL
FSSRRIRSIDGEKAIAWVEENLSIDLAEQQREAIKACFSEKLLIITGGPGTGKSTITQAILKIFEQVTHKIILAAPT
GKAAKRMTEITQKHSVTIHALLQYDFKTKSFRKNHDNPIDCDLIIVDESGMMDTHLLHHFLKALPDYTTLVFI
GDIHQLPSVGPNGILKDLITSNKMTVIRLNKIFRQVHDSGIVTNAHRVNEGELPILYSETGRRDFLFFQKDDQE
EALNHHIHLVTKFVPQKYHIYPQDIQVLAPMKKGTGLGIYNLNKALKHALNPKKANLHGRFQSYAVGDKVMQI
RNNYNKEVFNGDIGYVSTINFEDKAVVVRMEGKHVGYSFSELDDLVLAYATSVHKYQGSSEPCIIPIHTSHF
MMLYRNLLYTAITRGKKLVILVGTKKAIAIATRNNRVQHRCTGLAEVLKELDTKKNYADL

>core/78/4/Org4_Gene457

MLSFFYKHQKKFIGIVIAVVCVSGIGVGWGRFSREGSAESTSRRTVFTTASGKRYVEKDFMAMKKFFAHEAY
PFTGNPRAWNFINEGLLTDYFLTTRVGEKLFLKVYHPGEKIFSKEKAYQPYRRFDAPFISSEEVWKSSAPQLLE
ILKVFFQIENPISKEGFLARVKLFLEERRFPHYVLRQMLEYRRQMFALPPDEALSRGKDLRLFGYQTIQDWFG
DAYLSAAVELLIRFIDEQKKVLPRPSKQEARDDFYDKAKHAYTKISKNKEFSLSGFEEFVNSYFQFLEISESEFF
NMYRDILLCKRALLLLQGGVSFDFQPLTTFFVQGKDSIQVEFFRLPKEYSFKTKQELKAFEVYLKLVSLPKSD
SLDVPNEILPIATIKAKEPRLVGRRFSIDYKRVALQDLAATVPMVEVLHWQQNSEHFQEILQQFPDVETCQSY
KDFQHLKPALRDKISLFTRKEILRARPERILQSLQQVPKQSQEVLLSAGKNSALPGISDGQQLAKVLLENEVLD
LYSQDAETYYTIIVNSSFEKEEVLPYREVLKRDLASQLLTSHGHLVDMERLESALRTRYPGEEGASLWQRRRL
WKVVENHRLGRHLEGSFSWSLDRSLKTFSRGDKELPQEFDRIFSMKVGDYSSVFMSPNEGPCYYQCLSHLLY
DRPASVDKLFLAKSQLDEELLGSYMERFIEQGVR

>core/79/4/Org4_Gene258

MDYLEKLQVLIIEGQSANFLSLWEEYCFNDVVRGRELVEILEKVKSSSLASLFGKIVDTVVPWLWEKIEGKDK
DRVLQLILDQLTSNSQMFFDIATEYVNKKYSGEENFNEALRVVGLRDGRDFQFSLSRFDFLMHMHKGNFVFH
QGGWGVGEVMGVSFLQKQVLIEFEGIMSAKDISFETAFKSLTPLSGDHFLSRRFGDPDGFEAFAKENPIEVIEI
LLRDLGPKTAKEIKDELVDLVIPEADWNRWWQSAKTKIKKGTRIISPDNPKEPYVLSDAECSHMGQLERKLG
LSLNSAEKISLIYHFIRDLHSELKNIEIRKSLVKALQDLDVEEGNKSILQRELLSEYLGIKDASIDKEYITSLE
DDISRLLENMPIVALQKSFLSLVRKYSSFWQQVFMQILLYTTSPTMRDFVYKTIKNDPSSVEVLKKRLLDSA
HPMMFPELFFVWFFLKLGNHEDGLFDPEDKEVLRFLFLESALNFMYQVASTPHKELGKKLHHYLVGQRYLAVR
QMIEGASLPFLKELLLLSTKCPQFSSADLNVLQSLAEVVQPTLKKNKS NVEEENVLWSTSESFSRMKAKLQSL
VGKEMVDNAKEIEDARSLGDLRENSEYKFALEKRARLQEEIRVLSEEINRARIITKDLVFTDKVGVGCKVTL
KGDAGEVVEYITILGPWDADPDSCILSLQSKLAQNMLGKKLNDVVILQGKEYKISRISQIWEEHGA

>core/80/4/Org4_Gene433

MVDKLIHPWDLDLLVSGRQKDPHKLLGILASEDSSDHIVIFRPGAHTVAIELLGELHHAVAHRSGLFFLSVPK
GIGHGDYRVYHQNGLLAHDPAFPPLWGEIDSFLFHRGTHYRIYERMGAIPMEVQGIGSVLFLVLWAPHAQR
VSVVGDFNFWHGLVNPLRKISDQGIWELFVPGLGEGIRYKWEIVTQSGNVIVKTDOPYGKSFDPPPQGTARVA

DSESYSWSDHRWMERRSKQSEGPIAIEVHLGSWQWQEGRPLSYSEMAHRLASYCKEMHYTHVELLPITEH
PLNESWGYQVTGYAPTSRYGTLQEFQYFVDYLHKENIGVILDWVPGHFPVDAFALASFDGEPLYEYTGHS
QALHPHWNTFTFDYSRHEVTNFFLLGSALFWLDMHIDGLRVDASMLYRDYGREDGEWTPNIYGGKENL
ESIEFLKHLNSVIHKEFPGLTFAEESTAFPGVTKDVDQGGGLGFDYKWNLGWMHDTFHYFMKDPMYRKYH
QKDLTFSWYAFQESFILPLSHDEVVHGKGSVLNKLPGDTWTRFAQMRVLLSYQICLPGKKLLFMGGFEGQ
YGEWSPDRPLDWELLNHHYHKTLRNCVSALNALYMHQPYLWMQESSQECFWVDFHDIENNVIAYYRFA
GSNRSSALLCVHHFSASTFPSYVLRCEGVKHCELLNTDDESFGGSGKGNRAPVVCQDHGVAWGLDIELPPL
ATVIYLVTF

>core/81/4/Org4_Gene953

MNKFKTYLQTALIALFFSFPALSGSFSSIQAEITQQVNHPGAELLSEGSYIPGLQTFRLGIKITASKGSHIYWK
NPGEIGSPLKISWQLPKGFVVEEHWPTPKVFEEEGTTFFGYEDSALIVADVRAPEGYTPGQEVELRAQVEWL
ACGDSCLPGNVDLKLTLPYEEKEPSLYPDTHAEFTKTLHAQPRVLENDHSVQVAQKGKNEIILNISKKINATK
AWFVSEKADKLFAYAETSSEGTGTAWRLKVKNLSGVQKNEKLHGILLADHTGRPVESLTIHSEVLGQTGS
AVAGLSQYITILIMAFLLGGVLLNIMPCVLPLVTLKVYGLIKSAGEHRSSVIANGLWFTLGVVGCFWGLAGVAF
ILKVLGHNIGWGFQLQEPMFVATLIIVFFLFALSSLGLFEMGTMFANLGGKLQSSEMKSNNKAVGAFFNGIL
ATLVTTTPCTGPFLGSLGLVMSLSFLQQLLIFTAIGLGMASPYLVFSVFPKMLSVLPKPGGWMSTFKQLTGFM
LLATVTWLWVIFGSETSTTSVVVLLGGLWLAGLGAWILGRWGTPVSPKKQRCVACSLFFAFLGGAISVSGLA
SHYFAEPQQTVSVNEDSLWQPFSLKLAQLRAQGRPVFNFTAKWCLTCQMNKPVLYGDAVQKMFETHGI
VTLEADWTRKDPGITEELARLGRASVPSYVYYPGDNSAPVVLPEKITQNLLEDVVSFRVR

>core/82/4/Org4_Gene539

MIRSPLPFISSKRALNMLGLQDEFSCPEDVVDLFLSEIELLAQQDEPSEGYLALSRSLLMMTHNHPKVVKRVIF
YGVSYGLKHKSMSIFIDVLIYIDFLFEKLGISASDRLSLCSARTCINFELYSQTGEMKFLSEVVDNFRLLIEQLLK
MHPQLKNRLGWEHFRIGAKQEEVSLVASASVYQAVGRSFIELYHKHLELSDLACGMKCLALALDLSPPNAH
IHADYAKGLVVLGTRQGKSLIERGMEHFSKAIFLSFSRDGDTLAYQNYRYSYALASVKLFDLTYKKEHFDQ
AMNILYQTVQAFPNLSGLWMVWGELLIRSGWLNSNMKYIEVGLEKLASLQKKTNDPIALSGLLATGIAILGL
YLEEPNLFKESRHLISAMRTFPGNSALVHALGVVQLCSALYFNEDSHFASAISCFQSCLEWDLATGMWQK
LFDAYFSWGVKKKSARLLRKAVDVASRLCSLRPEAFLFWSDRGLALKCLAEATIDEAYKEIFLSESLHYQR
AWDLGRLEILELWGQSHYLLAELQQSLFHYDEAYTLLTKVDLTLSSSRVKLILAAVLLGKGRLLQDTPAE
EAREILEPLVEVYLEDENFLLLLKGKYLFLFWKNKNVCLGKLARTYLEKATSLGCPEAYYTLGKFYAVIKDV
NKAWGMVIRSAQYGVRITEAKWLNDPYLANLREIHTFREVVENQKGRLWLGKNTMKRN

>core/83/4/Org4_Gene518

MNKLLNFVSRTLGGDAALNMINKSSDLILALWMMGVVLMIIPLPPPVDLMITINLSISVFLLMVALYIPSAQ
LSVFPSSLITTFMRLGINISSSRQILLKAYAGHVIQAFGDFVVGNYVVGFIIFLIITIIQFIVVTKGAERVAEVA
ARFRLDAMPGKQMAIDADLRAGMIDATQARDKRAQIQKESELYGAMDGAMKFIKGDVIAGIVISLINIVGGL
TIGVAMHGMDLAQAAHVYTLLSIGDGLVSQIPSLLIALTAGIVTTTRVSSDKNTNLGKEISTQLVKEPRALLA
GAATLGVGFFKGFPLWSFSILALIFVALGILLTTKSAAGKKGGSGASTTVGAAGDGAATAGDNPDDYSLT
LPVILELGKDLKLIQHKTKSGQSFVDDMIPKMRQALYQDIGIRYPGIHVRTDSPSLEGYDYMILLNEVPYVR
GKIPPRHVLNEVEDNLSRYNLPFITYKNAAGLPSAWVSEDAKAIKAAIKYWTPLEVIIHLHSYFFHKSSQE

FLGIQEVRSMIEFMERSFPDLVKEVTRLIPLQKLTEIFKRLVQEQISIKDLRTILESLEWAQTEKDTVLLTEYVR
SSLKLYISFKFSQGQSAISVYLLDPEIEEMIRGAIKQTSAGSYLALDPDSVNLILKSMRNTITPTPAGGQPPVLLT
AIDVRRYVRKLIETEFPDIAVISYQEILPEIRIQPLGRIQIF

>core/84/4/Org4_Gene350

MYKRCVLDKILKGIVAGSLILLYWSSDLLERDIKSIKGNVRDIQEDIREISRVVKQQQTSQAIPAAPGVMLAPK
LVRDEAFALLSGDPSYPNLLSLDPYKQQTLPPELLGTNFHHPHGILRTAHVGKPENLSPFNGFDYVVGFDYDLCLPS
LASPHVGKYEESPD LAVKIEEHLVEDGSGDKEFHILRPNVFWRPIDPKAFPKHVQLDEVFQRPHPVTAHDI
KFFYDAVMNPYVATMRAVALRSCYEDVVSVSVENDLKL VVRWKAHTVINEEGKEERKVL YSAFSNTLSLQ
PLPRFVYQYFANGEKIHEDENIDTYRTNSIWAQNFTMHWANNYIVSCGAYYFAGMDDEKIVFSRNPFDYDPL
AALIDKR FVYFKESTD SLFQDFKTGKIDISYLPPNQ RDNFY SFMKSSAYNKQVAKGGAVRET VSADRAYTYI
GWNCFSLFFQSRQVRCAMNMAIDRERIEQCLDGQGYTISGPFASSSPSYNKQIEGWHYSPEEAARLLEEEGW
IDTDGDGIREKVIDGVIVPFRFRLCYVKS VTAHTIADYVATA CKEIGIECSLLGLDMADLSQAFDEKNFDALL
MGWCLGIPPEDPRALWHSEGAMEKGSANVVG FHN EEA D KIIDRLSYEYDLKERNRLYHRFHEIIEEAPYAF
LFSRHCSLLYKDYVKNIFVPTHRTDLIPEAQDET VNV TMVWLEKKEDPCLSTS

>core/85/4/Org4_Gene680

MKELRHESYNRALHKL SHQWVRYFLYTFVSCSFIVAI FTFAWLKVLYVPEYKAGEISRISLTAPMDFSLSWSA
HKFYKRTAHISEAFGKVYHLTLSPGSLLSKEGNADENTDYWFKKAADFLSTNFVDSSTQKCLKDL CIYPPLL
GKEKKTLEININSNKG NVIAQCFCCHKIFLIQENCPQPCFDAIMDILKIANFEMAVDKEMSGCVKGELLGKRCI
EKITKGTPILEKYQRIDDRDAKILKQLRAQLLSVHTL FSCRSLWGAI FVLLILLWGYGALKALCP EMLKSPQ
RFMLYIAILTL SLLWCRGTEIFCAYWVS YLSYPPILPFTAVLLGYFLGLPIAGFSCTFLALLYTLGSDLWNNSW
FLSINLLCSWRILVSLHRVSRLSSVFWACMKLGGVAMGSLLMFRIFTNTISREALYADGIESFVYSLITAISVVA
LIPVFEASFGASTNFSLLTYLSPENALLKRLFKEAPGTYQH SVLVGSLAEAAAQAIGADSLYCLVAAHYHDIG
KLINPGFFSENQKILQQSGHSLSPLECAKMIMRHIPEGVNLARQAGLPESFIQVIEEHHGTSVIRSAYYSHMVE
NPSTGSFDEELFRYSGNKPSSKET TIIMIADSFEAASRLKNASLPDLQRLIDQIIQGKLQDGQFSCSPVTLDELA
LISKSMVQTLYGALHSRMKYPEISYQISMDSCPKPSIGGT

>core/86/4/Org4_Gene714

MPEPLYTNKLITEKSPYLLLYAHTPVNWPWGAEAFHIAAIENKPVFLSIGCKHSRWCQVMLQESYTNPEIAA
MLNEYFVN VKVDKEELPYVAKLYGDLAQMLAVSGDHQETVSWPLNVFLTPDLIPFFSVNYLGNEGKLGLPS
FPQIIDKLHFMWEDAEEREALVEQAMKVLEIASFLEGCVRKEILDESSLKRTVAALYQDIDPHYGGVKA FPKR
LPGLLLQFFLRY SLEYQESRGLFFVDRSLSMVALGGVRDHIGGGVYSYTIDDKWLIPAFEKRLIDNALMALNY
LEAWACLGKEEYRGIGKQILSYILSELYSPEVGAFYSSEQAENWGAGGQNFYTWSVEEISNALGEDAEIFCDY
YGISREGFFNGRNILHIPVHREIEELSEKYHRSIEAIEDIVDRSRDILKGIRAQRSHRSKDDLSLTFNNGWMIYTF
AYAGRLLGEVEYIEIGKKCGEFVRNSLYKHHELYRRWREG EAKYRASLEDY GALILGVLALYESGCGSFWLS
FAEELMQEVVLSFRSEEGGFYSVDGRDSTLLIKQSPLSDGETISGNALICQCLLSLHLITEKKHYLTYAEDILQI
AQAYAHTHKFSSLGLLIASQNYFSRKHVKVLIALGDQEDRSPVLKCLSGFLPYLSLIWMTQENQEHL ETVLP
EYEHCLIPKGDCTATTIYVLEVDQCKRFKDLELFRRYLISL

>core/88/4/Org4_Gene697

MKRCFLFLASFVLMGSSADALTHQEAVKKKNSYLSHFKSVSGIVTIEDGVLNIHNNLRIQANKVYVENTVGQ
SLKLVAHGNVMVNYRAKTLVCDYLEYYEDTDSCLLTNGRFAMYPWFLGGSMITLTPETIVIRKGYISTSEGP
KKDLCLSGDYLEYSSDSLLSIGKTTLRVCRIPILFLPPFSIMPMEIPKPPINFRGGTGGFLGSYLGMSYSPISRKH
SSTFFLDSFFKHGVMGMFNLHCSQKQVPENVFNMKSYYAHLRAIDMAEAHRYRLHGDFRFTHKHVNFSGE
YHLSDSWETVADIFPNNFMLKNTGPTRVDCTWNDNYFEGYLTSSVKVNSFQANQELPYLTLRQYPISYNT
GVYLENIVECGYLNFAFSDHIVGENFSSLRLAARPKLHKTVPPLIGTSSLTGSSLIYYSDVPVISSRHSQLSAK
LQLDYRFLHKSIIQRRHIIPEFVTFITETRPLAKNEDHYIFSIQDAFHSLNLLKAGIDTSVLSKTNPRFPRIHAK
LWTTHILSNTESKPTFPKTACELSLPFGKKNTVSLDAEWIWKKHCWDHNMNIRWEWIGNDNVAMTLESLHRS
KYSLIKCDRENFILDVSRPIDQLLDSPLSDHRNLILGKLFVRPHPCWNYRLSLRYGWHRQDTPNYLEYQMILG
TKIFEHWQLYGVYERREADSRFFFFLKLDPKPKPPF

>core/89/4/Org4_Gene748

MNFQTISINLTEGKILVFETGKIARQANGAVLVRSGETCVFASACAVDLDDKVDLPLRVDYQEKFSSTGKTL
GGFIKREGRPSEKEILVSRLIDRSLRPSFPYRLMQDVQVLSYVWSYDQGQVLPDPLAICAASAALAISDIPQSNIV
AGVRIGCIDNQWVINPTKTELASSTLDLVLAGTENAILMIEGHCDFFTEEQVLDAIEFGHKHIVTICKRLQLWQ
EEIGKSKNLSAVYPLPTEVLTAVKECAQDKFTELFNIKDKKVHAATAHEIEENILEKLQREDDDLFSSFNIAA
CKTLKSDTMRALIRDREIRADGRSLTTVRPITIETSYLPRTHGSCLFTRGETQTLAVCTLGSEAMAQRYEDLNG
EGLSKFYLYQYFFPPFSVGEVGRIGSPGRREIGHGKLAEKALSHALPDSATFPYTIRIESNITESNGSSSMASVCG
GCLALMDAGVPISSPIAGIAMGLILDDQGAILSDISGLEDHLGDMDFKIAGSGKGITAFQMDIKVEGITPAIMK
KALSQAKQGCNDILNIMNEALSAPKADLSQYAPRIETMQIKPTKIASVIGPGGKQIRQIIETGVQIDINDLGVV
SISASSASAINKAKEIIIEGLVGEVEVGKTYRGRVTSVVAFGAFVEVLPGKEGLCHISEFSRQRIENISDVVKEGD
IIDVKLLSINEKGGLEKLSHKATLE

>core/90/4/Org4_Gene383

MSNQEFDLSAIRNIGIMAHIDAGKTTTTERILFYAGRTHKIGEVHEGGATMDWMAQEGERGITITSAATTVFW
LGAKINIIDTPGHVDFTIEVERSLRVLDGAVAVFDAVSGVEPQSETVWRQADKYGVPRIAFVNKMDRMGAD
YFAAVESMKEKLGANAFVHCPIGSESQFVGMVDLISQKALYFLDDTLGAKWEEKEIPEDLKERCAELRANL
LEELATIDESNEAFMMKVLEDPDSITEDEIHQVMRKGVIENTKINPVLCGTAFKNKGVQQLNVIVKWLPSPLD
RGNIRGINLKTQDEISLEPRRDGPLAALAFKIMTDPYVGRITFIRIYSGTLKKGAAILNSTKDKKERISRLLMH
ANERTDRDEFTVGDIGACVGLKFSVTGDTLCDDNQEIVLERIEFPDPVIDMAIEPKSKGDREKLAQALSSLSEE
DPTFRVSTNEETGQTIISGMGELHLDILRDRMIREFKVEANVGKPVSYKETITVSGNSETKYVKQSGGRGQY
AHVCLEIEPNEPGKGNEVVSKI VGGVIPKEYIPAVIKGVEEGLNTGVLAGYGLVDVKVSIVFGSYHEVDSSEM
AFKICGSMAVKDACRKAKPVILEPIMKVAVITPDDHLGDVIGDLNRRRGKILGQESSRGMAQVNAEVPLSEM
FGYTTSLRSLTSGRATSTMEPAFFAKVPQKIQEEIVKK

>core/92/4/Org4_Gene420

MYNLLHAHHDAAASPDGRLVSHLRKLSPHIYEGEVLIENIPAYFLGFHLPQQCIQVNLKSSLAQLGVEAVLNHL
ELNKARKEARLHVLFMSQDPIATAMLELLEPGSFVCKLFAADDRRLVRSPCYLNRMFTHTDRTGSPLLRFGK
KLEHFITLEIINDRLVVFLPILPGTICYEETIYGFLPLMSKSLTRPHLKIRKFLPLYQMVTDRPPVPEDHKILLIKT
EPLHIRTVFARVVQDLLPQGLRHTAADILEPTTQESGDIYEFYGSTSEPIERIPLEFFTLEPYKEHSFFFYRDMLQ
ETLESPQEVFRVFESIPEGEDQAAMFISKGSELLELSQDSWIIPRISPPDERHGREIQKYIEDQPCFPFLKAMET

DLITSQGVLFSTRYFPSAWLKGMFLSNYSRYYLQHIYFQIPSPTSGEFFSNRDRSFLLDLYFAGISVFWADLESK
RLLQYIKRRNKDVGMFVPKYQAEQFAQSYFIGIHGSCLIAGDYDEFLRELLTGMHTLSQQFTIPEFPPQTPLAI
LTGGGSGAMELANRVATELSILSCGNLISLDTTNAYVEAKMSYAIPDLLERQADFHVDLAVFVIGGMGTDFFE
LLELISLKTGKKALVPVFLIGPVDYWKSKITALYNSNHAVGTIRGSEWVHNCLFCLSSAKAGIEIFRRYLNHT
LPIGPEHPVPEDGFVIV

>core/93/4/Org4_Gene221

MKRSRRNFEQALENLEKLKEISLATSNDSYLNNPARFNQRKQTGSSVMEMKEALKNVENYLLEISCVSKSHA
DKALKESDFLIAGVQNVFSFLENQEDLYKSLLDEYSEVTKAYDEVKKNLKEVPTYDLSTDEETEEHKEPECFL
NNLVEVKRDRSYELFYMLDEQDKRFYNDALVQIIYKQNKLHETVNEGDP LTKTLLWNSEEVKNIASSLVIVN
DMPLRLFYQRALSHLDIEAVVKVHNAMALFFSRYEATMVFKSPKKHNIWYFND FLLFLREAWKDLNNNVI
DSQERKQTKLLASALS LGIFESKLVFEEASRYLYFNIQTKLENANGKKPLSPGQYLT DAYEELHRLISKYPNGP
LFKAMDRVLEHESRPYDPMILGILPSLEGTLKLHGKSIDIIRSPSPVTQSSILYANCNEEFLGFLNAKAHRSEVT
LVLNIQNRISRKERARSRVIEEALQEEHAPYVHAFSFPEPEELLQNLESIHGDIE TFADFFSILQEEFHKPLLAS
SFFLTKEKKEFVGSFLKEKLTALKDIFFAKKKILFRNDKLLLLHLLSYLIVFKLIERTNPNSIVV VSKDGLDYVS
VFIAGFAFFSREAFWDEHSLKLLL TNVLSPTLVARDRLVFVSHIELLSKFVNCLKKNRQGFSSLSKSF KDDIEG
WEFTGYLHELTEVSHKHNL

>core/94/4/Org4_Gene959

MQPCLNMSIVRNSALPLPCLSRSETFKKVRSHMKFMKV LTPWIYRKDLWVTAFL LTAIPGSFAHTLV DIAGEP
RHAAQATGVSGDGKIVIGMKVPDDPFAITVGFQYIDGHLQPLETVRPQCSVPYNGITPDGTVIVGTNYSPMM
GSVAVKWVNGKV FELPILPDTLDSVASAVSADGRVIGGNRNINLGASVAVKWEDDVITQLPSLPDAMNAYV
NGISSDGSIIVGTMDVDSWRNTAVQWIGDQLSVIGTLGGATSVANAISTDGTVIVGGSENADSQTHAYAYKN
GVMSDIGTLGGFYSLAHAVSSDGSVIVGVSTDSKHRYHAFQYADGQMIDLGTLGGSESYAQSVSGDGKVIV
GRAQVPSGDWHAFLCPFQAPSPAPVQGGSTVVT SQNPRGMVDINATYSSLKNSQQQLQRLLTQHSAKVQSV
SSGAPSFISVKDAISRQSPAVQNDVQKGTFLSYRSQVHGNVQNQQLLTGAFMDWKLVSAPRCGFKVALHYG
SQDALVERAALPYTEQGLGSSVLSGFGGQVQGRYDFNLGETVVLQPFMGIQVLHLSREGYSEKNVRFPVSYD
SVAYSAATSFMGAHLFASLSPKMSTAATVGVERDLNSHIDEFKGSVSAMGNFVLENSTVSVLRPFASLAMY
DLRQQQLVTL SVVMNQPLTGTL SLISQSSYNLSF

>core/95/4/Org4_Gene689

MGVVQNQVISSIRDVLKLVWELRFAEHKMLLLSRQSGSGGTFQLSCAGHEL AGVLAGKSLIPGKDWSFPYY
RDQGFPIGLGCDLSEIFASFLARTTPNHSSARMMPYHYSHKKLRIC CQSSVVG TQFLQAAGRAWAVKHSSAD
EVVYVSGGDGATSQGEFHEMLNFVALHQLPLITVIQNNHWAISVPFEDQCGADLASLGRCHQGLAVYEVDG
GNYTSLTETFSHAVDQARQHSVPALILIDVVRLSSHSNSDNQEKYRSALDLKLSMDKDPLILLEKEAINVFGLS
PFEIEEIKAEAEQEEVRRSCEIAEAFPFPSKGST SHEVFSPYTETLIDYENSESAQNLRNSEPKVMRDAISEALVEE
MTRDSGVIVFGEDVAGDKGGVFGVTRNLTEKFGPQRCFNSPLAEATIIGTAIGMALDGIHKPVVEIQFADYIW
PGINQLFSEASSIYYRSAGEWEVPLVIRAPSGGYIQGGPYHSQSIEGFLAHCPGIKVA YPSNAADAKALLKAAI
RDPNPVV FLEHKALYQRRIFSACPVFSHDYVLPFGKAAIVHPGKDLTIVSWGMPLVLSLEVAQELASQGISIEV
IDLR TIVPCDFATVLKSLEKTGRLLVIHEASEFCGFGSELVATMSEQGYAYLDAPIRRLGGLHAPVPYSKVLEN
EVL PQKESILQA AKSLAEF

>core/96/4/Org4_Gene920

MLKKPKRKPGRRTYGKSLKIFIPGTLFVHARKGFGFVSPDNPEEYPFDIFVPARDLRGALDGDHVIVSVLPYPR
DGQKLKGTISEVLARGKTTLVGTITSLVSPTSALAYTSMMSGSQLIPVELLPGRITYKIGDRILLSTPPWVDKPQE
GASPALQMLEFIGHITNAKADFQAIQAEYNLAEEFPPEVIEEASLFSQKHITQVLHSRKDLRDLLCFTIDSSTAR
DFDDAISLTYDHNNNYILGVHIADVSHYVTPHSHLDKEAAKRCNSTYFPGKVIPMLPSALSNDLCSLKPNVDR
LAVSVFMTFTKSGHLSDYQIFRSVIRSKYRMTYDEVNDNIEKKHSHPLSKILNEMATLSKKFSDIREERGCIKRFV
LPSVTMSLDNLQEPVALIENHQTFSHKLIEEFMLKANEVVAYHISHQGVSLPFRSHEPPNDENLLAFQELAKN
MGFDITFTPTQEPDYQYLLQTTSAGHPLEQVLHSQFVRSMKTASYSTENKGHYGLKLDYYTHFTSPIRRYIDL
IVHRLLFNPLSIDQTHLEIIVRACSTKERVSAKAENSFENLKKTRFINKFLQEOPKTTYHAYIITANHEGLSFVV
TEFCHEGFIAAAELPKEYSLKKNALPESIPDKMKPGASIKVTIDSVNLLTQKIVWSIVTTTEDKPKKIKKTPSKK
KGTKKRAS

>core/98/4/Org4_Gene818

MINKELDIGILGKIAGAIKQISIESIQKASSGHPGLPLGCAELAAAYLYGYVLRQNPRDPHWINRDRFVLSAGHG
SALLYSCLHLAGFDVSLEDLQEFRQLHSRTPGHPEYGETVGVEATTGPLGQGLGNAVGMALSMKMLESRFN
RPGHKIFNGKIYCLAGDGCMEGVCSFAGSLNLLNNLVVIYDYNVVLGDGYLNEISVEDTKKRFEAYG
WDVYEIDGYDFTHIHETFSIKRGQERPVLVIAHTIIGHGSPKEGTNKAHGSPLGIEGTHETKQFWHLPEEKFF
VPPAVKNFFAHKIQEDRKAQEQLDEVVRVWSKQFPELHEEFVALTSHKLPKNLESLVQSVEMPDSIAGRAAS
NKLIQVLVQHIPPYLIGGSADLSSSDGTWIANEKVIHTYDFSGRNIKYGVREFGMATIMNGLAYSQVFRPFGGT
FLVFSYMRNAIRLAALSKLPVIYQFTHDSIFVGEDGPTHQPVEQLMSLRAIPGLYVIRPADANEVKGAWIAG
LKHTGPTVIVLSRQALPTLPAHRPFKDGVGGRGAYIVLKESGEKPDYTLFATGSEVSLALSAKELEHLDKQV
RVVSFPCWELFEAQDVDYKQSIVGGDLGIRVSIEAGSALGWYKYIGSEGLAIAMDRFGYSGAPDDVSEECGF
TTEQILQRILSQ

>core/99/4/Org4_Gene480

MEKVSSYPSVPLPLGASKISPNNRYRFALYASQATEVILALTDENSEVIEVPLHPDTRMGAIWHIEIEGISDQW
SYAFRVHGPKKHGMQYSFKEYLADPYAKNIHSPQSFGSRKKQGDYAFCYLKEEPFPWDGDQPLHLPKEEMII
YEMHVSFTQSSSRVHAPGTFLGIEKIDHLHLKGINAVELLPIFEFDETAHPFRNSKFPYLCNYWGYAPLNFF
SPCRRYAYASDPCAPSREFKTLVKTLHQEGIEVILDVVFNHTGLQRTTCSLPWIDTPSYIILDAQGHFTNYSGC
GNTLNTNRAPTTQWILDILRYWVEEMHVDGFRFDLASVFSRGPSPGSLQFAPVLEAISFDPLLASTKIIAEPWD
AGGLYQVGYFPTLSRWSEWNGPYRDNVKAFLNGDQNLIGTFASRISGSQDIYPHGSPTNSINYVSCHDGFTL
CDTVTYNHKHNEANGEDNRDGTDANYSYNFGTEGKTEDPGILEVRERQLRNFFLTLMVSQGIPMIQSGDEY
AHTAEGNNNRWALDSNANYFLWDQLTAKPTLMNFLCDLIAFRKKYKTLFNRGFLSDKEISWVDAMGNPMT
WRPGNFLAFKIKSPKAHVYVAFHVGAQDQLATLPKASSNFLPYQIVAESQQGFVPQNVATPTVSLQPHTLIA
ISHAKEVT

>core/100/4/Org4_Gene621

MKEENSAHYLALCRELEDHDYSYYVLHRPRISDYEYDMKLRKLEIERSHPEWKVLWSPSTRLGDRPSGTF
SVVSHKEPMLSIANSYSKEELSEFFSRVEKSLGTSPTYVELKIDGIAVAIRYEDRVLVQALSRGNGKQGEDIT
LNIRTIRSLPLRLPEDAPEFIEVRGEVFFSYSTFQTINEKQQQLEKTIFANPRNAAGGTLKLLSPQEVAKRKLEIS

IYNLIAPGDNDSDHYENLQRCLEWGFPVSGKPRLCSTPEEVISVLKTIETERASLPMEIDGAVIKVDSLASQRVL
GATGKHWRWALAYKYAPEEAETLLEDILVQVGRTGVLTPVAKLTPVLLSGSLVSASLYNEDEIHRKDIRIG
DTVCVAKGGEVIPKVVRVCREKRPEGSEVWNMPEFCPVCHSHVREEDRVSVRCVNPECVAGAEIKIRFFVG
RGALNIDHLGVKVITKLFELGLVHTCADLFLQTTEDLMQIPGIRERSARNILESIEQAKHVDLDRFLVALGIPLI
GIGVATVLAGHFETLDRVISATFEELLSLEGVGEKVAHAIAEYFSDSTHLNEIKKMQDLGVCISPYHKSGSTCF
GKAFVITGTLEGMSRLDAETAIRNCGGKVGSSVSKQTDYLVMGNNPGSKLEKARKLGVSILDQEAFTNLIHL
E

>core/101/4/Org4_Gene655

MRLNIHKYLFIGNKADFFSASRELGVVEFISKKCFITTEQGHFVECLKVFDHLEAEYSLEALEFVKDESFSV
EDIVSEVLTLNKEIKGLETVKALRKEIVRVKPLGAFSSSEIAELSRKTGISLRFFYRTHKDNEDLEEDSPNVFY
LSTAYNFDYYLVLGVDLPRDRYTEIEAPRSVNELQVDLANLQREIRNRSDRLCDLYAYRREVLRGLCDYDN
EQLRHQAKECCEDLFDGKVFAVAGWVIVDRIKELQSLCNRYQIYMERSVPVDPDETIPTYLENKGVGMMGED
LVQIYDTPAYSDDKDPSTWVFFAFVLFFSMIVNDAGYGLLFLMSSLLFSWKFRKMKFSKHLRVLKMNTAILG
LGCICWGTTTTTSFFGMSFSKTSVFREYSMTHVLALKKAEYYLQMRPKAYKELTNEYPSLKAIRDPKAFLLAT
ETGSAGIESRYVVYDKFIDNLMELALFIGVIHLSLGMRLYLRYSYGIGWILFMVSAYLYVPIYLGTVSLIHY
LFHVPYELGGQIGYYGMFGGIGLAVVLAMIQRSWRGVEEISVIQVFSVDLSYLRIYALGLAGAMMGATFNQ
MGARLPMLLGSIVILLGHSVNIILSIMGGVIHGLRLNFIEWYHYHYSFDGGGRPLRPLRKIVCEDAEASGIHLDN
NSIV

>core/102/4/Org4_Gene414

MSEHKKSSKIIGIDLGTNSCVSVMEGGQAKVITSSEGTRTTSPSIVAFKGNEKLVGIPAKRQAVTNPEKTLGST
KRFIGNKYSEVASEIQTPYPTVTSKSGDAVFEVDGKQYTPEEIGAQILMKMKETAEEAYLGETVTEAVITVPA
YFNDSQRASTKDAGRIAGLDVKRIIPEPTAAALAYGIDKVGDKKIAVFDLGGGTDFDISILEIGDGVFEVLSTNG
DTHLGGDDFDEVIKWMIEEFKKQEGIDLSKDNMALQRLKDAAEKAKIELSGVSSTEINQPFITMDAQGPKHL
ALTLTRAQFEKLAASLIERTKSPCIKALSDAKLSAKDIDDVLLVGGMSRMPAVQETVKELFGKEPNKGVNPD
EVVAIGAAIQGGVLGGEVKDVLLLDVIPLSLGIETLGGVMTTLVERNTTIPTQKKQIFSTAADNQPAVTIVVLQ
GERPMAKDNKEIGRFDLTDIPPAPRGHPQIEVSFDIDANGILHVSADKDVASGKEQKIRIEASSGLQEDEIQRMV
RDAEINKEEDKKRREASDAKNEADSMIFRAEKAIDYKEQIPETLVKEIEERIENVRNALKDAPIEKIKEVTE
DLSKHMQKIGESMQSQSASAAAASAANAKGGPNINTEDLKKHSFSTKPPSNNGSSEDHIEEADVEIIDNDDK

>core/103/4/Org4_Gene466

MKLLLKAVLRHKNHLVILGCSLLAILGLTFSSQMEIFSLGMIKTGPDAFLLFGRKESGKLVKVSELSQKDILE
NWQAISKDSETLTVSDATTYIAEHGKSTASLTSKLSKFVRNYIDVSRFRGLAIFLICVAIFKAVTLFFQRFLGQV
VAIRVSRDLRQDYFKALQQLPMTFFHDHDIGNLSNRVMTDSASIALAVNSLMINYIQAPITFILTLGVCLSISW
KFSILVCVAFPIFILPIVVIARKIKNLAKRIQKSQDSFSSVLYDFLAGVMTVKVFRTEKFAFTKYCEHNNKISAL
EEKSAAYGLLPRPLLHTIASLFFAFVVVIGIYKFTIPPEELIVFCGLLYLIYDPIKKFGDENTSIMRGCAAERFY
EVLNHPDLHSQKEREIEFLGLSNTITFENVSGYQEDKHILKDLSTLHKGEALGIVGPTGSGKTTLVKLLPRL
YEVSQGKILIDSLPITEYNKGSLRNHIACVLQNPFLFYDTVWNNLTCGKDMEEEAVLEALKRAYADEFILELP
KGVHVSLEESGKNLSGGQQQLRAIARALLKNASILILDEATSALDAISENYIKNIIGELKGQCTQIIIAHKLTTLE
HVDRLVLIENGQKIAEGTKEELLQTCPEFLKMWELSGTKEYDRVFPDHKLVANPTDMAITT

>core/104/4/Org4_Gene837

MFSRLFFTSFSAEVLNNTFFESGMSEDTSPLLSKQNRKLSHNLPKLSAYLSLGTYLIALLSFWLHAKNLSNLFVV
FTFFLAGTPALIKSLDNICQKVVNIDILMTSAAFGSIFIGGALEGALLVLFAISEALGQMVSQKAKSTLVSLKQ
LAPTTGWLVLLEDGNLQKVAINKIEVGNILRIKSGEVVPLDGEILHGSSSINLMHLTGEKVPKSGHPGSIVPAGA
HNMEGSFDLRLVLTGSDSTIAHIINLVIQAQNSKPRLQQRLDKYSSVYALSIFAIASGIALLVPLFTSIPLLGQS
AFYRALAFLIAASPCALIIAIIPIAYLSAINACAKHGVLLKGGVILDRLVSCNSVVMMDKTGTLTGTGELTCIGCDYF
GPKNETFFPSVLALAEQSSSHPIAEAIVSYLMEQKVSSLPADRYLTVPGEGVRGYFNEQEAFVGRVETGLGKVP
SEYLEDIEQKIYQAKQHGEICSLAYVGNFSALFYFRDIPRPAKEIIQDLKDLGYPVSMLTGDHKVSAENTAIEI
LGISEVFFDLTPEDKLAKIRELATQRQIMMVGDGINAPALAQATVGIAMGEAGSATAIEAADIVLLHDSLSS
LPWHIQAQKQTKKVVSQNLALALAIILLVSWPASLGIPLWLAVILHEGSTVIVGLNALRLLKS

>core/105/4/Org4_Gene877

MTFQLHAPFAPCGDQPEAIARLSAGVRNQVKSQVLLGTTGSGKTFTIANVVANVNLPTLVLAHNKTLAAQL
YQEFREFFPNNAVEYFISYYDYYQPEAYIARSDTYIEKSLLINDEIDKLRLSATRSILERRDTLIVSSVSCIYGIGS
PENYTSMALVLEVGKEYPRNILTAQLVKMHYQASPIQRSASFRERGSVIDIFPAYESEALRLLEFLNDTLTSIE
YSDPLTMIPKESVSSATLYPGSHYVPEAIREQAIRTIQEELEERMAFFDDRPIEKDRIFHRTTHDIEMIKEIGFCK
GIENYSRHFTGAPPGAPPTCLLDYFPEDFLLVIDESHQTLPIRAMYRGDQSRKQSLVEYGFRLPSAFDNRPLT
YEEAQKYFRKVIYVSATPGDTEVQESSGHIVQQIIRPTGIPDPMPEIRPATGQVDDLLEEIRLRLSQKHEKILVIS
ITKKLAEDMAGFLSELEIPAAYLHSGIETAERTQILTDLRSGVIDVLIGVNLLREGLDLPEVSLVAILDADKEGF
LRSTSSLIQFCGRAARNINGKVIFYADQKTRSIEETLRETEERRRQIQLDYNKEHNIVPKPIIKAIFANPILQTSKDS
ESPKESQRPLSKEDLEEQIKKYEALMQRAAKEFRFNEAAKYRDAMQACKEQLLYLF

>core/106/4/Org4_Gene361

MATPAQKSPTFQDPSFVRELGSNHPVFSPLTLEERGEMAIAPVQQCGWNHTIVKVSFLFILALLTILGGGLLVGL
LPAVPMFIGTGLIALGAVIFALALILCLCDSQGLPEELPPVPEPQQIQIEYLRNETREVLEGTLLEVLLKDRDAK
DPAVPQVVVDCEKRLGMLDRKLRREEEILYRSTAHLKDEARYEFLLLELMRSLVADRLEFNRRSYERFVQG
IMTVRSEEGEKEISRLQDLIGLQQQTVQDLRSQIDDEQKRCWTSLQRIHQSQKDIQRAHDREASQRACEGTEM
DCAERHQLEKDLRRQLKSMREWIEMRGTIHQEKAWRKQNAKLERLQEDLRLTKIAFDEQPLFYREYKEY
LSQKLDQMOKILQEVNAEKSEKARLKS LVRDYEKQLEQQDANLKKAKAIWEEELGKQQLKDHEQTQEIKRLN
TFMLEYQDGLREAEQVAEQVRQDLRQLEEKYSHLQEEKQEKEKILEQSVNHFAERFEALQKENVVYKKKLA
DLEGAAAPTEIREEDGWILAGSASLSQKKIRELNEENQELLKLLAFKTRELTLAADVGEAEKEISKLREQIEE
QKEELRVLDTMHSEAVKDCEAAQRKCRDLEGLLSPVREDAGMRFELEIELQRLREENAQLRLEVERLEQEQL
QG

>core/107/4/Org4_Gene464

MSYRKIRSTLIVLGVFALYALLVLRYYKIQICEGDHWAEEALGQHEFCVRDPFRRGTFFANTTVRKGDKDLQ
QPFAVDITKFHLCADPLAIPCHRDEIIQGILQFIEGQTYDDLCLKDKKSRYCKLYPLLDVSVHDLRLSLWWK
GYATKHRLPTNALFFITDYQRSYPFGKLLGQVLHTLREIKDEKTGKAFPTGGMEAYFNHILEGDVGERKLLRS
PLNRLDTNRVIKLPKDGSDIYLTINPVIQTIAEEELERGVLEAKAQGGRLILMNSQTGEILALAQYPPFDPTNYK
EYFNNKERIEHTKVSFVSDVFEPGSIMKPLTVAIALQANKEASLKSQKKIFDPEEPIDVTRTLFPGRKGSPLKDI

SRNSQLNMYMAIQKSSNVYVAQLADRIIQSLGVAWYQQKLLALGFGRKTGIELPSEASGLVSPHRFHINGSP
EWSLSTPYSLAMGYNILATGIQMVQAYAILANGGYAVRPTLVKKIVSASGEEYHLPTKEKTRLFSEEITREVV
RAMRFTTLPGGSGFRASPKHHSSAGKTGTTEKMIHGKYDKRRHIASFIGFTPVESSEGNFPPLVMLVSIDDPEY
GLRADGTKNYMGGRCAPIFSRVADRTLTYLGILPDKKLRNCDEEAAALKRLYEEWNRSPK

>core/108/4/Org4_Gene269

MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSVNALMSLAD
KLGIASSNSSSSTSRADVDSTTATAPTPPPPTFDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNMKDT
AATDEETAIAAEWETKNADAVKVGAQITELAKYASDNQAILDSLGLKTSFDLLQAALLQSVANNNKAAELL
KEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNVIRDAYFAGQNASGAVENAKSNNSISNIDSAKAAIA
TAKTQIAEAQQKFPDSPILQEAEQMVIAEKDLKNIKPADGSDVPNP GTTVGGSKQQGSSIGSIRVSMLLDDA
ENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQAGAAKAAGDDSAAAALADAQKALEAALGKAGQQ
QGILNALGQIASAAVVSAGVPPAAASSIGSSVKQLYKTSKSTGSDYKTQISAGYDAYKSINDAYGRARNDAT
RDVINNVSTPALTRSVPRARTEARGPEKTDQALARVISGNSRTLGDVYSQVSALQSVMQMIQSNPQANNEEI
RQKLTSAVTKPPQFGYPYVQLSNDSTQKFIAKLESLFAEGSRTAAEIKALSFETNSLFIQQVLVNIGSLYSGYL
Q

>core/109/4/Org4_Gene379

MKKLVRLCVVLLSLLPNVLFSSDLLREEGIKKMMDKLIYHVDAQEVSTDILSRSLSSYIQSFDPHKSYLSNQE
VAVFLQSPETKKRLLKNYKAGNFAIYRNINQLIHESILRARQWRNEWVKNPKELVLEASSYQISKQPMQWSK
SLDEVKQRQRALLLSYLSHLGASSSRYEGKEEQLAALCLRQIENHENVYLGINDHGVAMDRDEEAYQFHI
RVVKALAHSLDAHTAYFSKDEALAMRIQLEKGMCGIGVV LKEDIDGVVVREIIPGGPAAKSGDLQLGDIIYR
VDGKDIEHLSFRGVLDCLRGGHGSTVVLDIHRGESDHTITLRREKILLEDRRVDVSYEPYGDGVIGKVTLHSF
YEGENQVSSEQDLRRAIQGLKEKNLLGLVLDIRENTGGFLSQAIVSGLFMTNGVVVVVSRYADGTMKCYRT
VSPKKFYDGPLAILVSKSSASAAEIVAQTLQDYGVALVVGDEQTYGKGTIQHQTITGDASQDDCFKVTVGKY
YSPSGKSTQIQGVKSDILIPSLY AEDRLGERFLEHPLPADCCDNVLHDPLTDLDTQTRPWFQKYYPNLQKQE
TLWREMLPQLMKNSEQRLSENSNFQAFLSQIKSSEKMDLSYGSNDLQLEESINILKDMILLQQCKK

>core/110/4/Org4_Gene711

MTSSSFPLLDLILSPADLKKLSSISQLPGLAEIIRYRIISVLSQTGGHLSSNLGIVELTIALHYVFSSPKDKFIFDVG
HQTYPHKLLTGRNNEGFDHIRNDNGLSGFTNP TESDHDLFFSGHAGTALSALGMAQTTPLESRTHVIPILGD
AAFSCGLTLEALNNISTDLSKFVILNDNNMSISKNVGAMSRIFSRWLHHPATNKLTQVEKWLAKIPRYGD
SLAKHSRRLSQC VKNLFCPTPLFEQFGLAYVGPIDGHNVKKLIPILQSVRNLPFPILVHVCTTKGKGLDQAQN
NPAKYHGVSANFNKRESAKHLPAIKPKPSFPDIFGQTLCELGEVSSRLHV VTPAMSIGSRLEGFKQKPERFFD
VGIAEGHAVTFSAGIAKAGNPVICSISTFLHRA LDNVFHDVCMQDLPVIFAIDRAGLAYGDGRSHHGIYDMS
FLRAMPQMIICQPRSQVVVFQQLLYSSLHWSSPSAIRYPNIPAPHGDP LTGDPNFLRSPGNAETLSQGEDVLI AL
GTL CFTALSIKHQLLAYGISATVVDPIFIKPFNDLFSLLLMSH SKVITIEEHSIRGGLASEFNNFVATFNFKVDI
LNFAIPDTFLSHGSKEALTKSIGLDESSMTNRILTHFNFRSKKQTVGDVRV

>core/111/4/Org4_Gene891

MTCISELNEAQRKAVTAPLNPVLVLGAGAGKTRVVTYRILHLINQGIAPREILAVTFTNKAARELKERIVNQ
CASTNEFDVPMVCTFHSLGVFILRRSINLLNRENNFTIYDQSDAEKLIKYALQQHNLKPNLASKIQAHISQAKN
RLLFPEDLDPNDYIDPVVSIYQEYQKKLIEANALDFDILLFTVRLRESPEAQELYNQLWKALLIDEYQDTN
HAQYTLMQLLSKQHRNVFAVGDPDQSIYSWRGANIHNLNFENDYPNAKVLCEENYRSYGNILNAANALIK
NNASRLEKELRSVKGPGEKIRLFLGSTDREEADFVAAEILQLHRVGNIKLRDICIFYRTNSQSRTFEDALLRRRI
PYEIIGGLSFYKRKEIQDILAFLRIFISKSDIVAFDRTVNLPKRGIGSTTIFALTQYAIAQGLPILKACQQALDTKD
VKLSKKQQEGLQEYLALFPQIEHAYNTLSLRDFIESVVRITGYLEILKEDADTFKDRKSNLEELYHKALESEQQ
NPKTHLELFLDDLALKGSDDDQNLTA DRVNLMTLHNGKGLEFRVSFLVGLLEEQLLPHANS LGGTyenIEEER
RLCYVGITRAQDLLYLTA AQVRS LWGTVRMMKPSRFLKEIPKDYMIQVR

>core/112/4/Org4_Gene643

MKQHYSLNKSRHILRSTYKLLKSKKLAHSPADKKQLQELLEQLEEAIFEHDQETASDLAQQALAFSNRY PNS
FGRKTYELIKALLFAGVVAFLVRQFWFELYEVPTGSMRPTILEQDRILVSKTTFGLHCPFAKKPLAFNPESVTR
GGLVVFTVGDLPIDADTKYFGLIPGKKRYIKRCMGRPGDFLYFYGGKIYGLDDAGKRIEFPSVHGLENLYH
VPYISFDGTTSSHTEGQKTIIDFKQFNQSYGRLIFPQTS MYGQFFDHKEWHQDEPNKLKDPHLSLVSYADLFG
MGNYAMVRILTEHQARTSHLLPNPGSPTKVYLEICHTANLSYPKPLL RHYEHQLSPTIQPMKTLLPLRKEHLH
LIRNNLTTSRFIVAQGCAYKYHQFKINTSGIAKAYAILLPKVPDGCYEYSKGEAYQIGFGGIRYKLKSSHPLTQ
LNDKQVIELFNCGINFSSINPVNPLQAPLPNRYAFFNQGNLYIMDSPVFIKNDPTLQKFVTSEKEKQEGSSET
QPYIAFVDKGLPPEDFKEFVEFIHNFGIQVPKGHVLVLGDNYPMSADSREFGFVPMENLLGSPLCTFWPIGRM
GRLTGVSAPTTL SGYLVSGIALATGLSLIGYVYYQKRRRLFPKKEEKNHKK

>core/113/4/Org4_Gene880

MIPFTKTIGFRLWLACAVAIAPLGINIVWLNLDQYRTIVSAISTALKENAAFKANTLTQIVPLNVDVLSLFS DV
LDDL DAGIPETPNVLLSNEMQKV FQGIYNEISLIKVF PNGDKIVVASSIPEHLGENYNHKIDIPENTPFLAALKQS
PKNQEVFSVMQANVFD AKTQELQGILYTTFSAESLLKDLLINKQSYLTVKTAILSKYGVILKASDPALHLHTV
YPDMTKEKFCQVFLNDDPCPIDSELGPLT LSPLDIGENFY SFKIKDTEIWGCIENVPSIDIAVLSYAKKEESFAPL
WRRARMYTAYFFCILLGSLIAFIVARRLSLPIRKLATAMIESRKNKNLYLTDDSLGFEINRLGHIFNAMVENLH
KQQYLAKTNFEMKENAQNALHLGEQAQQRLLPNTLPSYPHIELAKAYIPAITVGGDFFDV FVVGEGSEARLF
LIVADASGKGVNACGYSLFLKNMLR TFLSRSSSLQQA IQETSRLFYNN TKNSGMFVTLCVYCYHQTSNTMEY
YSCGHPPACYLDPDGETSWL FHPGMALGFLPEVANITSKL FHPKPGSLFVLYSDGITEAHNNNNDMFGEERL
QAAIQGLTGKSAADAVHRLMLS VKTFVGNSHQHDDITLLILKVLES

>core/114/4/Org4_Gene875

MIQVTC DQKNYEVLEGTTAAELAKQLKNSHQFIGVLINERPRDLSTHLNEGDTLVFLTSEDPEGREIFLHTSA
HLLAQAVLRLWPDAIPTIGPVIDHGFYYDFANLSISESDFPLIEDTVKQIVDEKL TISRFTYGD KQQA LAQFPQN
PFKTELIRELPENEEISAYSQGEFFDL CRGPHLPSTAHVKAFKVLRTSAAYWRGDPSRESLVRIYGT SFPTSKE L
RAHLEQIEEAKKRDHRVLGAKLDLFSQQESSPGMPFFHPRGMIVWDALIRYWKQLHTAAGYKEILTPQLMN
RQLWEVSGHWDNYKANMYTLQIDDEDYAIKPMNCPGCMLYYKTRLHSYKEFPLRVAEIGHVHRQEASGAL
SGLMRVRAFHQDDAHVFLTPEQVEEETLNILQLVSTLYGTFGLEYHLELSTRPEKDTIGDDSLWELATDALN
RALVQSGTPFIVRPGEGAFYGP KIDIHVKDAIQRTWQCGTIQLDMFLPERFELEYTTAQGTKSVPVMLHRALF

GSIERFLGILIENFKGRFPLWLSPEQVRIITVADRHIPGAKELEEAWKRLGLVVTLDDSSSESVSKIRNAQNMQ
VNYMITLGDHEINENVLAVRTRDNRVINDVSVERFLNTILEEKNSLSLTALL

>core/117/4/Org4_Gene882

MDENRKVIVVGGGLAGLSAAMQLANLGIIVELVSLTKVKRSHSVCAQGGINAALNLKPEEEDSPYVHAYDTI
KGGDFLADQPPVLEMCLAAPRIKMLDNFGCPFNRGPSGNLDVRRFGGTLYHRTVFCGASTGQQLMYTLDE
QVRRREHAGRVIKRENHEFVRLVTDHSGRACGIILMNLFNRLLEILRGDAVIIATGGPGVIFKMSTNSTFCTGA
ANGRLFLQGMAYANPEFIQIHPTAIPGRDKLRLISESVRGEGGRVWVPGDSSKRIVFPDGSERPCGETGAPWY
FLEDMPAYGNLVS RDVGARAILRVCEAGLGIDGRMEVYLDVTHLPEKTRHKLEVVLDIYKKFTGEDPNTV
PMRIFPAVHYSMGGAWVDWPAADDPDRDSRFRQMTNIPGCFNCGESDFQYHGANRLGANSLLSCLFAGLVS
GDEASRFIEAFGASQATSSDFDRALQQEKEENARLLSASGKENIFVLHEEIAKIMVRNVTVKRNNRDLQETM
DKLKEFRERLKNVSVLDSSPFANKSFHFVRQMGPMLLALAITKGALLRNEFRGSHYKPEPPERDDEHWLKT
TVVVYAPEEPEISYLPVDTRHVAPTLRDYTKSSTGKIELTNIPDNIRLPI

>core/118/4/Org4_Gene242

MTIIFYFILAALGILVLIHELGHLLVAKAVGMAVESFSIGFGPALFKKRIGGIEYRIGCIPFGGYVRIRGMERT
KEKGEKGKIDSVYDIPQGGFFSKSPWKRLVLVAGPLANILLAVLAFSILYMNGGRSKNYSDCSKVVGWVHPV
LQAEGLLPGDEILTCNGKPYVGDKDMLTTSLLEGHLNLEIKRPGYLTVPKSKEFAIDVEFDPTKFGVPCSGASY
LLYGNQVPLTKNSPMENSELRPNDRFVWMDGTLLFSMAQISQILNESYAFVKVARNDKIFFSRQPRVLASVL
HYTPYLRNELIDTQYEAGLKGWSSLYTLPYVINSYGYIEGELTAIDPESPLPQPQERLQLGDRILAIDGTPVSG
SVDILRLVQNHRSIIVQQMSPQELEEVS NRDADKRFIASYHSEDLLQILNHLGESHPVEVAGPYRLLDPVQPR
PWIDVYSSESLDKQLEVAKKIKNKDKQRYYLERLDAEKQKPSLGISLKD LKVRYNPSPVVMLSNITKESLITL
KALVTGHLSPQWLSGPVGIVQVLHTGWSVGFSEVLFWIGLISMNLAVLNLLPIPVLDGGYILLCLWEIVTRRR
LNMKIVERILVPFTLLIIFIFLTFQDLFRFFG

>core/119/4/Org4_Gene410

MRRSVCYVNP SIARAGQISTWKFLYSLATPLPAGTKCKFDLAGSGKPTDWEAPATDLSQTRNVIYAEMPEGE
IIEATAIPVKDNPVPQFEFTLPYELQVGETLTIVMGASPNHPQVDDAGNGAQLFAQRKPFYLYIDPTGEGNY
DEPDVFSMDIRGNVLKKIEIFTPSYVVKNKRFDITVRFEDEFGNLTNFSPEdTRIELSYEHLRENLNWQLFIPET
GFVILPNLYFNEPGIYRIQLKNLSTQEIFISAPIKCFADSAPNLMWGLLHGESERVDSEENIETCMRYFRDDRAL
NFYASSSFENQENLSPDIWKLINQTVSDFNEEDRFITLSGFQYSGEPHLEGVRHILHTKETKSHSKHKEYKHIPL
AKLYKSTVNHDMISIPSFTASKEHGFDNFYFEFERVVEIYNAGSSETTAALNNPFPIQGKDS EDPRTGTVIE
GLKKNLRF GFVAGGLDDRGIYKDYFDSPQVQYSPGLTAHCNKYTRESLVEALFARHCYATTGPRIVLSFNITS
APMGSELSTGSKPGLNVNRHISGHVAGTALLKTVEIIRNGEVLHTFFPDSNNLDY EYDDMVPLSSVTLKDPNG
KAPVFVYYLRVTQADNAMAWSSPIWVDLN

>core/120/4/Org4_Gene622

MESEKDIGARFLGDYRILYRKGQSLWSEDLLAEHRFIKKRYFIRLLLPNLGSSEPFMEAFHDVVVRLAKLNHP
GVLCIENVSESEGR CFLVTQE QNIPILSLTQYLKSIPRKLTELEIVDIVSQLAVLLDYVHSEGLVQEEWNLD SIYI
HVLNGVPKVLPDLGFASLIKERVLEGLISDEENRESKIKERVLLHTSEGKQGREDTYAFGAITYYLLFGFLPQ
GIFPMPSKVFSDFIYDWDFLISSCLSCFMEERAKELFPLIRKKT LGEELQNVVTNCIESSLREVDPDPLESSQNLPQ

AVLKVGETKVSHQQKESAHELFVLVEACSIDEAMDTAIESESSSGVEEEGYSLALQSLLVREPVVSRVVEAE
KEEPKPQPILTEMVLIEGGEFSRGSVEGQRDELPVHKVILHSFFLDVHPVTNEQFIRYLECCGSEQDKYYNELI
RLRDSRIQRRSGRLVIEPGYAKHPVVGVTWYGASGYAEWIGKRLPTEAEWEIAASGGVAALRYPCGEEIEKS
RANFFTADTTTVMSPNPYPGLYDMAGNVYEWQCQDWYGYDFYEISAQEPESPQGPAQGVYRVLRGGCWK
SLKDDLRCABHRNPNPGAVNSTYGFRCANIN

>core/121/4/Org4_Gene738

MKKGKLGAIVFGLLFTSSVAGFSKDLTKDNAYQDLNVIEHLISLKYAPLPWKELLFGWDLSQQTQQARLQLV
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MGIHEAIESLRFGRGSATDYSAAVRSLTSRSAAFGDAVPSGIAMKLRRPSGLIRSTPVRWRYTPEHIGDFSLV
APLIPEHKPQLPTQSCVLFSGVNSQSSSSSLFSSYMPYFWEELRVQNKQRFDSNHHIGSRNGFLPTFGPILW
EQDKGPYRSYIFKAKDSQGNPHRIGFLRISSYVWTDLEGLEEDHKDPSWELFGEIIDHLEKETDALIIDQTHNP
GGSVFYLYSLLSMLTDHPLDTPKHRMIFTQDEVSSALHWQDLLEDVFTDEQAVAVLGETMEGYCMDMHAV
ASLQNFSSQSVLSSWVSGDINLSKPMPLLGFAQVRPHPKHQYTKPLFMLIDEDDFSCGDLAPAILKDNGRATLI
GKPTAGAGGFVFQVTFPNRSGIKGLSLTGSLAVRKDGEFIENLGVAPHIDLGFTSRDLQTSRFTDYVEAVKTIV
LTSLSENAKKSEEQTSPQETPEVIRVSYPTTTSAS

>core/122/4/Org4_Gene670

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VRVLYETGHLVAFARENTCHSRLEVSHTVRAMTYFWDRFFSRHWNVGRFLVFYQNGGAYVQAALDSS
MHTQDIYVLGLSPTVYIRGNVHVQHRYVRGFWPSCLDLAACAENTSVLPGESSDGIFYPSLFSHTFDNAIR
YGERCLLVCEGMGMLPETQQQTSPLTSLEGGHEVALVLNPQQNPEALSIALRMHEERGGRLESNYMPGRS
SNPFMTSMYVLVRLNLAQIYLMSPYYSFQSNDIVCLIFISSAAVETVSYIFLTVTDSTCGRRYLVRPRLVCTG
LRNLALPTTLELLILSYPRSEGVFPNVRFILGYMCTTRVFFAWNLILHWPFRCLRHHGIQLFVHRSIIGHTLG
ARITDLTLASMRYAIVFPSIVSSCLLTALAHANTNILALDPYRLIESGDLRRPAFNDDDEMQQADNPWDAYSIGL
VINTCIYMLVLFANLIFMVYSVRRYHRSRR

>core/123/4/Org4_Gene489

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EKIKERLIALGLNIPLVADIHFFPQAAMLVADFADKVRINPGNYIDKRNMFKGTKIYTEASYAQSLRLLEEKFA
PLVEKCKRLGKAMRIGVNHGSLSERIMQKYGDTIEGMVASAIEYIAVCEKLNRYRDVVFSMKSSNPKIMVTAY
RQLAKDLDAAGWLYPLHLGVTEAGMGMDGIIKSAVGIGTLLAEGLGDTIRCSLTGCPTTEIPVCDSSLRHTKI
YLDLPEKKNPFSLQHSNFVSAKKPAKTTLWGDVYGVFLKLYPHHLTNFTPEELLEHLGVNPVTKEKAFTT
PEGVVVPPELKDAPITNVLREHFLVFHHHQVPCLYEHNEEIWDSPAVHQAPFVHFHASDPFIHTSRDFFFEKQG
HQGKPTKLVSFRDFDNKEEAISIAATEFGALLLDGLGEAVVLDLPNLPLQDVLEIAFGTLQONAGVRLVKTEYI
SCPMCGRTLFDLEEVTTRIRKRTQHLPGLKIAIMGCIVNGPGEMADADFGFVGSKTGMIDLYVKHTCVKAHIP
MEDAEELIRLLQEHGVWKDPEETKLTIV

>core/124/4/Org4_Gene336

MWTHPIAYDVIVVGAGHAGCEAAAYCSAKMGASVLMMLTSNLDIAKLSCNPAVGGIGKGHIVREIDALGGIM
AEVTDQSGIQFRILNQTKGPAVRAPRAQVDKQLYHIHMKRLLENTPGLHIMQATVESLLDKEGVISGVTTKE
GWMFSGKTVVLSSGTFMRGLIHIGDRNFSGGRLGDPSSQGLSEDLKKRGFPISRRLKTGTPPRLASSINFSCME
EQPGDLGVGFVHRTEPFQPPLPQLSCFITHTTTEKTKEIISANLHRSALYGGCIEGVGPRYCPSIEDKIVKFSDE
RHHVFLEPEGLHTQEIYANGLSTSMFPDVQYDMIRSVLGLENAIITRPAYAEYDYIHGNVIHPTLESKLIEGLF
LCGQINGTTGYEEAAAQGLIAGINAVNKVFNKPPFIPSRQESYIGVMLDDLTTQILDEPYRMFTGRAEHRLLL
RQDNACARLSHYGYELGLLSEERYELVKKQNQLLEEEKVRLQKTRQYQGSVSLAKALSREVSVDMLRE
AFPNDIRDLGTVLNASLEMEIKYSGYIDRQKILIQSLEKAESLLIPEDLDYKQITALSLEAQEKLAKFTPTLGS
ASRISGIASADIQVLMIALKKHAHH

>core/125/4/Org4_Gene629

MTTELKTEALPTRTQVDPEHCWDTTLMYANRKEWKKDFDLCSSGKDRSPIWPEFSPSHYQIDNPESLLELLS
KKFSVERKLDQLYVYAHLIHDQDITNPEGESDYQSIVYLYTLFSQEISWIQPALIALSEEKVAALLSSSVLALY
RFYLEKIFRLSPHTGTANEEKILASSFAALNVANKAFSSLSDAEIPFGIAKDSNGEEHPLSHALASLYMQSPDQ
ELRRTAYLAQFQRYDYRNTFANLLNGKVQAHLFEAKARNYPSCLEASLFQHNIPTTVYINLINETKKHTSLI
NRYFNLKKEALNLKEHFHYDVYAPISQTTSKNYSYEEGVDLVCKSLLPLGTHYVEILRNGLLSNRWVDRYEN
KHKRSGAYSSGCYDSAPYILLNYTNTLYDVS VIAHEAGHSMHSYFSREAQPYHDAQYPLFLAEIASTFNEML
LMEALSKSDQSKEDKIVIITKTLDITFATLFRQTFFAAFEYIEHSAAEQGTPLTEEFLSATYGNLQKEFYGGVVT
SDSLSALEWARIPHFYNFYVYQYATGIIAALSFAEKILTQEPGALELYLKFLKSGGSDFPLNILKKSGLDMTT
SAPLDKAFAFITKKIDLLSSLLSED

>core/126/4/Org4_Gene905

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QKLYREVIEQLAYWQEEKTRALAPLLNISIEQLLTDFLLDYISAHSLIEQKMFPEGRVILNRNINRLKHECEW
NAKTYDRIAILLSRSYFLELVESKSADIYFDYYEMVLFYLLKKIYILEQCPYAELLPEEELVSLIMEHVFILPKDK
LYPLIQLLEMWQKHVHPNSSLVVQILVDHFSTHMEGAIRFCEALVSFSGLEELHQQIITTFEELLSNKVQQIK
TEEAKQCVALLHILDPSISISEKLALSSDTLQNIVSGDDEQHTKLRNYLDLWEAIQSYDIDRQQVLVHHLVYGA
KDLWKKGGNDEKALNLLQLVLRFTSYDIECESVFLVFKQAYKQALSSSHAIARLLKLEKFISEANIPSIVISEA
EKANFLADAEYLF AHEDYDKCYLYSMWLTKVAPSPQSYRLAGLCLMENKRYDEALEFLCMLSPNDSINDY
KTQKALAFQCQKHQSKDRAAS

>core/127/4/Org4_Gene770

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WATHGVPTEINAH PHVDEGRSCAVVHNGI IENFKELRRELTAQG ISFASDTDSEIIVQLFSLYYQESQDLVFSF
CQTLAQLRGSVACALIHKDHPTILCASQESPLILGLGKEETFIASDARAFLKYTRHSQALASGEFAIVSQGKE
PEVYNLELKKIHKDVRQITCSEDASDKSGYGYMLKEIYDQPEVLEGLIQKHMDEEGHILSEFLSDVPIKSFK
ITIVACGSSYHAGYLAKYIIESLV SIPVHIEVASEFRYRRPYIGKDTLGILISQSGETADTLAALKELRRRNIAYL
LGICNVPESAIALGV DHCLFLEAGVEIGVATTKAFTS QLLLLVFLGLKLANVHGALTHAEQCSFGQGLQSLPD
LCQKLLANESLH SWAQPYSYEDKFLFLGRRLMYPV VMEAAKLKEIAYIEANAYPGGEMKHGPIALISKGTP

VIAFCGDDIVYEKMIGNMMEVKARHAHVIAIAPESEDIAAASDQQIFVPDCHFLAAPVLYTIVGQVMAYAM
ALAKGTEIDCPRNLAKSVTVE

>core/128/4/Org4_Gene772

MIPSGLVYLLYPLGFLASLFFGSAFSIQWWLSKKRKEVYAPRSFWILSSIGATLMIVHGTIQSQFPVTVLHVINL
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LIQWFYIESNNTKDFPLLFWKIGLLGGLLALVYFIRIGDPINILCYGCGLFPSIANLRLFYKEQRSTPYLDTHCFL
SAGEASGDILGGKLIQSIKSLYPNIRFWGVGGPAMRQEGQLPILNMEEFQVSGFAEVLGSLFRLYRNYRKILKT
ILKHKPATLIFIDFPDFHLLLIKLRKHGYRGKIIHYVCPSIWAWRPKRKRILEQHLDMLLLILPFEEGLFKNTSL
ETVYLGHPLVEEISDYKEQASWKEKFLNSDRPIVAAFPGSRRGDISRNLRIQVQAFLNSSLSTHGFVSSSSA
KYDEIIEDTLKAEGCQHSQIIPMNFYELMRSCDCALAKCGTIVLETALNQTPTIVMCRLRPFDFTFLAKYIFKIL
LPAYSLPNIIMNSVIFPEFIGGKKDFHPEEIIATDILLNQHSKEKQKEDCRKLCKVMTTGQIASSEFLKRIFDT
LPAV

>core/129/4/Org4_Gene881

MKHTFTKRVLFFFFLVIPIPLLLNLMVVGFFSFAAKANLVQVLHTHATNLSIEFEKKLTIHKLFLDRLANTLA
LKSYPSPAEPYAQAYNEMMALSNITDFSLCLIDPFDGSRVTKNPGDPFIRYLKQHPKMKKLSAAVVGKAFL
TIPGKPLLHYLILVEDVASWDSTTTSGLLVSFYPMSTFLQKDLFQSLHITKGNICLVNKYGEVLFCQDSESSFV
FSLDLPNLPQFQARSSSAIEIEKASGILGGENLITVSINKKRYLGLVLNKIPIQGTYTSLVPVSDLIQSALKVPL
NICFFYVLAFLMWIFSKINTKLNKPLQELTFCMEAAWRGNHNVRFEPQPYGYEFNELGNIFNCTLLLLLNS
IEKANIDYHSGEKLQKELGILSSLQSALLSPDFPTFPKVTFSQHLRGRQLSGHFNGWTVQDGGDTLLGIIGLA
GDIGLPSYLYALSARSLFLAYASLDVSLQKISKDTADSFSTTEGNEAVVAMTFIKYVEKDRSLELLSLSEGAP
TMFLQRGESFVRLPLETHQALQPGDRLICLTGGEDILKYFSQLPIEELLKDPLNPLNTENLIDSLTMMLNNETE
HSADGTLTILSFS

>core/130/4/Org4_Gene790

MRIEDFSLKLIPSSPGVYLMKDVHDQVLYIGKAKNLKNRLASYFHEKGDSRERIPFLMKKTASVETIVVSNET
EALLLENLIKQHHPKYNVLLKDDKTFFCLAISLSHWPKEAIRTKAITSSQRQLIFGPYVSAEACHTLLEVIS
QWFPLRTCSDREFALRKRPCILYDMKRCLAPCVGYCTPEEYQGTLDKAILFLKGKIEEVVKDLEKAIQKASD
NLEFEQAANYRRTLSTLIKQAMAKQQVEKFHFQNIADGLYRHKQRTILTLLTVRSGKLLGARHFSFFENAQE
DQDLLSSFILQYYVSQPYIPKEILTPLPLEFPTLSYVLNAESPRLRSPKTGYGKELLDLAYRNAKAYAATTLP
STLPYQDFQNILRMSQYPYRIECYDNAHMQGAHATGVYIVFENNGFDPKQYRTFSIDSEKTQNDLALLEEVL
LRRFHSLTALPDMIVVDGGKTHYNKTKKILQTLNLTGIQVVVIAKEKSNHSRGLNKEKIFCETFPEGFSLPPT
SNLLQFFQILRDEAHRFAISKHRKKRGKALFEQEIPGIGEVKRRKRLQKFKSWKQVMLSSQEELEAIPGLTK
KDIAVLLARQKDFNKSD

>core/131/4/Org4_Gene497

MKEYKIENIRNFSIIAHIDHGKSTIADRLLESTSTVEEREMREQLLDSMDLERERGITIKAHPVTMTYLHEGEV
YQLNLIDTPGHVDFSIEVSRSLSACEGALLIVDAAQGVQAQSLANVYLALERDLEIIPVLNKIDLPAADPVRIA
QQIEDYIGLDTTNIACSAKTGQGIPAILKAIIDLVPPPKAPEETELKALVFDSHYDPYVGIMVYVRIISGELKKG
DRITFMAAKCSSFEVLGIGAFLPKATFIEGSLRPGQVGFFIANLKKVKDVKIGDVTTKTKHPAKTPLEGFKEIN

PVVFAGIYPIDSSDFDTLKDALGRLQLNDSALTIEQESSHSLGFGFRCGFLGLLHLEIIFERIIREFDLDIIATAPS
VIYKVVLKNGKVLDDIDNPSGYPDPAIIEHVEEPWVHVNIITPQEYLSNIMNLCCLKRGICVKTEMLDQHRLVL
AYELPLNEIVSDFNDKLKSVTKGYGSFDYRLGDYRKGSIIKLEVLINPEPIDAFSCLVHRDKAESRGRSICEKL
VNVIPQQLFKIPIQAAINKKVIARETIRALSKNVTAKCYGGDITRKRKLWEKQKKGKKRMKEFGKVSIPNTAFI
EVLKLD

>core/132/4/Org4_Gene994

MVMVWSTNIKHEGLKSWIDEVAKLTTPKDIRLCDGSDAEYDELCTLMESTGTMIRLNPEFHPNCFLVRSSAD
DVARVEQFTFICTPTEAEAGPTNNWRDPQEMRRELHQLFRGCMQGRTLIVPFCMGPLDSPFSIVGVELTDSF
YVVC SMKIMTRMGDDVLRSLGTSGKFLKCLHSVGKPLSPGEADVSWPCNPKSMRIVHFQDDSSVMSFGSGY
GGNALLGKKCVALARLASYMAKSQGWLAEHMLIIGITNPEGKKKYFSASFPSACGKTNLAMLMPKLPGWKIE
CIGDDIAWIRPGRDGRLYAVNPEYGFFGVAPGTsertnpNALATCRSNSIFTNVALTADGDVWWEGLTEQPP
EPLTDWLKGPWKPGGSPAHPNSRFTAPLRQCPSLDPEWNSPQGVPLDAIIFGGRRSETIPLVYEALSWEHGV
TIGAGMSSTTTAAIVGQLGKLRHDPFAMLPFCGYNMAYYFQHWLSFAENRSLKLPKIFGVNWFRKNNQGEF
LWPGFSENLRVLEWIFQRTDGLEDIAERTPIGYLPNIQKFNLNGLNLDPQTVQELFSVDAEGWLAEEVENIGEY
LKIFGSDCPQQITDELLRIKSELKEK

>core/133/4/Org4_Gene278

MAAYTEASILSLASLDHIRLRAGMYIGRLGNGSQKEDGIYTLFKEVVDNGIDEFIMGHGKSLKISASDKQISIQ
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SKQGSTKDPDGTfVSFTPDPSIFPEFTFNHDFLKDKIRQYTYLHSGLEIRFNDEVFISHNGLKDLFDAEITEPPLY
SPLFFQNEDLTFIFSHLEGNTERYFSFVNGQETLDGGTHLTAFKEAIVKGVNEFFGKTFVSNDIREGIVGCIAIKI
ASPIFESQTKNKLNTQIRSSLIKDVKEAIVQALRKDKVAAELLEKIKFNEKTRKNIQFIKQDLKSKQKKVHY
KIPKLRDCKFHYNDRSLYGEASSIFLTEGESASASILASRNPLTQAVFSLRGKPMNVFSLEETKMYKNDELfYL
ATALGITQNGIQHLRYNKVILATDADVDGMHIRNLLITFFLKTLLPLVENNHLFILETPLFKVRNKTtTLYCYS
EQEKMQUALQQFGKKDSSLEITRFKGLGEISPKEFAAFIGPEIRLTPVTITSLESISSILQFYMgKNTKERKQFIMD
NLITDF

>core/134/4/Org4_Gene677

MKEVEQRIRSLYDAVTAENICRWLSNDCTQQDAKTILGWLDTDPAQLEDLFGATLTFTGTGGLRSLMGIGTNR
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VRYERAIGGVMITASHNPPNYNGYKVYMASGGQVLPPLDQEIVAACSAVNEILSVPSIDHPNIHLIGKEYEAL
YRDTLKQLQLYPEANRISGRSLSYSPLHGTGISLVPHVLKDWGFLSVHLVEKQAIGDGDfPTVQLPNPEDPE
ALTLGIEQMLANDDDLFIATDPDADRVGVVCLEDGQPYRFNGNQMASLLADHILGAWSKTRHLGEHDKLV
KSLVTTEMLSAIAKHVHVDLINVGTGFKYIGEKIESWRNSTNKFVFGAEESYGCLYGTHVEDKDAIIASALIA
EAALQQKLQGKTLRDALLSLYETYGYFANKTESVVFSAKTDEQEIRKKLSHLEEISSANFFSGKYQVEKFENY
KQGIGFNLLSKDSYALTLPKTSMLCYFSGGGRVIIRPSGTEPKIKFYFEMSTHYPERVTDKEIQKQREAESFQ
HLDDFIFDFKEKFSNL

>core/135/4/Org4_Gene658

MVTVSEQTAQGHVIEAYGNLLRVFRDGYVRQGEVAYVNVNDNTWLKAEVIEVADQEVKVQVFEDTQGACR
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LLGTVPEGRFTHKIMVPFSCFQEVTLTWVISEGTYNAHTVVAKARDAQGKEYAFTMVQRWPIKQAFIEGEKI
PAHKIMDVGLRILDTQIPVLKGGTFCTPGPFGAGKTVLQHHLISKYAAVDIVILCACGERAGEVVEVLQEFPHL
IDPHTGESLMHRTCIICNTSSMPVAARESSIYLGVTIAEYYRQMGLDILLADSTSRWAQALREISGRLEEIPGE
EAFPAYLSSRIAIFYERGGAITTKDGSEGSLTICGAVSPAGGNFEETVQSTLAVVGAFCGLSKARADARRYP
SIDPLISWSKYLNQVGQILEEKVSGWGGAVKKAQFLEKGSEIGKRMEVVGEEGVSMEDMEIYLKAELYDF
CYLQQNAFDPVDCYCPFERQIELFSLISRIFDAKFVFDSPDDARSFFLELQSKIKTNLGLKFLSEEYHESKEVIV
RLLEKTMVQMA

>core/136/4/Org4_Gene484

MTAPTESRSSSPTLLEETEPLSPNIPADIRIPRITISPPSPDVSTVASSAEDISVLIIEGGPRSSSSASVASDVYELVC
LCGGDEDPEPPDSEVRTLYVNGSWQTHQEAVQELLYISEVRGEAVRLLYNDGSGMSPWPISPCRTLPTHDP
LCQALLMVWEQFFSAPENQNSEFLVIFYGDASPIYQALQTSMYSQRIVVVGISPTVFIQGDVRVHNYRVSGD
FFSSLDRCGTRAENTTILPYSSGLEGVFLPSIRCPSFTWAVRFGEQCLITNRGEDVEDRGGRPQDIERSQLPHSE
RDLAVVIDSTDPSSMTRLVEWLNQGSPPSSDMEINPYPQRCPDVALSALYAIRSVSGLVQEWILASVHEGLDLQ
ICHSLILMHTTFAVRYFFLLFTNYPQCRERFRTARIVAQSLYLPSILVLVFDYGNVLRRLWMPQEILRAIFISAS
TISGSIVFVECTRWMGRLRHRVQQFVQQRVIGSGLPVGTVRASYRDRAGFIIGFLQTVHGGLYLPISIMVLN
QIAIQVPRTLVRPNNTAVYDLHNKSAEDSWNSGDVLAVGQTLNFILCAVFLVNLWFFVKSVLRHSRRRRR

>core/137/4/Org4_Gene741

MKKKFIFYFVIVFSLFLWEMTSRHRPTFSFLFPPSSIASSTLQSLPLLLTSAWHTLKAILGGFFLAITLSIVLAT
IMLSYKSAKDLLQPLFILLQCTPMFALAPLIVLWFGWGIGAVIVPTALTIFFPPLTLTIYQGILSTPDELIEQFVLC
GATKFQLLIKLRIPHALPHIFSGLKIAIGSAGFAAIAGEWVASQSGLGILMLESRRNYEMELALAGLATLSILTL
SLFQITLLIEKLIFSLFRVKRMSLKHKSVAKKALSVALIPIMLIPWKGNKSPDKKNLTSLLLDWTPNPNH
IPLYAGVAKGYFKQHGLDLQLQKNTDSSSAVPHVLFEQVDMALYHALGIMKTSIKGMPIQIVGRLIDSSLQGF
LYRSQDPIYKFEDLNGKVLGFCLNNSRDLNRLLETNLRNGVVPSEVKNVSSDLISPMLLNKIDFLYGAFYNIE
GVKLQTLGMPVKCFLSDTYDLPTGPQLIVFTKKGTKASEPEIVEAFQKALQESIIFSKDHPEDAFKLYAKETKS
IPKNLYQEYLQWEETFPLLAQSQDPLSKDLVDKLLETIIKRYPELASEVAKFSLNDLYNPSPLEEQSV

>core/138/4/Org4_Gene788

MYTEESLDNLRHSIDIVDLSEHIHLKRSGATYKACCPFHTEKTPSFIVNPAGAHYHCFGCGAHGDAIGFLMQ
HLGYSFTEAILVLSKKFQVDLVLQPKDSGYTPPQGLKEELRHINSEATFFRYCLYHLPEARHALQYLYHRGF
SPDTIDRFHLGYGPEQSLFLQAMEERKISQEQLHTAGFFGNKWFLFARRIIFPVHDALGHTIGFSARKFLENSQ
GGKYVNTPETPIFKKSRILFGLNFSRRRIAKEKKVILVEGQADCLQMIDSGFNCTVAAQGTAFTEEHVKELSK
LGVLKVFLFDSDSDEAGNKAALRVGDLCTAQMSVVFCKLPQGHDPDSFLMQRGSSGLIALLEQSQDYLTFLI
SEKMSSYPKFGPREKALLVEEAIKQIKHWGSPILVYHLKQLASLMMVPEDMVLSLANPQVTAEPQNILIKQK
VPKIHPIHIVMETDILRCMLFCGSNTKILYTAQFYFVPEDFKHPECKRKLFAFMISYYEKYRKNVPFDEACQVLS
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SELIP

>core/139/4/Org4_Gene434

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VALTVLAPGVPQAILLGIAISGVGIGGSIMKSLVYMVRDYMSPRMQESSRIKSALAVGTGFTVMGLVMKVG
ANFVPGGYGGLVGS LGSSAYS RGSQTTLASF SHYIYTKFFRSEK VAKGEKL TEAETIKEAKKLHYITLSIATIG
VGLAVLGILLAIAGTVLLGGTPATIAILAPPLISIGLTTVLQ TILHSSIGKWRAFLLTQEKKDLFVDTSLKDIRLE
KLPPSEVEESETSQSVIEVPDSEGIAETRISAE EIDTRLSLTTRQKVIFALATLLLLASIAAFIVTGFGGLTVMQVL
LVASVGS AVASVTLP MVSSGFSYVAYQLKARLNISKLRWKEAKNKKRVRQFLIESGVIASDREFNQMWKTV
YKKQIQKTDAAIREEV RNFEKGGEVN SALVGGILLGVGIGIMLLALVPAFAPIVPGILALGGSTLGIAGSILMR
KFVNWLYDEL VKLYERRRRNRRELLYGPESKMRSIATDLVVEALAASHDH LFDLDGPVDFIDVDVDIDGAA

>core/140/4/Org4_Gene373

MTNSDNASATGLLWAHPKEDPAFLGMIIKEFHL PPTVAQIFISRGFQTIQEIHKFLYSHLSSLYDPGLFLDMSK
AVERLLLARDRKEHVMIYGDSDVDGMTGVALLVEFLRDIDVHVS YFFLGAILKQHGETSTLIAKLKEEGITLL
ITVDCGITAGKEVSDITRQGIDVIITDHHMPTGKIPHC VATLNPKLRDHTYPNREL TGVGVAFKLARGVLNALI
SRNLVPK SQGSLKLLDLVTLGTITDVGVLLGENRVMVRYGIKEIARGARLGLNKL CALCGVEKSEVSSTDIV
LKIAPKLNSLGR LDDPAKGVELLLTQDDERVDALIMELDNINKERQRIEADV FQDVQEILNSNPEILNQAAIVL
SSTAWHARVPII SARLAKTYNKPVVIIAIQGGIGKGSARTIGSFLLGVLKKCSSLLLSYGGHDF AAGVIMKED
KVEDFKKKFVHLVNSSLKKGDTLPHLEIDAYADFDAIDYDLLASMELFEPFGKGNLMPIFYSKVRQVRYPKV
LPGNHLKLYLSQKERNLEGVAFGLGRHADALKARWHYPLEIAYTPRLSQTSGSGVIHLLVRDFRISSEPRFSD

>core/141/4/Org4_Gene515

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PLVYTESPTLTTPNLGMYRMQRFNQNTMGLHFQIQKGGMHLYEAEQKKQNLPVSVFLSGNPFLTLSAIAPL
PENVSELLFATFLQGAKLLYKKTNDHPHPLLYDAEFILVGKSPAGKRRPEGPF GDHFGYYSLQHDFPEFHCHK
IYHRKDAIYPATVVGKPYQEDFYIGNKLQEYLSPLFPLVMPGVRSLKSYGESGFHALTA AVVKERYWRESLT
TALRILGEGQLSLTKFLMVT DQEVPLDRFSVVLETILERLQPDRDLIIFSETANDTLDYTGPSLNKGSKGIFMGI
GKAIRDLPHRYQGGKIHGVQDIAPFCRGCLVLETSLEDRCIKSLLHHPDLKSWPLIILADNLRETIQSEKDFLW
RTFTRCAPANDLHALHSHFATHRPNYNFPFVIDALMKPSYPKEVEVDPSTKQKV SERWHEYFPNKETFYI

>core/142/4/Org4_Gene314

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LSVRGKVCPRLAGMENPNLATGHIEVEVASFEVL SKSQNL PFSIADDHINVNEELRLEYRYLDMRRGDII EKM
LCRHQVMLACRNFM DAQGFEIVTPVLGKSTPEGARDYL VPSRIYPGKFYALPQSPQLFKQLLMVGGLDRYF
QIATCFRDEDLRADRQPEFAQIDIEMSF GDTQDLFPIIEQLVATLFATQGIEIPLPLAKMTYQEAKDSYGTDKPD
LRFDLK LKDCRDYAKRSSFSIFLDQLAHGGTIKGFCVPGGATMSRKQLDGYTEFVKRYGAMGLVWIKNQEG
KVASNIAKFMDEEVFHELFA YFDAKDQDILLLIAALESVANQSLDHLRRLIAKERELYS DNQYNFVWITDFPL
FSLEDGKIVAEHHPFTAPLEEDIPLLETDP LAVRSSSYDLVLNGYEIASGSQRIHNPD LQSQIFTILKMSPESIQE
KFGFFIKALSFGTPPHLGIALGLDRLVMVLTA AESIREVIAFPKTQKASDLM MNAPSEIMSSQLKELSIKVAF

>core/143/4/Org4_Gene494

MSGKKDGVGRGMIFVPLSILVLIFLPLPQILLDFGLCISFALSLLTVCWVFTLNSSNSAKLFPPFFLYLCLLRLGLN
LASTRWIVSSGTASSLIVSLGSFFSLGSLWAATFACLLFFVNFLMVSKGSERIAEVRSRFFLEALPAKQMALD
SDLVSGRASYKAVKKQKNALIEEGDFFSAMEGVFRFVKGDAIISCILLVNVVSVTCLYYTSGYALEQMWFT
VLGDALVSQVPALLTSCAAATLISKIDKEESLLNYLFEYYKQLRQHFRVVSLLIFSLCCIPSSPKFPIILLASLLW
LAYRKEEPASEDSCIERAFSYVEGACPKEQESQFYQVYRAASEEVLEDLGVRLPVLTSRLRIERPWLRFVFGQN
VYLDEVTPEAVLPFLRNIAHEALNAEVVQKYLEESERVFGIAVEDIVPKKISLSSLVVLRSLLVRERVSLKLP
KILEAVAVYQNSGDSLEILAEKVRKSLGYWIGRSLWDQKQTLLEVITIDFHVEELINSSYSKSNPVMQENVIRR
VDSLLEERSVFKDFRAIVTSSETRFEMKKMLDPHFPDLLVLSHNELPKEIPISFLGIVSDEVLP

>core/144/4/Org4_Gene522

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KSEGVIPMSEFIDSSEGLVLGAEEVEVYLDQAEDEEGKVLSREKATRQRQWEYILAHCEEGSIVKGQITRKVK
GGLIVDIGMEAFLPGSQIDNKKIKNLDDYVGKVCEFKILKINVERRNVVSRRELLEAERISKKAELIEQISIGE
YRKGVVKNITDFGVFLDLGDIDGLLHITDMTWKRIRHPSEMVELNQELEVIILSVDKEKGRVALGLKQKEHN
PWEDIEKKYPPGKRVLGKIVKLLPYGAFIEIEEGIEGLIHVSEMSWVKNIWDPSEVVNKGDEVEAIVLSIQKDE
GKISLGLKQTEHNPWDNIEEKYPIGLHVNAEIKNLTNYGAFVELEPGIEGLIHISDMSWIKKVSHPSELFKKGN
SVEAVILSVDKESKKITLGVKQLSSNPWNEIEAMFPAGTVISGVVTKITAFGAFVELQNGIEGLIHVSELSDKPF
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>core/145/4/Org4_Gene873

MSTRRPIQLLDPLTINQIAAGEVIENSVSIVVKELIENSLDAGADEIEIETLGGGQGAIIRDNGCGFRAEDIPIALQ
RHATSKIREFSDIFSLNSFGFRGEALPSIASISKMEIQSSIEGDEGVRTVIHGGDIVSCEPCARQLGTTVIVNSLFY
NVPVRRGFQKSMQSDRLGIRKLIENRILSTANIGWSWISEGHHEIQIAKQQGFQERVAYVMGDHFMQDALT
DKEANGVRIVGVLGSPSFHRPTRQGQKIFINDRPIESLFISKKVGDAYALLPLHRYPVFVLKLYLPSSWCDFN
VHPQKIEARILKEELVGDCIKEAIVETLTCPPGILCRTHQEIEESDSVPLPMFRMLETSDVQEEESVEFNQNLFA
YSSDEVSLKQEYTSRGPKSQMDWMYSSDVRLTSLGRVLAEDLEGVHIIFTAAARKHLFFLSLMQENS
YQSQALLIPLRLQVTPEEAFFFSHHGRTLCDLGIEISQVGPCVFSIESTPTVIGEEELKEWLLLLAARGSTDINSE
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>core/146/4/Org4_Gene512

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EMQGFFLDASGMGGSSDISQLSLEALKSSAFSGARSLSLSSSESSSVASFGSFQKAIEPMSEEKVNAWTVARL
GGEMVSSLLDPNVETSSLVRRAMATGNEG MIDLSDLGQEEVSTAMTSPRAVEGKVKVSSSDSPEANPTGIPN
SNTLERAEEKEAEKQESREQLSEDQMMLARAMAGLLTGAAPQEVLSNSVWSGPSTVFPPPKFSGTLPTQRSGD
KSKHKSPGIEKSTNHTNFSPLREGTVKSAEVKSLPHPESMYRFPKDSIVSREEPEAVVKESTAFKNPENSSQNF
LPIAEESVFPKESGTGGALGSDAVSSSYHFLAQRGVSLAPLPRATDDYKEKLEAHKGPGGPPDPLIYQYRNV
AVEPPIVLRSPQPFSGSSRLSVQGKPEAASVHDDGGGGNSGGFSGDQRRGSSGQKASRQEKKKGKLSRDI

>core/147/4/Org4_Gene352

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NSEMVMLLPKDTRTWEMERRY MSTYEQLGILIKAKYRKKQEASVKKYQVAFEEKRQSPMPTLRHLEMKNE
GICLKRLQQRVDKMQRPYEMAQQAWN RATDNYRPFLMALTRIEHELRLADYNNWGQPEDLCIAYANVEKR
AEPYKKSLLAIRQVLEDYAKLRS AISFIQDKRLWIEKESEDLRILINPFFSSFWEDDAGGSREM NKYVPWWQ
LSRVTRKDLLAALVFGIRIALVVAGIGITALAIGIMIGLVSGYFGGTVD MILSRFTEIWETMPVLFILMLVISIT
QQKSLLLNTVLLGCFSWTGFSRYVRIEVLKQRDRGYVLAATNLGYSHYYIMVHQILPNAIVPVISLVPFAMM
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>core/148/4/Org4_Gene941

MTDFPTHFKGPKLNPIKVNPNFFERNPKVARVLQITAVVLGIIALLSGIVLIIGTPLGAPISMILGGCLLASGGAL
FVGGTIATILQARNSYKKA V NQKKLSEPLMERPEL KALDYS LDLKEVWDLHHSVVKHLKKLDLNLSETQRE
VLNQIKIDDEGPSLGECAAMISENYDACLKMLAYREELLKEQTQYQETRFNQNLTHRNKVLLSILSRITDNIS
KAGGVFSLKFSTLSSRMSRIHTTITVILALS AVVSVMVVAALIPGGILALPILLAV AISAGVIVTGLSYLVRQILS
NTRNRNQDFYKDFVKNVDIELLNQTVTLQRFLFEMLKGV LKEEEEEVSLEGQDWYTQYITNAPIEKRLIEEI
RVTYKEIDAQTKMKMTDLEFLENEVRSGRLSVASPS EDPSETPIFTQGKEFAKLRRQTSQNISTIY GPDNENIDP
EFSLPWMPKKEE EIDDSLEPVTKLEPGSREELL VEGVSPTLRELNMR IALLQQQLSSVRKWRHPRGEHYGNV
IYSDTELDRIQMLEGAFYNPLREAQEEITQSLGDLVDIQNRILGVIVEGDS DSRTEEE PQE

>core/149/4/Org4_Gene673

MANPTQSRPPSPEISIEEIELQELPGSSNTTETTSNTPPPSCAATAEEVSLFIEGGRRNSEDEEGLLGPCDVYDVVC
ITNQGDPEVRDHEVRVMYINGSGRTQHEGILDAVNICELRGEPVRFIHNSGYGLANCFLGTQNRIPPRDNVISQ
AIQARWNEFFVSPENANRNYIVLFSGNGGLYLQVALDNSIYSHILCVGIGSSYYIQGSYRVHNYRVTGDWT
TLLDRRGATAVNTTTL PYADSAEGLFLPSVRCPSYQWALRYGEQCLIMDNNQQGGFRPQDPSSEIALLVNLN
QDQGNWTRLIEWIDQGDSQAVLELNPQPSHCRDIALTALYATTRISSLLQECLMISVTYSPDV FVTYAIVTGY
SIMTLRYFILLLTNRPGCRQHFRVLR LAALGLQPLGFLT VLLDHINVTRRVNRRPPLISVIFCTASFATGSFIYV
DLTRMFFTSLSRSLQLFVQRRLTGRGLPLRRVCVNHLDSLRF SQNALTTFHGGLFMPLIIGFFNQLVIQVPRVV
IRPNTNAVYDLNQTSQEAWDSGDVLAIGQTINFLLCMILLVINTFFFVRSVRRNLHRRPHR

>core/150/4/Org4_Gene965

MFMN TQNSQATEVSSEEEESQKKLEELVALAKEQG FITYEEINEILPMSFDTPEQIDQVLIFLTGM DIQVLNQID
VERQKEKKKEAKELEGLARRTEGTPDDPVRMYLKEMGT VPLLTRREEVEISKRIEKAQVQIERIILRF RYSAK
EASIAHYLISGKERFDKIISEKEVEDKTHFLKLLPKLITLLKEEDTYLENLLLSLKQPDLSKQEAAKL NDSLEK
CRIRTQAYLRCFHCRHNVTEDFGEVVFKAYDSFLHLEQQINDLKVRAERNKFAAAKLAAAKRKL YKREVAA
GRTLEEFKKDVRMLQRWMDKSQEAKKEMVESNLRLVISIAKKYTNRGLSFLDLIQEGNMGLMKAVEKFEY
RRGYKFSTYATWWIRQAVTRA IADQARTIRIPVHMIETINKVLRGAKKLMMETGKEPTPEELAEELGLTPDR
VREIYKIAQHPISLQAEVGE GESSFGDFLED TAVESPAEATGYSMLKDKMKEVLKTLTDRERFVLIHRFGLL
DGKPKTLEE VGSAFNVTRERIRQIEAKALRKM RHPISKQLRAFLDLL EEEKTGTSKVKSLSKSK

>core/151/4/Org4_Gene685

MDTQSSIGNEEWRIAGTSIVSGMALGKVFFLGTSPLHVRELTLPQEEVEHEIHRYKALNRSKSDIVALEQEV
TGQQGLQEVSSILQAHLEIMKDPLLTEEVVNTIRKDRKNAEYVFSSVMGKIEESLTAVRGMPSVVDREVQDIH
DISNRVIGHLCCQHKSSLGESDQNLIIFSEELTPSEVASANSAYIRGFVSLVGAATSHTAIVSRAKSIPYLANISE
ELWNIKRYNGKLVLIDGYRGELIFNPKPATLQSCYKKELSVVAHTSQRLVRKSLHPIVSSHAGSDKDVEDLL
ENFPQTSIGLFRSEFLAVILGRLPTLREQVDLYEKLARFPGDSPSVLRLFDGFKPCPGIKNKKERSIQWLLDY
SVILEDQLQAIKASLQGSIKVLIPGVSDVSEIIEVKKKWEIQTFRPKGHKVSWGTMIEFPSAVWMIEEILPEC
DFLSIGTNDLVQYTLGISRESALPKHLNVTLPFAVIRMIHHVLQAAKQNPVPSICGEAAGQLSLTPLFIGLV
QELSVAMPVINRLRNHIALLELNSCLEITEALLQAKTCSEVEELLNRNNKITS

>core/152/4/Org4_Gene997

MVKVPWAFKNFIPKLYTSIKEGYSFNTFKKDFQAGITVGILAFPFAIAIAIGVGVSPIQGLLASIIGGLLASAMG
GSNVLISGPSSAFISILYCLSAKYGAELFTVTLLAGVFLIAFGLTGLGTFIKYMPYPVVTGLTTGLAVIIFSSQI
KDFLGLQMGANIPADFLPKWVAYWDHLWTWDSKSFVGLFTLLIMYFRNYKPRYPGVMIAIVTATTLVWL
LKIDIPTIGSRYGTLPTAIPKIPQLSITKILQLMPDALTIAVLSGLETLLSAVVADGMTGWRHQSNQCLVAQG
VANIGTSLFSGIPVTGSLSRTAASIKSGATTPIAGIVHSIFICILLAPLTVKIPLTCLAAVLILIAWNMSEIHHFI
HLFTAPKKDIVVLLTVFILTVMTTITAAVQVGMMLAAFLFMKQMSDLSDVISTAKYFDDDNQPKDSDFLSKA
EVPQNTIYEINGPFFFGIADRLKNLLNDIEKPPKIFILCMTRVPTIDASAMHALEEFFLECDRQGTLLLLAGVK
KTPLADLKRYHLDLIGVDHIFSNIKSALLFAQALTNLESKTSTRHLA

>core/153/4/Org4_Gene696

MGLFHLTLFGLLLCSLPISLVAKFPESVGHKILYISTQSTQQALATYLEALDAYGDHDFVLRKIGEDYLKQSI
HSSDPQTRKSTIIGAGLAGSSEALDVLSQAMETADPLQQLVLSAVSGHLGKTSDDLKALASPYPVIRLEA
AYRLANLNKNTKVIDHLHSFIHKLPEEIQCLSAAIFLRLETEESDAYIRDLLAAKKSARSATALQIGEYQQKRFL
PTLRNLLTSASPQDQEAVLYALGKLKDGQSYNIKKQLQKPDVDVTLAAAQALIALGKEEDALPVIKKQALE
ERPRALYALRHLPSIEGIPIALPIFLKTKNSEAKLNVALALLELGCDTPKLLEYITEWLVPHYNETLALSFSKG
RTLQNWKRVNIIVPQDPQERERLLSTTRGLEEQILTFLFRLPKEAYLPCIYKLLASQKTQLATTASFLSHTSHQ
EALDLLFQAAKLPGEPHIRAYADLAIYNLTKDPEKKRSLHDYAKKLIQETLLFVG TENQRPHPSMPYLR YQVT
PESRTKLMLDILETLATSKSSEDIRLLIQLMTEGDAKNFPVLAGLLIKIVE

>core/154/4/Org4_Gene416

MKTSQLFYKTSKNANKSAAVLSNELLEKAGYLFKVSKGVYTYTPLLWRVVSMMNIIREELNAIGGQELLLP
LLHNAELWQHTGRWEAFTSEGLLYTLKDREGKSHCLAPTHEEVICSFVAQWLSSKRQLPLHLYQIATKFRDE
IRPRFGLIRSRELLMEDSYTFSDSPEQMNEQYEKLRSYGYSKIFDRLGLAYAIVTADGGKIGKGKSEEFQVLCSL
GEDTICVSGSYGANIEAAVSIPPQHAYDREFLPVEEVATPGITTIEALANFFSIPLHKILKTLVVKLSYSNEEKFI
AIGMRGDRQVNLVKVASKLNADDIALASDEEIERVLGTEKGFIGPLNCPIDFFADETTSPMTNFVCAGNAKD
KHVVNVNWDRDLPPPQYGDFLLAEEGDTCPENPGHPYRIYQGIEVAHIFNLGTRYTDSFEVNFQDEHGQTQQ
CWMGTYGIGVGRTLAACVEQLADDRGIVWPKALAPFSITIAFNNGDTSQELAETLYHELQSQGYEPLDDR
DERLGFKLKDSDLIGIPYKLILGKSYQSSGIFEIESRSGEKYTVSPEAFPTWCQNHLA

>core/155/4/Org4_Gene263

MTVSVKKKSFRALVTTHFLTIINDNLYKFLLAFFLLEGKTLTENAKILSCVSFFFALPFLLLAPLAGSLADRFQ
KRNILATRFIEILCTILGTYFFFIQSVVGGYVVLILMACHTTIFGPAKLGILPEMLPSEQLSQANGIMTAATYTG
SILGSC LAPLLVDVTHRLGVNSYVWPTLMCVVVSIISTLISFCIRPSNVKNVKQKITLVSFKDLWKVLKDTRMI
HYLTVSIFLGSFFLLIGAYTQLEIIPFVEFTLKYPKHYGAYLFPIVALGVGMGSYITGKISGKDIKIGYVPLAAIG
LALVFMGLYAFACSILFVLFFLLALGFLGGVYQVPLHAYVQYASPEHKRGQILAANNFLDFFGV LVAAGVIR
VLGSNLGLSPETSFFYIGWFLAVSIWTLWIWREHVYRLLLGIILRRQLGYYLKIHQSSSPKCYFVAVQSYREI
RRVLAALTKTVRSRVIIDQKLVPGWRAWLLSWCVPTVSSVRDNDSEAQDAWAVLQANHLKTS LKKFPD
VSVVCLGLPKNVERFTSILQE QGIDLHP IQLVQKEGKKRVIYTLVFPHA

>core/156/4/Org4_Gene369

MSTLLSILSVICSQAIAKAFP NLEDWAPEITPSTKEHFGHYQCNDAMKLARVLKKAPRAIAEAIVAELPQEPFS
LIEIAGAGFINFTFSPVFLNQQLEHFRDALKLGFQVSQPKKIIIDFSSPNI AKDMHVGH LRSTIIGDSLARIFS YVG
HDVLRNLNHIGDWGTAFGMLISYLQENPCDYS DLEDLTSLYKKA YVCFTNDEEFKKRSQQNVVALQAKDPQA
IAIWEKICETSEKAFQKIYDILDIVVEKRGESFYNPFLPEIHEDLEKKGLLTVSND AKCVFHEAFSIPFMVQKSDG
GYNYATTDLAAMRYRIEEDHADKIIIVTDLGQSLHFQLLEATAIAAGYLQPGIFSHVGFGLVLD PQGKKLKTR
SGENVKLRELLDTAIEKAEEALREHRPELTDEEIQERAPVIGINA IKYSDLSSHRTSDYVFSFEKMLRFEGNTA
MFLLYAYVRIQGIKRRLGISQLSLEGPPEIQEPAEELLALTLLRFPEALESTIKELCPHFLT DYLYNLTHKFNGFF
RDCHI QDSPYAKSRLFLCALTEQVLATGMHLLGLKTLERL

>core/157/4/Org4_Gene377

MSKLIRRVTVLALTSMASCFASGGIEAAVAESLITKIVASAETKPAPVPVTAKKVRLVRKNKQPVEQKSRG
AFCDKEFYPC EEGRCQPVEAQQESC YGRLYSVKVND DCNVEICQSVPEYATVGSPYPIEILAIGKKDCVDVVI
TQQLPCEAEFVSSDPETTPTS DGKL VWKIDRLGAGDKCKITVWVKPLKEGCCFTAATVCACPELRSYTKCGQ
PAICIKQEGPDCACLRCPV CYKIEVVNTGSAIARNVTVDNPVPDGYSHASGQRVLSFNLGDMRPGDKKVFTV
EFCPQRRGQITNVATVTYCGGHKCSANVTTVVNEPCVQVNISGADWSYVCKPVEYSISVSNPGDLVLHDVVI
QDTLPSGVTVLEAPGGEICCNKV VWRIKEMCPGETLQFKLVVKAQVPGRFTNQVAVTSESNCGTCTSCAETT
THWKGLAATHMCVLDTNDPICV GENTVYRICVTNRGSAEDTNVSLILKFSKELQPIASSGPTKGTISGNTVVF
DALPKLGSKESVEFSVTLKGIAPGDARGEAILSSDTLTSPVSDTENTHVY

>core/158/4/Org4_Gene613

MELLSLNKSYFEIQRLRYRPEILTLETIRSKHIQETSSPLSPPPELQKHIPNL CRIVEVSIYTEQETSSKPLKIGVL
LSGGQAPGGHNVVIGLFDALRVFN PETRLFGFIKGPLGLTRGLYKDLDISVIYDY YNMGGFDMLSSSREKIKT
EEQKKNILNTVKKLKL DGLLIIGGNN SNTDTAMLA EYFLAHNCKTSVIGVPKTIDGDLKNCWIETSLGFHTSC
RTYSEMIGNLAKDALS AKKYHHFIRLMGQQASYTTLE CGLQTLPNIALISELIATR KISLKQLSEQLALGLVRR
YKSGKNYSTVLIPEGLIEHIFDTRKLIDELNVLLANGHSAIEKILSRLSPEALKTFHLFPKDIANQLLLARDSHG
NVRVSKIA TEELLAVMVKKEIEKIEPHMEFHSVSHFFGYEARAGFPSNFDCNYGIALGIISALFLVRQKTGYMI
TINNLARAYTEWQGGATPLYKMMHLENRCGTETPVIKTDSVDPKSPAVQHLLQQSDSCLVEDLYRFPGLQ
YFGKEELIDQRPLTFLWENQTHSPLL

>core/159/4/Org4_Gene237

MSSPPQAVASLTERIKTLLESNFCQIIVKGELSNVSLQPSGHL YFGIKDSQAFLNGAFFHFKSKYYDRKPKDGD
AVIIHGKLAVYAPRGQYQIVAHALVYAGEGDL LQKFEETKRRLTAEGYFATEKKKPLPFAPQCIGVITSPTGA
VIQDILRVLSRRARNYKILVYPVTVQGNSAAHEISKAIEVMNAENLADVLIARGGGSIEDLWAFNEEILVKAI
HASTIPIVSAVGHETDYLCDFASDVRAPTPSAAAEIVCKSSEEQVQVFEGYLRHLLSHSRQLLTSKKQQLLP
WRRFLDRAEFYT TAQQQLDSIEIAIQKGVQGGKI HESKQRYDNISRWLQGD LVSRMTCRLQSLKKMLSQALSH
KALSLQVRCHQLKKSLTYPRQIQQASQKLSPWRQQ LDTLISRRLHYQKEEYFHKHTRLKHAHNVLEQQLRS
HVQKLELLGRRLSRGCELNLQNQKIA YANVKETLATILERRYENSVARYSALKEQLHSLNPKNVLKRGYAM
LDFDNENSAMISVDSLQENARVRIQLQDGEAILTVTNIEICKLIK G

>core/160/4/Org4_Gene805

MDNSDNSFHTLETEQGSFLNDELAVEEVASTESTEMSDATLCFADEIQELPSPEKKVAFILNKMREALTGSSQ
GSDLRLFWDLRKQCLPLFNEIEDTAKRADHWRCYIELTKEGRHLKGLQDEEGSFVVGQIDLAITCLEKDILKF
QEGTEDKIFKDREDNFLESQALDKHQAFYKQHHTSLLWLSSFSSKIIDL RKELMNVGMRMRLKSKFFQRLSN
LGNQVFPKRKELIEKVSQTFAEDVDAFVAKYFIGSDKETLKKTVFFLRKEIKNLQHA AKRLFVSSHVFAETRL
KLSKCWDQLKGMEKEIRQE QGRLRVVSAENSKEVRQMLAEVSSLLIEGNDLSKVRKNLEGISKKIRALDLTH
DDVISLKKEMQQFLDQLREKQDAAEHSYQEQLAKDKQVKKEAARSLAERITTF SKTCSEGNITSESREEWQT
LKELLGKMSFLPPPEKISLDNQLNLALQTIVNFFEEQLLSSPDSREKLVNMRQVLKQRRERRQELKDKLEQDK
KLLGSSGLDFDRAMQYSALVEEDKRALEELDASILELKQQIQQLL

>core/161/4/Org4_Gene252

MPQKVLITSALPYANGPLHFGHIAGVYLPADVYARFRLLGDDVLYICGSDEF GIAITLNADREGLGYQEYV
DMYHKLHKDTFEKLG FALDFFSRTTNPFHAELVQDFYSQLKASGLIENRISEQLYSEQEQRFLADRYVEGTCP
RCGFDHARGDECQSCGADYE AIDLIDPKSKISGVELVKKETEHSYFLDRMKDALLSFIQGCYLPDHVRKFV
VDYIEHVRSRAITRDL SWGIPVPDFPGKV FYVWFDAPIGYISGTM EWAASQGNPDEWKRFWLEDGVEYVQFI
GKDNLPHFSVVPAMELGQKLDYKKVDALVVSEFYLL EGRQFSKSEGN YVDMDKFLSSYS LDKLRYVLAAT
APETSDSEFTFLDFKTRCNSELVGKFGNF INRVLAFAEKNHYDKLSYHSVVLEDSDRAFLEEARQLVRDAEK
CYREYSLRKATSVIMSLAALGNVYFNQQAPWKLLKEGTRERVEAILFCACYCQKLLALISYPIIPESAVAIWE
MISPKSLENCNLDTMYARDLWKEEILDVINEEFHLKSPRLLFTTVE

>core/162/4/Org4_Gene587

MHPSYFDLDTIISSYSPLPK EFQEAASLIAVPDTSHSKPVVPGVKTLFPQTYHLPYLKFVQGENVVHTPLKVG
VMFSGGPAPGGHNVIQGLFNSLKDFHPDSSLVGF INNGDGLTNNKSIDITEEF LSKFRNSGGFNCIGTGRKKIV
TPEAKEACLKTA EALDGLVIIGDG SNTATAILAEYFAKRRPKTSIVGVPKTIDGDLQHTFLDLTFGFD TAT
KFYSSIISNISRDAL SCKAHYHFIKLMGRSASHIALECALQTHPNIALIGEEIAEKNLPLKTIH KICSVIADRAAM
EKYYGVIL IPEGIIEFIPEIINLITEIESLSEYEDKISR LSPESQRLLKSFPAPIIEQILNDRDAHGNVYVSKISVDKLL
IHLVSNHLQQYFPNVPFNAISHFLGYEGRSGLPTKFDNTYGYSLGYGAGILVRNHCNGYLSTIESLACPFMKW
KLRAIPVVKMFTVKQQADGTLQPKIKKYLVDIGSTA FRKFKLYRKIWALED SYRFLGPLQIETPP EMHSDNFP
PLTLLLNHNFWQRHQGCIEIPDTTY

>core/163/4/Org4_Gene267

MSRKDNEVSLARSIFNILSGTFCSRITGIFREIAMATYFGADPIVAAFVLGFRTVFFLRKILGGLILEQAFIPHFE
FLRAQSLDRAAFFFRFRSRLIKGSIIFTLLIEAVLWVVLQYVEEGTYDMILLTMILLPCGIFLMMYNVNGALL
HCENKFFGVGLAPVVVNIIWIFFVIAARHSDPRERIIGLSVALVIGFFFEWLITVPGVWKFLQAKSPPQEHDSV
RALLAPLSLGILTSSIFQLNLLSDICLARYVHEIGPLYLMYSLKIYQLPIHLFGFGVFTVLLPAISRCVQREDHER
GLKLMKFVLTLTMSVMIIMTAGLLLLALPGVRVLYEHGLFPQSAVYAIVRVLRGYGASIIPMALAPLVSVLFY
AQRQYAVPLFIGIGTALANIVLSVLGRWVLKDVSGISYATSITAWVQLYFLWYYSSKRLPMYSKLLWESIRR
SIKVMGTTMLACMITLGLNILTQTTYVIFLNPLTPLAWPLSSITAQAIAFLSESCIFLAFLFGFAKLLRVEDLINL
ASFEYWRGQRGLLQRQHVMQDTQN

>core/164/4/Org4_Gene630

MAAKNIKYNEEARKKIHKGVKTLAEAVKVTLGPKGRHVVIDKSFGSPQVTKDGVTVAKEIELEDKHENMGA
QMVKEVASKTADKAGDGTTTATVLAELIYSEGLRNVTAGANPMDLKRIGDKAVKVVDDELKKISKPVQHH
KEIAQVATISANNDSEIGNLIAEAMEKVGKNGSITVEEAKGFETVLDVVEGMNFNRGYLSSYFSTNPETQECV
LEDALILIYDKKISGIKDFLPVLQQAESGRPLLIIEEIEGEALATLVNRLRAGFRVCAVKAPGFGDRRKAM
LEDIAILTGGQLVSEELGMKLENTTLAMLGKAKKVIVTKEDTTIVEGLGNKPDIQARCDNIKKQIEDSTSDYD
KEKLQERLAKLSGGVAVIRVGAATEIEMKEKKDRVDDAQHATIAAVEEGILPGGGTALVRCIPTLEAFLPML
ANEDEAIGARIILKALTAPLKQIASNAGKEGAIIICQQVLARSANEGYDALRDAYTDMIDAGILDPTKVTRSAL
ESAASIAGLLLLTTEALIADIPEEKSSSAPAMPSAGMDY

>core/165/4/Org4_Gene422

MFGSESLRYQLLIQDFAKVSEEGIDLLESKEYSLLQAKLVLRALAQNSSFDDWFRSFKKCQISYPELAHDRDV
LEEFGIQVLREGIENPSVTVRAVSVLAIGLARDFRLVPLLLQSCNDDSAIVRSLALQVAVNYGSESLKKAIVEL
ARNDDSIHVRITAYQVVALLQIEELLPFLRERAENKLVDGVERREAWKACLELSSQFLETGVAKDDIDQALFT
CEVLHNGMLPETTEIFTELLSVEHPEVQESLLLSALAWSHQLQNHKEFLSKVRHVMRTSPFAKVRFQAAALL
HLHGDSLGRDSLVEGLRSHQPLVCEAASAALCSLGIHGVPLAKEHLESLSRKAANLSILLVSREDIERAG
DVIARYLSNPEMCWAIEYFLWDAQWNLRGDAFPLYSDMIKREIGRKLIRLLAVARYSQAKAVTATFLSGQQ
AQGWSFFSGMFWEEGDVKTSEDLVTDACFAAKLEGALASLCQKKDQASLQRVSQLYNDSRWQDKLAILES
VAFSENHAVPFLDCCHEAPSLRSAAAGALFSIFK

>core/166/4/Org4_Gene318

MLRIFCFVISWCLIAFAQPDLRSFVSILGAACGYGLFWYSLEPLKKTSLPLRTLTVSCFFWIFTIEGIHFSWMLS
DQYIGKLIYLVWLTLLITILSVLFSGFSCLLVAIVRQKRTAFLWSLPGVWVAIEMLRFYGIFSGMSFDYLGWPM
TASAYGRQFGGFLGWAGQSFAVIAVNMSFYCLLLKKPHAKMLWVLTLLLPYTFGAIHYEYLKHAFQQDKR
ALRVAVVQPAHPPIRLKLKSPIVVWEQLLQLVSPIQPIDLLIFPEVVVPFGKHRQVYPYESCAHLLSSFAPLPE
GKAFLSNSDCATALSQHFQCPVIIGLERWVKKENVLYWYNsAEVISHKGISVG YDKRILVPGGEYIPGGKFGS
LICRQLFPKYALGCKRLPGTRSGVVQVPGLPRIGITICYEETFGYRLQSYKRQGAELLVNLTNDGWYPESRLP
KVHFLHGMLRNQEFGMPCVRACQTGVTA AVDSLGRILKILPYDTRETKAPSGVLETSPLPFNYKTLYGYCGD
YPMILIAFCAVSYLGGGFLGYRLLAKKEIR

>core/167/4/Org4_Gene338

MQSSEVKPFSRLRAYLCPIYKSEFSKFVPLFLLAFFVGFNYCLLKNMKDTLVIVGSDAGAEVIPFLKVGIVP
GAVIVTMVYGWLGSRYPRDTVFYCFMAAFLGFFFLFAVIIYPVGDSLHLNSLADKLQELLPQGLRGFVVMVR
YWSYIIYYVMSELWSSVVL SMLFWGLANQITTITEAGRFYALINTGLNLSSICAGEISYWMGKQTFVAYSFA
CDSWHSVMLNLTMLITCSGLIMIWL YRRIHHLTIDTSIPPSRRVLAEEAATANLKEKKKPKAKARNLFLHLI
QSRYLLGLAIIVLSYNLVIHLFEVVWKDQVSQIYSSHVEFNGYMSRITTLIGVVSVLA AVLTTGQCIRKWGWT
VGALVTPLVMLVSGLLFFGTIFA AKRDISIFGGVLGMTPLALAAWTGGMQNVLSRGTKFTFFDQTKEMAFIP
LSPEDKNHGKAAIDGVVSRIGKSGGSLIYQGLLVIFSSVAASLNVIALVLLIIMVVWIAVVAYIGKEYYSRAAD
AVATLKQPKEPSSSIVREAQESVEQEEMAVL

>core/168/4/Org4_Gene202

MHDQRNRGHNNHNLRLRPGSTLLEAFLILCSEHEEGIA CFDEHLGSLSYRELRNAIIA VAIKVSKFSEDRVGV
MMPASIGAFIAYFGILLAGKTPVMMNWSQGLRELRACTKTVEVRRVLT SQQFIKHLTEVQGFVEYPFDLMY
MEDVRKRLSWWEKCRIGLYSKCSVPWLLRIFGVSGVESDDTAVILFTSGTEKLPKAVPLTHKNLMENQEACL
KFFDPNTQDVMLAFLPPFHAYGFNSCGLFPLLMGVHVVFASNPLNPKKLVEFIDDKKVTFFGSTPVFFDYILK
TAKKQNSCLESRLVVIGGDALKDTLYEETKKLQPQIALYQGYGATECSPVISITTKESPRKSECVGMPIEGM
DVLIISKETHIPVSSGEQGLIVVRGNSVFSGYLG NHEHQSFVSLGGDQWYLTGDLGHIGPSGDLFLEGRLSRFV
KIGGEMVSLEALESILHEHFTENQNE DAGSLVVCGIPGDKVRLCLFTTLATTIHEVNDILKSAETSSIVKISYVH
QVESIPILGIGKPDYVSLNALAVSLFG

>core/169/4/Org4_Gene40

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LGHYHRFSSAALSRHSSATSGQIYARVIKREREGDYLGSTVQVIPHITNEIIQVILDAAKEHSPDVLIVEIGGTIG
DIESLPFLEAIRQFRYDHSEDCLNIHMTYVPYLQA ADEVKSKPTQHSVQTLRGIGIIPDAILCRSEKPLTQEVKS
KISLFCNVPNRAVFNVIDVKHTIYEMPLMLAQEKIANFIGEKLKLATVPENLDDWKVLVNQLSQDLPKVKIG
VVGKYVQHRDAYKSIFEALTHAALRLGHAAEIIPIDA EDENLTMELSQCDACLVPGGFGVRGWEGKIAAAKF
CREQGIPYFGICLGMQVLVVEYARNVLNLDQANSLEMDPNTPHPIVYVMEGQDPLVATGGTMRLGAYPCLL
KPGSKAHKAYNESSLIQERHRHRYEVNPDYIQSLEDHGLRIVGT CPPQGLCEIIEVSDHPWMIGVQFHPEFVSK
LISPHPLFIAFIEAALVYSKDASHV

>core/171/4/Org4_Gene594

MRKISVGICITILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNL SG
NIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLS
IDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPH
YYNQSQVETKTITIHFIPDANTA AKLFNQGKLNWQGPWGERIPQETLSNLQSKGHLHSFDVAGTSWLT FNIN
KFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIH SYPEHQKQEVAQRQAYAKKLFKEALEELQ
ITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIFGKEFALLQADLSSGNFSLATGGWFADFADPMAF
LTIFAYPSGVPPYAINHKDFLEILQNIEQE QDHQKRSELVSQASLYLET FHIIEPIYHDAFQFAMNKKLSNLGVS
PTGVVDFRYAKEN

>core/172/4/Org4_Gene908

MLGKEEEFTCKQKQCLSHFVTNLTSDVFAKLNLPVVKGALFSKYSRSLGLRALLLKEFLSNEEDGDVCDE
AYDFETDVQKAADFYQRVLDNFGDDSVGELGGAHLAMENVSILA AKVLEDARIGGSPLEKSTRYVYFDQKV
RGEYLYYRDPILMTSAFKDMFLGTCDFLFDTYSALIPQVRAYFEKLYPKDSKTPASAYATSLRAKVLD CIRGL
LPAATLTNLGFFGNRFRWQNLHKLQGHNL AELRRLGDESLTELMKVIPSFVSRAEPHHHHH QAMMQYRRA
LKEQLKGLAEQATFSEEMSSSPSVQLVYGDPDGIYKVAAGFLFPYSNRSLTDLIDYCKKMPHEDLVQILESSV
SARENRRHKSPRGLECFEFGFDILADFGAYRDLQRHRTL TQERQLLSTHHGYNFPVELLDTPMEKSYREAME
RANETYNEIVQEFPEEAQYVVP MAYNIRWFFHVNARALQWICELRSQPQGHQNYRTIATGLVREVVKFNPM
YELFFKFVDYSDIDLGRNLNQEMRKEPTT

>core/173/4/Org4_Gene624

MFVGGFVSFLLPIPDLECANNVTKTYDKKASVISRDLKLQEDCQKFWNLDPYKLESLCAYQVLYHDDYSSK
RIRELFPQIQKDEVPIFATMILT LGKVDRGFSPEEISLIQKLSYPGLSLASLRGSTEIDPNTDLARALVVSEFSGD
LGKNRADYYSNCLDILALRIHAERQRYLDQSPCVPGTSEFHKATIEAINTILFYEEAVRYPSKKEMFSDEFSFL
SSVTDRKFGVCLGVSSLYFSLSQRLDLPLEAVTPPGHIYLR YQGGEVNIETTAGGRHLPTASYCDCLDLEDLQ
VRTPEEMIGLTFMNQGSFALQKKKYKEAEEAYKKAQEYLGDEELQELLGFVQILGGKKKEGKSLIGKSPRAS
QKGSVAYDYLYKGRINIPTLALLFSYPGSNYEEIASYEEELKKAMKSSMPCCEGQRRLASVAFHLGKTAEAVA
LLEKCVEDIPNDLSLHLRLCKILCDRHDYTKALKYFIIAERLMEDQGFLKKDNRSFALFYEVKKIISKVAPQKA
NTLLLMESER

>core/174/4/Org4_Gene695

MSIVLDKIGKSLGTRILFDDVSVVFNPGNCYGLTGPNAGAKSTLLKIIMGMIEPTRGSISLPKKVGILRQNIDSF
HDTTVLDCVIMGNTRLWEALQRRDNLYLQEFTDAIGMELGEIEEIIIGEENGYRADSEAEELLTGIGIPNEMFD
KKMAMIPIDLQFRVLLCQALFGHPEALLLDEPTNHLDLYSINWLG NFLKDYEGTVIVVSHDRHFLNTITTHIA
DIDYDTIIHYPGNYDDMVEMKTASREQEKADIKSKEKKISQLKEFVAKFGAGSRASQVQSRLREIKKLQPQEL
KKSNIQRPYIRFPLSDKSSGKVVL SLEAITKDYGDHQVIHPFSLEIYQGDKLGIIGNGLGKTTLMKLLAGVEA
PSSGSIKLGHQAICSYPQNHSDVLADCGQETLFEWLRNRKTGINDQEIRSVLGKMLFGGDDAFKQIQALSGG
ETARLLMAGMMLNHNVLILDEANNHLDLESVSALS WAINDYKGTAIFVSHDRGLIQDCATKLLIFDKDKIT
FFDGTMADYTAGHKQLL

>core/175/4/Org4_Gene591

MKMHRLKPTLKS LIPNLLFLLLTLSSCSKQKQEPLGKHLVIAMSHDLADLDPRNAYLSRDASLAKALYEGLT
RETDQGIALALAESYTL SKDHKVYTFKLRPSVWSDGTPLTAYDFEKS IKQLYFEEFPSIHTLLGVKNSSAIHN
AQKSLETGLIHAKDDLTLVITLEQPPFYFLT LIARPVFSPVHHTLRESYKKGTPPSTYISNGPFVLKKHEHQNYL
ILEKNPHYD HESVKLDRVTLKIIPDASTATKLFKSKSIDWIGSPWSAPISNEDQKVLSQEKILTYSVSSTLLIY
NLQKPLIQNKALRKAIAHAIDRKSILRLVPSGQEAVTLVPPNLSQLNLQKEISTEERQKKARAYFQEAKETLSE
KELAELSILYPIDSSNSSIIAQEIQRQLKDTLGLKIKIQGMEYHCFLKKRRQGDFFIATGGWIAEYVSPVAFLSIL
GNPRDLTQWRNSDYEKTLEKLYLPHAYKENLKRAEMIIIEETPIIPLYHGKYIYAIHPKIQNTFGSLLGHTDLK
NIDILS

>core/176/4/Org4_Gene246

MPGSVSSPPLSPVIVRERVSSSSGSDLIQPHAVLKISILIFALVTILGIVLVVSSALGALPSLVLTVSGCIAIAVGLI
GLGILVTRLILSTIRKVDAMGYDAAVKEEQYLSRIELEASENREIRDNRAVEDQCAHLSEENKDLRDPEYLH
GMTERLIASLEIENQALVAENILLKDOWNASLSRDFRAYKQKFPLGALEPWKEDIACIMEQNLFLKPECIAMVK
SLPLETQRLFLYPKGFQSLVNRFAPRSRFFQTPKYEYNSRNENEDGKVAAVCARLKKEFFSAVLGACSYEELG
GICERAVALKETLPLPEAVYDTLVQEFPNLLTAESLWKEWCFYSYPYLRPYLSVDYCKRLFVQLFEELCLKLF
TTGSPEDQALVRLFSYYRNHIPAVLASFGLPPPETGGSVFVLLPKQENLLWSQIEVLATRYLKDTFVRNSEWT
GSFEMMFSYNEMCKEISEGRIRFAEDYETRHSEEFPPSPLSEEGEGEEFLPPCSEEEVSVLERPDLDVDSMWV
WHPPVPGGPL

>core/177/4/Org4_Gene793

MTARAEYLNHEDFLYRSHKLQELSALGVVPYPYEFPGVLSCEDIKKAFTGQELGNSEAAMSRSTPKVRFAGR
LVLFAMGKNAFGQILDHNQTIQVMFNSEFTSVHGLSKDAGVVPKIFIEKKLDLGDILGIDGYLFFTHSGELT
VLVETVTLLCKSLLSLPDKHAGLSDKEVRYRKRWLDLISSREVSDTFVKRSYIIKLIRNYMDAHGFLEVETPIL
QNIYGGAEAKPFTTKMEALHSEMFLRISLEIALKKILVGGAPRIYELGKVFRNEGIDRTHNPEFTMIEAYAAY
MDYQEVVMVFVENLVEHLVRAVNHDNTSLVYSHWKHGPQEVDFKAPWIRMTMKESIATYAGIDVDVHSDQ
KLKEILKKKTTLPETAFATASRGMILIAALFDELVSDNLIAPHHITDHPVETTPCLKTLRSGDTAFVERFESFCLG
KELCNAYSELNDPIRQRELLEQQHTKKELLPDSECHPIDEEFLEALCQGMPPAGGFGIGVDRLVMILTNAASIR
DVLVYFPVMRRFDAEKTN

>core/178/4/Org4_Gene593

MLRFFAVFISTLWLITSGCSPSQSSKGIFVVMKEMPRSLDPRKTRLIADQTLMRHLYEGLVEEHSQNGEIKPA
LAESYTISEDGTRYTFKIKNILWSNGDPLTAQDFVSSWKEILKEDASSVYLYAFLPIKNARAIFDDTESPENLG
VQALDKRHLEIQLETCAHFLHFLTLPFFPVHETLRNYSTSFEEMPITCGAFRPVSLEKGLRLHLEKNPMYHN
KSRVKLHKIIVQFISDPNTAAILFKHKKLDWQGPPWGEPIPEISASLHQDDQLFSLPGASTTWLLFNIQKKPW
NNAKLRLKALSLAIDKDMLTKVYQGLAEPTDHILHPRLYPGTYPERKQRNERILEAQQLFEEALDELQMTRE
DLEKETLTFSTFSFSYGRICQMLREQWKKVLKFTIPIVGQEFFIIQKNFLEGNYSLTVNQWTAAFIDPMSYLMIF
ANPGGISPYHLQDSHFQTLLIKITQEHTKHLRNQLIIEALDYLEHCHILEPLCHPNLRIALNKNKNFNLFVRRTS
DFRFIEKL

>core/179/4/Org4_Gene516

MNVLYTKHSSSAHAWKLIGTSPKHGIYLPFSIHTKNNSCGIGEFLDLVPLISWCQKQGFGVIQLLPLNDTGED
TSPYNSISSVALNPLFLSLSSLPNIDTIPEVAKKLQDMHELCSTPSVSYTQVKEKKWAFLREYYQKCKSSLEG
NSNFSEFLESERYWLYPYGTFRAIKHHMHGEPINNWPKSLTDQENFPDLTKKFHDEVLFSSYLQFLCYQQLCE
VKAYADQHHVLLKGDLPILISKDSCDVWYFRDYFSSSRVSGAPPDLYNSEGQNWHLPIYNFSQLAKDDYIW
WKERLRYAQNFYSVYRLDHIIGFFRLWIWDSSGRGRFIPDNPKDYIKQGTEILSTMLGASSMLPIGEDLGIIPQ
DVKTTLTHLGICGTRIPRWERNWESDSAFIPLKDYNPLSVTTLSTHDSDTFAQWWLNSPKEAKQFAKFLHLFP
QKTLTTETQIDILKLSHESASIFHINLFDNYLALCPDLVSKNLQRERINTPGTISKKNWSYRVRPSLEELAIHKK
FNGYIEKILTGL

>core/180/4/Org4_Gene733

MERKRFIDCDSTKILQELALNPLDLTAPGVLSAERIKKFSLLGGGFTFSFATERLDDAILAALISLAEERGLHES
MLAMQQGQVVNYIEGFPSEMRPALHTATRAWVTDSSFTGEAEDIAVRSRVEAQRLKDFLTKVRSQFTTIVQI
GIGGSELGPKALYRALRAYCPTDKHVFISNIDPDNGAEVLDTIDCAKALVVVVSXSGTTIETAVNEAFFADY
FAKKGLSFKDHFIAVTCEGSPMDDTGKYLEVFHLWESIGGRFSSTSMVGGVVLGFAYGFEVFLQLLQGASA
MDQIALQPNARENLPMLSALISIWNRNFLGYPTAVIPYSSGLEFFPAHLQCCMESNGKSITQDGRRVGFSTS
PVIWGEPTNGQHSFFQCLHQGTDIIPVEFIGFEKSQKGEDISFQGTSSQKLFANMIAQAIALACGSENTNPN
KNFDGMRPSSVLVSSQLNPYSLGELLSYYENKIVFQGFQWINSFDQEGVSLGKALANRVLELLEGADASNFP
EAASLLTLFNIKFR

>core/181/4/Org4_Gene501

MTKTEEKPFGLRSFLWPIHTHELKKVLPMLMFFCITFNYTVLRDTKDTLIVGAPGSGAEAIPIKFWLVVPC
AIIIFMLIYAKLSNLSKQALFYAVGTPFLIFFALFPTVIYPLRDVLPTEFADRLQAILPPGLLGLVAILRNWTF
AFYVLAELWGSVMLSLMFWGFANEITKIHEAKRFYALFGIGANISLLASGRAIWWASKLRASVSEGVDPWGI
SLRLLMAMTIVSGLVLMASYWWINKNVLTDPFRFYNPEEMQKGGKAKPKMNMKDSFLYLARSPYILLAL
LVIAYGICINLIEVTWKSQKLQYPNMNDYSEFMGNFSFWTGVVSVLIMLFVGGNVIRKFGWLTGALVTPVM
VLLTGIVFFALVIFRNQASGLVAMFGTTPLMLAVVVGAIQNILSKSTKYALFDSTKEMAYIPLDQEQKVKGK
AAIDVVAARFGKSGGALIQQGLVICGSIGAMTPYLAVILLFIIAIWLVSATKLNKFLAQSALKEQEVAQEEA
ASVQTRTQEDPAPASS

>core/182/4/Org4_Gene888

MVWVFKSQFEGLSALKRGVHALTKAVTPAFGPRGYNAVKKKGKAPIVLTKNIGIRIAKEIILQDAFESLGVKLA
KEALLKVVEQTGAGSTTALVVIDALFTQGLKGIAAGLDPQEIKAGILLSVEMVYQQLQRQAIELQSPKDVLP
VAMVAANHDVTLGTVVATVISQADLKGVFSSKDSGISKTRGLGKRVKSGYLSPYFVTRPETMDVVWEEALV
LILSHSLVSLSEELIRYLELISEQNTHPLVIIAEDFDQNVLRRTLILNKLNRNGLPVCAPKAPGSRELQVVLDAI
LTGATLIGQSENCEIPVSLDVLGRVKQVMITKETFTFLEGGGDAEIIQARKQELCLAIARSTSESECQELEERL
AIFIGSIPQVQITADTDTEQRERQFQLESALRATKAAMKGGIVPGGGVAFLRAAHAIEVPANLSSGMTFGFETL
LQAVRTPLKVLAQNCGRSSEEVIIHTILSHENPRFGYNGMTDTFEDLVDAGICDPLIVTTSSLKCAVSVSCLLLT
SSFFISSRTKT

>core/183/4/Org4_Gene964

MYQENLRLLERLLYNSFQKSYADRLFSYEKTKMVHDTPLIPWEEDKEKCAEAEKAFLEQQKILLDYGKSIFW
LNENDEINLNDPWSWGLNTRVTRKVFQEVDSDSERWNHVKVLIQKLEDDYEKLLLEESSKESTEANKLLSDLV
DRLEDAKTKFFLKKQEEVETRVKDLRAGYGGTVDPKQDTEAKKKVELEASLETFLDSIESELVQCLEDQDIY
WKEQDVKDLARRQEEQDVEAKREEAAEDLRSLNERLKSSKTMLDRAKWHIENAEDSITWWTSQIEMKD
MKARLKILKEDITSVLPEIDEIETCLSLEELPLLTRELLTKSYLKFKICSEKLLKMTSVFENNIYVQEYEVQLQ
NLGFKLQGISQRFQKQDDFANLEEQVALQKKRLRELTONFEIQGFNFMKEDFKAAAKDLYIRSTAEQKMN
FDVPCMELFRRYHEEVNKPILLEMYNCADSYRDAKKKLCSLRLDEKELLQKEIKKEEFYQKKQQRHADRSR
HTTYQKLRIAEELALELKKKI

>core/184/4/Org4_Gene966

MGPFVFPKQTSCEGDKDFSARNVSIHLGLNDVLKLCLLQRCPFALQWDNISVRRDYEEEEPVIKIRSLEPKVSQ
ISPTHGLLCSTLVQWASILGSEEQLFWLEETIKHLTFPKSLGSKDAVIDSEEVPLNANPTQDVPMPSTGTMKSTP
VVPETGDSLPTASTFAAAEDSTSEAGRESFSQRYALVLQGVPPYEPPEPLVMFTDQEKSLILEATRARMEL
DLYNGYLADYELSKDEIQKHVSDLPENWRTNWRWSERLYKFFFKTKKEGLEEIFLNKELGNMILARGLAAT
QSQARIKVFNSLVAWLLQGFNVGRSCTAKPLPTLKLDFKSEFESKPKNNILTEFLVASDEEILFKGLRVLEPG
IEGWYDHPDQAGEIRSVLEGLVQAGRISGYWENQPCGRFVLRGVGERRTELVELLESLVASGEIMQFFESSDE
EGAFIIDNEPSKTAMLKQRFKSCVRTLKLVGSFADESLPRGRFTILV

>core/185/4/Org4_Gene405

MVSLHLHKFLENASGKKGQSLASTAYLAALDHLLNAPFSIGERIIDEDELKSQRSHLKMIASENYSSLSVQLAMGN
LLTDKYCEGSPFKRFYSCCENVDAIEWECVETAKELFAADCACVQPHSGADANLLAVMAILTHKVQGPVAVS
KLGKTVNELTEEEYTLLKAEMSSCVCLGPSLNSGGHLTHGNVRLNVMSKLMRCFPYDVNPDTCECFDYAEI
SRLAKEYKPKVLIAGYSSYSRRLNFAVLKQIAEDCGSVLWVDMAHFAGLVAGGVFVDEENPIPYADIVTTTT
HKTLRGRGGLVLATREYESTLNKACPLMMGGPLPHVIAAKTVALKEALSVDFFKKYAHQVVNNARRLAER
FLSHGLRLLTGGTDNHMMVIDLGSLGISGKIAEDILSSVGIAVNRNSLPSDAIGKWDTS GIRLGT PALTTLG MG
IDEMEEVADIIVKVLNRNIRLSCHVEGSSKKNKGELPEAIAQEARDRVCNLLLRFLYPEIDLEALV

>core/186/4/Org4_Gene815

MSEQEKL SNYNADKKLFSGIDKLFQIVKGSYGPKQSLSPTSFFKERGIFYAISQTELSNSYENLGVDFAKAMVN
KIHKEHSDGATTGLILLHAILQESYAALEKGISTHKLIALSLKLQGEKLQEALQQQSWPIKDALKVRNIIFSSLH
MPTIADHFYNAFSVVGPEGLISITKERENEKTSMDVFQGFKIPAGYASTYFVSDTASRLTRIAHPLILITDRKIS
MIHSLPLLQEISEQNQHIIIFCEDIDPDALATLVVNKLQGLLQVTVTIPQLSTTNQELAEDIALFTGTHICPCQ
EASHVLAPEMVTLGSCLSIEISESQTTLIGGLHIPEVLTALKTRQLAEEIRTTSCLETKKRLIKRTNRLQSSVAILPT
DEDNEPLYTLALKIMESALSRGYVPGGGVALFYASLT LGTPKDDADENSIAISLLQKACCAPLKLLATNADLD
GDAVIAKLSSLGTTSLGISVFSREIEDLIAGGILDSLATTSTILAQALDTAILVLSSKILILENQYEISTL

>core/187/4/Org4_Gene775

MENEILLNIESKEIRY AHLKNGQLFDLIIERKKVRQLKGNIRGRVTNIRNIQSAFINIDERENGFIHISDILENS
KKFEQMFDMDVDALPEEASEAPLLSSEEAPIEEFLKLDSPVLVQVVKEPIGSKGARLTSNISIPGRYL VLLPNSP
HRGVSRKIEDPHMREQLKQLIRSFEMPQDMGLICRTASTTASTEALINEAHDLLLTWKTILEKFYSTEQPCLLY
SETDILKKAVITCIDKNYKRLIDDYATYQKCKHMLKKYSPDASIKIEYYRDSIPMFERFNIEKEIDKATRRKI
WLSSGGYLFFDKTEAMHTIDVNSGRSTQLES GVEETLVQINLEAAEEIARQLRLRNVGGLVIIDFIDMKSRKN
QRRVLERLKEHMKYDAARCTILSMSEFGLVEMTRQRNRESLMQTLFTLCPYCSGNAIKTPESVVIEIERDLK
KVINHKEHSHLCLVHPEIASYMKQENDDNEMINLAKQLKAKLQINTSDSVHLNHYQFFSLITGESIDL

>core/188/4/Org4_Gene929

MFNLFFFTANKETTASHELIYRKNQSFSLSPV TILCLLAISVLLLLGVVFALVGCHVLAAPLGLLVWGCAASV
CSMMAIVSLMCLYRGGKPLIEPSNEEKIDPTKD PESLKPVPVEGQSLPKERKTVSFKAKIPSIVEDDFKPYVIQS
TFYHQNKVYSKPIAERMQSLEKEITTLIVDFPRALEESSKSSGSLLRGVISEIKNLFLPRFLSRKVKYSLTACLR
RLGSIVEEYASSDLLILLTKPEFLNMVTQQLIAHLNSLKTEKQKLTSHMQKL VLSINFWFYGWSLEEK CIEKI
VAYDPNLLTDELKAHLEAGNIVQFLLSFQSSEM QREFRALFPSDAQELPSAKDGSNYVPAMNSSEYMYDFKD

LSVLKKSLSERLAFCEKIPSPSSWNFTSSVASHYKDFSLLFTFFSNQQSVILQNPFLLIELLHENPKCQTFKGLL
EKAMPMSNWAALFRPMLMGMLCSGIARKKELKIIAEHLGVPFKEITQAIASGKILDLLQHLFDF

>core/189/4/Org4_Gene442

MTLLRNFLTCSALFLALPAAQVVYLHESDGYNGAINNKSLEPRITCDPEGTSYIFLDDVRISNVKHDQEDAG
VFINRSGNLFFMGNRCNFTFHNLMTEGFGAAISNRVGDTTLTLSNFSYLAFTSAPLLPQGRGAIYSLGSVMIE
SEEVTFCGNYSLWGGAAIYTPYLLGSKASRPSVNLSGNRYLVFRDNVSQGYGGAISTHNLTLTTRGPSCFENN
HAYHDVNSNGGAIAIAPGGSISISVKSGLIFKGN TASQDGNTIHNSIHLQSGAQFKNLRAVSESGVYFYDPIS
HSESHKITDLVINAPEGKETYEGETISFSGLCDDHEVCAENLTSTILQDVTLAGGTLSLSDGVTQLHLSFKQEA
NSTLTMFPGTTLFCSGDARVQNLHILIEDTDNFVPVRIRAEDKDALVSLEKLIVTFEAYWSVYDFPQFKEAFTI
PLLELLGPSFDSLLLGETTLERTQVTTENDAVRGFWSLSWEEYPPSLDKDRRITPTKKTVFLTWNPEITSTP

>core/190/4/Org4_Gene568

MTNVVQETTGGNSPRTCPCILVIFGATGDLTARKLLPALYHLTKEGR LSDQFVCVGFARREKSNEQFRQE
MKQAVIQFSPSELDIKVWEDFQQRLFYHRSEFDNNTGYTSLKDSLEDLDKTYGTRGNRLFYLSTPPQYFSGIIE
NLNKHKL FYKNQDQGKPWSRVII EKPFGRDLDSAKQLQCCINENLNENSVYHIDHYLGKETVQNILTTRFAN
TIFESCWNSQYIDHVQISLSETIGIGSRGNFFEKSGMLRDMVQNHMMQLLCLLTMEPPTTFDADEIRKEKIKIL
QRISPFSEGSSIVRGQYGP GTVQGVSVLGYREEENVDKDSRVETYVALKTVINNPRWLGV PFYLRAGKRLAK
KSTDISIIFKKSPYNLFAAECSRCP IENDLLIIRIQPDEGVALKFNCKVPGTNNIVRPVKMDFRYDSYFQTTTPE
AYERLLCDCIIGDRTLFTGGDEV MASWKLFTPVLEEWDQDSSPSFPNYPAGSSGPKEADALIERDGRSWRPL

>core/191/4/Org4_Gene735

MSSWLSQASEVLLNQDPYIPDAPSSQESSVPKISYSITVAPQEAQKSLPKFFTQKFQSQCKSEPPITHHKTFIIAT
PRERILRFGSSFESQLHNTSQAQTSSPWNLF SQKNSTEASKALMQELTMPKSPEKTSEKALDKNLSSKQEGSC
KNFDTLHLQQLKLF GTVDSL YSQLDSEQQELLQSRREERSETYANQQSSEKKIETKVQIKDLCKDLFSQDQ
DSNQKQKKSPFQQDTSRKNRIAKAAQAVPVIPPSIGVFTLSYLLTKQGILSDFSSYACHKDSVESTQRELDAL
HEKRIETIKVSIEKEKRERLWGSLSDIIGWLAPFV SIGIGIVAILSGGGIFAFAGFFAGLISLVIKCLEKLK FWDW
LEKHLPIKNEELRRKIITIIQWVVYLTPVILSIC TLKVENLGFSP IIEGAIKGIQPAIESTMAALRCAILFSQAEIYK
LKGKLT KIQLDIELKS FDRDDHYERSQELLDNMESSFEALSRI LNYMRELDQVYLHSLRG

>core/192/4/Org4_Gene435

MAVGGVGGSRSLSPIPPNNRNS EDGKVSPKDNLGEHTVSSSDSSLASQGPTIEERKAQLGGTDKIPLPSVKEPG
DSQTSGRSGVLQRIWKG VKGVFKKTPQARPEVSSPRLPSHVQH GQRLPGFEGLRDRIQKRSENPEADLGKFQ
RSASEGDLTTQGRDSVGDA AEDSRSEGGEPSRSSSFLSGVRGA ASTVQ GALGDAKEKVSAFGEQAPGAIRS
APGNIRTRFQRSSSEGDL SNVNKA AKHLRKALENLEKVAPEQVSPEVASGVQSLLARMEQLTHQEPPTVEDLI
TFVESNVGSDSVEYASLDL FATPGESGVRGAGDSVEYASIVPQDGSQASAETA EAPETGGVERSAAQGAWK
ALRDFVVSIFQAVASFFRAIASRLSSARRESA VDDLASESNTQWFVEQEGVSNPSAAPSLSFAEESARRAAEM
SNRNAQSLEKLESGNV TDPVIQQGLGLARSFAPEGQ

>core/193/4/Org4_Gene619

MADILVIGANPTGLILANMLIQHGISVKVIDHRASPEDPSFLDCRKLPVILSCSSLELLHNSEMLGDFIQANHKI
FGARYHWKKRTLLFKFSQATDSPVPFSLSTTYQSLEQHLIDEFLKRGGVIDWSTRPVTLVDNSIFIESTKVSQN
FENREIYNPKWIIACEADNNLDIRDLVKSQLRARRINREVIFINCDEGEPEEDHIIHLLPITKNFLNFVFYNPQEK
TKQLCLPQGTHSISPKLKQKLLYTYNLVISDENFHIKTSHHAFPEHGNVFLGSLSENTLLLSYLNGIN TNIHAA
FNLAWKLLPVLKKAALKHLVITKEQEDGNILPYISPTTEKRAKKLPFSRFYTPALMYYFLKGCRKFNTTGEEY
YYPHQALKYRSSDIKMSPQDKEIHGPGPGMRAIDARLENGSFLLDPLKSSKHLLIFFKDIPDLKEALQEEYG
EWIEICNVKEPRILKLYHANPNSLFIIRPDRIYGYRTHTFKLHELISYLLRIFASEKTS

>core/194/4/Org4_Gene375

MNWENVVRVAPSTGDPHVGTAYMALFNEIFAKRFKGKMILRIEDTDRTRSRRDYEENIFSALRWCGIQW
DEGPDVGGPYGPYRQSERTKIYQGYVETLLKTDCAYKCFATPQELAEMRAVASTLGYRGGYDRRYRYSPE
EVASREAAGQPYTIRLKVPLSGECVFEDYSKGRVVPFWADVDDQVLKSDGFPTYHFANVIDDHLMGITHV
LRGEEWLSSTPKHLLLYEAFGWEPVFLHMPLLLNPDGTKLSKRKNPTSIFYRDSGYVKEAFVNFLTLMGY
SMEGDEEVYSLERIETFNPRRIGKSGAVFDIQKLDWMNKHLYLNHEGSPERLLKELQGWLLNDEFFLKILPLC
QSRITTLAEFINLTSFFFSGLLEYRVEELLPQVLSPEKAAILLYSYVKYLEKTDQWTKETCYLGSKWLAQAFN
VHHKKAIIPLLYVAITGKKQGLPLFDSIEILGKPRARARLVYAEKLLGGVPKKLAAAVDKFMQREDFEATFD
L

>core/195/4/Org4_Gene285

MDCRGDIPLPEPQVIGGYHVKKILSKKLRSRVVHGLHPETRHSTVIKVFSPSPSFTSRSVHNFLKEAQLHQIT
HPNIVKFHRYGKWQDCLYIAMEYIEGISLREYILAQFISLPQAIDIIFDIAQALEHLHSRNILHKDIKPENILITPQ
GKIKLIDFGLADWDTEIQRHPSVIGTPYYMSPEQRQGESHSPASDIYALGLLAYELILGHLSLGRVFLSLVPE
RISKILAKALQPSNNRYSSTREFIQDIHHYRMSGDMQEDLRIKDHTVALYEQLQTQRFWLAPETLRFDPDFISG
VLYHQGYPLYPHAYYDTLLEGDVFNLWLGYSISP NATIALSVVKS LVCQQDLQRPLLDVCEINECLIRMKIP
IDEMGISILCLEISKENKELSWIACGKT VFWIKRQGRVVQDFESFSPGLGKITS LQIRETKVAWEIGDEAVVRTL
ELEESVASLKTLSLAELQDRRQKAIFCPIESIHGGIQSRQHGSNSPSTLISLKRIR

>core/196/4/Org4_Gene462

MLKKFINSLWKLCQQDKYQRFTPIVDAIDTFCYEPIETPSKPPFIRDSVDVKRWMMMLVVIALFPATFVAIWNS
GLQSIVYSSGNPVLMEQFLHISGFGSYLSFVYKEIHIVPILWEGLKIFIPLLTISYVVGGTCEVLFAVVRGHKIAE
GLLVTGILYPLTLPPTIPYWMAALGIAFGIVVSKELFGGTGMNILNPALSGRAFLFFTFPAKMSGDVWVGSNP
GVIKDSLKMNSSTGKVLIDGFSQSTCLQTLNSTPPSVKRLHVDIAANMLHIPHVPTQDVIHSQFSLWTETHP
GWVLDNLTLTQLQTFVTAPVAEGGLGLLPTQFDSAYAITDVIYGIGKFSAGNLFWGNIGSLGETSTFACLLG
AIFLIVTGIASWRTMAAFGIGAFLTGWLFKFISVLIVGQNGAWAPARFFIPAYRQLFLGGLAFGLVFMATDPVS
SPTMKLGKWIYGFFIGFMTIVIRLINPAYPEGVMLAILLGNVFAPLIDYFAVRKYRKRRV

>core/197/4/Org4_Gene560

MKFEFSVALKYLIPGKGRLSSAIVSLFSVGIISLVVWLSIVFISVIHGLEQRWIEDLSQLHSPITILPSDTYYSSYY
YQIDKHSNLSNYTTKTLGEKIASPQVDPYPDES DYLLPETFPLKDCDLGGQKQDPVKMTLES LGPYLQSQHG
KVIEFEQGVGYLDIKTSLKLQKPQPRNLTHFLTYP SKLSYEDKVLPYDETDY TSAELNPFNRSPSGWQQDFHH
LEELYRGASIILPSTYKDSGYKVGDTGVFSTYSIENQKETQYTVHVIGFYNPGLSPLGGRTVFIDPDLARSIRSQ

SEGLGMSNGFHLFFPNTKRIVFVKKQIENILTSLGIDDYWEISSLYDYDYFQPILDQLQSDQVLFLFVCILILIVA
CSNIVTMSMLLVNNKKKEIGILKAMGTSSRSLKIIFACCGAFSGACGVVIGTIFAIITLKNLQFIVKALNYLQGR
ETFNTAFFGQNLPSVHPQAIYFLGLGTLFLAAVSGALPARKVAKMHVSEILKAD

>core/198/4/Org4_Gene481

MVLFHAQASGRNRVKADAIVLPFWHFKDAKNAASFEEFEPSTYLPALENFQGKTGEIELLYSSPKAKEKRIV
LLGLGKNEELTSDVVFQTYAKLTRVLRKAKCSTVNIILPTISELRLSAEFLVGLSSGIFSLNYDYPRYNKVDR
NLETPLSKVTVIGIVPKMADAIFRKEEAIFEGVYLTRDLVNRNADEITPKKLAEVALNLGKEFPSIDTKVLGKD
AIAKEKMGLLLAVSKGSCVDPQFIVVRYQGRPKSKDHTVLIGKGVTFDSGGLDLKPGKSMLTMKEDMAGG
ATVLGILSALAVLELPINVTGIIPATENAIDGASYKMGDVYVGMMSGLSVEICSTDAEGRLLADAITYALKYCK
PTRIIDFATLTGAMVVSLGEEVAGFFSNNDVLAEDLLEASAETSEPLWRLPLVKKYDKTLHSDIADMKNLGS
NRAGAITAALFLQRFLEESSVAWAHLDIAGTAYHEKEEDHYPKYASGFGVRSILYYLEKSLSK

>core/199/4/Org4_Gene736

MTVSYQSISTPPPEGEFDIFVDGNATEEAVVAAEVQVALPAGEQYAMLRATSELFCGILTQSECAITQALPPK
EKPLQEEQFLVKNLILMRSTSLPNLKPGQSQQTSLASHRNPLAQSTSSNSTGKASTETTSSSFPPFSCKAPEG
DSSVDKTFTVSVQTPKAQEQQEASASQSQAQFHVRSYSSSTIKEHSAKEKVSQSTKSAETQKHTQTKSDATLS
PMSLYSTLHKEAPQALSSTKSQQKDEEHRDQGGQEGYEQEQEQEKGKKTPWCTVESLQQTSSSNQVYESY
TPIIPDPIVEFALSESQLSVLAGKRVTNLDVLRICTELMKLMKSRANDTMTRLEERELMEREAEHLAASYSR
QAKYARWLGIATATLGILGAIAPMVGEISGDSILGFVQRISGRFKDATAKTFFKGIGKVFTSLSQLTEAASKVH
ELSESAVRAVAEYRKEVFRMRQDEVTRTIEEVKDNWKSMDNLFLLNLQTEHDAARSLYQ

>core/200/4/Org4_Gene870

MAASILSQELLDILPYTFLKKHCLLPIEESSEAITIAHATATSVIAQDEVKLLIKKPVRFVLKEESEILQRLQQLY
SNREGNVSDMLLTMKKEEDGTTISEEEDLLETDTIPVVRLLNLILKEAIEERASDIHFEPCEDSMRIRYRIDGVL
HDRHSPPSHLRSALTTRLKVLAKMDIAEHRLPQDGRIKIHIGGQEVDMRVSTVPVIYGERVVLRIIDKRNVL
DIAGLHMPKDTEILFKDTITAPEGILLVTGPTGSGKTTTLYSVLQELKGPLTNIMTIEDPPEYKLPQIAQIAVKP
KIGLTFARGLRHLLRQDPDILMVGEIRDQETAETIAIQAALTGHLVVSTLHTNDAISAIPRLLDMGIESYLLSATL
VGVVAQRLVRTICPYCKVAYTPENQEKSFLASLGKDTEMPLYRGQGCVHCFRSGYKGRQGIYEFLRPNTLFR
SEVASNRPHYHILRETAEQNGFLPILEHGIALAVSGETTLAEVLRVTKRCD

>core/201/4/Org4_Gene50

MNKKHASFSSRLGFIFSMIGIAVGAGNIWRFPVRVAAQNGGGAFLILWLCFLFLWSIPLIIHLSIGKLTKKAPIGA
LIKTAGKKFAWAGGFITLVTTCILAYYSTIVGWGLSYFYAVSGKIHGNDFAKLWTSHYQSSIPLWAHLTSL
GLAYLVIRKGIVHGIEKCNKILIPAFFLCTIALLLRAVTLPGAVQGQIKQLFSCDKSCFSNYKVWIEALTQNAWD
TGAGWGLLLVYAGFASKKTGVVSNGALTAICNNLVSLIMGIIIFSTCASLDILGTTQLQDGAGASSIGITFIYLP
ELFTRLPGGIYLTTLFSSIFFLAFSMAALSSMISMLFLLSQTLEFGIKPYISETLATIIAFVLGIPSALSLTFFSNQ
DTVWGVALIVNGLIFIYAALVYGFPKLKKEVINAAPGDLRLNKAFDYIIKYLLPIEGILLGWYFYEGLPENG
QWWNPISLYSLGSLVLQWSLGLIILWKFNKQLYLRFSRYNHEIL

>core/203/4/Org4_Gene351

MLKYILKRLVLIPLTLFAIVSIN FVILN AAPGDVLEE KSRDALGEAGKSDKMRSYKGPDRYLQFREHYGLTLPI
FFNTRPKITHKKIQTALQELANANNTTPSAKNAAKSLVYWGDCAKFVMPALLFEADDASRDDKYRHIAADL
FIRGGVLQGFVGP NLSPEQRAQNKEIAESNAFLVRQLNEEDLDTKVEALKGWFQDHGGTEVFCYSPKQFWK
TFFLETRFARYMSRVLRLDFGTLRND AHKTVISEVIKRLRCSLVLSILPMIVGFVLCQIFGMIMALKRNHWIDH
SLNFIFLILFSIPVFVAVPWILDNFVINKTIPFTTIPMPYSGLRSPPEVFNELSTLGRIFDLVSHGFLPFCVSYGAL
AAQSRLSRSIFLEVLSQDFICAAKARGLRWFDILYKHVGKNAAVSIVTSLASSLGTLLGGALVVETLFNIDGFG
NFFYQAILNRDHN VVLFVSVLVGSALSLVGYLLGDICYVLLDPRVQLEGRRI

>core/204/4/Org4_Gene904

MHTEFAPFLEDLVHQQVISLLDIAFASKHISDFEESFVFLAVSSALWRYGHPFLSLEENRIRPSLGGISETDLY
RGFHNLPKEVRDKLFVVVSGRLYLRSLYTIRSKLLDKLSLLCSATPNYFPPSIDSSILSEEQNFIFNKITQGCFSI
VSGGPGTGKTFLAAQLILSLVKQQPKLRIAIVSPTGKATSHIRQILMKYNIFDDMVLMQTVHHFLQEYAYRRY
NSIDVLLVDEGSMVTFDLLYSLVQTLQGYEKDKKLYTSSLIILGDTNQLPPIGIGVGNPLQDLIGYFHENTFFL
KTSHRAKTGAVDQLTQSVLRGEMIPFSPLPSISSAIEVLKDRFVKSLRQSEARLCVLTPMRHGPWGVNLNNTM
IHQRLARSDPDLRIPIMVTSRYETWGLFNGDTGLLCLKTQKLHFPQHEPIDSRALSQYVYNYVMSVHKSQGSE
YDEVIVIIPKGSEVFGVSILYTAITRAKYRVSVWGD PETLHKIIKKS NY

>core/205/4/Org4_Gene761

MNLD SKHFDINSANFLEEF AKFISFPSISADSDHLQDCENCAHFLVDHVNKIFDVELWETPGHPPIIYASYKSE
DPLSPTLM LYNHYDVQPAQLSDGWKGDPFILREENG NLYARGASDNKGQCFYTLKALQHYYESRGNFPLNII
WLIEGEEESGSLALFTWLEKKKEALHADYLLIVDGGFLSEKHPYVSIGARGIVSMKISLEEGNKDMHSGVLG
GIAYNTNRALSEILSSLHHPDNSIAIEGFYDDLALPSDSDRPDLPKSDTLRECEENLGFRPQGYEASYSPEESAL
RPTVEINGISGGYTGP GFKTVIPYRATAYLSCLVP NQDPDKAAHQVIHHLKQQVPSSLKFSYEILPGGSRGW
RSSANLPIVKVLQEIYSDLYNEECLRLMMPATIPIGPLLGEAAQTSPHICGTSYLSDDIHAAEEHFSIDQLKKGFL
SICQLLDKLPKIKE

>core/206/4/Org4_Gene249

MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTMESDATIAGASGKD KTSSTTKT
ETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSIEEASKSMESTLESLSLSAAQMKEV
EAVVVAALSGKSSGS AKLETPELPKPGVTPRSEVIEIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLG
LEKQAIKIDKERE EYQEMKAAEQKSKDLEGTMDTVNTVMIAVSVAITVISIVAAIFTCGAGLAGLAAGAAVG
AAAAGGAAGAAAATTVATQITVQAVVQAVKQAVITAVRQAITAAIKA AVKSGIKAFIKTLVKAIKAISKGI
SKVFAKGTQMIAKNFPKLSKVISSLTSKWVTVGVGVVVAAPALGKGIMQMQLSEMQQNVAQFQKEVGKLQ
AAADMISMFTQFWQQASKIASKQTGESNEMTQKATKLGAQILKAYAAISGA IAGAA

>core/207/4/Org4_Gene702

MYRYSALELAKAVTLGELTATGVTQHFFHRIEEAEGQVGAFISLCKEQALEQAELIDKKRSRGEPLGKLAGV
PVGIKDNIHVTGLKTT CASRML ENYQPPFDATVVERIKKEDG IILGKLN MDEFAMGSTTL YSAFHPTHPWD
LSRVPGGSSSGSAAAVSARFCPVALGSDTGG SIRQPAAFCGVVGFKPSYGAVSRYGLVAFASSLDQIGPLANT
VEDVALMMDVVFSGRDPKDATSREFFRDSFMSKLS TEV PKVIGVPRTFLEGLRDDIRENFFSSLAIFEGEGTHLV
DVELDILSHAVSIYYILASAEAA TNLARFDGVRYGYRSPQAHTISQLYDLSRGEGFGKEVMRRILLGNYVLSA

ERQNVYYKKATAVRKIVKAFRTAFEKCEILAMPVCSSPAFEIGEILDPVTLYLQDIYTVAMNLAYLPAIAVP
SGFSKEGLPLGLQIIGQQGQDQQVCQVGYSFQEHAQIKQLFSKRYAKSVVLGGQS

>core/208/4/Org4_Gene991

MQRDGRFKWLQDEDTSAHAEQRFRDINGCWEDLKQTIFWVGEHDCMDIETVRKSYMMWLDTRYADKFILR
EKEEKMKRHELPHATMVRKASGHAYAKAKAAFEKERSNENQRKVKDIEKWLSKGLAEFRNQESRRARERL
RELQTLYPGVSVEERVLERQRTKKVNLENLYADIEKKYHHCVREQEHWKEVENKEAEFRENREKVLSTEE
VLECLQRLEDCLTWSKQLTKAEGSVFEMMFDATEELGNKVLSDVTNRLEILCEDAEEMIFRIEEIEMTLRM
VELPLLFMKNTFEKASLQYNSCKEMLAKAEPHCKESAIRSSSEERLERLNRDLQTAYTNCHERLQGFSSKLESE
VRTCKDHLREQMKHFEVQGLNFINEELLWVGAEFLTQARLDLVATVPYMEFYLYHNIKREKVRSSQWMAK
TERYREIRQAFQGVMKEDLLAEDTILKEEDYWLLRDDWLLRDERKNRQRRLICNKIAAAQQRVKGF

>core/209/4/Org4_Gene637

MLGILLIASGHIIFLAVAIPGLSSAVALGLGCGMTALGTVLLITGLVSLIRSEQLALEQVEIKQARTRVNNELDQL
SQYVFYTENVDNLKRWSYRDLGFVRQAQEEVTNLEQDIEEIFLTRDIRNALDNEEFFMTHAKQCLAQVGE
SLFQDASIDEFINLAHLSEIRQHLDINDPRWSMITKKVKGTVVRFIYVSTMYKQIKSNFEKSDFGQLRKMLLN
NYKTIEEVLYQSFQKGYNRAALLSEKTRIIHTSSLLHWEKDEDKHLNIKNECASRLNFKKFRTLFLGLSEED
VIDFTGASGWDCSKLPRKELPLDGGKKKLRFKRTFADEQVGDWDRITSLEHMTPEEDPLDKLMDQVEQE
ATSVLKDQDRYWKEIETSEAKFRSLPQEDDFEKQSQIDSYIRDLDDHLSVWANQLSAAEDALIEVTDVQEHG
NREMLKNIQQGLELIEDAVKATLPRVDFIQELLEKEELPLVAARMSLENSYLKISS

>core/210/4/Org4_Gene705

MSFPCGNCDCCYYRETPSLNPGGEDIPLQEGGTPNPQMGHAI TNQPGHAAGISFGSDNLLGTVEQAGKMLDNL
LSSVRMQRLGHYCYRTGTPWCRTHC PGFLQWIWGGCCACCLEAVDDPENPSEICLRDLVDRFGPICVGM AF
QQLPRCTSKVEQGDPLDDEDQRNLETMCQEQLKLLKAAQPRCMGLSLIKILKNTDLGEGMRSESPSSLLLQA
VSEGSRPYITSIESVPTCWILQPDQHPSPPPPTDEEQLQGAVGGAPATQPKKNPAQECRV TCKLDFKVLLQKL
SKLDVYCLSTGYQG PLGRAARPVLDTVKRSLKRLVVREPMIFQAPGIGLSLESKIFELMILLCLLSQGFLPLDP
LNPEQPILDPRAGQPWQDILKEMLFTTMAGENIWRH THGEP RHPTPPSGNEIEIDGGGPQAAASGTGRGATR
RRDPTDDENTGRAGNLGMPLSDGDVDDDDDEDPWSPDNQRALLSTA FRVCNIFNLG

>core/211/4/Org4_Gene946

MHMSNPISLFS PAELIAKYNLIPKTSPIYPRRTELIILEENACQTRL TNVAQILHPSSLFSMSKKILNPCGCSGGPL
CWVILNILAFIITSVLFIILLPVNLIVAGLRLFMPLPPKKIVEDLSEPTTEETNEVIQPFIFALQALLFEDNKLRSFK
IVEQSVSKAPLPNPFLNRLVATSPQESQEAMRKIPDLCSQLKKVLKSLGVLTP EWKHMLKYFEG LKNEHDSN
PDKKTFPILIKLLIEALTGKSSFFSNLPKTPSTKEKMQAALFIASSCKTCKPTWGEVITRSLNRLYSIANEGDNQ
LLIWVQEFKERELMSIQDGDDAE EYRFAAQQHGERYTEAIEQVLRNESA AKLQWHVINTMKFFH GKNLGLV
TEHLQDTL GALTLRQT TVDTHQGREDADLSAALFLNKYLN SGNQLVNSVFKSMQKADPETKALIREFALDIL
YASRLRPQ TSAHTEVFSTLLMDPETYE PNKACIAYLLYVLKIIEL

>core/212/4/Org4_Gene701

MSAVYADWESVIGLEVHVELNTASKLFSSALNRFGDEPNTNISTVCTGLPGSLPVLNQSAVEKAVLFGCAVE
GEISLLSRFDRKSYFYPDSPRNFQITQFEHPIIRGGRIKAIVQGEERYFELAQTHIEDDAGMLKHFGEFAGVDYN
RAGVPLIEIVSKPCMFCEPDAVAYATSLVSLLDYIGISDCNMEEGSIRFDVNVSVRPKGSPELRNKVEIKNMNS
FAFMAQALEAEKQRQIDEYLNQPNKDPKLVIPAATYRWDPEKKKTVLMRLKESAEDYKYFPEPDLPTLQLTE
SYIEGIRKTLPELPYDKYHRYIQEYGLSEDIASILISDKNIATFFEVACKDCKNFRSLSNWVTVEFGGRCKTLGV
KLPSSGIFPEGVAQLVNAIDQGVITGKIAKEIADLMMESPGKNPEEILKEKPELLPMSDEGELQKIIAEVVLANP
ESIVDYKNGKTKALGFLVGQIMKRTAGKAPPKRVNELLLLLLELDKG

>core/213/4/Org4_Gene762

MITKQLRSWLAVLVGSSLLALPLSGQAVGKKESRVSELPQDVLLKEISGGFSKVATKATPAVVYIESFPKSQA
VTHPSPGRRGPYENPFDYFNDEFFNRFFGLPSQREKPSKEAVRGTGFLVSPDGYIVTNNHVVEDTGKIHVTL
HDGQKYPATVIGLDPKTDLAVIKISQNLPLYLSFGNSDHLKVGDWAIAGNPFGLQATVTVGVISAKGRNQL
HIADFEDFIQTDAAINPGNSGGPLLNDGQVIGVNTAIVSGSGGYIGIGFAIPSLMANRIIDQLIRDGQVTRGFLG
VTLQPIDAELAACYKLEKVYGALVTDVVKGSPADKAGLKQEDVIIAYNGKEVDSLSTFRNAVSLMNPDRIV
LKVVREGKVIEIPVTVSQAPKEDGMSALQRVGIRVQNLTPEAKKLGIAPETKGILIISVEPGSVAASSGIAPGQ
LILAVNRQKVSSIEDLNRTLKDSNNENILLMVSQGDVIRFIALKPEE

>core/214/4/Org4_Gene687

MWNRCQVFSSFFFRYPISSWLIRLRASCECFQQRHPIFLCGLYWLAGITSRGHPECSALILIFLGMFLPRNPKQ
WLPLASAWIISLMLTPAPFLHDGPISGTFVIHHAGGQGTYYGEALCIQTPCGKRAHHLSCQILSESRLLEKKVY
ELEGTLHHTSQIVFKSNACYKEIPRSRFYIMKEKCRESSCHFLNHRFPSSEVGPFASSLLLGTPLPQNLRDLFRQ
KGLSHLFAISGWHFSLCATTWMLCALLPLKIKKILSFIVLTSACIFPMSPSVWRSWISVTLLCFSWCFSGSCS
GLNRLGAGFILCSIFFSPFSPTFVLSFLATLGILLFFPKIFSFLYTPWTQFLSPFWLYPIRYLAMTLAISLSAQLFIV
LPIMQYFGSLPLEGLLYNLIVPFTILPIIVFLIATIILPCCSPITEALIQGFLSHPWLHNPNIKLTLSFAPVPPWMLTL
ASLILFFIGILRTNVSPYASISATSYRFIETL

>core/215/4/Org4_Gene853

MLKIAILGRPNVGKSSLFNRLCKRSLAIVNSQEGTTRDRLYGELHAFGVPAQVIDTGGVDHNSDYFQKHIYN
QALTGAKEADVLLLVIDIRCGITEEDAHLAKLLLPLKKPLILVANKADSRQEELQIHETYKLGIRDIVVTSTAH
DKHIDTLLQRIKLVANLPEPREEEGLEELSVDEHEESEAAALPSNTFPDFSEVFTEGFSPEEPCTIPESPQQAPKTL
KIALIGRPNVGKSSIINGLLNEERCIIDNTPGTTRDNIDILYSHKDRQYLFIDTAGLRKMKS VKNSIEWISSRTE
KAISRADICLLVIDATQKLSSYEKRILSLISKRKKPHIILINKWDLLEEVRMEHYCKDLRATDPYLGQAKMLCIS
ATTKRNLKKIFSAIDELHHVVS NKVPTPIVNKTLASALHRNHPQVIQGRRLRIYYAIQKTTTPLQFLLFINAKSL
LTKHYEYYLKNTLKSSFNLYGIPFDLEFKEKPKRHN

>core/216/4/Org4_Gene734

MNMPVPSAVPSANITLKEDSSTVSTASGILKTATGEVLVSCTALEGSSSTDALISLALGQIILATQQELLQSTN
VHQLLFLPPEVVELEIQVVDLLVQLEHTETITSEPQETQTQSRSEQTLPPQSSSKQSALSPRSLKPEISDSKQQQ
ALQTPKDSAVRKHSEAPSPETQARASLSQASSSSQSRSLPPQESAPERTLLEQQKASSFSPLSQFSAEKQKEALT
TSKSHELYKERDQDRQQREQHDRKHDQEEDAESKKKKKKRGLGVEAVAEEPGETLDIAALIFSDQMRPPAE
ETSKKETTFKKKLSPMSVFSRFIPSKNPLSVGSSIHGPIQTPKVENVFLRFMKLMARILGQAEAEANELYMRV

KQRTDDVDTLTVLISKINNEKKDIDWSENEEMKALLNRAKEIGVTIDKEKYTWTEEEKRLLKENVQMRKEN
MEKITQMERTDMQRHLQEISQCHQARSNVLKLLKELMDTFIYNLRP

>core/217/4/Org4_Gene729

MTSRTKSSKNLGTIALAGMVVSSMIGGGIFSLPQNMAATAGAGAVILSWILTGFGMFFIANTFRILSTIRPDLK
EGIYMYSREGFGPYIGFTIGWGYWLCQIFGNVGYAVITMDALNYFFPPYFQGGNTLPAILGGSILIWFNFIVL
KGIRQASIINVIGTIFKIIPLIIFIILTAFFFKLAVFKTDFWGHAVTKAQPSLGSVSSQLKGTMLVTLWAFIGIEGA
VVMSSGRAKNPLSVGKATVLGFLGCLTIYILLSLLPFGSLFQHQLANIPNPSTAGVLDILVGKWGEVLMNVGLII
AVLSSWLSWTIIVAEIPFSAAKNGTFPEIFTIENKEKSPSVSLYITSSVMQLAMLLVYFSSNAWNTMLSITGVM
VLPAYLASAAFLFKLSKSKTYPKKGSIKAPLAMITGILGVVYSLWLIYAGGLKYLFMALVLLALGIPFYIDAG
KKKKNAKTFFAKKEIVGMTFIGLLALTAIFLFSTGRIKI

>core/218/4/Org4_Gene651

MITRTKIICTIGPATNSPEMLAKLLDAGMNVARLNFSHSGSHETHGQTIGLLKELREQKRVPLAIMLDTKGPEIR
LGNIPQPISVSQGQKLRLVSSDIDGSAEGGVSLYPKGIFPFVPEGADVLIDDGYIHAVVVSSEADSLELEFMNS
GLLKSHKSLSIRGVDVALPFMTEKDIA DLKFGVEQNVDVVAASFVRYGEDIETMRKCLADLGNPKMPIIAKIE
NRLGVENFSKIAKLADGIMIARGDLGIELSVVEVPNLQKMMAKVSRETGRFCVTATQMLES MIRNVLPTRAE
VSDIANAIYDGSSAVMLSGETASGAHPVAAVKIMRSVILETEKNLSYDSFLKLDDSNSALQVSPYLSAIGLAGI
QIAERADAKALIVYTESGSSPMFLSKYRPKFPIIAVTPSTSVYYRLALEWGVYPMLTQESDRAVVRHQACIYG
IEQRILSNYDRILVLSRGACMEETNNLTLTIVNDILTGSEFPET

>core/219/4/Org4_Gene294

MGESVKVFLEEREDYPYGFVTPIESQGLTRGLSEETIEEIAALRNEPQFIIDFRLQAYRHWKQLHEPAWARLH
YGPIAYDDIVYFSSPKQKKPLGRLEDADPEILDTFKKLGIPLDEQKRLNVENVAVDLVFDSVSIGTTTFKEALE
KAGVIFCSLGEAIQEHPNLVKKYLGSVVSHRDNFFAALNAAVFSDGSFVYVPKGVKCPMDISTYFRINNKEA
GQFERTLIVVEDGGYASYLEGCTAPAYSSNQLHAAVVELVAHEHAVIRYSTVQNWYAGDKKTGKGGIYNFV
TKRGLCAGYRSKISWSQVEVGAAITWKYPSCILKGDES VGEFY SVALTSGKMQADTGTKMLHVGKRTTSTV
ISKGISSESKNTFRSLVSLGKKA EHSSNYTQCDSMLIGKASGAYTDPKIVVENSTSSIEHEATTSKLREDQLLY
LRSRGLSPEEAVSLVIHGFCREIIEQLPLEFAQEASKLLLIKLENSVG

>core/220/4/Org4_Gene465

MDLKELLHGVQAKIYGKVRPLEVRNLTRDSRCVGVGDIFIAHKGQRYDGNDFAADALANGAIAIASSLYNPF
LSVVQIITPNLEELEAELSAKYIEYPSSKLHTIGVTGTNGKTTVTCLIKALLDSYQKPSGLLG TIEHILGEGVIK
DGFTTPTPALLQKYLATMVRQNRDAVVMEVSSIGLASGRVAYTNFDTAVLTNITLDHLDHFHGTFEAYVAAK
AKLFSLVPPSGMVVINTDSPYASQCIESAKAPVITYGIESAADYRATDIQLSSSGTKYTLVYGDQKIACSSSFIG
KYNVYNLLAAISTVHASLRCDLEDLLEKIGLCQPPPGRLDPVLMGPCPVYIDYAHTPDALDNVLTGLHELLPE
GGRLIVVFGCGGDRDRSKRKLMAQVVERYGFAVVTSDNPRSEPPEDIVNEICDGFYSKNYFIEIDRKQAITYA
LSIASDRDIVLIAGKGHEAYQIFKHQTVAFDDKQTVCEVLASYV

>core/222/4/Org4_Gene496

MQTNIGLIGLAVMGKNLVLNMIDHGFSSVSYNRTPEKTRDFLKEYPNHRELIGFESLEDFVNSLERPRKIMLM
IQAGKPV DQSIHSLLPFLES GDVIIDGGNSYFKDSERRCKELQEK GILFLGIGISGGEEGARHGPSIMPGGNPEA
WPLVAPIFQSI AAKVQGRPCCSWVGTGGAGHYVKA VHNIGIEY GDIQLICEAY GILRDFLKL SPTAVATIFKEW
NTLEESYLIRIASEVLALKDPEGIPVIDTILDVVGQKGTGK WTAIDALNSGVPLSLIIEAVLARFLSSWKEIREQ
AARNYPGTPLIFEMPHDPSVFIQDVFHALYASKIISYAQGFMLLGEASKEYNWGLDLGEIALMWRGGCIIQSA
FLDVIHKGF AANPENTSLIFQEYFRGALRHAEMGWRRTVVTAIGAGLPIPCLA AAITFYDGYRTANSSMSLAQ
GLRDYFGAHTYERNDRPRGEFYHTDWVYTKTTERVK

>core/223/4/Org4_Gene277

MRDVSELFRTHFMHYASYVILERAIPHILDGLKPVQRRLWTLFLMDDGKMHKV ANIAGR TMALHPHGDAP
IVEALVVLANKGYLIDTQGNFGNPLTGDPHAAARYIEARLSPLARETLFNTDLIAFHDSYDGREKEPDILPAKL
PVLLLHGVDGIAVGM TTKIFPHNFAELLKAQIAILNDKKFTVFPDFPSGGLMDPSEYQDGLGSITLRASIDIIND
KTLVVKQICPQSTTETLIRSIENAAKRGTIKIDTIQDFSTDVPHIEIKLPKGSRAKEMLP LLFEHTECQVILYSKPT
VIYENKPVECSISEILKLHTTALQGYLEKELLLQEQLTLDHHHKTLEYIFIKHKLYDSVREALAINKKISADDL
HQA V LHALEPWLHELATPVTKQDTSQLASLTIKKILCFNEEACTKELLAIEKKQAAIQKDLGRIKEVTVKYLK
GLLRHGH LGERKTQITNFKTAKTSILKQQTLI

>core/224/4/Org4_Gene726

MLCATVSGPSFCEAKQQILKSLHLVDIIELRDLINELDDQELHTLITTAQNPILTFRQHKEMSTALWIQKLYSL
AKLEPKWMDIDVSLPKTALQTIRKSHPKIKLILSYHTDKNEDLD AIYNEMLATPAEIKIVLSPENSSEALNYI
KKARLLPKPSTVLCMGTHGLPSRVLSP LISNAMNYAAGISAPQVAPGQPKLEELLSYNYSKLSEKSHIYGLIG
DPVDRSISHL SHNFLLSKLSLNATYIKFPVTIGEVVTFFSAIRDLPFSGLSVTMPLKTAIFDHVDALDASAQLCE
SINTLVFRNQKILGYNTDGEGVAKLLKQKNISVNNKHIAIVGAGGAAKAIAATLAMQGATLHIFNRTLSSAA
ALATCCKGKAYPLGSLENFKTIDIINCLPPEVTFPWRFPPIVMDINTKPHPSPYLERAQKHGSLIIHGYEMFIEQ
ALLQFALWFPDFLTPESCD SFRNYVKNFMAKV

>core/225/4/Org4_Gene923

MMSRLRFRLAALGIFFILLVPNFVSAKTIVASDNEKVGVLVYDNSVEAFQQILDCIDHANSYVELCPCMAGGR
TLKEMVDHLEARM DLVPELCSYIIIQPTFTNAEDQKLLKALKERHPNRFFYVFTGCPPSTSILAPNVIEMHIKLS
IIDGKYCILGGTNFE EFMCTPGDKVPENVDN PRLFVSGVRRPLAFRDQDIMLRSTAFGLQLREEYHKQFAMW
DYAAHMMWFIDNPEQFAGACPPLTLEQAEETVFPGF DKHEDLVLDSSKIRIVLGGPHDKQPNPVTQEYLKLI
QGARSSVKLAHMYFIPKDELLNALVDVSHNHGVHLSLITNGCHELSPAITGPYAWGNRINYFALLYGKRYPL
WKKWFCEKLPYERVSIEFAIWETQLHKKCMIIDDEIFVIGSYNFGKKSDAFDYESIVVIESPEVA AKANKV
FNKDIGLSIPVSHGDIFSWYFHPVHHTLGH LQLTYMPA

>core/226/4/Org4_Gene784

MRIVQVAVEFTPIVKVGGLGDAVASLSKELAKQNDVEVLLPHYPLIFKFSSSQVLSERSFYEFLGKQQAS AIS
YSYEGTLTITILDSQIELFSTTSVYSENNVVRFS AFAAAAAAYLQEADPADIVHLHDWHVGLLAGLLKNPLN
PVH SKIVFTIHNFYRGYCSTQLLAASQIDDFHLSHYQLFRDPQTSVLMKGALYCSDYITTVSLTYVQEIINDY
SDYELHDAILARNSVFSGIINGIDEDVWNPKTDPALAVQYDASLLSEPDLFTKKEENRAVLYEKLGISSDYFP
LICVISRIVEEKGPEFMKEIILHAMEHSYAFILIGTSQNEVLLNEFRNLQDCLASSPNIRLILDFNDPLARLTYAA

ADMICIPSHREACGLTQLIAMRYGTVPLVRKTGGLADTVIPGVNGFTFFDTNNFNEFRAMLSNAVTTYRQEP
DVWLNLIESGMLRASGLDAMAKHYVNLYHSLLS

>core/227/4/Org4_Gene792

MAFSHIEGLYFYNTASQKKELFFPNHTPVRLYTCGPTVYDYAHIGNFRITYVFEDILKRTL VFFGYSVTHVMNI
TDVEDKTIAGASKKNIPLQEYTPYTEAFFEDLDLNLIAKADFYPHATHYIPQMIQAITKLLEQGIAYIGQDAS
VYFSLNRFPNYGKLSHLDLSSLRCCSRISADEYDKENPSDFVLWKAYNPERDGVIIYWESPFGKGRPGWHLEC
SIMAMELLGDSLDIHAGGVDNIFPHHENEIAQSEALSGKPFVRYWLHSEHLLIDGKKMSKSLGNFLTLDLLH
QGFTGQEVRYMLLQSHYRTQLNFTEEALLACRHALRRLKDFVSRLEGVDLPGESPLPRTL DSSSQFIEAFSRA
LANDLNVSTGFASLDFVHEINTLIDQGHFSKADSLYILDTLKKVDTVLGVLP LTTSVCIPETVMQLVAEREEA
RKTKNWAMADTLRDEILAAGFLVEDSKSGPKVKPL

>core/228/4/Org4_Gene430

MDTIDTPGEQGSQSFGNSLGARFDLPRKEQDPSQALAVASYQKKTDSQVVEEHLDELISLADSCGISVLETRS
WILKTPSASTYINVGKLEEIEEILKEFPSIGTLIIDEIITPSQQRNLEKRLGLVVLDRTELILEIFSSRALTAENIQ
VQLAQARYLLPRLKRLWGHLSRQKSGGGSGGFVKGEGEKQIELDRRMVRRERIHKL SAQLKAVIKQRAERRK
VKSRRGIPTFALIGYTNSGKSTLLNLLTAADTYVEDKLFATLDPKTRKCVLPGRHVLLTDTVGFIRKLPHTL
VAAFKSTLEAAFHEDVLLHVVDASHPLALEHVQTTYDLFQELKIEKPRIITVLNKVDRLPQGSIPMKLRLLSPL
PVLISAKTGEGIQNLLSLMTEIIQEKS LHVTLNFPYTEY GKFTELCDAGVVASSRYQEDFLVVEAYLPKELQKK
FRPFISYVFPEDCGDDEGRGPVLESSFGD

>core/229/4/Org4_Gene49

MDSRTSHLDDELSFKLEKAFTCLSTDIHSHDLSKIVIEYNPIDLAYAVSCLPSESRAILYKNLSCITAKVAFIINT
DSASRWAI FRRLSDSEVCALIEQMPPDEAVWVLDDIPDRRYRRILELIDSKKALKIRDLQKHGRNTAGRLMTN
EFAFLMETTVKDV SACIRSNPGIDLTRLVFVLDFK GELQGVVTDRSLIINPPMSLKQIMNQIEHKVLPDATR
EEVVDLVERYKIAALPVVDEENFLIGAITYEDVVEAIEDIADETIARMAGTTEDVGYQTCHVVQRFLLRAPWL
LVTLFAGLISASVMAYFQKISPALLALIIFFIPLINGMSGNVGVQCSTILVRSMATGTLSFGRRRRETIFKEMSIGL
LTGVVLGILCGLVVYLMGFLGLNIFSGGGIQLGVT VATGVLGASLTATTLGVLS PFFFAKLGVDPALASGPIV
TALNDIMSMIIFFLIAGGINFLFFN

>core/230/4/Org4_Gene244

MNKKKRFLSLLFLTAVLLGIWFSPHPASINSNAWQLFAIFTT TIMGIIFQPVPMGAIAIIGISTLLL TQTLTLEQG
LSGFHNPIAWLVFLSFSIAKGIIKTGLGERIAYFFVSALGKSPLGLSYGLVITDFFLAPAIPSVTARAGGILYPVV
TSLSDSFGSSAEKGTQDLIGSFLIKVAYQSSVITSAMFLTAMAGNPLVAALAGHVGVSLSWVLWAKAAIIPGL
LSLFLMPIILYKLYPPKITSCEEAIRSAKLRLKEMGPLKKEEKTILMIFFLVVLWTFGDLLGISATTAALIGLSL
LILTNI LDWQKDVIANTTAWETFIWFGALIMMASFLNQLGFIPLVGDSAAALVSGLSWKIGFPLFLIYFYSHY
LFASNTAHIGAMYPIFLAVSISLGTNPIFAALTAFASNLF GGLTHYGSGPAPLYFGSHL VTVQEWWRSGFALS
IVNIVIWIGIGSLWWKALGLI

>core/231/4/Org4_Gene559

MTTKSLGSFNSVISKNKIHFIISLGCSRNLVDSEVMLGILLKAGYESTNEIEDADYLILNTCAFLKSARDEAKDY
LDHLIDVKKENAKIIVTGCMTSNHKDELKPWMSHIHYLLGSGDVENILSAIESRESGEKISAKSYIEMGEVPRQ
LSTPKHYAYLKVAEGCRKRCAFCIIPSIK GKLRSKPLDQILKEFRILVNNGVKEIILIAQDLGDY GKDLDSTRSS
QLESLLHELLKEPGDYWLRLMLYLYPDEVSDGIIDLMRSNP KLLPYVDIPLQHINNRI LKQMRRTTSREQILGFL
EKLRAKVPQVYIRSSVIVGFPGETQE EFQELADFIGEGWIDNLGIFLYSQEANTPAAELPDQIPEKV KESRLKIL
SQIQKRNVDKHNQKLIGEKIEAVIDNYHPETNLLL TARFYGQAPEVDPCIIVNEAKLVSHFGERC FIEITGAAG
YDLVGRVVKKSQNQALLKASKA

>core/232/4/Org4_Gene540

MHSHSKPTKPLGTFTVGM LSLAVVISLRNLPLTAKHGLSTLFFYGLAVICFMIPYALISAELASFKPQGIYIWA
RDALGKWWGFFAIWMQWFHNMTWYPAMLA FIASTIVYKINPELAHNKVYIATVILAGFWILTFFN FLGITSS
ALFSSICVIIGTLIPGVILVSLALFWIFSGNP IAIISLSWGNLLPDFSNVSSLVLLAGM LLLALCGLEANANLASDM
VNPRKNYPKAVFIGAIA TLTILVLGSLSIAIVIPKEEISLVSGLVKTFTLFFDKYNLSWMTGIVVVM TIAGSLGE
LNAWMFAGTKGLFISTQNDCLPRLFKKVNSKNVPTNMLFQGIVVTIFTLLFLCLDSADLVY WILTALSVQM
YLAMYICLFLAGPILRIKEPRAQRLYSVP GKFLGICTMSILGILSCAFALWVSFLPPRELAQISEGSKIGYTTFL
LAFSLNCLIPFGIYFTHKRLSKKS

>core/233/4/Org4_Gene337

MDKSTAVPLPSPPHSKESEMIVLGCMLTG VHYLNLAANQLYEEDFYYLEHKIIFRVLQDAFKQDKPIDVHLA
GEELKRRNQITVIGGPSYLITLAEFAGTAAY LEEYVDIIRSKSILRKMISTAKEIEKRALEQPKNVAEALDEAQN
SFFKISQSTSVSQYTLVADKLRLGLTTT TDKPYLVLQLERQELFLQNAQGDNKSFFTGIPTHFIDLDQLIHGFSPS
NLMILAAPAMGKTALALNIAENLCFQNR LPIGIFSLEMTVDQLIHRMICS RSEVDSKKISIGDLSGHD FQRIVS
VINEMQEHTLLIDDQPGLKVSDLRARARRM KESYDIQFLIIDYLQLLSGSGTLRATESRQTEISEISRMLKTLAR
ELNIPILCLSQRKVEDRANHRPMMSDLRESGSIEQSD LVMFLLRREYYDPNDKPGTAELIIAKNRHGSIGS
VPLVFEKELARFRNYSAFECIS

>core/234/4/Org4_Gene160

MKITVNRGLDLSLQGSPKESGFYNKIDPEFVSIDLRPFQPLSLKLKVEQGDAVCSGAPIAEYKHFPNTYITSHV
SGVVTAIRRGNKRSLLDVIKKKTPGPTSTEY TYDLQTLRSDDLSEIFKENGLFALIKQRPFDIPA IPTQTPRDVFIN
LADNRPFTPSPEKHLALFSSREEGFYVFVVG VRAIAKLFGLRPHIVFRDRLTLPTQELKTIAHLHTVSGFPFSGS
PSIIHHSVAPITNEKEVVFTLSFQDVL TIGHLFLKGRILHEQVTALAGTALKSSLRRYVITTKGASFSSLINLNDI
SDNDTLISGDPLTGR LCKKEEPPFLGFRDHSISVLHNPTKRELFSFLRIGFNKPTFTKTYLSGFFKKKRTYTNPD
TNLHGETRPIIDTDIYDKVMPMRIPVVPLI KAVITKNFDLANELGFLEVCGEDFALPTLIDPSKTEMLTIVKESLI
EYAKESGILTPHQD

>core/236/4/Org4_Gene342

MKEERSSEILPKVKETKKHAYVSMQE KSCVGECAVVASESEEAESVTVTKIAKLQRMGIEELNILARQYGVK
NIGSLTKSQVVFEIVKAKSERPDELLIGEGVLEVLPDGF GFLRSPTYNYLPSAEDIYVSPAQIRRFDLKKGD TIIG
TIRSPKEKEKYFALLKVDKINGSTPDKAKERVLFENLTPLYPNQ RIVMEMGKDHLAERVLDLTAPIGKGQRG
LIVAPPRSGKTVILQSI AHAIAVNNPDIVLIVLLIDERPEEVTDMIRQVRGEVVASTFDEQPERHIQVAEMVIEK
ARRLVEHGNDVVILLDSITRLARAYNTVQPHSGKILTGGVDASALHKPKRFFGAARNIEGGGSLTILATALIDT

>core/241/4/Org4 Gene527

MRAWEEFLLLQEKEIGTNTVVDKWLRSLKVLCFDACNLYLEAQDSFQITWFEEHIRHKVKSGLVNNNNKPIRV
HVTSDKAAPFYKEKQMQQEKTAYFTMHYGSVNPEMTFSNFLVTPENDLPFRVLQEFTKSPDENGGVTFNPI
YLFSGPEGSGLTHLMQSAISVLRSEGGKILYVSSDLFTEHLVSAIRSGEMQKFRSFYRNIDALFIEDIEVFSGKSA
TQEEFFHTFNSLHSEGKLIVVSSSYAPADLVAVEDRLISRFEWGVAPIHPLVQEGLRSFLMRQVERLSIRIQET
ALDFLIYALSSNVKTLHLALNLLAKRVMYKKLSHQLLYEDDVKTLLKDVLEAAGSVRLTPLKIIRNVAQYYG
VSQESILGRSQSREYVLPRQVAMYFCRQKLSLSYVRIGDVFSRDHSTVISSIRLIEQKIEENSHDIHMAIQDISKN
LNSLHKSLEFFPSEEMII

>core/242/4/Org4_Gene740

MRQEKDSLGLIVEVPEDKLYGAQTMRSRNFFSWGPELMPYEVIRALVWIKKCAAKANQDLGFLDSKHCDMIV
AAADEILEGGFEEHFPLKVWQTGSGTQSNMNVNEVIANLAIRHHGGVLGSKDPIHPNDHVNKSQSSNDVFPT
AMHIAAVISLKNKLIPALDHMIRVLDAKVEEFRHDVKIGRTHLMDAVPMTLGQEFSGYSSQLRHCLESIAFSL
AHLIELAIGATAVGTGLNVPEGFVEKIIHYLRKETDEPFIPASNYFSALSCHDALVDAHGSLATLACALTKIAT
DLSFLGSGPRCGLGELFFPENEPGSSIMPGKVNPTQCEALQMVCAQVLGNNQTVIIGGSRGNFELNVMKPVII
YNFLQSVDLLSEGMRAFSEFFVKGLKVNKARLQDNINNSLMLVTALAPVLGYDKCSKAALKAFHESISLKEA
CLALGYLSEKEFDRLVVPENMVGNI

>core/243/4/Org4_Gene423

MNFSLFLFFLIAIQGICLYVGRRGSKKVEDRESYFLAGRSLKIFPLMMTFIATQIGGGVLLGAAEEAFICYGYGV
ILYPLGVALGLIFLGMGPGKRLAEGSLTTVVSIFEVIFYGSKKLRKIAFLLSAGSLFFILVAQVIALDRLFSSFPFG
KYVTVAFWIVLASYTSTGGFRGVVRTDVIQAGFLLIQAVLVCVSVVWLSVPKSLPVLDPFQSLPCAKLSNWIF
MPMLFMLVEQDMVQRCVAASSPKRLQWAAVGAGLVLLFNFIPLFLGSLGAKAGLKAGCPLIDTIAYFCNPS
LAAVMAAAIGVAILSTADSLMNAVAQLIAEEYPTLKAPYYRYLVGLAVAAPLVAIGFTNIVDVLILSYSLSV
CCLSVPGFYLLAPKGRRVSGAAAWAGVLVGALGYGWVQIVSLGMFGELLAWVGSVAFSFGFIEITWK
NKVKQT

>core/244/4/Org4_Gene771

MQQSVRKLFGTDGVRGRANFEPMTVETTVLLGKAVARVLREGRSGKHRVVVGKDTRLSGYMFENALIAGL
NSMGIETLVLGPIPTPGVAFITRAYRADAGIMISASHNPYRDNGIKIFSSEGFKISDVLEQRIETMVSEADFGPLP
EDHAVGKNKRVIDAMGRYIEFVKATFPKGRTLKGLKIVLDCAHGASYKVAPSVFEELDAEVICYGCEPTGINI
NEHCGALFPQVIQKVVEIHQAHLGIALDGDGDRIIMVDEKGHIVDGDMLISICAGDLKKRSALPHNRVVATIM
TNFGVLKYLEGLGLQVFTSPVGDRHVLHAMLEHEVTLGGEQSGHMIFLDYNTTGDGIVSALQVLRIMIESES
TSLDLTAPIVKSPQTLINAVREKIPLIETIPLIERTLRDVQDALGPSGRILLRYSGTENICRVMVEGHKKHQVDC
LAKALADVIDAELGTGSRE

>core/245/4/Org4_Gene368

MQIAQVFGGGRLNGEVKVSAGAKNAATKLLVASLLSDQKCTLRNVDPDGDVSLTVELCKSLGAHVSWDKETE
VLEIYTPEIQCTRVPTFSNVNRIPILLGALLGRCPEGVYVPTVGGDAIGERTLNFHFEGKQLGVQISSDSSG
YYAKAPRGLKGNYIHLPPSVGATENLILAAIHAKGRTVIKNVALEAEILDVLFLQKAGADITTDNDRTIDIF
GTGGLGSVDHTILPDKIEAASFGMAAVVSGGRVFVRNAKQELMIPFLKMLRSIGGGFLVSESGIEFFQERPLV
GGVVLETDVHPGFLTDWQQPFAVLLSQAQGSSVIHETVHENRLGYLHGLQHMGAECQLFHQCLSTKACRY

AIGNFPHSAVIHGATPLRASHLVIPDLRAGFAYVMAALIAEGGGSIIENTHLLDRGYTNWVGKLRSLGAKIQIF
DMEQEELTTSPKSLALRDASL

>core/246/4/Org4_Gene191

MLYFIEQLNKLSTSFCVFPMILLGGFLTWKLRGLQFHGLKLGFNMLQNKLDDSSSKANEVSSYEAVAGIL
AGNFGTGNIAGMAVALACGGPGALVWVWLAALLGAIVQYAGSYLGSKYRKPEGNTGEFIGGPIACLAFGM
RKKILAGFFALFTIMTAFCAAGNCVQVSCIVPLCAEGTPGKLLVGILLALVVIPVLAGGNNRILRFSARVIPFIAG
FYCISCGIILFQHASAILPAIKLICSSAFGIKAGLAGIGGYTLSQVISTGINRAVMATDCGSGMVSIQANTKSKN
PVVDGLVTLVPPVIVMVVCSITMLVLIVSGAYSSGAQGTLMVMSAFKNSLGSLSVIVILAMALFGYTTILT
FACAEKSLQYMIPGRRANLWLKAIYVLIPLGGVIDMRMIWALSDTGFSGMVILNCIALIALKDVLTNRDV
ALLKERECSVADPVRNLDA

>core/247/4/Org4_Gene821

MFNVNFKFLEGLHQAPRYTSYPTALEWEPDAAPALLAFQRIRENPPQLSLYFHIPFCQSMCLYCGCSVVLN
RREDIVEAYINTLIQEMKLVVETIGFRPQVSRIHFGGGTPSRLSRELFTLLFDHIHKLFDLSHAEEIAIEVDPRSL
RNDMEKADFFQNVGFNRVSLGVQDTQADVQEAARRRQSHEESLKAYEKFELGFQSSINIDLIYGLPKQTKES
FSKTIQDILAMYPDRLALFSFASVPWIKPHQKAMKASDMPSMEEKFAIYSQSRHLLTKAGYQAIGMDHFSLP
HDPLTLAFKNKTLIRNFQGYSLPPEEDLLGLGMTSTSFIRGIYLNQAKTLEEYHNTVLRGTFATVKSILTEDD
RIRKWAIHKLCTFTINKEEFYNLFGYEFDTYFIESRDLISMETTGLIHNSPGSLKVTPLGELFVRVIATAFDH
YFLNKVSKKECFASI

>core/248/4/Org4_Gene328

MTTLRQFFLITELRQKLFYTFALLAACRVGVFIPVPGINGELAVAYFKQLLGSGQNLFQLADIFSGGAFAQMT
VIALGVVPYISASIIVQLFLVFMPALQREMRESPDQGKRRIGRLTRLFTVALAVIQSLLFAKFALRMNLTIPGIV
LPTLLSSKLFQVWPWIFYITTVVVMTTGTLLLMWIGEQISDKGIGNGISLIILGILSSFPSVLGSIWNKLNLSQD
SSDLGLISILILALVFVFLITLIIIEGVKIPVQYARRVIGRREVPGGGSYLPLKVNYAGVIPVIFASSLLMFPA
TIGQFIASESSWMKRIAALLAPGSLVYSICYVLLIIFTYFWTATQFHPEQIASSEMKKNNAFIPGIRQGKPTQHY
LEYTMNRVTLLGALFLAAIAILPSLLGCLLRVDSNVSYFLGGTAMLIVVGVVLDTMKQVDAFLLMRRYDSVL
KTDRTKGRH

>core/250/4/Org4_Gene139

MNVWTKFFQPPKHIKEIEDQEVVKKKYKYWRIRIFYSMFIGYIFYFTRKSFTFAMPTLIADLGFDKAQLGIIG
STLYFSYGISKFVSGVMSDQSNPRYFMAIGLMTGLTNIFFGMSSSIVLFALWWGLNGWFQGWGWPPCARLL
THWYAKSERGTWWSVWSTSHNIGGALIPILTGFIIDYSGWRGAMYVPGILCIGMGLVLINRLRDTPQSLGLPPI
EKYKRDPHHAHHEGKSASEGTEEIERELSTREILFTYVLTNQWLWFLAAASFFIYIVRMAVNDWSALFLIETK
HYAAVKANFCVSLFEIGGLFGMLVAGWLSKISKGNRGP MNVLFSLGLLFAILGMWFSRSHNQWWVDGTL
LFVIGFFLYGPQMMIGLAAAELSHKKAAGTASGFTGWFAFYFGATFAGYPLGKVTDVWGWKGFFIALLACAS
IALLLFLPTWNATEKNTRSKA

>core/251/4/Org4_Gene606

MKKVLIANRGEIAVRIIRACHDLGLSTVAVYSLADQEALHVLLADEAVCIGEPQAAKSYLKISNILAACEITGA
DAVHPGYGFLSEANFASICESCGLTFIGPSSESIAMMGDKIAAKSLAKKIKCPVIPGSEGIIEDESEGLKIAEKI
GFPIVIKAVAGGGGRGIRIVKEKDEFYRAFSAARAEAEAGFNNPNVYIEKFIENPRHLEIQVIGDTHGNYVHLG
ERDCTIQRRRQKLIEETPSPILNAEIRAKVGKVAVDLARSAGYFSVGTVEFLLDKDKKFYFMEMNTRIQVEHT
ITEEVTGIDL VKEQIHVAMGNKLPWKQKNIEFSGHIIQCRINAEDPTNNFSPSPGRLDYYLPPAGPSIRVDGAC
YSGYAIPPPYDSMIAKVIAKGKNREEAIAIMKRALKEFHIGGVQSTIPFHQFMLDNPKFLESNYDINYIDNLLA
QGNSFFKEF

>core/252/4/Org4_Gene10

MATKTKTQWTCNQC GATAPKWLGQC PGCHNWN SLVEEYVPQARS GTSSRSSTSAIALSSIELENESRIFIDHA
GWDRILGGGVVRGSLTLLGGDPGIGKSTLLLQTAERLASQKYKVLVVCGEESVTQTS LRAKRLNISSPLIYLF
PETNLDNIKQQIATLEPDILIIDSIIQIFNPTLNSAPGSVAQVREVTYELMQIAKSAQITTFIIGHVTKSGEIAGPRV
LEHLVDTVLYFEGNSHANYRMIRSVKNRFGPTNELLI L SMHADGLKEVSNPSGLFLQEKTGPTTGSMIPIIEG
SGALLIELQALVSSSPFANPVRKTAGFDPNRFSLLLAVLEKRAQVKLFTMDVFLSITGGLKII EPAADLGALLA
VASSLYNRLLPNNSIVIGEVLGGEIRHVAHLERRIKEGKLMGFEGAILPEGQISSLPKEIRENFRLQG VKTIKD
AIRLLL

>core/253/4/Org4_Gene831

MLKILKIKVLVFPLALLMGCNSIGYAGPQGS LQTNSQTKVKIGSEVWIEQKL RQYPELLWLTESGGAPLLTST
PIDMAYSEKLFNKKVPALDIAIRSMIHLHLLIQGSRQSYMQLSQILPSEEGMTFKQFQTAHKQLLFFLN SPKS
FDNTRLRIETAIVLRHVGC SAKAVTTFKPYFTDSCPQS FYAKALHVLRTFPELCP SYARLSPEQQEVLLSLRRL
GNYDSLNLNTEVPSAQLLSAWRTRRSLAILDLYLYCLDTCGDKNCSQEFYVNFAPLLSMLQQHATIEEAFSR
YFTYRANRLGFEGTSRTD MTLVRLATLMNLS PSEASTLAWSFKNLPSDEAENLVNSFYTVQGEHIPLTFRGLP
SLVAGLSVATHGSTVSPENRLRQVYSTMLSLLVKS LRSREMLNKQLLPQGTVLDFSETTLSSGGLDVFAESI
AVRIHLNGAVSINL

>core/254/4/Org4_Gene598

MRKRHSFDSTSTKKEAVSKAIQKIIKIMETTDPS LNVETPNAEIESILQEIKEIKQKLSKQAEDLGLLEKYCSQE
TLNLENTNASLKL SIGSVIEELASLKQLVEESIEESLGQQDQLIQSVLIEISDKFLSSIGGTLSGNLDMNQNVIQ
GLLIKENPEKSEAASVGYVQTLLEPLSKRIGETHEKVATHDVNISSLQFHMMSVAGGRFRGHIDMNGYRVLG
LGEPKNGEDAVSKDYLER YVSSQLTIDKVEDKPITKPNKGKLLYSQGTSPKLESPLPLGLLTSGISGFTWKSAS
KSNDGSFPFSALRHKETESD TDCFQITSTTLSGNQAGTYTWSLSLKVLVPSIFQIEKPEVQLSLVYSYEDWLPID
NIFNMSQPRTIPLALLGQTMLAGQKYDILELAAHQTNQ TLMISPNC SRFSLQLKQTNQFENSPVDFYIVHAAH
SCLWSGF

>core/255/4/Org4_Gene84

MLTCNECTTWEQFLNYVKTRCSKTAFENWISPIQVLEETQEKIRLEV PNIFVQNYLLDNYKRDLC SFVPLDVH
GEPALEFVVAEHKKPSAPVASQKESNEGISEVFEETKDFELKLNLSYRFDNFIEGPSNQFVKSAAVG IAGKPGR
SYNPLFIHGGVGLGKTHLLHAVGHYVREHHKNLRIHCITTEAFINDLVYHLKSKSVDKMKNFYRSLDLLLV D
DIQFLQNRQNFEFFCNTFETLINLSKQIVITSDKPPSQLKL SERI IARMEWGLVAHVGI PDLETRVAILQHKA E
QKGLLIPNEMAFYIADHIYGNVRQLEGAINKLTAYCRLFGKSLTETT VRETLKELFRSPTKQKISVETILK SVA

TVFQVKLNDLKGNSRSKDLVLARQIAMYLAKTLITDSLVAIGAAFGKTHSTVLYACKTIEHKLQNDETLKRQ
VNLCKNHIVG

>core/256/4/Org4_Gene778

MILPPYSYSLKIGAAVLFFCSILHTFLTPWLYTLCQSYEHKKLVFPECWKRYVRLSELFRILSRVEIVFFLWAVP
LFFWFLYTEGYRISMAYFNERNYGFVFMVILILLESRPVYFAELVLSSIAKLGKTSPKSWWWTLMIAPPLL
SCLLKETGAMIIIGATLLMRHFYVFSPSRRFAYATMGLLFSNISIGGLTSYVSSRALFLIFPALKWEHSSFFLSHFA
WKAIVAILISTTIYYFIFRKEFKKFPDIPSDKDPSVEKVPWWIICVNIIFVGSILSRSTPLFMGALLLFYLGFKFT
IFYQDPINLPKVCYVGLFYAGLVVFGDLQEWVVLNLMQGLSDFGYMTVSYTSLIFLDNALVNYLVHNLSVA
TDCYHYLVVAGCMAAGGLTLVSNIPNIVGYLILRSAFPSSTIHMGWFLGALGPSIISLGVFVWLLKNVPEFLYC
FFR

>core/257/4/Org4_Gene901

MSEPRFVCLSLGSNLGNRFKNLQIARTLLGEQAVLGLRSSVILETEALLPGSPPEWDLPYFNSVLVGETTSL
RELLVTIKQIEKVVGRAEESPPWSPRTIDIDILLYGDESFCCDHTEITIPLSNLLSRPFLIALIASLCPYRRFCTQGS
PYHNFTFGELAHHLSPPPGMIRRSLSPTDMLMGVVNVTNDSMSDGGMFLDPEKAVAQAELFTEGAVIDF
GAQATNPVKVKQFLSVDQEWERLEPVLRLKETSNSRKQYPIISLDTFYPEILRAMDIYPIQWINDVSGGSQS
MAEVARDCELSLVMNHSSSLPVDPKNILSFSVPIGEQLLSWGEKQLKMFSDVGLNANQVIFDPGIGFGKGAA
QSLATLYEIAKFKRLGCPILIGHSRKSFLSLFGNHDPKDRDWETVGLSILLQQQGVVDYLRVHNVAAHQKALS
VAACEACAPI

>core/258/4/Org4_Gene393

MNRLLSLLSVFDDFFWSYVAFILIIVLGVFSWSRFFQFTKFSQFCKLFRYYSQNPQERETKQGVHPLKVFFA
SAGGNIGIGNVVGIVTAACIGGPGALFWVWIAGIFGSIVKYSEVYLGIFRKLDRDGVYQGGPMYFLTKAFKT
PVVSVIVAILLCIYGVEIYQFSVITDSLHCWNLPKVYPMLGLLFLVFYAIRGGLQRIQKICSIVLPFFMMLLYCA
LSLYILVKEFHTLPHLLSTVFSSAFKQGSALGGFAGCTVATTIHQGISRAAYSGDIGIGFDSIIQSESSAKDPSTQ
AQLSIVGIAIDNICTLSLLMVLASGSWSLGLENASQVVEHTLASYFPMVKFFLPTFFFVTGYTTIISYFLVGKK
CAKFLYGNTGAKIYTYGLLILPLFCFLSQNTALLIMSVSGALLLCFNLLGVFILRKEVIFPARAASLTETSLST
E

>core/259/4/Org4_Gene505

MLSCVFSDTIFLSSFLAVTLICMTTALWGTILLISKQPLLSESLSHASYPGLLVGALMAQYVFSLQASIFWIVLF
GCAASVFGYGIIVFLGKVCKLHKDSALCFVLVVFFAIGVILASYVKESSPTLYNRINAYLYGQAATLGFLEAT
LAAIVFCASLFALWWWYRQIVVTTFDKDFAVTCGLKTVLYEALSIFISLVIVSGVRSVGIVLISAMFVAPSLG
ARQLSDRLSTILISAFFGGISGALGSYISVAFTCRAIIGQQA VPVTLPTGPLVVICAGLLAGLCLLFSPKSGWVI
RFVRRKHFSFSKDQEHLKVFVWHISHNRLNENISVRDFVCSYKYQEYFGPKPFPRWRVQILEWQGYVKKEQDY
YRLTKKGRSEALRLVRAHRLWESYLVNSLDFSKESVHELAEIEHVLTEELDHTLTEILNDPCYDPHRQIIPNK
KKEV

>core/260/4/Org4_Gene641

MINSLSQKLSSIFSSLVSSRRINEENISESIREVRLALLDADVNYHVVKDFISKVKEKILGEEIWKHVSPGQQFIR
CLHEELVAFLSDGREEFTIQKTPSIILLCGLQGAGKTTTAAKLADYVIKNNKAKKVLVVPCLDKRFAAVDQL
KILVAQTKAEFYQSQENKPIDVVVKALAYAKENGHDFVILDTAGRLNIDNELMEELTAIQKVSQANERLFVM
NVAMGQDVLATVQAFDQSLDLTGVILSMTDGDARAGAVFSIKHVLGKPIKFEGCGERIQDLRSFDPQSMAER
ILGMGDTINFKEMREYISEEEDAELGKKLVTAFTYEDYYKQMKAFRRMGPLRKLLGMMPGFNNAKPSQ
KEIEDSEKQMKRTEAIIISMTPEERKELVELDMSRMKRIASGCGLTLGDVNQFRKQMSQSKKFFKGMSKGK
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>core/261/4/Org4_Gene648

MDALILSRIQFGLFITFHLYFVPLSMGLSMMLVIMEGLYLVTKKQIYKQMTWFWVGIFALTFVLGVVTGIMQI
FSFGSNWANFSEYTGNI FGTLGSEGVFAFFLESGFLGILLFGRHKVSKKMHHFSTCMVALGAHMSAFWIICA
NSWMQTPSGYEMVMHKGKLI PALTSFWGVVFSPTTIDRFIHAVLGTWLSGVFLVISVSAYYLWKKRHHEFA
KQGMKIGTICAVIVLVLQLWSADVTARGVAKNQPAKLAAFEGIFKTEEYTPIWAFGYVDMEKERVIGLPIPG
ALSFLVHRNIKTPVTGLDQIPRDEWPNVQAVFQLYHLMIMLWGVMVALTLISWSAYKGWRWALKPFFLVIL
TFSVLLPEICNECGWCAAEMGRQPWVVQGLLKTDAVSPIVQANQIVQSLVMFSLVFIALLTLFITVLCKKIK
HGPEEENDLTEFEVK

>core/262/4/Org4_Gene814

MRAMLLEDWVSLMLS DVSCPKCDKKITGFAIDSQQVQPGDLFFALPGNATDGHQFLKHAATAGAVAAVVS
HDYQGDSFGLELIRVDDTKSALQEAGSNQCNLFQGTLVGITGSVGKTTTKEFSKITLSSYKTHASPKSYNSQL
TVPLSLLMAEGDEDVMILEMGVSEPGNMQDLLRIVQPEIAVITHINDQHMHFPQGIQEILKEKSYILQKSKL
QLLPKDSPYYLDLRSCSPTAEKFSFSFNDPLADFCYKAISRDSVVIQTPEENYCLPIAFSYKPAYTNLLIAVALS
WILEVPEEGVIRSLPELKLPPMRFEHSMRNGMQVINDAYNACPEAMIAALDALPLPSDGGKIILILGHMAELG
RYSEEGHALVAEKAASRGDMIFFIGEKWIPVQSVLKSYSCEVSFFSSAQDVKDILKQVARYGDVILLKGSRAL
ALESLLACF

>core/263/4/Org4_Gene500

MNNITSPVIQNNRSCNYYFELKNSTTIHIVISAILLCGALIAFLCVAAPVSYILSGALLGLGLLIALIGVILGIKIT
PMISSKEQVFPQELVNRIRAHYPKFVSDFVSEAKPNLKDLSIFIDLLNQLHSEVGSSTNYNVSEELQQKIDTFG
GIARLKNEVRTASLKRLESAASSRPLFPSPKILQKLFPPFSLGEFISAGSKVVELHRVKKIGGSLEEDLSDYIKP
EMLPTYWLIPLDFRPTNSSILNLHTLVLARVLTRDVFQHLKYAALNGEWNLNHSDLNTMKQQLFAKYHAAY
QSYKHLSQLQEDEFYNLLLCIFKHRYSWKQMSLIKTVPADLWENLCCLTLDHTGRPQDMEFASLIGTLYT
QGLIHKESAEFLSSLTLLSLDQFKTIRRQSTNIAMFLENLATHNSTFRSLPPITVHPLKRSVFSQPEEDESLLIG

>core/264/4/Org4_Gene963

MVITNLSINADTIYGKNPINIVASAANKNITLTGTLALVNADGAFYENHTLQDSQDYSFVKLSPGAGGTIITQD
ASQKPLQVAPSRPHYGYQGHWNVQVIPGTGNQPSQPILEWVRTGYLPNPERQGSLVPNSLWGSFVDQRAIQE
IMVNSSQILCQERG VWGAGIANFLHRDKINEHGYRHSGVGYLVGVGTHAFSDATINAAFCQLFSRDKYVVS
KNHGTSYSGVVFLD TLEFRSPQGFYTDSSSEACCNQVVTIDMQLSYSHRNNDMKTKYTTTYPEAQGSWAND
VFGLEFGATTYYYPNSTFLFDYYSPFLRLQCIYAHQEDFKETGGEVRHFTSGDLFNLA VPIGVKFERFSDCKR

GSYELTFAYVPDVIRKDPKSTATLASGAAWSTHGNNLSRQGLQLRLGNHCLINPGIEVFSGHAIELRGSSRNY
NINLGGKYRF

>core/265/4/Org4_Gene724

MLTYKVSPSSVYGNAPSSKSHLTRAILWASVAEGKSIINYLDSPDTEAMICACKQMGASIKKFPQILEIVG
NPLAIFPKYTLIDAGNSGIVLRFMTALACVFSKEITVTGSSQLQRRPMAPLLQALRNFGASFHFSSDKSVLPFT
MSGPLRSAYS DVEGSDSQFASALAVACSLAEGPCSFTIIEPKERPWFDSLWWLEKLHLPYSCSDTTYSFPGSS
HPQGFSYHVTGDFSSAAFIAAAALLSKSLQPIRLRNLDILDIQGDKIFFSLMQSLGASIQYDNEEILVFPSSFSGG
SIDMDGCIDALPILTVLCCFADSPSHLYNARSAKDKESDRILAITEELQKMGACIQPTHDGLLVNPSPLYGAVL
DSHDDHRIAMALTIAALYASGDSRIHNTACVRKTFPNFVQTLNIMEARIEECHDNYSMWSTHKRKVFARESF
G

>core/266/4/Org4_Gene874

MTSGVSGSSSQDPTLAAQLAQSSQKAGNAQSGHDTKNVTKQGTQAEVAAGGFEDLIQDASAQSTGKKEATS
STTKSSKGEKSEKSGKSKSSTSVASASETATAQAVQGPGLRQNNYDSPSLPTPEAQTINGIVLKKGMGTAL
LGLVMTLMANAAGESWKASFQSQNQAIQSQVESAPAIGEAIKRQANHQASATEAQAKQSLISGIVNIVGFTV
SVGAGIFSAAKGATSALKSASFAGETGASAAGGAASKALTSASSSVQQTASTAKAATTAASSAGSAATKAA
ANLTDDMAAAASKMASDGASKASGGLFGEVLNKPWSEKVS RGMNVVKTQGARVASFAGNALSSSMQMS
QLMHGLTAAVEGLSAGQTGMEVAHHQRLAGQAEQAQAEVLKQMSSVYGQQAGQAGQLQEQAMQSFNTAL
QTLQNIADSQTQTTS AIFN

>core/267/4/Org4_Gene684

MTLQPYQASSRKYRPQIFREILGQSSVAVLKNALIFNRAAHAYLFSGIRGTGKTTLARILAKALNCVHLS
GEDVVEFQCHGGFFACSQILDALIALGARPALPGEFSQRAFLNGKIDLVQAEAIQNLIVAENIDAFRIAQTHFQ
EPPQHVKFFATTEIHKIPGTILSRCQKMHLQRIPEKTILEKLSLMAQDDHIEASQEALAPIARAAQGSLRDAES
LYDVISLFPKSLSPDTVAQALGFASQDSLRTLDNAILQRDYATALGIVTDFLNSGVAPVTFLHDLTLFYRNLL
LTNSTTSKFSSQYKTEQLLEIIDFLGESAKHLQNTIFEQTLETVIIHIIRYQRPVLSELISSIKSRQFEGLRNIKEP
TLTQQVSAPQPQPTYKEQSFLEKKNQPAAEGKIISVEVKSSASIKSAAVDTLQFAVVEFSGILRQ

>core/268/4/Org4_Gene857

MLKHDTIAAIATPPGEGSIAVVRLSGPQAIVIADRIFSGSVASFASHTIHLGQVIFEETLIDQALLLLMRSPRSFT
GEDVVEFQCHGGFFACSQILDALIALGARPALPGEFSQRAFLNGKIDLVQAEAIQNLIVAENIDAFRIAQTHFQ
GNFSKKIQEIHTLIEALAFLEVLADFPEEEQPDLLVPQEKIQNALHIVEDFISSFDEGQRLAQGTSILLAGKPNV
GKSSLLNALLQKNRAIVTHIPGTTRDILEEQWLLQGKRIRLLDTAGQRTTDNDIEKEGIERALSAMEEADGIL
WVIDATQPLEDLPKILFTKPSFLLWNKADLAPPFPDLTSLPQFAISAKTGEGLTQVKQALIQWMQKQEAGKTS
KVFLVSSRHHMILQEVARCLKEAQQNLYLQPPEIALELREALHSIGMLSGKEVTESILGEIFSKFCIGK

>core/269/4/Org4_Gene850

MPRSLSNEQFSVDLEESPGCIVSALVKVSPEVLNKNLQKALKKIKKEITLPGFRKGKAPDDVIASRYPTNVRK
ELGELVTQDAYHALSTVGDRRPLSPKAVRSNSITQLDLQEGAKVEFSYEAFPAISDLPWENLSLPQEEAASEIS
DSDIEKGLTNIGMFFATKTPVERPSQEGDFISISLHVSKSNDENASSAAIFENKYFKLSEEEMTDAFKEKFLGIS

TGHRVVETITSPEIQSFLRGDTLTFTVNAVIEVSIPEIDDEKARQLQAESLDDLKAKLRIQLEKQAKDKQLQKR
FSEAEDALAMLVDFELPTSLLEERISLITREKLLNARLIQYCSDEELEKRKSELIKEAEEDATKALKLLFLTHKI
FSDEKLTISREELQYMMDVCSRERFGQQPPKDISNDTLQELVMSARDRLTYSKAIEHVLRKAELLASTPSA

>core/270/4/Org4_Gene282

MDQLTTDFDTLMSQLGDVNLTTVVGRITEVVGMLIKAVVPNVRVGEVCLVKRNGMEPLVTEVVGFTQSFAF
LSPLGELSGVSPSSEVIPTGLPLHIRAGNGLLGRVLNGLGEPIDVETKGPLQNVDQTFPIFRAPPDPLHRAKLQR
ILSTGVRCIDGMLTVARGQRIGIFAGAGVGKSSLLGMIARNAEEADVNVIALIGERGREFIEGDLGEEGM
KRSVIVVSTSDQSSQLRLNAAAYVGTAIAEYFRDQGKTVVLMMDSVTRFARALREVGLAAGEPPARAGYTPS
VFSTLPRLLERSGASDKGTITAFYTVLVAGDDMNEPVADEVKSILDGHIVLSNALAQAYHYPAIDVLASISRL
LTAIVPEEQRRRIIGKAREVLAKYKANEMLRIGEYRRGSDREVDFDAIDHIDKLNRLKQDIHEKTNYEEAAQQL
RAIFR

>core/271/4/Org4_Gene855

MWLVILWALAASLAIALVAKGYRFFVYFRRYAVQVIREVRLSMELKEWALAEQQLLPILKKRSYRRQCLFE
YMRILRKMQRFESEKLLAEAKKLGLRGPYFFLEIAYKAYRFGAFKECAQAFASVPQDLFEEEDAACKYASAL
VRLGDLDAACSLIEPWISPLSHQETFVTMGHIYFTSKRYKDAIDFYNRANALGVCPEVTYNLAQAYRITSSY
AKAGKLFRKLLSNPVYKEEALFNIGLCEQKLGRPGKALLIYQSSDLWSRGDALLMKYAAMAAMDQRDYVL
AERCWELALRCSTFAKDYKCGLGYGFSCLRLRKYGDAERVYCNLIQNFPPECLTACKALAWLCGVGYATLL
GSEGLMYAKKAVELDHSCETLELLSACEARCGNFDAAYEIQSFLSSRDTSLQDKQRRSQILRILRKKLPLND
HHIVEVDALLAA

>core/272/4/Org4_Gene344

MIENDFPEASNFESSHFYRDKVGVILCGGEGKRLSPLTNCRCCKPTVSFGGRYKLIDIPISHAISAGFSKIFVIGQ
YLTYTLQQHLFKTYFYHGVLDQDIHLLAPEARQGDQIWYQGTADAIRKNLLYFEDTEIEYFLILSGDQLYNM
DFRSIVDTAIRTHVDMVLVAQPIPEKDAYRMGVLDIDSKGKLIDFYEKPQEKEVLKRFQLSSEDRIHKLTED
SGDFLGSMGIYLFRRDSLFSLLQEEEGNDFGKHLIQAQMKRGVQVQTLLYNGYWTDIGTIESYYEANIALTQKP
HAEKRGLNCYDDNGMIYSKNHHLPGAITDSMISSLLCEGCVIDTSHVSRSVLGIRSKIGENSVVDQSIIMGN
ARYGSRSMPSLGIGKDCEIHKAIIDENCCIGNGVKLQNLKGYIEYDSPDKKL FVRDNIIVPQGTHIPDNYIF

>core/273/4/Org4_Gene627

MLNCSNQKHTVTFEEACQVFPGGVNSPVRACRSVGVTPPIVSSAQGDIFLDTHGREFIDFCGGWGALIHGHSH
PKIVEAIQKTALKGTSYGLTSEEEILFATMLLSSLKLKEHKIRFVSSGTEATMTAVRLARGITNRSIIKFIGGYH
GHPDTLLGGISITEETIDNLTSLIHTSPHSLILSPYNNSQILHHVMEALGPQVAGIIFEPICANMGIVLPKAEFL
DDIHELCKRFGSLSIMDEVVTGFRVAFQGAQDIFNLSPDITIYGKILGGGLPAAALVGHRISLDHLMPEGTIFQA
GTMSGNFLAMATGHAAIQLCQSEGFDHLSQLEALFYSPIEEIRSQGFPVSLVHQGTMFSLFFTESAPTNFDE
AKNSDVEKFQTFYSEVFDNGVYLSPLSPLEANFISSAHTENLTYAQNIIDS LIKIFDSSAQRFF

>core/274/4/Org4_Gene892

MFQQKQKLSLKYLP SLRMQQGLQMLQSPLTELSSYVVQEIIDNPFFDLSSLEEEEWSPCYRPTNSTFSYLNQTP
GPQESLYTRLLPQIEEAFSTAEERFIAHQIAGNLSDEGLFLRNPEDFAQELELPLEKIHKVWDTIQNLSPEGIASP

SLQSYWMKLLRNSSHQQAYSIVRDCYPLMTNCEFAPIMKKFSLSLSELRNILKKALGSIPWCPAAACTVKPM
VSTPLPDIYLFYSSGSWKIEVSTRGLPSIKLNKETFFHYEHLPKKEEQKNLSQQILSAKWLIKNLRKREQTLLQV
METLLPKQEDFLLGKIPAPYPLGIKDLAEDLSFHSTIFRAIENKAVAAPIGIFPLKHLFPRGIHQDSSHSKENVL
QWIRQWIAEQTPLSDSVISDRITAKGIPCARRTVAKYRAQLKILPANKRRIQM

>core/275/4/Org4_Gene717

MSKIVYKFGGTSLATAENICLVCDIICKDKPSFVVVSAIAGVTDLLVDFCSSSLREREEVLRKIEGKHEEIVKNL
AIPFPVSTWTSRLLPYLQHLEISDLDFARILSLGEDISASLVRAVCSTRGWDLGFEARSVILTDDSYRRASP
DLMKAHWHQLELNQPSYIIQGFISNGLGETVLLGRGGSDYSATLIAELARATEVRIYTDVNGIYTMDPKVIS
DAQRIPELSFEEMQNLASFGAKVLYPPMLFPCMRAGIPIFVTSTFDPEKGGTWVYAVIDKSVSYEPRIKALSLS
QHQSFCSDYTVLGCGLLEEILGILESHGIDPELMIAQNNVVGFMDDDIISQEAQEHLDVLSLSSVTRLHHS
VALITMIGDNLSSPKVVSTITEKLRGFQGPVFCFCQSSMALSFVVAASELAEGIIIEELHNDYVKQKAIVAT

>core/276/4/Org4_Gene657

MQTIYTKITDIKGNLITVEAEGARLGELATITRSDGRSSYASVLRFDLKKVTLQVFGGTSGSLSTGDHVTFLGRP
MEVTFGSSLLGRRLNGIGKPIDNEGECFGEPIEIAPTFNPVCRIVPRSMVRTNIPMIDVFNCCLVKSQKIPIFSSSG
EHHNALLMRIAQAQTDADIVVIGGMGLTFVDYSFFVEESKKLGFADKCVMFHKAVDAPVECVLVPDMALAC
AEKFAVEEKKNVLLVLLTDMTAFADALKEISITMDQIPANRGYPGSLYSDLALRYEKAVEIADGG SITLITVTT
MPGDDITHPVPDNTGYITEGQFYLRNNRIDPFGSL SRLKQLVIGKVTREDHGD LANALIRLYADSRKATERMA
MGFKLSNWDKKLLAFSELFETRLMSLEVNIPLLEEALDIGWKILAQSFTSEEVGIIKAQLINKYWPKAACLSK

>core/277/4/Org4_Gene728

MISFRLLLLSGLCALGISSYAETPKETTGHYHRYKARIQKKHPESIKESAPSETPHHNSLLSPVTNIFC SHPWKD
GISVSNLLTSVEKATNTQISLDFSILPQWFYPHKALGQTQALEIPSWQFYFSPSITWTLYDSPTAGQGIVDFS
LIRYWQTNGVDANQAAGTASGMNDYSNRENNLAQLTFSQTFPGDFLT LAIGQYSLYAIDGTLYDNDQYSGFI
SYALSQNASATYSLGSTGAYLQFTPNSEIKVQVGFQDSYNIDGTNFSIYNLT KSKYNFYGYASWTPKPCSGDG
QYSVLLYSTRKVPEQNSQVTGWSLNAAQHIHEKLYLFGRINGATGTALPINRSYVLGLVSENPLNRHSQDLL
GIGFATNKVNAKAISNVNKLRRYESVMEAFATIGFGPYISLTPDFQLYIHPALRPERRTS QVYGLRANLSL

>core/278/4/Org4_Gene616

MMLRGIHRIFKCFYDVVLVCAFVIALPKLLYKMLVYGKYKKSLAVRFG LKKPHVPGEGPLVWFHGASVGEV
RLLL PVLEKFCEEFPGWRCCLVTSC TELGVQVASQVFIPMGATVSILPLDFSIIKS VVAKLRPSLVVFSEGDCWL
NFIEEAKRIGATTLVINGRISIDSSKRFKFLKRLGKNYFSPVDGFL LQDEVQKQRFLSLGIPEHKLQVTGNIKTY
VAAQTALDLEREAWRDLRLPTDSKLVLVLSMHRSDAGKWLPVVQK LIKEGVSVLWVPRHVEKTKDVEES
LHRLHIPYGLWSRGANFSYTSVVVVDEIGLLKQLYVAGDLAFVGGTFDPKIGGHN LLEPLQCEVPLIFGPHITS
QSELAQRLLLSGAGLCLDEIEPIIDTVSFLNNQEMREAYVQKGKVFLKAETASFDRTWRALKSYIPLYKNS

>core/279/4/Org4_Gene307

MKRPFPTYLCIIFYGSCASLSLHAGLSFPEVRGATAAVVHADSGKV FYDKDIDAVIYPASMTKIATALFILKHY
PTVLDTLIKVKQDAIASITPQAKKQSGYRSPPHWLETDGSTIQLHL REELLGWDLFHALLVCSANDAANVLA
MACCGSVEKFMDKLNFFLKEEIGCTHTHFNNPHGLHHPNHYTTTRDLISIMRCALKEPPFRGVISTTSYKIGAT

NLHGERILSPTNKL LLLPGSTYHYPPALGGKTGTTKTAGKNLIMAAEKNNRLLVTIATGYSGPVSDLYQDVIAL
CETVFNEPLL RKELVPPSDCLQLEIANLGKLSCLPEGLYYDFYASEDREPLSVSFIAHADAFPIEQGDLLGHW
VFYDDEGKKISSQPFYAPCRFERTIKPWKLYMKRVFTSYRTYISITMLLMYFRIRKHRKYKNLKHYSKI

>core/280/4/Org4_Gene822

MKRAIIIGAGISGLAAGWWLHKKFPQAEILVLDKEAYAGGFVRTE SPQGFSFDLGPKGFLTRGDGEYTLKLIH
ELGLQNSLIFS DRAAKNRFVYYRGKAHKISTWTLLRKGLLPSLIKDFRAPCYAQDSSVQDFLKRHSSQNFTSY
ILDPLITAIRAGHSSILSTHMAFPELAKREASSGSLRSYLKNRSPKKS KTD RYLASLSPSMGTLITTIQEKLPAT
WKFSTSVTHIDCSPKEACV TTPSETFFADMVIYTGPLHQLPVLLPNYGIENLSKRVLPWNLSSISLGWHHANFS
LPKGYGMLFADELPLL GIVWNSQIFPQATPGKTVLSLLIEGKWRESEAHAF AIAALSEYLNINQKPD AFALFSS
QDGMPPQH AVGFLERKERILPHLPGNLKIVGQNIAGPGLNRCIASAYHAICDLHTEETLAQPQSSL

>core/281/4/Org4_Gene592

MFSRWITL FLLFISLTGCSSYSSKHKQSLIPIHDDPVAFSPEQAKRAMDLSIAQLLFDGLTRETHRESNDLELAI
ASRYTVSEDFCSY TFFIKDSALWSDGTPITSEDIRNAWEYAQENSPHIQIFQGLNFSTPSSNAITIHLDSPNPDPF
KLLAFPAFAIFK PENPKLFSGPYTLVEYFPGHNIHF KKNPNYYDYHCVSINSIKLLIIPDIYTAIHLLNRGKVDW
VGQPWHQGIPWELHKQS QYHYTYTPVEGAFWLCLNTKSPHLNDLQNRHRLATCIDKRSIIEEALQGTQQPAE
TL SRGAPQPNQYKKQKPLTPQEKLVL TYPSEDILRCQRIAELLKEQWKAAGIDLILEGLE YHLFVNKRKVQDY
AIATQTGVAYYPGANLISEEDKLLQNF EIPIYYLSYDYL TQDFIEGVIYNASGAVDLKYTYFP

>core/282/4/Org4_Gene521

MNKNLVAIFD YMEKEKGIQRSTIIGAIESALKIAAKKTLRDDANISVNINSRTGDIEVFCEKEIVEICQNPSKEIP
LDKAREYDPDCQIGQYMDVPFVSDNFGRIA AHAARQIIGQKLRHAERDVIYEEYRHRVNEILSGVVKRFAKG
SNLIIDL GKVEAILPTRFY PKTEKHKIGDKIYALLYEVQESENGGAEVILSRSHA EFKQLFIQEVPELEEGSVEI
VKIAREAGYRTKLAVRSSDPKTD PVGAFVGMGRGSRVKNIIRELNDEKIDIVNYS PVESTELLQNLLYPIEQKIAI
LEDDKVIAIVNDADYATVIGKRGINARLISQILDYELEVQRMSEYNKLL EIQRLQLAEFDSPHLDQPLEMEGI
SKLVIQNLEHAGYDTIRRVLLASANDLASVPGISLELAYKILEQVSKYGESKVDEKPEIED

>core/283/4/Org4_Gene499

MSMTIVPHALFKNHCECHSTFPLSSRTIVRIAIASLFCIGALAALGCLAPPVSYIVGSVLAFIAFVILSLVILALIF
GEKKLPPTPRIIPDRFTHVIDQAYGLSISAFVREQQVTLAEFRQFSTALLCNISPEEKIKQLPSELRSKVESFGISR
LAGDLEKNNWP IFEDLLSQTCPLYWLQKFISAGDPQVCRDLGVPRECYGY YWLGPLGYSTAKATIFCKETHH
ILQQLTKEDVLLLKNKALQEKWDTDEVKAIVERIYTTYTARGTLKTEAGGLTKETISKELLLL SLHGYSFDQL
QLITQLPRD TDWDLCSVDNSTAYNLQLCALVGALSSQNLLDESSIDFDVNLGLYVIQDLKEAVQAFSASDEP
KKELGKFLLRHLSSVSKRLESVLRQGLHRIA LEHGNARARVYDVNFVTGARIHRKTSIFFKD

>core/284/4/Org4_Gene187

MNHLNKEKLHIHNWQPYRACGLLSKVSGN LIEVDGLSACL GELCKISSTKDPNLLAEVIGFHNHTTLLMSLSP
LHSVALGTEVLPLRRPPSLHLS DHLLGRVLD AFGNPIDKKEDLPKTHRKP LLSLPPSPMMRQPIDQIFPTGIKAI
DAFLT LGKGQRIGVFSEPGSGKSSLLSAIALGSKSTINVIALIGERGREVREYIEKHSNALKQQRTIIIAAPA HET
APTKVIAGRAAMTIAEYFREQGHEVL FIMDSLRSWIAALQEVALARGETLSAHQYAASVFHHVSEFTERAGN

NDKGSITALYAILYYPKHPDIFTDYLSLLDGHFFLTSQGKALASPPIDILSSLSRSAQALALPHHYAAAERLRS
LLKVYNEALDIIHLGAYTPGQDEELDKAVKLLPSIKAFLAQPLSSYCYLDNTLKQLEALADS

>core/285/4/Org4_Gene944

MLKPMYVLSKRLYRWVNQLIKLGDLVKNSRSFSVEWVFISALLLIFGCLGCASVVKVSLVPFLLLSFLAFPLI
LCFRGKGYALLLGVFVTLVYAKYVVGETLYVSFWLSGLGVSFLLAFGLFLQGVWLAQEEEMVKGKEQLRL
SEDLDAQRSAYEDLLLTQSKEKEFLDARAQGLDRELTECQELLKAAYQKQEYLTIDLKILADQKNSWLEDY
AELHNKYIELVSKNGDVVFPWVAEPSVGESQGSEKVDVSRWVSALQEKEESLERLRNEILVEKQRCSDYEHR
CQELGLLLQNFTALERRCEELQNLLNQKETQINELHQLVCKSEEKVSVEPSAHAETSCVEEKQYKGLYSQLQ
EQFLEKSETLSLVRKKLFAVQEKYLTLLKKKEELTKQDMSFDDISMIQGLLERIEILEEEVSHLEELVSRSLSL

>core/286/4/Org4_Gene171

MLRQLCFQVFFFCFASLVYAEELVVVRSEHITLPIEVSCQTDTKDPKIQKYLSSLTEIFCKDIALGDCLQPTAA
SKESSSPLAISRLHVPQLSVVLLQSSKTPQTLCSTISQNLSDVRQKIHHAADTVHYALTGIPGISAGKIVFALS
SLGKDQKLKQGELWTTDYDGKNLAPLTTECSLSITPKWVGVSNGFPYLYVSYKYGVPKIFLGSLENTGKKV
LPLKGNQLMPTFSRKKLLAFVADTYGNPDLFIQPFSLTSGPMGRPRLLNENFGTQGNPSFNPEGSQLVFISN
KDGRPRLYIMSLDPEPQAPRLLTKKYRNSSCPAWSPDGKKIAFCSVIKGVRQICIYDLSSGEDYQLTTSPTNKE
SPSWAIDSRHLVFSAGNAEESLEYLISLVTKKTNKIAIGVGEKRFPSWGAFPPQPIKRTL

>core/287/4/Org4_Gene826

MTWLSGLYFICIASLIFCAIGVILAGVILLSRKLFIKVHPCKLKINDNEELTKTVESGQTLLVSLSSGIPIPCG
GKATCKQCKVRVVKNADEPLETDRSTFSKRQLEEGWRLSCQCKVQHDMSEIEERYLNASSWEGTVVSND
NVATFIKELVVAVDPNKPIPFKPGGYLQITVPSYKTNSSDWKQTMapeYYSDWEHFHFLDQVIDNSQLPADS
ANKAYSLASYPaelptIKFNIRIATPPFINGKPNSEIPWGVCSYVFSCLKPGDKITVSGPYGESFMKDDDRPLIFL
IGGAGSSFGRSHILDLLLNNKHSKREIDLWYGARSLKENIYQEEYENLERQFPNFHYHLVLSEPLPEDIAAGWD
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>core/288/4/Org4_Gene313

MTVTLPKGVFDIFPYLADAKQLWRHTSLWHSVEKAIHTVCMLYGFCEIRTPIFEKSEVFLHVGEESDVVKKE
VYSFLDRKGRSMTLRPEGTAADVRSFLEHGASHRSDNKFYYILPMFRYERQQAGRYRQHHQFGVEAIGVRH
PLRDAEVLALLWDFYSRVGLQHMQIQLNFLGGSETRFRYDKVLRAYLKESMGELSALSQQRFSTNVLRILDS
KEPEDQEIRQAPPILDYVSDEDLKYFNEILDALRVLEIPYAINPRLVRGLDYSDLVFEATTTTFQEVSYALGGG
GRYDGLISAFGGASLPACGFGVGLERVIQTLLAQKRIEPQFPHKLRLIPMEPDADQFCLEWSQHLRRLGIPTEV
DWSHKKVKGALKAASTEQVSFVCLIGERELISQQLVIKNMSLRKEFFGTKEEVEQRLLYEIQNTPL

>core/289/4/Org4_Gene600

MFRKLFPPFSKKKTGQKQRLRNNGLLQAIISIKVLLHNEASKEACVLSYYGLLTCVPILVFFLRLSQHLFTNLN
WKEWLIIFPDYKKPIVAIVEAAYHATESNIGLVVGSSFFVFCWAGILMLLSLEDGLNKIFRTSWTPISLKRLV
SYFVITLVSPMIFIHVCGSWIYITQIMPIQYAKLFSLSHSM TALYFISRFVYLLLYLALFCCY AFLPRVAIQK TSA
LISTLIIGSVWIVFQKAFFSLQVSIFNYSFTYGALVALPSFLLLLYIYAMIYLFGGALTFIIQNRGCTFIFLGDKILP

SCYLQLITSTYILALTTRQFNEGLSPLTAQFIAKQSKVPIGEVSQCLDVLEKEGFLFPYNNGYQPVFNFSELITK
DIADKLLHREIFKKFNPDLGITFIENSFQNFNQASKNKENLTLSEIARRIK

>core/290/4/Org4_Gene215

MVCENNILSGRGLELLKKKSNITLTPTIYSVSNHNIKLDKDFSPHALSVIKTLRKAGYIAYIVGGCIRDLLLNTTP
KDFDISTSAKPEEIKAFKNCILVGKRFRLAHIRFSKQIEVSTFRSGSTDEDVLITKDNLWGTPEEDVLRRDFTI
NGLFYDPEHEEIIDYTGGVNDLRNRYLRTIGDPFTRFKQDPVRMLRLLKILSRSPFTVETQTQEALICRQELIK
SSQARVFEELIKMLNSGAANKNFFQLLIENHLLLEILFPYMDKAFRLNRALEEQTATYLKALDDKILKKEAEYDR
HQLMAIFLFPVNFNVRYKHQKHPYLSLTSVFDYIKNFLEQFFADSFTSCSKNFILTALILQMQYRLTPLIPTK
KALFFNKLLHHTRFLEALSLEIRSIVYPKLDKVYVAWIRHHQTLKCKKDSHSQK

>core/291/4/Org4_Gene58

MISLLKMPKLSPTMEVGTIVKWHKKSNDQVSFGDVIVEISTDKAILEHTANEDGWIREILRHEGEKIVIGTPIA
VLSTEANEPFNLEELLPKTEPSNLEASPKGSSEEVSPATTPQAASATFTAFTFKPEPPLSSPLVFKHVGTNNLS
PLARQLAKEKNIDVSSIQSGPGGRIVKKDLEKAPPKSIAGFGYPESPEVPPGSYHEENLSPIREVIAARLQAAK
ISIPHFYVRQQVYASPLNLLKELQAQGIKLSINDCIVRACALALKEFPSINSGFNSVDNKIVRFDTIDISIAVAIP
DGIITPIIRCADRKNLGMISAEIKSLALKARNQSLQDTEYKGGSCVSNLGMTGITEFTAIVNPPQAAILAVGSV
TEQALVLDGEITIGSTCNLTLSVDHRVIDGYPAAMFMKRLQKILEAPAVLLN

>core/293/4/Org4_Gene255

MFEAVIADIQAREILDSRGYPTLHVKVTSTGSGVEARVPSGASTGKKEALEFRDTSPPRYQGKGVLQAVKN
VKEILFPLVKGCSVYEQSLIDSLMMDSDGSPNKETLGANAILGVSLATAHAAAATLRRPLYRYLGGCFACSLP
CPMMNLINGGMHADNGLEFQEFMIRPIGASSIKEAVNMGADVHTLTKLLHERGLSTGVGDEGGFAPNLAS
NEEALELLLLAIEKAGFTPCKDISLALDCAASSFYNVKTGTYDGRHYEEQIAILSNLCDRYPIDSIDGLAEED
YDGWALLTEVLGEKVQIVGDDLFVTNPILILEGISNGLANSVLIPNQIGTLTETVYAIKLAQMAGYTTIISHR
SGETTDTTIADLAVAFNAGQIKTGSLRSERVAKYNRLMEIEEELGSEAIFTDSNVFAYEDSEE

>core/294/4/Org4_Gene897

MDIKKLFCLFLCSSLIAMSPIYGKTGDYEKLTLTGINIIDRNGLSETICSKEKLKKYTKVDFLAPQPYQKVMRM
YKNKRGDNVSCLTAYHTNGQIKQYLECLNNRAYGRYREWHVNGNIKIQAIEVIGGIADLHPSAESGWLFQDT
TFAYNDEGILEAAIVYEKGLLEGSSVYYHTNGNIWKECPYHKGVPQGKFLTYTSSGKLLKEQNYQQGKRHG
LSIRYSEDSEEDVLAWEEYHEGRLLKAEYLDPQTHEIYATIHEGNIGIAIYGKYAVIETRAFYRGEPYGVKVS
FDNSGTQIVQTYNLLQGAKHGEEFFYPETGKPKLLLNWHEGILHGIVKTWYPGGTLESCHELNNKKSGLL
TIYYPEGQIMATEEYDNDLLIKGEYFRPGDRHPYSKIDRGCGTAVFFSSAGTITKKIPYQDGKPLL

>core/295/4/Org4_Gene939

MKKTMVIDTSVFIYDPEALFSFENTRIIPFPVIEELEAFGKFRDESAKNASRALSNIRLLLLENAKTKVTDGVLLP
NGSELRIEVAPLSNDDRRGKLLTLELLKIIATREPMVFVTKSLGRRVRAEALQIESRDYESKRFSFRSLYRGFR
ELQVSQEDIENFYKNGYLDLPLDVVPSNEYFFMSAGENHFALGRYYVSQGKIIALKAMDKSVWGKPLNTE
QRCALDLLLRDDVKLVTLIGQAGSGKTILALAAAMHKVFDKETYNKVLVSRPIVPMGRDIGFLPGLKEDKL

MHWMQPIYDNMEVLF SINQMGNSS SEALQALMDAKKLEMEALTYIRGRSLPKAFIIIIDEAQNLTPHEIKTIISRA
GKGTKIVLTGDPTQIDSLYFDENSNGLT YLVGKFHHLALYGHMFMTRTERSELAAAAATIL

>core/296/4/Org4_Gene835

MLDIKIIRKTPEECETRLRKKDPKISLEPVLSLDKEVRQLKTDSETLQAQRRLLSQDIHKAKTQGV DATNLIQE
VETLAADLEKIEQHLDQKNAQLHELLSHLPNYPADDIPVSEDKAGNQVIKSVGDLPTFSFPPKHHLELNQELD
ILDFQAAAKTTGSGWPAYKNR GV LLEWALLTYMLQKQAAHGFQLWLPPLL VKKEILFGSGQIPKFDGQYYR
VEDGEQYLYLIPTAEVVLN GFRSQDILTEKELPLYAACTPCFRREAGAAGA QERGLVRVHQFHKVEMFAFT
TPNQDDIAYEKMLSIVEEMLTELKLPYRLSLLSTGDMSFTASKTIDAEVWLPGQKAFYEVSSISQCTDFQSRRS
GTRYKDSQGKLQFVHTLNGSGLATPRLLV AILENNQQADGSVVIPEVLRPYLG GLEILLPKDQ

>core/297/4/Org4_Gene301

MLPLIIFVLLCGFYTSWNIGANDVANAVGPSVSGSVLTLRQAVVIAAIFEFFGALLLGDRVAGTIESSIVSVTN
PMIASGDYMYGMTAALLATGVWLQLASFFGWPVSTTHSIVGAVIGFGLVLGKGTHIYWNSVGIILISWILSPF
MGGCVAYLIFS FIRRHIFYKNDPVLAMVRVAPFLAALVIMTLGTVMISGGVILKVSSTPWAVSGVLVCGLLSY
VITFYVYVHTKHCSYISDTPKKGSLTYRLKERGGNYGRKYL VVERIFAYLQIIVACFMAFAHGSNDVANAIAPV
AGVLRQAYPASYSYTLIGLMAFGGIGLVIGLAIWGW RV IETVGCKITELTPSRGFSVGMGSALTIALASILGL
PISTTHVVVGAVLGIGLARGIRAINLNIIKDIVLSWFITLPAGALLSILFFFALRALFH

>core/298/4/Org4_Gene961

MIMGLQSRLQHCIEVSQNSNFDSQVKQFIYACQDKTLRQSVLKIFRYHPLLKIHDIA RAVYLLMALEEGEDLG
LSFLNVQQYPSGAVELFSCGGFPWKGLPYPAEHA EFGLLLLQIAEFYEE SQAYVSKMSHFQQALFDHQGSVF
PSLWSQENSRLLEKTTLSQSFLFQLGMQIHPEYSLEDPALGFWMQRTRSSSAFVAASGCQSSLGAYSSGDV
GVIAYGPCSGDISDCYYFGCCGIAKEFVCQKSHQTTEISFLTSTGKPHPRNTGFSYLRDSYVHLPIRCKITISDK
QYRVHAALAE TT SAMTFSIFCKGKNCQVVDGPRLRSCSLDSYKGP GNDIMILGENDAINIVSASP YMEIFALQ
GKEKFWNADFLINIPYKEEGVMLIFEKK

>core/299/4/Org4_Gene722

MDKQSSGNSGCIWHPFTQSALDSTPIKIVRGEGAYLYAESGTRYLDAISSWWCNLHGHHGHPYITKKLCEQAQ
KLEHVIFANF THEPALELVSKLAPLLPEGLERFFFSDNGSTSIEIAMKIAVQYYYNQN KAKSHFVGLSNAYHG
DTFGAMSIAGTSPTTVPFHDLFLPSSTIAAPYYGKEELAI AQAKNVFSES NVA AFIYEPLLQGAGGMLMYNPE
GLKEILKLAKHYGVLCIADEILTGFGRTGPLFA SEFTDIPPDII CLSKGLTG GYLPLALT VTTKEIHDAFVSQDR
MKALLHGHTFTGNPLGCSAALASLDLTL SPECLQQRQMIERCHQEFQEAHGSLWQRCEVLGTVLALDYP AE
ATGYFSQYRDHLNRFFLERGVLLRPLGNTLYVLPPYCIQEEDLRIIYSHLQDALCLQPQ

>core/300/4/Org4_Gene688

MAEISTPSLPDSSIVSQKTPPVDPDPDSSPDHIPTIPTQAPFKPQRKKETPSSIVNAIAFAILAFLSCLGGVFAICLGC
SLEITMPLFILTA VFIAFTLLYFIHYLEKPKIPELPTPLPKLSPPPSPTLRAPTLTPEIPVPAPGIPLPPTLPKVDRT
KLTCNPDIHYPSTYDPKACSSLLKQLFSLDPETRPEDRKYSNKLASILRSKEKPGFRFHC FKGHFSHDKILNK
KSGAVVISSHSSMDFSTTLGRAFAVTTCLQRSCWEKIKNNIPTPEKHLPIGSCVSGPWDVEEGAQLYTSHLIVI

NPPTLETLIKEKMRRAVTLKDFSMKEAFTNLVLAYLQCFDICIEHNLESVQLEVFGLNLSADQEEFTTWESC
CHLALLESVRILLASKEEYALSNSVNSIPQVPLQTACRALFLN

>core/301/4/Org4_Gene268

MKKQVYQWLASVVLLALTISGYAELPLSEQVKVSHTYTTLDEVKDYLSKRGFVETRKQDGVLRAGDVRAR
WLYFREDIKNPSDKDKYNPLPVNRYRSEFYLYIDYRAERNWLSSKMNWTAIAGGENTAAGVDINRAFLGYR
FYKNPETRTDFFMEIGRSGLGDLFESEVQFQSNFDGLHIYWTRELSKDYPYQVIVHGGPFVVMNTKKHYAW
VVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVPWINGQKKPLYL
YGAFLMNPLAKATKTTLNGKENLAWFVGGTLGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKF
WFAQAIAANYDPKEANGFTNYKGFSALYMYGITDSLFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF

>core/302/4/Org4_Gene495

MQSWLQSLQERNILENFTAGLDSVEGPAAAYLGFDPTAPALHIGHWIGICFLKRLAALGITPIALVGGATGMV
GDPSGKQSERSLLQTSEVFDNSQKITACLQRYLPGVTLVNNADWLQEISLIDFLRDIGKHFRLGQMLAKDTIK
QRVHSDEGISYTEFSYLILQSYDFYHLFKNYGTILQCGGSDQWGNITSGIDFIRRKGLGQAYGLTYPLLNAQ
GKKIGKTESGTVWLDSDLTSPFELYQYLLRLPDDTIPKIARTLTLLSNEEIQDIDRRVQTDPVAVKEFVAQDIL
RAIHGDLGLEEALSVTRSMHPGNLSSLSEKDFHELFAGGMGASLDKSEVLGKRWLDLFLVLGLCKSKGEIRR
LIEQKGVYINNVPANEHSVCEEQDICYGHYVLLAQGKKRKLVLNLN

>core/303/4/Org4_Gene431

MTVAEVKGTFLVCLGCRVNQYEVQAYRDQLTILGYQEVLDSIADLCIINTCAVTASAESSGRHAVRQLC
RQNPTAHIVVTGCLGESDKEFFASLDRQCTLVSNKEKSRLIEKIFSYPDTPFEFKIHSFEGKSRAFIKVQDGCNS
FCSYCIIPYLRGRSVSRPAEKILAEIAGVVQGYREVVIAGINVG DYCDGERSLASLIEQVDQIPGIERIRISSIDP
DDITEDLHRAITSSRHTCPSSHLVLQSGSNSILKRMNRKYSRGDFLDCVEKFRASDPRYAFTTDVIVGFPGESD
QDFEDTLRIIEDVGFIKVHSPFSARRRTKAYTFDNQIPNQVIYERKKYLAEVAKRVGQKEMMKRLGETTEVL
VEKVTGQVAMGHSPYFEKVSFPVVGTVAINTLVSVRLDRVEEEGLIGEIV

>core/304/4/Org4_Gene851

MNKKNLTICSFCGRSEKDVEKLIAGPSVYICDYCIKLCSGILDKKPSSTISSAPVSETPSQPSDLRVLTPKEIKKH
IDEYVIGQERAKKTIAVAVYNHYKRIRALLHNKQVSYGKSNVLLLGPTGSGKTIAKTLAKILDVPFTIADAT
TLTEAGYVGEDVENIVLRLQLAADYDVARAERGIIYIDEIDKIGRTTANVSITRDVSGEGVQQALLKIVEGTTA
NVPPKGGRKHPNQEYIRVNTENILFIVGGAFVNLDKIIAKRLGKTTIGFSDDQADLSQKTRDHLAKVETEDLI
AFGMIPFVGRFNCIVNCEELSLDELVAILTEPTNAIVKQYIELFAEENVKLVFKKEALYAIKKAKQAKTGA
RALGMILENLLRDLMFEPDPTVEAIIHQEDTIAENKAPIIIRRTPEAIA

>core/305/4/Org4_Gene975

MIKFLSQLFIRHWPRKVVS LGFAIIIWILVGQSVTITRTL TNVPVRIVDLHPDQTVLGLQKSGFLNKKVSLTITG
NKNTVQDLRPSNLEVVISAAHNHTESWIATIDKHNLSVDHEINIRKDIHSVDANDIFVRLTQYVTE DILLTITKP
IGSPPKGYEYLDVWP KYLNQKVSGPKKEYINALKEQGLELTFNLNKISFEELERNRIAQGS HDEIIFPIPK EWKKI
LIPFENTFMDLNDPQADFLRLFLKRECIPLNLNLPVFLFFPVTFIQTMNPLEYSLDPVPPIILNHGIHQINIPLYV

KDVSQRQLDVVKNNMALTIVMPSPQDPSSINWAIEFLDEKTLENTFLQTIIAQEHGILHDIALIDEAGIRHRFRE
YLRKLALFTADGEPLNLIAEIKNNKVVIQTKTKETTKLYKKEW

>core/306/4/Org4_Gene739

MLKLQLCALFLFGYLAIVFEHIVRVNKSALALAMGGLMWLVCFSHIPMADHMILVEEIADMSQVIFFLFSAM
AIVELIDAHKGFSVIVKFCRIQSRTLLLWALIGLSFFLSAALDNLTSHHHISILKRLVKAREDRLLLGAICVIAVNA
GGAWTPLGDVTTTMLWINNKITSWGIIRALFVPSLVCVLVAGFCGQFFLRKRGSTLIAKDVELQSAPPKSLWII
FIGLGSLLMVPVWKACLGLPPFMGALLGLGLVWLTSDWIHSPHGEDRYHLRVPHILTKIDISSITFFIGILLAVN
ALSFANLLTDFSLWMDKIFSRNVVAIVIGLLSSVLDNVPLVAATMGMYNLPLDDTLWKLIAYAAGTGGSILII
GSAAGVAFMGLEKVDLWYFKRISWIALASYFGGLFSYFVLESNFFI

>core/307/4/Org4_Gene585

MSSAIARDCFPSPSPQPSSTLGVHPPKYKSLILSVSLIVLGALLLCVGMLLLVAIFSFSVLTVGLGGAGVFLGS
LLLILGLIFFVSYHRKLSEATRSLEQKITLEYQPWADLRKELNEVQEWSNFLLDEWEDFKEVVAQHKSQFATF
EGDLLLFGREVEKEYETIWKELDGRDVALLTELKNIWGPLEFLGKKGDRLQCEIDKLRKEVMKVGKSGLKLA
CELTKFKSALKDVKIEQECYRDKRKVEKLEVLPEGYRRELLEVLKTRLSVEKEIQLFEEVVSFAFEKSLASLHR
TVFSEELQEALDKAKAELLDIQVRKSVVEDLSCEPTLIQYHLLRLYEYVQCRIVEQFLTQTFSSSEQEKVLEEYE
ALKARIRKTLRVKLDQVRANVAFVASTTDLSSASESLDGNDSVFEDAHDFFLD

>core/309/4/Org4_Gene833

MIETREEVGSANFVSLERAIEDLRAGKFVIVVDEASREDEGDLIIAGEKITVEKMTFLLQHTTGVVCAALSQER
LLSLDLPPMVKDNRCRFTPTVSVDAAHGVTTGVSAADRRTKVQQLADPKSKPEDFISPGHFFPLASSPGGV
LKRAHTESTVDLMELAGLQPCGVLAELVNEDYSMMRLPQILEFARKHNIAPVIPVTSIIAHRMLSDRLVSKIS
SARLPTIYGDFTIHVYESLLDGMQHLALVKGNVAGKSNVLVRVHSECVTGDILGSKRCDCEQLSSAMSZIA
EKGTVGLVYLRGQEGRGIGLGHKVRAYALQDNGYDTVDANLAMGFPVDSREYGIGAQILVDLKLTTIKLIT
HNPQKYFGLQGFGLSITERVPLPVRISEDNEQYLRTKQERMGHWLDLPCCNNRVQ

>core/310/4/Org4_Gene951

MLCYSPNYVTDLYSISLSAEESLGGIRAFPQAESLLGGACALNFPDLEERLPDLRKELLFLGSNDRPDACGGKF
SLQLASSKECYIAALKERVYLNVTSSRGPVYSFSPKGVPTELWIECFVSMDGRVEVKVRLQGLHKLISKP
RDCETLFLNPPANKLDCWEIAGFRVDASFPVKQKIRRIGVDKFLLMHGGAEYADKATKERVDFVSSDEENYS
RYLAVGDVLLWDGNCWQTCGEFQGASSRAPLFEVKRIDDKVMADLWNVGGTQRQTISLVKGVPSPIEINE
VIREIEFTGMRSWSKPIVLVGGQRLILSPDDWILRTAKGWEKLSRADQIQDYVTGKVTGPLLVFEKLEKDLRG
FVLRGHMFNAQRTLVTETISLPLKQGFEPASQEVSSNTRSAAAHPGATNRGGS

>core/311/4/Org4_Gene450

MSQPPINPLGQPQVPAAASPSGQPSVVKRLKTSSTGLFKRFITVPDKYPKMRYVYDIGIIALAAIAILSILLTASG
NSLMLYALAPALALGALGVTLLISDILDSPKAKKIAEAITAIVVPIIVLAIAAGLIAGAFVASGGTMLVFANPMF
VMGLITVGLYFMSLNKLTNLNYFRREHLLRMEKKTQETAEPILVTPSADDAKKIAVEKKKDLASARMEEHEA
SQRQDARHRRIGREAQGSFFYSSRNPEHRRSFGSLSRFKTKPSDAASTRPASISPPFKDDFQPHHFKDLRSSSFG

SGASSAFTPIMPASSRSPNFSTGTVLHPEPVYPKGGKEPSIPRVSSSSRRSSRDRQDKQQQQQNQDEEQKQQSK
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>core/312/4/Org4_Gene813

MCQRILILGTGITGKSVARFLYQQGHYLGADNSLESLSVDHLHDLRLMGASEFPENVDLVIRSPGIKPYHPW
VEQAVSLKIPVVTDIQVALKTPEFQRYPSFGITGSNGKTTTTLFLTHLLNTLGIPAIAMGNIGLPILDHMGQPGV
RVVEISSFQLATQEEHIPALSGSVFLNFSRNHLDYHRNLDAYFDAKLRIQKCLRQDKTFWVWEECSLGNSYQI
YSEEIEEILDKGDALKPIYLHDLRDNCAAYALANEVGVWSPEGFLKAIRTFEKAHRLEYLGEKDGVDHYINDS
KATTVTAVEKALMAVGKDVIVILGGKDKGGDFPALASVLSQTTKHVIAMGECRQTIADALSEKIPLTLKDL
QEAVSIAQTIAQEGDTVLLSPGCASFDDQFQSFEERGAYFKLLIREMQAVR

>core/313/4/Org4_Gene804

MSKKRVVVTGFGVVSCLGNEVDTFYDNLLAGVSGVRPITSFPCEDYATRFAGWIPEFNPEPYVDKKQARRV
DPFITYAMVAAKKAIAMSRWDKDHLPSPDPVRCGVIVGSGMGGLSTLDQGMERLLVIHKKLSPFFIPYIITNMA
PALIAMDFGLMGPNYSTACATGNYCIDAAYQHLVSGRADMIICGGTEAAVNRIGLEGFIANRALSERNDAP
DQASRPWDRDRDGFVLGEGAGILVLETLESALRRDAPIFAEMLGSYVTCDAFHITAPRDDGEGITACVLGAL
NSAGIPKERVNYVNAHGTSTPLGDLSEVLAVKKAFGSHVRNLRMNSTKSLIGHCLGAAGGVEAIVAIQAILT
GKLHPTINLDNPIAEIEDFDVVANKAQDWDIDVAMSNFSGFGGHNSTILFSRYVP

>core/314/4/Org4_Gene296

MLVSIETFSSIASGSPVQKAAEACYTQYSKQPSSKEVLSSFSWIQELSLFPDRYNLATGASELIKQHWLHNNHS
LAFECILINGKYEPSLSQLPEGVIVCGIDEARGSLSSFMQGFVDNKHPLAFLNAVCSEDRGVVIIPEEMQTSDP
IFVRHISFPTVSDHDVIFSPRIVVILGQRASAIQISHDVLDMVGSSKTIVNGVTLEFVGEADLTVFMVPRYS
EEDTLWSSTIATVEKDAVCRMTHNLLESCQGFQWFDNTSYIVGKKGHAESLVLVQSPRKTWVNNLMASHDA
EETVSRQNIKSILYSGHFLFEGTISISSQGDLSDAYQKHDTLLLSSEARVSTFPRLEIETDEVKASHGATVGPLD
PQQIFYMRSRGMTEAEAQEKLIHGFLKQGLVSDTFLGSSFQLNQTS

>core/315/4/Org4_Gene838

MRYHKYFRYVNSWVFLVVLTLMLLSVVVISSMDPTAMLVTSKGLLTNKSIMQLRHFALGWVVFICAYFD
YHLFKRWAWVLYFFMICALVGLFFVPSVQNVHRWYRIPFIHMSVQPSEYGKL VIVIMLSYILES RKADITSKT
TAFLACLVALPFFLILKEPDLGTALVLCVTLTIFYLSNVHSLLVKFCTVVATIGIIGSLLIFSGIVSHQVKPY
ALKVIKEYQYERLSPSNHHQRASLISIGLGGIRGRGWKTGEFAGRGWLPYGYTDSVFSALGEEFGLLGLLFTL
GLFYCLICFGCRTVAVATDDFGKLLAAGITVYLAMHVLINISMMCGLLPITGVPLILISYGGSSVISTMASLGV
LQSIYSRRFAKY

>core/316/4/Org4_Gene400

MKLWMKIFIGLVGVTLGLVLEDKAIFFKPIGDIFLNLLSMVVYPLVFCSMVLGASISDMKKLGRIGIKSVGL
YLGTTALAIVIGLCFAWIFSPGNGCDFAQTQSMDSAVTVIDSNKTASYFLSIIAQVFPSNPVRSFAEGNILQIIIF
AIFLGIALRLSGERGRPVERFIDGFSEIMLRMVNMIMSFAFYGVGASMAWISGNHGLGVWLWQLGKFIIAYYLA
CLFHATLVFGGLVRFVGCKMSFSKFLSSMMDAISCAVSTASSSATLPVTMRCVSKNLGVSAEVSGFVLP LGAT

VNMNGTAIFQGMAAVFIAQAYNCPLSLSSLLLLVVTATFSAVGSAGVPGGGMITLGSVLASVGLPIQGIAILA
GIDRLRDIVGTPMNILGDAVVATYVASGEGELSPSESIKQESVETT

>core/317/4/Org4_Gene889

MKRIFYSFVLLSCIFPYVGCAQVFVGLDRIFSEGEYTRCIQGKKIALISHSAAINSRGQDALSVFYSRKHDCTVE
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KASERYGKQLIVLDRPNPMGGRIVDGPLPNPTTSGSLAIPYCYGMTPGELALFFKKTYPNANVVVVPMKGW
NRSMTFDETGLIWMPSTSPQMPDPQSPFFYAATGILGALSVASIGVGYTLPFKVLGAPWMDGEKVADELNRM
KLPGVFLPFFYEPFFGKYKMEMCSGVLLVLQDPKIFYPVETQCTIWGVLKALYPKQVEQTLKSIERIPARRSS
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>core/318/4/Org4_Gene859

MKKNASHKTNDKKSLSIWSIGGSIFAMFFGAGNIVFPLALGYHYNAHPWSAYFGMMLTAVCVPLLGLVSML
FYSGDYQKFFFSIGRIPGMIFITAILLIGPFGGIPRAIAVSHATLISLSEHKSAFIPSLPIFSAICCVLIYIFSCKLSRL
IQWLGSVFFPIMLVTLWVHIRSFMIPHPMVQEFIPNARQAWLAGFIEGFNTMDLLAAFFFCSIVLISLRQLVA
EEKHPTEEEIPLSFQGISKKNKRSLALGFFLAAILLGVTYLGFLVLSAARHAGLLVNVSKGHILGRISAIALGPNSI
LTGVSVFIACLTTEIALVGIVADFLARVVSFKKLVYASAVICTLIPTYLISILNFETISHLLLPLLQLSYPALIVLA
CGNIAAYKLWNFRYSPVLFYLTLSLTIVLKLVN

>core/319/4/Org4_Gene573

MDKETLENIYRHFYRFLKLNILPAFLGLLLLCSPNTLNNTQVDVIFSDRLCGCLLIFLAIASLTRSLLWL
LGIWVTLFACVAGRSPTIFANDTLIGFAILAVVCISPTRPEALEVGPTLPEGFSYNPSAGGRRRAAVLFLSLLGWL
EARYLTASSLGITSSQSSNFLLLYSSIMTVYSLVVLVSLAGSERRWHTRPKIVIATALALTGVIIITLLPIILHQLR
YDCWLCLCLTIEPALAVVFAYDETRATLRYIAQFLGDKRALTRASFFGSEYYKHTLSWEERTVLPLRKAYKQ
AFEGISFPINQLLAILVATVFVKVNSSMGLPTFPRNFLNICCWFIIVLFILAFESLRHLRWMNLIFSAAILFSPVL
FHIPVESPMFLPIIVTGLLIIISIGKRRRTKRKL

>core/320/4/Org4_Gene477

MIPTMLMFFHICFTLCSGFISLSQIALFSLPTSLISHYKRSKSKKQQRVATLLLHPHLLITLIFCDIGLNIAIQNCF
AILFGDAASWWFTVGLPLAITLILGEILPKAVALPFNTQIASSVAPLILCVTKIFKPLLHWGIVGINYVVQWILS
KQQIDIIQPQELKEVLQCKDFGVVNQEESSRLLYGYLSLSDCSVKERMQPRQDILFYDIQTPLENLYLLFSKQH
CSRVPVCNDNLQNLLGICTARSLLLHDKPLQSSDDLPLKKPYMPETISAKMALCQMAAEDETLGMIIDE
YGSIEGLITQEDLFEIVAGEIVDQRDNKILYTTSGADVIIASGTLELREFSEIFDINLPTNNNIATIGGWLIEQIGTI
PTTGMKLSWNNLLFQVLDAAPNRIRRVYIRKLYD

>core/321/4/Org4_Gene986

MDESDGEEASKDSAFSASFYSYEFVKSSTRESKNTVTHSTASRTLYILRQDCSYDPRALKVDDEFYRWVEKRL
DAKNPDSLNAFVKEVGTHYVTSVTYGGIGFQVLKMSYLQVEELEKEKISISVAAASSLLKSKTSNATEKGYSS
YQSESSAQTVFLGGTVLPDLQQDKLDFKDWSESVPNEPIPLAISVSSITDLIPELFPSEDAQVLSQKKKSALGKVI
LNYLESHKPKEEGPKPVQITSGFNSSSSVFTLQAAKAPKTVSFPYIDYWSTIPYLFPTLKETSGAQPLSFYLRFD

DIFEQQNLVHNTSYILASTSVRLGYFGDSYRDYDALSFYGSWPQAYFDWAGYKDRCTWTLEKLNTTGDLFIR
SGDEIRLKHNTSGKYLATTSMSDGYQTLTCTTQTSDSVFIITV

>core/322/4/Org4_Gene759

MNLPVSLACLLLSGCVFFLGVFVSSSLYARKKRAFLEKIQKLEHENQLLQTSNLNLSRHQEQLIEDFSNRLALSS
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LTDILKHPGSRGRWGIEQLERILELAGMLKYCDYDSQTTSAQGAFRADIIIRLPQDRCLIIIDAKAPISDSYFSVE
EIDKGDLVDKIKEHIKTLKSKSYWEKFHQSPYVILFLPGESLFNDAIRLAPELMEIGASSNVILSSPLTLLALLK
TIAVMWKQENLQKQIQEVGLLGKELHRRQLQVVFTHFQKIGKNLNQTVQSYNDMASSFQYRVLPTLRKFEG
ETSSSHQIEPTPIESLATSFPHTCDIDTNLAVIESLEKQD

>core/323/4/Org4_Gene241

MKTAHSCYSWFCWLFSFLVLFVGGIAGGEPLCPDCKYETKSVLRSDQLPDHLWNYENDCYLTGYVQSLLD
MHFLDSRTQVVIEKNRAYLFLSLPVDSSLSEAITNFVRDLPFICAVEICERPYGECITRSSAERPLLPEKTLGMP
FCGKEGVWLPQNTILFSPLIADPRQVTNSAGIRFNEKVVGNRVGATIFGGDFILLRLFDVSRFHVDCDFGIQGG
VFSVFDLDHPESCMVNSDFFVAGLWSGAIDKWSFRFRLWHLSSHLGDEFILTHPNFPRFNLSDGVDLFI
YTPQIRLYGGCGYIVSRDLTFPERPFYCEWGAELRPFGLREGNLHAQPIFAMHFRCWEEQKFGLDQSYILGME
WAKFQEIGRKIRAVLEYHQFSKEGQFIREPCNYYGFRLTYGF

>core/324/4/Org4_Gene852

MTTIAIEAAKKVLIKLRNAGYQAYFVGGCVRDMLMNRPLEDIDIATNASPTIVSTIFPDVISIGVAFGIIVVKQD
GRLFEVATFRSDGEYKDGRHPDRIIFSSMREDALRRDFTVNGMYYPDFFEDKVDFDVEGTRDIEKKVIRAIGH
RLRFSEDKLRILRAIRFSSSLGFTLDPTTERAIKEAPALVNSVSPERIWQELKKMLKRQPHGALSLLLKLKVLIF
IFPELRDIPYSLRRTTIEFARKFNPTHFPEILFLLPLFQGVSEEAATVAFGRRLRISNKLKLIESWYEALPHFQ
SNRVFWAHFLASPTAPLFLFLSALQKQDPSRQQHFISRVQELESRLQFILRIKTSSPVVSAPDLIAKGITPGRLL
GDLLREAEILSIENECLDKEKILLLLQEKGFWK

>core/325/4/Org4_Gene297

MKNLKEDFPIFAAKAKENEPFIYLD SAATTQKPQQVIDAVANFYTSSYATVNRAIYSSSRNVTEAYAAVREK
VRKWVSAASDSEIVFTRGTTAGLNLLAISVNDLWIPKGGVVLVSEAEHHANVLSWEIACRRRGSLVKKIRVH
DSGLIDLDDLEKLLNEGAQFVSIPHVSNTGCVQPLQQVAELVHRYDAYLAVDGAQGAPHLPIDVQLWDVD
FYVFSSHKIYGPTGIGVLYGKKDLLDQLPPVEGGGDMVAIYDHQNPEYLPAPMKFEAGTPNIAGVLGLGAAL
DYLDGLSAKFIYDKEIALTTYLHKELLEIPGVEILGPSIEEPRGALISMTIDGAHPLDLGFLDLRGIAVRTGHQ
CAQPAMERWNVGHVLRVSLGIYNDEDDINQFILVLQDSLDKIRR

>core/326/4/Org4_Gene933

MVVVALFILGIFFLSGSLAFLVHTSCGVLLGAALPILCIGLVLLAVALIVFLCHKHKTRQDLDDYDQDLDSLVI
HKKEIPNDISELRVTFEKLQNLQFHTKDFSDLSQELQGKFINCMEKWLTLDEVTKFLIVRDRFLETRRNFTT
FGEQVKEIQSNIFDLHEEKSSLYLELYRLRKDLQVLLNFFLLPPGILKVDYDEIEAIKGLFIRLTSRLDKLDVKA
QERKKFINEMSREFKEVEKAFFDIVDRATKKLMDRAKKESPARLFMGRTESLLEMKKNEEALKNQGLDPENL

SHPELFSPYQQLLILNYLNSEIVLHHYEFLISGAVTSGLTLEECENRMRAASTRLNAFLVRKLQFRGAIKSAYF
EKLTEIEKELRSLQDVIKSLELELIHKIKDIVTEET

>core/327/4/Org4_Gene492

MTDSNPLPSYTDASLYRTPAKHSYPRLPLNRTDRIEKILKIVTLTLALACALGFSIAAGILAMPIFSASVVITLA
IAAVSLYSLLKKPKLYEILPQIEPESEESSLSPSPQPPEQQDLPLQIDPLDPESLPEVSLADLTTPPEELTAITVTP
GYEALLQQNWDLLPSLAAVDPSFTTETPQQPCFIWKLKDSKLIFISTSGDIAVPRIKTQGRVMIVNAANENISR
EGGGTNKALSLATSLQCWNASRLPRAHSRSGSQLQPGECRSKAWENS DHTSNDHVP GKAHFLAQLLGPEAA
KCNNDPKQAFEVSKKAFHNL FQEA EIIGVDVIQLPLIGCNLFAPSRLNLGKTRAEWIEAVKLALITSLQDFG
WEQDNQEEQKIILTDQDQPPIIPPLFDLTP

>core/328/4/Org4_Gene537

MKKQRSHYTKNNLLLLLSILVGLGLGSVQSPWIVYSAECIANTFLKFLRLLSIPLVFCALGSTITSIQNFNTMVT
LGKRILYYTLLTTVIAASIGLLLFFLLRPQMITQDALATTTKCNPLGYLDVLSDTLPENIFKPFLQGNVISAACL
AVLLGTASLFLQEKEKHFVNQFFNSFFSIFLNLARGGLKLLPIAMLGFSVILFKELKDQSNLTMFAKYLLCVIG
ANLAQGFIVLPILLKINKVSPLKVAKAMSPALVTAFFSKSSAATLPLTMELAEDDLKINKNLSRFSFPLCSVIN
MNGCAAFILITVLFVATSNGMIISPLMSLGWIFIATLAAIGNAGVPMGCYFLTSLTSMNVPLSILGLILPFYT
VIDMIETSLNVWSDCCVVS LANQQLSKKLSL

>core/329/4/Org4_Gene476

MTNSALFWIGVNIICIVLQGFYSMMEMACVSFNRVRLQYYLTKDHKKARYINFLIRRPYRLF GTVMLGVNIA
LQVGSESSRNCYRALGITPDYAPFTQIFIVVIFAELLPLTISRKIPEKLALWGAPILYYSHYIFYPLIQLIGSLTEGL
YYLLNIKKEKLNSTLSRDEFQKALETHHEEQDFNTIATNIFSLSATCADQVCQPLEQVTMLPSSANVKDFCRTI
KNTDINFIPVYHKARKNVIGIAHPKDFVNKALDEPLINNLHSPWFITAKSKLIRILKEFRDNRSSVAVVLNASG
EPIGILSLNAIFKILFNTT NIAHLKPKTISVIERTFPGNSRIKDLQKELDIQFPKYPVETLAQLVLQLLDSPA EVGT
SVIINNLLLEVKEMSLSGIKTVSIKNLLS

>core/330/4/Org4_Gene142

MDKLTVQDLSPEEKKVLVRVDFNVPMQDGKILDDIRIRSAMPTINYLLKKHAAVILMSHLGRP KGQGFQEEY
SLQPVVDVLEGYLGHVPLAPDCVGEVARQAVAQLSPGRVLLLENLRFHIGEEHPEKDPTFAAELSSYGDFY
VNDAFGTSHRKHASVYVVPQAFPGRAAAGLLMEKELEFLGRHLLTSPKRPFTAILGGAKISSKIGVIEALLNQ
VDYLLLAGGMGFTFLQALGKSLGNSLVEKSALDLARNVLKIAKSRNVTIVLPSDVKAAENLQSKESVISIDQ
GIPPHLQGF DIGPRTTEEFIRIINQSATVFWNGPVG VYEVPPFDSGSIAIANALGNHPSAVTVVGGGDAAAVVA
LAGCSTKVSHVSTGGGASLEFLEQGFLPGTEVLSPSKS

>core/331/4/Org4_Gene825

MSTMQNCPHFGVCGGCSFPQSNYSDSLKKKEELLHQLFAPLVPSDMIAPIPCSPSLRGRNKMESFFQTYEGE
KSLGFISSTKPKKGIPVTTCLLIEQTM DILKLTREWWDKHPELMAYFPPKNKGSLCTLTVRTGSPQQNFMVI
LTTSGTPEYRVNEACIDEWKEILLSSSLNIASIY WEEKVAARGISTYYETKLLYGAPSIQQKLSLPSDDNSASFS
LRPRSFFQPQITQAAKIIETAKEFINPEGSETLLDLYCGAGTIGIMLSPYVKNVIGVEIIPDAVASAQENIKANNK

EDCVEVYLEDAKAFCKRNENCKAPDVIVIDPPRCGMQSKVLKYILRIESPKIVYISCNPKTQFQECADLISGGY
RIKKMQPIDQFPYSTHLENIILLEREIDL

>core/332/4/Org4_Gene163

MLLVRKWLHTCFKYWIYFLPVVTLTLLPLVCYPFLSISQKIYGYFVFTTISSLGWFFALRRRENQLKTAADVQLL
QTKIRKL TENNEGLRQIRESLKEHQESAQLQIQSQKLKNSLFHLQGLLVKTKGEGQKLETLLLHRTEENRCL
KMQVDSL IQECGEKTEEVQTLNRELAETLAYQQALNDEYQATFSEQRNMLDKRQIYIGKLENKVQDLMYEI
RNLLQLES DIAENIPSQESNAV TGNISLQLSSELKKIAFKAENIEAASSLTASRYLHTDTSVHNYSLECRQLFDS
LREENLGMLFVYARQSQR AVFANALFKTWTGYCAEDFLKFGSDIVISGGKQWMEDLHSSREECSGRLVIKT
KSRGHLPFRYCLMALNKGPLCYHVLGVLYPLHKEVLQS

>core/333/4/Org4_Gene646

MRMLQISM LLLALGTAINSPA IYAADSQSVSFPEQLLSSFTGEIKGNHVRMRLAPHTDGTIREFSKGDLVAVI
GESKDYYVISAPPGITGYVFRSFVLDNVVEGEQVNVRLPSTSAPVLVRLSRGTQIQPASQEPHGKWLEVVLP
SQC VFYVAKNFVANKGPIELYTQREGQKKIAMDLINSALNFAHIELEKSLNEIDLEAIYKKINLVQSEEFKDVP
GIQGLIQKALEEIQDAYLSKSLESQNTSIASSQCSTPKVSSSSEVTTSLLSRHIRKQTALKTAPLTQGRENLEYSL
FRIWASMQQGNDHSEALTQEAFYRAEQKKKQVLGVLEVYPHVVKNNPGDYLLKAQENTIAFLYGTSINLE
QWLGKRVTVECLPRPNNHFAFPAYYVVGIKEAS

>core/334/4/Org4_Gene62

MAASGGTGGLGGTQGVNLA AVEAAAAKADAAEVVASQEGSEMNM IQQSQDLTNPAAATR TKKKEEFQT
LESRKKGEAGKAEKKSESTE EKPDTDLADKYASGNSEISGQELRGLRDAIGDDASPEDILALVQEKIKDPALQ
STALDYL VQTTPPSQGKLKEALIQARNTHTEQFGR TAIGAKNILFASQEYADQLNVSPSGLRSLYLEVTGDTH
TCDQLLSMLQDRYTYQDMAIVSSFLMKGMATELKRQGPYVPSAQLQVLMTETRNLQAVLTSYDYFESRVPI
LLDSLKAEGIQTPSDLNFVKVAESYHKIINDKFPTASKVEREVRNLIGDDVDSDVTGVLNLFFSALRQTSSRLFS
SADKRQQLGAMIANALDAVNINNEDYPKASDFPKPYPWS

>core/335/4/Org4_Gene931

MVYFMVFFPSSES VVKANSVVR SNFCYFLENKFVSPSESTEVMFSEIMNGRVPDIESLFDRPTDMMMTGFKA
AQNLGNLFNSFGILIMCFSQCKSCQTPEKETS AIVLGATLLFFVIALILGPTLGALVYCA YKVYTLGKMIYSLN
KAKAKVLRHPAQNVFHRAAGVATIRSSEEAVKACKLYKSAMIGSLVVSLIASLALIALTAGIVLALFFVAPGA
APVITAAMIGCCAAGGGALLISLLGLWIAMVRKAKHQEACVGHLTNVVLHTAVSEALLHDP SHFQTNALAR
DLFLTDCLSHYGHLFSNEEVAQLVQGGAPGGGSRPSQHYGGPSDYQNR RGNGNFGGSHFGGGGGFAGSHF
GAGYPTAPT MPSAPPPPPYNPAFNPPFPFPAYDTIYG

>core/336/4/Org4_Gene90

MLSVTIVLVGLEMARSKVSKRDSKILDILFATTELYLKTGQPVGSKTLKESFCSDLSTATIRNYFAELEAEGFL
KKNHTSGGRIPTDLALRHYVDHQEECPAEISAPIFDKISQLPSES RNIIKDLQKATELLGEILDLP TFFSSPRFEN
DSVTNIQITQVDKQRAVTILSTEFQGIFTDTLWLPEACDTLSIKRIEKFLQNYIRKLPTNEELSKKEEHL SMSLY
NEVVVRYLTRYCNFSEEDLYQTGMSKLLKYEAFKDPEVLALGLSLFENRRQMCELLNIGMHKGRATAFIGK

ELSDILGTSNPGCSVITIPYYMNRSP LGALGILGPINLPYKEALPLLKLFANKINETLTQSFYKFKLSFRRPLTSN
CKLSNEPILRTEYSSIKLLPSKETL

>core/337/4/Org4_Gene419

MRRNPHFSLLKPQYLFSEISKKLAQFRKENPEISVIDLSIGDTTQPLCRSITQAIKEFCVSQEKQETYRGYGPET
GLEKLRTKIASEVYENRISPEEIFISDGAKPDIFRLFSFFGPEKTLGLQDPVYPAYRDIAHITGIRDIPLACRKET
GFIPELPNQQLDILCLCYPNNPTGTVLTFQQLQALVNYANQHGTVLIFDAAYSAFVSDPSLPKSIFEIPEAKYC
AIEINSFSKSLGFTGMRLAWNVIPKELTYDNNPEMINDWKRLFATTENGASLLMQEAGYYGLDLFPTPPAISL
YLTNAQKLKKSLETAGFSVHGGDHAPYLWVELPEGISDEEAFDFFLHQYHIAVTPGHGFGSCGQGFVRFSA
AQPQNIALACDRLCTASLKETMVLA

>core/338/4/Org4_Gene769

MSNKVLGGSLLIAGSAIGAGVLAVPVLTA KGGFFPATFLYIVSWLFSIASGLCLLEVMTWMKESKNPVNMLS
MAESILGHVKGKISICLVYLFFFYSLIA YFCEGGNILCRVFN CQNLGISWIRHLGPLGFAILMGPIIMAGTKVIDY
CNRFFMFGLTVAFGIFCALGFLKIQPSFLVRSSWLT TINAFPVFFLAFGFQSIPTLYYYMDKKVGDVKKAILIG
TLIPLVLYVLWEVVVLGAVSLPILSQAKIGGYTAVEALKQAHRSWAFYIAGELFGFFALVSSFVGVALGVMD
FLADGLKWNKKSHPF SIFFLTFIPLAWAVCYPEIVLTCLKYAGGFGAAVIIGVFPTLIVWKGRY GKQHHREK
QLVPGGKFTLFLMFL LIVINVVSLYHEL

>core/339/4/Org4_Gene498

MVNIQPVYRNTQVNYSKATPFSVCQPALSLIIVSVVAAVLAI VALVCSQSLLSIGLGIALVLVSLILFASAMFMI
YKMRQEPKELLIPKKIMELIQEHYPSIVVDFIRDQEVSIYEIHHLSILNKTSVFDKAPVYLQEKLLQFGIEKFKD
VHPSKLPNFEEILLQHCPHLHWLGR LVYPMVPDVTPTGTYGY YWCGPLGLYENAPSLFERRSLLLLKKMSFGEF
ALLEDGLKKNTWSSSELVQIRQNL FTRYADKEEVDEAELNADYEQFNSLLHLIFSHKLSWKQVQLFQYMN
ESGWDWLCDFDSQGE GFQLSRLVGLLHSSWALYEAKEQFYLP EVSLLTWEELIEMQWLSKPAKHGVAKDL
CNVFEKHFQRFRQYLGSLESKSKVRKYLLELS

>core/340/4/Org4_Gene259

MSFFNHIPTFSPDAILGLQNVFFADKRPEKVNLVIGVYEH PPKRYGGLSCIRKAQTVILEEEQNKSYLPISGLQI
FLDEMREL VFGAVDPSAIVGFQSLGGTGALHLGARLLSVAKGSGKVYVPEQTWSNHIRIFSQEGLEVIRYPY
SKEQKQLLFEPLIAFLKEVEKNSVILLHGCCHNPTGVDFTE DMWKELAILMKERELIPFFDTAYQGFAQGIEL
DRKPIEIFISEGNTVLVAASSSKNFALYGERVGYFAVHSTFTDELVKIRSFLEEKIRGEYSSPQRWGVEIVSTILS
NPYLKEEWQSELNFIRESLGKMRTFRVQALRKVAGHTFD FLLSQHGFFAYPGFSDKQVFLFLREQHAVYTTAG
GRMNLNGITEKNIDHV VQSFIQAYEL

>core/341/4/Org4_Gene932

MVVSIIYSEILSFSELTSCKHSLFPFGPIETASIRIHHVFN VVIVCLIIILGTLFVCLGMVFLGVFSTYLLGMSSMILG
LLLSIGLALLKFKERYGLEPKELFGVEGGFDKKLPSEIIQM QDQIADLARELDLEQKKDTLIRGFSARLDVLE
GSKTEKKQILKIGVPRNLSEIQERAQELNSILEQCKEALLFR RKS AQEIFKKLYDRKAAFWRSYREDLWCYSEI
HVS KKALS NLYIGDVFE GTAPHFLMEAYAMC RTAKNLRNYVKVCVEDMRMRIDE EKKRAKQLSVSELLCC

CTEIETDLENETNLFTSDSEDVLEEYQIH CIRVTMLHALWAIYNDEVVCRKPIDTLDRVRARMAVEDCIETFEE
LQMCVVHTKTLELEIAQLYVDILLEA

>core/343/4/Org4_Gene16

MSKETFQRNKPHINIGTIGHVDHGKTTLTAAITRALSGDGLASFRDYSSIDNTPEEKARGITINASHVEYETPN
RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSATDGAMPQTKEHILLARQVGVPYIVVFLNKVDMISQE
DAELIDL VEMELSELEEKGKGCPIIRGSALKALEGDANYIEKVRELMQAVDDNIPTPEREIDKPFLMPIEDV
FSISGRGTVVTGRIERGIVKVSDKVQLVGLGETKETIVTGVEMFRKELPEGRAGENVGLLLRGIGKNDVERG
MVVCQPNSVKPHTKFKSAVYVLQKEEGGRHKPFFSGYRPQFFFRTTDTGVVTLPEGTEMVMPGDNVELDV
ELIGTVALEEGMRFAIREGGRTIGAGTISKINA

>core/344/4/Org4_Gene960

MFEFRFPKIGETSSGGSIVRWLKNLGDHVARDEPLIEVSTDKIATELPSPKAGRLVRFCVNEGDEVASGDVLG
LIELEEISEADDESTSCPLTSCETKSEAGSSSSSAWFSPAVLSLAQREGIGLDNLQKIAGTGKGGRVTRQDLEA
YISESQQVSIPETFQGEVNRIPMSPLRRAIASSLSKSSDEVPHASLVVDVDVTDLMNLISGERQRFLDTHGVKL
TITSFIVQCLAQTLRQFPLLNGSLDGTITVMKKS VNVGVA VNLNKEGVVVPVIHNCQDRGLVSIKALADLSS
RARLNKLDPSEVQDGSVTVTNFGMTGALIGMPIIRYPEVAILGIGTIQKRVVVRDDDSLAIKRMVYVTLTFDH
RVLDGIYGSEFLTSLKNRLESVTMG

>core/345/4/Org4_Gene690

MDYYISILGISKTASAEIEKKAYRKLAVKYHPDKNPGDAEAEKRFKEVSEAYEVLSDPQKRDSYDRFGKDGP
AGAGGFGGAGGMGNMEDALRTFMGAFGGEFGGGSFFDGLFGGLGEAFGMRSDPAGARQGASKKVHINLTF
EEAAHGVEKELVVSQYKSCETCSGQGA VNPQGIKSCERCKGSGQV VQSRGFFSMAS TCPEC GGEGRIITDPCS
SCRGQGRVKDKRSVHVHIPAGVDSGMRLKMEGYGDAGQNGAPSGDLYVFIDVESHVPVFERRGDDLILELPIG
FVDAALGMKKEIPTLLKTEGSCRLTVPEGIQSGTILKVRNQGFNPVHGKGRGDLLVRISVETPQNLSEEQKEL
LRTFASTEKAENFPKKRSFLDKIKGFFSDFTV

>core/346/4/Org4_Gene602

MSSPVNNTPSAPNIPAPTTPGIPTTKPRSSFIEKVII VAKYILFAIAATSGALGTILGLSGALTPGIGIALLVIFV
SMVLLGLILKDSISGGEERRLREEVSRFTSENQRLTVITTTLETEVKDLKAAKDQLTLEIAFRNENGNLKT
EDLQEQVSKLSEQLEALERINQLIQANAGDAQEISSELKKLISDWDPKVVEQINTSIQALKVLLGQEWVQEAQ
THVKAMQEQIQALQSEILEMHNQSTALKKSVENLLVQDQALTRVVGDLLSEKKLSQACSA LREEIEKLAQH
ETSLQQRIDMMLAQEQNLAEQVASLEKMKQEAQQAQSDFIACVRDRTFGRRET PPPPTPPVVKGDESQEED
GSTPPVSPSSPVDRATGDGQ

>core/347/4/Org4_Gene869

MPRYRYTYLDPKERRKRGYLEALHIQEAREKLAQENIQVLDIREVALRRMSIKSTELIVFTKQLLLLLRSGLPL
YESLVSLRDQYHGQKMGLLLTSFMETLRSGGSLSQAMAAHPNIFDHFYCSGVAAGESVGNLEGCLQNIIVL
EERAQITKKMIGALSYPCVLLVFSFAVMLFFLLGVIPALKETFENMEVKGLTKIVFGVSDCLSAYRYLFLGFAS
ALITVGILMRHRIPWKKILEKLLFALPGTKKFVVKVAVNRFCSVASAILKGGGT LIEGLDLGCDAIPYDRLKTD

MRDIVQAVIGGGSLSQELAQRSWVPKLAIGMIALGEESGDLADVLGYVAHIYNEDTQKTLASITSWCQPVILI
FLGGLIGVIMLAILIPLTSNIQTL

>core/348/4/Org4_Gene847

MHPKIEKRNSLPLTAVAPVFEEASYHPSVATTVDYVDATTLSRHLTVLKDVIKEARNLDLGKAFLTSMKQGFI
NTGTELAIIQASLADQSSRESRKKEEKIFHQHLGKAAPQASTATSGVQPTADPVADKMPLQSAFAYVLLDKYI
PAQEEALYALGRELNLSGYAQNLFSPLLDMIKSFNSAPINYNLGSYISQTSGTANFAYGYEMILSRYNNEVSQ
CRLDIAS TVKAKAALANMSASVKANVSLTDAQKKQIEDIIASYTKSLDVIHTQLTDVMTNLASITFVPGLNKY
DPSYRIVGGDLSIIALQNDEKVLVDGKVDITTA VNEGGLLNFFTTVLTDVQNYGD LAQTQQQLMLDLELKAM
QQQWSLVSASLKLLNGMYTTVISGFKN

>core/349/4/Org4_Gene291

MKKLLKSALLSAAFAGSVGSLQALPVGNPSPDLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFD
RILKVDAPKTFMSGAKPTGSATANYTTAVDRPNPAYNKHLDHDAEWFTNAGFIALNIWDRFDVFC TLGASNG
YIKGNSTAFNLVGLFGVKGTSVAANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGCATLGAEFQYAQ
SKPKVEELNVICNVAQFSVNKPKGYKGVAFLPTDAGVATATGTKSATINYHEWQVGASLSYRLNSLVPYIG
VQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGNTTTLPTSDSFSDFMQIVSCQINKFKSRKACGVTVGA
TLVDADKWSLTAEARLINERAAHVSGQFRF

>core/350/4/Org4_Gene921

MMKQGVGQDAKELYTFLSRGNENYQPCLWFSLEEELGFLFDEKMLCAPLSEDHYCHSYLVDLVDQHLKDLI
LSMFLDPQNISGGELLKVSINIGDSLSPQQQKDFLSMVLRDETEKNVVVVSQGVLSLPATQVCKLVEELNTKD
YSYLNIFSCHADSSPQLLRKELEGTSGRYFTVICTLYLGADMRSLQLASERIMVSREFGLV DAYAARCKLL
KIDHTNWRPGTFSRHADFADA VDVSAGFNSKEFKLITQANQGILESGELPLPSKTFWEGFLAFCDRVTVTRHF
VPMLDAAIKQAVWTHKHPSLIDKECKALDLKTQCLPSIVSYLEYVTNSQEKT SKVPFIQKEIIVDCSPLKEALF
PGSDEDVPSTSEDPSDDHPSDLEDS

>core/351/4/Org4_Gene304

MGTPISGDDGDRNTISDPLEESA AEEGDS DLEDRVSESATQVIETIADTGIPEATPSEG TNSDLNSDLVDRVEY
EARGSLLTMLARIRKAVSQIWMHVKTKRHPKEQGVRSLGDIPCDLLKATRLPKETAEP PFYFALETALASC
RSFFFHVFLRLFTLLRRQHPEAPLDLCGTDPI SPEAAVAFALILRSCCKWVATDAVQEGLPLEVIEEAGIYNAF
SLEATTTVEEVSKRLSELLYSDKRIDGLANVRGITKIITSPYLGAGQCVSVDNLKTYDLGRNYTQVLACASQ
IDEFADKGENEALVMKDILYLVRQDRSKELGDFLMMWSEEHASEVNYDVVLAILEVNLP ILEEDYRSHPLAY
QKKLNYVICQFFCSERLTSIEPKD

>core/352/4/Org4_Gene93

MLHILLAIFCILLFLAFGLTQPSCHGSSKFLKTLNQRFFKDKGREYPPFPSAPTILATLLCILY GALGTKLYTLLP
PKTAHKDLLFWPLYSLSALIAYGFLPPWISTKVPKETTAHLRFLASVFQLGLFPLQLLFYRRRPNQQVRSSTS F
QSQLSEALS AFDNLIVREVMIPKVDIFALPEETTLQEALVLVSEEGYSRVPVYKKNLDNITGILLVKDLLLYT
SSHDLSQPISSVAKPPFYAPEIKKASSLLQEFRQKHRHLAIIVNEYGFTEGIATMEDIIEEII GEIAD EHDVQENTP

YKKIGSSWIVDGRMNISDAEEYFNLKIDHENSYDTLGGHV FHKVGAVPQKGMRIHHENFDIEIITCTERNVGK
LKITPRKRKFNIS

>core/353/4/Org4_Gene360

MAIKNILVVDDEPLLRDFLSELLTSQGFIPDTAENLRNALQMIRTRDYDLVISDMSMPDGSGLDLIKIHKQSSPH
TPVLVVTAYGSIENAVEAMHQGAFNYLTKPFSSEALFAFISKAEEELKNLVHENLFLHSQTTPDSHPLIAESKA
MKDLLAIAKKAASSSANIFIHGESGCGKEVLSFFIHHNSPRANHPIYKVNCAAIPETLLESELFGEKGAFTGA
TTKKAGRFE LAHKGTLLLDEITEVPVNLQAKLLRAIQEKEIEHLGGTKTLSVDVRILATSNRNLKEAIDDKSFR
QDLYYRLNVIPLHLPPLRDRQDDILPLANYFLNKFCRMNNTPLKTLSPKAQELLNYPWPGNIRELSNVLERV
VILENTSLLTEDMLALA

>core/354/4/Org4_Gene767

MHLHEYQAKDLLASYDVPIPPYWVVSSEEEGELLITKSGLDSAVVKVQVHAGGRGKHGGVIVAKSSAGILQ
AVAKLLGMHFTSNQTADGFLPVEKVLISPLVAIQREYYVAVIMDRKHRCPVLMLSKAGGMDVEEVAQSSPE
QILTLP LTSYGHYSYQLRQATKFMeweGEVMHQGVQLIKKLAKCFYENDVSLLEINPLVLTLEGELLVLDSK
ITIDDNALYRHPNLEVLYDPSQENVRDVLAKQIGLSYIALSGNIGCIVNGAGLAMSTLDILKLHGGNAANFLD
VGGGASQKQIQEAVSLVLSDES VKVLFINIFGGIMDCSVVASGLVAVMETRDQVVPTVIRLEG TNVELGKEIV
QQSGIPCQFVSSMEEGARRAVELSM

>core/355/4/Org4_Gene811

MKWFVISCLLGIFSLGLIMVFDTS SAEVLDRSLECSTHKALIRQVTYLILGLGVASLLYMMEW RDFLKISPVL
SGATLALICVFIPGLGICRNGARRWLGF GQLTIQPSEFVKYLVPIVALYFLTFSSLYQKQLKMFLKLTAILFIPIL
LIAIEPDNGSAAVISASLIPVFIMTSVRLRYWLLPLL CVLIAGGALAYRMPYVRYRLNVYLHPELDIKGRGHQP
YQAKIAAGSGKLLGKGPGASLQKLTYLPEAQNDYIAAIYAEEFGFLGMLVLILLYMCFVYGGY AIAIKASSLE
GAALAMVITLIISMQA FMNLGVVSGLLPSKGVNLPFFSQGGSSLIANMCGVTLLLKVYDEENSKSSLGCRRFR
RPHCPSSLGKGSFFS

>core/356/4/Org4_Gene417

MSSVNQSSGTPNPEEVTSPESTEENKNVVSSDEAQATHAVALPIVTQLSLPEGVGTSP EETASNPKVDEIVA EV
SSSRAVVDQISSLVERVGELLDDLQGVQSLFTSFQSELKNCLPAWKSSTRRLETRGAGDNADIARLELFRSDY
EAVLDHVNQFHGDAHLTSLKLTDIHHKLQGNSREDLFLAFDNNDRVLEHLGSLGLDVDAEGNWSLSCERGI
PRLVLTADSM LVQIKKVNLP TVEELRTLQGTTESSDPRVEESLSCERLLNELRRLWANFVGVFISSCYDNIVF
VLMWIMRRINLLPGQGCLPFHNP DASQEDHRSSSGERSTRRERLSRRSDLSEEEMIVRAEGESIHPESPHGDGR
NQPSRGDKQDSDSEEETEL

>core/357/4/Org4_Gene841

MEKPQNRKAPRIFWLNNQVAIPPSERVKESYALHSDIFSLPPGSALKLA EKTEESIRQLVGLKD SHIFRVPHFP
HV VHVLAALVENLSMFQGRNHIILPAHDQQLINSLCRHQGLGTTYDWVTVNHEGRIVEEQ LIETLSPRSLLF
SLSAAHGLTGVIQPLDLLSLCKDRRILLHLDISDILGRAPLTPEILNADIITFSSVALGGMGSIGGIFIRKSLERV
FSSWFPHTSASLCFSAVAAMQTACEERISALPLFTFHTSNLCKKLIQELQSVLPSIQLAFSEVQNRLPNIVVAA

IPDIPAESLAFHLHQGGIYPSLGYERFQPLAQVLQNCGISPFLCHSALHFSLTERSKDLEFSKLARAMHDAVKH
LTPLLGSSS

>core/358/4/Org4_Gene305

MILDFQFSIGYYLRVLELAIRDGTRILAYDRKRLLLDWVPVNDPLPTNYDTSVSTIRQVIHELFSWSAISYSISS
RLLAIHELRLHEEKPQTGWLYRLFFPSKYHIKKAIVDKLCMFKSLILFESKRPVDKIVHAANKVFSKGKSNFSS
WEDFTHEVTVSEVQTPLAGEVQGRLAADASLQMIIEALTTLLEGHTAYLPLSLELLNQFIGEKAQPLKTLSEK
SYVLLRELIQLFSWSAEDFQTIIMSIIISDSLSEVLANSIGNQPLTFHGKTFVGLWQETALVSPEDSKLALGFLA
EVLRKVIVEKKLHVSKSDNTTPEEVGNIYSIRDQNPALWDKMITMLLMRWLLDYDRDIGIALRKAAEYYNPH
PSFWRQFLRLWQRRP

>core/360/4/Org4_Gene567

MSAMISLSSSHEASIASNTQVRDVLVSLAMDEFVEHNTEILPIKVFLARGTLSSTAIIDDLKDVVETEGEHHFQ
VYSNISLKMIIYQRFEEKIFGIGCCPLLLVTDSSHDTPCGALITGIFAAVLFTVLAIVFGPTLGILCYSAYKIYQLT
KKISSLSRTHTEVINSVQKSDPFIHRSGAVAAAAASQSTIKACKVFRQSTLIFFVLGLIITISLAALIVGLVFALFF
LGPGAPAVMTAAMIGCCAAGGTGILLSVIGFLLASVYSVQKSKEGVHHMHTALLRCMVSNTIIQMPYLPITP
GTKKVLTQSIRRYQQFFSDDEYRDIESEVPLTPPPSYETLFHEEGSDGSSNVIPRESPPAYSTIDSSNSFPSSSP
PYYR

>core/361/4/Org4_Gene996

MSETHITTPHVVKLISNFFQKKLFSSISTAYPLVIITDVSQQHLLGPILDHIKMLGYQVIVLTFPPGEPNKTWET
FISLQYQLVDQNISPKSSIIIGGGTVLDMTGFLAATYCRGLPLYLIPTTITAMVDASIGGKNGINLRGIKNRLG
TFYLPKEVWMCPQFLSTLPREEWYHGIAEAIKHGFIADAYLWEFLNSHSMKMLFSSSQILHEFIKRNQCIIKAAIV
AEDPYDRSLRKILNFGHSIAHAETLAKGTVNHGQAVSVGMMIETRISLAEGVMKTPQLIDQLERLLKRFNLP
STLKDLQSIVPEHLHNSLYSPENIITYTLGYDKKNLSQHELKMIMIEHLGRAAPFNGTYCASPMEILYDILWSE
CHVMRHC

>core/362/4/Org4_Gene721

MSCQQFLIEALARRKSKHTYRSLSLNSHLIDFTSNDYLGFASSPELRKEYITKLHAIESLGATGSRLLTGHSQLC
QRIEEQLAAYHNFESCLIFNTGYTANLGLLYALATDQDRILHDLYIHASIYDGIRLSKAQSFPFNHNDLNHLEK
RLASSHLGRTFVCVESVYSLHGSAVPLQAISELCERY SAYLIVDEAHAVGVFGDQGEGLVSALGLQDKVLAT
VYTFGKALGTHGAAIAGSSILKDYLINFCRPFIYTTAQPPHALTAIELAYEHNQRAFNQREHLSALIIHFFREKA
QNLGLQLMKDNTTTPIQSICVSGSHRARQAALQIQNSGYDVRPIVSPTVKQREELLRICLHAFNTKNEIDHLLH
TLEQIFLCNVSSL

>core/363/4/Org4_Gene538

MSCFNLTSTNESLRPISPKASFQGWQSYFRSALRKHSNTLSVSVCKVNKYDVNLFVRLTVIALAVVGVLI
LFSIMLASIQGTLVITSWPLVTAAILIPTILLTGGMYLHRLGKKVDVISGVCIPPFSSRCWVPISCSHTLEKFDE
KHVSACSYPDISTLSADGSGIAAVYQCPPLLFRAFPFCGIPCAMPFVALLRMIYNLIRFLVVPFYIIFRMIYEHFF
CKHLPEDDRFICKDIAREMGRSLAAFLKAPFYASACMIGAFYSLLDPLAGRVLMGSVERDWNNDNVILARSVS

LANEAHSLFRFEGGGGRKGLGQHAFYMLCCQPQSVFLFDKGEIVSGAHPSIQLPERRGLDTSGRYPHISVIPD
SGNDSAKNFIV

>core/364/4/Org4_Gene303

MGINPSGNRSPDDVWVRGAQGDSSSTQGTGATNSNLGAHNVTSTSQPQVASRAKQLWQMVKEFFLGKKS
PDSSQGASGPAMQSPSGPTIRPTRPAPPPPTMGGVNAKRPATHGKGPAQPPTTGSSSGSEQPTAMSPEVVKL
VSELKDAVHSHAESQKVLKKVSQELQTKWSDWENNKGPDYSLHGYYRVVTRALQQTYTEQSMLIEGTSSTGP
VPQAVTVAKDAVTQTVREAVKNLENPKPGNDPDGVLMQVVTSLGIEGPTLDPGESIQNFLETRVSDFGGDDS
DIDYTGDIARLGAALDRVRENHPNEMPRIWIALARELGAAVHSHATSVRIANAGKNHTRDVVRMANESSRL
LQGMKVLSVGAWANTMTVLIGDLFE

>core/365/4/Org4_Gene797

MIPSPTPINFRDDTILETDPKPSLIMFSSKKTEIASERRKAHPTLFKVLGTIWNIVKFIISIILFLPLALLWVLKKTC
QFFILPSSIISQSMSTAVAIRRMFTLSHIKQLLSLKEISAADRVVIQYDDLVDLSLAIKIPHALPHRWILYSQGN
SGLMENLFDRGDSSLHQLAKATRSNLLVFNYPGIMSSKGEVKRENLIKSYQACVRYLRDEETGPKANQIIAFG
YSLGTSVQAAALDREVTGSDGTSWIVVKDRGPRSLADVANQICKPIASAIKLVGWNIDSVKPSERLRCPEIF
IYNSNHDQELISDGLFERENCVATPFLELPEVKTSGTKIPIPERDLLHLNPLSPNVVDRLAAVISNYLDSNRKS
QQPD

>core/366/4/Org4_Gene507

MKHLAVLGSTGSIGRQTLEIVRRYPSEFKIISMASYGNNPRLFFQQLLEEFAPLAAAVYNEEVYNEACQRFPHM
QFFLGQEGLTQLCIMDTVTTVVAASSGIEALPAILESMKKGKALALANKEILVCAGELVSKTAKENGIVLPI
DSEHNALYQCLEGRITIEGIKKLILTASGGPLLKNSLEELSCVTQKQDVLNHPINWNGSKVTVDSSTLVNKGLEII
EAYWLFGLNVEILAVIHPQSLIHGMVEFLDGSVISIMNPPDMLFPIQYALTAPERFASPRDGMDFSKKQTLEF
FPVDEERFPSIRLAQQVLEKQGSSGSFFNAANEVLVRRFLCEEISWCDILRKLTTLMECHKVYACHSLEDILEV
DGEARALAEI

>core/367/4/Org4_Gene954

MKDLGTLGGTSSTAKTVSPDGKVMGRSQIADGSWHAFMCHTDFSSNNVLFDLNTYKTLRENGRQLNSIF
NLQNMMLQRASDHEFTEFGRSNIVLGAGLYVNALQNLPSNLAAQYFGIAYKIRPEYRLGVFLDHNFSHVPN
NFNVSHNRLWMGAFIGWQSDALGSSVKVSFGYGKQKATITREQLENTEAGSGESHFEGVAAQIEGRYGKS
LGGHVRVQPFLGLQFVHITRKEYTENGVOFPVHYDPIDYSTGVVYLGIGSHIALVDSLHVGTTRMGMEQNFAA
HTDRFSGSIASIGNFVFEKLDVTHTRAFAEMRVNYELPYLQSLNLILRVNQPLQGVMGFSSDLRYALGF

>core/368/4/Org4_Gene834

MEDFSEQQLFFMRRAIEIGEKGRITAPPNPWVGCVVVQENRIIGEGFHAYAGGPHAEELAIQNASMPISGSDV
YVSLEPCSHFGSRPPCANLLIKYKVS RVFVALVDPDPKVAGQGIAMLRQAGIQVYVGIGESEAQASLQPYLY
QRTNFPWTILKSAASVDGQVADSQGKSQWITCPEARHDVGKLRAESQAILVGSRTVLSDDPWLTARQPQG
MLYPKQPLRVVLDSESVPPSTSKVFDKTSPTLYVTTERCPKNYIKVLDSLDPVLLTESTPSGVDLHKVYEYL
AQKKILQVLVEGGTTLHTSLLKERFVNLSVLYSGPMILGDQKRPLVGVLGNLLESASPLTLKSSQILGNSLKV
VWEISPQVFPIRN

>core/369/4/Org4_Gene796

MNLSNRSDILSGIFSNPHVSYFSSTHAKQLSDFSKQHPILTKIVTIIVKIFKLLIGLIILPLGIYWLCQSVCSLALF
PRSSMLYSVLKTCFKKYRLEQEIQDYFVKNLDPSPFKDPAVSESKRITIQDHLTIDTLAIHFSTARPKRWLLISL
GSGDFLEDMIGLKDSLFLSWKELAKLLGANILIYNYPGVKSSTGKLNLENLATAHNLCAYLQDKIQGPGAN
EIITYGYSLGGVVQSAALQKNPFTNSETSWVAVKDRAPHSLPAAANSFFGPIGKLIAVLAGWKMDAEKNSRE
LPCPEILVYSADRFPRSEVGDDIALLPFTLAHAIKRTPFARSKKFIGEVNLLHSSPLKHPTIQKLAEAILLESLSR
KN

>core/370/4/Org4_Gene625

MNTSLKRPLKSHFDVVGSLRPEHLKKTRESLEEGSISLDQLMQIEDIAIQDLIKKQKAAGLSFITDGEFRRAT
WHYDFMWGFHGVGHHRATEGVFFDGERAMIDDTYLTDKISVSHHPFVDHFKFVKALEDEFTTAKQTLPPAPA
QFLKQMIFPNNIEVTRKFYPTNQELEDIVAGYRKVIRDLYDAGCRYLQLDDCTWGGGLVDPRVCSWYGIDEK
GLQDLIQQYLLINNLVIADRPDDLNVNLHVCGRGNYHSKFFASGSYDFIAKPLFEQTNVDGYYLEFDDERSGDF
SPLTFISGEKTVCLGLVTSKTPTLENKDEVIARIHQAADYLPLERLSLSPQCGFASCEIGNKLTEEEQWAKVAL
VKEISEEVWK

>core/371/4/Org4_Gene329

MSDNAHNLLYDKFELPEAVKMPLVEGLPIDKHARFIAEPLERGMGHTLGNALRRALLIGLEAPAIISFAMTGV
LHEYMAIEGVIEDVTNIIILNLKGALLKKYPMQDSSLGRTTQVLKASISIDASDLAAANGQKEVTLQDLLQEGD
FEAVNPDQVIFTVTQPIQLEVVLRIFAIFGRGYTPSERIVLEDKGVYEIILDAAFSPVTLVNYFVEDTRVGQDADF
DRLVLIVETDGRVTPKEALAFSTQILTKHFSIFENMDEKKIVFEEAISIEKENKDDILHKLILGINEIELSVRSTNC
LSNANIETIGELVIMPEPRLLQFRNFGKKSLCEIKNKLKEMKLELGMDLTQFGVGLDNVKEKMKWYAEKIRA
KNTKG

>core/372/4/Org4_Gene485

MNGKSPLALYIHIPFCTKKCRYCSFYTIPYKSESVSLYCNAVIEGLRKLAPIQETHFVETVFFGGGTPSLVSHL
DLKRILKELAPHAQEITLEANPENLTASYLRQLQETPINRISVGVQTFDDSLQLLGRTHSSSVAITALQECHNH
GFSNLSIDLIIYGLPTQSLEIFLSDLHQALTLPITHISLYNLTIDPHTSFYKHKRILVPTIAQEEILAEMSLLAENLLL
SQGFQRYELASYAKPGYPKHNLYYWTDPRFLGLGVSAQSQYLHGERSKNYSRISHYLRAVRKNLPTQETSEI
LPEKERIKEALALRLRLGAYLAEFPSTLISMLTQDVKLQNLFSVHGQFLTLNRQGRLFHDTIAEEIMGYSF

>core/373/4/Org4_Gene374

MSIAIAREQYAAILDTHPKPSIAMFSSEQARTSWEKRQAHPYLYRLLEIIWIVVKFLLGLVFFIPLGLFWVLQKI
CQNFILPGAGGWIFRPICRDSNLLRQAYAARLFSASFQDHVSSVRRVCLQYDKVFIDGLELRPNAPDRWM
LISNGNSDCLEYRTVLQGENDWIFRIAEESQSNILIFNYPGVMKSQGNITRDNVVKSQYACVRYLRDEPAGPQ
ARQIVAYGYSLGASVQAEALSKEITDGSDSVRWVVKDRGARSTGAVAKQFIGSLGVWLANLTHWNINSEK
RSKDLHCPELFIYGKDSQGNLIGDGLFKKETCF AAPFLDPKNLEECGKKIPVAQTGLRHDHILSDDVIKEVAG
HIQRHFDN

>core/374/4/Org4_Gene581

MALKFHLLHKSKKSQARVGQIETSHGVIDTPAFVPVATHGALKGVIDHSDIPLLCNTYHLLLHPGPEAVAKL
GGLHQFMGRQAPIITDSGGFQIFSLAYGSVAEEIKSCGKKKGMSLVKITDEGAWFKSYRDGRKLFLSPELSV
QAQKDLGADIIPLDELLPFHTDQEYFLTSCSRTYVWEKRSLEYHRKDPRHQSMYGVHGGLDPEQRRIGVRF
VEDEPFDGSAIGGSLGRNLQEMSEVVKITTSFLSKERPVHLLGIGDLPSIYAMVGFIDSFDSSYPTKAARHGLI
LSKAGPIKIGQQKYSQDSSSTIDPSCSCLTCLSGISRAYLRHLFKVREPNAI WASIHNLHMQVMKEIREAIL
KDEI

>core/375/4/Org4_Gene795

MAPIHGSNAFVEDILHSHPSQATYFSSTHAQKLHEFKDRHPVLTIRASVIIKIFKVLIGLIILPLGIYWLCQTL
TNSILPSKNIEENLLTIFKKKPNTKTLRTNYLRALQDYSSKNRVASMRVPILQDNVLIDTLEICLSQAPTNRWM
LISLGSDCSLEEIACKEIFDSWQRFAKLIGANILVYNYPGVMSSSTGSSSLKDLASAHNICTRYLKDKEQGP
GAK EIITYGYSLGGLIQAELRDQKIVANDDTTWIAVKDRCPLFISPEGFHSCRRIGKLVARLFGWG
TKAVERSQDL PCLEIFLYPTDSLRRSTVRQNKLLAPELTLAHAIKNSPYVQNKEFIEGRLSSDIDPIDSKTRVALATPILKKLS

>core/376/4/Org4_Gene491

MSTTEPNLTNVNLTMPISSKSMPTQLASHKLKGLDLVAFILIIGIAVSSGTAAIILGIPLLILTALAVLA
FSILLY FLLREPKSPISVTHQPTPIIKDIDLPPVPPLALTPVPTEAMLEEPPLPSPRTHQTLLQENWDRIPDLQANTDMPFI
AADNQTYGAWHLKNSNLTLISTLGPKEPRYKTQGIVMIVNAATPNMANNVKGTSALAKATSVRCWEN
SK KSPDPLRSKQPLQLGECRSGKWENLNGTTNAGKAGLPQFLGQLLGPKASDYNYNPNDAFTFCRQAY
LNCLN EAKRRKTTVVQLPLLSSHFPSSPKDEETSLRLQWIDGVKLALIDALQTFGSEAENQNQPWV
IILTTLARHPLI TP

>core/377/4/Org4_Gene284

MAVAADPSASWLKSRNDFLSSLGKTEEQVAAPQFPKELCQHKIREKFRLEDVQVSIKFRGSITAVEATKEFGV
HLLIQPMVVQPWEVENLLFLTSEEDLQELMVAVFDDASLASYFYEKDRLLGFHYFVAEACKLFEELQWVP
SLSAKVGGDAIFTATSLQGSFQVVDISLRDLGKNVRCRLLLPEDTFQSCQKFFSGLHDESDLHNIDQTQ
QISLS VEVGYSQLTQEEWHQVVPGSFIMLDSCLYDPETEESGALLTVQKHQFFGGRFLTPSSGEFKITSY
PNLTHEDP PLPENPQAPAAPLPGYSLVVEVARYSLAVSEFIKLNLSILSLGNHPAYGVDIILDGAKVGR
GEIIALGDVVLGIRVLEV

>core/378/4/Org4_Gene475

MIYLDNNAMTPPERGLLEFLQKTFLIEGTYANPSSVHQLGKKSRQLVLEASHWMQKVLSFQGRVLYTSGATE
SLNLAIASLPKDSHVITSGSEHPAILEPLKHSSLSVSYLNPEEGRCVLTIEQIERAVTPKTSAILGWVN
SETGAK ADIAAIAHFAQEQLQFIVDATAIVGKERIVLPSGVTMAAFSGHKFHALLSGIGALLVSPGVKL
HPQLWGGGQ QGGLRAGTENLWGIASLLYIFKYLDLHQRISQEILTHRNGFENAIKARIPDVHIHCADQPR
ANNVSAIAFPPL EGEVLQIALDIEGVACGYGSACSSGATAPFKSLVSMGVDEELTLATLRFSSHLLQED
VERAVGIIKVVVERL KNS

>core/379/4/Org4_Gene947

MTTSDVIDFVTNDFLGFAVSPTIYCEVSKRFQIHCQQFPHEKLGIRGSRLMVGSSSVIDDLEAKIASYH
GAPNA FIVNSGYMANLGLCHHVSRSTDVLLWDEEVHMSVVHLSLSAISGQHHTFHNDLEHLESLLQCYRI
SSKGRIFI

FVSSVYSFRGTLAPLEQIIALSKKYHAHLIVDEAHAMGIFGDDGKGLCHALGYENFYAVLVITYGKALGTMG
ASLLTSSEVKYDLMQNSPPLRYSTSLSPHTLISIGTAYDFLASEGEIARKQVFKLKEHFHECFDSHAPGCVQPIF
LPHTCLEEAISVLETTGIHVGVAFAKHPFLRVNLHAYNTVDEVNLLAQVMKPYLEKSSHRVHINHEFHLWR
ELCQH

>core/380/4/Org4_Gene764

MEVYSFHPAVRTSFQHRVMAGLDNWFFLGGYRLKVVFLDKNNCGWACQKLVSISKTEKILKILSYLLVPIVL
IALLIRCFLHARFKCTWNRDSLIDSRVPSDVRPFHDFRLFNNQERLNIWKNRIYVSGVDVLVASVDYLKSQFS
GFNHIPKAIRCENYVRNGQFSEEGKKSYLGRMLTHIVGYILSVDETYWEDVILKIPAMNILSEAAYSRSVSTDP
NYQHHGVYLFDLKSLQVPARHVLGEGNMLNTAKWMHIRAERPGKEGECIAKQFLKDYCKKHLEVMNCPDF
IESLLDEKIREFHCPSVLNSAVCDIIDHKCQEHLKAIINEANRRLPGMKNSSFTMCGDQVLFYTVFSPPKLPPA
ASSAYF

>core/381/4/Org4_Gene409

MTTCLPQPPKTSPLYSIFEKLDQAERLSSDALHLLLLTNKEDQRTLWNFADQVRKQRVGDTVYYSSSTLYLY
PTNFCDFSCFKCSFYAKPGDPKGWLYSPNHLLQQIQNIKTPIEVHIVGGCFPSCNLQYYSDLFTKIKEYDPQIH
IKALTAIEYAYLSDLDNLSIRDVLLTLKDAGLDSIPGGGAEILVDKIRNFLAPKRLSSSDFLNIHKMAHQLGIHS
NITMLCYHKEGPEDLVTHMVKVRDLQDETQGFKNFILLKFAQENNVLGKRLRKSGQGHAIPKSLMAVARIF
LDNFSNMKALWNYLGIEAALDLLSCGANDLSSTHMGEKVFQMASSKEPIKMDAEGMAALITQQGRTPCLTN
SSHV

>core/382/4/Org4_Gene972

MRRQVREIMQRTVIVAMSGGVDSSVVAYLFKKFTNYKVIGLFMKNWEEDSEGGLCSSTKDIEDVERVCLQL
DIPYYTVSFAKEYRERVFARFLKEYSLGYTPNPDILCNREIKFDLLQKKVQELGGDYLATGHYCRLNTELQET
QLLRGCDPQKDQSYFLSGTPKSALHNVLFPLGEMNKTEVRAIAAQAALPTAEKKDSTGICFIGKRPFKFLEK
FLPNKTGNIIDWDTKEIVGQHQAHAHYTIGQRRGLDLGGSEKPCYVVGKNIEENSIYIVRGEDHPQLYLRELT
ARELNWFTPPKSGCHCSAKVRYRSPDEACTIDYSSDDEVKVRFSQPVKAVTPGQTIAFYQGDTCLGSGVIDVP
MIPSEG

>core/383/4/Org4_Gene470

MTKIAFSEKAKNFPVEALKKWFENKRSRSLPWRDNPTPYSVVWSEVMLQQTRAEVVIDYFNQWMERFPTLES
LAAAKEEDVIKLWEGLGYYSRARHLLEGARMVMEEFHGKIPDDAISLAQIRGVGPYTVHAILAFAFKRRAAA
VDGNVLRVLSRIFLIETSIDLESTRTWVSRIAQALLPHKSPEVIAEALIELGACICKKVPQCHRCPPVRQACGAW
RENKQFVLPVRHARKKVIFLHRLVAIVLYDGSLVVEKRRPKEMMAGLYEFPYIEVEPEEGLQDIEGFTKKME
LSLESPLEFLGNLKEQRHAFTNHKVHLCPIIFKATSLPQFGELHRLSDIDHLAFSSGHKKIKDALLIYLGDVRS
GESIGV

>core/384/4/Org4_Gene984

MQENLDKRLEVL RTEISLAARSLFDLDDKKQKELQVLEESSEENFWQDSVHAGKISEQIVSLRRQIQEYQELK
SKIDAIEFFLEDADALEDPAICEDLEKEFLFCEKKLAVWETQRLLSGEADKNSCFLTINAGAGGTESCDWVEM
LFRMYSRWATKHQWALEVVDRLDGEVAGIKHVTVKFSGMYAYGYAKAERGVHRLVRISPFDSNGKRHTSF

ASVDVFPEIDDDQIKIEIRPNDLRIDTFRSSGAGGQHVNVTESAVRITHLPSGVVVSCQNERSQIQNRESCMKML
QAKLYQQVLQERLEKQSLDRKDKKEIAWGSQIRNYVFQPYTLVKDVRTGHETGNVQAMLDGELLDEFIKAY
LAEFGEVS

>core/385/4/Org4_Gene672

MAVEGRVNSSQALNQDCQEVLANQSKGLLRCRILSIVVAVITFIAGVVLIALTASILTSVPYLALGVFLLLV
TLGCIIFALCSEKIKKVPPTPISHKEEIIAWFEERKNIDMEKEKEDPEHFGRTATDIPMRSALDQFNHSCHHIHES
PTLTETRYRGHQDVLLFKDWCPVTLPDVTSEEEVLIRSVVGSYLLIEACVPKVSMLIDELHNKLLKSPSERECLFI
DKKTLQRKASFLFTQKDLATFFLAYTRVNDGHLAPFRAGAKWILIHVRLRRQHNQNDFFTPGHSCYYARL
AFNQTQRLYHQLFNVEKLRSIYANMEKDPLCHPWAFIPIYDLLKTEDHGDGFLEQQEDREYPSRAAQDQFW
G

>core/386/4/Org4_Gene185

MSPHRNLFKLKNFSNRLYNRALGRFDKVFNFSSGNVIGDLGTANTLVYVRGRGIVLSEPSVVAVDAQTHAVL
AVGHKAKAMLGKTPRKIMAVRPMKDGVIADFEIAEGMLKALIKRVTPSRSVFRPRILIAVPSGITGVEKRAVE
DSALHAGAQEVLIEEPMAAAIGVDLPVHEPAASMIIDIGGGTTEIAIISLGGIVESRSLRIAGDEFDECIINYMR
RTYNLMIGPRTAEIKITIGSAYPLGDQELEMEVRGRDQVAGLPITKRINSVEIRECLAETPIQQIIECVRLTLEKC
PPELSADLVERGMVLAGGGALIKGLDKALSKNTGLSVITAPHLLAVCLGTGKALEHLDQFKKRKGNLV

>core/387/4/Org4_Gene508

MKFVVSRNELGNLIKKIQSVVPQNTPIPVLTHTVLIETYNDELVFTATDLTVSTRCVTKAKVYEKGAISIPSKRF
FQLVKELTEANLEISSSAGEMAQITSGSSCFRLLSMEKEDFPMLPDIQNALRFSLPAEQLKTMQLQRTSFAVSRE
ESRYVLTGVLLAIANGVATIVGTDGKRLAKIDAEVTLDKSFSGEYIPIKAVEEIIKMCSDGEATIFLDQDKIA
VECDNTLLITKLLSGEFPDFSPVISTESNVKLDLHREELITLLKQVALFTNESSHSVKFSFLPGELTLTANCTKV
GEGKVSMVAVNYSSELLEIAFNPFFFLDILKHSKDELVCLGISDSYNPGIITDSASGLFVIMPMRLHDD

>core/388/4/Org4_Gene222

MLIWKRHLLTRFWFALTSLVLALIFYASIHHSHTLKGASTAASGASVKLSILYYLAQISLKAFLMPQLVA
VATTSTLFAMQNKREIILLQASGLSLKSLMHPLLLSGAVIMMVLYANFQWLHPICEKISITKENMDRGTDDKE
QGKIPALYLKDQTVLLYSSIEPKTLTLNNVFWIKDPKTIYTMEKLAFTTSLPIGLNVTQFFANDSENLELKEFF
DMKEFPEIEFNFYENPFSLKFSAGNKNRLSEFFKAIPWNATGLGLSTQVPQRILSLLAQFYVVLISPLACMAAII
LSAYLCLRFSRTPTVTLAYLIPLGTVNIFFVFLKAGIVLASSSVLPTLPVMAFPLIVLFLLTNYAYAKLQ

>core/389/4/Org4_Gene104

MKFPRISISDLIPTQMVIWWRGGGNVHYVPNAQNLPKKILGGVLACFGLALLGCAAFAGVCQTIFPCIGLMI
LGLVLLGFAYLQYSKGWSRFRPLFRETKVFEKPINWLGCSSLQSWKKIRPGCYYPGCPQVEICEGSQEIV
TKIFQKKS DRNTSIFLIQEMDQIALRQGIEKSSLSRKTF AIDPSVVSSLLSEIQREEQQYLDPKVISWSSDQASD
RTHPKSAIYVNISDAAQEPQGRCYIDAYTKAFFTVLDQIGDPNIVKKHTIYVLTPILGVPDALPKEEQENLKL
SQAFLYSAEQVAKRMREEKQDSIRIKFIFTDPTSPTSLSLYFSPHSSSTPHSVTPISLSGFVGEQESYTFA

>core/390/4/Org4_Gene879

MSKKITVLGYLKLRTLFRRLVLCAAALSNIGYASTSQESPYQKSIEDWKGHTFTDLELLSKEGWSEAHAISGNG
SSIVGASGANQGSATAVIWESHLIKHLGTLGGEASSAEGISKDGEVVVGWSDTREGHTAHFVFDGRDMKDL
GTLGATYSVARGVSGDGSIIVGVSATAHGEDYGWQVGVKWEKGKIKQLKLLPQGLWSEAHAISEDGTVIVG
RGEISRDHIVAVKWNKNNAVYSLGTLGGSVASAEAISANGKVIVGWSTTNNGETHAFMHKDETMHDLGTLG
GSFSVATGVSADGRAIVGFSVKTGEIHAFYYAEGEMADLTTFGGEEARVFDISSEGNDIIGSIRTDAGAERA
YLFHIHK

>core/391/4/Org4_Gene399

MKKRFPSTLFLFYRRVTIAISLEGILGWGWLGSLLSKVFAFLVACWNRFSWSTPYRARSTVISVGNIVVGGAG
KTPTVLWLAEALRLRGYSCGVLSRGYKSQSSRQKKLTVVDSKVHSASYVGDEPLLMAEKLPEGSVWVHKD
RRISAARAAEKFDILLDDGLQYRKLHKDVEIAVVNGQDPLGGRAFFPKGRLRDFPLRLKTVDAIIVNGGGKE
AGTVVKRVSNAPQIFVKPTIASVVWTHNGERIPKEALRELRVGVFCGLGFPQGFLNMLREEGIHILGKYLLPD
HAAITKKELNYFCQQMAMRQGQGLLCTEKDSVKLPRLSGEVSLPIAKVEMRLSVNQDDTLSLLNMIEQIHK
NRGN

>core/392/4/Org4_Gene362

MNVPDSKNLHPPAYELLEIKARITQSYKEASAILTAIPDGILLSETGHFLICNSQAREILGIDENLEILNRSFTD
VLPDTCLGFSIQEALSLKVPKTLRLSLCKDSKEKEVELFIRKNEISGYLFIQIRDRSDYKQLENAIERYKNIAEL
GKMTATLAHEIRNPLSGIVGFASILKKEISSPRHQRMMLSSIISGTRSLNNLVSSMLEYTKSQPLNLKIINLQDFFS
SLIPLLSVSFPNCKFVREGAQPLFRSIDPDRMNSVWVNLVKNVETGNSPITLTLHTSGDISVTNPGTIPSEIMD
KLFTPFFTTKREGNGLGLAEAQKIIRLHGGDIQLKTSDSAVSFFIIPELLAALPKERAAG

>core/393/4/Org4_Gene61

MSHTECGIVGLPNVGKSGLFNALTGAQVASCNYPFCTIDPNVGIVPVIDERLEALAKISNSQKIIYADMKFVDI
AGLVKGASDGAGLGNRFLSHIRETHAIAHVVRFCDDPDVTHVSGKVNPVEDIEVINLELIFSDFSSAKNIHSKL
EKLAKGKREVGALLPLFDTHAHLEKGLPLRTLTLTPEQIVALKPYPFLTMKPMFYIANVDESSLPDMNDYV
AAVREVAAKENSKVVPICVRIEEIVSLPIEERLEFLMSLGLKESGLHRLVRAAYDTLGLISYFTTGPQESRAW
TVVRGSSAWEAAGEIHTDIQKGFIRAEVITFEDMIECQGAAARELGKLIHIEGRDYIVQDGDTMLFLHN

>core/394/4/Org4_Gene487

MTTEVRIPNIAESISEVTVASLLVTEGALIQUENQGLLEIESDKVNQLIYAPASGRIFWEVSEGDVVPVGGVVGKI
EPAGEGEELGDSQSKETIEAEIICFPQSGVRQSPPENKTFIPLRDQMDQGSQGLSAGDRGETRERMTSIRKTISR
RLLSALHESAMLTTFNEVYMTPLLHLRKEKQEEFLSRYGVKLGFMSSFFVKAVLEALKAYPRVNAIDGEEIV
YRHHYDISIAVGTDRGLVVPVIRDCDKLSNGEIEQKLADLALRAREGLLAIGELEGGGFTITNGGVYGSLLSTP
IINPPQVGILGMHKIEKRPVVDNEIVIADMMYVALSYDHRLIDGKEAVGFLVKVKEDLENPTSLLDL

>core/395/4/Org4_Gene306

MVPFRQHHAYQLLKQLHTSAISEADRVSYFYFKQNRSLGSKDRQWIQNIIFNILRHRRLLETILDSGEQVTPEA
LVAKVNEGVLNLDSSAIPWPVRYISDDLHFLVQDYGEEQAEIIAKIWLTEAPITIRVNTDKISVKELQE
LEYPSCPGELPEALHFSKRHPLQSTEAFFRRGFFEIQDENSQRISQGISLTDKDIVLDFCAGAGGKSLIFAQKAKH

VVINDSRKAILQTAKHRLLRAGARNFSLADQLRLGSFSVVIVDAPCSGTGVFRRHPEHKWQFSKKLLLNYVR
VQKSILKQASAYVGPRGRLVYITCSLLKEENEAHVAYMHSLGWKEVHRKTLPLQVGKGDAFFTSHFQKI

>core/396/4/Org4_Gene713

MKLYQTLRGIVLVSTGCIFLGMHGGYAAEVPVTSSGYENLLESKEQDPSGLAIHDRILFKVDEENVVTTLDVI
HKLNLLFYNSYPHLIDSFPARSQYYTAMWPVVLESVIDEFLMVADAKAKRIATDPTAVNQEIEEMFGRDLSP
LYAHFEMSPNDIFNVIDRTLTAQRVMGMMVRSKVMLKVTPGKIREYYRKLEEEASRKVIWKYRVLTIKANT
ESLASQIADKVRARLNEAKTWDKDRLTALVISQGGQLVCSEEFSSRENSLSQSHKQELDLIGYPKELCGLPKA
HKSGYKLYMLLDKTSGSIEPLDVMESKIKQHLFALEAESVEKQYKDRLRKRYGYDASMIKLLSEEAPPLFS
LL

>core/397/4/Org4_Gene355

MAFKRKTRWLWQVLILSLGLNMLFLLLFYSAIFRKDIYKLHLFSGPLIAKSSRKVYLSEDFLNEISQASLDDLI
SLFKDERYMYGRPIKLWALSVAIASHHIDITPVLSKPLTYTELKGSSVRWLLPNIDLKDFPVILDYLRCHKYPY
TSKGLFLLIEKMVQEGWVDEDCLYHFCSTPEFLYLRTLLVGADVQASSVASLARMVIRCGSERFFHFCNEESR
TSMISATQRQKVLKSYLDCEESLAALLLVHDSDVVLHEFCDEDELEKVIRLMPQESPYSQNFFSRLQHSPRRE
LACMSTQRVEAPRVQEDQDEEYVVQDGDSDLWLIKRFGIPMDKIIQKNGLNHHRLFPKGVLKLPKQKS

>core/398/4/Org4_Gene718

MAVVSTPFFNQNLWYRLLSSRFSLWKSYPFRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP
HQYLSLLQDRYFPIASVMRTLDDKNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ
RIQTLQSNLIAIIRCFWFTVESGLIENHEGRKAYGAVLISSPQELRHAFIDNVRVLPLELDQIIRLPFNTSTPQETL
FSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVLCQ

>core/400/4/Org4_Gene640

MKIDILSLFPGYFDGPLQTSILGRAIKQRLLDVQLTNLRDFGLGKWQVDDTPFSGGGMLLMAEPVTSAIRSV
RKENSKVIYLSPOGALLTAEKSRELAASHLILLCGHYEGIDERAIESEVDEEISIGDYVLTNGGIAALVLIDAV
SRFIPGVLGNQESAERDSLGNLLEGPQYTRPREFEGKEVPEVLLQGDHKAISQWRLEQSERRTYERRPDLYL
NYLCKRSIDHKFDEETTTNRDHFCDKISVVLEVNKLKRAKNFYCKVFGLDAMSCENKFCLPHEGKTIFWLR
EVQAEKKNIVTSLSLDCACEEDFCYLLRRWELFGGKLLLEKQADEHAVWALAQDLGDHAWIFSWHRMK

>core/401/4/Org4_Gene519

MGEKTEKATPKRLRDARKKGQVAKSQDFPSAVTFIVSMFTAFLSLSTFFFKHLGGFLVSMLSQAPTRHDPVITL
FYLKNCLMLILTASLPLLGAVAVVGIVGFLIVGPTFSTEVFKPDIKKFNPIENIKQKFKIKTLIELIKSILKIFGA
ALILYITLKSQVSLIETAGVSPITTAQIFKEIFYKAVTSIGIFFLIVAVLDLVYQRHNFAGELKMEKFVKQEFKD
TEGNPEIKGRRRQIAQEIAYEDSSSQVKHASTVVSNNPKDIAVAIGYMPEKYKAPWIIAMGINLRAKRILDEAEK
YGIPIMRNVPLAHQLLDEGKELKFIPESTYEAIGEILLYITSLNAQNPNKNTNQPDL

>core/402/4/Org4_Gene57

MSEAPVYTLKQLAELLQVEVQGNIEPTISGVEDISQAQPHHIAFLDNEKYSSFLKNTKAGAILSRSQAMQHA
HLKKNFLITNESPSLTFQKCIELFIEPVTSGFPGIHPTAVIHPTARIEKNVTIEPYVVISQHAHIGSDTYIGAGSVIG

AHSVLGANCLHPKVVIRERVLMGNRVVVQPGAVLGSCFGYITNAFGHHKPLKHLGYVIVGDDVEIGANTT
IDRGRFKNTVIHEGTKIDNQVQVAHHVEIGKHSIIVAQAGIAGSTKIGEHVIIGGQTGITGHISIADHVIMIAQTG
VTKSITSPGIYGGAPARPYQETHRLIAKIRNLPKTEERLSKLEKQVRDLSTPSLAEIPSEI

>core/403/4/Org4_Gene402

MSGPSRTESSQVSVLSYVPRDKEIAPKKQFTIAKISTLAILASLALGALVAGISLTIVLGNPVFLALLITTALFSV
VTFLVYHQMTSKVSSNWQKALEQNFKPLGKAWQEKNVDCYSNEMQFYNNHLNPKFKVAIQTDASQPFQPT
FLTGLRVIEKNQSTGIIFNVPVGTNLIDNTATNLSTILYSTLKDKSVWDTCQREGDPAKGEDPFSPTEVVRVK
LPNEALDQTFNLNLSSAEKKSILPTFLGHVCGPKSEELPNQQEYYRQALLAYENCLKAAIESHAAIVALPLFTS
VYEVPP EEILPKEGTFYWDNQTQAFCKRALLDAIQNTALRYPQRSLLVILQDPFNTIESQSRSEE

>core/404/4/Org4_Gene725

MKNSFGSLFSFTTWGESHGPSIGVVIDGCPAGLELHESDFVPAMKRRRPGNPGTSSRKENDIVQILSGVYK GK
TTGTPLSLQILNTDVDSTPYENSERLYRPGHSQYTYEKKFGIVDPNGGGRSSARETACRVAAGVVAEKFLAN
QNIFTLAYLSSLGSLTLPHYLKISPELIHKKIHTSPFYSPLPNEKIQEILTSLHDDSDSLGGVISFITSPIHDFLGEPLF
GKVHALLASALMSIPAAKGFEIGKGFASAQMRGSQYTDPFVMEGENITLKSNNCGGTLGGITIGVPIEGRIAF
KPTSSIKRPCATVTKTKKETTYRTPQTGRHDPCVAIRAVPVVEAMINLVLADLVLYQRCSKL

>core/405/4/Org4_Gene287

MTLPNDLLETLVKRKESPQANKVWPVTTFSLARNLSVSKFLPCLSKEQKLEILQFITSHFNHIEGFGEFIVLPLK
DTPLWQKEFLLEHFLLPYDLVGNPEGEALVVSRS GDFLA AINFQDHLVLHGIDFQGN AEKTL DQLVQLDSYL
HSKLSFAFSSEFGFLTTPNPKNCGTGLKSQCFLHIPALLYSKEFTNLIDEEVEIITSSLLPGVTGFPGNIVVLSNRC
SLGLTEEQLLSSLRITASKLSVAEVA AAKKRLSEENSGDLKNLILRSLGLLTHSYQLELKETLDALSWIQLGIDL
GLIQVTENHPLWNPLFWQIRRAHLALQKQAEDSRDLQKDTISHLRASVLKELTKGLSPESF

>core/406/4/Org4_Gene948

MMKKIRKVALAVGGSGGHIVPALSVKEAFSREGIDVLLLGKGLENHPSLQQGISYREIPSGLPTVLNPIKIMSR
TSLCSGYLKARKELKIFDPDLVIGFGSYHSLPVLLAGLSHKIPLFLHEQNLVPGKVNQLFSRYARGVGVNFSP
VTKHFRCPAEEVFLPKRSFSLGSPMMKRCTNHTPTICVVGGSQGAQILNTCVPQALVKLVNKYPNMYVHHIV
GPKSDVMKVQH VYNRGEVLCCVKPFEEQLLDVLLAADLVISRAGATILEEILWAKVP GILIPYPGAYGHQEV
NAKFFVDVLEGGTMILEKELTEKLLVEKVTFALDSHNREKQRNSLAAYSQQRSTKTFHAFICECL

>core/407/4/Org4_Gene25

MKKKVAEYLNRLAEVEIKISNPEIFSNSKEYSALSKEHSYLLELKNA YDKILNLEKVLADDDKQALAEKDP
VVMLEEGINENKVELEKLNKILESLLVPPDPDDDLNVIMELRAGTGGEAAALFVGDCVRMYHLYASSKGWK
YEVLSASESDLKGYKEYVMGISGTGVKRLQYEAGTHRVRVPETETQGRVHTSAITIAVLPEPSEEDTELLI
NEKDLKIDTFRASGAGGQHVNVTD S AVRITHLPTGVVVTCQDERSQHKNKDKAMRILKARIRDAEMQKRHN
EASAMRSAQVGSGDRSERIRTYNFSQNRVTDHRIGLTLYNLDKVMEGDLDPITTAMVSHAYHQLLEHGN

>core/408/4/Org4_Gene750

MPILWKVLIFRYLKTAAFCTLSLICISIISSLQEIVAYIAKDVPHYDTVLRLMAYQIPYLLPFILPGSCFVSAFSLFR
KLSDNNQMTFLRASGASQSIIMFPVLMVSGAICCLNFYTCSELASICRYQTCKEIANMAMTSPALLLQTLQKK
ENNRIFIAVDHCAKSKFDNVIVALKGNNEISHVGIKSIIPDTTKDVTAKADVVFISKLPDSLTESSSPSSQRFYIE
TLDELLIPKITSTLFAGKSYLKTRTDYLPWKQLVKQSLKSHLPETLRRVAIGFLCITLTYAGMILGIHKPRFRK
SIALYFIFPILDILLIVGKNTKNLPLAFMLFVFPQLVSWVVF AARAYRESRGYA

>core/409/4/Org4_Gene924

MSLLSGHRLEGFPPIAEVMAACDRCSMDFC EILKSQSMDLWADAASRVDGLLQDPFWSTAIASGIAKSSLQE
TEFECESKVMVLSSWGEQGAQVCSPFNLERICMSFP SLKVFS LKKNGCENMGIQLSASCMNLLMSIFFVATN
GGSTPIWITKENLMALVALVLSHYQCYFVPATGDPQRGNILGNPEVNAILARGMGMRVDLERKRGAYRTHK
GKVFAKVHHQERESSSSRYLELAARCFENSLTKTSLSDANNVQERDKCLLQMSTSLMHTAGLNLQRPPVPT
PSGVT AHPQPQDPVVT SQPSSLGARERSPVSSRGRFPVVLPLSVISPRSHPGRVERRDLEDEEEVVMF

>core/410/4/Org4_Gene872

MSHDRILRAQRALSEHNLDAILVEKSEDLAYFLHDEAIA GILLIGQQEVMFFVYRMDKDLYSHIQRVPLTFLT
QDVVADLSLYVQKQRYQKIGFDSASTVYHKFAQRQVLPCLWEPLECFTEKIRSIKSEEEIRRMQEAAALGSA
GYDYVL TLLREGITEKEVVRQLRAFWAEAGAEGPSFPPIIAFGEHSAPHSIPADRPLKKGDIVLIDIGVLLNGY
CSDMTRMTALGTPHPKLLESYPVVVEAQKRAMALCKEGVLWGDIDAEAVRVLREHHLDTYFIHGIGHGVG
RNIHEYPCSPRGSQVKLESGMTITVEPGVYFPGIGGIRIEDTLCIDKNKNFSLTARPVISELVCL

>core/411/4/Org4_Gene514

MNKRQKDKLKICVIISTLILVGIFARAPRGDTFKTFLKSEEAIYSNQCNE DMRKILCDAIEHADEEIFLRIYNLS
EPKIQQSLTRQAQAKKKVTIYYQKFKIPQILKQASNVTLVEQPAAGRKL MHQKALSIDKKDAWLGSANYTNL
SLRLDNNLILGMHSSELCDLIITNTSGDFS IKDQTGKYFVLPQDRKIAIQAVLEKIQT TQKTIQVAMFAL THSEII
QALHQAKQRGIHVDIIIDRSHSKLTFKQLRQLNINKDFVSINTAPCTLH HKFAVIDNK TLLAGSINWSKGGFSL
NDESLIILENLTKRQNQKL RMIWKDLAKHSEHPTVDDEEKEIIEKSLPVEEQEAA

>core/412/4/Org4_Gene165

MNLPDRKKALEAAVAYIEKQFGAGSIMSLGRHSATHEISTIKTGALSLDLALGIHGVPKGRVIEIFGPES SGKT
TLATHIVANAQKMGGVAAYIDAEHALDPSYASLIGVNIDDL MISQPDCGEDALSIAELLARSGAVDVVIDSV
AALVPKSELEGDIGDVHVGLQARMMSQALRKLTATLSRSQTC AVFINQIREKIGVSFGNPETTTGGRALKFY S
SIRLDIRRIGSIKGS DNSDIGNRIKVKVAKNKLAPPFRIA EFDILFNEGISSAGCILD LAVEYNIEKKGSWFNYQE
KKLGQGREFVREELKRN RKLFEIEKRIYDVIAANKTPSVHANETPQEVPAQTVEA

>core/413/4/Org4_Gene806

MNLCKRISFEEGLELFVSSPIERLQERADAIKERYPSNEV TYVLDANPNYTNICKIDCTFCAFYRKPKSPDAY
LLSFDEARSLLQRYVSSGVKTVLLQGGVHPRLGIDYLEELVRITVQEFP SIHPHFFSAVEIEHACRVSGISIEQG
LQRLWDAGQRTIPGGGAEILSERVRKIISP KKMQPGGWINLHKL AHLMGFRTTATMMFGHVENPEDIL IHLQ
TLRDAQDSCPGFY SFIPWSYKPGNTALRRNVPQQASIETY YRILALGRIFLDNFDHVAASWFGEGKSLGAKAL
HYGADDFGGVILDES VHKATGWSIQSSEEEICNIIRSEGFIPVERNTFYQHISCTVSSL

>core/414/4/Org4_Gene801

MKYSLNFKKIDYERVIEVTCSEVRLHAIHQTAVGPALGGVRASLYSSFEDACTDALRLARGMTYKAI
SNTGTGGGKSVIILPQDAPSLTEDMLRAFGQAVNALEGTYICAEDLGVSINDISIVAEETPYVCGIADVSGDPSI
YTAHGGFLCIKETAKYLWGSSSLRGKKIAIQGIGSVGRRLQLSLFFEGAELYVADVLERAVQDAARLYGATIV
PTEEIHAECDIFSPCARGNVIRKDNLADLNCKAIVGVANNQLEDSSVGMMLHERGILYGPDYLVNAGGLLN
VAAAIEGRVYAPKEVLLKVEELPVVLSKLYNQSKTTGKDLVALSDSFVEDKLLAYTS

>core/417/4/Org4_Gene48

MLNIHDILGNDDENLLSYQCKHITKDKLTLPSHDFVDKVFGLSDRNNRVLRLSLQTMFSHGRLANSGYLSILPV
DQGIEHSAGASFAINPIYFDPENIVKLAIESGCSAVASTYGTLSLLSRKYAHKIPFMLKLNHNELLSYPTKYHQI
FFTQVEAAYSMGAVAVGATVYFGSETSNEEIVAVSNAFAKARSLGLATVLWCYLRNPAFVANGVDYHTAA
DLTGQADHLGATLGADIVKQKLPTCQGGFKAINFGKTDERVYSELSSNHPIDLCRYQVLNSYCGKVGLNSG
GPSGKNDFTEAARTAVINKRAGGMGLILGRKAFQRPLSEGIQLNLVQDIYLDPNITIA

>core/418/4/Org4_Gene197

MIPLIPMFLKQSLFFSLALTGMTTLVLTVALGVPVMKWLKRKNYRDYIHKEYCEKLEMLHKDKAEVPTGGG
VLLFISLIASLLVWLPWGKFSTWFFIILLTCYAGLGWYDDRIKIKRKQGHGLKAKHKFMVQIAIAAFTLIALPY
IYGSTEPLWTLKIPFMEGMLSPLFWLGKVFCLGLALVAIIGTSNAVNLTGGLDGLAAGTMSFAALGFIFVALR
SSTPIAQDVAYVLAALVGACIGFLWYNGFPAQLFMGDTGSLLGGLLGSCAVMLRAECILVVGGVFVAAEA
GSVILQVLSCLRLKKRLFLCSPLHHHYEYQGLPETKIVMRFWIFSVCAGLGIAAVLWR

>core/419/4/Org4_Gene730

MRIAVLGAGYAGLSVTWHLHLSQGTATIDLFDPIPLGEGASGMSSGLLHAFTGKKALKPPLADQGINATHA
LITEASKALNPVIVISQGILRPAIDEDQAQLFMKRVEEFPKEVEWWEKARCEISIPSMVIPPNLGALFIKSGVTL
NNDLYIQGLADACMKLGTQFYDELIEDLADIEEFYDHIIVTPGANASILPELKDMPVNKVKGQLEISWPKDL
AMPSFSINAHKYMVANTQKNTCILGATFEHNQPEETPDPAIAYQEIMPPVLSLFPGLKDAQVLHCYAGMRSSS
KSRLPVISRISEKLWFLGGLGSKGLLYHGITGDMLAQAVLRKSTAYIAKEFLFTI

>core/420/4/Org4_Gene204

MILLQNIKRCSLKQLKVLATLLLSLSLPTLEAAENRDSDSIVWHLDYQEALQKSKEAELPLLVI FSGSDWNGP
CMKIRKEVLESPEFIKRVQGKFVCVEVEYLKHRPQVENIRQQNLALKSKFKINELPCMILLSHEEREIYRIGSFG
NETGSNLGDSLCHIVESDSLLRRAFPMMTSLSLSELQRYYRLAEELSHKEFLKHALELGVRSDDYFFLSEKFR
LLVEVGKMDSEECQRIKKRLLNKDPKNEKQTHFTVALIEFQELAKRSRAGVRQDASQVIAPLESYISQFGQQD
KDNLWRVEMMIAQFYLDSDQWHHALQHA EVAFEAAPNEVRSHISR SLEYIRHQS

>core/421/4/Org4_Gene384

MYLQEKFKAQVPLVLRELLSCSDSINDSDPVYRIVFDSNDTTISYKVGDALGVLPENSKEVSEHVLQLLGYS
PTTLVNVKKTSEKVSQAQFIQGYVDLDKIPAKLNSFFPKDPKITLYDAIQEYHPQIPIELFAESVFPLLPFRFYI
ASSPDLHPKSIELLVKHVSYPGKYQKRFGVCSSFLCSELQVND SAYIFVQPTKHFTLSTQIEGKPLVMIGAGTG

IAPYKAFLEERLFNKDPGNNLLFFGERKEKVNFFYYREFWNHSEEEGKLKLFLAFSRESQKVVVQDLLRIQK
DEV RKAYEEGGFFVFCGRKVLGIEVKHALEEILGKDTLASLRKEHRYVVDVY

>core/422/4/Org4_Gene531

MDVSRKINRHTQFYVDSIDGVIKKFDQKPSSEKSRDHEELEEKLLTITKRIVASAEFQNRKTDSKNYYLKKT
QWLPFKNEELEQTKELFAMLTSMKKIAQLFFYSPGCSSDWVEFTEVICHNLNDSIGLGGVLLCCGLFEQQCEH
VVTVNKKLDLPLLLGTTVVNSLRYYLTYRNLNLCQSMSELGKELGDVLKQHGVAFTLIFKEIVDIDLLNYA
KLIQGLKRSGNIQARIYDNDVPTLPSVSSSPIALRYS LANTIRGLALHVD FSSLKFISPSILSNTEHTAKALNSGG
ECFIFSNLDEFNLGMKIVMQLLRTGKISPEILNKNIMKILMIKRRVRSLYI

>core/423/4/Org4_Gene218

MEADILDGKLKRVEVSKKGLVNCNQVDVNQLVPIKYKWAWEHYLNGCANNWLPTEVPMARDIELWKSDE
LSEDERRVILLNLGFFSTAESLVGNNIVLAIFKHITNPEARQYLLRQAFEEAVHTHTFLYICESLGLDEGEVFNA
YNERASIRAKDDFQMTLTVDVLDPNFSVQSSEGLGQFIKNLVGYYIIMEGIFYSGFVMILSFHRQNKMTGIGE
QYQYILRDETIHLNFGIDLINGIKEENPEVWTTTELQEEIVALIEKAVELEIEYAKDCLPRGILGLRSSMFIDYVRH
IADRRLERIGLKPIYHSRNPFPWMSETMDLNKEKNFFETRVT EYQTAGNLSW

>core/426/4/Org4_Gene647

MELSLTSLPLAWYVILGVAVFAYSFGDGF DLGLGAVY LKAKEDKERRILLNSIGPVWDGNEVWLVIIVGGL
FAGFPACYATLLSIFYMPIWTLVLLYIFRGCSLEFRSKSES VSWKTFWDIIFICSGTAISFFLGTIVGNLILGLPLS
PDTSYASLSWILFFRPYAALCGAVVASAF AIHGSCFALMKTSDSLNARIAQQFPYILSSFLVFYVFLGASLISIP
KRFDAPPTYPLILLIALTSCCCVAAKTSVSKKRYGYAFIYSTLNLLSLILSAATLTFPNILLSTVDPQYSYTIYN
SAVETKTLKSLLIHVLIGLPFIITYTCYIYRVFRGKT NFPSIY

>core/427/4/Org4_Gene846

MNSKMLKHLRLATLSFSMFLGIVSSPAVYALGAGNPAAPVLPGVNPEQTGWCAFQLCNSYDLFAALAGSLK
FGFYGDYIFSESAHITNVPVITSVTTS GTTPTITSTTKNVDFDLNNSISSSCVFATIALQETSPA AIPLLDIAFT
ARVGGLKQYYRLPLNAYRDFTSNPLNAESEVTDGLIEVQSDYGIVWDL SLQKVLWKDGVSFVGV SADYRH
GSSPINYIIVYNKANPEIYFDATDGNLSYKEWSASIGISTYLNDYVLPYASV SIGNTSRKAPSDSFTELEKQFTN
FKFKIRKITNFDRVNF CFGTTCCISNFFYYSVEGRWGYQRAINITSGLQF

>core/428/4/Org4_Gene978

MMEVYSFSPSVRTSFQHRVMAGLDNWFFLG GHRLKVVS LDSCNSGRVCEEYVPISMTEKILKILSYLLIPV II
ALLIRYLLHSNFTAKVSPKPWLKTLQLGIDIKSFILPSSHVNTMDSATL FKAHLEGKRVDVEYHRLHSSDKV V
FYIPAQKL PDDLRLTHWLPEKETRKTEYVRHMLAHVMGYLTSQGKERLQQV VQDSRSSTSLGAEKVLQYRF
IDHPQSQGEFQRLLENITTKGSEDKEVVQSDLFDMAFQCWWPQFISVIQSPTFSEELVHEMSQKLDLDCIYPE
DDEFEQTF LNTLLKAVLYHGFQGISVASMGVIFLICLDSLELQIPFLRNQK

>core/429/4/Org4_Gene876

MNKKKRVL TGDRPTGKLHLGHWVGS IKNRLELQNSPEYDCFFIADLHTLT TTKIRKEEVLDVDNHIYEV LAD
WLSVGIDPTKSIHYLQSAIPEIYELHLLFSMLISINRVMGIPSLKDMARNASIEEGGLSYGLIGYPILQSADILLAK

AQFVPVGKDNEAHVELTRDIARNFNRLYGQVFPEPEVLQGELTSLVGIDGQGKMSKSANNAIYLSDS DATITE
KVRKMYTDPNRIRATTPGRVEGNPLFIYHDIFNPHKDEVVEEFKARYRQGCIDIEVKARLAEELIHLKPIKER
RLEFLSKPLALQNVLEDGTHKMREVAKATMEEVHDKFGFSGHSHKWRSLK

>core/430/4/Org4_Gene595

MLTLGLESSCDEACAIVNEDKQILANIIASQDIHASYGGVPELASRAHLHIFPQVINKALQQANLLIEDMDL
IAVTQTPGLIGSLSVGVFHFGKGIAIGAKKPLIGVNHVEAHLAAAYMAAQNVQFPALGLVVSGAHTAAFFIENP
TSYKLIGKTRDDAIGETFDKVGRFLGLPYAGPLIEKLALLEGSEDSYPFSPAKVPNYDFSFSGLKTAVLYAIKG
NNSSPRSPAPEISLEKQRDIAASFQKAACTTIAQKLPTIIKEFSCRSILIGGGVAINEYFRSAIQTACNLPVYFPPA
KLCSDNAAMIAGLGGENFQKNSIPEIRICARYQWESVSPFSLASP

>core/431/4/Org4_Gene632

MENAMSSSFVYNGPSWILKTSVAQEVFKKHGRGIQVFLSTSVMLFIGLVCAFIFPQYLIVFVLTIALMLAIS
LVLFLIRSVRSSMVDRLWCSEKGYALHQHENGPFDLKHVQQVLLRSPYIKVRALWPSGDIPEDPSQAAVL
LLSPWTFSSVDVEALLPSPQEKEGKYIDPVLPKLSRIERVSLLVFLSAFTLDDLNEQGVNPLMNNEEFLFFINK
KAREHGIQDLKHEIMSSLEKTGVPLDPSMSFQVSQAMFSVYRYLRQRDLTSSSELRCFHLLSCFKGDVVHCLA
SFENPKDLADSDFLEACKNVEWGEFISACEKALLKNPQGSIKDLKQFLVR

>core/432/4/Org4_Gene530

MDSSAPYNIASQGIEKSTVERILDLYGPASCIKFLKQMVLIREFEARGEAAYLEGLVGGFYHSYAGQEAVATA
AIANTGLDPWVFSSYRCHALAILLNIPLQEIAAELLGKETGCALGRGGSMMHMCNPNPFGGFIVGGQIPLAAG
AAFTIKYQEQKNRVSLCFIGDGAVAQGVFHETLNFVSLHQLPLMLIENNGWGMGTSLNRAVAKQPIAESQG
SSYDIRAVTVNGFDLFLNSLLGFREAYRYMVDTESPVLVECLCSRFRGHSISDPNLYRSKEEMQCLFKKDPIVL
AKDWLIRLEVLTEEEFQNIHQECKTAVLEAFSNAKLSSDPSVTTLLEEGVYA

>core/433/4/Org4_Gene611

MKLYSISSAVDTPWIFQLMSKVDSYLFLGGNRIKVVSIVMQEPNLIIGKVENVQISTIVKILKILSFLIFPLILIAL
ALHYFLHAKYANHLLVSKILERAPQYVPIPRSGDTTSHYKLTTLVPISQKNLQAMGSPLEVEAALRTTKPS
FFCVPAKYRQIISSHGIRFSLDLEQLADDINLDSVSWPTEYLNSTMDFCADKRVIQNVRLQTGTYINSVG
KRSLLKFMLRYLFDIGHIIQENPEALPNNTSGRLTLFPGVPYIYSRFTPNPTIWPQVFFRQGPLDEDRGGGFEIL
EQLQELGVRFPICPSQGPDPNPNFKGFQGIRIYWEDSYQPNKEV

>core/434/4/Org4_Gene807

MLPFEFENNTSSPECVCLDPQKLFVKLFKRTIVLLSGPTGSGKTDVSLALAPMIDGEIVSVDSMQVYQGMD
IGTAKVSLKARQEIPHHLLDIRHVQEPFNVVDFYYEAIQACQNILSRNKVPILVGGSGFYFHAFLSGPPKGPA
DPQIREQLEAIAEEHGVSALYEDLLLKDPEYAQTITKNDKNKIIRGLEIIQLTGKKVSDHEWDIVPKASREYCC
RAWFLSPETEFLKNNIQMRCEAMLQEGLLVEVRGLLNQGIENPSAFKAIGYREWIEFLDNGEKLEKYEETKR
KFVSNSWHYTKKQKTWFKRYSIFRELPTLGLSSDAIAQKIAKDYLLYS

>core/435/4/Org4_Gene843

MFFQNLAKKLTALGISPLGCLLIGGVVSCAILFGRSSNPSLAPTQVKTEKTSGNWLKLTQMGNPKLIESLTKK
EQLEKDLTSFHPIASAKVAIALSTEDDVMSPHLHLSVILTLRKEESLTPSLLFSITDYLCSSLPGLKREHISLSDNL
GNLYIPESITVNSLFIHTLENYL GKIFPKEHFALAYHAKAEKPTLQLTLNENYIAHLAKEESEKIVAHTKHLY
QNYDDSYDIVIETLPFARLQNKKSFPKAVLIGSMILVISLMIVALASFYLARHAYERVSPEPRKIKRGINISKLLE
IIQESPEKIALILSYLDPKKA EALLNRLPEDLKHQVLKYKL

>core/436/4/Org4_Gene541

MSEQHSPHISVQDVSKKLGDHILLSKVSFSVYPGEVFGIVGHSGSGKTTLLRCLDFLDMPTSGSISVAGFDNSLP
IQKFSRRNFSKKVAYISQNYGLFSSKTVFENIAYPLRIHHEMSKSEVEEQVYDTLNFLNLYHRHDAYPGNLS
GGQKQKVAIARAIVCQPEVVLCDEITSALDPKSTEDIIERLLQLNQERGITLVLVSHEIDVVKKICSHVLVMHQ
GAVEELGTTEELFLNSENSITNELFHEDINIAALSSCYFAEDREEVLRNLNFSKELAIQGIISKVIQTGLVSINILSG
NINLFRKSPMGFLIIVLEGEVEQRKKAKELLIELGVVKEFY

>core/437/4/Org4_Gene418

MTILRKLSQYLLFFSLLCSFIYVATCGSQPDSVSSPKIAIFLSFPHPLLEDCKSKSCIETLKDFENLPEIVVLNAEDSI
VKARKIARSLHTDKNVVAIVTLGTIATKVM SHIETQKPVIIAAVPDRESLTLPKNTMNIYGVNDTLDINQYCF
AIQAVATNAQSIVYLKPSEPFPSDLQKEIVKKLHASGIEVIEIPITSSTFKTRIRQAIDKRPSAIFIPLSPLSHKEGT
AFLQEILKEKIPIITDDTSLISEGACIACSVDYKKSGKQIAKIVHHLLYNNHDVDSL RKIIAQPLSPTTTFNEDIK
YLGIKLHKTERNQFLSFKSKKLEKSEKGKNVAVS

>core/438/4/Org4_Gene751

MEMKEEIEAVKQQFHSELDQVNSSQALADLKVRYLGKKGIFRSFSEKLKQCTDKAKLGS LINDFKTYVEDLL
QEKSLVLLASEQAEAFSKEKIDSSLPGDSQHSGGRHILKSILDDVVDIFVHLGFCVREAPNIESEANNFTLLNFT
EDHPARQMHDTFYLNATTVLRTHTSNVQARELKKQOPPIKV VAPGLCFRNEDISARSHVLFHQVEAFYVDH
NVTFSDLTAILSAFYHSFFQRKTELRF RHSYFPFVEPGIEVDVSCECCGKGKALCKHTGWLEVAGAGMIHPQV
LRNGNVDPEIYSGYAVGMGIERLAM LKHGISDIRLFSENDLRFLQQFS

>core/439/4/Org4_Gene957

MATISPISLTVDHPLVDTKKKSCSNFDKIQSRILLITAIFAVLVTIGTLLIGLLL NIPVIYFLTGISFIAVVLSNFILY
KRATTLKPCACGKHKEIKPKRVSTNLQYSSISIAINRSKENWEHQPKDLQNL PAPSALLTDNPYEIWKAKHS
LFSLVSLPGGNPEHLLISASENLGKTL LIEETSQNAPISSYVDTPSPKSLLNEAIQETRVEINTELPAGDSGERL
YWQPDFRGRVFLPQIPTTPEAIYQYYYALYVTYIQTAINNTQIIQIPLYSLREHLYSRELPPQSRMQQSLAMIT
AVKYMAELHPEYPLTIACVERSLAQLPQESIEDLS

>core/440/4/Org4_Gene293

MEEAAKHLAKEFLCSGINLFLSGEYEQAEKRLKETLELDSTAALAYCYLGIIALETGRVPEALNWCSKGLASE
PGDSYLR YCYGVALDRGNQYEAIEQYSAYVALHPDDVECWFSLSVYHRLKRLQEALDCFDKILALDPW
NPQSLYNKAVILSEMDDEAESIRLLEVA VAKNPLYWKA WVKLGFLLSRSKRWDKATEAYERVVQLRPDLS
GHYNLGLCYLTLDKTRLALKAFQEALFLNAEDADAHFYVGLAHMDLKQMREAYEAFNSALSINLEHERAH
YLLGYLHHMQGETDKATKELLFLQKKDSTFAPLLQKTVVSDPSSMQFERRLDTIS

>core/441/4/Org4_Gene279

MVLGVVGISYREAALKERERAIQYLQSFEKNLFLAQRFLGKGGAFIGLLTCHRAELYYYSESPEIAQAALLSEL
TSQGIRPYRHRGLSCFTHLFQVTSGIDSLIFGETEIQQQVKRAYLKGSKERDLPFDLHFLFQKALKEGKEYRSRI
GFPDHQVTIESVVQEILLSYDKSIYTNFLFVGYSINRKYAAAYLYQHGYHRITFCSRQQVTTTPYRTLSRETLSF
RQPYDVIFFGSSESASQFSDLSCESLSSIPKRIVFDNFVPRFTLWKETPTGFVYLDIDFISECVQKRLQCTKEGVN
KAKLLLTCAAQKQWEIYEKKSSHITQRQISSPRIPSVLSY

>core/442/4/Org4_Gene635

MFPSANPESRTRNVPLGIFHGLVACLYWGIVFVIPNFLGSFGDLDIVLTRYTIFGIFSLIACAIGNPSVIKKTPLYI
WRKSLWTLINPVYYFGITLGIRYVGSATVVIAGLAPIAVLYHSNTKQKELPYSLFSAISSVIITGVILTHLSA
LNLPTAASPLYSILGVIAVILSTSLWVIYVIRNQSLLEKHPNLTPDTWSYLIGISALIICLPMIILDLCGITHATHN
LISHTPGSERLLFLLCSAMGIFSSAKALTAWNKASLNLSPALLGAILIFEPIFGLVLTLYLSQSLPSLQEGIGIFL
MLGGSLLCLVLFGRKVQKSLENSQVSSSNE

>core/443/4/Org4_Gene878

MKKTCFQNYRSIGVVFSVVLFLVLTQTFLAGHFIDIGTSGLYSWARGVSGDGRVVVGYEAGNAFKYVDGEK
FLLEGLVPRSEVLVFKASYDGSVIIGISDQDPSCRAVKWVNGALVDLGIFSEGMQSFAEGVSSDGKTIVGCLY
SDDTETNFAVKWDETGMVVLPNLPEDRHSYAWDASEDGSVIVGDAMGSEEIAKAVYWKDGEQHLLSNIPG
AKRSSAHAVSKDGSFIVGEFISEENEVHAFVYHNGVIKDITLGGDYSVATGVS RDGKVIVGHSTRTDGEYR
AFKYVDGRMIDLGTLLGGSASFAGVSDDGKTIVGKSETELGECHAFIYLLDD

>core/444/4/Org4_Gene478

MTHQVAVLHQDKKFDVSLRPKGLEEFYQHHLLKERLDLFLCAALQRGEVPGHCLFFGPPGLGKTSLAHIVA
YTVGKGLVLASGPQLIKPSDLLGLLTSLQEGDVFFIDEIHRMGKVAEEYLYSAMEDFKVDITIDSGPGARSVR
VDLAPFTLVGATTRSGMLSEPLRARFAFSARLSYYSQDLKEILVRSSHLLGIEADSSALLEIAKRSRGTPRLA
NHLLRWVRDFAQIREGNCINGDVAEKALAMLLIDDWGLNEIDIKLLTTIIDYYQGGPVGKTLTSAVGEDIKT
LEDVYEPFLILKGLIKKTTPRGRMVTQLAYDHLKRHAKNLLSLGEGQ

>core/445/4/Org4_Gene260

MSYSLRNKKTICVYIIIALGILSFRSIPQEVYDKIRSSFVSLHVKFFPKIKQAPSSHLANLELENLVLKERVASL
EEKLKLVEVSNHTPPLFPEILTPYFHKLVGKVVYRDYTHWSSSCWVNVGKTHGIKKNSPVLSGNVLVGLVD
YVGEHQSRIRLITDVGMKPSVAMRGDIQSWWIKHSLRELIRQVEQISHAYILEKDKYEKISQLQELDSLQGE
GENQALLRGILSGVGGALWKEGSLCEGEGFYFSEGKTLLPGDILVTTGLDGVFPGLLVARVTKVKAPRDG
ACAFKIEAQSLLEKLMELDQLFILPPLEFNPNDRPDIFGLLWD

>core/446/4/Org4_Gene331

MKVVINGFGRIGRLVLRQILKRNSSVEVLAINDLVPGDALTYLKFDFSTHGRFPEDVRCEADHLIVGKRKIQF
LSERNVQNLPWKDLGVDLVIECTGLFTKKEDAEKHIQAGAKRVLISAPGKGDIPTFVMGVNHKTFNPEKDFV
ISNASCTTNCLAPIAKVLLDNFGITEGLMTTVHAATATQLVVDGPSKKDWRGGRGCLQNIIPASTGAAKAVT

LCLPELKGKLTGMAFRVPIEDVSVVDLTVRLDKSTTYDDICKAMKQASETDLKGILDYTDEQVVSSDFIGSEY
SSIFDALAGIALNDRFFKLVAWYDNEIGYATRIVDLLEYVEKNSK

>core/447/4/Org4_Gene386

MFVDQITLELRAGKGGNGVVAWRKEKYLPKGGPYGGNGGNGGSGVII EATTNVYSFEAYRNIRFLKAPDGQS
GATNNRTGRSGKDLIVSVPTGTLLRDAETGEILHDFTVDGERLLVSQGGKGGKGNTFFKTSVNRAPT KATPG
KPGEIRQVELEKLIADIGLVGFPNAGKSTLFNTLAHTEVKVGAYPFTTLAPSLGLVLCNDRLYQKPWIIADIP
GIIEGAHQNKGLGLDFLRHIERTLLLLFVIDVSKRERNSPEEDLETLIHELHSHQPDFEKKDMLVALNKIDDLL
PDEQEECLQSFQKRFPSTFVLISGLTGEGVDGLYRFFTQRLAV

>core/448/4/Org4_Gene54

MWFSVNKNKKAIIWATGSYLPEKVLSNADLEKMVDTSDEWIVTRTGIKERRIAGPQEYTSLMGAIAAEKAI
ANAGLSKDQIDCIIFSTAAPDYIFPSSGALAQAHLGIEDVPTFDCQAACTGYLYGLSVAKAYVESGTYNHVLLI
AADKLSSFVDYTDNRNCTCVLFGDGGAACVIGESRPGSLEINRLSLGADGKLGELLSLPAGGSRCPASKETLQSG
KHFIAMEGKEVFKHAVRRMETAAKHSIALAGIQEEDIDWFVPHQANERIIDALAKRFEIDESRVFKSVHKYGN
TAASSVGIALDELVHTESIKLDDYLLLVAFGGGLSWGAVVLKQV

>core/449/4/Org4_Gene895

MAAPIFIKNILLRSSIVYAPLAGFS DYPYRCMSALYQPGLMFCEMVKVEGMLYAPERTSKLLDYNENMRPIG
AQLCGSNPETSGEAAKILEGLGFDLIDLNCGCPTDKITKD GSGSGLLKTPELIGRILDKIINSVSIPVTVKIRSGW
DMEHINIEDTVRIIRDAGASAVFVHGRTRAQGYHGPSNQEYISRAKAAAGKEFPVFGNGDIFSPEAAQAMLT
GCDGVLVARGTMGAPWIGKQIQDYLTG SYEKIPFIKRKA AFLEHMRLVEDYYQSETKFLSETRKLCGHYLI
SAAKVRFLRSSLA KATS YQEVYQLVNDYEEADDSSLET FVKC

>core/450/4/Org4_Gene668

MSTPLSSGGISPSEQYVPQELFC DRLSSSRNSPDSNASGDSPIVSPPI SALVALTDLKLVPYNQNSFSWTTRLK
NAAEKIGLFLQRNWKYILLYILAWALILVCHHTVALTLTIWLGVLGIGVVF GIFTATCLDKENKHRHVNSL
WNLINHGILQLDPNGTRQILLATMIASISALIYAVPQAVGLVIGFSIGNQLSINTVYGARLGDEATY AIDRKAH
KKRIENIEQAINQHQIIKHQMINQKQLNALIEINRNNQTD PATANLLASLKLNLNQPM PYCFSMPEC GVTSSYL
DLNNNSPDDIIRADQCIMTLSQTLQQIKKEPDRIIESNH

>core/451/4/Org4_Gene863

MVRRSVSFCLFFLMTLLCCTGCNSRSLIVHGLPGRDANEIVVLLVSKGVAAQKLPQAAAATAGAA TEQMWD
IAPVSAQITEALAILNQAGLPRMKGTSLDLFAKQGLVPSELQEKIRYQ EGLSEQMASTIRKMDGIVDASVQIS
FTTENEDNLPLTASVYIKHRGVLDNPN SIMVSKIKRLIASAVPGLVPENVS VSDRAAYS DITINGPWGLTEEI
DYVSVWGIILAKSSLTKFRLIFYVLILILFVISCGLLWVIWKTH TLMTMGGTKGFFNPTPYTKNALEAKKAEG
AAADKEKKEDADSQGESKNAETS DDKDSSDKDAPEGSNEIEGA

>core/452/4/Org4_Gene845

MKQHIGYLG MGIWGFCLASLLANKGYPVVAWSRNPDLIKQLQEERRHPLAPNVVISPNLSFTT DIKEAIHNAF
MIVEGVTSAGIRPVAEQLKQITDLSVPFVITSKGIEQNTGLLLSEIMLEVLGDSVTPYLG YLSGPSIAKEVLNGS

PCSVVVSAYDSQTLKQIHEAFSLPTFRVYPNTDIKGAALGGALKNVIAIACGIAEGLSFGNNAKAGLVTRGLH
EMRKLAAIMDCKPETLNGLAGLDLCVTCFSESSRNLRFGHLLAQGLTFEQAKAKIGMVVEGAYTALSAYQ
VAKHHKIDMPITTTGIYRVLYENLDLKEGIALLLQRNTKEEFL

>core/453/4/Org4_Gene348

MKPLGFQENLEALCNKTSRQLLKYLKQILFVCGASLLIALEFSFFLYFFLFSGETVIPAFCLACFFLTLFVCLVT
RLYLLSGKGDFEDLASEYLQGAVPPNKR SQNIVEEQSHLAAAATKLSINLQNQEYSLLSEIFKFLPKHDLIRK
FSCFCFWKDYFLFRECLLQKAIEAYIKVVQAIPVDLSAHVSLADAYVALSGLYADPRKYPEFDANYWIPSGR
YSAEIQEKFFATARRAIEEFQILNEYAPGNAWVHAQLAYSYHDLQMPMEEIQEYEIVLKLKPNDVETMSKLG
LYFQQGMNAKGLRIYEEIKRDIYKKSQKLIKFYGVEYKY

>core/455/4/Org4_Gene180

MQPFIFTLLCLTSLVSLVAFDAANARKRCACAQTIERGENFFSIKRSACAEIEYQEKS RHASAIERISKDKGKV
TPKQIAKVATKKKQRYRLLQVPFSRPPNNSRYNLYALLSEPPECYSDTASWYAIFIRLLRRAYVDTGNVPPGS
EYAIANALISNKQEILERGAQLGPDVIETLTLPEEQAEIFYKMLKGSSNSQSLLNFLHYEEKSLGHCKLNLIFM
DPLLLEAVLDHPDAYRETSLLRDGIWEAVKRQEHAIQEHGQAAALELFKTRTDFRLELRDKMQLLLSRYDLL
PLLNKKMFDTLGSAGDYLFLVDPDTKAISRCRCPSKSIKL

>core/456/4/Org4_Gene321

MATNAIRLAGSAASKMLLPVAKEPAAVSSFAQKGIYCIQQFTNPGNKLAKFVGATKSLDKCFKLSKAVSDC
VVGSL EEAGCTGDALTSARNAQGMLKTTREVVALANVLNGAVPSIVNSTQRCYRYTRQAFELGSKTKERET
PGEYSKMLLTRGDYLLAASREACTAVGATTYSATFGVLRPLMLINKLTAKPFLDKATVGNFGTAVAGIMTIN
HMAGVAGAGCGIALEQKLYKRAKESLYNERCALENQSQSLSGDVILSAERALRKEHVATLKRNVLTLEKA
LELVVDGVKLIPLPITVACSAAISGALTAASAGIGLYSIWQKTKSGK

>core/457/4/Org4_Gene235

MRIAVLGVTGLVGQKFVALLHKWYRDWVIAEVVASNSKYGQSYGDACIWQEPGMPPEMVRDLPIRKIEEV
QSDIVVSFLPSSAESMEAYCLSQGKVVFSNASTYRMHSSVPIIPEVNSDHFQLLEE QPYPGKIITSPNCCVSGIT
LALAPLRKFSLDHVHIVTLQSASGAGYPGVPSLDLLANTVPHIVGEEKILRETVKILGSSKQPLPCKLSVT VH
RVPVAYGHTLSLHVTF SKDVDLDEILYSYQEK NK EFPNTYQLYDNPWSPQARKHLSHDDMRVHLGPITYGG
DFRTIKMNVLIHNLVRGAAGTLLASMENYFFDYLKREMCLR

>core/458/4/Org4_Gene339

MKTLWHFVSKAFLSIVGLCCGVVLA FVVIFALIASSLGNGDATFVSLPDAQGEVKDLGKTAPIIAVIEMKDVI
ASSKNTAKTIQNILEGFEKAPLKDRVKGIVIDMDCPGGEVFEIDRIYSMLRFWKERKGFPIIYVNGLCASGGY
YVSCAATKIYATSSSLIGSIGVRSGPFFNVKEGLNRYGVESDLLTAGKDKAPMNPYIPWTSHDREERQATLDF
LYGQFVDIVTQNRPLL TKEKL VHTLGARIFSPEKAKQEGYIDVVGATKEQVLQDIVAVCKIEDNYRVIGSGGD
GWWKRVASAAASSPLVTGMIKHDILPLSHDAA YIPPYLAL

>core/460/4/Org4_Gene916

MSSLTLSRRPRRNKRTAAIRDLLAETHLSPKDLIAPFFVKYGNNIKEEIPSLPGVFRWSLDLLLKEIERLCAYGL
RAVMLFPIIPDDLKDAYGSYSSNPKNILCHSIHEIKNAFPHLCLISDIALDPYTTHGHDGIFLNGEVLNDESVRIF
GNIATLHAEMGADIVAPSDMMDGRIGYIRSKLDQSGYSKTSIMSYSVKYASCLYSPFRDALSSHVTSGDKKQ
YQMNPKNVLEALLESSLDEEEGADILMVKPAGLYLDVIYRIRQNTCLPLAAYQVSGEYAMILSAFQQGWLD
KETLFHESLIAIKRAGADMIISYSAPFILELLHQGF

>core/461/4/Org4_Gene615

MNIYQFSPGVSPNWQASLMARLDSYFCLGGETVTRIISLRPSGLILAKKEKAVVSIAAKILKILSFILFPLVLTAL
AIRYLLYNKFNKDLDRVFFIPTEITKTEELIIAKNPALVKEAALNVSPFFYSLPKKYQRMKVETPEGKFYKITE
SVNLDLLVEDLHLETLDWPTTELLKNRPFDFTHGPEEEKLIKIDILLKEEGNEYFSLESKLLARHMMHNIVVL
SEEPGRSAFLGRTAFFPNKYPIAKGGVGIPSTTSNLFTHWYCFYFYRAATPQSDHPDGC GFILLERLKLGAEFF
YCDLRESNTTGFTLLFEGSNKGVLKNHLFIRDE

>core/462/4/Org4_Gene614

MSNIYSFSPGICPNWQAGLMSKLDLCCFGGETATRIFSMTPSGFSLATEEKVHISTAEKVIKILALIFFPIILIAL
AIRYFLHRKFDRKCFVIPQDTPKELELILAANPQLVEKAAREVHPGFFALPTKYQSMYIQTSGQPPKITLSINI
DLLLEDLDTDSIPWPKLYLDEDFDFAYYPESKAIIDTVTKLEKNNPGEEFCLESKKILAHYLLEQLFKLETGLN
FPTSTIDGGRESFLIKFSHETKKPTVWAFIYFYHHSNGPKLEKDFKQAGCEVHNRLNLGLKYRPQAGAQN
DGCDDGGPYGPRGFLIVWEENYGSVLKDHGFIKDN

>core/463/4/Org4_Gene776

MQFSRYLRYAFDNQYLPEPLYQKFSVFHQNYIDAATKKAAADQAEALCLQWVKVIIEDLKNPFIFPPYHKKI
RAPIDLFRLSIDFFSLVIDDKNSRILNLHRLKEIEEYIARGDNVLLANHQTECDPQLMYIALGKTHPELMEN
MIFVAGDRVTSDPLARPFMSMGCDLLCIYSKRHIATPPELREEKLLHNQKSMQILKTLLNEGKFIYVAPAGGR
DRKNAEGKLYPSEFSPESIEMFRLAKASNQTTTFYFPALKTYDILPPPKIENAIGEQR AIFAPVFFNFGAELF
FDALCSKEELIHCDKHAQRTLRAEKVFSIVKNLYEEL

>core/464/4/Org4_Gene720

MREETVSWSLDIREIYHTPVFELIHKANAILRSNFPHSELQTCYLISIKTGGCVEDCAYCAQSSRYHHTVTPPEP
MMKIVDVVERAKRAVELGATRVCLGAAWRNAKDDRYFDRVLAMVKSITDLGAEVCCALGMLSEEQAKKL
YDAGLYAYNHNLDSSPEFYETIITTSYEDRLNTLDVVNKSISTCCGGIVGMGESEEDRIKLLHVLATRDHIP
ESVPVNLLWPIDGTPLQDQPPISFWEVLRTIATARVVFPRSMVRLAAGRAFLTVEQQTL CFLAGANSIFYGDK
LLTVENNDIDEDAEMIKLLGLIPRSSFGIERGNPCHANNS

>core/465/4/Org4_Gene432

MIDIMQHFKPYTMVPGQKLPIPGSLLYAQVFPTLWRLFSSKHEILNEQTLQVQGPKRFAVFQDLHRGGLAV
TSERYKYLLPSGECTQSIKGLPSAAQAGPLLSLGVHKKHADWQKVRRRRDLKEILPLWFRFAAMAPKGSY
RDLETTAIGSLVKTAHQSVLHRETTEIAPALLSIALAGFSECFLPRSYDEEFQGILPQDGDPEGGVPFELLSYSF
GMIQDIFLRHQQLVEILPALPPEFPCGRLIHVALPNLGTLSIVWTKKTIRQVELHAEYSGEVFLKFCSSLCSAR
LREWSERRLSGSKRLSLGETLEIKAGTTYLWDCFBK

>core/466/4/Org4_Gene820

MSAFFDLLKSQTASHPPIWLLRQVGRYMPYPYQELKGSQSLKTFFHNTAIVEATLLGPSLLHVDAAILFADILS
ILDGFAVTYDFAPGPRIQFFPEQPFTFTSDPQTIFSYYLLDAIRTLKQKLPVPLIVFAASPFTLACYLIDGGASKDF
SKTMSFLYAYPEKFDQLISTHIEGTAIYLKTQMDAGAAAVQLFESSRLRLPSALFTRYVTEPNRRLIAKLKEQAI
PVSLFCRCFEENFYTLQATQADTLHPDYHVDLHRIQKNLMPSLQGNLDPALFLLPQEKLLHYVEAFLVPLRTY
PNFIFNSGHGILPETPLENVQLVVSYVQRQL

>core/467/4/Org4_Gene401

MPSPMISTDVCQDILGKQKEAVDFFFQAFQPKAMQLAEKILGHSGWVFFSGVGKSGCVARKLVATLQSLSE
RALFFSPVDLLHGDGLVSPGDIVCLFSKSGETQELLDTPVPHLKSARGAILVAITSMYPYSNLAALSDLVVILPSV
AELDPFNLIPTNSTTCQMIFGDFLAMLFFHSRGVSLSTYGKNHPSGQVGMKANGKVKDFMFPKTEVPFCHLG
DKVSFSLEVFSAYGCGCVCIVDPQFRLMGIFTDGDRLRRSLASYGGEVLSLSLDMVTANPRCITEDSDIAIALQ
LMESSPVAVLPVLDNEENRHVTGLLHMHTLAKAGLL

>core/468/4/Org4_Gene732

MAFKEVVRVAVTGGTGQIAYNFLFALAHGDVFGVDRGVDLRIYDVPGTERALSGVRMELDDGAYPLLHHL
RVTTSLNDAFDGIDAAFLIGAVPRGPGMERGDLLKQNGQIFSLQGAALNTAAKRDALFVVGPNPVNTNCWIA
MKHAPRLHRKNFHAMLRDLQNRMHSM LAHRAEIPLEEVSRVVIWGNHSAKQVPDFTQARISGKPAAEVIGD
RDWLENILVHSVQNRGSAVIEARGKSSAASASRALAEAARSIFCPKSDEWFSSGVCSDHNPYGIPEDLIFGFPC
RMLPSGDYEIIPGLPWEPPFIRNKIQISLDEIAQEKAASVSSL

>core/469/4/Org4_Gene529

MPKHKTLEIREALREAIDEEMSRDPNVCILGEEIGDYNAYKVTKGLLDKWGPKRVIDTPISEAAAFSGIGIGAA
LSGLRPIIEFMSWNFSFVALDQIISHAAKMFMFTGGKFSVPVFRGPNGAAAQVSCQHSHCVESLYANIPGLIII
APSNPYDAKGLLKS AIRNNNPVLFLENELEYNLKGEVPTEEYLVPIGKAHRVQEGNDLTIITYSRMVSITKEAC
SLAKKRWGLSIEIIDLRTIKPLDISTILSSVRKTSRCIVVEEGHYFAGISSEIILITEHVFDSDLAPPLRVCQKETP
MPYSKILEQATLPNVNRILDTIEKVMR

>core/470/4/Org4_Gene662

MSNQFDQLKKLSTIVCDSDGPELVKASGSQDATTNPSLILKVAQEPKFQELLNEAVVWGIRQNGDDLQTLSEI
LDKIQVNFALIEIKNIPGRISLEIDARLSFNVEAMVQRAVFLSQLFEAMGGDKRLLVKIPGTWEGIRAVEFLE
AKGIACNVTLIFNLVQAIAAAKAKATLISPFVGRIDWWIAAYGDEGYSIDADPGVASVSNIYAYYKKFGIPT
QIMAASFRTKEQVLALAGCDLLTISPKLLDELKKSQDPVKKELDPAEAKKLDVQPIELTESVFRFLMNEDAM
ATEKLAEGIRIFAGDTQILETAITEFIKQIAAEGA

>core/471/4/Org4_Gene115

MTTPAYLLANFGGPRHAKDLQEFLISLLTDRDVTGTFLPRVLHRHLFTFIAKKRVPKVLPQYQSLQNWSPYIF
DTETLAKTLSEILRAPVIPFHRYLPSTHEKTLLALRTLHTRHVIGIPLFPHTYSVTGSIVRFFMKHVPEIPISWIP
QFGSDSKFVSLITCHIRDFLQKLGILEKECCFLSVHGLPVRYISQGDYPYSKQCYESFAITTNFKQSENFLCFQS

KFGPGKWLS PSTAQLCQNIDTDKPNVIVVPFGFISDHLETLYEIERDYLP LLRSRGYRALRIPAIYSSPLWVSTL
VDIVKENSTVVAEELIKSGKKHTGIR

>core/472/4/Org4_Gene503

MDAKMGYIFKVMRWIFCFVACGITFGCTNSGFQNANSRPCILSMNRMIHDCVERVVGNRLATAVLIKGSLDP
HAYEMVKGDEDKIAGSAVIFCNGLGLEHTLSLRKHLENNPNSVKLGERLIARGVFVPLEEDGICDPHIWMDL
SIWKEAVIEITEVLIEKFPEWSAEFKANSEELVCEMSILDSWAKQCLSTIPENLRYLVSGHNAFSYFTRRYLATP
EEVASGAWRSRCISPEGLSPEAQISVRDIMAVVDYINEHDVSVVPEDTLNQDALKKIVSSLKKSHLVRLAQK
PLYSDNVDDNYFSTFKHNVC LITEELGGVALECQR

>core/473/4/Org4_Gene406

MMTYPVPQNPLLLRILRLMDAFSKSDDERDFYLDRVEGFILYIDLDKDQEDLNKIYQELEENAERYCLIPKLT
FYEVKKIMETFINEKIYDIDTKEKFLEILQSKNAREQFLEFIYDHEAELEKWQQFYVERSRIIIEWLRNNKFHF
VFEEDLDFTKNVLEQLKIH LFDKVGKEITQARQLLSNKAKIYYSNEALNPRPKRGRPPKQSAK VETETTISSD
IYTKVPQAARRFLFLPEITSPSSITFSEKFDTEEEFLANLRGSTRVEDQLNLTNLSERFASLKELSAKLG YDSLST
GDFFGDDEEEEEVVT KTKGSKRGRKKSS

>core/474/4/Org4_Gene201

MHSELPNYQNIVESVVTEITTQLLNYSERHRLVPFWEKSDGSFITAADYGSQYYLKQQLAKAFNPFIGEETL
YPDQDNEKIPEILKFTRLLTSSVSRDDLSTLVPPPSTSLFWLVDPIDGTAGFIRHRAFAVAISLIYEYRPILSVM
ACPAYNQTFKLYSAAKGHGLSIVHSQNLD RRFVYADRKQTKQFCEASLAALNQHHATRKL SLGLPNT PSP
RRVESQYKYALVAEGA VDFIRYPFIDSPARAWDHVPGAFLVEEAGGRVTDALGAPLEYRKESLV LNNHAVI
LASGDQETHETTLAALQNQLNVVPTDKLIAL

>core/475/4/Org4_Gene155

MKTVTSFTVCKENSGRLDKYLTEVHPKYSRAFYQEHL SGLVQINGQINTRVATRLNCGDIVTIDIQEKEELLE
LLPEAIPLDKVYEDGMILVINKPRDMVVHPAPGHFHGTLVHALLHEIGERLKEEFPEEPWRPGIVHRLDKDTS
GLIITAKTRQAKKVSELFSTKRLKKS YLAVCIGKPRSTTIHTHISRHQNKRKEMTVSSQGKEAVTHCQVLAF
NGKLSFVALSPETGRTHQLRVHMKHLGTPILGDPVYGIPSMNSSYGLDKQQLHAYSVDFTHPETRQFCSLKA
GLPEDMRSLLIKEFRNETTILNKNLLESILKEQ

>core/476/4/Org4_Gene549

MTIDMHCDLLSHPHFCRKDPAVRCSPEQLLSGGVRQQVCAIFVPHSQGEPHCDKQNSLFFSLPNQYPDIGLLS
YEEEENGSSSQKKSLSLIRSIENASALGDDTAPLGTL LAKLIHLTKQGPLAYLGIVWKGDNRFGGGTEAPKRL
SNDGKVLLDIMYELGVPIDLSHCSDKLAEDILDY TADKLPNLAVIASHSNFRSVLDHRRNLVDAHAK EIVRRK
GVIGLNLVRSYVGDSLGDLEKHVLHAENLGILSSIVLGSDFFYANEDENFFFNECSSAE AHPVLNQLIHRIFSK
GKAESILSSRAEKFLKQVIVEQVNRKITDVKL

>core/478/4/Org4_Gene631

MIEFAFVPHTSVTADRIEDRMACRMNKLSILAITSLCVLISSVCIMIGILCISGTVGTYAFVVGIIFSVLALVACV
FFLYFFYFSSEEFK CASSQEFRFLPIPAVVVSALRSYEYISQDAINDVIKDTMQLSTLSSLLDPEAFFLEFPYFNSLI

VNHSMKEADRLSREAFLILLGEITWKNCETKILPWLKDPNITPDDFWKLLKDHFGFKKRIATWIRKAYPE
IRLPKKHCLDKSIYKGCCKFLLPAENDVQYQRLHKKVCYFSGEFPAMVLGLGCEVPMVLGLPKVPKDLTWE
MFMENMPVLLQSKREGHWKISLEDVASL

>core/479/4/Org4_Gene77

MELLPHEKQVVEYEKAIAEFKEKNKNSLLSSSEIQKLEKRLDKLKEKIYSDLTPWERVQICRHPSRPRTVNYI
EGMCEEFFVELCGDRTFRDDPAVVGGFVKIQGQRFVLIGQEKGCDTASRLHRNFGMLCPEGFRKALRLGKLA
EKFGLPVVFLVDTPGAYPGLTAEERGQGWAIKKNLFELSRLATPVIIIVIGEGCSGGALGMAVGDSVAMLEH
SYYSVISPEGCASILWKDPKKNSEAAASMLKMHGENLKQFGIIDTVIKEPIGGAHHPALVYSNVREFIIQEWLR
LKDLAIEELLEKRYEKFRSIGLYETTSSESGPEA

>core/480/4/Org4_Gene300

MASNPILQIEDLSITLAKQRQQYPIVQSLSFTINEGQTLAIIGESGSGKSVSAHAILRLLPCPPFSVSGQVNFQGH
NLLTASRSIQKKIIGTEISMIFQNPQASLNPVFTIEQQFREIIHHTLALTAEVAKEKMLYALEETGFHDPRLCLNL
YPHQLSGGMLQRICIAMALLCSPKLLIADEPTTALDVSQYQILQLLKTQKKTGMSLLIITHNMGVVAETAD
DVLVLYAGRMVECAPAVQIFHNPSHPYTRDLLASRPSLQPQPLGSFNPIPGQPPHYTAFPSGCRYHPRCSKILN
RCSAEAPEIYPVREGHKVRCWLYDD

>core/481/4/Org4_Gene506

MALGPSPYYGVSFQFFSVFFSRLFSGSLFTGSLYIDDIQIIVFLAISCAGAFAGTFLVLRKMAMYANAVSHTVL
FGLVCVCLFTHQLTTLISLGTTLAAMATAMLTGFLIYFIRNTFKVSEESSTALVFSLLFSLSLVLLVFMTKNAH
IGTELVLGNADSLTKEDIFPVTIVILANAVITIFAFRSLVCSSFDSVFASSLGIPIRLVDYLIIFQLSACLVGAFKA
VGVLMAFLIIPSLIAKVIKSIKSLMAWSLVFSIGTAFLAPASSRAILSAYDVGLSTSGISVVFLTMMYIVVK
FISYFRGYFSKNFEKISEKSSQY

>core/482/4/Org4_Gene299

MTTNFPQPLIQATSLTKHYKRSFWFQGKTIASRPVDDVSFSLYSRRVGLIGESGSGKSTLALALAGLLPLTS
GFLTNGTPIKLHSHKHGRHQLRSQVRLVFQNPQASLNPRKTILDSLGHSLLYHKLVPKEKVLATVREYLELVG
LSEEFYRYPHQLSGGQQQRVSIARALLGVPQLIICDEIVSALDLSIQAQILNMLAELQKKLSLTYLFISHDLAV
VRSFCTEVFIMYKGQIVEKGNTERIFSDPQHPYTRMLLNAQLPETPDQRQSKPIFQEYHKDSEESCSTGCSFYN
RCPQKQEACKSETSPNQGDAHHTYRCIH

>core/483/4/Org4_Gene265

MEKKYYALAYYYITRVDNPHEEIALHKKFLEDLDVSCRIYISEQGINGQFSGYEPHAELYMQWLKERPNFSKI
KFKIIHHIKENIFPRITVKYRKELAAALGCEVDLSKQAKHISPQEWHEKLQENRCLILDVRNNYEWKIGHFDNAT
LPDIQTFREFPEYAEKLAQECPETTPVMMYCTGGIRCELYSPVLLEKGFKEVYQLDGGVIAYGQQVGTGKW
LGKLFVFDDRLAIPIDESDPDVAPIAECCHCQTPSDAYYNCANTDCNALFLCCDECIHQHQGCCGEECSQSPR
VRKFDSSRGNKPFRRHLCEISENSESTSCCLI

>core/484/4/Org4_Gene113

MKQLLFCVCVFAMSCSAYASPRRQDPSVMKETFRNNYGIIVSGQEWVKRGSDGTITKVLKNGATLHEVYSG
GLLHGEITLTFPHTTALDVVQIYDQGRLVSRKTFFVNGLP SQEELFNEDGTFVLTRWPDNNDSDTITKPYFIET
TYQGHVIEGSYTSFNGKYSSSIHN GEGVRSVFSSNNILLSEETFNEGVMVKYTTFFYPNRDPESITHYQNGQPHG
LRLTYLQGGIPNTIEEWRYGFQDGTTFVKNGCKTSEIAYVKGVKEGLELRYNEQEIVAEVSWRNDFLHGER
KIYAGGIQKHEWYYRGRSVSKAKFERLNAAG

>core/486/4/Org4_Gene320

MNLKV VYFGTPTFAATVLQDLLHHKIPITAVVTRVDKPQKRSAQLIPSPVKTIALTHGLPLLQPSKASDPQFIE
ELRAFNADV FIVVAYGAILRQIVLDIPRYGCYNLHAGLLPAYRGA APIQRCIMEGATESGNTVIRMDAGMDT
GDMANITRVPIGPDMTSGELADALASQGA EVLIKTLQQIESGQLQLVSQDAALATIAPKLSKEEGQVPWDKP
AKEAYAHIRGVTPAPGAWTLFSFSEKAPKRLMIRKASLLAEAGRYGAPGTVVVTDRQELAIACSEGAICLHE
VQVEGKGSTNSKSFLNGYP AEKLKIVFTLNN

>core/488/4/Org4_Gene461

MSKGSSKHTVRINQ TWYIVSFILGLSLFAGVLLSTIYYVLSP IQEQAATFDRNKQMLLA AHILDFKGRFQIQEK
KEWVAATFDKKTQLLEVATKKVSAVSYPELELYAERFVRPLLTDAQ GKVFSFEEKNLNPIEFFEKYQKSPPC
QQSLLPFYVILENSTRTENMSGADVAKDLSTVQALIFPISGFWGPIHGYLG VKNDGDTVLTAWYQQGET
PGLGANITNPEWQE QFYGKKIFLQDSSGTTNFATTDLGLEVIKGSVRTTLGDSPKALSAIDGISGATLTCNGVT
EAYVQSLACYRQLLINFSNLTHEKKTGE

>core/489/4/Org4_Gene333

MRLLSILKLHLFSLRSSSSLSPHYHSCSR SMLHLLCRWKDADIMEWQQICNILSGVCSRMSGKLVSLQKETQ
DSCHQEHERIHLQYREQLSALEEEYRRREEAKNQDLEKLQQENTWLQNRLAEKLQQIRHQSDIIDEIKKELLQ
SVQRTEISEGRRLCYEHKIKQLEEQLQRYVSQHGAPSIEIEDKSSAAYAEINRLKKSLIDLQQEKDIYIKTYHS
EIAKLREKLQRQEGAQTSSEVCSIEKLTEVQTDLAEKKKAIAL LQDIVEDQYCQLRDLHKEKGMAMPSNTKL
DHLKGLLGKEPECEVDVVFSESKSLGS

>core/490/4/Org4_Gene774

MEVQIGIDLMGGDHSPLV VVQVLVDVLKSQSSTIPFAFTLFASEEIRKQIQEEFISNLPQEKFPKIISAENFVAM
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VGANISVKPEEMVGFARMGLAYRQCLGDSKIPTIGLLNIGSEERKGTEAHRQTFRMLRDTFGEAFLGNIESGA
VFDGAADIVVTDGFTGNIFLKTAEGVFEFLQRILGDKLEADIQRRLDYTFYPGSVVCGLSKLVIKCHGKACGS
SLFHGILGSINLAQARLCKRILSNLI

>core/491/4/Org4_Gene365

MLISISLATLPILAFSWASFIEPNWLRTTAIPWRLPKKHAHLHGLRIAQISDLHFHKRVPEKFLNKVSKSIKNFSP
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LFSSPSYRYDPNLTPQEPHPDLLKLLKNTPLTLLHNTTHVIPNTLNIVGLGDLFARQFHPEQAFKNYDPSLPGL
LLSHNPDGITRLQQYPGDFVLSGSHGPQVTL SWPKFARKFFERLSGLENPYLARGYFVTKEGKQLYVNRGL
GGLKRIRFCSPPEICYITCSYD

>core/492/4/Org4_Gene749

MVLSSDLLRDDKQLDLFFASLDVKKRYLLALSGGSDSLFLFYLLKERGVSFTAVHIDHGWIRSTSAQEAKELE
ELCAREGVPFVLYTLTAAEQGDKDLENQARKKRYAFLYESYRQLDAGGIFLAHHANDQAETVLKRLLESAAH
LTNLKAMAERSYVEDVLLLRPLLHIPKSSLKEALDARGISYVQDPSNEDERYLRARMRKKLFPWLEEVFGKN
ITFPLLTLGEESAELSEYLEKQAQPFFSAATHQDSQGELPCPDCLIQQAFCKWVMKKFFNNAGIAVSRHFLQ
MVYDHLSRSSCATLRMRNKIVIIKPGVVMID

>core/493/4/Org4_Gene311

MKFLLYVPLLLVLVSMGCDAPVSFEPFSGKLSTQRFEPQHSAAEYFSQGQEFLLKKNFRKALLCFGIITHHFP
KDILRNQAQYLYGVCYFKQDHPDLADKAFASYLQLPDAEYSEELFQMKYAIAQRFAQGKRKRICRLEGFPKL
MNADEDALRIYDEILTAFPSKDLGAQALYSKAALLIVKNDLTEAIKTLKKLTLQFPLHILSSEAFVRLSEIYLQ
QAKKEPHNLQYLHFAKLNEEAMKKQHPNHPLNEVVSANVGAMREHYARGLYATGRFYEKKKKAEEAANIY
YRTAITNYPDTLLVAKCQKRLDRISKHTS

>core/494/4/Org4_Gene89

MNRRKARWVVALFAMTALISVGCCPWSQAKSRCIDKYIPVVRNLLEVCGLP EAENVEDLIESSSAWVLTPE
ERFSGELVSICQVKDEHAFYNDLSLLHMTQAVPSYSATYDCAVVFGGPLPALRQRLDFLVREWQRGVRFKKI
VFLCGERGRYQSIEEQEHFFDSRYNPFPTENWESGNRVTPSSEEEIAKFVWMQMLLPRAWRDSTSGVRVTF
LLAKPEENRVVANRKDTLLLFRSYQEAFPGRVLFVSSQPFIGLDACRVGQFFKGESYDLAGPGFAQGVLKYH
WAPRICLHTLAEWLKETNGCLNISEGCFG

>core/495/4/Org4_Gene618

MRKVAFLVSCLFSSAIGASAAPVRVPGFPQIPEDLVQIKTEVCPKQEVCLAVTIKCDDHNLIGVLHLPNTPTPE
GGFPTVVLFHGFRTKFGGLTGAYRKLGRKFAAAGIATLRVDMAGCGDSEGVAEEVPIETYLRDAQTILETV
QEHPDLNAYRLGISGFSLGCHIAFELAKIYNPRDLNIKALSVWAPIADGGILLKELYENFSKHGEGDIISVGKDF
GFGPPPLIVCSGDVDLLIRIQDHVTANSLPTKPYILHQQGIDDTLVSRTQQTLFKNTAPGRMTFISYPNTGHNL
ATAPDLDMILDQIVSHFQRTL

>core/496/4/Org4_Gene452

MFKLLFHIAAFAGHVLSTPIFIVQDACGIDEEACKNPPRPFSQVQYLKVNDKFKKLPHQTIGYRQYDGT
LCTLPITEHSGLLFSTGYIGADIQWKSSLPISETDPNGLGWATFQDTSFYNYVLLSLGAYTLNKNWQWSIILS
GLVDPKNIEMGYGLYQGVLSGKYQATEKLSAIFGVINETGLHQEKAWPLVGVSYKATDQLTLNCIYPVNFSI
DYRSTSVCNLGLAYRLTRFRKKLHKNHLTSSRGIFEYQGREIEANVKLTPWPGSFIKGFYGWSIGNDISIADDDH
NNNKTSHTFKTSAFFGGSAVMNF

>core/497/4/Org4_Gene985

MLVELEALKKEFAHLKDQKPTSDQEITSLYQRLDHLEFVLLELGQDKFLKATEDEDMLFESQKAIDAWNALL
TKARDALGLGDIGAIYQTIEFLGAYLSKVNRRAFCIASEIHFLKTAIRDLNAYYLLDFRWPLCKIEEFVDWGN
DCVELAKRKLCTFEKETKELNESLLREEHAMEKCSIQDLQRKLSDIIEHLDVSLFCFSKTPSQEEYQKDCLYQ

SRLRYLLLLYEYTLCKTSTDFQEQAARAKEEFIREKFSLLELQKGIKQTKELEFAIAKSKLERGCLVMRKYEA
AAKHSLSMFEEETVKSPRKDTE

>core/498/4/Org4_Gene482

MTLPMQKSLTSFDDFSQAYAEKVPAIALIGSALEDDKDALIELLVSESFKELDGQGLMPATLMSWTETFALFQ
EHETLGIIHAEKFPLATKEFLSRYARNPQPHLTILIFTTKQECFRELSKALPSALSLSLFGWPADRQKRIIRLLL
QRAERVGISCSQSLASFLRALASTSLPDILSEFDKLLCSVGKKTSLDHSDIKELVVKKEKASLWKFRDSLLKR
DPVEGHQQLHFLLLEDGEDPLGIIAFLRTQCLYGLRSIEEGSKENKHRMFVLYGKERLHQALNSLFYAETLIKN
NVQDPIVAVETLVIRMVNL

>core/499/4/Org4_Gene590

MFSYIKNRILFNLLSLWIVLTLTFLVMKTIPGDPFNDEGCNVLSEEVLQTLKSRYGLDKPLYQQYTQYLHSIAK
LDFGNSLVYKDRKVTNIISTAFPISAILGLQSLFLSIGGGIALGTIAALKKKKQRRYILGASILQISIPAFIFATLLQ
YVFAVKIPLLPACWGSFTHLTPLALAVTPMAFIIQLTYSSVSAALNKDYVLLAYAKGLSPLKVVIKHILPYA
IFPTISYSAFLITTVITGTFAIENIFCIPGLGKWFICSIKQRDYPVALGLSVFYGTFLMLSSLLSDLIQSIIDPQIRYA
HGKEKKRK

>core/500/4/Org4_Gene509

MAMLPKFFLVLLCLGLCSCSQKTTTIEGEQMTIFYRIVLGTSLSAKEKASLSQQIDRCFHKIDSIYNNWNPHSE
LSIINRAPADVPIITLSVELSEFLDQVDTLYKLSEGRFDPTVGPLKTLWLLHLKSQTLPPKDVWEQHYKDMGW
QHLEFQSNTKTLIKKNPHVQIDLCGVVKGYYAVDCLNEICNTFCPNNYVEWGGEIKTSGHHPSGRPWRIFSEA
AGTILDIDDMAIATSGNHIQKWCVEGKIYTHILDTRTGKPLELSSYPIQSVSVVHPSCAYADAIATVLMTFDSK
IEAKQWAEHHILTYINDGASS

>core/501/4/Org4_Gene381

MWRVVLRLFIIFILGRAVFPLRASESFSWETSTCLTVLGIPFIDIILTNEDEFVAQCGLQIGTISSTNNATIKEIFLI
YKEKFPETSISFKRKEPLNLSQSHLSDLGILCMRNGETYAEGMANKENGPAKQPKDLRLVLRCPNQPDITLLY
SEKEAEKGIETNICLCNQGYTLLDGQLILYGDSIEKFLKETKRKNHNLVDLCDSQVVTTFLSRFWSLLNYIQV
LFLSEDSAKILAGIPDLAQTQLLSHTVPLLFIYTNDHSIHIEQGKESSFTYNQDLTEPILGFLFGYINRGSMYECF
NCAQSSLGET

>core/502/4/Org4_Gene694

MIASIYFLDYLMVKASASPHTLRNYCLDLNGLKIFLEERGNLAPSSPLQLATEKRKVSELPFSLFTKEHVRM
YIAKLIENGKAKRTIKRCLSSIKSFAHYCVVQKILLENPAETIHGPRLPKELPSPMTYAQVEVLMATPDISKYH
GLRDRCLMELFYSSGLRISEIVAVNKQDFDLSTHLIRIRGKGKKERIIPVTSNAIQWIQTYLNHPDRKRLEKDP
QAIFLNRFGRRISTRSIDRSFQEYLRRSGLSGHITPHTIRHTIATHWLESGMDLKTQIALLGHSSLETTTVYTQV
SVKLKKQTHQEAPHA

>core/503/4/Org4_Gene523

MIHSRLIIIGSGPSGYTAAIYASRALLHPLLFEGLFFSGISGGQLMTTTEVENFPGFPEGILGPKLMDNMKEQAVR
FGTKTLAQDIISVDFSVRPFILKSKEETYSCDACIIATGASAKRLEIPGAGNDEFWQKGVTACAVCDGASPIFK

NKDLYVIGGGDSALEEALYLTRYGSHVYVVHRRDKLRASKAMEARAQNNEKITFLWNSEIVKISGDSIVRSV
DIKNVQTQEITTREAAGVFFAIGHKPNTDFLGGQLTLDESGYIVTEKGTSTSPGVFAAGDVQDKYYRQAV
TSAGSGCIAALDAERFLG

>core/504/4/Org4_Gene227

MRKLILCNPRGFCSGVVRAIQVVEVALEKKGAPIYVKHEIVHNRHVVNALRAKGAIFFEELVDVPEGERVIY
SAHGIPPSVRAEAKARKLIDIDATCGLVTKVHSAAKLYASKGYKIILIGHKKHVEVIGIVGEVPEHITVVEKVA
DVEALPFSSDTPLFYITQTTLSDDDVQEISSALLKRYPSIITLPSSSICYATTNRQKALRSVLSRVNYVYVVGDV
NSSNSNRLREVALRRGVPADLINNPEDIDTNIVNHSGDIAMTAGASTPEDVVQACIRKLSSLIPGLQVENDIFA
VEDVVFQLPKELRCS

>core/505/4/Org4_Gene862

MKCRPTLNTDQPRVRKKLPERFPKWLRPLPQGPAFHATDATIKRSGMPTVCEEALCPNRAECWSRKTATY
LALGDVCTRSCGFCNIGHSKTPPALDPTEPERIALSAKELGLKHVVITMVARDDLEDGGAQGLVDIIRKLGEE
LPQATTEVLASDFQGNVSALHTLLDSGITYNHNIETIERLTPLVRHKATYARSMFMLEQAANYLPNLKIKSGI
MVGLGETEGEVKQTLQDLASVGVRIVTIGQYLRPSRKHIQVKSIVTPETFDYYRRVGTAMGLFVYAGPFVRS
SFNADMILTSVQDKASAQQT

>core/507/4/Org4_Gene53

MKKRYAFLFPGQGSQYVGMGQDLYMEYPEVRELFDFANERLGFSLTSIMFEGPEDLLMETVHSQLAIYLHS
MAVVKVLSQRSSIQPSLVSGLSLGEYTALVASDRISVLDGLELVRKRGQLMNEACNQSPGAMAALLGLPSEV
IEENITSLGQGIWIANYNAPKQLVVAGIAEKVDQAIELFRDLGCKKAVRLKVSGAFHTPLMQVAQDGLAPDI
YALCMKDSSLPLVSHVVGKSLVNTEEMRECLARQMTSPTLWYQSCYHIESEVDEFLELPGPKVLAGLNRSIG
ISKPITSLGTFAQIEKFLSEV

>core/508/4/Org4_Gene371

MLNSNKFKSKTGAYGDLFQRVVHSLVLTFLVLLLYSSLFPLTSFALGFITATCGAVGTYEYSSMAKAKMHY
PLSTFSAIGSFLFLALSFLSIRWGHSLPGFFDALPWTLIVVWVWSIFRVRKSTIGALQLSGVTLFSILYVGPIRL
FLHVLYGFIHTQEPYLGIIWWASFLIATTKGADIFGYFFGKAFGNKKITPQISPNTVVGVFVAGCLGATLISFIF
LQIPTRFASYFPMPAILPLGLALGITGFFGDIIESIFKRDAHLKNSNKLKAVGGMLDTLDSLLLSTPIAYLFLIT
QSKEFIG

>core/509/4/Org4_Gene12

MRLFSYDKPKIKVQKIKADGFSGLKCNHCHEMIHANELGQNYNCCPKCSYHYRITAIERVKLLADKDSWR
PLYTDLKSQDPLEFIDTDTYANRLEKARKNTTESEGVIVGICTIGLHPVALAVMDNFNFMAGSMGAVVGEKLT
RLIEEAIETRLPVIIVSASGGARMQESVFSLMQMVKTSAAALAKLHEAGLPYISVLTNPTSGGVTASFAALGDIII
AEPKALICFAGPRVVAQVIGEDLPEGAQKSEFLLEHGMIDKIVERKELKTTLQTLDDYFLAQEYTGKSKAPR
DLSKRLKEIFLLTDDSE

>core/510/4/Org4_Gene520

MEIAYSLTSSFSVDSVTVGFFDGCHLGHSNLLSILTSYSGSSGVITFDSPQTVLSLNHTKLINTKEERLQLLQT
FPIDWLGVLTFDLNFANQSAEEFLTLLHRNLKCKRLILGYDSCIGKEQQSNTEALDTIGKPLGIEVIKIPPYRMD
NIVVSSKAIRQFLSAGNLECAHRFLGHPY AISGKITEGSGIGSSLGFATINLPREESLIPLGVYACEIRYDSTTCQ
GVMNLGTAPTFGRESLYAEAHIFSFAENLYGKEVSIIPRKFLREEKKFQSKETLIRAIEKDILDAQDWFAKGSF
NYEGTA

>core/511/4/Org4_Gene693

MSSRELIILGCSSQQPTRTRNQGAYLFRWNGEGLLFDPGEGTQRQFIFANIAPTTVNRIFVSHFHGDHCLGLGS
MLMRLNLDKVSHPIHCYYPASGKKYFDRLRYGTIYHETIQVVEHPISEEGIVEDFGSFRIEARRLQHQVDTLG
WRITEPDTIKFLPKESRGIRGPPIQDLIRDQEISIGGSTVYLSDVSYVRKGDSIAIIADTLPCQAAIDLAKNSCM
MLCESTYLEQHRHLAESHFHMTAKQAATLAKRAATQKLILTHFSARYLNLDIFYKEASAVFPNVSVAQEYR
SYPFPKNPLLNK

>core/512/4/Org4_Gene866

MRSIFRFFLCFFTLVSCCFADASLYENSCPSRCQPTPPPSNSNPLNVVQQPVAASSVPSYMPVFNADDVLPRD
HLSDGFSFDTPDITTAAILIFLALSPFLVMLLTSYLKIIITLVLLRNALGVQQTTPPSQVLNGLIALILSIYVMFPT
GVAMYKDARKEIEANTIPQSLFTAEGAETVFVALNKSKEPLRSFLIRNTPKAQIQSFYKISQKTFPSEIREHLTA
SDFVIIIIPAFIMGQIKNAFEIGVLIYLPFFVIDLVTANVLVAMQMMMLSPLSISLPLKLLIVMVDGWTLLLQGL
MISFK

>core/513/4/Org4_Gene755

MKESAPVHFPPVRRSVWLNRYSTFRIGGPANYFKAIHTIEEAREVIRFLHSINYPFLIIGKGSNCLFDDRGRFDG
FVLYNAIYGKQFLEDARIKAYSGLSFAALGKATAYNGYSGLEFAAGIPGSVGGAI FMNAGTNESDISSVVRNV
ETINSEGELCSYSVEELELSYRSSRFHRQQEFILSATFQLSKKQVSADHSKSILQHRLMTQPYTQPSAGCIFRNP
EGTSAGKLIDAAGLKGLAIGGAQISPLHANFIINTGKATSDEVKQLIAIIQSTLKTQGIDLEHEIRIIPYQPKIHSP
VSEK

>core/514/4/Org4_Gene949

MSLFLVFLTAFIWSSSFALSKLVMNASAPIFATGARMVIAGAILALAAWFRGGFVGISKKIFLYIVLLALTGFY
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QIGLPELLILGAASLASFGWTLLRQIEKQSTLSVTAINAYAMLIAGILSIMHS AVVEPWRPLPVQDISQFLYATL
ALVVISNLCYNYAKLLRKYSSTFLSFCNLVMPLYSGFYGWILLGEKGVSLGLVLAVAFMVAGCRLIYHEEF
RQGYIVS

>core/515/4/Org4_Gene856

MQKPQYIDRITKKKVIEPIFYEKTMLFLYNSKLGGKLSVFLSTHPIFSRIYGWLQRCSWTRRQIRPFMNRYKIS
EKELTKPVADFTSFNDFFTRKLKPEARPIVGGKEVFITPVDGRYLVYPNVSEFDKFIVKSKAFSLPKLLGDHEL
TKLYAHGSIVFARLAPFDYHRFHFPDCDFPQKTRCVNGALFSVHPLAVKDNFILFCENKRTVTVLETEQFGNV
LYLEV GAMNVGSIVQTFSPNQTYPKGDEKGFFAFGGSTVILLFLPNAIRFDNDLLKNSRMGMFETRCLMGQSLG
RSQREEI

>core/516/4/Org4_Gene230

MTMPSTQFHTTILEQFSLFLSVDRGLCQQSIAAYRQDISSFLTISAISSPQDISQNSVYIFAEELYRRKEAETTLA
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GVRVSELCDLRLGHVSDDCIRVTGKGSKTRLVPLGSRAREAIDAYLCPFRDQYQKKNPHEDHLFLSTRGHKL
ERSCVWRRIHNYAKQVTSKPVSPHSLRHAFATHLLDNKADLRVIQEMLGHARIASTEVYTHVAADSLIEKFL
AHHPRNL

>core/517/4/Org4_Gene73

MLKIDLTGKVAFVAGIGDDQGYGWGIAKLLAEAGATIIVGTWVPIYKIFSQSWELGKFNESRKLSNGTLLEIA
KIYPMDASFDSPEDVPEDIAENKRYKGITGFTISEVAEQVKKDFGHIDILVHSLANSPEISKSLLETSRKGYLAA
LSASSYSFVSLLSHFGSIMNRGGSTISLTYLASMRAVPGYGGGMSSAKAALES DTKTLAWEAGRRWGIRVNT
ISAGPLASRAGKAIGFIERMVDYYQEWAPIPEAMNAEQVGAVAAFLASPLASAITGETLYVDHGANVMGIGP
EMFPKDS

>core/518/4/Org4_Gene707

MPPPLVVTLT TSAQNNLRDRLKEKNFLFSQPQNTVFQARSNTVTCTLYPSGKLV IQGKGSEEFIEFFLEPEILHT
FTHARVEQDLRPRLGVDES GKGDFFGPLCIAGVYASNAEILKKLYENKVQDSKNLKD TKIASLARIIRSLCVC
DVIIYPEKYNELYGKFQNLNTLLAWAHATIINN LAPKPAGDVFAISDQFAASEYTLLKALQKKETDITLIQKP
RAEQDVVVAAASILARDAFVQSIQKLEE QYQVQLPKGAGFNVKAAGREIAKQRGKELLAKISKTHFKTFDEI
CSGK

>core/519/4/Org4_Gene546

MHLEENQGWEALLRKVYHQEMPPAILLHGFTLPVLQDKAEQLASEILLSSSPGSEHKVSQKIHPDIYQFFPE
GKGRLHSIDLPRGIKKQIYISPFEANYKIYIIHEADRMTLAAISAF LKVFEPPKHAVIILTAKVQRLPKTIISRS
LSIFIERGEKILCSKETFSYLFYQAQCEIPVTEVSQIIKESSETDKQVLRDKVQRFMEV LLELYRDRYTLNLGLK
ASALNYPEHVKEILQLPLLPLDKVLLIVESACRSLNNSSSAASVLEWVAIQLVSLQYKEKELVSVSPGQDLSN

>core/520/4/Org4_Gene551

MRLNYFLNLVNFKYSIFSILFLSASTVFALSINEISQNL SFKEGFKISVFGATAFVFARTTGIVVNQCIDRFIDKK
NTRTSKRVL PANLVSLNFAWVLSLFC SFLFLCKILHIFSLGIASLTLMIVYPYMKRVTF FCHWGLGLVYTVA
ILMNFCFAESGLSMRLCFLAFLWGGSVGMVIAANDIYAIQDTEFDRE EGLRSVPAHYGEKKAVEIAKVNL
WVSYLAYIFSGFVGSLDKEFYFTAIIPLVVILKVVRMYSNYSKKDQEGESKFFLANIAIALSFLVSMTLFWSL
R

>core/521/4/Org4_Gene81

MSERAHIPVLVEECLALFAQRPPQTFRDVTLGAGGHAYAFLEAYPSLTCYDGSDRDLQALAI AEKRLET FQD
RVSF SHASFEDLANQPTPRLYDGV LADLVSSMQDLTSLRGFSFQGEKEELDMRMDQTQELSASDV LNSLKE
EELGRIFREYGEEPQWKSAAKAVVHFRKHKKILSIQDVKEALLGVFPHYRFHRKIHPLTLIFQALRVYVNGED
RQLKSLTSAISWLAPQGRLVIISFCSSEDRPVKWFFKEAEASGLGKVITKKVIQPTYQEVRRNPRSRSAKLRC
FEKASQ

>core/522/4/Org4_Gene883

MSRREICPEVSHKKGKYYSTFIFRCIHSLAGIAFTFFLCEHLFTNMLASSYFSQGKGFVAMVNGFHKIPGLKIIIE
VVGLALPCLCHAIIGIVYLFQGKSNCYSGDGRPHLRYAKNYSYTWQRWTAWILLFGIAFHVVHLRFIRYPV
HVDIHGTTYAAVDIQPFYRDVIVRGTKGFLTLNLPNTEASSIEVSRHDLGGADAALLSEGNSYLLTPSAGTAF
LYVVRDALGSLFIALLYTILVIAAAFHGFNGLWTFCCRWGVVVSRLMQGVLRIVCYLAMIVVTFMGVSVVW
NLYSVA

>core/524/4/Org4_Gene570

MRRFLFLILSSLPLVAFSADNFTILEEKQSPLSRVGIIFALPEVTPVSFDGNCPIPWFSHKKTLLEGQRIYYSGDS
FGKYFVVSALWPNKVSSAVVACNMILKHRVDLILIIGSCYSRSQDSRFGSVLVSKGYINYDADVRPFFERFEIP
DIKKSVMFATSEVHREAILRGGEFISTHKQEIEELLKTHGYLKSTTKTEHTLMEGLVATGESFAMSRNYFLSLQ
KLYPEIHGFDSVSGAVSQVCYEYSIPCLGVNILLPHPLESRSNEDWKHLQSEASKIYMDTLLKSVLKELCSSH

>core/525/4/Org4_Gene44

MSHGPRPTKFSFPLYFSKTLNFWFILGGFLAACGVQMVLVPNELIDGGIVGLSIIASHFLGHKALPFCLVLFNLPF
VFLAFKQIGKYFVIQMLTAVIIFSCSLWLIDQLPSWLGMSPFVFKGSEMETVVLGGAIIGVGCGLIIRHGGSTD
GTEILGIIINKKKGYTVGQIILFVNFFIFALSGIVYKNWHTAFVSFLTGYGIATKVMMDMVILGLEDTKSVTIITSSP
RKLGHILMETLGIGLTYIHAEGGYSGEPRNLLYVVVERLQLSQLKEIVHREDPSAFIAIENLHEVINGRRT

>core/526/4/Org4_Gene816

MQEKPRHVHRIIHISDVHFHVLVPNPVHCFNKRLKGLLRKVFGVLVHFQATTIGQRFKVVRSLGADSVICITGD
FSLTAMDGEFLLAKHFVETLAKHSSVYLLPGNHDVYTPKSLAQQTIFYTHFPNDQLQQNKVSFHKITDHWL
ILLDCSCLNGWFSANGVVHLAQISAIETFLLSLSPEENVIIANHYPLLSSQNPSHDLINNTHLQNVLKKYPKVRL
YLHGHEHQAAVYNCA DTSPSYILNSGSISLPTNSRFHVIDLYPEKYQVHTMILKNLLDFDAPLEIANEATWDC
QKL

>core/527/4/Org4_Gene468

MEKLLVTDIDGTITHQSHHLDKKVYERLYALHQAGWKLFFLTGRYYKYAARLFSDFDAPYLLGCQNGASV
WSSTSSNLLYSKSLPSDLLCILQDCMEGATALFSVESGAPYGDHYRFSPTPIAQDLHEYVDPRYFPNAKEREI
LFETRSLKDDYAFPSFAAAKVFGRLDEVIRIQKELERQEALTSVATMTLMRWPFDFRYAILFLTDKSVSKGKA
LDRVVNILDGKKPFVMASGDDANDLDLIERGDFKIVMSSAPEEMHVVHADFLAPPADKNGILSAWEAGVRY
YDELMSL

>core/528/4/Org4_Gene140

MKKLILYFAAFVASLFCGVFLWDRVPCAQKIMRLAADHSSEVFSKSCRFRVKISGFEELQVFERHVSPEQALA
LFPEYRDGKSFVELAFIPHTLMHVRFSKEEPVKKHIISQEGEILWSLVNGEMVLHTGTWTCCKGFRECLLLHA
GKQDMRVIQTLATLGGTTSRESLAQALALKNIRAERVIKECQKKKLIFASGNQIGTHFQQFQPIRGCTTTLNN
NPVWLQKPRHAAVFPAQYSEDRVRHLVKMIFGDNFLIVRSSMVYVPVYKISLVSADNSVRVEYINAVTGKSF
QDL

>core/529/4/Org4_Gene217

MFHSLSKNTPIITQGITGKAGSFHTEQCLAYGTNFVGGVTPGKGGTLWLDLPVYDSVLEAKQATGCRATMIF
VPPPYAAEAILEAEAEAGIELIVCITEGIPVRDMLEVARVMDNSTSQLIGPNCPGIIKPGECKIGIMPGYIHLPGNI
GVVSRSGTLTYEAVWQLTQLKIGQSICVGIGGDPLNGTSFIDVLQALEEDPYTELILMIGEIGGSAEEEEAAAWI
QAHCTKPVVAFIAGVTAPKGKRMGHAGAIISGNSGDAKSKIQVLRESGVTVVESPAHIGKTVDAVLRAKEL

>core/530/4/Org4_Gene817

MSKHTSESRIAQDMLERYSGSNVKQFCPYLLL TNFSYIIQTFAKLHGVPIFEGSMFSAAHAPHLKTSILDFKLG
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EVLEDDKKANYHIGITHTTNIRFWEFNKKFRKKLYETKAQSAEMECATLFAAGYRRNLPIGALLLISDLPLRKE
GIKTKSSGNFVFNTYTEDHILTGQEVIENTLEKVMLKRAASDHKKDQQYRGLPHMEVGEADDTMASGSETSD
SDY

>core/531/4/Org4_Gene266

MKVLPPPSIPLLGAHTSTAGGLKNAIYEGRDIGASTVQIFTANQRQWQRRALKEEVIEDFKAALKETDLSYIM
SHAGYLINPGAPDPVILEKSRIGIYQEILDCITLGISFVNFHPGAALKSSKEDCMNKIVSSFSQSAPLFDSSPPLV
VLLETTAGQGTLIGSNFEELGYLVQNLKNQIPIGVCDTCHIFAAGYDITSPQGWEDVLNEFDEYVGLSYLRA
FHLNDSMFPLGANKDRHAPLGEGYIGKESFKFLMADERTRKIPKYLETPGGPENWQKEIGELLKFSKKQR

>core/532/4/Org4_Gene919

MLSSLIRDSFPLLILLPTFLAALGASVAGGVMGTIYIVVKRIVSISGSISHAILGGIGLTLWIQYKLHLSFFPMYGA
IVGAIFLALCIGKIHLKYQEREDSLIAMIWSVGMAIGIIFISRLPTFNGELINFLFGNILWVTPSDLYSLGIFDLLV
LGIVVLCHTRFLALCFDERYMALNHCSVQLWYFLLLVLTAITIVMLIYVMGTILMLSMLVLPVAIACRFSYK
MTRIMFISVLLNILCSFSGICIA YCLDFPVGPTISLLMGLGYTASLCVKKRYNPSTPSPVSPEINTNV

>core/533/4/Org4_Gene945

MKRNDPCWCGSGRKWKQCHYPQPPKMSPEALKQHYASQYNILLKTPEQKAKIYNACQVTARILDELCKAS
QKGVTTNELDELSQELHKKYDAIAAPFHYGSPFPKTICTSLNEVICHGIPNDIPLKGDIMNIDVSCIVDGY
GDCSRMVMIGEVP EIKKKICQAAL ECLNDSIAILKPGIPLCEIGEAIEARADTYGFSVVDQFVGHGVGIEFHENP
YVPHYRNRSMIPLAPGMIFTIEPMINVGKKEGVVDPKNQWEARTCDNQPSAQWEHTIAITETGYEILTLLND

>core/534/4/Org4_Gene716

MHLLTATVTPFFPNGTIDFASLERLLSFQDAVGNGVVLLGSTGEGLSLTKKEKQALICFACDLQLKVPLFVGT
SGTLLEEVLWDWIHFCNDLPISGFLMTTPITYTKPKLCGQILWFEAVLNAAKHPAILYNIPSRAATPLYLDTV
KALAHHPQFLGIKDSGGSVEEFQSYKSIAPHIQLYCGDDVLWSEMAACGAHGLISVLSNAWP EEA
REYVLPNPQEQDYRSLWMETCRWVYTTTNPIGIKAILAYKKAITHAQLRLPLSIEDFDLENVSPAVESMLAWPKLR
TSVFSYS

>core/535/4/Org4_Gene216

MFKFFRNKLQSLFKKNISLDLIEDAESLFYEADFGTELTEELCARLRRTKKADASTIKDLITVLLRESLEGLPSQ
ASQSSQTRPIVSLLLGTNGSGKTTTAAKLAHYYKERSESVMLVATDTFRAAGMDQARLWANELGCGFVSGQ
PGGDAAAIAFDGIQSAIARGYSRVIIDTSGRLHVHGNLMKELSKIVSVC GKALEGAPHEIFMTVDSTLGNN
AIEQVRVFHDVVPLSGLIFTKVDGSAKGGTLFQIAKRLKIPTKFIGYGESLKD LNEFDLDFLNKLFPEVEKI

>core/536/4/Org4_Gene556

MKRRNLQKILPNASTPSTNVAENTGIKDQNLFLDQATLNVDGSVDVENFLETRDLKVADTITSPCEFTVGGAL
LSAESSQFKATTLRSGLEITSEDQNGRVPKFINVSDPQSPRDALTYNYYRNTGCQALNMYTFYDGLYSAQPTT
VGKPIEPVSQNPGPPTYHTSASAKIYDAIGTTPYVEFKAPGIYQVTIQVLRDLGQHSGNDYPNLYLNLMIGNN
KTLLCASDTRGYSGGHRTSVAVTGTFTLLEIVTTPPRDYPWLFLLETTIGLNIKSMSTCIIWFPPQSNFAEVD

>core/537/4/Org4_Gene251

MQIPRSIGTHDGSFHADEVTAALLIIFDLVDENKIIRS RDPVVL SKCEYVCDVGGVYSIENKRFDHHQVSYDG
SWSSAGMILHYLKEFGYMDCEEYHFLNNTLVHGVDEQDNGRFFSKEGFCFSFSIIKIYNPREEEETNSDADFS
CALHFTIDFLCRLRKKFQYDRVCRGIVREAMETEDMCLYFDRPLAWQENFFFLGGEKHPAAFVCFPSCDQWI
LRGIPPNLDRRMEVRVPFPENWAGLLGKELSKVSGIPGAVFCHKGLFLSVWTNRESCQRALRLTLQDRGII

>core/538/4/Org4_Gene867

MGISLPELFSNLGSAYLDYIFQHPPAYVWSVFLLLLARLLPIFAVAPFLGAKLFPSPIKIGIGLSWLAIIFPKVLA
DTQITNYMDNNLFYVLLVKEMIIGIVIGFVLAFFYAAQSAGSFITNQQGIQGLEGATSLISIEQTS PHGILYHYF
VTIVFWLVGGHRIVISLLLQTLEVIPIHSFFPAEMMSLSAPIWITMIKMCQLCLVMTIQLSAPAALAMLMSDLF
LGIINRMAPQVQVIYLLSALKAFMGLLFLTLAWWFIHKQIDYFTLAWFKEVPIMLLGSNPQVL

>core/539/4/Org4_Gene161

MLHALD TYRPSIESAIEKALEGFGPIGHPIRSPVEYALQGGGKRLRPGLVCMMAQGLGLNHDVMDSALAVEF
VHTSTLIADDLPCMDNDDERRGRPTVHKAFDEATALLASYALIPAAAYSHLRLNAKKLKEQGCDPREIDIAYN I
IGDITDKNIGCSGVLGGQYDDMFFSNRGQEHVQSIMIKKTGSLFEIACISGWLFGGGDPQFAPIITSFSNNFGLL
FQIKDDFSDLQKDSQQIGLNYALLFGEKAALELLARSQNNCLELLDRLSAGGLKNSSEFETIISSLGSF

>core/540/4/Org4_Gene557

MSNPTPKTKISIPTFVRFNVSINLTEDQKKTALT VGGKVT TENTVVGGDLTCTDGGLTCQSDLT IQKDINIRP
TSTNSMVFDGRLNLSNSPLSYKNSQGQDITDYEKISSGKPQEYVPFGYYKRTQIMMAQRGATSSGHVSGSV
PSGSYVPWNKFDQTSVQKTSGETIYIDPNDGTKLVFEVNSKVPKLFRIIIMAKNGSWLDNGTGADVLLAANE
YEQSGGKIKVTELAMTSSRGTSYYETRPLQVVCVTYYAKNNGYFTFQNRAGGGFRVSFFSWNIVSLPYVE

>core/541/4/Org4_Gene704

MLKIQKKRMCVSVVITVGAIVGFFNSADAAPKKKKIPIQILYSFTKVSSYLKNEDASTIFCVDVDRGLLQHRY
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TLHSLLRQNLSFQKRSIASESFLKIDSAPSDASVFYKGVLF RGETAIVDALSQLFAQLDLSPKKIIFLGEDPEV
VRAVGSACIGWGMNFLGLVYYPAQESLFSYVHPYSTATELQEAQGLQVISDEVAQLTLNALPKMN

>core/542/4/Org4_Gene692

MSHLIPSLRNSVTSYFHKPQPIKQAAPSKSIRDICNIAYLIIICVLV VVVVLVGAMLCMFIPSVGIPLCLSSLALLV
LLSIFNPCLINWISTKKTKEIAPKDASESQPTKSASRKGSPQLSPHHDHEPKNFIRTQLEKGVNYVTNKFKSGEE
SPHISDEHHSRQSKRSSEIESSDESSPELHRKAKGKAPHTATT KESKTSTTESSKKKKKTKHSLHRTTSSIHKR
SAPKPMVPSKKRKPVPLKKPVPLPIEDLEHQSSGNESSDSSSPPPVQRKAILPWFCQPTDP

>core/543/4/Org4_Gene26

MEIKKAIQEGTAYLDYYGVPLSDCEALYILMDLLEVSSRAKLFDLVGISETMLMEYRKRLALRGQRCPTAYL
NGAVSFLGLRLRVDSRVLIPRTETELLA EYIINYLLSHSEIQTFYDICC GSGCLGLAIKKSCPHVEVVLSDVCPQ
AVAVANENAKSNGLDVKILLGDL SAPYTRPADAFVCNPPYLSFNEIIHIDPEVRCYEPWKALVGGSTGLEFYQ
RIAQELPKIVTSTGVGWLEIGSSQGESIKNIFSKHGIYGR LHQDLSGRDRIFFLEMDGRDPVSSGAYS

>core/544/4/Org4_Gene982

MAVIYWDRSKIVWSFEPWSRLTWYGVFFTVGIFLACLSARYLALSYYGLKDHL SFSKSQLRVALENFFIYSI
LFIVPGARLAYVIFYGWSFY LQHPEEIIQIWHGGLSSHGGILGFL LWAAIFSWIYKKKISKLTFLFLTDLCGSVF
GIAAFFIRLGNFNWQEIVGTPTSLPWGVVFS DPMQGVQGVVHPVQLYEGISYLVVSGILYFLSYKRYLHLGK
GYVTSIVCISVALIRFLAEYVKSHQGVLAEDCLLTIGQILSIPLFLFGVALLIICSLKARRHRSHI

>core/545/4/Org4_Gene510

MLLRGIPAAEKILQRLKEEISQSPTSPGLAVVLIGNDPASEVYVGMKVKKAAEIGIISK A HKLPDSTLSSVLKL
IERLNQDPSIHGILVQLPLPKHLDSEVILQAISPDKDVDGLHPVNMGKLLLGNFDGLLPCTPAGI IELLNYYEIP
LRGRHAAIVGRSNIVGKPLAALMMQKHPQTNCTVTVLHSQSENLPKILKTADIIAALGAPLFIKETMVAPHA
VIVDVGTTRVPADNAKGYTLLGDVDFNNVVTKCAAITPVPGGVGPMTVAMLSNTWRCYQNFS

>core/546/4/Org4_Gene144

MTEEISKDTIIEVAIDDIRVSPFQPRRVFSNEELQELIASIKAVGLIHPPV VREICTGDRVLYELIAGERRWRAM
QLAGATTIPVILKHVIADGTAAEATLIENIQRVNLNPIEMAEAFKRLIHVFGLTQDKVAYKVGKKRSTVANYL
RLLALS KTIQESLLQGQITLGHAKVILTLEDPILREKLNEIIIQEHLAVREAELIAKQLISEEGSSI ELKPTPLDMA
ESSKQHEELQQR LSDL CGYKVQIKTRGSKATVSFHLQNTQDLQKLEAWLSSHGTLSESLS

>core/547/4/Org4_Gene548

MPDKKAQITFSLPEVMSAIHQGKIVALPTDTVYGVFLSLYASEAEERLYALKDREPSKAFALYVNSIEDIENIS
GYPLSPTAKKLAQLFPGAITLVVKHRNPRFPKETLAFRIVDHSVVREIVDHC GTLIGTSANLSEFP SALTAEV
FADFADHDL CIFDGP CSHGLESTVVASDPLYIYREGLISRSVIENIAGTEAKIFHRTSHAFSKHIKIYTVKNQEQ
LVSFSLGSLDFKGVVCEHPKPKNFYTRLREALKKKTPSIVFIYDINTSDYPELFPFLSPYYIE

>core/548/4/Org4_Gene555

MTTTNNQDNNECYFKLDSTVDGDLLASNIQTFDTQAKGISSTETFSVEGNATFKDQVSATGLTSASTYKLNA
TGPAPSSITIDMKNNRLSNPALPKNPCDPVPANYVRSPQYFFCSKPIEGTFTFDGSSRYLPITGDGSNYTLYQSN
KAGDVFRFVSWDQNSKKLNLGGNTAIQLLAAGTYILTFTIGKRWGWNNGWGG SIRLFEGKFTGDGTILCGST
VYSGGGYSTIGYLSTAVYRDHSDVDPDPNNPSNRYMNNFLFVRNGDSSAVIGNYSFTLLYFAGDKV

>core/549/4/Org4_Gene425

MHEVLILTFTYPLPRTLKQHPDEVHTVPISP NLSFGEGSPILIAGPCTLESYEHTVSSALT VKEAGA QVFRGSIR
KPRTSPFSFQWEKECVLWHKEAQRIHGLPTETEVL DVRDVEITA EHV DILRIGAKNMHNTPLLQE VSKSHRP
IILKRSPAATLEEWLCAA EYILASPSCPGVILCERGIRTFEHSTRYTLDLNTVALLKEISSLPVIVDPSHAAGKRS
LVLPLASAGLSVGADGLMIEVHAHPEKALCDAKQQITPEELRLFAKKHFCPSESRAHAIS

>core/550/4/Org4_Gene563

MKHYLSFSPSADLFSKQGAJETQVLFGERVLVKGSTCYAYSQLFHNELLWKPYPGHSFRSTLVPCTPEFHIHP
NVSVVSVDAFLDPWGIPLPFGTLLHVNSQNTVIFPKDILNHMNTIWGSGTPQCDPRHLRRLNYNFFAELLIKD
ADLLLNFPYVWGGRSVHESLEKPGVDCSGFINILYQAQGYNVPRNAADQYADCHWISSFENLPSGGLIFLYP
KEEKRISHVMLKQDSSTLIHASGGGKKVEYFILEQDQKFLDSTYLFRRNNQRGQAFFGIPRKRKAFL

>core/551/4/Org4_Gene36

MDNYLLNIKDLTITSTNPKRTLIENTSLQLKENRNLALVGESGSGKTTITKAILGFLPENCLIKTGSILFEDIDIT
KLSPKELHKIRGQKIATILQNAMGSLTPSMRIGMQIIETLRQHHKMNKEEAYNKAMQLLTDVCIPNPKYSFSQ
YPFELSGGMRQRVVIAIALASQPKLILADEPTTALDSMSQAQVLRILRNIQQKQATILLVTHNLSLVKELCND
ICIIKDGLIETGTVEEIFLSPKHPYTLKLLNAVSKIPIKKTSSPILKNKFQPLMSMQGGL

>core/552/4/Org4_Gene589

MENLSSAPSRSIWKSIIQNKMLVLGLTTLIILILGALLLPWFYQDYEQTSLKDILVSPCSRFPFGTDTLGRCMFA
RTLRLGLRLSLLIATLATLIDVCVGLLWATVAISGGKKIDFLMMRTTEILFSLPRIPHIILLVIFHHGLLPLILAMTI
TGWIPISRIIYGQFLLLKNKPFVLSAKAMHASTFHILKKHLLPNTLAPIISTLIFTIPNAIYTEAFISFLGLGIQPPQ
ASLGLTVKEGINAIDYYPWLFFFPSLIMIALSISFNLIGEGAKTLCLEEGSHG

>core/553/4/Org4_Gene607

MKQPMSLIFSSICLGLGLGSLSSCNQKPSWNYHNTSTSEEFFVHGNKSVSQLPHYPSAFRTTQIFSEEHNDPYV
VAKTDEESRKIWREIHKNLKIKGSIPISTYGSLMHPKSAALTLKTYRPHPIWINGYERSFNIDTGKYLKNGSR
RRTSHDGPKNRAVLNLIKSSGRRCNAIGLEMTEEDFVIARRREGVYSLYPVEVCSYPQGNPCGIAYAWIADES
ACSKEVLPVKGYYSLVWESVSSSDSLNAFGDSFAEDYLRSTFLANGTSILCVHESYKKVPPQP

>core/554/4/Org4_Gene130

MFKKFKPVTPGTRQLVLPADFELTTRGELRGTKSKRSLRPNKKLSFFKKSSGGRDNLGHISCRHRGGGAKQL
YRVVDFKRNDGITAKVVTVVEYDPNRSAYIALLSYEDGEKRYILAPKGIQRGDVVVSGEGSPFKPGCCMTLK
SIPLGLSVHNIEMRPSSGGKLVRSAGLAAQVIAKSPGYVTLKMPSGEFRMLNEGCRATIGEVSADHNLNRVD
GKAGRRRWMGVRPTVRGTAMNPVDHPHGGGEGRHNGYIPRTPWGKVTGLKTRDKNKSNKWIVKDRRK

>core/556/4/Org4_Gene319

MASIHPTAIIEPGAKIGKDVVIEPYVVIKATVTLCDNVVVKSAYAYIDGNTTIGKGTTIWPSAMIGNKPQDLKYQ
GEKTYVTIGENCEIREFAIITSSTFEGTTVSIGNNCLIMPWAHVVAHNCTIGNNVVLSNHAQLAGHVQVGDYAIL
GGMVGVHQFVRIGAHAMVGALSGIRRDVPPYTIGSGNPYQLAGINKVGLQRRQVPFTTRLALIKAFKKIYRA
DGCFFESLEETLEETLEEYGDIEVKNFIEFCQSPSKRGIERSIDKQALEEESADKEGVLI

>core/557/4/Org4_Gene289

MSDFSMETLTKTLRQQTGVGLTKCKEALEACGGNLEEAVVYLRKLGLASAGKKEHRETKEGIIAAKTDANGT
ALIEVNVETDFVANNAVREFVSNLLNDILKYKVDTEALSQAASSQDPSLSVDELRAVTMQTVGENIRISRV
AYFPAKANSTVGIYSHGNGKTVALTMLSGSSTADSLAKDIAMHVVAQAQPFLSKESVPAEIAAKEKEVIASQI
QGKPQEVIEKIVTGKLNTHFFQEACLEQPFIKNADLSIQSLIDDFSKTSGSSVAIEQFILWKIGA

>core/558/4/Org4_Gene133

MLERTQRTLKREVRYSVGVIHLGKSSSTLHLQPAQTNTGIVFQRQSASGNYENVPALLDHVYTTGRSTTL SRG
SAVIATVEHLMAALRSNNIDNLIQCSGEEIPIGDGSSNVFVELIDQAGICEQEDKVSIALRTRPVYYQH QDIFL
AAFPSDELKISYTLHY PQSSTIGTQYKSLVINEESFRQEIAPCRTFALYNELCFLMEKGLIGGGCLDNA VVFKD
DGIISRGQLRFADEPVRHKILDLIGDLSLVGRPFVAHVLA VSGHSSNIAFGKKILEALEL

>core/559/4/Org4_Gene903

MATAHLGRQALLHLRSWTPAIRTSGNLFRQQSMSLHNNILFAGDIIGA IKNSTAISRYALGSSHHAAHALQKT
EGFLGAADGVNTAVAGAMLWGQLLNGSMIFETDEETGELRRCNEADAEGCRTQKLQRRSALTITGKVARL
ASKTLGTATFLHEMDVVS LGANANKIGCKVTSCNLVATGCSL TESSISLYRILSTRPETISDPENRNKPSAEF
AARSKAIRNAFI AWLGDMVDLVCDALGTLSLFLPAILGVH AVLIMAILGLISCVIN FVKDYAKIG

>core/560/4/Org4_Gene974

MVLMNKRLKIILTND DGITAKGMSCLVSALLEANIGDIYIAAPQAEQSGKSMAISLNQVVCASPYAYPQP VKE
AWAVGGSP TDCVRLGLRTL FESVSPDLVISGINCGNNICKNAWYSGTVGA AKQALVDGIPSMALSQDNHISF
FQQYKAPEILKALVIYLLSQPFPCLTGLNINFPTSPGGSSWEGMRLVPPGDEFFYE EPQYLGSVNKNQYYVGKI
SGVRIGEHPSEELACMLENHISVSPIFSQNSPIGLMTLEEFQKTQENFNASLLSSEL TTKIF

>core/561/4/Org4_Gene283

MELKKTAESLYSAKTDNHTVHQNSPEPRDSRDVKVFSLEGKQTRQEKT TSSKGNTRTESRKFADEEEKRVGD
EIAEVGSKEEEQESQEFC LAENAFAGMSLIDIAAAGSAEAVVEVAPIAVSSMDTQWIENIILSTVESM VISEING
EQLVELVLDASSSVPEAFV GANLTLVQSGQDLSVKFSSFVDATQMAEAADLV TNNPSQLSSLVSALKGHQLT
LKEFSVGNLLVQLPKIEEVQTPLHMIASTIRHREEKDQRDQNQKQKQDDKEQDSYKIEEARL

>core/563/4/Org4_Gene731

MRQSFDELSQNAFKNIFNKQRFCFIFCSLCCFGFVFALFLKLCSRLA PEISLSTLGLGAFFCAFSVICASAIIVQF
LLHKESQGETSKLCCA IKNTWSSLWLSLLVSMPPFIAMVAVVTVM LSSFLGSLPWVGKLFHTVLIFIPYLSA
TALILLFLGSFSLFFCIPVLHNQESIDYRKLLDCFRGNILRQFIGVVIALV PLALCSWLALDSFYLMTHLVEIA
DIHTWSFLAQMFVLIVPIALILTPAVSFFFNFSFSFYLA KQEEEEKALVK

>core/564/4/Org4_Gene388

MHKVIVFVFLTLYSLKSYGNDVIDKPHVLVSIAPYKFLVEQIAEETCFVY AIVTNHYDPHTYELPPRQIKELRQ
GDLWFRIGEAFEKTCERNL TCQQVDLSQNVSLIQGKPCCNQHTTNYDHTW LSPKNLKVQVETIVTTLSKKY
PEHATLYQSNGEKLLLALDQLNEEILTITSKAKQRHILVSHGAFGYFCRDY NFSQHTIEKSSHVEPSPKDVARV
FRDIEQYKISSVILLEYSGRRSSAMLADRFHMHTVNLDPYAENVLVNLKTIATTFSSL

>core/565/4/Org4_Gene332

MYFTRDPVIETVITSREGYKLSVRNTKHFSQDPFMVEAIEVISLGNICFFRN CDHSPFLVPAGDYEVMEVRDT
KINLKAVGLDRGVK IAGGREALIKLTKSTPLPVIDEKPLADSPEEGTEPTSPSKKEKKEARKDSFKGEKWKEK
KKLSRRRNHKEIAEVTGASQEILD TVKEELWEESQENEIVEQKKFSLPPP AKLISEVISQTVVDPVVT SADLN
ESLQALVRESSDVINALLSADDAIHFPETEEPTSASFEESSAMFFPETSSATEEE

>core/566/4/Org4_Gene712

MTRSSPAQLSRLLEIQNKPKKSLSQNFLVDQNIVKKIVATSEVIPQDWVLEIGPGFGALTEELIAAGAQVIAIE
KDPMFAPSLEELPIRLEIIDACKYPLDQLQEYKTLGKGRVVANLPYHITTPLLTKLFLEAPDFWKTVTVMVQD
EVARRIVAQPGGKDYGSLTIFLQFFADIHYAFKVSASCFYPKPQVQSAVIHMKVKETLPLSDEEIPVFFTLTRT
AFQQRKVLANTLKGLYPKEQVEQALKELGLLLNVRPEVLSLNDYLALFHKMQAG

>core/567/4/Org4_Gene290

MESQSCKLTIKDLMSAGAHFGHQTRRWHPKMKLYIFEEKNGLYIINLAKTLQQLRNALPHIRKVIQDNKTVL
FVGTKKQAKCVIREAAIEAGEFFVAERWLGGMLTNMTTIRNSIKTLDKIEKDLSRNQAYLTKKEAALLAKRH
QKLLRNLEGIRYMKKAPGLLVVVDPSYEKIAVAEAKKLGIPVLALVDTNCDPTPIDHVIPCNDDSLKSIRLIIN
VIKENIIEAKHKLGIEIVSPVKSLEVPDLSAFESSQDDESEENREEDLLAKKFDSEAN

>core/569/4/Org4_Gene864

MTANTFGTLDILMKHSEDDLSRFLPKNLLVESPHPEEIPLKSLSFTMSWLPTIHPSWITIAMKEFPPEIQGQLL
AWLPEPLVQEILPLPGISMAPHRCAPFGAFYLLDMLSCKIRPCGITTEIFLPASSANAILYYTGPKIALINCLG
LYSIAKELKHILDKVVIERVKNALSPTEKLFLTQYCSHPMKHLETTNLFSSWTTDAELRQFVHKQGLEFLGKA
LTKENASFLWYFLRRLDVGRAYIVEQTLKTYDHPYVDYFKSRLEQCMKVLVK

>core/570/4/Org4_Gene397

MDYKLLDSGDGNKLECFGPVTLIRPSSIAVWPKSRLPELWSQAQLQYVREGERGAWKNFKRLPEEWEVAFSD
VRCLLKRTPFGLHGVFPEHMGFWPALKQAIEKHKECQVLNLFAYTGAGSIFAACGARVTHVDASQA AVR
WAQRNVEKNAFPERRIFWVIEDVISFLKKEIRRNKKYQVILLDPPSYGRGPDGDVFKIDKDLFPLLSLCSKLLA
DDASYFLLTSHTPGHTPEFLRAIARRSVPTLVSEAWSCGESFCGEGVGALPSGSFVQWIA

>core/571/4/Org4_Gene612

MITGVVLEKHEQRTMFSLTLLNNFTTFGVLHTPLHYNPPYPIVILLHGLASDKTGSKRSHVRLAQELTRLGIA
ALRVDLLGHGDGEGELMDFSLENYKQNIREIIEYTHSLHIDQERLAIFGSSLGGTLALQTLPPFDKIKALAVW
APTISGELMAAEAQKNAPEVITMSQKGAITYAGMTLNPDFYTQFLKIDIVKELMPSARNLPPILYMQGEQDHL
VSMNHRTLFTFAFANQDKPITILTYPDVDHAFPPFAESSALSDLTQWLKRELTSRE

>core/572/4/Org4_Gene272

MLLGFLCDCPCASWQCAAVANCYDSVFMSRPEHKPNIPYITKATRRGLRMKTLAYLASLKAARQLAYDFLK
DPGSLARLAKALIAPKEALQEGNLFFYGCSNIEDILEEMRRPHRILLGFSYCQPKACPEGRFNDACRYDPSH
PTCASC SIGTMMRLNARRYTTVIPTFIDIAKHLHTLKKRYPGYQILFAVTACELSLKMFGDYASVMNLKGVG
IRLTGRICNTFKAFKLAERGKPGVTILEEDGFEVLARILTEYSSAPFPRDFCEIH

>core/573/4/Org4_Gene703

MRRYLFMVLAALCLYRAAPLEAVVIKITDAQAVLKFAREKTLVCFNIEDTVVFPKQMVGQSAWLYNRELDLK
TTLSEEQAREQAFLEWMGISFLVDYELVSANLRNVLTGLSLKRSWVLGISQRPVHLIKNTLRILRSFNIDFTSC
PAICEDGWL SHPTKDTTTFDQAMAIEKNILFVGS LKNGQPMDAALEVLLSGISSAPSQIIYVDQDAERLRSIGAF
CKKANIYFIGMLYTPAKQRVESYNPKLTAIQWSQIRKNLSDEYYESLLSYVSKSG

>core/574/4/Org4_Gene645

MKVKINDQLICIPPFISARWSQIAFIESQEGENKDQGTLRLHLIDGKIISIPNLDQSIIDIAFQEHLLEYLETSQSGKE
DSRDDDKLGVGVLMNVLQQITKGNDIQVLPKNLISPLFSGTNPIEAILQHTPEHKDHPDAPTDVLEKMADVIR
VLSGNNATLLPKPEPHCNCMHCQIGRVMNEEDTLAVSDKDLTFRTWDIMQSGDKLYIVTNPLNPSEQFSVYL
GSPIGCTCGEPNCEHIKAVLYT

>core/575/4/Org4_Gene479

MKLLKNVLLGLFFSMSISGFSEVKVSDTFVKQDTVVEPKIRVLLSNESTTALIEAKGPYRIYGDNVLLDTAIQG
QRCVVHALYEGIRWGEFYPLGLQCLKIEPVDDTASLFFNGIQYQGSLYVHRKDNHCIMVSNEVTIEDYLKSVL
SIKYLKELDKEALSACIILERTALYEKLLARNPQNFHWVKAEEEGYAGFGVTKQFYGVVEEAIDWTARLVVDS
PQGLIIDAQGLLQSNVDRLAIEGFNARQILEKFYKDVDVVFVIESWNEELDGEIR

>core/576/4/Org4_Gene542

MKKKLSLLVGLIFVLSSCHKEDAQNKIRIVASPTPHAELLESQEEAKDLGIKLIKILPVDDYRIPNRLLLDKQV
DANYFQHQAFLLDDECERYDCKGELVVIKVVHLEPQAIYSKKHSSLESLSQKKLTIAIPVDRTNAQRALHLL
ECGLIVCKGPANLNMTAKDVCCKENRSINILEVSAPLLVGSLPDVDAVIPGNFAIAANLSPKKDSLCLDLS
VSKYTNLVVRSEDVGSPPMIKLQKLFQSPSVQHFFDTKYHGNILMTQDNG

>core/577/4/Org4_Gene429

MVRDIQSESIGKLVFLGTGNPEGIPVPFCSCRVCQNTGIHRLRSSVLIQYQNKTLVIDAGPDFRTQMLVAGVSE
LDGVFLTHPHYDHIGGIDDLRAWYIVTQRSPLVLSASTYRFLNKAKEYLFATPNVESSLPAVLEFTILNEDYG
QEEFQGIPYTYVSYYQKSCHVTGFRFGNLAYLTDLCSYDAKIFSYPDNDVETLILSAGPSETPIAFQGHKSSHLT
VEEAKAFANHAGIKNLIITHISHCLEAERDQHLEVTFAIDGMEVLWTL

>core/578/4/Org4_Gene247

MIRFFKTLFPPGPQYSLCYASILIVLSSLVCVPTFCWLFLPELSLSKFNPSPIRNLFLVSSTLSKVPPTAIAEHLR
LSADAPTYLHEFSIKEAESSLHALGIFSSLVIEKSPDNKGITIFYTLQTPIAYVGNRSNTLCNLEGSCFLGQPYFP
SLNLPQIFFSQEDLKMQKLPKEKMLFTKILLKELAMESPKIIDLSLSDAYPGEIIVTLSSGSLLRLPIKTLDRALD
LYKHMKKSPVIESEKQYVYDLRFPNFKLLKAL

>core/579/4/Org4_Gene274

MFNNKMILIAGPCVIEGEDITLEIAGKLQSILAPYSDRIQWFFKSSYDKANRSSLNSFRGPGLTEGLRILAKVKE
TFGVGILTDVHTPQDAYAAAEVCDILQVPAFLCRQTDLLIATAETGAIVNLKKGQFLSPWDMEGPINKVLSTG
NNKILLTERGCSFGYNNLVSDMRSIPVLSRSGFPVIFDATHSVQLPGALSTESGGQTEFVPTLSRAALAAGAHG
LFIETHNPKIAKSDAASMLSLEEFAALLPTWDQLFTCVSSFDMVSA

>core/580/4/Org4_Gene918

MTKVALLIAYQGTAYSGWQQQPNDLSIQEVISSLKKITKTRTPLIASGRTDAGVHAYGQVAHFRAPDHPLF
ANPNLTKKALNAILPKDIVIRDVALFDDNFHARYLAIKEYRYSLSRLAKPLPWQRHFCYTTPRHPFSTELMQE
GANLLIGTHDFASFANHGRDYNSTVRTIYTLTDIVDKGDSLSIICRGNGFLYKMRNLVGALLDVGKGAYPPE
HLLDILEQKNRREGPSAAPAYGLSLHHVCYSSPYNNFCCEQCSVSTSNEG

>core/582/4/Org4_Gene20

MTQYYFLSSFLPTQLPESVPLFSISDLDDLLYLNLSENDLCNYGLLKRFFDFENFAFFWAGKPIPFSGEVTQE
NVERMLSSQQWSDDNDFEDFFKDFLMNHKSSQDRLNHFSDLFREFLSYHQTNSSKFLQDYFRFQQQLRVVL
AGFRARVLNMDVSYVLRDEDEDSSDPVVLEVLMQKDSPNYELPEEFSDLQGVLDLDDYGLLPHTLNRALALYQFH
KLEGFCSDSYFDGNVILARCATYMFAIRNSLASVEKGREIINHIEKAIKW

>core/583/4/Org4_Gene601

MHSKFLSRRKKNSSHKEETSWDCIASSYNKIVQDKGHYYHRETILPQLPSLTLNSKSSVLDIGCGQGFLERA
LPKECRYLGIDISSRLIALAKKMRSVNSHQFKVADLSKRLEFVEPTLFSHAVAILSLQNMEFPGEAIRNTATLL
EPLGQFFIVLNHPCFRIPRASSWHYDENKKAISRHDYRLSPMKIPIMAHPGQKDSPSTLSFHFPLSYWFKELSS
HGFLVSGLEEWTSSTKTSTGKRAKAENLCRKEFPLFLMISCIKIK

>core/584/4/Org4_Gene842

MTLPLEPMIFWSSLSAKVMKKFLTPHCAGTFSEEDAEAKEAHLVTGKQGHRLMGNCVTFYWLVDKKNNGVI
LDAKFQYFGHPYLIPLAEAVCNLVCCKSYSEAYKMTLDDIDKSLRVHAHQPALPEDSISLYHFVIDALDTAVE
QCLEIPLEDGSLPFQNSPMNLDFEDANPYSQSDWEALTHEQKLYALRATIAEKIGPYIAMDGGEVTVESLENFI
VTIAYSGNCSGCPSSLGSTLNSIGQLLRAYIYPELQVKVDESSLNLSHP

>core/585/4/Org4_Gene193

MQGFFPLASGSKGNSAYLGTDSCKILIDLGVSKQVVTRELLSMNIDPEDIQAIFVTHEHSDHISGIKSFVKAYN
TPIVCNLETARALCHLLDSHPEFKIFSTGSSFCFQDLEVQTFNVPHDAVDPVAFIFHYREEKLGFCITDLGWVTS
WITHELCDYLLIESNHSPELVRQSQRPDVYKKRVLSKLGHISNQECCGQLLQKIITPKLKKLYLAHLSTECNT
AELALSTVSESIASITSIAPEIALAQGITSPIYFSRLEVACPR

>core/586/4/Org4_Gene758

MAGLDLEARGKRRVVTNPAITAFGLCCGLFIIFKSVLRTSSSVELFHRLQGLSLLLISAMIADFSDGAIARIMKA
ESAFGAQFDSLSDAVTFGIAPPLIAIKSLDGIYVGNFFSSLLITSIIYSLCGVLRLVRYNLFSSQKTVDVSKPYCFI
GLPIAAAASIVSLALFLASDFFPDLPALQRLVGLLSFALLFIGGLMISPWKFPKGVKHFRFNVSSFLLVVTIGLAA
CLFFSGLVDHFVEVFFLVSWLYTLVGFPIFSIIYRKRS

>core/587/4/Org4_Gene686

MKKPDNDSTFDVRSFFPFVLCIEQLRKEMSWEVVSAKIPRLPRGWYELMGLSKEDRIDFCLDFWCSVLGIE
HKESPSICRFFSLLETIEVYIYRLEKGPYQLKMFYVFRDGRCGFQGEPPLLDFLGHHRLPPLGDRHYEKFFSIHN
GFGKWEDEGIFPMRSLAKVQQKLRQQLVVMNKMQAEDNCYSLGIFPFYGYEFPAYQSFFFDPEIRRDLPSP
NVLLNEESLEHRSLETIELLHLSKSYPSFLSWLENYLHSEEVYNE

>core/590/4/Org4_Gene398

MDCIGKHNPLVKEALALKRSRCRKSSWFLVEGAREIQKALRAGYLCQHVFCSTHLSEKEKEFLYELKRNSTK
ILYCLDSTLAQLSFKEHDSFVAVIQKRVWNKEDFLIQRKNAQPFYLIIEQVEKPGNVGAILRIADGAGVDGVI
LCNPVDLYNPNVVRSSLGAVFSLPILSISREEGKELFKQEGWTVFVTSPRAETMYFSKNYLGPTALVFGSEKD
GLTEDWFSEDFSEIALPMLGESDSLNLATSVAAYEVVRQRWVN

>core/591/4/Org4_Gene977

MGSSMHVGVIGCSGRTGKVIVSALEQSSEYTLGPGFSRSSALTSQVIAHNDVLVDFSHPLLTKEVVAHLLISP
KPLIIGTTGFP GKCKE A HDSLEELTHIVPVVCPNASLGAYIHKRLVMLLSQLCNPQFDIRIRETHHRYKKDSL
SGTAQDLLDTIQQVKQEDWGEEYEVGQRDSSKKTIEVQSSRVGDIPGEHEVAFISSGEQILVRHTVFSRNVFG
QGILSILDWLKTLNPQPGLYSLGDDTLELVLRNEHCLLKTTDH

>core/592/4/Org4_Gene893

MEKLEFVTSLSPPDDDLITFNKQGLIAGPEEEKVAFLVRSNAMLDAGPETPASFPESLREQFDIFPEYVEVLYS
NEGLDVWEAGCTWILNNEVTIQLRKHLRKASRWLGMYSRDEVLAHEAVHAVRMKFHEPVFEEVLAYQTSR
WGWRRFFGPLFRSPGESYLLFFFTILGLGISLWYPAGILIMLVLP MYFLMRLCMAQSYLYRAMKKIRKMLGV
PPLWVLLRLTDKEIKMFAKEPIPVLEHYARKRKLENVRWKQIYQSYFV

>core/593/4/Org4_Gene408

MPNQLQPRISLGCVSYINSFPLSLQLIKRNDILCVLAPPADLLNLLIEGKLDVALTSSLGAISHNLGYVPGFGIA
ANQRILSVNLYAAPTFFNSPQPRIATLESRSSIGLLKVLCRHLWRIPTPHILRFITTKVLRQTPENYDGLLLIGD
AALQHPVLPGFVTYDLASGWYDLTKLPFVFALLHSTSWKEHPLPNLAMEEALQQFESSPEEVLKEAHQHTG
LPPSLLQEYYALCQYRLGEEHYESFEKFREYYGTLYQQARL

>core/594/4/Org4_Gene79

MKLT KYLNTKQLRSMISRLFVRYSLPMSKQLSFFALCVLGSHPIFAQTPNPPQVRVRSEVIFIDPGHGGKDQGT
ASKELHYEEKSLTSLALTVQSYLKRMGYKPQLTRSSDVYVDLGKRVALSNRGQGDVFISIHCHNSSNAAAF
GTEVYFYNGKVGSPTRNRMSEVLGKNILAAMEKNGILKSRLGTANFVVIRDTSMPAVLVETGFLSNSRERA
ALQDARYRMHVAKGIAEGVHNFLSGPSFQKPKQNI AKIRKPQIQAN

>core/597/4/Org4_Gene23

MPFDITYYTTPLEIILWVMLNYLLKFFWGTRAMDVVFGLLAFLFLVLADKLHLPIIRRLMLHVVNIAAIVV
FIIFQPEIRLALSRI RFHGKKFFIDTQE QFVEQLAASIYQLSERQIGALVVLENKDSFDEYLSFSSVKINATFSEEL
LETIFEPSSPLHDGAVILRGDILAYARVVLPLAHDTTQLSRSMGTRHRAALGASQRSDALIITVSEENGSVLSR
DGLLTRGVKIDRFKAVLRSILSPKEHKRKPLFSWIWKR

>core/599/4/Org4_Gene588

MTTLLSIKDLSTIRGKKILNHINLNLIKGSCLTIVGPSGSGKSSLALTILDLLKPTTGTITFHMDPKIPRARKVQ
VIWQDIDSSLNPCMSIKGIISEPLNIIGTYSKAEQNKEIYNVLDLVNLPKSVLHLKPYKLSGGQKQRIAIKALV
SKPELLICDEPLSSDLTLNQSLILDLFQTIKKEYQNTLLFITHDMSAAYYIADTIAVMDQGSLVEHACREKIFST
PEHTTTQDLLDAIPIFSLISTEMEPSEEYELQVASK

>core/600/4/Org4_Gene727

MKTWLFFTFLFSCSSFYASCRYAEVRSIHEVAGDILYDEENFWLILDLDLDDTLLQGGEALSHSIWKS KAIQGLQ
KQGIPEQEAWEAVVPFWLEIQEMGTVQPIESAIFLLIEKIQKQGKTTFFVYTERPKTAKDLTLKQLHMLNVSL
DTAPQPQAPLPKNLLYTSGILFSGDYHKGPGLDLFLEICTPLPAKIIYIDNQKENVLRIGDLCQKYGIAYFGITY
KAQELQPPIYFDNIAQVQYNYSKLLSNEAAALLLRHQMHE

>core/601/4/Org4_Gene885

MMKYLPYIAITACIHGGILLLVFASPLPKRRLQPKAFQEKLVTIQPKPPVPTPSVVVDPAKTIRPSVATQPQQQ
AKCSPPQENVQKALKKPIPKVVKTEPPKPSAPTVAKKTATEKPPPSTTKKNTQLSKTQLQTLSEVAQALFL
HVDKIEKSETSLKNISWPSTAQLTMHSELKATQEDELCELFRTIALPSKGYVRIKLVLSPNGEIQECSFLSEVS
AADKQLLTQRIQALPFQKFLEKYKVSKNISFHIKLVSNES

>core/602/4/Org4_Gene173

MDLADAHVHLSDDAFEEDINSVLQRAQDSGVSLVVNVTTTEKELNRSFAYAERFPKIRFCHVGGTPPQDVDQ
DIEEDYRNFHAAAHSKKLAAIGEVLGYCFATEEGIARQKEVLQRYLALSLECELPLVVHCRGAFNDFFRML
DQYYHNDPRSRPGMLHCFTGTLEEAQELISRGWFSISGIVTFKNAQDLRDLVVELPLEHLLIETDAPFLAPVP
YRGKKNEPAHVLHTINAVANVKGMFPQELAAALAYKNVLRFLHG

>core/603/4/Org4_Gene6

MFLQFFHPIVFSQSLSFLPYLGKSSGIIKCSNIVEHYLHLGGDTSVIITGVSGATFLSVDHALPISKSEKIIKILS
YILILPLILALFIKIVLRILFFKYRGLILDVKKEDLKKTLTPDQENLSLPLSPPTTLKKIHALHILVRSGKTYNELI
QEGFSFTKITDLGQAPSPKQDIGFSYNLLPNFYFHSLVSVPNISGEERALNYHKEQQEEMAVKLKTMQACSF
VFRSLHLPMSQTKDKKAGFGLLTFFPWKIYPL

>core/605/4/Org4_Gene75

MILTAAFSPCPNDIFLFRSFLKDPQFRPLLNQVTIADIETLNTLALQRRLSLMKMSAALFPLVSDYYNLMDVG
NTLGYNSGPIVLSLDPECSLDTLATPGEMTTAHALCKLYYPKAKLIPMPYDKILSAILQGKVDGGALIHEERFS
YDLQLTLRADFGELWRRKTIFPLPLGCLAIAKYVPMATVDALTAALRKSILCSLKDPITAGAKAVEYSKNKN
VTVIHRFIGTYINKETFQLSKTGKKALHMLWKANECCQYT

>core/606/4/Org4_Gene426

MIKQIGRFFRAFIIMLLSLTSCESKIDRNRIWIVGTNATYPPFEYVDAQGEVVGFDIDLAKAISEKLGKQLEVR
EFAFDALILNLKKHRIDAILAGMSITPSRQKEIALLPYYGDEVQELMVVSKRSLETPLVPLTQYSSVAVQTGTF
QEHYLLSQPGICVRSFDSTLEVIMEVRYGKSPVAVLEPSVGRVVLKDFPNLVATRLELPPECWVLGCGLGVA
KDRPEEIQTIQQAITDLKSEGVISLTKKWQLSEVAYE

>core/607/4/Org4_Gene634

MLRNQVLVYCSEGVSPYYLRHTIRFLKHYSTQEGAFDILRVDGNFLIKNPFWEETTRLVFPGGADRPYHRV
LHGLGTARIFQYVSEGGNFLGICAGAYFGSKMIYFYEPGAPLQGARDLGFFPGTAKGPAYRGNFSYVSPSGV
RVSPQLFSDFGLYAMFNNGRFFEGSEGYPGVNIESRYDDLPGKPASIVSRIVGKGLAVLSGPHIEYLPHYCR
MVEENVQKTREFLQREGTTLDRYCQNLVRRLLQPAFSKVDC

>core/608/4/Org4_Gene504

MNVKDETFWSVHNLCVNYEHAAVLYHISFSLGKGS�TAILGPNGAGKSTLLKASLGLIKPSSGTVYFFNQKF
KKVRQRIAYMPQRASVDWDFPMTVLDLVLGMCYSYKGMWGRISSDDRREAFHILERVGLESVADRQIGQLS
GGQQQRAFLARALMQADLYLMDELFSIDMASFKTSVGVQLQELRDQGKTIVVVHHDLSHVRQLFDHVVL
LNKRLICCGPTDECLNGDTIFQTYGCEIELLEQTLKLSRGKQFGSC

>core/609/4/Org4_Gene137

MNRRWNLVLATVALALSVASCDVRSKDKDKDQGSLVEYKDNKDTNDIELSDNQKLSRTFGHLLARQLRKS
EDMFFDIAEVAKGLQAELVCKSAPLTETEEYEEKMAEVQKLVFEEKSKENLSLAEKFLKENSKNAGVVEVQP
SKLQYKIIKEGAGKAISGKPSALLHYKGSFINGQVFSSEGNNEPILLPLGQTIPGFALGMQGMKEGETRVLVI
HPDLAYGTAGQLPPNSLLIFEINLIQASADEVAAPVQEKNQGE

>core/611/4/Org4_Gene952

MENLETFILKIYRGIPGKQYWESFELPLHPGENVISALMEIEKRPVNILGEKVNPPVWEQGCLEEVCGSCSILV
NGVPRQACTALIQEYIDATQSREIVLAPLTKFPLIRDLIVDRSIMFDNLERIQGWVAADIEGETFGPQVTQEQQ
ELLYALSQCMTCGCCTEACPQIDNKSDFIGPAAISQARYFNTYPGDKQSKKRWRALMGKGGIEGCGQAHNC
VRVCPKKLPLTESISAMGREISKFSLRSLFSALFKKKK

>core/613/4/Org4_Gene472

MSKFILLLSLGVAALASKNFFIWPAPSGKTPLKLRQVLFGGALLVFSSLVALSVSSQTAELLSTMTGISLAFAP
LFYLLFLPKDITRAILFSGERPIKTSWRALGSAIRMWIIIPVTQLIGIMMSKFLTLVLPTQEIHTEVTQEVQNSL
PITGHYISMILNLGVLTTPFGEEVFFRGILQTFLLKNKMTRIAAVLCSSIIFSFIHIEHSLGSWVFVPVLFVFSLSAGF
LYEKDRHILSPIALHGLFNLTSLLFVGIK

>core/614/4/Org4_Gene94

MAFYSPSTISKYFIYSGAGNRFLGETLPEVEDVRFLCQETRVDGFLYLPSSCADAQLIIFNSDGSRPTMCGN
GLRCAIAHLASQKGKSDISVSTDSGLYSGYFYSWDRVLVDMTLADWRASVHRLESRPDPLPKEVVCIHTGVP
HAVVILPEISTLDLSILGPFLRYHQTFSPDGVNVNFVQILGHCQLRVRTYERGVEGETAACGTGALASALVVS
NSYGWKESIQTHTWGGELMTVSQNRGRVYLQGSVTRDL

>core/615/4/Org4_Gene31

MFKLLKNLFLIGCCIVGYFWMRKESIVEQWLSNRLHTQVTVGRVSIRTSGIKIRHICIHNPASERFPYAAEIEY
ADVRFSSISMLLTQKLEISELIIHGANFTIFPYDSHGKTNWSLVWKNFHPQKETPSNLWIDRAPVLIRRCFLN
TRLYGLRANHGDIPHLSPSLEFHSHTSSAKELPKLSEALPSLLYLALLESYHLNLPGDIIKPLSQQAHKHFYS
SYPQFQDRLNDINTPGTPTTEEIIGFIRGLFFH

>core/616/4/Org4_Gene940

MVSPLSLFHKMLLENWTPVEEPFPWPPAEKNQKIFAWALNQSKLIFVSTSGNIAQPRLVTDSMSMMIVNAAN
RTMSRDGAGTNQVLAAVSVDSWGLSQQPLNPERRGTPLNEGECRAGMWRNADGSNHTGKQGKPHYLAQ
LLGPKAVDHHNESQAAFDCCKNAYLNCFRLAQTGLGVTFLLQIPLISSGIYAPPENRKKPNSEENKVRLRWIHAV
KCALVAAMQEFGNPEGNADRKMLIVLTDLKTPAITDPKKKSHL

>core/617/4/Org4_Gene65

MKTQQTQNIIEVWNFYWETQEIEYRDSLIEFYLPVKSVVHRLISGMPSHVKTEDLYASGVEGLVRAVERYN
PERSRRFEGYAVFLIKAAIIDDLRKQDWVPRSVHQKANKLSGAMDSLRLQSLGKEPTDLELCEYLNISQQELSG
WVVSARPALIVSLNEEWPSQSDEGAGMALEERIPDERAETGYDVVDKQEFSLCLANAIQEELEEKERKVMALY
YYEELVLKEIGKVLGVSESRSVSIHISKALLKLRAALSAFR

>core/618/4/Org4_Gene86

MWLGAYTWLNVFGILLQAAFIQNILLANFLGMCSYLACSTRVSTANGLGMSVALVLTVTGSINWFWHAFITG
PKALTWISPSLASVNLGFLELIIFIVVIAAFTQILELLEKVSRNLYLSLGFPLIAVNCAILGGVLFGITRSPFIP
MMIFSLGAGCGWWLAIVILATIKEKLAYS DIPKNLQGMGISFITTGLIAMAFMSLTGIDISKPSAKIQRAPLETE
VVENTTNPLKESSSKHQPSISKARTQRRSL

>core/619/4/Org4_Gene295

MLKIKHLHASCNDVKILDDFNLNIPGTMHVIMGPNGAGKSTLAKILAGDESVLVSSGEIALQEQNLLSMLPE
ERSRAGLFGVGFQMPPEIPGVNNKMFLRDAYNARRRANQEGDISIDEFNTLLSTVLETYEYNTTTDLFLDRNVN
EGFSGGERKRNEICQMLVLEPEMVLLDEPD SGLDVDALRLICRVLEKYRELHPTSSLCIVTHNPKLGNLIRPD
VVHLLLDGRVALSGDVSLMHELEAKSYQEVTKRVAWR

>core/621/4/Org4_Gene176

MKTIAVNSFKGGTAKTSTTLHLGAALAQYHQARVLLIDFDAQANLTSGLGDPDCYDSLAVVLQGEKEIQE
VIRPIQDTQLDLIPADTWLERIEVSGNLAADRYSHERLKYVVLG SVQDKYDYVIIDTPPSLCWLTESALIAADYA
LICATPEFYSVKGLERLAGFIQGISARHPLTILGVALSFWNCRGKNNSAFAELIHKTTPGKLLNTKIRRDITVSE
AAIHGKPVFATSPSARASEDYFNLTKE LLILLRDI

>core/622/4/Org4_Gene710

MTRQSYVLGNWKMHKTIQEAKKEYVQTLASLLQGEPLSCTIGIAPPFTSLRAIHEMINTTGAFWLGAQNVHP
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VIKKQLLLGLEQMDNGSEFLIAYEPVWAIGTGKVAEASDVQDIHMF CREVVAERFSEATAEEISILYGGSVKV
DNAQRFGQCSDVDGLLVGGASLEAQSFFEVAKNFNV

>core/623/4/Org4_Gene96

MHDALLSILAIQELDIKMIRLMRVKKEHQKELAKVQSLKSDIRRKVQEKELEMENLKTQIRDGENRIQEISEQI
NKLENQQA AVKKMDEFNALTQEMTTANKERRSLEHQLSDLMDKQAGGEDLIVSLKESLASTENSSSVIEKEI
FESIKKINEEGKALLEQRTELKHATNP ELLSIYERLLNNKKDRVVVPIENRVCSGCHIVLTPQHENLV RKKDRL
IFCEHCSRILYWQESQVNAQENSTAKRRRRRAAV

>core/624/4/Org4_Gene569

MKPEESECLCIGVLPARWNSSRYPGKPLAKIHGKSLIQRTYENASQSSLLDKIVVATDDQRIIDHVTD FGGYA
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KKVKCVFDSEGRALYFSRSPIFILKKATPVYLHIGVYAFKREALFRYLQHSSTPLSDAEDLEQLRFLEHGGKI
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>core/625/4/Org4_Gene800

MLIKLWRATYEGMYTFLVGALLKLRYRMQVEGWDTLNINPKQGCLFLANHVAEVDPIILEYLFWSRFHVRP
MAVEYLFHSRIVRWFLNSVRSIPIQLVPGKESKRS LERMNVCYEEASRALNRGESLLLYPSGRLSRTGKEEIV
NQYSAYVLLHRVMECNVVLVRVSGLWGSAFSRYKQNSTPKLGPAFKEAFRALLRRGIFFMPKR FVKITLCQ
VDHLFLKQFPTKQDLNTFLASWFNQGDDNLPIEVPYA

>core/626/4/Org4_Gene357

MQICVTGVVLRSRPLGKNHTLTTLFTPEGLFTFFAKQGQTLQCDYRETLVPISLGKYTLHRNGSRLPKLTHGD
ILNAFEAIKQTYALLEASGKMIQALLASQWKEKPSHKLFSLFLNFLHRIPESSNNPEFFAAIFVLKLLQYEGILDL
TPACSLCKASLPYACYRYQGHKLCKKHQHKQAISIEKEEEEQILQAIHAKQFSELLAIAEFPIAIAEKIFYLFDSL
QEEKKSERNSSSEDPYHEILRLSKVVHPY

>core/627/4/Org4_Gene146

MLIVLAFRQVFFSHSRSQLDRLKKNYLRLLLKQNFALTLPKERTSKGHSLMLTFDFASFDFYTNIFPFLEEQKIPAV
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LTTEILLSRHHIETITGAKPLAFLFPFGKSDPTSRKLAADHYPYSFLLGNTINRKLKTHNIYRLDIKPMQYVCPS
LFQSSRYLKNWIKESKQLYLKKQLPKR

>core/628/4/Org4_Gene38

MLMDISHILEDLAYDEGILPREAIEAAIVKQMQITPYLLHILHDATQRVPEIVNDGSYQGHLYAMYLLAQFRE
SRALPLIIKLFAFEDDTPHAIAGDVLTEDLPRILASVCNDDSLIKELIETPKINPYVKAAASGLVTLVGAGKIPR
DKVIRYFAELLNYRLEKQPSFAWDNLIAGICTLYPGELFYPISKAFDGGGLVDTSFISMEDVENIHEETVESCIH
TLCSSTELINDTLEEMEKWLEDFPIEP

>core/629/4/Org4_Gene628

MNVADLLSHLETLLSSKIFQDYGPNGLQVGDPQTPVKKIAVAVTADLETIKQAVAAEANVLIVHHGIFWKG
MPYPITGMIYKRIQLLIEHNIQLIAYHLPLDAHPTLGNNWRVALDLNWHDLKPFGSSLPYLGVQGSFSPIDIDS
FIDLLSQYYQAPLKGSALGGPSRVSSAALISGGAYRELSSAATSQVDCFITGNFDEPAWSTALESNINFLAFGH
TATEKVGPKSLAEHLKSEFPIPTTFIDTANPF

>core/630/4/Org4_Gene642

MKKQGKTLFLFLFLSFLFSTAFSGLFASQTSSLRTIQENIFLAKTGDYTVLSRGSQRTFVLVKSTTPKTVWIEIHH
FPCIAYKERPSLEQASWKTVIHQLESQSQVFVVSLSSEGSQFFSLNTRTKSLEPVGKSTTVPAFLQIFDLPLSPAP
ANVIKTKGKENKPWSRVSFEGAPLTSISVNAWQGLWPKDRGPLSETGILMYFTQPDISVFPLWVSIETPKGT
SIVRAVDIGHGATSPYVYSLPHSKTQ

>core/632/4/Org4_Gene105

MSLATNNAESKFPSLQRLPNHVAIIMDGNRRWYKKHREECGHTHTSGHYYGAKVLPNILNAVLDLGIKVLTL
LYTFSTENFGRPKEEIQEIFNIFYTQLDKQLPYLMENEICLRCIGDLSKLPKGIQTKINHVSMTASFSRLELVLA
VNYGGKDELVRAFKKLHVDILNKKISSDDLSESLISSYLDTSGLTDPDLLIRTGGEMRVSNFLLWQIAYTELYI
TDTLWPDFTPQDLFEAINVYQQRSRRGK

>core/633/4/Org4_Gene175

MGNLKTLLSRFKKNTPTKMEALARKRMEGDPSPLAVRLSNPTLSSKEKEQLRHLLQHYNFREQIEEPDLTQ
LCTLSAEVKQIIHHQSVLLHGERITKVRDLLKSYREGAFSSWLLLTYGNRQTPYNFLVYYELFTLLPEPLKIEM
EKMPRQAVYTLASRQGPQEKKEEIRNYRGERKSELLDRIRKEFPLVETDCRKTSPVKQALAMLTGKSQILTK
CTSLSSDEQIILEKLIKKEKVKSNLFPDTKV

>core/634/4/Org4_Gene347

MKIKFSWKVNFLICLLAVGLIFFGCSRVKREVLVGRDATWFPKQFGIYTSDINAFLNDLVSEINYKENLNINIV
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VLVAQNIPDAVISLYQHVPALAEALTSNCYDALLAPVIEVTALLETAYKGRLKIISKPLNADGLRLAILKGTNG
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>core/635/4/Org4_Gene317

MSLLKDTVFTCLDCEMTGLDVKKDRIIEIAAVRFTFDSVISSIEFLINPERVVSASQRVHHISNAMLRDQPKIA
EVFPQIKAFFKEGDYIVGHSVGFDLQVLSQEMERIGETFLSKYTIIDTLRLAKEYGDSPNNSLES LAVHFNPY
DGNHRAMKDVEININIFKHLCKRFRITLEQLKQVLAKPIKMKYMPLGKHKGRCFSEIPLAYLQWASKMDFDS
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>core/636/4/Org4_Gene533

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CVQKFLDKHNKIDILVNNAGITRDNLLMRMSEDDWQSVISTNLTSLYTCSVIRHMIKARSGSIINVASIVAK
IGSAGQNTNYAAAKAGIIAFTKSLAKEVAARNIRVNCLAPGFIETDMTSVLNDNLKAEWLKSIPLGRAGTPEDV
ARVALFLASQLSSYMTAQTLVVDGGLTY

>core/637/4/Org4_Gene836

MTQDPHDHFKSRTPEDHIKHVRDKHRVCKGEPHTTFKGFFYHLANNALSTGVFIFFIRTLFFLIPTNRALQVKS
LISLGVGWTFYHGCLKARKAWAYMELSHRSMLEEKNEIEENFEQEKIELRILFENQGFKDPLLQEMVEYVCS
DSTLLLDTMIREELYIRKEDLPHP LIQGGSRILGGLCGLAIFLPLVLCISYTLAGVFSALMVLVLSFLKAKILEN
DKISEMVWVLGIFITSASIISSLMKLL

>core/638/4/Org4_Gene488

MTLSFHTHPLNYWTFEEFDGLPIRHGVFSKQKDAEGTVFAAKNPEIASALQSPKYCDLHQRHGTSVRCVTPT
SPTYQPADGVCTQSPLLSLHIRHSDCQAAIFYDREHHAIANVHSGWRGLLGNIYAVTVGTMKKLFHTKPQDL
FVASGPSIGPDYAIYPDYATLFP RSFLPFMNPKNHFDLRAIARKQLTNLGISKDRIFISDLCTYTEHDAFFSSRYL
AHPDPNLTGQH SKNRNNVTAVLLLPRD

>core/639/4/Org4_Gene288

MAKQTRRVLFKISGEALSKDSSNRIDEMRLSRLVSELRAVRNNDIEIALVIGGGNLRGLAEQKELQINRVSAD
QMGMLATLINGMAVADALKAEDIPCLLTSTLSCPQLADLYTPQKSIEALDQGKILICTTGAGSPYLTTDTGAA
LRACELNVDVLIKATMHVDGVYDKDPRLFPDAVKYDFVSYKDFLSNQLGVMDAS AISLCMDSHIPRVFSFL
QHSLEKALFDPTIGTLISEDVNHVCSPRH

>core/640/4/Org4_Gene660

MKFFFILFILIVAQFPAFSAQPRTQVSASHSKQAKARRTSRTRSSATTNASVSRYKTRAAARKKTGKFEKKPSLS
PVQWVRYSGKNYSIQTPSLWQCIDDKTQLPEKLDILLIGKGKGNLTPTINIAQEITSKSSKEYIEEILAYHKANE
MTLESGIFTQIQSPSGEFTIIKTEKNSSWGRVFCLQATTVIDHTAYIFTSTATLDDYAELSFTFLKVVSSFQIRGG
KEATSGDAILEKALEALQENK

>core/641/4/Org4_Gene345

MHIYGLADLHLALGVPEKTMVEVFGDPWIGYHQKICSEWQAVVHPEDIVLLPGDISWAMNLSEAHKDFAFIG
DLPGTKYMIRGNHDYWSSASTSKILQALPPSLYLNQGFALLTPHLAVVGVRLWDSPTICVKKENFLNPSTQ
EQSYTEQDEKIFLRELGRLLKRAFAALPKEVSEVIVMTHYPPISSDGTGPVSEFLEADGRVSLCLFGHIIHKVQR
PIDGFGNIRGIHYILVAADYVNFVPQEV

>core/642/4/Org4_Gene164

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YLTKKWGILIPSAGIDESNVEGYFVLYPRDFLLSVNTLGDWLRNFYHLEHCGIIISDSHTTPLRRGTMGLGLC
WNGFFPLYNYVGKPDGCFGRALKMTYSNLLDGLSAAAVLCMGEGDEQTPIAIIIEAPKITFHSSPTTLQDMSTL
AIAEDEDLYGPLLQSMAWETPAPTS

>core/643/4/Org4_Gene474

MDFDYFGLSDIGRVRARNEDFWQVNLMSQVVAVADGVGGRLGGDIASQEAVTSLMELIDEQQSKLMGYED
DQYKETLKKILLEVNGVVYEHGQMEEHLQGMGTTLFSIQFRKDRAWLHFVGDRIYRIREGELRCLTEDHSL
ENQLKNRYGLPKQSDKVYSYRHILT NVLGSRPYVMPDIRNLPCEKEDLYCLCSDGLTNMVPDIDIRDILNQPA
TLEERGNALISLANTRGGDDNATVVLVRIQ

>core/644/4/Org4_Gene387

MTIRILAEGLAFRYGSKGPNIIHDVSFSVYDGDFIGIIGPNGGGKSTLTMLILGLLTPTFGSLKTFPSHSAGKQTH
SMIGWVPQHFSYDPCFPISVKDVVLSGRLSQLSWHGKYKKKDFEAVDHALDLVGLADHHHHCF AHLSGGQI
QRVLLARALASYPEILILDEPTTNIDPDNQQRILSILKKLNRTCTILMVTHDLHHTTNYFNKV FYMNKTLTSLA
DTSTLTDQFCCHPYKNQEFSCSPH

>core/646/4/Org4_Gene737

MSYFNYQKNSVVLRLSLGLLAKFFSRLLYRVFFSFREGIYLFSSLYLKYPRLFFYDLGKYVYSLRHCPYAKLGR
LPGASLLKEGNVYGETPWSVLAKISQAFDITSQDILYDLGCGLGKVCFWFSHVRCQVIGIDNQPNFIRFSSN
MHRKLSSGFALFDTEEFKNVLSQASYVYFYGSSFSRLLNEIILKLEMAPGSVVISISFPLDSFSKGKECFFT
EKSCSVRFPWGKTIA YKNIRKGS

>core/647/4/Org4_Gene553

MSTSLNPPWMKAGKRIESLVRKALYTHTMLANHHKIVVALSGGKDSL TLLLMLKAISGRGFPDLDLHAVNI
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TALLNLLHKA EFAGMLPVLD MVHFGVTILRPLIFTPEFWIRKFAKENG FARVTCRCPVVSLRSKAEQSLK LLE
EVFPLARHNIALAIQEHGSSKSQKI

>core/648/4/Org4_Gene547

MTDYSFFRRKIGNIEAIECPGNPQDPPIILCHGYGSLADNL TFFPSICSFSKLRPTWIFPNGILPLENDFRGSRAWF
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NPYAGALIFAGARLFNQGWEEGLKQCAQVPFLQSHGYEDEILPYHLGAHLNDLLLTKLNGQFVSFHGGHEIP
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>core/650/4/Org4_Gene156

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HRARLGIGYLAQEPTIFKELTVQDNLICILEIHYKARKQQSHLLNTLVDDLQLGSLHKKAGTSSGGERRRLEI
ACVLALNPSVLLLDEPFANVDPLVIQNVKYLIKILAGRGIGILITDHNAKELLSIADRCYLIIDGKIFFEGSSSQM
ISNPMVKQHLYLGDSFSY

>core/651/4/Org4_Gene456

MKVRIVDSGKSSVASHMAKDRDLLESQDGELILHLYEWENPCSLTYGHFMRPEKFLVSNPDLGLDAAVR
PTGGGFVFHKGDYAFSVLMSATHPSYSSSVLENYHTVNSFVAKVLEKVFRIQGMLAPEDENSSSRDSGNFCM
AKTSKYDVLFGDKKIGGAAQRKVQQGFLHQGSLFLSGSSSEFYQRFLKPEVLEEIIIEQIQIHAFPLGLESAD
VLQEARQQVKEAFIKLFCGERL

>core/652/4/Org4_Gene483

MTLYLLPNTLGTRAVETLPSVIGELVHRLDGLIVESDRGGRAFLSLWKIPEVHKFPLAILSKHARLPKAWDFY
LEPIVKHGENWGLISDAGLPCIADPGASLVRRARALGIPVQAFSGPCSITLALMLSGLPQSFTFLGYLPQSPKE
RVKSIKKAATSKEVSTSVCIETPYRNVYTFESLLDTLPSYAELCVASDLSAPSELVLTRQVKSWRTNEDLGSV
KQSITKVPTIFLFHIPN

>core/653/4/Org4_Gene367

MAGHSKWANTKHKRERADHKKGKIFSRIIKELISAVKLGGADPKSNARLRMVIQKAKENNIPNENIERNLKK
ATSAEQKNFEEVTYELYGHGGVGIIVEAMTDNKNRTASDMRIAINKRGGSLVEPGSVLYNFARKGACTVAK
SSIDEEVLFSYAIEAGAEDLDTEDEENFLVICAPSELASVKEKLISQGATCSEDRLIYLPLRLVDCDEKDG
EANLALIDWLEQIEDVDDVYHNMS

>core/654/4/Org4_Gene135

MDISGAVKQKLLQFLGKQKKPELLATYLFYLEQALSLRPVVFVRDKIIFKTPEDAVRILEQDKKIWRETEIQIS
SEKPQVNENTKRIYICPFTGKVFADNVYANPQDAIYDWLSSCPQNMEKQGGVRIKRFLVSEDPDVIKEYAVPP
KEPIIKTVFASAITGKLFHSLPPLLEDFISSYLRPMTLEEYQNQTKFQLESSFLSLLQDALVEDKIAAFIESLADD
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>core/655/4/Org4_Gene768

MGLYDRDYIQDSRMQGTASRVYGWMTAGLIVTSCVALGLYFSGLYRSLFSFWWWCFATLGVSFFINSKI
QTLSVSAVGGLFLLYSTLEGMMFFGTLLPVYAAQYGGGVIWAAFGSAALVFGLAAVYGAFTKSDLTKISKIMT
FALIGLLLVTLVFAVSMFVSMPLIYLLICYLGLVIFVGLTAADAQAIRRISSTIGDNNTLSYKLSLMFALKMY
CNVIMVFWYLLQIFSSSGNRD

>core/656/4/Org4_Gene678

MHPPIDITAIEAKLNFTFTQPKLLEIALTHPSYKNESAVQIEDSERLEFLGDAVLGLIVTEHLFLLFSPMDEGTLS
TARASLVNAKACCRYTTTTLGIGDYLLIGKGEKIQSERGRLSAYANLFESILGAVYLDGGLSPARKLTVPLLP
R EEILPLMSGNPKNLLQQFTQKQFRVLPVYQSTAVTDAQGNVSYQIQVLVNQEVWGEKNASSKKEAEKIAAQ
QALDTYGNKNQNTMDV

>core/657/4/Org4_Gene407

MEPSTNKPDCCKIFDSIASKYDRINTILSLGMHHFWNRS LIQILGSGHSLLDLCAGTGKVAKRYIAAHPQASVT
LVDFSSAMLDIAKQHLPQGSCSFIHSDINQLPLENHSYPLAAMAYGLRNLSDPHKALQEISRVLMPSGKLGILE
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>core/658/4/Org4_Gene253

MDVLIFYDTETTGTQIERDRIIEIAAYNSVTDESFLT YVNPEIPIPEASKI HGITTD AVL SAPKFPEAYEGFRKF
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ALDDVVILHKVFTSLIGDLPPQQVLDLLQQSYHPKVFKMPFGKYKGQPLVDIPKSYFEWLENQGALDKPENK
DIKAAIAL LHQPT

>core/659/4/Org4_Gene890

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VILGQDPYPGKGQAHGLSFSVPEGQRLPPSLINIFRELKTD LGIENHKGCLQSWANQGVLLNTVLT VRAGEP
FSHAGKGWELFTDAIVTKLIQERTHIIFVLWGAAARKKCELLFNSKHQHAVLSSPHPSPLAAHRGFFGCSHFS
KINYLLNKLNKPMINWKLP

>core/660/4/Org4_Gene60

MDLAVELKEGILLVDKPQGRTSFSLIRALTKLIGVKKIGHAGTLD PFATGVMVMLIGRK FTRLSDILLFEDKEY
EAIAHLGTTTDSYDCDGKVVGGRSKIPSLEEVL SAAEYFQGEIQQLPPMFSAKKVQGKKLYEYARKGLS IERH
HSTVQVHLQITKYEYPLLHFVVSCSKGTYIR SIAHELGTMLGCGAYLEQLRRLRSGRFSIDECIDGNLLDHPDF
DISPYLRDAHGNSL

>core/661/4/Org4_Gene906

MIGDKIILFVTEDLSLSSQLKDLASQRS DYQILVSPVFPTSFEAVAIFCEYLLLPEQIFSPGIFPEEDLIVLFDTFQE
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GILKKLLINRGHLCLRKNLLAEIKGNTKEI IARNVDVHIASLRKKLGPYGSKIVTIRGVGYLFSDDDSIPLQNH D
NTAHPNEE

>core/662/4/Org4_Gene839

MTKVRLNKFLASAGVASRRKCDEIIFSGSVTVNGRVAEGP FVLVDPEDKVQVGGTSVHLTKKVYFMVHKAI
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KDLEKLMEGTFIDGKHVRPVSVTKIRRGTVKIVVSE GKKHEIRLFADAAGLPILELKRIRIGSLVLGGLRYGEY
RELTAELGT YMKLSD

>core/663/4/Org4_Gene571

MLQAHRLCYSYDNQVILKDASFQASPGTITIILGSSGVGKTTLFRLLAGFLPLQEGELLWNGSPLNCKDVAYM
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KPILLLDEPFSSLDVLLKEQLYQDIVALAKKENKT VLLVTHDFHDV SCLGDVLYVIKNKTLTPVPLDPSMRSL
NNGLCFIKDLKKHLYT

>core/664/4/Org4_Gene746

MRVIFPDKHNNFPNLSKLLKKLPSVILVTSCIAPFFSYIINKFFGIPGLLEILALSVKGIQKHFWQFLTYPLITAD
SLSLNKDQSFEITQRLLLLRNVLDFFLFYKAIQHILIRKLGAFSVLVVISGQALIIGAVLWGFMALIHSSQSFFGPE
SIICGVLTQIFLDPEKRFTIGPTPLSVSRKWGFLFVLGFYCCILIFSGAFLLLLASMLAIVLAILFCKKEKIPNPY
TTSLRF

>core/665/4/Org4_Gene335

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HTTFLWDIDLKLSYYLPIPQQQPTYRNQRSHEEFLTTLRPWFPSRDDFLERIKASGSLLFTWEEFLDNELEEIL
AQPHRKATTVLN

>core/666/4/Org4_Gene679

MLSVCYSDPFLSDFCQGKRPLRIASRNSNLAKAQVHECISLLRSWYPKLWFQLSTTETTGD RDKKIPLHLVEN
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AVLKQLFPQGQILDIRGTIEERLDQLHRGHYDAIVLAKAASRLHLHHAYSIELPPPYHALQGSLAITAKDHA
GKWKQLFTPIHCHSS

>core/667/4/Org4_Gene865

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PELKNIVEYADSLILTAKPDVTPGGCHETEAGIINAQLDVQLDALEKAFSTILKAKNPVDEPSETSSSTDSASLS
NDQDKKE

>core/668/4/Org4_Gene812

MNRRDMVITAVVVNAILLVALFVTSKRIGVKDYDEGFRNFASSKVTQAVVSEEKVIEKPVVAEVPSRPIAKET
LAAQFIESKPVIVTTPVPVSETPEVPTVAVPPQPVRET VKEEQAPYATVVVKKGDFLERIARANHTTVAKL
MQINDLT TTTQLKIGQVIKVPTSQDVSNEKTPQTQTANSENYIYVQEGDSPWTIALRNHIRLDDLLKMNDLDEY
KARRLKPGDQLRIR

>core/669/4/Org4_Gene995

MFFIVCFGFLIHKKHTILPPKAHIPTNAKHFP TIGNPYAPINITVFEEPSCSACAEFTTEVFPLLKKHYIDTGEISF
TLIPVCFIRGSKPAAQALLCIYHHDPRQADIDAYMEYFHRILTYPKEEGSHWATPEVLT KLAEGLKTNSGRSIN
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>core/670/4/Org4_Gene884

MVHFShNPiiQAYTEADFFGKSIFFLILSVCTWTVLHQKLAIQKKFLKAGKSLKDFLIKNRHAPLSLDIHPEL
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NTNL

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GPGISIDTRELMA

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LISKKYSV

MLQSCKKALLSIVVSILAFHPIPGMGVEAKSGFLGKVKGWFSKKEIQEEARILPVKDSLSWKRYDYTSSSGFS
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QPDNPIPPYYIADSLKLQQPEESNNFLDVTMDICGNNPEFKILKERQCIMKQSIEKQMAGETKKAPTCKKPA
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MYLEDYDVFFFDLDGLLVDTEPCFYRAFLQACAEFSLEVHWDFSTYYSHHTLGTEIFSKKFIEQYPQAEYM
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ARPKPYGDSYDYAYRTFAREGMKVIGFEDSVKGLRALSKIPATLVCINSMAEITPEDYPELKGKEFFSYPSFD
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MNTSHRKTLVFSYLSSTFTLLLVLNLVLSSKLIPTTFFNFIIPGGILYPLTFLISDVVNEIFGPKKARVMIFS
AFI
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SNGS
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QP

>core/678/4/Org4_Gene603

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SFLPNTIEKIAFARHAIKTLGLKDSCLIEVDGGIDQQSAPLCRDAGADILVTASYLFEADSLAMEDKILLRGEN
YGVK

>core/679/4/Org4_Gene583

MKGFLSVNELIFGFQTFSSVVVLGVFFASRGKAWLTGWLSLLSSIMNVFVLKQIHLWGFEVTSADVYVIGLLT
CLNYAREHYEKNDVNDAMLC SWVISIAFLVLTQLHLFLIPSPNDSSQKHFLALFSSTPRIVVASLVTLIFVQIVD
IKLFTFLQRVFSKKYFAMRSTISLLFSQLIDTIIFSFLGLYGLVSNLCDVMIFAMLVKGIVITLAIPTLTVTKAVL
DRRS

>core/680/4/Org4_Gene359

MRPHRKHVSSKSLASKQSTSTHVEITTKAFRLSMPLKQLILEKSDHLPPMETIRVVLTSHKDKLGTEVHVVAS
HGKEILQTKVHNANPYTAVINAFKKIRTMANKHSNKRKDRTKHDLGLAAKEERIAIQEEQEDRLSNEWLPVE
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EPSLKPGFCI

>core/681/4/Org4_Gene840

MALLILLRHGQSVWNEKNLFSGWVDIPLSQQGIEEAFSAGRAIQNLPIDCIFTSTLVRSLMTALLAMTNHHSK
KIPYIVHEDPKAKEMSRIYSAEEENNMIPLYQSSALNERMYGELQGKNKKQTAEQFGEEQVKLWRRSYKTAP
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HKIEKHPEFFG

>core/682/4/Org4_Gene572

MSSQPLVTTSSSLSRVYVLTGEEKVACYKKAFNHIWHGAPAILAAALLMFCIFGFVLGSILLGAPLEGASILY
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EGLGT

>core/683/4/Org4_Gene561

MSLLIEAKNLSKTIQQNQNISILTDVSLSLHAGETISITGASGNGKTTLLHLLGTLDVPSSGSLRFFDKDLKNQ
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GEKQRVAIARALINEPAILLADEPSGNLDEETSEQIHNLLLEQASALCGILIVTHNKHLSRCSREGVLSNGKLF
FHNS

>core/684/4/Org4_Gene597

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DEPTSALDPFATASFRHLLLETLRDQELTVGLTTHDMQFVHSCLDRIYLIDQGTVAGVYDKRDGELDSDHPLS
KYIHSAQ

>core/685/4/Org4_Gene675

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KYSLYKAIHRGGVLCDVVVHSKEEALQYASKYIAQKFQLDESVLFEMLFHRENLMSTGIGEGIALPHAKDFLI
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VKEWESQTH

>core/686/4/Org4_Gene363

MILRISTVSLLTSCSFSKNSRTCFVTPERITSQKDCPVLLHPKSTTISPLYDWISPNREVITAYSFYCRGQGNSII
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>core/687/4/Org4_Gene798

MENSQNFHDTLCQLLDYSEELYPTLASLLNVTLPNTAISASVSPICEKAVEVPNAEPQPITPPPPTNLSQEKTK
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>core/688/4/Org4_Gene756

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QPSFVQEISRLQDSAVFALATDDKTYLLESIEALQTRLAPRMETPYIYKMTDTYGNSWFENLWRTKGQEIFY
TEFIKKAGI

>core/689/4/Org4_Gene150

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MTTQLG

>core/690/4/Org4_Gene899

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QVCVEKIRGLKEYFGVSARGYAYFTVHQEADIKHASEEKEMLQTLVGRENPD AVLQGSQEVLDLWNFLSS
FINSTEPSCSK

>core/691/4/Org4_Gene323

MVLLSKFDFSGNKIGEEVADSLFADEGDGLQLIKDYIVAIRANKRQWSACTRNRSEVSHSTKKPQKQGTG
NARQGCLASPQFRGGGIVFGPKPKFNQHVRI NRKERKAAIRLLLAQKIQTNKLTVVDDTVFVDALTAPKTQS
ALKFLKDCNVECRSILFIDHLDHVEKNENLRSLRNLTA VKGFVYGININGYDLASAHNIVISKKALQELVER
LVSETKD

>core/692/4/Org4_Gene143

MQTLARLFGQSPFAPLQAHLEMVVSCVEYMLPIFTALRDGRYEELLEMAKLVSDKEYQADCIKNDMRNHLP
AGLFMPISRAGILEIISIQDSIADTAEDVAILLTIRRLNFYPSMETLFFRFLEKNLEAFELTMTLLHEFNQLLESSF
GGRKADKARLLVGRVAKSEHESDVLQRELMQIFFSDDFIPEKEFYLWLQVIRRTAGISDSSEKLAHRINMTLE
EK

>core/693/4/Org4_Gene723

MSTTTVKHFIHTASRWEPLKEIVASNYWHAQWINTLSFLENSGAKKISASEHPTEVKEEVLKHAAEEFRHA
HYLKTQISRISSETSLPDYTSKNLLGGLLTKYYLHLLDLRTCRVLENEYSLSGQTLKTAAYILVTYAIELRASEL
YPLYHDILKEAQSKITVKSIILEEQGHLQEMERELKDLPHGEELLGYACQFEGELCLQFVERLEQMIFDPSSTF
TKF

>core/694/4/Org4_Gene576

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>core/695/4/Org4_Gene91

MKKYFITGLVILLPLAITIAIVTMIMNFLTQPFVGLASEFFEKFSFYTKHRALLKFVLQIILLFGLFFATVLLGFL
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GEKEDDPLVTVFIPTTPNPTSGFLTFRKSDIVFLDMKIEDAFKYIISCGVLSTPMACSSPLPDELHQDQGS

>core/696/4/Org4_Gene325

MGQKGCPIGFRTGVTKKWRSLWYGNKQEFGKFLIEDVRIREFLRKKPSCQGAAGFVVRMSGKIEVTIQTAR
PGLVIGKKGAEVDLLKEELRALTGKEVWLEIAEIKRPELNAKLVDNIARQIERRVSFRRAMKKAMQSVMD
AGAVGVKIQVSGRLAGAEIARSEWYKNGRVPLHTLRADIDYATACAETTYGIIGIKVWINLGENSSSTTPNNP
AAPSAAA

>core/697/4/Org4_Gene404

MTLYLGLNQKTARKYQAHYLPILTLFPYAKSTPQNKRALQFLPQATHVILTSPSSTHLFLSRMTSLLSKATLK
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TVKPRKLKKNILSKYKEIIFTSPSTVRAFAKIFPRFPEKTYWCQGRMTLQEFQKFYSQKQVSLLETLGKSRTSP

>core/698/4/Org4_Gene264

MLMMLMMIIGITGGSGAGKTTLTQNIKEIFGEDVSVICQDNYYKDRSHYTPEERANLIWDHPDAFDNDLLISD
IKRLKNNEIVQAPVDFVLGNRSKTEIETIYPSKVILVEGILVFENQELRDLMDIRIFVDTDADERILRRMVRDV
QERGDSVDCIMSRYLSMVKPMHEKFIEPTRKYADIIVHGNYRQNVVTNILSQKIKNHLENALESDETYYMVN
SK

>core/699/4/Org4_Gene47

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VHLISCSTLAGFVGGGGLGQLLLQYGYRRFEWSVTTSVLVITLVLIESVRILGDFWGRRVLKYRGIL

>core/700/4/Org4_Gene829

MSTVTTEPCSSIHISLNNDWRDSLPPYSLDRASELLHFRFLPSLVFSNWKVEQQIETLCRKSEKRRRLISPLAKWL
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RYFTIDSGKQGNVTRFINHSEQPNAEAIGVFCEGLFHVIIRTIAPIYAGQEICYHYGPLYWKHRKKREEFIPEEE

>core/701/4/Org4_Gene322

MRSHISVMGKKEGMIHIFDKDGSLVACSVIRVEPNVVAQIKTKESDGYFSLQMGAEE MNAPAHTITKRVSKP
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SHGSGFHRHAGSIGMRSTPGRCFPGSKRPSHMGAENVTVKNLEVIKVDLEKKVLLVKGAIPGARGSIVIVKHS
SRT

>core/702/4/Org4_Gene234

MQRHIVGIDTGVGKTIVSAILARALNAEYWKPIQAGNLENSDSNIVHEL SGAYCHPEAYRLHKPLSPHKAQI
DNVSIEESHICAPKTTSNLIETSGGFLSPCTSKRLQGDVFSSWSCSWILVSQAYLG SINHTCLTVEAMRSRNLN
ILGMVVNGYPEDEEHWTQEIKLPIIGTLAKEKEITKTIISCYAEQWKEVWTSNHQGIQGVSGTPSLNLH

>core/703/4/Org4_Gene76

MNAVNTPKKILCIVADYREISPLIEQLDFTQINEHLYSYRCTDYHLDLYIVHVWGSTAVLNALQSYCQAYTDY
DLWINPGFVGACSP EIPLGQCYTIEKIANLTDTTPVLSEDPPYIFDALPDSL PKSSLVTSPVLYHYGFHKTFKL
LDMEGYAIASQAAEH HIPCSFLKITSDYTVPGDCPFSRLEEVSQKLTQTLVELLMERAIPP KLLLPCP

>core/704/4/Org4_Gene428

MLGSLPCYPGAGNIEEYKNRYFYCQLCAEVVSPYVVPVVVVVDVQGAPPTGILQVLRCKQH KFKQGLPVHGPIT
SLWALEPVGKGAPQLESAMYELCSQVRNFDICSIVSWVFGGLCIFAGLIVGVMVEAPLIAGLSAWVIPCIIIGI
GAILCLFAILMAYLGRGRVREWLNLSHEYITQCHCRQIQAHSQNYSVITEYPATCALSQPITKLPNGSRRDN

>core/705/4/Org4_Gene596

MDHWLAIARLLL RGCYTLCVSGIGILCGSILGLLIGTVTSLYFPSKLT KLLANSYVTVIRGTPLFIQILIVYFGL
PEVLP I EPTPLVAGIIALSMNSAAYLAENIRGGINSLSIGQWESAMVLGYKKYQIFIYIYPQVFKNILPSLTNEF
VSLIKESSILMVVGVP ELTKVTKDIVSRELNPME MYLICAGLYFLMTTAFSCISRLSEKRRSYDN

>core/706/4/Org4_Gene830

MKRFIYKTIFCGLTLLTSLSSCSLDPKGYNLETKNSGDLNQESVILKENRETPSLVKRLSRRSRRLFARRDQTQ
KDTLQVQANFKTYAEKISEQDERDLSFVVSAAEKSSISLALSQGEIKDALYRIREVHPLALIEALAENPALIEG
MKKMQGRDWIWNFFLTQLSEVFSQAWSQGVITEEDIAAFAS TLGLDSGTVASIVQGERWP ELVDIVIT

>core/707/4/Org4_Gene145

MQKL VHNIWKKFYSFSSAIAICIVLASFLSLKIVSNTYKHSQAKRNSILLLTRA AEVAVSQGFLPSKSALSSLEQ
AYHLGGESMKPYAGFLASCFYIHNEPLRGAYYAGLAYNNSQALQLPHPIQKLLKEISEAQADQLYDVALSKS
YQLLQTANSSPEYPTLSFLTLLRVIELKELLHQDVSQDFAALKSSPLFHQFERMYSDGEWTLSKRFGKKG

>core/708/4/Org4_Gene106

MIITIDGPSGTGKSTTAKALADHLHFNYCNTGKMYRTLAYARLQSPWATLPLTKFLEEPPFSFTFATGQPLESF
FNGHLLTSELTTQEVANAASELSQLPEVRAFMQDLQRRYAQLGNCVFEGRDMGSKVFPNADLKIFLTSSPEV
RAQRRLKDLPEGTLSPEQLQAELVKRDAADAQRAHDPLVIPENGIVIDSSDLTIRQVLEKILALLFRNEL

>core/709/4/Org4_Gene473

MRKMLVLLASLGLLSPTLSSCTHLGSSGSYHPKLYTSGSKTKGVIAMLPVFHRPGKSLEPLPWNLQGEFTEEI
SKRFYASEKVFLIKHNASPQTVSQFYAPIANRLPETVIEQFLPAEFIVATELLEQKTGKEAGVDSVTASVRVRV
FDIRHHKIALIYQEII ECSQPLTTLVNDYHRYGWN SKHFDSTPMGLMHSRLFREVVARVEGYVCANYS

>core/710/4/Org4_Gene802

MSKKPLYVAHPWHSPTLTQDNYESLCCYIEITPYDSVKFELDKTTGLLKVDRPQKFSNFCPCLYGLLPQTYCG
TASGNYSGEQTRREGIQGDKDPLDVCVLTEKNIHHGNILLQARPIGGLRIIDSGEADDKIIAVLEDDL VFAEIED
ISDCPGTVLDMIQHYFLTYKATPDHLIKGSPAKIEIVGIYGKKEAQKVIQLAHEDYLSYIGDTAEVN

>core/711/4/Org4_Gene302

MSVNPSGNSKNDLWITGAHDQHPDVKESGVTSANLGSHRVTASGGRQGLLARIKEAVTRFFSRMSFFRSGAP
RGSQQPSAPSADTVHSPLPGGDARATEGAGRNLIKKGYQPGMKVTIPQVPGGGAQRSSGSATLKPTRPAPPP
KTGGTNAKRPATHGKGPAQPQPKIGGTNAKRAATHGKGPAQPQPKILKQPGQSGTSGKKRVSWSEDESM

>core/712/4/Org4_Gene639

MNTSISEIQRFLSMIAFEKELVSEGFVSVAGIDEAGRGPLAGPVVASACILPKGKVFPGVNDSKKLSPKQRAQV
RDALMQDPEVCFGIGVISVERIDQVNILEATKEAMLQAISSLPISPDILLVDGLYLPHDIPCKKIIQGDAKSASIA
AASILAKEHRDDLMLQLHRLYPEYGFDRHKG YGTS LHVEAIRRYGPSPCHRKSFSPIKQMCAIV

>core/713/4/Org4_Gene564

MTKGSVFIIMGPPGSGKGTQSQYLANRIGLPHISTGDLLRAIIQEGTPNGLKAKAYLDKGAFVPSDFVWEILKE
KLQSQACSKGCIIDGFPRTL DQAHL LDSFLMDVHSNYTVIFLEISEDEILKRVCSRFLCPSCSRIYNTSQGHTEC
PDCHVPLIRSDDTPEIIKERLKKYQERTAPVIAYYDSLGLKLCRVSSSENKEDLVFEDILKCIYK

>core/714/4/Org4_Gene460

MTSKKSYRSYFFDPLWSNNQILAILGICSALAVTTTVQTAITMGIAVSIVTGCSSFFVSLLRKFTPD SVRMITQ
LIISLVFVIDQFLKAFFFDISKTL SVFVGLIITNCIVMGRSESLARHVTPIPAFLDGFASGLGYGWVLLVIGVIRE
LFGFGTLMGFRIIPQFVYASETHPDGYQNLSLMVLAPSAFFLLGIMIWLVNIRDSKKRKR

>core/715/4/Org4_Gene691

MYFYKYVIIDTSGYYPFLAYVDNQQVLEHWSLPVGPDLGIVLEFLFKSKNLSFQGVAAVALGPGNFSATRIGIS
FAQGLAMAKNVPLLGYSSLEGYLLSKDEKKALMLPLGKRGGVLTLSSEIPEEGLNEKRRGVGPGALLSYEEA
SDYCVAHGYYHVISPNPQLFASSFSDKITVEEVAPSVEQIRRHVISQFMFVEYDKQLSPDYRSYSCIF

>core/716/4/Org4_Gene453

MATSVAPSPVPPESSPLSHATEVLNLPNAYITQPHPIPAAPWETFRSKLSTKHTLCFALTLLLTLGGTILAGYAG
YTGNWIICGIGLGIIVLTLLALLLAIPLKNRQTGTKLIDEISQDISSIGSGFVQRYGLMFSTIKSVHLPETTTQNNQ
EKTRILNEIEAKKESIQNLELKITECQNKLAQKQPKRKSSQKSFMHSIKHRSKNP

>core/717/4/Org4_Gene370

MIFRICKFFTWVAFSLFYKLKVYGVKKNFIFKGPAAIAVNHNSFLDPIALHMCVHECIYHLARASLFNIPWLWK
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FNRHQKIPHVWKTITCVFGTPMYFDDIIQNPEIKNKETYQIITNQTMNKIAELKAWYESGCKGDVP

>core/718/4/Org4_Gene364

MIKSSLILLSGGQGTRFGSKIPKQYLPLNGTPLVLHSLKILSSLPQIAEVIVVCDPSYQETFQEYPVSFAIPGERR
QDSVFSGLQQVSYPWVIIHDGARPFYIPDEIHDLLETAEKIGAAALASPIPYTIKQRNPVRTLDRDNLAIHTPQ
CIKTEILREGLALAKEKQLTLVDDIEAAEIIGKPSQLVFNKHPQIKISYPEDLTIAQALL

>core/719/4/Org4_Gene917

MMNYEDAKLRGQAVAILYQIGAIFGKHILASGEETPLYVDMRLVISSPEVLQTVATLIWRLRPSFNSSLLCG
VPYTALTLATSISLKYNIPMVLRRKELQNADPSDAIKVEGLFTPGQTCLVINDIVSSGKSIETAAALEENGLVV
REALVFLDRRKEACQPLGPQGQIKVSSVFTLPTLIKALIAYGKLSSGDLTLANKISENLEIES

>core/720/4/Org4_Gene158

MARYCGPKNRVARRRFGANIFGRSRNPLLKKPHPPGQHGMQRKKKSDYGLQLEEKQKLKACYGMIMEKQLV
KAFKEVIHKQGNVAQMFLERFECRLDNMVYRMGFAKTIFAAQQLVAHGHILVNGRRVDRRSFFLRPGMQIS
LKEKSKRLQSVKDALESKDESSLPSYISLDKTGFKGELLVSPEQDQIEAQLPLPINISVVCEFLSHRT

>core/721/4/Org4_Gene858

MKQFILRTLNTLFPNPKPSLEGWSSPFQLLIAILLSGNSTDKAVNSVTPQLFAKAPDAQSILDLP PGKLYQLIAP
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EKKSPSAAEKDLARFFGHENTPKLHLQLIYYARQYCPALHHKIDNCPICSYLAKEANSTRT

>core/722/4/Org4_Gene656

MSVQVKLTKNSFRLEKQKLARLQTYLPTLKLKKALLQAEVQNAVKDAAERDKDYVQAYERIYFAELFSIP
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ILEEELRAVSIRVNLFEKKLIPETTKILKKIAVFLSDRSITDVGVKMAKKKIELRKARGDECV

>core/723/4/Org4_Gene659

MANLNADDKLKQICDALRLDTLKPAAEDEAAALLHNAKEQAKRIIQEAQEEARKILETAEERAHQKIKQGEVALSQQGGKRALEALKQAVENKIFRESLVEWLEHVTDDPEVSTKLIQALVQALEAQGVSGNLTAYIGKHVSPRAVNELLGKAVTTKLRRKKSVVVGGFVGGVQLKVEEKNWVLDLSSSALLEIFTRYLQKDFREMIFQGS

>core/724/4/Org4_Gene907

MTYLASSIFSPEDFLYPEIISKAHYTWDILDMDQMLENHVFSGIHGTVESGVTLKNIEKIEIAEGAYVESGAYIVGPCILGSQTEVRHGAYLRLGNVITGSRCSVVGHCTEIKNSYLGHHTKAAHFAYLGDSVLSSEVNLGAGVRCANFRLDGRNIYVRSTSDKSKKIDTGRRKLGAF LGKGVAIGCNVVINPGQHILPHTRIRPGQVI

>core/726/4/Org4_Gene676

MSFVPYSLPELPYDYDALEPVISSEIMILHHQKHHQTYINNNAALKRLDAAETQQNLNELIALEPALRFNGG GHINHSFLWETLAPIDQGGGQPPKHELLSLIERFWGTMDNFLKKLIEVAAGVQGGSGWAWLGFCPAKQELVL QATANQDPLEPLTGKLP LLGVDVWEHAYYLQYKNVRMDYLKAFPQIINWGYIENRFSEIISSEI

>core/727/4/Org4_Gene118

MYDYIRGTLTYVHTGAIVIECQGIGYHIAITERWAIECIRALHQDFLVFTHVIFRETEHLLYGFHSREERE CFRLISFSGIGPKLALAILNALPLKVLCSVVRSEDIRALASVSGIGKKTA EKLMVELKQKLPDLLPLDSRVETSQTHTTSSCLEEGIQALAA LGYSKIAAERMIAEAIKDLPEGSSLT DILPIALKKNFSGVNKD

>core/728/4/Org4_Gene250

MKIVIASSSHGYKIRETKTFLKRLGDFDIFSLSDFPDYKLPQE QEDSITANALTKGIHAANHLGCWVIADDTMLRVPALNGLPGPLSANFAGVGAYDKDHRKKLLDLMSSLESLVDRSAYFECCVVLVSPNQEIFKTYGICEGYISHQ EKGSSGFGYDPIFVKYDYKQTF AE SEDVKNQVSHRAKALQKLAPHLQSLFEKHLLTRD

>core/729/4/Org4_Gene785

MGLPNYITFSRLFITPIFMILYLKGKWFGITPVVLPYPVLLALLAISELTD AIDGYVARKFSQVTDLGKLLDPMA DSIYRISIYLTFTQPPVNLPLLLVFIFLARDSVISTLRTVCAFRGRVVAARASGKLKAILQGV SFFLILLVMIPHSLGLLSQNGLEIFASVTVSIIAVYSIASGIEYFWMNKNFLSQR AKTKDSEKNHESKE

>core/730/4/Org4_Gene45

MFIVIEGGEGSGKSSLAKALGDQLVAQDRKVLLTREPGGCLIGERLRDLILEPPHLELSRCCELFLFLGSRAQH IQEVIIPALRDGYIVICERFHDSTIVYQGIAEGLGAD FVADLCSKVVGPTPFLPNFVLLLDIPADIGLQRKHRQKVFDKFEKKPLSYHNRIREGFLSLASADPSRYLVLDARES LASLIDKVMLHTQLGLCT

>core/731/4/Org4_Gene638

MNKILVDSPFSPDHQKCCPKLFTISAPAGVGKTTLVRLMLEQEFSSAFAETISVTTRKPREGEVPGKDYHFVSHE EFQRLLD RQALLEWVFLFGEYYGTSMLEIERIWSLGKHAVAVIDIQGALFIRSRMP SVSIFIAPPSQEELERRLASRGSEEGSQRKERLEHSLIELAAANQFDYVIINDDLNQAYKVLKSIFIAEEHRNIL

>core/732/4/Org4_Gene887

MHAKLSFFILLSLLFSGIDCCRLHAAGRSPSLQGVLAIEIDISAKLASHEVEIVMLSERLDEQDSKCQKWTAAK
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YADFSDPVPENIYIVREGDSLAKKYKLSVTELKKINKLDSDAIYAGQRLCLQRNKQ

>core/733/4/Org4_Gene956

MIGAQQKQSGKKTASRAVRKPAKKVAAKRTVKKATVRKTAVKKPAVRKTAAKKTVAKKTTAKRTVRKTV
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KPVARKTTVAKGSPKAAAACALACHKNHKHTSSCKRVCSSTATRKHGSKSRVRTAHGWRHQLIKMMSR

>core/734/4/Org4_Gene535

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GFTGVLPQVALLMQGETNLIWAMVSGSIICFIALIGTLGLILTNNKNTPLRAS

>core/735/4/Org4_Gene184

MTLVPYVVEDTGRGERAMDIYSRLLKDRIVMIGQEITEPLANTVIAQLLFLMSEDPKKDIQIFINSPGGYITAG
LAIYDTIRFLGCDVNTYCIGQAASMGALLLSAGTKGKRHALPHSRMMIHQPSGGIIGTSADIQLQAAEILTLKK
HLANILSECTGQPVEKIIEDSERDFFMGAEAAISYGLIDKVVTSAKETNKDTSST

>core/736/4/Org4_Gene341

MLKLLKVSITGDLSSGKTEACQVFQELGAYVVSADIEISHSFLIPHTRIGRRVIDLLGSDVVVDGAFDAQAIAA
KVFYNSVLLQGLEAILHPEVCRIIEEQYHQSIQDGDYPLFVAEVPLLYEIHAKWFDSVILVMANEDIRRRERFM
KKTGRSSEDFDQRCRSLNVEEKLAQADVVENNGTKKELHQKIEEYFYALKGAL

>core/737/4/Org4_Gene742

MLTLLNLSLLFYVLFDSPGSIPVFVALLKNFSRKKQQRVILRECLFALGALILFVTFGRSFFQFLDISLYAFQIIG
GFLFLTYSIKMMLAPMPEKAKDDTSKTEPIFFPLAFPVITGPAVITALLSYMEEGIYSREIIFTAMIIAWAFSLFT
LLCSSFFDRLFGNFGLLALERLFGIALLLMSVNLMLKGISIAFNIGFYIG

>core/738/4/Org4_Gene396

MMSGIIQELGEVCFFEAQGNGLSLGIKSTPLFVSPLVTGDSVAVDGVCLTLTSCNESKIFFDVIPETLACTTLGE
KRCSDQVNLEAALKMGDSIGGHLLSGHVFGTAEIFLIKENRYYFRGSKELSQYLFEEKGFIAIDGISLTLVSVDS
DTFSVGLIPETLQRTTLGKKREGERVNIEIDMSTKIQVDTVKRILASSGKD

>core/739/4/Org4_Gene219

MFAYRTLTHNVVQVSHEIFKTTVVPGDTVIDATCGNGNDSLFLARLLQGEGRLVVYDIQKEALSNAALLFE
THLSEQERSVIEMKEQSHEHILEKDVKLIHYNLGYLPKGNKEITTLARTTEISLEYALNIVRPDGLITVVCYPGH
PEGEKETHSVESLAQRLHPKEWCVSSFYVANRCRAPRLFIFQRQGSSESSVDKG

>core/740/4/Org4_Gene55

MTRYPDYLSKLIFFLRKLPGIGFKTAEKLAFELISWDSEQLKILGNAFHNVASERSHCPLCFTLKESEADCHF
CREERDNQSLCIVASPKDVFFLERSKVFVKGRYHVLGSSLSPITGKHIENERLSILKSRIETLCPKEIILAI DATLEG
DATAFLKQELQHFSVNISRLALGLPIGLSFDYVDSGTLARAFSGRHSY

>core/741/4/Org4_Gene111

MGFACRYLFFFIVLFASGSFGNQLLSVPCWLSEESFYTHRFDfsksYPDMENMEIQAQRKKRVEFNLTGEFP
KLETNLNYQGSFGHLRAKCRGVYPVLYALNFSCSSCKMDMDFRGKWNRSSSTITISNQKESINLKLPKDVGIV
NTKTSLKGNVCPGSTFIKQGWGVWNKIYHNDLVGFSEVTLIFNVSSSEGGTITFS

>core/742/4/Org4_Gene310

MRLFSLGTIYLFFSLALSSCCGYSLNSPYHLSSLGKSLLQERIFIAPIKEDPHGQLCSALTYELSKRSFAISGRSS
CAGYTLKVELLNGIDENIGFTYAPNKLGDKTHRHFIVSNEGRLSLSAKVQLINNDTQEVLDQCVAESVDFD
FEPDLGTANAHEFALGQFEMHSEAIKSARRILSIRLAETIAQQVYYDLF

>core/743/4/Org4_Gene935

MNWAPKTMDHVDPKSETNIRLVISCYKLIKACQLEFPSLVDEVLLGMKCCAWESFKLVRQYQEQAKTVSAK
NAPLFCLTRSYYRDGHLTPLRAGPRAALSNYLDLRRRENSEKFFNPGHPCYYARLAFNETIQIYRTLFDISKLQ
IMFESGDYEKGQRENIAVILNFVKTLDDNEKVNFLLRHNDTRIPGRESATVFCS

>core/744/4/Org4_Gene211

MRIALSLLSLLMIFPIFGEESRPGSEDGNSNTQEIVGSQDTQVCLYHSYEQGLQASRIEGKPLVIVVLCNSGDD
GQACTIGLSETCEEVLSVLSGSIFSELANFVVLVPSGVNPLIYPPIEDPILAEIVKFKELFKDESFTGLSIIVGV
TPEGPGDIIIVSPVSLTVEEEETLPSEQTTEVESTSELQSEDPAIA

>core/745/4/Org4_Gene378

MSSNLHPVGGTGTGAAATESVLNIVEETAASGSVTAGLQAITSSPGMVNLLIGWAKTKFIQPIRESKLFQSRA
CQITLLVLGILLVVAGLACMFIFHSQLGANAFWLIPATIGLIKLLVTSLCFDEACTSEKLMVFQKWAGVLEDQ
LDDGILNNSNKIFGHVKTEGSNSRATTPVPTSEGRGTPILSPLVSKIARV

>core/746/4/Org4_Gene4

MSLPLVLGSSSPRRKFILEKFRVPFTVIPSNFDESKVSYSGDPIAYTQELAAQKAYAVSELHSPCDCIILTGDITV
SYDGRIFTKPQDKADAIQMLKTLRNQTHDVVTSIAVLHKGKLLTGSETSQISLTMIPDHRIESYIDTVGTLNNC
GAYDVCHGGLILKKVHGCYVNVQGLPIQTLKYLLEELNIDLWDYSI

>core/747/4/Org4_Gene413

MLQEHFFLSEDEVITLAQQLLGHKLITTHEGLITSGYIVETEAYRGPDDKACHAYNYRKTQRNRAMYLKGGSA
YVYRCYGMHLLNVVTGPEDIPHAVLIRAILPDQGKELMIQRRQWRDKPPHLLTNGPGKVCQALGISLGNN
KQRLNTPALYISKEKISGTLTATARIGIDYAQEYRDVPWRFLSSEDSGKVLS

>core/748/4/Org4_Gene169

MTLSLVGKEAPDFVAQAVVNGETCTVSLKDYLGYVVLFFYPKDFTYVCPTELHAFQDALGEFHTRGAEVI
GCSVDDIATHQQWLATKKKQGGIEGITYPLLSDEDKVISRSYHVLKPEEELSFRGVFLIDKGGIIRHLVVNDLP
LGRSIEEELRTLDALIFFETNGLVCPANWHEGERAMAPNEEGLQNYFGTID

>core/749/4/Org4_Gene85

MFRRTGKGPFDVQTLYEEETSSPSSYSPYSRSERPETPPSLFDNPKASEARPLNHNLTEESSLPQWSSTPRTES
LLPLEEPETTLGEGVTFKGEALAFERLLRIDGTGEGILVSKGKIIIGPKGVVKADIQLQEAIIIEGVVEGNITVSGKV
ELRGGAIIKGDIIQANTLCVDEGVRIILGYLAIAGITDHSEERERDL

>core/750/4/Org4_Gene232

MAYGTRYPTLAFHTGGIGESDDGMPPQPFETFCYDSALLQAKIENFNIVPYTSVLPKELFGNIVPVDTCVKSFK
HGAVLEVIMAGRGAALSDGTHAIATGIGICWGKDKNGELIGGWAAEYVEFFPTWINDEIAETHAKMWLKK
LQHELDLRSIAKHSEFQFFHNYINIKQKFGFCLTALGFLNFENAEPKVN

>core/751/4/Org4_Gene166

MKKWISILILSFLSLLSILPVLAITINHVKISQRWSDLNSQILTLKVIRDHEDQVIKHNARISKDRNNLSIESLNAS
CKQLRPLSKERERLNKLNSNSLLAQSKVWERKRALEKSNHQLVWNCEQMHNDFAFVRLEQATEMDNEDI
ESLFSLFNPENPVAPLVFFTCWKMTKQTTPLGNEVWLTHAEAISRWI

>core/752/4/Org4_Gene886

MNIHSLWKLCLILLALLALPACSLSPNYGWEDSCNTCHHTRRKKPSSFGFVPLYTEEDFNPNTFTGEYDSKEEK
QYKSSQVAAFRNITFATDSYTIKGEENLAILTNLVHYMKKNPKATLYIEGHTDERGAASYNLALGARRANAI
KEHLRKQGISADRLPTISYGKEHPLNSGHNELAWQQNRRTEFKIHAR

>core/753/4/Org4_Gene463

MVLFSLLFPKLCYGCQAPGAYFCSNCLEKLLVEDREGRCLHCFRYLGSSETRLCSQCSPSSQLQAFSLYLPSQ
TALSVYARACEGKRPALQFFSKSIAFELASLDETPSCIAYITSTISREIVVEVAKLEKLLRIPLWPWLPKKRQIEK
LPKGECICFLSAYPLSQWMQAIVGGSASPVVVISLFLSQNDQ

>core/754/4/Org4_Gene552

MKRYVVGISGASGVILAVKLIKELVNAKHQVEVIISPSGRKTLYYELGCQSFDALFSEENLEYIHTHSIQAISS
LASGSCPVEATIIIPCSMTTVAAISIGLADNLLRRVADVALKERRPLILVPRETPLHTIHLNLLKLSRSGATIFPP
MPMWYFKPQSVEDLENALVGKILAYLNIPSDLTKQWSNPE

>core/755/4/Org4_Gene190

MKVIYYEIEEIPSTNTMAKSYMHLWDPYALTVISTKCQTAGTGKFGKSWKSSKGDLLNTFCFFITDLHIDVSR
LFRLGTEAVVALCKDLGITEAKIKWPNDVLVHGEKLCGVLPETLPVEGLLGVLGIGLNGNTTKQALKDVG
QPATSLQEILGHPIDLETTRELLIHLLGVLQENLPDSLATKSNRGN

>core/757/4/Org4_Gene95

MADGEVHKLRLDIEKELLEARRVFFSEPVTEKSASDAIKKLWYLELKDPGKPIVVFVINSPPGGSVDAGFAVWDQ
IKMLTSPVTTVVVTGLAASMGSVLSLCAAPGRRFATPHSRIMIHQPSIGGPITGQATDLDIHAREILKTKARIIDV
YVEATNQPRDIEKAIDRDMWMTANEAKDFGLLDGILFSFNDL

>core/758/4/Org4_Gene671

MIKKFFIYSLIFSCSFSAPLKGICNEDVSSQSRIEEDPDVLITQLNGLIETLIEEGKEIRNELQAISDGQKSSEEIEES
CGTSDSEGLSEKTDEESSNEYVLDFDMSVQRLEGISKMCQSGQVAQIIDCFNREFDIRNRELELKNRELELRE
KDLEFKKSILDWNKEKVSRELAHQREQDIKQTLMLLKK

>core/759/4/Org4_Gene70

MSIKEDKWIREMALNADMIHPFVNGQVNVNEETGEKLISYGLSSYGYDLRLSREFKVFTNVYNSVVDPKCFT
EDIFISITDDVCIVPPNSFALARSVEYFRIPRNVLTMCIGKSTYARCGIIVNVTPFEPEWEGHVTIEISNTTPLPAK
IYANEGIAQVLFFESSTTCEVSYADRKGGKYQKQQGITVPCV

>core/760/4/Org4_Gene196

MVRVSTSEFRVGLRIEIDGQPYLILQNDVFKPGKGQAFNRIKVKNFLTGRVIERTYKSGESVETADIVERSMRL
LYTDQEGATFMDDETFEQEVVFWEKLENIRQWLLEDTIYTLVLYNGDVVAVEPPIFMELSIAETAPGVRGDT
ASGRVLKPAVTNTGAKIMVPIFIDEGELVKVDTRTGSYESRVSK

>core/762/4/Org4_Gene938

MMKIPYARLEKGSLLVASPDMNQGVFARSVILLCEHSLNGSFGLILNKTLGFEISDDIFTFEKVSNNHNRFCMG
GPLQANQMMLLHSCSEIPEQTLEICPSVYLGGLPFLQEIASSESGPEINLCFGYSGWQAGQLEKEFLSNDWFL
APGNKDYVFYSEPEDLWALVLKDLGGKYASLSTVPDNLN

>core/763/4/Org4_Gene708

MIRLEYYGSPILRKKSSPIAEITDEIRNLVSDMCDTMEAHRGVGLAAPQVGKNVSLFVMCVDRETEDGELIF
SESPRVFINPVLSDPSETLIIGKEGCLSIPGLRGEVFRPQKITVTAMDNLNGKIFTEHLEGFTARIIMHETDHLNGV
LYIDLMEEPKDPKKFKASLEKIKRRYNTHLSKEELVS

>core/764/4/Org4_Gene753

MALNFKINRQIRAPKVRLIGSAGEQLGILAIKDALDLAREAGLDLVEVASNSEPPVCKIMDYGKYRYDLTKKE
KDSKKAQHQVRIKEVKLKPNIENDFSTKLKQARTFVEKGNKVKITCMFRGRELAYPEHGFKVVQKMSQGL
EDIGFVEAEPKLAGRSLICVVAPGTVKTKKKQEKSHAQDENQ

>core/766/4/Org4_Gene346

MRILAGKYKGKSLKTFSNPHIRPTSGLVKEAFFSICREDIEGAFLDLFAGMGAIGFEALSARGAACVVFDISI
KAIQLIHTNSALLGEQLPVVIFRQDAQSAIQRLIKQKRSFDLIYIDPPYELCNRYVQTLLQKIVSGNILNPEGTLF
LENASDEEIIACEGLTLRRRRKLKGTYLAEYIVEKDP

>core/768/4/Org4_Gene783

MELVVTSRETGKKSFLKKIRQQGGIPAVVYSAGKSLANITVDALVFKKFLSNLESGALSSTVFSLSYEGRIIKA
LVKDIQYQITTYDVIHLDFEELVEDRPVKLNIPRCINAVDCIGVKLGGSLRQVIRAVRVVCKPKDIVPFLELDV
QSVGLSQTRKLSDIKIPAGIETITPLKEVAITVSRR

>core/770/4/Org4_Gene604

MVLSSQLSVGMFISTKDGLYKVTSVSKVAGPKGESFIKVALQAADSDVVVERNFKATQEVKEAQFETRRTLEY
LYLEDESYLFLDLGNYEKLFIPOEIMKDNFLFLKAGVTVSAMVYDNNVFSVELPHFLELMVSKTDFPGDSL
SGGVKKALLETGIEVMVPPFVEIGDVIKIDTRTCEYIQRV

>core/771/4/Org4_Gene415

MTDTPPENEEQHESNVQNENEVEHLQQEIVTLKTELKEKNDKYLMAESENSRKRLQKERQELMQYALEN
TLIDFLNPIESMEKALGFATQMSDDVKNWALGFNMILNQFKQIFEEKGIIYSSIGQKFNPFLEAVETEETSE
VPEGTILEEFAKGYKIGERPIRVAKVKVAKAPTPKENKE

>core/772/4/Org4_Gene174

MAAKTKTLELEDNVFLLLEGNLKRIFATPIGYTTFREFQNVVFNCAANGQQEIANFFFEMLINGKLTQELAPQQ
KQAAHSLIAEFMMPIRVAKDIHERGEFINFITSMDLTQQERCIFLNRLARVDGQEFLLMTDVQNTCHLIRHLL
ARLLEAQKNPVGEKNLQEIQEEITSLKNHFDDELTKALQ

>core/773/4/Org4_Gene107

MVETVLHNFQRYLSKYLYRVFRFPCRKKTFLSSHRVLARPSFPVDYCPGKIYDLQEIYEELNAQLFQGALRLQ
IGWFGKATRKGKSVVLGLFHENEQLIRIHRSLDRQEIPRFFMEYLVYHEMVHVSVPREYSLSGRSIFHGKKF
KEYEQRFPLYDRAVAWEKANAYLLRGYKKRVGGGYGRA

>core/775/4/Org4_Gene943

MNFAKIDHNHLYLTCLGDLGVACPILSTDCLPNYSEKASHEVLVYSKFRCSGEP SRLATSGNDTYYSIVSLPI
GLRYEVTSPSGRHDFNIDMHVAPKIGAVLSHGAREAKEIPGSSKDYAFFSLTARESLMLSEKLAMTFQVSEVI
QNCYSQCTKVTKTNLKEQYRHLSHNTGFELSVKSAF

>core/776/4/Org4_Gene326

MSRKAREPILLPQGVESIQDDKIIIVKGPKGSLTQKLVEVEITLKDNSIFVHAAPHVVD RPSCMQGLYWALI
SNMVQGVHLGFEEKRLEMIGVGFRASVQGAFLDLSIGVSHPTKIPISTLQVSVEKNTLISVKGLDKQLVGEFA
ASIRAKRPPEPYKGKGIRYENEYVRRKAGKAAKTGKK

>core/777/4/Org4_Gene667

MYKWYVVQVFTAQEKVKKALEDFKESSGMTDFIQEIILPIENVMEVKKGEHKVVEKYIWPGYLLIKMHLT
DESWLYVKSTAGVVEFLGGGVPVALSEDEVRSILTDIEEKKSGVVQKHQFEVGSRVKINDGVFVNFIMGVSE
VFHDKGRLSVMVSIFGRETRVDDLEFWQVEEVAPGQESE

>core/778/4/Org4_Gene358

MSLLNLPSSQDSASEDSTSQSQIFDPIRNRALVSTPEEKVRQRLLSFLMHKLNYPKKLIIEKELKTLFPLLMRK
GTLIPKRRPDILIITPPTYTDAQGNTHNLGDPKPLLLIECKALAVNQNALKQLLSYNYSIGATCIAMAGKHSQV
SALFNPKTQTLDIFYPLPEYSQLLNYFISLNL

>core/779/4/Org4_Gene82

MVEIFNYSTSIYEQHASNNRIVSDFRKEIQMEGISIRDVAKHAQILDMNPKPSALTSLLQTNQKSHWACFSPPN
NFYKQRFSTPYLAPSLGSPDQQDEIDIEKISSFLKVLTRGKFSYRSQITPFLSYKDKEEEEDPEEDDDDDPRVQ
QGKVLLKALDLGVKSTNVMIDYVISRIFQFVQG

>core/780/4/Org4_Gene580

MSKESIRSYSEISTPTPIFRETPSKEGVAYKLQLRSPAKDCILRNRVSLKGALLRSIPFYGSFLGAKRIHSAWSA
KDAPCTTRVYHYLVGGLELLGLGVVVLACKVLATALKFLFSKASSKIKQMKWREKARNLAAKDTVQSIKEF
CSVDLTSCFTRCFRLRNRVVEEGESENQTVREIIV

>core/781/4/Org4_Gene898

MTDPKIEKSALRKLFISIRRDLESEERKHEASSAVASFVRSFSKESVVLSFVSFNHEIDMQEANRILIQKCTLALP
KIDQENLYPVLIPSIDDLISVVHPKDPFSKQTPISSDKITHVLVPGLAFDQQGYRLGYGHGFYDRWLAQHPYPS
IRTIGIGYCEQKIDKLPQESHDIPLSQIYLC

>core/782/4/Org4_Gene124

MSRLKKFYTEEIRKSLFEKFGYANKMQIPVLKKIVLSMGLAEAAKDKNLFQAHLEELTMISGQKPLVTKARN
SIAGFKLREGQGIGAKVTLRGIRMYDFMDRFCNIVSPRIRDFRGFSNKGDGRGCYSVGLDDQQIFPEINLDRV
KRTQGLNITWVTTAQTDDDECTTLELMGLRFKKAQ

>core/784/4/Org4_Gene782

MAKLIVAIGNPGHGYANTRHNAGFLLADRLVEELQGPPFKPLSKCHALMTLVESSSGPLVFIKPTTFVNLSGK
AVVLAKKYFNVALSHILVLADDVNRSFGKLRLCFNGSGGHNGLKSITASLGSNEYWQLRFGVGRPLEEGV
ELSNFVLGKFSEENLQLGSIFVEASTLFTEWCSKF

>core/785/4/Org4_Gene147

MSVLQDTEKKMAAALDFFHKEVKSFRGTGKAHPALVETVVVDVYGTTMRLSDIASISVADLRQLVISPYDGN
NASAIAKGIIAANLNLQPEVEGSIIRIKVPEPTADYRQEMIKQLRRKCEEAKINVRNIRREANDKLKKDSALTE
DVVKGNEKKIQELTDKFCKQLDELTKQKEAEIASI

>core/786/4/Org4_Gene188

MTTPQSPGSLSQSHLPHPHDPWDTEPTSLPEDPNDKASQELHSLVHLFRKLSIHLLSEVEKTVQQLKPDLELA
LLICEKFLYKKLENPQELALLLSTALQRHTTLRSLTPIKVFLHPEDLKTLTDWISTHELPMIKHAEFFPDTSCRR
SGFKIETPNGILRQEISEELDHLLSVLTA

>core/787/4/Org4_Gene103

MACEQHEGCYEEEREIEIEDIKSDTKWVSITQAAKLHNVTQAIYVAIKQKKLKASKETRWEIDIKDLEEY
KRNRYSRKKSLYQGELVFDNGKGCYSINQVAQILGIPVQKVYYATRTGTIRGERKGAAWVIHVSEIERYKNE
YLSKQAAKKLKGAEPKEHQAPNFEPPTTEIFPESN

>core/789/4/Org4_Gene233

MTIILCGLPTSGKSSLGKALAKFLNLPFYDLDDLIVSNYSSALYSSSAEIKAYGDQKFSECEARILETLPPEDA
LISLGGGTLMYEASYRAIQTRGALVFLSVELPLIYERLEKRGLPERLKEAMKTKPLSEILTERIDRMKEIADYIF
PVDHVDHSSKSSLEQASQDLITLLKS

>core/790/4/Org4_Gene536

MSAPIPTPQELSDQITCLNVQYQQVSELARENKGDIEGLKTLTAALTAHAGIQPSADEIYSLQTAAALILSASE
KPGSGPSGSTEGSVTVQSPCKFKKVLAVVLTHALIAIAVLIACIVAACGGFPLLLSALNLYTIGACVSLPIIASAS
VALICLCTFVANSLTKPVITVHTAR

>core/791/4/Org4_Gene99

MDRDNEVPLPKPKWIYRTGIGQDSHRFLPESSTKPCILGGIIFDHCPGFQANSDDIIFHAICNAISSVTNKIILG
KVADELLQTRGITDSGIYLEEALKSLKPNQKISHVAITIEGSRPKFLCKLSALRQNIQVMNLTPTDIGITATSG
EGLSDFGCGDGVQCFCVLTVMHEYCD

>core/793/4/Org4_Gene189

MGYVFYVIAGSIFLGISLGAYCQLYYSVKSVLFSWYLLTVYALEKRHALLALSQLVGEEDAQSQKEIDFLSQC
DKLSWRAFLKNSYEIPTFKEMEDLLSERVQGFLIESIETIAEHDRAILCIENFWASKNLDFEIAAYEEAVEKYL
KLRQRAPRLASKLFRFLDVPSIRFSS

>core/794/4/Org4_Gene256

MDCVDNLKLYIFRLKLPDTERISYSISPEYIREKGEEELLSPIEVEGSLGRIDSDQWILSLSLKTQLGLCCPVC
NNFFSHSVCLPDLQRVISHDEVGSGVFDCRPLIRQELLLESDFEESGQGCPERKNILKFLEDRKKHEGNNPF
EYL

>core/795/4/Org4_Gene454

MSSTLNGIFPSSLPEESADLFITNKEIVALGEKGNVFLTHSIPMHIAAITILVIVALAGIAIICLGCYSQSILLIAVGI
VLTILTLLCLQALVGFIKFIRQLPQQLHTTVQFIREKIRPESSLQLVTNAQRKTTQDTLKL YEELCDLSQKEFKL
QSTLYQKRFELSHKNEKTNQ

>core/796/4/Org4_Gene745

MSIQPVSNTTTKADKVIPDSTKVISDSITINKQSAFYFCISVMLRLSESTTEYGKSILAVLEDNTIVQQQRVKELI
NLPLLKVPDLQKKDGSDEYKNQNEIQAYQSSNQQISANRQMIQQELSSAQQRAQANQKSVNSTTTESMQIL
QATSSMLSTLKELTIKANLTNSPSD

>core/797/4/Org4_Gene226

MWIIDPLSAKKPLQAAINVPGTPITGGPNTATADDIIAKFSKDSNPLIVTVYYVYQSVLVAQDNLSIIAQELQA
NSSAQTYLNNQEALYQYVSIPKNKLNDNSSSYLQNIQSDNQAIGASRQAIQNQISSLGNAAQVISSNLNTNNNI
IQQSLQVGQALIQTFSSQIVSLIANI

>core/798/4/Org4_Gene353

MADDTLIPKLMKNSLSQACSEGLLIAKYPPLQVIVHFDNNLVVKTHLSVAPVFSCLFLGPAAHKAMQELVLW
CSRYANKEHPPFSSHFAKDLIPSQYLEILNCVAEIPFGEQQTYAEIAKKTDTHPRTVGAACKQNPFLFFPCHR
VVGSHGERNYVLGPVIHEILLKFENSY

>core/799/4/Org4_Gene451

MGFKNICKQGSQLYLNGIFPERILARKLKNCASYPRALTIEVLVSSVLGALKVILIPCASTYAALTPLRALF
NAIKTKSCQHASYAMAWLFHILTIAVIIGLVFSLVFIPPPVVFISLGLLMSVTTSVTLFQVHKNLFPPEPLPSR
PHTPPPFAD EYVPLISESYFD

>core/800/4/Org4_Gene228

MSHLNYLLEKIAASSKEDFPFPDDLESYLEGYVPDKNIALDTYQKIFKISSEDEK VYKEGYHAYLDKDYAKS
ITVFRWL VFFNPVSKFWFSLGASLHMSEQYSQALHAYGVTAVLRDKDPYPHYAYICYTLTNEHEEAEKAL
EMAWVRAQHKPLYNELKEEILDIRKHK

>core/802/4/Org4_Gene511

MPVHTTPRKCFILCILSMFTLPTLFPKAHLILFSPYIVLCFYCFSKDKGLVLALGCGVLSDLALGSRGVFLLLYP
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CAINSGIHKMMSFFRRLVCY

>core/803/4/Org4_Gene148

MVHSPTHQCYHCQQPATICYTEIDKDKVIRSYVCATCPCPSHYNNNEHLSLSKGVGVLTLECGNCKTVWHS
KQDDEQLLGCHQCYTNFKNQITSKLKSERVSSSFTMEKGQGS LHIGRAPGEASNTNPLLKLIALNEALQDTL
EREDYEQA AVIRDQINHLKTKNPDDPS

>core/804/4/Org4_Gene366

MTAEKQNTGIPGLEIRYTLPSDATYMLKWLNPKILRGFPIQTEAEIRETVNFWVGFYRYHSSLTAVYNGNV
AGVATLVLNPYVKVSHHALISIIVGEEFRNKGIGTALLNNLIHLAKTRFKLEVLYLEVYEGNPALHLYQRFGF
VEVGRQNR FYKDEIGYLAKTTEMEKDL

>core/805/4/Org4_Gene56

MKKLLFSTFLLVLGSTSAAHANLGYVNLKRCLEESDLGKKETEELEAMKQQFVKNAEKIEEELTSIYNKLQD
EDYMESLSDSASEELRKKFEDLSGEYNAYQSQQYQSINQSNVKRIQKLIQEVKIAAESVRSKEKLEAILNEEA
VLAIAPGTDKTTEIIAILNESFKKQN

>core/806/4/Org4_Gene636

MSEVKPLLLKNSDFDLATQRFQNLINMLQEQAIEYNEYEEKNARVQNEIKEQKDSVKRCIEDFEARGLGVLK
EELASLTRDFHDKAKAETSMLIECPCIGFYYSIHQEEQRQRQERLQKMAERYRDCKQVLEAVQVEQKDMISP
RVVVDDSYFEEEEKQKVDNRKKEQD

>core/807/4/Org4_Gene900

MCKNRGVRGIVACDPRGVIGLEGKLPWHYPEDLQFFSETIQKFPIVMGRKTTWETLPRKYFVDRAVVVFSHEK
RQGVHGEIWVTSLEEFLLLDLSSPTFLIGGGELYSLFLENQIVRDIFFISHIKKEYAGDTFFPLSLETWTKTVLR
DTQEIITCYENHHSQNTKNISL

>core/808/4/Org4_Gene665

MKQEKTLLLQEVEDKISAAQGFILLRYLGFTAAYSREFRNSLSGVSAEFEVLKKRIFFKAIEAAGLEVDCSDTD
GHLGVVFSYGDVPVSAAKQVLDFNKQHKDSLVLFLAGRMDNASLSGA EVEAVAKLPSLKELRQQVVGLFAAP
MSQVVGIMNSVLSGVISCVDQKAEKN

>core/809/4/Org4_Gene22

MQRLGLSNLFHCLLLFLRYYYSKLVFGLTVLLAAISVICLLGCSEPSLSSFTEYVGPEYSAAAQLSIEQSCHDE
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>core/810/4/Org4_Gene781

MKQQLLLLEDVDGLGRSGDLITARPGYVRNYLIPKKKAVIAGAGTLRLQAKLKEQRLIQAAADKADSERIAQ
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EVTSDNEYVTVLAQGKQTEENQEG

>core/811/4/Org4_Gene543

MIINVRAPAFGITSVQQFSTNFQAAIPILNIVIGCSRISSTYAEDIEEVAQEKSEKSTHSKSSTSVNLWAHRVRGV
VEILGGGIVILALEITALVLQVIIKLIKCLIDVLCVCLFGLGVCVVAIIIGAIAFCVVVVVKYLGFCSQGEELEPIE
VKTLISPDKPYPTVVYV

>core/812/4/Org4_Gene334

MSELIIGVDPGTIVAGYAIIAVEQRYQLRPYSYGAIRLSSDMPLPMRYKTLFEQLSGVLDDTQPNAMVLETQF
VNKNPQSTMKLAMARGIVLLAAAQRDIPIFEYAPNVAKKAVVGKGHASKRQVQVMVSKILNVPEVLHPSNE
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>core/813/4/Org4_Gene116

MRQFCNLLSLSRLWLALYFCQEKLHIRLLAIVGAMLSDVLDGYLARRYKATSRLGSILDPITDKVFVFCITV
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VALGFLYFLERIMDYKKQFLR

>core/814/4/Org4_Gene394

MATRFRSTLLVITLFLVLDWVTKLVVLLQYKDLQILTHPTLYTHSWGRFSFSIAPVFNEGAAFGFLFSNYKYFLF
LLRIFVILGLLAYLFLKKKSIQSTTQTALVLLCAGAIGNVGDIIIFYGHVVDVFISFNYKQWAFPTFNVADVLSLG
TLLLVYKFYFPTKQTEKKR

>core/815/4/Org4_Gene149

MAKYPLEPVLAIKKDRVDRAEKVVKEKRRLLIEQEKLREKEAERDKVKNHYMQKIQQLRDLLDEGTTSDA
VLQIKSYIKVAVQLSEEEKVNKQKEVLAASKELEKAEVNLAKRRKEEEKTRLHKEEWMKEALKEEARA
EEKEQDEMGQLLFQLRQKKKRESGGS

>core/816/4/Org4_Gene502

MAVEQSHIKEEIEKLIGKAIKKVCGNKENDLCRYLPGPSGGYMHHTLKKMKSAAPEQLLKMLKTFILESETP
RTINPKPRAPRGSKKRRDFINFTKTDIERVLELARQVGDKDLLARFSPKKPLTSLKRELIRSIRNGIVSVELWNA
YVEAVKAVSSPNLEVTSPFV

>core/817/4/Org4_Gene605

MDLKQIEKLMIAMGRNGMKRFAIKREGLELELERDTGEGNRQEPVFYDSRLFSGFSQERPIPTDPKKDTIKET
TTENSETSTTTSSGDFISSPLVGTFYGGSPAPDSPAFVKPGDIVSEDIVCIVEAMKVMNEVKAGMSGRVLEVLI
TNGDPVQFGSKLFRIAKDAS

>core/819/4/Org4_Gene554

MSKKINRNDLCPCGSNKKYKQCCLKKEEQTARYTTEGKFKFSAEVLSSSEQGEAGDNCTKLFQRLSQSLTSE
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DFIPTQEDFRISENSQKPPVEED

>core/820/4/Org4_Gene69

MSRQNAEENLKNFAKELKLPDVAFDQNNTCILFVDGEFSLHLTYEEHSDRLYVYAPLLDGLPDNTQRKLALY
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SVDTMPQMPQGGGGMQPPPTGIRA

>core/821/4/Org4_Gene203

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ARMGFEPGGGAAYVSKVKSALKLR

>core/822/4/Org4_Gene382

MSRRHSAEKRDIPGDIYGSVILEKFINKVMMHGKKS VARKIVYSALERFGKKLNLE NVLEGFEEALENAKPI
LEVRSR RVGGATYQVPVEVASERRNCLAMQWIIKHARSKPGKSMEVGLATELIDCFNKQGATIKKREDTHR
MAEANKAFAHYKW

>core/823/4/Org4_Gene327

MSLSKNSHKEDQLEEKVLVNNRCSKVVKGGRKFSFSALILVGDGKGRLGYGFAKANELTDAIRKGGEEAAKK
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AFKALTGLSPRKDLLRRGAIND

>core/826/4/Org4_Gene273

MTKFLYCGLFYSLGLLVLAFGTMVAIIQVDQICDVSCMNKHFQESPPFLKIKKVVNVSKQICSPEERFFHCKIDK
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SSSGGMKTLYLSLFRN

>core/827/4/Org4_Gene787

MMHRYFIPLLALLIFSPSLVKAELQPSNRKGGWPTQLSCAEGSQLFCKFEAAYNNAIEEGKPGILVFFSERPT
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AQCQAVLPLETKI

>core/828/4/Org4_Gene744

MSITTLGTLPTVNTINSSRPPEPLNTPKIGAVLFSIYELLLQAIEIRQQTVLTQSQQLNNDNTNIQQQLNQETNQI
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VNQLNKPLG

>core/829/4/Org4_Gene467

MTTWTLNQNNLTFLKSSDEEPFLERESGLTYINIQANGNELPLFFVIRSEGEILQLICYLPYQLHESHKASTAR
LLHLLNRDIDIPGFGMDDEEQGLIFYRLVLPCLNGKIHDTLRIYIDTIKLVCDSSFHAIGLISSGNMNLDELRRQ
ALQEQQEKRNE

>core/831/4/Org4_Gene754

MATLSPEKFSGSPISISKEFPQQKMREIILQMLYALDMAPSAEDSLVLLMSQTAVSQKHVLVALNQTKSILEK
SQELDLIIGNALKNKSFDSLDELVEKNVLRRLTFEHFYSPINKAILIAEAIRLVKKFSYSEACPFHAILNDIFTDS
SLNENSLSI

>core/832/4/Org4_Gene973

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MYAGYGQEQQYVCEDEVFPF

>core/834/4/Org4_Gene582

MSKKVFFESYEDFANVASSWPKSLRALVQGRYFVDSELKETPYRIHDFKKTPIHHRLYRSLPIISTIGGIIRLIEA
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EAVNFLA

>core/835/4/Org4_Gene74

MFFNFLFSLVFKLSDELALAETIQEPISVHEMFPGSMKLEMFKMLGSLILLLTIFGFGVWAFKKFVRSRSHGFGG
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KQQTND

>core/837/4/Org4_Gene14

MPSYCQNQQDFSLFSLSPRLVMFLGKHSRDEILQDLTDLVDAAGLLEDKQAFFDALVRRENIMSTGIGMGV
AIPHGKLESCSNFFIAIGIHTQGILWDAIDGALVRLVFLIGGPENAEYLKLLSTLTLREESRRQQLQVNT
IEEVMNVFVGM

>core/838/4/Org4_Gene181

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QDTSNKPS

>core/839/4/Org4_Gene412

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RKKHALLTA

>core/841/4/Org4_Gene209

MLPISILLFYVILGCLSAYIADKKKRNVIWFFAGAFFGFIGLVVLLLLPSRRNALEKPQNDPFDNSDLFDDLK
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VPSLQQALKEASK

>core/842/4/Org4_Gene513

MRIIRFDYPYGALSAQSIKDSRQNSPLVEKISEEIIATNEAIRLALLAIGDREQUEKKQRHRYKLLGQKQAKVLL
SQLRHVHLDFFKKLHCDSKKKEDQEKDEKNKQKRSIKVTKKKKGISLGAAASQAIAAAAEAWVISRNKGVLE
TASTLFYQKDEEA

>core/843/4/Org4_Gene791

MEKQNLKLDVKEIEFPETVFSRDIETRVIQVIILHCLAKINGVSLGGLNLIDALFGRDIERMKGIVVEQDSKNHL
VKVRVEVNVDYGVSIPEKTEEIQGCIVSEISEYTGLHVAAVHVIIKGLTQPKDRIDEEIEEEVPVQDLSPEDFL
LENSEG

>core/844/4/Org4_Gene608

MTVISNSPSPALNPESLIPPTLVSSGTQTSLAYTIPAQGRRSTLRIILDIFIILGLATIISTFIVIFFLNGLNLLSTP
SISSSCLIIVGLLFLIMGLYFMISSLDQGLVGLLQKELSQAEEEREEYIQEIEALRGAPRAESPTEPSTWL

>core/845/4/Org4_Gene136

MRVV LHCPDIPQNTGNIGRTCVALGAELILVRPLGFSLADKFVKRAGMDYWDKLQLTVVDSIEEALHDVPED
QIFCLSTKGSASYTEFSLPSSGTYVFGSESKGLPKEILKKYYKNCLRIPMQQDIRSLNLATSVGIVLYEVVRQKT
VALQKNPTV

>core/846/4/Org4_Gene747

MEKDIFFMQQAFKEARKAYDQDEVPGCVIVKDDKIIARAHNSVEKLKDATAHAELCIGSAAQDLDNWRL
LDTVLYCTLEPCLMCAGAIQLARIPRIVWAAPDVRLGAGGSWVNIFTEKHPFHTV SCTGGVCSEEA EHLMKK
FFVEKRREKSEK

>core/847/4/Org4_Gene493

MRYLPVSATDVL FESPAAPLINSANTQNQELIELKGKQQAESSPRITTSVILEVLLLIGCCLIVLSLLAIYPALQF
TLETGHPAAIAVLAVSGTILLVAVIILFCFLAAVPFAAKKTYEYVKTVDDYASWHS HKQTPTLTGTIFSGIVYAE
SQAQL

>core/848/4/Org4_Gene134

MLKKKPVSFSCIDGHIYKIFPNDLNANNTVFGGLLSLLDRLALVVAERHTESVCVTAFVDALRFYAPAYMG
ENLICKAAVNRTWRTSLEVGVK VWAENIYKQERRHITSAYFTFVAVNEDNQPIPVHQIVPETPEEKRRYNEA
DRRRQARLELK

>core/849/4/Org4_Gene832

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DAIVACGVLIQGETDHYNQIVNQVAAGIGALSLEFCLPITLSIVAAPSAEIAWQRSGIKGCHLGVSGMTTAIEM
ATLFTQI

>core/850/4/Org4_Gene861

MPFAKETEMQRTCWKCEGSVSMHVPQCPYCSAFLQDPPVASGGFSSCHISFSEGASKEEAEDLFAVSSSEDWE
AVLGDQNPTQETNKQVIPEWTWLQSWPLAALFLGIGLLAFAFLILLFSTDSGLVLTWPKNRAYSYGIIGAAVA
YRGYRKLPL

>core/851/4/Org4_Gene11

MRSALHLQHLRHFHNHGSILFENLLTIKDCFLLETKLQNFIKASKTIDTVRWRENIFRSMPEIYTVVRKRRLD
FFAAELVHRPKLSLVRDLWVFPGEEILEGEEDCMLFLLLSGDRAGSGIFFTG PYPSDLYELEKGTTGLLLAFSS
VGIPVI

>core/852/4/Org4_Gene132

MNQPSVIKLRELLDLLPHRYPFLLVDKVL SYDIEARSITAQKNVTINEPFFMGHFPNAPIMPGVLILEALAQAA
GVLIGLVLENDRNKRIALFLGIQKAKFRQAVRPGDVLTLQADFSLISSKGGKAWAQARVDSQLVTEAELSFA
LVDKESI

>core/853/4/Org4_Gene97

MQCPFCNHGELKVIDSRNAPEANAIKRRRECLKCSQRFTTFETVELTLQVLKRDGRYENFQESKLIHGLNAAAS
SHTRIGQDQVHAIASNVKSELLGKQNREISTKEIGELVMKYLLKKADMIAYIRFACVYRRFKDVGELMEVLLS
ATPDMEK

>core/854/4/Org4_Gene927

MAQKEIVSNRKALRNYEVIETLEAGIVLTGTEIKSLRDHGGNLGDAYVIVSKGEGWLLNASIAPYRFGNIYNH
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MKRRHH

>core/855/4/Org4_Gene525

MARNIKYFLILFPGILWISAGMKLLLKATAIALDPLSSFFTYCLLSMISWGLASLKHRYLLSKTIRKQLSLSSEF
FSQKITWIAYIKQTFISRRFLIMVIMIAFSLVLRRYISNPQALFVIRATVGYALIKTAIAYFSKLQNALMENPEGN

>core/856/4/Org4_Gene41

MSKPSSCKAYLGIDYGKKRIGLAYAAEPLLLTLPIGNIEAGKNLKLSSAEALHKKIILSRNITCVVLGNPLPMQKG
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LTL

>core/857/4/Org4_Gene803

MMKTKYEYSFGVPIKFFGTPDKSTLKACFICHTRGKHWFPGKHSEDKEGPQEAERELVEETGLSVVNFFP
KVLIEQYSFNNEEQVFVRKEVTYFLAEVRGDIHADPMEICDSQWLSLQEGLRLLSFPELRDLTVEADKFINNY
LFSS

>core/858/4/Org4_Gene192

MQLLSPAFAYGAPIPKKYTCQGAGISPPLTFVDVPGAAQSLALIVEDPDVPKEIRSDGLWIHWIVYNLSTTITN
LAEGAEIFAVQGLNTSGKPVYEGPCPPDKQHRYFFTLFALDVVLPEEENVTRDQLYEAMEFHIEQAELMGTY
EKS

>core/859/4/Org4_Gene562

MEKRKDTKTIVKSSETTKSWYVVDAAGKTLGRLSSEVAKILRGKHKVTTYTPHVAMGDGVIVINAEKVRLT
GAKKGQKIYRYTGYISGMREIPFENMMARRPNYIIEHAIKGMMPRTRLGKKQLKSLRIVKGDSYETFESQKP
ILLDI

>core/860/4/Org4_Gene669

MEFICPLQHARCLKKQHKIIEKLFPEPFQKDHLYLKLMENSSSRDAFDKKRMLKENLVVGCQSDLYLYEVYQ
DGILFFFTYTKALMSSGIASLFTEVYSGETPSTILTCKPIFFQRLTPYLSFGRLNGGESLYMRMKQIAVQYLKPP
QT

>core/861/4/Org4_Gene151

MADLEVFQADFULLFEAGLLAIKQGDEDSARKLFQSLHILNPNHYGHDLGLALISLHKMDLFD AEERLSALIK
GNEDNWSIKAFLSLTHMLIVLHQSSFEVRRESLESCLKFADQVIANCKIESTRALAQSVLDWHDTLVAKSA
GPLG

>core/863/4/Org4_Gene68

MKSERLKKLESELHDLTQWMQLGLVPKKEISRHQEEIRILEHKKIYEEKERLQLLKENGEEIEEYVTPRRSPAKTV
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W

>core/864/4/Org4_Gene925

MKTKMNSRKKAGQWAFNSPTPGVSSTLVLAWTPWGYDVKDVQDILERKDPMSSSLSDKDSKEFLKNLFVD
LLENGFTSVHIIHAEAEFTPLDHTGKPHFKRDNVYLP GKLLGALNEAAVQANVSADTQFTLFLTQDDRNPFHD
KKKRD

>core/865/4/Org4_Gene979

MSNIMGSRRKLKRSFLLIEVLMALSLVCAVLLPCIRFYIAIHRSFEEDIFNLQLPALIDHCFLSVEEKMRQQMA
EGTVFTSGKGQTVSLAYTSQGIGYRIPYGYNVDIRQEVRGDNLKMKVCLADVVELFPDQKQAVSVQRCLC
VTL

>core/866/4/Org4_Gene35

MKKKVTIDEALKEILRLEGAATQEELCAKLLAQGFATTQSSVSRWLRKIQAVKVAGERGARYSLPSSTEKTT
TRHLVLSIRHNASLIVIRTVPGSASWIAALLDQGLKDEILGTLAGDDTIFVTPIDEGRLPLLMVSIANLLQVFLD

>core/867/4/Org4_Gene517

MQNQYEQLLES LAPLLNTTLAPDKNNSCLIRFSDTQVPVQIEEDGNSGDLAVSTLLGTLPENVFRERIFKAALS
VNGSFQSSIKGILGYGEVTQQLYLSDILSMNYLNGEKLFEYLKLFSLHAKIWME SLRTGNLPDLHVLGIYYVA

>core/868/4/Org4_Gene809

MEEFVAYIVKNLVTNPEAVEIRSIEDEDNESIKLEIRVAAEDIGKII GRRGNTIHALRTILRRVCSRLKKKVQIDL
IQPENGTDVIADQDYICDNDSSNSTEDTFGESDTCCSGHCHYDEDLNQEELDQEEQEEDNMHHSCECSNHH

>core/869/4/Org4_Gene33

MSLEKELLEETPLVLLNFYKLVSFCNYAGMILGTEEKKFAIYGHVSMGQAFQGADTEGHSPQRPF AHDLLNF
VFSGFDIQVLRVVINDYKDNVIFYTRLFLEQKDREFLYVVDVDARPSDSIPLAL THKIPILCVKSVFD AVVPYEE

>core/870/4/Org4_Gene584

MNPVTFDRIQVDFIPEDTSLRINSYIVAGGLLILGVVLSILSVICLDIGLVGLSAGAAFTLGLGCLIFALFLFSFSL
ILLLSQEKRVPDVLCLYLEKEVPQYETPLYKEDLESERDMSAISERLGIIEEKLRIA EKFRYSDSVFV

>core/871/4/Org4_Gene13

MTVFCELDSSGGELPEYTTPGAAGADLRANIEEPIALLPGQRALIPTGIKAEIPEGYELQVRPRSGLALKHGITVL
NSPGTIDSDYRGEIRVILINFGDSTFIIPEKMRQAQVVLSPVVQATFVVKQESLAETARGSGGFGHTGAS

>core/872/4/Org4_Gene309

MTFFEGETVFPVAVLSELHSMMLDLIKRAGKQSKCPQEKLLKLELACEELLVNIISYAYQGGNSPGTIAISCISHRG
DLEVVIKDHGPSFNPLAVSINIQEDLPLEQRKLGGLGIFLAKSSVDEFLYAREDHCNIVHLKILNSQHS

>core/873/4/Org4_Gene117

MEQTLSEIKPDSVSKAHIGEILSIFEQSGLRIAAMKMMHLSQTEAEGFYFVHRERPFFQELVDFMVSGPVVVLV
LEGANAVSRNRELMGATNPAAEASGTIRAKFGESIGVNAVHGSDTLENAAVEIAYFFSKIEVVNASKPLV

>core/874/4/Org4_Gene121

MIKLESLFDISERKRRKLLGRGPSSGHGKTSGRGHKGDGSRSGYKRRFGYEGGGVPLYRRVPTRGFSHKRF
DKCVEEITTGRLAELFQEGEAITLDALKAKKAIARQAVRVKVLKGDLEKTFVWQDTAVVLSQGVQNLLGIT

>core/875/4/Org4_Gene566

MACSIFFRMSQGDYDDEPLSKKTACLVDTMLYPVIAVVCVVSVVLLILKVLFLLLSFPFKLCSASSALPGE
RVSLGSHFKCLYGGGLPDLLACLLIVPVIGTAIHGVIISHRTSEDDRLSSAIVFMQAPILQLAGMSGLIK

>core/876/4/Org4_Gene706

MQEHVHKELLHLGEIFRSSREFQSLSLKDVEAATSIRYSCLEAIEQGCLGKLISPVYAQGFIIKKYATYLGLDGD
SILQEHPYVMKIFKEFSHDNMEMLLDLESMGGRNSPERAIHSWSNLWWAGLIIGGIVVWWLGSLSIF

>core/877/4/Org4_Gene308

MSLDFFEEFYHQSIKNTGTSFPEGYLNAEILSHPHCTDANADFLCSQSDNDFIAESKDKLTLFNADFAIWLVP
ELVQGGQAVTRGYIAVSQGEKNYEPMAFEASGQYNQSSLILEALQLYLKDIKDTENALRSFRFNNDH

>core/878/4/Org4_Gene330

MQHARKKFRVGRVTSSHNRCMLANMLKSLIHHERIETTLPAKELRRHADKMITLAKKNSLAARRIAIGRLM
VRYNKLTSKEARQAKGGDTSVYNVDRLVVNKLDELGNRFVERKGGYTRILKLQNRIGDNAQKCIIEFLAS

>core/879/4/Org4_Gene159

MNSKSAQKIIDSIIKQILTIYNIDFDPSFGSSLSSDSDADYEYLITKTQEKIQELDKRAQEILTQTGMSKEQMEVF
ANNPDNFSPEEWLALEKVRSSCDEYRKETENLINEITLDLHPTKESKRPKQKLSSTKKNKKKNWIPL

>core/880/4/Org4_Gene83

MLDNEWKAILGWGDDELEELRISGYSFLRQGHYSKAILFFEALVILDPLSIYDHQTLGGLYLQIGENSQALAV
LDQALRMQGDHLPDLLNKTKALFCLGRIEEATAIATYLSSCPIPAIANDAEALLMSYSKATKKNAALVR

>core/881/4/Org4_Gene316

MGRYRRVSHSSQETLLLGTGLGQVLVPGAVLLLFGDYGAGKTEFVRGIVSGYLGDTIAEEVASPSFSILHVG
NEPKRLCHYDLYRIDQKNQEYIFQDAEEDDVLCIEWADRLPKPRFCDTINIYIAML TNMEREIIIIEKR

>core/882/4/Org4_Gene18

MSVKKVIKIIKLQIPGGKANPAPPIGPALGAAGVNIMGFCKEFNAAATQDKPGDLLPVVITVYADKTFTFITKQP
PVSSLIKTLNLESGSKIPNRNKVGKLTQAQVEAIAEQMKMDIVLLES AKRMVEGTARSMGIDVE

>core/883/4/Org4_Gene21

MIDMSVVGPA LVGLAMIGSAIGCGMAGVASHAVMSRIDE GHGKLIGMSAMPSSQSIYG FILMLLMQAAIKN
GTLSPVGGAIGLSVGAALLVSSVMQ GKCCVSGIQAYARSSSIYGKCYAAIGIVESFSLFAVV FALLLL

>core/885/4/Org4_Gene205

MHPLTLPKQSRVLKRKQFLYITRSGFCCRG SQATFYVVP SRHPGTCRMGITVSKKFGKAHERNSFKRVVREV
FRHVRHQLPNCQIVVFPKGHKQRPVFSKLLQDFINQIPEGLHRLGKTKATTGGECTPKSEKCVTAPR

>core/886/4/Org4_Gene129

MLMPKRTKFRKQQKGQFAGLSKGATFVDFGEYAMQTLERG WVTSRQIEACRVAINRYLKRRGKVWIRIFPD
KSVTKKPAETRMGKGKGAPDHWVAVVRPGRILFEVANVSKEDAQDALRRAAAKLG IKTFRV KRVERV

>core/887/4/Org4_Gene51

MNLIDRAFLKKTIIFQSLDMDLLL TIADKTETIIFKPGSNVFSIGQPGFSFYIIVEGYITISKEKLESPLNLKPLDC
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>core/888/4/Org4_Gene579

MVNRYKSSAEFSADHYYDDNLLRMGYKRNL RGLAPVENEVCLFEENNLL ESVMASIPIMGSILGLGRLHSV
WSTQDPKDSKISHIIFHTALGILETLGLGIIVLLIKITITILLILFTPCLLCYFMYSAAYSDFHPI

>core/889/4/Org4_Gene574

MINFIRSYALYFAWVISCAGTLISIFYSYILNVEPCILCYYQRICLFPLTVILGISAYREDSSIKLYTLPQAVLGLGI
SIYQVFLQEIPGMQLDICGRVSCSTKIFLSYVTIPMASVVAFGAIVCLLVLT KKCRG

>core/890/4/Org4_Gene172

MKYRFTEEIEEEPLVNLTPLIDIVFVILMAFIVAVPLIKLDSIALAPGTQE QEVLSSENDSIAVIKVFADHSLTLN
EHPITLQELTVRLTLLHKAYPEKTPLLLQDGETSFRTYQNVKNAIEAAGFHELHVALQN

>core/891/4/Org4_Gene43

MAKSTIQESVATGRRKQAVSSVRLRPGSGKIDVNGKSFEDYFPLEIQRTTILSPLKKITEDQSQYDLIIRVSGGG
IQGQVIATRLGLARALLKENEENRQDLKSCGFLTRDPRKKERKKYGHKKARKSFQFSKR

>core/892/4/Org4_Gene902

MIAIERYQLISKFRMWLFLGCSVEERHFKQPVLISVTFSYNEVPSACLSDKLSDACCYLEVTSLEEIVNTKPY
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>core/893/4/Org4_Gene575

MPYYANTLEFIQGTQSLCPLFKYGFVRHHNKGQLEIEDASHDWDWFLEPPSTWKRTLAAIPILGSIIGLGRLFSI
WSIREPQDSQEYKSIFWHTLCAVLEILGLGIVALILKILATFIMAMPGLKRVATFLFYs

>core/894/4/Org4_Gene123

MGMTSDSIADLLTRIRNALMAEHLVYDVEHSKMREAIVKILKHKGFVAHYLVKEENRKRMRVFLQYSDD
RKPVIHQKRVSKPSRRVYVSAKIPYVFGNMGISVLSTSQGVMEGSLARSKNIGGELLCLVW

>core/895/4/Org4_Gene119

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QDAAKTAMNSGLKEVEVCLKGTGAGRESAVRALISAGLVVSVIRDETTPVPHNGCRPRKRRRV

>core/896/4/Org4_Gene199

MNFVSTLTGSDFYAPVLEKLEEFADTTGQVILFSSSPDFIVHPIAQQLGISSWYASCYRDQSAEQTIYKKCLT
GDKKAQILSYIKKINQARSHTFSHDILDLPLMLGEEKTVVRPQGRLKKMAKKYYWNIV

>core/898/4/Org4_Gene930

MSQCQSSSISTWEWMKSFVPNWSTEPKYSTPLSSPTPSEDEFTLAYESFVLKGDPENAPANPPGTPTPNSengi
DDLNPPLGQPNEQNNANNPGTSGSNPISLPAPERLPETEENSQEEEQGSQNSedlig

>core/899/4/Org4_Gene153

MLEKLIKNFATYMGITSTLELDADGAYVLPiseVVKVRAQQNADNEIVLSASLGALPPSADTAKLYLQMMIG
NLFGRETGGSALGLDSEGNVVMVRRFSGDTTYDDFVRHVESFMNFSETWLSDLGLGKQ

>core/900/4/Org4_Gene471

MRDHAFSKLIGTVRAMVVEGRCPWSLQQSLVSMVEHILGECQEFHEAVLQGKTAQEVGSEAGDVLTLVLIL
CFLLEREGVLASEDVANEAIEKLRRRAPYIFAEDYKPVsIEEADRLWELAKHREKNEST

>core/901/4/Org4_Gene661

MDYKSQLVFSCPCCCKGNVCFSVFNLDVILTCNVCSSTYTFDSIRNEIRQFVALCKRIHDANSILGNATVSVS
VEDNQMDIPFQLLFSRFPVVLNLSLDGKKIAIRFLFDALNTSILHQESDLIS

>core/902/4/Org4_Gene968

MCDKIVAQKNFLFTLDAVIKQAGWRSQEKLNLFYVESQALGREIKVSLEEYIQSMVGILGSQRTKKSFKFSVD
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>core/903/4/Org4_Gene19

MTTESLETLVEKLSNLTVLELSQLKKLLEEKWDVTASAPVVAAGGGGEAPVAAEPTEFAVTLEDVPADK
KIGVLKVREVTGLALKEAKEMTEGLPKTVKEKTSKSDAEDTVKKLQDAGAKASFKGL

>core/904/4/Org4_Gene170

MKFTVALFGAEKGSYDTAYFCRSLVDLHNYLGDVSSPGITLAIKTLLSDYNVYFRVREEGYCVDSYFFGL
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>core/905/4/Org4_Gene937

MRAGGSLVTTYPKGRRLRSPEQLRVLDDLVSYPNHLHAIELDCDAIPQDLIGATYIITFADFSTYILSLRSY
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>core/906/4/Org4_Gene577

MLIGRYSSDDQFTEATKNTPTIIKLGFVRDNLGLTNPISEMVSETSSSIKDSVLRSLPILGSILGCARLYSTLST
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>core/908/4/Org4_Gene395

MPLSDDEIEQFKKRLLMKAKLSHTLEGNAQEVKKPNEATGYSQHQAQGTDTFDRITISLEVTTKEYELLRQ
INRALEKINESSYGICDVSREEIPLARLIAIPYATMTVKAQEQFEKGLLSGN

>core/909/4/Org4_Gene122

MESSLCKKSLMKRRRALRVKVLKGSPTKPRLSVVKTNKHIYVQLIDDSIGKTLASVSTLSKLNKSQGLTKK
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>core/910/4/Org4_Gene101

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>core/911/4/Org4_Gene824

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>core/912/4/Org4_Gene868

MKRQKRKQSITLIEMMVVITLIGIIGGALAFNMRGSIHKGKVFQSEQNCAKVYDILMMEYATGGSSLKEIIAH
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>core/913/4/Org4_Gene844

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>core/914/4/Org4_Gene120

MPRIIGIDIPAKKKLKISLTYIYGIGSARSDEIHKLLKLDPEARASELTEEEVGRLNSLLQSEYTVEGDLRRRVQS
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>core/915/4/Org4_Gene126

MIQQESQLKVADNTGAKKVKCFKVLGGSRRRYATVGDVIVCSVRDVEPNSSIKKGDVIKAVIVRTRRHITRK
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>core/917/4/Org4_Gene524

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>core/918/4/Org4_Gene28

MVNLLKELEQEQCRNDLPEFHVGDTIRLATKISEGGKERVQVFQGTVMARRGGGSGETVSLHRVAYGEGME
KSFLNSPRIVSIEIVKRGKVARARLYYLRGKTGKAAKVKEFVGPRSSKK

>core/919/4/Org4_Gene752

MVRATGSVASRRRRKRILKQAKGFWGDRKGHIRQSRSSVMRAMAFNYMHRKDRKGDFRSLWIARLNVASR
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>core/920/4/Org4_Gene578

MRELNAFELTQPEEYRNRWVLMPCCLKRFCRTQHAKVWSYRCVHEASLYEKNCFLLTYDDKHLPQYGSL
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>core/921/4/Org4_Gene528

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>core/922/4/Org4_Gene59

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>core/923/4/Org4_Gene177

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>core/924/4/Org4_Gene392

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>core/925/4/Org4_Gene200

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>core/926/4/Org4_Gene67

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>core/927/4/Org4_Gene27

MALKIRLRQQGRRNHVVYRLVLADVESPRDGKYIELLGWYDPHSSINYQLKSERIFYWLERGAQLSSKAEAL
VKQGAPGVYSALLSKQEARKLVVRKKRRAYRQRRSTQREEAAKDATK

>core/928/4/Org4_Gene976

MSLNKEIGMTVLFYAFLFIFLFCVILCGLILVQESKSMGLGSSFGVDSGDSVFGVSTPDILKKVTSWCAVAF
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>core/929/4/Org4_Gene194

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>core/930/4/Org4_Gene411

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>core/932/4/Org4_Gene46

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>core/933/4/Org4_Gene71

MSKVSVRKKNWGFRLLEEVMIKSWWVIFSILIGGFVYDRAIQELRTEELRLQSKVSSLCQDILSAQEKQRQLQ
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>core/934/4/Org4_Gene87

MWYSDYHVWILPVHERVVRLGLTEKMQKNLGAILHVDLPSVGSLSCKEGLVILESSKSAIEVLSPVSGEVID
INLDLVDNPQKINEAPEGEGWLAVVRLDQDWDPSNLSLMDEE

>core/936/4/Org4_Gene212

MGKKENQLYEGAYVFSVTLSEEARRKALDKVISGITNYGGEIHKIHDQGRKKLAYTIRGAREGYYYFIYFSVS
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>core/937/4/Org4_Gene808

MTAVLILTSFPSEESARSLARHLITERLASCVHVFPKGTSTYLWEGKLCESSEHHIQUIKSIDIRFSEICLAIQEFSG
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>core/938/4/Org4_Gene324

MFKATARYIRVQPRKARLAAGLMRNLSVQEAEQQLGFSQLKAGRCLKKVLNSAVANAELHENIKRENLSVI
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>core/939/4/Org4_Gene125

MKKQNIRVGDKVFILAGNDKGKEGKVLSLTEDKVVVEGVNVRIKNIKRSQQNPKGKRISIEAPIHISNVRLTIA
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>core/940/4/Org4_Gene459

MTTLPKYVPRSRQNPDTLTFLKRYSSVLLHSENSLSYRIFAKVLAILLTSLAVAFVTLFSCEGSQLRVCALYI
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>core/943/4/Org4_Gene131

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>core/945/4/Org4_Gene421

MTVFKQIIDGLIDCEKVFENENFIAIKDRFPQAPIHLLIIPKKPIPRFQDIPGDEMILMAEAGKIVQELAAEFGIAD
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>core/946/4/Org4_Gene198

MNLSAKEYGDIIVIYLQGS�DAVSVPVQEQYLEQFIQKKHLKIALNFTDVSYISSAGIRLLLSNFKLVQSLGGK
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>core/947/4/Org4_Gene403

MASSATPGFDGTAPSLFPPATRPRYNFKLALFVTIAIALVWLALIATTIAIGLCIHPLCSSIFLTAIPLYFISRYIFS
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>core/948/4/Org4_Gene24

MKKNTHPEYRQVLFVDSSTGYKFVCGSTYQSEKTEVFEGKEYPVCYVSVSSSSHPFFTGSKKFVDAEGRVDK
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>core/949/4/Org4_Gene8

MNEPTRTYLESEKDTQDQIEELQATCIVKNAAGIHVRPAGVIVRLFDGEPCDVHFTYAGKTINAKSIMSILML
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>core/950/4/Org4_Gene926

MSTSPIGVPSMLNAATSLNATTSKAPLPTSTLSERIKEWLPCILLIVGAIFTIAGCIVMALTKQILYGLLCVVG
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>core/952/4/Org4_Gene114

MDEITPNYPLLRQDSLWNRVRVSWRADLSVSSRYEIASAAILGLLVAFCASAAVSIIFTANPLAQVFIDGCLA
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>core/954/4/Org4_Gene98

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>core/955/4/Org4_Gene276

MSFTYFLALPVDRLMQERFLCSPKRWAPFINSPLYLTLIADHDTPLYAKNLDKFPLPVEQWEKTVLHVSSLLK
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>core/956/4/Org4_Gene110

MNERTLLLLLKKKKGLFLAILDLTQTESSLTPPELEKVLKQKKIFLSCIDRVDLQIKEFRHAFSSSELPQDIQEEL
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>core/957/4/Org4_Gene100

MKQQKQKIRIRLKGFDQGGQLDRSTADIVETAKRTGARVVGPIPLPTKREVYTVLRSPHVDKKSREQFEIRTHK
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>core/958/4/Org4_Gene490

MSSPVVTGTSSASPVEQTALGEFLERLSGSGRCIKFAFAASTALLLNFTVSGIVAIAIMIFVATSVGAYFTVIGP
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>core/959/4/Org4_Gene112

MSFKRFLQQIPVRICLLIYLYQWLISPLLGSCCRFFPSCSHYAEQALKSHGFLMGCWLSIKRIGKCGPWHPPGI
DMVPKTALQEVLEPYQEIDGGDSSHFE

>core/961/4/Org4_Gene315

MVKIISSENFDSFIASGLVLVDFFAEWCGPCRMLTPILENLAAELPHVTIGKINIDENSKPAETYEVSIIPTLILFK
DGNEMARVVGLKDKEFLTNLINKHA

>core/962/4/Org4_Gene32

MSDQATTLLRIKPLGDRILVKREEEETARGGIILPDTAKKKQDRAEVLVLGTGKRTDDGTLLPFEVQVGDIIIL
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>core/963/4/Org4_Gene458

MDPASPVAPNVLQDHVQLSSEELSALSSGVS RVKKLTIAIMILSLIAISLVACGLFLTGSAPLQLSIWIAASCITL
SMLVCACWRYKISNALEKTKVAHES

>core/964/4/Org4_Gene208

MAKKSSVAREAKRRRLVEANFKKRSDLRKIVKSLSVSEEEKENARISLNKMKRDTSPTRLHNRCLLTGRPRG
YLRKFAISRICFRQMASMGEIPGVIKASW

>core/965/4/Org4_Gene3

MEQFHLDREEILLAKASALQLSEELIQEYQTSLSAVITSMKEALAIEIDDADSCESLFMHVVNVEDLREDSVT
SDFNREEFLRNVPESLGGLVKVPAVIK

>core/967/4/Org4_Gene391

MFRSNHKPKKTKCKRFRWLRGVLFGGFIATLLTCLFTP KSGVQLRKKILKVKN SGAKKSRVFFKNSKQHTKS
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>core/968/4/Org4_Gene78

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PIHIPARRAVKFTP GKRMKRLIETPNKHS

>core/969/4/Org4_Gene162

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VKRGIFKDNKAARIKSKATLKV NARAS

>core/970/4/Org4_Gene229

MKKVVTLShIFFATYCASELSAVTVVAVPLSEAPGKIQVRPVVGLQFQEEQGSVPYSFYYPYDYGYYYPETYG
YTKNTGQESRECYTRFEDGTIFYECD

>core/971/4/Org4_Gene154

MEPRHIYIRKPETPKAPDVEKPGVPEYMTMANTPTFEGPVKTLDQLRRALIEQRGAEEGQKMYDNFIQSILIST
FGLVHKDMDRAQKASKRMRSVYKEQ

>core/972/4/Org4_Gene649

MCLIDCLGQGFEAAINTVCCCSDSSESKANVAKVSAGLLALTAIVSFILIILICTGVLGASGMTFGMSNVA AVL
VLVVTILLSMFLSGACFAAKREILR

>core/974/4/Org4_Gene167

MLSyllRTAINVYSFLILAYIFASWVPDCQSARWYQLVSKCVD PFLNFFRRFVPRIGFIDPSPFVGLLCLGILPF
VILRVLRFIILNIFHSPWLLQYL

>core/975/4/Org4_Gene64

MGKPKKSRTDRALAQEIQKKSTEVLKKPARIKAKNRRKFLIAKEQKTLKHRAQEYDQLVRSLLDSQKKDTD
KVLIFNYENGFVFTDKDHFSKYSIRL

>core/976/4/Org4_Gene29

MIKKDRFTNEKLNKLFDSPFSLVNYAIKQAKIKIAKGDVRSSNVAIETLVLLDREGIQPEFTEEIVVTASPTVER
KRSEHTNSRKKDPSAYTWSDVK

>core/977/4/Org4_Gene380

MASPTPGQLHLQQKVESKVYDYSRSLAMIATALLFFIVALILSGLSLLPQVLLPFSGAYFIIGSFLAFIALGILLI
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>core/978/4/Org4_Gene9

MGSYAKKKKEAKIMEQQFLEMEASLLEKRYEGQAGNGLVSVVINGKCDLISVKVQPTCLDPEDPEVIEDLF
RAAFKLAKEQMDQEMSLMRSTMPF

>core/979/4/Org4_Gene80

MNKSRLRLCCCLCFGSLFYFYINKQNSLTKLRLEIPCLSVRLRQLEQQNISLRFLIDKIERPDHLMEDIAALPE
YQYLEYPSEESISLLSYELP

>core/980/4/Org4_Gene182

MLAFFATSFKSVLFEYSYQSLLLILIVSAPPIILASIVGIMVAIFQAATQIQEQTFAFVKLVVIFGTLMISGGWL
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>core/982/4/Org4_Gene343

MLIRLFLGISLPKGFPLYVEPPLVLATFQGTQFVGTYSEATNPLYIDNLNLNYHYTQELLYKAVPCNYKPIYRE
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>core/983/4/Org4_Gene2

MLGKIIRGLSSLIVILCALNVGLIGITHNKLNIIAKLCCGGVSTPATQITYIIIGIAGVICLLSFCPFCSKKSRRHSHGD
SCSSGGCHSHHSDKN

>core/988/4/Org4_Gene66

MAKLVITSDDEQQEFELEDNSEIAEPCESMGIPFACTEGVCGTCVIEVLEGRENLSEFTEPEYDFLGEPEDSNER
LACQCRIKGGCVKVTF

>core/989/4/Org4_Gene88

MDDSWILEVKVTPKAKENKIVGFDGQALKVRVTEPPEKGKANDAVISLLAKALSLPKRDVTLIAGETSRKKK
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>core/990/4/Org4_Gene102

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>core/991/4/Org4_Gene224

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DTERYKNLITRLNLRK

>core/992/4/Org4_Gene63

MSRKCPLTGKRPRRGYSYTLRGIACKKKGIGLKVTGKTKRRFFPNMLTKRLWSTEENRFLKLKISASALRHID
KLGLEKVLERAASKNF

>core/993/4/Org4_Gene239

MSRSLRKGPFVDHLLKKVRAMNIEEKKTPIKTWSRRSMITPEMIGHTFEVHNGKKFLTVFVSETMVGHKLG
EFSPTRIKSHPVKKG

>core/994/4/Org4_Gene934

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GYENREREVWVYLD

>core/996/4/Org4_Gene108

MSQKNKNSAFMHPVNISTDLAVIVGKGPMRTEIVKKVWEYIKKHNCQDQKNKRNILPDANLAKVFGSSDPI
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>core/997/4/Org4_Gene210

MKSFKFLLPFLSVILCCGNLLSSPRSRAISVTESIGMSAVKTLVLSEKAHEFLEGIGYGVGASSILRDWQTQQW
LEIESLLAQNEVM

>core/998/4/Org4_Gene127

MASEPRGSRKVKIGVVVSAMKMEKTVVVRVERIFSHQPQYLKVVRRSSKKYYAHTELKVSEGDKVKIQETRPLSK
LKRWRVIEHVGVS

>core/999/4/Org4_Gene236

MVEIHHKDP SLK KLFALQQSLETNLNSLSDIVATYEAMFSLIYEGLNKALRKDQLCYLLSVNSKGELLKSPSGD
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>core/1000/4/Org4_Gene152

MATNKSCTAFDFNKMLDGVCTYVKG VQQYLTELETSTQGTVDLGTMFNLQFRMQILSQYMESVSNILTAVN
TEMITMARAVKGS

>core/1001/4/Org4_Gene385

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>core/1003/4/Org4_Gene17

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>core/1004/4/Org4_Gene281

MFNMENTAKEEKNSQPLLDLEQDMQDHNRAQELKASVQDKVHKLHALLREGSDKESFGQQQSLLAGYVA
LQKVLGRINRKMI

>core/1005/4/Org4_Gene213

MNKPVHNNEHRRKRfNKKCPFVSAGWKTIDYKDVETLKKFITERGKVLPRRITGVSSRFQGVLSQAIKRARH
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>core/1007/4/Org4_Gene942

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RGPAPIWLLW

>core/1009/4/Org4_Gene52

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QAEQ

>core/1012/4/Org4_Gene275

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>core/1013/4/Org4_Gene240

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>core/1014/4/Org4_Gene168

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LVPSE

>core/1015/4/Org4_Gene225

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QEN

>core/1016/4/Org4_Gene248

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>core/1018/4/Org4_Gene157

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>core/1019/4/Org4_Gene245

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>core/1021/4/Org4_Gene15

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>core/1022/4/Org4_Gene743

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>core/1023/4/Org4_Gene779

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>core/1025/4/Org4_Gene128

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>core/1027/4/Org4_Gene238

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>core/1028/4/Org4_Gene138

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>core/1031/4/Org4_Gene349

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>core/1034/4/Org4_Gene424

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>core/1037/4/Org4_Gene376

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>core/1045/4/Org4_Gene214

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>core/1046/4/Org4_Gene141

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>core/1050/4/Org4_Gene7

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>core/1054/4/Org4_Gene72

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>core/1058/4/Org4_Gene92

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>core/1067/4/Org4_Gene231

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>core/1068/4/Org4_Gene298

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>core/1069/4/Org4_Gene207

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>core/1070/4/Org4_Gene206

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>core/1073/4/Org4_Gene971

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>core/0/5/Org5_Gene64

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>core/1/5/Org5_Gene1033

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>core/2/5/Org5_Gene781

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>core/3/5/Org5_Gene954

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>core/4/5/Org5_Gene914

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>core/5/5/Org5_Gene432

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LAILLYVSLRFEWQYAFSAVCALIHDL LATCAVL FIAHFFLKKIQIDLQAIGALMTVLGYSLNNTLIIFDRIRED
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>core/6/5/Org5_Gene1029

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INDKHIEIIVRQMLQKVRITDPGDTTLLFGEDVNKKEFY EENRRTEEDGGKPAQAVP VLLGITKASLGTESFIS
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>core/7/5/Org5_Gene52

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DVRPMVDA

>core/8/5/Org5_Gene526

MTWIPLHCHSQYSVLDAMSSIKDFVAKGQEFGIPALALTDHGNLYGAVDFYKECTQKGIQPIIGCECYIAPGS
RFDKKKEKRSRAAHLILLCKNEQGYRNLCILTSALFTEGFYYFPRIDKDLLRQYSEGLICLSGCLSSSVSDAA
LKSPEALLLELQWFQDLFKDDYFTEVQLHKMSEESIAGFKEEWLKQEYYSLEIKQIKVNTAVLEASKRLGIPT
VATNDIHYINANDWQAHEILLNVQSGETVRIAKQNTHIPNPKRKVYRSREYYFKSPAQMAELFKDIPEVISNT
LEVAKRCDFTFDFSCKKHYPYVPESLKTLNSYTEEDRYQASAVFLKQLAEEALPKKYSSEVLAKKFPHRD
PIDIVKERMDMEMAIIIPKGMCDYLLIVWDIIHWAKANGIPVGPGRGSGAGSVLLFLLGITEIEPIRFDLFFERFI
NPERLSYPDIDIDICMAGRERVINYAIERHKGDNVAQIITFGTMKAKMAVKDVGRTLDMALSKVNHIKHIPD
LNTTLSKALETDPDLHQLYINDAESAQVIDMALCLEGSIRNTGVHAAGVHICGDQLTNHIPICISKDSTMITTQY
SMKPVESVGMLKVDLLGLKTLTSINIAMSIEKKTGQSLAMATLPLDDATTFSLHKGKTMGIFQMESKGMQ
ELAKNLRPDLFEEIIMGALYRPGPMDMIPSFINKHKGKEIIEYDHPLMESILKETYGIMVYQEQVMQIAGALA
SYSLGEGDVLRRAMGKKDFQQMEQEREKFCKRACNNGIDPELATVIFDKMEKFAAYGFNKSHAAAYGLITY
TTAYLKANYPKEWLAALLTCDSDDIEKIGKLIREAQSMGIPILPPHINVSSNHFVATDEGIRFAMGAIKGIGRG
LIESIVEERDHHGPYESIRDFIQRSDLKKVSKKSIESLIDAGCFDCFDNSNRDLLASVEPLYEAIKDKKEAASG
VMTFFTLGAMDRKNEVPICLPKDIPTRSKKELLKKEKELLGIYLTEHPMDTVRDHLSRLSVVLAGEFENLPHG
SVVRTVFIIDKVTTKISSKAQKKFAVLRVSDGIDSYELPIWPDMYEEQQELLEEDRLIYAILVLDKRSDSLISC
RWMKDLNENIIECDQAFDRIKNQVQKMSFTMSTSGKETKAKGNKPNENGHTQALAPVTLSLDLNLNR
HSHLCILKKIVQKHPGSRTLVLVFTQDNERVASMSPDDAYFVCEDEELRQELVTADLPVRVITV

>core/9/5/Org5_Gene675

MVLEALAIQRQDAMQHLLKHRKEIVVDFCEDSYTIRIPDEEAPEGYWLSTLKLQDIDRLTFASCSCPDGECCL
HLMTAYFAVYDALGLHPLHDKFRHSFWYAVFSHFFLDIPLQAQGEMVYTLESHPITLTIECLSEEVFQDWLR
TIHASEEPTVFTNKTFLKSALYRTAKKFFFLNEEGAELTIGENSQGFPESHFLQWQGLVFKAELDFPTLEDIFP
KLELAHTSLENVSHDISITNVTVCAGEAKVNFTLSPVIHKKDRENHPKTRIGSVEYVAKTHEMITGPKAIALPI
YAIPLLADKFKDQLLSLLCYDSLEYRLRYDIRLLRDASFSSAYLVTPGDLDNGSLIYPNYCYSPTKGLMQVV

GMLSPKQAFIVKSEQVEDFLNERGHLIQEPGFQTFINERPEGHLTYNVTEQGVLLFHYDVGDPSSSTEIRFGTWT
YYTNQGGFFLEKKNDLPIQDGLIVEPQDIPAFIVKNDAAALRRLPNFFSSPPNLKDLLIEVHRQSRGKGLDLKPILV
GLGESRCWLFGVFLYREDIGFSLIPTPLQGLCFLPRVIPPENVPQFLTQYAQHERILFPNPQTRPPESYELVIQSI
HRPHPASPLHLQLELKTNLGSPIGIALQGLKSKHTFLFTQAGFLDLKQNLQFLKQFLSTQKCVIAENTVIANI
TDVFKLDALAPLSVTDDTIANPEDLQFFSQLKAACLPPIPQNLFSSDHQLRPYQNSGLLWMWFLYNHRLSGLL
CDEMGLGKTHQATALLDIVFQSSQPSARPKFLIVCPTSVLPHWEHILSNHLPGVSIFSFHGPKNKPSSELPPADILL
TSYGTLRQNYDKFYKIAFTIVVFDEIHMAKNKSSQIHKILCRIDAQMKGLTGTPIENNLLFEKGLLDIILPNYL
PSDALFKKLFTKRCSSSEEEIIPSQDLLLLKLTRPFILRRTKKLVLPELPDKVESIIACSLSPDQEKLYMATLQRE
KSHIQKLETPEEPATNFLHIFALLNHLKQICDHPAVFFKDPDQYKNYESGKWNAFVKLLKESLNAGYKVVVF
SQYIHMIRIITLYLEEIGIKYASIQGKSLNRKEEIEFTTDPNCQVFVGSLLAAGTGINLTAGNVVIMYDRWWN
PAKENQALDRVHRIGQKNTVFIYKLITEDTLEERIHYLEKKIRLLDKVIASQDSNILHMLNREDLLTILSYKDE
HGTSDSEESPVDA PVEDDTGVLPPEDS

>core/10/5/Org5_Gene686

MLNFRKLRRDFSANILQDGKKLFEQGAVIDAKILSMNGETVCISAQVRGLYDNIYECEIEVDRSES DTVDSNC
DCSYNYDCQHIVALLFYLEQYFNEMVVAYARSADLET DHEINEEVKKELKETFVAAATKEEERK DREHQKEI
LREYVHAANALSANPFFLPLEYLEKDSAELAVLFVSVNEDTFAPANQPIEFQLVLR LPCR SKPFYISNIRTFLEG
VLYQEPIVLNRRFFFTMQSFNASDRKLIDLLIRYVRYPNHTTEEKLLKSAYLMPPALGVILAKMFEHQ LADR
GGGSLGEKESFSGLFCGNLEEPLCWSLTPAKMKFNLDFFDMPYKALLMTPVILVDDDEVQPEQTM LLES DAP
GIIHHFVYHRFSPQIKRAHLRSFSRLRDIAIPEALFGSFRENALPVFQEYAEIANVHLLNSFVTLPYVDEVRAIC
DMSYLDGELEAKLHFLYGS LRVPAASLALQYQDVRAFISDEGILARNLVEERKM LEEVFSGFIYDERDGAFR
VKSEKKIVEFMTETIPANQHRITFNCPENLSGQFIYDETIFELSFREGSDINYYEADLKVHGLLKGVP LDDLWD
CISAKKRFLLEPKAGQQSKGTRRGKVN SGKLP CILVLDLEKIAPVVQIFNEIGFKVLDDL VQKCPLWSLTGISL
DQFEALPVNFMSERLIEIQKQIRGEIEFDFQDVPQQIQATLSYQTEGVHWLERLRKMHLNGILADD MGLGK
TLQAIHAVTQSKLEKSGCSLIVCPTSLVYNWKEEFRKFNP EFRTLVIDGVPSQRRKQLTALADR DVAITSYNL
LQKDVELYKSFRFDYVVLDEAHHIKNR TTRNAKSVKMIQSDHRLILGTPIENSLEELWSLFDFLMPGL LSSY
DRFVGKYIRTGNMGNKADNMVALKKKVSPFILRRMKEDVLKDLPPVSEILYHCHLTESQKELYQSYAASA
KQELSRLVKQEGFERIHHV LATLTRLKQICCHPAIFAKDAPEPGDS AKYDMLMDLLSSLVDSGHKT VVFSQY
TKMLGIIKKDLESRGIPFVYLDGSTKNRLDLVNQFNEDPSLLVFLISLKAGGTGLNLVGADTVIHYDMWWNP
AVENQATDRVHRIGQSRSVSSYKLVTLNTIEEKILTLQNRK KSLVKKVINS DDEVVSKLTWEEVLELLQI

>core/12/5/Org5_Gene878

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LAVNQLQYDVS VAYGAIRDLPTRAWRVDEHGHKQLIPVRKH YIMCLSELLSQELHLDREAIEDAIHAKASVL
GSVPYLVAANVSERTYLKLKMLSKDWPGLHVEAVVRRHYPQESVASDILGYVGPISLQEYKRV TQELS QLR
ECVRA YEEGEDPKLPEGLASIDQVRALLESVESNAYS LNALVGKMGVEACWDSKLRGKIGKKPILVDRRGNF
IQEMEGAVPEAPGTKLQTL SAELQAYADALLLEYEKTETFRSAKSLKKREKL PPLFPWIKGGAIHALDPNNG
EILAMASSPRYRNND FVNAKVAEDSKAVRSSIYRWLENKEHIAEIYDRKVPLIRERRNPLTGLCYEEILPLTFD
CFLDFLPENSVIKLQLKRNSFVGQAIEVQNLVTRLLSLFPYEEGTCPCSAIFDAVFPNEEGHILIQEVISLXEQK
WIMECLNQHKADIEELKEALDQVFNELPANYDKILYTDILRLIVDPERFSPVLPSEVHRLSLSEFTELQGRYVV
LRS AFSTILED AFIEVHFKSWRKSEFLQYLA AKRQEEALRKQRYPTPYVDYLEEEKTRQYKMFCQEHLDTFL

AYLFSKTPYKEGLEPYDYDILDLWINELDNGAHRALSWNEHYLFLKERVSHLSEHLPALFSTFREFNELQRPLL
GKYPISIVRNKRQTEQDLAASFYPVYGYGYLRPHAYGQAATLGSIFKLVSAYSVLSQRILWGHNEEPANPLVI
IDKNSFGYRSSKPHVGFVKDGTPIPTFFRGGSLPGNDFMGRGFIDLVSALEMSNNPYFSLLVGEGLGDPEDLAD
AASLFGFGEKTGLGLPGEYAGRVPHDLAYNRSGLYATAIGQHTLVVTPLQTAVMLASLVNGGVVYVPKLLL
GEWEGEHVSYLSSKKKRTIFMPDAVVEVLKTGMRNVIWGQYGTARAIQSQFPPQLLSRIIGKTSTAESIMRVG
LDREYGTMMKMDIWFAAVGFSDQDLSLPTIVVIVYLRLGEFGRDAAPMAVKMIDMWEKIQQRESFLRG

>core/13/5/Org5_Gene721

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PVEFPSSEIDLSPKLVNIDAVGKRDHLLYSLNQHRAPIFCVTTLKALLEKTRSPQATSQQHLDLAVGDVLDPE
ATTELCKSLGYSQVMLTSEKGEFSCRGGIVDIFPLSSPEPFRIEFWGEKIISIRSYNPSDQLSTGKVSKISISPAYT
EEASGGNYSHSLLDYFSTPPLYLFDNLEILEDFADISGTLSSLPDRFFSIGTLYDRISTSQVYFSETPFPNVKN
LKENRVIIIEAFHRNMEASRQAIPILYPEQIIQNDENPLLAFLQHLQEYMPPHGKPLKLAISTKTKSLKEARAL
AETVARGDVEIYEKTGNLTSSFALVNEAFAAISLSEFASTKVLRRQKQORTHFSVTTEEVFVPIPGETVVHIHNG
IGKFLGIEKKPNHLNIETDYLVEYADKARLYVPSNQAYLISRYVGTSDKAADLHHLNSSKWKRSDLTEKS
LIVYAEKLLQLEAQRSTTPAFVYPPHGESVIKFAETFPYEETPDQLKTIDQIYNDMMSPKLMDRLICGDAGFG
KTEVIMRAAVKAVCDGHRQVIVMVPTTILATQHYETFKERMAGLPIEIAVLSRFSQAKVQKLICEQVASGQID
IIIGTHKLINKSLEFKNPGLLIIDEEQRFQVVKVDNLKERYPMIDCLTVSATPIPRTLHMSLSGARDLSVIAMPPL
DRLPVSTFVMEHNTETLTAALRHELLRGGQAYVIHNRIESIYTLAETIRNLIPEARIGVAHGQMGAEDLSNIFT
KFKNQKTDILVATALIENGIDIPNANTILIDHADKFGMADLYQMKGRVGRWNKKAYCYFLVPHLDRLSGPA
AKRLAALNKQEYGGGMKIALHDLEIRGAGNILGTDQSGHIGTIGFNLCKLLKKAVSALKKHTSPLLFNDDV
KIEFPYNSRIPDTYIETGSMRIEFYQKIGNAESSEELTAIQEEMRDRFGPLPQEICWLFALAEIRLFALQHGISSIK
GTANALYVQKCLSKSEQTKKTLPYALSPTPELLVKEVIESIERGFLINAS

>core/14/5/Org5_Gene1031

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LPTPPTLPKGPEPKTIEIAKQPPKDGEDKKPDVVPKPGTPPPEDTPPPPKAPSPASPKVPKQPADKKPTPPPEAPP
PPVRVATPMPLRPSSQGYWQCLNRMVSMVLRRAPLPLPAMQVDPILGDFNPHFVASYPNRIDNEPMYFQIKQ
FKKIAQNPDLPQQHRRRLAQLSLEQALYLNDNYLNVNPGDGNCFYRAYAVGWLSALYEESSRNDIVFEQEA
TRLDDLFPASSSPANANLCAEMAELLQLCSTYCSFIDLVDGVILSQKHTATLIAFLRKLSAYAIRQQAASSNEE
TARALFISDMQDDLLPSVLEFLAANRPYSELFQNLIDHSALPYMQSRDKLFLLLEHLPALFLTDAELQKMSPE
DQQLRKQYEREIREAFAKLSRRIADSGWDTERFNAIVKDYLPEAIRCQYSRFLATIENRRSGDLPWSPALSFFA
FLCTCPSVRFHKLCAFYKSLEDIIIASAPPQRSIQEILQISNASLSYLNEDLDSSWQREVISSNIMTILTTHESLTL
ESSMPQLETLHKRIANLLKNVISTSFETPPLSNQPDLLSNLVNKLVAIHSKLELKEHFNTVCSARSLRLTRDE
GSGLSQEQLLYTQAVQLLFFILQHPQVNNRPETKDAVKELKMLLPFLQYAFKKVENEKKLQKLLRSILGS
LVLKPPARYPSTPSNKKETFCFKFWSRHPEVMVLDPILEKNCMQFLRATFPNYQLETEAILLEKEIESTFRNG
WNVFLTRLNLFGSKLGSPSSPTALSDQFSKSFLIFCFLNNYPKLLQKKTPLAARLDAFQREASHRFTQVKDKL
LLSLKYGFPLATATINQYSRARDQLICNLLKNTVTASDGFCRSGFRQSLIGYLHSLSSNELGDILDDVKEQAEA
NDVAAMTTVPLQPFVCLIMSDRDTVSEENIENFVAMHGFLNTISPERDARIFLIRFPNHYGCLLPNPRTEQDQ
NSKPDSSNP

>core/15/5/Org5_Gene875

MKPFNIFDSNSSIQGKFFLEASAGTGKTFTTIEQIVLRALIEGSLTHVEHALAITFTNASTNELKVRIKDNLAQTL
RELKAVLNSQPASLPTYLDINCNVKQIYMQVRNALATLDQMSLFTIHGFCNFVLEQYFPKTRLIHKKPALTHS
QLVLHHITNYLKQDLWKNVLFQEQFHLLAVRYNVTSKHTSSLVDKLLASYTQPISSYFSSRVERLEQISLWHQ
QIYNSLLEIPKQVFLDQLTAHISGFKKQPFSILDDLHHFVDLLYTSETHSSLFSFFKIAETFNFKHRLARYKPCA
AFTVLENMSWVERTLEFCNLDRIENTLLVDLQEYLKQNYTPWLSPDESVFALEKLLSSSEAQPVVQALREQY
QLVLIDEFQDQDKQQWSIFSNNLFIKFTGSLFLIGDPKQSIYEWRSADLPTYLTAKSSFSSEDKQLQLVNNYRST
PKLMEAINQIFGKISPFLEIPGYLPIEYHALNPQSSETFENPPHAPIHFFFYETIKDQALWIFSEALRLQKEQKIPL
GNMVVLVSDSNQAFELISYATIPVSFSKNKSIFHLTETHILTALLEAILHPENYEKISKILFSSSLFGLSLDEVTTK
KEDFTIYFQSLHSYISHHGLLATFYRVMTTQGNVLFSSPRGDLIFQEMEKLKCYLDTISSYPYHQLLHLKNFSE
TGRWEEELAISSYSEDLETLKITTIHSSKGLEVDIVFCPGIEKSKKNKSSSELLREMYVACTRAKKQLYLPISTQ
PPSLQRSSALTNYVKLEGTQSSAYDLAIHLHQHPDLFSYSLPKDHGHATTVLNLPLLETFALKVTPPKTIFSFS
STKFLDTHKDSQSIPYSKLPISKQQLPLGEKTGILHKILESIFSLQDTEYLMSTIMRFIKHHTHLEGFEETILK
LLSKTFFSPLTFSSQTFSLSQVLPNKIFRETSFLFLENQELWQGVIDLFFEHEGKYIIDWKTSFLGETNSDYKSN
NLSIYIKQEKLDYQGRIYVKA VRKFLNQFEIDDDVELGVIFIRGIDTQGNNGFFALNSSSEDIPNPNPKAIQKCQAY
H

>core/16/5/Org5_Gene796

MVEVEEKHYTIVKRNGMFVFPFNQDRIFQALEAAFRDTRSLETSSPLPKDLEESIAQITHKVVKEVLAKISEGQ
VVTVERIQDLVESQLYISGLQDVARDYIVYRDQRKAERGNSSSIIAIIRRDGGSAKFNPMKISAALEKAFRATL
QINGMTTPPATLSEINDLTRIVEDVLSLHGEEAINLEEIQDIVEKQLMVAGYYDVAKNYILYREARARARANK
DQDGQEEFVPQEETYVVQKEDGTTYLLRKTDLKRFWSACKRFPKTTDSQLLADMAFMNLYSGIKEDEVTT
ACIMAARANIEREPDYAFIAAELLTSSLYEETLGCSSQDPNLSEIHKKHFKKEYILNGEEYRLNPQLKDYLDDAL
SEVLDSLSDQQFSYMGVQNLVDRYFNLHEGRRLTAQIFWMRVSMGLALNEGEQKNFWAITFYNNLLSTFRY
TPATPTLFNSGMRHSQLSSCYLSTVKDDLISHYKVISDNALLSKWAGGIGNDWDVDRATGAVIKGTNGKSQG
VIPFIKVANDTAIAVNQGGKRKGAMCVYLENWHLDYEDFLELRKNTGDERRRTHDINTASWIPDLFFKRLEK
KGMWTLFSPDDVPGLHEAYGLEFEKLYEEYERKVESGEIRLYKKVEAEVLWRKMLSMLEYTGHPWITFKDP
SNIRSNQDHVGVVRCNLCTEILLNCSESETAVCNLGSINLVEHIRNDKLDEEKLKETISIAIRILDNVIDLNFPY
TPEAKQANLTHRAVGLGVMGFQDVLVELNISYASQEAVEFSDECSEIIAYYAILASSLLAKERGTYASYSGSK
WDRGYLPLDTIELLKETRGEHNVLDVTSSKKDWTVPVRTIQKYGMRNSQVMAIAPTATISNIIGVTQSIEMYP
KHLFVKSNLSGEFTIPNTYLIKKLKLGLWDAEMLDDLKYFDGSLLEIERIPNHLKKLFLTAFEIEPEWIIECTS
RRQKWIDMGVSLNLYLAEPDGKKLSNMYLTAWKKGLKTTYLLRSQAATSVEKSFIDINKRGIQPRWMKNK
SASTSIVVERKTPVCSMEEGCESCQ

>core/17/5/Org5_Gene962

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FSSTWKTMDASFMESVWWVFQSLYNQGLVYEGTKVVPFSTALGTPLSNFEASQNYKEVDDPSLVVRMPLQ
NDSASLLVWTTTPWTLPSNMAIAVGETLVYVRIQDKKSQGEQWILSQGCVSRWFSNPEEFVILEFSFGKDLVG
RTYEPPFTFFQSKREEGAFRVIAASFVEESEGTGVVHMAPAFGEGDFLVCKENHVPLVCPVDAHGSFTEEIPQ

YQGQYIKHADKEIIFLKKKEGRIFYYGTVKHRYPCWRTDTPLIYKAVNSWFVAVEKIKDKMLRANSSIHV
PEHIQEGRFKWLLEGARDWAISRNYWGTPPIWKSADGEILVVGSIREEELTGTQITDIHRHFIDDLNIVKD
GKPFHRIPIYVFDWFDGAMPYAQNHYPFENQKETEEAFPADFIAEGLDQTRGWFYTLTVISAILFDRPAFRN
AIVNGIILAEDGNKMSKRLNNYSPKYVLDYTGADALRLYLLHSVVVKAEDLRFSDKGIEGVLKQILLPLTNV
LSFFNTYAELYGFDPKSQDIEPAYTEIDQWILSNLYSVVGKVRRESMSQYHLNFAVEPFVTFIDDLTNWYIRRC
RRRFWEAEDTPDRRAAFSTLYEVLTVFCKVIAPFVPFLAEDIYQKLKLEKEPESVHLCDFPQVEMDKILPDLE
KXMHDIRIVGLGHSLRKEHKLKVRQPLANFYVVGSKDRLSLLKTFEGLIAEELNVKNVIFYEEAPSFIYTTV
KPNFRMLGKKVGSKMKEVQKALSELPNNAIDKLIQEETWVLTIDDREIALDGDDVVICRHTDPGYIARSSALF
SVILDCQLREPLIVEGIARELVNKINTMRRNQQLHVS DRIALRIKTTEAVHRAFLDYENYICEETLIIAYDFTQD
SDFQGENWDINGHATQIEITVSSIDS

>core/18/5/Org5_Gene876

MNATKHCRASFSNSPRHLLAQLAEDITSTHQPFTKRWILVANATTGHWIKNQLVHVLSDHIFMGSTIFTASD
SIVKHLFLGSGCSQPNIPDYLTLPLINNILEEISKASKFENGREFLSPTTYETTKKLAAAFKQFHTFSQRPTKNA
SHYQELFQILESHFSSYEEMFTTILNNRTQEEDCSLHIFGYAHLPKHLAEFFINLSTYFPVYFYCFSPCREYFGD
LLSDRAIDFFWNQLPDSPIKNAWEHYVLSDRQALLANLAHKSQSSQNFFLDREIDYQEMFLPSKHDSSLGVIQ
NSILDLKPTSPQDFSQTKQTICIYRALNIPREVQEVFCKVTELLHRGVSPEEIFILSSHIESYKVHLNAIFNPHVPI
YFTDEVDPRAE DLRNKILLSSILQTQGD LHYILQLLTHPQLQQPIDQNKVPYLIKLSSEWGKISSKDRASGQ
QMKALGDLILEEYPFHQEGGRVSQVEVWETTVPLIYFIQERINLYLSSSQHSYEDLFQNVFSCLEKIFVLSPEET
SFITTLRNSLFPTFATSSCSLLFFTFCLDFLLHFHKPSPLYDKPGPYIGSLSSLIPKGYVFILGANKTTSSDIFD
LLNRTTTHEELAFSSTEDEENFHFLQILVSTKHELHISYISSAAQFNLPSPFLNHIKETLDLPVETLPTQPYLSAFF
KNKACLHTSQEYNYS LAHAFYSKKALLPSLFIPTVKQVNL PQHLSLNEIIGIFSPLDLFLKTNYNLRISYPEHL
KKQQKLFP TKHQIEDFWNECFVDKEHDLIPSISPHAEELFTYYREKTILLRNGLDKDPKHSPYTVTFSSSIFEER
PYHESYLFPPLSLSFQGNPVQIHGTIHGVCNEGLYLCSIDPGDSLKKTTRTLGSLPETSSEQKQLLERYVALAV
LQMSQHLSSDSALIKLTSFNXKENHHPFSDPEXYLRKVLEVYHLMSSQPIPLLSPLCWKTLDDDEEFHQAVL
SAISEEAKNPSLPFWQFHNRNIEEILNHVGASERLKILSLFRGPCEAV

>core/19/5/Org5_Gene1037

MESFVSEHPLTLQSMIATILRFWSEQGCVIHQGYDLEV GAGTFNPATFLRALGPEPYKAAYVEPSRRPQDGRY
GVHPNRLQNYHQLQVILKVPENFLSLYTESLRAIGL DLRDHDRIHDDWENPTIGAWGLGWEVWLNNGMEI
TQLTYFQAIGSKPLDTISGEITYGIERIAMYLQKKTSIYDVLWNDTLTYGQITQASEKAWSEYNFDYANTEMW
FKHFEDFAEEALRTLKNGLSVPAYDFVIKASHAFNILDARGTISVTERTRYIARIRQLTRLVADS YVEWRASLN
YPLLSLSSTSEPKETSES VVPMISSTEDL LLEIGSEELPATFVPIGIQQLES LARQVLT DHNIVYEGLEVLGSPRRL
ALLVKNVAPEVVQKA FEKKGPMLTSLFSPDGDVSPQGGQFFASQGV DISHYQDL SRHASLAIRTVNGSEYLF
LLHPEIRLRTADILMQELPLLIQRMKFPK KMVWDNSGVEYARPIRWLVALYGEHILPITLGTIIASRNSFGHRQ
LDPRKISSPQDYVETLRQACVVVSQKERRMIIEQGLRAHSSDTISA IPLRLIEEATFLSEHPFVSCGQFSEQF
CALPKELLIAEMVNHQKYFPTHETSSGAISNFFIVVCDNSPNDTIEGNEKALTPRLTDGEFLFKQDLQTPLTTF
IEKLKSVTYFEALGSLYDKVERLKAHQRVFSTFSSLAASEDLDAIQYCKADLVSAVVNEFP ELQGIMGEYYL
KHANLPTASAVAVGEHLRHITMGQKLSTIGTLLSLLDRLDNLLACFILGLKPTSSHDPYALRRQSLEVLTLVS
ASRLPIDLASLLDRLADHFPSTIEEKVWDKSKTIHEILEFIWGR LKTFMGSLEFRKDEIAAVLIDSATKNPIELD

TAEALQLLKEEHTEKLAVITTTTHNRLKKILSSSLKLSMTSSPIEVLGDRESNFKQVLDAFPGFPKETSAAHAFLEY
FLSLADLSNDIQDFLNTVHIANDDGAI RNLRISLLL TAMDKFSLCHWESVAV

>core/20/5/Org5_Gene637

MYSCYSKGISHNYLLHPMSRLDIFVFDSLIANQDQNLLEEIFCSEDTVLFKAYRTTALQSPLAAKNLNIARKV
ANYILADNGEIDTVKLVEAIHHL SQCTYPLGPHRHNEAQDREHLLKMLKALKENPKLKESIKTLFVPSYSTIQ
NLIRHTLALNPQTILSTIHVRQAALTALFTYLRQDVGSCFATAPAILHQEYPERFLKDLNDLISSGKLSRIVNQ
REIAVPINLSGCIGELFKPLRILDLYPDPLVKLSSSPGLKKAFSAANLIETLGDSEAQQQLLSHQYLMQKLQNV
HETLTANDIIKSTLLHYYQLQESTVRAIFFKEGLFSKEQVAFSTQHPRELSEIQRVYHYLHAYEEAKSAFIHDT
QNPLLKAWEYTLATLADASQPTISNHIRLALGWKSEDPHSLVSLVTHFVEEEVENIRILVQQCEQTYHEARSQ
LEYIEGRMRNPLNNQDSQILTMDHMRFRQELNKALYEWDSAQEKAKKFLHLPEFLLSFYTKQIPLYFRSSYD
AFIQEFAHLYANAPAGFRILFTHGRTHPNTWSPYISINEFIRFLSEFFTSTESELLGKHAVINLEKETSRLVHNIT
AMLHTDVFQEALLTRILEAYQLPVPPSILNHL DQLSQTPWVYVSGGTVDTL LLDYFESSEPLTLTEKHPENPH
ELAAFYADALKDLPTGIKSYLEEGSHSLSSSPTHVFSIIAGSPLFREAWDNDWYSYTWLRDVVWKQH QDFL
QDTILPQLSIYAFIENFCNKYALQHVVHDFHDFCSDHSLTPELYDKGSRFLSSLFTKDKTVALIYIRRLLYLM
VREVPYVSEQQLPEVLDNVSSYLGISSRITYEKFRSLIEETIPKMTLLSSADLRHIYKGLLMQSYQKIYTEEDTY
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NPIDYGMPPPPGYRSRLPKEFF

>core/21/5/Org5_Gene910

MPLSFKSSSFCLLACLCSASCAFAETRLGGNFVPPITNQGEEILLTSDFVCSNFLGASFSSSFINSSSNLSLLGKG
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TSATPAITTVTTGASALQPTDSLTVENISQSIKFFGNLANFGSAISSSPTAVVKFINNTATMSFSHNFTSSGGGVI
YGGSSLLFENNSGCIIFTANSCVNSLKGVT PSSGTYALGSGGAICIPTGT FELKNNQGKCTFSYNGTPNDAGAI
YAETCNIVGNQGALLLDSNTAARNNGGAICAKVLNIQGRGPIEFSRNRAEKGGAIFIGPSVGDPAKQTSTLILA
SEGNIAFQGNMLNTKPGIRNAITVEAGGEIVSLSAQGG SRLVFYDPITHSLPTTSPSNKDITINANGASGSVVFT
SKGLSSTELLLPANTTTILLGTVKIASGELKITDNAVVNVLGFATQGGGQLTLGSGGT LGLATPTGAPAAVDFT
IGKLAFDPFSFLKRDFVSASVNAGTKNVTLTGALVLDEHDVTDLYDMVSLQSPVAIPIAVFKGATVTKTGFPD
GEIATPSHYGYQGKWSYTW SRPLIPAPDGGFPGGPSPSANTLYAVWNSDTLVRSTYILDPERYGEIVSNSLW
ISFLGNQAFSDILQDVLLIDHPGLSITAKALGAYVEHTPRQGHEGFSGRYGGYQAALSMNYTDHTTLGLSFGQ
LYGKTNANPYDSRCSEQMYLLSFFGQFP IVTQKSEALISWKAAYGYSKNHLNTTYLRPDKAPKSQGGQWHNN
SYYVLISA EHPFLNWCLLTRPLAQAWDL SGFISAEFLGGWQSKFTETGDLQRSFSRGKGYNVSLPIGCSSQWF
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KNGFTNHRVSTGLKSTF

>core/22/5/Org5_Gene793

MKAGDTYRNFIKSKKDLPEIESKLLAEHKPTGASIMMIVNND EENVFNICFRTCPQTSNGVAHVLEH MVLC
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NSENHLCYTGVVFNEMKGAMMSGEARLSEALNAAIFPSVTYGVNSGGEPREIVTL SHEDVRAFHQSQYSINR
CLFYFYGNIKPSRHLD FLEEKLLRQATKLEKQAVSVPLQKRKFEPVRNILTYPVDHQEEDKVLFGISWLTCSIL
EQQELLALHVLEIILMGTDASPLKSRLKSGFCKQTEMSIENDIREIPMTLVCKGCSPAGA QKLEALIFASLEEII

REGISENIVEGAVHQLELSRKEITGYSLPYGLSLFFRSGLLKQHGGSAEDGLRIHSLFSELRNSLKNSDYLAKLI
RKYFLDNPHFARVILLPDTELVAKDNKDEQQLLLSVSEKLTDENKEKIQQNVRELTESQEQKEDLNGILPNLA
LDKVPTSGKEFPLIKEGLSQGEVLHHECFNDIVFIDVVLDIPPLSGEELPWLRLLVFLMLQLGCGGRSYKEHL
EFLLEHTGGVDVSYDFSPHANKNSFLSPSVSIRGKALSSKSEKLCGIVSDMLTSDVFTDIPRIRELLMQHNEAL
TNSVRNSPMSYAVSMACSGNSITGAMSYLTGLPYVKKIRELTKNFDQNIDEAVVILQRLYTKCFSGKRQIVI
SGSAHNYQQLKDNKFYGLLDYLIVIEPWENPSINLYVTSRGLHIPARAAFNALAFPIGDIAYDHPDAAALTV
AAEILDNVVLHTKIREQGGAYGSGAAANLSRGSFYCYSYRDPEIATTYKTFLKGVSEIASGNFTKEDIYEGAL
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LRNNVLTLDKDFPIVPAI

>core/23/5/Org5_Gene350

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YATTPMLFTNNDLSILFQYNRSAGFGAAIRGTSITIENTKKSLLFNGNGSISNGGALTGSAAINLINNSAPVIFSTN
ATGIYGGAIYLTGGSMILTSGNLSGVLFVNNSSRSGGAIYANGNVTFSSNNSDLTFQNNTASPQNSLPAPTPPPTP
PAVTPLLGYGGAIFCTPPATPPPTGVSLTISGENSVTFLENIASEQGGALYGKKISIDSNKSTIFLGNTAGKGGAI
AIPESGELSLSANQGDILFNKNLSITSGTPTRNSIHFGKDAKFATLGATQGYTLYFYDPITSDDL SAASAAATV
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DAGTTLATNGANNTDGAITLNKLVINLDSLDGTAAVVNVQSTNGALTISGTLGLVKNSQDCCDNHGMFN
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GFGQLFTKSKDYLVGHGHSNVYFATVYSNITKSFLGSSRFFSGGTSRVTYSRNEKVKTSYTKLPKGRCWS
NNCWLGELEGNLPITLSSRILNLKQIIPFVKAEVAYATHGGIQENTPEGRIFGHGHLNVAVPVGVRFKNSH
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>core/24/5/Org5_Gene680

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TVNDYLAQRDCEWVGSVLRWLGLTTGVLVSGTLLEKRKKIYQCDVVYGTASEFGFDYLRDNSIATRL EEQV
GRGYYFAIIDEVDSILIDEARTPLIISGPGEKHNPVYFELKEKVASLVYLQKELCSRIAEARRGLDSFLDVDILP
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LLRAQLLMERDVDYIVRDDQIVIIDEHTGRPQPGRRFSEGLHQAIEAKEHVTIRKESQTLATVTLQNFFRLYEK
LAGMTGTAITESREFKEIYNLYVLQVPTFKPCLRIDHNDEFYMTEREKYHAIVNEIATIHGKGNPILVGTESVE
VSEKLSRILRQNRIHTVLNAKNHAQEAIEIAGAGKLGAVTVATNMAGRGTDIKLDNEAVIVGGLHVIGTTR
HQSRRIDRQLRGRCARLGDPGA AKFFLSFEDRLMRLFASPKNLTLIRHFRPPEGEAMSDPMFNRLIETAQKRV
EGRNYTIRKHTLEYDDVMNKQRQAIYAFRHDVLHAESVFDLAKEILCHVSLMVASLVMSDRQFKGWTLPNL
EEWITSSFPIALNIEELRQLKDTDSIAEKIAAELIQEFQVRFDHMVEGLSKAGGEELDASAICRDVVR SVMVMH
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VATSFHNNVNYGPLELTVVTDSEDQD

>core/26/5/Org5_Gene357

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TGAAATTSAKTAARHSFSLGFAQMFSKTRERQSPSTTSSHNYFAGLRFDSELLFRDFISTGLSLGYSYGDHML
CHYTEILKGSSKAFFNNHTLVASLDCTFLPARITRTLELQPFISAIALRCSQASQFETGDHIRKFHPKHPLTDLSS
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>core/27/5/Org5_Gene410

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VLCQNNISYGPGGALLLQGRKSKALFFRDNRGTILFLKNKAVNQDESHPGYGGAVSSISPGSPITFADNQEILF
QENEGELGGAIYNDQGAITFENNFQTTSSFSNKASFGGAVYSRYCNLYSQWGDTLFTKNAAAKVGGAIHAD
YVHIRDCKGSIVFEENSATAGGAIAVNAVCDINAQGPVRFINNSALGLNGGAIYMQATGSILRLHANQGDIEF
CGNKVRSQFHSHINSTSNFTNNAITIQGAPREFSLSANEGHRICFYDPIISATENYNSLYINHQRLLLEAGGAVIFS
GARLSPEHKKENKNKTSIINQPVRLCSGVLSIEGGAILAVRSFYQEGGLLALGPGSKLTTQGKNSEKDKIVITN
LGFNLLENLDSSDPAEIRATEKASIEISGVPRVYGHTEFYEYASKPYTTSIILSAKKLVTAAPSRPEKDIQNLII
AESEYMGYGYQGSWEFSWSPNDTKEKKTIIASWTPTGEFSLDPKRRGSFIPTTLWSTFSGLNIAASNIVNNNYL
NNSEVIPLQHLCVFGGPVYQIMEQNPKQSSNNLLVQHAGHNVGARIPFSFNTILSAALTQLFSSSSQQNVADK
SHAQILIGTVSLNKSQALSLRSSFSYTEDSQVMKHVFPYKGTSRGSRWNYGWSGSVGMSSYAYPKGIRYLK
MTPFVDLQYTKLVQNPVETGYDPRYFSSSEMNTNLSLPIGIALEMRFIGSRSSLFLQVSTSYIKDLRRVNPQSSA
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>core/28/5/Org5_Gene904

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PNASNFAADTCTGGAVLCSKNVTISKNGTAYFINNKAQSSGGAIQAAIINIKDNTGPCLFFNNAAGGTAGGAL
FANACRIENNSQPIYFLNNQSGLGGAIRVHQECILTKNTGSVIFNNNFAMEADISANHSSGGAIYCISCISIKDNP
GIAAFDNNTAARDGGAICTQSLTIQDSGPVYFTNNQGTWGGAIMLRQDGACTLFADQGDIIFYNNRHFKDTEF
SNHVSVNCTNRNLSLTVGASQGHSAFTYDPILQRYTIQNSIQKFNPNPHEHLGTILFSSAYIPDTSTSRDDFISHFR
NHIGLYNGTLALEDRAEWKVKFDQFGGTLRLGSRAVFSTTDEEQSSSSVGSVINNNLAINLPSILGNRVAPK
LWIRPTGSSAPYSEDNNPIINLSGPLSLLDENLDPYDTADLAQPIAEVPLLYLLDVTAKHINTDNFYPEGLNT
TQHYGYQGVWSPYWIETITTSSTSEDVNTLHRQLYGDWTPGTGYKVNPNENKGDIALSAFWQSFHNLFATL
RYQTQQGQIAPTASGEATRLVHQNNSNDAKGHMEATGYSLGTTSTNTASNHSFGVNFSQLFSNLYESHSDN
SVASHTTTVALQINNPWLQERFSTSASLAYSYSNHHIKASGYSGKIQTEGKCYSTTLGAALSCSLSLQWRSRP
LHFTPFIQAIIVRSNQTAQESGDKARKFSVHKPLYNLTVPLGIQSAWESKFRLPTYWNIELAYQPVLYQQNP
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>core/29/5/Org5_Gene776

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LFINPKFRQEDLDREKYAVHQEFAAHPLSDGRRVHRIQQLVAPQGHPCARFGCGNASTLTPVTTEKMAEWF
KLHYPENMCAIAYTSAPLSKAKKQFSKIFSQIPRSKNYERQEPFLPSGDTSSLKNLYINQAIQPTS N L E I Y W H I
YESSHPIPLGCYKALAEVLRNESKNSLVSLKNEQLITDL D V E F R S S L N T G E F Y I S Y E L T E K G D K H Y S Q V I D S T
FQYLR Y I Q E H G I P N Y T L E E I S T I N A L N Y C Y S S K S P L F D L L C K Q I V S L G N E D L S T Y P Y H S L V Y P K Y S S E D E S A L L N
LVSDPEQARFVLSSKNSEHWEEATQLHDPIDMTYYVKALDGVQDYGKVQSLKPIALPKPNLFIPKEVTLP
VHLLKKQEFPPAPALSYQDDKLTLYHCE DH Y Y T A P K L S S Q I R I R S P Q I S R S S P Q F L V A T E L Y C L A V N D Q L L R E Y
YPATQAGLSFTSALGGDGLRVSGYTTTVPALLNSILTSLPNLEISYETFLVYKKQLLELYQGALLNCPVRSG
LDELASQVMKETYSNTTKLSALEKLSFSEFQAFASNLFNSVHLEVMVLGNLSEQQKKDYLEMLQVFTASRSS
HATKPFYYELQSQEISEIHHDYPLTANGMLLLLQDKSSPSIQGKVC A E M L F E W L H H I T F E E L R T Q Q Q L G Y M V
GARYREFASRPFGLYIRSDAYSPEELLA K T S L F L N K V S A S P E K F G I S Q E K F A N I R K A Y I N K I L E P E H S L D M M N S
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>core/30/5/Org5_Gene62

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KRMSGFEVCWIPGTDHAGIATQAVVERHLQASEGKRRTDYSREDFLKHIWAWKEKSEKVVLSQLRQLGCSC
DWDRKRFTMEPLANRAVKKAFKTLFENGYYIRGYLVNWD P V L Q T A L A D D E V E Y E E K D G W L Y Y I R Y R M V
GSQESIVVATTRPETS LGDTGIAVSPNDERYASWIGASVEVPFVNRQIPIGDASVDPTFGTGAVKVTPAHDKD
DYLMTGNHHLPMINILTPSGGINENGPFAGMAKEKAREEILIALEEQGLFVRKEPYKL RVGVSYRSGAVIEP
YLSKQWFVSVSEFRGALREFVESQDIKIFPKDFVKNYLSWVNHLRDWCISRQLWWGHRIPVWYHKNDDERV
LCYDGE GI P E E V A Q D P D S W Y Q D P D V L D T W F S S G L W P L T C L G W P D E N S P D L K K F Y P T A L L V T G H D I L F F W V T
RMVLLCSSMSG E K P F S E V F L H G L I F G K S Y K R Y N D F G E W S Y I S G K E K L A Y D M G E A L P D G V V A K W E K L S K S K G
NVIDPLEMIATYGTDAVRLTLCSCANRGEQIDLDYRLFEEYKHFANKVWNGARFIFGHISDLQGKDLLAGIDE
DSLGLEDFYILDGFNQLIHQLEEAYATYAFDKVATLAYEFFRNDLCSTYIEIHKPTLFGKQGNEASQSTKRTLL
AVLLINVLGVLHPVAPFITESLFLRIQDTLGALPEGDGDAFTGHALRMLRSRACMEAPYPKAFDV K I P Q D L R E
SFTLAQRLVYTIRNIRGEMQLDPRHLKAFVVCSDTTEIQSCIPILQALGGLESIQLLDKEPEKGLYSFGVVDTI
RLGIFVPEEHL L K E K R L E K E R V R L E R A V E N L E R L L G D E S F C Q K A N P N L V V A K Q E A L K N N R I E L Q G I L D K L A S
FA

>core/31/5/Org5_Gene355

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TNNLGQGT F V D N L A L N K G G A L Y T E T N L S I K D N K G P I I K Q N R A L N S D S L G G G I Y S G N S L N I E G N S G A I Q I T S N S S
GSGGGIFSTQTLTISSNKKLIEISENSAFANNYGSNFPNGGGGLTTTFC T I L N N R E G V L F N N N Q S Q S N G G A I H A K
SIIKENG P V Y F L N N T A T R G G A L L N L S A G S G N G S F I L S A D N G D I I F N N N T A S K H A L N P P Y R N A I H S T P N M N L Q I G
ARPGYRVLFYDPIEHELPSFPILFNFETGHTGTVLFSGEHVHQNFTDEMNFSSYL R N T S E L R Q G V L A V E D G A
GLACYKFFQRGGTLLLGQGA V I T T A G T I P T S S T P T T V G S T I T L N H I A I D L P S I L S F Q A Q A P K I W I Y P T K T G S T Y T
EDSNPTITISGTLTLRNSNNE DPYDSLDSLH S L E K V P L L Y I V D V A A Q K I N S S Q L D L S T L N S G E H Y G Y Q G I W S T Y
WVETTTITNPTSLLGANTKHKLLYANWSPLGYRPH P E R R G E F I T N A L W Q S A Y T A L A G L H S L S S W D E E K G H A
ASLQGIGLLVHQDKNGFKGFRSHMTGYSATTEATSSQSPNFSLGFAQFFSKAKEHESQNSTSSH Y F S G M C I

ENTLFKEWIRLSVSLAYMFTSEHTHTMYQGLLEGNSQGSFHNHTLAGALSCVFLPQPHGESLQIYPFITALAIR
GNLAAFQESGDHAREFSLHRPLTDVSLPVGIRASWKNHHRVPLVWLTEISYRSTLYRQDPELHSKLLISQGTW
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>core/32/5/Org5_Gene913

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GNLSLTGNSQIIFTQNFSSDNGGVINTKNFLLSGTSQFASFNRQAFTGKQGGVVYATGTITIENSPGIVSFSQN
LAKSGGALYSTDNCSITDNFQVIFDGNSAWEAAQAQGAICCTTTDKTVTLTGKNLSFTNNTALTYGGAI
SGLKVSISAGGPTLFQSNISGSSAGQGGGGAINIASAGELALSATSGDITFNNNQVTNGSTSTRNAINIIDTAKV
TSIRAATGQSIYFYDPITNPGTAASTDTLNLNLADANSEIEYGGAIVFSGEKLSPTKEAIAANVTSTIRQPAVLA
RGDLVLRDGVTVTFKDLTQSPGSRILMDGGTTLSAKEANLSLNLAVNLSSLDGTNKAALKTEAADKNISLS
GTIALIDTEGSFYENHNLSASTYPLLELTTAGANGTITLGALSTLTLQEPETHYGYQGNWQLSWANATSSKI
GSINWTRTGYIPSPERKSNLPLNSLWGNFIDIRSINQLIETKSSGEPFERELWLSGIANFFYRDSMPTRHGFRRHS
GGYALGITATTPAEDQLTFAFCQLFARDRNHITGKNHGDYTGASLYFHHTEGLFDIANFLWGKATRAPWVLS
EISQIPLSFDKFSYLHTDNHMKTYTDTNSIIKGSWRNDAFCADLGASLPFVISVPYLLKEVEPFVKVQYIYA
HQQDFYERYAEGRAFNKSELINVEIPIGVTFERDSKSEKGTYDLTLMYILDAYRRNPKCQTSLIASDANWMA
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>core/33/5/Org5_Gene356

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CNGDFTISQNQGTFFVNNNSVNNWGGALSTNGHCRIQSNRAPLLFFNNTAPSGGGALRSENTTISDNTRPIYF
KNNCGNNGGAIQTSVTVAIKNNSGSVIFNNNTALSGSINSGNGSGGAIYTTNLSIDDNPGTILFNNNYCIRDGG
AICTQFLTIKNSGHVYFTNNQGNWGGALMLLQDSTCLLFAEQGNIAFQNNNEVFLTTFGRYNAIHCTPNSNLQ
LGANKGYTTAFFDPIEHQHPTTNPLIFNPANHQGTILFSSAYIPEASDYENNFISSSKNTSELRNGVLSIEDRA
GWQFYKFTQKGGILKLGAASIATTANSETPSTSVGSQVIINNLAINLPSILAKGKAPTLWIRPLQSSAPFTEDN
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QGIADGLFVHQNSIPGAPGFRIQSTGYSLQASSETSLHQKISLGAQFFTRTKEIGSSNNVSAHNTVSSLYVELP
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>core/34/5/Org5_Gene63

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LFSEAVILDWGAACVACGEEEDLLDIDVSKEEVLSSRMTPGRIVGTPDYMAPERLLGHPASKSTDIYALGVVL
YQMLTSLFPYRRKKGKKIVLDGQRIPSPQEVAPYREIPPFLSAVVMRMLAVDPQERYSSVTELKEDIESHLKG
SPKWTLTTALPPKSSSWKLNEPILLSKYFPMLEVSPASWYSLAISNIESFSEMRLEYTLSSKKGLNEGFGILLPT
SENALGGDFYQGYGFWLHIKERTLSVSLVKNSLEIQRCSQDLESDEKETFLLIALEQHNHSLSLFVDGTTWLIHM

NYLPSRSGRVAIIVRDMEDILEDIGIFESSGLRVSCLAVPDAFLAEKLYDRALVLYRRIAESFPGRKEGYEARF
RAGITVLEKASTDNNEQEFAIAIEEFSKLHDGVAAPLEYLGKALVYQRLQEYNEEIKSLLLALKRYSQHPEIF
RLKDHVVYRLHESFYKRDRLALVFMILVLEIAPQAITPGQEEKILVWLKDKSRATLFCLLDPTVLELRSSKME
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FLFAIQSIFNKEDAEEKIFVSNDQLSPILLVYIFDLFANRALLESQGEAIFQALDLIRSKVPENFYHDYLRNHEIRA
HLWCRNEKALSTIFENYTEKQLKDEQHELFVLYGCRYLALIQQGAEEAAKQHFDVCREDRIFPASLLARNYNRLG
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>core/35/5/Org5_Gene912

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NNKGETGGGALGFEASSITQNSSLFFSGNTATDAAGKGGAIYCEKTGETPTLTISGNKSLTFAENSSVTQGG
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SAKITNLRAAQGQSIYFYDPIASNTTGASDVLINQPDNSPLDYSGTIVFSGEKLSADEAKAADNFTSILKQPL
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KSGTMTWVTTGYNPNPERRASVVPDSLWASFTDIRTLQQIMTSQANSIYQQRGLWASGTANFFHKDKSGTN
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MLKDIPLILNAQLSYSYTKNDMDTRYTSYPEAQGSWTNNSGALELGGSLALYLPKEAPFFQGYFPFLKFQAV
YSRQQNFKESGAEARAFDDGDLVNCSIPVGIRLEKISEDEKNNFEISLAYIGDVYRKNPRSRSTLMVSGASWT
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>core/37/5/Org5_Gene346

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IQSNYSCYFGQNFSNDNGGALQGSSISLSLNPNTFAKNKATQKGGALYSTGGITINNTLNSASFSENTAANN
GGAIYTEASSFISSNKAISFINNSVTATSATGGAIYCSSTSAPKPVLTLSDNDELNFIGNTAITSGGAIYTDNLVL
SSGGPTLFGKNNSAIDTAAPLGGAIAIADSGSLSLSALGGDITFEGNTVVKGASSSQTTTRNSINIGNTNAKIVQL
RASQGNTIYFYDPITTSITAALSDALNLNGPDLAGNPAYQGTIVFSGEKLSEAEAAEADNLKSTIQQPLTLGG
QLSLKSGVTLVAKSFSQSPGSTLLMDAGTTLETADGITINNVLNVDSLKETKKATLKATQASQTVTLSGSLS
LVDPGSGNVYEDVSWNNPQVFSCLTLTADDPANIHTDLAADPLEKNPIHWGYQGNWALSQEDTATKSKAA
TLTWTKTGYNPNPERRGTLVANTLWGSFVDVRSIQQLVATKVRQSQETRGIWCEGISNFFHKDSTKINKGFR
HISAGYVVGATTTLASDNLITAAFCQLFGKDRDHFINKNRASAYAASLHLQHLATLSSPSLLRYLPGESESEQP
VLFDAQISYIYSKNTMKTYYTQAPKGESSWYNDGCALELASSLPHTALSHEGLFHAYFPFIKVEASYIHQDSF
KERNTTLVRSFDSGDLINVSPIGITFERFSRNERASYEATVIYVADVYRKNPDCTTALLINNTSWKTTGTNLS
RQAGIGRAGIFYAFSPNLEVTSNLSMEIRGSSRSYNADLGGKFQF

>core/38/5/Org5_Gene348

MKTSIPWVLVSSVLAFSCHLQSLANEELLSPDDSFNGNIDSGTFTPKTSATTYSLTGDVFFYEPGKGTPLSWSC
FKQTTDNLTFLGNGHSLTFGFIDAGTHAGAAASTTANKNLTFSGFSLLSFDSSPSTTVTTGQGTLSAGGVNL

ENIRKLVVAGNFSTADGGAIKGASFLLTGTSGDALFSNNSSSTKGGAIATTAGARIANNTGYVRFLSNIASSTSG
GAIDDEGTSILSNNKFLYFEGNAAKTTGGAICNTKASGSPELIISNNKTLIFASNVAETSGGAIHAKKLALSSGG
FTEFLRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTTGSTDTPKRNAINIGSNGKFTELRAAKNHT
IFFYDPITSEGTSSDVLKINNGSAGALNPYQGTILFSGETLTADELKVADNLKSSFTQPVSLSGGKLLLQKGV
LESTSFSEAGSLLGMDSGTTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYES
HMFSDQLFSLLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGGQWNVNWTDTATNTKEATATWTKTGF
VPSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFVWSSMTNFLHKTGDENRKGFRHTSGGYVI
GGSHTPKDDLFTFAFCHLFARDKDCFIAHNSRITYGGTLFFKHSHTLQPQNYLRLGRAKFSESAIEKFPREIP
LALDVQVSFSHSDNRMETHYTSPESEGSWSNECIAGGIGLDLPFVLSNPHPLFKTFIPQMKVEMVYVSQNSF
FESSDGRGFSIGRLLNLSIPVGAKFVQGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDSWKIRGGNLSR
QAFLLRGSNNYVYNSNCELFHYAMELRGSSRNYNVDVGTKLRF

>core/39/5/Org5_Gene936

MQRVLRLLFNLHHGEEKRAFLFLLGLVWGIGCYGTLSLAEGLFIEKLGSALPKIYLGSSLILCVLSSLILYNL
FKKHISATALFLIPVLSILCNFYLILSSIFAIDPPRSPLFFYRIVIWSLTILSYTSFWGFVDQFFNLQDGKRHFCIF
NAIIFLGDAIGSGHIASLVHTIGIQGILILFTAALVLTPIVFYVSKSLKSLSDDHDLFIDTGHPPPPLSKALKLCFYD
KYTFYLLCFYFLMQLLAIAATEFNYLKIFEIQFASKEEFELVAHIGKCSLWISLGNMCFALFAYSRIKRLGVNNI
ILFAPLCFLSLFLFWTFKTTLSIAVLAMVVREGVTYALDDNNLQLLIYGVPNKIRNQIRIVVESFIEPIGMLVWS
LVCFLSSQQYVFCLISLIATILVCLVRSYYAKAILKNLSAQALQLTRSMQDWIKSMTVKQKRQVELFLLAHL
KHPSERHQTFAFQHLLNLASRSVLPSSLAHMNKLKSLPNKLTITEMVKSSLWAKDFLTLELLKRWTSIFPHPAI
ASAIHLYFAEHDLLHITHIAEDLYDTVGDRLLAAILTVRRQEAYGPYRDLADKRLKELLNSDQPEDIVMGLTI
LKLEKNPQNFPILLDFLNTKNEDILIVTCKALHTSVRANHKKPYCPELLKRLRQCSDHNDASQYLLKTISIALDIS
FVKDLLMTTSQKNTSRKYAEAMIGELDKEVAPAFQLVLTDEGTHNRCRILAAKALCKIDNWLLKKHAYKI
VKSKASKALFYSYHGHIYQKKYPTYNLSLLANTLNSNYAEVNFMLSLLGILGSMEHSGVLIRALTSKNQKI
KAQALESLEKNCDSHLFSLLEPFVNQPGMCYSEKYYFKCGVIPLTLKELNMMENSPSSLNKLTAQQLKEEL
SYCDPDFQSVNTIYNQEHEDFRTEESETLISFLSI

>core/40/5/Org5_Gene981

MRFSLCGFPLVFSFTLLSVFDTLSATTISLTPEDSFHGDSSQNAERSYNVQAGDVYSLTGDVSISNVDNSALNK
ACFNVTSGSVTFAGNHHGLYFNNISSGTTKEGAVLCCQDPQATARFSGFSTLSFIQSPGDIKEQGCLYSKNAL
MLLNNYVVRFEQNQSKTKGGAISGANVTIVGNYDSVSFYQNAATFGGAIHSSGPLQIAVNQAEIRFAQNTAK
NGSGGALYSDGDIDIDQNAAYVLFRENEALTTAIGKGGAVCCLPTSGSSTPVPIVTFSDNKQLVFERNHSSIMGG
GAIYARKLSISSGGPTLFINNISYANSQNLGGAIAIDTGGEISLSAEKGTITFQGNRTSLPFLNGIHLLQNAKFLK
LQARNGYSIEFYDPITSEADGSTQLNINGDPKNKEYTGTLFSGEKSLANDPRDFKSTIPQNVNLSAGYLV
GAEVTVSKFTQSPGSHLVLDLGTKLIASKEDIAITGLAIDIDSLSSSSTAATAVIKANTANKQISVTDSEI
LISPTGNAYEDLRMRNSQTFPLLSLEPGAGGSVTVTAGDFLPVSPHYGFQGNWKLAWTGTGNKVGEFFWDKINYKPRP
EKEGNLVPNILWGNAVDVRSLMQVQETHASSLQTDRLWIDGIGNFFHVSASEDNIRYRHNSGGYVLSVNN
EITPKHYTSMAFSQLFSRDKDYAVSNNEYRMYLGSYLYQYTTSLGNIFRYASRNPNVNVGILSRRFLQNPLMI
FHFLCAYGHATNDMKTIDYANFPMVKNSWRNNCWAIECGGSMPLLVFENGRLFQGAIPFMKLQLVYAYQG
DFKETTADGRRFSNGSLTSISVPLGIRFEKLALXQDVLYDFSFSYIPDIFRKDPSCEAALVISGDSWLVPAAHVS
RHAFVGS GTGRYHFNDYTELLCRGSIECRPHARNYNINCGSKFRF

>core/41/5/Org5_Gene559

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KSHTKKTTPGSIPSKVFSKFDATQDKTFQKTSGSAFPAKPTTLKELEERKKPRPERRTTADV KRSRFLPTQEV
EEPVPAASKEQLDSIQVWEEKQNYARRAVNAINLSIKKQLEEQTSTVTEKDVQPKTQATPHASKKNVASPST
SMPGIEKAATTVAVPQDKSEEEKVKERLTKRELTCEDLKDNGYTVNFEDISILELLQFVSKISGTNFVFDNDL
QFNVTVSHDPTSVDDLSTILLQVLKMHDLKVVEQGNVLIYRNP HLSKLSTVVT DSSLKETCEAVV VTRVFR
LYSVSPSAAVNIIQPLLSHDAIVSASEATRHVIISDIAGNVDKVSDLLAALDCPGTSVDMTEYEVKYANPAALV
SYCQDVLGTLAEDDAFQMFIQPGTNKIFVSSPRLANKAEQLLKSLDVP EMAHTLDDPASTALALGGTGTTS
PKSLRFFMYKLKYQNGEVIANALQDIGYNLYVTTAMDEDFINTLNSIQWLEVNNSIVIIGNQGNVDRVIGLLN
GLDLPPKQVYIEVLIDTSLEKSWDFGVQWVALGDEQSKVAYASGLLNNTGIATPTKATVPPGTPNPGSIPLP
TPGQLTGFS DMLNSSSAFGLGIIGNVL SHKGKSFLT LGGLLSALDQDGD TVIVLNPRIMAQDTQQASFFVGQT
VPYQTTNTIIQETGTVTQNIDYEDIGVNLVVTSTVAPNNVVT LQIEQTISELHSASGSLTPVTDKTYAATRLQIP
DGCFLVMSGHIRDKTTKV VSGVPLLNSIPLIRGLFSRTIDQRQKR NIMMFIKPKVISSFEEGTRVTNKEGYRYN
WEADEGSMQVAPRHAPECQGPPSLQAESDFKIIIEAQ

>core/43/5/Org5_Gene809

MSKDKMKPEPKKNFPTVFFLLFGVVFGVVA FQNFLAGKKARVGF SHQIEHLVNLRLIVPEDSHKIALNDN
LVSF GGRFRDVQTQEGQLRYHYLELIDQGHRLDL DQETSKSLTTLGKEVTNSILWFS AISGSP IPEQGYAISY
PSEVSGSVLTEPLVVTGPATPQLINLHSLQERYPTLSRSPEALRTY GSDLYELIGKYLSPVLGIGSETLKRELKD
LYQQVEVSLTQETDTEAAYTLYGQVLSTLNRISSSLV VSEGGERFSQLRSVRLYREEWNKYHKLVEARDLNQ
AQLEKLRGELSQT VWFYFNNQELSSRSLEKQDPEVFGHWFAGAKEEWTAFKFNHSLSFKAPDQPRNLVLEKT
FKSQEPSPHYLG YLFTFLPIILVLLFVYLVFSRQMRGMSG SAMSFGKSPARMLLKGNKVTFADVAGIEEAKE
ELIEIVDFLKNPNKFTSLGGRIPKGVLLIGPPGTGKT LIAKAVSGEADRPFFSIAGSDFVEMFVGVGASRIRDMF
EQA KRNAPCII FIDEIDAVGRHRGAGIGGGHDEREQTLNQLLVEMDGFGTNEG VILMAATNRPDVLDKALLR
PGRFDRRVVMNLPDIKGRFEILMVHAKRIKLDPTVDLM AVARSTPGASGADLENLLNEAALLAARKDRTAV
TAVDVAEARDK VLYGKERRSLEMDAEERKTTAYHESGHAVVGLCVQH GDPVDKV TIIPRGLSLGATHFLPE
KNKLSYWK KELYDQLAVLMGGRAAE EIFLGDISSGAQQDISQATKLVRSMVCEWGMSPQLGNVTYDERSD
GLTGYGGYHEKSYSEETA KTIDTELRMLLDAAYQRALDIINEHKAEIELMTQMLIEFETLDSKDVKEIMDHT
WDPEKKRARLKEEGMLFKKSSDDLPPPPPKEDTLPGLGFNAT

>core/44/5/Org5_Gene289

MDSEFVGQVYSSDMDWIESMYQRFMNHETLDPSWKYFFEGYQLGQAASPSEASTKISGNETIAMLQEQKSQ
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CTPELQEFVWNLMEKRQVERFAEQLLSYKDLCKATFFEEFLQIKFTGQKRFSLEGGETLVPMLEHLVHYGS
ALGISNYVLGMAHRGRLNVL TNVLGKPYRYVFMEFEDDPAARGLESVGDVKYHKGYVLKSHQKDRETTFV
MLPNASHLESVDPIVEGVVAALQH QGHAGKEQSSLA ILVHGDAAFSGQG VVYETLQLSRVPGYSTEGTLHIV
VNNYIGFTA VPRESRSTPYCTDI AKMLGIPVFRVNSEDDVACIEAIEYALQVRERFSCDVIIDLCCYRKYGHNE
SDDPSVTAPLLYDQIKRKKSIRELFRQYLLEGQFADISEETLASIEKEIQESLNREFQVLKGTDPEFPKKECHH
CDRLNNGELILHDCDVSLDRET L FHMSSRLCGFPDNFHPHPKIKTLLEKRMKMAEGGVGYDWAMAEE LAFA
SLLIEGYNLRLSGQDSIRGTFSQRHLVWSDTVTGD TYSPLYHLSAEQGSVEMYN SPLSEYAILGFEYGYAQQA

LKTLVLWEAQFGDFANGAQIIFDQYISSGIQKWDLHSDIVLLLPHGYEGQGPEHSSSRIERYLQLAANWNFQV
VLPSTPVQYFRILREHAKRDLPLVIFTPKLLRYPQCVSSIEEFTEPGGFRAILEDADPNYDASILVLCSGKIY
YDYAEMLPQDRRKDFSCLRISLYPLALEDLVSLIDKYSHLKHFWLQEESKNMGAYDYMFMALQDILPEK
LLYIGRPRSSSTASGSAKLSRQELVTCMETLFSLR

>core/45/5/Org5_Gene933

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SPESTSRIRAKNRSSFSSSEESSAHIPVDTSEPAPVSIADPEPELEVVDDEVCDDESPEVHPVAEVLPEQPVLPET
PPQEKELEPKPVKPAEPKSVVMIKSKFGPTGKHINLLAKTFKAPAKEEKVVAGSKSTKPVASDKTGKPGTSE
GGEQNNREKQFNPANRSPASGPKRDAGKKNLTDFRDRSKKSDESLKAFTGRDRYGLNEGGEEDRWRKKRV
YKPKKHYDEASIQRPTHIKISLPITVKDLATEMCLKASEVIQKLFHGMTYVVNDILDSETAVQFIGLEFGCTID
IDYSEQDKLCLSNDTVRDEIQSTDPSKL VIRSPIVAFMGHVDHKGKTTLIDSLRKSNAATEAGAITQHMGAF
CSTPVGDITILDTPGHEAFSAMRARGAEVCDIVVLVVAGDEGIKEQTLEAIEHAKAADIAIVVAINKCDKPNF
NSETIYRQLSEINLLPEAWGGSTVTVNTSAKTGEGELSEMLELALQAEVLELKADPSARARGLVIESELHKGL
GPVATVLIQNGSLKLGEALVFNDYCYGKVKTMHNEHNELMKEAGPSIPVLITGLSDIPKAGDPFFVVKNEKTA
RDIEARSAGQQRFALQQKKRPNFDSMLQNKKTLKLMIKADVQGSIEALVSSISKIKSEKVDVEILTNSVGEIS
ESDIRLAAASKAVLIGFHTGIESHAEPLIKSLGVRVELFTVIYHAIDAIKEIMTSLLDPIAEEKDEGSAEIKEIFRS
SQVGSYGCIVTEGIMTRNHKVRVLRNKEILWKGTLSLKRKVKEDVKEVRKGLECGILLEGYQQAQIGDVLQ
CYEVIYHPQKL

>core/46/5/Org5_Gene722

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RIFRLTDKDNFWSMANTGPCGYCSELLFDRGPSFGNASSPLDDTDGERFLEYWNLVFMEFNRTSEGSLALP
NKHVDTGAGLERLVSLIAGHTTVFEADVLELIAKTEQLSGKVYHPDDSGAAFRVIADHVRSLSFAIADGLLP
GNTERGYVLRKILRRSVNYGRRLGFRNPFLAEIVPSLADAMGEAYPELKNSLSQIQKVLTL EEESFFKTLDRG
GNLLQQVLKSSSSSSCISGEDAFKLKDTYGMPIDEISLLAKDYDYSVDMDTFHKLEQEAKERSRKNVVSQSG
TSESIYNELHLTSEFIGYDHLSCDTFIEAISKDHIVSSLQEKQEGAIVLKVSPFYAEKGGQVGDSGEIFCSEGTFI
VTHTTSPKAGLIVHHGRISQGSALTVEAAVTAQVNRYRRKRIANNHTACHLLHKALEITLGDHIRQAGSYVDD
TKIRLDFTHPQAISPEDLLCIETLVNESIRENEPVDIREALYSDVMNSSEIKQFFGDKYSDVVRVVSAGHSHEL
GGTHAEATGDIGFFRITKEHAVAMGIRRIEAVTGEKAEATVHQQSEVLEEIATLLQVPRDQIVSRLTATLDER
KQQDKRLNELENSLIQTKLDKLIHNCHQRQGITCLVHHLAEHENHRLQQYAQCLHQRIPEKLISLWTTEKNG
KYIVLSRVSDDLITQGVHAQDLLKAVLTPCGGRWGGKDQSAQGSAPALPATEVLNETLWQWISTQLI

>core/47/5/Org5_Gene583

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PTTSWTDYKHSRPQASSPRAPSSQTPTDIVSAAALALVLVIDGGLAELVASVTEIDL GALSTISTVRQLMASYL
GLTTLTAEQEKVVFSSSYPSEKNLLEHVKQEKAAEIQAKQEEIKAVLEAKGVSTEEIEAILKEYPDIYAADFF
KEFIEEPLHTYRAKVGAPIQEMNENAIQLLTPPAITPDNVNEVNGMNTLSTILQAIDDAIKQAPALGGDQEIT
ILQTLVPLVDKTTFTKAEFDLIYTATQLPNTASLKL YLTDRQIAEYRGKITKVYQNSIQNLSETKRVVENNRSM
LETQLSMFQQAQNCFTWISQANALNIAITNKYISAVLTTSMEMYGGLLCLSYMYERLADDEKAIFDKSVNE

YLPPIHVGGSWVNGWIAKMAAYQELAEYSLGTAVTSQDQIKAYLQTRGNEFKATRHHFFHNIGDQMYQFAN
ETVFGNCLTTANGAIQPDLGGFIREAMTNVGTVEADYVSNAQRILNEFNATAAHVLQLQLQIAELQKKADD
LDPGKASFTENRKFVAAWITSESLGDALISMILNSQLPKQEAFKPLIEEINFNNLAANALNSLLQITNEFSTT
SVYYSLSSYLVSQKTGQNLFAGDYYETLLAAAREREYIYRDTARCKQAINLVNGLLQKINSLPGATSAQKQE
MLNATYYQYSLSVTLNQLTVLESLLAGLKMTLQTTSNNKYDKSVFKIESFDDWIPTLAALESFLTSGFPNIS
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>core/48/5/Org5_Gene619

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KVYLSPDPDREGAIAWHIANQLPDSPLIQRVSFNaitKNAVTEALKHPRTIDMALVNAQQARRLLDRIVGYK
ISPILSRKLQQRSGISAGRVQSVALKLVVDREKAIDAFVPVEYWNLRVLMQDPKTTKTFWAHLYAVQGKKW
EKEIPEGKTENDVLLINSEEKARHYAELLEKSSYTITRVEAKAKRRFAPPPFITSTLQQEASRHRFSASRTMSI
AQTLYEGVDLSESTGLITYMRTDSVRVDPEALTTVREYIQQTFGKEYLPEKANVYTTKKMTQDAHEAIRP
TDINLTPDKLKNKLSDDQFKVYNLIWKRFVASQITPAIYDTLAVQITTDTEIDLRASGSLLKFKGFLAVYEEKQ
DDENDQEEDHPLPPLHAQDALIKEEVSQEQAFKPLPRFTEASLVKELEKSGIGRPSTYATIMNKIQSREYTTK
ENQRLRPTELGKIISQFLETNFPRI MDIGFTALMEDELELIADNKKPWKLLLQEFWTTFLPVVITAEKEAVIPRI
LTNIECSKCHKGKLVKIWSKNSYFYGCSEYPECDYRTSEEELAFNKEDYAEDTPWDSPCPLCGGVMKVRHG
RYGTFLGCEKYPECRGITISIHKKGEEIEQEEPIPCPAIGCNGKIFKKRSRYNKIFYSCSEYPECSVIGNSIDAVITK
YSGTEKIPYKKKTPTKKKSSAKTTKAAKTPSKKGKAKSSVKKSSSEKKTGPLFLPSPDLAKMIGNEPVSARGEAT
KKIWDYIKEHQLQAPENKKLLVPDNNLATIIGPNPIDMFQLSKHLSQHLLTKVSNDESSASS

>core/49/5/Org5_Gene477

MKKLFLVDASGFIFRAYFALPEMKNHQGQATQAVFGFIRSLNKLIFESPEYMISSVFDGPNNKQSRQAIYADY
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VAWNPWADQGVVGISEVIERYGIPPGNIPDYLALVGDSSDNIPGLPGCGPKKAAALLKQFGSVEGLLENLDA
VKGLSQTMLSERQETLKL SKRLALLDSNIPVPIESLTFPQHPVDEEKLIHFYIQQGFKTLVPSKQTEAATVDV
QIIKDAESLTNINLVQGGDIAFAVAYTGNHLLSLKLEGLALTQGSGVFFIALEEETKILPILKDFFLREDLTF
YGYNLKRDCHALLNAGIVIREISYDLALAEHLTNGGGKISFQSLLVNHGFTETAHRFAKEWGN SGLPIGRLPE
QPEQYFGEFVAYLPIIKDAILEEINRKNLNHILSDIEMPLEKVLFSMERAGVPLDVEELAILEALFETELAVLTE
EIYDLSGRPFNIKSPKQLSDILYNELGLRPIDKAKSTRAEVLEALRSEHPHIEKLLAFRTIEKLLSTYVKALPKQV
DSHTQRIHPSFDQTGAVTGRLACRDPNLQNIPIRSERGILLRKAFLRSEKNSYFLSADYSQIELRFLAHLSDKS
LKFAFESGEDIHAFASQVFHVPLEQVSKEQRMQAKTVNFGIVYQQAFGLAKVLKISIGEAQELIQAYFSRY
PEIAHFVEETIQQAADLRVTTMLGRERIIDSWNEFPGSRAASGRFAVNTRIQGSAAELIKLAMLDISQAIKQQ
QMKSRMLLQIHDELLFEVPEEEIEEMQRLVREKMESAMTLSVPIVVNIGKNWAEC

>core/50/5/Org5_Gene102

MEKFSDAVSEALEKAFELAKSSKHTYVTENHLLLALLENTESLFYLVIKDIHGPNGLLNTAVKDALSREPTVV
EGEVDPKPSPGLQTLLRDAKQEAKTLGDEYISGDHLLLAFWSSNKEPFNSWKQTTKVSFKDLKNLITKIRRG
RMDSPAESNFQGLEKYCKNLTAAREGKLDPVIGRDEEIRRTIQVLSRRTKNNPMLIGEPGVGKTAIAEGLA
LRLIQGDVPESLKGKQLYVLDMGALIAGAKYRGEFEERLKSVLKDVESGDGEHIIFIDEVHTLVGAGATDGA
MDAANLLKPALARGTLHCIGATTLENYQKYIEKDAALERRFQPIFVTEPSLEDAVFILRGLREKYEIFHGVRIT

EGALNAAVLLSYRYIPDRFLPDKAIDLIDEAASLIRMQIGSLPLPIDEKERELAALIVKQEAIKREQSPSYQEEA
DAMQKSIDALREELASRLGWDEEKKLISGLKEKKNSLES MKFSEEEAERVADYNRVAELRYS LIPQLEEEIK
QDEASLNQRDNRLQEEVDERLIAQVVANWTGIPVQKMLEGAEKLLILEESLEERVVGQPFASVAVSDSIR
AARVGLNDPQRPLGVFLFLGPTGVGKTELAKALADLLFNKEEAMVRFD MSEYMEKHSISK LIGSSPGYVGYE
EGGSLSEALRRRPYSVVLFDIEKADKEVLNILLQVFDDGILTDGKKRKVNCKNALFIMTSNIGSPELADYCS
KKGSELTKEAILS VVSPVLKRYLSPEFMNRIDEILPFVPLTKEDIVKIVGIQMRRIAQRLKARRINLSWDDSVIL
FLSEQGYDSAFGARPLKRLIQKVVILLSKALLKGDIKPDTSIELTMAKEVLVFKKVETPS

>core/51/5/Org5_Gene569

MAVRLIVDEGPLSGVIFVLEDGISWSIGRDSSANDIPIEDPKLGASQAIINKTDGSYYITNLDDTIPIVNVNGVAIQ
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KLTKDQGSSDPITSGDQELADAFASAKAEKNQPRAKVAKKGLKESSNESLNPKEQNAKDSPKG EERTNK PQ
NAIMEDNGASPRQDPQPKSAEPSLKNTARDETPLKENKPVEEKANKKATPDSPEKKDQPEEGSKKEGSKIEA
TPLDSQKESEDKEAEEAFVQEEEEENLTEDNKEDSDSAADANDDTASDH TAEDNKETPKKVENEKS AVLSPFH
VQDLFRFDQTIFPAEIDDI AKKNISVDLTQPSRFLKVL AGANIGA EFHLDSGKTYILGTDPTTCDIVFNDLSVS
HQAKITVGN DGGILIEDLDSKNGVIVEGRKIDKTSTLSSNQVVALGTTFLFLIDHHAPADTIVASLSPDDYSL
FGRQQDAEALERQEAQEEEEKQKRATLPAGSFILTLFVGGLAILFGIGTASLFHTKEVVPLENIDYQEDLAQVI
NQFPTVRYTFNKTNSQLFLIGHVKNSTDKSELLYKVDALS FVKSVDNDVIDDEAVWQEMNILLSKRPEFKGIS
MHSPEPGKFIITGYVKTEEQAACLVDYLNHFNYLSLLENKVVVETQMLKAIAGHLLQGGFANIHVAFVNGE
VILTYVNNDDAEKFRAVVQELSGIPGVRLVKNFAVLLPAEEGIIDLNLRYPNRYRVGTGYSRYGEISINVVVN
GRILTRGDVIDGMTVTSIQPNAIFLEKEGLKYKIDYNK

>core/52/5/Org5_Gene918

MF EKFTNRAKQVIKLAKKEAQRLNHNYLGTEHILLG LLKLGQGVAVNVLRNLGIDFDTARQEVERLIGYGPE
IQVYGD PALTGRVKKS FESANEEASLLEHNYVGTEHLLGILHQSDSVALQVLENLHIDPREVRKEILKELETF
NLQLPPSSSSSSSSSR SNPSSSKSPLGHSLGSDKNEKLSALKAYGYDLTEMVRESKLDPVIGRSSEVERLILILCR
RRKNNPVLIGEAGVGKTAIVEGLAQKIILNEVPDALRKKRLITLDALMIAGTKYRGQFEERIKAVMDEV RKH
GNILLFIDELHTIVGAGAAEG AIDASNILKPALARGEIQCIGATTIDEYRKHIEKDAALERRFQKIVVHPPSVDE
TIEILRGLKKKYEEHNVFITEEALKAAATLSDQYVHGRFLPDKAIDLLDEAGARVRVNTMGQPTDLMKLEA
EIENTKLAK EQAIGTQEYEKAAGLRDEEKKLRERLQSMKQEWENHKEEHQVPVDEEAVAQVVS LQTGIPSA
RLTEAESEKLLKLEDTLRRKVIGQNDAVTSICRAIRRSRTGIKDPNRPTGSFLFLGPTGVGKSLLAQQIAIEMFG
GEDALIQVDMSEYMEKFAATKMMGSPPGYVGHEEGGHLTEQVRRRPYCVVLFDIEIEKAHPDIMDLMLQILE
QGRLTDSFGRKVDFRHAIIMTSNLGADLIRKS GEIGFGLKSHMDYKVIQEKIEHAMKKHLKPEFINRLDESVI
FRPLEKESLSEIIHLEINKLDSRLKNYQMALNIPDSVISFLVTKGHSPEMGARPLRRVIEQYLEDPLAELLKES
CRQEARKLRATLVENRVAFEREEEEQE AALPSPHLES

>core/53/5/Org5_Gene8

MKIPLRFL LISLVPTLSMSNLLGAATTEELSASNSFDGTTSTTSFSSKTSSATDGTNYVFKDSVVIENVPKTGET
QSTSCFKNDAAAGDLNFLGGGFSFTFSNIDATTASGAAIGSEAANKTVTL SGFSALSFLKSPASTVTNGLGAIN
VKGNLSLLDNDKVLIQDNFSTGDGGAINCAGSLKIANNKSLSFIGNSSSTRGGAIHTKNLTLS SGGETL FQGN T
APTAAGKGGAIAIADSGTLSISGDSGDIIFEGNTIGATGTVSHSAIDLGTSAKITALRAAQGHTIYFYDPITVTGS

TSVADALNINSPDTGDNKEYTGTIVFSGEKLTEAEAKDEKNRTSKLLQNVAFKNGTVVLKGDVVLSANGFSQ
DANSKLIMDLGTSLVANTESIELTNLEINIDSLRNGKKIKLSAATAQKDIRIDRPVVLAIKDESFYQNGFLNEDH
SYDGILELDAGKDIVISADSRSIDAVQSPYGYQGKWTINWSTDDKKATVSWAKQSFNPTAEQEAPLVPNLLW
GSFIDVRSFQNFIELGTEGAPYEKRFVWAGISNVLHRSGRENQRKFRHVSGGAVVGASTRMPGGDTLSLGFA
QLFARDKDYFMNTNFAKTYAGSLRLQHDASLYSVVSILLGEGGLREILLPYVSKTLPSCSFYQGQLSYGHTDHR
MKTESLPPPPPTLSTDHTSWGGYVWAGELGTRVAVENTSGRGFFQEYTPFVKVQAVYARQDSFVELGAISR
FSDSHLYNLAIPLGKLEKRFQAEQYYHVAMYSPPVCRSNPKCTTTLLSNQGSWKTGKSNLARQAGIVQASG
FRSLGAAAEELFGNFGFEWRGSSRSYNVDAGSKIKF

>core/54/5/Org5_Gene939

MFNKDEIIVPKNLEEEMKESYLRYSMSVIISRALPDIRDGLKPSQRRVLYAMKQLSLSPGAKHRKCAKICGDT
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VDIVPNYDETKHEPVVFPKFPNLLCNGSSGIAVGMATNIPPHNLGELIEATLLLLANPQASVDEILQVMPGPD
FPTGGIICGSEGIRSTYTTGRGKIKVRARLHVEENEDKHRESIIITEMPNVNVKSRLIEQIANLVNEKTLAGISDV
RDESDKDGIRVVLEIKKGESSEIIINRLYKFTDVQVTFGANMLALDKNLPRTMSIHRMISAWIRHRKEVIRRT
RYELNKAETRAHVLEGYLKALSCLDALVKTIRESGNKEHAKERIIESFGFTEPQALAILRLYQLTGLEAEKI
QKEYEELLNKIAYYKQVLSDEGLVKDIIRNELQDLLKHHKVARRTTIEFDADDIRDIEDIITNESVIITISGDDY
VKRMPVKVFKEQRRGGHGVGTGDMKKGAGFLKAVYSAFTKDYLIFTNFGQCYWLKVWQLPEGERRAKG
KPIINFLEGIRPGEELAAILNIKNFDNAGFLFLATKRGVVKVSLDAFSNPRKKGIRALEIDEGDELIAACHIVS
DEEKVMLFTHLGMVRFPHKVRPMGRTARGVRGVSLKNEEDKVVSQCIVTENQSVLIVCDQGFGKRSLVE
DFRETNRGGVGVRILINERNGNVLGAIPVTDHDSILLMSSQGQAIRINMQDVRVMGRSTQGVRLVHLKEGD
ALVSMEKLSSNENDDEVLSGSEEECSDTVSLR

>core/55/5/Org5_Gene1035

MIYSTSISTFYKKLSLVSSMHSFAQRHRESLEHIANYEKTTAERDILKRLIEVLDQRASERYRSAVEKLHKYEV
ERATVAKSIPVAAIHEKPLSSTHASVQVTASTPAATGSGVGAYYNAVKKQWAQDLIVELNTVMTTIMASVNS
KNPANKDVFDKLNTELQALVAAGNNLTEENFQTLYNFPFEEIFTAIQRADTFTGGMKTDFTNQLAGKYGNQA
TLTQTFADGRVEGFKDILTAVQGVLTPEQFTIFAEIATELQALADHVGNFDEAGLQRIEDAGEKLA VINSSD
LTRNDKIMFCQHITDLYSDQVAALGSFDTVLDASIYVNQHQGTMFSNLSSFVGSGLIGTFAPIDLSSSQGDISSA
ALAGALQTARGLNSRFNELTAEQQKLINECIKSLVTFKCGEHLGAIWAYFTASTVVALNPTATMDHVKAAIL
EEAKELDNSSFQLASSIKSAMTSIVNSSGSFSVTVNSSTLQYTIYSEKNGKVEINQILLNYGSTGFLPEITKLAKT
NAESTARSYFRFKALAAVESENVQNKIEDLQSQLQQFTNMKTELFDGQLLSQASELRALPLPSAVASVLIDRY
MPKEVDYLNIEYKKLYYSNLGSSVGNSIIDAISQYVNGATYFNFASYVGQQPAVGAGGANAFPGSQESAQAK
LDQERKQAALYLQETRGALTVIEEQRARVLKDDKITNEQRSTILDSLRYEDNINSISGSLVLLQNYLQPLSIA
GGSVAGTFEVKEGQEQWQARLQILEEALVSGLVGNMINGGMFPLQSTIQSDQQSFADMGNFQLDLQMHLT
SMQQEWTVVATSLQLLNQMYLSLARSLTG

>core/56/5/Org5_Gene997

MTEKKPTPMMEQWHQCKEKAGDSVLLFRMGDFYEA FYDDAVLLSQHLELTLTQRQGIPMSGIPVSTVDITYV
DRLIGKGFKVAVAEQFGEPAKEKESKKIGPMARDIQRFTPGTLLSSTLLQEKFNYYIVAINRIGSLFGFACLD
LSTGSFFIEECENTKELVDEICRLAPSEVLSCNKFYNKETAIVMQLQQHLKLTSTYADWAFEHKFASQKLTT

HFQVASLDGFGKGLVPAINAAGGLLSYIQDKLLLPTKHIAIPQTRGKQQKLLIDTASQVNLELLAPLNDPQG
KNSLLRIMDHTSTPMGGRLLRQILISPFYNPKEILVRQDAVEFFLRQVTLRKNIKTYLCQVRDIERLMTKVTTG
LAGPRDIGTLRDSFSAGAQIYEQLASATLPEFFIDKCSLDTKLASLIALLSKSLNGDLPLRVSDGNIFVDEFHND
LKRLRHNQEHSQEWIWEYQERIRKETGIKKLKICFAQALGYIIEVSSEFAPQLPKDFIRQRSRLHAERFTTIEL
QQFQDDMSNISEKLQTLTETQFFKDLCSHILQLRTEILALSQSLADLDYIISLADLAHAQGYCRPRVDMSDTLCI
YRGCHPVAKTLVDTGKFIPNDTEMRGSQTRMILLTGPNMAGKSTYIRQIALLVIMAQMGSYIPAKSAHIGVID
KIFTRIGAGDNLSKGMSTFMVEMAETANILHNATDRSLVILDEVGRGTSTYDGLAIAQAVVEYLLFTDKKKA
KTLFATHYKELTTLEDHCPHVENFHAGVKDKAGQPVFLYEILKGHSQKSFGIHVARLAGFPLCVVSRAQQIL
RQLEGPESTRPAQDKMQQLTLF

>core/57/5/Org5_Gene236

MEDFSSFDKNKVSVDMSMKRAILDRLYLSVVQSPESASPRDIFTAVAKTVMEWLAKGWLKTQNGYYKNDVK
RVYYLSMEFLLGRSLKSNLLNLGILDLVRKALKTLNYDFDHLVEMESDAGLGNGGLGRLAACYLDSMATLA
VPAYGYGIRYDYGIFDQRIVNGYQEEAPDEWLRYGNPWEICRGEYLYPVRFYGRVIHYTDSRGKQVADLVD
TQEVLAMAYDIPIPGYGNDTVNSLRLWQAQSPRGFEFSYFNHGNYIQAIEDIALIENISRVLYPNDSITEGQELR
LKQEYFLVSATIQDIIRRYTKTHICLDNLADKVVVQLNDTHPALGIAEMMHILVDREELPWDKAWEMTTVIF
NYTNHTILPEALERWPLDLFSKLLPRHLEIHYEINSRWLEKVGSRYPKNDDKRRSLSIVEEGYQKRINMANLAV
VGSAKVNGVSSFHSQLIKDTLFKEFYEFFPEKFINVTNGVTPRRWIALCNPRLSKLLNETIGDRYIIDLSHLSLIR
SFAEDSGFRDHWKGVKLKNKQDLTSRIYNEVGEIVDPNSLFDCHIKRIHEYKRQLMNILRVIIYVYNDLKENP
NQDVVPTTVIFSGKAAPGYVMAKLIKLINSVADVNNQDSRVNDKCLKVLFLPNYRVSMAEHIIPGTDLSEQIS
TAGMEASGTGNMKFALNGALTIGTMDGANIEMAEHIGKENMFIFGLLEEQIVQLRREYCPQTICDKNPKIRQ
VLDLLEQGFFNSNDKDLFKPIVHRLHHEGDPFFVLADLESYIAAHENVNKLKFEPDSWTKISYNTAGMGFFS
SDRAIQDYARDIWHVPTKSCSGEGN

>core/58/5/Org5_Gene1005

MKKLYHPTLFLRPLIRLSLIFALSLTLISGNFPQQKSFGHCCADMHSALISGKNCEELFADFIERVLA DRET LTA
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CHESLQDHLLFELYTVTLHSGYENRKQDMLLAKEQG DYKKAIELAKELVA ALEKGSCSPHPEIVQIEKTFLQ
KTLLALQIKVAQEAQESCDALLTPYCLSEIAYTEAMDALVLRARGEVSRTNEVDSVLLSHALQHLPFAREKA
IPELEVLI DHGAYLESTLLYYAYFSLLELYHQNKDFASLERLLEKGD AVFVPEHPYFPEYGFFLGAYFYAKGK
YESAEKVFLQIIDPAVKLGATFARAYEYLGCIAYVQNHYEKAEEYFLRAYKSWG REESGIGLFLAYAVQKKK
TACEDMLYHPKFSFTYRHLLDSLCSLSYPHGENKGSSAIQRVHRAVPELSEIYSRCIYDMIKYRNV TYTHPIIE
LAYNQVRNLEKRNLEEICRDAQDPEYDKALAFWGALQSGASVPRSLIESSDVDEAGITIRCYEALYFHNPD AI
AMLPQAFSEECNSWQTALRLVWTLVRPKGAPNHAKYWDHLVLRPHGDSL YFFGYDLQEY LIGKEDALKHL
SVFAELFPKSSLLSLVYYLQGYSESSALRKVGWVFKALEEFTEISWSGEHMKTWAYIYYMVKLDLADTYISL
GNFSQAVHILEEVKEDWQVASHPKLHFLKGEDCYLAMELRWVEGLAYAYFQLHETAHLSNHLLEHVEKNLI
SPRSYRDYYGESLQRTLGLCQRFLGV

>core/59/5/Org5_Gene108

MRYDPNLIKWKWQFWKEHRSFQANEDEDKVKYYVLDMFPYPSGAGLHVGH LIGYTATDIVARYKRARGF
SVLHPMGWDSFGLPAEQYAIRTGTHPKVTTQKNIANFKKQLSAMGFSYDEGREFATSDPDYHWTQKLFLF

LYDQGLAYMADMAVNYCPELGTVLSNEEVENGFSIEGGYPVERKMLRQWILKITAYADKLLEGLDALDWP
ENVKQLQKNWIGKSEGALVTFHLTQEGSLEAFTTRLDTLLGVSFLVIAPEHPDLDSIVSEEQRDEVTAYVQES
LRKSERDRISSVKTKTGVTGNVYAKHPITGNLLPVWISDYVVLGYGTGVVMGVPAHDERDREFAEMFSLPIH
EVIDDNGVCIHSNYNDFCLNGLSGQEAKDYVINYLEMRSLGRAKTMYRLRDWLF SRQRYWGEPIPIIHFEDG
THRPLEDDELPLPPNIDDYRPEGFGQGPLAKAQDWVHIYDEKTGRPGCRETYTMPQWAGSCWYYLRFCDA
HNSQLPWSKEKESYWMPVDLYIGGAEHAVLHLLYSRFWHRVIFYDAGLVSTPEPFKKLINQGLVLASSYRIPG
KGYVSIEDVREENG TWISTCGEIVEVRQEKMSKSKLNGVDPQVLIIEYGADALRMYAMFSGPLDKNKTWSN
EGVGGCRRFLNRFYDLVTSSEVQDIEDRDGLVLAHKL VFRITEHIEKMSLNTIPSSFMEFLNDFS KL PVYSKRA
LSMAVRVLEPIAPHISEELWVILGNPPGIDQAAWPQIDESYLVAQTVTFV VQVNGKL RGRLEVAKEAPKEEVL
SLSRSVVAKYLENAQIRKEIYVPNKL VNFVL

>core/60/5/Org5_Gene15

MDSTTNSDSPILDPNPEDVEKLLDESEEESEDQSTERLLPSELFILPLNKRPFPGMAAPILIESGPYYEVLKVLA
KSSQKYIGLVLT KKENADILKVSFNQLHKTGVAARILRIMPIEGGSAQVLLSIEERIRIIEPIKDKYLKARVSYH
ADNKELTEELKAYSISIVSVIKDLLKLNPLFKEELQIFLGHSDFTEPGKLADFSVALTTATREELQEVLETTNM
HDIRIDKALILLKKELDL SRLQSSINQKIEATITKSQKEFFLKEQLKTIKKELGLEKEDRAIDIEKF SERLRKRHVP
DYAMEVIQDEIEKLQTLETSSAEYTVCRNYLDWLTIIPWGIQSKEYHDLKKA EIVLNKDHYGLDEIKQRILELI
SVGKLSKGLKGSII CLVGPPGVGKTSIGRSIAKVLHRKFFRFSVGGMRDEAEIKGHRRTYIGAMP GK MVQALK
QSQAMNPVIMIDEVDKIGASYHGD PASALLEVLDP EQNKDFLDHYLDVRVDLSNVLFILTANVLD TIPDPLLD
RMEILRLSGYILEEKLQIAKKYLVPKARKEIGLTASEVNFQPEALKYMINNYAREAGVRTLN GN IKKVLRKVA
LKIVQNQEKP KSKITFKISSKNLQTYLGKPIFSSDRFYESTPVGVATGLAWTSLGGATLYIESVQVSSLK TDM
HLTGQAGEVMKESSQIAWTYLHSALHRYAPGYTFFPKSQVHIHIPEGATPKDGPSAGITMVTSLLSLLLETPV
VNNLGMTGEITLTGRVLGVGGIREKLIAARRSRLNILIFPEDNRRDYEELPAYLKTGLKIH FVSHYDDVLKVA
FPKLLK

>core/61/5/Org5_Gene732

MKGTPQYHF IGIGGIGMSALAHILLDRGYEVSGSDLYESYTIESLKAKGARCFSGHDS SHVPHDAVVVYSSSI
APDNVEYLTAIQRSSRL LHRAELLSQLMEGYESILVSGSHGKTGTSSLIRAI FQEAQKDPSYAIGGLAANCLNG
YSGSSKIFVAEADESDGSLKH YTPRAVVITNIDNEHLN NYAGNLDNLVQVIQDFSRKVTDLNKV FYNGDCPIL
KGNVQGISYGYSPECQLHIVSYNQAWQSHFSFTFLGQEYQDIELNLPQHNAANAAAACGVALTFGIDINII
RKALKKFSGVHRRLERKNISESFLFLEDYAHHPVEVAHTLRSVRDAVGLRRVIAIFQPHRFSRLEECLQTFPKA
FQEADEVILTDVYSAGESPRESIILSDLAEQIRKSSYVHCCYVPHGDIVDYL RNYIRIHDVCVSLGAGNIYTIGE
ALKDFNPKKLSIGLVCGGKSCEH DISLLSAQHVS KYISPEFYDVSYFIINRQGLWRTGKDFPHLIEETQGDSPLS
SEIASALAKVDCLFPVLHGPFGE DGTIQGF FEILGKPYAGPSLSLAATAMDKLLTKRIASAVGVPPVVPYQPLN
CFWKRNP ELCIQNLIETFSFPMIVKTAHLGSSIGIFLVRDKEELQEKISEAFLYD TDVFVEESRLGSREIEVSCIG
HSSSWYCMAGPNERCGASGFIDYQEKYGF DGIDCAKISFDLQLSQESLDCVRELAERVYRAMQGKG SARIDF
FLDEEGNYWLSEVNPIPGMTAASPFLQAFVHAGWTQE QIVDHFII DALHKFDKQQTIEQAFTKEQDLVKR

>core/62/5/Org5_Gene713

MIRERKKS RHPRLPTLPLAAKASLYLFFACFSGLSLWSFH RDQPCTQNWIGLLGWSFSSFLLYFFGAAAFFIPL
YFLWLSFLYFRRTPRPLFFYKAA AFLSLPFCSAILLSMLSPVGTLPALLDTRL PKFILGNPPVS YVGGIPFYLF

YEQSFCLKHLIGSVGTALIFGFVMLFSVLYLCGGIALLLKKKTFQDGVKKAFCSSFFQTCFKNLKKLINRRNYL
PKPSVPFVSKNPFSCTKSQPSRRVSETIILDGSISPLQEEIPGSKKESFFLTPHPCKRFLTTFVEPQENKAKEGK
TIALSSTPTVVRESKGKERAALPKLKSLAVPENDLPQYHLLSKNREARPESLQAELERKALILKQTLTSFGIDA
DLGNICSGPTLAAFEVLPHSGVKVQKIKSLENDIALKLQASSIRIIAPIPGKAAVAGIEIPTFPFQAVNFRDLLEDY
QKTNRKLQIPLLLGKKANGDNLWADLATMPHLIIAGTTGSGKSVCCINTIVMSMIMTTLPSEIKLVIIDPKKVEL
TGYSQLPHMLSPVITESREVYNALVWLVKEMESRYEILRYLGLRNIQAFNSRTRNKTIIEASYDREIRETMPFM
VGIIDELSDLLSSSQDIETPIRLAQMARAVGIHLILATQRPSREVITGLIKANFSPSRISFKVSNKVNSQIIIDEPG
AENLMGNGDMLVLLPSVFGTIRAQGAYICDEDINKVIQDLCSRFTQYVIPSFHAFDDSDSDNSGEKDPLFAQ
AKTLILQTGNASTTFLQRKLKIGYARAASLIDQLEEARIIGPSEGAQPRQILIQNPLEG

>core/63/5/Org5_Gene209

MDPKENYDASAITVLEGLQAVRERPGMYIGDTGITGLHHLVYEVDNSIDEAMAGYCSRIDVRILEDGGIVI
VDNGRGIPIEVHERESAKQGREVSALEVVLTVLHAGGKFDKDSYKVSGGLHGVGVSCVNALSEKL VATVFK
DKKCYQMEFSRGIPVTPLQYVSVSDRQGTEIVFYPDPKIFSTCTFDRSILMKRLRELAF LN RGITIVFEDDRDVS
FDKVTFFYEGGIQSFSYLNQNKESLFSEPIYICGTRVGDDGEIEFEAALQWNSGYSELVYSYANNIPTRQGGT
HLTGFTALTRVINTYIKAHNLA KNNKLALTGEDIREGLTAVISVKVPNPQFEGQTKQKLGNSDVSSVAQQV
VGEALTIFFEENPQIARMIVDKVFVAAQAREAAKKARELTLRKSALDSARLPGLIDCLEKDPEKCEMYIVEG
DSAGGSAKQGRDRRFQAILPIRGKILNVEKARLQKIFQNQEIGTIIAALGCGIGADNFNLSKLRYYRIIIMTDAD
VDGSHIRTLTLLTFFYRHMTALIENECVYIAQPPLYKVSKKKDFRYILSEKEMDSYLLMLGTNESSILFKSTERE
LRGEALESFINVILDVESFINTLEKKAIPFSEFLEMYKEGIGYPLYLAPATGMQGGRYLYSDEEKEEALAQEE
THKFIIELYKVAVFVDIQNLKEYGLDISSYLIPQKNEIVIGNEDSPSCNYSCYTLEEVINYLNKLGKRGIEIQR
YKGLGEMNADQLWDTTMNPEQRTLHVSLKDAVEADHIFTMLMGEEVPPRREFIESHALSIRINNLDI

>core/64/5/Org5_Gene934

MNKRTLLFVSLIGIAFVGCQIFFGYNEFRSCKNLA EKQRKISEQTLAAVESVGLSVASWDTDVNGEEHKNNY
AVRVGDKLFLHNGEAAQSVYSSGESWSFVDHKCGFDNIHLALYRQQGSSFNPTNTGKVFLPTNHEGLPVL
VVEFRNNKEPLVFLGEYAQGRISNKDSTIFGTALVFWRSGSDYIPLGLYDSREEKLVS L DLPITRAVIFGNDQD
SAKSSDTANHYYVLFNDYMQIIVSEESGSIEGINLPFASTNNKSIVNEIGFDRDLASEKSPEALFPGLSSKLPDGQ
QAKNSIGGYYP LLRRGLLSDSKKLLPLEYHALNVVSGRELATPVALRYRVLSYTPHSIQLES LDRSVQKVYKL
PENPEEKPYVFETAITLTKETEDVWVTSGVPEVEIMSNASAPTIKYRVIKKNKGS LDKVKLPKVKEPLAVRRG
VYPQWILNSNGYFGIILTPLSEIASGYGSLYISGSTAPTRLAISPKNQLYPVSKYPGYETLLPLPKDAGTHRFL
VYAGPLAEPTLKVLDKTITQEKGENPEYLD SISFRGVFAFITAPFAALLFIIMKFFKLVTGSWGISIILLTVFLKL
LLYPLNAWSIRSMRRMQILSPYIQQIQQKYKNEPKRAQMEIMGLYKTNKVN PITGCLPLLIQLPFLIAMFDLLK
SSFLLRGASFIPGWIDNLTA PDVLFWSWQTSIWFIGNEFHLLPILLGIVMFLQQKVTS LHKKG PVT DQQKQQQV
MGNMMAILFTAMFYNFPSGLNIYWLSSMILGVVQQWITNKILDSKHLKNEVVLNNKKHR

>core/65/5/Org5_Gene886

MRIPITLLQTYFSEPLSTKEILEACDHIGIEAEIENTTLYSFASVITAKILHTIPHPNADKLRVATLTDGEKEHQV
VCGAPNCEAGLIVALALPGAKLFDSEGQAYTIKKSKLRGVESQGMCCGADELGLDELQIQERALLELPEATP
LGEDLATVLGNTSLEISLTPNLGH CASFLGLAREICHVTQANLVIPKEFSFENLPTTALDMGNDPDICPFFSYV
VITGISAQPSPIKLQESLQALKQKPINAIVDITNYIMLSLGQPLHAYDASHVALDSL RVEKLSTPESLTLLNGET

VLLPSGVPVVRDDHSLGLGGVMGAKAPSFQETTTTTVIKAAAYFLPEALRASQKLLPIPSESAYRFTRGIDPQN
VVPALQAAIHYLEIFPEATISPIYSSGEICRELKEVALRPKTLQRILGKSFSIEILSQKLQSLGFSTTPQETSLLVK
VPSYRHDINEEIDLVEEICRTESWNIETQNPVSCYTIYKLRKRETAGFLANAGLQEFTPDLLDPETVALTRKE
KEEISLQGSKHHTTVLRSSLLPGLLKSAATNLNRQAPSVQAFEIGTVYAKHGEQCQETQTLAILLTEDGESRSW
LPKPSLSFYSLKGWVERLLYHHHLSIDALTLESSALCEFHYPYQQGVLRHKKQSFATLGQVHPELAKKAQIKHP
VFFAELNLDLLCKMLKKTTKLYKPYAIYPSSFRDLTLTPEDIPANLLRQKLLHEGSKWLESVTIISIYQDKSL
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>core/66/5/Org5_Gene230

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YLKRGYFASSVDYSLEHNQEKGHIDVLIKINEGPCGKIKQLTFSGISRSEKSDIQEFIQTKQHSTTTSWFTGAGL
YHPDIVEQDSLAITNYLHNNGYADAIVNSHYDLDDKGNILLYMDIDRGSRYTLGHVHIQGFEVLPKRLEKQS
QVGPNDLYCPDKIWDGAHKIKQTYAKYGYINTNVDFLIPHATRPYDVITYEVSEGSPYKVGLIKITGNTHTK
SDVILHETSLFPGDTFNRLKLEDTEQRLRNTGYFQSVSVYTVRSQLDPMGNADQYRDIFVEVKETTTGNLGLF
LGFSSLDNLFGGIELSESNDLFGARNIFSFGFRCLRGGEHLFLKANFGDKVTDYTLKWTCPHFLNTPWILGI
ELDKSINRALSKDYAVQTYGGNVSTTYILNEHLKYGLFYRGSQTSLHEKRFLLGPNIDSNKGFVSAAGVNL
NYDSVDSRPTPTTGIRGGVTFEVSGLGTYHFTKLSLNSSIYRKLTRKGILKIKGEAQFIKPYSNNTAEGVPVSE
RFFLGGETTVRGYKSFIIGPKYSATEPQGGLSSLLISEEFQYPLIRQPNISAFVFLDSGFVGLQEYKISLKDLRSS
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>core/67/5/Org5_Gene974

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AEFVELQQILCQEGRLLEFVINQTRYIGRDLFKREDSLYKLWEWLGYPVSGDVRGERLKKSAREVVDRFMRT
TCNIRKIAMTFDRHVYSVAKTAFEKAFFGALETCVYESMRESYREAFCEYEKAKLLGDEEKSAHAEQRFQDIK
NRWEDVKDAFFWVKEDGKIEIDDAIGNSCKWSERYEEHRITRARWYKVAEHQLFNATMRVKDSLREHNEA
RVAFEKERSKENQRQVQKKKEKRLRDLKELHDQELPRAQERLRELQALYPEIAVSVVEARREVASDLEKAH
ESIDKHYSQSCVREQELY

>core/68/5/Org5_Gene903

MASGIGGSSGLGKIPPKDNGDRSRSPSPKGELGSHEISLPPQEHGEEGASGSSHIHSSSSFLPEDQESQSSSSAAS
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ENPSQGVPESSGPEPQRLFSLPSVKKQSGGLGRLVQTVRDRIVLPSGAPPTDSEPLSLYELNLRSSLRQELSDI
QSNQDLTPEEKAEATVTIQQLIQITEFQCGYMEATQSSVSLAEARFKGVETSDEINSLCSELTDPQLQELMSDG
DSLQNLDETADDLEAALSHARLSFSLDDNPTPIDNNPTLISQEEPIYEEIGGAADPQRTRENWSTRLWNQIRE
ALVSLLGMILSILGSLHRLRIARHAAAEAVGRCCTCRGEECTSSSEEDSMSVSGSPSEIDETERTGSPHDVPRRN
GSPREDSPLMNALVGWAHKGHAKTKESSESSTPEISISAPIVRGWSQDSSVSFIVMEDDHIFYDVPRRKDGIYD
VPSSPRWSPARELEEDVFGDYEVPITSAEPSKDKNYMTPLATPAIYDLPSRPGSSGSSSRSPSSDRVRSSSPNR
RGVPLPPVSPAMSEEGSIYEDMSGASGAGESDYEDMSRSPSPRGDLDEPIYANTPEDNPFTQRNIDRILQERS

GGASASPVEPIYDEIPWIHGRPPATLPRPENTLTNVSLRVSPGFGPEVRAALLSESVSAVMVEAESIVPPTEPGD
GESEYLEPLGGLVATTKILLQKGWPRGESNA

>core/69/5/Org5_Gene980

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LNFLINGGRSLMMTAESESLDLFHVSKRLGYLPSGDVRGEGLLKKSACEIVARLMSLHCEIHKVAVAFDRNSY
AMAEKAFKALGALEESVYRSLTQSYRDKFLESERAKIPWNGHITWLRDDAKSGCAEKKLRDAEERWKKF
RKAVFWVEEDGGFDINNLLGDWGTVLDPYRQERMDEITFHELYEKTTFLLKRLHRKCALAKTTFEKKRSKKN
LQAVEEANARRLKYVRDWDYQGEFQKAGERLEKLHALYPEVSVSIRENKIQETRSNLEKAYEAEIENYRCCVR
EQEDYWKEEEKREAEFRERGNKILSPEELESSLEQFDHGLKNFSEKLMELEGHILKLQKEATAEVENKILSDA
ESRLEIVFEDVKEMPCRIEIEKTLRMAELPLLPTKKAFEKACSQYNSCAEMLEKVKPYCKESLAYVTSKERL
VSLDEDLRRAYTECQKRFQGDGSEVRACREQLRERIQEFETQGLDLVEKELLCVSSRLRNTECDCVSGV
KKEAPPGKKFYAQYYDEIYRVRVQSRWMTMSERLREGVQACNKMLKAGLSEEDKVLKEEEYWLIREERK
NKEKRLVGTKIVATQQRVAAFESIEVPEIPEAPEEKPSLLDKARSLFTREDHS

>core/70/5/Org5_Gene1024

MLFSKNFSTDNGGAIKATLSLTGTTMSALFSENTSSKKGGAIQTSDALTITGNQGEVSFSDNTSSDSGAAIFT
EASVTISNNAKVSFIDNKVTGASSSTTGDMSSGAICAYKTSTDTKVTLTGNQMLLFSNNTSTTAGGAIYVKKL
ELASGGLTLFSRNSVNGGTAPKGGAAIAIEDSGELSLSADSGDIVFLGNTVTSTTPGTNRSSIDLGTSAKMTALR
SAAGRAIYFYDPITTSSTTVTDVLKVNTPADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSGGT
LSLKHGVTLQTQAFTQQADSRLEMDVGTTLPEADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLL
DPTGTFYENHSLRNPQSYDILELKASGTVTSTAVTPDPIMGEKFHYGYQGTWGPVWGTGASTTATFNWTKT
GYIPNPERIGSLVPNSLWNAFIDISSLHYLMETANEGLOGDRAFWCAGLSNFFHKDSTKTRRGFRHLSGGYVI
GGNLHTCSDKILSAAFCQLFGRDRDYFVAKNQGTVYGGTLYYQHNETYISLPCKLRPCSLSYVPTEIPVLFSG
NLSYTHTDNDLKTKYTTYPTVKGSWGNDSSFALEFGGRAPICLDESALFEQYMPFMKLQFVYAHQEGFKEQG
TEAREFGSSRLVNLALPIGIRFDKESDCQDATYNLTLYGTVDLVRSPDCTTTLRISGDSWKTFTGTNLARQAL
VLRAGNHFCFNSNFEAFSQFSFELRGSSRNYNVDLGAKYQF

>core/71/5/Org5_Gene689

MTLQPSYINFTPNVTTALSGGKIDTSAIELSCSALFFQELQDKAQGLKHALGLVQELSAEALRPAQVQTSISYL
PTEESSRPGISAGIIDRTMPTFTDDEVKAILQNPNFETSKIFVEGLDKVFKSYLDSVTPPEGIDPSNPESAILNYIT
LLNNLKPKFAAGSTPTDADYNALYALPGDFVKEIEALKAADAPPKSKVHAFWQEIMTIYNNMQVLSYPVTD
YLVNQIADLSLNITAAQEVQQYLKNFYLSILKDILNPGWTDPPQATHYPADA EYNARDAGVIQSLNLSGNYRQ
LTENMLPNTDTSLPQEIIAQIRSFQNGVNGTIIASNTLLPTTMRLDTLLGVIYTYQCCATIFGMSYGTSTPAKQN
YIDAINQEKSYWQARANGFDVTSQVFDQFATNIQSGTSYRGIDLFKNNKVNEINPIFLSQAASFLRYPYNLM
SRSMYQTIEDAANRSITALDGLISGWSTQIATFQTQKNSLDPSLLKYFDTMKANKESFVTTAPLQMVYSSLML
DKYLPTQQNVIASLGIQMTYSNKAAYLNELIKEITTFQSADIYYSLSIYLLKQMNLLQAVADPIGKAVGVLNDE
KTRAMADITRCNKIKAAIDKMLVEIKADAELSKSQIRELVDTLTNFKSQSDDLIRNLSCLLGFLSGLTLKAVN
DPNATYEAFTAEIFTEPFNNWKRQLATFESFVIQGGQNGITPGGQQQLLQAMESSQQDFSTFNQNNQQLALQLE
SSAMQQEWTLVSAALALLNQMVSKIARRIKS

>core/75/5/Org5_Gene656

MVFFRNSLLHLVALSGMLCCSSGVALTIAEKMASLEHSGRGADDYEGMASFNANMREYSLQLSKLYEEARK
LRASGTEDEALWKDLIRRIGEVRGYLREIEELWAAEIREKGGNLEDYALWNHPETTIYNLVTDYGTEDSIYLI
PQEIGAIIKIATLSKFVVPKESFEDCLTQILSRLGIGVRQVNSWIKELYMMRKEGCSVAGVFSSRKDLEALPETA
YIGFVLNSNVDAHTNQHVLLKKFINPETTHVDVIAGRVWIFGSAGEVGELLKIYNFVQSESIRQEYRVIPLTKID
PGEMISILNAAFREDLTKDVSEESLGLRVVPLQYQGRSLFLSGTAALVQQALTLIRELEEGIENPTDKTVFWYN
VKHSDPQELAALLSQVHDFVSGENKASVGAADGCGSQLNASIQIDTTVSSSAKDGSVKYGNFIADSKTGTLI
MVVEKEVLPRIQMLLKKLDVPPKMVRIEVLLEFERKLAHEQKSGNLNLLRLGEEVCKKGCSPSVSWAGGTGILE
FLFKGSTGSSIVPGYDLAYQFLMAQEDVRINASPSVVTMNQTPARIAVVDMSIAVSSDKDKAQYNRAQYGI
MIKMLPVINVGEEDGKSYITLETDTITFDTTGKNHDDRPDVTRRNITNKVRIADGETVIIGGLRCKQMSDSHDGI
PFLGDIPGIGKLFGMSSTSDSLTEMFVFITPKILENPVEQKERKEEALLSSRPGEREEYYQALAASEAAARAAH
KKLEMFASGVSLSQVERQEYDGC

>core/76/5/Org5_Gene749

MGYIESSTFRLYAEVIVGSNINKVLDYGVPENLEHITKGTAVTISLRGGKKVGVYQIKTTTQCKKILPILGLSD
SEIVLPQDLLDLFWISQYYFAPLGKTLKLFLPAISSNVIQPKQHRYRVVLKQSKAKTKEILAKLEVLHPSQGAV
LKILLQHASPPGLSSLMETAKVSQSPIHSLEKLGLDIVDAAQLELQEDLLTFFPPAPKDLHPEQQSAIDKIFSSL
KTSQFHTHLLFGITGSGKTEIYL RATSEALKQGKSTILLVPEIALTVQTVSLFKARFGKDVGVLLHHKLSDSKDS
RTWRQASEGSLRILIGPRSAFCPMKNLGLIIVDEEHPAYKQTESPPCYHARDVAVMRGKLAHATVVLGSA
TPSLESYTNALSGKYVLSRLSSRAAAAHPAKISLINMNLEREKSKTKILFSQPVLKKIAERLEVGEQVLIFFNRR
GYHTNVSCTVCKHTLKCPCPHCDMVLTFHKYANVLLCHLCNSSPKDLPQSCPKCLGTMTLQYRGSGETEKIEKIL
QQIFPQIRTIRIDSDDTKFKGSHETLLRQFATGKADVLIGTQMIAKGMNFSAVTLAVILNGDSGLYIPDFRASEQ
VFQLITQVAGRSGRSHLPGEILIQSFLPDHPTIHSAMRQDYSAFYSQEITGRELCEYPPFIRLIRCIFMGKCPKQT
WEEAHRVHNILKEQLESTNPLMPVTPCGHFKIKDTFRYQFLIKSAYVIPVNKKLHHALMLAKLSPKVKFMID
VDPMTTFF

>core/77/5/Org5_Gene86

MEKICGYLEQILVENKDSGDITAYIKIPNKTTPILIKGKLPQPLELGSPIQIYGVWSHSPSNTKYFQIHSYDSPLL
YEYRGVFHYLTSKLIKIGPKIAEKIIEKFQEKTCYVLDITPERLSEVSGISETRCVSICKQLCEQKILRKTLFLQ
EYNIPIHYGVRIFFKYYQEKSIKICEDPFLAREMEGIGFKTADFIAMKLGVPNRNSESRLCAGIQHSLEELQEEG
HTCYPIELLIDVVAKLLNQDVFDTPITLEEIDTQILNMQKRKLLHIQDISGTLHVWTRYLHLAEKTIVSDLKRIL
FSSRRIRSIDGEKAIAWVEENLSIDLAEQQREAIKACFSEKLLIITGGPGTGKSTITQAILKIFEQVTHKIILAAPT
GKAAKRMTEITQKHSVTIHALLQYDFKTKSFRKNHDNPIDCDLIIVDESGMMDTHLLHHFLKALPDYTTLVFI
GDIHQLPVSGPGNLIKDLITSNKMTVIRLNKIFRQVHDSGIVTNAHRVNEGELPILYSETGRRDFFQKDDQE
EALNHHIHLVTKFVPQKYHIYPQDIQVLAPMKGTLGIYNLNKALKHALNPKANLHGRFQSYAVGDKVMQI
RNNYNKEVFNGDIGYVSTINFEDKAVVVRMEGKHVGYSFSEDDLVLAYATSVHKKYQGSSEPCIIPIHTSHF
MMLYRNLLYTAITRGKKLVILVGTKKAIAIATRNNRVQHRCTGLAEVLKELDTKKNYADL

>core/78/5/Org5_Gene341

MRIYQQDLFCRLCRDPAWFFSLLSFTLRFYCLGRGWTTLSFFYKHQKKFIGIVIAVVCVSGIGVGWGRFSRKG
SAESTSRRTVFTTASGKRYVEKDFMAMKKFFAHEAYPFTGNPRAWNFINEGLLTDYFLTTRVGEKLFLKVYH
PGEKIFSKEKAYQPYRRFDAPFISSEEVWKSSAPQLEILKVQQIENPISKEGFLARAKLFLEERRFPHYVLRQ
MLEYRRQMFALPPDEALSRGKDLRLFGYQTIQDWFGDAYLSAAVELLIRFIDEQKKVLPRPSKQEARDDFYD
KAKHAYTKISKNEFSLGFEEFVNSYFQFLEISESEFFNMYRDILLCKRALLLQGGVSFDFQPLTTFFVQGKD
SIQVEFFRLPKEYSFKTKQELKA FEVYLKL VSLPKSDSLDVPNEILPIATIKAKEPRLVGRRFSIDYKRVALQDL
AATVPMVEVLHWQQNSEHFQEILQQFPDVETCQSYKDFQHLKPALRDKISLFTRKEILRARPERILQSLQQVP
KQSQEVLLSAGKNSALPGISDGQQLAKVLLENEVLDLYSQDAETYTYIIVNSSFEKEEVLPYREVLKRDLASQ
LLTSHGHLVDMERLESALRTRYPGEEGASLWQRRLLWKVVENHRLGRHLEGSFSWSLDRSLKTFSRGDKELP
QEFDRIFSMKVGDYSSVFMSPNEGPCYYQCLSHLLYDRPASVDKLFLAKSQLDEELLGSYMERFIEQGVR

>core/79/5/Org5_Gene595

MDYLEKLQVLIIEGQSANFLSLWEEYCFNDVVRGRELVEILEKVKSSSLASLFGKIVDTVVPLWEKIPEGKDK
DRVLQLILDQLTSNSQMFFDIATEYVNKKYSGEENFNEALRVVGLRDGRDFQFSLSRFDFLMHMHKGNFVFH
QGGWGVGEVMGVSFLQQKVLIEFEGIMSAKDISFETA FKSLTPLSGDHFLSRRFGDPDGFEAFAKENPIEVVEI
LLRDLGPKTAKEIKDELVDLVIPEADWNRWWQSAKTKIKKGTRIISPDNPKEPYVLS DAGCSHMGQLERKLG
LSLNSAEKISLIYHFIRDLHSELKNIEIRKSLVKALQDL DVEEGNKSLILQRELLSEYLGIKDASIDKEYITSLS
DDTSRLLENMPIVALQKSFLSLVRKYSSFWQQVFMQILLYTTSPTMRDFVYKTIKNDPSSVEVLKKRLLDSA
HQPMMFPELFWVFFLKLGNHEDGLFDPEDKEVLRLFLESALNFMYQVASTPHKELGKKLHHYLVGQRYLAVR
QMIEGASLPFLKELLLLSTKCPQFSSDLNVLQSLAEVVQPTLKKHKSNVEEENVLWSTSESF SRMKAKLQSL
VGKEMVDNAKEIEDARSLGDLRENSEYKFALEKRARLQEEIRVLSEEINRARILTKDLVFTDKVGVGCKVTL
KGDAGEVVEYITILGPWDADPDSCILSLQSKLAQNMLGKKLNDVVILQGKEYKISRISQIWEEHGA

>core/80/5/Org5_Gene359

MVDKLIHPWDLDLLVSGRQKDPHKLLGILASEDSSDHIVIFRPGAHTVAIELLGELHHAVAYRSGLFFLSVPK
GIGHGDYRVYHQNGLLAHDPAFPPLWGEIDSFLFHRGTHYRIYERMGAIPMEVQGISGVLFVLWAPHAQR
VSVVGD FNF WHGLVNPLRKISDQGIWELFVPGLGEGIRYKWEIVTQSGNVIVKTDPTYGKSFDPPPQGTARVA
DSESYSWSDHRWMERRSKQSEGPVTIYEVHLGSWQWQEGRPLSYSEMAHRLASYCKEMHYTHVELLPITEH
PLNESWGYQVTGYAPTSRYGTLQEFQYFVDYLHKENIGIILDWVPGHFPVDAFALASFDGEPLYEYTGHSQ
ALPHHWNTFTFDYSRHEVTN FLLGSALFWLDKMHIDGLRVDAVASMLYRDYGREDEGWTPNIYGGKENLE
SIEFLKHLNSVIHKEFSGLTFAEESTAFPGVTKDVDQGGGLGFDYKWNLGWMHDTFH YFMKDPMYRKYHQ
KDLTFS LWYAFQESFILPLSHDEVVHGKGS LVNKLPGDTWTRFAQMRVLLSYQICLPGKKLLFMGGEFGQY
GEWSPDRPLDWELLNHHYHKTLRNCVSALNALYIHQPYLWMQESSQECFHWVDFHDIENNVIAYYRFAGS
NRSSALLCVHHFSASTFPSYVLRCEGVKHCELLLNTDDESFGGSGKGNRAPVVCQDQGVAVGLDIELPPLAT
VIYLVTF

>core/81/5/Org5_Gene633

MIAPFFSFPALSGSFSSIQAEIEITQQVNHPGAELLSEGSYIPGLQTFRLGIKITASKGSHIYWKNPGEIGSPLKISW
QLPKGFVVEEEHWPTPKVFEEEGTTFFGYEDSALIVADVRAPEGYTPGQEV ELRAQVEWLACGDSCLPGNV
DLKLTLPYEEKEPSLYPDTHAEFTKTLHAQPRVLENDHSVQVAQGKGNEIILNISKKINATKAWFVSEKADKL
FAYAETSYSGGTGTAWRLKVKNLSGVQKNEKLHGILLADHTGRPVESLTIHSEVLGQTGSAVAGLSQYITIL

IMAFLGGVLLNIMPCVLPVTLKVYGLIKSAGEHRSSVIANGLWFTLGVVGCFWGLAGVAFILKVLGHNIGW
GFQLQEPMFVATLIIVFFLFALSSLGLFEMGTMFANLGGKLQSSEMKSSNNKAVGAFFNGILATLVTTTPCTGP
FLGSVLGLVMSLSFLQQLLIFTAIGLGMASPYLVFSVFPKMLSVLPKPGGWMSTFKQLTGFMLLVTVTWLWV
IFGSETSTTSVVVLLGGLWLAGLGAWILGRWGTPVSPKKQRCASLLFFAFLGGAISVSGLASHYFAEPQQT
SVNEDSLWQPFSLKLAQLRAQGRPVFVNFTAKWCLTCQMKNKPVLYGDAVQKMFETHGIVTLEADWTRKD
PGITEELARLGRASVPSYVYYPGDNSAPVVLPEKITQNLLEDVVSFRVR

>core/82/5/Org5_Gene220

MIRSPLPFISSKRALNMLGLQDEFSCPEDVVDLFLFSEIELLAQQDEPSEGYLALSRSLLMMTHNHPKVVKRVIF
YGVSYGLKHKSMSIFIDVLTYIDFLFEKLGISASDRLSLCSARTCINFELYSQTGEMKFLSEVVDNFRLLIEQLLK
MHPQLKNRLGWEHFRIGAKQEEVSLVASASVYQAVGRSFIELYHKHLELSDLACGMKCLALALDLSNNAH
IHADYAKGLVVLGTRQGKSLIERGMEHFSKAIFLSFSRDGDTLAYQNYRYSYALASVKLFDLTYKKEHFDQ
AMNILYQTVQAFPNLSGLWMVWGELLIRSGWLNSNMKYIEVGLEKLASLQKKTNDPIALSGLLATGIAILGL
YLEEPNLFKDSRHRLISAMRTFPGNSALVHALGVVQLCSALYFNEDSHFASAISCFQSCLEWDLDATGMWQK
LFDAYFSWGIKKKSARLLRKAVDVASRLCSLRPEAFLFWSDRGLALKCLAEATIDEAYKEIFLSESLHYQRA
WDLGRLEILELWGQSHYLLAELQQSLFHYDEAYTLLTKVDLTLSSSRVKLILAAVLLGKGRLQDTPAEE
AREILEPLVEVYLEDENFLLLLGKVYLFLFWKNKNVCLGKLARTYLEKATSLGCPEAYYTLGKFYAVIKDVN
KAWGMVIRSAQYGVRITEAKWLNDPYLANLREIHAFREVVENQKGRLWLGNKTEMKRN

>core/83/5/Org5_Gene249

MNKLLNFVSRTLGGDTALNMINKSSDLILALWMMGVVLMIIPLPPPVDLMITINLSISVFLLMVALYIPSAQ
LSVFPSLLLITTMFRLGINISSSRQILLKAYAGHVIQAFGDFVVGNGYVVGFIIFLIITIIQFIVVTKGAERVAEVA
ARFRLDAMPQKQMAIDADLRAGMIDATQARDKRAQIQKESELYGAMDGAMKFIKGDVIAGIVISLINIVGGL
TIGVAMHGMDLAQAAHVYTLLSIGDGLVSQIPSLLIALTAGIVTTRVSSDKNTNLGKEISTQLVKEPRALLA
GAATLGVGFFKGFPLWSFSILALIFVALGILLTKKSAAGKKGGGSGASTTVGAAGDGAATVGDNPDDYSLT
LPVILELGKDLKLIQHKTSGQSFVDDMIPKMRQALYQDIGIRYPGIHVRTDPSLEGYDYMILLNEVPYVR
GKIPPHHVLTNEVEDNLSRYNLPFITYKNAAGLPSAWVSEDAKAILEKAAIKYWTPLEVILHLSYFFHKSSQE
FLGIQEVRSMEFMERSFPDLVKEVTRLIPLQKLTEIFKRLVQEQISIKDLRTILESLEWAQTEKDTVLLTEYVR
SSLKLYISFKFSQGQSAISVYLLDPEIEEMIRGAIKQTSAGSYLALDPDSVNLIKSMRNTITPTPAGGQPPVLLT
AIDVRRYVRKLIETFPDIAVISYQEILPEIRIQPLGRIQIF

>core/84/5/Org5_Gene464

MYKRCVLDKILKGIVAGSLILLYWSSDLLERDIKSIKGNVRDIQEDIREISRNVKQQQTSQAIPAAPGVMLAPK
LVRDEAFALLFGDPSYPNLLSLDPYKQQTLPPELLGTNFHHPHGILRTAHVGKPENLSPFNGFDYVVGFDYDL
LASPHVGKYEEFSPDLAVKIEEHLVEDGSGDKEFHILRPNVFWRPIDPKALPKHVQLDEVFQRPHPVTAHDI
KFFYDAVMNPYVATMRAVALRSCYEDVVSVSVENDLKLVRWKAHTVINEEGKEERKVLVSFAFSNTLSLQ
PLPRFVYQYFANGEKIHEDENIDTYRTNSIWAQNFTMHWANNYIVSCGAYYFAGMDDEKIVFSRNPFDYDPL
AALIDKRFVYFKESTDLSLQDFKTGKIDISYLPPNQRDNFYFSFMKSSAYNKQVAKGGAVRETVSADRAYTYI
GWNCFSLFFQSRQVRCAMNMAIDRERIEQCLDGQGYTISGPFASSSPSYNKQIEGWHYSPEEAARLLEEEGW
IDTDGDGIREKVIDGVIVPFRRLCYVKSVAHTIADYVATACKEIGIECSLLGLDMADLSQAFDEKNFDALL

MGWCLGIPPEDPRALWHSEGAMEKGSANVVG FHNEEADKIIDRLSYEYDLKERNRLYHRFH EIIHEEAPYAF
LFSRHCSLLYKDYVKNIFVPTHRTDLIPEAQDET VNVTMVWLEKKEDPCLSTS

>core/85/5/Org5_Gene27

MKELRHESYNRALHKL SHQWVRYFLYTFVSCSFIVAI FTFAWLKVLYVPEYKAGEISRISLTAPMDFSLSWSA
HKFYKRTAHISEAFGKVYHLTLSPG SLLSKEGNADENTDYWFKKAADFLSTNFVDSSTQKCLKDL CIYPPLL
GKEKKTLEININSNKG NVIAQCFCCHKIFLIQENCPQPCFDAIMDILKIANFEVAVDKEMSGCVKGELLGKR CI
EKITKGTPILEKYQRIDDRDAKILKQLRAQLLSVHTL FSCRSLWGAIFVLLILLWGYGALKALCP EMLKSPQ
RFMLYIAILTLSLLWCRGTEIFCAYWVS YLSYPPILPFTAVLLGYFLGLPIAGFSCTFLALLYTLGSDLWNNSW
FLSINLLCSWRILVSLHRVSRLSSVFWACMKLGGVAMGSLLMFRIFTNTISREALYADGIESFVYSLIT AISVVA
LIPVFEASFGASTNFSLLTYLSPENALLKRLFKEAPGT YQHSVLVGSLAEAAAQAIGADSLYCLVAAHYHDIG
KLINPGFFSENQKILQQSGHSLSPLECAKMIMRHIPEGVNLARQAGLPESFIQVIEEHHGTSVIRSAYYSHMVE
NPSTGSFDEELFRYSGNKPSSKETTIIMIADSFEAAS RSLKNASLPDLQRLIDQIIQGKLQDGQFSCSPITLDELA
LISKSMVQTLYGALHSRMKYPEISYQISMDSCPKPSIGGT

>core/86/5/Org5_Gene859

MPEPLYTNKLITEKSPYLLLYAHTPVN WYPWGAEAFHIAAIENKPVFLSIGCKHSRWCQV MLQESYTNPEIAA
MLNEYFVN VKVDKEELPYVAKLYGD LAQMLAVSGDHQETVSWPLNVFLTPDLVPFFSVNYLGN EGKLGLP
SFPQIIDKLHFMWEDAEEREALVEQAMKVLEIASFLEGCVRKEILDESSLKRTVAALYQDIDPHYGGVKA FPK
RLPGLLLQFFLRYSLEYQESRGLFFVDRSL SMVALGGVRDHIGGGVYSYTIDDKWLIPAF EKRLIDNALMALN
YLEAWACLGKEEYRGIGKQILSYILSELYSPEVGAFYSSEQAENWGAGGQNFYTWSVEEISNALGEDAEIFCD
YYGISREGFFNGRNILHIPVHREIEELSEKYHRSIEAIEDIVDRSRDILKGIR AQRSRSHRSKDDL SLTFNNGWMIYT
FAYAGRLLGEVEYIEIGKKCGEFVRNSLYKHHEL YRRWREGEAKYRASLEDYGALILGVLALYESGCGSFWL
SFAEELMQEVLVLSFRSEEGGFYSVDGRDSTLLIKQSPLSDGETISGNALICQCLLSLHLITEKKHYLT YAEDILQ
IAQACAHTHKFSSLGLLIASQNYFSRKHV KVLIALGDQEDRSPVLKCLSGLFLPYLSLIWMTQENQE HLETVL
PEYEHCLIPKGDCTATTIYVLEVDQCKR FKDLLELFRRYLISL

>core/88/5/Org5_Gene9

MKRCFLFLASFVLMGSSADAL THQEAVKKKNSYLSHFKSVSGIVTIEDGV LNIHNNLRIQANKVYVENTVGQ
SLKLVAHG NVMVNYRAKTLVCDYLEYYEDTDSCLLTNGRFAMYPWFLGGSMITLTPETIVIRKGYISTSEGP
KKDLCLSGDYLEYSSDSLLSIGKTTLRVCRIPILFLP PFSIMPMEIPKPPINFRGGTGGFLG SYLGMSYSPISRKH F
SSTFFLDSFFKHGVMGFNLHCSQKQVPENVFNMKSYYA HRLAIDMAEAHDYRLHGDFCFTHKHVNFSGE
YHLSDSWETVADIFPNNFMLKNTGPTRVDCTWNDNYFEGYLTSSVKVNSFQNaNQELPYLT LRQYPISIYNT
GVYLENIVECGYLNFAFS DHIVGENFSSLRLAARPKLHKTVPLPIGTLSSTLGSSLIYYSDVPEISSRHSQLSAKL
QLDYRFL LHKSYYIQRRIIEPFVTFITETRPLAKNEDHYIFSIQDAFHSLNLLKAGIDTSVL SKTNPRFPRIHAKL
WTTHILSNTESKPTFPKTACELSLPFGKKNTVSLDAEWIWK KHCWDHNMNIRWEWIGNDNVAMTLES LHRSK
YSLIKCDRENFILDVSRPIDQLLDSPLSDHRNLILGKL FVRPHPCWNYRLSLRYGWHRQDTPNYLEYQMILGT
KIFEHWQLYGVYERREADSRFFFFLKLDPKKPPF

>core/89/5/Org5_Gene810

MNFQTISINLTEGKILVFETGKIARQANGAVLVRSGETCVFASACAVDLDDKVDFLPLRVQDYQEKFSSTGKTL
GGFIKREGRPSEKEILVSRLIDRSLRPSFPYRLMQDVQVLSYVWSYDGQVLPDPLAICAASAALAISDIPQSNIV
AGVRIGCIDNQWVINPTKTELASSTLDLVLGATENAILMIEGHCDFFTEEQVLDAIEFGHKHIVTICKRLQLWQ
EEVGKSKNLSAVYPLPAEVLTAVKECAQDKFTELFNIKDKKVHAATAHEIEENILEKLQREDDDLFSSFNKA
ACKTLKSDTMRALIRDREIRADGRSLTTVRPITIETSYLPRTHGSCLFTRGETQTLAVCTLGSEAMAQRYEDLN
GEGLSKFYLYFFPPFSVGEVGRIGSPGRREIGHGKLAEKALSHALPDSATFPYTIRIESNITESNGSSSMASVC
GGCLALMDAGVPISSPIAGIAMGLILDDQGAILSDISGLEDHLGDMDFKIAGSGKGITAFQMDIKVEGITPAIM
KKALSQAKQGCNDILNIMNEALSAPKADLSQYAPRIETMQIKPTKIASVIGPGGKQIRQIIEETGVQIDVNDLG
VVSISASSASAINKAKEIIEGLVGEVEVGKTYRGRVTSVVAFGAFVEVLPGKEGLCHISECSRQRIENISDVVKE
GDIIDVKLLSINEKGQLKLSHKATLE

>core/90/5/Org5_Gene419

MSNQEFDLsAIRNIGIMAHIDAGKTTTTERILFYAGRTHKIGEVHEGGATMDWMAQEQRGITITSAAATTVFW
LGAKINIIDTPGHVDFTIEVERSLRVLDGAVAVFDAVSGVEPQSETVWRQADKYGVPRIAFVNKMDRMGAD
YFAAVESMKEKLGANAFVHCPIGSESQFVGMVDLISQKALYFLDDTLGAKWEEKEISED LKERCAELRANL
LEELATIDESNEAFMMKVLEDPDSITEDEIHQVMRKGVIENKINPVLCGTAFKNKGVQQLNVIVKWLPSPLD
RGNIRGINLKTQEISLEPRRDGPLAALAFKIMTDPYVGRITFIRIYSGTLKKGSAILNSTKDKKERISRLEMH
ANERTDRDEFTVGDIGACVGLKFSVTGDTLCDDNQEIVLERIEFPDPVIDMAIEPKSKGDREKLAQALSSLSEE
DPTFRVSTNEETGQTIISGMGELHLDILRDRMIREFKVEANVGKPVSYKETITVSGNSETKYVKQSGGRGQY
AHVCLEIEPNEPGKGNEVVSKIVGGVIPKEYIPAVIKGIEEGLNTGVLAGYGLVDVKVSIVFGSYHEVDSSEM
AFKICGSMAVKDACRKAKPVILEPIMKVAVITPEDHLGDVIGDLNRRRGKILGQESSRGMAQVNAEVLPLSEM
FGYTTSRLSLTSGRATSTMEDIAFAKVPQKIQEEIVKK

>core/92/5/Org5_Gene368

MYNLLHAHHDAASPDGRLVSHLKKLSPHIYEGEVLIENIPAYFLGFHLPQQCIQVNLKSSLAQLGVEAVLNHL
ELNKARKEARLHVLFMSQDPIATAMLELLEPGSFVCKLFAADDRRLVRSPCYLNRMFTHTDRTGSPLLRFGK
KLEHFITLEIINDRLVVFLPILPGTICYEETIYGFLPLMSKSLTRPHLKIRKFLPLYQMVTDRPPVPEDHKILLIKT
EPLHIRTVFARVVQDLLPQGLRHTAADILEPTTQESGDIYEFYGSTSEPIERIPLEFFTLEPYKEHSFFFYRDMLQ
ETLESPQEVFRVFESIPEGEDQAAMFISKGSSELLELSQDSWIIPRISPSDERHAREIQKHIEDQPCFPFLKAMET
DHITSQGVLFsRYFPSASLKGMFLSNYSRYYLQHIYFQIPSPTSGEFFSNRDRSFLLDLYFAGISVFWADLESKR
LLQYIKRRNKDVGMFVPKHQAEQFAQSYFIGIHGSLIAGDYDEFLRELLTGMHTLSQQFTIPEFPPQTPLAIL
TGGGSGAMELANRVATELSILSCGNLISLDTTNAIVEAKMSYAIPDLLERQADFHVDLAVFVIGGMGTDFEL
LLELISLKTGKKALVPVFLIGPVDYWKSKITALYNSNHAVGTIRGSEWVHNCLFCLSSAKAGIAIFRRYLNHTL
PIGPEHPVPEDGFVIV

>core/93/5/Org5_Gene805

MKRSRRNFEQALENLEKLKEISLATSNDsYLNNPARNQQRKQTGSSVMEMKEALKNVENYLLEISCVSKSHA
DKALKESDFLIAGVQNVFSFLENQEDLYKSLLDEYSEVTKAYDEVKKNLKEVPTYDLSTDEETEEHKEPECFL
NNLVEVKRDRSYELFYMLDEQDKRFYNDALVQIIYKQNKLHETVNEGDPLTKTLLWNSEEVKNIASSLVIVN
DMPLRLFYQRALSHLDIEAVVKVHNAMALFFSRYEATMVFKSPKKHNIWYFNDFLLFLREAWKDLNNVI
DSQERKQTKLLASALSIGIFESKLVFEEASRYLYFNIQTKLENANGKKPLSPGQYLTDAYEELHRLISKYPNGP

LFKAMDRVLEHESRPYDPMILGILPSLEGTLKLHGKSIDIIRSPSPVTQSSILYANCNEEFLGFLNAKAHRSEVT
LVLNIQNRISRKERARSRVIEEALQEEHAPYVHAFSFPEPEELLQNLESIHGDIETFADFFSILQEEFHKPLLAS
SFFLTKEKKEFVGSFLKEKLTALKDIFFAKKKILFRNDKLLLLHLLSYLIVFKLIERTNPNSIVVVS KDGLDYVS
VFIAGFAFFSREAFWDEHSLKLLL TNVLSPTLVARDRLVFVSHIELLSK FVNCLKKNRQGFSSLSKSF KDDIEG
WEFTGYLHEL TEVSHKHNL

>core/94/5/Org5_Gene641

MQPCLNMSIVRNSALPLPCLSRSETFKKVRSHMKFMKVLTWPWIYRKDLWVTAFLLLTAIPGSFAHTLVDIAGEP
RHAAQATGVSGDGKIVIGMKVPDDPFAITVGFQYIDGHLQPLEAVRPQCSVYPNGITPDGTVIVGTNYAIGM
GSVAVKWVNGKVSELPMPLDTLDSVASAVSADGRVIGGNRNINLGASVAVKWEDDVITQLPSLPDAMNAC
VNGISSDGSIIVGTMV DVSWRNTAVQWIGDQLSVIGTLGGTTSVASAISTDGT VIVGGSENADSQTHAYAYK
NGVMSDIGTLGGFYSLAHAVSSDGSVIVGVSTNSEHRYHAFQYADGQMVDLGT LGGPESYAQGVSGDGKVI
VGRAQVPSGDWHAFLCPFQAPSPAPVHGGSTVVT SQNPRGMVDINATYSS LKNSQQQLQRLLIQHSAKVESV
SSGAPSFTSVKGAISKQSPAVQNDVQKGTFLSYRSQVHGNVQNQQLLTGAFMDWKLASAPKCGFKVALHY
GSQDALVERAALPYTEQGLGSSVLSGFGGQVQGRYDFNLGETVVLQPFMGIQVLHLSREGYSEKNVRFPVSY
DSVAYSAA TSFMGAHV FASLSPKMSTAATLGVERDLNSHIDEFKGSVSAMGNFVLENSTVSVLRPFASLAMY
YDVRQQQLVTL SVVMNQPLTGTL SLVSQSSYNLSF

>core/95/5/Org5_Gene20

MGVVQNQVISSIRDVLKLVWELRFAEHKMLLLSRQSGSGGTFQLSCAGHEL AGVLAGKSLIPGKDWSFPYY
RDQGFPIGLGCDLSEIFASFLARTTPNHSSARMMPYHYSHKKLRICCCSSVVG TQFLQAAGRAWAVKHSSAD
EVVYVSGGDGATSQGEFHEMLNFVALHQLPLITVIQNNHWAISVPFEDQCGADLASLGRCHQGLAVYEVDG
GNYTSLTETFSHAVDQARQHSVPALILIDVVRLSSHNSNDNQEKYRSALDLKLSMDKDP LILLEKEAINVFGLS
PFEIEEIKAEAQEEVRKSCEIAEALPFPSKGST SHEVFSPYTETLIDYENSESAQNLRNSEPKVMRDAISEALVEE
MTRDSGVIVFGEDVAGDKGGVFGVTRNLTEKFGPQRCFNSPLAEATIIGTAIGMALDGIHKPVVEIQFADYIW
PGINQLFSEASSIYYRSAGEWEVPLVIRAPSGGYIQGGPYHSQSIEGFLAHCPGIKVAYPSNAADAKALLKAAI
RDPNPVVFLEHKALYQRRIFSACPVFSHDYVLPFGKAAIVHPGKDLTIVSWG MPLVLSLEVAQELASRGISIEV
IDLRTMVPCDFATVLKSLEKTGRLLVIHEASEFCGFGSELVATMSEQGYAYLDAPIRRLGGLHAPVPYSKVLE
NEVLPHKESILQAAKSLAEF

>core/96/5/Org5_Gene380

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GASPALQMLEFIGHITNAKADFQAIQAEYNLAE EFPPEVIEEASLFSQKHITQVLHSRKDLRDL LCFIDSSTAR
DFDDAISLT YDHNNNYILGVHIADVSHYVTPHSHLDKEAAKRCNSTYFPGKVIPMLPSALSDNLCSLKPNVDR
LAVSVFMTFTKSGHLSDYQIFRSVIRSKYRMTYDEVDNIEKKHSHPLSKILNEMATLSKKFSDIREERG CIRFV
LPSVTMSLDNLQEPVALIENHQTFSHKLIEEFMLKANEVVAYHISHQGVSLPFRSHEPPNDENLLAFQELAKN
MGFDITFTPTQEPDYQYLLQTTSAGHPLEQVLHSQFVRSMKTASYSTENKGHYGLKLDYYTHFTSPIRRYIDL
IVHRLLFNPLSIDQTHLEIIVRACSTKERVSAKAENSFENLKKTRFINKFLQE QPKTTYHAYIITANHEGLSFVV
TEFCHEGFIAAAELPKEYSLKKNALPESIPDKMKPGASIKVTIDSVNLLTQKIVWSIATT TEDKPKKIKKTPSKK
KGTKKRAS

>core/98/5/Org5_Gene1003

MINKELDIGILGKIAGAIKQISIESIQKASSGHPGLPLGCAELAAAYLYGYVLRQNPRDPHWINRDRFVLSAGHG
SXLLYSCLHLAGFDVSLEDLQEFRQLHSRTPGHPEYGETVGV EATTGPLGQGLGNAVGMALSMKMLESRFN
RPGHEIFNGKIYCLAGDGCMEGVSHEVCSFAGSLNLNLLVVIYDYNVVLVDGYLNEISVEDTKKRFEAYG
WDVYEIDGYDFTHIHETFSSIKRGQERPVLVIAHTIIGHGSPKEGTNKAHGSPLGVEGTHETKQFWHLPEEKFF
VPPAVKNFFAHKIQEDRKAQEQLWDEV RVWSKQFPELHEEFVALTSHKLPKNLESLVQSVEMPD SIAGRAAS
NKLIQVLVQHIPPYLIGGSADLSSSDGTWIANEKVIHTYDFSGRNIKYGVREFGMATIMNGLAYSQVFRPFGGT
FLVFS DYMRNAIRLAALSKLPVIYQFTHDSIFVGEDGPTHQPVEQLMSLRAIPGLYVIRPADANEVRGAWIAG
LKHTGPTVIVLSRQALPTLPAAHRPFKDG VGRGAYIVLKESGEKPDYTLFATGSEVSLALSVAKELEHLDKQV
RVVSFPCWELFEAQDVDYKQSIVGGDLGIRVSIEAGSALGWYKYIGSEGLAIAMDRFGYSGASDDVSEECGF
TTEQILQRILSQ

>core/99/5/Org5_Gene298

MEKVSSYPSVPLPLGASKISPNRYRFALYASQATEVILALTDENSEVIEVPLYPDTHRTGAIWHIEIEGISDQSS
YAFRVHGPKKHGMQYSFKEYLADPYAKNIHSPQSFGSRKKQGDYAFCYLKEEPFPWDGDQPLHLPKEEMIIY
EMHVRSTQSSSRVHAPGTFLGII EKIDHLHKLGINAVELLPIFEFDETAHPFRNSKFPYLCNYWGYAPLNFFS
PCRRYAYASDPCAPSREFKTLVKTLHQEGIEVILDVVFNHTGLQGTTCSLPWIDTPSYIILDAQGHFTNYS GC
GNTLNTNRAPTTQWILDILRYWVEEMHVDGFRFDLASVFSRGPSPQLQFAPVLEAISFDPLLASTKIIAEPWD
AGGLYQVG YFPTLSRWSEWNGPYRDNVKAFLNGDQNLIGTFASRISGSQDIYPHGSPTNSINYVSCHDGFTL
CDTVTYNHKHNEANGEDNRDGT DANYSYNFGTEGKTEDPGILEVRERQLRNFFLTLMVSQGIPMIQSGDEY
AHTAEGNNNRWALDSNANYFLWDQLTAKPTLMHF LCDLIAFRKKYKTLFNRGFLSNKEISWVDAMGNPMT
WRPGNFLAFKIKSPKAHVYVAFHVGAQDQLATLPKASSNFLPYQIVAESQQGFVPQNVATPTVSLQPHTTLIA
ISHAKEVT

>core/100/5/Org5_Gene106

MKEENSQAHYLALCRELEDHDYSYYVLHRPRISDY EYDMKLRKLL EIERSHP EWKVLWSPSTR LGDRPSGTF
SVVSHKEPMLS IANSYSKEELSEFFSRVEKSLGTSPRYTVELKIDGIAVAIRYEDRVLVQALSRGNGKQGEDIT
SNIRTIRSLPLRPEDAPEFIEVRGEVFFSYSTFQI NEKQQQLEKTIFANPRNAAGGTLKLLSPQEVAKRKLEISI
YNLIAPGDND SHYENLQRCLEWGFPVSGKPRLCSTPEEVISVLKTIETERASLPMEIDGAVIKVDSLASQ RVLG
ATGKH YRWALAYKYAPEEAETLLEDILVQVGRTGVLTPVAKLTPVLLSGSLVSRASLYNEDEIHRKDIRIGDT
VCVAKGGEVIPKVVRVCREKRPEGSEVWNMPEFCPVCHSHVVREEDRVSVRCVNPECVAGAIEKIRFFVGR
GALNIDHLGVKVITKLFELGLVHTCADL FQLTTEDLMQIPGIRERSARNILESIEQAKHVDLDRFLVALGIPLIG
IGVATVLAGHFETLDRVISATFEELLSLEGIG EKVAHAIAEYFSDSTHLNEIKKMQDLGVCISPYHKSGSTCFG
KAFVITGTLEGMSRLDAETAIRNCGGKVGSSVSKQTDYVVMGNNPGSKLEKARKLGVSILDQEAFTNLIHLE

>core/101/5/Org5_Gene965

MRLNIHKYLFIGNKADFFSASRELGVVEFISKKCFITTEQGH RFVECLKVFDHLEAEYSLEALEFVKDES VSV
EDIVSEVLTLNKEIKG LLETVKALRKEIVRVKPLGAFSSSEIAELSRKTGISLRFFYRTHKDNE DLEEDSPNVFY
LSTAYNFDYYLV LGVVDLPRDRYTEIEAPRSVNELQVDLANLQREIRNRSDRLCDLYAYRREVLRGLCN YDN
EQLRHQAKECCEDLFDGKVF AVAGWVIVDRIKELQSLCNRYQIYMERVVPDPDETIPTYLENKGVGXMGED

LVQIYDTPAYSDKDPSTWVFFAFVLFFSMIVNDAGYGLLFLMSSLLFSWKFRKMKFSKHLRMLKMTAILG
LGCICWGTTTTTSFFGMSFSKTSVFREYSMTHVLALKKAEYYLQMRPKAYKELTNEYPSLKAIRDPKAFLLAT
EIGSAGIESRYVVYDKFIDNLMELALFIGVVHLSLGMRLYLRYSYGIGWILFMVSAYLYVPIYLGTVSLIHY
LFHVPYELGGQIGYYGMFGGIGLAVVLAMIQRSWRGVEEISVIQVFSVDLSYLRIYALGLAGAMMGATFNQ
MGARLPMLLGSIVILLGHSVNIILSIMGGVIHGLRLNFIEWYHYHYSFDGGGRPLRPLRKIVCEDAEASGIHLDN
NSIV

>core/102/5/Org5_Gene379

MSEHKKSSKIIGIDLGTNSCVSVMEGGQAKVITSSEGTRTTSPSIVAFKGNEKLVGIPAKRQAVTNPEKTLGST
KRFIGRKYSEVASEIQTVPYTVTSGSKGDAVFEVDGKQYTPEEIGAQILMKMKETA EAYLGETVTEAVITVPA
YFNDSQRASTKDAGRIAGLDVKRIIPEPTAAALAYGIDKVGDKKIAVFDLGGGTDFDISILEIGDGVFEVLSTNG
DTLLGGDDFDEVIIKWMIEEFKKQEGIDLSKDNMALQRLKDAAEKAKIELSGVSSTEINQPFITMDAQGPKHL
ALTLTRAQFEKLAASLIERTKSPCIKALSDAKLSAKDIDDVLLVGGMSRMPAVQETVKELFGKEPNKGVNPD
EVVAIGAAIQGGVLGGEVKDVLLLDVIPLSLGIETLGGVMTTLVERNTTIPTQKKQIFSTAADNQPAVTIVVLQ
GERPMAKDNKEIGRFDLTDIPPAPRGHPQIEVSFDIDANGIFHVSAKDVASGKEQKIRIEASSGLQEDEIQRMV
RDAEINKEEDKKRREASDAKNEADSMIFRAEKAIKDYKEQIPETLVKEIEERIENVRNALKD DAPIEKIKEVTE
DLSKHMQKIGESMQSQSASAAASSAANAKGGPNINTEDLKKHSFSTKPPSNNGSSEDHIEEADVEIIDNDDK

>core/103/5/Org5_Gene919

MKLLLKAVLRHKNHLVILGCSLLAILGLTFSSQMEIFSLGMIAKTGPDAFLLFGRKESGKLVKVSELSQKDILE
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VVAIRVSRDLRQDYFKALQQLPMTFFHDHDIGNLSNRVMTDSASIALAVNSLMINYIQAPITFILTLGVCL SIS
WKFSILICVAFPIFILPIVVIARKIKNLAKRIQKSQDSFSSVLYDFLAGVMTVKVFRTEKFAFTKYCEHNNKISA
LEEKSAAYGLLPRPLLHTIASLFFAFVVVIGIYKFAIPPEELIVFCGLLYLIYDPIKKFGDENTSIMRGCAA AERF
YEVLNHPDLHSQKEREIEFLGLSNTITFENVSFQYQEDKHILKNLSFTLHKGEALGIVGPTGSGKTTLVKLLPR
LYEVSQGKILIDSLPITEYNKGSLRNHIACVLQNPFLFYDTVWNNLTCGKDMEEEAVLEALKRAYADEFILKL
PKG VHSVLEESGKNLSGGQQQLAIARALLKNASILILDEATSALDAISENYIKNIIGELKGQCTQHIAHKL TTL
EHVDRVLYIENGQKIAEGTKEELLQTCPEFLKMWELSGTKEYNRVFPDHLKLVANPTDMAITT

>core/104/5/Org5_Gene702

MFSRLFFTSFSAEVVNTFFESGMSEDTSPLLSKQNRKLSHNLPLKSAYLSLGTLYLIALLSFWLHAKNLSNLFVV
FTFFLAGTPALIKSLDNICQKVVNIDILMTSAAFGSIFIGGALEGALLVLFAISEALGQMVSGKAKSTLVSLKQ
LAPTTGWLVL EDGNLQKVAINKIEVGNILRIKSGEVVPLDGEILHGSSSINLMHLTGEKVPKSCHPGSIVPAGA
HNMEGSFDLRVLRGTSDSTIAHIINLVIQAQNSKPRLLQRLDKYSSVYALSIFAACGIALLVPLFTSIPLLG PQS
AFYRALAFLIAASPCALIIAIIPIAYLSAINACAKHGVLLKGGVILDRLVSCNSVVM DKTGTLT TTGELTCIGCDYF
GSKNETFFPSVLAL EQSSSHPIAEAIVSYLMEQKVSSLPADRYLTVPGEGVRGYFNEQEAFVGRVETGLGKVP
SEYLEDIEQKIYQAKQHGEICSLAYVGN SFALFYFRDIPRPQAKEIIQDLKDLGYPVSM LTGDHKVSAENTA EI
LGISEVFFDLTPEDKLAKIRELATQRQIMMVGDGIN DAPALAQATVGIAMGEAGSATAIEAADIVLLHDSLSS
LPWIIQKAKQTKKVVSQNLALALAILLVSWPASLGIIPLWLAVILHEGSTVIVGLNALRLLKS

>core/105/5/Org5_Gene644

MTFQLHAPFAPCGDQPEAIARLSAGVRNQVKSQVLLGTTGSGKTFTIANVVANVNLPTLVLAHNKTLAAQL
YQEFREFFPNNAVEYFISYYDYYQPEAYIARSDTYIEKSLLINDEIDKLRLSATRSILERRDTLIVSSVSCIYGIGS
PENYTSMALVLEVKEYPRNILTAQLVKMHYQASPIQRSASFRERGSVIDIFPAYESELALEFLNDTLTSIE
YSDPLTMIPKESVPSATLYPGSHYVPEAIREQAIRTIQEELEERMAFFDDRPIEKDRIFHRTTHDIEMIKEIGFCK
GIENYSRHFTGAPPGAPPTCLLDYFPEDFLLIIDESHQTLQPIRAMYRGDQSRKQSLVEYGFRLPSAFDNRPLT
YEEAQKYFRKVIYVSATPGDTEVQESSGHIVQQIIRPTGIPDPMPEIRPATGQVDDLLEEIRLRLSQKHEKILVIS
ITKKLAEDMAGFLSELEIPAAYLHSGIETAERTQILTDLRSGVIDVLIGVNLLREGLDLPEVSLVAILDADKEGF
LRSTSSLIQFCGRAARNINGKVIFYADQKTRSIEETLRETERRRQIQLDYNKEHNIVPKPIIKAIFANPILQTSKDS
ESPKESQRPLSKEDLEEQIKKYEALMQRAAKEFRFNEAAKYRDAMQACKEQLLYLF

>core/106/5/Org5_Gene452

MATPAQKSPTFQDPSFVRELGSNHPVFSPLTLEERGEMAIARVQQCGWNHTIVKVSLIILALLTILGGGLLVGL
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DPAVPQVVVDCEKRLGMLDRKLRREEEILYRSTAHLKDEERYEFLLLELMRSLVADRLEFNRRSYERFVQG
IMTVRSEEKEISRLQDLISLQQQTVQDLRSRIDDEQKRCWTALQRINQSQKDIQRAHDREASQRACEGTEM
DCAERQQLEKDLRRQLKSMQEWIEMRGTIHQEKAWRKQNAKLERLQEDLRLTGIAFDEQSLFYREYKEYY
LSQKLDMMQKILQEVNAEKSEKACLESVHDYEQLEQKDANLKKAAAVWEEELGKQQQEDYEQTQEIRRL
STFILEYQDSLREAEKVEKDFQELQQRYSRQEEKQVKEKILEESMNHFADLFEKAQKENMAYKKKLADLE
GAAAPTEIGEDDDWVLTDASLSQKKIRELVEENQELLKALAFKSNELTQLVADAVEAEKEISKLREHIEEQK
EGLRALDKMHAQAIKDCEAAQRKCCDLESLLSPVREDAGMRFELEVELQRLQEENAAQLRAEVERLEQEQQFQ
G

>core/107/5/Org5_Gene326

MSYRKSTLIVLGVFALYALLVLRYYKIQICEGDHWAEEALGQHEFCVRDPFRRGTFFANTTVRKGDKDLQ
QPFAVDITKFHLCADPLAIPCHRDEIIQGILQFIEGQTYDDLCLKDKKSRYCKLYPLLDVSVHDLRLSLWWK
GYATKHRLPTNALFFITDYQRSYPFGKLLGQVLHTLREIKDEKTGKAFTGGMEAYFNHILEGDVGERKLLRS
PLNRLDTNRVIKLPKDGSDIYLTINPVIQTIAEEELERGVLEAKAQGGRLILMNSQTGEILALAQYPFFDPTNYK
EYFNNKERIEHTKVSFVSDVFEPGSIMKPLTVAIALQANEEASLKSQKKIFDPEEPIDVTRTLFPGRKGSPLKDI
SRNSQLNMYMAIQKSSNVYVAQLADRIIQLSGVAWYQQKLLALGFGRKTGIELPSEASGLVPSPHRFHINGSL
EWSLSTPYSLAMGYNILATGIQMVQAYAILANGGYAVRPTLVKKIVSASGEEYHLPTKEKTRLFSEEITREV
RAMRFTTLPGSGFRASPKHHSSAGKTGTTEKMIHGKYDKRRHIASFIGFTPVESSEGNFPPLVMLVSIDDPEY
GLRADGTKNYMGGRCAAPIFSRVADRTLLYLILPDKKLRNCDEEAAALKRLYEEWNRSPKQGGTR

>core/108/5/Org5_Gene584

MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSVNALMSLAD
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ATDEETAIAAEWETKNADAVKVGAQITELAKYASDNQAILDSLGLKTSFDLLQAALLQSVANNNKAAELLK
EMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNABDAYFAGQNASGAVENAKSNNSISNIDSAKAAIAT
AKTQIAEAQKKFPDSPILQEAQMVIAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAE
NETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAACAAGDDSAALADAQKALEAALGKAGQQQ
GILNALGQIASAAVVSAGVPPAAASSIGSSVKQLYKTSKSTGSDYKTQISAGYDAYKSINDAYGRARNDATR

DVINNVSTPALTRSVPRARTEARGPEKTDQALARVISGNSRTLGDVYSQVSALQSVMQIIQSNPQANNEEIRQ
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>core/109/5/Org5_Gene424

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QWSKSLDEVKQRQRALLLSYLSHLAAGASSRYEGKEEQLAALCLRQIENHENVYLGINDHGVAMDRDEEA
YQFHIRVVKALAHSLDAHTAYFSKDEALAMRIQLEKGMCGIGVVLKEDIDGVVVREIIPGGPAAKSGDLQLG
DIIYRVDGKDIEHLSFRGVLDCLRGHGHSTVVLDIHRGESDHTIALRREKILLEDRRVDVSYEPYGDGVIGKVT
LHSFYEGENQVSSEQDLRRAIQGLKEKNLLGLVLDIRENTGGFLSQAIVSGLFMTNGVVVVSRYADGTMKC
YRTVSPKKFYDGPLAILVSKSSASAAEIVAQTLQDYGVALVVGDEQTYGKGTIQHQTITGDASQDDCFKVTV
GKYYSPPSGKSTQLQGKSDILIPSLYAEDRLGERFLEHPLPADCCDNVLHDPLTDLDTQTRPWFQKYYPNLQ
KQETLWREMLPQLTKNSEQRLSENSNFQAFLSQIKSSEKTDLSYGSNDLQLEESINILKDMILLQQCRK

>core/110/5/Org5_Gene862

MTSSSCPLLDLILSPADLKKLSSISQLPGLAEEIRYRIISVLSQTGGHLSSNLGIVELTIALHYVFSSPKDKFIFDVG
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AAFSCGLTLEALNNISTDLKSFVVILNDNMSISKNVGAMSRIFSRWLHHPATNKLTKQVEKWLAKIPRYGD
SLAKHSRRLSQCVKNLFCPTPLFEQFGLAYVGPIDGHNVKKLIPILQSVRNLPFVILVHVCTTKGKGLDQAQN
NPAKYHGVVRANFNKRESAKHLPAIKPKPSFPDIFGQTLCELGEVSSRLHVVTAMSIGSRLEGFKQKFPERFFD
VGIAEGHAVTFSAGIAKAGNPVICSIIYSTFLHRAIDNVFHDVCMQDLPVIFAIDRAGLAYGDGRSHHGIYDMS
FLRAMPQMIICQPRSQVVVFQQLLYSSLHWSSPSAIRYPNIPAPHGDPLTGDPNFLRSPGNAETLSQGEDVLIIL
GTLCFTALSIKHQLLAYGISATVVDPIFIKPFNDLFSLLLMSHSKVITIEEHSIRGGLASEFNNFVATFNFKVDI
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>core/111/5/Org5_Gene622

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NRLLPEDLDPNDYIDPVVSIYQEYQKKLIEANALDFDILLFTVRLLRESPEAQELYNQLWKALLIDEYQDT
NHAQYITLMQLLSKQHRNVFAVGDPDQSIYSWRGANIHNLNFENDYPNAKVLCEENYRSYGNILNAANALI
KNNASRLEKELRSVKGPGEKIRLFLGSTDREEADFVAAEILQLHRVGNIKLRDICIFYRTNSQSRTFEDALLRR
RIPYEIIGGLSFYKRKEIQDILAFLRIFISKSDIVAFDRTVNLPKRGIGSTTIFALTQYAIAQGLPILKACQQALDT
KDVKLSKKQQEGLQEYLALFPQIEHAYNTLSLRDFIESVVRITGYLEILKEDADTFKDRKSNLEELYHKALESE
QQNPKTHLELFLDDLALKGSDDDLNLTA DRVNLMTLHNGKGLEFRVSFLVGLLEEQLLPHANS LGGTyenIEE
ERRLCYVGITRAQDLLYLTAQVRSLWGTVRMMKPSRFLKEIPKDYMIQVR

>core/112/5/Org5_Gene75

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GGLVVFTVGDLPIDADTKYFGLIPGKKRYIKRCMGRPGDFLYFYGGKIYGLDDAGKRIEFPSVHGLENLYH
VPYISFDGTTSSHTEGQKTIIDFKQFNQSYGRLIFPQTSMYGQFFDHKEWHQDEPNKLDPHLSPVSYADLFG

MGNYAMVRILTEHQARTSHLLPNPGSPTKVYLEICHTANLSYPKPLLRHYEHQLSPAIQPMKTLLPLRKEHLH
LIRNNLTTSRFIVAQQCAYKYHQFKINTSGIAKAYAILLPKVPDGCYEYSKGEAYQIGFGEIRYKLKSSHPLTQ
LNDKQVIELFNCGINFSSIYNPVNPLQAPLPNRYAFFNQGNLYIMDSPVFIKNDPTLQKFVTSETEKQEGSSET
QPYIAFVDKGLPPEDFKEFVEFIHNFQVPGKHVVLVLDNYPMSADSREFGFVPMENLLGSPLCTFWPIGRM
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>core/113/5/Org5_Gene639

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LDLDAGIPETPNVLLSNEMQKVFGGIYNEISLIKVPNGDKIVVASSIPEHLGENYNHKIDIPKNTPFLAALKQS
PKNQEVFSVMQANVDAKTQELQGILYTTFSAESLLKDLLINKQSYLTVKTAILSKYGVILKASDPALHLHTV
YPMTEKEKFCQVFLNDDPCPIDSELGPLTSLPDIGENFYSFKIKDTEIWGCIENVPSIDIAVLSYAKKEESFAPL
WRRARMYTAYFFCILLGSLIAFIVARRLSLPIRKLATAMIESRKNKNCLYTDDSLGFEINRLGHIFNAMVENLH
KQQHLAKTNFEMKENAQNALHLGEQAQQRLLPNTLPSYPHIELAKAYIPAITVGGDFFDVVFVGEESKARLF
LIVADASGKGVNACGYSLFLKNMLRFTLSRSSSLQQAQIETSRLFYNNTKNSGMFVTLVCVYCYHQTSTNTMEY
YSCGHPPACYLDPDGETSWLFHPGMALGFLPEVANITSKLHFKPGSLFVLYSDGITEAHNNNNNDMFGEERL
QAAIQGLTGKSAADAVHRLMLSVKTFVGNSHQHDDITLLILKVLES

>core/114/5/Org5_Gene649

MIQVTCQKNYEVLEGTTAAELAKQLKNSHQFIGVLINERPRDLSTHLNEGDTLVFLTSEDPEGREIFLHTSA
HLLAQAVLRLWPDIAIPTIGPVIDHGFYYDFANLSISESDFPLIEDTVKQIVDEKLAISRFTYGDKQQALAQFPQ
NPFKTELIRELPENEEISAYSQGEFFDLCRGPHLPSTAHVKAFAKVLRTSAAYWRGDPSRESLVRIYGTSFPTSKE
LRAHLEQIEEAKKRDHRVLGAKLDLFSQQESSPGMPFFHPRGMIVWDALIRYWKQLHTAAGYKEILTPQLM
NRQLWEVSGHWDNYKANMYTLQIDDEDYAIKPMNCPGCMLYYKTRLHSYKEFPLRVAEVGHVHRQEASG
ALSGLMRVRAFHQDDAHVFLTPEQVEEETLNILQLVSTLYGTFGLEYHLELSTRPEKDTIGDDSLWELATDAL
NRALVQSGTPFIVRPGEGAFYGPKIDIHVKDAIQRTWQCGTIQLDMFLPERFELEYTTAQGTKSVPVMLHRAL
FGSIERFLGILIENFKGRFPLWLSPEQVRIITVADRHIPRAKELEEAWKRLGLVVTLDDSESVSCKIRNAQNM
QVNYMITLGDHEINENVLAVRTRDNRVINDVSVERFLNTILEEKNSLSLTALL

>core/117/5/Org5_Gene636

MDENRKVIVVGGGLAGLSAAMQLANLGIIVELVSLTKVKRSHSVCAQGGINAALNLKPEEEDSPYVHAYDTI
KGGDFLADQPPVLEMCLAAPRIIKMLDNFGCPFNRGPSGNLDVRRFGGTLYHRTVFCGASTGQQLMYTLDE
QVRRREHAGRVIKRENHEFVRLVTDHSGRACGIILMNLFNRLLEILRGDAVIIATGGPGVIFKMSTNSTFCTGA
ANGRLFLQGMAYANPEFIQHPTAIPGRDKLRLISESVRGEGGRVWVPGDSSKRIVFPDGSERPCGETGAPWY
FLEDMPAYGNLVSRDVGARAILRVCEAGLGIDGRMEAYLDVTHLPEKTRHKLEVLDIYKKFTGEDPNTV
PMRIFPAVHYSMGGAWVDWPAADDPDRDSRFRQMTNIPGCFNCGESDFQYHGANRLGANSLLSCLFAGLVS
GDEASRFIEAFGASQATSSDFDRALQQEKEENARLLSASGKENIFVLHEEIAKIMVRNVTVKRNNRDLQETM
DKLKEFRERLKNVSVLDSSPFANKSFHFVRQMGPMLELALAITKGALLRNEFRGSHYKPEFPERDDEHWLKT
TVAVYAPEEPEISYLPVDTRHVAPTTLRDYTKSSTGKIELTNIPDNIRLPI

>core/118/5/Org5_Gene928

MTIIYFILAALALGILVLIHELGHLLVAKAVGMAMESFSIGFGPALFKKRIGGIEYRIGCIPFGGYVRIRGMERT
KEKGEKGKIDSVYDIPQGFFSKSPWKRLVLVAGPLANILLAVLAFSILYMNGGRSKNYSDCSKVVGWVHPV
LQAEGLLPGDEILTCNGKPYVGDKDMLTTSLLEGHLNLEIKRPGYLTVPKSKEFAIDVEFDPTKFGVPCSGASY
LLYGNQVPLTKNSPMENSELRPNDRFVWMDGTLLFSMAQISQILNESYAFVKVARNDKIFFSRQPRVLASVL
HYTPYLRNELIDTQYEAGLKGWSSLYTLVPYVINSYGYIEGELTAIDPESPLPQPQERLQLGDRILAIDGTPVSG
SVDILRLVQNHRSIIVQQMSPQELEEVSNSRDADKRFIASYHSEDLLQILNHLGESHPVEVAGPYRLLDPVQPR
PWIDVYSSES LDKQLEVAKKIKNKDKQRYYLRLDAEKQKPSLGISLKD LKVRYNPSPVVMLSNITKESLITL
KALVTGHLSPQWLSGPVGIVQVLHTGWSVGFSEVLFWIGLISMNLAVLNLLPIPVLDGGYILLCLWEIVTRRR
LNMKIVERILVPFTFLLIFFIFLTFQDLFRFFG

>core/119/5/Org5_Gene388

MRRSVCYVNP SIARAGQISTWKFLYSLATPLPAGTKCKFDLAGSGKPTDWEAPATDLSQTRNVIYAEMPEGE
IIEATAIPVKDNPVPQFEFTLPYELQVGETLTIVMGASPNHPQVDDAGNGAQLFAQRRKPFYLYIDPTGEGNY
DEPDVFSMDIRGNVLKKIEIFTPSYVVKNKRFDITVRFEDEFGNLTNFSPEETRIELSYEHLRENLNWQLFIPET
GFVILPNLYFNEPGIYRIQLKNLSTQEIFISAPIKCFADSAPNLMWGLLHGESERVDSEENIETCMRYFRDDRAL
NFYASSSFENQENLSPDIWKLINQTVSDFNEEDRFITLSGFQYSGEPHLEGVRHILHTKETKSHSKHKEYKHIPL
AKLYKSTVNHD MISIPSFTASKEHGDFDFENFYPEFERVVEIYNAWGSSETTAALNNPFPIQGKDESDPRGTVIE
GLKKNLRF GFVAGGLDDRGIYKDYFDSPQVQYSPGLTAIICNKYTRESLVEALFARHCYATTGPRIVLSFNITS
APMGSELSTGSKPGLNVNRHISGHVAGTALLKTVEIIRNGEVLHTFFPDSNNLDYEYDDMVPLSSVTLKDPNG
KAPFVFYYLRVTQADNAMA WSSPIWVDLN

>core/120/5/Org5_Gene955

MESEKDIGAKFLGDYRILYRK GQSLWSEDLLAEHRFIKKRYLIRLLL PDLGSSQPFMEAFHDVVVKLAKLNHP
GILSIENVSESEGR CFLVTQE QDIPILSLTQYLKSIPRKLTELEIVDIVSQLASLLDYVHSEGLAQEEWNLD SVYI
HILNGVPKVILPDLGFASLIKERILDGFISDEENRESKIKERVLLHTSEGKQGREDTYAFGAITYYLLFGFLPQGI
FPMPSKVFSDFIYDWD FLISSCLSCFMEERAKELFPLIRKKTLGEELQNVVTNCIESSLREVDPLESSQNLPQA
VLKVGETKASHQQKESA EHLEFVLVEACSIDEAMDTAIESESSSGVEEEGYSLALQSLLVREP VVSRYVEAEK
EEP KPQPILTEMVLIEGGEFSRGSVEGQRDEL PVHKVILHSFFLDVHPVTNEQFIRYLECCGSEQDKYYNELIRL
RDSRIQRRSGRLVIEPGYAKHPVVGVTWYGASGYAEWIGKRLPTEAEWEIAASGGVAALRYPCGEEIEKSRA
NFFTADTTTVM SYPPNPYGLYDMAGNVYEWCQDWYGYDFYEISAQEPESPQGP AQGVYRVLRGGCWKSLK
DDLRC AHRHRNNPGAVNSTYGFRC AKNIN

>core/121/5/Org5_Gene989

MKKGKLGAIVFGLLFTSSVAGFSKDLTKDNAYQDLNVIEHLISLKYAPLPWKELLFGWDLSQQTQQARLQLV
LEEKPTTNYCQKVLSNYVRS LNDYHAGITFYRTESAYIPYVLKLSEDGHVFVVDVQTSQGDIYLGDEILEVDG
MGIREAIESLRFGRSATDYSA AVRSLTSRSAAFGDAVPSGIAM LKLRRPSGLIRSTPVRWRYTPEHIGDFSLV
APLIPEHKPQLPTQSCV LFRSGVNSQSSSSSLFSSYMVPYFWEELRVQNKQRFDSNHHIGSRNGFLPTFGPILW
EQDKGPYRSYIFKAKDSQGNPHRIGFLRISSYVWTDLEGLEEDHKDSPWELFGEIIDHLEKETDALIIDQTHNP
GGSVFYLYSLLSMLTDHPLDTPKHRMIFTQDEVSSALHWQDLLEDVFTDEQAVAVLGETMEGYCMDMHAV
ASLQNFQSQSVLSSWVSGDINLSKPMPLLGFAQVRPHPKHQYTKPLFMLIDEDDFSCGDLAPAILKDNGRATLI

GKPTAGAGGFVFQVTFPNRSGIKGLSLTGSLAVRKDGEFIENLGVAPHIDLGFTSRDLQTSRFTDYVEAVKTIV
LTSLENAKKSEEQTSPQETPEVIRVSYPTTTSAL

>core/122/5/Org5_Gene968

MFGTLVSTLCCPANSE RDWEDHEVN CIYIASTSDTQLEAVQGGMHITELRGEPVRVLYETGHLYAFARENTC
HSRLEVSH TVRAMTYFWDRFFSRHWNVGR RFLVFYQGN GGAYVQAALDSSMHTQDIYVLGLSPTVYIRGN
YHVQH YRVRGFWPSCLD SLAACAE NTSVLPYGESSDGIFYP SLFSHTFDNAIRYGERCLLVCSEGMGMLPET
QQQTSPLTSLEGGHEVALVLNPQQNPEALS IASRLMHEERGGRLESNYMPGRSSNPFMTSMYVLVRLNTLAQ
IYLMSPYY SFQSN DIVCLIFISSAAVETVSYIFLTVTDSTCGRRYLRVPRLVCTGLRNLALPTTLLELLILSYPRS
VEGV PFNVRFILGYMCTTRVVFFAWNLILHWPFRCLRHGIQLFVHRSIIGHTLGARITDLTLASMRYAIVFPSI
VSSCLLTALAHANTNILALDPYRLIESGDLRRPAFNDDDEMQQADNPWDAYSIGLVINTCIYMLILFANLIFMV
YSVRRYHRSRR

>core/123/5/Org5_Gene284

MTLITPAINSSRRKTH TVRIGNLYIGSDHSIKTQSM TTTLTDDIDSTVEQIYALAEHNCDIVRVTVQGIKEAQAC
EKIKERLIALGLNIPLVADIHFFPQAAMLVADFADKVRINPGNYIDKRNMFKGTKIYTEASYAQSLRLLEEKFA
PLVEKCKRLGKAMRIGVNHGSLSERIMQKYGDTIEGMVASAIEYIAVCEKLN YRDVVFSMKSSNP KIMVTAY
RQLAKDL DARGWLYPLHLGVTEAGMGVDGIIKSAVGIGITLLAEGLGDTIRCSLTGCPTTEIPVCDSLLRHTKI
YLDLPEKKNPFSLQHS ENFVSAAEKPAKTTLWGDVYGVFLKLYPHHLTDFTPEELLEHLGVNPVTKEKAFTT
PEGVVVPPELKDAPITDVLREHFLVFHHHQVPCLYEHNEEIWDSPAVHQAPFVHFHASDPFIHTSRDFFEKQG
HQGKPTKL VFSRDFDNKEEAAISIA TEFGALLDGLGEAVVLDLPNLPLQDVLKIAFGTLQNAGVRLVKTEYI
SCPMCGRTLFDLEEVTTRIRKRTQHLPGLKIAIMGCIVNGPGEMADADFGFVGSKTGMIDLYVKHTCVKAHIP
MEDAEELIRLLQEHGVWKDPEETKLT V

>core/124/5/Org5_Gene481

MWTHPIAYDVIVVGAGHAGCEAA YCSAKMGVSVLMLTSNLDTIAKLSCNPAVGGIGKGHIVREIDALGGIM
AEVTDQSGIQFRILNQTKGPAVRAPRAQVDKQLYHIHMKRLLENTPGLHIMQATVESLLDKEGVISGVTTKE
GWMFSGKTVVLSSGTFMRGLIHIGDRNFSGGRLGDPSSQGLSEDLKRGFPISR LKTGTPPRL LASSINFSCME
EQPGDLGVGFVHRTEPFQPPLPQLSCFITH TMEKTKAIISANLHRSALYGGCIEGVGP RYCPSIEDKIVKFSDKE
RHHVFLEPEGLHTQEIYANGLSTSM PFDVQYDMIRSVLGLENAIITR PAYAIEYDYIHGNVIHPTLESK LIEGLF
LCGQINGTTGYEEAAAQGLIAGINAVNKVFNRPPFIPSRQESYIGVMLDDLTTQILDEPYRMFTGRAEHRLLLLR
QDNACARLSHYGYELG LLSEERYELVKKQNQLLEEEKVRLQKTFRQYQSVVSLAKALSRPEVSYDMLREA
FPNDIRDLGAVLNASLEMEIKYSGYIDRQKILIQSLEKAESLLIPEDLDYKQITALSLEAQEKLAKFTPRTL GSA
SRISGIASADIQVLMIALKKHAHH

>core/125/5/Org5_Gene95

MTTELKTEALPTRTQVDPKHCWDTTLMYANREEWKKDFDL CSSGKDRSPIWPEFSPSHYQIDNPESLLELLS
KKFSVERKLDQLYIYAH LIHDQDITNPEGESDYQSIVLYTLFSQEISWIQPALIALSEEKVAALLSSSVLAPYR
FYLEKIFRLSPHTGTANEEKILASSFAALNVSNKAFSSLSDAEIPFGIAKDSNGEEHPLSHALASLYMQSPDQEL
RRTAYLAQFQRYDYRNTFANLLNGKVQAHLFEAKARNYPSCLEASLFQHNIPTTVYINLINETKKHTSLINR
YFNLKKEALNLKEFH FYDVYAPISQTT SKNYSYEEGVDLVCKSLLPLGTHYVEILRNGLLSNRWVD RYENKH

KRSGAYSSGICYDSAPYILLNYTNTLYDVS VIAHEAGHSMHSYFSREAQPYHDAQYPLFLAEIASTFNEMLLM
EALSKSDQSKEDKIVIITKTLDTIFATLFRQTFFAAFEYEIHSAAEQGTPLTEEFLSATYGNLQKEFYGGVVTSD
SLSALEWARIPHFYNFYVYQYATGIIAALSFAEKILTQEPGALELYLKFLKSGRSDFPLNILKKSGLDMTTSA
PLDKAFAFITKKIDLLSSLLSED

>core/126/5/Org5_Gene1023

MFRCILFGIFLLTCFSSGGVLYYLFCSHDFSIGPKEKSRSVWIEEEKEFTDSVLHHLPSQHHLHILCFQGFLQ
KQQKFSQAEEKIFSKVYDEAQDGPFLFKEEILGSR LINSFFLEKTDVMETILCLLNQRCPNSPYYHLFKALVCYK
QKLYREVIEQLAYWQEEKTRALAPLLNISIEQLLTDFLLDYISAHSLIEQKMFPEGRVILNRNINRLLKHECEW
NAKTYDRIAILLSRSYFLELVESKSADIYFDYYEMVLFYLLKKIYILEQCPYAELLPEEELVSLIMEHVFILPKDK
LYPLIQLLEMWQKHVHPNSSLVVQILVDRFSTHMEGAIRFCEALVSFSGLEELHQQIITTFEELLSNKVQQIK
TEEAKQCVALLHILDPSISISEKLALSSDTLQNI VSGDDEQHTKL RNYLDLWEAIQSYDIDRQQLVHHLVYGA
KDLWKKGGNDEKALNLLQLVLRFTSYDIECESV VFLFIKQAYKQALSSHA IARLLKLEKFISEANIPSIVISEAE
KANFLADAEYLF AHEDYDKCYLYSMWLT KVAPSPQSYRLAGLCLMENKRYDEALEFLCMLSPNNSINDYK
TQKAL AFCQKHQSKDRAAS

>core/127/5/Org5_Gene994

MCGIFGYLGNQDGV SIVLEGLAKLEYRGYDSAGLA AVVEQELFIRKTVGRVQELSNLFQEREIPTASVIGHTR
WATHGVPTEINAHPHVDEGRSCAVVHNGIIENFKELRRELTAQG ISFASDTDSEIIVQLFSLYYQESQDLVFSF
CQTLAQLRGSVACALIHKDHPTILCASQESPLILGLGKEETFIASDSRAFFKYTRHSQALASGEFAIVSQGKEP
EVYNLELKKIHKDVRQITCEDASDKSGYGY YMLKEIYDQPEVLEGLIQKHMDEEGHILSEFLSDVPIKSFKEI
TIVACGSSYHAGYLA KYIIESLV SIPVHIEVASEFRYRRPYIGKDTLGILISQSGETADTLAALKELRRRNIA YLL
GICNPESAIALGVDHCLFLEAGVEIGVATTKAFTS QLLLLVFLGLKLANVHGALTHAEQCSFGQGLQSLPDL
CQKLLANESLH SWAQPYSYEDKFLFLGRRLMYPV VMEAAKLKEIAYIEANAYPGGEMKHGP IALISKGTPV
IAFCGDDIVYEKMIGNMMEVKARHAHVIAIAPESREDIAAVSDQ QIFVPDCHFLAAPVLYTIVGQVMAYAMA
LAKGMEIDCPRNLAKSVTVE

>core/128/5/Org5_Gene783

MIPSGLVYLLYPLGFLASLFFGSAFSIQWWLSKKRKEVYAPRSFWILSSIGATLMIVHGTIQSQFPVTVLHVINL
IYLRNLNITSSRPISFRATLVLMALSVV FVTL PFLYVNMEWMASPNIFHLPLPPAQLSWHLIGCLGLAIFSGRF
LIQWFYIESNNTKDFPLLFWKIGLLGGLLALVYFIRIGDPINILCYGCGLFPSIANLRLFYKEQRSTPYLDTHCFL
SAGEASGDILGGKLIQSIKSLYPNIRFWGVGGPAMRQEG LQPILNMEEFQVSGFAEVLGSLFRLYRN YRKILKT
ILKHKPATLIFIDFPDFHLLLIKLRKHGYRGKIIHYVCPSIWAWRPKRKRILEQHLDMLLLILPFEEGLFKNTSL
ETVYLGHPLVEEISDYKEQASWKEKFLNSDRPIVA AAFP GSRRGDISRNLRIQVQAFLNSSL SQTHQFVSSSSA
KYDEIIEDTLKAEGCQHSQIIPMNF RYELMRSCDCALAKCGTIVLETALNQTPTIVMCRLRPFD TFLAKYIFKIL
LPAYSLPNIIMNSVIFPEFIGGKKDFHP EEIAT ALDLLNQHGSKEKQKEDCRKLCKVMTTGQIASEEFLKRIFDT
LPAV

>core/129/5/Org5_Gene638

MKHTFTKRVLFFF LVIPIPLLLNLMVVGFFSFSAAKANLVQVLHTRATNLSIEFEKKLTIHKLFLDRLANTLA
LKSYASPSAEPYAQAYNEMMALSN TDFSLCLIDPFDG SVRTKNPGDPFIRYLKQHP EMKKKLSAAVGKAFL

TIPGKPLLHYLILVEDVASWDSTTTSGLLVSFYPM SFLQKDLFQSLHITKGNICLVNKYGEVLFCAQDSESSFV
FSLDLPNLPQFQARSPSAIEIEKASGILGGENLITVSINKKRYLGLVLNKIPIQGTYTLSLVPVSDLIQSALKVPL
NICFFYVLAFLLMWWIFSKINTKLNKPLQELTFCMEAAWRGNHNVRFEPPYGYEFNELGNIFNCTLLLLLNS
IEKADIDYHSGEKLQKELGILSSLQSALLSPDFPTFPKVTFSQHLLRRRQLSGHFNGWTVQDGGDTLLGHIIGLA
GDIGLPSYLYALSARSLFLAYASSDVSLQKISKDTADSFSKTTEGNEAVVAMTFIKYVEKDRSLELLSLSEGAP
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HSADGTLTILSFS

>core/130/5/Org5_Gene764

MRIEDFSLKLIPSSPGVYLMKDVHDQVLYIGKAKNLKNRLASYFHEKGDSRERIPFLMKTASIETIVVSNETE
ALLENNLIKQHHPKYNVLLKDDKTFFCLAISLSHSWPKVEAIRTKAITSSQRQLIFGPYVSAEACHTLLEVISQ
WFPLRTCSDREFALRKRPCILYDMKRCLAPCVGYCTPEEYQGTLDKAILFLKGKIEEVVKDLEKVIQKASDNL
EFEQAANYRTLSLIKQAMAKQQVEKFHFQNIDALGLYRHKQRTILTLLTVRSGKLLGARHFSFFENAQEDQ
DLLSSFILQYYVSQPYIPKEILTLPLEFPTLSYVLNAESPRLRSPKTGYGKELLDLAYRNAKAYAATTLPSS
LPYQDFQNILRMSQYPYRIECYDNAHMQGAHATGVYIVFENNGFDPKQYRTFSIDSEKTQNDLALLEEVLLR
RFHSLTTALPDMIVVDGGKTHYNKTKKIIQTLNLTGIQVVTAIEKESNHSRGLNKEKIFCETFPPEGFSLPPTS
NLQFFQILRDEAHRFAISKHRKKRGKALFEQEKIPGIGEVKRKRLQKFKSWKQVMLSSQEELEAIPGLTKKDIA
VLLARQKDFNKSD

>core/131/5/Org5_Gene272

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YQLNLIDTPGHVDFSIEVSRSLSACEGALLIVDAAQGVQAQSLANVYLALERDLEIIPVLNKIDLPAADPVRIA
QQIEDYIGLDTTNIACSAKTGQIPAILKAIIDLVPKKAPAE TELKALVFDSHYDPYVGIMVYVRIISGELKKG
DRITFMAAKGSSFEVLGIGAFLPKATFIEGSLRPGQVGFFIANLKKVKDVKIGDVTTKTKHPAKTPLEGFKEIN
PVVFAGIYPIDSSDFDTLKDALGRLQLNDSALTIEQESSHSLGFGFRCGFLGLLHLEIIFERIIREFDLDIIATAPS
VIYKVVLKNGKVLDDIDNPSGYDPDPAIIEHVVEEPWVHVNIITPQEYLSNIMNLCCLKRGICVKTEMLDQHRLVL
AYELPLNEIVSDFNDKLKSVTKGYGSFDYRLGDYRKGSIIKLEVLNIEPIDAFSCLVHRDKAESRGRSICEKL
VDVIPQQLFKIPIQAANKKVIARETIRALSKNVTAKCYGGDITRKRKLWEKQKKGKKRMKEFGKVSIPNTAFI
EVLKLD

>core/132/5/Org5_Gene688

MVWSTNIKHEGLKSWIDEVAKLTTPKDIRLCDGSDTEYDELCTLMESTGTMIRLNPEFHPNCFLVRSSADDV
ARVEQFTFICTSTEA EAGPTNNWRDPQEMRRELHQLFRGCMQGRTLYIVPFCMGPLDSPFSIVGVELTDS
PYVVC
SCMKIMTRMGDDVLRSLGTSGKFLKCLHSGKPLSPGEADVSWPCNPKSMRIVHFQDDSSVMSFGSGYGG
NALLGKKCVALRLASYMAKSQGWLAEHMLIIGITNPEGKKKYFSASFPSACGKTNLAMLMPKLPGWKIECIG
DDIAWIRPGRDGRLYAVNPEYGFFGVAPGTsertNPNALATCRSNSIFTNVALTADGDVWWEGLTEQPPEPL
TDWL
GKPKPGGSPA
AHPNSRFTAPLRQCPSLDPEWNSPQGVPLDAIIFGGRRSETIPLVYEALSWEHGVTIG
AGMSSTTTAAIVGQLGKLRHDPFAMLPFCGYNMAYYFQHWLSFAENRSLKLPKIFGVNWFRKNNQGEFLW
PGFSENLRVLEWIFQRTDGLEDIAERTPIGYLPNIQKFNLNGLNLDLQTVQELFSVDAEGWLAEEVENIGEYLKI
FGSDCPQQITDELLRIKSELKEK

>core/133/5/Org5_Gene572

MAAYTEASILSLASLDHIRLRAGMYIGRLGNGSQKEDGIYTLFKEVVDNGIDEFIMGHGKSLKISASDKQISIQ
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SKQGSTKDPDGTFSFTPDPSIFPEFTFNHDFLKDKIRQYTYLHSGLEIRFNDEVFISHNGLKDLFDAEITEPLY
SPLFFQNEDLTFIFSHLEGNTERYFSFVNGQETLDGGTHLTAFKEAIVKGVNEFFGKTFVSNDIREGIVGCIAIKI
ASPIFESQTKNKLGNLTQIRSSLIKDVKEAIVQALRKDKVAPELLLEKIKFNEKTRKNIQFIKQDLKSKQKKVHY
KIPKL RDCKFHYNDRSLYGEASSIFLTEGESASASILASRNPLTQAVFSLRGKPMNVFSLEETKMYKNDEL FYL
ATALGITQNEIQHLRYNKVILATDADVDGMHIRNLLITFFLKTLLPLVENNHLEFILETPLFKVRNKTTTTLYYS
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NLITDF

>core/134/5/Org5_Gene970

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INLFTIRRTTQGLVQVLR AHLPHPGDPMRVVVGCDTRHNSIEFAQETAKVL AGNGCEVFLFQYPEPLALVSFT
VRYERAIGGVMITASHNPPNYNGYKVYMASGGQVLPPLDQEIVAACSAVNEILSVPSIDHPNIHLIGKEYEAL
YRDTLKQLQLYPEANRISGRSLSISYSPLHGTGISLVPHVLKDWGFLSVHLVEKQAIGDGDFTVQLPNPEDPE
ALTLGTEQMLANDDDLFIATDPDADRVGVVCLEDGQPYRFNGNQMASLLADHILGAWSKTRHLGEHDKLV
KSLVTTEMLSAIAKH YHVDLINVGTGFKYIGEKIESWRNSTNKFVFGAEESYGCLYGTHVEDKDAIIASALIA
EAALQQKLQGKTLCDALLSLYETYGYFANKTESVVFSAKTDEQEIRKKLSHLEEISSANFFSGKYQVEKFENY
KQGIGFNLLSKDSYAL TLPKTSMLCYFSGGGRVIIRPSGTEPKIKFYFEMSTHYPERVTDKEIQKQREAESFQ
HLDDFIFDFKEKFSNL

>core/135/5/Org5_Gene57

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GALVTFSGHLLEAELGPGLLQGIFDGLQNRLEVLAEDSSFLQRGKHVNAISDHNLWNYTPVASVGDTLRRGD
LLGTVPEGRFTHKIMVPFSCFQEVTLTWVISEGTYNAHTVVAKARDAQGKECAFTMVQRWPIKQAFIEGEKI
PAHKIMDVGLRILDTQIPVLKGGTFCTPGPFGAGKTVLQHHL SKYAAVDIVILCACGERAGEVVEVLQEFPHL
IDPHTGKSLMHR TCHICNTSSMPVAARESSIYLGVTIAEYYRQMGLDILLADSTSRWAQALREISGRLEEIPGE
EAFPAYLSSRIA AFYERGGAITTKDGSEGS LTICGAVSPAGGNFEETVPTQSTLAVVGAF CGLSKARADARRYP
SIDPLISWSKYLNQVGQILEEKVSGWGGA VKKAAQFLEKGSEIGKRMEVVGEEGVSMEDMEIYLKAELYDF
CYLQQNAFDPVDCYCPFERQIELFSLISRIFDAKFVFDSPDDARSFFLELQSKIKTNLGLKFLSEEYHESKEVIV
RLLEKTMVQMA

>core/136/5/Org5_Gene292

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PLCQALLTVWEQFFSAPENQNREFLVIFYGDASPYIQQALTQSRHSPRIVVVGISPTVFIQGD FRVHNYRVSGD
FFSSLCDRGTRAENTTILPYSSGLEGVFLPSIRCPSFTWAVRFGEQCLVANRGEDVEDRGGLS QDAERSQLPHS
ERDLAVVIDSTDPSSMSRLVEWLNQGSPSSDMEINYPQRCPDVALSALY AISRVSGLAQEWILASVHEGLDL
QICYSLILMHTTFAVRYFFLLFTNYPQSRERFRTARIVAQSLYLPSILVLVFD CGNVLRKLWMPQEILRAIFISA

STISGSIVFVECTRWMGRGLRHRVQQFVQQRVIGSGLPVGTVRASYRDRAGFIIGFLQTVHGGLYLPVSIMVL
NQIAIQVPRILVRPNNTAVYDLHNKSAEENWSSGDVLA VGQTLNFILCAFVLVNLWFFVKSVLRHSRRRRR

>core/137/5/Org5_Gene821

MKKKFIFYFVIVFSLLFLWEMTSRHRPTFSFFCPPPSSIASSTLQSLPLLLTSAWHTLKAILGGFFLAITLSIVLAT
IMLSYKSAKDLLQPLFILLQCTPMFALAPLIVLWFGWGIGAVIVPTALTIFFPPLTLTIYQGILSTPEELIEQFVLC
GATKFQLLIKLRIPHALPHIFSGLKIAIGSAGFAAIAGEWVASQSGLGILMLESRRNYEMELAFAGLATLSILTL
SLFQITLLIEKLIFSLFRVKRMSLKHKSVAKKALSVLALIPIMLIPWKGNKSPDKKNLTSLTLLLDWTPNPNH
IPLYAGVAKGYFKQHGLDLQLQKNTDSSSAVPHVLFEQVDMALYHALGIMKTSIKGMPIQIVGRLIDSSLQGF
LYRSQDPIYKFEDLNGKVLGFCLNNSRDLNRLLETNLRNGVVPSEVKNVSSDLISPMLLNKIDFLYGAFFYNIE
GVKLQTLGMPVKCFLSDTCDLPTGPQLIVFTKKGTKASEPEIVEAFQKALQESIIFSKDHPEDAFKLYAKETKS
IPKNLYQEYLQWEETFPLLAQSQDPLSKDLVDKLLLETIIKRYPELASEVAKFSLNDLYNPSLPPEEQSV

>core/138/5/Org5_Gene765

MYTEESLDNLRHSIDIVDLSEHIHLKRSGATYKACCPFHTEKTPSFIVNPAGAHYHCFGCGAHGDAIGFLMQ
HLGYSFTEAILVLSKKFQVDLVLPKDSGYTPPQGLKEELRHINSEAEFFRYCLYHLPEARHALQYLYHRGF
SPDTIDRFHLGYGPEQSLFLQAMEERKISQEQLHTAGFFGNKWFLFARRIIFPVHDALGHTIGFSARKFLENSQ
GGKYVNTPETPIFKKSRILFGLNFSRRRIAKEKKVILVEGQADCLQMIDSGFNCTVAAQGTAFTEEHVKELSK
LGVLKVFLLFDSDEAGNKAALRVGDLCQTAQMSVFVCKLPQGHDPDSFLMQRGSSGLIALLEQSQDYLTFLI
SEKMSSYPKFGPREKALLVEEAIRQIKHWGSPILVYEHLKQLASLMMVPEDMVLSLANPQVTAEPQNIPIKQK
VPKIHPIHIVMETDILRCMLFCGSNTKILYTAQFYFVPEDFKHPECRKLFAFMISYYEKYRKNVPFDEACQVLS
DSQILQLLTKRRLNTEALDTIFVQSLQKMADRRWREQCKPLSLNQNIQDKKLEILEDYVQLRKDRITIITLLDPE
SELIP

>core/139/5/Org5_Gene358

MSTSPISNDPRYLSLSNATEKTSLLANSRSLSPVPNSLVPSNPEDTGLRKSIFTHSVTLFAGLVVLLVAVSVVV
VALTVLAPGVPQAILLGIAISGVGIGGSIMKSLVYMVRDYMSPRMQESSRIKSALAVGTGFTVMGLVMKVG
ANFVPGGYGGLVGS LGSSAYSRSQTTLASFHYIYTKFFRSEKVAKGEKLTEAETIKEAKKLHYITLSIATIG
VGLAVLGILLAIAGTVLLGGAPATIAIILAPPLISIGLTTVLQTIHSSIGKWRAFLTQEKKDLFVDTSLKDIRLE
KLPPSEVEESETSQSVIEVPDSEGIAETRISAEIDTRLSLTTRQKVIFALATLLLLASIAAFIVTGFGGLTVMQVL
LVASVGSASVSTLPMVSSGFSYVAYQLKARLNISKLRWKEAKNKKRVRQFLIESGVIASDREFNQMWKTV
YKKQIQKTDAAIREEVNFEKGGEVNSALVGGILLGVGTGIMLLALVPAFAPIVPGILALGGSTLGIAGSILMR
KFVNWLYDELVKLYERRRRNRRELLYGPESKMRSIATDLVVEALAASHDHLFDLDGPVDFIDVDVDIDGAA

>core/140/5/Org5_Gene431

MTNSDNASAAGLLWAHPKEDPAFLGMIIKEFHLPPTVAQIFISRGFQTIQEIHKFLYSHLSSLYDPGLFLDMSK
AVERLLLARDRKEHVMIYGDSDVDGMTGVALLVEFLRDIDVHVSYFFLGAILKQHGETSTLIAKLKEEGITLL
ITVDCGITAGKEVSDITRQGIDVIITDHHMPTGKIPHC VATLNPKLRDHTYPNRELTVGVVAFKLARGVLNALI
SRNLVPK SQGSLKLLDLVTLGTITDVGVLLGENRVMVRYGIKEIARGARPGLNKLCALCGVEKSEVTSTDIV
LKIAPKLNSLGRLLDDPAKGVELLLTQDDERVDALIMELDNINRERQRIEAEVFQDVQEILNSNPEILKQAAIVL
SSTAWHARVPIISARLAKTYNKPVVIIAIQRGIGKGSARTIGSFLLGVLLKKCSSLLLSYGGHDFAGVIMKED

KVEDFKKKFVHLVNSSLKKGDTLPHLEIDAYADFDAIDYDLLASMELFEPFGKGNLMPIFYSKVRQVRYPKV
LPGNHLKLYLSQKERNLEGVAFGLGRHADALKASWHYPLEIAYTPRLSQTSGSGVIHLLVRDFRISSEPRFSD

>core/141/5/Org5_Gene254

MSFLRRHISLFRSQKQLIDVFAPVSPNLELAEIHRRVIEDQGPALLFHNVISSFPVLTNLFGTKHRVDQLFSQA
PDNLIARVAHLISSTPKLSSLWKSRLDKRISSGLKKARFRRFPFVSMSSVNL DHLPLLT SWPEDGGAFLTLP
LVYTESPTLTTPNLGMYRVQRFNQNTMGLHFQIQKGGGMHLYEAEQKKQNL PVS VFLSGNPFLTLSAIAPLP
ENVSELLFATFLQGAKLLYKKTNDHPHPLLYDAEFILVGESPAKRRPEGPFGDHFGYYSLQHDFFEFHCHKI
YHRKDAIYPATVVGKPYQEDFYIGNKLQEYLSPLFPLVMPGVRRLKSYGESGFHALTAAVVKERYWRESLTT
ALRILGEGQLSLTKFLMVTDQEVPLDRFSVLETLERLQPDRLIIFSETANDTLDTGPSLNKGSKGIFMGIG
KAIRDLPBGYQGGKIHGVDIAPFCRGCLVLETSLEDRCIKSLLHHPDLKSWPLIILADNLRETIQSEKDFLWR
TFTRCAPANDLHALHSHFATHRPNNYFPFVIDALMKPSYPKEVEVDPSTKQKVSERWHAIFYPNKETFYI

>core/142/5/Org5_Gene522

MKYRTHRCNELTSNHIGENVQLAGWVHRYRNHGGVVFIDLRDRFGITQIVCREDEQPELHQRLDAVRSEWV
LSVRGKVCPRLAGMENPNLATGHIEVEVASFEVLSSKSNLPFSIADHDHINVNEELRLEYRYLDMRRGDIEKL
LCRHQVMLACRNFMDAQGFTEIVTPVLGKSTPEGARDYL VPSRIYPGKFYALPQSPQLFKQLLMVGGLDRYP
QIATCFRDEDLRADRQPEFAQIDIEMSFSGDTQDLLPIIEQLVATLFATQGIEIPLPLAKMTYQEAKDSYGTDP
DLRFDLKLKDCRDYAKRSSFSIFLDQLAHGGTIKGFVPGGATMSRKQLDGYTEFVKRYGAMGLVWIKNQE
GKVASNIAKFMDEEVFHELFAFYFDAKDQDILLLIAAPESVANQSLDHLRRLIAKERELYSDNQYNFVWITDFP
LFSLEDGKIVA EHHPTAPLEEDIPLLETDPLAVRSSSYDLVLNGYEIASGSQRIHNPDLQSQIFTILKISPESIQE
KFGFFIKALSFGTPPHLGIALGLDRLVMVLTAESIREVIAFPKTQKASDLMMNAPSEIMSSQLKELSIKVAF

>core/143/5/Org5_Gene275

MSGKKDGVGRGMIFVPLSILVLIFLPLPQILLDFGLCISFALSLLTVCWVFTLNSSNSAKLFPPFFLYLCLLRLGLN
LASTRWIVSSGTASSLIVSLGSFFSLGSLWAATFACLLFFVNFLMVSKGSERIAEVRSRFFLEALPAKQMALD
SDLVSGRASYKAVKKQKNALIEEGDFFSAMEGVFRFVKGDAAISCILLVN NVSVTCLYYTSGYALEQMWF
VLGDALVSQVPALLTSCAAATLISKIDKEESLLNYLFEYYKQLRQHFRVVSLLIFSLCCIPSSPKFPIVLLASLL
WLAYRKEEPASEDSCIERAFSYVEGACPKESQFYQVYRAASEEVFEDLGVRLPVLTSRLIEERPWL RVFGQ
NVYLDGMTPEAVLPFLRNIAHEALNAEVVQKYLEESERVFGIAVEDIVPKKISLSSLVLSRLLVRERSVLKLF
PKILEAVAVYQNSGDSLEILAEKVRKSLGYWIGRSLWDQKQTLVITIDFHVEELINSSYSKSNPVMQENVIRR
VDSLLERSVFKDFRAIVTSCETRFEMKKMLDPHFPDLLVLSHDELPKEIPISFLGIVSDEVLP

>core/144/5/Org5_Gene243

MPKQAEYTWGSKKILDNIECLTEDVAEFKDLLYTAHRITSSEEDSDNEIQPGAILKGTVVDINKDFVVDVGL
KSEGVIPMSEFIDSSEGLVLGAEEVEVYLDQAEDEEGKVLSREKATRQRQWEYILAHCEGSIVKGQITRKVK
GGLIVDIGMEAFLPGSQIDNKKIKNLDDYVGKVCEFKILKINVERRNIVSRRELLEAERISKKAELIEQISIGEY
RKGVVKNITDFGVFLDLGDIGLLHITDMTWKRIRHPSEMVELNQELEVIILSVDKEKGRVALGLKQKEHNP
WEDIEKKYPPGKRVLGKIVKLLPYGAFIEIEEGIEGLIHISEMSWVKNI VDPSEVVNKGDEVEAIVLSIQKDEGK
ISLGLKQTERNPWDNIEEKYPIGLHVNAEIKNL TNYGAFVELEPGIEGLIHISDMSWIKKVSHPSSELFKKGNSV

EAVILSVDKESKKITLGVKQLSSNPWNEIEAMFPAGTVISGVVTKITAFGAFVELQNGIEGLIHVSELSDKPFA
KIEDIISIGENVSAKVIKLDPDHKKVSLSVKEYLADNAYDQDSRTELDFKDSQGPKERKKKKGK

>core/145/5/Org5_Gene654

MSTRRPIQLLDPLTINQIAAGEVIENSVSVVKELIENSLDAGADEIEIETLGGGQGAIIRDNGCGFRAEDIPIALQ
RHATSKIREFSDIFSLNSFGFRGEALPSIASISKMEIQSSIEGDEGVRTVIHGGDIVSCEPCARQLGTTVIVNSLFY
NVPVRRGFQKSMQSDRLGIRKLIENRILSTANIGWSWISEGHHEIQIAKQQGFQERVAYVMGDHFMQDALTI
DKEANGVRIVGVLGSPSFHRPTRQGQKIFINDRPIESLFISKKVGDAYALLPLHRYPVFVLKLYLPSSWCDFN
VHPQKIEARILKEELVGDCIKEAIVETLACPPGILCRTHQEIEESDSVPLPMFRMLETSDVQEEESVEFDQNLFA
YSSDEVSLKQEYTSRGPKSQMDWIYSSDVRFSLTSLGRVVLAEDLEGVHIIFTAAARKHLFFLSLMQENSRM
YQSQALLIPLRLQVTPEEAFFFSHHGRTLCDLGIEISQVGPCVFSIESTPTVIGEEELKEWLLLLAARGSTDINSE
ALTALMKETLTQATFSKHQHVFVDVSWLKLLWSVGKPEKGFDFGARIRRLILDSDFMEG

>core/146/5/Org5_Gene256

MAVSGGGGVQPSSDPGKWNPALQGEQAEGPSPLKESIFSETKQASSAAKQESLVRSGSTGMYATESQINKAK
YRKAQDRSSTSPKSKLKGTFSKMRASVQGFMSGFGSRASRVSAKRASDSGEGTSLLPTEMMDVALKKGNRISP
EMQGFFLDASGMGGSSSDISQLSLEALKSSAFSGARSLSLSSSESSSVASFGSFQKAIEPMSEEKVNAWTVARL
GGEMVSSLLDPNVETSSLVRRAMATGNEG MIDLSDLGQEEVSTAMTSPRAVEGKVKVSSSDSPEANPTGIPN
SNTLERAEEKAEKQESREQLSEDQMMLARAMAGLLTGAAPQEVLSNSVWSGPSTVFPPPKFSGTLPTQRSGD
KSKHKSPGIEKSTNHTNFSPLREGTVKSAEVKSLPHPESMYRFPKDSIVSREEPEAVVKESTAFKNPENSSQNF
LPIAVESVFPKESGTGGALGSDAVSSSYHFLAQRGVSL LAPLPRATDDYKEKLEAHKGPGGPPDPLIYQYRNV
AVEPPIVLRSPQPFSGSSRLSVQGKPEAASVHDDGGGGNSGGFSGDQRRGSSGQKASRQEKKGKKLSTDI

>core/147/5/Org5_Gene462

MQKHPSFYQRFLSAYYKNLLASLSWKFFISVALIGIYAPLFASSKPLLVTWHGEIFFPLRLRYLFFPGYYTKPVD
LFFNVLMVTFPFFILSFKLTRGWLRRWLLGLCIISQCMIFAWAYSGKVQDPALAENLKKMRAEKVRENISKV
NSEMVMLLPKDTRTWEMERRY MSTYEQLGILIKAKYRKKQEASVKKYQVAFE EKQRQSPMPTLRHLEMKNE
GICLKRLQQRVDKMQRPYEMAQQA WN RATDN YRPFLMALTRIEHELRLADYNNWGQPEDLCIAYANVEKR
AEPYKKSLLAIRQVLEDYAKLRS AISFIQDKRLWIEKESEDRLILNPFSSFWEDDAGGSREM NKYVPWWQ
LSRVTRKDLLAALVFGIRIALV VAGIGITIALAIGIMIGLVSGYFGGTVD MILSRFTEIWETMPVLFILMLVISIT
QQKSLLLNTVLLGCFSWTGFSRYVRIEVLKQRDRGYVLAATNLGYSHYYIMVHQILPNAIVPVISLVPFAMM
AMISCEAGLTFLGLGEESSASWGNLMREGVTGFPAESAVLWPPAILTMLLIAIALIGDGV RDALDPRLQDS

>core/148/5/Org5_Gene1027

MTDFPTHFKGPKLNPIKVNPNFFERNPKVARVLQITAVVLGIIALLSGIVLIIGTPLGAPISMILGGCLLASGGAL
FVGGTIATILQARNSYKKAVNQKKLSEPLMERPELKALDYSLDLKEVWDLHHSVVKHLKKLDLNLSETQRE
VLNQIKIDDEGPSLGECAAMISENYDACLKMLAYREELLKEQTQYQETR FNQNLTHRNKVLLSILSRITDNIS
KAGGVFSLKFSTLSSRMSRIHTTTT VILALSAVVSVMVVAALIPGGILALPILLAVAISAGVIVTGLSYLVRQIL
SNTKRNRQDFYKDFVKNVDIELLNQTVTLQRFLFEMLKGV LKEEEEVSLEGQDWYTQYITNAPIEKRLIEIR
VTYKEIDAQTKKMKTDLEFLENEVRSGRLSVASPS EDPSETPIFTQGKEFAKLRRQTSQNISTIYGPDNENIDPE

FSLPWMPKKEEEIDHSLEPVTKLEPGSREELLLVEGVNPTLRELNMRIALLLQQQLSSVRKWRHPRGEHYGNVI
YSDTELDRIQMLEGAFYNHLREAQEEITQSLGDLVDIQNRILGIIVEGSDSDSRTEEEPQE

>core/149/5/Org5_Gene41

MANPTQSRPPSPEISIEEELQELAGSSNTETISNTPPPSCAATAEEVSLFIEGGRRNSEDEEGPLGSCEVYDVVC
ITNQGDPEVRDHEVRVMYINGSGRTQHEGILDAMNICDLRGEPVRFIHNSGYGLGSCFLGIRNRIPPRDNVISQ
AIQARWNEFFIFAENANRDYIVLFSGNGGLYLQVALDNSIYSHHILCVGIGSSYYIQGNRYVHNYRVTGDWTT
LLDRRGATAVNTTTLPYADSAEGLFLPSVRCPSYQWALRCGEQCLIMDNNQQVGFRPQDSSSEIALVVNLNQ
DHSTWTRLIEWIDRGDSQAVLELNPQPSHCRDIALTALYATTRISSLLQECLMISVTYAPEVFVTYAIVTGYSI
MTLRYFILLTNRPGCRRHFRVLRALGLQSLGFLTVLDDHINVTRRVNRRPPLISVIFCTASFATGSFIYVDL
TRMFFTSLRSRLQLFVQRRLTGRGLPLRRVFNHLDSLRF SQNALITFHGGFLMPLIIGFFNQLVIQVPRVVIRP
NTTAVYDLNQTSQEAWDSDVLAIGQTINFLLCMILLVINTFFFVRSVRRNLHRRPHR

>core/150/5/Org5_Gene607

MFMNTQNSQATEVSSEEEESQKKLEELVALAKEQGFITYEEINEILPMSFDTPEQIDQVLIFLTGMDIQVLNQID
VERQKEKKKEAKELEGLARRTEGTPDDPVRMYLKEMGTVPLLTREEVEISKRIEKAQVQIERIILRFYSAK
EASIAHYLISGKERFDKIISEKEVEDKTHFLKLLPKLITLLKEEDTYLENLLLSLKQPDLSKQEA AKLND SLEK
CRIRTQAYLRFCFHC RHNVTEDFGEVVFKAYDSFLHLEQQINDLKVRAERNKFAAAKLAAAKRKLKREVAA
GRTLEEFKKDVRMLQRWMDKSQEAKKEMVESNLRLVISIAKKYTNRGLSFLDLIQEGNMGLMKAVEKFEY
RRGYKFSTYATWWIRQAVTRAADQARTIRIPVHMIETINKVLRGAKKLMMETGKEPTPEELAEELGLTPDR
VREIYKIAQHPISLQAEVGESESSFGDFLEDTAVESPAEATGYSMLKDKMKKEVLKTLTDRERFVLIHRFGLL
DGKPKTLEEVGSAFNVTRERIRQIEAKALRKM RHPISKQLRAFLDLLEEEKTGTSKVKSLKSK

>core/151/5/Org5_Gene975

MDTQSSIGNEEWRIAGTSVVSGMALGKVFFLGTSPHVR ELTLPQEEVEHEIHRYYKALNRSKSDIVALEQEV
TGQQQLQEVSSILQAHLEIMKDPLLTEE VVNTIRKDRKNAEYVFSSVMGKIEESLTAVRGMPSVVDRVQDIH
DISNRVIGHLCCQH KSSLGESDQNLIIFSEELTPSEVASANSAYIRGFVSLVGAATSHTAIVSRAKSIPYLANISE
ELWNI AKRYNGKLV LIDGYRGELIFNP KPATLQSCYKKELSVVAHTSQRLVRKSLHPIVSSHAGSDKDVEDLL
ENFPQTSIGLFRSEFLAVILGRLPTLREQVDLYEKLARFPGDSPSVLRLFD FGEDKPCPGIKNKKERSIRWLLDY
SVILEDQLQAIKASLQGSIKVLIPGVSDVSEIIEVKKK WETIQTRFPKGHKVSWGTMIEFPSAVWMIEEILPEC
DFLSIGTNDLVQYTLGISRESALPKHLNVTLP PAVIRMIHHVLQAAKQNQVPVSICGEAAGQLSLTPLFIGLGV
QELSVAMPVINRLRNHIALLELNSCLEITEALLQAKTCSEVEELLNRNNKITS

>core/152/5/Org5_Gene823

MKVPWAFKNFIPKLYTSIKEGYSFNTFKKDFQAGITVGILAFPFAIAIAIGVGVSPIQGLLASIIGLLASAMGG
SNVLISGPSSAFISILYCLSAKYGA EALFTVTLLAGVFLIAFGLTGLGTFIKYPYPVVTGLTTGLAIIIFSSQIKD
FLGLQMGANIPADFLPKWIA YWDHLWTWDSKSFAVGLFTLLIMIYFRNYKPRYPGVMI AIVTATTLVWLLKI
DIPTIGSRYGTLPTAIPLPKIPQLSITKILQLMPDALTIAVLSGLETLLSAVVADGMTGWRHQSN CQLVAQGVA
NIGTSLFSGIPVTGSLSR TAASIKSEATTPIAGIVHSIFICFILLLLAPLTVKIPLTCLAAVLILIAWNMSEIHHFIHL
FTAPKKDIVVLLTVFILTVMTTITA AVQVGMMLAAFLFMKQMSDLSDVISTAKYFDKDSDFLSKA EVPQNTEI

YEINGPFFFGIADRLKNLLNDIEKPPKIFILCMTRVPTIDASAMHALEEFFLECDRQGTLLLLAGVKKTPLADLK
RYHLDELIGVDHIFSNIKSALLFAQALTNLESKTSTRHLV

>core/153/5/Org5_Gene10

MGLFHLTLFGLLLCSLPISLVAKFPESVGHKILYISTQSTQQALATYLEALDAYGDHDFVLRKIGEDYLKQSI
HSSDPQTRKSTIIGAGLAGSSEALDVLSQAMETADPLQQLVLSAVSGHLGKTSDDLKALASPYPVIRLEA
AYRLANLKNKTKVIDHLHSFIHKLPEEIQCLSAIFLRLETEESDAYIRDLLAAKKSARSATALQIGEYQQKRFL
PTLRNLLTSASPQDQEAILYALGKLKDGQSYNIKKQLQKPDVDVTLAAAQALIALGKEEDALPVIKKQALE
ERPRALYALRHLPSEIGIPIALPIFLKTKNSEAKLNVALALLELGCDTPKLLEYITERLVQPHYNETLALSFSKG
RTLQNWKRVNIIVPQDPQERERLLSTTRGLEEQILTFLFRLPKEAYLPCIYKLLASQKTQLATTAISFLSHTSHQ
EALDLLFQAAKLPGEPPIRAYADLAIYNLTKDPEKKRSLHDYAKKLIQETLLFVDTENQRPHPSMPYLRQVT
PESRTKLMLDILETLATSKSSEDIRLLIQLMTEGDAKNFPVLAGLLIKIVE

>core/154/5/Org5_Gene376

MKTSQLFYKTSKNANKSAAVLSNELLEKAGYLFKVSKGVYTYTPLLWRVVSKMMNIIREELNAIGGQELLLP
LLHNAELWQHTGRWEAFTSEGLLYTLKDREGKSHCLAPTHEEVICSFVAQWLSSKRQLPLHLYQIATKFRDE
IRPRFGLIRSRELLMEDSYTFSDSPEQMNEQYEKLRSAYSKIFDRLGLAYVIVTADGGKIGKGKSEEFQVLCSL
GEDTICVSGSYGANIEAAVSIPPQHAYDREFLPVEEVATPGITTIEALANFFSIPLHKILKTLVVKLSYSNEEKFI
AIGMRGDRQVNLVKVASKLNADDIALASDEEIERVLGTEKGFIGPLNCPIDFFADETTSPMTNFVCAGNAKD
KHVNVNWDRLDLPQYGDFLLAEEGDTCPENPGHPYRIYQGIEVAHIFNLGTRYTDSFEVNFQDEHGQTQQ
CWMGTYGIGVGRTLAACVEQLADDRGIVWPKALAPFSITIAFNGGDTVSQLAETIYHELQSQGYEPLDDR
DERLGFKLKDSDLIGIPYKLILGKSYQSSGIFEIESRSGEKYTVSPEAFPTWCQNHLA

>core/155/5/Org5_Gene592

MTVSVKKKSFRALVTTHFLTIINDNLYKFLLAFFLLEGKTLTENAKILSCVSFFFALPFLLLAPLAGSLADRFQ
KRNILATRFIEILCTILGTYFFFIQSVVGGYVVLILMACHTTIFGPAKLGILPEMLPSEQLSQANGIMTAATYTG
SILGSC LAPLLVDVTHRLGVNSYVWPTLMCVIVSIISTLISFCIRPSNVKNVKQKITLVSFKDLWKVLKDTRMI
HYLTVSIFLGSFFLLIGAYTQLEIIPFVEFTLKYPKHYGAYLFPIVALGVGTGSYITGKISGDKIKIGYVPLAAIGL
ALVFMGLYAFACSILFVLFFLLALGFLGGVYQVPLHAYVQYASPEHKRGQILAANNFLDFFGVLVAAGVIRV
LGSNLGLSPETSFFYIGWFLAVSIWTLWIWREHVYRLLLGIIILRRQLGYLYLKIHQSSSPKCYFVAVQSYREIR
RVLAALTKTVRSRVIILDQKLVPGWRAWLLSWCVPTVVSVRDNDSEAQDAWAVLQANHLKTSKKKFPDV
SVVCLGLPKNVERFTSILQEQQIDLHPIQLVQKEGKKRVIYTLVFPHA

>core/156/5/Org5_Gene438

MSTLLSILSVICSQAIAKAFPNLEDWAPEITPSTKEHFGHYQCNDAMKLARVLKKAPRAIAEAIVAELPQEPFS
LIEIAGAGFINFTFSPVFLNQQLHEFKDALKLGFQVSQPKKIIIDFSSPNIAKDMHVGHRLSTIIGDSLARIFS YVG
HDVLRNLNHIGDWGTAFGMLITYLQENPCDYSLEDLTSLYKKAYVCFTNDEEFKKRSQQNVVALQAKDPQA
IAIWEKICETSEKAFQKIYDILDIVVEKRGESFYNPFLPEIIEDLEKKGLLTVSNDAKCVFHEAFSIPFMVQKSDG
GYNYATTDLAAMRYRIEEDHADKIIIVTDLGQSLHFQLLEATAIAAGYLQPGIFSHVGFGLVLDPQGKKLKTR
SGENVKLRELLDTAIEKAEEALREHRPELTDEAIQERAPVIGINAIKYSDLSSHRTSDYVFSFEKMLRFEGNTA

MFLLYAYVRIQGIKRRRLGISQLSLEGPPEIQEPAEELLALTLLRFPEALESTIKELCPHFLTDYLYNLTHKFNGGF
RDSHIQDSPYAKSRLFLCALAEQVLATGMHLLGLKTLERL

>core/157/5/Org5_Gene426

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AFCDKEFYPCEEGRCQPVEAQQESC YGRLYSVKVND D CNVEICQSVPEYATVGSPYPIELAIGKKDCVDVVI
TQQLPCEAEFVSSDPETTP TSDGKL VWKIDRLGAGDKCKITVWVKPLKEGCCFTAATVCACPELRSYTKCGQ
PAICIKQEGPDCACLRCPVCYKIEVVNTGSAIARNVTVDNPV PDGYSHASQRVLSFNLGDMRPGDKKVFTV
EFCPQRRGQITNVATVTYCGGHKCSANVTTVVNEPCVQVNISGADWSYVCKPVEYSISVSNPGDLVLHDVVI
QDTLPSGVTVLEAPGGEICCNKV VWRIKEMCPGETLQFKLVVKAQVPGRFTNQVAVTSESNCGTCTSCAETT
THWKGLAATHM CVLDTNDPICVGENTVYRICVTNRGSAEDTNVSLILKFSKELQPIASSGPTKGTISGNTVV F
DALPKLGSKESVEFSVTLKGIAPGDARGEAILSSDTLTSPVSDTENTHVY

>core/158/5/Org5_Gene951

MELLSLNKSYFEIQRLRYRPEILTLETIRSKHIQETSSPPSPPELQKHIPNLCRIPEVSIYTEQETSSKPLKIGVL
LSGGQAPGGHN VVIGLFDALRVFNPKTRLFGFIKGPLGLTRGLYKDLDISVIYDYNNMGGFDM LSSSREKIKT
EEQKKNILNTVKQLKLDGLLIIGGNSNTDTAMLA EYFLAHNCKTSVIGVPKTIDGDLKNCWIETSLGFHTSC
RTYSEMIGNLAKDALS AKKYHHFIRLMGQQASYTTLE CGLQTLPNIALISELIATR KISLKQLSEQLALGLVRR
YKSGKNYSTVLIPEGLIEHIFDTRKLIDELNVLLANGDSSIEKILSKLSPETLKT FHLFPKDIANQLLLARD SHGN
VRVSKIA TEELLAVMVKKEIEKIKPHMEFHSVSHFFGYEARAGFPSNFDCNYGIALGIISALFLVRQKTGYMIT
INNLAQSYTEWQGGATPLYKMMHLENRCGTETPVIKTDSVDPKSPAVQHLLQQSDSCLVEDLYRFPGPLQYF
GKEELIDQRPLTLLWENQTHSPLL

>core/159/5/Org5_Gene864

MSSPPQAVASLTERIKTLLESNFCQIIVKGELSNVSLQPSGHL YFGIKDSQAFLNGAFFHFKSKYYDRKPKDGD
AVIIHGKLAVYAPRGQYQIVAHALVYAGEGDL LQKFEETKRRLTAEGYFATEKKKPLPFAPQCIGVITSPTGA
VIQDILRVLSRRARNYKILVYPVTVQGN SAAHEISKAIEVMNAENLADVLI IARGGGSIEDLWAFNEEILVKAI
HASTIPIVSAVGHETDYTLCD FASDVRAPTPSAAAEIVCKSSEEQVQVFEGYLRHLLSHSRQLLTSKKQQLLP
WRRFLDRAEFYT TAQQQLDSIEIAIQKG VQGKI HESKQRYDNISRWLQGD LVSRMTCRLQSLKKMLSQALSH
KALSLQVRCHQLKKSLTYPRQIQQASQKLSPWRQQLDTLISRRLHYQKEEYFHKHTRLKHAHNVLEQQ LRS
HVQKLELLGRRLSRGCELNLQNQKIAYANVKETLATILERRYENSVARYSALKEQLHSLNPKNVLKRGYAM
LDFDNENSAMISVDSLQENARVRIQLQDGEAILTVTNIEICKLIK G

>core/160/5/Org5_Gene1000

MDNSDNSFHTLETEQGSFLNDELA VEEVAYTESTEISDATLCFADEIQELPSPEKKVAFILNKMREALTGSSQG
SDLRLFWDLRKQCLPLFNEIEDTAKRADHWRCYIELTKEGRHLKGLQDEEGSFVVGQIDLAITCLEKDILKFQ
EGTEDKIFKDREDNFLESQALDKHQA FYKQHHTSLLWLSSFSSKIIDL RKELINVGMRLKSKFFQRLSNLG
NQVFPKRKELIEKVSQTFAEDVDAFVAKYFIGSDKETLKKT VFFLRKEIKNLQHAAKRLFVSSHVFAETRLKL
SKCWDQLKGMEKEIRQE QGRLRVVSAENSKEVRQMLAEVSSLLIEGNDLSKVRKDLEGISKKIRALDLTHDD
VISLKKEMQQQLFDQLREKQDAAEHSYQEQLAKDKQVKKEAARSLAERITTF SKTCSEGNITSESREEWQTLK

ELLGKMSFLPPPEKISLDNQLNLALQTIVNFFEEQLLSSPDSREKLVNMRQVLKQRRERRQELKDKLEQDKKL
LGSSGLDFDRAMQYSALVEEDKRALEELDASILELKQQIQQLL

>core/161/5/Org5_Gene960

MPQKVLITSALPYANGPLHFGHIAGVYLPADVYARFRLLGDDVLYICGSDEFGIAITLNADREGLGYQEYV
DMYHKLHKDTFEKLGFAldFFSRTTNPFAELVQDFYSQLKASGLIENRISEQLYSEQEQRFLADRYVEGTCP
RCGFDHARGDECQSCGADYEALDLIDPKSKISGVLEVKKETEHSYFLLDRMKDALLSFIQGCYLPDHVRKFV
VDYIEHVRSRAITRDLSWGIPVPDFPGKVIFYVWFDAPIGYISGTMewaASQGNPDEWKRFWLEDGVEYVQFI
GKDNLPFHSSVFPAMELGQKLDYKKVDALVSEFYLLERQFSKSEGNyVMDKFLSSYSldKLRYVLAAT
APETSDSEFTFLDFKTRCNSELVGKFGNFIRVLAFAEKNHYDKLSYHSSVLEDSDRAFLEEVRLVRDAEK
CYREYSLRKATSVIMSLAALGNVYFNQQAPWKLLKEGTRERVEAILFCACYCQKLLALISYPIIPESAVAIWE
MISPKSLENCNLDtMYARDLWKEEILDVINEEFHLKSPRLlFTTVE

>core/162/5/Org5_Gene151

MHPLYVDLDTISSYSPLPKEFQEAASLIAVPDTSHSKPVVPGVKTLFPQTYHLPYLKFVQGENVVHTPLKVG
VMFSGGPAPGGHNVIQGLFNSLKDFHPDSSLVGVFNNGDGLTNNKSIDITEEFLSKFRNSSGGFNCIGTGRKKIV
TPEAKEACLKTAEALDLDGLVIIGGDGSNTATAILAEYFAKRRPKTSIVGVPKTIDGDLQHTFLDLTFGFDTAT
KFYSSIISNISRDALSCKAHYHFIKLMGRSASHIALECALQTHPNIALIGEEIAEKNLPLKTIHhKICSVIADRAAM
EKYYGVILPEGIIEFIPEIINLITEIESLSEYEDKISRlSPESQRLLKSFPAPIIEQILNDRDAHGNVYVSKISVDKLL
IHLVSNHLQQYFPNVPFNAISHFLGYEGRSGLPtkFDNTYGYSLGYGAGILVRNHCNGYLSTIESLACPFMKW
KLRAIPVVKMFTVKQQADGTLQPKIKKYLVDIGSTAFRKFKLYRKIWALEDsYRFLGPLQIETPPeMHSdNFP
PLTLLLNHNFWQRHQGCIEIPDTTY

>core/163/5/Org5_Gene586

MSRKDNEVSLARSIFNILSGTFCsRITGIFREIAMATYFGADPIVAAFWLGFRTVFFLRKILGGLILEQAFIPHFE
FLRAQSLDRAAFFFRFSRLIKGSTIIFTLLIEAVLWVVLQYVEEGTYDMILLTMILLPCGIFLMMYNVNGALL
HCENKFFGVGLAPVVVNIIWIFFVIAARHSDPRERIIGLSVALVIGFFFEWLITVPGVWKFLLEAKSPpQEHDSV
RALLAPLSLGILTSSIFQLNLLSDICLARYVHEIGPLYLMYSLKIYQLPIHLFGFGVFTVLLPAISRCVQREDHER
GLKLMKFVLTLTMSVMIIIMTAGLLLLALPGVRVLyEHGLFPQSAVYAIVRVLRGYGASIIPMALAPLVSVLfY
AQRQYAVPLFIGIGTALANIVLSVLGRWVLKDVSGISYATSITAWVQLYFLWYYSSKRLPMYSKLLWESIRR
SIKVMGTTMLACMITLGLNILTQTTYVIFLNPLTPLAWPLSSITAQAIAFLSESCIFLAFLFGFAKLLRVEDLINL
ASFEYWRGQRGLLQRQHVMQDTQN

>core/164/5/Org5_Gene93

MAAKNIKYNEEARKKIHKGVKTLAEAVKVTLGPKGRHVVIDKSFGSPQVTKDGVTVAKEIELEDKHENMGA
QMVKEVASKTADKAGDGTTTATVLAEAIYSEGLRNVTAGANPMDLKRgidKAVKVVVDELKKISKPVQHH
KEIAQVATISANNDSEIGNLIAEAMEKVGKNGSITVEEAKGFETVLDVVEGMNFNRGYLSSYFSTNPETQECV
LEDALILIYDKKISGIKDFLPVLQQVAESGRPLLIIEEIEGEALATLVVNRLRAGFRVCAVKAPGFGDRRKAM
LEDIAILTGGQLVSEELGMKLENTTLAMLGKAKKVIVTKEDTTIVEGLGNKPDIQARCDNIKKQIEDSTSDYD
KEKLQERLAKLSGGVAVIRVGAATEIEMKEKKDRVDDAQHATIAAVEEGILPGGGTALVRCIPTLEAFLPML

ANEDEAIGTRILKALTAPLKQIASNAGKEGAIICQQVLARSANEGYDALRDAYTDMIDAGILDPTKVTRSALE
SAASIAGLLLTTEALIADIPEEKSSSAPAMPSAGMDY

>core/165/5/Org5_Gene366

MFGSESLRYQLLIQDFAKVSEEGIGLLESKEYSLLQAKLVLRALAQNSSFDDWFRSFKKCQISYPELAHDRDV
LEEFGIQVLREGIENPSVTVRAVSVLAIGLARDFRLVPLLLQSCNDDSAIVRSLALQVAVNYGSESLKKAIVEL
ARNDDSIHVRITAYQVVALQIEELLPFLRERAENKLVDSEVERREAWKACLELSSQFLETGVAKDDIDQALFT
CEVLRNGMLPETTEIFTELLSVEHPEVQESLLLSALAWSHQLQNHKEFLSKVRHVMCTSPFAKVRFQAAALL
HLHGDPLGRDSLVEGLRSPQPLVCEAASAALCSLGIHGVPLAKEHLESLSSRKAANLSILLLVSRREDIERAGD
VIARYLSNPEMCWAIEYFLWDAQWNLRGDTFPLYSDMIKREIGRKLIRLLAVARYSQAKAVTATFLSGQQA
QGWSFFSGMFWEEGDVKTSEDLVTDACFAAKLEGALASLCQKKDQASLQRVSQLYNDSRWQDKLAILESV
AFSENLDVAPFLDCCHHEAPSLRSAAAGALFSIFK

>core/166/5/Org5_Gene513

MLRIFCFVISWCLIAFAQPDLSGFVSILGAACGYGFFWYSLEPLKKPSLPLRTL FVSCFFWIFTIEGIHFSWMLS
DQYIGKLIYLVWLTILITLSVLFSGFSCLLVAIVRQKRTAFLWSLPGVWVAIEMLRFYGIFSGMSFDYLGWPM
TASAYGRQFGGFLGWAGQSFAVIAVNMSFYCLLLKKPHAKMLWVLTLLLPYTFGAIHYEYLKHAFFQQDKR
ALRVAVVQPAHPPIRPKLKSPIVVWEQLLQLVSPIQPIDLLIFPEVVVPFGKHRQVYPYESCAHLLSSFAPLPE
GKAFLSNSDCATALSQHFQCPVIIGLERWVKKENVLYWYN SAEVISHKGISVG YDKRILVPGGEYIPGGKFGS
LICRQLFPKYALGCKRLPGRRSVVQVRGLPRIGITICYEETFGYRLQSYKRQGAELLVNL TNDGWYPESRLP
KVHFLHGM LRNQEFGMPCVRACQTGVTA AVDSLGRILKILPYDTRETKAPSGVLETS LPLFNYKTLYGYCGD
YPMILIAFCAVSYLGGGFLGYRLLAKKEIR

>core/167/5/Org5_Gene479

MQSSEVKPFSRLRAYLCPIYKSEFSKFVPLFLLAFFVGFNYCLLKNMKDTLVIVGSDAGAEVIPFLKVWGIVP
GAVIVTMVYGWLGSRYP RDTVFYCFMAAFLGFFFLFAVIIYPVGDSLHLNSLADKLQELLPQGLRGFIVMVR
YWSYSIIYYMSELWSSVVL SMLFWGLANQITTITEAGRFYALINTGLNLSSICAGEISYWMGKQTFVAYSFA
CDSWHSVMLNLTMLITCSGLIMIWL YRRIHHLTIDTSIPPSRRVLAEEGAATANLKEKKKPKAKARNLFLHLI
QSR YLLGLAIIVLSYNLVIHLFEVVWKDQVSQIYSSHVEFN GYMSRITT LIGVVSVLA AVL LTGQCIRKWGWT
VGALV TPLVMLVSGLLFFGTIFA AKRDISIFGGVLGMTPLALAAWTGGMQNVLSRGTKFTFFDQTKEMAFIP
LSPEDKNHGKAAIDGVVSRIGKSGGSLIYQGLLVIFSSVAASLN VIALVLLIIMVVWIAVVAYIGKEYYSRAAD
AVATLKQPKEPSSSIVREAAQESVEQEEMAVL

>core/168/5/Org5_Gene747

MHDQRNRGHNHNHNLRLRPGSTLLEAFLILCSEHEEGIACFDEHLGSLSYREL RNAIIA VAIKVSKFSEDRVGV
MMPASIGAFIAYFGILLAGKTPVMMNWSQGLRELRACTKTVEVRRVLTSQQFIKHLTEVQGFVEYPFDLMY
MEDVRKRLSWWEKCRIGLYSKCSVPWLLRIFGVSGVESDDTAVILFTSGTEKLPKAVPLTHKNLMENQEACL
KFFDPNTQDVMLAFLPPFHAYGFNSCGLFPLLMGVHVVFASNPLNPKKLVEFIDDKKVTFFGSTPVFFDYILK
TAKKQNSCLESRLV VIGGDAL KDTLYEETKKLQPQIALYQGYGATECSPVISITTKESPRKSECVGMPIEGM
DVLIISKETHIPVSSGEQGLIVVRGNSVFSGYLG NHEHQSFVSLGGDQWYLTGDLGHIGPSGDLFLEGRLSRFV

KIGGEMVSLEALESILHEHFTENQNEDAGSLVVCGIPGDKVRLCLFTTLATTIHEVNDILKSAETSSIVKISYVH
QVESIPILGIGKPDYVSLNALAVSLFG

>core/169/5/Org5_Gene941

MPFKCIFLTGGVVSSLGKGLTAASLALILERQRLNVAMLKLDPYLNVDPGTMNPFEGHEIYVTDDGVETDLD
LGHYHRFSSAALSRHSSATSGQIYARVIKREREGDYLGSTVQVIPHITNEIIQVILDAAKEHSPDVLIVEIGGTIG
DIESLPFLEAIRQFRYDHSEDCLNIHMTYVPYLQAADEVKSKPTQHSVQTLRGIGIIPDAILCRSEKPLTQEVKS
KISLFCNVPNRAVFNVIDVKHTIYEMPLMLAQEKIANFIGEKLKLATVPENLDDWRVLVNQLSQDLPKVKIG
VVGKYVQHRDAYKSIFEALTHAALRLGHAAEIIPIDAEDENLTMELSQCDACLVPGGFGVRGWEGKIAAAKF
CREQGIPYFGICLGMQVLVVEYARNVLNLDQANSLEMDPNTPHPIVYVMEGQDPLVATGGTMRLGAYPCLL
KPGSKAHKAYNESSLIQERHRHRYEVNPDYIQSLEDHGLRIVGTCPPQGLCEIIEVSDHPWMIGVQFHPEFVSK
LISPHPLFIAFIEAALVYSKDASHV

>core/171/5/Org5_Gene140

MRKISVGICITILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNLSG
NIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLS
IDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPH
YYNQSQVETKTITIHFI PDANTA AKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLT FNIN
KFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSPYEHQKQEMAQRQAYAKKLFKEALEELQ
ITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMA
FLTIFAYPSGVPPYAINHKDFLEILQNIEQE QDHQKRSELVSQASLYLET FHHIIEPIYHDAFQFAMNKKLSNLGV
SPTGVVDFRYAKEN

>core/172/5/Org5_Gene600

MLGKEEEFTCKQKQCLSHFVTNLTSDFV FALKNLPEVVKGALFSKYSRSVLGLRALLLKEFLSNEEDGDVCDE
AYDFETDVQKAADFYQRVLDNFGDDSVGELGGAHLAMENVSILA AKVLEDARIGGSPLEKSTRYVYFDQKV
RGEYLYYRDPILMTSAFKDMFLGTCDFLDFTYSALIPQVRAYFEKLYPKDSKTPASAYATSLRAKVLDCIRGL
LPAATLTNLGFFGNRFRWQNLIIHKLQGHNLAE LRRLLGDESLTELMKVIPSFVSRAEPHHHHHQAMMQYRRA
LKEQLKGLAEQATFSEEMSSSPSVQLVYGDPDGIYKVAAGFLFPYSNRSLTDLIDYCKKMPHEDLVQILESSV
SARENRRHKSPRGLECVFEGFDILADFGAYRDLQRHRTL TQERQLLSTHHGYNFPVELLDTPMEKSYREAME
RANETYNEIVQEFPEEAQYMVP MAYNIRWFFHV NARALQWICELRSQPQGHQNYRTIATGLVREVVKFNPM
YELFFKFVDYSDIDLGRNLNQEMRKEPTT

>core/173/5/Org5_Gene103

MFKSFIVRYMFVGGGLVSFLLPIPDLECANNVTKTYDKKASVISRDLKLQEDCQKFWNLDPYKLESLCAYQVL
YHDDYSSKRIRELFPQIQKDEVPIFATMILTLGKVDRGFSPEEISLIQKLSYPGLSLASLRGSTEIDPNTDLARAL
VVSEFSGDLGKNRADYYSNCLDILALRIHAERQRYLDQSPCVPGTSEFHKATIEAINTILFYEEAVRYP SKKEM
FSDEFSFLSSVTDRKFGVCLGVSSLYFSLSQRLDLPLEAVTPPGHIYLYRYQGGEVNIETTAGGRHLPTASYCDC
LDLEDLQVRTPEEMIGLTFMNQGSFALQKKKYKEAEEAYKKAQEYLGDEELQELLGFVQILGGKKKKEGKSLI
GKSPRASQKGSVAYDYLKGRINIPTLALLFSYPGSNYEEIASYEEELKKAMKSSMPCCEGQRRLASVAFHLGK

TAEAVALLEKCVEDIPNDLSLHLRLCKILCDRHEYTKALKYFIIAERLMEDQGFLKKDNRSFALFYEVKKIISK
VAPQKANTLLLMESER

>core/174/5/Org5_Gene12

MSIVLDKIGKSLGTRILFDDVSVVFNPGNCYGLTGPNAGAGKSTLLKIIMGMIEPTRGSISLPKKVGILRQNIDSF
HDTTVLDCVIMGNTRLWEALQRRDNLYLQEFTDAIGMELGEIEEIIIGEENGYRADSEAEELLTGIGIPNEMFD
KKMAMIPIDLQFRVLLCQALFGHPEALLLDEPTNHLDLYSINWLGNFLLKDYEGTVIVVSHDRHFLNTITTHIA
DIDYDTIIIPGNYDDMVEMKTASREQEKADIKSKEKKISQLKEFVAKFGAGSRASQVQSRLREIKKLQPQEL
KKSNIQRPYIRFPLSDKSSGKVVLSEAITKDYGDHQQVIHPFSLEIYQGDKLGIIGNNGLGKTTLMKLLAGVEA
PSSSGIKLGHQAICSYFPQNHSDVLADCGQETLFEWLRNRKTGINDQEIRSVLGKMLFGGDDAFKQIQALSGG
ETARLLMAGMMLNHNVLILDEANNHLDLESVSALSWAINDYKGTAIFVSHDRGLIQDCATKLLIFDKDKIT
FFDGTMDVDTAGHKQLL

>core/175/5/Org5_Gene143

MHRLKPTLKSILPNLLFLLTLSSCSKQKQEPLGKHLVIAMSHDLADLDPRNAYLSRDASLAKALYEGLTRET
DQGIALALAESYTLKDHKVYTFKLPSVWSDGTPLTAYDFEKSQKLYFEFSPSIHTLLGVKNSSAIHNAQ
KSLETGLQAKDDLTLVITLEQPPFYFLTILIARPVFSPVHHTLRESYKKGTTPSTYISNGPFVLKKHEHQNYLIL
EKNPHYDHESVKLDREVTLKIIPDASTATKLFSKSIDWIGSPWSAPISNEDQKVLSQEKILTYSVSSTLLIYN
LQKPLIQNKALRKAIAHAIDRKSILRLVPSGQEAUTLVPPNLSQLNLQKEISTEERQTKARAYFQEAKETLSEK
ELAELSILYPIDSSNSSIIAQEIQRQLKDTLGLKIKIQGMEYHCFLKKRRQGDFFIATGGWIAEYVSPVAFLSILG
NPRDLTQWRNSDYEKTLEKLYLPHAYKENLKRAEMIIIEETPIIPLYHGKYIYAIHPKIQNTFGSLLGHTDLKN
IDILS

>core/176/5/Org5_Gene986

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GLGILVTRLILSTIRKVDAMGYDAAVKEEQYLSRIRELESENREIRDNRNRAVEDQCAHLSEENKDLRDPEYLH
GMTERLIASLEIENQALVAENILLKDOWNASLSRDFRAYKQKFPLGALEPWKEDIACIMEQNLFKPECIAMVK
SLPLETQRLFLYPKGFQSLVNRFAPRSFFQTPKYEYNSRNENEDGKVAAVCARLKKEFFSAVLGACSYEELG
GICERAVALKETLPLPEAVYDTLVQEFPNLLTAESLWKEWCFYSYPYLRPYLSVDYCKRLFVQLFEELCLKLF
TTGSPEDQALVRLFSYYRNHIPAVLASFGLPPPETGGSVFVLLPKQENLLWSQIEVLATRYLKDTFVRNSEWT
GSFEMMFSYNEMCKEISEGRIRFAEDYETRHSEEFPPSPLSEEGERGEEFLPPCSEEEVSVLERPDLDVDSMWV
WHPPVPKGPL

>core/177/5/Org5_Gene755

MTARAEYLDHEDFLYRSHKLQELSELGVVLYPYEFPGVFSCEDIKKTFFASQELGNSEAAMSRSTPRVRFAGR
LVLFRAMGKNAFGQILDHNQTIQVMFNREFTSVHGLSEDAEITPIKFIEKKLDLGDILGIDGYLFFTHSGELTV
LVETVTLCKSLLSLPDKHAGLSDKEVRYRKRWLDLISSREVSDTFVKRSYIIKLIRNYMDAHGFLEVETPILQ
NIYGGAEAKPFTTTMEALHSEMFLRISLEIALKKILVGGAPRIYELGKVFRNEGIDRTHNPEFTMIEAYAAAYMD
YKEVMVFVENLVEHLVRAVNHNDNTSLVYSYWKHGPQEVDFKAPWIRMTMKESIATYAGIDVDVHSDQKLL
EILKKKTTFPETAFAFATASRGMLIAALFDELVSDNLIAPHHITDHPVETTPLCCKTLRSGDTAFVERFESFCLGKEL

CNAYSELNDPIRQRELLEQQHTKKELLPDSECHPIDEEFLEALCQGMPPAGGFGIGVDRLVMILTNAASIRDVL
YFPVMRRFDAEKTN

>core/178/5/Org5_Gene141

MLRFFAVFISTLWLITSGCSPSQSSKGIFVVMKEMPRSLDPGKTRLIADQTLMRHLYEGLVEEHSQNGEIKPA
LAESYTISEDGTRYTFKIKNILWSNGDPLTAQDFVSSWKEILKEDASSVYLYAFLPIKNARAIFDDTESPENLG
VRALDKRHLEIQLETPCAHFLHFLTLPDIFFPVHETLRNYSTSFEEMPITCGAFRPVSLEKGLRLHLEKNPMYHN
KSRVKLHKIIVQFISNANTAAILFKHKKLDWQGPPWGEPIPEISASLHQDDQLFSLPGASTTWLLFNIQKKPW
NNAKLRKALS LAIDK DMLTKVVYQGLAEPTDHILHPRLYPGTYPERKRQNERILEAQQLFEEALDELQMTRE
DLEKETLTFSTFSFSYGRICQMLREQWKKVLKFTIPIVGQEFFTIQKNFLEGNYSLTVNQWTA AFIDPMSYLM I
FANPGGISPYHLQDSHFQTLLIKITQEHHKKHLRNQLIIEALDYLEHCHILEPLCHPNLRIALNKNIKNFNLFVRR
TSDFRFIEKL

>core/179/5/Org5_Gene252

MNVLYKYTKHSPSAHAWKLGITSPKHGIYLPFSIHTKNNSCGIGEFLDLIPLISWCQKQGFSVIQLLPLNDTGEDT
SPYNSISSVALNPLFSLSSLPNIDTIPEVAKKLQDMHEL CSTPSVS YTVKEKKWAFLREYYQKCKSSLEGN
SNFSEFLESERYWLYPYGTFRAIKHHMHGEPINNWP KSLTDQENFPDLTKKFHDEVLF FSYLQFLCYQQLCEV
KAYADQHHVLLKGDLPIISKDSCDVWYFRDYFSSSR SVGAPPDLYNSEGQNWHLPIYNFSQLAKDDYIWW
KERLRYAQNFYSVYRLDHIIGFFRLWIWDSSGRGRFIPDNPKDYIKQGTEILSTMLGASSMLPIGEDLGIIPQDV
KTTLTHLGICGTRIPRWERNWESDSA FIPLKDYNPLSVTTLSTHDSDTFAQWWLNSPKEAKQFAKFLHLPFQK
TLTTETQIDILKLSHESASIFHINLFNDYLALCPDLVSKNLQRERINTPGTISKKNWSYRV RPSLEELAIHKKFN
GYIEKILTGL

>core/180/5/Org5_Gene987

MERKRFIDCDSTKILQELALNPLDLTAPGVLSAERIKKFSWLGGGFTFSFATERLDDAILAALISLAEERGLHES
MLAMQQGQVVNYIEGFPSEMRPALHTATRAWVTDSSFTGEAEDIAVR SRVEAQRLKDFLTKVRSQFTTIVQI
GIGGSELGPKALYRALRAYCPTDKHVHFISNIDPDNGAEVLDTIDCAKALVVVVS KSGTTIETAVNEAFFADY
FAKKGLSFKDHFIAVTCEGSPMDDTGKYLEVFHLWESIGGRFSSTSMVGGVVLGFAYGFEVFLQLLQGASA
MDQIALQPNARENLPMLSALISIWNRNFLGYPT EAVIPYSSGLEFFPAHLQQCCMESNGKSIVQDGRRVGFST
SPVIWGEPTNGQHSFFQCLHQGTDIIPVEFIGFEKSQKGEDISFQGTSSQKLFANMIAQAIALACGSENTNPN
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EAASLLTLFNIKFR

>core/181/5/Org5_Gene267

MTKTEEKPFGLRSFLWPIHTHELKKVLP MFLMFFCITFNYTVLRDTKDTLIVGAPGSGAE AIPFIKFWLVVPC
AIIFMLIYAKLSNLSKQALFYAVGTPFLIFFALFPTVIYPLRDVLHPTEFADRLQAILPPG LLGLVAILRNWTF A
AFYVLAELWGSVMLSLMFWGFANEITKIHEAKRFYALFGIGANISLLASGRAIWASKLRASVSEGVPWGI
SLRLLMAMTIVSGLVLMASYWWINKNVLTDPRFY NPEEMQKKGKKGAKPKMNMKDSFLYLARSPYILL LAL
LVIAYGICINLIEVTWKSQKLQYPNMNDYSEFMGNFSFWTG VVSVLIMLFVGGNVIRKFGWLTGALVTPVM
VLLTGIVFFALVIFRNQASGLVAMFGTTPLMLAVVVGAIQNILSKSTKYALFDSTKEMAYIPLDQE QKVKGK

AAIDVVAARFGKSGGALIQGGLVICGSIGAMTPYLAVILLFIIAIWLVSATKLNKLFLAQSALKEQEVAQEDS
APASS

>core/182/5/Org5_Gene1019

MVWVFKSQFEGLSALKRGVHALTKAVTPAFGPRGYNVVIKKGKAPIVLTKNGIRIAKEIILQDAFESLGVKLA
KEALLKVVEQTGDGSTTALVVIDALFTQGLKGIAAGLDPQEIKAGILLSVEMVYQQLQRQAIELQSPKDV LH
VAMVAANHDTVLTGTVVATVISQADLKGVFSSKDSGISKTRGLGKRVKSGYLSPYFVTRPETMDVVWEEALV
LILSHSLVSLSEELIRYLELISEQNTHPLVIIAEDFDQNVLRRTLILNKLNRNGLPVCVKA PGSREL RQVVLEDLAI
LTGATLIGQESENCEIPVSLDVLGRVKQVMITKETFTFLEGGGDAEIIQARKQELCLA IAGSTSESECQELEERL
AIFIGSIPQVQITADTDTEQRERQFQLESALRATKAAMKGGIVPGGGVAFLRAAHAIEVPANLSSGMTFGFETL
LQAVRTPLKVLAQNCGRSSEEVIIHTILSHENPRFGYNGMTDTFEDLVDAGICDPLIVTTSSLKCAVSVSCLLLT
SSFFISSRTKT

>core/183/5/Org5_Gene7

MYQENLRLLERLLYNSVQKSYADRLFSYEKTKMVHDTPLIPWEEDKEKCAEAEKAFLEQQKILLDYGKSIFW
LNENDEINLNDPWSWGLNTVRTRKVFQEVD DSERWNHKVLIQKLEDDYEKLL EESSKESTEANKKLLSDLV
DRLEDAKTKFFLKKQEEVETRVKDLRARYGGTVDPKQDTEAKKKVELEASLETFLDSIESELVQCLEDQDIY
WKEQDVKDLARTQELEEQDIEAKREEAAEDLRSLNERLKKSKTMLDRAKWHIENAEDSITWWTSQIEMKD
MKARLKILKEDITSVLPEIDEIETCLSLEELPLLTRELLTKSYLKFKICSETLLKMTSVFENNIYVQEYEVQLQ
NLGFKLQGISQRFQKKQDDFANLEEQVALQKKRLRELTQNFEIQGFNFMKEDFKAAAKDLYIRSTAEQKMN
FDVPCMELFRRYHEEVNKPLLELMYNCADSYRDAKKKLC SLRLDEKELLQKEIKKEEFYQKKQQRHADRSR
HTTYQKLRIAEELALELKKKI

>core/184/5/Org5_Gene894

MVARGLCDFP TLVPNERLPIGPFFVPQHTSGAKGKEFAKRNF SIISGLDDILKLCILQRRPFALQWDNLSVKSD
YEEAGPAIGIRSLEPQVSQISPAHGRLCSTLVQWAPILGSEERLVWLEETMKRLKFPKSLGSKDAVIVDSEMP
VNANPTQEIPAASETVESSPVAPGNTTDTMPAASGTTDTTSGVSEAAAAEATVDSTPGTEEPSFSRLYALVV
QNVPPYPEPPKEPEVMFTDEEKSLILEATRARMELDLYNGYLADYELSKDEIQKHVPDLPENWRTNWRWSE
RLYKFFFKTKKEGLEEIFLNKELGNMILARGLAATQSQARIKVFNSLVAWLLQSFNVGRSCTAKPLPTSKLDL
FKSEFESKPKNNILTEFLVASDEEILFKGLRVLEPGIEGWYDHPDQAGEIRSVLEGLVQAGRISGYWENQPFGR
FVLRGVGERRTELVELLESLVASGEIMQFFESSDEEGAFIIDNEPSKTAMLKQRFKSCVRTKLVG SFADESLPR
GRFTILV

>core/185/5/Org5_Gene394

MLKVFEKFKKFAIVEIFTKVAVVSL LHKFLENASGKKGQSLASTAYLAALDHLLNAFPSIGERIIDE LKSQRS
HLKMIASENYSSLSVQLAMGNLLTDKYCEGSPFKRFYSCCENVDAIEWECVETAKELFAADCACVQPHSGA
DANLLAVMAILTHKVQGPVAVSKLGYKTVNELTEEEYTLLKAEMSSCVCLGPSLN SGGHLTHGNVRLNVMSK
LMRCFPYDVNP DTECFDYAEISRLAKEYKPKVLIAGYSSYSRRLNFAVLKQIAEDCGSVLWVDMAHFAGLV
AGGVFVDEENPIPYADIVTTTTTHKTLRGPRGGLVLATREYESTLNKACPLMMGGPLPHVIAAKTVALKEALS
VDFKKYAHQVVNNARRLAERFLSHGLRLLTGGTDNHMMVIDLGSLGISGKIAEDILSSVGIAVNRNSLPSDAI

GKWDTSGIRLGTPALTTLGMGIDEMEEVADIIVKVLNRNIRLSCHVEGSSKKNKGELPEAIAQEARDVRNLLL
RFPLYPEIDLEALV

>core/186/5/Org5_Gene727

MSEQEKLSNYNADKKLFSGIDKLFQIVKGSYGPKQSLSPTSFFKERGFYAISQTELSNSYENLGVDFAKAMVN
KIHKEHSDGATTGLILLHAILQESYAALEKGISTHKLIALSKLQGEKLQEALQQQSWPIKDALKVRNIIFSSLH
MPTIADHFYNAFSVVGPEGLISITKERENDKTSMDVFGFKIPAGYASTYFVSdTASRLTRIAHPLILITDRKIS
MIHSLPLLQEISEQNQHIIIFCEDIDPDVLATLVVNKLQGLLQVTVVTIPQLSTTNQELAEDIALFTGTHICPCQ
EASHVLAPEMVTLGSCLSIIESESQTTLIGGLHIPEVLTLKTRQLAEEIRTTSCLETKKRLIKSTNRLQSSVAILPT
DEDNEPLYTLALKIMESALSRGYVPGGGVALFYASLTLGTPKDDADENSIAISLLQKACCAPLKLLATNADLD
GDAVIAKLSSLGTTSLGISVFSREIEDLIAGGILDSLATTSTILAQALDTAILVLSSKILILENQYEISTL

>core/187/5/Org5_Gene778

MENEILLNIESKEIRYAHKNGQLFDLTIERKKVRQLKGNIYRGRVTNILRNIQSAFINIDERENGFIHISDILENS
KKFEQMFDMDVDALPEEASEAPLLSSEEAPIEEFLKLDSPVLVQVVKEPIGSKGARLTSNISIPGRYLVLNPNSP
HRGVSRKIEDPHMREQLKQLIRSFEMPQDMGLICRTASTASTEALINEAHDLLLTWKTILEKFYSTEQPCLLY
SETDILKKAVITCIDKNYKRLIDDYATYQKCKHMLKKYSPDASIKIEYYRDSIPMFERFNIEKEIDKATRRKI
WLSSGGYLFFDKTEAMHTIDVNSGRSTQLESGVEETLVQINLEAAEEIARQLRLRNVGGLVIIDFIDMKSRKN
QRRVLERLKEHMKYDAARCTILSMSEFGLVEMTRQRNRESLMQTLFTLCPYCSGNAIIKTPESVVIEIERDLK
KVINHKEHSHLCLVVHPEIASYMKQENDDNEMINLAKQLKAKLQINTSDSVHLNHYQFFSLITGESIDL

>core/188/5/Org5_Gene218

MFNLFFFTANKETTASHELIYRKNQSFSLSPVTILCLLAISVLLLLGVVFALVGCHVLAAPLGLLVWGCAASV
CSMMAIVSLMCLYKGGKPLIEPSNEEKIDPTKDLEIKDPESLKPVPVEGQSLPKERKTVSFKAKIPSIVEDDFKP
YVIQSTFYHQNKVYSKPIAERMQSLEKEITTLIVDFPRALEESSKSSGSLRGVISEIKNLFLPRFLSRKVKYSLT
ACLRRLGSIVEEYASSDLLILLTKPEPLNMVTQQLIAHLNSLKTEKRKLTPHMQKLVLINFWFYGWSLEEK
CIEKIVAYDPNLLTDELKAHLEAGNIVQFLSFQSSEMQRERFALFPSDAQELPSAKDGSNYVPAINSEYMY
DFKDL SVLKKSLSERLAFCEKIPSPSSWNFTSSVASHYKDFSLLFTFFSNQQSVILQNPFLLIELLHENPKCQTF
KGLLEKAMPMSNWAALFRPMLMGMLCSGIARKKELKIIAEHLGVPFKEITQAIASGKILDLLQLHLFDF

>core/189/5/Org5_Gene349

MTILRNFLTCSALFLALPAAQVVYLHESDGYNGAINNKSLEPKITCYPEGTSYIFLDDVRISNVKHDQEDAG
VFINRSGNLFFMGNRCNFTFHNLMTEGFGAAISNRVGDTTLTLSNFSYLAFTSAPLLPQGQGAIFYSLGSVMIE
SEEVTFCGNYSSWSGAAIYTPYLLGSKASRPSVNLSGNRYLVFRDNVSQGYGGAISTHNLTLTTRGPSCFENN
HAYHDVNSNGGAIAIAPGGISISVKSGLIFKGNTASQDGNTIHNSIHLQSGAQFKNLRAVSESGVYFYDPIS
HSESHKITDLVINAPEGKETYEGETISFSGLCDDHEVCAENLTSTILQDVTLAGGTLSLSDGVTLQLHSFKQEA
SSTLTMSPGTTLLCSGDARVQNLHILIEDTDNFVPVRIRAEDKDALVSLEKLKVAFEAYWSVYDFPQFKEAFT
IPLLELLGPSFDSLLLGETTLERTQVTTENDAVRGFWLSWEEYPPSLDKDRRITPTKKTVFLTWNPEITSTP

>core/190/5/Org5_Gene179

MTNVVQETIGGLNSPRTCPPCILVIFGATGDLTARKLLPALYHLTKEGRLSDQFVCVGFARREKSNELEFRQEM
KQAVIQFSPSELDIKVWEDFQQRLFYHRSEFDNNMGYTSLKDSLEDLDKTYGTRGNRLFYLSTPPQYFSRIEN
LNKHKLFYKNQDQGKPWSRVIIKPFGRDLDSAKQLQQCINENLNENSVYHIDHYLGKETVQNILTTFRANTI
FESCWNSQYIDHVQISLSETIGIGSRGNFFFEKSGMLRDMVQNHMMQLLCLLTMEPPTTFDADEIRKEKIKILQR
ISPFSEGSSIVRGQYGPQTVQGVSVLGYREEENVDKDSRVETYVALKTVINNPRWLGVPFYLRAGKRLAKKS
TDISIIFKKSPYNLFAAECSRCPIENDLLIIRIQPDEGVALKFNCKVPGTNNIVRPVKMDFRYDSYFQTTTPEAY
ERLLCDCIIGDRTLFTGGDEVMAWKLFTPVLEEWDQDSSPSFPNYPAGSSGPKEADALIERDGRSWRPL

>core/191/5/Org5_Gene828

MSSWLSQASEVLLNQDPYIPDAPRSQESSVPKISYSITVAPQEAQKSLPKFFTQKFQSQCKSEPPITHHKTFIAT
PRERILRFGSSFESQLHNTSQAQTSSPWNLFQKNSTEASKALMQELTMPKSPEKTSEKALDKNLSSKQEGSC
KNFDTLHLQQHLKLFQTVDSLVSQSLDSEQQELLQSRREERSETYANQQSSEKKIETKVQIKDLCKDLFSQDQ
DSNQKQKKSPFQQDTSRKNRIAKAAQAVPVIPPSIGVFTLSYLLTKQGILSDFSSYGCHKDSVESTQRELDAL
HEKRIETIKVSIEKEKRERLWGSLSDIIGWLAPFVVISIGIVAILSGGGIFAFAGFFAGLISLVIKCLEKLKFWDW
LEKHLPIKNEELRRKIITHIQWVVYLTPVILSICTLKVENLGFSPHIEGAIKGIQPAIESTMAALRCAILFSQAEIYK
LKGKLTQIQLDIELKSFDRDDHYERSQELLDNMESSFEALSRLNYMRELDQVYLHSLRG

>core/192/5/Org5_Gene902

MAVGGVGGSRSPPIPPNRRNSEDGKVSPKDNLGEHTVSSSDSSLASQGPTIEERKAQLGGTDKIPLPSVKEPG
DSPTSGRSGVLQRIWKGVKGVFKKTPQARPEVSSPRLPSHVQHGQRLPGLEGFRDRIQKRSENPEADLGKMK
RSYSDGDLDRVGHDSNEDSTEDSRSEGGEPSKSSSFLSGVRGAVSKVHGALGDIKGFQRSASEDDLTTQG
EDSAGDTVKERRSEEAEASSKSSSFLSGVRGATSTVQGALGDAKEKVSAFGEQAAGAIRSAPGNIRTRFQRSS
SEGDLNVNKAAKHLRKALLENLEKVAPEQVSPEVASRVQSLLARMEQLTHQEPTVEDLITFVESNVGSDSV
EYASIVPDGGSQAPAETAETAPETGGVEGSAAQGAWKALRDFVVSIFQAVASFFRAIASRLSSARRESAVDDL
ASESNTQWFVEQEGVSNPSAAPSLSFAEEIARRAAEMSNRNAQSLEKLESGNVTDPVIQQGLGLARSFAPEGQ

>core/193/5/Org5_Gene107

MADILVIGANPTGLILANMLIQHGISVKVIDHRASPEDPSFLDCRKLVPVILSCSSLELLHNSEMLGDFIQANHKI
FGARYHWKKRTLLFKFSQATDSPVPFSLSTTYQSLEQHLIDEFLKRGGVIDWSTRPVTLVDNSIFIESTKVSQN
FENREIYNPKWIIACEADNNLDIRDLVKSQLRARRINREVIFINCDEGEPEEDHIIHLLPITKNFLNFVFYNPQEK
TKQLCLPQGTHSISPKLKQKLLYTYNLVISDENFHIKTSHHAFPEHGNVLFGLSLSNTLLLSYLNGINNTNIHAA
FNLAWKLLPVLKKAALKHLVITKEQEDGNILPYISPTTEKRAKKLPFSRFYTPALMYFLKGCRKFNTTGEEY
YYPHQALKYRSSDIKMSPQDKEIHGPGPMRAIDARLENGSFLLDPLKSSKHLLIFFKDIPDLKEALQEEYG
EWIEICNVKEPRILNLYHANPNLSFIIRPDRIYIGYRTHTFKLHELISYLLRIFASEKTS

>core/194/5/Org5_Gene429

MNWENVVRVAVAPSTGDPHVGTAYMALFNEIFAKRFKGMILRIEDTDRTRSRQDYEEENIFSALRWCGIQW
DEGPDVGGPYGPYRQSERTKIYQGYVETLLKTDCAYKCFATPQELAEMRAVASTLGYRGGYDRRYRYSPE
EVASREAAGQPYTIRLKVPLSGECVFEDYSKGRVVPWADVDDQVLVKSDFPTYHFANVIDDHLMGITHV
LRGEEWLSSTPKHLLLYEAFGWEPVFLHMPLLLNPDGTKLSKRKNPTSIFYRDSGYVKEAFVNFLTLMGY
SMEGDDEVYSLERIIETFNPRRIGKSGAVFDIQKLDWMNKHLYLNHEGSPECLLKELQGWLLNDEFFLKILPLC

QSRITTLAEFINLTSFFFSGLLEYRVEELLPQALSPEKAAILLYSYVKYLEKTDQWTKETCYLGSKWLAQAFN
VHHKKAIIPLLYVAITGKKQGLPLFDSIEILGKPRARARLVYAEKLLGGVPKKLAATVDKFMQREDFEEATFD
L

>core/195/5/Org5_Gene560

MDCRGGIPLPEPQVIGGYHVKKILSKKLRSRVVHGLHPETRHSTVIKVFSPSPSFTSRSVYNFLKEAQSLHQIT
HPNIVKFHRYGKWQDCLYIAMEYIEGISLREYILAQFISLPQAIDIIFDIAQALEHLHSRNILHKDIKPENILITPQ
GKIKLIDFGLADWDTEIQRHPSVIGTPYYMSPEQRQGESHSPASDIYALGLLAYELILGHLSSLGRVFLSLVPE
RISKILAKALQSPNNRYSSTREFIQDIHHYRMSGDMQEDLRIKDHTVALYEQLQTQRFWLAPETLRFPDFISG
VLYHQGYPLYPHAYDTLLEGDVFNLWLGYSNISNATIALSVVKSLSVCQQDLQRPLLDRCVCEINECLIRMKIPI
DEMGISILCLEISKENKELSWIACGKTVFWIKRQGRVVQDFESFSPGLGKITSLQIRETKVAWEIGDEAVVCTL
ELEESVASLKTLSLAELQDRRQKAIFCPIESIHGGIQSRQHGSNSPSTLISLKRIR

>core/196/5/Org5_Gene334

MLKKFINSLWKLCQQDKYQRFTPIVDAIDTFCYEPIETPSKPPFIRDSVDVKRWMMMLVVIALFPATFVAIWNS
GLQSIVYSSGNPVLMEQFLHISGFGSYLSFVYKEIHIVPILWEGLKIFIPLLTISYVVGGTCEVLFAVVRGHKIAE
GLLVGTGILYPLTLPPTIPYWMAALGIAFGIVVSKELFGGTGMNINLPALSGRAFLFFTFPAKMSGDVWVGSNP
GVIKDSLMMKNSSTGKVLIDGFSQSTCLQTLNSTPPSVKRLHVDAIAANMLHIPHVPTQDVIHSQFSLWTETH
PGWVLDNLTLTQLQTFVTAPVAEGGLGLLPTQFDSAYAITDVIYIGIGKFSAGNLFWGNIIISLGETSTFACLLG
AIFLIVTGIASWRTMAAFGIGAFLTGWLFFKISVLIVGQNGAWAPARFFIPAYRQLFLGGLAFGLVFMATDPVS
SPTMKLKGKWIYGFFIGFMTIVIRLINPAYPEGVMLAILLGNVFAPLIDYFAVRKYRKRGV

>core/197/5/Org5_Gene189

MKFEFSVALKYLPGRGRLYSAIVSLFSVGIISLVVWLSIVFISVIHGLEQRWIEDLSQLHSPITILPSDTYYSSYY
YQIDKHSSLSNYTTKTLGEKIASPQVDPYPDES DYLLPETFPLKDCDLGGQQKDPVKMTLES LGPYLQSQH GK
VIEFEQGVGYLDIKTSLKLQKPQPRNLTHFLTYP SKLSYEDKVL PYDET DYTS AELNPFNRSPSGWQQDFHHL
EELYRGASIILPSTYKDSGYKVGDTGVFSTYSIENEKETQYTVHVIGFYNPGLSPLGGRTVFIDPDLARSIRSQS
EGLGMSNGFHLFFPNTKRIVFVKQIENILTSLGVDDYWEISSLHDYDYFQPILDQLQSDQVLFLFVCILILIVA
CSNIVTMSMLLVNNKKKEIGILKAMGTSSRSLKIIFACCGAFSGACGVVIGTIFAITLKNLQFIVKALNYLQGR
ETFNTAFFGQNLPSVHPQAIYFLGLGTL LLA AVSGALPARKVAKMHVSEILKAD

>core/198/5/Org5_Gene295

MVLFHAQASGRNRVKADAIVLPFWHFKDAKNAASFEEFEP SYLPALENFQGKTGEIELLYSSPKAKEKRIV
LLGLGKNEELTSDVVFQTYATLTRVLRKAKCSTVNILPTISELRLSAEEFLVGLSSGILSNYDYPRYNKVDR
NLETPLSKVTVIGIVPKMADAIFRKEAAIFEGVYLTRDLVNRNADEITPKKLAEVALNLGKEFPSIDTKVLGKD
AIAKEKMGLLLAVSKGSCVDPHFIVVRYQGRPKSKDHTVLIGKGVTFDSGGLDLKPGKSMLTMKEDMAGG
ATVLGILSALAVLELPINVTGIIPATENAIDGASYKMGDVYVGM SGLSVEICSTDAEGRILILADAITYALKYCK
PTRIIDFATLTGAMVVSLGEEVAGFFSNNDVLAEDLLEASAETSEPLWRLPLVKKYDKTLHSDIADMKNLGS
NRAGAITAALFLQRFLEESSVAWAHLDIAGTAYHEKEEDRYPKYASGFGVRSILYYLENSLSK

>core/199/5/Org5_Gene827

MTVSYQSISTPPPEGEFDIFVDGNATEEAVVAAEVQVALPAGEQYAMLRATSELFCGILTQSECA LTQALPPK
EKPLQEEQFLVKNGILMRSTSLPNLKPGQSQQTSLASHRNPLAQQSTSSNSTGKASTETTSSSFPFFSCKAPEG
DSSVDKTFTVSVQTPKAQEQQEASASQSQAQFHVRSYSSSTIKEHSAKEKVSQSTKSAETQKHTQTKSDATLS
PMSLYSTLHKEVPQALSSTKSQQKDEEHRDQRQQEGYEQEQEQQEKGKKTPWCTVESLQQTSSSNQVYESY
TPIIPDPIVEFALSESQLSVLAGKRVTNLDVLRICTELMKMLKSRANDTMTRLEERELMEREAEHELAASYSR
QAKYARWLGIATATLGILGAIAPMVGEISGDSILGFVQRISGRFKDATAKTFFKGIGKVFTSLSQLTEAASKVH
ELSESAVRAVAEYRKEVFRMRQDEVTRTIEEVKDNWKSMDNFLLNILQTEHDAARSLYQ

>core/200/5/Org5_Gene657

MAASILSQELLDILPYTFLKKHCLLPIEESSEAITIAHATATSVIAQDEVKLLIKKPVRFVLKEESEILQRLQQLY
SNREGNVSDMLLTMKKEEDGTTISEEEDLLETTDTIPVVRLLNWILKEAIEERASDIHFEPCEDSMRIRYRIDGVL
HDRHSPPSHLRSALTTRLKVLAKMDIAEHRLPQDGRIKIHIGGQEVDMRVSTVPVIYGERVVLRIIDKRNVL
DIAGLHMPKGTEILFKDTITAPEGILLVTGPTGSGKTTTLYSVLQELKGPLTNIMTIEDPPEYKLPGIAQIAVKP
KIGLTFARGLRHLLRQDPDILMVGEIRDQETAETAEIAQAALTGHLVVSTLHTNDAISAIPRLLDMGIESYLLSATL
VGVVAQRLVRTICPYCKVAYTPENQEKSFSLASLGKDTEMPLYRGQGCVHCFRSGYKGRQGIYEFLRPNTLFR
SEVASNRPYHILRETAEQNGFLPILEHGIALAVSGETTLAEVLRVTKRCD

>core/201/5/Org5_Gene937

MNKKHASFSSRLGFIFSMIGIAVGAGNIWRFPRVAAQNGGGAFLILWLCFLFLWSIPLIIIELSIGKLTKKAPIGA
LIKTAGKKFAWAGGFITLVTTCILAYYSTIVGWGLSYFYAVSGKIH LGNDFAKLWTSHYQSSIPLWAHLTSL
GLAYLVIRKGI VHGIEKCNKILIPAFFLCTIALLLRAVTLPGAVQGKQLFSCDKSCFSNYKVWIEALTQNAWD
TGAGWGLLLVYAGFASKKTGVVSNGALTAICNNLVSLIMGIIIFSTCASLDILGTTQLQDGAGASSIGITFIYLP
ELFTRLPGGIYLTTLFSSIFFLAFSMAALSSMISMLFLLSQT LAEFGIKPYISETLATIIAFVLGIPSALSLTFFSNQ
DTVWGVALIVNGLIFIYAALVYGFPKLKKEVINAAPGDLRLNKAFDYIIKYLLLLIEGILLLGWYFYEGFLPENG
QWWNPISLYSLGSLVLQWSLGLIILWKFNKQLYLRFSRYNHEIL

>core/203/5/Org5_Gene463

MLKYILKRLVLIPLTLFAIVSINFVILNAAPGDVLEEKS RDALGEAGKSDKMRSYKGPDRYLQFREHYGLTLPI
FFNTRPKITHKKIQTALQELANANNTTPSAKNAAKSLVYWGDCAKFVMPALLFEADDASRDDKYRHIAADL
FIRGGVLQGFVGP NLSPEQRAQNKEIAESNAFLVRQLNEEDLDTKVEALKGWFQDHGGTEVFCYSSKQFWK
TFFLETRFARYMSRVLR LDFGTLRND AHKTVISEVIKRLRCSLVLSILPMIVGFVLCQIFGMIMALKRNRWIDH
SLNFIFLILFSIPVFVAVPWILDNFVINKTIPFTTIPMPYSGLRSPPEVFNELSTLGRIFDLVSHGFLPFCVSYGAL
AAQSRLSRSIFLEVLSQDFICAAKARGLRWFDILYKHVGKNAAVSIVTSLASSLGTLLGGALVVETLFNIDGFG
NFFYQAILNRDHNVVLF SVLVGSALSLVGYLLGDICYVLLDPRVQLEGRRI

>core/204/5/Org5_Gene1022

MHTEFAPFLEDLVHQQVISPLDIAFASKHISSDFEESFVFLAVSSALWRYGHPFLSLEENRIRPSLGGISETDLY
RGFHNLPKEVRDKLFVVVSGRLYLRSLYTIRSKLLDKLSLLCSATPNYFPSPSIDSSILSEEQNFI FNKITQGCFSI
VSGGPGTGKTFLAAQLILSLVKQQPKLR IAIVSPTGKATSHIRQILMKYNIFDDMVLMQTVHHFLQEYAYRRY
NSIDVLLVDEGSMVTFD LLYSLVQTLQGYEKDKKLYTSSLIILGDTNQLPPIGIGVGNPLQDLIGYFHENTFFL
KTSHRAKTGVVDQLTQSVLRGEMISFSPLPSISSAIEVLKNRFVKSLRQSEARLCVLT PMRHGPWGVLNLNTM

IHQRLARSDPDLRIPIMVTSRYETWGLFNGDTGLLCLKTQKLHFPQHEPIDSRALSQYVYNYVMSVHKSQGSE
YDEVIVIIPKGSEVFGVSILYTAITRAKYRVSVWGDPE TLHKIIKKS NY

>core/205/5/Org5_Gene792

MLNHAKKHAKPYVLIFSTKDKLSYCDIIFNNCSGKPMNLDSKHFDINSANFLEEF AKFISFPSISADSDHLQD
CENCAHFLVDHVNKIFDVELWETPGHPPIIYASYKSEDPLSPTLMLYNHYDVQPAQLSDGWKGDPFILREEN
GNLYARGASDNKGQCFYTLKALQHYYESQGNFPLNIIWIEGEEESGSLALFTWLEKKKEALRADYLLIVDG
GFLSEKHPYVSIGARGIVSMKISLEEGNKDMHSGVLGGIAYNTNRALSEILSSLHHPDNSIAIEGFYDDLALPS
DSDRPDLPKSDTLRECEENLGFRPQGYEASYSPEESALRPTVEINGISGGYTGPFGKTVIPYRATAYLSCRLVP
NQDPDKAAHQVIHHLKQQVPSSLKFSYEILPGGSRGWRSSANLPVKVLQEIYSDLYNEECLRLVMPATIPIGP
LLGEAAQTSPHICGTSYLSDDIHAAEEHFSMDQLKKGFLSICQLLDKLPKIKE

>core/206/5/Org5_Gene1015

MSISSSSGPDNQKNIMSQVLTSTPQGVPPQDKLSGNETKQIQQTRQGKNTMESDATIAGASGKDKTSSTTKT
ETAPQQGVAAGKESSESQKAGADTGVS GAAATTASNTATKIAMQTSIEEASKSMESTLESLSAAQMKEV
EAVVVAALSGKSSGSAKLETPELPKPGVTPRSEVIEIGLALAKAIQTLGEATKSALS NYASTQAQADQTNKLG
LEKQAIKIDKEREYQEMKAAEQKSKDLEGTMDTVNTVMIAVSVAITVISIVAAIFT CGAGLAGLAAGAAVG
AAAAGGAAGAAAATTVATQITVQAVVQAVKQAVITAVRQAITAAIKAAVKSGIKAFIKTLVKAIAKAISKGI
SKVFAKGTQMIAKNFKLSKVISSLTSKWVTVGVGVVVAAPALGKGIMQMQLSEMQQNVAQFQKEVGKLG
AAADMISMFTQFWQQASKIASKQTGESNEMTQKATKLGAQILKAYAAISGA IAGAA

>core/207/5/Org5_Gene3

MYRYSALELAKAVTLGELTATGVTQHFFHRIEEAEGQVGAFISLCKEQALEQAE LIDKKRSRGEPLGKLAGV
PVGIKDNIHVTGLKTTCASRVLENYQPPFDATVVERIKKEDGILGKLN MDEFAMGSTTLYSAFHPTHNPWDL
SRVPGGSSGGSAAAVSARFCPVALGSDTGGSIRQPA AFCGVVGFKPSYGAVSRYGLVAFASSLDQIGPLANT
VEDVALMMDVFSGRDPKDATSREFFRDSFMSKLS TEVPKVIGVPRTFLEGLRDDIRENFFSSLAIFEGEGTHLV
DVELDILSHAVSIYYILASAEAA TNLARFDGVRYGYRSPQAHTISQLYDLSRGEGFGKEVMRRILLGNYVLSA
ERQNVYYKKATAVRAKIVKAFRTAFEKCEILAMPVCSSPAFEIGEILD PVTLYLQDIYTVAMNLAYLPAIAVP
SGFSKEGLPLGLQIIGQQGQDQQVCQVGYSFQEHAQIKQLFSKRYAKSVVLGGQS

>core/208/5/Org5_Gene1057

MNGCWEDLKQTIFWVGEHDCTDIETVRKSCMWLD RYADKFILREKEEKMERHEL FHATMVRKASGHAYA
KAKAAFEKERSNENQRKVKDVEKWLSKGLAEFRNQESRRARERLRELQ TLYPEVSVEERVLERQRTKKVNL
ENLYADIEKKYHHCVREQEHYWKEVENKEAEYRENGEKVLSAE EVSECLQRLEDCL ETWSKKLTKAESVF
EMKFDATEKLGKVLSDVTNRLEILCEDAEEMIFRIEEIEMTLRMVELPLLF MKNTFEKASLQYNSCKEMLA
KVPEPQCKESPTYRSSQERLERLNQDLQTAYTNCQERLQGFSDLESKVRTCRDHLREQMKHFEVQGLNFINEE
LLWVGAEFLTQARLDLVATVPYMEFYLYHNIKREK VRSQWMAKTERYREIRQAFQGV MKEDLLAEDTIL
KEEDYWLLRDDWLLRDERKNRQRRLICNKIAAAQQRVKGF

>core/209/5/Org5_Gene959

MLGILLIASGIIFLAVAIPGLSSAVALGLGCGMTALGTVLLITGLVLLIRSEKLALAEQVEIKQARTRVNNELDQL
SQYVFYTENVLNLRWSYRDLGFVRQAQEEVTNLEQDIEEIFLTRDIRNALDNEEFFMTHAKQCLAQVGE
SLFQDASIDEFINLAHLSEIRQHLNDINDPRWSMITKKVKGTVVRFIYVSTMYKQIKSNFEKSDFGQLRKMLLN
NYKTIEEVLYQSFQRGYNRAALLSEKTRIIHTSSLLHWEKDEDEKHLNIKNECASRLNFKKFRTLFLGLSEEDV
IDFTGASGWDCSKLPRKEVPLDGGGKKLRFKRTFADEQVGDWDRTTSLEHMTPQEEDPLDRLMDQVEQEAT
SVLKDQDRYWKEIETSEAKFRSLPREDDFEKQSQIDSYIRDLDDHLSVWANQLSAAEDALIEVTDVQEHGNR
EMLKNIQQGLELIEDAVKATLPRVDFIQELLEKEELPLVAARMSLENS

>core/210/5/Org5_Gene871

MTFPCGNCNCYYRETPPPNPGGEDIPLQEGGQSGSQGGRVITQQPGTGGREMGISLGSDNVLGMVEQAGSLL
NNLLDSARMQRLGHYCYRTGTPWCREHCPGFLQWIWGGCCACCLETVDDPDNPSAQFLQQLIQQYGPICVG
MSFQQLPHCTQKIEQGEPLGDGDKQEVENGCKLHRELLKAAQPRCMGESLVKLLQNNGLGEDMQQTTPWS
LILQAVSEGALSFVTSSDNPPTCWILQPEQQPCPPPTDEEQLQGAVGGAPAPQQKKHPAQECRVTCCLNFRT
LLQKLSRLEVLSLESYGKGPLGQAAKQIVDLIKKSLKRLVASDLATFLGPGIGLSLESQVFEVLVLLCLLSKGY
LPLDPLHPEQTVLDPRVQGPWQRILRKVLVTTTAGENIWRQTQGEAPRQAPPPDPWDDDEIERDGIVTGGG
FGIPCQCLRCWRKLPTEKRPNRWL

>core/211/5/Org5_Gene782

MHMSNPISLFSAPAEIAKYNLIPKTSPIYPRRTELIILEENACQTRLTNVAQVLHPSSLFMSKKILNPCGCSGGP
LCWVILNILAFIITSVLFIILLPVNLIVAGLRLFMPLPPKKIVEDLSEPTTEETNEVIQPFIFALQALLFEDNKLRSF
KIVEQSVGKAPLPNPFLNRLVAISPQESQEAMRKIPDLCSQLKKVLKSLGVLTPEWKHMLKYFEGLKNEHDS
NPDKKTFPILIKLLIEALTGKSSLPKTPSTKEKMQAALFIASSCKTCKPTWGEVITRSLNRLYSIANEGDNQLLI
WVQEFKERELMSIQDGDAAEEYRFAAQQHGERYTEAIEQVLRNESAAKLQWHVINTMKFFHGKNLGLVTE
HLQDTLGALTLRQTTVDTHQGREDADLSAALFLNKYLNsgnQLVNSVFKSMQKADPETKALIREFALDILYA
SLRLPQTSAHTEVFSTLLMDPETYEPNKACIAYLLYVLKIIEL

>core/212/5/Org5_Gene4

MSAVYADWESVIGLEVHVELNTASKLFSSALNRFGDEPNTNISTVCTGLPGSLPVLNQSAVEKAVLFGCAVE
GEISLLSRFDRKSYFYPDSPRNFQITQFEHPIIRGGRIKAIVQGEERYFELAQTHIEDDAGMLKHFGEFAGVDYN
RAGVPLIEIVSKPCMFCPEDAVAYATSLVSLLDYIGISDCNMEEGSIRFDVNVSVRPKGSPELRNKVEIKNMNS
FAFMAQALEAEKQRQIDEYLNQPNKDPKLVIPAATYRWDPEKKKTVLMRLKESAEDYKYFPEPDLPTLQLTE
SYIERIRKTLPELPYDKYHRYIQEYGLSEDIASILISDKNIATFFEVACKDCKNFRSLSNWVTVEFGGRCKTLGV
KLPSSGIFPEGVAQLVNAIDQGVITGKIAKEIADLMMESPGKNPEEILKEKPELLPMSDEGELQKIIAEVVLANP
ESIVDYKNGKTKALGFLVGQIMKRTAGKAPPKRVNELLLLLLELDKG

>core/213/5/Org5_Gene992

MITKQLRSWLAVLVGSXLLALPLSGQAVGKKESRVSELPQDVLLKEISGGFSKVATKATPAVVYIESFPKSQA
VTHPSPGRRGPYENPFDYFNDEFFNRFFGLPSQREKPSKEAVRGTGFLVSPDGYIVTNNHVVEDTGKIHVTL
HDGQKYPATVIGLDPKTDLAVIKISQNLPLYLSFGNSDHLKVGDWAIAGNPFGLQATVTVGVISAKGRNQL
HIADFEDFIQTDAAINPGNSGGPLLNIIDGQVIGVNTAIVSGSGGYIGIGFAIPSLMANRIIDQLIRDGQVTRGFLG
VTLQPIDAELAACYKLEKVYGALVTDVVKGSPADKAGLKQEDVIIAYNGKEVDSLSMFRNAVSLMNPDTRI

VLKVVREGKVIEIPVTVSQAPKEDGMSALQRVGIRVQNLT PETAKKLGIA PETKGILIISVEPGSVAASSGIAPG
QLILAVNRQKVSSIEDLNRTLKDSNNENILLMVSQGDVIRFIALKPEE

>core/214/5/Org5_Gene976

MWNRCQVFSSFFFRYPISSWLIRLRASCECFQQRHPIFLCGLYWLAGITSRGYPECSALILIFLGMFLPRNPKQ
WLPLASAWIISLMLTPAPFLHDGPISGTFVIHHAGGQGTYYGEALCIQTPCGKRAHHLSCQILSESRLKLVY
ELEGTLHHTSQIVFKSNACYKEIPRSRFYIMKEKCRESSCHFLNHRFPSSEVGPFASSLLGTPLPQNLRDLFRQ
KGLSHLFAISGWHFSLCATTWMLCALLPLKIKILSFIVLTSLACIFPMSLSVWRSWISVTLLCFSWCFSGSCS
GLNRLGAGFILCSIFFSPFSPTFVLSFLATLGILLFFPKIFSFLYTPWTQFLSPFWLYPIRYLAMTLAISLSAQLFIV
LPIMQYFGSLPLEGLLYNLIVPFTILPIIVFLIATILPCCSPITEALIQGFLSHPWLHNPNIKTLTSFAPVPPWMLTL
ASLILFFIGILRTNVSPYASTSATSRYFIETL

>core/215/5/Org5_Gene681

MLKIAILGRPNVGKSSLFNRLCKRSLAIVNSQEGTTRDRLYGELHAFGVPAQVIDTGGVDHNSDYFQKHIYN
QALTGAKEADVLLLVIDIRCGITEEDAHLAKLLLPLKKPLILVANKADSRQEELQIHETYKLGIRDIVVTSTAH
DKHIDTLLQRIKLVANLPEPREEEEEGLEELSVDEHEESEAAALPSNTFPDFSEVFTEGFSPEEPTIPESPQQAPK
TLKIALIGRPNVGKSSIINGLLNEERCIIDNTPGTTRDNIDILYSHKDRQYLFIDTAGLRKMKSVKNSIEWISSR
TEKAISRADICLLVIDATQKLSSYEKRILSLISKRKKPHIILINKWDLLEEVRMEHYCKDLRATDPYLGQAKML
CISATTKRNLKKIFSAIDELHHVVS NKVPTPIVNKTLASALHRNHPQVIQGRRLRIYYAIQKTTTPLQFLFINA
KSLTKHYEYYLKNTLKSSFNLYGIPFDLEFKEKPKRHN

>core/216/5/Org5_Gene988

MNMPVPSAVPSANITLKEDSSTVSTASGILKTATGEVLVSCTALEGSSSTDALISLALGQIILATQQELLQSTN
VHQLLFLPPEVVELEIQVVDLLVQLEHAETITSEPQETQTQSRSEQTLPPQSSSKQSALSPRSLKPEISDSKQQQ
ALQTPKGS AVRKHSEAPSPETQARASLSQASSSSQSRSLPPQESAPERTLLEQQKASSFSPLSQFSAEKQKEALT
TSKSHELYKERDQDRQQREQHDRKHDQEEDAESKKKKKKRGLGVEAVAEEPGENLDIAALIFSDQMRPPAE
ETSKKETTFKKKLSPMSVFSRFIPSKNPLSVGSSIHGPIQTPKVENVFLRFMKLMARILGQAEAEANELYMRV
KQRTDDVDTLTVLISKINNEKKDIDWSENEEMKALLNRAKEIGVTIDKEKYTWTEEEKRLLKENVQMRKEN
MEKITQMERTDMQRHLQEISQCHQARSNVLKLLKELMDTFIYNLRP

>core/217/5/Org5_Gene985

MTSRTKSSKNLGTIALAGMVVSSIIGGGIFSLPQNMAATAGAGAVILSWILTGFGMFFIANTFRILSTIRPDLKE
GIYMSYREGFGPYIGFTIGWGYWLCQIFGNVGYAVITMDALNYFFPPYFQGGNTLPAILGGSILIWVFNFIVLK
GIRQASIINVIGTIFKIIPLIIFIILTAFFFKLAVFKTDFWGHAVTKAQPSLGSVSSQLKGTMLVTLWAFIGIEGAV
VMSGRAKNPLSVGQATVLGFLGCLTIYILFSLLPFGSLFQHQLANIPNPSTAGVLDILVGKWGEVLMNVGLIIA
VLSSWLSWTIIVAEIPFSAAKNGTFPEIFTIENKEKSPSVSLYITSSVMQLAMLLVYFSSNAWNTMLSITGVMV
LPAYLASAAFLFKLSKSKTYPKKGSIKAPLAMITGILGVVYSLWLIYAGGLKYLFMALVLLALGIPFYIDAGK
KKKNAKTFFAKKEIVGMTFIGLLALTAIFLFSTGRIKI

>core/218/5/Org5_Gene65

MITR TKI ICTIGPATNSPEMLAKLLDAGMNVARLNFSGSHETHGQAIGFLKELREQKRVPLAIMLDTKGPEIR
LGNIPQPISVSQGQKLRLVSSDIDGSAEGGVSLYPKGIFPFVPEGADVLIDDGYIHAVVVSSEADSLELEFMNS
GLLKSHKSLSIRGVDVALPFMTEKDIALDKFGVEQNMDDVVAASFVRYGEDIETMRKCLADLGNPKMPIIAKI
ENRLGVENFSKIAKLADGIMIARGDLGIELSVVEVPNLQKMMAKVSRETGHFCVTATQMLES MIRNVLPTRA
EVSDIANAIYDGSSAVMLSGETASGAHPVAAVKIMRSVILETEKNLSHDSFLKLDDSNSALQVSPYLSAIGLA
GIQIAERADAKALIVYTESGSSPMFLSKYRPKFPPIAVTPSTSVYYRLALEWGVYPMLTQESDRAVVRHQACI
YGIEQGILSNYDRILVLSRGACMEETNNLTLTIVNDILTGSEFPET

>core/219/5/Org5_Gene551

MGESVKVFLEEREDYPYGFVTPIESQGLTRGLSEETIEEIAALRNEPQFIIDFRLQAYRYWKQLHEPAWARLH
YGP IAYDDIVYFSSPKQKKPLGRLEDADPEILDTFKKLGIPLDEQKRLNVENVAVDLVFDSVSIGTTTFKEALE
KAGVIFCSLGEAIQEHPNLVKKYLGSVVSHRDNFFAALNAAVFSDGSFVYVPKGVKCPMDISTYFRINNKEA
GQFERTLIVVEDGGYASYLEGCTAPAYSSNQLHAAVVELVAHEHAVIRYSTVQNWYAGDKKTGKGGIYNFV
TKRGLCAGYRSKISWSQVEVGAAITWKYPSCILKGDES VGEFY SVALTSGKMQADTGTKMLHVGKRTTSTV
ISKGISSESKNTFRSLVSLGKKA EHSSNYTQCDSMLIGKASGAYTDPKIVVENSTSSIEHEATTSKLREDQLLY
LRSRGLSPEEAVSLVIHGFCREIIEQLPLEFAQEASKLLLIKLENSVG

>core/220/5/Org5_Gene325

MDLKELLHGVQAKIYGKVRPLEVRNLTRDSRCVSVGDIFIAHKGQRYDGNDFAVDALANGAIAIASSLYNPF
LSVVQIITPNLEELEAELSAKYEYEPSSKLHTIGVTGTNGKTTVTCLIKALLDSYQKPSGLLG TIEHILGEGVIK
DGFTTPTPALLQKYLATMVRQNRDAVVMEVSSIGLASGRVAYTNFDTAVLTNITLDHLDFHGT FETYVAAK
AKLFSLVPPSGMVVINTDSPYASQCIESAKAPVITYGIESAADYRATDIQLSSSGTKYTLVYGDQKIACSSSFIG
KYNVYNLLAAISTVHASLRCDLEDLLEKIGLCQPPPGRLDPVLMGPCPVYIDYAHTPDALDNVLTGLHELLPE
GGRLIVVFGCGGDRDRSKRKLMAQVVERYGFAVVTSDNPRSEPPEDIVNEICDGFYSKNYFIEIDRKQAITYA
LSIASDRDIVLIAGKGHEAYQIFKHQTVAFDDKQTVCEVLASYV

>core/222/5/Org5_Gene273

MQTNIGLIGLAVMGKNLVLMIDHGFVSVYNRTPEKTRDFLKEYPNHREL VGFESLEDFVNSLERPRKIML
MIQAGKPV DQSIHALLPFLEPGDVII DGGNSYFKDSERRCKELQEKGILFLGVGISGGEEGARHGPSIMPGGNP
EAWPLVAPIFQSIAAKVQGRPCCSWVGTGGAGHYVKAVHNGIEYGD IQLICEAYGILRDFLKL SATAVATILK
EWNTLELESYLIRIASEVLALKDPEGIPVIDTILDVVGQKGTGKWT AIDALNSGVPLSLIIGAVLARFLSSWKEI
REQAARNYPGTPLIFEMPHDPSVFIQDVFHALYASKIISYAQGFMLLGEASKEYNWGLDLGEI ALMWRGGCII
QSAFLDVIHKGFAANPENTSLIFQEYFRGALRHAEMGWRRTVVTAIGAGLPIPCLA AAITFYDGYRTASSSMS
LAQGLRDYFGAHTYERNDRPRGEFYHTDWVHTKTTERVK

>core/223/5/Org5_Gene573

MRDVSELFRTHFMHYASYVILERAIPHILDGLKPVQRRLLWTLFLMDDGKMHKVANIAGR TMALHPHGDAP
IVEALVVLANKGYLIDTQGNFGNPLTGDPHAAARYIEARLSPLARETLFNTDLIAFHDSYDGREKEPDILPAKL
PVLLLHGVDGIAVGM TTKIFPHNFAELLKAQIAILNDKKFTVFPDFPSGGLMDPSEYQDGLGSITLRASIDIIND
KTLVVKQICPQSTTETLIRSIENAAKRGTIKIDTIQDFSTDVPHIEIKLPKGSRAKEMLP LLFEHTECQVILYSKPT
VIYENKPVECSISEILKLHTTALQGYLEKELLLLQEQLTLDHYHKTLEYIFIKHKLYDSVREVLAINKKISADDL

HQAVLHALEPWLHELATPVTQDTSQLASLTIKKILCFNEEACTKELLAIEKKQAAIQKDLGRIKEVTVKYLK
GLLERHGHLLGERKTQITNFKTAKTSILKQQTLI

>core/224/5/Org5_Gene839

MLCATVSGPSFCEAKQQILKSLHLVDIIELRDLINELDDQELHTLITTAQNPILTFRQHKEMSTALWIKLYSL
AKLEPKWMDIDVSLPKTALQTIRKSHPKIKLILSYHTDKNEDLDAIYNEMLATPAEIIYKIVLSPENSSEALNYI
KKARLLPKPSTVLCMGTHGLPSRVLSPNISNAMNYAAGISAPQVAPGQPKLEELLSYNYSKLSEKSHIYGLIG
DPVDRSISHLSHNFLLSKLSLNATYIKFPVTIGEVVTFSSAIRDLPFSGLSVTMPLKTAIFDHVDALDASAQLCE
SINTLVFRNQKILGYNTDGEDEVAKLLKQKNISVNNKHIAIVGAGGAAKAIAATLAMQGANLHIFNRTLSSAA
ALATCCKGKAYPLGSLENFKTIDIINCLPPEVTFPWRFPPIVMDINTKPHPSPYLERAQKHGSLIIHGYEMFIEQ
ALLQFALWFPDFLTPESCDSFRNYVKNFMAKV

>core/225/5/Org5_Gene342

MMSRLRFRLAALGIFFILLVPNSVSAKTIVASDKEKVGVLVYDNSVEAFQQILDCIDHANFYVELCPCMTGGR
TLKEMVDHLEARMDLVPELCSYIIIQPTFTDAEDQKLLKALKERHPNRFFYVFTGCPPSTSILAPNVIEMHIKLS
IIDGKYCILGGTNFEFEMCTPGDEVPEKVDPNRLFVSGVRRPLAFRDQDIMLRSTAFGLQLREEYHKQFAMW
DYYAHMWFIDNPEQFAGACPPLTLEQAEETVFPGFDKHEDLVLDSSKIRIVLGGPHDKQPNPVTQEYLKLI
QGARSSVKLAHMYFIPKDELLNALVDVSHNHGVHLSLITNGCHELSPAITGPYAWGNRINYFALLYGKRYPL
WKKWFCEKLKPYERVSIYEFAIWETQLHKKCMIIDDEIFVIGSYNFGKKSDAFDYESIVVIESPEVAAKANKV
FNKDIGLSIPVSHGDIFSWYFHSVHHTLGHLQLTYMPA

>core/226/5/Org5_Gene770

MRIVQVAVEFTPIVKVGGLGDAVASLSKELAKQNDVEVLLPHYPLISKFSSSQVLSERSFYIEFLGKQQASAI
YSYEGTLTITLDSQIELFSTTSVYSENNVVRFSFAAAAAAYLQEADPADIVHLHDWHVGLLAGLLKNPLN
PVHISKIVFTIHNGFYRGYCSTQLLAASQIDDFHLSHYQLFRDPQTSVLMKGALYCSDYITTVSLTYVQEIINDY
SDYELHDAILARNSVFSGIINGIDEDVWNPKTDPALAVQYDASLLSEPDLFTKKEENRAVLYEKLGISSDYFP
LICVISRIVEEKGPFEFMKEIILHAMEHSYAFILIGTSQNEVLLNEFRNLQDCLASSPNIRLILDFNDPLARLTYAA
ADMICIPSHREACGLTQLIAMRYGTVPVLRKTGGLADTVIPGVNGFTFFDTNNFNEFRAMLSNAVTTYRQEP
DVWLNLIESGMLRASGLDAMAKHYVNLYQSLLS

>core/227/5/Org5_Gene756

MAFSHIEGLYFYNTASQKKELFFPNHTPVRLYTCGPTVYDYAHIGNFRTYVFEDILKRTL VFFGYSVTHVMNI
TDVEDKTIAGASKKNIPLQEYTPYTEAFFEDLDTLNIARADFYPHATHYIPQMIQAITKLLEQGIAYIGQDAS
VYFSLNRFPNYGKLSHLDLSSLRCCSRISADEYDKENPSDFVLWKAYNPERDGVIIYWESPFGKGRPGWHLEC
SIMAMELLGDSLDIHAGGVDNIFPHHENEIAQSEALSGKPFARYWLHSEHLLIDGKKMSKSLGNFLTLRDLH
QEFTGQEVRYMLLQSHYRTQLNFTEEALLACRHALRRLKDFVSRLEGVDLPGESPLPRTL DSSSQFIEAFSRA
LANDLNVSTGFASLDFVHEINTLIDQGHFSKADSLYILDTLKKVDTVLGVLP LTTSVCIPETVMQLVAEREEA
RKTKNWAMADTLRDEILAAGFLVEDSKSGPKVKPL

>core/228/5/Org5_Gene900

MDTIDTPGEQGSQSFGENSLGARFDLPRKEQDPSQALAVASYQNKTDSQVVEEHLDELISLADSCGISVLETRS
WILKTPSASTYINVGKLEEIEEILKEFPSIGTLIIDEIITPSQQRNLEKRLGLVVLDRTELILEIFSSRALTAEANIQ
VQLAQARYLLPRLKRLWGHLSRQKSGGGSGGFVKGEGEKQIELDRRMVRERIHKL SAQLKAVIKQRAERRK
VKSRRGIPTFALIGYTNSGKSTLLNLLTAADTYVEDKLFATLDPKTRKCVLPGGRHVLLTDTVGFIRKLPHTL
VAAFKSTLEAAFHEDVLLHVVDASHPLALEHVQTTYDLFQELKIEKPRIITVLNKNVDRLPQGSIPMKLRLLSPL
PVLISAKTGEGIQNLLSLMTEIIQEKS LHVTLNFPYTEYGKFTELCDAGVVASSRYQEDFLVVXAYLPKELQK
KFRPFISYVFPEDCGDDEGRGPVLESSFGD

>core/229/5/Org5_Gene219

MDSRTSHLDDELSFKLEKAFTCLSTDIHSHDLSKIVIEYNPIDLAYAVSCLPSESRAILYKNLSCITAKVAFIINT
DSASRWAIFRRLSDSEVCALIEQMPPDEAVWVLDDIPDRRYRRILELIDSKKALKIRDLQKHGRNTAGRLMTN
EFFAFLMETTVKDVSA CIRS NPGIDLTRLVFVLDFK GELQGVVTDRSLIINPPEMSLKQIMNQIEHKVLPDATR
EEVVDLVERYKIAALPVVDEENFLIGAITYEDVVEAIEDIADETIARMAGTTEDVGYQTCHVVQRFLLRAPWL
LVTLFAGLISASVMAYFQKISPALLALIIFFIPLINGMSGNVGVQCSTILVRSMATGTLSFGRRRETIFKEMSIGL
LTGVVLGILCGLVVYLMGFLGLNIFSGGGIQLGVTVATGVLGASLTATTLGVLSPFFFAKLGVDPALASGPV
TALNDIMSMIIFFLIAGGINLFFN

>core/230/5/Org5_Gene943

MNKKKRFLSLLFLTAVLLGIWFSPHPASINSNAWQLFAIFTTTIMGIIFQPVPMGAIAIIGISTLLLLTQTLTLEQG
LSGFHNPIAWLVFLSFSIAKGIIKTGLGERIAYFFVSALGKSPLGLSYGLVITDFFLAPAIPSVTARAGGILYPV
TSLSDSFGSSAEKGTQDLIGSFLIKVAYQSSVITSAMFLTAMAGNPLVAALAGHVGVSLSWVLWAKAAIIPGL
LSLFLMPIILYKLYPPKITSCEEAIRSAKLRLKEMGPLKKEEKTILMIFLLVVLWTFGDLLGISATTAALIGLSL
LILTNI LDWQKDVIANTTAWETFIWFGALIMMASFLNQLGFIPLVGDSAAALVSGLSWKIGFPLLFLIYFYSHY
LFASNTAHIGAMYPIFLAVSISLGTNPIFAALTLAFASNLFGG LTHYGSGPAPLYFGSHL VTVQEWWRSGFALS
IVNIVIWIGIGSLWWKALGLI

>core/231/5/Org5_Gene1049

MTTKSLGSFNSVISKNKIHFI SLGCSRNLVDSEVMLGILLKAGYESTNEIEDADYLILNTCAFLKSARDEAKDY
LDHLIDVKKENAKIIVTGCMTSNHKDELKPWM SHIH YLLGSGDVENILSAIESRESGEKISAKSYIEMGEVPRQ
LSTPKHYAYLKVAEGCRKRCAFCIIPSIKGKLRSKPLDQILKEFRILVNKSVKEIILIAQDLGDY GKD LSTDRSS
QLESLLHELLKEPGDYWLRLMYLYPDEVSDGIIDLMQSNPKLLPYVDIPLQHINDRILKQMRRTTSREQILGFL
EKLRAKVPQVYIRSSVIVGFPGETQEEFQELADFIGEGWIDNLGIFLYSQEANTPAAELPDQIPEKV KESRLKIL
SQIQKRNV D KHNQKLIGEKIEAVIDNYHPETNLLL TARFYGQAPEVDPCIIVNEAKLVSHFGERC FIEITGTAG
YDLVGRVVKKSQNQALLKTSKA

>core/232/5/Org5_Gene216

MHSHSKPTKPLGTFTVGMLSLAVVISLRNLPLTAKHGLSTLFFYGLAVICFMIPYALISAELASFKPQGIYIWA
RDALGKWWGFFAIWMQWFHNMTWYPAVLAFIASTIVYKINPELAHNKVYIATVILAGFWILTFN FLGITSS
ALFSSICVIIGTLIPGVILVSLALFWIFSGNP I AISLSWGNLLPNFSNVSSLVLLAGMLLALCGLEANANLASDM
VNPRKNYPKAVFIGAIA TL TILVLGSLSIAIVIPKEEISLVSGLVKTFTLFFDKYNLSWMTGIVVVM TIAGSLGE
LNAWMFAGTKGLFISTQNDCLPRLFKKVNSKNVPTNMLFQGIVVTIFTLLFLCLDSADLVYWILTALSVQM

YLAMYICLFLAGPILRIKEPRAQRLYSVPGKFLGICTMSILGILSCAFALWVSFLPPRELAQISEGSKIGYTTFL
LAFSLNCLIPFGIYFTHKRLSKKS

>core/233/5/Org5_Gene884

MDKSTGVPLPSPPHSKESEMIVLGCMLTGVHYLNLAANQLYEEDFYYLEHKIIFRVLQDAFKQDKPIDVHLA
GEELKRHNQITVIGGPSYLITLAEFAGTAAYLEEVVDIIRSKSILRKMISTAKEIEKRALEQPKNVAEALDEAQN
SFFKISQSTSVSQYTLVADKLRGLTTTTDKPYLVQLQERQELFLQNAQGDNKSFFTGIPTHFIDLDQLIHGFS
NLMILAAPAMGKTALALNIAENLCFQNRPLIGIFSLEMTVDQLIHRMICSSEVDSKKISIGDLSGHDFQRIVS
VINEMQEHTLLIDDQPGLKVSDLRARARRMKESYDIQFLIIDYLQLLSGSGTLRATESRQTEISEISRMLKTLAR
ELNIPILCLSLSRKVEDRANHRPMMSDLRESGSIEQSDSLVMFLLRREYYDPNDKPGTAELIIAKNRHGSIGS
VPLVFEKELARFRNYSAFECIS

>core/234/5/Org5_Gene597

MKITVNRGLDLSLQGSPKESGFYNKIDPEFVSIDLRPFQPLSLKLKVEQGDVCSGAPIAEYKHFPNTYITSHV
SGVVTAIRRGNKRSLLDVIIKKTGPTSTEYTYDLQTLRSDDLSEIFKENGLFALIKQRPFDIPAIPQTQPRDVF
LADNRPFPSPEKHLALFSSREEGFYVFVVGVRRAIAKLFGLRPHIVFRDRLTLPTQELKTIAHLHTVSGFPFSGS
PSIIHSVAPITNEKEVVFTLSFQDVLTIHGLFLKGRILHEQVTALAGTALKSSLLRYVITTKGASFSSLINLNDI
SDNDTLISGDPLTGRCLKKEEPPFLGFRDHSISVLHNPTKRELFSLRIGFNKPTFTKTYLSGFFKKKRTYTNPD
TNLHGETRPIIDTDIYDKVMPMRIPVVPLIKAVITKNFDLANELGFLEVCGEDFALPTLIDPSKTEMLTIVKESLI
EYAKESGILTPHQD

>core/236/5/Org5_Gene475

MKEERSSEILPRVKETKKHAYVSMQEKSCVGECAVVAESEEAESVTVTKIAKLQRMGIEELNILARQYGVK
NIGSLTKSQVVFEIVKAKSERPDELLIGEGVLEVLPDGFGLRSPTYNYLPSAEDIYVSPAQIRRFDLKKGDTIIG
TIRSPKEKEKYFALLKVDKINGSTPDKAKERVLFENLTPLYPNQRIVMEMGKDHLAERVLDLTAPIGKGQRG
LIVAPPRSGKTVILQSIAHAIAVNNPDIVLIVLLIDERPEEVTD MIRQVRGEVVASTFDEQPERHIQVAEMVIEK
ARRLVEHGNDVVILLDSITRLARAYNTVQPHSGKILTGGVDASALHKPKRFFGAARNIEGGGSLTILATALIDT
GSRMDEVIFEEFKGTGNMELVLDRRLSDRRTYPAIDLIKSGTRKEELLYHPSELERVYLFRQAIADLTIDAM
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>core/237/5/Org5_Gene616

MNFKLPVYHIGLTKAENNTIKIAILQKTCKGWIVCHCEQIPEGKTWSLPKKYFAAPTTFSLQGSDILVKSSSSS
LKNRKNILKVALTNLEASLALPWESLIVQPQLGKPTDRGETPLTLWIAQKNTLKKELSFLSQAQIFPDKLSCRA
ADIFFLAEQSPKSLPAYLLIYGGSEEVTCIFVKNHAI AVARSFSNHSTKKSCDDIHATLQYIQETFPQTVLPAIH
VAQISPNLQKILEQKLSLPLVVCQSM TYGVEDEDWEIYGDTIAAAHHGASRRPLTFPYDATSVSPAQKHWL
LRSSLLIGKYALMATVVVSLGSVLKLSLSSASNHFAFACPEEGVLPRSLKAAEKT VKAIGKKNSASNYPLL
PTIPTSEQTLKFLALGKSSPSIKFSYFSYTM TSYP SKDNPSLPYSALVEVKGGQPEDIPQFLKKISSHPKLQHV
SESLEDQRSFKLQFTLSS

>core/238/5/Org5_Gene693

MTESVYSPSAMHVNSLADKLKAINQEHLDIWPSLSPKQQQRLFQQQLTSVDIDFFRKQQQLLSSPTAILKDFHP
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AGQPLPLAFMTSPLNTRQTRSFFESNDYFHLDPNQVDFFCQPLWPLLTLSGDLFLEDMDTLALGPNGNGCIAT
LLYTSGVWEKWKNAGIEMVSVIPIDNPLALPFDVELCGFHAMSNNEVTIKAALRQTAIEDVGILVKSHDSGK
TSVIEYSEIPQNERFALNEDGKLKYCLANIGLYCLSMDFIRHAAYQQLPLYKVHKKHAKQLGHTSLNEKNAWK
FEEFIFDLFCYSDHCQTLVYPRQECFAPLKNLEGNHSPDTVRQALSDRERQLFHKVTGKKLSPNTTTFEADDF
YYPSTSTSLHWENKAFFEEPFEAS

>core/239/5/Org5_Gene673

MTQEFDCCVIGAGPSGYVAAITAAQSKLRTALIEEDQAGGTCLNRGCIPSKALIAGANVVSHIKHAEQFGIHV
DGYTIDYPAMAKRKNTVVQGIRQGLEGILRSNKITVLKGTGSLVSSTEVKVIGQDTTIIKANHIILATGSEPRPF
PGVPFSSRILSSTGILELEVLPKKLAIIGGGVIGCEFASLFHTLGVEITVIEALDHILAVNNKEVSQTVTNKFTKQ
GIRILTKASISAIEESQNQVRITVNDQVEEFDYVLVAIGRQFNTASIGLDNAGVIRDDRGVIPVDETMRTNVPNI
YAIGDITGKWLLAHVASHQGVIAAKNISGHHEVMDYSAIPSVIFTHPEIAMVGLSLQEAQQNLPAKLTKFPPF
KAIGKAVALGASDGFAAIVSHEITQQILGAYVIGPHASSLIGEMTLAIRNELTLPCIYETVHAHPTLSEVWAEG
ALLATNHPLHFPPKS

>core/240/5/Org5_Gene38

MMSSKRTSKIAVLSILLTFTHSIGFANANSSVGLGTVYITSEVVKKPQKGSEKQAKKEPRARKGYLVPSSRT
LSARAQKMKNSSRKESSGGCNEISANSTPRSVKLRRNKRAEQKAAKQGFSAFSNLTLKSLLPKLPSKQKTSIH
EREKATSRFVNESQLSSARKRYCTPSSAAPSLFLETEIVRAPVERTKELQDNEIHIPVVQVQTNPKQNTKTTK
QLASQASIQQSEGTEQSLRELAQGASLPVLVRSNPEVSVQRQKEELLKELVAERRQCKRKSVRQALEARSLT
KKVARGGSVTSTLRYDPEKAAEIKSRRNCKVSPEAREQKYSSCKRDARANGKQDKTTPSEDASQEEQQTGA
GLVRKTPKSQVASNAQNFYRNSKNTNIDSYLTANQYSCSSEETDWPCSSCVSKRRTHNSISVCTMVVTVIAMI
VGALIIANATESQTTSDPTPTPTP

>core/241/5/Org5_Gene238

MRAWEEFLLLQEKEIGTNTVDKWLRSLKVLCFDACNLYLEAQDSFQITWFEEHIRHKVKSGLVNNNNKPIRV
HVTSDVKAAPFYKEKQMQQEKTAYFTMHYGSVNPEMTFSNFLVTPENDLPFRVLQEFTKSPDENGGVTFNPI
YLFSGPEGSGKTHLMQSAISVLRSEGGKILYVSSDLFTEHLVSAIRSGEMQKFRSFYRNIDALFIEDIEVFSGKSA
TQEEFFHTFNSLHSEGKLIVVSSSYAPVDLVAVEDRLISRFEWGVAPIHPLVQEGLRSFLMRQVERLSIRIQET
ALDFLIYALSSNVKTLHLALNLLAKRVMYKKLSHQLLYEDDVKTLLKDVLEAAGSVRLTPLKIIRNVAQYYG
VSQESILGRSQSREYVLPRQVAMYFCRQKLSLSYVRIGDVFSRDHSTVISSIRLIEQKIEENSHDIHMAIQDISKN
LNSLHKSLEFFPSEEMII

>core/242/5/Org5_Gene822

MRQEKDSLGLIVEVPEDKLYGAQTMRSRNFFSWGPELMPYEVIRALVWIKKCAAQANQDLGFLDSKHCDMIV
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AMHIAAVISLKNKLIPALDHMIRVLDAKVEEFRHDVKIGRTHLMDAVPMTLGQEFSGYSSQLRHCLESIAFSL
AHLIELAIGATAVGTGLNVPEGFVEKIIHYLRKETDEPFIPASNYFSALSCHDALVDAHGSLATLACALTKIAT
DLSFLGSGPRCGLGELFFPENEPGSSIMPGKVNPTQCEALQMVCQAQVLGNNQTVIIGGSRGNFELNVMKPVII

YNFLQSVDLLSEGMRAFSEFFVKGLKVNKARLQDNINNSLMLVTALAPVLGYDKCSKAALKAFHESISLKEA
CLALGYLSEKEFDRLVVPENMVGNH

>core/243/5/Org5_Gene365

MLKGNIFHLGCGVLYFMNFSLFLFFLIAIQGICLYVGRRGSKKVEDRESYFLAGRSLKIFPLMMTFIATQIGGG
VLLGAAEEAFICYGYGGILYPLGVALGLIFLGMGPGKRLAEGSLTTVVSIFEVFGSKKLRKIAFLLSAGSLFFI
LVAQVIALDRLFSSFPFGKYVTVAFWIVLASYTSTGGFRGVVRTDVIQAGFLIAVLVCGVSVWLSVPKSLSV
LDPFQSLPCAKL SNWIFMPMLFMLEQDMVQRCVAASSPKRLQWAAVGAGLVLLLNFNFIPLFLGSLGAKAG
LKAGCPLIDTIA YFCNP SLAAVMAAAIGVAILSTADSLMNAVSQLIAEEYPTLKAPYYRYLVGLAVAAPLVA
IGFTNIVDVLILSYSLSVCCLSVPVGFYLLAPKGRRVSGAAAWAGVLVGALGYGWVQIVSLGMFGELLAWV
GSLVAFSFVGFIEITWKNKVKTQT

>core/244/5/Org5_Gene784

MQQSVRKLFGTDGVRGRANFEPMTVETTVLLGKAVARVLREGRSGKHRVVVGKDTRLSGYMFENALIAGL
NSMGIETLVLGPIPTPGVAFITRAYRADAGIMISASHNPYRDNGIKIFSLEGFKISDVLEQRIETMVSEADFGPLP
EDHAVGKNKRVIDAMGRYVEFVKATFPKGRTLKGLKIVLDCAHGASYKVAPSVFEELDAEVICYGCEPTGIN
INEHCGALFPQVIQKAVIEHQAHLGIALDGDGDRIIMVDEKGHIVDGDMLICSAGDLKKRSALPHNRVVATI
MTNFGVLKYLEGLGLQVFTSPVGDRHVLHAMLEHEVTLGGEQSGHMIFLDYNTTGDGIVSALQVLRIMIESE
SMLSDLTAPIVKSPQTLINAVREKIPIETIPLIERTLRDVQDALGPSGRILLRYSGTENICRVMVEGHKKHQV
DCLAKALADVIDAELGTGSRE

>core/245/5/Org5_Gene439

MQIAQVFGCGRLNGEVKVSGAKNAATKLLVASLLSDQKCTLRNVPDIGDVSLTVELCKSLGAHVSWDKETE
VLEIYTPEIQCTRVPPTFSNVNRIPILLGALLGRCPEGVYVPTVGGDAIGERTLNFHFEGCLKQLGVQISSDSSG
YYAKAPRGLKGNYIHLPPPSVGATENLILAAIHAKGRTVIKNVALEAEILDVLFLQKAGADITTDNDRTIDIF
GTGGLGSVDHTILPDKIEAASFMAAVVSGGRVFVRNAKQELLIPFLKMLRSIGGGFLVSESGIEFFQERPLVG
GVVLETDVHPGFLTDWQQPFAVLLSQAQGSSVIHETVHENRLGYLHGLQHMGAEQCLFHQCLSTKACRYAI
GNFPHSAVIHGATPLWASHLVIPDLRAGFAYVMAALIAEGGGSIIENTHLLDRGYTNWVGKLRSLGAKIQIFD
MEQEELTTSPKSLALRDASL

>core/246/5/Org5_Gene710

MLYFIEQLNKLSTSFVCPMILLGGFLTWKLRGLQFHGLKLGFNMLQNKLDDSSSKANEVSSYEAVAGIL
AGNFGTGNIAGMAVALACGGPGALVWWLAALLGAIVQYAGSYLGSKYRKPEGNTGEFIGGPIACLAFGM
RKKILAGFFALFTIMTAFCAAGNCVQVSCIVPLCAEGTPGKLLVGILLALVIPVLAGGNNRILRFSARVIPFIAG
FYCISCGIILFQHASAILPAIKLICSSAFGIKAGLAGIGGYTLSQVISTGINRAVMATDCGSGMVSILQANTKSKN
PVVDGLVTLVPPVIVMVVCSITMLVLIVSGAYSSGAQGTLMVMSAFKNSLGSLSGVIVILAMALFGYTTILT
FACAEKSLQYMIPGRRANLWLKAIYVLIPLGGVIDMRMIWALSDTGFSGMVILNCIALIALLKDVLSTNRDV
ALLKERECSVADPVRNLDA

>core/247/5/Org5_Gene719

MFNVNFKFLEGLHQAPRYTSYPTALEWEPSSDAAPALLAFQRIRENPPQLSLYFHIPFCQSMCLYCGCSVVLN
RREDIVEAYINTLIQEMKLVVETIGFRPQVSRIHFGGGTPSRLSRELFTLLFDHIHKLFDLSHAEEIAIEVDPRSL
RNDMEKADFFQNVGFNRVSLGVQDTQADVQEAARRRRQSHEESLKAYEKFELAFQSINIDLIYGLPKQTKES
FSKTIQDILAMYPDRLALFSFASVPWIKPHQKAMKASDMPSMEEKFAIYSQSRHLLTKAGYQAIGMDHFSLP
HDPLTLAFKNKTLIRNFQGYSLPPEEDLLGLGMTSTSFIRGIYLNQAKTLEEYHNTVLRGTFATVKSKILTEDD
RIRKWAHKLMTFTINKEEFFNLFGYEFDTYFIESRDRRLISMETTGLIHNSPGSLKVTPLGELFVRVIATAFDH
YFLNKVSKKECFASI

>core/248/5/Org5_Gene492

MTTLRQFFLITELRQKLFYTFALLTACRVGVFIPVPGINGELAVAYFKQLLGSGQNLFQLADIFSGGAFAQMT
VIALGVVPYISASIIVQLFLVFMPALQREMRESSDQGKRRIGRLTRLFTVALAVIQSLLFAKFALRMNLTIPGIV
LPTLLSSKLFQVPWIFYITTVVVMTTGTLLLMWIGEQISDKGIGNGISLIILGILSSFPSVLGSIYNKLNLSQD
SSDLGLISILILALVFVFLITLIIIEGVRKIPVQYARRVIGRREVPGGGSYLPLKVNYAGVIPVIFASSLLMFPA
TIGQFIASESSWMKRIAALLAPGSLVYSICYVLLIIFFTYFWTATQFHPEQIASSEMKNNAFIPGIRQGKPTQHY
LEYTMNRVTLLGALFLAAIAILPSLLGCLLRVDSNVSYFLGGTAMLIVGVVLDTMKQVDAFLLMRRYDSVL
KTDRTKGRH

>core/250/5/Org5_Gene525

MNVWTKFFQPPKHIKEIEDQEVVKKKYKYWRIRIFYSMFIGYIFYFTRKSFTFAMPTLIADLGFDKAQLGIIG
STLYFSYGISKFVSGVMSDQSNPRYFMAIGLMTGLTNIFFGMSSSIVLFALWWGLNGWFQGWGWPPCARLL
THWYAKSERGTWWSVWSTSHNIGGALIPILTGFIIDYSGWRGAMYVPGILCIGMGLVLINRLRDTQPQSLGLPPI
EKYKRDPHHAHHEGKSASEGTEEIERELSTREILFTYVLTNQWLWFLAAASFFIYIVRMAVNDWSALFLIETK
HYAAVKANFCVSLFEIGGLFGMLVAGWLSDKISKGNRGP MNVLFSLGLLFAILGMWFSRSHNQWWVDGTL
LFVIGFFLYGPQMMIGLAAAELSHKKAAGTASGFTGWFA YFGATFAGYPLGKVTDVWGWKGFFIALLACAS
IALLLFLPTWNATEKNTRSKA

>core/251/5/Org5_Gene948

MKKVLIANRGEIAVRIIRACHDLGLSTVAVYSLADQEALHVLLADEAICIGEPQAAKSYLKISNILAACEITGA
DAVHPGYGFLSEANFASICESCGLTFIGPSSESIAMMGDKIAAKSLAKKIKCPVIPGSEGIIEDESEGLKIAEKI
GFPIVIKAVAGGGGRGIRIVKEKDEFYRAFSAAAEAEAGFNNPNVYIEKFIENPRHLEIQVIGDTHGNYVHLG
ERDCTIQRRRQKLIEETPSPILNAEIRVKVGKIAVDLARSAGYFSVGTVEFLDKDKKFYFMMENRIQVEHTI
TEEVTGIDL VKEQIHVAMGNKLPWKQKNIEFSGHIIQCRINAEDPTNNFSPSPGRLDYYLPPAGPSIRVDGACY
SGYAIPPPYYDSMIAKVIAKGKNREEAIAIMKRALKEFHIGGVQSTIPFHQFMLDNPKFLESNYDINYIDNLLAQ
GNSFFKEF

>core/252/5/Org5_Gene31

MATKTKTQWTCNQCGATAPKWLGQCPGCHNWNLSLVEEYVPQARSGTSSRSSTSAIALSSIELENESRIFIDHA
GWDRILGGGVVRGSLTLLGGDPGIGKSTLLLQTAERLASQKYKVLVYVCGEESVTQTSRAKRLNISSPLIYLF
PETNLDNIKQQIATLEPDILIISIQIIFNPTLNSAPGSVAQVREVTYELMQIAKSAQITTFIIGHVTKSGEAGPRV
LEHLVDTVLYFEGNSHANYRMIRSVKNRFGPTNELLILSMHADGLKEVSNPSGLFLQEKTGPTTGSMIPIIEG
SGALLIELQALVSSSPFANPVRKTAGFDPNRFSLLLAVLEKRAQVKLFTMDVFLSITGGLKIIIPAADLGALLA

VASSLYNRLLPNNSIVIGEVGLGGEIRHVAHLERRIKEGKLMGFEGAILPEGQISSLPKEIRENFRLQGVKTIKD
AIRLLL

>core/253/5/Org5_Gene708

MLKILKIKVLVFPLALLMGCNSIGYAGPQGSLLQTNSTKVKIGSEVWIEQKLRQYPELLWLTESGGAPLLTST
PIDMAYSEKLFNKKVPALDIAIRSMIHLHLLIQGSRQSYMQLSQILPSEEGGMTFKQFQTAHKQLLFFLNPKS
FDNTRLILETAIVLRHVGCSAKAVTTFKPYFTDSCPQSFYAKALHVLRTFPELCPSYARLSPEQQEVLLSLRRL
GNYDSLLNLTEVPSAQLLSAWRTRSLAILDLYLYCLDTCGDKNCSQEFYINFAPLLSMLQQHATIEEAFSRY
FTYRANRLGFEGTSRTDMLVRLATLMNLSPEASTLAWSFKNLPSDEAENLVNSFYTVQGEHIPLTFRGLPS
LVAGLSVATHGSTVSPENRLRQLYSTMSSLVKSLRSHREMLNKQLLPQGTVLDFSETTLSSGGLDVFAESIA
VRIHLNGAVSINL

>core/254/5/Org5_Gene945

MRKRHSFDSTSTKKEAVSKAIQKIIKIMETTDPSLNVETPNAEIESILQEIKEIKQKLSKQAEDLGLLEKYCSQE
TLNLENTNASLKL SIGSVIEELASLKQLVEESIEESLGQQDQLIQSVLIEISDKFLSSIGETLSGNLDMNQNVIQ
GLLIKENPEKSEAASVGYVQTLLEPLSKRIGETHKKVATHDVNISSLQFHMMSVAGGRFRGHIDMNGYRVLG
LGEPKNGEDAVSKDYLERIVSSQLTIDKVEDKPITKPNKGKLLYSQGTSPKLEGPLPLGLLTSGISGFTWKSAS
KSNDGSFPFSALRHKETESDTCFQITSTTLSGNQAGTYTWSLSLKVLVPSIFQIEKPEVQLSLVYSYEDWLPID
NIFNMSQPRTIPLALLGQTMLAGQKYDILELAAHQTNQTLMISPNCSTRFSLQLKQTNQFENSPVDFYIVHAAH
SCHWSGF

>core/255/5/Org5_Gene331

MLTCNECTTWEQFLNYVKTRCSKTAFENWISPIQVLEETQEKIRLEVNPVIFVQNYLLDNYKRDLCFSVPLDVH
GEPALEFVVAEHKKPSAPVASQKESNEGISEVFEETKDFELKLNLSYRFDNFIEGPSNQFVKSAAVGIAGKPGR
SYNPLFIHGGVGLGKTHLLHAVGHYVREHHKNLRIHCITTEAFINDLVYHLKSKSVDKMKNFYRSLDLLLVD
DIQFLQNRQNFEEFECNTFETLINLSKQIVITSDKPPSQLKLSERIIARMEWGLVAHVGIPDLETRVAILQHKAE
QKGLLIPNEMAFYIADHIYGNVRQLEGAINKLTAICRLFGKSLTETTRETLEKELFRSPTKQKISVETILKSVA
TVFQVKLNDLKGNSRSKDLVLARQIAMYLAKTLITDSLVAIGAAGFKTHSTVLYACKTIEHKLQNDETLKRQ
VNLCKNHIVG

>core/256/5/Org5_Gene775

MILPPYSYSLKIGAAVLFFCSILHTFLTPWLYTLCQSYEHKKLVFPECWKRYARLSELFRILSRVEIVFFLWAVP
LFFWFLYTEGYRISMAYFNSRNYGFAVFIMVILILLESRPVYFAELVLSSIAKLGKTSPKSWWWTLMIAPLL
SCLLKETGAMIIIGATLLMRHFYVFSPSRRFAYATMGLLFSNISIGGLTSYVSSRALFLFPALKWEHSFFLSHFA
WKAIVAILISTTIYYFIFRKEFKKFPDIPSDKDPSVEKVPWWIICVNIIFVGSILSRSTPLFMGALLFYLGFKFT
IFYQDPINLSKVCYVGLFYAGLVVFGDLQEWVVLNLMQGLSDFGYMTVSYTSLIFLDNALVNYLVHNLSVA
TDCYHYLVVAGCMAAGGLTLVSNIPIVGYLILRSAPSSTIHMGWFLGALGPSIISLGVFVWLLKNVPEFLYC
FFR

>core/257/5/Org5_Gene609

MSEPRFVCLSLGSLGNRFKNLQIARTLLGEQAVLGLRSSVILETEALLPGSPPEWDLPYFNSVLVGETTSL
RELLVTIKQIEKVVGRAEESPPWSPRTIDVDILLYGDESFCCDHTEITIPLSNLLSRPFLIALIASLCPYRRFCTQG
SPYHNFTFGELAHHLPSPPGMIRRSLSPTMLMGVVNVTNDSMSDGGMFLDPEKAVAQAIEKLFTGAAVIDF
GAQATNPKVKQFLSVDQEWERLEPVLRLKETSNSNRKQYPIISLDTFYPIILRAMDIYPIQWINDVSGGSQS
MAEVARDCELSLVMNHSSSLPVDPKNILSFSVPIGEQLLSWGEKQLKMFSDVGLNANQVIFDPGIGFGKGAA
QSLATLYEIAKFKRLGCPILIGHSRKSFLSLFGNHDPKDRDWETVGLSILLQQQGVVDYLRVHNVAAHQKALS
VAAACEACAPI

>core/258/5/Org5_Gene407

MNRLLSLLSVFDDFFWSYVAFILIIVLGVFSWSRFFQFTKFSQFCKLFRYYSQNPQERETKQGVHPLKVFFA
SAGGNIGIGNVVGIVTAACIGGPGALFWVWIAGIFGSIVKYSEVYLGIFRKLDRDGVYQGGPMYFLIKAFKT
PVVSVIVAILLCIYGVEIYQFSVITDSLAHCWNLPKVYPMLGLLFLVFYAIRGGLQRIGKICSIVLPFFMLLYCA
LSLYILVKEFHTLPHLLSTVFSSAFKQGSALGGFAGCTVATTIHQGISRAAYSGDIGIGFDSIIQSESSAKDPSTQ
AQLSIVGIAIDNLICTLSLLMVLASGSWSLGLENASQVVEHTLASYFPMVKFFLPTFFFVTGYTTIISYFLVGKK
CAKFLYGNTGAKIYTLYGLLILPLFCFLSQNTALLIMSVSGALLLCFNLLGVFILRKEVIFPARAASLTETSLST
E

>core/259/5/Org5_Gene263

MLSCVFSDTIFLSSFLAVTLICMTTALWGTILLISKQPLLSESLSHASYPGLLVGALMAQYVFSLQASIFWIVLF
GCAASVFGYGIIVFLGKVCKLHKDSALCFVLVFFAIGVILASYVKESSPTLYNRINAYLYGQAATLGFLEAT
LAAIVFCASLFALWWWYRQIVVTTFDKDFAVTCGLKTVLYEALSLIFISLVIVSGVRSVGIVLISAMFVAPSLG
ARQLSDRLSTILLSAFFGGISGALGSYISVAFTCRAIIGQQA VPVTLPTGPLVVICAGLLAGLCLLFSPKSGWVI
RFVRRKHFSFSKDQEHLKVFVWHISHNRLNENISVRDFVCSYKYQEYFGPKPFPRWRVQILEWRGYVKKEQDY
YRLTKKGRSEALRLVRAHRLWESYLVNSLDFSKEVHELAEIEHVLTEELDHTLTEILNDPCYDPHRQIIPNK
KKEV

>core/260/5/Org5_Gene961

MINSLSQKLSSIFSFLVSSRRINEENISESIREVRLALLDADVNYHVVKDFISKVKEKILGEEIWKHVSPGQQFIR
CLHEELVAFLSDGREEFTIQKTPSIILLCGLQGAGKTTTAAKLADYVIKNNKAKKVLVVPCLDKRFAAVDQL
KILVAQTKAEFYQSQENKPIDVVVKALAYAKENGHDFVILDTAGRLNIDNELMEELTAIQKVSQANERLFVM
NVAMGQDVLATVQAFDQSLDLTGVILSMTDGDARAGAVFSIKHVLGKPIKFEGCGERIQDLRSFDPQSMAER
ILGMGDTINFKEMREYISEEEDAELGKKLVTAFTYEDYYKQMKAFRRMGPLRKLLGMMPGFNNAKPSQ
KEIEDSEQQMKRTEAIIISMTPEERKELVELDMSRMKRIASGCGLTLGDVNQFRKQMSQSKKFFKGMSKGK
MEQVRKKMSGGNQWR

>core/261/5/Org5_Gene68

MDALILSRIQFGLFITFHLYFVPLSMGLSMMLVIMEGLYLVTKKQIYKQMTWFWVGIFALTFVLGVVTGIMQI
FSFGSNWANFSEYTGNI FGTLGSEGVAFFLESGLGILLFGRHKVSKKMHHFFSTCMVALGAHMSAFWIICA
NSWMQTPSGYEMVMHKGLIPALTSFWGVVFSPTTIDRFIHAVLGTWLSGVFLVISVSAYYLWKKRHHEFA
KQGMKIGTICAVIVLVLQLWSADVTARGVAKNQPAKLAAFEIGFKTEEYTPIWAFGYVDMEKERVIGLPIPG
ALSFLVHRNIKTPVTGLDQIPRDEWPNVQAVFQLYHLMIMLVGVMVALTLISWSAYKGWRWALKPFFLVIL

TFSVLLPEICNECGWCAAEMGRQPWVVQGLLTKDAVSPIVQANQIVQSLVIFSLVFIALLTLFITVLCKKIKH
GPEEENDLTEFEVK

>core/262/5/Org5_Gene1002

MRAMLLEDWVSLMLSDVSCPKCDKKITGFAIDSQKVQPGDLFFALPGNATDGHQFLKHAATAGAVAAVVS
HDYQGDSFGLELIRVDDTKSALQEAGSNQCNLFQGTLVGITGSVGKTTTKEFSKITLSSYKTHASPKSYNSQL
TVPLSLLMAEGDEDVMILEMGVSEPGNMQDLLRIVQPEIAVITHINDQHMHFPQGIQEILKEKSYILQKSKL
QLLPKDSPPYYLDRSCSPTAEKFSFSFNDPLADFCYKAISGDSVVIQTPEENYCLPIAFSYKPAYTNLLIAVALS
WILEVPEEGVIRSLPELKLPPMRFEHSMRNGMQVINDAYNACPEAMIAALDALPLPSDGGKIILILGHMAELG
RYSEEGHALVAEKAASRGDMIFFIGEKWIPVQSVLKSYSCEVSFFSSAQDVKDILKQVARYGDVILLKGSRAL
ALESLLACF

>core/263/5/Org5_Gene1052

MSNITSPVIQNNRSCNYYFELKNSTTIHIVISAILLCGALIAFLCVAAPVSYILSGALLGLGLLIALIGVILGIKKIT
PMISSKEQVFPQELVNRIRAHYPKFVSDFVSEAKPNLKDLSIFIDLLNQLHSEVGSSTNYNVSEELQQKIDTFEG
IARLKNEVRTASLKRLESAASSRPLFPKSLAKILQKVFPFFWLGEFISAGSKVVELHRVKKIGGSLEEDLSDYIKP
EMLPTYWLIPLDFRPTNSSILNLHTLVLARVLTRDVFQHLKYAALNGEWNLNHSDLNTMKQQLFAKYHAAY
QSYKHLSPSLQEDXFYNLLLCIFKHRYSWKQMSLIKTVPADLWENLCCLTLDHTGRPQDMEFASLIGTLYT
QGLIHKESAEFLSSLTLLSLDQFKTIRRQSTNIAMFLENLATHNSTFRSLPPITVHPLKRSVFSQPEEDESSLIG

>core/264/5/Org5_Gene1026

MVITNLSINADTIYGKNPINIVASAANKNITLTGTLALVNADGAFYENHTLQDSQDYSFVKLSPGAGGTIITQD
ASQKPLEVAPSRPHYGYQGHWNVQVIPGTGTQPSQANLEWVRTGYLPNPERQGS�VPNSLWGSFVDQRAIQ
EIMVNSSQILCQERGVBWAGIANFLHRDKINEHGYRHSGVGYLVGVGTHAFSDATINA AFCQLFSRDKDYV
VSKNHGTSYSGVVFLEDTFEFRSPQGFYTDSSSEACCNQVV TIDMQLSYSHRNNDMKTKYTTTYPEAQGWA
NDVFGLEFGATTYYYPNSTFLFDYYPFLRLQCTYAHQEDFKETGGEVRHFTSGDLFNLA VPIGVKFERFSDC
KRGSYELTFAYVPDVIRKDPKSTATLASGATWSTHGNNLSRQGLQLRLGNHCLINPGIEVFVSHGAIELRGSSR
NYNINLGGKYRF

>core/265/5/Org5_Gene843

MLTYKVSPSSVYGNAFIPSSKSHTLRAILWASVAEGKSHIYNYLDSPDTEAMICACKQMGASIKKFPQILEIVG
NPLAIFPKYTLIDAGNSGIVLRFMTALACVFSKEITVTGSSQLQRRPMAPLLQALRNFGASFHFSSDKSVLPFT
MSGPLRSAYS DVEGSDSQFASALAVACSLAEGPCSFTIIEPKERPWFDSLWWLEKLHLPYSCSDTTYSFPGSS
HPQGFSYHVTGDFSSAAFIAAAALLSKSLQPIRLRNLDILD IQGDKIFFSLMQNLGASIQYDNEEILVFPSSFSGG
SIDMDGCIDALPILTVLCCFADSPSHLYNARSAKD KESDRILAITEELQKMGACIQPTHDGLLVNPSPLYGAVL
DSHDDHRIAMALTIAALYASGDSRIHNTACVRKTFPNFVQTLNIMEARIEECHDNYSMWSTHKKRVFARESF
G

>core/266/5/Org5_Gene651

MTSGVSGSSSQDPTLAAQLAQSSQKAGNAQSGHDTKNVTKQGAQAEVAAGGFEDLIQDASAQSTGKKEATS
STTKSSKGEKSEKSGKSKSSTSVASASETATAQAVQGPKGLRQNNYDSPSLPTPEAQTINGIVLKKGMGTAL

LGLVMTLMANAAGESWKASFQSQNQAIRSQVESAPAIGEAIKRQANHQASATEAQAKQSLISGIVNIVGFTV
SVGAGIFSAAKGATSALKSASFAGETGASAAGGAASKALTSASSSVQQTMASTAKAATTAASSAGSAATKA
AANLTDDMAAAASKMASDGASKASGGLFGEVLNKNPNWSEKVS RGMNVVKTQGARVASFAGNALSSSMQ
MSQLMHGLTAAVEGLSAGQTGIEVAHHQRLAGQAEQAQAEVLKQMSSVYGQQAGQAGQLQEQAMQSFNTA
LQTLQNIADSQTQTTS AIFN

>core/267/5/Org5_Gene24

MTLQPYQASSRKYRPQIFREILGQSSVAVLKNALVFNRAAHAYLFSGIRGTGKTTLARILAKALNCVHLS
EDGEPNCQCFSCKEIASGSSLDVLEIDGASHRGIEDIRQINETVLFTPVKAKFKIYIIDEVHMLTKEAFNALLKTLE
EPPQHVKFFFATTEIHKIPGTILSRCQKMHLQRIPEKTILEKLSLMAQDDHIEASQEALAPIARAAQGSLRDAES
LYDVISLFPKSLSPDTVAQALGFASQDSLRLDNAILQRDYATALGIVTDFLNSGVAPVTFLHDLTLFYRNLL
LTNSTTSKFSSQYKTEQLLEIIDFLGESAKHLQNTIFEQTLETVIIIIRIYQRPVLS ELISSIKSRQFEGLRNIKEP
TLTQQVSAPQPQPTYKEQSFLEKKNQPAAEGKIISVEVKSSASIKSAAVDTLQFAVVEFSGILRQ

>core/268/5/Org5_Gene677

MLKHDTIAAIATPPGEGSIAVVRLSGPQAIVIADRIFSGSVASFASHTIHLGQVIFEETLIDQALLLLMRSRPSFT
GEDVVEFQCHGGFFACSQILDALIALGARPALPGEFSQRAFLNGKIDLVQAEAIQNLIVAENIDAFRIAQTHFQ
GNFSKKIQEIHTLIEALAFLEVLADFPEEEQPDLLVPQEKIQNALHIVEDFISSFDEGQRLAQGTSLILAGKPNV
GKSSLLNALLQKNRAIVTHIPGTTRDILEEQWLLQGKRIRLLDTAGQRTTDNDIEKEGIERALSAMEEADGIL
WVIDATQPLEDLPKILFTKPSFLLWNKADLTPPPFLDTSLPQFAISAKTGEGLTQVKQALIQWMQKQEAGKTS
KVFLVSSRHHMILQEVARCLKEAQQNLYLQPPEIIALELREALHSIGMLSGKEVTESILGEIFSKFCIGK

>core/269/5/Org5_Gene685

MPRSLSNEQFSVDLEESPGCIVSALVKVSPEVLNKLNKQALKKKIKEITLPGFRKGKAPDDVIASRYPTNVRK
ELGELVTQDAYHALSTVGDRRPLSPKAVRSNSITQFDLQEGAKVEFSYEAFPAISDLPWENLSLPQEEAASEIS
DSDIEKGLTNIGMFFATKTPVERPSQEGDFISISLHVSKSNDENASSAAIFENKYFKLSEEEMTDAFKEKFLGIS
TGHRVVETITSPEIQSFLRGDTLTFTVNAVIEVSIPEIDDEKARQLQAESLDDLKAKLRIQLEKQAKDKQLQKR
FSEAEDALAMLVDFELPTSLLEERISLITREKLLNARLIQYCSDEELEKRKSELIKEAEEDATKALKLLFLTHKI
FSDEKLTISREELQYMMDVCSRERFGQQPPKDISNDTLQELVMSARDRLTYSKAIEHVLRKAELLASTPSA

>core/270/5/Org5_Gene564

MDQLTTDFDTLMSQLGDVNLTTVVGRITEVVGMLIKAVVPNVRVGEVCLVKRNGMEPLVTEVVGFTQSFAF
LSPLGELSGVSPSSEVIPTGLPLHIRAGNGLLGRVLNGLGEPIDVETKGPLQNVDQTFPIFRAPPDPLHRAKL
RQILSTGVRCIDGMLTVARGQRIGIFAGAGVGKSSLLGMIARNAEEADVNVIALIGERGREVREFIEGDLGEEGM
KRSVIVVSTSDQSSQLRLNAAYVGTAIAEYFRDQGKT VVLMMDSVTRFARALREVGLAAGEPPARAGYTPS
VFSTLPRLLERSGASDKGTITAFYTVLVAGDDMNEPVADEVKSILDGHIVLSNALAQAYHYPAIDVLASISRL
LTAIVPEEQRRRIIGKAREVLAKYKANEMLRIGEYRRGSDREIDFAIDHIDKLNRLFLKQDIHEKTNYEEAAQQL
RAIFR

>core/271/5/Org5_Gene679

MWLVILWALAASLAIALVAKGYRFRVYFRRYAVQVIREVRLSMELKEWALAEQQLLPILKKRSYRRQCLFE
YMRILRKMQRFESEKLLAEAKKLGLRGPYFFLEIAYKAYRFGAFKECAQAFASVPQDLFEEEDAACYASAL
VRLGDLDAACSLIEPWISPLSHQETFTVMGHIYFTSKRYKDAIDFYNRANALGVCPEVTYNLAQAYRITSSY
AKAGKLFRKLLSNPVYKEEALFNIGLCEQKLGRPGKALLIYQSSDLWSRGDALLMKYAAMAAMDQRDYVL
AEPCWELALRCSTFAKDYKCGLGYGFSLCRLRKYGDAERVYCNLIQNFPECLTACKALAWLCGVGYATLLG
SEGLMYAKKAVELDHSCETLELLSACEARCGNFDAAYEIQSFLSSRDTSLQEKQRRSQILRILRKKLPLNDH
HIVEVDALLAA

>core/272/5/Org5_Gene472

MIENDFPEASNFESSHFYRDKVGVIIICGGEGKRLSPLTNCRCCKPTVSFGGRYKLIDIPISHAISAGFSKIFVIGQ
YLYTYTLQQHLFKTYFYHGVLDQDIHLLAPEARQGDQIWYQGTADAIKRNLLYFEDTEIEYFLILSGDQLYNM
DFRSIVDTAIRTHVDMVLVAQPIPEKDAYRMGVLDIDSEGKLIDFYEKPEKEVLKRFQLSSDDRRIHKLTEDS
GDFLGSMGIYLFRRDSLFSLLREEEGNDFGKHLIQAQMKRGQVQTLLYNGYWADIGTIESYYEANIAITQKP
HAEKRGLNCYDDNGMIYSKNHHLPGAITDSMISSLLCEGCVINTSHVSRSVLGIRSKIGENSVVDQSIIMGN
ARYGSPSPSLGIGKDCEIRKAIIDENCCIGNGVKLQNLKGYIKYDSPDKKLFVRDNIIVPQGTHIPDNYIF

>core/273/5/Org5_Gene956

MLNCSNQKHTVTFEEACQVFPGGVNSPVRACRSVGVTPPIVSSAQGDIFLDTHGREFIDFCGGWGALIHGHSH
PKIVKAIQKTALKGTSYGLTSEEEILFATMLLSSLKLKEHKIRFVSSGTEATMTAVRLARGITNRSIIKFIGGYH
GHADTLLGGISTTEETIDNLTSLIHTSPHSLISLPYNNSQILHHVMEALGPQVAGIIFEPICANMGIVLPKAEF
LDDIIELCRFGSLSIMDEVVTGFRVAFQGAKDIFNLSPDITIYGKILGGGLPAAALVGHRSDHLMPEGTIFQ
AGTMSGNFLAMATGHAAIQLCQSEGFYDHLSQLEALFYSPIEEEIRSQGFPVSLVHQGTMFSLFFTESAPTNFD
EAKNSDVEKFQTFYSEVFDNGVYLSPSPLEANFISSAHTENLTYAQNIIDSIIKIFDSSAQRFF

>core/274/5/Org5_Gene621

MFQQKQKLSLKYLPRLMQQGLQMLQSPLTELSSYVVQEIIDNPFFDLSSLEEEEWSPCYRPTNSTFSYLNQTP
GPQESLYTRLLPQIEEAFSTAEERFIAHQIAGNLSDEGLFLRNPEDFAQELELPLEKIHKVWDTIQNLSPEGIASP
SLQSYWMKLLRNSSHQQAYSIVRDCYPLMTNCEFAPIMKKFSLSLSELRNILKKALGSIPWCPAAACTVKPM
VSTPLPDIYLFYSSGSWKIEVSTRGLPSIKLNKETFFHYEHLPKKEEQKNLSQQILSAKWLIKNLRKREQTLLQV
METLLPKQEDFLGKIPAPYPLGIKDLAEDLSFHSTIFRAIENKAVAAPIGIFPLKHLFPRGIHQDSSHSENVL
QWIRQWIAEQTPLSDSVISDRITAKGIPCARRTVAKYRAQLKILPANKRKKLFYIRSSNSHFRDRQF

>core/275/5/Org5_Gene984

MSKIVYKFGGTSLATAENICLVCDIICKDKPSFVVVSAIAGVTDLLVDFCSSSLREREEVLRKIEGKHHEIVKNL
AIPFPVSTWTSRLLPYLQHLEISDLDFARILSLGEDISASLVRAVCSTRGWDLGFEARSVILTDDSYRSASPNL
DLMKAHWHQLELNQPSYIIQGFISNGLGETVLLGRGGSDYSATLIAELARATEVRIYTDVNGIYTMDPKVIS
DAQRIPELSFEEMQNLASFGAKVLYPPMLFPCMRAGIPIFVTSTFDPEKGGTWVYAVDKSVSYEPRIKALSLS
QYQSFCSDYTVLGCGLLEEILGILESHGIDPELMIAQNNVVGFMDDDIISQEAQEHLDVLSLSSVTRLHHS
VALITMIGDNLSSPKVVSTITEKLRGFQGPVFCFCQSSMALSFVVAASELAEGHIEELHNDYVKQKAIVAT

>core/276/5/Org5_Gene58

MQTIYTKITDIKGNLITVEAEGARLGELATITRSDGRSSYASVLRFDLKKVTLQVFGGTSGLSTGDHVTFLGRP
MEVTFGSSLLGRRLNGIGKPIDNEGECFGEPIEIA TPTFNPVCRIVPRSMVRTNIPMIDVFNC LVKSQKIPIFSSSG
EHHNALLMRIA AQT DADIVVIGGMGLTFVDYSFFVEESKKLG FADKCV MFIHKA VDAPVECVLVPDMALAC
AEKFAVEEKKNVLVLLTDMTAFADALKEISITMDQIPANRGYPGSLYSDLALRYEKA VEIADGGSITLITVTT
MPSDDITHPVPDNTGYITEGQFYLRNNRIDPFGSL SRLKQLVIGKVTREDHGD LANALIRLYADSRKATERMA
MGFKLSNWDKKLLAFSELFETRLMSLEVNIPL EEALDIGWKILAQSFTSEEVG IKAQLINKYWPKACLSK

>core/277/5/Org5_Gene837

MISFRLLLLSGLCALGISSYAETPKETTGHYHRYKARIQKKHPESIKESAPSETPHHNSLLSPVTNIFCSHPWKD
GISVSNLLTSVEKATNTQISLDFSILPQWFYPHKALGQTQALEIPSWQFYFSPSTTWTLYDSPTAGQGIVDFS YT
LIHYWQTNGVDANQAAGTASSMNDYSNRENNLAQLTFSQTFPGDFLTLAIGQYSLYAIDGTLYDNDQYSGFI
SYALSQNASATYSLGSTGAYLQFTPNSEIKVQLGFQDSYNIDGTNFSIYNLT KSKYNFYGYASWTPKPS CGDG
QYSVLLYSTRKVPEQNSQVTGWSLNAAQHIHEKLYLFGRINGATGTALPINRSYVLGLVSENPLNRHSQDLL
GIGFATNKVNAKAISNVNKLRRYESVMEAFATIGFGPYISLTPDFQLYIHPALRPERRTSQVYGLRANLSL

>core/278/5/Org5_Gene952

MMLRGVHRIFKCFYDVVLVCAFVIALPKLLYKMLVYGKYKKS LAVRFG LKKPHVPGEGLVWFHGASVGE
VRLLL PVLEKFCEEFPGW RCLVTSC TELGVQVASQVFIPMGATVSILPLDFSIIKSVVAKLRPSLAVFSEGDC
WLN FIEEAKRIGATT LVINGRISIDSSKRFKFLKRLGKNYFSPVDGFL LQDEVQKQRFLSLGIPEHKLQVTGNIK
TYVAAQTALHLERETWRDRLRLPTDSKL VILGSMHRSDAGKWLPVVQKLIKEGVSVLWVPRHVEKTKDVE
ESLHRLHIPYGLWSRGANFSYVPVVVVDEIGLLKQLYVAGDLAFVGGTFDPKIGGHN LLEPLQCEVPLIFGPH
ITSQSELAQRLLL SGAGLCLDEIEPIIDTVSFLNNQEVREAYVQKGKVFVKAETASFDRTWRALKSYIPLYKN
S

>core/279/5/Org5_Gene531

MKRPFPTYLCIIFYGSCASLSLHAGLSFPEVRGATAAVVHADSGKV FYDKDIDAVIYPASMTKIAT ALFILKHY
PTVLDTLIKVKQDAIASITPQAKKQSGYRSPPHWLETDGSTIQLHLREELLGWDLFHALLVCSANDAANVLA
MACCGSVEKFMDKLNFFLKEEIGCTHTHFNNPHGLHHPNHYT TTRDLISIMRCALKEPPFRGVISTTSYKIGAT
NLHGERILSPTNKLLLPGSTYHYPPALGGKTGTTKTAGKNLIMAAEKNRLLVTIATGYSGPVS DLYQDVIAL
CETVFNEPLL RKELVPPSDCLQLEIANLGKLS CPLPEGLYYDFYASEDREPLSVSFIAHADAFPIEQGDLLGHW
VFYDDEGKKISSQPFYAPCRFERTIKPWKLYMKRVFTSYRTYMSITMLLMYFRIRKHRKYKNLKHYSKI

>core/280/5/Org5_Gene1004

MKRAIIIGAGISGLAAGWWLHKKFPQAEILVLDKEAYAGGFVRTESPQGFSFDLGPKGFLTRGDGEYTLKLIH
ELGLQNSLIFSDRAAKNRFVYYRGKARKISTWTLLRKGLLPSLIKDFRAPCYTQDSSVQDFLKRHSSQNFTSYI
LDPLITAIRAGHSSILSTHMAFPELAKREASSGSLLRSYLKNRSPKSKTD RYLASLSPSMGTLITTIQEKL PAT
WKFSTSVTHIDCSPKEACVTTTPSETFFADMVIYTGPLQQLPVLLPNYGIENLSKRVL PWNLSSISLGWHHANFS
LPKGYGMLFADELPLL GIVWNSQIFPQATPGKTVLSLLIEGKWRESEAHAF AIAALSEYLNINQKPDAFALFSS
QDGMPQHAVGFLE RKERILPHLPGNLKIVGQNIAGPGLNRCIASAYHAICDLHTEETLAQPQSSL

>core/281/5/Org5_Gene142

MFSRWITLFLLFISLTGCSYSSKHKQSLIPIHDDPVAFSPEQAKRAMDLSIAQLLFDGLTRETHRESNDLELAI
ASRYTVSEDFCSYTFFIKDSALWSDGTPITSEDIRNAWEYAQENSPHIQIFQGLNFSTPSSNAITIHLDSPNPDPF
KLLAFPAFAIFKPENPKLFSGPYTLVEYFPGHNIHLKKNPNYYDYHCVSINSIKLLIIPDIYTAIHLNLRGKVDW
VGQPWHQGIPWELHKQSQYHYTYTPVEGAFWLCLNTKSPHLNDLQNRHRLATCIDKRSIIEEALQGTQQPAE
TLSRGAPQPNQYKKQKPLTPQEKLVLTYPSDILRCQRIAEILKEQWKAAGIDLILEGLEYHLFVNKRKVQDYA
IATQTGVAYYPGANLISEEDKLLQNFEEIPIYYLSYDYLTDQDFIEGVIYNASGAVDLKYTYFP

>core/282/5/Org5_Gene244

MNKNLVAIFDYMEKEKGIQRSTIIGAIESALKIAAKKTLRDDANISVNINSRTGDIEVFCEKEIVEICQNPSKEIP
LDKAREYDPDCQIGQYMDVPFVSDNFGRIAHAARQIIGQKLRHAERDVIYEEYRHRVNETLSGVVKRFAKG
SNLIIDLKGVAILPTRFYPKTEKHKIGDKIYALLYEVQSENGGAEVILSRSHAEFVKQLFIQEVPELEEGSVEI
VKIAREAGYRTKLAVRSSDPKTDVPVGAFFVGMGRGSRVKNIIRELNDEKIDIVNYSVPSTELLQNLLYPIEQKIAI
LEDDKVIAIVNDADYATVIGKRGINARLISHILDYELEVQRMSEYNKLLIQRLQLAEFDSPHLDQPLEMEGI
SKLVIQNLEHAGYDTIRRVLLASANDLASVPGISLELAYKILEQVSKYGESKVDKPEIED

>core/283/5/Org5_Gene1051

MSMTIVPHALFKNHCECHSTFPLSSRTIVRIAIASLFCIGALAALGCLAPPVSYIVGSVLAFIAFVILSLVILALIF
GEKKLPPTPRIIPDRFTHVIDEAYGLSISAFVREQQVTLAEFRQFSTALLCNISPEEKIKQLPSELRSKVESFGISR
LAGDLEKNNWPIFEDLLSQTCPLYWLQKFISAGDPQVCRDLRVPRECYGYWLGPLGYSTAKATIFCKETHH
ILQQLTKEDVLLLKNKALQEKWDTDEVKAIVERIYTTYTARGTLKTEAGGLTKETISKELLLLHLHGYSFDQL
QLITQLPRDAWDWLCFVDNSTAYNLQLCALVGALSSQNLLDESSIDFDVNLGLYVIQDLKEAVQAQFSASDEP
KKELGKFLRLSSVSKRLESVLRQGLHRIALEHGNARARVYDVNFVTGARIHRKTSIFFKD

>core/284/5/Org5_Gene1010

MNHLNKEKLHIHNWQPYRACGLLSKVSGNLIIEVDGLSACLGELCKISSTKDPNLLAEVIGFHNHTTLLMSLSP
LHSVALGTEVLPLRRPSSLHLSHDLLGRVLDAFGNPIDKKEDLPKTHRKPLLSLPPSPMMRQPIDQIFPTGIKAI
DAFLT LGKGQRIGVFSEPGSGKSSLLSAIALGSKSTINVIALIGERGREVREHIEKHSNALKQQRTHIAAPAHET
APTKVIAGRAAMTIAEYFREQGHEVLFIMDSLRSWIAALQEVALARGETLSAHQYAASVFHHVSEFTERAGN
NDKGSITALYAILYYPKHPDIFTDYLSLLDGHFFLTSQGKALASPPIDILSSLSRSAQALALPHHYAAAERLRS
LLKVYNEALDIIHLGAYTPGQDEELDKAVKLLPSIKAFLAQPLSSYCYLDNTLKQLEALADS

>core/285/5/Org5_Gene819

MLKPMYVLSKRLYRWVNQLIKLGDLVKNSRSFSVEWVFISALLIFGCLGCASVVKVSLVPFLLLFSFLAFPLI
LCFRGKGYALLLGVFVTLYVAKYVVGETLYVSFWLSGLGVSFLLAFGLFLQGVWLAQEEEMVKGKEQLRL
SEDLDAQRSAYEDLLLTKSKEKEFLDARAQGLDRELTECQELLKAAYQKQEYLTIDLKILADQKNSWLEDY
AELHNKYIELVSKNGDVVFPWVAEPSVGESQGSERVDVSRWVSALQEKEESLERLRNEILVEKQRCSDYEHR
CQELGLLLQNFTALERRCEELQNLLNQKETQINELHQLVCKSEEKVSVEPSAHAETSCVEEKQYKGLYSQLQ
EQFLEKSETLSLVRKKLFAVQEKYLTLLKKKEELTKQDISFDDISMIQGLLERIEILEEEVSHLEELVSRSLSL

>core/286/5/Org5_Gene630

MLRQLCFQVFFFCFASLVYAAEELEVVRSEHITLPIEVSCQTDTKDPKIQKYLSSLTEIFCKDIALGDCLQPTAA
SKESSSPLAISRLHVPQLSVVLLQSSKTPQTLCSFTISQNLSDVRQKIHHAADTVHYALTGIPGISAGKIVFALS
SLGKDQKLKQGELWTTDYDGKNLAPLTTECSLSITPKWVGVGSNFPYLYVSYKYGVPKIFLGSELENTEGKKV
LPLKGNQLMPTFSRKKLLAFVADTYGNPDLFIQPFSLTSGPMGRPRLLNENFGTQGNPSFNPEGSQLVFISN
KDGRPRLYIMSLDPEPQAPRLLTKKYRNSSCPAWSPDGKKIAFCSVIKGVRQICIDYDLSSGEDYQLTTSPTNKE
SPSWAIDSRHLVFSAGNAEESELYLISLVTKKTNKIAIGVGEKRFPSWGAFPPQPIKRTL

>core/287/5/Org5_Gene716

MTWLSGLYFICIASLIFCAIGVILAGVILLSRKLFIVHPCKLKINDNEELTKTVESGQTLLVSLSSGIPIPCG
GKATCKQCKVRVVKNADEPLETDRSTFSKRQLEEGWRLSCQCKVQHDMSLEIEERYLNASSWEGTVISNDN
VATFIKELVVAVDPNKPIPFKPGGYLQITVPSYKTNSDDWKQTMapeyySDWEHFHLDQVIDNSQLPADSA
NKAYSLASYPaelptikfniriatppfingKPNSEIPWGVCSsyVfSLKPGDKITVSGPYGESFMKDDDRPLIFLI
GGAGSSfGRSHILDLLNKHskREIDLWYGARSLKENIYQEEYENLERQFPNFHYHLVLSEPLPEDIAAGWDK
DDPTKTNFLFRAFNLGQLSRLDNPEDYLYYVCGPPLHNSSILKLLGDYGVERSSIILDDFGS

>core/288/5/Org5_Gene523

MTVTLPKGVFDIFPYLADAKQLWRHTSLWHSVEKAIHTVCMlyGFCEIRTPIFEKSEVFLHVGEESDVVKKE
VYSFLDRKGRSMTLRPEGTAavvRSFLEHGASHRSDNKFYYILPMFRYERQQAGRYRQHHQFGVEAIGVRH
PLRDAEVLALLWDFYSRVGLQHMQIQLNfLGgSETRFRYDKVLRAYLKESMGELSALSQQRFSTNVLRILDS
KEPEDQEiIRQAPPILDYVSDEDLKYfNEILDALRVLEIPYAINPRLVRGLDYYSdlVFEATTTfQEVSYALGGG
GRYDGLISAFGGASLPACGFGVGLERAIQTLLAQKRIEPQfPHKLRLIPMEPDADQfCLEWSQHlRRLGIPTEV
DWSHKKVKGALKAASTEQVSfVCLIGERELISQQLVIKNMSLRKEffGTKEEVEQRLLYEIQNTPL

>core/289/5/Org5_Gene947

MFRKLFpFSKkkTGQKQRLRNNGLLQAIIQSIKVLLHNEAXKEACVLSYYGLLTCVPILVFFLRLSQHLFTNL
NWKEWLIikFPDYKKPIVAIVEAAyHATESNIGLVLVGSFFVFCWAGILMLLSLEDGLNKIFRTSWTPISLKRL
VSYFVITLVSPMIFIIVCGSWIYITQIMPIQYAKLFSLSHSMtALYfISRFVPYLLLYLALFCCYAFLPRVAIQKTS
ALISTLIIGSVWIVFQKAFFSLQVSIFNYSfTYGALVALPSfLLLLYIYTMIYLFGGALTfIIQNRGCTfIFLGDKIL
PSCYLQLITSTYILALTTRQfNEGLSPLTAQfIAKQSKVPIGEVSQCLDVLEKEGFLFPYNNGYQPVFNFSElTI
KDIADKLLHREIFKKfNPDLGITfIENSfQNIFNQASKNKENLTlSEIARRIK

>core/290/5/Org5_Gene995

MVCENNILSGRGLELLKKKSNIltPTIYSVSNHNIKLKDFSPHALSVIKTLRKAGYIAYIVGGCIRDLLLNTTP
KDFDISTSAKPEEIKaIFKNCILVGKRFRLAHIRfSKQIIEVSTfRSgSTDEDVLITKDNLWGTPEEDVLRrdFTI
NGLFYDPEHEEIIIDYTGGVNDLRNRYLRTIGDPfTRFKQDPVRMLRLLKILSRSPfTVETQTQEALIAcRQELIK
SSRARVFEELIKMLNSGAakNffQLLIENHLLAILFPYMDKALRLNRALEEQTATYlKALDDKILKKEAEYDR
HQLMAIFLFPVLVNFNVRYKHQKHPYLSLTSVFDYIKNFLEQFFADSFtSCSKKNfILTALILQMqYRLTPLIPTK
KALFFNKLLHHTRfLEALSLEIRSIVYPKLDKVYVAWIRHHQTLKCKKDSHSQK

>core/291/5/Org5_Gene235

MISLLKMPKLSPTMEVGTIVKWHKKSNDQVSFGDVIVEISTDKAILEHTANEDGWIREILRHEGEKIVIGTPIA
VLSTEANEPFNLEELLPKTEPSNLEASPKGSSEEVSPATTPQAASATFTA VTFKPEPPLSSPLVFKHVGTTNNLS
PLARQLAKEKNIDVSSIQSGPGGRIVKKDLEKAPPKSIAGFGYPESPEVPPGSYHEENLSPIREVIAARLQAAK
ISIPHFYVRQQVYASPLLNLLKELQAQGIKLSINDCIVRACALALKEFPSINSGFNSVDNKIVRFD TIDISIAVAIP
DGIITPIIRCADRKNLGMISAEIKSLALKARNQSLQDTEYKGGSFVSNLGMTGITEFTAIVNPPQAAILAVGSV
TEQALVLDGEITIGSTCNLTLSVDHRVIDGYPAAMFMKRLQKILEAPAVLLN

>core/293/5/Org5_Gene1016

MFEAVIADIQAREILDSRGYPTLHVKVTTSTGSGVEARVPSGASTGKKEALEFRD TDS PRYQGGKGV LQAVKN
VKEILFPLVKGCSVYEQSLIDSLMMDSDGSPNKETLGANAILGVSLATAHAAAATLRRPLYRYLG GCFACSLP
CPMMNLINGGMHADNGLGFQEFMIRPIGASSIKEAVNMGADV FHTLKKLLHERGLSTGVGDEGGFAPNLAS
NEEALELLLLAIEKAGFTP GKDISLALDCAASSFYNVKTGT YDGRHYEEQIAILSNLCD RYPIDSIEDGLAEED
YDGWALLTEVLGEKVQIVGDDLFVTNP ELILEGISNGLANSVLIKPNQIGTLTETVYAIKLAQMAGYTTIISHR
SGETTDTTIADLAVAFNAGQIKTGSLRSERVAKYNRLMEIEEELGSEAIFTDSNVFSYEDSEE

>core/294/5/Org5_Gene614

MDIKKLFCLFLCSSLIAMSPIYGKTGDYKLTLTGINIIDRNGLSETICSKEKLKKYTKVDFLAPQPYQKVMRM
YKNKRGDNVSCLTAYHTNGQIKQYLECLNNRAYGRYREWHVNGNIKIQAEVIGGIADLHPSAESGWLF DQT
TFAYNDEGILEAAIVYEKGLLEGSSVYYHTNGNIWKECPYHKGV PQGKFLTYTSSGKLLKEQNYQQGKRHG
LSIRYSEDSEEDVLAWEEYHEGRLLKAEYLDPQT HEIYATIHEGNQIAIYGKYAVIETRAFYRGEPYGKVTR
FDNSGTQIVQTYNLLQGAKHGEEFFYPETGKPKLLLLNWHEGILNGIVKTWYPGGTLESCKELVNNKKSGLL
TIYYPEGQIMATEEYDNDLLIKGEYFRPGDRHPYSKIDRGCGTAVFFSSAGTITKKIPYQDGKPLL N

>core/295/5/Org5_Gene72

MKKT MVIDTSVFIYDPEALFSFENTRIIPFPVIEELEAFGKFRDES AKNASRALSNIRLLLLENAKTKVTDGVLLP
SGSELRIEVAPLSNDDRRGKLLTLELLKIIAKREPMVFVTKSLGRRVRAEALQIESRDYESKRFSFRSLYRGFRE
LQVSQEDIENFYKNGYLDLPLDVSSPNEYFFMSAGENHFALGRYYVSEGKIIALKAMDKS VWGIKPLNTEQ
RCALDLLLRDDVKLVTLIGQAGSGKTILALAAAMHKVFDKETYNKVLVSRPIVPMGRDIGFLPGLKEDKLM
HWMQPIYDNMEVLFSINQMGNSSSEALQALMDAKKLEMEALTYIRGRSLPKAFIIIIDEAQNLTPHEIKTIISRAG
KGTKIVLTGDPTQIDSLYFDENSNGLTYLVGKFHHLALYGHMFMTRTERSELAAAAATIL

>core/296/5/Org5_Gene704

MLDIKIIRKTPEECETRLRKKDPKISLEPVLSLDKEVRQLKTDSETLQAQRRLLSQDIHKAKTQGV DATNLIQE
VETLAADLEKIEQHLDQKNAQLHELLSHLPNYPADDIPVSEDKAGNQVIKSVGDLPIFSFP PKHHLELNQELDI
LDFQAAAKTTGSGWPAYKNRGVLL EWALLTYMLQKQAAHGFQLWLPPLL VKKEILFGSGQIPKFDGQYYR
VEDGEQYLYLIPTAEVVLNGFRSQDILTEKELPLYAACTPCFRREAGAAGA QERGLVRVHQFHKVEMFAFT
TPNQDDIAYEKMLSIVEEMLTELKLPYRLSLLSTGDM SFTASKTIDAEVWLPGQKAFYEVSSISQCTDFQSRRS
GTRYKDSQGKLQFVHTLNGSGLATPRLLVAILENNQQADGSVVIPEVLRPYLG GLEILLPKDQ

>core/297/5/Org5_Gene539

MLPLIIFVLLCGFYTSWNIGANDVANAVGPSVSGSVLTLRQAVVIAAIFEFFGALLLGDRVAGTIESSIVSVTN
PMIASGDYMYGMTAALLATGVWLQLASFFGWPVSTTHSIVGAVIGFGLVLGKGTHIYWNSVGIIISWILSPF
MGGCVAYLIFSIRRHIFYKNDPVLAMVRVAPFLAALVIMTLGTVMISGGVILKVSSTPWAVSGVLVCGLLSY
IITFYVHTKHCSYISDTPKKGSLTYRLKERGGNYGRKYLVERIFAYLQIIVACFMAFAHGSNDVANAIAPV
AGVLRQAYPASYSYTLIRLMAFGGIGLVIGLAIWGWVRIETVGCKITELTPSRGFSVGMGSALTIALASILGL
PISTTHVVVGAVLGIGLARGIRAINLNIIKDIVLSWFITLPAGALLSILFFFALRALFH

>core/298/5/Org5_Gene322

MTLIFVIIIIVWCNAFLIKLCVIMGLQSRLQHCIEVSQNSNFDSQVKQFIYACQDKTLRQSVLKIFRYHPLLKIHD
IARAVYLLMALEEGEDLGLSFLNVQQYPSGAVELFSCGGFPWKGLPYPAEHAIEFGLLLLQIAEFYEESQAYVS
KMSHFQQALFDHQGSVFPSSLWSQENSRLLEKKTLSQSFLFQLGMQIHPEYSLEDPALGFWMQRTRSSSAFV
AASGCQSSLGAYSSGDVGVIAYGPCSGDISDCYYFGCCGIAKEFVCQKSHQTTEISFLTSTGKPHPRNTGFSYL
RDSYVHLPIRCKITISDKQYRVHAALAEATSAMTFSIFCKGKNCQVVDGPRLRSCSLDSYKGPGNDIMILGEN
DAINIVSASPYMEIFALQGKEKFWNADFLINIPYKEEGVMLIFEKKVTSEKGRFFTKMN

>core/299/5/Org5_Gene845

MDKQSSGNSGCIWHPFTQSALDSTPIKIVRGEGAYLYAESGTRYLDAISSWWCNLHGHGHPYITKKLCEQAQ
KLEHVIFANFTHEPALELVSKLAPLLPEGLERFFFSDNGSTSIEIAMKIAVQYYYNQNKAKSHFVGLSNAYHG
DTFGAMSIAGTSPTTVPFHDLFLPSSTIAAPYYGKEELAIAQAKTVFSESNIAAFIYEPLLQGAGGMLMYNPEG
LKEILKLAKHYGVLCIADEILTGFGRGTGPLFASEFTDIPPDIIICLSKGLTGGYLPLALTVTTKEIHDAFVSQDRM
KALLHGHFTFTGNPLGCSAALASLDLTLSPECLQQRQMIERCHQEFQEAHGSLWQRCEVLGTVLALDYPAEAT
GYFSQYRDHLNRFFLERGVLLRPLGNTLYVLPYCIQEEDLRRIYSHLQDALCLQPQ

>core/300/5/Org5_Gene1054

MAEISTPSLPDSSIVSQKTPPVDPDPDSSPDHIPTIPTQAPFKPQRKKETPSSIVNAIAFAILAFLSCLGGVFAICLGC
SLEITXPLFILTAVFIAFTLLYFIHYLEKPKIPEPLTPPPSPTLRAPTLTPEIPAPAPGIPLPPTLPKVDRTKLTCP
DIHYPSTYDPKACFSLLKQLFSLDPETRPEDRKYSNKLASILLRSKEKSGFRFHCFCGHFSDKILNKKSGAVV
ISSHSSMDFSTTLGRAFAVTTCLQRSCWEKIKNNIPTPEKHLPIGSCVSGPWDVEEGAQLYTSHLIVINPPTLET
LIKEKMRRAITLKDFSMKEAFTNLVLAYLQCFDICIEHNLESVQLEVFGLNNLSADQEEFTTWESCCHLALLE
SVRILLASKEEYALSNSVNSISQVPLQTACRALFLN

>core/301/5/Org5_Gene585

MKKQVYQWLASVLLALTISGYAELPLSEQKVKSHTYTTLDEVKDYLKRGFVETRKQDGVLRAGDVRAR
WLYFREDIKNPSDKDKYNPLPVNRYRSEFYLYIDYRAERNWLSSKMNWTAIAGGENTAAGVDINRAFLGYR
FYKNPETRTDFFMEIGRSGLDLFESEVQFQSNFDGLHIYWTRELSKDYPYQVIVHGGPFVVMNMTKKHYAW
VVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVPWINGQKKPLYL
YGAFMLNPLAKATKTTLNGKENLAWFIGGTGGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFW
FAQAIAANYDPKEANGFTNYKGFSALYMYGITDSLFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF

>core/302/5/Org5_Gene1043

MAILNYVRSLMQSWLQSLQERNILENFTAGLESVEGPAAAYLGFDPTAPALHIGHWIGICFLKRLAALGITPIA
LVGGATGMVGDPSGKQSERSLLQTSEVFDNSQKITACLQRYLPGVTLVNNADWLQEISLIDFLRDIGKHFRLG
QMLVKDTIKQRVHSDEGISYTEFSYLILQSYDFYHLFKNYGTILQCGSDQWGNITSGIDFIRRKGLGQAYGL
TYPLLTNAQGKKIGKTESGTVWLSDLTSPFELYQYLLRLPDDTIPKIARTLTLLSNEEIQDIDRRVQTDPAVAV
KEFVAQDILSAIHGDLGLEEALSVTRSMHPGNLSSLSEKDFHELFAAGMGASLDKSEVLGKRWLDLFLVLGL
CKSKGEIRRLIEQKGVYINNVPANEHSVCEEQDICYGHYVLLAQGKKRKLVLNLN

>core/303/5/Org5_Gene901

MTVAEVKGTFLVCLGCRVNQYEVQAYRDQLTILGYQEVLDSIADLCIINTCAVTASAESSGRHAVRQLC
RQNPTAHIVVTGCLGESDKEFFASLDRQCTLVSNKEKSRLIEKIFSDDTTFPEFKIHSFEGKSRAFIKVQDGCNS
FCSYCIIPYLRGRSVSRPAEKILAEIAGVVDQGYREVVIAGINVGCDYCDGERSLASLIEQVDQIPGIERIRISSIDP
DDITEDLHRAITSSRHTCPSSHLVLQSGSNSILKRMNRKYSRGDFLDCVEKFRASDPRYAFTTDVIVGFPGESD
QDFEDTLRIIEDVGFIVHSPFSARRRTKAYTFDNQIPNQVIYERKKYLAEVAKRVGQKEMMKRLGETTEVL
VEKVTGQVATGHSPYFEKVSFPVVGTVAINTLVSVRLDRVEEEGLIGEIV

>core/304/5/Org5_Gene683

MNKKNLTICSFCGRSEKDVEKLIAGPSVYICDYCIKLCSGILDKKPSSTISSAPVSETPSQPSDLRVLTPKEIKKH
IDEYVIGQERAKKTIAVAVYNHYKRIRALLHNKQVSYGKSNVLLLGPTGSGKTIAKTLAKILDVPFTIADAT
TLTEAGYVGEDVENIVLRLQLAADYDVARAERGIIYIDEIDKIGRTTANVSITRDVSGEGVQQALLKIVEGTTA
NVPPKGGRKHPNQEYIRVNTENILFIVGGAFVNLDKIIAKRLGKTTIGFSDDQADLSQKTRDHLLAKVETEDLI
AFGMIPEFVGRFNCIVNCEELSLDELVAILTEPTNAIVKQYMELFAEENVKL VFKKEALYAIKKAKQAKTGA
RALGMILENLLRDLMEIPSDPTVEAIIHQEDTIAENKAPIIIIRRTPEAIA

>core/305/5/Org5_Gene66

MIKFLSQLFIRHWPRKVVSLSGFAIIIWILVGQSVTITRTLTVNPVRIVDLHPDQTVLGLQKSGFLNKKVSLTITG
NKNTVQDLRPSNLEVVISAAHNTESWIATIDKHNLVSDHEINIRKDIHSVDANDIFVRLTQYVTEIDILLTITKP
IGSPPKGYEYLDVWPKYLNQKVSGPKKEYINALKEQGLELTFNLNKISFEELERNRIAQGSHEIIFPIPKWKI
LIPFENTFMDLNDPQADFLRLFLKRECIPLNLNPVFLFFPVTFIQTMNPLEYSLDPVPPHILNHGIHQINIPLYV
KDVSQRFLDVVKNNMVLTVMPSPQDPSSINWAIEFLDEKTLNTEFLQTIIAQEHGILHDIALIDEAGIRHRFRE
YLRKLALFTADGEPLNLIAEIKNNKVVIQTKTKETTKLYKKEW

>core/306/5/Org5_Gene824

MLKLQLCALFLFGYLAIVFEHIVRVNKSALALAMGGLMWLVCFSHIPMADHMILVEEIADMSQVIFFLFSAM
AIVELIDAHKGFSVIVKFCRIQSRTLWALIGLSFFLSAALDNLTSSIIISILKRLVKAREDRLLLGAICVIAVNA
GGAWTPLGDVTTTMLWINNKITSWGIIRALFVPSLVCVLVAGFCGQFFLRKRGSTLIAKDVELQSAPPKSLWII
FIGLGSLLMVPVWKACLGLPPFMGALLGLGLVWLTSDWIHSPHGEDRYHLRVPHILTKIDISSITFFIGILLAVN
ALSANLLTDFSLWMDKIFSRNVVAIVIGLLSSVLDNVPLVAATMGMYTLPLDDTLWKLIAYAAGTGGSILII
GSAAGVAFMGLEKVDLWYFKRISWIALASYFGGLFSYFVLESNFFI

>core/307/5/Org5_Gene157

MSSAIARDCFPSPSPQPSSTLGVHPPKYKSLILSVSLIVLGVLLLCVGMLLL VNAIFSFSVLT VGLGGAGVFLGS
LLLILGLIFFVSYHRKLSEATRSLEQKITLEYQPWADLRKELNEVQEWSNFLDDEWEDFKEVVAQHKSQFATF
EGDLLLFGREVEKYETIWKELDGRDVALLTELKNIWGPLEFLRKKGDRLQCEIDKLRKEVMKVGKSGLKLA
CELTkFksALKDVKIEQECYRDKRKVEKLEVFPEGYRRELLEVLKTRLSVEKEIQLFEEVVS AFEEKLASLHR
TVFSEELQEALDKAKAELLDIQVRKSVVEDLSCEPTLIQYHLLRLYEYVQCRIVEQFLTQTFSSSEQEKVLEEYE
ALKARIRKTLRVKLDQVRANVAFVASTTDLLSESES LDGNDSVFEDAHD DFLD

>core/309/5/Org5_Gene706

MIETREEVGSANFVSLERAIEDLRAGKFVIVVDEASREDEGDLIAGEKITVEKMTFLLQHTTG VVCAALSQER
LLSLDLPPMVKDNRCRfKTPFTVSVDAAHGVT TGVSAA DRTKV VQLLADPKSKPEDFISPGHFFPLASSPGGV
LK RAGHTESTVDLMELAGLQPCGVLAELVNEDYSMMRLPQILEFARKHNIAVIPVTSIIAHRMLSDRLVSKIS
SARLPTIYGDFTHVYESLLEGMQHLALVKGNVAGKSNVLVRVHSECVTGDILGSKRCD CGEQLSSAMSYIA
EKGTGVLVYLRGQEGRGIGLGHKVRAYALQDNGYD TVDANLAMGFPVDSREYGIGA QILVDLKLTTIKLIT
HNPQKYFGLQGFGLSITERVPLPVRISEDNEQYLRTKQERMGHWLDLPCCNNRVQ

>core/310/5/Org5_Gene1014

MLCYSPTYVTDLYRISLSAEESLGGIRAFPAESLLGGACALNFPDLEERLPDLRKELLFLGSNDRPDACGGK
FSLQLASSKECYIAALKERVYLVNTNSSRGPVYSFSPKGVPTELWIECFVSVDGRVEVKVRLQGLHKELISKP
RDCETLFLNPPANKLDCWEIAGFRVDASFPVKQKIRRIGVDKFLLMHGGAEYADKATKERVDFVSSDEENYS
RYLAVGDVLLWDGNCWQTCGEFQGASSRAPLFEVKRIDDKVM IADLWNVGGTQRQTISLVKGVPSPIEINE
VIREIEFTGMRSWSKPIVLVGGQRLILSPDDWILRTAKGWEKLSRADQIQDYVTGKVTGPLL VFEKLEKDLRG
FVLRGHMFNAQRTL VETISLPLKQGFEP AVASQEVSSNTRSAAAHPGATNRGGS

>core/311/5/Org5_Gene915

MSQPPINPLGQPQVPAAASPSGQPSVVKRLKTSSTGLFKRFITVPDKYPKMRYVYDTGIIALAAIAILSILLTAS
GNSLMLYALAPALALGALGVTLLISDILDSPKAKKIGEAITAIVVPIIVLAIAGLIAGAFVASSGTMLVFANPM
FVMGLITVGLYFMSLNKLTLDYFRREHLLRMEKKTQETAEPILVTPSADDAKKIAVEKKKDL SASARMEEHE
ASQRQDARHRRIGREAQGSFFYSSRNPEHRSFSGLSRfKTKPSDAASTRPASISPPFKDDFQPYHFKDLRSSSF
GSGASSAFTPIMPASSRSPNFSTGTVLHPEPVYPKGGKEPSIPRVSSSSRRSPRDRQDKQQQQQNQDEEQKQQS
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>core/312/5/Org5_Gene728

MCQRILILGTGITGKSVARFLYQQGHYLGADNSLESLSVDHLHDRLLMGASEFPENIDL VIRSPGIKPYHPW
VEQAVSLKIPVVTDIQVALKTPEFQRYPSFGITGSNGKTTTTLFLTHLLNTLGIPAIAMGNIGLPILDHMGQPGV
RVVEISSFQLATQEEHIPALSGSVFLNFSRNHLDYHRNLDAYFDAKLRIQKCLRQDKTFWVWEECSLGNSYQI
YSEEIEEILDKGDA LKPIYLHDRDNYCAAYALANEVGWVSPEGFLKAIRTFEKPAHRLEYLGKKDGVHYIND
SKATTVTAVEKALMAVGKDVIVILGGKDKGGDFPALASVLSQTTKHVIAMGECRQTIADALSEKIPLTLSKD
LQEAVSIAQTIAQEGDTVLLSPGCASFQFQSFKERGAYFKLLIREMQAVR

>core/313/5/Org5_Gene741

MSKKRVVVTGFGVVSCLGNEVDTFYDNLLAGVSGVRPITSFPCEDYATRFAGWIPEFNPEPYVDKKQARRV
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PALIAMDFGLMGPNYSISTACATGNYCIDAAYQHLVSGRADMIICGGTEAAVNRI GLEGFIANRALSERNDAP
DQASRPWDRDRDGFVLGEGAGILVLETLESALRRDAPIFAEMLGSYVTCDAFHITAPRDDGEGITACVLGAL
NSAGIPKERVNYVNAHGTSTPLGDLSEVLAVKKAFGSHVRNLRMNSTKSLIGHCLGAAGGVEAVVAIQAILT
GKLHPTINLDNPIAEIEDFDVVANKAQDWDIDVAMSNSFGFGGHNSTILFSRYVP

>core/314/5/Org5_Gene549

MLVSIETFSSIASGSPVQKAAEACYTQYSKQPSSKEVLSSFSWIQELSLFPDRYNLATGASELIKQHWLHNNHS
LAFECILINGKYEPSLSQLPEGVIVCGIDEARGSLSSFMQGFVDNKHPLAFLNAVCSSEDRGVVIYIPEEMQTSDP
IFVRHISFPTVSDHDVIFSPRIVVILGQRASAQIQISHDVDLEMVGSSKTIVNGVTELFVGEGADLTVFMVPGYS
EEDTLWSSTIATVEKDAICRMTQNLLDESCQGFGWFDNTSYIVGKKGHAESLVLVQSPRKTWVNNLMSHDAE
ETVSRQNIKSILYSGHFLFEGTISISSQGDLSANQKHDTLLLSSEARVSTFPRLEIETDEVKASHGATVGPLDP
QQIFYMRSRGMTEAEAQEKLIHGFLKQGLVSDTFLGSSFQLNQTS

>core/315/5/Org5_Gene701

MHIGFCHCVRGGNFFYFVINNFHILEIYSLLNSNTIMRYHKYFRYVNSWVFLVVLTLMLLSVVVISSMDPTAM
LVTSSKGLLTNKSIMQLRHFALGWVFFICAYFDYHLFKRWAWVLYFFMICALVGLFFVPSVQNVHRWYRI
PFIHMSVQPSEYGKL VIVIMLSYILES RKADITSKTTAFLACL VVALPFFLILKEPDLGTALVLCPTLTIFYLSN
VHSLLVKFCTVVATIGIIGSLLIFSGIVSHQKV KPYALKVIKEYQYERLSPSNHHQRASLISIGLGGIRGRGWKT
GEFAGRGWLPYGYTDSVFSALGEEFGLLGLLFTLGLFYCLICFGCRTVAVATDDFGKLLAAGITVYLAMHVL
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>core/316/5/Org5_Gene399

MKLWMKIFIGL FVGVT LGLVLEDKAIFFKPIGDIFLNLLSMVVYPLVFCSMVLG IASISDMKKLGRIGIKSVGL
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AIFLGIALRLSGERGRPVERFIDGFSEIMLRMVNMIMSFAPYGVGASMAWISGNHGLGV LWQLGKFIIAYYLA
CLFHATLVFGGLVRFGCKMSFSKFLSSMMDAISCAVSTASSSATLPVTMRCVSKNLGVSAEVSGFVLPLGAT
VNMNGTAIFQGMAAVFIAQAYNCPLSLSSLLLLVVTATFSAVGSAGVPGGGMITLGSVLASVGLPIQGIAILA
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>core/317/5/Org5_Gene625

MKKIFYSFVLLSCIFPYVGCAQVFVGLDRIFSEGEYTRCIQGKKIALISHSAAINSRGQDALSVFYSRKHDCTVE
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KASERYGKQLIVLDRPNPMGGRIVDGPLPNPTTSGSLAIPYCYGMTPGELALFFK KTYAPNANVVVIPMKGW
NRSMTFDETGLIWMP TSPQMPDPQSPFFYAATGILGALSVASIGVGYTL PFKVLGAPWMDGEKVADELNRM
KLPGVLF LPPFFYEPFFGKYKMEMCSGVLLVLQDPKIFYPVETQCTIWGVLKALYPKQVEQTLKSIERIPARRSS
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>core/318/5/Org5_Gene1013

MKKNASHKTNDKKSLSIWSIGGSIFAMFFGAGNIVFPLALGYHYNAHPWSAYFGMMLTAVCVPLLGLVSM
FYSGDYQKFFFSIGRIPGMIFITAIILLIGPFGGIPRAIAVSHATLISLSEHKSAFIPSLPIFSAICCVLIYIF
SCKLSRLIQWLGSVFFPIMLVTLWVIIRSFMIPTHPMVQEIPNARQAWLAGFIEGFNTMDLLAAFFFC
SIVLISLRQLVAEEKHPTEEEIPLSFQGISKKNKRSALGFFLAAILLGMTYLG FVLSAARHAGLLVNV
SKGHILGRISAIALGPNSILAGVSVFIACLTTEIALVGIVADFLARVVSFKKLNYSASAVICTLIPT
YLISILNFETISHLLLPLLQLSYPALIVLACGNIAYKLWNFRYSPVLFYLTLSLTIVLKLVN

>core/319/5/Org5_Gene172

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AVLFLSLLGWL EARYLTASSLGITSSQSSNFLLYSSIMTVYSLLVVLSLAGSERRWHTRPKI
VIATALALTGVIIITLLPIILHQLRYDCWLCLCLTIEPALAVVFAYDETRATLRYISQFLGDKRAL
TRASFFGSEYYKHTLSWEERTVLPLRKAYKQAFEGISFPINQLLAILVATVFVKVNSSMGLPT
FPRNFLNICCWFIIVLFILAFaesLRHLRWMNLIFSAAILFSPVL FHIPVESPMFLPIHVTGL
ILHLSIGKRRRTKRKL

>core/320/5/Org5_Gene303

MIPTMLMFFIICFTLCSGFISLSQIALFSLPTSLISHYKRSKSKKQQRVATLLLHPHLLITLIFCDI
GLNIAIQNCF AILFGDAASWWFTVGLPLAITLILGEILPKAVALPFNTQIASSVAPLILCVTKIF
KPLLHWGIVGINYVQWILSKQQIDIIQPQELKEVLQSCKDFGVVNQEEsRLLYGYLSLSDCSVKERM
QPRQDILFYDIQTPLENLYLLFSKQHCSRVPICNDNLQNLGICTARSLLLHDKPLQSSDDLPL
LKKPYMPETISAKMALCQMAAEDETGMIIDEYGSIEGLITQEDLFEIVAGEIVDQRDNKILYTT
SGADVIIASGTLELREFSEIFDINLPTNNNIATIGGWLIEQIGTIP TTGMKLSWNNLLFQVLDA
APNRIRRVYIRKLYD

>core/321/5/Org5_Gene949

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RYWVEKRL DAKNPDSLNAFVKEVGTHYVASVTYGGIGFQVLKMSYLVQEELEKEKISISVAAAS
SLLKSKTSNATEKGYSYQSESSAQTVFLGGTVLPDLQQDKLDFKDWSESI PN EPI LAISVSSIT
DLIPELFPSEDAQVLSQKKSALGQVILNYLESHKPKEEGPKPVQITSGFNSSSSVFTLQAAKAP
KTVSFPYIDYWSTIPYLFPTLKETSGAQPLSFYLRFD DIFEQQNLVHNTSYILASTSVRLGYF
GDSYRDYDALSFYGSWPQAYFDWAGYKDRCTWTLEKLNTTGDLFIRSGDEIRLKHNTSGKYL
ATTSMSDGYQTLTCTTQTSDSVFIITV

>core/322/5/Org5_Gene794

MNLPVSLACLLLSGCVFFLGVFVSSSLYARKKRAFLEKIQKLEHENQLLQTSNLNLSRHQEQLIED
FSNRLALSS HKLIKDMKEEAQNYFGDTSKSFQSILSPIQTTLTTFKQSLETFETKHAEDRGR
LKEQISQLLAVEKKLEHETHV LTDILKHPGSRGRWG EIQ LERILELAGMLKYCDYDSQTTS
AQGAFRADIIIRLPQDRCLIIDAKAPISDSYFSVE EIDKGDLVDKIKEHIKTLKSKSYWEK
FHQSPEYVILFLPGESLFNDAIRLAPELMEIGASSNVILSSPLTLLALLK TIAYMWKQENLQK
QIQEVSLLGKELHRRQLQVVFTHFQKIGKNLNQTVQSYNDMTSSFQYRVLPTLRKFEGLE
TSSSHQIEEPTPIESLATSFPHTCDIDTNLAVIESLEKQD

>core/323/5/Org5_Gene369

MHFLDSRTQVVIEKNRAYLFSLPVDSSLSEAITNFVRDLPFICAVEICERPYGECITRSSAERPLLPEKTLGMPI
FCGKEGVWLPQNTILFSPLIADPRQVTNSAGIRFNEKVVGNRVGATIFGGDFILLRLFDVSRFHVDCDFGIQGG
VFSVFDLDHPESCMVNSDFFVAGLWSGAIDKWSFRFRLWHLSSHLGDEFILTHPNFPRFNLSDEGVDLFISFR
YTPQIRLYGGCGYIVSRDLTFPERPFYCEWGAELRPFGLREGNLHAQPIFAMHFRCWEEQKFGLDQSYILGME
WAKFQEIGRKIRAVLEYHQGFSKEGQFIREPCNYYGFRLTYGF

>core/324/5/Org5_Gene682

MTTIAIEAAKKVLIKLNRNAGYQAYFVGGCVRDMLMNRPLEDIDIATNASPTIVSTIFPDVISIGVAFGIIVVKQD
GRLFEVATFRSDGEYKDGRHPDRIIFSSMREDALRRDFTVNGMYYPDVEDKVFDFVEGTRDIEKKVIRAIGHP
RLRFSEDKLRILRAIRFSSSLGFTLDPTTERAIKEAPALVNSVSPERIWQELKKMLKRQPYGALSLLLKLKVLIF
IFPELRDIPYSLRRTTIEFARKFNPTHFPEILFLLPLFQGVSEEAATVAFGRRLISNKKELKLIESWYEALPHFQNQS
GNRVFWAHFLASPTAPLFLELFSALQKDPSRQQHFISRVQELESRLQFILRIKTSSPVVSAPDLIAKGISPGRLL
GDLLREAEILSIENECLDKEKILLLLQEKGFWK

>core/325/5/Org5_Gene548

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VRKWVSAASDSEIVFTRGTTAGLNLLAISVNDLWIPKGGVVLVSEAEHHANVLSWEIACRRRGSLVKKIRVH
DSGLIDLDDLEKLLNEGAQFVSIPHVSNTGCVQPLQQVAELVHRYDAYLAVDGAQGAPHLPIDVQLWDVD
FYVFSSHKIYGPTGIGVLYGKKDLLDQLPPVEGGGDMVAIYDHQNPEYLPAPMKFEAGTPNIAGVLGLGAAL
DYLDGLSAKFIYDKEIALTTYLHKELLEIPGVEILGPSIEEPRGALIGMTIDGAHPLDLGFLDLRGIAVRTGHQ
CAQPAMERWNVGHVLRVSLGIYNDEDDIDQFILVLQDSLDKIRR

>core/326/5/Org5_Gene156

MVVVALFILGIFFLSGSLAFLVHTSCGVLLGAALPILCIGLVLLAVALIVFLCHKHKTRQDLDDYDQDLDSLVI
HKKEIPNDISELRVTFEKLQNLQFHTKDFSDLSQELQGKFINCMEKWLTLEDEVTKFLIVRDRFLETRRNFTT
FGEQVKGIQSNIFDLHEEKSSLYLELYRLRKDLQVLLNFFLLPPGILKVDYDEIEAIKGLFIRLTSRLDKLDVKA
QERKKFINEMSREFKEVEKAFDIVDRATKKLMDRAKKESPARLFMGRTESLLEMKKNEEALKNQGLDPENL
SHPELFSPYQQLLILNYLNSEIVLHHYEFLISGTVTSGLTLEECENRMRAASTGLNALLVRKLQFRGAIKSAYF
EKLTEIEKELRSLQDVIKSLELELIHKIKDIVTEET

>core/327/5/Org5_Gene280

MTDSNPLPSYTDASLYRTPAKHSYPIRLPLNRTDRIEKILKIVTLTLALACALGFSIAAGILAMPIFS AVVVITLA
IAAVSLYSLLKKPKLYEILPQIEPESEQSSLSPSPQPPEQQDLPLQIDPLDPESLPEVSLADLTPPEELTAITVTP
GYEALLEQNWDLLPSLAAVDPSFTTETPQQPCFIWKLKDSKLIFISTSGDIAVPRIKTQGRVMIVNAANENISR
EGGGTNKALSLATSLQCWNASRLPRAHSRSGSQLQPGECRSAKWENS DHTSNDHVP GKAHFLAQLLGPEAA
KCNNDPKQAFEVSKKAFHNLFQEA EIIGVDVIQLPLIGCNLFAPSRLNLGKTRA EWIEAIKLALITSLQDFGW
EQDNQEEQKIILTDKDKQPPHIPPRFDLTPP

>core/328/5/Org5_Gene938

MKKQRSHYTKNNLLLLLSILVGLGLGSVQSPWIVYSAECIANTFLKFLRLLSIPLVFCALGSTITSIQNFNTMVT
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AVLLGTASLFLQEKEKHFVNQFFNSFFSIFLNLARGGLKLLPIAMLGFSVILFKELKDQSNLTMFAEYLLCVIG
ANLAQGFIVLPILLKINKVSPLKVAKAMSPALVTAFFSKSSAATLPLTMELAEDDLKINKNLSRFSFPLCSVIN
MNGCAAFILITVLFVATSNGMIISPLMSLGWIFIATLAAIGNAGVPMGCYFLTLSLLTSMNVPLSILGLILPFYT
VIDMIETSLNVWSDCCVSLAN

>core/329/5/Org5_Gene304

MTNSALFWIGVNIICIVLQGFYSMMEMACVSFNRVRLQYYLTKDHKKARYINFLIRRPYRLFQTVMLGVNIA
LQVGSESSRNCYRALGITPDYAPFTQIFIVVIFAELLPLTISRKIPEKLALWGAPILYYSHYIFYPLIQLIGSLTEGL
YYLLNIRKEKLNSTLSRDEFQKALETHHEEQDFNTIATNIFSLSATCADQVCQPLEQVTMLPSSANVKDFCRTI
KNTDINFIPVYHKARKNVIGIAHPKDFVNKALDEPLINNLHSPWFITAKSKLIRILKEFRDNRSSVAVVLNASG
EPIGILSLNAIFKILFNTTNIHLKPKTISVIERTFPGNSRIKDLQKELDIQFPQYPVETLAQLVLQLLDSPAIEVGT
SVIINNLLLEVKEMSLSGIKTVSIKNLLS

>core/330/5/Org5_Gene538

MDKLTVQDLSPEEKVLRVDFNVPMQDGKILDDIRIRSAMPTINYLLKKHAAVILMSHLGRPQGGFQEEY
SLQPVVVDVLEGYLGHVPLAPDCVGEVARQAVAQLSPGRVLLLENLRFHIGEEHPEKDPTFAAELSSYGDFY
VNDAFGTSHRKHASVYVVPQAFPGRAAAGLLMEKELEFLGRHLLTSPKRPFTAILGGAKISSKIGVIEALLNQ
VDYLLLAGGMGFTFLQALGKSLGNSLVEKSALDLARNVLKIAKSRNVTIVLPSDVKAAENLQSKEYSVISIDQ
GIPPHLQGFIDIGPRTTEEFIRIINQSATVFWNGPVGVEVPPFDSGSIAIANALGNHPSAVTVVGGGDAAAVVA
LAGCSTKVSHVSTGGGASLEFLEQGFLPGTEVLSPSKS

>core/331/5/Org5_Gene1006

MSTMQNCPHFGVCGGCSFPQSNYSDSLKKKEELLHQLFAPLVPSDMIAPIIPCSPSLRGRNKMESFFQTYEGE
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LTTSGTPEYRVNEACIDEWKEILLSSSLNIASIYWEKVAARGISTYYETKLLYGAPSIQQKLSLPSDGNSASFS
LRPRSFFQPQITQAAKIIETAKEFINPEGSETLLDLYCGAGTIGIMLSPYVKNVIGVEIIPDAVASAQENIKANNK
EDCVEVYLEDAKAFCKRNENCKAPDVIIIDPPRCGMQSKVLKYILRIGSPKIVYISCNPKTQFQECADLISGGY
RIKKMQPIDQFPYSTHLENIILLEREIDL

>core/332/5/Org5_Gene606

MLLVRKWLHTCFKYWIYFLPVVTTLLPLVCYPFLSISQKIYGYFVFTTISSLGWFFALRRRENQLKTAAVQLL
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KMQVDSLIECEKTEEVQTLNRELAETLAYQQALNDEYQATFSEQRNMLDKRQIYIGKLENKVQDLMYEI
RNLLQLES DIAENIPSQESNAV TGNISLQLSSELKKIAFKAENIEAASSLTASRYLHTDTSVHNYSLECRQLFDS
LREENLGMLFVYARQSQRVAFANALFKTWTGYCAEDFLKFGSDIVISGGKQWMEDLHSSREECSGRLVIKT
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>core/333/5/Org5_Gene70

MRMLQISM LLLALGTAINSPAIYAADSQSVSFPEQLPSSFTGEIKGNHVRMRLAPHTDGTHREFSKGDLVAVI
GESKDYYVISAPPGITGYVFRSFVLDNVVEGEQVNVRLPSTSAPVLVRLSRGTQIQPASQEPHGKWLEVVLV
SQC VFYVAKNFVANKGPIELYTQREGQKKIAMDLINSALNFAHIELEKSLNEIDLEAIYKKINLVQSEEFKDVP

GIQGLIQKALEEIQDAYLSKSLESQNTSIASSQCSTPKVSSSEVTTSLLSRHIRKQTALKTAPLTQGRENLEYSLF
RIWASMQQGNDHSEALTQEAFYRAEQKKKQVLAGVLEVYPHVVKNNPGDYLLKAQENTIAFLYGTSINLEQ
WLGKRVTVECLPRPNNHFAFPAYYVVGIKEAS

>core/334/5/Org5_Gene250

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STALDYLVTTPPSQGKLKEALIQARNTHTEQFGRTAIGAKNILFASQEYADQLNVSPSGLRSLYLEVTGDTH
TCDQLLSMLQDRYTYQDMAIVSSFLMKGMATELKRQGPYVPSAQLQVLMTETRNLQAVLTSYDYFESRVPI
LLDSLKAEGIQTPSDLNFVKVAESYHKIINDKFPTASKVEREVRNLIGDDVDVSVTGVLNLFFSALRQTSSRLFS
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>core/335/5/Org5_Gene940

MVYFMVFSPPSESVVKANSVVRSNFCYFLENKFVSPSESTEVMFSEIMKGRVPDIESLFD RPTDMMMTGFKA
AQNLGNLFNSFGILIMCFSQCKSCQTPEKETS AIVLGATLLFFVIALILGPTLGALVYCA YKVYTLGKMIYSLN
KAKAKVLRHPAQNVFHRAAGVATIRSSEEAVKACKLYKSAMIGSLVVS LIASLALIALTAGIVLV LFFVAPGA
APVITAAMMGCCAAGGGALLISLLGLWIAIVRKAKHQEACVGH LTNVVLHTAVSEALLHDPSHFQTNALAR
DLFLTDCLSHYGHLFSNEEVAQLVQGGAPGGGSRPSQHYGGSSDYQNR RGNGNFGGSHFGGGGGFAGSHF
GAGYPTAPT MPSAPPPFPPPAYDTIYG

>core/336/5/Org5_Gene377

MLSVTIVLVGLEMARSKVSKRDSKILDILFATTELYLKTGQPVGSKTLKESFCSDLSTATIRNYFAELEAEGFL
KKNHTSGGRIPTDLALRHYVDHQEECPAEISAPIFDKISQLPSES RNIKD LQKATELLGEILDLP TFFSSPRFEN
DSVTNIQITQVDKQRAVTILSTEFQGIFTDTLWLPEACDTLSIKRIEKFLQNYIRKLPTNEELSKKEEHL SMSLY
NEVVVRYLTRYCNFSEEDLYQTGMSKLLKYEAFKDPEVLALGLSLFENRRQMCELLNIGMHKGRATAFIGK
ELSDILGTSNPGCSVITIPYYMNRSP LGALGILGPINLPYKEALPLLKLFANKINETLTQSFYKFKLSFRRPLTSN
CKLSNEPILRTEYSSIKLLPSKETL

>core/337/5/Org5_Gene373

MRRNPHFSLLKPQYLFSEISKKLAQFRKENPEISVIDLSIGDTTQPLCRSITQAIKEFCVSQEKQETYRGYGPET
GLEKLRTKIASEVYENRISPEEIFISDGAKPDIFRLFSFFGSEKTLGLQDPVYPAYRDIAHITGIRDIIP LACRKET
GFIPELPNQQLDILCLCYPNNPTGTVLTFQQLQALVNYANQHGTVLIFDAAYSAFVSDPSLPKSIFEIPEAKYC
AIEINSFSKSLGFTGMRLAWNVIPKELTYDNN EPMINDWKRLFATTFN GASLLMQEAGYYGLDLFPTPPAISL
YLTNAQKLKKSLETAGFSVHGGDHAPYLWVELPEGISDEEAFDFFLHQYHIAVTPGHGFGSCGQGFVRFSAL
TQPQNIALACDRLCTASLKETMVLA

>core/338/5/Org5_Gene785

MSNKVLGGSLLIAGSAIGAGVLAVPVLTA KGGFFPATFLYIVSWLFSMASGLCLLEVMTWMKESKNPVNML
SMAESILGHVGKISICLVYLFLFYSLLIAYFCEGGNILCRVFNCQNLGISWIRHLGPLGFAILMGPIIMAGTKVID
YCNRRFFMFGLTVAFGIFCAGFLKIQPSFLVRSSWLTTINAFPVFFLAFGFQSIPTLYYYMDKKVGDVKKAILI
GTLIPLVLYVLWEVVVLGAVSLPILSQAKIGGYTAVEALKQAHRSWAFYIAGELFGFFALVSSFVGVALGVM

DFLADGLKWNKKSHPFISIFLTFIIPLAWAVCYPEIVLTCLKYAGGFGA AVIIGVFPTLIVWKGRY GKQH HRE
KQLVPGGKFALFLMFL LIVINV VSIYHEL

>core/339/5/Org5_Gene270

MVNIQP VYRNTQVNYSQATQFSVCQPALSLIIVSVVA AVLAI VALVCSQSLLSIELGTALVLVSLILFASAMFM
IYKMRQEPKELLIPKKIMELIQEHYPSIVVDFIRDQEVSIYEIHHLISILNKTNVFDKAPVYLQEKLLQFGIEKFK
DVHPSKLPNFEEILLQHCHPLHWLGRLVYPMVSDVTPGTYGYYWCGPLGLYENAPSLFERRSLLLLKKISFGEF
ALLEDGLKKNTWSSSELVQIRQNLFTRYADKEEVDEAELNADYEQFDSLHLIFSHKLS

>core/340/5/Org5_Gene594

MSFFNHIPTFSPDAILGLQNVFFADKRPEKVNLVIGVYEHPPQKRYGGLSCIRKAQTVILEEEQNKSYLPISGLQI
FLDEMRELVFGAVDPSAIVGFQSLGGTGALHLGARLLSVAKGSGKVYVPEQTWSNHIRIFSQEGLEVIRYPYY
SKEQKQLLFEPLIAFLKEVEKNSVILLHGCCHNPTGVDFTEDMWKELAILMKERELIPFFDTAYQGFAHGIEL
DRKPIEIFISEGNTVLVAASSSKNFALYGERVGYFAVHSTFTDELVKIHSFLEEKIRGEYSSPQRWGVEIVSTILS
NPYLKEEWQSELNFIRESLGKMRTFRVQALRKVAGHTFDLLSQHGFFAYPGFSDKQVFLFLREQHAVYTTAG
GRMNLNGITEKNIDHV VQSFIQAYEL

>core/341/5/Org5_Gene155

MVVSIIYSEILSFSELTSCKHSLFPFGPIETASIRIHVFNVVIVCLII LGTLFVCLGMVFLGVFSTYLLGMSSMILG
LLISIGLALLKFKERYGLEPKELFGVEGGFDKKLPSEIIQM QDQIADLARELDLEQKKDTLIRGFSARLDVLE
GSKTEKKQILKIGVPRNLSEIQERAQE QNSILEQCKEALLFRRKSAQEIFKKLYDRKAAFWR SYREDLWCYSEI
HVSKKALS NLYIGDVFEGTAPHFLMEAYAMCRTAKNLRNYVKVCVEDMRVNEEKKRAKQLSVSELLCCCT
EIETDLENETNLFTSDSEDVLEEYQIH CIRVTMLHALWAIYNDEVVSRKPIDTLDRVRARMAVEDCIETFEELQ
MCVVHTKTLELEIAQLYVDILLEA

>core/343/5/Org5_Gene46

MSKETFQRNKPHINIGTIGHVDHGKTTLTAAITRALSGDGLASFRDYSSIDNTPEEKARGITINASHVEYETPN
RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSATDGAMPQTKEHILLARQVGVPYIVVFLNKVDMISQE
DAELIDL VEMELSELEEKG YKGCPIIRGSALKALEGDANYIEKVRELMQAVDDNIPTPEREIDKPFLMPIEDV
FSISGRGT VVTGRIERGIVKVSDKVQLVGLGETKETIVTGVEMFRKELPEGRAGENVGLLLRGIGKNDVERG
MVVCQPNSVKPHTKFKSAVYVLQKEEGGRHKPFFSGYRPQFFFRTTDVTGVVTLPEGTEMVMPGDNVELDV
ELIGTVALEEGRFAIREGGRTIGAGTISKINA

>core/344/5/Org5_Gene891

MIFEFRFPKIGETSSGGSIVRWLKNLGDHVARDEPLIEVSTDKIATELPSPKAGRLVRFCVNEGDEVASGDVLG
LIELEEISEADDESTSCPLTSCETKSEAGSSSSSVWFSPA VLSLAQREGIGLDNLQKIAGTGKGGRVTRQDLEA
YISESQQVSIPEIFQGEVNRIPMSPLRRAIASSLSKSSDEVPHASLVVDVDVTDLMNLISGERQRFLDTHGVKLT
ITSFIVQCLAQTLRQFPLLNGSLDGTTIVMKKSVNVGVAVNLNKEGVVVPVIHNCQDRGLVSIKALADLSSR
ARLNKLDPSEVQDGSVTVTNFGMTGALIGMPIIRYPEVAILGIGTIQKR VVVRDDDSLAIKRMVYVTLTFDHR
VLDGIYGSEFLTSLKNRLESVTMG

>core/345/5/Org5_Gene19

MDYYISILGISKTASAEIKKAYRKLAVKYHPDKNPGDAAAEKRFKEVSEAYEVLSDPQKRDSYDRFGKDGPF
AGAGGFGGAGGMGNMEDALRTFMGAFFGGEFGGGSFFDGLFGGLGEAFGMRS DPAGARQGASKKVHINLTF
EEAAHGVEKELVVS GYKSCETCSGQGAVNPQG IKS CERCKGSGQVVQSRGFFSMAS TCPEC GGEGRIITDPCS
SCR GQGGRVKDKRSVHVHIPAGVDSGMRLKMEGYGDAGQNGAPSGDLYVFIDVESHVPVFERRGDDLILELPIG
FVDAALGMKKEIPTLLKTEGSCRLTVPEGIQSGTILKVRNQGFNPVHGKGRGDLLVRISVETPQNLSEEQKEL
LRTFASTEKAENFPKKRSFLDKIKGFFSDFTV

>core/346/5/Org5_Gene134

MSSPVNNTPSAPNIPIAPTTPGIPTTKPRSSFIEKVIIIVAKYILFAIAATSGALGTILGLSGALTPGIGIALLVIFV
SMVLLGLILKDSISGGEERRLREEVSRFTSENQRLTVITTTLETEVKDLKAAKDQLTLEIEAFRNENGNLKT
EDLEEQVSKLSEQLEALERINQLIQANAGDAQEISSELKKLISGWDSKVVEQINTSIQALKVLLGQEWVQEAQ
THVKAMQEQIQALQAEILGMHNQSTALQKSVENLLVQDQALTRVVGELLESENKLSQACSA LRQEIEKLAQ
HETSLQQRIDAMLAQEQLAEQVTALEKMKQEAQKA ESEFIACVRDRTFGRRET PPPTTPVVEGDESQEEDE
GGTPPVSQPSSPVDRATGDGQ

>core/347/5/Org5_Gene658

MPRYRYTYLDPKERRKRGYLEALHIQEAREKLAQENIQVLDIREVALRRMSIKSTELIVFTKQLLLLLRSGLPL
YESLVSLRDQYHEQKMGLLLTSFMETLRSGGSLSQAMAAHPNIFDHFYCSGVAAGESVGNLEGCLQNIIVL
EERAQITKKMVGALSYPVLLVFSFAVMLFFLLGVIPSLKETFENMEVKGLTKIVFGVSDCLSAYRYLFLGFA
SALITVGILMRHRIPWKKILEKLLFALPGTKKFVVKVAVNRFCSVASAILKGGGT LIEGLDLGCD AIPYDRLKT
DMRDIVQAVIGGGSLSQELAQRSWVPKLAIGMIALGEESGDLADVLGYVAHIYNEDTQKTLASITSWCQPVI
LIFLGGLIGVIMLAILIPLTSNIQTL

>core/348/5/Org5_Gene690

MHPKIEKRNSLPLTAVAPVFEE SYHPSVATTVDYVDATTLSRH LTVLKDV IKEARNLDLGKAFLTSMKQGFI
NTGTELAIIQASLADQSSRESRKKEEKIFHQHLGKAAPQAATATSGVQPTADPVADKMPLQSAFAYVLLDKYI
PAQEEALYALGRELNLSGYAQNLFSPLLD MIKSFNSAPINYNLGSYISQTS GTANFAYGYEMILSRYNNEVSQ
CRLDIAS TVKAKAALANMSASVKANVSLTDAQKKQIEDIIASYTKSLDVIHTQLTDVMTN LASITFVPGLNKY
DPSYRIVGGDLSIIALQNDEKVLVDGKVDITTAVNEGGLLNFFTTVLT DVQNYGDLAQTQQQLMLDLELKAM
QQQWSLV SASLKLLNGMYTTVISGFKN

>core/349/5/Org5_Gene553

MKKLLKSALLSAAFAGSVGSLQALPVGNPSDPSLLIDGTIWE GAAGDPCDPCATWCD AISLRAGFYGDYVFD
RILKVDAPKTFSMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDV FCTLGASNG
YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGCATLGA EFQY AQ
SKPKVEELNVICNVSQFSVNKPKGYKGVAFFPLPTDAGVATATGTKSATINYHEWQVGASLSYRLNSLVPYIG
VQWSRATFDADNIRIAQPKLP TAVLNLTAWNPSLLGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVG
ATLVDADKWSLTAEARLINERAAHVSGQFRF

>core/350/5/Org5_Gene353

MMKQGVGQDAKELYTFLSRGNEHYQPCLWFSLEEELGFLFDEKMLCAPLSEDHYCHSYLVDLVDQHLKDLI
LSMFLDPQNISAGELLKVSINVGDSFSPLQQKDFLSMVLREDTGKNVVVVFKGVLSLPATQVCKLVEELNSK
DYSYLNIFSCHGDSSPQLLFRKELEGTSGRYFTVICALYLGDTDMRSLQLASERIMVSREFDLVDAYAARCKL
LKIDHTNWRPGTFSRHADFADAVDVSAGFNSREFKLITQANQGILESSELPLPSKTFWEGFLAFCDRVTVTRH
FIPMLDAAIKQAVWTHKHPSLIDKECEALDLKTQCLPSIVSYLEYVTNSHEKTSKGPFIQKEIADCSPLKEALF
PGSDEDVPSTSEDPSDDHPSDLEDS

>core/351/5/Org5_Gene535

MGTPISGNDGDRNTISDPLEESAAEEGSDLEDREVSESATQVIETIADTGIPEATPSEGNSDLNSDLVDRVEY
EARGSLLTMLARIRKAVSQIWMHVKTKRHPKEQGVRSLGDIPCDLLKATRLPKETAEPYFYALETALASC
RSFFFHVFLRLFTLLRRQHPEAPLDLCGTDPIPEAAVAFALILRSCCKWVATDAVQEGLPLEVIEEAGMYNA
FSLEATTTVEEVSKRLELLYSDKRIDGLANVRGITKIITSPYLGAGQCVSVVDNLKTYDLGRNYTQVLACAS
QIDEFADKGENEALVMKDILYLVRQDRSKELGDFLMMWSEEHASEVNYDVVLAILEVNLPILEEDYRSHPLA
YQKKLNYVICQFFCSERLTSIEPKD

>core/352/5/Org5_Gene386

MLHILLAIFCILLFLAFGLTQPSCHGSSKFLKTLNQRFFKDKGREYPPFPSAPTILATLLCILYGALGTKLYTLLP
PKTAHKDLLFWPLYSLSALIAYGFLPPWISTKVPKETTAHLRFLASVFQLGLFPLQLLFYRRRPNQQVRSSTSF
QSQLSEALSAFDNLIVREVMIPKVDIFALPEETTLQEALVLVSEEGYSRVPVYKKNLDNITGILLVKDLLLLYT
SSHDLSQPISSVAKPPFYAPEIKKASSLLQEFRQKHRHLAIVNEYGFTEGIATMEDIIEEIIIGEIADEHDVQENTP
YKKIGSSWIVDGRMNISDAEEYFNLKIDHENSYDTLGGHV FHKVGAVPQKGMRIHHENFDIEIITCTERNVGK
LKITPRKRKFNIS

>core/353/5/Org5_Gene453

MAIKNILVVDDEPLLRDFLSELLTSQGFIPDTAENLRNALQMIRSRDYDLVISDMSMPDGSGLDLIKIIKQSSPH
TPVLVVTAYGSIENAVEAMHQGAFNYLTKPFSSEALFAFISKAEEELKNLVHENLFLHSQTPDSHPLIAESKA
MKDLLAIAKKAASSSANIFIHGSGCGKEVLSFFIHHNSPRANHPIYKVNCAAIPTLLESELFGEKGAFTGA
TTKKAGRFE LAHKGTLLLDEITEVPVNLQAKLLRAIQEKEIEHLGGTKTLSVDVRILATSNRKLKEAIDDKSFR
QDLYYRLNVIPLHLPPLRDRQDDILPLANYFLNKFCRMNNTPLKTLSPKAQELLNYPWPGNIRELSNVLERV
VILENTSLLTEDMLALA

>core/354/5/Org5_Gene788

MHLHEYQAKDLLASYDVPIPPYWVVSSEEEGELLITKSGLDSAVVKVQVHAGGRGKHGGVIVAKSSAGILQ
AVAKLLGMHFTSNQTADGFLPVEKVLISPLVAIQREYYVAVIMDRKHRCVLMMLSKAGGMDIEEVAHSSPEQ
ILTLPLTSYGHIYSYQLRQATKFMeweGEVMHQGVQLIKKLAKCFYENDVSLLEINPLVLTLEGELLVLDSKI
TIDNALYRHPNLEVLYDPSQENVRDVLAKQIGLSYIALSGNIGCIVNGAGLAMSTLDILKLHGGNAANFLDV
GGGASQKQIQEAVSLVLSDESVKVLFINIFGGIMDCSVVASGLVAVMETRDQVVPTVIRLEGTNVELGKEIVQ
QSGIPCQFVSSMEEGARRAVELSM

>core/355/5/Org5_Gene730

MKWFVISCLLGIFSLGLIMVFDTS SAEVLDRSLECS THKALIRQVTYLILGLGVASLLYMMEW RDFLKISPVLL
SGAALALICVFIPGLGICRNGARRWLGF GQLTIQPSEFVKYLVPIVALYFLTFSSLYQKQLKMFLKLTAILFIPIL
LIAIEPDNGSAAVISASLIPVFIMTSVRLRYWLLPLL CVLIAGGALAYRMPYVRYRLNVYLHPELDIKGRGHQP
YQAKIAAGSGKLLGKGPGASLQKLTYLPEAQNDYIAAIYAE EFGFLGMLVLILLYMCFVYGGYAIAIKASSLE
GAALAMVITLIISMQA FMNLGVVSGLLPSKGVNLPFFS QGGSSLIANMCGVTLLLKVYDEENSKSSSLGCRRFR
RPHCPSSLGKGSFFS

>core/356/5/Org5_Gene897

MSSVNQSSGTPNP EEVTSPESTEENKNVVS SDEAQATHAVALPIVTQLSLPEGVGTSS EETASNPKVDEIVA EV
SSSRAVADQISSL VERVGELLDDLKGAQSLF TSFQSELKNCLPAWKSSTRRLETRGAGDNADIARLELFRSDY
EAVLGHANQFHGKAHLILSKLTDVHHKLQGLSREDLSLAFDNNDRVLEHLGSLGLDVDAEGNWSLSCERGI
PRLVLTADSM LVQIKKVNLP TVEELRTLQGTTESSDPRVEESLSCCERLLNELRRLWANFVGFISSCYDNIVF
VLMWIVRRINLLPGLGCLPFHNP DASQEDQRSSSGERSTRRERLSRRSDLSEEEMIVRAEGESIHPESPHGDGR
NQPSRGDKQDS DSEEETEL

>core/357/5/Org5_Gene697

MEKPQNRKAPRIFWLN NQVAIPPSERVKESYALHSDIFSLPPGSALKLA EKTEESIRQLVGLKD SHIFRFVPHFP
HVVHIVLAALVENLSMFQGRNHIILPAHDQQLINSLCRHQGLGTTYDWVTVNHEGRIVEEQ LIETLSPRSLLF
SLSAAHGLTGVIQPLDPLLSLCKDRRILLHLDISDILGRAPLTPEILNADIITFSSAALGGMGSIGGIFIRKSLERV
FSSWFPPTSASLCFSAVAAMQTACEERISALPLFTFHTSNLCKKLIQELQSVLPSIQLAFSEVQNR LPNIVVAA
IPDIPAESLAFHLHQQGIYPSLGYERFQPLAQVLQNCGISPFLCHSALHFSLTERSKDLEFSKLARAMHDAIKHL
TPLLGSSS

>core/358/5/Org5_Gene534

MILDFQFSIGYYLRVLELAIRDGTRILAYDRKRLLLD AWPVNDPLPTNYDTSVSTIRQVIHELFSWSAISYSISS
RLLAIIELRLHEEKPQTGWLYRLFFPSKYHIKKAIVDKLCMFKSLILFESKRPVDKIVQAANKVFSKGKSNFSS
WEDFTHEVTVSEVQTPLAGEVQRRLAADASLQMIIEALT TLLEGHTAYLPLSLELLNQFIGEKAQPLKTLSEK
SYVLLRELIQLFSLSAEDFQTIIMSIISDSLSEVLANS LIGNQPLTFHGKTFVGLWQETALASPEDSKLALGFLAE
VLRKVIVEKKLHVSKSDNTTPEEVGNIYSIRDQNPALW DKMITMLLMRWLLDYDRDIGIALRKAAEYYNPHP
SFWRQFLRLWQRRP

>core/360/5/Org5_Gene181

MSAMISLSSSHEASIASNTQVRDVLVSLAMDEFVEH NTEILPIKVFLARGTLSSTAIIDDLKDVVETEGEH HFQ
VYSNISLKM IYQRFFEKIFGIGCCPLLLVTDSHHTD PCGALITGIFAAVLFTVLAIVFGPTLGILCY SAYKIYQLT
KKISSLSRTHTEVINSVQKSDPFIHRSGAVAAAAA SQTIKACKVFRQSTLIFFVLGLIITISLAALIVGLVFALFF
LDPGAPAVMTAAMIGCCAAGGTGILLSVIGFLLASVYSVQKSQEGVHHMHTALLRCIVSNTI IQMPYLPITPG
TKKVLTQSIRRYQQFFSDDEYRDIESEVPLNRQTTPPSYETL FHEEGSDGSSNVIPRESPPAYSTIDSSNSPFPSS
SPPPYR

>core/361/5/Org5_Gene840

MLQTMSETIITTPHVVKLISNFFQKKLFSSISTAYPLVIITDVSQVQHLLGPILDHIKMLGYQVIVLTFPPGEPN
KTWETFISLQYQLVDQNI SPKSSIIIGGGTVLDMTGFLAATYCRGLPLYLIPTTITAMVDTSIGGKNGINLRGI
KNRLGTFYLPKEVWMCQPFLSTLPREEWYHGIAEAIKHGFIADAYLWEFLNSHSMMLFSSSQILHEFIKRNCQI
KAAIVAEDPYDRSLRKILNFGHSIAHAETLAKGTVNHGQAVSVGMMIETRISLAEGVMKTPQLIDQLERLLK
RFNLPSTLKDQLQSIVPEHLHNSLYSPENIIYTLGYDKKNLSQHELKMIMIEHLGRAAPFNGTYCASPMEILYD
ILWSECHVMRHC

>core/362/5/Org5_Gene847

MLCQQFLIEALARRKSKHTYRSLSLNSHLIDFTSNDYLGFASSPELRKEYITKLHAIESLGATGSRLLTGHSQL
CQRIEEQLAAYHNFESCLIFNTGYTANLGLLYALATDQDRILHDLYIHASIYDGIRLSKAQSFPFNHNDLNHLE
KRLASSHLGRTFVCVESVYSLHGSAVPLQAISEL CERYSAYLIVDEAHAVGVFGDQGEGLVSALGLQDKVLA
TVYTFGKALGTHGAAIAGSSILKDYLINFCRPFIYTTAQPPhALTAIELAYEHNQRAFNQREHLSALIHFFREK
AQNGLGLQMKDNTTTPIQSICVSGSHRARQAALQIQNSGYDVRPIVSPTVKQREELLRICLHAFNTKNEIDHLL
HTLEQIFLCNVSSL

>core/363/5/Org5_Gene221

MSCFNLTSTNESLRPISPKASFPKQGWQSYFRSALRKHRSDTLSVSVCKVNKYDANLFVRLTVIALAVVGVLI
LFSIMLASIQGTLVITSWPLVTAAILIPTILLTGGMYLHRLGKKVDVISGVCIPPF SRRCWVPISSHTLEKFDEK
HVSACSYLDISTLSADGSGIAAVYQCPPLLFRAPFCFGIPCAMPFVALLRMIYNLIRFLVVPFYIIFRMIYEHFFC
KHLPEDDRFIYKDVAREMGRSLAAFLKAPFYASACMIGAFYSLLDPLAGRVLMGSVERDWNNDNVILARSVS
LANEAHSLFRFEGGGGRKGLGQHAFYMLCCQPQSVFLFDKGEIVSGAHPSIQLPERRGLDTSGRYPHISVIPD
SGNDSAKNFIV

>core/364/5/Org5_Gene536

MGINPSGNRSPDDVWVRGAQGDSSSTQGTGATNSNLGAHNVTSTSQPQVASKAKQLWQTVREFFLGKKSP
DSSQGASGPAMQSPSGPTIRPTRPAPPPPTTGANAKRPATHGKGRAPQPPTAGSSSGSEQPTAMSSEVAKLV
SELKDAVHSHAESQKVLKKVSQELQTKWTDWENNRGPDYLLHGYRVIARALQQTYTEQSMLEGTSTSTGPV
PQAVTVAKDAVTQTVRGAIKNLENPKPGNDPDGVLMQVVISL GIEGPTLDPGESIQNFLETRVSDFGGDDSDI
DYTSDIARLGSALDRVRENHPNEMPRIWIALARELGA AVHSHATSVRIANAGKNHTRDVVRMANESSRLQ
GMKVLSVGAWANTMTVLIGDLFE

>core/365/5/Org5_Gene752

MIPSPTPINFRDDTILETDPKPSLIMFSSKKTEIASERRKAHPTLKFVLGTIWNIVKFIISIILFLPLALLWVLKKTC
QFFILPSSIIQSMSKTAVAIRRM TFLSHIKQLLSLKEISAADRVVIQYDDLVDLSLAIKIPHALPHRWILYSQGN
SGLMENLFDRGDSSLHQLAKATGSNLLVFNYPGIMSSKGEAKRENLVKSYQACVRYLRDEETGPKANQIIAF
GYSLGTSVQAAAALDREVTDGSDGTSWIVVKDRGPRSLADV ANQICKPIASAIKLVGWNIDSVKPSERLRCPEI
FIYNSNHDQELISDGLFERENC VATPFLELPEVKTSGTKIPIPERDLLHLNPLSPNVVDRLAAVISNYLDSEN RK
SQQPD

>core/366/5/Org5_Gene927

MKHLAVLGSTGSIGRQTLEIVRRYPSEFKIISMASYGNNLRLFFQQLEEFAPLAAAVYNEEVYNEACQRFPHM
QFFLGQEGLTQLCIMDTVTTVVAASSGIEALPAILESMKKGKALALANKEILVCAGELVSKTAKENGIVLPI
DSEHNALYQCLEGRITIEGIKKLILTASGGPLLNKSLEELSCVTKQDVLNHPINWNGMSKVTVDSSTLVNKGLEII
EAYWLFGLNEXEILAVIHPQSLIHGMVEFLDGSVISIMNPPDMLFPIQYALTAPERFASPRDGMDFSKKQTLEF
FPVDEERFPSIRLAQQVLEKQGSSGSFFNAANEVLVRRFLCEEISWCDILRKLTTLMECHKVYACHSLEDILEV
DGEARALAEI

>core/367/5/Org5_Gene1061

MIVGQAQTADKSVHAFQYYNGEMKDLGTLGGTSSTAKTVSPDGKVIMGRSQIADGSWHAFMCHTDFSSNN
VLFDLDNTYKTLRENGRQLNSIFNLQNMMLQRASDHEFTEFGRSNIALGAGLYVNALQNLPNLAQAQYFGIA
YKIRPKYRLGVFLDHNFSHVNNFNVSHNRLWMGAFIGWQSDALGSSVKVSFGYGKQKATITREQLENT
EAGSGESHFEGVAAQIEGRYGKSLGGHVRVQPFLGLQFVHITRKEYTENAVQFPVHYDPIDYSTGVVYLIGIS
HIALVDSLHVGTMRMGMEQNFAAHTDRFSGSIASIGNFVFEKLDVTHTRAFAEMRVNYELPYLQSLNLILRVN
QQPLQGVMGFSSDLRYALGF

>core/368/5/Org5_Gene705

MEDFSEQQLFFMRRAIEIGEKGKITAPPNPWVGCVVVQENRIIGEGFHAYAGGPHAEELAIQNASMPISGSDV
YVSLEPCSHFGSCPPCANLLIKHKVSRVFVALVDPDPKVAGQGIAMLRQAGIQVYVGIGESEAQASLQPYLY
QRTNFPWTILKSAASVDGQVADSQGKSQWITCPEARHDVGKLRAESQAILVGSRTVLSDDPWLTARQPQG
MLYPKQPLRVVLDSRGSPPTSKVFDKTSPTLYVTTERCPENYIKVLDSLDVPVLLTESTPSGVDLHKVYEYL
AQKKILQVLVEGGTTLHTSLLKERFVNSLVLYSGPMILGDQKRPLVGVNLLESASPLTLKSSQILGNSLKV
VWEISPQVFPIRN

>core/369/5/Org5_Gene753

MNLSNRSDILSGIFSNPHVSYFSSTHAKQLSDFSCKHPILTKIVTIIVKIFKLLIGLIIPPLGIYWLCQLVCSLALF
PRSSMLYSVLKTCFKKYRLEQEIQDYFVKNLDPSFKDPAVSESKRITIQDHLTIDTLAIHFSTARPKRWLLISL
GSGDFLEDMIGLKDSLFLSWKELAKLLGANILIYNYPGVKSSTGKLNLENLATAHNLCAKYLQDKIQGPGAN
EIITYGYSLGGVVQSAALQKNPFTNSETSWVAVKDRAPHSLPAAANSFFGPIGKLI AVLARWKMDAEKNSRE
LPCPEILVYSADRFPSVGGDDTALLPEFTLAHAIKRTPFARSKKFGEVNLLHSSPLKHPTIQKLAEAIKESLSR
KN

>core/370/5/Org5_Gene101

MNTSLKRPLKSHFDVVGSLRPEHLKKTRESLKEGSISLDQLMQIEDIAIQDLIKKQKAAGLSFITDGEFRRAT
WHYDFMWGFHGVGHHRATEGVFFDGERAMIDDTYLTDKISVSHHPFVDHFKFVKALEDEFTTAKQTL PAPA
QFLKQMIFPNNIEVTRKFYPTNQEIEDIVAGYRKVIRDLYDAGCRYLQLDDCTRGGGLVDPRVCSWYGIDEK
GLQDLIQQYLLINNVIADRPDDL VVN LHVCGRGNYHSHKFFASGSYDFIAKPLFEQTNVDGYYLEFDHERSGDF
SPLTFISGEKTVCLGLVTSKTPTLENKDEVIARIHQAADYLPLERLSLSPQCGFASCEIGNKLTEEEQWAKVAL
VKEISEEVWK

>core/371/5/Org5_Gene1034

MSDNAHNLLYDKFELPEAVKMLPVEGLPIDKHARFIAEPLERGMGHTLGNALRRALLIGLEAPAIISFAMTGV
LHEYMAIEGVIEDVTNIILNLKGALLKKYPMQDSSLGRTTQVLKASISIDASDLAAANGQKEVTLQDLLQEGD
FEAVNPDQVIFTVTQPIQLEVVLRIFAFRGYTPSERIVLEDKGVYEIVLDAAFSPVTLVNYFVEDTRVGQDADF
DRLVLIVETDGRVTPKEALAFSTQILTKHFSIFENMDEKKIVFEEAISIEKENKDDILHKLILGINEIELSVRSTNC
LSNANIETIGELVIMPEPRLLQFRNFGKKSLCEIKNKLKEMKLELGMDLTQFGVGLDNVKEKMKWYAEKIRA
KNIKG

>core/372/5/Org5_Gene291

MNGKAPLALYIHIPFCTKKCRYCSFYTIPYKSESVSLYCNAVIEGLRKLAPIQETHFIETVFFGGGTPSLVSPL
DLKRILKELAPHAREITLEANPENLTVSYLRQLQETPINRISVGVQTFDDSLQLLGRTHSSSAITALQECQNH
GFSNLSIDLIYGLPTQSLEIFLSDLHQALTLPTHISLYNLTIDPHTSFYKHRKILVPTIAQEEILAEMSLLAENLLL
SQGFQRYELASYAKPDYPAKHNLYYWTDPRPFLGLGVSSASQYLHGERSKNYSHISHYLRAVRKNLPTQETSEI
LPKKERIKEALALRLRLLEGADLAEPSTLISMLTQDVKLQNLFSVHGQCLALNRQGRLFHDTIAEEIMGYSF

>core/373/5/Org5_Gene889

MSIAIAREQHAAILDMHPKPSIAMFSSEQARTSWEKRQAHPYLYRLLEIHWGVVKFLLGLIFFIPLGLFWVLQK
ICQNFILLGAGGWIFRPICRDSNLLRQAYAARLFSASFQDHVSSVRRVCLQYDEVFIDGLELRPNAPDRWM
LISNGNSDCLEYRTVLQGEKDWIFRIAEESQSNILIFNYPGVMKSQGNITRNNVKSQACVRYLRDEPAGPQ
ARQIVAYGYSLGASVQAEALSKEIADGSDSVRWFVVKDRGARSTGAVAKQFIGSLGVWLANLTHWNINSEK
RSKDLHCPELFIYGKDSQGNLIGDGLFKKETCFAAPFLDPKNLEECSGKKIPVAQTGLRHDHILSDDVIKEVAG
HIRRHFDN

>core/374/5/Org5_Gene161

MALKFHLIHQSKKSQARVGQIETSHGVIDTPAFVPVATHGALKGVIDHSDIPLLCNTYHLLLHPGPEAVAKL
GGLHQFMGRQAPIITDSGGFQIFSLAYGSVAEEIKSCGKKKGMSLVKITDEGAWFKSYRDGRKLFLSPELSV
QAQKDLGADIIPLDELLPFHTDQEYFLTSCSRTYVWEKRSLEYHRKDPRHQSMYGVHGGLDPEQRRIGVRF
VEDEPFDGSAIGGSLGRNLQEMSEVVKITTSFLSKERPVHLLGIGDLP SIYAMVGFGIDSFDSSYPTKAARHGLI
LSKAGPIKIGQQKYSQDSSTIDPSCSCLTCLSGISRAYLRHLFKVREPNAAIWASIHNLHHMQQVMKEIREAIL
KDEI

>core/375/5/Org5_Gene998

MAPIHGSNAFVEDILHSHPSQATYFSSTRAQKLHEFKDRHPVLTRIASVIIKIFKVLIGLILPLGIYWLCQTLCT
NSILPSKNLLKIFKKQPNTKTLKTNYLRLALQDYSSKNRVASMRRVPILQDNVLIDTLEICLSQAPTNRWMLISL
GSDCSLEEIACKEIFDSWQRFKALIGANILVYNYPGVMSSSTGSSSLKDLASAHNICTRYLKDEKEQGPMAKEIIT
YGYSLGGLIQAEALRDQKIVANDDTTWIAVKDRCPLFISPEGFHSCRRIGKLVARLFGWGTKAVERSQDLPLCL
EIFLYPTDSLRRSTVRQNKLLAPELTLAHAIKNSPYVQNKEFIEVRLSSDIDPIDSKTRVALATPILKKLS

>core/376/5/Org5_Gene281

MSTTEPNLTNVNLTMLISSESMPTQLASHKLKGLDLVAFILIIGIAVSSGTAAIILGIPLLILTALAVLAFSILLY
FLLREPKSPISVTHQPTPIIKDIDLPPVPPLALTPVPTEAVLEEPPLSPRTHQTLLQENWDRIPDLQANTDMPFI
AADNQTYAWHLKNSNLTLISTLGPKEKPRYKTQGIVMIVNAATPNMANNVKGTSALAKATSVRCWENSK

KSPDPLRSKQPLQLGECRSAKWENLNGTTNAGKAGLPQFLGQLLGPKASDYNYNPNDAFTFCRQAYLNCLN
EAKRRKTTVVQLPLLSSHFPGPSKDEETTSRLQWIDGVKLALIDALQTFGSEAENQNQPWVILTTLARHPLI
TP

>core/377/5/Org5_Gene561

MAVAADSSASWLKSRNNFLSSLGKTEEQVAAPFEPKELCQHKIREKFRLEDVQVSIKFRGSITAVEATKEFGV
HLLIQPMVVQPWEVENLLFLTSEEDLQELMVAVFDDASLASYFYEKDKLLGFHYFVAEACKLFEELQWVP
SLSAKVGGDAIFTATSLQGSFQVVDISLRLDGKNVRCRLLLPEDTFQSCQKFFSGLHDESDLHNIDQTQQISLS
VEVGYSQLTQEEWHQVVPGSFIMLDSCLYDPETEESGALLTVQKHQFFGGRFLTPSSGEFKITSYPNLTHEDP
PLPENPQASAAPLPGYSRLVVEVARYSLAVSEFIKLNLSILSLGNHPAYGVDIILDGAKVGRGEIHALGDVLGI
RVLEV

>core/378/5/Org5_Gene305

MIYLDNNAMTPPERGLLEFLQKTFLIEGTYANPSSVHQLGKKSRQLVLEASHWMQKVLSFQGRVLYTSGATE
SLNLAIASLPKDSHVITSGSEHPAILEPLKHSSLSVSYLNPEEGRCVLTIEQIERAVTPKTSAILGWVNSETGAK
ADIAAIAHFAQERQLQFIVDATANVGKERIVLPSGVTMAAFSGHKFHALSGIGALLVSPGVKLHPQLWGGGQ
QGGLRAGTENLWGIASLLYIFKYLDLHQERISQEILTHRNGFEKAIAKARIPDVHIHCADQPRANNVSAIAFPPL
EGEVLQIALDIEGVACGYGSACSSGATAPFKSLVSMGVDEELTLATLRFSFSHLLLQEDVERAVGIIKVVVERL
KNS

>core/379/5/Org5_Gene748

MTTSDVIDFVTNDFLGFARSPTIYCEVSKRFQIHCQQFPHEKLGIRGSRLMVGPPSSVIDDLESKIASYHGAPNA
FIVNSGYMANLGLCHHVSRSTDVLLWDEEVHMSVSVHLSAISGQHHTFHNNLEHLESLQCYSRISKGRIFI
FVSSVYSFRGTLAPLEQIIALSCKYHAHLIVDEAHAMGIFGDDGKGLCHALGYENFYAVLVITYGKALGTMG
ASLLTSSEVKYDLMQNSPPLRYSTSLSPHTLISIGTAYDFLASEGEIARKQVFKLKEHFHECFDSHAPGCVQPIF
LPHTCLEEAISVLETTGIHVGVVAFAKHPFLRVNLHAYNTVDEVNLLAQVMKPYLEKSSHRVHINHEFHLWR
ELCQH

>core/380/5/Org5_Gene1039

MMLVYCFDPSVPTSPEHRLMAALDRWFFLGHRVRILTLEGNHYRAFQENMSISTVEKILKLISYLLIPIVLIA
LLIRCFLHSRFGKNWKCDLSLDARVPHDVQPFNDFQLFNNQERLNIWKNRRYVSGIDVLMVPVDYLRSQFPG
FKEIPEAIRCENYVSDGQFSEESKTSYLRAMLTDIVGYILSLDETYWTNVILKIRAMCITFESFPGKEADPNYSP
RVTHHYFDESWKALARHVLGEGNMVNRLDEALIRTEKPGKEGECITKQFLKDYCKKHLEVMSCPDFIESLV
DEKIREFRCP SILNSAVCDVIDRKCQEHLKAIINEANRRRLPGMKNSSFTMRGNQVLFYTIFSPPKLPPAASSVY
F

>core/381/5/Org5_Gene389

MTTCLPQPPKTSPLYSIFEKLDAQERLSSDALHLLLLTNKEDQRTLWNFADQVRKQRVGDTVYYSSTLYLY
PTNFCDFSCFKCSFYAKPGDPKGWLYSPDDLQIQNIKTPITEVHIVGGCFPSCNLQYYSDLFTKIKEYDPQIH
IKALTAIEYAYLSDLNLSIRDVLLTLKDAGLDSIPGGGAEILVDKIRNFLAPKRLSSSDFLNIHKMAHQLGIHS
NITMLCYHKEGPEDLVTHMVKVRDLQDETQGFKNFILLKFAQENNVLGKRLRKSGQGHAIPKSLMAVARIF

LDNFSNMKALWNYLGIEAALDLLSCGANDLSSTHMGEKVFQMASSKEPIKMDAEGMAALITQQGRTPCLTN
SSHV

>core/382/5/Org5_Gene1059

MRRQVREIMQQTIVIVAMSGGVDSSVVAYLFFKKFTNYKVIGLFMKNWEEDSEGGLCSSTKDYEDVERVCLQ
LDIPYYTVSFAKEYRERVFARFLKEYSLGYTPNPDILCNREIKFDLLQKKVQELGGDYLATGHYCRLNTELQE
TQLLRGCDPQKDQSYFLSGTPKSALHNVLFPLGEMNKTEVRAIAAQAALPTAEKKDSTGICFIGKRPFKEFLE
KFLPNKTGNVIDWDTKEIVGQHQAHAHYTIGQRRGLDLGGSEKPCYVVGKNIEENSIYIVRGEDHPQLYLRE
LTARELNWFTPPKSGCHCSAKVRYRSPDEACTIDYSSGDEVKVRFSQPVKAVTPGQTIAFYQGDTCCLGSGVID
VPMIPSEG

>core/383/5/Org5_Gene310

MTKIAFSEKAKNFPVEALKKWFENKRSRSLPWRDNPTPYSVVWSEVMLQQTRAEVVIDYFNQWMERFPTIES
LAAAKEEDVIKLWEGLGYYSRARHLLLEGARMVMEEFHGGIPDDAISLAQIRGVGPYTVHAILAFAFKRRAAA
VDGNVLRVLSRIFLIETSIDLESTRTWVSRIAQALLPHKSPEVIAEALIELGACICKKVPQCHRCPPVRQACGAW
RENKQFVLPVRHARKKVIFLHRLVAIVLYDGSLVVEKRRPKEMMAGLYEFPYIEVEPEEGLQDIEGFTKKME
LSLESPLEFLGNLKEQRHAFTNHKVHLCPIIFKATSLPQFGELHLLSDIDHLAFSSGHKKIKDALLIYLGDVRSR
ESIGV

>core/384/5/Org5_Gene444

MQENLDKRLEALRTEISLAARSLFDLDDKKQKELQVLEESSEENFWQDSVHAGKISEQIVSLRRQIQEYQELK
SKIDAIEFFLEDADALEDPAICEDLEKEFLFCEKKLAVWETQRLLSGEADKNSCFLTINAGAGGTESCDWVEM
LFRMYSRWATKHQWALEVVDRDLGDEVVGKIHVTVKFSGMYAYGYAKAERGVHRLVRISPFDSNGKRHTSF
ASVDVFPEIDDQIKIEIRPNDLRIDTFRSSGAGGQHVNVTESAVRITHLPSGVVVSCQNERSQIQNRESCMKML
QAKLYQQVLQERLEKQSLDRKDKKEIAWGSQIRNYVFQPYTLVKDVRTGHETGNVQAMLDGELLDEFIKAY
LAEFGEVS

>core/385/5/Org5_Gene42

MAVEGRVNSSQALNQDCQEVLANQSKGLLRCRILSIVVAVITFIAGVVLIALTASILTSVPYLALGVFLLIV
TLGCIIFALCSEKIKKVPPTPISHKEEIIAWFEERKNIDMEKEKEDPEHFGRTATDIPMRSALDQFNHSCHHIHES
PALTETYRSHQDVLLFKDWCPVTLPDVTSEEEVLIRSVVGSYLLMEACVPKVSMLIDELHNKLKSPSERECLF
IDKKTQQRKASFLFTQKDLATFFLAYTRVNDGHLAPFRAGAKWILIHVRLRRQHNQNDFFTPGHSCYYARL
AFNQTQRLYHQLFNVEKLRSIYANMDKDPLCHPWAFIPIYDLLKTEDHGDGFLEQQEDREYPSRAAQDQFW
G

>core/386/5/Org5_Gene687

MSPHRNLFKLKNFSNRLYNRALGRFDKVFNFSSGNVGIDLTANTLVYVRGRGIVLSEPSVVAVDAQTHAVL
AVGHKAKAMLGKTPRKIMAVRPMKDGVIADFEIAEGMLKALIKRVTPSRSVFRPRILIAVPSGITGVEKRAVE
DSALHAGAQEVLIEEPMAAAIGVDLPVHEPAASMIIDIGGGTTEIAIISLGGIVESRSLRIAGDEFDECIINYMR
RTYNLMIGPRTAEEIKITIGSAYPLGDQELEMEVRGRDQVAGLPITKRINSVEIRECLAETPIQQIIECVRLTLEKC
PPELSADLVERGMVLAGGGALIKGLDKALSKNTGLSVITAPHPLAVCLGTGKALEHLDQFKKRKGNLV

>core/387/5/Org5_Gene930

MKFFVSRNELGNLIKKIQSVVPQNTPIPVLTHVLIETYNDELVFTATDLTVSTRCVTKAKVVEKGAISIPSKRF
FQLVKELTEANLEISYSAGEMAQITSGSSCFRLLSMEKEDFPMPLDIQNALRFSLP AEQLKTMLQRTSFAVSRE
ESRYVLTGVLLAIANGVATIVGTDGKRLAKIDAEVTLDKSFSGEYIPIKAVEEIIKMCSDGEATIFLDQDKIA
VECDNTLLITKLLSGEFPDFSPVISTESNVKLDLHREELITLLKQVALFTNESSHSVKFSFLPGELTLTANCTKV
GEGKVSMAVNYSGELLEIAFNPFFFLDILKHSKDEL VSLGISDSYNPGIITDSASGLFVIMPMRLHDD

>core/388/5/Org5_Gene806

MLIWKRHLLTRFWFALTSLLV LALIFYASIHSLHTLKGASTAASGASVKLSILYYLAQISLKA EFLMPQLVA
VATTSTLFAMQNKREIILLQASGLSLKSLMHPLLLSGAVIMMVLYANFQWLHPICEKISITKENMDRGTTDKE
QGKIPALYLKDQTVLLYSSIEPKTLTLNNVFWIKDPKTIYTMEKLAFTTSLPIGLNVTQFFANDSENLELKEFF
DMKEFPEIEFNFYENPFSKLF SAGNKNRLSEFFKAIPWNATGLGLSTQVPQRILSLLAQFYVVLISPLACMAAII
LSAYLCLRFSRTPTVTLAYLIPLGTVNIFFVFLKAGIVLASSSVLPTLPVMAFPLIVLFLLTNYAYAKLQ

>core/389/5/Org5_Gene433

MKFPRISISDLIPTQMVIWWRGGGNVHYVPNAQNLPKKILGGVLACFGLALLGCAAF AAGVCQTIFPCIGLMI
LGLVLLGFAYLQYSKGWSRFRPLFRETKVFEKPINWLGCLSLLQSWKKIRPGCYYPGCPQVEICEGSQEIV
TKIFQKKSDRNTSIFLIQEMDQIALRQGIEKSSLSRKTF AIDPSVVSSLLSEIQREEQQYLDPKVISWSSEDQASD
RTHPKSAIYVNISDAAQEPQGRCYIDAYTKAFFTVLDQIGDPNIVKKHTIYVLTPI LGVPDALPKEEQENLKL
SQA AFLYSAEQVAKRMREEKQDSIRIKFIFTDPTSPTS LYFSPHHSSTPHSVTPISLSGFVGEQESYTFA

>core/390/5/Org5_Gene1017

MSKKIKVLGHLTLCTLFRGVLCAAALSNIGYASTSQESP YQKSIEDWKGYTFTDLELLSKEGWSEAH AISGNG
SRIVGASGAGQGSVTAVIWESH LIKHLGTLGGEASSAEGISKDGEVVVGWSDTREGYTHAFVFDGRDMKDL
GTLGATYSVARGVSGDGSIIVGVSATARGEDYGWQVG VKWEKGKIKQLKLLPQGLWSEANAISEDGTVIVG
RGEISRNHIVAVKWNKNAVYSLGTLGGSVASAE AISANGKVIVGWSTTNNGETHAFMHKDETMHDLGTLG
GGFSVATGVSADGRAIVGFSAVKTGEIHAFYYAEGEMEDL TTLGGEEARVFDISSEGNDIIGSIKTDAGAERA
YLFHIHK

>core/391/5/Org5_Gene400

MKKRFPSTLFLFYRRVTIAISLEGILGWGWLGSLLSKVFAFLVACWNRF SWSTPYRARSTVISVGNIVVGGAG
KTPTVLWLAEALRLRGYSCGVLSRGYKSQSSRQK KLTVVDSKVHSASYVGDEPLLMAEKLPEGSVWVHKD
RRISAARAAEKFGILLDDGLQYRKLHKDVEIAV VNGQDPLGGRAFFPKGRLRDFPLRLKTVDAIIVNGGGKE
AGTVVKRVSNAPQIFVKPTIASVWVTHNGERIPKEALREL RVGVFCGLGFPQGFLNMLREEGIHILGKYLLPD
HAAITKKELNYFCQMAMRQGQGLLCTEKDSVKLPRLSGEV SLLPIAKVEMRLSVNQDDTL SLLNMIEQIHK
NRGN

>core/392/5/Org5_Gene451

MNVPDSKNLHPPAYELLEIKARITQSYKEASAILTAIPDGILL LSETGHFLICNSQAREILGIDENLEILNRSFTD
VLPDTCLGFSIQEALES LKVPKTLRLSLCKESKEKEVELFIRKNEISGYLFIQIRDRSDYKQLENAIERYKNIAEL

GKMTATLAHEIRNPLSGIVGFASILKKEISSPRHQ RMLSSIISGTRSLNNLVSSMLEYTKSQPLNLKIINLQDFFS
SLIPLLSVSFPNCKFVREGAQPLFRSIDPDRMNSV VWNLVKNAVETGNSPITLTLHTSGDISVTNPGTIPSEIMD
KLFTPFFTTKREGNGLGLAEAQKIIRLHGGDIQLK TSDSAVSFFIIPELLAALPKERAAS

>core/393/5/Org5_Gene247

MSHTECGIVGLPNVGKSGLFNALTGAQVASCNYPF CTIDPNVGIVPVIDERLEALAKISNSQKIIYADMKFVDI
AGLVKGASDGAGLGNRFLSHIRETHAIAHVVRCFDD PDVTHVSGKVNVEDIEVINLELIFSDFSSAKNIH SKL
EKLA KGKREVGALLPLFDTHAHLEKGLPLRTLELT PEQIVALKPYPFMTMKPMFYIANVDESSLPDMDNDYV
AAVREVA AKENSKVVPICVRIEEEIVSLPIEERLEF LMSLGLEKSGLHRLVRAAYDTLGLISYFTTG PQESRAW
TVVRGSSAWEAAGEIHTDIQKGFIRAEVITFEDMIEC QGRAAAARELGKLHIEGRDYIVQDGD TMLFLHN

>core/394/5/Org5_Gene288

MTTEVRIPNIAESISEVTVASLLVTEGALIQENQGL LEIESDKVNQLIYAPVSGRIFWEVSEGDVVPVGGVVGKI
EPAGEGEELGDSQSKETIEAEIICFPQSGVRQSPPE NKTFIPLRDQMDQGSQGLSAGDRGETRERMTSIRKTISR
RLLSALHESAMLTTFNEVYMTPLFHLRKEKQEEFLS RYGVKLGFMSSFFVKAVLEALKAYPRVNAYIDGEEIV
YRHYIDISIAV GIDRGLVVPVIRDCDKLSNGEIEQKL ADLALRAREGLLAIAELEGGGFTITNGGVYGSLLSTPI
INPPQVGILGMHKIEKRPVVDNEIVIADMMYVALSYD HRLIDGKEAVGFLVKVKEGLENPASLLDL

>core/395/5/Org5_Gene533

MVPFRQHHAYQLLKQLHTSAISEADRVSYFYFKQNR SLGSKDRQWIQNIIFNILRHRRLLETILDSGEQVTPEA
LVAKVNEGVLNLDSSAIPWPVRYISDDLAHFLVQDY GEEQAEEIAKIWLTEAPITIRVNTDKISVKELQEK
LEYPPSPGELPEALHFSKRHPLQSTEAFRRGFFEIQD ENSQRISQGISLTDKDIVLDFCAGAGGKSLIFAQKAKH
VVINDSRKAILQTAKHRLLRAGARNFSLADQLRLGS FSFVVIVDAPCSGTGVFRRHPEHKWQFSKKLLLNYVR
VQKSILKQASAYVGPRGRLVYITCSLLKEENEAHVA YMHSLGWKEVHRKTLPLQVGKGDAFFTSHFQKI

>core/396/5/Org5_Gene860

MKLYQTLRGIVLVSTGCIFLGMHGGYAAEVPVTSSG YENLLESKEQDPSGLAIHDRILFKVDEENVVTALDVI
HKLNLLFYNSYPHLIDSFPARSQYYTAMWPVVLESV IDEFLMVADAKAKRIATDPTAVNQEIEMFGRDLSP
LYAHFEMSPNDIFNVIDRTLTAQRVMGMMVRSKVMLK VTPGKIREYYRKLEEEASRKVIWKYRVLTIKANT
ESLASQIADKVRARLNEAKTWDKDRLTALVISQGGQL VCSEEFSSRENSLSQSHKQELDLIGYPKELCGLPKA
HKSGYKLYMLLDKTSGSIEPLDVMESEKIKQH LFALEAESVEKQYKDRLRKRYGYDASMIAKLLSEEAPPLFS
LL

>core/397/5/Org5_Gene887

MAFKRKTRWLWQVLILSVGLNMLFLLLFYSAIFRKDI YKLHLFSGPLIAKSSRKVYLSEDFLNEISQASLDDLI
SLFKDERYMYGRPIKLWALSVAIASHHIDITPVLSK PLTYTELKGSSVRWLLPNIDLKDFPVILDYLRCHKYPY
TSKGLFLLIEKMVQEGWVDEDCLYHFCSTPEFLYL RTLLVGADVQASSVASLARMVIRCGSERFFHFCNEESR
TSMISATQRQKVLKSYLDCEESLAALLLVHDSDVVL HEFCDEDLEKVIRLMPQESPYSQNFFSRLQHSPRRE
LACMSTXRVEAPRVQEDQDEEYVVQDGD SLWLIAKRFGIPMDKIIQKNGLNHHRLFP GKVLKLPKQAS

>core/398/5/Org5_Gene850

MHYCERTLDPKYILKIALKLRSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLL
FVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYPFRFFLDYLEAFGLLSDFLDHQAVIKF
FELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMG
RLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLP
LELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVLCQ

>core/400/5/Org5_Gene81

MKIDILSLFPGYFDGPLQTSILGRAIKQRLLDVQLTNLRDFGLGKWKQVDDTPFSGGGMMLMAEPVTSAIRSV
RKENSKVIYLSPPQGALLTAEKSRELAASHLILLCGHYEGIDERAIESEVDEEISIGDYVLTNGGIAALVLIDAV
SRFIPGVLGNQESAERDSLLEGLGPQYTRPREFEGKEVPEVLLQGDHKAISQWRLEQSERRTYERRPDLYL
NYLYKRSIDHKFDEETTTNRDHFCKDKISVVLEVNKLKRAKNFYCKVFGLDAMSCENKFCLPHEGKTIFWLR
EVQAEKKNIVTSLSLDCACEEDFCYLLRRWELFGGKLEKQADEHAVWALAQDLGDHAWIFSWHRMK

>core/401/5/Org5_Gene248

MGEKTEKATPKRLRDARKKGQVAKSQDFPSAVTFIVSMFTAFLSLSTFFFKHLGGFLVSMLSQAPTRHDPVITL
FYLKNCLMLILTASLPLLGAVAVVGIVGFLIVGPTFSTEVFKPDIKKFNPIENIKQKFKIKTLIELIKSILKIFGA
ALILYITLKSKVSLIETAGVSPITAQIFKEIFYKAVTSIGIFFLIVAILDLVYQRHNFAKELKMEKFEVKQEFKD
TEGNPEIKGRRRQIAQEIAIEDSSSQVKHASTVVSNPKDIAVAIGYMPEKYKAPWIIAMGINLRAKRILDEAEK
YGIPIMRNVPLAHQLLDEGKELKFIPESTYEAIGEILLYITSLNAQNPNKNTNQPDL

>core/402/5/Org5_Gene232

MSEAPVYTLKQLAELLQVEVQGNIEPISGVEDISQAQPHHIAFLDNEKYSSFLKNTKAGAILSRSQAMQHA
HLKKNFLITNESPSLTFQKCIELFIEPVTSGFPGIHPTAVIHPTARIEKNVTIEPYVVISQHAHIGSDTYIGAGSVIG
AHSVLGANCLIHKPVVIRERVLMGNRVVVQPGAVLGSCGFGYITNAFGHHKPLKHLGYVIVGDDVEIGANTT
IDRGRFKNTVIHEGTKIDNQVQVAHHVEIGKHSIIVAQAGIAGSTKIGEHHVIGGQTGITGHISIAHDVIMIAQTG
VTKSITSPGIYGGAPARPYQETHRLIAKIRNLPKTEERLSKLEKQVRDLSTPSLAEIPSEI

>core/403/5/Org5_Gene892

MSGPSRTESSQVSVLSYVPRDKEIAPKKQFTIAKISTLAILASLALGALVAGISLTIVLGNPVFLALLITTALFSV
VTFLVYHQMTSKVSSNWQKVLEQNFKPLGKAWQEKNVDCYSNEMQFYNNHLNPKFKVAIQTDASQPFQPT
FLTGLRVIEKNQSTGIIFNPVGPTNLIDNTATNLSTILYSTLKDKSVWDTCKQREGXPAKGEDPFSPTEVRVVK
LPNEALDQTFNLNLSSAEKKSILPTFLGHVCGPKSEELPNQQEYYRQALLAYENCLKAAIESHAAIVALPLFTS
VYEVPPPEILPKEGTFYWDNQTQAFCKRALLDAIQNTALRYPQRSLLVILQDPFNTIESQSRSEE

>core/404/5/Org5_Gene841

MKNSFGSLFSFTTWGESHGPSIGVVIDGCPAGLELHESDFVPAMKRRRPGNPGTSSRKENDIVQILSGVYKKG
TTGTPLSLQILNTDVDSSPYENSERLYRPGHSQYTYEKKFGIVDPNGGGRSSARETACRVAAGVVAEKFLAN
QNIFTLAYLSSLGSLTLPHYLKISPELIHKKIHTSPFYSPLNEKIQEILTSLHDDSDSLGGVISFITSPIHDFLGEPLF
GKVHALLASALMSIPAAGFEIGKGFASAQMRGSQYTDPFVMEGENITLKSNNCGGTGGITIGVPIEGRIAF
KPTSSIKRPCATVTKTKKETTYRTPQTGRHDPCVAIRAVPVVEAMINLVADLVLYQRCSKL

>core/405/5/Org5_Gene877

MTLPNDLLETLVKRKESPQANKVWPVTTFSLARNLSVSKFLPCLSKEQKLEILQFITSHFNHIEGFGEFIVLPLK
DTPLWQKEFLLFLLPYDLVGNPEGEALVVSRSGLAALVQDHLVLHGIDFQGNVEKTLQDLVQLDSYL
HSKLSFAFSSEFGFLTTPNPKNCGTGLKSQCFLHIPALLYSKEFTNLIDEEVEIITSSLLLGVTFPGNIVVLSNRC
SLGLTEELLSSLRITASKLSVAEVAACKRLSEENSGDLKNLILRSLGLLTHSCQLELKETLDALSWIQLGIDLG
LIKVTENHPLWNPLFWQIRRAHLALQKQAEBSRDLQKDTISHLRASVLKELTKGLSPESF

>core/406/5/Org5_Gene731

MMKKIRKVALAVGGSGGHIVPALSVKEAFSREGIDVLLLGKGLKNHPSLQQGISYREIPSGLPTVLNPIKIMSR
TSLCSGYLKARKELKIFDPDLVIGFGSYHSLPVLLAGLSHKIPLFLHEQNLVPGKVNQLFSRYARGIGVNFSP
VTKHFRCPAEVFLPKRSFSLGSPMMKRCTNHTPTICVVGGSQGAQILNTCVPQALVKLVNKYPNMYVHHIV
GPKSDVMKVQHVNVRGEVLCCVKPFEEQLLDVLLAADLVISRAGATILEEILWAKVPGILIPYPGAYGHQEV
NAKFFVDVLEGGTMILEKELTEKLLVEKVTFALDSHNREKQRNSLAAYSQQRSTKTFHAFICECL

>core/407/5/Org5_Gene78

MKKKVAEYLNRLAEVEIKISNPEIFSNSKEYSALSKEHSYLLELKNAYDKILNLEKVLADDKQALAIEKDPEM
VVMLEEGINENKVELEKLNKILESLLVPPDPDDDLNVIMELRAGTGGEEAALFVGDCVRMYHLYASSKGWK
YEVLSASESDLKGYKEYVMGISGTGVKRLQYEAGTHRVRVPETETQGRVHTSAITIAVLPEPSEEDTELLI
NEKDLKIDTFRASGAGGQHVNVTDASVRITHLPTGVVVTCQDERSQHKNKDKAMRILKARIRDAEMQKRHN
EASAMRSAQVGSGDRSERIRTYNFSQNRVTDHRIGLTLYNLDKVMEGDLDPITTAMVSHAYHQLLEHGN

>core/408/5/Org5_Gene807

MPILWKVLIFRYLKTAAFCTLSLICISIISSLQEIVAYIAKDVPYDTVLRLMAYQIPYLLPFILPGSCFVSAFSLFR
KLSDNNHMTFLRASGASQSIIMFPVLMVSGAICCLNFYTCSELASICRYQTCKEIANMAMTSPALLQTLQKK
ENNRIFIAVDHCAKSKFDNVIVALKGNNEISHVGIKSIIPDTTKDTPVAKDVVFISKLPDSLTESSSPSSQRFYIE
TLDELLIPKITSTLFAGKSYLKTRTDYLPWKQLVKQSLKHSHPETLRRVAIGFLCITLTYAGMILGIHKPRFRK
SIALYFIFPILDILLIVGKNTKNLPLAFMLFVFPQLVSWVVF AARAYRESRGYA

>core/409/5/Org5_Gene312

MSLLSGHRLEGFPPIAEVMAACDRCSMDFC EILKSQSMDLWADAASCVDGLLQDPFWSTAIASGIAKSSLQE
TEFECESKVMVLSSWGEQGAQVCSPFNLERICMSFPSLKVFSCLKNGCENMGIQLSASCMNLLMSIFFVATN
GGSTPIWITKENLMALVALVLSHYQCYFVPATGDPQQRGNILGNPEVNAILARGMGMRVDLERKRGGESSSR
YLELAARCFENSLTKTSLSDANNVQERDKCLLQMSTSLMHTAGLNLQRPPVPTPSGVT AHPQPQPDVVTS
QPSLLGARERSPVSSRGRFPVVLPLSVISPRSHPGRVERRDLEDEEEV MF

>core/410/5/Org5_Gene655

MSHDRILRAQRALSEHNLDAILVEKSEDLAYFLHDEAIA GILLIGQQEVMFFVYRMDKDLYSHIQRVPLTFLT
QDVVADLSLYVQKQRYQKIGFDSASTVYHKFAQRQVLPCLWEPLECFTEKIRSIKSEEEIRRMQEAAALGSA
GYDYVLTLLREGITEKEVVRQLRAFWAEAGAEGPSFPPIIAFGEHSAPHSIPTDRPLKKGDIVLIDIGVLLNGY

CSDMTRMTALGTPHPKLLESYPVVVEAQKRAMALCKEGVLWGDIDAEAVRVLREHHLDTYFIHGIGHGVG
RHIHEYPCSPRGSQVKLESGMTITVEPGVYFPGIGGIRIEDTLCIDKNKNFSLTARPVISELVCL

>core/411/5/Org5_Gene931

MNKRQKDKLKICVIISTLILVGIFARAPRGDTFKTFLKSEEAIYSNQCNXDMRKILCDAIEHADEEIFLRIYNLS
EPKIQQSLTRQAQAKNKVTIYYQKFKIPQILKQASNVTLEQPPAGRKLMMHQKALSIDKKDAWLGSANYTNL
SLRLDNNLILGMHSSELCDLIITNTSGDFSIKDQGTGKYFVLPQDRKIAIQAVLEKIQTAQKTIQVAMFALTHSEII
QALHQAKQQRGIHVDIIIDRSHSKLTFKQLRQLNINKDFVSINTAPCTLHHKFAVIDNKTLLAGSINWSKGRFSL
NDESLIILENLTKQQNQKLRLMIWKDLAKHSEHPTVDDEEKEIIIEKSLPVEEQEAA

>core/412/5/Org5_Gene612

MNLPDRKKALEAAVAYIEKQFGAGSIMSLGRHSATHEISTIKTGALSDDLALGIHGVPKGRVIEIFGPESGKT
TLATHIVANAQKMGGVAAYIDAEHALDPSYASLIGVNIDDLMSQPDCGEDALSIAELLARSGAVDVVIDSV
AALVPKSELEGDIGDVHVGLQARMMSQALRKLATLSRSQTCAVFINQIREKIGVSFGNPETTTGGRALKFY
SIRLDIRRIGSIKGSDNSDIGNRIKVKVAKNKLAPPFRIAEDILFNEGISSAGCILDALAVEYNIIKKGSWFNYQE
KKLGQGREFVREELKRNRKLFEEIEKRIYDVIAANKTPSVHANETPQEVPAQTVEA

>core/413/5/Org5_Gene738

MNLCKRISFEEGLELFVSSPIERLQERADAIKERYPSNEVTYVLDANPNYTNICKIDCTFCAYRKPKSPDAY
LLSFDEVRSLLQRYVSSGVKTVLLQGGVHPGLGIDYLEELVRITVQEFPSIHPHFFSAVEIEHACRVSGISIEQG
LQRLWDAGQRTIPGGGAEILSERVRKIISPKKMQPGGWINLHKLALHLMGFRTTATMMFGHVENPEDILHLQ
TLRDAQDSCPGFYSPFWSYKPGNTALRRNVPQQASIETYRILALGRIFLDNFDHVAASWFGEGKSLGAKAL
HYGADDFGGVILDESVMKATGWSIQSSEEEICNIIRSEGFIPVERNTFYQHISCTVSSL

>core/414/5/Org5_Gene744

MKYSLNFKEIKIDDYERVIEVTCSEKVRLLHAIHQTAVGPALGGVRASLYSSFEDACTDALRLARGMTYKAI
SNTGTGGGKSVIILPQDAPSLTEDMLRAFGQAVNALEGTYICAEDLGVSINDISIVAEETPYVCGIADVSGDPSI
YTAHGGFLCIKETAKYLWGSSSLRGKKIAIQGIGSVGRRLQLSLFFEGAELYVADVLERAVQDAARLYGATIV
PTEEIHAECDIFSPCARGNVIRKDNLADLNCKAIVGVANNQLEDSSAGMMLHERGILYGPDYLVNAGGLLN
VAAAEIGRVYAPKEVLLKVEELPIVLSKLYNQSKTTGKDLVALSDSFVEDKLLAYTS

>core/417/5/Org5_Gene215

MLNIHDILGNDDENLLSYQCKHITKDKLTLPSHDFVDKVFGLSDRNNRVLRLSLQTMFSHGRLANSGYLSILPV
DQGIEHSAGASFAINPIYFDPENIVKLAIESGCSAVASTYGTLSLLSRKYAHKIPFMLKLNHNELLSYPTKYHQI
FFTQVEAAYSMGAVAVGATVYFGSETSNEEIVAVSNAFAKARSLGLATVLWCYLRNPAFVANGVDYHTAA
DLTGQADHLGATLGADIVKQKLPTCQGGFKAINFGKTDERVYSELSSNHPIDLCRYQVLNSYCGKVGLINS
GPSGKNDFTEAARTAVINKRAGGMGLILGRKAFQRPLSEGIQLNLVQDIYLDPNITIA

>core/418/5/Org5_Gene1001

MIPLIPMFLKQSLFFSLALTGMTTLVLTVSLGVPVMKWLRKKNYRDYIHKEYCEKLEMLHKDKAEVPTGGG
VLLFISLIASLLVWLPWGKFSTWFFIILLTCYAGLGWYDDRIKIKRKQGHGLKAKHKFMVQIAIAAFTLIALPY

IYGSTEPLWTLKIPFMEGMLSLPFWLGKVFCLGLALVAIIGTSNAVNLTGDLGDLAAGTMSFAALGFIFVALR
SSTIPIAQDVAYVLAALVGACIGFLWYNGFPAQLFMGDTGSLLLGGLLGSCAVMLRAECILVVIGGVFVAEA
GSVILQVLSCLRLRKKRLFLCSPLHHHYEYQGLPETKIVMRFWIFSVCAGLGIAAVLWR

>core/419/5/Org5_Gene835

MRIAVLGAGYAGLSVTWHLLLHSQGTATIDLFDPIPLGEGASGMSSGLLHAFTGKKALKPPLADQGINATHA
LITEASKALNPVIVISQGILRPAIDEDQAQLFTERVEEFPEKEVEWWEKARCEISIPSMVIPPNLGALFIKSGVTLN
NDLYIQGLADACMKLGTQFYDELIEDLADIEEFYDHHIIVTPGANASILPELKDMPVNKVKGQLLEISWPKDLA
MLSFSINAHKYMVANTQKNTCILGATFEHNQPEETPDPAIAYQEIMPPVLSLFPGLKDAQVLHCYAGMRSSS
KSRLPVISRIREKLWFLGGLGSKGLLYHGITGDMLAQAVLRKSTAYIAKEFLFTI

>core/420/5/Org5_Gene757

MILLQNIKRCSLKQLKVLATLLLSLSLPTLEAAENRDSDSIVWHLDYQEALQKSKEAELPLLVI FSGSDWNGP
CMKIRKEVLESPEFIKRVQGKFVCVEVEYLKHRPQVENIRQQNLALKSKFKINELPCMILLSHEEREIYRIGSFG
NETGSNLGDSLCHIVESDSLLRRAFPMMTSLSLSELQRYYRLAEELSHKEFLKHALELGVRSDDYFFLSEKFR
LLVEVGKMDSEECQRIKKRLLNKDPKNEKQTHFTVALIEFQELAKRSRAGVRQDASQVIAPLESYISQFGQQD
KDNLWRVEMMIAQFYLDSDQWHHALQHA EVAFEAAPNEVRSHISR SLEYIRHQS

>core/421/5/Org5_Gene417

MYLQEKFKAQQVPLVLRELLSCSDSINDSDPIYRMVFDSNDTTISYKVGDALGVLPENSKEVSEHVLQLLGYS
PTTLVNVKKTSEKVSQAQKFIQGYVDLDKIPAKLNSFFPDKDPKITLYDAIQEYRPQIPIELFAESVFLLPRFYSI
ASSPDLHPKSIELLVKHVSYPGKYQKRFGVCSSFLCSELQVNDSAYIFVQPTKHFTLSTQTEGKPLVMIGAGT
GIAPYKAFLEERLFNKDPGNNLLFFGERKEKVN FYREFWNHAE EEGKLKLF LAFSRERDQKVYVQDLLRIQ
KDEVRKAYEEGGFFFVCGRKVLGIEVKHALEEILGKDTLASLRKEHRYVVDVY

>core/422/5/Org5_Gene935

MDVSRKINRHTQFYVDSIDGVIKNFDHKPSEDKSRDHEELEEKLLTITKRIVASAEFQNRKTDSKNYYLKKT
QWLPFKNEELEQTKELFAMLTSMDDKIAQLFFYSPGCSSDWVEFTEVICHNLNDSIGLGGVLLCCGLFEQQCEH
VVTVNKKLDLPLLLGTTVVNSLRYYLT YRNLNLCQSMSELGKELGDVLKQHGVAFTLIFKEIVDIDLLNYV
KLIQGLKRSGNIQARIYDNDVPTLPSVSSS PIALRYGLANTIRGLALHVDFSSLKFISPSILSNTEHTAKALNSGG
ECFIFSNLDEFNLGMKIVMQLLRTGKISPEILNKNIMKILMIKRRVRSLYI

>core/423/5/Org5_Gene797

MEADILDGKLKRVEVSKKGLVNCNQVDVNQLVPIKYKWAWEHYLN GCANNWLPTEVPMARDIELWKSDE
LSEDERRVILLNLGFFSTAESLVGN NIVLAIFKHITNPEARQYLLRQAFEEAVHTHTFLYICESLGLDEGEVFNA
YNERASIRAKDDFQMTLTVDVLPNFSVQSSEGLGQFIKNLVGYYIIMEGIFYSGFVMILSFHRQNKMTGIGE
QYQYILRDETIHLNFGIDLINGIKEENPEVWTTTELQEEIVALIEKA VELEIEYAKDCLPRGILGLRSSMFIDYVRH
IADRRLERIGLKPIYHSRNPFPWMSETMDLNKEKNFFETRVT EYQTAGNLSW

>core/426/5/Org5_Gene69

MELSLTSLPLAWYVILGVAVFAYSFGDGFDLGLGAVYLKAKEDKERRILLNSIGPVWDGNEVWLVIIVGGL
FAGFPACYATLLSIFYMPIWTLVLLYIFRGCSLEFRSKSESVSWKIFWDIIFICSGTAISFFLGTIVGNLILGLPLSP
DTSYASLSWILFFRPYAALCGAVVASAFAIHGSCFALMKTSDSL NARIAQQFPYILSSFLVFYVFLGASLISIP
KRFDAPPTYPLILLIALTSCCCVAAKTSVSKKRYGYAFIYSTLNLLSLILSAATLTFPNILLSTVDPQYSYTIYN
SAVETKTLKSLLIIVLIGLPFIITYTCYIYRVFRGKTNFPSIY

>core/427/5/Org5_Gene691

MNSKMLKHLRLATLSFSMFFGIVSSPAVYALGAGNPAPVLPGVNPEQTGWCAFQLCNSYDLFAALAGSLK
FGFYGDYVFSESAHITNVPVITSVTTS GTGTPTITSTTKNVDFDLNNSISSSCVFATIALQETSPAAIPLLDIAF
TARVGGLKQYYRLPLNAYRDFTSNPLNAESEVTDGLIEVQSDYGIVWGLSLQKVLWKDGVSVFVGVSADYRH
GSSPINYIIVYNKANPEIYFDATDGNLSYKEWSASIGISTYLNDYVLPYASVSIGNTSRKAPSDSFTELEKQFTN
FKFKIRKITNFDRVNF CFGTTCCISNNFYYSVEGRWGYQRAINITSGLQF

>core/428/5/Org5_Gene790

MMEVYSFSPSVRTSFQHRVMAALDNWFFLGGRRLKVVS LDSCNSGQACEEYVPISTTEKVLKILSYLLIPIVII
ALLIRYLLHSNFTAKVSQKPWLKTLQLGIDIKSFILPGSHVNTMDSATLFKAIRLEGKRVDVEYHRLHSSDKV
VFYIPAQKLPDDLRLTHWLPEKETRKTEYVRHMLAHVMGYLTSQGKERLQQVVQDSRSSTSLGAEKVLQYR
FIDHPQSQGEFQRLLENITTKGSEDKEVVQSDLFDMAFQCWWPQFISVIQSPTFSEELVHEMSQKLDLDCIYP
EDDEFEQKFLNTLLKAVLHHGFEGISVASMGVIFLICPDSLALQIPFLRNQK

>core/429/5/Org5_Gene645

MNKKKRVL TGDRPTGKLHLGHWVGSIKNRLELQNSPEYDCFFIADLHTLTTKIRKEEVLVDVDNHIYEV LAD
WLSVGIDPTKSIHYLQSAIPEIYELHLLFSMLISINRVMGIPSLKDMARNASIEEGSLSYGLIGYPILQSADILLAK
AQFVPVGKDNEAHVELTRDIARNFNRLYGQVFPEPEVLQGELTSLVGIDGQGKMSKSANNAYLSDS DATITE
KVRKMYTDPNRIRATTPGRVEGNPLFIYHDIFNPHKDEV EEFKARYRQGCIDIEVKARLAEELIHFLKPIKER
RSEFLSKPLALQNVLEDGTHKMREVAKVTMEEVHDKFGF SHKWRSLLK

>core/430/5/Org5_Gene139

MLTLGLESSCDE TACAIVNEDKQILANIIASQDIHAS YGGVPELASRAHLHIFPQVINKALQQANLLIEDMDL
IAVTQTPGLIGSLSVGVHFGKGIAIGAKKSLIGVNHVEAHL YAAymaaQNVQFPALGLVVSGAHTAAFFIENP
TSYKLIGKTRDDAIGETFDKVG RFLGLPYAGPLIEKLAL EGSSESYPFSPAKVPNYDFSFSGLKTAVLYAIKG
NNSSPRSPAPEISLEKQRDIAASFQKA ACTTIAQKLPTIIEKFSCRSILIGGGVAINEYFRSAIQ TACNLPVYFPPA
KLCSDNAAMIAGLGGENFQKNSSIPEIRICARYQWESVSPFSLASP

>core/431/5/Org5_Gene91

MENAMSSSFVYNGPSWILKTSVAQE VFKKHKGKGIQVLLSTSVMLFIGLGVC AFIFPQYLIVFVLTIALLM LAIS
LVLFLLIRSVRSSMVDRLWCSEKGYALHQHENGPF LDVVKRVQQILLRSPYIKVRALWPSGDIPEDPSQA AVL
LSPWTFSSVDVEALLPSPQEKEGKYIDPVL PKLSRIERVSLLVFLSAFTLDDLNEQGVNPLMNNEEFLFFINK
KAREHGIQDLKHEIMSSLEKTGVPLDPSMSFQVSQAMFSVYRYLRQRDLT TSELRCFHLLSCFKGDVVHCLA
SFENPKDLADSDFLEACKNVEWGEFISACEKALLKNPQG ISIKDLKQFLVR

>core/432/5/Org5_Gene233

MDSSAPYNIASQGTEKSTVERILDLYGPASCIKFLKQMVLIREFEARGEAEAYLEGLVGGFYHSYAGQEAVATA
AIANTGLDPWVFSSYRCHALAILLNIPLQEIAAELLGKETGCALGRGGSMMHMCNPFPGGFIVGGQIPLAAG
AAFTIKYQEQKNRVSLCFIGDGA VAQGVFETLNFVSLHQLPLMLIENNGWSMGTSLNRAVAKQPIAESQG
SSYDIRAVTVNGFDLNFSLLGFREAYRYMVDTESPVLVECLCSRFRGHSISDPNLYRSKEEMQCLFKKDPIVL
AKDWLIRLEVLTEEEFQNIHQECKTAVLEAFSNAKLSSDPSVTTLLEEGVYA

>core/433/5/Org5_Gene115

MKLYSISSDVDTPWIFQLMSKVDSYFLGGNRIKVVSIVMQEPNLIIGKVENVRISTIVKILKILSFLIFPLILIAL
ALHYFLHAKYANHLLVSKILERAPQYVPIPGRSGDTASHYKLTTLPVVSQKNLQAMGSNPLEVEAALRTTKP
SFFCVPKAYRQIISSHGIRFSLDLEQLADDINLDSVSWPTEYLNSTMDFCADKRVIQNVQNLRTGTYINSV
GKRSLLKFMLQHLFIDGITQENPEALPNNTSGRLTLFPSVRYIYSHFTPNPTIWPQVFFRQGPLDEDRGGGFEL
LEQLQELGVRFPICPSQGPDPNPNFQGFQGIRIYWEDSYQPNKEV

>core/434/5/Org5_Gene737

MLPFEFEFNTTSSPECVCLDPQKLFVKLFKRTIVLLSGPTGSGKTDVSLALAPMIDGEIVSVDSMQVYQGM
IGTAKVSLKARQEPHHLIDIRHVQEPFNVVDFYYEAIQACQNILSRNKVPILVGGSGFYFHAFSLGPPKGPAA
DPQIREQLEAIAEEHGVSALEYDLLLLKDPEYAQTTKNDKNKIIRGLEHQLTGKKVSDHEWDIVPKASREYCC
RAWFLSPETEFLKNNIQMRCEAMLQEGLLSEVRGLLNQGIENPSAFKAIGYREWIEFLDNGEKLEEYEETKR
KFVSNNSWHYTKKQKTWFKRYSIFRELPTLGLSSDAIAQKIAKDYLLYS

>core/435/5/Org5_Gene696

MFFQNLAKKLTAALGISPLGCLLIGGVVSCAILFGRSSNPSLAPTQVKTEKTSGNWLKLTQMGNPKLIESLTKK
EQLEKDLTSFHPIASAKVAIALSTEDDVMSPLHLSVILTLRKEESLTPSLLFSITDYLCSSLPGLKREHISLSDNL
GNLYIPESITVNSLFIHTLENYLGKIFPKEHFALAYHAKAEKPTLQLTLNENYIAHLTKEESEKIVAHTKHLY
QNYDDSYDIVIETLPFARLQNKKSFPKAVLIGSMILVISLMIVALASFYLARHAYERSPEPRKIKRGINISKLE
IIQKESPEKIALILSYLDPKKAEEALLNRLPEDLKHQVLKYKL

>core/436/5/Org5_Gene214

MSEQHSPIISVQDVSKKLGDHILLSKVSFSVYPGEVFGIVGHSGSGKTTLLRCLDFLDMPTSGSISVAGFDNSLP
TQKFSRRNFSKKVAYISQNYGLFSSKTVFENIAYPLRIHHSEMSKSEVEEQVYDTLNLFLNLYHRHDAYPGNLS
GGQKQKVAIARAIVCQPEVVLCDEITSALDPKSTENIIRLLQLNQERGITLVLSHEIDVVKKICSHVLVMHQ
GAVEELGTTEELFLNSENSITNELFHEDINIAALSSCYFAEDREEVLRLNFSKELAIQGIISKVIQTGLVSINILSG
NINLFRKSPMGFLIIVLEGEVEQRKKAKELLIELGVVIKEFY

>core/437/5/Org5_Gene898

MTILRKLSQYLFFFSLFCFSFIYVATCGSQPDSVSSPKIAIFLSFPHPLLEDCKSKSCIETLKDFENLPEIVVLNAEDSI
VKARKIARSLHTDKNVVAIVTLGTIATKVMISHIETQKPVIIAAVPDRESLTPPKNTMNIYGVNDTLNINQYCF
AIQAVATNAQSIVYLPSEPFPSDLQKEIVKKLHASGIEVIEISITSSTFKTRIRQAIDKRPSAIFIPLSPLSHKEGT

AFLQEILKEKIPITDDTSLISEGACIACSVDYKKSGKQIAKIVHHLLYNNHDVDSLRKIIAQRLSPTTTFNEDIK
YLGIKLHKTERNQFLSFKSKKLEKSEKGKNVAVS

>core/438/5/Org5_Gene804

MEMKEEIEAVKQQFHSELDQVNSSQALADLKVRYLGKKGIFRSFSEKLKQCTDKAKLGSINDFKTYVEDLL
QEKSLVLLASEQAEAFSKEKIDSSLPGDSQPSGGRHILKSILDDVVDIFVHLGFCVREAPNIESEANNFTLLNFT
EDHPARQMHDTFYLNATTVLRTHTSNVQARELKKQPPKVVAPGLCFRNEDISARSHVLFHQVEAFYVDH
NVTFSDLTAILSAFYHSFFQRKTELRFHSYFPFVEPGIEVDVSCECCGKGCALCKHTGWLEVAGAGMIHPQV
LRNGNVDPEIYSGYAVGMGIERLAMLYGVSDIRLFSENDLRFLQQFS

>core/439/5/Org5_Gene277

MATISPISLTVDHPLVDTKKKSCSNFDKIQSRILLITAIFAVLVTIGTLLIGLLLNIPIYIYFLTGISFIAVVLNSFILY
KRATTLLKPRACGKHKEIKPKRVSTNLQYSSISIAINRSKENWEHQPKDLQNLPAAPSALLTDNPYEIWKAKHS
LFSLVSLLPGGNPEHLLISASENLGKTLLEETSQNAPISSYVDTTPSPKSLLEAIQETRVEINTELPAGDSGER
LYWQPDFRGRVFLPQIPTTPEAIYQYYYALYVTYIQTAINNTQIIQIPLYSLREHLYSRELPPQSRMQQSLAMI
TAVKYMAELHPEYPLTIACVERSLAQLPQESIEDLS

>core/440/5/Org5_Gene552

MEEAAKHLAKEFLCSGINLFLSGEYEQAERLKETLELDSTAALAYCYLGIIALETGRVSEALNWCSKGLASE
PGDSYLRICYGVALDRGNQYEAIEQYSAYVALHPDDVECWFSLGSVYHRLKRLQEALDCFDKILALDPW
NPQSLYNKAVILSEMDDEAESIRLLEVAVAKNPLYWKAWVKLGFLSRSKRWDKATEAYERVVQLRPDLSD
GHYNLGLCYLTLDKTRLALKAFQEALFLNAEDADAHFYVGLAHLDLKQMREAYEAFNSALSINLEHERAHY
LLGYLHHMQGETDKATKELLFLQKKDSTFAPLLQKTVSDPSSMQFERRLDNIS

>core/441/5/Org5_Gene571

MVLGVVGISYREAALKERERAIQYLQSFEKNLFLAQRFLGKGGAFIPLLTCHRAELYYYSESPEIAQAALLSEL
TSQGIRPYRHRGLSCFTHLFQVTSIGDSLIFGETEIQGQVKRAYLKGSKERELPFDLHFLFQKALKEGKEYRSRI
GFPDHQVTIESVVQEILLSYDKSIYTNFLFVGYSINRKVAAYLYQHGYHRITFCSRQQVTAPYRTLSRETLSF
RQPYDVIFFGSSESASQFSDLSCESLASIPKRIVFDNFVPRFTLWKETPTGFVYLDIDFISECVQKRLQCTKEGV
NKAKLLLTCAAKKQWEIYEKKSSHITQRQISSPRIPSVLSY

>core/442/5/Org5_Gene89

MFPSANQESRTRNVPLGIFHGLVACLYWGIVFVIPNFLGSFGDLDIVLTRYTIFGIFSLIACAIPNPSVIKKTPLYI
WRKSLWTLINPVYYFGITLGIRYVGSAITVVIASLAPTAVLYHSNTKQKELPYSLLFAISSVIITGVILTHLSA
LNLPTAASPLYSILGVIAVILSTSLWVIYVIRNQSLLEKHPNLTPDTWSYLIGISALIICLPMIILDLGITHVTHN
LISHTPGSERLLFLLCSAMGIFSSAKALIAWNKASLNLSPALLGAILIFEPIFGLVLTLYLSQSLPSLQEGIGIFL
MLGGSLLCLVLFGRKVQKSLENSQVSSSNE

>core/443/5/Org5_Gene642

MKKTCCQNYRSIGVVFSVVLFLVLTQTFLAGHFIDIGTSGLYSWARGVSGDGRVVVGYEAGNAFKYVDGEK
FLLEGLVPRSEALVFKASYDGSVIIIGISDQDPSCRAVKWVNGALVDLGIFSEGMSQFAEGVSSDGKTIVGCLY

SDDTETNFAVKWDETGMVVLNLPEDRHSCAWDASEDGSVIVGDAMGSEEIAKAVYWKDGEQHLLSNIPG
AKRSSAHAVSKDGSFIVGEFISEENEVHAFVYHNGVIKDIGTLGGDYSVATGVS RDGKVIVGHSTRTDGEYR
AFKYVDGRMIDLGTLLGGSASFAFGVSDDGKTIVGKFETELGECHAFIYLLDD

>core/444/5/Org5_Gene922

MTHQVAVLHQDKKFDVSLRPKGLEEFYGQHHLKERLDLFLCAALQRGEVPGHCLFFGPPGLGKTSLAHIVA
YTVGKGLVLASGPQLIKPSDLLGLLTSLQEGDVFFIDEIHRMGKVAEEYLYSAMEDFKVDITIDSGPGARSVR
VDLAPFTLVGATTRSGMLSEPLRTRFAFSARLSYYSQDLKEILVRSSHLLGIEADSSALLEIAKRSRGTPRLA
NHLLRWVRDFAQIREGNCINGDVAEKALAMLLIDDWGLNEIDIKLLTTIIDYYQGGPVGKTLSSAVGEDIKT
LEDVYEPFLILKGFIKKTTPRGRMVTQLAYDHLKRHAKNLLSLGEGQ

>core/445/5/Org5_Gene593

MSYSLRNKKTKICVYIIIALGILSFRSIPQEVYDKIRSSFVSLHVKFFPKIKQAPSSHLANLELENLVLKERVASL
EEKLKL YEVS NHTPPLFPEILTPYFHKLVEGKVYVRDYTHWSSSCWVNVGKTHGIKKNSPVLSGNVLVGLVD
YVGEHQSRIRLITDVGMKPSVVAMRGDIQSWWIKHSLRELIRQVEQISHAYILEKDKYEKISQLQELDSL IQGE
GENQALLRGILSGVGGALWKEGSLCLEGEGFYFSEGKTLLPGDILVTTGLDGVFP PGLLVARVTKVKAPRDG
ACTFKIEAQSLEEKLMELDQLFILPPLEFNPNDRPDIFGLLWD

>core/446/5/Org5_Gene488

MKV VINGFGRIGRLVLRQILKRNSSVEVLAINDLVPGDALTYLKF FDSTHGRFPEDVRCEADHLIVGKRKIQF
LSERNVQNLPWKDLGVDLVIECTGLFTKKEDA EKHIQAGAKRVLISAPGKGDIPTFVMGVNHKTFNPEKDFV
ISNASCTTNCLAPIAKVLLDNFGITEGLMTTVHAATATQLVVDGPSKKDWRGGRGCLQNIIPASTGA AKAVT
LCLPELKGKLTGMAFRVPIEDVS VVDLTVRLDKSTTYDDICKAMKQASETDLKGILDYTDEQVVS SDFIGSEY
SSIFDALAGIALNDRFFKLVAWYDNETGYATRIVDLLEYVEKNSK

>core/447/5/Org5_Gene413

MFVDQITLELRAGKGGNGVVAWRKEKYLPGGPGYGGNGGNGG SVIIEATTSVYSFEAYRNIRFLKAPDGQS
GATNNRTGRSGKDLIVSVPTGTLLRDAETGEILHDFTVDGERLLVSQGGKGGKGN TFFKTSVNRAPTKATPG
KPGEIRQVELELKLIADIGLVGFPNAGKSTLFNTLAHTEVKVGAYPFTTLAPSLGLVLCKDRLYQKPWIIADIP
GIIEGAHQNKGLGLDFLRHIERTLLLLFVIDVSKRERNSPEEDLET LIHELHSHQPDFEKKDMLVALNKIDDLL
PDEQEECLQSFQKRFPSTYTFVLISGLTGEGVDGLYRFFTQRLAV

>core/448/5/Org5_Gene228

MWFSVNKNKKAIIWATGSYLPEKVLSNADLEKMVDTSDEWIVTRTGIKERRIAGPQEY TSLMGAIAAEKAI
ANAGLSKDQIDCIIFSTAAPDYIFPSSGALAQAHLGIEDVPTFDCQA ACTGYLYGLSVAKAYVESGTYNHVLLI
AADKLSSFVDYTDNRNCTVLFGDGGAACVIGESRPGSLEINRLSLGADGKLGELL SLPAGGSRCPASKETLQSG
KHFIAMEGKEVFKHAVRRMETA AKHSIALAGIQEEDIDWFVPHQANERIIDALAKRFEIDESRVFKSVH KYGN
TAASSVGIALDELVHTESIKLDDYLLLVAFGGGLSWGAVVLKQV

>core/449/5/Org5_Gene618

MAAPIFIKNILLRSSIVYAPLAGFSDYPYRCMSALYQPGMLFCCEMVKVEGILYAPERTSKLLDYNENMRPIGA
QLCGSNPETSGEAAKILEGLGFDLIDLNCGCPTDKITKDGS GSGLLKTPELIGRILDKIINSVSIPVTVKIRSGWD
MEHINVEDTVRIIRDAGASAVFVHGRTRAQGYHGPSKQEYISRAKAAAGKEFPVFGNGDIFSPEAAQAMLT
GCDGVLVARGTLGAPWIGKQIQDYLTGTSYEKIPFIKRKAAFLEHMRLVEDYYQSETKFLSETRKLCGHYLIS
AAKVRFLRSSLAKATSYQEVYQLVNDYEEADDSLET FVKC

>core/450/5/Org5_Gene44

MSTPLSSGGISPSDQYVPQELFCDLRSSSRNSPDSNASGDSPIVSPISALVALTDLKLV PYNQNSFSWTTRLK
NAVEKIGLFLQRNWKYILLYILAWALILVCHHTVALTLTIWLGVLGIGVVFGIFTATCLDKENKHRHVNSL
WNLINHGILQLDPNGTRQILLATMIASISALIYAVPQAVGLVIGFSIGNQLSINTVYGARLGDEATY AIDRKAH
KKRIENIEQAINQHQQIKHQMINQKQLNALIEINRNNQTDPATANLLASLKLNLNQPMPCFSMPEC GVTSSYL
DLNNNSPDDIARADQCIMTSLSQTLLQIKKEPDRIIESNH

>core/451/5/Org5_Gene669

MVRRSISFCLFFLMTLLCCTSCNSRSLIVHGLPGREANEIVLLVSKGVAAQKLPQAAAATAGAA TEQMWDI
AVPSAQITEALAILNQAGLPRMKGTSLLDLFAKQGLVPSELQEKIRYQEG LSEQMASTIRKMDGVVDASVQIS
FTTENEDNLPLTASVYIKHRGVLDNPN SIMVSKIKRLIASAVPGLVPENVS VVSDRAAYS DITINGPWGLTEEI
DYVSVWGIILAKSSLTKFRLIFYVLILILFVISCGLLWVIWKTHLTIMTGGTKGFFNPPTPYTKNALEAKKAEG
AAADKEKKEDADSQGESKNAETSDKDSSDKDAPEGSNEIEGA

>core/452/5/Org5_Gene692

MKQHIGYLG MGIWGFCLASLLANKGYPVVAWSRNPDLIKQLQEERRHPLAPNVVISPNLSFTTDMKEAIHNA
FMIVEGVTSAGIRPVAEQLKQITDLSVPFVITSKGIEQNTGLLLSEIMLEVLGDSVTPYLYGLSGPSIAKEVLNG
SPCSVVVSAYDSQTLKQIHEAFSLPTFRVYPNTDIKGAALGGALKNVIAIACGIAEGLSFGNNAKAGLVTRGL
HEMRKLAAIMDCKPETLNGLAGLDLCVTCFSESSRNLRFGHLLAQGLTFEQAKAKIGMVVEGAYTALSAY
QVAKHHKIDMPITTGIYRVLYENLDLKEGIALLLQRNTKEEFL

>core/453/5/Org5_Gene467

MKPLGFQENLEALCNKTSRQLLKYLKQILFVCGASLLIALEFSFFLYFFLFSGKTVIPAFCLACFFLTLFVCLV
TRLYL LSGKGDF FEDLASEYLQGA VPPNKRSQNIVEEQSHLAAAATKLSINLQNQEYSLLSEIFKFLPKHDLIR
KFSCFCFWKDYFLFRECLLQKAIEAYIKVVQAIPVDLSAHVSLADAYVALSGLYADPRKYPEFDANYWIPSG
RYS AEIQEKFFATARRAIEEFQILNEYAPGNAWVHAQLAYSYHDLQMPMEEIQEYEIVLKLKPNDVETMSKL
GILYFQQGMNAKGLRIYEEIKR DYKKSQKLIK FYGVEYKY

>core/455/5/Org5_Gene662

MQPFIFTLLCLTSLVSLVAFDAANARKRCACAQTIERGENFFSIKRSACAEIEYQEKS RHASAIERISKDKGKV
TPKQIAKVATKKKQRYRLLQVPFSRPPNNSRYNLYALLSEPPECYS DTASWYAIFIRLLRRAYVDTGNVPPGS
EYAIANALISNKQEILERGAQLGPDVIETLTLPEEQAEIFYKMLKGSSNSQSLLNFLHYEEKSLGHCKLNLIFM
DPLLLEAVLDHPDAYRETSLLRDGIWEAVKRQEHA IQEHGQAAAELFKTRTDFRLELRDKMQLLLSRYDLL
PLL NKKMF DYTLGSAGDYFLVDPDTKAISRCRCPSKSIKL

>core/456/5/Org5_Gene509

MATNAIRSAGSAASKMLLPVAKEPAAVSSFAQKGIYCIQQFFTNPGNKLAKFVGATKSLDKCFKLSKAVSDC
VVGSLLEEAGCTGDALTSARNAQGMLKTTREVVALANVLNGAVPSIVNSTQRCYQYTRQAFELGSKTKERKT
PGEYSKMLLTRGDYLLAASREACTAVGATTYSATFGVLRPLMLINKLTAKPFLDKATVGNFGTAVAGIMTIN
HMAGVAGAVGGIALEQKLFRKAKESLYNERCALENQSSQLSGDVILSAERALRKEHVATLKRNVLTLLEKA
LELVVDGVKLIPLPITVACSAAISGALTAASAGIGLYSIWQKTKSGK

>core/457/5/Org5_Gene852

MRIAVLGVTGLVGQKFVALLHKWYRDWVIAEVVASNSKYGQSYGDACIWQEPIGPMPPEMVRDLPIRKIEEV
QSDIVVSFLPSSAESMEAYCLSQGKVVFNSASTYRMHSSVPIIPEVNSDHFQLLEEQYPYPGKIITSPNCCVSGIT
LALAPLRKFSLDHVHIIVTLQSASGAGYPGVPSLDLLANTVPHIVGEEEEKILRETVKILGSSKQPLPCKLSVTVH
RVPVAYGHTLSLHVTFSKDVDLDEILYSYQEKNEFPNTYQLYDNPWSPQARKHLSHDDMRVHLGPITYGG
DFRTIKMNVLIHNLVRGAAGTLLASMENYFFDYLKREMCLR

>core/458/5/Org5_Gene478

MKTLWHFVSKAFLSIVGLCCGVVLAFFVIFALIASSLGNGDATFVSLPDAQGEVKDLGKTAPIIAVIEMKDVI
ASSKNTAKTIQNILEGFEEKAPLKDRVKGIVIDMDCPGGEVFEIDRIYSMLRFWKERKGFPIIYIVNGLCASGGY
YVSCAATKIYATSSSLIGSIGVRSGPFFNVKEGLNRYGVESDLLTAGKDKAPMNPYTPWTSHDREERQATLDF
LYGQFVDIVTQNRPLLTKEKLVHTLGARIFSPEKAKQEGYIDVVGATKEQVLQDIVAVCKIEDNYRVIGSGGD
GWWKRVASAAASSPLVTGMIKHDILPLSHDAAAYIPPYLAL

>core/460/5/Org5_Gene598

MSSLTLRRPRRRNRKTAAIRDLLAETHLSPKDLIAPFFVKYGNNIKEEIPSLPGVFRWSLDLLLKEIERLCTYGL
RAVMLFPIIPDDLKDAYGSYSSNPKNILCHSIHEIKNAFPHLCLISDIALDPYTTHGHDGIFLNGEVLNDESVRIF
GNIATLHAEMGADIVAPSDMMDGRIGYIRSKLDQSGYSKTSIMSYSVKYASCLYSPFRDALSSHVTSGDKKQ
YQMNPKNVLEALLESSLDEEEGADILMVKPAGLYLDVIYRIRQNTCLPLAAYQVSGEYAMILSAFQQGWLD
KETLFHESLIAIKRAGADMIISYSAPFILELLHQGFEF

>core/461/5/Org5_Gene111

MNIYQFSPGASPNWQASLMAQLNSYFCLGGETVTRIISLRPSGLILAKKEKAVVSTAEEKILKILSFILFPLVLIAL
AIRYLLYNKFNKDLDRVFFIPTTEITKAELIIAKNPALVKEAALTVSPLFYSLPKKYQLMKVETP

>core/462/5/Org5_Gene112

MLLEDLDTDSIPWPKLYLSEDFDFAYYPESKAIIDTVAKLEKNNPGEEFCLESKKILARYLLEQLFKLETGLNF
PTSTIDGGRESFLIEFSHETKKPTVWAFIYFYHYHSNGPKLEKDFKQAGCEVHNRLNLGLKYRPQAGAQN
GRNGGPYPGPIGFLIVWEENYGSVLKDHGFIKDN

>core/463/5/Org5_Gene777

MQFSRYLRYAFDNQYLPEPLYQKFSVFHQNYIDAATKKAAADQAEVLCLQWVKVIIEDLKNPFIFPPYHKKI
RAPIDLFRLSIDFFSLVIDDKNSRIILNLHRLKEIEEYIARGDNVLLANHQTECDPQLMYALGKTHPELMEN
MIFVAGDRVTSIDPLARPFSGMCDLLCIYSKRHIATPPELREEKLLHNQKSMQILKTLLNEGKFIYVAPAGGR

DRKNAEGRLYPSEFSPESIEVFRLAKASNQTTHFYPFALKTYDILPPPKIENAIGEQRAIFFAPVFFNFGAELF
FDALCSKEELIHCDKHAQRTLRAEKVFSIVKNLYEEL

>core/464/5/Org5_Gene848

MREETVSWSELDIREIYHTPVFELIHKANAILRSNFLHSELQTCYLISIKTGGCVEDCAYCAQSSRYHTHTVTEP
MMKIVDVVERAKRAVELGATRVCLGAAWRNAKDDRYFDRVLAMVKSITDLGAEVCCALGMLSEEQAKKL
YDAGLYAYNHNLDSSPEFYETIITTSYEDRLNTLDVVNKSISTCCGGIVGMGESEEDRIKLLHVLATRDHIP
ESVPVNLLWPIDGTPLQDQPPISFWEVLR TIATARVVFP RSMVRLAAGRAFLTVEQQTLCFLAGANSIFYGDK
LLTVENNDIDEDAEMIKLLGLIPRPSFGIERGNPCYANNS

>core/465/5/Org5_Gene360

MIDIMQHFKPYTMVPGQKLPIPGSLLYAQVFPTLWRLFSSKHEILNEQTLQVQGPKRFAVFQDLHRGGLAV
TSERYKYLLPSGECTQSIKGLPSAAQAGPLLSLGVHKKHADWQKVRCRRDLKEILPLWFRFAAMAPKGSY
RDLETTAIGSLVKTAHQRVLHRETTEIAPALLSIALAGFSECFLPRS YDEEFQ GILPQDGDPEGGVPFELLSYSF
GMIQDIFLRHQGQLVEILPALPPEFPCGRLIHVALPNLGTLSIVWTKKTIRQVELHAEYSGEVFLKFCSSLCSAR
LREWSERRLSGSKRLSLGETLEIKAGTTYLWDCFBK

>core/466/5/Org5_Gene720

MSAFFDLLKSQTASHPPIWLLRQVGRYMPYQELKGSQSLKTFFHNTEAIVEATLLGPSLLHVDAAILFADILS
ILDGFAVTYDFAPGPRIQFSPEQPFTFTSDPQTIFS YLLDAIRTLKQKLPVPLIVFAASPFTLACYLIDGGASKDF
SKTMSFLYVYPEKFDQLISTHIEGTAIYLKTQMDAGAAAVQLFESSLR LPSALFTRYVTEPNRRLIAKLKEQAI
PVSLFCRCFEENFYTLQATQADTLHPDYHVDLHRIQKNLM LSLQGNLDP AIFLLPQEKLLHYVEAFLVPLRTY
PNFIFNSGHGILPETPLENVQLVVSYVQRQL

>core/467/5/Org5_Gene398

MPSPMISTDVCQDILGKQKEAVDFFFQAFQPK EAMQLAEKILGHSGWVFFSGVGKSGCVARKLVATLQSLSE
RALFFSPVDLLHGDGLVSPGDIVCLFSKSGETQELLDTVPHLKSRRAILVAITSM PYSNLAALSDLVVILPSV
AELDPFNLIPTNSTTCQMIFGDFLAML LFHSRGVSLSTYGKNHPSGQVGMKANGKVKDFMFPKTEVPFCHLG
DKVSFSLEVFSAYGCGVCIVDPQFRLMGIFTDGD LRRSLASYGGEVLSLSLEKVM TANPRCITEDSDIAIALQ
LMESSPVAVLPVLDNEENRHVTGLLHMHTLAKAGLL

>core/468/5/Org5_Gene833

MAFKEVVRVAVTGGKGQIAYNFLFALAHGDVFGVDRGVDLRIYDVP GTERALSGVRMELDDGAYPLLHRL
RVTTSLNDAFDGIDA AFLIGAVPRGPGMERGDLLKQNGQIFSLQGAALNTAAK RDAKIFVVGNPVNTNCWIA
MKHAPRLHRKNFHAMLR LDQNRMHSM LAHRAEVPLEEVS RVVIWGNHSAKQVPDFTQARISGKPAAEVIG
DRDWLENILVHSVQNRGSAVIEARGKSSAASASRALAEAARSIFCPKSDEWFSSGVCSDHNPYGIPEDLIFGFP
CRMLPSGDYEIIPGLPWEFPFIRNKIQISLDEIAQEKASVSSL

>core/469/5/Org5_Gene234

MPKHKTLEIREALREAIDEEMSRDPNVCILGEEVGDYNGAYKVTKGLLDKWGPKRVIDAPISEAAFSGIGIGA
ALSGLRPIIEFM SWNFSFVALDQIISHAAKM HFM TGGKFSVP I VFRGPNGAAAQVSCQHSHCVESLYANIPGLI

IIAPSNPYDAKGLLKS AIRNNNPVL FLENELEYNLKG EVPTEEYL VPIGKAHRVQEGNDLTIITYSRMVSITKEA
CSLAKKRWGLSIEIIDLRTIKPLDISTILSSVRKTSRCIVIEEGHYFAGISSEIIALITEHVFDSLDAPPLRVCQKETP
MPYSKILEQATLPNVNRILDTIEKVMR

>core/470/5/Org5_Gene53

MSNQFDQLKKLSTIVCDSGDPELVKASGSQDATTNP SLILKVAQE PKFQELLNEAVVWGIRQNGDDLQTL SFI
LDKIQVNFAL EIIKNIPGRISLEIDARLSFNVEAMVQRAVFLSQLFEAMGGDKKRLLVKIPGTWEGIRAVEFLE
AKGIACNVTLIFNLVQAIAAAKAKATLISPFVGRIYDWWIAAYGDEGYSIDADPGVASVSNIYAYYKKFGIPT
QIMAASFRTKEQVLALAGCDLLTISPKLLDELKKSQHPVKKELDPAEAKKLDVQPIELTESFFRFLMNEDAMA
TEKLAEGIRIFAGDTQILETAITEFIKQIAAEGA

>core/471/5/Org5_Gene468

MTTPAYLLANFGGPRHAKDLQEFLISLLTDRDVTGTFLPRVLHRHLFTFIAKKRVPKVL PQYQSLQNWSP IYF
DTETLAKTLSEILRAPVIPFHRYLPSTHEKTLLALRTLHTRHVIGIPLPHFTYSVTGSIVRFFMKHVPEIPISWIP
QFGSDSKFVSLITCHIRDFLQKLGILEKECCFLFSVHGLPVRYISQGDPYSKQCYESFSAITTNFKQSENFLCFQS
KFGPGKWLS PSTAQLCQNIDTDKPNVIVVPFGFISDHLETLYEIERDYLP LLRSRGYRALRIPAIYSSPLWVSTL
VDIVKENSTVVAEELIKSGKKHTGIR

>core/472/5/Org5_Gene265

MDAKMGYIFKVMRWIFCFVACGITFGCTNSGFQNANSRPCILSMNRMIHDCVERVVGNRLATAVLIKGSLDP
HAYEMVKGD KDKIAGSAVIFCNGLGLEHTLSLRKHLENNPN SVKLGERLIARGAFVPLEEDGICDPHIWMDL
SIWKEAVIEITEVLIEKFPEWSAEFKANSEELVCEMSILDSWAKQCLSTIPENLRYLVSGHNAFSYFTRRYLATP
EEVASGAWRSRCISPEGLSPEAQISVRDIMAVVDYINEHDVSVVPEDTLNQDALKKIVSSLKKSHLVRLAQK
PLYSDNVDDNYFSTFKHNVCLITEELGGVALECQR

>core/473/5/Org5_Gene391

MMTYPVPQNPLLLRILRLMDAFSKSDDERDFYLDRVEGFILYIDLDKDQEDLNKIYQELEENAERYCLIPKLT
FYEVKKIMETFINEKIYDIDTKEKFLEILQSKNAREQFLEFIYDHEAELEKWQQFYVERSRIIIEWLRNNKFHF
VFEEDLDFTKNVLEQLKIH LFDKVGKEITQARQLLSNKAKIYYSNEALNPRPKRGRPPKQSAK VETETTISD
IYTKVPQAARRFLFLPEITSPSSITFSEKFDTEEEFLANLRGSTRVEDQLNLTNLSERFASLKELSAKLG YDSLST
GDFFGDDDEKVVT KTKGSKRGRKKSS

>core/474/5/Org5_Gene745

MHSELPNYQNIVESVVTEITTQLLNYSERHRLVPFWEKSDGSFITAADYGSQYYLKQQLAKAFNPFIGEETL
YPDQDNEKIPEILKFTRLLTSSVSRDDLSTLVPPPSP TSLFWLVDPIDGTAGFIRHRAFAVAISLIYEYRPILSVM
ACPAYNQTFKLYSAAKGHGLSIVHSQNLDRRFVYADRKQTKQFCEASLAALNQQHHATRKL SLGLPNT PSP
RRVESQYKYALVAEGAVDFFIRYPFIDSPARAWDHVPGAFLVEEAGGRVTDALGAPLEYRKESLV LNNHAVI
LASGDQETHETTLAALQNQLNVVPTDKLIAL

>core/475/5/Org5_Gene576

MKTVTSFTVCKENSGRLDKYLTEVHPKYSRAFYQEHLISGLVQINGQINTRVATRLNCGDIVTIDIQEKEELLE
LLPEAIPLDKVYEDGMILVINKPRDMVVHPAPGHFHGTLVHALLHEIGERLKEEFPEEPWRPGIVHRLDKDTS
GLIITAKTRQAKKVSELFSTKRLKKSYLAVCIGKPRSTTIHTHISRHQNKRKEMTVSSQGKEAVTHCQVLAF
NGKLSFVALSPETGRTHQLRVHMKHLGTPILGDPVYGIPSMNSSYGLDKQQLHAYSVDFTHPETRQFCSLKA
GLPEDMRSLLIKEFRNETTILNKNLLESILKEQ

>core/476/5/Org5_Gene204

MTIDMHCDLLSHPHFCRKDPAVRCSPEQLLSGGVRQQVCAIFVPHSRGEPNCDKQNSLFFSLPNQYPDIGLLS
YEEENGSSSQKKSLSLIRSIENASALGDDTAPLGTLAKLIHLTKQGPLAYLGIVWKGDNRFGGGTEAPKRL
SNDGKVLLDIMYELGVPIDLSHCSDKLAEDILDYTADKLPNLAVIASHSNFRSVLDHRRNLVDAHAKIVRRK
GVIGLNLVRSYVGDSLGDLEKHVLHAENLGILSSIVLGSDDFYANEDENFFFNECSSAEAHVPLNQLIHRIFSK
GKAESILSSRAEKFLKQVIVEQVNPKITDVKL

>core/478/5/Org5_Gene957

MIEFAFVPHTSVTADRIEDRMACRMNKLSTLAITSLCVLISSVCIMIGILCISGTVGTYAFVVGIIFSVLALVACV
FFLYFFYFSSEEFKCASSQEFRFLPIPAVVVSALRSYEYISQDAINDVIKDTMQLSTLSSLLDPEAFFLEFPYFNSLI
VNHSMKEADRLSREAFLILLGEITWKDCETKILPWLKDPNITPDDFWKLLKDHFDLKDFKKRIATWIRKAYPE
IRLPKKHCLDKSIYKGCKFLLLAENDVQYQRLHKKVCYFSGEFPAMVLGLGSEVPMVLGLPKVPKDLTWE
MFMENMPVLLQSKREGHWKISLEDVASL

>core/479/5/Org5_Gene321

MELLPHEKQVVEYEKAIAEFKEKNKNSLLSSSEIQKLEKRLDKLKEKIYSDLTPWERVQICRHPSRPRTVNYI
EGMCEEFFVELCGDRTFRDDPAVVGGFVKIQGQRFVLIGQEKGCDTASRLHRNFGMLCPEGFRKALRLGKLA
EKFGLPVVFLVDTPGAYPGLTAEERGQGWAIKCNLFELSRLATPVIIIVIGEGCSGGALGMAVGDSVAMLEH
SYYSVISPEGCASILWKDPKKNSEAASMLKMHGENLKQFGIIDTVIKEPIGGAHHPALVYSNVREFIIQEWLRL
LKDLAIEELLEKRYEKFRSIGLYETTSSESGPEA

>core/480/5/Org5_Gene541

MASNPILQIEDLSITLAKQRQQYPIVQSLSFTINEGQTLAIIGESGSGKSVSAHAILRLLPCPPFSVSGQVNFQGH
NLLTASRSIQKKIIGTEISMIFQNPQASLNPVFTIEQQFREIIHHTHALTAEVAKKMLYALEETGFHDPRLCLNL
YPHQLSGGMLQRICIAMALLCSPKLLIADEPTTALDVSQYQILQLLKTQKKTGMSLLIITHNMGVVAETAD
DVLVLYAGRMVECAPAVQMFHNPSHPYTRDLLASRPSLQPQQLGSFNPPIPGPPHYTAFPSGCRYHPRCSKIL
NRCSAEAPEIYPVREGHKVRCWLYDD

>core/481/5/Org5_Gene262

MALGPSPPYYGVSFQFFSVFFSRLFSGSLFTGSLYIDDIQIIVFLAISCSGAFAGTFLVLRKMAMYANAVSHTVL
FGLVCVCLFTHQLTTLISLGTTLAAMATAMLTGFLIYFIRNTFKVSEESSTALVFSLLFSLSLVLLVFMTKNAH
IGTELVLGNADSLTKEDIFPVTIVILANAVITIFAFRSLVCSSFDSVFASSLGIPIRLVDYLIIFQLSACLVGAFKA
VGVLMAFLIIPSLIAKVIKSIKSLMAWSLVFSIGTAFLAPASSRAILSAYDLGLSTSGISVVFLTMMYIVVK
FISYFRGYFSKNFEKISEKSSQY

>core/482/5/Org5_Gene542

MTTNFPQPLIQATSLTKHYKRSFWFQGKTIASRPVDDVSFSLYSRRVGLIGESGSGKSTLALALAGLLPLTS
GFLTNGTPIKLHSHKHGRHQLRSQVRLVFQNPQASLNPRKTILDSLGHSLLYHKLVPKEKVLATVREYLELVG
LSEEFYRYPHQLSGGQQQRVSIARALLGVPQLIICDEIVSALDLSIQAQILNMLAELQKKLSLTYLFISHDLAV
VRSFCTEVFIMYKGQIVEKGNTKRIFSDPQHYPYTRMLLNAQLPETPDQRQSKPIFQEYHKDSEESCSTGCYFY
NRCPQKQEACKSEIPNQGDAAHHTYRCIH

>core/483/5/Org5_Gene590

MEKKYYALAYYYITRVDNPHEEIALHKKFLEDLDVSCRIYISEQGINGQFSGYEPHAELYMQWLKERPNFSKI
KFKIHHIKENIFPRITVKYRKELAALGCEVDLSKQAKHISPQEWHEKLQENRCLILDVRNNYEWKIGHFDNAT
LPDIQTFREFPEYAEKLAQECDPETTPVMMYCTGGIRCELYSPVLLEKGFKEVYQLDGGVIAYGQQVGTGKW
LGKLFVFDDRLAIPIDESDPDVAPIAECCHCQTPSDAYYNCANTDCNALFLCCDECIHQHQGCCGEECSQSPR
VRKFDSSRGNKPFRRHLCEISENSESASCCLI

>core/484/5/Org5_Gene460

MKQLLFCVCFAMSCSAYASPRRQDPSVMKETFRNNYGIIVSGQEWVKRGSDGTITKVLKNGATLHEVYSG
GLLHGEITLTFPHTTALDVVQIYDQGRLVSRKTTFFVNLPSQEELFNEDGTFVLTRWPDNNDSDTITKPYFIET
TYQGHVIEGSYTSFNGKYSSSIHNGEGVRSVFSSNNILLSEETFNEGVMVKYTTFYPNRDPESITHYQNGQPHG
LRLTYLQGGIPNTIEEWRYGFQDGTTIVFKNGCKTSEIAYVKGVKEGLELRYNEQEIVAAEEVSWRNDFLHGER
KIYAGGIQKHEWYYRGRSVSKAKFERLNAAG

>core/486/5/Org5_Gene881

MNLKVVFYFGTPTFAATVLQDLLHHKIQITAVVTRVDKPQKRSAQLIPSPVKTIALTHGLPLLQPSKASDPQFIE
ELRAFNAADVFIIVVAYGAILRQIVLDIPRYGCYNLHAGLLPAYRGAAPQRCIMEGATESGNTVIRMDAGMDT
GDMANITRVPIGPDMTSGELADALASQGAEVLIKTLQQIESGQLQLVSQDAALATIAPKLSKEEGQVPWDKP
AKEAYAHIRGVTPAPGAWTLFSFSEKAPKRLMIRKASLLAEAGRYGAPGTVVVTDRQELAVACSEGAICLHE
VQVEGKGSTNSKSFLNGYPAKKLKIVFTLNN

>core/488/5/Org5_Gene335

MSKGSSKHTVRINQTWYIVSFILGLSLFAGVLLSTIYYVLSPIQEQAATFDRNKQMLLAHILDFKGRFQIQEK
KEWVPATFDKKTQLLEVATKKVSEVSYPELELYAERFVRPLLTDQGKVFSFEENLNPIEFFEKYQESPPCQ
QSPLPFYVILENSTRTENMSGADVAKDLSTVQALIFPISGFGLWGPIHGYLGVKNDGDTVLTAWYQQGETP
GLGANITNPEWQEQQFYGKKIFLQDSSGTTNFATTDLGLEVVKGSVRTTLGDSPKALSAIDGISGATLTCNGVT
EAYVQSLACYRQLLINFNLTHEKKTGE

>core/489/5/Org5_Gene486

MRLLSILKLHLFSLRSSSSLSPHYHSCSRSMHLHLLCRWKDADIMEWQQICNILSGVCSRMSGKLVSLQKETQ
DSCHQEHERIHLQYREQLSALEEEYRRREEAKNQDLEKLQQENTWLQNRLAEKLQQIRHQSDIIDEIKKELLQ
SVQRTEISEGRRLCYEHKIKQLEEQLQRYVSQHGAPSIIEEDKSSAAYAEINRLKKSLLDLQQEKDIYIKTYHS

EIAKLREKLQRQEGAQTSSEVCSIEKLTEVQTDLAEEKKAIALLLQDIVEDQYCQLRDLHKEKGMAMPSNTKL
DHLKGLLGKEPESEVDVVFSESKSLGS

>core/490/5/Org5_Gene780

MEVQIGIDLMGGDHSPLVVWQVLVDVLKSQSSTIPFAFTLFASEEIRKQIQEEFISDLPQEKFPKIISAENFVAM
EDSPLAAIRKKSSSMALGLDYLQEDKLDAFISTGNTGALVTLARAKIPLFPAVSRPALLVCVPTMRGHAVILD
VGANISVKPEEMVGFARMGLAYRQCLGDSKIPTIGLLNIGSEERKGTEAHRQTFRMLRETFGAFLGNIESGA
VFDGAADIVVTDGFTGNIFLKTAEGVFEFLQRILGDKLEADIQRRLDYTFYPGSVVCGLSKLVIKCHGKACGS
SLFHGILGSINLAQARLCKRILSNLI

>core/491/5/Org5_Gene446

MLISISLATLPILAFSWASFIENWLRRTTAIPWRLPKKHAHLHGLRIAQISDLHFHHRVPEKFLNKVSKSIKNFSP
DLIVFCGDLLCRARLEDKERLETFLNTLEAPLGVFAILGNHDYSSYISRNTKGEITCIPEEKSRIPIQRAIIAVMQG
LFSSPSYRYDPNLTPQEPHPDLLKLLKNTPLTLLHNTTHVIPNTLNIVGLGDLFARQFHPEQAQFKNYDPSLPGL
LLSHNPDGITRLQQYPGDFVLSGSHSGPQVTLSPWPKFARKFFERLSGLENPYLARGYFVTKEGKQLYVNRGL
GGLKRIRFCSPPEICYITCSYD

>core/492/5/Org5_Gene808

MVLSSDLLRDDKQLDLFFASLDVKKRYLLALSGGSDSLFLFYLLKERGVSTAVHIDHGWSTSAQEAKELE
ELCAREGVPFVLYTLTAEQGDKDLENQARKKRYAFLYESYRQLDAGGIFLAHHANDQAETVLKRLLESAAH
LTNLKAMAERSYVEDVLLLRPLLHIPKSSLKEALDARGISYLQDPSNEDERYLRARMRKKLFPWLEEVFGKNI
TFPLLTLGEESAELSEYLEKQAQPFFSAATHQDSQGELPCPDCLIQQAFLCKWVMKKFFNNAGIAVSRHFLQ
MVYDHLRSSCATLRMRNKIVIIKPGVVVID

>core/493/5/Org5_Gene880

MKFLLYVPLLLVLVSTGCDAPVSFEPFSGKLSTQRFEPQHSAAEYFSQGQEFLLKGNFRKALLCFGIITHHFP
RDILRNQAQYLIGVCYFTQDHPDLADKAFASYLQLPDAEYSEELFQMKYAIAQRFAQGKRKRICRLEGFPKL
MNADEDALRIYDEILTAFPSKDLGAQALYSKAALLIVKNDLTEATKTLKKLTLQFPLHLSSEAFVRLSEIYLQ
QAKKEPHNLQYLHFAKLNEEAMKKQHPNHPMNEVVSANVGAMREHYARGLYATGRFYEKKKKAEAAANIY
YRTAITNYPDTLLVAKCQKRLDRISKHTS

>core/494/5/Org5_Gene375

MNRRKARWVVALFAMTALISVGCCPWSQAKSRCSIDKYIPVVNRLLVCGLPEAENVEDLIESSSAWVLTPE
ERFSGELVSICQVKDEHAFYNDLSLLHMTQAVPSYSATYDCAVVFGGPLPALRQRLDFLVREWQRGVRFKKI
VFLCGERGRYQSIEEQEHFFDSRYNPFPTENWESGNRVTPSSEEEIAKFVWMQMLLPRAWRDSTSGVRVTF
LLAKPEENRVVANRKDTLLLFRSYQEAFPGRVLFVSSQPFIGLDACRVGQFFKGESYDLAGPGFAQGVLKYH
WAPRICLHTLAEWLKETNGCLNISEGCFG

>core/495/5/Org5_Gene953

MRKVAFLVSCFLSVAIGASAAPVRVPGFPQIPEDLVQIKTEVCPKQEVCLAVTIKCDDHNLIGVLHLPNTPTPE
GGFPTVVLFHGFRGTKFGGLTGAYRKLGRKFAAAGIATLRVDMAGCGDSEGVAEEVPIETYLRDAQTILETV

QEHPDLNAYRLGISGFSLGCHIAFELAKIYNPRDLNIKALSVWAPIADGGILLKELYENFSKHGEGDIISVGKDF
GFGPPPIIVCSGDVDLLIRIQDHVTANSLPTKPYILHQQGIDDTLVSRTQQTLFKNTAPGRMTFISYPNTGHNLA
TAPDLDMILDQIVSHFQRTL

>core/496/5/Org5_Gene917

MFKLLFHIAAFAGHVLSTPIFIVQDACGIDEEACKNPPPRPFSAQVQYLKVNDKFKKLPHQTIGYRQYDGT
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GLVDPKNIEMGYGLYQGVLSGKYQATEKLSAIFGVINETGLHQEKAWPLVGVSYKATDQLTLNCIYPVNFSI
DYRSTSVCNLGLAYRLTRFRKKLYKNHLISSRGIFEYQGREIEANVKLTPWPGSFIKGFYGWSIGNDISIADDH
NNNKTSHTFKTSAFFGGSAVMNF

>core/497/5/Org5_Gene153

MLVELEALKREFAHLKDQKPTSDQEITSLYQCLDHLEFVLLGLGQDKFLKATEDEDVLFESQKAIDAWNALL
TKARDVLGLGDIGAIYQTIEFLGAYLSKVNRRAFCIASEIHFLKTAIRDLNAYYLLDFRWPLCKIEEFVDWGN
DCVEIAKRKLCTFEKETKELNESLLREEHAMEKCSIQDLQRKLSDIIEHLDVSLFCFSKTPSQEEYQKDCLYQS
RLRYLLLLLYEYTLCKTSTDFQEQUARAKEEFIREKFSLLELEKGIGKQTKLEFAIAKSKLERGCLVMRKYEAA
AKHSLDSMFEEETVKSPRKDTE

>core/498/5/Org5_Gene293

MTLPMQKSLTSFDDFSQAYAELKVPALIGSALEDDKDALIELLVSESFKELGGQGLMPATLMSWTETFALFQ
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QRAERVGISCSQSLASFLRALASTSLPDILSEFDKLLCSVGKKTSLDHSDIKELVVKKEKASLWKFRDSLLKR
DPVEGHQQLHFLLEDGEDPLGIITFLRTQCLYGLRSIEEGSKENKHRMFVLYGKERLHQALNSLFYAETLIKN
NVQDPIVAVETLVIRMVNL

>core/499/5/Org5_Gene144

MFSYIKNRILFNLLSLWIVLTLTFLVMKTIPGDPFNDEGCNVLSEEVLTQLKSRYGLDKPLYQQYTQYLHSLAK
LDFGNSLVYKDRKVTNIISTAFPIAAILGLQSLFLSIGGGIALGTIAALKKKKQRRYILGASILQISIPAFIFATLLQ
YVFAVKIPLLPIACWGSFTHTILPTLALAVTPMAFHQLTYSSVSAALNKDYVLLAYAKGLSPLKVVIKHILPYA
IFPTISYSAFLT TTTVITGTFAIENIFCIPGLGKWFICSIKQRDYPVALGLSVFYGTFLMLSSLLSDLIQSIIDPQIRYA
HGKEKKRK

>core/500/5/Org5_Gene261

MAMLPKFFLVLLCLGLCSCSQKTTTIEGEQMTIFYRIVLGTSLSAKEKASLSQQIDRCFHKIDSIYNNWNPNYSE
LSIINRAPADVPIITLSVELSEFLDQVDTLYKLSEGRFDPTVGPLKTLWLLHLKSQTLPPKDVWEQHYKDMGW
QHLEFQSNTKTLIKKNPHVQIDLCGVVKGAVDCLNEICNTFCPNNYVEWGGEIKTSGHHPSGRPWRIFSEA
AGTILDIDDMAIATSGNHIQKWCVEGKIYTHILDTRTGKPLELSSYP IQSVSVVHPSCAYADAIATVLMTFDSK
IEAKQWAEHHILTYINDGASS

>core/501/5/Org5_Gene422

MWRVVLRFLIIFILGRAVFPLRASESFSWETSTCLTVLGIPFIDIILTNNEDFVAQCGLQIGTISSTNNAKIKEIFLI
YKEKFPEASISFKRKEPLNLSQSHLSDLGILCMRNGETYAEGMANKENGPALKQPKDLRLVLRCPNQPDITLL
YSEKEAEKGIE TNTCLCNQGYTLLDGGQLILYGDSIEKFLKETKRKNHNTLVLDLCSQVVTTFLGRFWSLLNY
VQVLFLSEDSAKILAGIPDLAQATQLLSHTVPLLFIYTNDHSIHIEQ GKESSFTYNQDLTEPILGFLFGYINRGSM
EYCFNCAQSSLGET

>core/502/5/Org5_Gene13

MIASIYSFLDYLMVKSSASPHTLRNYCLDLNGLKIFLEERGNLAPSSPLQLATEKRKVSELPSLFTKEHV
YIAKLIENGKAKRTIKRCLSSIKSFAHYCVIQKILLENPAETIHGPRLPKELPSPMTYAQVEVLMA
TPDISKYHG
LRDRCLMELFYSSGLRISEIVAVNKQDFDLSTHLIRIRGKGKKERIIPVTSNAIQWIIQIYLNHPDRKRLEKDPQA
IFLNRFGRRISTRSIDRSFQEYLRRSGLSGHITPHTIRHTIATHWLESGMDLKTIQALLGHSSLETTTVYTQVSV
KLKKQTHQEAPHA

>core/503/5/Org5_Gene242

MIHSRLIIIGSGPSGYTAAIYASRALLHPLLFEGLFFSGISGGQLMTTTEVENFPGFPEGILGPKLMN
NMKEQAVR
FGTKTLAQDIISVDFSVRPFILKSKEETYSCDACIATGASAKRLEIPGAGNDEFWQKGV
TACAVCDGASPIFK
NKDLYVIGGGDSALEEALYLTRYGSHVYVHRRDKLRASKAMEARAQNNEKITFLWNSEIVKISGDSIVRSV
DIKNVQTQEITTREAAGVFFAIGHKPNTDFLGGQLTLDESGYIVTEKGTSKTSVPGVFAAGDVQDKY
YRQAV
TSAGSGCIAALDAERFLG

>core/504/5/Org5_Gene825

MRKLILCNPRGFCSGVVRAIQVVEVALEKWGAPIYVKHEIVHNRHVVNALRAKGAIFVEELVDVPEGE
RVIY
SAHGIPPSVRAEAKARKLIDIDATCGLVTKVHSAKLYASKGYKIILIGHKKHVEVIGIVGEVPEHITV
VEKVA
DVEALPFSSDTPLFYITQTTLSDDDVQEISSALLKRYPSIITLPSSSICYATTNRQKALRSVLSRVN
YVYVVG
DV
NSSNSNRLREVALRRGVPADLINNPEDIDTNIVNHSGDIAMTAGASTPEDVVQACIRKLSSLIPLGLQV
ENDIFA
VEDVVFQLPKELRCS

>core/505/5/Org5_Gene672

MKCRPTLNTDQPRVRKKLPERFPKWLRPLPQGSFAHATDATIKRSGMPTVCEEALCPNRAECWSRKTATY
LALGDVCTRSCGFCNIGHSKTPPALDPTEPERIALSAKELGLKHVVITMVARDDLEDGGAQGLVDIIQK
LREE
LPQATTEVLASDFQGNVSALHTLLDSGITYNHNHNVETVARLSPLVRHKATYARSMFMLEQAANYLPDL
KIKS
GIMVGLGEMEGEVKQTLQDLASIGVRIVTIGQYLRPSRKHLQVKSYVTPETFDYYRRVGEAMGLFVYAG
PFV
RSSFNADMILASVQDKASA

>core/507/5/Org5_Gene227

MKKRYAFLFPQGGSQYVGMGQDLYMEYPEVRELFDFANERLGFSLTSIMFEGPEDLLMETVHSQLA
IYLHS
MAVVKVLSQRSSIQPSLVSGLSLGEYTALVASDRISVLDGLELVRKRGQLMNEACNQSPGAMAALLGLP
SEV
IEENITSLGQGIWIANYNAPKQLVVAGIAEKVDQAIELFRDLGCKKAVRLKVSGAFHTPLMQVAQDGLAP
DI
YALCMKDSSLPLVSHVVGKSLVNTEEMRECLARQMTSPTLWYQSCYHIESEVDEFLELGP
GKVL
AGL
NRSIG
ISKPITSLGTFAQIEKFLSEV

>core/508/5/Org5_Gene435

MLNSNFKFSKTGAYGDLFQRVVVHSLVLTFLVLLLYSSLFPLTSFALGFITATCGAVGTYEYSSMAKAKMHY
PLSTFSAIGSFLFLALSFLSIRWGHSLPGFFDALPWTLIVWVWWSIFRVRKSTIGALQLSGVTLFSILYVGPIRL
FLHVLYSFIHTQEPYLGIIWWASFLIATTKGADIFGYFFGKAFGNKKIAPQISPNTVVGVFVAGCLGATLISFIF
LQIPTRFASYFPMPIPLGLALGITGFFGDIIESIFKRDAHLKNSNKLKAVGGMLDTLDSLLLSTPIAYLFLIT
QSKEFIG

>core/509/5/Org5_Gene35

MRLFSYDKPKIKVQKIKADGFSGWLKCNHCHEMIHANELGQNYNCCPKCSYHYRITAIERVKLLADKDSWR
PLYTDLKSQDPLEFIDTDTYANRLEKARKNTTESEGVIVGICTIGLHPVALAVMDFNFMAGSMGAVVGEKLT
RLIEEAIETRLPVIIVSASGGARMQESVFSLMQMVKTSAAALAKLHEAGLPYISVLTNPTSGGVTASFAALGDIII
AEPKALICFAGPRVVAQVIGEDLPEGAQKSEFLEHGMIDKIVERKELKTTLQTLDDYFLAQEYTGKSKAPR
DLSKRLKEIFLLTDDSE

>core/510/5/Org5_Gene932

MPMEIAYSLTSSFSVDSVTVGFFDGCHLGHSNLLSILTSYSGSSGVITFDSHPQTVLSLNHTKLINTKEERLQLL
QTFPIDWLGVLTFDLNFANQSAEEFLTLLHRNLKCKRLILGYDSCIGKEQQSNTEALDTIGKPLGIEVIKIPPYR
MDNIVVSSKAIRQFLSAGNLECAHRFLGHPY AISGKITEGSGIGGSLGFATINLPREESLIPLGVYACEIRYDSTT
CQGVMMNLGTAPTFERESLYAEAHIFSFAENLYGKEVSIIPRKFLREEKKFQSKETLIRAIEKDILDAQDWFAKG
SFNYEGTA

>core/511/5/Org5_Gene14

MSSRELIILGCSSQQPTRTRNQGAYLFRWNGEGLLFDPGEGTQRQFIFANIAPTTVNRIFVSHFHGDHCLGLGS
MLMRLNLDKVSHPIHCYYPASGKKYFDRLRYGTIYHETIQVVEHPISEEGIVEDFGSFRIEAQRLQHQVDTLG
WRITEPDTIKFLPKESRGIRGLIIQDLIRDQEISIGGSTVYLSDVSYVRKGDSIAHADTLPCQAAIDLAKNSCM
MLCESTYLEQHRHLAESHFHMTAKQAATLAKRAATQKLILTHFSARYLNLDIFYKEASAVFPNVSV AQEYR
SYPPFPKNPLLNK

>core/512/5/Org5_Gene666

MRSIFRFLCFFTLVSVCCFADASLYENSCPSRCQPTPPPSNSNPLNVVQQPVAASSVPSYMPPLNADDVLPRD
HLSDGFSFSDTYPDITTQAIIILFLALSPFLVMLLTSYLKIIITLVLLRNALGVQQTTPPSQVLNGIALILSIYVMFPT
GVAMYKDARKEIEANTIPQSLFTAEGAETVFVALNKSKEPLRSFLIRNTPKAQIQSFYKISQKTFPSEIRAHLTA
SDFVIIIAPAFIMGQIKNAFEIGVLIYLPFFVIDLVTANVLVAMQMMMLSPLSISLPLKLLIVMVDGWTL LLQGL
MISFK

>core/513/5/Org5_Gene991

MKEAAPMHFPFPVRRSVWLNRYSTFRIGGPANYFKAIHTIEEAREVIRFLHSINYPFLIIGKGSNCLFDDR GFD
GFVLYNAIYGKQFLEDARIKAYSGLSFAALGKATAYNGYSGLEFAAGIPGSGVGAIFMNAGTNESDISSVVRN
VETINSEGELCSYSVEELELSYRSSRFHRQQEFILSATLQLSKKQVSADHKSILQHRLMTQPYTQPSAGCIFRN

PEGTSAGKLIDAAGLKGLAIGGAQISPLHANFIINTGKATSDEVKQLIAIIQSTLKTQGIDLEHEIRIIPYQPKIHS
PVSEK

>core/514/5/Org5_Gene650

MSLFLVFLTAFIWSSSFALSKLVMNASAPIFATGARMVIAGAILALAAWFRGGFVGISKKIFLYIVLLALTGFY
LTNIFEFIGLQSLSSSKTCFIYGLSPLMSALFSYIQLKEKVTLKKVLGLSLGLVSYICYLTFGGGGDDSQPWTW
QIGLPELLILGAASLASFGWTLLRQIEKQSTLSVTAINAYAMLIAGMLSIMHSAVVEPWRLPVQDISQFLYAT
LALVVISNLICYNLYAKLLRKYSSTFLSFCNLVMPLYSGFYGWILLGEKGVSLGLVLAVAFMVAGCRLIYHEE
FRQGYIVS

>core/515/5/Org5_Gene678

MQKPQYIDRITKKKVIEPIFYEKTMLFLYNSKLGGKLSVFLSTHPIFSRIYGWLQRCSWTRRQIRPFMNRYKIS
EKELTKPVADFTSFNDFFTRKLKPEARPIVGGKEVFITPVDGRYLVYPNVSEFDKFIVKSKAFSLPKLLGDHEL
TKLYAHGSIVFARLAPFDYHRFHPCDCLPQKTRCVNGALFSVHPLAVKDNFILFCENKRTVTVLETEQFGNV
LYLEV GAMNVGSIVQTFSPNQTYAKGDEKGFFAFGGSTVILLFLPNAIRFDNDLLKNSRMGFETRCLMGQSL
GRSQREEI

>core/516/5/Org5_Gene831

MTMPSTQFHTTILEQFSLFLSVDRGLCQQSIAAYRQDISSFLTISAISSPQDISQNSVYIFAEELYRRKEAETTLA
RRLIALKVFFLFLKDQQLLPYPPIIEHPKIWKRLPSVLTPEVDALLAVPLQMEKNPRHLAFRDTAILHTLYST
GVRVSELCDLRLGHVSDDCIRVTGKGSKTRLVPLGSRAREAIDAYLCPFRDQYQKKNPHEDHLFLSTRGHKL
ERSCVWRRIHNYAKQVTSKPVSPHSLRHAFATHLLDNKADLRVIQEMLGHARIASTEVYTHVAADSLIEKFL
AHHPRNL

>core/517/5/Org5_Gene314

MLKIDLTGKVAFVAGIGDDQGYGWGIAKLLAEAGATHIIVGTWVPIYKIFSQSWELGKFNESRKLSNGTLLEIA
KIYPMDASFDSPEDVPEDIAENKRYKGITGFTISEVAEQVKKDFGHIDILVHSLANSPEISKSLLETSRKGYLAA
LSASSYSFVSLLSHFGSIMNRGGSTISLTYLASMRAVPGYGGGMSSAKAALESDTKTLAWEAGRRWGIRVNT
ISAGPLASRAGKAIGFIERMVDYYQEWAPIPEAMNAEQVGAVAAFLASPLASAITGETLYVDHGANVMGIGP
EMFPKDS

>core/518/5/Org5_Gene869

MPPPFVVTLTTS AQNNLRDQLKEKNFIFSQPQNTVFQARSNTVTCTLYPSGKLVIQGKGSEEFIEFFLEPEILHT
FTHARVEQDLRPLRGVDESGKGDFFGPLCIAAVYASNAEILKKLYENKVQDSKNLKDTKIASLARIIRSLCVC
DVIIYPEKYNELYGKFQNLNTLLAWAHATVINNLAPKPGADVFAISDQFAASEYTLLKALQKKETDITLIQK
PRAEQDVVVAASILARDAFVQSIQKLEEQYQVQLPKGAGFNVKAAGREIAKQRGKELLAKISKTHFKTFDE
ICSGK

>core/519/5/Org5_Gene207

MHLEENQGW EALLRKVYHQEVPPAILLHGFTLPVLQDKAEQLASEILLSSSPGSEHKVSQKIHPDIYQFFPEG
KGRLHSIDLPRGIKKQIYISPF EANYKIYIIHEADRMTLAAIS AFLKVFEPPKHAVIILTAKVQRLPKTIISRSLS

IFIERGEKILCSKETFSYLFYQAQCEIPVTEVSQIIKESSETDKQVLRDKVQRFMEVLLELYRDRYTLNLGLKAS
ALNYPEHVKEILQLPLLPLDKVLLIVESACRSLNNSSSAASVLEWVAIQLVSLQYKEKELVSVSPGQDLSN

>core/520/5/Org5_Gene200

MRLNYFLNLVNFKYISIFSILFLSASTVFALSINEISQNL SFKEGFKISVFGAIAFVFARTTGIVVNQCIDRFIDKKN
TRTSKRVL PANLVSLNFAWVLSLFC SFLFLCKILRIFSLG IASLTLMIVYPYMKRV TFFCHWGLGLVYTVAI
LMNFCAFAESGLSMRLCFLALLWGGSVGMVIAANDIYAIEDTEFDREGLRSVPAHYGEKKAVEIAKVN LW
VSYLAYIFSGFVGSLDKEFYFTAIPLVVILKVVRMYSNYSKKDQEGESKFFLANIAIALSFLVSMTLFWSLSR

>core/521/5/Org5_Gene328

MSERAHIPVLVEECLALFAQRPPQTFRDVTLGAGGHAYAFLEAYPSLTCYDGSDRDLQALAI AEKRLET FQD
RVVSF SHASFEDLANQPTPRLYDGV LADLGVSSMQLD TLSRGFSFQGEKEELDMRMDQTQELSASDV LNSLKE
EELGRIFREYGEEPQWKSAAKAVVHFRKHKKILSIQDVKEALLGVFPHYRFHRKIHPLTLIFQALRVYVNGED
RQLKSLTSAISWLAPQGRLVIISFCSSEDRPVKWFFKEAEASGLGKVITKKVIQPTYQEVRRNPRSRSAKLRC
FEKASQ

>core/522/5/Org5_Gene635

MSRHEICPEVSHKKGKYYSTFIFRCIHSLAGIAFTFFLCEHLFTNMLASSYFSQGKGFVAMVNGFHKIPGLKII E
VAGLVLPFLCHAIIGIVYLFQGKSNCYSGDGRPHLRYAKNYSYTWQRWTAWILLFGIAFHVVHLRFIRYPVH
VDIHGTTYAYVDIQPSRYDVIVRGTKGFLTNLNPTEASSIEVSRHDLGGADAALLSERNSYLLTPSAGTAFLY
VVRDALGSLFIALLYTILVIAAAFHGFNGLWTFCCRWGVVVS LRMQGVLRIVCYLAMIVVTFMGVSAVWNL
YSVA

>core/524/5/Org5_Gene942

MRRFLFLILSSLPLVAFSADNFTILEEKQSPLSRVSIIFALPGVTPVSFDGNCSIPWF SHSKKTLEGQRIYYSGDSF
GKYFVV SALWPNKVSSAVVACNMILKHRVDLILIGSCYSRSQDSRFGSVLVSKGYINYDADVRPFFERFEIPD
IKKSVFATSEVHREAILRGGEFISTHKQEIEELLKTHGYLKSTTKTEHTLMEGLVATGESFAMSRNYFLSLQK
LYPEIHGFDSVSGAVSQVCYEYSIPCLGVNILLPHPLESRNEDWKHLQSEASKIYMDTLLKSVLKELCSSH

>core/525/5/Org5_Gene198

MSHGPRPTKFSFPLYFSKTL SWFILGGFLAACGVQMVLVPNELIDGGIVGLSIIASHFLGHKALPFCLVLFNL PF
VFLAFKQIGKYFVIQMLTAVIIFSCSLWLIDQLPSWLGMSPFVFKGSEMETVVLGGAIIGVGCGLIIRHGGSTD
GTEILGIIIINKKKGYTVGQIILFVNFFIFALSGIVYKNWHTAFVSFLTYGIATKVM DMVILGLEDTKSVTIITSSP
RKLGHILMETLGIGLTYIHAEGGYSGEPRNLLYVVVERLQLSQLKEIVHREDPSAFIAIENLHEVINGRRT

>core/526/5/Org5_Gene726

MQEKPRHVHRIIHISDVHFHVLPVNPVHCFNKRLKGLLRKVFGLVHFQATTIGQRF PKVVRS LGADSV CITGD
FSLTAMDGEFL LAKHFVETLAKHSSVYLLPGNH DVYTLKSLAQQTFYTHFPNDQLQQNKVSFHKITDHWL
ILLDCSCLNGWFSANGVVHLAQISAIETFLLSLSP EENVIIANHYPLLSSQNPSHDLINNTHLQNV LKKYPKVRL
YLHGHEHQAAVYNCA DTSPSYILNSGSISLPTNSRFHVIDLYPEKYQVHTMILKNLLDFDAPLEIANEATWDC
QKL

>core/527/5/Org5_Gene315

MEKLLVTDIDGTITHQSHHLDKKVYERLYALHQAGWKLFFLTGRYYKYAARLFSDFDAPYLLGCQNGASV
WSSTSSNLLYSKSLPSDLLCILQDCMEGATALFSVESGAPYGDHYYRFSPTPIAQDLHEYVDPRYFPNAKEREI
LFETRSLKDDYAFPSFAAAKVFGRLDEVIRIQKELERQEALTSVATMTLMRWPFDFRYAILFLTDKSVSKGKA
LDRVVNILYDGKKPFVMA SGDDANDLDLIERGDFKIVMSSAPEEMHVVHADFLAPPADKNGILSAWEAGVRY
YDDLMSL

>core/528/5/Org5_Gene527

MKKLILYFAAFVASLFCGVFLWDRVPCAQKIMRLAADHSSEVFSKSCRFRVRKISGFEELQVFERHVSPEQALA
LFPEYRDGKSFVELAFIPHTLMHVRFSSKEPVKKHIISQEGEILWSLVNGEMVLHTGTWTC SKGFRECLLLHA
GKQDMRVIQTLATLGGTTSRESLAQALALKNIRAERVIKECQKKKLIFASGNQIGTHFQQFQPIRGCTTTLNN
NPVWLQKPRHAAVFPAQYSEDRVRHLVKMIFGDNFLIVRSSMVYVPVYKISLVSADNSVRVEYINAVTGKSF
QDL

>core/529/5/Org5_Gene789

MFHSLSKNTPIITQGITGKAGSFHTEQCLAYGTNFVGGVTPGKGGTLWDLVPYDSVLEAKQATGCRATMIF
VPPPYAAEAILEAEEAGIELIVCITEGIPVRDMLEVARVMDNSTSQLIGPNCPGIIKPGECKIGIMPGYIHLPGNI
GVVSRSGTLTYEAVWQLTQLKIGQSICVGIGGDPLNGTSFIDVLQALEEDPYTELILMIGEIGGSAEEEEAAWI
QAHCTKPVVAFIAGVTAPKGKRMGHAGAIISGNSGDAKSKIQVLRESGVTVVESPAHIGKTVD AVLRAKEL

>core/530/5/Org5_Gene723

MSKHTSESRIAQDMLERYSGSSVKQFCPYLLL TNFSYYIQTFAKLHGVPVFEGSMFSAAHAPHLKTSILDFKL
GSPGAALTIDLC SFLPDLKAALMLGMCGLRSHYQVG DYFVPVASIRGEGTSDAYFPPEVPALANFVVQKAT
TEVLEDKKANYHIGITHTTNIRFWFNKKFRKKLYETKAQSAEMECATLFAAGYRRNLPIGALLLISDLPLRK
EGIKTKSSGNFIFNTYTEDHILTGQEV IENLEKVMLKRAASDHKKDQQYRGLPHMEVGEADDTMASGSETSD
SDY

>core/531/5/Org5_Gene588

MKVLPPPSIPLLGAHTSTAGGLKNAIYEGRDIGASTVQIFTANQRQWQRRALKEEVIEDFKAALKETDLSYIM
SHAGYLINPGAPDPVILEKSRIGIYQEILDCITLGISFVN FHPGAALKSSKEDCMNKIVSSFSQSAPLFDSSPPLV
VLLETTAGQGTLIGSNFEELGYLVQNLKNQIPIGVCDTCHIFAAGYDITSPQGWEDVLNEFDEYVGLSYLRA
FHLNDSMFPLGANKDRHAPLGEGYIGKESFKFLMTDERTRKIPKYLETPGGPENWQKEIGELLKFSKNRDS

>core/532/5/Org5_Gene412

MLSSLIRDSFPLLILLPTFLAALGASVAGGVMGTIYIVVKRIVSISGSISHAILGGIGLTLWIQYKLHLSFFPMYGA
IVGAIFLALCIGKIHLKYQEREDSLIAMIWSVGMAIGIIFISRLPTFN GELINFLFGNILWVTPSDLYSLGIFDLLV
LGIVVLCHTRFLALCFDERYTALNHCSVQLWYFLLLVLTAITIVMLIYVMGTILMLSMLVLPVAIACRFSYKM
TRIMFISVLLNILCSFSGICIA YCLDFPVGPTISLLMGLGYTASLCVKKRYNPSTPSPVSPEINTNV

>core/533/5/Org5_Gene820

MKRNDPCWCGSGRKWKQCHYPQPPKMSPEALKQHYASQYNILLKTPEQKAKIYNACQITARILDELCKASQ
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DCSRMVMIGEVEIKKKICQAALECLNDSIAILKPGIPLCEIGEAEARADTYGFSVVDQFVGHGVGIEFHENPY
VPHYRNRSMIPLAPGMIFTIEPMINVGKKEGVVDPKNQWEARTCDNQPSAQWEHTIAITETGYEILTLLND

>core/534/5/Org5_Gene853

MHLLTATVTPFFPNGTIDFASLERLLSFQDAVGNVGVLLGSTGEGLSLTKKEKQALICFACDLQLKVPLFVGT
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AHHPQFLGIKDSGGSVEEFQSYKSIAPHIQLYCGDDVFWSEMAACGAHGLISVLSNAWPEEAREYVLNPQEQ
DYRSLWMETCRWVYTTTNPIGIKAILAYKKAITHAQLRLPLSIEDFDLENVSPAVESMLAWPKLRTSVFSYS

>core/535/5/Org5_Gene787

MFKFFRNKLQSLFKKNISLDLIEDAESLFYEADFGTELTEELCARLRRTKKADASTIKDLITVLLRESLEGLPSQ
ASQSSQTRPIVSLLLGTNGSGKTTTAAKLAHYYKERSESVMLVATDTFRAAGMDQARLWANELGCGFVSGQ
PGGDAAAIAFDGIQSAIARGYSRVIIDTSGRLHVHGNLMKELSKIVSVCCKALEGAPHEIFMTVDSTLGNAIE
QVRVFHDVVPLSGLIFTKVDGSAKGGTLFQIAKRLKIPTKFIGYGESLKDLEFDLDFLNKLFPEVEKI

>core/536/5/Org5_Gene194

MKRRNLQKILPNASTPSTNVAENTGIKDQNLFLDQATLNVNVDGNVDIENFLETRDLKVADTITSPCEFTVGGGL
SAESSQFKATTLSKGLEITSEDQDGRVPKFTNVSDPQSPRDALTYNYYRNTGCQALNLYTTYSSSQPTTVGKP
IETVCQNPNPETYRISASAKIYDAVTRFPYIQFKAPGIYQVTIQIRRESGQHSGLDNPNLYLNLNLMIGNNKTLLCA
SDTRGYSGGHRTSIAVTGTFTLTEIVATPPHDYPWLFLETTIGLDIKSMSTCVIWFPPQANFAEVD

>core/537/5/Org5_Gene1032

MQIPRSIGTHDGSFHADEVTAALLIIFDLVDENKIIRSBDPVVLSKCEYVCDVGGVYSIENKRFDHHQVSYDG
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CALHFTIDFLCRLRKKFQYDRVCRGIVREAMETEDMCLYFDRPLAWQENFFFLGGEKHPAAFVCFPSCDQWI
LRGIPPNLDRRMEVRVPFPENWAGLLGKELSKVSGIPGAVFCHKGLFLSVWTNRESCQRALRLTLQDRGII

>core/538/5/Org5_Gene664

MGISLPELFSNLGSAYLDYIFQHPPAYVWSVFLLLLARLLPIFAVAPFLGAKLFPSPIKIGISLSWLAIIFPKVLA
DTQITNYMDNNLFYVLLVKEMIIIGIVIGFVLAFFYAAQSAGSFITNQQGIQGLEGATSLISIEQTSPhGILYHYF
VTIIFWLVGGHRIVISLLLQTLEVIPIHSFFPAEMMSLSAPIWITMIKMCQLCLVMTIQLSAPAALAMLMSDLFL
GIINRMAPQVQVIYLLSALKAFMGLLFLTALWWFIIKQIDYFTLAWFKEVPIMLLGSNPQVL

>core/539/5/Org5_Gene601

MLHALD TYRPSIESAIEKALEGFGPIGHPIRSPVEYALQGGGKRLRPGLVCMMAQGLGLNHDVMDSALAVEF
VHTSTLIADDLPCMDND DERRGRPTVHKAFDEATALLASYALIPAAAYSHLRLNAKKLKEQGCDPREIDIA YNI
IGDITDKNIGCSGVLGGQYDDMFFSNRGQEHVQSIMIKKTGSLFEIACISGWLFGGGDPQFAPIITSFSNNFGLL
FQIKDDFSDLQKDSQQIGLNYALLFGEKAALELLARSQNNCLELLDRLSAGGLKNSSEFETIISLGSF

>core/540/5/Org5_Gene193

MSNPTPKTKISIPTFVRFNISINLTEDQKKTTFTVGGKVTTENTVVRGDLTCTDGGLTCQSDLTIQKDINIRPT
STNSMVFDGRLNLSNSPLSYKNSQGQDITDYEKMSSGKPQEYVPFGYYKRTQIMMAQRAAHSSGYVGGGSV
PSGSYVPWNKFDQTSTQKTSGETIYIDPNDSTKLVEVNNKVPKLFKRISVIMAKHGSWLDNGTGADILLAANE
YEQGGGRINVTDLAMTTSRGSSYYETRPLQVVCVTTYAQNNGYFTFQNRAGGGLRVSFFSWNIVALPYVE

>core/541/5/Org5_Gene873

MLKIQKKRMCVSVVITVGAIVGFFNSADAAPKKKKIPIQILYSFTKVSSYLKNEDASTIFCVDVDGRLLQHRY
LGSPGWQETRRRQLFKSLENQSYGNERLGEETLAIDIFRNKECLESEIPEQMEAILANSSALVLGISSFGITGIPA
TLHSLLRQNLSFQKRSIASESFLKIDSAPSDASVFYKGVLFRRGETAIVDALSQLFAQLDLSPKKIIFLGEDPEV
VQAVGSACIGWGMNFLGLVYYPAQESLFSYVHPYSTATELQEAQGLQVISDEVAQLTLNALPKMN

>core/542/5/Org5_Gene978

MSHLIPSLRNSVTSYFHKPQPIKQAAPSKSIRDICNIAYLIIICVLVVVVLVGAMLCMFIPSVGIPLCLSSLALLV
LLSIFNPCLINWISTKKTKEIAPKDASESQPTKSASRKGSPQLSPHHDHEPKNFIRTQLEKGVNYVTNFKKSGEE
SPHISDEHHSPRQSKRSSEIESSDESSPELHRKAKGKAPHTATTKGSKTSTTESSKKKKKTKHSLHRTTSSIHKR
SAPKPMVPSKKRKPVLLKKTVPPLIEDLEHQSSGNESSDSSSPPPVQRKAILPWFCCKQPTDP

>core/543/5/Org5_Gene79

MEIKKAIQEGTAYLDYYGVPLSDCEALYILMDLLEVSSRAKLFDLVGISETMLMEYRKRLALRGQRCPTAYL
NGAVSFLGLRLRVDSRVLIPRTETELLA EYIINYLLSHSEIQTFYDICC GSGCLGLAIKKSCPHVEVVLSDVCPQ
AVAVANENAKSNGLDVKILLGDLSAPYTRPADAFVCNPPYLSFNEIIHIDPEVRCYEPWKALVGGSTGLEFYQ
RIAQELPKIVTSTGVGWLEIGSSQGESIKNIFSKHGIYGRLLHQDLSGRDRIFLEMDGRDPVSSGAYS

>core/544/5/Org5_Gene239

MAVIYWDRSKIVWSFEPWSLRLTWYGVFFTVGIFLACLSARYLALSYYGLKDHLSFSKSQLRVALENFFIYSI
LFIVPGARLAYVIFYGWSFYQLQHPEEIIQIWHGGLSSHGGVLGFLWAAIFSWIYKKKISKLTFLFLTDLCGSVF
GIAAFFIRLGNFWNQEI VGTPTSLPWGVVFS DPMQGVQGVVHPVQLYEGISYLVVSGILYFLSYKRYLHLGK
GYVTSIACISVAFIRFFAEYVKSHQGKVLAE DCLLTIGQILSIPLFLFGVALLIICSLKARRHRSHI

>core/545/5/Org5_Gene260

MLLRGIPAAEKILQRLKEEISQSPTSPGLAVVLIGNDPASEVYVGMKVKKATEIGIISKAHKLPSDSTLSSVLKL
IERLNQDPSIHGILVQLPLPKHLDSEVILQAISPDKDVDGLHPVNMGKLLLGNFDGLLPCTPAGIHELLNYYEIP
LRGRHAAIVGRSNIVGKPLAALMMQKHPQTNCTVTVLHSQSENLP EILKTADIIIAALGAPLFIKETMVAPHA
VIVDVGTTRVPADNAKGYTLLGDVDFNNVVTKCAAITPVPGGVGPMTVAMLSNTWRCYQNFS

>core/546/5/Org5_Gene543

MTEEISKDTIIEVAIDDIRVSPFQPRRVFSNEELQELIASIKAVGLIHPPVVREICTGDRVLYYELIAGERRWRAM
QLAGATTIPVILKHVIADGTAAEATLIENIQRVNLNPIEMAEAFKRLIHVFGLTQDKVAYKVGKKRSTVANYL
RLLALSKTIQESLLQGQITLGHAKVILTLEDPIREKLN EIIQEH LAVREAELIAKQLISEEGSSI ELKPTPLDMA
ESSKQHEELQQRSLDCGYKVQIKTRGSKATVSFHLQNTQDLQKLEAWLSSHGTLSESLS

>core/547/5/Org5_Gene205

MPDKKAQITFSLPEVMSAIHQGKIVALPTDTVYGFVLSLYASEAEERLYALKDREPSKAFALYVNSIEDIENIS
GYPLSPTAKKLAQLFPGAITLVVKHRNPRFPKETLAFRIVDHSVVREIVDHCGLTIGTSANLSEFPSALTAQEIF
ADFADHDLCIFDGPCSHGLESTVVASDPLYIYREGLISRSVIENIAGTEAKIFHRTSHAFSKHIKIYTVKNQEQL
VSFLSGSLDFKGVVCEHPKPKNFYTRLREALKKKTPSIVFIYDINTSDYPELFPFLSPYYIE

>core/548/5/Org5_Gene192

MKNNINNNECYFKLDSTVDGDLLAANLKTFTDQAQGISSTETFSVQGNATFKDQVSATGLTSGTTYNLNAQ
NFTSSQISIDFKNNRLSNCALPKEDCDVPANYVRSPEYFFCSKPLIGDFDFNSGESYLPLTGSEYTLYQSRNVN
SIFRFIGWKQSTRELTVGGNATAQFLAAGTYIVSFTVGKRWGWNGWGGAIIYINNGLGQVQCESTIYSGGGY
ATIGTLGTSIYRASVDVAPNPNDPNASDRYRAGIFYLSNGGSSAGIGNYSFSLLYYPDDR

>core/549/5/Org5_Gene363

MHEVLILTFTYPLPRTLKQHPDEVHTVPISPNSFGEGSPILIAGPCTLESYEHTVSSALTVKEAGAQVFRGSIR
KPRTSPFSFQGEKECVLWHKEAQSIHGLPTETEVLDVRDVEITAEHVDILRIGAKNMHNTPLLQEVSKSHRP
IILKRSPAATLEEWLCAA EYILASSPSCPGVILCERGIRTFEHSTRYTLDLNTVALLKEISSLPVIVDP SHAAGKR
SLVLPLASAGLSVGADGLMIEVHAHPEKALCDAKQKITPEELHLFAKKHFCPSESRAHAIS

>core/550/5/Org5_Gene185

MKHYSFSPSADFFSKQGA IETQVLFGERVLVKGSTCYAYSQLFHNELLWKPYPGHSFRSTLVPCTPEFHIHP
NVSVVSVDAFLDPWGIPLPFGTLLHVNSQNTVIFPKDILNHMNTIWGSGTPQCDPRHLRRLNYNFFAELLIKD
ADLLLNFPYVWGGRSVHESLEKPGVDCSGFINILYQAQGYNVPRNAADQYADCHWISSFENLPSGGLIFLYP
KEEKRISHVMLKQDSSTLIHASGGGKKVEYFILEQDGKFLDSTYLFFRNNQRGRAFFGIPRKRKAFL

>core/551/5/Org5_Gene944

MDNYLLNIKDLTITSTNPKRTL IENLSLQLKENRNLALVGESGSGKTTITKAILGFLPENCLIKTGSILFEDIDIT
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YPFELSGGMRQRVVIAIALASQPKLILADEPTTALDSMSQAQVLRILRNXQQKQATILLVTHNLSLVKELCN
DICIHKDGKLIETGTVEEIFLSPKHPYTLKLLNAVSKIPIKKTSSPILKNKFQPLMSMQGGL

>core/552/5/Org5_Gene145

MENLSSAPRSIWKSIIQNKMLVLGLTTLIILMLGALLPWIFYQDYEQTSKLDILVSPCSRFPFGTDTLGRCMF
ARTLRGLRLSLLIATIALIDVCVGLLWATVAISGGKKIDFLMMRTTEILFSLPRIPHIILLVIFHHGLLPLILAM
TITGWIPISRIIYGQFLLLKNKPFVLSAKAMHASTFHILKKHLLPNTLAPIISTLIFTIPNAIYTEAFISFLGLGIQP
QASLGTLVKEGINAIDYYPWLFFFPSLIMIALSISFNLIGEGAKTLCLEEGSHG

>core/553/5/Org5_Gene127

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VVAKTDEESRKIWREIHKNLKI KGSYIPISTYGSLMHPKSAALTLKTYRPHPIWINGYERSFNIDTGKYLKNGS
RRRTSHDGPKNRAVLNLIKSSGRRCAIGLEMTEEDFVIARRREGVYSLYPVEVCSYPQGNPFVIAIYAWIADE
SACSKEVLVPKGYYSLVWESVSSDSLNAFGDSFAEDYLRSTFLANGTSILCVHESYKKVPPQP

>core/554/5/Org5_Gene505

MFKKFKPVTGTRQLVLPADFELTTRGELRGTKSKRSLRPNKLSFFKKSSGGRDNLGHISCRHRGGGAKQL
YRVVDFKRNDGITAKVVTVVEYDPNRSAYIALLSYEDGEKRYILAPKGIQRGDVVVSSEGSPFKPGCCMTLK
SIPLGLSVHNIEMRPSSGGKLVRSAGLAAQVIAKSPGYVTLKMPSGEFRMLNEGCRATIGEVSNADHNLRV
GKAGRRRWMGVRPTVRGTAMNPVDHPHGGGEGRHNGYIPRTPWGKVTGLKTRDKNKSNKWIVKDRRK

>core/556/5/Org5_Gene510

MASIHPTAIIPEGAKIGKDVVIEPYVVIKATVTLCDNVVVKSAYAYIDGNTTIGKGTTIWPSAMIGNKPQDLKYQ
GEKTYVTIGENCEIREFAIITSSTFEGTTVSIGNNCLIMPWAHVVAHNCTIGNNVVLSNHAQLAGHVQVGDYAIL
GGMVGVHQFVRIGAHAMVVGALSIGIRRDVPPYTIGSGNPYQLAGINKVGLQRRQVPFATRLALIKAFKKIYRA
DGCFFESLEETLEEYGDIPVKNFIEFCQSPSKRGIERSIDKQALEEESADKEGV LIES

>core/557/5/Org5_Gene555

MSDFSMETLKTLRQQTGVGLTKCKEALEACGGNLEEAVVYLRKLGLASAGKKEHRETKEGIIAAKTDANGT
ALIEVNVETDFVANNAVREFVSNLLNDILKYKVDTVEALSQAASSQDPSLSVDELRAVTMQTVGENIRISRV
AYFPKATNSTVGIYSHGNGKTVALTMLSGSSTADSLAKDIAMHVVAAPQFLSKESVPAEIAIAKEKEVIASQI
QGKPQEVIEKIVTGKLN TFFQEAC LLEQPFIKNADLSIQSLIDDFSKTSGSSVAIEQFILWKIGA

>core/558/5/Org5_Gene512

MLERTQRTLKREVRYSVGIHLGKSSTLHLQPAQTNTGIVFQRQSASGNYENVPALLDHVYTTGRSTTL SRG
SAVIATVEHLMAALRSNNIDNLIQCSGEEIPIGDGSSNVFVELIDQAGICEQEDKVSIA RLTRPVYYQH QDIFL
AAFPSDELKISYTLHYPQSSTIGTQYKSLVINEESFRQEIAPCRTFALYNELCFLMEKGLIGGGCLDN AVVFKD
DGIISRGQLRFADEPVRHKILDLIGDLSLVGRPFVAHVLA VSGHSSNIAFGKKILEALEL

>core/559/5/Org5_Gene604

MATAHLGRQALLHLRSWTPAIRASGNLFRQQSMSLHNNVLFAGDIVGAIKNSTAISRHALGSSHYAHAALQK
TEGFLGAADGVNTAVAGAMLWGQLLNGSMIFETDEETGELRRCNEADAEGCMTQKLQRRSALTITGKVAR
LASKTLGTATFLHEMDVVS LGANANKIGCKVTSCNLVATGCSL TESSISLYRILSTRPETISDPENRNKPSAEF
AARSKAIRNAFI AWLGDVVDLVCDALGTLSLFLPAILGVHAVLIMAILGLISCVIN FVKDYAKIG

>core/560/5/Org5_Gene197

MVLMNKRLKIILTNDGITA KGMSCLVSALLEANIGDIYIAAPQAEQSGKSMAISLNQVVCASPYAYPQPVKE
AWAVGGSP TDCVRLGLRTL FESVSPDLVISGINCGNNICKNAWYSGTIGA AKQALVDGIPSMALSQDNHISFF
QQDKAPEILKALVIYLLSQPF PCLTGLNINFPTSPGGSSWEGMRLVPPGDEFFYE EPQYLGSVNKNQYYVGKIS
GVRIGEHPSEELACMLENHISVSPIFSQNSPIGLMTLEEFQKTQENFNASLLSSELT TKIF

>core/561/5/Org5_Gene562

MELKKTAESLYSAKTDNHTVYQNSPEPRDSRDVKVFSLEGKQTRQEKT TSSKGNTRTESRKFADEEKR VDD
EIAEVGSKEEEQESQEFCLAENAFAGMSLIDIAAAGSAEAVVEVAPIAVSSIDTQWIENIILSTVESM VISEINGE
QLVELVLDASSSVPEAFVGANLTLVQSGQDLSVKFSSFVDATQMAEAADLVTNNPSQLSSLVSALKGHQ LTL
KEFSVGNLLVQLPKIEEVQTPLHMIAS TIRHREEKDQRDQNQKQKQDDKEQDSYKIEEARL

>core/563/5/Org5_Gene834

MLWGVSMRQSFDELSQNAFKNIFNKQRFCFIFCSLCCFGFVFALFLKLCSRLAPEISLSTLGLGAFFCAFSVICA
SAIIVQFLLHKESQGETSKLCCAIAKNTWSSLWLSLLVSMPPFIAMVAVVTVAMLSSFLGSLPWVGKLFHTVLIF
IPYLSATALILLFLGSFSCFFCIPVLHNQESIDYRKLLCEFRGNILRQFIGVVIALVPLALCSWLALDSFYLMTH
LVEIADIHTWSFLAQMFVLIVPIALILTPAVSFFFNFSSFYLAKEEEKALVK

>core/564/5/Org5_Gene890

MHKVIVFIFLTLYSLKSYGNDVIDKPHVLVSIAPYKFLVEQIAEETCFVYAIVTNHYDPHTYELPPQIQIKELRQ
GDLWFRIGEAFEKTCERNLTCQQVDLSQNVSLIQGKPCCNQHTTNYDHTWLSPKNLKVQVETIVTTLSKKY
PQHATLYQSNGEKLLLALDQLNEEILTITSAKQRHILVSHGAFGYFCRDYNFSQHTIEKSSHVEPSPKDVAR
VFRDIEQYKISSVILLEYSGRRSSAMLADRFHMHTVNLDPYAENXLVNLKTIATTFSSL

>core/565/5/Org5_Gene487

MYFTRDPVIETVITSREGYKLSVRNTKHFSQDPFMVEAIEVISLGNICFFRNCDHSPFLVPAGDYEVMVRDT
KINLKAVGLDRGVKIAAGGREALIKLTKSTPLPVIDEKPLADSP EEGTEPTSPSKKEKKEARKDSFKGEKWKEK
KKLSRRRNHKEIAEVTGASQEILDTVKEELWEESQENEIVEQKKFSLPPP AKLISEVISQTVVDPVVT SADLN
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>core/566/5/Org5_Gene861

MTRSSPAQLSRFLSEIQNKPKKSLSQNFLVDQNIVKKIVATSEVIPQDWVLEIGPGFGALTEELIAAGAQVIAIE
KDPMFAPSLEELPIRLEIIDACKYPLDQLQEYKTLGKGRVVANLPYHITTPLLTKLFLEAPDFWKTVTVMVQD
EVARRIVAQPGGRDYGSLTIFLQFFADIHYAFKVSASCFYPKPQVQSAVIHMKVKETLPLSDEEIPVFFTLTRT
AFQQRKVLANTLKG LYPKEQVEQALKEGLLLNVRPEVLSLNDYLALFHKMQAG

>core/567/5/Org5_Gene554

MESQSCKLTIKDLMSAGAHFGHQTRRWNP KMKLYIFEEKNGLYIINLAKTLQQLRNALPHIRKVIQDNKTVL
FVGTKKQAKCVIREAAIEAGEFFIAERWLGGMLTNMTTIRNSIKTLDKIEKDL SRNQAYLTKKEAALLAKRH
QKLLRNLEGIRYMKKAPGLLVVVDPSYEKIAVAEAKKLGIPVLALVDTNCDPTPIDHVIPCNDDSLKSIRLIIN
VIKENIIEAKHKLGIEIVSPVKSLEV PDL SAFESSQDDDESDEENREEDLLAKKFDGEAN

>core/569/5/Org5_Gene668

MTANTFGTLDILMKH SKEDDL SRFLPKNLLVESPHPEEIPLKSLSFTMSWLPTIHPSWITIAMKEFPPEIQGQLL
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YSIAKELKHILDKVVIERVKNALSPTEKLFLTYCQSHPMKHLETTNFLSSWTTDAELRQFVHKQGLEFLGKAL
TKENASFLWYFLRRLDVGRAYIVEQTLK TWYDHPYVDYFKSRLEQCMKVLVK

>core/570/5/Org5_Gene402

MDYKLLDSGDGNKLECFGPVTLIRPSSIAVWP KSRPELWSQAQLQYVREGERGAWKNFKRLPEEWEVAFSD
VRCLLKRTPFGLGVFPEHMGFWPALKQAIEKHKERQVLNLFAYTGAGSIFAAKCGARVTHVDASQA AVR
WAQRNVEKNAFPERRIFWVIEDVISFLKKEIRRNK KYQVILLDPPSYGRGPDGEVFKIDKDLFPLLSLCSKLLA
DDASYFLLTSHTPGHTPEFLRAIARRSVPTLVSEAWSCGESFCGEGVGALPSGSFVQWIA

>core/571/5/Org5_Gene114

MITGVVLEKHEQRTMFSLTLLNNFTTFGLLHTPLHYNPPYPIVILLHGLASDKTGSKRSHVRLAQELTRLGIAA
LRVDLLGHGDCEGELMDFSLENYKQNIREIIEYTHSLLHIDQERLAIFGSSLGGTLALQTLPPFNKIKALAVWA
PTISGELMAAEAQKNAPEVITMSQKGAITYAGMTLNPDFYTQFLKIDIVKELMPSARNLPPILYMQGEQDLLV
SINHRTLFTFAFANQDKPITILTYPDVDHAFPPFAESSALSDLTQWLKRELTSGE

>core/572/5/Org5_Gene581

MLLGFLCDCPCASWQCAAVANCYDSVFMSRPEHKPNIPYITKATRRGLRMKTLAYLASLKDARQLAYDFLK
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PTCASCISIGTMMRLNARRYTTVIIPTFIDIAKHLHTLKKRYPGYQILFAVTACELSLKMFGDYASVMNLKGVG
IRLTGRICNTFKAFKLAERGVKPGVTILEEDGFEVLARILTEYSSAPFPRDFCEIH

>core/573/5/Org5_Gene874

MRRYLFMVLALCLYRAAPLEAVVIKITDAQAVLKFAREKTLVCFNIEDTVVFPKQMVGQSAWLYNRELDLK
TTLSEEQAREQAFLEWMGISFLVDYELVSANLRNVLTGLSLKRSWVLGISQRPVHLIKNTLRILRSFNIDFTSC
PAICEDGWLSHPTKDTTTFDQAMAIEKNILFVGSLKNGQPMDAALEVLLSGISSPPSQIYVDQDAERLRSIGAF
CKKANIYFIGMLYTPAKQRVESYNPKLTAIQWSQIRKNLSDEYYESLLSYVKSKG

>core/574/5/Org5_Gene71

MLLIYCKKKEIHLQWPQTAKIRFTPKIAMKVKINDQLICIPPFISARWSQIAFIESQEGENKDQGTLLRLHLIDGKI
ISIPNLDQSIIDIAFQEHLLYLETSQSGKEDSRDDDKLGVGVLNMVLLQQITKGNDIQVLPKNLISPLFSGTNPIEA
ILQHTPEHKDHPDAPTDVLEKMADVIRVLSGNNATLLPRPEPHCNCMHQCIGRVMNEEDTLAVSDKDLTFR
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>core/575/5/Org5_Gene299

MKLLKNVLLGLFFSMSISGFSEVKVSDTFVKQDTVVEPKIRVLLSNESTTALIEAKGPYRIYGDNVLLDTAIQG
QRCVVHALYEGIRWGEFYPLQLCKIEPVDDTASLFFNGIQYQGSLYVHRKDNHCIMVSNEVTIEDYLKSVL
SIKYLEELDKEALSACIILERTALYEKLLARNPQNFHWVKAEEEGYAGFGVTKQFYGVEEAIDWTARLVVDS
PQGLIIDAQGLLQSNVDRLAIEGFNARQILEKFYKDVDVFVIESWNEELDGEIR

>core/576/5/Org5_Gene212

MKKKLSLLVGLIFVLSSCHKEDAQNKIRIVASPTPHAELLESQEEAKDLGIKILPVDDYRIPNRLLLDKQV
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EECGLIVCKGPANLNMTAKDVCCKENRSINILEVSAPLLVGSLPDVDAAVIPGNFAIAANLSPKKDSLCELDL
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>core/577/5/Org5_Gene361

MVRDIQSESIGKLVFLGTGNPEGIPVPFCSCRVCQNTGIHRLRSSVLIQYQNKTLVIDAGPDFRTQMLVAGVSE
LDGVFLTHPHYDHIGGIDDLRAWYIVTQRSPLVLSASTYRFLNKAKEYLFATPNVESSLPAVLEFTILNEDCG
QEEFQGIPYTYVSYYQKSCHVTGFRFGNLAYLTDLCSYDAKIFSYPDNDVETLILSAGPSETPIPFQGHKSSHLT
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>core/578/5/Org5_Gene735

MIIKNNELMIRRFKTLFPPGPQYSLCYASILIVLSSLVCVPTFCWLFLPELSLSKFNPSPIRNLFLVSSTLSKVPP
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FLGQPYFPSLNLPIFFSQEDLKMQKLPKEKMLFTKILLKELAMESPKIIDLSLSDAYPGEIIVTLSSGSLLRLPIK
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>core/579/5/Org5_Gene578

MFNNKMILIAGPCVIEGEDITLEIAGKLQSILAPYSDRIQWFFKSSYDKANRSSLNSFRGPGLTEGLRILAKVKE
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GNNKILLTERGCSFGYNNLVSDMRSIPVLSRSGFPVIFDATHSVQLPGALSTESGGLTEFVPTLSRAALAAGAH
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>core/580/5/Org5_Gene888

MTKVALLIAYQGTAYSGWQQQPNDLSIQEVISSLKKITKTRTPLIASGRTDAGVHAYGQVAHFRAPDHPLF
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GANLLIGTHDFASFANHGRDYNSTVRTIYTLDIVDKGDSLSIICRGNGFLYKMMVRNLVGALLDVGKGAYPPE
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>core/582/5/Org5_Gene966

MTQYYFLSSFLPTQLPESVPLFSISDLDDLTYLNLSENDLCNYGLLKRFFDFENFAFFWAGKPIPFSGEVTQE
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AGFRARVLNMDVSYVLRDEDDSDPVVLEVLMMQKDSPNYELPEEFSDLQGVLDYGLLPHTLNRALALYQFH
KLEGFCSDSYFDGNVILARCATYMFAIRNSLASVEKGREIINHIEKAIKW

>core/583/5/Org5_Gene135

MHSKFLSRRKKNSSHKEETSWDCIASSYNKIVQDKGHYYHRETILPQLPSLTLGSKSSVLDIGCGQGFLERA
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EPLGQFFIVLNHPCFRIPRASSWHYDENKKAISRHDYRLSPMKIPIMAHPGQKDSPSTLSFHFPLSYWFKELSS
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>core/584/5/Org5_Gene1009

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EQCLEIPLEDGSLPLQNSPMNLDFEDANPYSQSDWEALTHEQKLYALRATIAEKIGPYIAMDGGEVTVESLEN
FIVTIAYSGNCSGCPSSLGSTLNSIGQLLRAYIYPELQVKVDESSLNLSHP

>core/585/5/Org5_Gene712

MQGFFPLASGSKGNSAYLGTDSCKILIDLGVSKQVVTTRELLSMNIDPEDIQAIFVTHEHSDHISGIKSFVKAYN
TPIVCNLETARALCHLLDSHPEFKIFSTGSSFCFQDLEVQTFNVPHDAVDPVAFIFHYREEKLGFCITDLGWVTS
WITHELCDYLLIESNHSPELVRQSQRPDVYKKRVL SKLGHISNQECGQLLQKIITPKLKKLYLAHLSTECNT
AELALSTVSESIASITSIAPEIALAQGITSPIYFSRLEVACPR

>core/586/5/Org5_Gene795

MAGLDLEARGKRRVVTNPNAITAFGLCCGLFIIFKSVLRTSSSVELFHRLQGLSLLLISAMIADFSDGAIARIMKA
ESAFGAQFDSLSDAVTFGIAPPLIAIKSLDGIYVGNFFSSLLITSIIYSLCGVLRRLVRYNLFSQKTVDVSKPYCFI
GLPIAAAASIVSLALFLASDFFPDLPALQRLVGLLSFALLFIGGLMISPWKFPGVKHFREFNVSSFLLVVTIGLAA
CLFFSGLVDHFVEVFFLVSWLYTLVGFPIFSIIYRKKS

>core/587/5/Org5_Gene21

MKKPDNDSTFDVRSFFPFDVLCIEQLRKEMSWEVVSAKIPRLPRGWYELMGLSKEDRIDFCLDFWC SVLGIE
HKESPSICRFFSLLETIEVYIYRLEKEPYQLKMFYVFRDGRGCGFQGEPLLDLFLGHHRLPPLGDRHYEKFFSIHN
GFGKWEDEGIFPMRSLAKVQQKL RQQLVVMNKMQAEDNCYSLGIFPFYGYEFPAYQSFFFDPEIRRDLPSP
NVLLNEESLEHRSLETIELLHLSKSYYP SFLSWLENYLHSEEVYNE

>core/590/5/Org5_Gene401

MDCIGKHNPLVKEALALKRSRCRKSSWFLVEGAREIQKALRTGYLCQHVCSTHLSEKEKEFLYELKRNSTK
ILYCLDSTLAQLSFKEHDSFVAVIQKRVWNKEDFLIQRKNAQPFYLIIEQVEKPGNVGAILRIADGAGVDGVI
LCNPIVDLYNPNVVRSSLGAVFSLPILSISREEGKELFKQEGWTVFVTSPRAETMYFSKNYLGPTALVFGSEKD
GLTEDWFSEDFSEIALPMLGESDSLNLATSVA AVAYEVVRQRWVN

>core/591/5/Org5_Gene851

MGSSMHVGVIGCSGRTGKVIVSALEQSSEYTLGPGFSRSSALTLFQVIAHNDVLVDFSHPLL TKEVVAHLLISP
KPLIIGTTGFP GKCKEAHDSLEELTHIVPVVCPNASLGAYIHKRLVMLLSQLCNPQFDIRIRETHHRYKKDSL
SGTAQDLLDTIQVKQEDWGEEYEVGQRDSSKKTIEVQSSRVGDIPGEHEVAFISSGEQILVRHTVFSRNVFG
RGILSILDWLKTLNPQPGLYSLGDTLELVLRNEHCLLKKTDDH

>core/592/5/Org5_Gene620

MEKLEFVTSLSPPDDDLITFNKQGLIAGPEEEKVAFLVRSNAMLDAGPETPASFPESLREQFDIFPEYVEVLYS
NEGLDVWEAGCTWILNNEVTIQLRKHHRKASRWLGMYSRDEVLAHEAVHAVRMKFHEPVFEEVLAYQTSR
WGWRRFFGPLFRSPGESYLLFFTILGLGISLWYPAGILIMLVLP MYFLMRLCMAQSYLYRAMKKIRKMLGV
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>core/593/5/Org5_Gene895

MSNQLQPCISLGCVSYINSFPLSLQLIKRNDIRCVLAPPADLLNLLIEGKLDVALTSSLGAISHNLGYVPGFGIA
ANQRILSANLYAAPTFFNSPQPRIATLESRSSIGLLKVL CRHLWRIPTPHILRFITTKVLRQTPENYDGLLLIGD
AALQHPVLPGFV TYDLASGWYDLTKLPFVFALLHSTSWKEHPLPNLAMEEALQQFESSPEEVLKEAHQHTG
LPPSLLQEYYALCQYRLGEEHYESFEKFREYYGTLYQQARL

>core/594/5/Org5_Gene324

MKLTKYLNTKQLRSMISRLFVRYSLPMSKQLSFFALCVLGSHPIFAQTPNPPQRRVRSEVIFIDPGHGGKDQGT
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GTEVYFYNGKVGSPTRNRMSEVLGKNILAAMEKNGILKSRGLKTANFVVIRDTSM PAVLVETGFLSNSRERA
ALQDARYRMHVAKGIAEGVHNFLSGPSFQKPKQNI AKIRKPQIQAN

>core/597/5/Org5_Gene67

MPFDITYYTTPLLEIILIWVMLNYLLKFFWGTRAMDVVFGLLAFLFLVLADKLHLPIIRRLMLHVVNIAAIVV
FIIFQPEIRLALSRIRFHGKKFFIDTQEQFVEQLAASIYQLSERQIGALVVLENKDSFDEYLSFSSVKINATFSEEL
LETIFEPSSPLHDGAVILRGDILAYARVVLPLAHDTTQLSRSMGTRHRAALGASQRSDALIITVSEENGSVSLSR
DGLLTRGVKIDRFKAVLRSILSPKEHKRKPFSWIWKR

>core/599/5/Org5_Gene146

MTTLLSIKDLSTIRGKKILNHINLNLIKGSYLTIVGPSGSGKSSLALTILDLLKPTTGTITFHMDPKIPRARKVQ
VIWQDIDSSLNPCMSIKGIISEPLNIIGTYSKAEQNKEIYNVLDLVNLPKSVLHLKPYKLSGGQKQRIAAKALV
SKPELLICDEPLSSLDTLNQLSLDLFQTIKKEYQNTLLFITHDMSAAYYIADTIAVMDQGSLVEHACREKIFST
PKHTTTQDLLDAIPFSLISTEMEPSEEYELQVASK

>core/600/5/Org5_Gene838

MKTWLFFFTFLFSCSSFYASCRYAEVRSIHEVAGDILYDEENFWLILDLDLDDTLLQGGEALSHSIWWSKAIQGLQ
KQGTPEQEAWEAVVPFWIEIQEMGTVQPIESAIFLLIEKIQKQKGTTFVYTERPKTAKDLTLKQLHMLNVSLE
DTAPQPQAPLPKNLLYTSGILFSGDYHKGPGLDLFLEICTPLPAKIIYIDNQKENVLRIGDLCQKYGIAYFGITY
KAQELHPPIYFDNIAQVQYNYSKKLLSNEAAALLLRHQMH

>core/601/5/Org5_Gene1064

MHSELKATQEDELCELFRTIALPSKGYVRIKLVLSPNGEIQECSFLSEVSAADKQLLTQRIHALPFQKFLEKY
KVSKNISFHIKLVSNES

>core/602/5/Org5_Gene634

MDLADAHVHLSDDAFEEDINSVLQRAQDSGVSLVVNVTTTEKELNRSFAYAERFPKIRFCHVGGTPPQDQDQ
DIEEDYRNFHAAAHSKKLAAIGEVLGYCFATEEGIARQKEVLQRYLALSLECELPLVVHCRGAFNDFFRML
DQYYHNDPRSRPGMLHCFTGTLEEAQELISRGWFISISGIVTFKNAQDLRDLVVELPLEHLLIETDAPFLAPVP
YRGKKNEPAHVLHTINAVANVKGMFPQELAAALAYKNVLRFLHG

>core/603/5/Org5_Gene16

MFLQFFHPIVFSQSLSLPYLGKSSGIIKCSNIVEHYLHLGGDTSVIITGVSGATFLSVDHALPISKSEKIIKILS
YILILPLILALFIKIVLRILFFKYRGLILDVKKEDLKKTLTPDQENLSLPLSPPTTLKKIHALHILVRSGKTYNELI
QEGFSFTKITDLGQAPSPKQDIGFSYNSLLPNFYFHSLVSVPNISGEERALNYHKEQQEEMAVKLKTMQACSF
VFRSLHLPMSQTKDKKAGFGLLTFFPWKIYPL

>core/605/5/Org5_Gene319

MILTAAFSPCPNDIFLFRSFLKDPQFRPLLNQVTIADIETLNTLALQRRLSLMKMSAALFPLVSDYYNLMDSG
NTLGYNSGPIVLSLDPECSLDTLATPGEMTTAHALCKLYYPKAKLIPMPYDKILSAILQGKVDGGALIHEERFS
YDLQLTLRADFGELWRRKTIFPLPLGCLAIAKYVPMATVDALTAALRKSILCSLKDPITAGAKAVEYSKNKN
VTVIHRFIGTYINKETFQLSKTGKKALHMLWKANECQYT

>core/606/5/Org5_Gene899

MIKQIGRFFRAFIFIMPLSLTSCESKIDRNRIWIVGTNATYPPFEYVDAQGEVVGFIDDLAKAISEKLGKQLEVR
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QEHYLLSQPGICVRSFDSTLEVIMEVRYGKSPVAVLEPSVGRVVLKDFPNLVATRLELPPECWVLGCGLGVA
KDRPEEIQTIQQAITDLKSEGVISLTKKWQLSEVAYE

>core/607/5/Org5_Gene90

MLRNQVLVYCSEGVSPYYLRHTIRFLKYYSTQEGAFDILRVDGNFLIKNPFWEETTRLLVFPGGADRPYHRV
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RVSPQLFSDFLGYAMFNGGCFEGSEGYPGVNIESRYDDLPGKPASIVSRIVSKGLAVLSGPHIEYLPHYCR
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>core/608/5/Org5_Gene264

MNVKDETFWSVHNLCVNYEHA AVL YHISFSLGKGSLTAILGPNGAGKSTLLKASLGLIKPSSGT VYFFNQKF
KKVRQRIAYMPQRASVDWDFPMTVLDLALMGCSYKGMWGRISSDDRREAFHILERVGLSVADRQIGQLS
GGQQQRAFLARALMQKADLYLMDELFS AIDMASFKTSVGVLQELRDQGKTIVVVHHDLSHVRQLFDHVVL
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>core/609/5/Org5_Gene521

MNRRWNLVLATVALALSVASCDVRSKDKDKDQGSLVEYKDNKDTNDIELSDNQKLSRTFGHLLARQLRKS
EDMFFDIAEVAKGLQAELVCKSAPLTET EYEEKMAEVQKL VFEKKSKENLSLA EKFLKENS KNAGVVEVQP
SKLQYKIIKEGAGKAISGKPSALLHYKGSFINGQVFS SSEGNNEPILLPLGQTIPGFALGMQGMKEGETRVLYI
HPDLAYGTAGQLPPNSLLIFEINLIQASADEVA AVPQEGNQGE

>core/611/5/Org5_Gene1018

MMENLETFILKIYRGVPGKQYWESFELPLHPGENVISALMEIEKRPVNILGEKVNPVVWEQGCLEEVCGSCSI
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QQELLYALSQCMT CGCCTEACPQIDNKSDFIGPAAISQARYFNTYPGDKQSKKRWRALMGKGGIEGCGQAH
NCVRVCPKKLPLTESISAVGREISKFSLRSLFSALFKKKK

>core/613/5/Org5_Gene308

MSKFILLLSLGVAALASKNFFIWPAPSGKTPLKLRQVLFGGALLVFSSLVALSVSSQTAELLSTMTGISLAF AF
LFYLLFLPKDITRAILFSGERPVKTSWRALGSAIRMWIIIPVTQLIGIMMSKFLTLVLPTQEIH TQEVTQEVQNS
LPITGHYISMILNLGVLT PFGEEVFFRGILQTFLKNKMTRIAAVLCSSIIFSFIHIEHSLGSWVFVPVLFVFSLSAG
FLYEKDRHILSPIALHGLFNLTSLFLGIK

>core/614/5/Org5_Gene392

MAFYSPSTISKYFIYSGAGNRFLGETLPEVEDVRFLCQETRVDGFLYLKPSSCADAQLIIFNSDGSRPTMCGN
GLRCAIAHLASQKGKSDISVSTD SGLYSGYFYSWDRVLVDMTLADWRASVHRLESRPDLPKEVVCIHTGVP
HAVVILPEISTLDLSILGPFLRYHQTFSPDGVNVNFVQILGHCQLRVRTYERGVETAACGTGALASALVVS
NSYGWKESIQTWGGELMTVSQNRGRVYLQGSVTRDL

>core/615/5/Org5_Gene92

MFKLLKNLFLIGCCIVGYFWMRKESIVEQWLSNRLHTQVTVGRVSIRTSGIKIRHICIHNP LASERFPYAAEIEY
ADVRFSSISMLLTKQLEISELIIHGANFTIFPYDSHGTKTNWSLVWKNFHPQKETPSNLWIDRAPVLIRRCLFLN
TRL YGLRANH KDIPHLSVPSLEFHSHTSSAKELPKLSEALPSLLYLAL EESLYHLNLP GDIIKPLSQQA HKHFYS
SYPQFQDRLNDINTPGTPT EEIIGFIRGLFFH

>core/616/5/Org5_Gene73

MVSPLSLFHKMLLENWTPVEEPFPWPPAEKNQKIFAWALNQSKLIFVSTSGNIAQPRLVTDSMSMMIVNAAN
RTMSRDGAGTNQVL SAAVSVD SWGLSQRPLNPERQGTPLNEGECRAGMWRNADGSNHTGKQGKPHYLAQ
LLGPKAVDHHNKSQA AFDRCKNAYLNCFSLAQTLGVTF LQIPLISSGIYAPPENRKKPNSEENKVRMRWIHA
VKCALVAAMQEFGN EPGNTDRRMLIVLTDLKTPAITDPKKKSHL

>core/617/5/Org5_Gene274

MKTQQTQNIIEVWNFYWETQEIEYRDSLIEFYLPVKSVVHRLISGMPSHVKTEDLYASGVEGLVRAVERYN
PERSRRFEGYAVFLIKAAIIDDLRKQDWVPRSVHQKANKLSGAMD SLRQSLGKEPTDLELCEYLNISQQELSG
WVFSARPALIVSLNEEWPSQSDEGAGMALEERIPDERAETGYDVVDKQEFSLCLANAIQELEEKERKVMALY
YYEELVLKEIGKVLGVSESRVSQIHSKALLKLRAALSAFR

>core/618/5/Org5_Gene337

MWL GAYTWLNVFGILLQAAFIQNILLANFLGMCSYLACSTRVSTANGLGMSVALVLTVTGSINW FVHAFITG
PKALTWISPSLASVNLGFLELIIFIVVIAAFTQILEL LLEKVSRLYLSL GIFLPLIAVNCAILGGVLFGITR SYPFIP
MMIFSLGAGCGWWLAIVILATIKEKLAYS DIPKNLQGMGISFIT TGLIAMAFMSLTGIDISKPSAKIQRAPLETE
VVENTTNPLKESSSKHQPSISKARTQRRSL

>core/619/5/Org5_Gene550

MLKIKHLHASCNDVKILDDFN LNIQPGTMHVIMGPNGAGKSTLAKILAGDESVLVSSGEIALQEQNLLSMLPE
ERSRAGLFGVGFQMPPEIPGVN NKMFLRDAYNARRRANQEGDISIDEFNTLLSTVLETYEYNATTDLFLDRNV
NEGFSGGERKRNEICQMLVLEPEMVLLDEPD SGLDVDALRLICRVLEKYRELHPTSSLCIVTHNP KLGNLIRP
DVVHLLLDGRVALSGDVSLMHELEAKSYQEVTKRVAWR

>core/621/5/Org5_Gene648

MKTIAVNSFKGGTAKTSTTLHLGAALAQYHQARVLLIDFDAQANLT SGLGLDPDCYDSLAVVLQGEKEIQE
VIRPIQDTQLDLIPADTWLERIEVSGNLAADRYSHERLK YVLG SVQDKYDYVIIDTPPSLCWLTESALIAADYA
LICATPEFYSVKGLERLAGFIQGISARHPLTILGVALSFWNCRGKNNSAFAELIHKTFPGKLLNTKIRRDITVSE
AAIHGKPVFATSPSARASEDYFNLT KELLILLRDI

>core/622/5/Org5_Gene982

MTRQSYVLGNWKM HKTIQEAK EYVQTLASLLQGEPLSCTIGIASPFTSLRAIHEMINTTG AFLWLGAQNVHP
ELSGAFTGEISLPMLKEVGVEFVLVGH SERRHIFGESDAFIASKVKSVAQAGLVPVLCVGESLEVREEGKAHQ
VIKKQLLLGLEQMDNGSEFLIAYEPVWAIGTGKVAEASDVQDIHMFCREVVAERFSEATAEEISILYGGSVKV
DNAQRFGQCSDVDGLLVGGASLEGQSFFEVAKNFNV

>core/623/5/Org5_Gene397

MHDALLSILAIQELDIKMIRLMRVKKEHQKELAKVQSLKSDIRRKVQEKELEMENLKTQIRDGENRIQEISEQI
NKLENQQA AVKKMDEFNALTQEMTTANKERRSLEHQLSDLMDKQAGGEDLIVSLKESLASTENSSSVIEKEI
FESIKKINEEGKALLEQRTELKHATNPPELLSIYERLLNNKKDRVVVPIENRVCSGCHIVLTPQHENLVRKKDRL
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>core/624/5/Org5_Gene177

MKPEESECLCIGVLPARWNSSRYPGKPLAKIHGKSLIQRTYENASQSSLLDKIVVATDDQHIIDHVTDFGGYA
VMTSPTCSNGTERTGEVARKYFPKAEIIVNIQGDEPCLNSEVVDALVQKLRSPEAELVTPVALTTDREEILTE
KKVKCVFDSEGRALYFSRSPFILKKATPVYLHIGVYAFKREALFRYLQHSSTPLSDAEDLEQLRFLEHGGKI
HVCIVDAKSPSDYPEDIAKVEQYITCLSNAYF

>core/625/5/Org5_Gene746

MLIKLWRATYEGMYTFLVGALLKLRYRMQVEGWDTLNINPKQGCLFLANHVAEVDPIILEYLFWSRFHVRP
MAVEYLFHSRVVQWFLNSVRSIPIQLVPGKESKRSLERMNVCYEEASRALNRGESLLLYPSGRLSRTGKEEI
VNQYSAYVLLHRVMECNVVLVRVSGLWGSAFSRYKQNSTPKLGPAFKEAFRALLRRGIFFMPKRFVKITLC
QVDHLFLKQFPTKQDLNTFLASWFNQGDDNLPIEVPYA

>core/626/5/Org5_Gene456

MQICVTGVVLRSRPLGKNHTLTTLFTPEGLFTFFAKQGQTLQCDYRETLVPISLGKYTLHRNGSRLPKLTHGD
ILNAFEAIKQTYALLEASGKMIQALLASQWKEKPSHKLFSLFLNFLHRIPESSNPEFFAAIFVLKLLQYEGILDL
TPACSLCKASLPYACYRYQGHKLCKKHQHKQAISIEKEEQILQAIHAKQFSELLAIAEFPIAIAEKIFYLFDL
QEEKKSERNSSDPYHEILRLSKVVHPY

>core/627/5/Org5_Gene547

MLIVLAFRQVFFSHSRSQLDRLKKNYLRLLLKQNFALTLPKERTSKGHSLMLTFDFASFDFYTNIFPFLEEQKIPAV
VGVASRYIPSNAAQDLHPSHRLKPSETLAFQDEIFSNYMPFCCQNELIEMAKSPYIQLASSGFAIRNLMNPPY
LTTEILLSRHIIETITGAKPLAFLFPFGKSDPTSRKLAADHYPYSFLLGNTINRKLKTHNIYRLDIKPMQYVCPS
LFQSSRYLKNWIKESKQLYLKKQLPKR

>core/628/5/Org5_Gene150

MLMDISHILEDLAYDEGILPREAIEAAIVKQMQITPYLLHILHDATQRVPEIVNDGSYQGHLYAMYLLAQFRE
SRALPLIIKLFAFEDDTPHAIAGDVLTEDLPRILASVCNDDSLIKELIETPKINPYVKAA AISGLVTLVGAGKIPR
DKVIRYFAELLNRYRLEKQPSFAWDNLIAGICTLYPGELFYPISKAFDGGLVDTSFISMEDVENIIHEETVESCIH
TLCSSTELINDTLEEMEKWLED FPIEP

>core/629/5/Org5_Gene96

MNVADLLSHLETLLSSKIFQDYGPNGLQVGDPQTPVKKIAVAVTADLETIKQAVAAEANVLIVHHGIFWKG
MPYPITGMIHKRIQLLIEHNIQLIAYHLPLDAHPTLGNNWRVALDLNWHDLKPFGSSLPYLG VQGSFSPIDIDS
FIDLLSQYYQAPLKGSALGGPSRVSSAALISGGAYRELSSAATSQVDCFITGNFDEPAWSTALESNINFLAFGH
TATEKVGPKSLAEHLKSEFPISTTFIDTANPF

>core/630/5/Org5_Gene76

MKKQGKTLFLFLSFLSTAFSGLFASQTSSLRTIQENIFLAKTGDYTVLSRGSQRTFVLVKSTTPKTVWIEIIH
FPCIAHKERPSLEQASWKTVIHQLESQSQVFVVSLSSEGSQFFSLNTRTKSLEPVGKSTTVPAFLQIFDLPLSPAP
ANVIKTKGKENKPWSPKVSFEGAPLTSISVNAWQGLWPKDRGPLSETGILMYFTQPDISVFPLWVSIETPKGT
SIVRAVDIGHGATSPYVYSLPDSKTQ

>core/632/5/Org5_Gene434

MSLATNNAESKFPSLQRLPNHVAIIMDGNRRWYKKHREECGHTHTSGHYYGAKVLPNILNAVLDLGIKVL
LYTFSTENFGRPKEEIQEIFNIFYTQLDKQLPYLMENEICLRIGDLSKLPKGIQTKINHVSMTASFSRLELVLA
VNYGGKDELVRAFKKLHVDILNKKISSDDLSESLISSYLDTSGLTDPDLLIRTGGEMRVSNFLLWQIAYTEL
YITDLWPDFTPQDLFEAINVYQQRSRRGK

>core/633/5/Org5_Gene647

MGNLKTLLSRFKKNTPTKMEALARKRMEDPSPLAVRLSNPTLSSKEKEQLRHLLQHYNFREQIEEPDLTQ
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EKMPRQAVYTLASRQGPQEKKEEIRNYRGERKSELLDRIRKEFPLVETDCRKTSPVKQALAMLTGKSQILTK
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>core/634/5/Org5_Gene469

MKIKFSWKVNFLICLLAVGLIFFGCSRVKREVLVGRDATWFPKQFGIYTSDTNAFLNDLVSEINYKENLNINIV
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VLVAQNIPDAVISLYQHVPIALEALTSNCYDALLAPVIEVTALLETAYKGRLKIISKPLNADGLRLAILKGTNG
DLLEGFNAGLVKTRRSGKYDAIKQRYRLP

>core/635/5/Org5_Gene515

MSLLKDTVFTCLDCEMTGLDVKKDRIIEIAAVRFTFDSVISSIEFLINPERVVSAESQRVHHISNAMLRDQPKIA
EVFPQIKAFFKEGDYIVGHSVGFDLQVLAQEMERIGETFLSKYTIIDTLRLAKEYGDSPNNSLES LAVHFNVPY
DGNHRAMKDVEININIFKHLCKRFRFTLEQLKQVLAKPIKMKYMPLGKHKGRCFSEIPLAYLQWASKMDFDS
DLLFSIRHEIKHRQKGTGFSQVNNPFMEL

>core/636/5/Org5_Gene226

MDITLVGKKVIVTGGSRGIGLGIVKLFLENGADVEIWGLNEERGQAVIESLTGLGGEVSFARVDVSHNGGVK
DCVQKFLDKHNKIDILVNNAGITRDNLLMRMSEDDWQSVISTNLTSYYTCSSVIRHMIKARSGSIINVASIVA
KIGSAGQTNAAAAGIIAFTKSLAKEVAARNIRVNCLAPGFIETDMTSVLNDNLKAEWLKSIPLGRAGTPED
VARVALFLASQLSSYMTAQTIVVDGGLTY

>core/637/5/Org5_Gene703

MTQDPHDHFKSRTPEDHIKHVRDKHRVCKGEPHTTFKGFFYHLANNALSTGVFIFFIRTLFFLIPTNRALQVKS
LISLGVGWTFYHGCLKARKAWAYMELSHRSMLEEKNEIEENFEQEKIELRILFENQGFKDPLLQEMVEYVCS
DSTLLDLMIREELYRKEDLPHPLIQGGSRLGGLCGLAIFLPLVLCISYTLAGVFSALMVLVLSFLKAKILKN
DKISEMVWVLGIFITSASIISSLMKLL

>core/638/5/Org5_Gene285

MTLSFHTHPLNYWTFEEFDGLPIRHGVFSKQKDAEGTVFAAKNPEIASALQSPKYCDLHQRHGTSVRCVTPT
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FVAIGPSIGPDYAIYPDYATLFPRSFLPFMNPKNHFDLRAIARKQLTNLGISKDRIFISDLCTYTEHDAFFSSRYL
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>core/639/5/Org5_Gene556

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>core/640/5/Org5_Gene55

MKFFILFILIVAQFPAFSAQPRTQVSASHSKQAKARRTSRIRSSAATNASVSRYKTRAAARKKIGKFEKKPSLSP
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>core/641/5/Org5_Gene471

MHIYGLADLHLALGVPEKTMEVFGDPWIGYHQKICSEWQAVVHPEDIVLLPGDISWAMNLSEAHKDFAFIG
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QSYTEQDEKIFLRELGRLLKRAFAALPKEVTEVIVMTHYPPISDGTGPISEFLEADGRVSLCLFGHHKVRPI
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>core/642/5/Org5_Gene1021

MKITTVKTPKIYPYDDLYSILESSLPKLNERSIVVITSKIVSLCEGAVVELEKVSKDELKQEADAYVFVEKYGI
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WNGFFPLYNYVGKPDGFRALKMTYSNLLDGLSAAAVLCMGEGDEQTPIAIIIEAPKITFHSSPTTLQDMSTL
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>core/643/5/Org5_Gene921

MDFDYFGLSDIGRVRARNEDFWQVNLMSQVVAIADGVGGRLGGDIASQEAVTSLMELIDEQQSKLMGYED
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ENQLKNRYGLPKQSDKVYSYRHILTNNVLSRPPYVMPDIRNLPCEKEDLYCLCSDGLTNMVPDIDIRDILNQPA
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>core/644/5/Org5_Gene411

MTIRILAEGLAFRYGSKGPNIIHDVSFSVYDGDFIGIIGPNGGGKSTLTMLILGLLTPTFGSLKTFPSHSAGKQTH
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QRVLLARALASYEILILDEPTTNIDPDNQQRILSILKKLNRTCTILMVTHDLHHTTNYFNKV FYMNKTLTSLA
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>core/646/5/Org5_Gene826

MSYFNYQKNSVVLRLSLGLLAKFFSRLLYRVFFSFREGIYLFSSLYLKYPRLFFYDLGKYVYSLRHCPYAKLGR
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MHRKLSSGFALFDTEEFKNVVLSQLASYVYFYGSSFSRLLNEIILKLSEMAPGSVVISISFPLDSFSRGKECFFT
EKSCSVRFPWGKTIAYKNIRKGS

>core/647/5/Org5_Gene196

MSTLLLNPPWMKAGKRIESLVRKALYTHTMLANHRKIVVALSGGKDSLTLMLKAISGRGFPDLDLHAVNI
GGKYSCGAENVKPYLTRICDQLCIPFRTIPSPYAPETPECYPCSQARRRLLFQAAKEIGASAIAGHHRDDLQV
TALLNLLHKAEFAGMLPVLDMVHFGVTILRPLIFTPEFWIRKFAKENG FARVTCRCPVVSLSKAEQSLKLL
EVFPLARHNIALAIQEHGSSKSQKI

>core/648/5/Org5_Gene206

MTDYSFFRRKIGNIEAIECPGNPQDPPIILCHGYGSLADNLTFFPSICSFSKLRPTWIFPNGILPLENDFRGSRA
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NPYAGALIFAGARLFNQGWEEGLKQCAQVPFLQSHGYEDEILPYHLGAHLNDLLTKLNGQFVSFHGGHEIP
SVVFQKMQVTPVNWIDPARG

>core/650/5/Org5_Gene580

MPILSVCNLVKKYNKKPVTNDVSFQINPGEIVGLLGPNGAGKTTAFYLTVGLIRPDSGKIIFKNVDVTKKTMD
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ACVLALNPSVLLLDEPFANVDPLVIQNVKYLIKILAGRGIGILITDHNAKELLSIADRCYLIIDGKIFFEGSSSQ
MISNPMVKQHLYLGDSFSY

>core/651/5/Org5_Gene343

MKVRIVDSGKSSAASHMAKDRDLLESQDGELILHLYEWENPCSLTYGHFMRPEKFLLSNYADLGLDAAVR
PTGGGFVVFHKGDYAFSVLMSATHPSYSSSVLENYHTVNSFVAKVLEKVFRIQGMLAPEDENSSSRDSGNFCM
AKTSKYDVLFGDKKIGGAAQRKVQQGFLHQGSLFLSGSSSEFYQRFLKPEVLEEIIIEQIQIHAFPLGLEAADE
VLQEARQQVKEAFIKLFCGEG

>core/652/5/Org5_Gene923

MTLYLLPNTLGTRAVETLPSVIGELVHRLDGLIVESDRGGRAFLSLWKIPEVHKFPLAILSKHARLPKAWDFY
LEPIVKHGENWGLISDAGLPCIADPGASLVRARALGIPVQAFSGPCSITLALMLSGLPSQSFTFLGYLPQSPKE
RVKSIKKAATSKEVSTSVCIETPYRNVYTFESLLDTLPSYAELCVASDLSGPSELVLTRQVQSWRTTEDLG
SVKQSITKVPTIFLFHIPN

>core/653/5/Org5_Gene441

MAGHSKWANTKHKRERADHKKGKIFSRIIKELISAVKLGGADPKSNARLRMVIQKAKENNIPNENIERNLKK
ATSAEQKNFEEVYELYGHGGVGIIVEAMTDNKNRTASDMRIAINKRGGSLVEPGSVLYNFARKGACTVAK
SSIDEEVIFSAYAIEAGAEDLDTEDEENFLVICAPSELASVKEKLISQGATCSEDRLIYLPRLVDCDEKDG
EANLALIDWLEQIEDVDDVYHNMS

>core/654/5/Org5_Gene518

MDISGAVKQKLLQFLGKQKKPELLATYLFYLEQALSLRPVVFVRDKIIFKTPEDAVRILEQDKKIWRETEIQIS
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KEPIIKTVFASAITGKLFHSLPPLLEDFISSYLRPMTLEEYVQNQTKFQLESSFLSLLQDALVEDKIAAFIESLADD
TAFHVYISQWVDTEE

>core/655/5/Org5_Gene786

MGLYDRDYIQDSRVQGTFFASRVYGWMTAGLIVTSCVALGLYFSGLYRSLFSFWVWVWCFATLGVSFFINSKI
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FALIGLLLVTLVFAVVSVMFVSMPLIYLLICYLGLVIFVGLTAADAQAIRRISSTIGDNNTLSYKLSLMFALKMY
CNVIMVFWYLLQIFSSSGNRD

>core/656/5/Org5_Gene32

MHPPIDITAIEAKLNFTFTQPKLLEIALTHPSYKNESAVQIEDSERLEFLGDAVLGLIVTEHLFLLFSPMDEGTLS
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REEILPLMSGNPKNLLQQFTQKQFRVLPVYQSTAVTDAQGNVSYQIQVLVNQEVWGEGNASSKKEAEKIAA
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>core/657/5/Org5_Gene390

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>core/658/5/Org5_Gene318

MSSQTMDVLIFYDTETTGTQIERDRIIEIAAYNSVTDESFLTYYVNPEIPIPEASKIHGITTDVLSAPKFPEAYE
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QAHRALDDVVILHKVFTSLIGDLPPQQVLDLLQQSYHPKVFKMPFGKYKGQPLVDIPKSYFEWLENQGALDK
PENKDIKAAIALLHQPT

>core/659/5/Org5_Gene623

MQNATIDQLPVSWQEQLPLCWREQLKEEWSKPVMQQLLIFLKQEYKEHTVYPEENCVFSALRSTPFDQVRV
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SHAGKGWELFTDAIVTKLIQERTHIIFVLWGAAARKKCELLFNSKHQHAVLSSPHPSPLAAHRGFFGC SHFSKI
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>core/660/5/Org5_Gene246

MDLAVELKEGILLVDKPQGRTSFSLIRALTKLIGVKKIGHAGTLDPFATGVMVMLIGRKFTRLSDILLFEDKEY
EAI AHLGTTTDSYDCDGKVVGRSKIPSLEEVL SAAEYFQGEIQQLPPMFSAKKVQGKKLYEYARKGLSIERH
HSTVQVHLQITKYEYPLLHFVVSCSKGTIYRSIAHELGTMLGCGAYLEQLRRLRSGRFSIDECIDGNLLDHPDF
DISPYLRDAHGNSL

>core/661/5/Org5_Gene603

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GILKKLLINRGHLCLRKNLLAEIKGNTKEIHARNVDVHIASLRKKLGPYGSKIVTIRGVGYLFSDDDSIPLQNHD
NTAHPNEE

>core/662/5/Org5_Gene1008

MTKVRLNKFLASAGVASRRKCDEIIFSGSVTVNGRVAEGPFVLVDPEDKVQVGGTSVHLTKKVYFMVHKAI
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KDLGKLMEGTFIDGKHVRPVSVTKIRRGTVKIVVSEGKKHEIRLFADAAGLPILELKRIRIGSLVLGGLRYGEY
RELTD AELGTYMKLSD

>core/663/5/Org5_Gene174

MLQAHRLCYSCDNQVILKDASFQASPGTITIILGSSGVGKTTLFRLLAGFLPLQEGELLWNGSPLNRKDVAYM
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KPILLLDEPFSSLDVLLKEQLYQDIVALAKKENKTVLLVTHDFHDV SCLGDVLYVIKNKTLTPVPLDPSMRPL
NNGLCFIKDLKKHLYT

>core/664/5/Org5_Gene814

MRVIFPDKHNNFPNLSKLLKKLPSVILVTSCIAPFFSYIINKFFGIPGLLEILALSVKGIQKHFWQFLTYPLITAD
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SIICGVLT VQIFLDPEKRFTIGPTPLSVSIKWGFLFVLGFYCCILIFSGAFLLLASMLAIVLAILFCKKEKIPNPYT
TSLRF

>core/665/5/Org5_Gene482

MPTTNCIFLDLRGHSILHQLQIEEALLRVANQNFCIINSGAKDSIVLGISRNLNQDVHISRAQADHIPIIRRYSGG
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AQPHRKATTVLN

>core/666/5/Org5_Gene30

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AVLKQLFPQGQILDIRGTIEERLDQLHRGHYDAIVLAKAASRLHLHHAYSIELPPPYHALQGSLAITAKDHA
GKWKQLFTPIHCHSS

>core/667/5/Org5_Gene667

MKFFSLIFKDDDVSPNKKVLSPEAFSAFLDAKELLEKTKADSEAYVAETE QKCAQIRQEAKDQGFKEGSESW
SKQIAFLEEETKNLRIRVREALVPLAIASVRKIIGKELELHPETIVSIISQALKELTQNKHIIISVNPKDLPLVEKSR
PELKNIVEYADSLILTAKPDVTPGGCIIETEAGIINAQLDVQLDALEKAFSTILKAKNPVDEPSETSSSTDSSSL
NDQDKKE

>core/668/5/Org5_Gene729

MNRRDMVITAVVVNAILLVALFVTSKRIGVKDYDEGFRNFASSKVTQAVVSEEKVIEKPVVAEVPSRPIAKET
LAAQFIESKPVIVTTPVPVSETPEVPTVAVPPQPVRETVKEEQAPYATVVVKKGDFLERIARANHTTVAKL
MQINDLTTLTKIGQVIKVPSTSQDVSNEKTPQTQTANPENYYIVQEGDSPWTIALRNHIRLDDLLKMNDLDEY
KARRLKPGDQLRIR

>core/669/5/Org5_Gene170

MNKKILVLCTAMFFIVCFGLIHKHTILPPKAHIPTNAKHFTIGNPYAPINITVFEPPSCSACAEFTTEVFPLL
KKHYIDTGEISFTLIPVCFIRGSKPAAQALLCIYHHDPRQADIDAYMEYFHRILTYPKEEGSHWATPEVLTKLA
EGLKINSGRSVNPKGLEQCIASGQYNEQIKNNLYGSQVLGGQLATPTAVVGDYLIEDPTFHEIERAIQHIRQL
QAVEGDHDD

>core/670/5/Org5_Gene632

MVHFSHNPIIQAYTEADFFGKSIFFCLLILSVCTWTVLHQKLAIQKNFLKAGKSLKDFLIKNRHAPLSLDIHPEL
SPFADLYFTIKRGTLLELDKNRQSAPDRGPILSSEDIQSLETLLGAIMPKYKALLHKNSFIPATTISLAPFLGLLG
TVWGILVAFTHISSGSSGNSAIMEGLATALGTTIIGLFVAIPSLIAFNLYKAHSSSELISEIEQTAYLLLNSIEVKYR
NTNL

>core/671/5/Org5_Gene49

MTKHGKRIRGILKNYDFSKSYSLREADILKQCPPVRFDQTVDVSIKLGIDPKKSDQQIRGAVFLPNGTGKTLR
ILVFASGNKVKEAVEAGADFMGSDDLVEKIKSGWLEFDVAVATPDMMREVGKLGKVLGPRNLMPTPKTGT
VTTDVAKAISELRKGKIEFKADRAGVCNVGVGKLSFESSQIKENIEALSSALIKAKPPAAKGQYLVSFTISSTM
GPGISIDTRELMA

>core/672/5/Org5_Gene99

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LNPEKFSSDLTVDGADEVDPQLRMKGGGGAIFREKILLRAAKRSIILVDESKLVPVLGKFRVPLEISRFRSA
IIEIRHLGYEGEWRLQDTGDLFITDSSNYIYDIFSPNSYPNPEKDLLKLIQIHGVIEVGVFVIEKVEVWSSNSQGL
ISKKYSV

>core/673/5/Org5_Gene176

MLQSCKKALLSIVVSILAFHPIPGMGVEAKSGFLGKVKGWFSKKEIQEEARILPVKDSLWKRYDYTSSSGFS
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QVLFMQARQIQGHKALEFWIVCEDVYFRGMLISVNHTLYQVFMVYKNKNPQALDKEYEAFSFSFKITKIREP
RTIPSSVKKKVSL

>core/674/5/Org5_Gene201

MALDEINNQNPNPSQQIASSTSQTSKINQDRKTFACVTLLVVATLMILSGIVLLFTIGSLGLSVPLSGILGTFAV
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YLQLGLCAGLVGLGTALFVAGLARMSPRSLADQEGSGSADSQSNIVGIGEPKAAQEQQWKYKMAVVRGEDGI
PTAIRLTPEK

>core/675/5/Org5_Gene653

MSKPSPRNANQPQKPSASFNNKTRSRRLAELAAQKKAKADDLEQVHPVPTEEEIKKALGNIFEGLSNGLDLQQI
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KSKTTTNKKSGKKR

>core/676/5/Org5_Gene448

MYLEDYDVFFFDLDGLLVDTEPCFYRAFLQACAEFSLEVHWDFSTYYSHHTLTGTEIFSKKFIEQYPQAEYM
AEIFAKRLQIYYKSLEHAGPALMPGVEAFIELVLSLNKTFGVVTNSPRDATHLTRMTYPILNKFLFWVTRENY
ARPKPYGDSYDYAYRTFAREGMKVIGFEDSVKGLRALSKIPATLVCINSMAEITPEDYPELKKGKEFFSYPSFD
VLTEHCSQQKLL

>core/677/5/Org5_Gene849

MNTSHRKTLLVFSYLSSTFTLLLVLNLVLSSKLIPTTFFNFIIPGGLILYPLTFLISDVVNEIFGPKKARVMIFSAPI
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TWISQIPDTFIVDTCILYFGMGLSFPQTLNIMFYSIYKITFCVLTTPLFYLAVENTIRKFLGMPSTKIANTVPLIN
QP

>core/678/5/Org5_Gene133

MKKQESVLVGPSIMGADLTCLGVEAKKLEQAGSDFIHIDIMDGHFVFNLTFGPGIIAAINRSTDLFLEVHAMII
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SFLPNTIEKIAFARHAIKTLGLKDSCLIEVDGGIDQQSAPLCRDAGADILVTASYLFEADSLAMEDKILLRGEN
YGVK

>core/679/5/Org5_Gene159

MKGFLSVNELIFGFQTFSSVVVLGVFFASRGKAWLTGWLSLLSSIMNVFVLKQIHLWGFEVTSADVYVIGLLT
CLNYAREHYEKNDINDAMLCWSVISIAFLVLTQLHLFLIPSPNDSSQEHFLALFSSTPRIVVASLVTLIFVQIVDI
KLFTFLQRVFSKKYFAMRSTISLLFSQLIDTIIFSFLGLYGLVSNLCDVMIFAMLVKGIVITLAIPTLTVTKAVLD
RRSS

>core/680/5/Org5_Gene454

MRPHRKHVSSKSLALKQSASTHVEITTKAFRLSMPLKQLILEKSDHLPPMETIRVVLTSHKDKLGTEVHVVAS
HGKEILQTKVHNANPYTAVINAFKKIRTMANKHSNKRKDRTKHDLGLAAKEERIAIQEEQEDRLSNEWLPVE
GLDAWDSLKTLGYVPASAKKKISKKKMSIRMLSQDEAIRQLESAAENFLIFLNEQEHKIQCIYKKHGDGNYVLI
EPSLKPGFCI

>core/681/5/Org5_Gene698

MALLILLRHGQSVWNEKNLFSGWVDIPLSQQGIEEAFSAGRAIQNLPIDCIFTSTLVRSLMTALLAMTNHHSK
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PQGESLYDTKQRTLPHYFEKNILPQLQNGKNVVFVSAHGNSLRSLIMDLEKLSEEEVLSLELPTGKPVVYQWKN
HKIEKHPEFFG

>core/682/5/Org5_Gene173

MSSQPLVTTSSSLSRVYVLTGEEKVACYKKAFNHIWHGAPAILLAAALLMFCIFGFVLGSILLGAPLEGASILY
DVILPWLLPSILVFVLLVLPLNIYAYSHHKQVLALHERITQSNYKEIYDHCEKEKKTTPNKKALSLYIESQVLVP
EYSKRFFSSMILGKTLKIIPKKDSPESLKHDELIQKALERAKENIYMNKNQREKRDEREAKKEAKNASKTNPLW
EGLGT

>core/683/5/Org5_Gene188

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DLANFRNQHIGFVFQNFYLLEDDTVLKNVLMPALIARKNISKGSPVYTRALELLDLVNLEDKVRTRCSKLSG
GEKQ RVAIARALINEPAILLADEPSGNLDEETSEQIHNLLLEQASALCGILIVTHNKHLSRCSREGVLSNGKLF
FHNS

>core/684/5/Org5_Gene136

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FDEPTSALDPFATASFRHLLLETLRDQELTVGLTTHDMQFVHSCLDRIYLIDQGT VAGVYDKRDGELDSGHPLS
KYIHSAQ

>core/685/5/Org5_Gene969

MDLKLDEVASLLDVSEHTVLQWLKEGAIPSYSMNNEYRFSREEIEDWLLHNQALMIQERGEDKEALKDLSL
KYSLYKAIHRGGVLCDVVVHSKEEALQYASKYIAQKFQLDESVLFEMLSHRENLMSTGIGEGIALPHAKDFLI
NAYYDIVVPMFLAEPIEYGALDGKPVGILFFLFACQDKSHLNLVNKIVHLGMSLNARSFFKNYPNKDQLLAY
VKEWESQTH

>core/686/5/Org5_Gene449

MILRISTVSLLTSCSFNSRTCFVTPERITSQKDCPVLLHPKSTTISPPLYDWISPNREVITAYSFYCRGQGNSII
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FALDPPLPMEKLLATIKKLYKKNSDPSLSNFIVTEATLTNPRLTQQDLGSHTTEITVEILDNLQNKEALSSA

>core/687/5/Org5_Gene750

MENSQNFHDTLCQLLDYSEELYPTLASLLNVTLNPNTAISASVSSIPEKAVEVPNAEPQPITPPPPTNLSQEKT
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TNIFVNNPNFFLALAPLNVIRYKIPTTDYHQSLTQNGCIFLPLYSSLEYEKDSQLKRNLWAILNRLPFAYTPKSS

>core/688/5/Org5_Gene798

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QPSFVQEISRLQDSAVFALATDDKTYLLESIEALQTHLAPRMETPYIYKMTDTYGNWFWENLWRTKGQEIFY
TEFIKKAGI

>core/689/5/Org5_Gene565

MIDPVECFPNLDGDAEAQSITQNSGTPLASELKKDISPFALGSYAAPKDTTLVQGFKNPMAMMQDQNSNLI
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DKEEGSVTRKIIDWVSSGEEVLNRALLYFSDRDGNRESLANFLKVQYAVQRATQRAELFASIVGTSVSSVKTI
MTTQLG

>core/690/5/Org5_Gene611

MTSWIELLDKQIEDQHMLKHEFYQRWSEGKLEKQQLQAYAKDYLLHIKAFPCYLSALHARCDDLQIRRQIL
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FINSTEPSCSK

>core/691/5/Org5_Gene507

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ALRFLKDCNVECRSILFIDHLDHVEKNENLRSLRNLTAVKGFVYGININGYDLASAHNIVISKKALQELVERL
VSETKD

>core/692/5/Org5_Gene540

MQTLARLFGQSPFAPLQAHLEMVVSCVEYMLPIFTALRDGRYEELLEMAKLVSDDKEYQADCIKNDMRNHLP
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GGRKADKARLLVGRVAKSEHESDVLQRELMQIFFSDDFIPEKEFYLWLQVIRRTAGISDSSEKLAHRINMTLE
EK

>core/693/5/Org5_Gene844

MSTTTVKHFIHTASRWEVLKEIVASNYWHAQWINTLSFLENSGAKKISASEHPTEVKEEVLKHAAEEFRHG
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TKF

>core/694/5/Org5_Gene167

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>core/695/5/Org5_Gene382

MKKYFITGLVILLPLAITIAIVTMIMNFLTQPFVGLASEFFEKFSFYTKHRALLKFVLQIILLFGLFFATVLLGFL
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>core/696/5/Org5_Gene883

MGQKGCPIGFRTGVTKKWRSLWYGNKQEFGKFLIEDVRIRQFLRKKPSCQGAAGFVRRMSGKIEVTIQTAR
PGLVIGKKGAEVDLLKEELRALTGKEVWLEIAEIKRPELNAKL VADNIARQIERRVSFRRAMKKAMQSVMD
AGAVGVKIQVSGRLAGAEIARSEWYKNGRVPLHTLRADIDYATACAETTYGIIGIKVWINLGENSSSTTPNNP
AAPSAAA

>core/697/5/Org5_Gene395

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>core/698/5/Org5_Gene591

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QEQQGDSVDCIMSRYL SMVKPMHEKFIEPTRKYADIIVHGNYRQNVVTNILSQKIKNHLENALESDETY YMVN
SK

>core/699/5/Org5_Gene213

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VHLISCSTLAGFVGGGGLGQLLLQYGYRFEWSVTTSVLVITLVLIESVRILGDFWGRRVLKYRGIL

>core/700/5/Org5_Gene1007

MSTVTTEPCSSIHISLNNDWRDSQPYS LDRASELLHFRFLPSLVFSNWKVEQQIETLCHKSEKRRLISPLAKWL
GKLHKQDLLCPPAPPVSVCWINAHVGYGV FARDEIAPWTYIGEYTGILRRHQAIWMDENDYCFRYPMPLFTL
RYFTIDSGKQGNVTRFINHSEQPNAEAIGVFSEGLFHVIIRTIAPIYAGQEICYHYGPLYWKHRKKREEFIPEEE

>core/701/5/Org5_Gene508

MRSHISVMGKKEGMIHIFDKDGS LVACSVIRVEPNVVTQIKTKESDGYFSLQIGAEEMNAPAHTITKRVSKPK
LGHLRKAGGRVFRFLKEVRGSEEALNGVSLGDAFGLEVFEDVSSVDVRGISKGKGFGQVMKKFGFRGGPGS
HGSGFHRHAGSIGMRSTPGRCFPGSKRPSHMG AENVTVKNLEVIKVDLEKKVLLVKGAIPGARGSI VIVKHSS
RT

>core/702/5/Org5_Gene846

MQRHIVGIDTGVGKTIVSAILARALNAEYWKPIQAGNLENSDSNIVHEL SGAYCHPEAYRLHKPLSPHKAAQI
DNVSIEESHICAPKTTSNLIETSGGFLSPCTSKRLQGDVFSSWSCSWILVSQAYLG SINHTCLTVEAMRSRNLN
ILGMVVNGYPEDEEHWTQEIKLPIIGTLAKEKEITKTIISCYAEQWKEVWTSNHQGIQGVSGTPSLNLH

>core/703/5/Org5_Gene320

MNAVNTPKKILCIVADYREISPLIEQLDFTQINEHLYSYRCTDYHLDLYIVHVWGSTAVLNALQSYCQAYTDY
DLWINPGFVGACSP EIPLGQCYTIEKIANLTDTPPVLSEDPPYIFDALPDSL PKSSLVTSPVLYHYGFHKTFKL
LDMEGYAIASQAAEH HIPCSFLKITS DYTVPGD C PFSRLEEVSQKLTQTLVELLPELMERAIPP KLLLPCP

>core/704/5/Org5_Gene362

MLGSLPCYPGAGNIEEYKNRYFYCQLCAEVVSPYVVPVIVVDVQGAPPTGILQVLRCKQHKFQGLPVHGPIT
SLWALEPVGKGAPQLESAMYELCSQVRNFDICSIVSWVFGGLCIFAGLIVGVMVEAPLIAGLSAWVIPCIIGGV
GAILCLFAILMAYLGRGRVREWLNLSHEYITQCHCRQIQAHSQNYSVITEYPATCALSQPITKLPNGSRRDN

>core/705/5/Org5_Gene137

MDHWLAIARLLLRCGYTLCVSGIGILCGSILGLLIGTVTSLYFPSKLTKLLANSYVTVIRGTPLFIQILIIFYGLP
EVLPIEPTPLVAGIIALSMNSAAYLAENIRGGINSLSIGQWESAMVLGYKKYQIFVYIIPQVFKNILPSLTNEFV
SLIKESSILMVVGVPPELTKVTKDIVSRELNPMEYLIACAGLYFLMTTSFSCISRLSEKRRSYDN

>core/706/5/Org5_Gene709

MKRVIYKTIFCGLTLLTSLSSCSLDPKGYNLETKNRDLNQESVILKENRETPSLVKRLSRRSRRLFARRDQTQ
KDTLQVQANFKTYAEKISEQDERDLSFVVSSAAEKSSISLALSQGEIKDALYRIREVHPLALIEALAENPALIEG
MKKMQRDWIWNFLTQLSEVFSQAWSQGVISEEDIAAFASLTGLDSGTVASIVQGERWPPELVDIVIT

>core/707/5/Org5_Gene546

MQKL VHNIWKKFYSFSSAIAICIVLASFLSLKIVSNTYKHSQAKRNSILLTRAAEVAVSQGFLPSKSALSSLEQ
AYHLGGESMKPYAGFLASCFYIHNEPLRGAYYAGLAYNNSQALQLPHPIQKLLKEISEAQADQLYDVALSKS
YQLLQTANSSPEYPTLSFLTLLRVIELKELLHQDVSQDFAALKSSPLFHQFERMYSDEWTL SKRFGKKG

>core/708/5/Org5_Gene436

MIITIDGPSGTGKSTTAKALADHLHFNYCNTGKMYRTLAYARLQSPWATLPLTKFLEPPFSFTFATGQPLESF
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RAQRRLKDLPEGTLSPPEQLQAELVKRDAADAQRAHDPLVIPENGIVIDSSDLTIRQVLEKILALLFRNEL

>core/709/5/Org5_Gene307

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SKRFYASEKVFLIKHNASPQTVSQFYAPIANRLPETIIEQFLPAEFIVATELLEQKTGKEAGVDSVTASVRVRVF
DIRHHKIALIYQEIIICSQPLTTLVNDYHRYGWNSKHFDSTPMGLMHSRLFREVVARVEGYVCANYS

>core/710/5/Org5_Gene743

MSKKPLYVAHPWHSPTLTQDNYESLCCYIEITPYDSVKFELDKATGLLKVDRPQKFSNFCPCLYGLLPQTYC
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DISDCPGTVLDMIQHYFLTYKATPNHLIKGSPAKIEIVGIYGKKEAQKVIQLAHEDYLSYIGDTAEVN

>core/711/5/Org5_Gene537

MSVNPSGNSKNDLWITGAHDQHPDVKESGVTSANLGSHRV TASGGRQGLLARIKEAVTGFFSRMSFFRSGAP
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KTGGTNAKRPATHGKGPAQPPKTGGTNAKRAATHGKGPAQPPKGILKQPGQSGTSGKKRVSWSD

>core/712/5/Org5_Gene83

MNTSISEIQRFLSMIAFEKELVSEDFSVVAGIDEAGRGLAGPVVASACILPKGKVFPGVNDSKKLSPKQRAQV
RDALMQDPEVCFGIGVISVERIDQVNILEATKEAMLQAISSLPISPDILLVDGLYLPHDIPCKKIIQGDAKSASIA
AASILAKEHRDDLMLQLHRLYPEYGFDRHKGYGTSLHVEAIRRYGPSPCHRKSFSPIKQMCAIV

>core/713/5/Org5_Gene184

MTKGSVFIIMGPPGSGKGTQSQYLANRIGLPHISTGDLLRAIIREGTPNGLKAKAYLDKGAFVPSDFVWEILKE
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PDCHVPLIRRSDDTPEIHKERLTKYQERTAPVIAYYDSLGLKLCRVSSSENKEDLVFEDILKCIYK

>core/714/5/Org5_Gene336

MTSKKSYKSYFFDPLWSNNQILAILGICSALAVTTTVQTAITMGIAVSIVTGCSSFFVSLLRKFTPDSVRMITQ
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LFGFGTLMGFRIIPQFVYASETHPDGYQNLSLMVLAPSAFFLLGIMIWLVNIRDSKKRKR

>core/715/5/Org5_Gene17

MYFYKYVIIIDTSGYYPFLACVDNQQVLEHWSLPVGPDLGIVLEFLFKSKNLSFQGVAAVALGPGNFSATRIGIS
FAQGLAMAKNVPLLGYSSLEGYLLSKDEKKALMLPLGKRGGVLTLSSEIPEEGLNEKRRGVGPGALLSYEEA
SDYCVAHGYYHVISPNPQLFASSFSKITVEEVAPSVEQIRRHVISQFMFVEYDKQLSPDYRSYSCIF

>core/716/5/Org5_Gene345

MATSVAPSPVPESSPLSHATEVLNLPNAYITQPHPIPAAPWETFRSKLSTKHTLCFALTLLLTLGGTISAGYAG
YTGNWIICGIGLGIIVLTILALLLAIPLKNKQTGTKLIDEISQDISSIGSGFVQRYGLMFSTIKSVHLPETTQNQ
EKTRILNEIEAKKESIQNLELKITECQNKLAQKQPKRKSSQKSFMRSIKHLKSNPVILFDC

>core/717/5/Org5_Gene437

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FNRHQKIPHVWKTITCVFGTPMYFDDIIQNPEIKNKETYQIITNQTMNKIAELKAWYESGCKGDVP

>core/718/5/Org5_Gene447

MIKSSLILLSGGQGTRFGSKIPKQYLPLNGTPLVLHSLKILSSLPQIAEVIVVCDPSYQETFQEYPVSFAIPGERR
QDSVFSGLQQVSYPWVIIHDGARPFYIPDEIHDLLETAEKIGATALASPIPYTIKQRNPVRTLDRDNLAIHHPQ
CIKTEILREGLALAKEKQLTLVDDIEAAEIIGKPSQLVFNKHPQIKISYPEDLTIAQALL

>core/719/5/Org5_Gene473

MMNYEDAKLRGQAVAILYQIGAIFGKHILASGEETPLYVDMRLVISSPEVLQTVATLIWRLRPSFNSSLLCG
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VREALVFLDRRKEACQPLGPQGIVSSVFTVPTLIKALIAYGKLSSGDLTLANKISEILEIES

>core/720/5/Org5_Gene589

MARYCGPKNRVARRFGANIFGRSRNPLLKKPHPPGQHGMQRKKKSDYGLQLEEKQKLKACYGMIMEKQLV
KAFKEVIHKQGNVAQMFLERFECRLDNMVYRMGFAKTIFAAQQLVAHGHLVNGRRVDRRSFFLRPGMQIS
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>core/721/5/Org5_Gene676

MKQFILRTLNALFPNPKPSLEGWSSPFQLLIAILLSGNSTDKAVNSVTPQLFAKAPDAQSILDLPPGKLYQLIAP
CGLGERKSAYIYQLSQILVRDFHGEPPNDMALLTQLPGVGRKTASVFLGIAYGKPTFPVDTHILRLAQRWKIS
EKKSPSAAEKDLARFFGHENTPKLHLQLIYYARQYCPALHHKIDNCPICSYLAKEANSTRT

>core/722/5/Org5_Gene59

MSVQVKLTKNSFRLEKQKLARLQTYLPTLKLKKALLQAEVQNAVKDAAECDKDYVQAYERIYAFELFSIP
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ILEEELRAVSIRVNLFEKKLIPETTKILKKIAVFLSDRSITDVGVKMAKKKIELRKARGDECV

>core/723/5/Org5_Gene56

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LSQAGKRALEALKQAVENKIFRESLVEWLEHVTDDPEVSTKLIQALVQALEAQGVSGNLTAYIGKHVSPRAV
NELLGKAVTTKLRRKKSVVVGSFVGGVQLKVEEKNWVLDLSSSALLEIFTRYLQKDFREMIFQGS

>core/724/5/Org5_Gene602

MTYLASSIFSPEDFLYPEIISKAHYTWDILDLMQMLENHVFSGIHGTVESGVTLKNIEKIEIAEDAYVESGAYI
VGPCILGSQTEVRHGAYLRGNVITGSRVVGHCTEIKNSYLGHHTKAAHFAYLGDSVLSSEVNLGAGVRCA
NFRLDGRNIYVRSTSDKSKKIDTGRRKLGAFLGKGVAIGCNVINPGQHILPHTRIRPGQVI

>core/726/5/Org5_Gene34

MSFVPYSLPELPYDYDALEPVISSEIMILHHQKHHQIYINNNAALKRLDAAETQQNLNELIALEPALRFNGGG
HINHSLFWETLAPIDQGGGQPPKHELLSLIERFWGTMDNFLKKLIEVAAGVQGSWAWLGFCPAKQELVLQ
ATANQDPLEPLTGKLPLLGVDVWEHAYYLQYKNVRMDYLLKAFPQIINWGHENRFSEIISSEK

>core/727/5/Org5_Gene484

MYDIYRGTLTYVHTGAIVIECQGIGYHIAITERWAIECIRALHQDFLVFTHVIFRETEHLLYGFHSREERECFRI
LISFSGIGPKLALAILNALPLKVLCSVVRSEDIRALASVSGIGKKTAEKLMVELKQKLPDLLPLDSRVETSQTHT
TSSCLEEGIQALAAALGYSKIAAERMIAEAIKDLPEGSSSLTDILPIALKKNFSGVVKD

>core/728/5/Org5_Gene1020

MKIVIASHHGYKIRETKTFLKRLGDFDIFSLSDFPDYKLPQEQEDSITANALTKGIHAANHLGCWVIADDTMLR
VPALNGLPGPLSANFAGVGAYDKDHRKKLLDLMSLESLVDRSAYFECCVVLVSPNQEIFKTYGICEGYISHQ
EKGSSGFGYDPIFVKYDYKQTFAELEDVKNQVSHRAKALQKLAPHLQSLFEKHLLTRD

>core/729/5/Org5_Gene769

MGLPNYITFSRLFITPIFMILYLK GKWFGITPVVLPYVLLALLAISELTD AIDGYVARKFSQVTDLGKLLDPMA
DSIYRISIIYLTFTQPPVNLPLLLVFIFLARDSVISTLRTVCAFRGRVVAARASGKLKAILQGV SFFLILLVMIPHS
GLLSQNGLEIFASVTVSIIAVYSIASGIEYFWMNKNFLSQRAKTKDSEKNHESKD

>core/730/5/Org5_Gene208

MFIVIEGGEGSGKSSLAKALGDQLVAQDRKVLLTREP GGCLIGERLRDLILEPPHLELSRCCELFLFLGSRAQH
IQEVIIPALRDGYIVICERFHDSTIVYQGIAEGLGADFVADLCSKVVGPTPFLPNFVLLLDIPADIGLQRKHRQK
VFDKFEKKPLSYHNRIREGFLSLASADPSRYLVLDARES LASLIDKVMLHTQLGLCT

>core/731/5/Org5_Gene84

MNKILVDSPFSPDHQKCCPKLFTISAPAGVGKTTLVRMLEQEFSSAFAETISVTTRKPREGEVPGKDYHFVSHE
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SRGSEEGSQRKERLEHSLIELAAANQFDYVIINDDLNQAYRVLKSIFIAEEHRNIL

>core/732/5/Org5_Gene628

MHAKLSFFILLSLLFSGIDCSRLHAAGRSPSLQGVLA EIEDISAKLASHEVEIVMLSERLDEQDSKCQKWTA
AKPETLAQKIRELESDQKALAKTLAVLTTSVKDLQTNLQSKLQEIQKDHRA LAQDLRLVRRSLLALVDSSSPGA
YADFSDPVPENIYIVREGDSLSKI AKKYKLSVTELKKINKLDSDAIYAGQRLCLQRNKQ

>core/733/5/Org5_Gene294

MIGAQQKKQSGKKTASRAVRKPAKKVAAKRTVKKATVRKTAVKKPAVRKTA AKKTVAKKTTAKRTVRKTV
AKKPAVKKVA AKRVVKKTVAKKTTAKRAVRKTVAKKPVARKTTVAKGSPKKAACALACHKNHKHTSSC
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>core/734/5/Org5_Gene223

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LGFTGVLPQVALLMQGETNLIWAMVSGSIICFIALIGTLGLILTNKNTPLPAS

>core/735/5/Org5_Gene684

MTLVPYVVEDTGRGERAMDIYSRLLKDRIVMIGQEITEPLANTVIAQLLFLMSEDPKKDIQIFINSPGGYITAG
LAIYDTIRFLGCDVNTYCIGQAASMGALLLSAGTKGKRHALPHSRMMIHQPSGGIIGTSADIQLQAAEILTLKK
HLANILSECTGQPVEKIIEDSERDFFMGAE E AISYGLIDKVVTSAKETNKDTSST

>core/736/5/Org5_Gene476

MLKLLKVSITGDLSSGKTEACQVFQELGAYVVSAD EISHSFLIPHTRIGRRVIDLLGSDVVVDGAFDAQAIAA
KVFYNSVLLQGLEAILHPEVCRIIEEQYHQSIQDGNYP LFVAEVPLLYEIH YAKWFDSVILVMANEDIRRERFM
KKTGRSSEDFDQRCRFLNVEEKLAQADV VVENNGTKKELHQKIEEYFYALKGAL

>core/737/5/Org5_Gene990

MLILLNLSLLFYVLFDSPGSIPVFVALLKNFSRKKQQRVILRECLFALGALILFVTFGRSFFQFLDISLYAFQIIG
GFLFLTYSIKMMLAPMPEKAKDDTSKTEPIFFPLAFPVITGPAVITALLSYMEEGIYSREIIFTAMIIAWAFSLFT
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>core/738/5/Org5_Gene403

MFSGIIQELGEVCFFEAQGNGLSLGIKSTPLFVTPLVTGDSVAVDGVCLTLTSCNESKIFFDVIPETLACTTLGE
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DTFSVGLIPETLQRTTLGKKREGERVNIEIDMSTKIQVDTVKRILASSGKD

>core/739/5/Org5_Gene799

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THLSEQERSVIEMKEQSHEHILEKDVKLIHYNLGYLPKGNKEITTLARTEISLEYALNIVRPDGLITVVCYPGH
PEGEKETHSVESLAQRLHPKEWCVSSFYVANRCRAPRLFIFQRQGSSESSVDKG

>core/740/5/Org5_Gene229

MTRYPDYLSKLIFFLRKLPGIGFKTAEKLAFELISWDSEQLKILGNAFHNVASERSHCPLCFTLKESKEADCHF
CREERDNQSLCIVASPKDVFFLERSKVFKGRYHVLGSLSPITGKHIENERLSILKSRIETLCPKEIILAIDATLEG
DATAFLKQELQHFSVNISRLALGLPIGLSFDYVDSGTLARAFSGRHSY

>core/741/5/Org5_Gene457

MGFACRYLFFFIVLFASGSFGNQLLSVPCWLSEEEESFYTHRFDFSKSYPDMMENMEIQAQRKKRVEFNLTGEFP
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NTKTSCLKGNVCPGSTFIKQGWGVWNKIYHNDLVGFSEVTLIFNVSSSEGGTITFS

>core/742/5/Org5_Gene528

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CAGYTLKVELLNGIDKNIGFTYAPNKLGDKTHRHFIVSNEGRLSLSAKVQLINNDTQEVLDQCVARESVDFF
FEPDLGTANAHEFALGQFEMHSEAIKSARRILSIRLAETIAQQVYYDLF

>core/743/5/Org5_Gene117

MNWVPKTIHVDPESEIDIRKVVSICYKLIKECQPEFRSLISELLGVIRCGLRLLKRSKYQEARTVSDDEDAPLF
CLTRSYYQDGYLTPLRAGPRDLINHYIHLRRRENPKHFFSPKHPCYYARLAFNESVCVYRELFDIERLTKMYV
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>core/744/5/Org5_Gene768

MRIALSLLSLLMIFPIFGESRPGSEDGNSNTQEIVGSQDTQVCLYHSYEQGLQASRIEGKPLVIVVLCNSGDD
GQACTIGLSETCEEVLSVLGSIFSELANFVVLVPSGVNPLIYPPIEDPILAEIVKFELFKDESFTGLSIIVGV
TPEGPGDIIIVSPVSLTVEEEETLPSEQTTEVESTSELQSEDPAIA

>core/745/5/Org5_Gene425

MSSNLHPVGGTGTGAAAPESVLNIVEEIAASGSVTAGLQAITSSPGMVNLLIGWAKTKFIQPIRESKLFQSRAC
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DDGILNNSNKIFGHVKTGNTSRATTPVLNDGRGTPVLSPLVSKIARV

>core/746/5/Org5_Gene11

MSLPLVLGSSSPRRKFILEKFRVPFTVIPSNFDESKVSYSGDPIAYTQELAAQKAYAVSELHSPCDCIILTGDTIV
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GAYDVCHGGLILKKVHGCVYNVQGLPIQTLKYLLEELNIDLWDYSI

>core/747/5/Org5_Gene381

MLQEHFFLSEDVITLAQQLLGHKLITTHEGLITSGYIVETEAYRGPDDKACHAYNYRKTQRNRAMYLKGGSA
YLYRCYGMHLLNVVTGPEDIPHAVLIRAILPDQGKELMIQRRQWRDKPPHLLTNGPGKVCQALGISLENNR
QRLNTPALYISKEKISGTLTATARIGIDYAEYRDVPWRFLSPEDSGKVLS

>core/748/5/Org5_Gene626

MTLSLVGKEAPDFVAQAVVNGETCTVSLKDYLGYVVVFFYPKDFTYVCPTELHAFQDALGEFHTRGAEVI
GCSVDDIATHQQWLATKKKQGGIEGITYPLLSDEDKVISRSYHVLKPEEELSFRGVFLIDKGGIIRHLVVNDLP
LGRSIEEELRTLDALIFFETNGLVCPANWHEGERAMAPNEEGLQNYFGTID

>core/749/5/Org5_Gene332

MFRRTGKGPFEDVQTLYEEETSSPSSYSPYSRSERPETPPSLFDNPKASEARPLNHNLTEESSLPQWSSTPRTES
LLPLEEPETTLGEGVTFKGEAFERLLRIDGTFEGILVSKGKIIIGPKGVVKADIQLQEAIIEGVVEGNITVSGKV
ELRGGAIKGDIQANTLCVDEGVRLGYLAAGITDHSEERDL

>core/750/5/Org5_Gene836

MAYGTRYPTLAFHTGGIGESDDGMPPQPFETFCYDSALLQAKIENFNIVPYTSVLPKELFGNIVPVDTCVKSFK
HGAVLEVIMAGRGAALSDGTHAIATGIGICWGKDKNGELIGGWAAEYVEFFPTWINDEIAETHAKMWLKKS
LQHELDLRSIAKHSEFQFFHNYINIKQKFGFCLTALGFLNFENAEPKVN

>core/751/5/Org5_Gene615

MKKWISILILSFLSLLSILPVLAITINHVKISQRWSDLNSQILTLKVIRDHEDQVIKHNRISKDRNNLSIESLNAS
CKQLRPLSKERERLNKLNSNSLLAQSKEVWERKRALEKSNHQLVWNCEQMHNDFAFVRLEQATEMDNEDI
ESLFSLFNPENPVAPLVFFTCWKMTKQTTPLGNEVWLTHAEAISRWI

>core/752/5/Org5_Gene629

MNIHSLWKLCTLLALLALPACSLSPNYGWEDSCNTCHHTRRKKPSSFGFVPLYTEEDFNPNTFGEYDSKEEK
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>core/753/5/Org5_Gene333

MVLFSLLPKLCYGCQAPGAYFCSNCLEKLLVEDREGRCLHCFRYLGSSETRLCSQCSPSSQLQAFSLYLPSQ
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>core/754/5/Org5_Gene199

MKRYVVGISGASGVILAVKLIKELVNAKHQVEVIISPSGRKTLYYELGCQSFDALFSEENLEYIHTHSIQAIESS
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>core/755/5/Org5_Gene700

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QPATSLQEILGHPIDLETTRELLIHLLGVLQENLPDSLATKSNRGN

>core/757/5/Org5_Gene393

MADGEVHKLRDIEKELLEARRVFFSEPVTEKSASDAIKKLWYLELKDPGKPIVFVINSPPGGSVDAGFAVWDQ
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>core/758/5/Org5_Gene43

MIKKFFIYSLIFSCSFSAPLKGICNEDVSSQSRIEEDPEVLITQLNELIETPIEEGKEIRNELQAISDGQKSSEEIEES
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>core/759/5/Org5_Gene301

MSIKEDKWIREMALNADMIHPFVNGQVNVNEETGEKLISYGLSSYGYDLRLSREFKVFTNVYNSVVDPKCFT
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>core/760/5/Org5_Gene724

MVRVSTSEFRVGLRIEIDGQPYLILQNDFVKPGKGQAFNRIKVKNFLTGRVIERTYKSGESVETADIVERSMRL
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>core/762/5/Org5_Gene97

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>core/763/5/Org5_Gene868

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>core/764/5/Org5_Gene801

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>core/766/5/Org5_Gene470

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>core/768/5/Org5_Gene996

MELVVTSRETGKKSFLKKIRQQGGIPAVVYSAGKSLANITVDALVFKKFLSNLESGALSSTVFSLSYEGRIIKA
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>core/770/5/Org5_Gene132

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>core/771/5/Org5_Gene378

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>core/772/5/Org5_Gene646

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>core/773/5/Org5_Gene442

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>core/775/5/Org5_Gene856

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>core/776/5/Org5_Gene496

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>core/777/5/Org5_Gene967

MYKWYVVQVFTAQEKKVKKALEDFKESSGMTDFIQEIILPIENVMEVKKGEHKVVEKYIWPGYLLVKMHLT
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FHDKGRLSVMVSIFGRETRVDDLEFWQVEEVAPGQESE

>core/778/5/Org5_Gene455

MSLLNLPSSQDSASEDSTSQSQIFDPIRNRELVSTPEEKVRQRLLSFLMHKLNYPKKLIIIEKELKTLFPLLMRK
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SALFNPKTQTLD FYPGLPEYSQLLNYFISLNL

>core/779/5/Org5_Gene329

MVEIFNYSTSIYEQHASNNRIVSDFRKEIQMEGISIRDVAKHAQILDMNPKPSALTSLLQTNQKSHWACFSPPN
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>core/780/5/Org5_Gene162

MSKESIRSYSEISTPTPIFRETPSKEGVAYKLQLRSPAKDCILRN RVSLKGALLRSIPFYGSFLGAKRIHSAWSA
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>core/781/5/Org5_Gene613

MTDPKIEKSALRKLFI SIRRDLSEERKHEASSAVASFVRSFSKESVVLSFVSFNHEIDMQEANRILIQKCTLALP
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IRTIGIGYCEQKIDRLPQESHDIPLSQIYLC

>core/782/5/Org5_Gene498

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>core/784/5/Org5_Gene771

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>core/785/5/Org5_Gene557

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DVVKGNEKKIQELTDKFCKQLDELTKQKEAEIASI

>core/786/5/Org5_Gene695

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>core/787/5/Org5_Gene430

MACEQHEGCELEEREIEIEDIKSDTKWVSITQAAKLHNVTRQAIYVAIKQKKLKASKETRWEIDIKDLEEY
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YLSKQAAKKLKGAEPKEHQAPNFEPPTTEIFPESN

>core/789/5/Org5_Gene842

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PVDHVDHSSKSSLEQASQDLITLLKS

>core/790/5/Org5_Gene222

MSAPIPTPQELSDQITCLNVQYQQVSELARENKGDIEGLKTLTAALTADAGIQPSADEIYSLQTAAALILSASE
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>core/791/5/Org5_Gene416

MDRDNEVPLPKPKWIYRTGIGQDSHRFLPESSTKPCILGGIIFDHCPGFQANSDDIIFHAICNAISSVTNKIILG
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>core/793/5/Org5_Gene699

MGYVFYVIAGSIFLGISLGAYCQLYYSVKSVLFSWYLLTVYALEKRHALLALSQLVGEEDAQSQKEIDFLSQC
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>core/794/5/Org5_Gene1063

MSLVSYLSNPQKALVLGSKGFSMDCVDNLKLYIFRLKLPDTERISYSISPEYIREKGEEELLNSPIEVEGSLGR
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CPERKNILKFLEDRKKHEGNNPFEYL

>core/795/5/Org5_Gene344

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>core/796/5/Org5_Gene815

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>core/797/5/Org5_Gene816

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IQQSLQVGQALIQTF SQIVSLIANI

>core/798/5/Org5_Gene461

MADDTLIPKLMKNSLSQACSEGLLIAKYPPQLQVIVHFDNNLVVKTHLSVAPVFSCLFLGPAAHKAMQEIVLW
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>core/799/5/Org5_Gene916

MGFKNICKQGSQLYLNGIFPERILARKLKNC AKSYPR TALTIEVLVSSVLGALKVILIPCASTYAALTPLRALF
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PHTPPPFAD EYVPLISESYFD

>core/800/5/Org5_Gene829

MSHLNYLLEKIAASSKEDFPFPDDLESYLEGYVPDKNIALDTYQKIFKISSEDLEKVYKEGYHAYLDKDYAKS
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EMAWVRAQHKPLYNELKEEILDIRKHK

>core/802/5/Org5_Gene259

MSVHITPRKCFILCILSMFTLPTLFPKAHLILFSPYIVLCFYCF SKDKGLVLALGCGVLSDLALGSRGVFLLLYP
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>core/803/5/Org5_Gene558

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>core/804/5/Org5_Gene443

MTAEKQNTGILGLEIRYTLPSDATYMLKWLNDPKILRGFPIQTEAEIRETVNFWVGFYRYHSSLTAVYNGNV
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VEVGRQNRFYKDEIGYLAKTTEMEKDL

>core/805/5/Org5_Gene231

MKKLLFSTFLLVLGSTSAAHANLGYVNLKRCLEESDLGKKETEELEAMKQQFVKNAEKIEEELTSIYNKLQD
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>core/806/5/Org5_Gene87

MSEVKPLFLKNDSDLATQRFQNLINMLQEQAIEYNEYEEKNARVQNEIKEQKDFVKRCIEDFEARGLGVLK
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RVVVDDSYFEEEEKQKVDNRKKEQD

>core/807/5/Org5_Gene610

MCKNRGVRGIVACDPRGVIGLEGKLPWHYPEDLQFFSETIQKFPIVMGRKTWETLPRKYFVDRAVVVFSHEK
RQGVHGEIWVTSLEEFLLLDLSSPTFLIGGGELYSLFLENQIVRDFFISHIKKEYAGDTFFPLSLLETWTKTVLR
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>core/808/5/Org5_Gene50

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GHLGVVFSCGDPVSAAKQVLDFNKQHKDSLVLFLAGRMDNASLSGAEEVAVAKLPSLKELRQQVVGLFAAP
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>core/809/5/Org5_Gene61

MQRLGLSNLFHCLLLFLRYYYSKLVFGLTVLLAAISVICLLGCSEPSLSSFTEYVGPEYSAAAQLSIEQSCHDE
VYGQQVVVTWSLPSRMRKCLPVTLYLWVYYGNGKVEKLTYEVNQSAGYRVYCLKGLEYSYRVA
LCSGNQEIVSRRHHLWMEVISLDSP

>core/810/5/Org5_Gene774

MKQQLLLLEDVDGLGRSGDLITARPGYVRNYLIPKKKAVIAGAGTLRLQAKLKEQRLIQAAADKADSERIAQ
ALKDIVLEFQVRVDPDNNMYGSVTIADIIAEAAKKNIFLVRKNFPHAHYAIKNLGKKNIPLKLKEEVTATLLV
EVTSDNEYVTVLAQGKQTEENQEG

>core/811/5/Org5_Gene211

MIINVRAPAFGITSVQQFSTNFQAAIPILNIVIGCSRISSTYAEDIEEVAQEKLEKSTHSKSSTSVNLWAHRVRGV
VEILGGGIVILALEITALVLQVIIKLIKCLIDVLCVCLFGLGVCVVAIIIGAIAFCVVVVVVKYLGFCSQGEELEPIE
VKTLISPDKPYPTVVVYV

>core/812/5/Org5_Gene485

MSELIIGVDPGTIVAGYAIHAVEQRYQLRPYSYGAIRLSSDMPLPMRYKTLFEQLSGVLDDTQPNAMVLETQF
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>core/813/5/Org5_Gene480

MRQFCNLLSLSRLWLALYFCQEKLHIRLLAIVGAMLSDVLDGYLARRYKATSRLGSILDPITDKVFVFCITV
LYMEGSLSIAHLFFICARDLFLIIFVCYLSLVKGWKGYDYGSLSFWGKIFTVVQFILLGVTAGGEIPWTGLVPL
VALGFLYFLERIMDYKKQFLR

>core/814/5/Org5_Gene406

MATRFRSTLLVITLFLIDWVTKLVVLLQYKDLQILTHPTLYTHSWGRFSFSIAPVFNEGAAFGFLFSNYKYFLF
LLRIFVILGLLAYLFFKKKSIQSTTQTALVLLCAGAINVGDIIIFYGHIVDFISFNYKQWAFPTFNVADVLISLGT
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>core/815/5/Org5_Gene563

MAKYPLEPVLAIKKDRVDRAEKVVKEKRRLLEIEQEKLREKEAERDKVKNHYMQKIQQLRDLLDEGTTSDA
VLQIKSYIKVVAVQLSEEEKVNKQKEVLAASKELEKAEVNLAKRRKEEEKTRLHKEEWMKEALKEEARA
EEKEQDEMGLLFQLRQKKKRESGGS

>core/816/5/Org5_Gene266

MAVEQSHIKEEIEKLIKAIKRVCGNKENDLCRYLPGPSGGYMHHTLKKMKSAAPEQLLMLKTFILESETP
RTINPKPRAPRGSKKRRDFINFTKTDIERVLELARQVGDKDLLARFSPKKPLTSLKRELIRSIRNGIVSVELWNA
YVEAVKAVSSPNLEVTSPFV

>core/817/5/Org5_Gene131

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NGDPVQFGSKLFRIAKDAS

>core/819/5/Org5_Gene195

MSKKINRNDLCPCGSNKKYKQCCLKKEEQTARYTTTEGKFKFSAEVLASASEQGEAGDNCTKLFQRLSQSLTSE
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DFIPTQEDFRISENSQKPPVEED

>core/820/5/Org5_Gene297

MSRQNAEENLKNFAKELKLPDVAFDQNNTCILFVDGEFSLHLTYEEHSDRLYVYAPLLDGLPDNTQRKLALY
EKLLEGSM LGGQMAGGGVGVATKEQLILMHCVLDMKYAETNLLKAFAQLFIETVVKWRTVCADICAGREP
SVDTMPQMPQGGGGMQPPPTGIRA

>core/821/5/Org5_Gene751

MKFWLQGC AFVGCLLLTLPCCAARRRASGENLQQTRPIAAANLQWESYAEALEHSKQDHPICLFFTGSDW
CMWCIKMQDQILQSSEFKHFAGVHLHMVEVDFPQKNHQPEEQRQKNQELKAQYKVTGFPELVFIDAEGKQL
ARMGFEPGGGAAYVSKVKSALKLR

>core/822/5/Org5_Gene420

MSRRHSAEKRDIPGDIYGSVILEKFINKVMMHGKKS VARKIVYSALERFGKKLNLENVLEGFGEALENAKPI
LEVRSR RVGGATYQVPVEVASERRNCLAMQWIIKHARSKPGKSMEVGLATELIDCFNKQGATIKKREDTHR
MAEANKAFAHYKW

>core/823/5/Org5_Gene494

MSLSKN SHKEDQLEEKVLVVNRC SKVVKGGRKFSFSALILVGDGKGRLGYGFAKANELTDAIRKGGEEAAKK
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KALTGLSPRKDLLRRGA AIND

>core/826/5/Org5_Gene579

MTKFLY CGLFYSLG LLVLAFGTMVAIIQVDQICDVSCMNKHFQESPPFLKIKKVNVS KQICSPEERFFHCKIDK
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SSSGGMKTLYLSLFRN

>core/827/5/Org5_Gene767

MMHRYFIPLLALLIFSPSLVRAELQPS ENRKGGWPTQLSCAEGSQLFCKFEAAYNNAIEEGKPGILVFFSERPT
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AQCQAVLPLETKN

>core/828/5/Org5_Gene817

MSITTLGTLPTVNTINSSRPPLNTPKIGAVLF SIYELL LQAIEIRQQT VLTQSQQ LNDNTNIQQQLNQETNQI
KYAIVSAGAKEDEITRVQNQNQNYS AQRSNIQDELVTTRQNGQIILSHASTNINIQQQSSQDSSFIKTTNSIGST
VNQLNKPLG

>core/829/5/Org5_Gene317

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LLHLLNRDIDIPGFGMDEEQGLIFYRLVLPCLNGEIHDTLLRIYIDTIKLVCD SFSHAIGLISSGNMNLDELRRQ
ALQEQQEKRNE

>core/831/5/Org5_Gene800

MATLSPEKFSGSPISISKEFPQQKMREIILQMLYALDMAPSAEDSLVLLMSQTAVSQKHVLVALNQTKSILEK
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SLNENSLSI

>core/832/5/Org5_Gene296

MMFGHFAGYLGADPEERMTSKGKRVITLRLGVKTRVGMKDETVWCKCNIWHNRYDKMLPYLKKGSGVIV
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MYAGYGQEQQYVCEDVPF

>core/834/5/Org5_Gene160

MSKKVFFESYEDFANVASSWPKSLRALVQGRYFVDSELKETPYRIHDFKKTPIHHRLYRSLPIISTIGGIIRLIEA
HSGPIHPRDKMKYRFEVLQAVIEILGLGVLLVFDIIGCFLAFLVAIILSLLLYCNSTFTCVQNLSFTERMLEGIG
EAVNFLA

>core/835/5/Org5_Gene316

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KQQTNQD

>core/837/5/Org5_Gene37

MPSYCQNQQDFSLFSLSPRLVMFLGKHSRDEILQDLTDLVDAAGLLEDKQAFFDALVRRENIMSTGIGMGV
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IEEVMNVFVGM

>core/838/5/Org5_Gene663

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QDTSNKPS

>core/839/5/Org5_Gene385

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RKKHALLTA

>core/841/5/Org5_Gene762

MLPISILLFYVILGCLSAYIADKKKRN VIGWFFAGAFFGFIGLVVLLLLPSRRNALEKPQNDPFDNSDLFDDLK
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VPSLQQALKEASK

>core/842/5/Org5_Gene255

MRIIRFDPYGALSAQSIKDSRQNSPLVEKISEEIATNEAIRLALLAIGDREQEEKQRHRYKLLGQKQAKVLL
SQLRHVHLDFFKKLYCDSKKKEDQEKDEKNKQKRSIKVTKKKKGISLGAAASQAIAAAAEAWVIARNKGVLE
TASTLFYQKDEEA

>core/843/5/Org5_Gene763

MEKQNLKLDVKEIEFPETVFSRDIETRVIQVIILHCLAKINGVSLGGNLIDALFGRDIERMKGIYVEQDSKNHL
VKVRVEVNVDYGVSIPEKTEEIQGCIVSEISEYTGHLVAAVHVIIKGLTQPKDRIDEEIEEEVSVQDLSPEDFL
LENSEG

>core/844/5/Org5_Gene125

MIMTTISNSPSPALNPESLIPPTLVSSGTQTSLAYTIPAQGRRSTLRIILDIFIILGLATIISTFIVIFFLNGLNLS
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>core/845/5/Org5_Gene520

MRVVLHCPDIPQNTGNIGRTCVALGAELILVRPLGFSLADKFVKRAGMDYWDKLQLTVVDSIEEALHDVPED
QIFCLSTKGSASYTEFSLPSSGTYYVFGSESKGLPKEILKKYYKNCLRIPMQQDIRSLNLATSVGIVLYEVVRQKT
VALQKNPTV

>core/846/5/Org5_Gene812

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LDTVLYCTLEPCLMCAGAIQLARIPRIVWAAPDVRLGAGGSWVNIFTEEHPFHTVSVCTGGVCSEEAHLMKK
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>core/847/5/Org5_Gene278

MGYLPVSATDVLFESPAAPLINSANTQNQKLIELKGKQQAESSPRTITSVILEVLLVIGCCLIVLSLLAIRPALQF
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SQAQL

>core/848/5/Org5_Gene514

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DRRRQARLELK

>core/849/5/Org5_Gene707

MKTLKGHLSAKNLRIAIVGSCFNQAMADALVSGTQETFLKFGGSEDGLMTIRVPGA FEIFPCTIKKLLSSERKF
DAIVACGVLIQGETDHYNQIVNQVAAGIGALSLEFCLPITLSIVAAPSAEIAWQRSGIKGRHLGVSGMTTAIEM
ATLFTQI

>core/850/5/Org5_Gene674

MPFAKETEMQRTCWKCEGSVSMHVPQCPYCSAFLQDPPVASGGFSSCHISFPEGASKEEAEDLFAVSSSEDWE
AVLGDQNPTQETNKQVIPEWTWLQSWPLAALFLGIGLLAFAFLILLFSTDSGLVLTWPKNRAYFYGIIGAAVA
YRGYRKLPL

>core/851/5/Org5_Gene33

MRSALHLQHLRHFHNHGSILFENLLTIKDCFLLETKLQNFIKASKTIDTVRWRENIFRSMPEIYTVVRKRRLD
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VGIPVI

>core/852/5/Org5_Gene511

MNQPSVIKLRELLDLLPHRYPFLLVDKVLSDIEARSITAQKNVTINEPFFMGHFPNAPIMPGVLILEALAAQAA
GVLIGLVLENDNRNKRIALFLGIQKAKFRQAVRPGDVLTLQADFSLISSKGGKAWAQARVDSQLVTEAELSFA
LVDKESI

>core/853/5/Org5_Gene404

MQCPFCNHGELKVIDSRNAPEANAIKRRRECLKCSQRFTTFETVELTLQVLKRDGRYENFQESKLIHGLNAAS
SHTRIGQDQVHAIASNVKSELLGKQNREISTKEIGELVMKYLKKADMIAYIRFACVYRRFKDVGELMEVLLS
ATPDMEK

>core/854/5/Org5_Gene1056

MAQKEIVSNRKALRNYEVIETLEAGIVLTGTEIKSLRDHGGNLGDAYVIVSKGEGWLLNASIAPYRFGNIYNH
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MKRRHH

>core/855/5/Org5_Gene240

MARNIKYFLILFPGILWISAGMKLLLKATAIALDPLSSFFTYCLLSMVSWGLASLKHRYLLSKTIRKQLSLSEF
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>core/856/5/Org5_Gene178

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LTL

>core/857/5/Org5_Gene742

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YLFSS

>core/858/5/Org5_Gene711

MQLLSPAFAYGAIPKKYTCQGAGISPPLTFVDVPGAAQSLALIVEDPDVPKEIRSDGLWIHWIVYNLSTTITN
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EKS

>core/859/5/Org5_Gene187

MEKRKDTKTTIVKSSETTKSWYVVDAAGKTLGRLSSEVAKILRGKHKVTTYTPHVAMGDGVIVINAEKVRLT
GAKKGQKIYRYTGYISGMREIPFENMMARKPNYIIEHAIKGMMPRTRLGKKQLKSLRIVKGDSYETFESQK
PILLDI

>core/860/5/Org5_Gene1028

MEFICPLQHARCLKKQHKIIEELFPEPFQKDHLYLKLMENSSSRDAFDKKRVLKENLVVGCQSDLYLYEVYQ
DGILFFFTYTKALMSSGIASLFTEVYSGETPSTILTCKPIFFQRLTPYLSFGRLNGGESLYMRMKQIAVQYLKPP
QT

>core/861/5/Org5_Gene566

MADLEVFQADFALLFEAGLLAIKQGDEDSARKLFQSLHILNPNHYGHDLGLALISLHKMDLFD AEERLSALIK
GNEDNWSIKAFLSLTHMLIVLHQSSFEVRRESLESCLKFADQVIANCKIESTRALAQSVLDWHD TLVAKSA
GPLG

>core/863/5/Org5_Gene290

MKSERLKKLESELHDLTQWMQLGLVPKKEISRHQEEIRILEHKKIYEEKERLQLLKENG EIEEYVTPRRSPAKTV
YPDGPSMSDIEFVEPTETEIDIDPGETVELELTDEGRE DGAVEVDYSHEDDEDPFSDRNRWRRGGIIDPDANE
W

>core/864/5/Org5_Gene287

MKTKMNSRKKAGQWAFNSPTPGVSSTLVLA WTPWGYDYDKDVQDILERKDPMSSSLSEKDSKEFLKNLFVD
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KKRG

>core/865/5/Org5_Gene660

MSNIMGSRRKLKRSFLLIEVLMALSLVCAVLLPCIRFY YAIHRSFEEDIFNLQLPALIDHCFLSVEEKMRQQMA
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VTL

>core/866/5/Org5_Gene138

MKKKVTIDEALKEILRLEGAATQEELCAKLLAQGFATTQSSVSRWLRKIQAVKVAGERGARYSLPSSTEKTT
TRHLVLSIRHNASLIVIRTVPGSASWIAALLDQGLKDEILGTLAGDDTIFVTPIDEGRLPLLMVSIANLLQVFLD

>core/867/5/Org5_Gene251

MQNQYEQLLES LAPLLNTTLAPDKNNSCLIRFS DTHVPVQIEEDGNSGDLAVSTLLGTLPENVFRERIFKAALS
VNGSFQSSIKGILGYGEVTQQLYLS DILSMNYLN GEKLF EY LKLFSLHAKIWME SLRTGNLPDLHVLGIYYVA

>core/868/5/Org5_Gene733

MEEFVAYIVKNLVTNPEAVEIRSIEDEDNESIKLEIRVAAEDIGKIIIGRRGNTIHALRRTILRRVCSRLKKKVQIDL
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>core/869/5/Org5_Gene98

MSLEKELLEETPLVLLNFYKLVSFCNYAGMILGTEKKFAIYGHVSMGQAFQGADTEGHSPQRPFADLLNF
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>core/870/5/Org5_Gene158

MNPVTFDRIQVDFIPEDTSLRINSYIVAGGLLILGVVLSILSVICLDIGLVGLSAGAAFTLGLGCLIFALFLFSFSL
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>core/871/5/Org5_Gene36

MTVFCELDSGGELPEYTTPGAAGADLRANIEEPIALLPGQRALIPTGIKAEIPEGYELQVRPRSGLALKHGITVL
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>core/872/5/Org5_Gene529

MTFFEGETVFPAVLSELHSMMLDLIKRAGKQSKCPQEKLKLELACEELLVNIISYAYQGENSPGTIAISCISHRG
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>core/873/5/Org5_Gene483

MEQTLSIIKPDSVSKAHIGEILSIFEQSGLRIAAMKMMHLSQTEAEGFYFVHRERPFFQELVDFMVS GPVVVLV
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>core/874/5/Org5_Gene493

MIKLESLFDISERKRRKKLLGRGPSSGHGKTSGRGHKGDGSRSGYKRRFGYEGGGVPLYRRVPTRGFSHKRF
DKCVEEITTGRLAELFQEGEAITLDALKAKKAIARQAVRVKVLKGDLEKTFVWQDTAVVLSQGVQNLLGIT

>core/875/5/Org5_Gene182

MACSIFFRMSQGDYDDEPLSKKTACLVDTMLYPVIAVVCVVSVVLLILKVLFLLLSFPFKLCSASSALPGE
RVSLGSHFKCLYGGGLPYLLACLLIVPIGTAIHGFIISHRTSEDARLSSAIVFMQAPILQLAGMSGLIK

>core/876/5/Org5_Gene870

MQEHIHKELLHLGEIFRSSRESQSLSLKDVEAATSIRYSCLEAIEQGCLGKLISPVYAQGFIIKKYATYLGLDGD
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>core/877/5/Org5_Gene530

MSLDFFEEFYHQSI LNTGTSFPEGYL NIAEILSYPHCTDANTDFLCSQSDNDFIIAESKDKLT LFNADFAIWLVP
ELVQQQAVTRGYIAVSQGE GNYEP EMAFEASGQYNQSSLILEALQLYLKDIKDTENALRSFRFNNDH

>core/878/5/Org5_Gene489

MQHARKKFRVGR TSSHNR CMLANMLKSLIHYERIETTL PKAKELRRHADKMITLAKKNSLAARRIAIGRLM
VRYNKLT SKEARQAKGGDTSVYNVDRLV VNKLFDELGNRFVERKGGYTRILKLQNRIGDNAQKCIIEFLAS

>core/879/5/Org5_Gene596

MNSKSAQKIIDS IKQILTIYNIDFDPSFGSSLSSDSDADYEYLITKTQE KIQELDKRAQEILTQTGMSKEQMEVF
ANNPDNFSPEEWLALEKVRSSCDEYRKETENLINEITLDLHPTKESKRPKQKLSSTKKNKKKNWIPL

>core/880/5/Org5_Gene330

MLDNEWKAILGWGDDELEELRISGYSFLRQGHYSKAILFFEALVILDPLSIYDHQTLGGLYLQIGENSQALAV
LDQALRMQGDHLP TLLNKTKALFCLGRIEEATAIATYLSSCPIPAIANDAEALLMSYSKATKKNAALVR

>core/881/5/Org5_Gene517

MGRYRRVSHSSQETLLLGT ELGQVLVPGAVLLLFGDYGAGKTEFVRGIVSGYLGDTIAEEVASPSFSILHVYG
NEPKRLCHYDLYRIDQKNQEYIFQDAEEDDVLCIEWADRLPKPRFCDTINIYITMQTNMEREIIIEKR

>core/882/5/Org5_Gene48

MSVKKVIKIIKLQIPGGKANPAPP IGPALGAAGVNIMGFCKEFNAATQDKPGDLLPVVITVYADKTFTFITKQP
PVSSLIKTLNLESGSKIPNRNKVGKLTQAQVEAIAEQMKMDIVLLES AKRMVEGTARSMGIDVE

>core/883/5/Org5_Gene60

MIDMSVVG PALVLGLAMIGSAIGCGMAGVASHAVMSRIDE GHGKLIGMSAMPSSQSIYGFILMLLMQAAIKN
GTLSPVG GIIAGLSVGAALLVSSVMQ GKCCVSGIQAYARSSSIYGKCYAAIGIVESFSLFAVV FALLLL

>core/885/5/Org5_Gene758

MHPLTLPKQSRVLKRKQFLYITRSGFCCRG SQATFYVVP SRHPGTCRMGITVSKKFGKAHERNSFKRVVREV
FRHVRHQLPNCQIVVFPKGHKQRPVFSKLLQDFINQIPEGLHRLGKTKATTGGECTPKSEKCVTAPR

>core/886/5/Org5_Gene503

MLMPKRTKFRKQQKGQFAGLSKGATFVDFGEYAMQTLERG WVTSRQIEACRVAINRYLKRRGKVWIRIFPD
KSVTKKPAETRMGKGKGAPDHWVAVVRPGRILFEVANVSKEDAQDALRRAAAKLG IKTFRVVKRVERV

>core/887/5/Org5_Gene224

MNLIDRAFL LKKTIIFQSLDMDLLLTIADKTETIIFKPGSNVFSIGQPGFSFYIIVEGYITISKEKLESPLNLKPLDC
FGEESLFNNKPREYNASANTQVRMLVLSKGQILNIVEECPSVALSFLELYAKQIKFREP

>core/888/5/Org5_Gene163

MVNRYKSSAEFSADHYYDDNLVRMGYKRNL RGLAPVENEVCLFEENNLL ESVMASIPIMGSILGLGRLHSV
WSTQDPKDSKISII FHTALGILETLGLGIIVLLIKITITILLILFTPCLLCYFMYSAAYSDFHPI

>core/889/5/Org5_Gene169

MINFIRSYALYFAWAISCAGTLISIFYSYILNVEPCILCYYQRICLPLTVILGISAYREDSSIKLYILPQAVLGLGI
SIYQVFLQEIPGMQLDICGRVSCSTKIFLSYVTIPMASVVAFGAIVCLLVLTKKYRG

>core/890/5/Org5_Gene631

MKYRFTEEIEEEPLVNLTPIDIVFVILMAFIVAVPLIKLDSIALAPGTQEQEVLSSENDSIAMIKVVFADHSLTLN
EHPITLQELTVRLTLLHKAYPEKTPLLLQDGETSFRTYQNVKNAIEAAGFHELHVALQN

>core/891/5/Org5_Gene186

MAKSTIQESVATGRRKQAVSSVRLRPGSGKIDVNGKSFEDYFPLEIQRTTILSPLKKITEDQSQYDLIIRVSGGG
IQGQVIATRLGLARALLKENEENRQDLKSCGFLTRDPRKKERKKYGHKKARKSFQFSKR

>core/892/5/Org5_Gene608

MIAIERYQLISKFRMWLFLGCSVEERHFKQPVLISVTFSYNEVPSACLSDKLSDACCYLEVTSLEEIANTKPY
ALIEHLANELFDSLVISFGDKASKIDLEVEKERPPVPNLLNPIKFTISKELCPSPVLSA

>core/893/5/Org5_Gene168

MPYYANTLEFIQGTQSLCPLFKYGFVRHHYKGQLEIEDASHDWDWFLEPPSTWKRTLLAAIPILGSVGIGRLFS
IWSIREPQDSQEYKSIFWHTLCAVLEILGLGIVALILKILATFIMAMPGLKRVATFLFYS

>core/894/5/Org5_Gene497

MGMTSDSIADLLTRIRNALMAEHLVYDVEHSMREAIKILKHKGFFVAHYLVKEENRKRMRVFLQYSDD
RKPVIHQKRVSKPSRRVYVSAKIPYVFGNMGISVLSTSQGVMEGSLARSKNIGGELLCLVW

>core/895/5/Org5_Gene490

MVKNQAQAKKSVKRKQLKNIPSGVVHVKATFNNTIVSITDPAGNVISWASAGKVGYSGRKSSAFAATVAA
QDAAKTAMNSGLKEVEVCLKGTGAGRESAVRALISAGLVVSVIRDETPVPHNGCRPRKRRRV

>core/896/5/Org5_Gene999

MNFVSTLTGSDFYAPVLEKLEEFADTTGQAILFSSSPDFIVHPIAQQLGISSWYASCYRDQSAEQTIYKKCLT
GDKKAQILSYIKKINQARSHTFSDHILDLPFLMLGEEKTVVRPQGRLKKMAKKYYWNIV

>core/898/5/Org5_Gene203

MSQCQSSSTSTWEWMKSFVPNWKNPTPPLSPIPSEDEFILAYEPFVLPKTDPENANPPGTSTPNVENGIDDL
NPLLGQPNEQNNANPNPGTSGSNPTSLPAPERLPETEENSQEEEQGSQNNEDLIG

>core/899/5/Org5_Gene570

MLEKLIKNFATYMGITSTLELDADGAYVLPISVVKVRAQQNADNEIVLSASLGALPPSADTAKLYLQMMIG
NLFGRETGGSALGLDSEGNVVMVRRFSGDTTYDDFVRHVESFMNFSETWLSDLGLGKQ

>core/900/5/Org5_Gene309

MRDHAFSKLIGTVRAMVVEGRCPWSLQQSLVSMVEHILGECQEFHEAVLQGKTVQEVGSEAGDVLTLVLIL
CFLLEREGVLASEDVANEAMEKLRRRAPYIFAEDYKPVSIIEADRLWELAKHREKNEST

>core/901/5/Org5_Gene54

MKNKMDYKSQLVFSCPCCKGNVCFSVFNLDVILTCNVCSSSTYTFDSVIRNEIRQFVALCKRIHDANSILGNA
TVSVSVEDNQMDIPFQLLFSRFPVVLNLSLDGKKIAIRFLFDALNTSILHQESDLIS

>core/902/5/Org5_Gene351

MREEGSVSFREYFRAYMCDKIVAQKNFLFTLDAVIKQAGWRSQEKLNLFYVESQALGREIKVSLEEYIQSMV
GILGSQRTKKSFKFSVDFTPLEQALQERCSSDDDEDATATSTATGATASPTDMHEDE

>core/903/5/Org5_Gene51

MTTESLETLVEKLSNLTVLELSQLKKLLEEKWDVTASAPVVAVAAGGGGEAPVAAEPTEFAVTLEDVPADK
KIGVLKVVREVTGLALKEAKEMTEGLPKTVKEKTSKSDAEDTVKKLQDAGAKASFKGL

>core/904/5/Org5_Gene627

MKFTVALFGAEKGSYDTAYFCRSLVDLHNYLGDVSSPGITLAIKTLLSDYNVVYFRVREEGYCVDSYFFGL
HFLNTQTTLKNIIAIGLPGVGNQHIIASRSLCQKHNSLLLFFDHDLYDLLTFNQPF

>core/905/5/Org5_Gene950

MRAGGSLVTTYPKQGRLRSPEQLRVLDDL VQSYPNHLHAIELDCGAIPQDLIGATYIITFADFSXYILSLRSY
QANSPSDDTWGIWFGSIDDPVQAVISFLKDHGFALPSTLAQDPLLCTNK

>core/906/5/Org5_Gene165

MLIGRYSSDDQFTEATKNTPTIIKLG FVRDNLEGLTNPIS EIVSETSSSIKDSVLRSLPILGSILGCARLYSTLSTN
DPLDETQEKIWH TIFGALET LGLGILILLFKIIFVILHCIFHLVIGFCK

>core/908/5/Org5_Gene405

MPLSDDEIEQFKKR LLEMKAKLSHTLEGNAQEVKKPNEATGYSQH QADQGTDTFDR TISLEVTTKEYELLRQ
INRALEKINESSY GICDVS GEEIPLARLIAIPYATMTVKAQE QFEKGLLSGN

>core/909/5/Org5_Gene495

MESSLCKKSLMKRRRALRV RKVLKGSPTKPRLSVVKTNKH IYVQLIDDSIGKTLASVSTLSKLNKSQGLTKK
NQEVAKVLGTQIAELGKNLQLDRVVFDRGPFKYHGIVSMVADGAREGGLQF

>core/910/5/Org5_Gene421

MPTINQLIRKRRKSSLARKKSPALQKCPQKRGVCLQVKT KTPKKPNSALRKVAWVRLSNGQEVIAYIGGEGH
NLQEHSIVLIQGGRVKDLPGVRYHIVRGTLDCAAVKNRKQSR SRYGAKRPK

>core/911/5/Org5_Gene718

MALKDTAKMKDLLDSIQHDLAKAEKGNKAAAQRVRTDSIKLEKVAKLYRKESIKAEKSGLLKRPSTKAP
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>core/912/5/Org5_Gene659

MKRQKRKQSITLIEMMVVITLIGIIGGALAFNMRGSIHKGKVFQSEQNCAKVYDILMMEYATGGSSLKEIIAH
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>core/913/5/Org5_Gene694

MRDRLGSLSLILKVKIHKYLDTLHNQKRLALTVSRNIQATNKRIADLHLERYEHFISRDNIKHYDILLEYLKTL
QSSLYKQQSESLRFLEIHHQQLQELINRRKIIKIKNNKYSKDQEIGT

>core/914/5/Org5_Gene491

MPRIIGIDIPAKKKLKISLTYIYGIGSARSDEIHKKLKDPEARASELTEEVGRLNSLLQSEYTVEGDLRRRVQS
DIKRLIAIHSYRGQRHRLSLPVRGQRTKTNSRTRKGKRKTVAGKKK

>core/915/5/Org5_Gene500

MIQQESQLKVADNTGAKKVKCFKVLGGSRRRYATVGDVIVCSVRDVEPNSSIKKGDVIKAVIVRTRRHITRK
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>core/917/5/Org5_Gene241

MEIIHIGTDIIISRIREAIAATHGNRLNLRIFTEAEQKYCLEKTDPIPSFAGRFAGKEAVAKALGTGIGSVVAWKD
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>core/918/5/Org5_Gene82

MVNLLKELEQEQRNDLPEFHVGDITRLATKISEGGKERVQVFQGTVMARRGGGSGETVSLHRVAYGEGME
KSFLNNSPRIVSIEIVKRGKVARARLYYLRGKTGKAAKVKEFVGPRSSKK

>core/919/5/Org5_Gene803

MVRATGSVASRRRRKRILKQAKGFWGDRKGHIRQSRSSVMRAMAFNYMHRKDRKGDFRSLWIARLNVASR
IHSLSYSRLINGLKCANISLNRKMLSEIAIHNPEGFAEIANQAKKALEATV

>core/920/5/Org5_Gene164

MRELNAFELTQPEEYRNRWVLMPCCLKRFCRTQHAKVWSYRCVHEASLYEKNCFLLTYDDKHLPQYGSL
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>core/921/5/Org5_Gene237

MATVAQTPQTTQPQPSVSHKATHRYCSWVFFKPILVSLGLLLASLTTLGLVIASGVTLISLGIGIVLAIQIVLAGI
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>core/922/5/Org5_Gene245

MTENRRIKRVNALLQEAIKVILKDVKHPKISNLWITVTRVSLSKDLHSARVYVSVMPHENTKEEAEALKV
SAGFIAHRASKNVVLKYFPELHFYLDDIFSPQDYIENLLWQIQEKEKS

>core/923/5/Org5_Gene652

MNKKPKKTKKAVQSKAAPVKRVPEESQEAAIQQLELAVSDLYKELPLAQTFASLTDKNQINSIIAALSGTLES
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>core/924/5/Org5_Gene408

MDNYLLGSLIFCCVLLSIGMCTIFVMTICFLRQLNKILKNIHRVTTLNFEAKILAPLMLGKKLLCGWLKKRKN
RGSLSIEDIDELLDEKKQRSWKKNLDQGIKWCAALVLIWKVFRNKD

>core/925/5/Org5_Gene740

MDSFCFDLLKVAAKAIDDKKGNNLVVLDVRTISEFTDYFVFVEGSVNVHVKALANTIVEELKKQKVSPLHVE
GITDGNWVVIDYGFIVVHVVFVSEIRGKYRLEELWKDGFIVTSKLLAS

>core/926/5/Org5_Gene282

MPVSSAPLPTSHRPSSGNLGLMEPNKALKAKHQDKTTKTIKLLVKILVAILVIEVLGIIAAFFIPGTPPICLIILG
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>core/927/5/Org5_Gene80

MALKIRLRQQGRRNHVVYRLVLADVESPRDGKYIELLGWYDPHSSINYQLKSERIFYWLERGAQLSSKAEAL
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>core/928/5/Org5_Gene867

MSLNKEIGMTVLFYAFLFIFLFLCVILCGLILVQESKSMGLGSSFGVDSGDSVFGVSTPDILKKVTSWCAVAFC
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>core/929/5/Org5_Gene717

MLSRIVTCFLFLLSSLPLFAEEEEAAQSKNTFVQPAVMLAIAILFFYFILWRPEQKRRKAMEKRKNDLAKGDKV
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>core/930/5/Org5_Gene387

MSDIQKEEHGSTTIFHLHGKLDGISSPEVQENISQSLAAGSKNIILDCAHLDYMSSAGIRVLLQSYHQVGQHSG
KIVLTTVPKTIEQTLYVTGFLSYFKIFNTVDEAIQTLNKDGD

>core/932/5/Org5_Gene210

MFLKRKKRGGSQVQNKRTASPIKHAKHYLHNYLQELQKIMAARPHDAIDAWNQVFRDKYKGMSQAIGFRD
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>core/933/5/Org5_Gene302

MSKVSVRKKNWGFRLLEEVMIKSWWVIFSILIGGFVYDRAIQELRTEELRLQSKVSSLCQDILSAQEKQRQLQ
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>core/934/5/Org5_Gene340

MWYSDYHVWILPVHERVVRLGLTEKMQKNLGAILHVDLPSVGSLSCKEGEVLVILESSKSAIEVLSPVSGEVID
INLDLVDNPQKINEAPEGEGWLAVVRLDQDWDPSNLSLMDEE

>core/936/5/Org5_Gene772

MGKKENQLYEGAYVFSVTLSEEARRKALDKVISGITNYGGEIHKIHDQGRKKLAYTIRGAREGYYYFIYFSVS
PGAITELWKEYHLNEDLLRFMTLRADSVKEVLEFASLPE

>core/937/5/Org5_Gene734

MTAVLILTSFPSEESARSLARHLITERLASCVHVFPKGTSTYLWEGKLCESSEHHIQKSIDIRFSEICLAIQEFSG
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>core/938/5/Org5_Gene504

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>core/939/5/Org5_Gene499

MKKQNIRVGDKVFILAGNDKGKEGKVLSTEDKVVVEGVNVRIKNIKRSQQNPKGKRISIEAPIHISNVRLTIA
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>core/940/5/Org5_Gene338

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>core/943/5/Org5_Gene506

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>core/945/5/Org5_Gene367

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>core/946/5/Org5_Gene736

MNLSAKEYGDIIVIYLQGS�DAVSVPVQEQYLEQFIQKKHLKIALNFTDVSYISSAGIRLLLSNFKLVQSLGGK
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>core/947/5/Org5_Gene396

MASSATPGFDGTAPSLFPPATRPRYNFKLALFVTIAIALVWIALIATTIAIGLCIHPLCSFIFLTAIPLYFISRYICS
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>core/948/5/Org5_Gene77

MKKNTHPEYRQVLFDVSSTGYKFVCGSTYQSEKTEVFEGKEYPVCYVSVSSSSHPFFTGSKKFVDAEGRVVK
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>core/949/5/Org5_Gene22

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>core/950/5/Org5_Gene925

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>core/952/5/Org5_Gene466

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>core/954/5/Org5_Gene415

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>core/955/5/Org5_Gene575

MSFTYFLALPVDRLMQERFLCSPKRWAPFINSPLYTLTIADHDTPYLAKNLDFPLPVEQWEKTVLHVSSLLK
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>core/956/5/Org5_Gene450

MNERTLLLLLKKKKGLFLAILDLTQTESSLTPPELEKVLKQKKIFLSCIDRVDLQIKEFRHAFSSELPQDIQEEL
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>core/957/5/Org5_Gene418

MKQQKQKIRIRLKGFDQGGQLDRSTADIVETAKRTGARVVGPIPLPTKREVYTVLRSPHVDKKSREQFEIRTHK
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>core/958/5/Org5_Gene283

MSSPVVTGTSSASPVEQTKLGEFLERLSGSGRCIKIAFAASTALLLNFTVSGIVAIAMIFVATSVGAYFTVIGP
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>core/959/5/Org5_Gene459

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>core/961/5/Org5_Gene519

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>core/962/5/Org5_Gene94

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>core/963/5/Org5_Gene339

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>core/964/5/Org5_Gene761

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>core/965/5/Org5_Gene2

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>core/967/5/Org5_Gene409

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>core/968/5/Org5_Gene323

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>core/969/5/Org5_Gene605

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>core/970/5/Org5_Gene830

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>core/971/5/Org5_Gene574

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>core/972/5/Org5_Gene963

MCLIDCLGQGFEAAINTVCCCSDSSESKANVATVSAGLLALTAIVSFILILICTGVLGASGMTFGMSNVA AVL
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>core/974/5/Org5_Gene617

MLSyllRTAINVYSFLILAYIFASWVPDCQSARWYQLVSKCVDPFNLFFRRFVPRIGFIDPSPFVGLLCLGILPF
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>core/975/5/Org5_Gene258

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>core/976/5/Org5_Gene85

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>core/977/5/Org5_Gene423

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IALGILLINCVC DLKQYLTSS

>core/978/5/Org5_Gene23

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>core/979/5/Org5_Gene327

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>core/980/5/Org5_Gene665

MLAFFATSFKSVLFEYSYQSLLLILIVSAPPIILASIVGIMVAIFQAATQIQEQTFAFV KLVVIFGTL MISGGWL
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>core/982/5/Org5_Gene474

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>core/983/5/Org5_Gene1

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>core/988/5/Org5_Gene276

MAKLVITSDDDEQQEFELEDNSEIAEPCESMGIPFACTEGVCGTCVIEVLEGRENLSEFTEPEYDFLGEPEDSNER
LACQCRIKGGCVKVTF

>core/989/5/Org5_Gene374

MDDSWILEVKVTPKAKENKIVGFDGQALKVRVTEPPEKGKANDAVISLLAKALSLPKRDVTLIAGETSRKKK
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>core/990/5/Org5_Gene427

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>core/991/5/Org5_Gene811

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>core/992/5/Org5_Gene253

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>core/993/5/Org5_Gene882

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>core/994/5/Org5_Gene128

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>core/996/5/Org5_Gene445

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>core/997/5/Org5_Gene766

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>core/998/5/Org5_Gene501

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>core/999/5/Org5_Gene863

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>core/1000/5/Org5_Gene567

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>core/1001/5/Org5_Gene414

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>core/1003/5/Org5_Gene47

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>core/1012/5/Org5_Gene577

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>core/1016/5/Org5_Gene725

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>core/1018/5/Org5_Gene582

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>core/1031/5/Org5_Gene885

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>core/1033/5/Org5_Gene802

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>core/1034/5/Org5_Gene364

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>core/1037/5/Org5_Gene428

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>core/1045/5/Org5_Gene779

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>core/1046/5/Org5_Gene532

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>core/1050/5/Org5_Gene18

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>core/1054/5/Org5_Gene306

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>core/1056/5/Org5_Gene1044

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>core/1058/5/Org5_Gene384

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>core/1067/5/Org5_Gene832

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>core/1069/5/Org5_Gene760

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>core/1070/5/Org5_Gene759

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