

Sequence of Cytoplasmic proteins

>core/3/1/Org1_Gene886

MASSSNSTKQDGIPSWVNPVQWNRASQVGDQEANSLTPEAQTSRSWFSDRKHFLVLDVSLEEMENNDLKKYSRYKTIILATLV
TVAITCIVPISMVFGIPMWVPCILIFGAGLSSAFLSHRLQSKCKEIHLYRAYQIYRQQLLSQYPDLRKSTLYKYSITHVKPKKGFVGKLVE
NLRPDLHKNKDDGGAAADSRLDFAGYGVKHYQTDALLGVSGVNSVEWQRLASLIMSVKNDILNDVGSREPIDKAQRSALVVSQKDIG
GEIQPGGILDISRDILAICGYGMNVGVEAKKAIDQYKKWYLNSTFIWNPQLPAIAQSYLLEQQRHLDYAAKIFQDLSALTTAHGTGQ
ALEDLSLLCYDQLIESKGVGEKIIASHQKHLDLAMQDSCDQEHLLKWSNLYHVFSITIKEFTEGKLEQNEVVSRIQRLRGKLEKSKCSI
LGNCRTNAEYATKSEKKLADYLLQIGDREPFLTGMHKAIAATGKAIQKQVEGVISQHPKQIMMLRCSIERLEGMLRREDWGAILQKNE
DEVLALKSTMEAQLQGFKDLVGTWEGKYQEFKKNKLSKVLVYDFTKSYSNLLNRLEVLAESSTDDLVLHVDRMSEDLLKKTIEIDGNL
FQVTPEELSLAREYQGLMNELPLIVQEGNRLQEAISSEGVSSQGLMLLNLLNRDEKINKNIESSRKNLVIAIAKQARSDARNIDSQGLAPL
IQRNRASLDNILQNMFLNGSIRNIHALDTETLVATSSNMFSAMHTFDWNIYTNLLDVLEIQSKPAPAPMENPDLPGALPEEVQDAVA
EDVSGTHRLHHQVLKRRCADLKNMISQLQKSINKWGMKAIVLGIVAVLFCVLSAIFIGQNILSLLILSCVGLLLTQVCPLIFDRISKSKEFE
KQVLETAQSLIPATKILPSEFNNDLNLRLAKLQDNLNLEGGPTWARNIVSDLEGIPTKEKSLKDLTKEFRKDSKNLNLKRIKRRFKEGLGQ
EAPVVRPTIPQDIRGAEVFAELHRELEHLQKQKEEISIRGDALVQERMGLCLEKSKYDNEKAHAAAMTKKVGLQNIIDRLQKNNETYV
RIQNFRTLIQEKLRDRTVQEIDVVKEAKELHELAIIYGNSTSGKSQKQRAKKQFKENVLHIAAGKGQLELLEAYLNVTASQGLCRHQM
ASFRERILLNPDGAKHGEAERTLASREEMKTLGLSYLTPFVRFSSPESTQSGYNQILKVREQLFDIEQRLQNQETVSPEDYAAVQAALA
AYVRKHESLIVSTYGLGAQEGQTSSKVTTLMRDLHAVEELVEMGVETRYLRNRSQDILHRVHVSVLHSHLRDSDSSNGIIDVVKKLFELLN
NNGNNPNDPECQKYMQILLDAPVSLLYGAFKSFKNFLLNFTELNIANSTKAAEEEAKRYVEEKGRGFETYWEEAKQRLEAIAAELDDL
RNQETLLEQEIRLANLKISIFSDLNLREKVSVEKAAEEEEIQGIEQYAEQQGIEDLELKQKFEDLQKKLEALEERLLQIGRRIDSSVDKQKE
LLGLLGREEAA

>core/8/1/Org1_Gene500

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LLCKNEQGYRNLCILTSLAFTGEFYFPRIDKDLLRQYSEGLICLSGLSSVSDAALKSPEALLLELQWFQDLFKDDYFTEVQLHKMSEESI
AGFKEEWLQKEYSLIEKQIKVNTAVLEASKRLGIPTVATNDIHYINANDWQAHEILLNVQSGETVRIAKQNTHIPNPKRKVYRSREYFF
KSPAQMAELFKDIPEVISNTLEVAKRCDFTDFSKKHYPYVPESLKTLSYTEEDRYQASAVFLKQLAEALPKKYSSEVLAHIAKKFPHR
DPIDIVKERMDMEMAIIIPKGMCDYLLIVWDIIHWAKANGIPVGPGRGSGAGSVLLFLLGITEIEPIRFDLFFERFINPERLSYDPIDIDICM
AGRERVINYAIERHGKDNVAQIITFGTMKAKMAVKDVGRITLDMALSKVNHIKHIPDLNTTLSKALETDPDLHQLYINDAESAQVIDM
ALCLEGSIRNTGVHAAGVIICGDQLTNHIPICISKDSTMITTQYSMKPVESVGMLKVDLLGLKTLTSINIAMSIAIEKKTGQSLAMATLPLD
DATTFSLLHQGKTMGIFQMESKGMQELAKNLRPDLFEEIIMAGALYRPGPMDMIPSFINRKHGKEIEYDHPLMESILKETYGIMVYQE
QVMQIAGALASYSLGEGDVLRRAMGKKDFQQMEQEREKFKRACNNGIDPELATVIFDKMEKFAAYGFNKSHAAAYGLITYTTAYLK
ANYPKEWLAALLTCDSDDIEKIGKLIREAQSMGIPILPHINVSSNHVFATDEGIRFAMGAIGIGRGLIESIVEERDHHGPYESIRDFIQRS
DLKKVSKKSIESLIDAGCFDCFDSNRDLLASVEPLYEAIKDKKEAASGVMTFFTLGAMDRKNEVPICLPKDIPTRSKELLKKEKELGIY
LTEHPMDTVRDHLSRSLSVVLAGEFENLPHGSVVRTVFIIDKVTTKISSKAQKKFAVLVSDGIDSYELPIWPDMYEEQQELLEEDRLIYAIL
VLDRSDSLRISCRWMKDLNENIIECDQAFDRIKNQVQKMSFTMSTSGKETAKGNKPNENGHTQALAPVTLSDLNLRLHSHL
CILKKIVQKHPGSRTLVLVFTQDNERVASMSPDDAYFVCEIDIELRQELVTADLPVRVITV

>core/12/1/Org1_Gene955

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DLPTRAWRVDEHGHKQLIPVRKHYIMCLSELLSQELHLDREAIEDAIHAKASVLGSVPYLVAANVSERTYCLKMLSKDWPGLVHVEAVV
RRHYPQESVASDILGYVGPISLQEYKRVTELSQLRECVRAYEEGEDPKLPEGLASIDQVRALLESVESNAYSLNALVGKMGVEACWDS
KLRGKIGKKPILVDRRGNFQEMEGAVPEAPGTKLQLTSAELQAYADALLEYEKTETFRSAKSLKKREKLPLFPWIKGGAIALDPNNG
EILAMASSPRYRNNDNFVNAKVAEDSKAVRSSIYRWLENKEHIAEIYDRKVPLIRERRNPLTGLCYEEILPTFDCFLDFLPENSVIKLQKLR
NSFVGQAIEVQNLVTRLLSLFPYEEGTCPCSAIFDAVFPNEEGHILIQEVISLREQKWIMECLNQHKADIEELKEALDQVFNELPANYDKIL
YTDILRLIVDPERFSPVLPSEVHRLSLSEFTELQGRYVVLRSASFSTILEDAFIEVHFKSWRKSEFLQYLAARKQEEALRKQRYPTPYVDYLEEE
KTRQYKMFCEHLDTFLAYLFSKTPYKEGLEPYDILDWINELDNGAHRALSWHEHYLFLKERVSHLSEHLPALFSTFREFNELQRPLL
KYPISIVRNKRQTEQDLAASFYPVYGYGLRPHAYGQAATLGSIFKLVSAYSVLSQRILWGHNEEPANPLVIIDKNSFGYRSSKPHVGF
DGTPIPTFFRGGSLPGNDFMGRGFIDLVSALMSSNPYFSLLVGEGLDPEDLADAASLFGFGEKTGLGLPGEYAGRVPHDLAYNRSGL
YATAIGQHTLVVTPVLTAVMLASLVNGGVVYVPKLLGEWEGEHVSYLSSKKKRTIFMPDAVVEVLKTGMRNVIWGQYGTARAIQSQ
FPPQLLSRIIGKTSTAESIMRVGLDREYGTMMKMDIWFAAVGFSDQDLSLPTIVVIVYLRGEGFRDAAPMAVKMIDMWEEKIQQRESF
LRG

>core/24/1/Org1_Gene643

MLGFLKRFFGSSQERILKKFQKLVDKVNIDEMLTPLSDDELNRKTAELKQRYQNGESLDSMLPEAYGVVKNVCRRLAGTPVEVSGYH
QRWDMVPYDVQILGAIAMHKGFIEMQTGEGKTLTAVMPLYLNALTGKPVHLVTVNDYLAQRDCEWVGSVLRWLGLTTGVLVSGT
LLEKRKKIYQCDVVYGTASEFGFDYLRDNSIATRLEEQVGRGYFFAIIDEVDSILIDEARTPLIISGPGEKHNPVYFELKEKVASLVYLQKELC
SRIALEARRGLDSFLDVDILPKDKKVLEGISEFCRSLWLVSKGMPNLRVLRVREHPDLRAMIDKWDVYHAEQNKESLERLSELYIIVD
EHNNDFELTDKGMQQWVEYAGGSTEEFVMMMDMGHEYALIENDETSPADKINKKIAISEEDTLRKARAHGLRQLLRAQLLMERD
YIVRDDQVIIDEHTGRPQPGRRFSEGLHQAIEAKEHVIRKESQTLATVTLQNFFRLYEKLAGMTGTAITESREFKEIYNLYVLQVPTFKP
CLRIDHNDEFYMTEREKYHAIVNEIATIHGKGNPILVGTESVEVSEKLSRILRQNRIEHTVLNAKNHAQEAIIAGAGKLGAVTVATNMA
GRGTDIKLDNEAVIVGGLHVIGTTRHQSRRIDRQLRGRCARLGDPGAFFLSFEDRLMRLFASPKLNTLIRHFRPPEGEAMSDPMFNR
LIETAQKRVEGRNYTIRKHTLEYDDVMNKQRQAIYAFRHDVLHAESVFDLAKEILCHVSLMVASLVMSDRQFKGWTLPLNEEWITSSF
PIALNIEELRQLKDTDSIAEKIAAELIQEFQVRFDHMEVGLSKAGGEELDASAICRDVVRSVMVMHIDEQWRIHLVDMDLLRSEVGLRT
VGQKDPLEFKHESFLLFESLIRDIRITIARHLFRLELTVEPNPRVNNVIPTVATSFHNNVNYGPLELTVVTDSEDQD

>core/58/1/Org1_Gene679

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RKGDCDYGVKILQKLLALRLPKDARKDLQILWHRLNPEQAPLRDVVDQLFTIGCHESLQDHLLFELYTVTLHSGYENRKQDMLLAKEQG
DYKKAIELAKELVAALEKGSCSPHPEIVQIEKTFLOKTLALQIKVAQEAQESCDALLTPYCLSEIAYTEAMDALVLRARGEVSRTNEVDS
VLLSHALQHLPFAREKAPELEVLIDHGAYLESTLLYYAFSLLELYHQNKDFASLERLLEKGDVAVFVPEHPYFPEYGFLLGAYFYAKGKYES

AEKVFLQIIDPAVKLGATFARAYEYLGCIAYVQNHYEKAEYFLRAYKSWGREESGIGLFLAYAVQKKKTACEDMLYHPKFSFTYRHLLDS
LCSLSYPHGENKGSSAIQVRVHRAVPELSEIYSRCIYDMIKYRNVITYTHPIELAYNQVRNLEKRNLEEICRDAQDPEYDKALAFW GALQSG
ASVPRSLIESSDVDEARITIRCYEALYFHNPDIAI MLPQAFSEECNSWQTALRLVWTLVRPKGAPNHAKYWDHLVLRPHGDSLYFFGY
DLQEYLGKEDALKHLSVFAELFPKSSLLSLVYYLQGYSESSALRKVGWVFKALEEFTEISWSGHEMKTWAYIYYMVKLDLADTYISLGNF
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RFLGV

>core/65/1/Org1_Gene438

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GAKLFDSEGQAYTIKKSKLRGVESQGMCCGADELGLDELQIQERALLELPEATPLGEDLATVLGNTSLEISLTPNLGH CASFLGLAREICH
VTQANLVIPKEFSFENLPTTALDMGNDPDCPFFSYVVITGISAQPSPIKLQESLQALKQKPINAIVDITNYIMLSLGQPLHAYDASHVALD
SLRVEKLSTPESLTLNGETVLLPSGVPVVRDDHSLGLGGVMGAKAPSFQETTTTTVIKAAAYFLPEALRASQKLLPISESAYRFRTRGIDP
QNVVPALQAAIHYLEIFPEATISPIYSSGEICRELKEVALRPKTLQRILGKSFSIEILSQKLQSLGFSTTPQETSLLVKVPSYRHDINEEIDLVEE
ICRTESWNIETQNPVSCYTPYIKLKRETAGFLANAGLQEFFTPDLLDPETVALTRKEKEEISLQGSKHTTVLRSSLLPGLLKS AATNLNRQA
PSVQAFEIGTVYAKHGEEYQETQTLAILLTEDGESRSWLPKPSLSFYSLKGWVERLLYHHHLSIDALTLESSALCEFPYQQGVLR IHKQS
FATLGQVHPELAKKAQIKHPVFFAELNLDLLCKMLKKTTKLYKPYAIYPSSFRDLTLTPEDIPANLLRQKLLHEGSKWLESVTIISIYQDKS
LETRNKNVSLRLVFQDYERTLSNQDIEEEYCRLVALLNELLTDTKGTINS

>core/67/1/Org1_Gene856

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ILDQLPQELDQLDRYIQEVFACLGPLKDLKYEDQGFLQDVKEEFQVDFVQKDMIAEFVELQQILCQEGRLLLEFVINQTRYIGRDLFKRE
DSLYKLWEWLGYPSPGDVRGERLKKSAREVVDRFMRTTCNIRKIAMTFDRHVYSVAKTAFEKAFGALET CVYESMRESYREAFCEYEK
AKLLGDEEKSAHAEQRFQDIKNRWEDVKDAFFWVKEDGKIEIDDAIGNSCKWSERYEEHRITRARWYKVAEHQLFNATMRVKDSLRE
HNEARVAFEKERSKENQRQVQKKKEKRLRDLKELHDQELPRAQERLRELQALYPEIAVSVVEARREVASDLEKAHESIDKHYQSCVREQ
ELY

>core/69/1/Org1_Gene1003

MLLLISGALFTLGIPGLSAAISFGLGIGLSALGGVLMISGLLCLLVKREIPTVRPEEIEGVS LAPSEEPALQAAQKT LAQLPKELDQLDTDI
QEVFACLRKLDKSKYESRSFLNDAKKELRVDFVVEDTLSEIFELRQIVAQEGWDLNFLINGGRSLMMTAESESLDFHVSKRLGYLPSG
DVRGEGLKKSAAKEIVARLMSLHCEIHKVAVAFDRNSYAMA EKAFAKALGALEESVYRSLTQSYRDKFLESERAKIPWNGHITWLRDDAK
SGCAEKKLRDAEERWKKFRKAVFWVEEDGGFDINNLLGDWGTVLDPYRQERMDEITFHELYEKTTLKRLHRKCALAKTTFEKKRSKK
NLQAVEEANARRLKVVRDWYDQEFQKAGERLEKLHALYPEVSVSIRENKIQETRSNLEKAYEAIEENYRCCVREQEDYWKEEEKREAEF

RErgnkILSPeelessleQFDHGLKNfSEKLMELEGHILKLQKEATAEVENKILSDAESrLEIVFEDVKEMPCRIEEIEKTLRMAELPLLPtk
KAFekACSQYNSCAEMLEKVKPYCKESLAYVTSKERLVSLDEDLRRAYTECQKRfQGDSGLESEVRACREQLRERIQEFETQGLDLVEKE
LLCVSSRLRNTECDCVSGVKKEAPPgKKFYAQYYDEIYRVRVQSRWMTMSERLREGVQACNKMLKAGLSEEDKVLKEEEYWLYREER
KNKEKRLVGTKIVATQQRVAAFESIEVPEIPEAPEEKPSLLDKARSLFTREDHT

>core/76/1/Org1_Gene708

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YFAPLGKTLKLFLPAISSNVIQPKQHyrVVLKQSKAKTKEILAKLEVLHPSQGAVLKILLQHASPPGLSSLMETAKVSQSPIHSLEKLGILDIV
DAAQLELQEDLLTFFPPAPKDLHPEQQSAIDKIFSSLKTSQFHTHLLFGITSGKTEIYLRATSEALKQGKSTILLVPEIALTvQTVSLFKARF
GKDVGVLHHKLSDSDKSRTWRQASEGSLRILIGPRsALFCPMKNLGLIIVDEEHDPAYKQTESPPCYHARDVAVMRGKLAHATVVLGs
ATPSLESYTNALSGKYVLSRLSSRAAAAHpAKISLINMNLEREKSKTKILFSQPVLKKIAERLEVGEQVLIFFNRRGYHTNVsCTVCKHTLKC
PHCDMVLTFHKYANVLLCHLCNssPKDLPQSCPCLGTMTLQYRGSGTEKIEKILQQIFPQIRTIrIDSdTTKfKGSHEtLLRQFATGKAD
VLIGTQMIAKGMNFSaVTLAVILNGDSGLYIPDFRASEQVFQLITQVAGRSGRSHLPGEILIQSFLPDHPTIHSAMRQDYSAFYsQEITGR
ELCEYPPFIRLIRCIFMGKCPKQTwEEAHRVHNILKEQLESTNPLMPVTPCGHfKIKDTFRYQFLIKSAYVIPVNKKLHHALMLAKLSPKV
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>core/79/1/Org1_Gene564

MDYLEKLQVLIIEGQsANFLSLWEEYCFNDVVRGRELVEILEKVKSSSLASLFGKIVDTVVPLWEKIPEGKDKDRVLQLILDlQTSNSQM
FFDIATEYVNKKYSgeENfNEALRVVGLRDGRDFQfSLSRFDfLMHMHKGNFVFHQGGWGVGEVMGVSFLQQKVLIIEFEGIMSAKD
ISFETAfKSLTPLSGDHFLSRRFGDPDGFEAFAKENPIEVVEILLRDLGPKTAKEIKDELVDLVIPEADWNRWWQSAKTKIKKGTRIISPDN
PKEPYVLSdagCSHMGQLERKLGLSLNSAEKISLIYHFIRDLHSELKNIEIRKSLVKALQDLdVEEGNKSLILQRELLSEYLGIKDASIDKEYI
TSLSEDDTSRLLENMPiVALQKSfSLVRKYSSFWQQVfMQILLYTTsPTMRDFVYKTIKNdPSSVEVLKKRLDSAHQPMMPeLFVW
FFLKLGNHEDGLFDPEDKEVLRlFLESALNFMYQVASTPHKELGKKLHHYLVGQRYLAVRQMIEGASLPFLKELLLSTKCPQfSSSDLNv
LQSLAEVVQPTLKKHKSNVEEENVLWSTSESfSRMKAKLQSLVGKEMVDNAKEIEDARSLGDLRENSeyKFALEKRARLQEEIRVLS EEI
NRARILTKDLVFTDKVGVGCKVTLKGdAGEVVEYtILGPWDADPDSCILSLQSKLAQNMLGKKLNDVVLQgKEYKISRIQSIWEEHGA

>core/82/1/Org1_Gene205

MIRSPLPFISSKRALNMLGLQDEFSCPEDVVDfLFSIEllaQQDEPSEGYLALSrSLLMMTHNHPKVVKRVIFYGVSyGLKHKsMSIFID
VLTYIDFLFEKLGISASDRLSLCSARTCINFELYSQTGEMKFLSEVVdNfRLIEQLLKMHPQLKNRLGWEHFRIGAKQEEVSLVASASVYQ
AVGRSfIELYHKHLESLdACGMKCLALALDLSPNNAHIHAdYAKGLVVLGTRQGKSLliERGMEHFskAIFLSfSRDGDtLAYQNYRYS
YALASVKLFDLTyKKEHFDQAMNilyQTVQAFPNLSGLWMVWGELLIRSGWLNSNMKYIEVGLEKLASLQKKTNDPIALSGLLATGIAI
LGLYLEEPNLFKDSRHRLISAMRTfPGNSALVHALGVVQLCSALYFNEDSHfASAIscfQSCLEWDLdATGMWQKLFDAYfSWGIKKK

SARLLRKAVDVASRLCSLRPEAFLWSDRGLALKCLAEATIDEAYKEIFLSESLHYQRAWDLSGRLEILELWGQSHYLLAELQQSLFHYD
EAYTLTKVDLTLSSSRVKLILAAVLLGKGRLQDTPAEEAREILEPLVEVYLEDENFLLLKGKVVFLFWKNKNVCLGKLARTYLEKATSL
GCPEAYYTLGKFYAVIKDVNKAWGMVIRSAQYGVRITEAKWLNDPYLANLREIHAFREVVENQKGRLWLGNKTEMKRN

>core/84/1/Org1_Gene997

MYKRCVLDKILKGIVAGSLILLYWSSDLLERDIKSIKGNVRDIQEDIREISRNVKQQQTSQAIPAAPGVMLAPKLVRDEAFALLFGDPSYP
NLLSLDPYKQQTLPPELLGTNFHHPHGILRTAHVGKPENLSPFNGFDYVVGFDYDLCLPSLASPHVGKYEESPD LAVKIEEHLVEDGSGDKEF
HIYLRPNVFWRPIDPKALPKHVQLDEVFQRPHPVTAHDIKFFYDAVMNPYVATMRAVALRSCYEDVVSVSSENDLKLVRWKAHTVI
NEEGKEERKVLVSFAFNTLSLQPLPRFVYQYFANGEKIIEDENIDTYRTNSIWAQNFTMHWANNYIVSCGAYYFAGMDDEKIVFSRNP
DFYDPLAALIDKRFVYFKESTDLSLQDFKTGKIDISYLPPNQRDNFYSFMKSSAYNKQVAKGGAVRETVSADRAYTYIGWNCFSLFFQSR
QVRCAMNMAIDRERIEQLDGGQYTGISGPFASSSPSYNKQIEGWHYSPEEAARLLEEGWIDTDGDGIREKVIDGVTVPFRFRLCYVY
KSVTAHTIADYVATACKEIGIECSLLGLDMADLSQAFDEKNFDALLMGWCLGIPPEDPRALWHSEGAMEKGSANVVGFFHNEEADKIID
RLSYEYDLKERNRLYHRFHEIIEEAPYAFLFSRHCSLLYKDYVKNIFVPTHRTDLIPEAQDET VNVMTMVWLEKKEDPCLSTS

>core/92/1/Org1_Gene351

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QDPIATAMLELLEPGSFVCKLFAADDRRLVRSPCYLNRMFTHDRTGSPLLRFGKKLEHFITLEIINDRLVVFLPILPGTICYEETIYGFLPL
MSKSLTRPHLKIRKFLPLYQMVTDTRPPVPEDHKILLIKTEPLHIRTVFARVVQDLLPQGLRHTAADILEPTTQESGDIYEFYGSTSEPIERIPL
EFFTLEPYKEHSFFFYRDMLQETLESPQEVFRVFESIPEGEDQAAMFISKGSSELLELSQDSWIKPRISPSDERHAREIQKHIEDQPCFPFLK
AMETDHITSQGVLSRYFPSASLKGMFLSNYSRYLQHIYFQIPSPTSGEFFSNRDRSFLDLDFAGISVFWADLESKRLLQYIKRRNKDV
GMFVPKHQAQEQFAQSYFIGIHGSLIAGDYDEFRELLTGMHTLSQQFTIPEFPQTPLAILTGGGSGAMELANRVATELSILSCGNLISL
DTTNAYVEAKMSYAIPDLLERQADFHVLDLAVFVIGGMGTDFELLELISLKTGKKALVPVFLIGPVDYWKSKITALYNSNHAVGTIRGSE
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>core/93/1/Org1_Gene763

MKRSRRNFEQALENLEKLKEISLATSNDSYLNNPARFNQRKQTGSSVMEMKEALKNVENYLLEISCVSKSHADKALKESDFLIAGVQNV
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KQKNLHETVNEGDLTKTLLWNSEEVKNIASSLVIVNDMPLRLFYQRALSHLDIEAVVKVHNAVMALFFSRYEATMVFKSPKKHNIWY
FNDFLLFLREAWKDLNNNVIDSQERKQTKLLASALSLGIFESKLVFEEASRYLYFNIQTKLENANGKKPLSPGQYLTDAYEELHRLISKYPN
GPLFKAMDRVLEHESRPYDPMILGILPSLEGTCLKHKGSIIRSPSPVTQSSILYANCNEEFLGFLNAKAHRSEVTLVNIQNRISRKERAR
SRVIEEALEQEEHAPYVHAFSFPEPEELLQNLESIHGDIETFADFFSILQEEFHKPLASSFFLTKEKLFVGSFLKEKLTALKDIFFAKKKILFR
NDKLLLLHLLSYLIVFKLIERTNPNSIVVVS KDGLDYVSFIAGFAFFSREAFWDEHSLKLLLTNVLSPTLVARDRLVVFVSHIELLSKFNCLK
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>core/105/1/Org1_Gene609

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YYDYYQPEAYIARSDTYIEKSLINDEIDKLRLSATRSILERRDTLIVSSVSCIYGIGSPENYTSMALVLEVKEYPRNILTAQLVKMHYQASPI
PQRSFRERGSVIDIFPAYESELALRLEFLNDTLTSIEYSDPLTMIPKESVPSATLYPGSHYVPEAIREQAIRTIQEELEERMAFFDDRPIEKD
RIFHRTTHDIEMIKEIGFCKGIENYSRHFTGAPPGAPPTCLLDYFPEDFLIIDESHQTLQPQIRAMYRGDQSRKQSLVEYGFRLPSAFDNRP
LYEEAQKYFRKVIYVSATPGDTEVQESSGHIVQQIIRPTGIPDPMPEIRPATGQVDDLLEEIRLRLSQKHEKILVISITKKLAEDMAGFLSE
LEIPAAYLHSGIETAERTQILTDLRSGVIDVLIGVNLLREGLDLPEVSLVAILDADKEGFLRSTSSLIQFCGRAARNINGKVIFYADQKTRSIEE
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EQLLYLF

>core/107/1/Org1_Gene306

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PECHRDEIIQGILQFIEGQTYDDLCLKDKKSRYSCKLYPLLDVSVHDRLSLWWKGYATKHRLPTNALFFITDYQRSYPFGKLLGQVLHRTL
EIKDEKTGKAFPTGGMEAYFNHILEGDVGERKLLRSPNLRLDTNRVIKLPKDGSDIYLTINPVIQTIAEEELERGVLEAKAQGGRLILMNS
QTGEILALAQYPFFDPTNYKEYFNNKERIEHTKVSFVSDVFEPGSIMKPLTVAIALQANEEASLSQKKIFDPEEPIDVTRTLFPGRKGSPL
KDISRNSQLNMYMAIQSSNVVYAQLADRIIQSLGVAWYQQKLLALGFGRKTGIELPSEASGLVPSPHRFHINGSLEWSLSTPYSLAMG
YNILATGIQMVQAYAILANGGYAVRPTLVKKIVSASGEEYHLPTKEKTRLFSEEITREVV RAMRFTTLPGGSGFRASPKHHSSAGKTGTTE
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ALKRLYEEWNRSPKQGGTR

>core/123/1/Org1_Gene268

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DIHFFPQAAMLVADFADKVRINPGNYIDKRNMFKGTKIYTEASYAQSLLRLEEFAPLVEKCKRLGKAMRIGVNHGSLSERIMQKYGDT
IEGMVASAIEYIAVCEKLNVRDVVFSMKSSNPKIMVTAYRQLAKDL DARGWLYPLHLGVTEAGMGVDGIIKS AVGIGTLLAEGLGDTIR
CSLTGCPTTEIPVCDLRLRHTKIYLDLPEKKNPFSLQHSENFVSAAEKPAKTTLWGDVYGVFLKLYPHHLTDFTPEELLEHLGVNPVTKEK
AFTTPEGVVVPPELKDAPITDVLREHFLVFHHHQPCLYEHNEEIWDSPAVHQAPFVHFHASDPFIHTSRDFFEKQGHQKPTKLVSFR
DFDNKEEA AISIATEFGALLDGLGEAVVLDLPNLPQDVLKIAFGTLQNAGVRLVKTEYISCPMCGRTLFDLEEVTTRIRKRTQHLPGLKI
AIMGCIVNGPGEMADADFGVGSKTGMIDLYVKHTCVKAHIPMEDAEELIRLLQEHGVWKDPEETKLTV

>core/126/1/Org1_Gene572

MFRCILFGIFLLTCFSSGGVLYYLFCSHDFSIGPKEKSRSVWIEEEKEFTDSVLHHLPSQHQLHLILCFQGFLQKQKFSQAEKIFSKVYDE
AQDGPFLFKEEILGSRLINSFFLEKTDVMETILCLLNQRCNPSPYYHLFKALVCYKQKLYREVIEQLAYWQEEKTRALAPLLNISIEQLLTDF
LLDYISAHSLIEQKMFPEGRVILNRNINRLLKHECEWNAKTYDRIAILLSRSYFLELVESKSADIYFDYYEMVLFYLLKKIYILEQCPYAEELLPEE
ELVSLIMEHVFILPKDKLYPLIQLLEMWQKHVHPNSSLVVQILVDRFSTHMEGAIRFCEALVSFSGLEELHQQIITTFEELLSNKVQQIKT
EEAKQCVALHILDPSISISEKALSSDTLQNIIVSGDDEQHTKLRNYLDLWEAIQSYDIDRQQLVHHLVYGAKDLWKKGGNDEKALNLLQ
LVLRFTSYDIECESVVFLFIKQAYKQALSSHAIRLLKLEKFISEANIPSIVISEAEKANFLADAEYLF AHEDYDKCYLYSMWLTKVAPSPQSY
RLAGLCLMENKRYDEALEFLCMLSPNDSINDYKTQKALAFQCQKHQSKDRAAS

>core/130/1/Org1_Gene722

MRIEDFSLKLIPSSPGVYLMKDVHDQVLYIGKAKNLKNRLASYFHEKGDSRERIPFLMKKTASIIETIVVSNETEALLENLIKQHHPKYN
VLLKDDKTFCLAISSLHSPKVEAIRTKAITSSQRQLIFGPYVSAEACHTLLEVISQWFPLRRTCSDREFALRKRPCILYDMKRCLAPCVGY
CTPEEYQGTLDKAILFLKGKIEEVVKDLEKVIQKASDNLEFEQAANYRTLSLIKQAMAKQQVEKFHFQNI DALGLYRHKQRTILTLLTVR
SGKLLGARHFSFFENAQEDQDLLSSFILQYYVSQPYIPKEILTPLLEFPTLSYVLNAESPRLRSPKTGYGKELDLAYRNAKAYAATTLPS
TLPYQDFQNILRMSQYPYRIECYDNAHMQGAHATGVYIVFENNGFDPKQYRTFSIDSEKTQNDLALLEEVLLRRFHSLLTALPDMIVVD
GGKTHYNKTKKIIQTLNLTGIQVVTIAKEKSNHSRGLNKEKIFCETPPEGFSLPPTS NLLQFFQILRDEAHRFAISKHRKKRGKALFEQEKIP
GIGEVKRKRLLQFKFSWKQVMLSSQEELEAIPGLTKKDIAVLLARQKDFNKS

>core/138/1/Org1_Gene723

MYTEESLDNLRHSIDIVDLSEHIHLKRSGATYKACCPFHTEKTPSFIVNPAGAHYHCFGCGAHGDAIGFLMQHLGYSFTEAILVLSKKFQ
VDLVLQPKDSGYTPPQGLKEELRHINSEATFFRYCLYHLPEARHALQYLYHRGFSPDTIDRFHLGYGPEQSLFLQAMEERKISQEQ LHT
AGFFGNKWFLFARRIIFPVHDALGHTIGFSARKFLENSQGGKYVNTPETPIFKKSRI LFGFNFSRRRIAKEKKVILVEGQADCLQMIDSGF
NCTVAAQGTAFTEEHVKELSKLGVLVFLLFDSDEAGNKAALRVGDL CQTAQMSVFVCKLPQGHDPDSFLMQRGSSGLIALLEQSQD
YLTLFISEKMSSYPKFGPREKALLVEEAI RQIKHWGSPILVYEHKQLASLMMVPEDMVLSLANPQVTAEPQNIPIKQKVPKIHPHIVME
TDILRCMLFCGSNTKILYTAQFYVPEDFKHPECRKLFAFMISYYEKYRKNVPFDEACQVLSDSQILQLLTKRRLNTEALDTIFVQSLQKM
ADRRWREQCKPLSLNQNIQDKKLEILEDYVQLRKDRITIITLLDPESELIP

>core/140/1/Org1_Gene409

MTNSDNAASAAGLLWAHPKEDPAFLGMIIEFHLPPPTVAQIFISRGFQTIQEIHKFLYSHLSSLYDPGLFLDMSKAVERLLLARDRKEHVM
IYGDSVDGDMTGVALLEFLRDIDVHVSYFFLGAILKQHGETSTLIAKLKEEGITLLITVDCGITAGKEVSDITRQGIDVIITDHHMPTGKIP
HCVATLNPKL RDHTYPNRELTVGVVAFKLARGVLNALISRNLPK SQGSLKLLDLVLTGTITDVGVLLENRMVMVRYGIKEIARGARPG

LNKLCALCGVEKSEVTSTDIVLKIAPKLNSLGRLLDDPAKGVELLTQDDERVDALIMELDNINRERQRIEAEVFQDVQEILNSNPEILKQA
AIVLSSTAWHARVIPIISARLAKTYNKPVVIIAIQRGIGKGSARTIGSFPLLGVLLKCCSSLLSYGGHDFAAAGVIMKEDKVEDFKKKFVHLVN
SSLKKGDTLPHLEIDAYADFDAIDYDLLASMELEFPFGKGNLMPIFYSKVRQVRYPKVLPGNHLKLYLSQKERNLEGVAFGLGRHADALK
ASWHYPLEIAYTPRLSQTSGSGVIHLLVRDFRISSEPRFSD

>core/141/1/Org1_Gene240

MSFLRRHISLFRSQQLIDVFAPVSPNLELAEIHRRVIEDQGPALLFHNVIGSSFPVLTNLFGTKHRVDQLFSQAPDNLIARVAHLISSTPK
LSSLWKSRLDKRISSGLKKARFRRFPFVSMSSVNL DHPLLTSWPEDGGAFLTLPVYTESPTLTTPNLGMYRVQRFNQNTMGLHFQI
QKGGGMHLYEAEQKKQNLPVSFVLSGNPFLTLSAIAPLPENVSELLFATFLQGAKLLYKKTNDHHPHLLYDAEFILVGESPAKRRPEGP
FGDHFYGYSLQHDFEFHCHKIYHRKDAIYPATVVGKPYQEDFYIGNKLQEYLSPLFPLVMPGVRRLKSYGESGFHALTAAVVKERYWR
ESLTTALRILGEGQLSLTKFLMVTDQEVPLDRFSVVLETILERLQPDRLIIFSETANDTLDYTGPSLNKSGSKGIFMGIGKAIRDLPHGYQG
GKIHGVDIAPFCRGCLVLETSLEDRCIKSLLHHPDLKSWPLIILADNLRETIQSEKDFLWRTFTRCAPANDLHALHSHFATHRPNYNFPF
VIDALMKPSYPKEVEVDPSTKQKVSRWHAYFPNKETFYI

>core/150/1/Org1_Gene576

MFMNNTQNSQATEVSSEESQKKLEELVALAKEQGFITYEEINEILPMSFDTPEQIDQVLIFLTGMDIQVLNQIDVERQKEKKKEAKELEG
LARRTEGTPDDPVRMYLKEMGTVPLLTREEEVEISKRIEKAQVQIERIILFRYSAKEAISIAHYLISGKERFDKIISEKEVEDKTHFLKLLPKLI
TLLKEEDTYLENLLLSLKQPDLSKQEAAKLNDLSLEKCRIRTQAYLRCFHCRRHNVTEDFGEVVFAYDSFLHLEQQINDLKVRAERNKFAAA
KLAAAKRKLYKREVAAGRTLEEFKKDVRMLQRWMDKSQEAKKEMVESNLRLVISIAKKYTNRGLSFLDLIQEGNMGLMKAVEKFEYR
RGYKFSTYATWWIRQAVTRAADQARTIRIPVHMIETINKVLRGAKKLMMETGKEPTPEELAEELGLTPDRVREIYKIAQHPISLQAEVG
EGSESSFQDFLED TAVESPAEATGYSMLKDKMKEVLKLTDRERFVLIHRFGLLDGPKTLEEVGSFAFNVTRERIRQIEAKALRKMRRPIR
SKQLRAFLDLLEEEKTGTSKVKSLKSK

>core/151/1/Org1_Gene901

MDTQSSIGNEEWRIAGTSIVSGMALGKVFFLGTSPLHVRELTLPQEEVEHEIHRYKALNRSKSDIVALEQEV TGQQGLQEVSSILQAHL
EIMKDPLLTEEVVNTIRKDRKNAEYVFSSVMGKIEESLTAVRGMPSVVDVQDIHDISNRVIGHLCCQHKKSSLGESDQNLIIIFSEELTPSE
VASANSAYIRGFVSLVGAATSHTAIVSRAKSIPYLANISEELWNI AKRYNGKLV LIDGYRGELIFNPKPATLQSCYKKELS VVAHTSQRLVR
KSLHPIVSSHAGSDKDVEDLLENFPQTSIGLFRSEFLAVILGRPLTLREQVDLYEKLARFPGDSPSVLR LFD FGEDKPCPGIKNKKERSIRWL
LDYSVILEDQLQAIKASLQGSIKVLIPGVSDVSEIIEVKKKWETIQTRFPKGHKVSWGTMIEFPSAVWMIEEILPECDFLSIGTNDLVQYT
LGISRESALPKHLNVTLP PAVIRMIHHVLQAAKQNQVPVSICGEAAGQLSLTPLFIGLVQELSVAMPVINRLRNHIALLELNSCLEITEAL
LQAKTCSEVEELLNRNNKITS

>core/153/1/Org1_Gene899

MGLFHLLTFLGLLCSLPISLVAKFPESVGHKILYISTQSTQQALATYLEALDAYGDHDFVLRKIGEDYLKQSIHSSDPQTRKSTVIGAGLAG
SSEALDVLSQAMETADPLQQLLVLSAVSGHLGKTSDDLKALASPYPVIRLEAAYRLANLKNKTKVIDHLHSFIHKLPEEQCLSAAIFLRLE
TEESDAYIRDLLAAKKSARSATALQIGEYQQKRFLPTLRNLLTSASPQDQEAILYALGKLKDGQSYNNIKKQLQKPDVDVTLAAAQALIAL
GKEEDALPVIKKQALEERPRALYALRHLPSEIGIPIALPIFLKTKNSEAKLNVALALLELGCDTPKLLEYITERLVQPHYNETLALSFSKGRTLQ
NWKRVNIIVPQDPQERERLLSTTRGLEEQILTFLFRLPKEAYLPCYKLLASQKTQLATTASFLSHTSHQEALDLLFQAAKLPGEPIIRAYAD
LAIYNLTKDPEKKRSLHDYAKKLIQETLLFVDTENQRPHPSMPYLRVQVTPESRTKLMLDILETLATSKSSEDIRLLIQLMTEGDAKNFPVL
AGLLIKIVE

>core/159/1/Org1_Gene813

MSSPPQAVASLTERIKTLLESNFCQIIVKGELSNVSLQPSGHLVFGIKDSQAFLNGAFFHFKSKYYDRKPKDGDVAVIIHGKLAVYAPRGQY
QIVAHALVYAGEGDLQKFEETKRRLTAEGYFATEKKKPLPFAPQCIGVITSPTGAVIQDILRVLSRRARNYKILVYPVTVQGNAAHEISK
AIEVMNAENLADVLIARGGGSIEDLWAFNEEILVKAIHASTIPVSAVGHETDYTLCDFASDVRAPTPSAAAEIVCKSSEEQVQVFEGYL
RHLLSHSRQLLTSKKQQLPWRRFLDRAEFYTTAQQQLDSIEIAIQKGVGQKIHESKQRYDNISRWLQGDVSRMTCRLQSLKKMLSQ
ALSHKALSQVRCHQLKKSILTYPRQIQQASQKLSPWRQQLDITLISRLHYQKEEYFHKHTRLKHAHNVLQQLRSHVQKLELLGRRLSR
GCELNLQNQKIAYANVKETLATILERRYENSVARYSALKEQLHSLNPKNVLKRGYAMLFDFNENSAMISVDSLQENARVRIQLQDGEAI
LTVTNIEICKLIKG

>core/160/1/Org1_Gene973

MDNSDNSFHTLETEQGSFLNDELAVEEVASTESTEISDATLCFADEIQELPSPEKKVAFILNKMREALTGSSQGSDDLRLFWDLRKQCLPL
FNEIEDTAKRADHWRCYIELTKEGRHLKGLQDEEGSFVVGQIDLAITCLEKDILKFQEGTEDKIFKDREDNFLESQALDKHQAFYKQHHT
SLLWLSSFSSKIIDLKELINVGMRLKSKFFQRLSNLGNQVFPKRKELIEKVSQTFAEDVDADFVAKYFIGSDKETLKKTVFFLRKEIKNL
QHAARKLFVSSHVFAETRLKLSKCWDQLKGMEKEIRQEGRRLRVVSAENSKEVRQMLAEVSSLLIEGNDLSKVRKDLEGISKKIRALDLT
HDDVISLKKEMQQFLDQLREKQDAAEHSYQEQLAKDKQVKKEAARSLAERITTFSKTCSEGNITSESREEWQTLKELLGKMSFLPPPEKI
SLDNQLNLALQTIVNFFEEQLSSPDSREKLVNMRQVLKQRRERRRQELKDKLEQDKLLGSSGLDFDRAMQYSALVEEDKRALEELDAS
ILELKQIQQLL

>core/162/1/Org1_Gene140

MHPLYVDLDTIISYSPPLPKEFQEAASLIAVPDTSHSKPVVPGVKTLPQTYHLPYLKFVQGENVVHTPLKVGVMFSGGPAPGGHNVI
QGLFNSLKDFHPDSSLVGFVNNGDGLTNNKSIDITEEFLSKFRNSGGFNICIGTGRKKIVTPEAKEACLKTAEALDLDGLVIIGDGSNTAT
AILAEYFAKRRPKTSIVGVPKTIDGDLQHTFLDLTFGFDATATKFYSSIIISNRDALSCAHYHFIKLMGRSASHIALECALQTHPNIALIGEEI
AEKNLPLKTIHHKICSVIADRAAMEKYYGVILPEGIIEFIPEIINLITEIESLSEYEDKISRSPESQRLLKSFPAPIIEQILNDRDAHGNVYVSKIS
VDKLLIHLVSNHLQQYFPNVFPNAISHFLGYEGRSGLPTKFDNTYGYSGLYGAGILVRNHCNGYLSTIESLACPFMKWKLRAIPVVKMFT
VKQQADGTLQPKIKKYLVDIGSTAFRKFKLYRKIWALEDYSYRFLGPLQIETPPMHSDNFPPLTLLLNHNFWQRHQGCIEIPDTTY

>core/165/1/Org1_Gene349

MFGSESLRYQLLIQDFAKVSEEGIGLLESKEYSLLQAKLVLRALAQNSSFDDWFRSFKKCQISYPELAHDRDVLEEFGIQVLRGIENPSVT
VRAVSVLAIGLARDFRLVPLLLQSCNDDSAIVRSLALQVAVNYGSESLKKAIVELARNDDSIHVRITAYQVVALQIEELLPFLRERAENKL
VDSVERREAWKACLELSSQFLETGVAKDDIDQALFTCEVLRNGMLPETTEIFTELLSVEHPEVQESLLLSALAWSHQLQNHKEFLSKVRH
VMCTSPFAKVRFQAAAALLHLHGDP LGRDSLVEGLRSPQPLVCEAASAALCSLGIHGVPLAKEHLESLSRKAANLSILLVSRDIERAG
DVIARYLSNPEMCWAIEYFLWDAQWNLRGDTFPLYSDMIKREIGRKLIRLLAVARYSQAKAVTATFLSGQQAQGWSFFSGMFWEEG
DVKTSEDLVTDACFAAKLEGALASLCQKKDQASLQRVSQLYNDSRWQDKLAILESVAFSENLDAPVFLDCCHHEAPSLRSAAAGALFS
IFK

>core/172/1/Org1_Gene568

MLGKEEEFTCKQKQCLSHFVTNLTSDFALKNLPEVVKGALFSKYRSVLGLRALLKEFLSNEEDGDVCDEAYDFETDVQKAADFYQR
VLDNFGDDSVGELGGAHLAMENVSILAANKVLEDARIGGSPLEKSTRYVYFDQKVRGEYLYYRDPILMTSAFKDMFLGTCDFLFDTSALI
PQVRAYFEKLYPKDSKTPASAYATSLRAKVLDCIRGLLPAATLTNLGFFGNRGRFWQNLHKLQGHNLAE LRRLGDES TELMKVIPSFVS
RAEPHHHHHQAMMQYRRALKEQLKGLAEQATFSEEMSSSPSVQLVYGDPDGIYKVAAGFLFPYSNRSLTDLIDYCKKMPHEDLVQIL
ESSVSARENRRHKSPRGLECFEGFDILADFGAYRDLQRHRTLQERQLLSTHHGYNFPVELLDTPMEKSYREAMERANETYNEIVQEF
PEEAQYMVPMAYNIRWFFHVNARALQWICELRSQPQGHQNYRTIATGLVREVVKFNPMYELFFKFVDYSIDLGRNLNQEMRKEPTT

>core/178/1/Org1_Gene132

MLRFFAVFISTLWLITSGCSPSQSSKGIFVVNMKEMPRSLDPGKTRLIADQTLMRHLYEGLVEEHSQNGEIKPALAESYTISEDGTRYTFK
IKNILWSNGDPLTAQDFVSSWKEILKEDASSVYLYAFLPIKNARAIFDDTESPENLGVRALDKRHLEIQLETPCAHFLHFLTLPFFPVHETL
RNYSTSFEEMPITCGAFRPVSLEKGLRLHLEKNPMYHNKSRVKLHKIIVQFISNANTAAILFKHKKLDWQGPPWGEPPIPEISASLHQQD
QLFSLPGASTTWLLFNIQKKPWNNAKLRKALS LAIDKDM LTKVVYQGLAEPTDHILHPRLYPGTYPERKRQNERILEAQQLFEEALDELQ
MTREDLEKETLTFTSFYSYGRICQMLREQWKKVLKFTIPIVGQEFFTIQKNFLEGNYS LTVNQWTA AFIDPMSYLMIFANPGGISPYHL
QDSHFQTLKITQEHHKHLRNQLIIEALDYLEHCHILEPLCHPNLR LIALNKNIKNFNLFVRRTSDFRFIEKL

>core/183/1/Org1_Gene5

MYQENLRLLERLLYNSVQKSYADRLFSYEKTKMVHDTPLIPWEEDKEKCAEAEKAFLEQQKILLDYGKSIFWLNENDEINLNDPWSWG
LNTVRTRKVFQEVDSDSERWNHKKVLIQKLEDDYEKLLKESSKESTEANKKLLSDLVDRLEDATKFFLKKQEEVETRVKDLRARYGGTVDP
KQDTEAKKKVELEASLETFLDSIESELVQCLEDQDIYWKEQDVKDLARTQELEEQDIEAKREEAAEDLRSLNERLKKSKTMLDRAKWHIE
NAEDSITWWTSQIEMKDMKARLKILKEDITSVLPEIDEIETCLSLEELPLLTRELLTKSYLKFICSETLLKMTSVFENNIYVQEYEVQLQNL
GFKLQGISQRFQKQDDFANLEEQVALQKKRLRELTQNFEIQGFNFMKEDFKAAAKDLYIRSTAEQKMNFDVPCMELFRRYHEEVNK
PLLELMYNCADSYRDAKKKCLSLRLDEKELLQKEIKKEEFYQKKQQRHADRSRHTTYQKLRIAEELALELKKKI

>core/184/1/Org1_Gene996

MVARGLCDFTLPVNERLPIGPFFVPQHTSGAKGKEFAKRNFSISGLDDILKLCILQRRPFALQWDNLSVKSDYEEAGPAIGIRSLEPQV
SQISPAHGRCLSTLVQWAPILGSEEQLVWLEETMKRLKFPKSLGSKDAVIDDSEMVPVNANPTQEIPAASETVESSPVAPGNTTDTMP
AASGTTDTTSGVSEAAAAEATVDSTPGTEEEPSFSRLYALVVQNVYPPEPPKEPEVMFTDEEKSILEATRARMELDLNGYLADYELS
KDEIQKHVPDLPENWRTNWRWUSERLYKFFFKTKKEGLEEIFLNKELGNMILARGLAATQSQARIKVFNSLVAWLLQSFNVGRSCTAKP
LPTSKLDLFKSEFESKPKNNILTEFLVASDEEILFKGLRVLEPGIEGWYDHPDQAGEIRSVLEGLVQAGRISGYWENQPFGRFVLRGVGER
RTELVELLESVASGEIMQFFESSDEEGAFIIDNEPSKTAMLKQRFKSCVRTKLVGSGFADESLPRGRFTILV

>core/186/1/Org1_Gene686

MSEQEKLSNYNADKKLFSGIDKLFQIVKGSYGPKQSLSPTSFFKERGFYAISQTELSNSYENLGVDFAKAMVKNKIHKEHSDGATTGLILLH
AILQESYAALEKGISTHKLIALSLKQGEKLQEALQQQSWPIKDALKVRNIIFSSLHMPTIADHFYNAFSVVGPEGLISITKERENDKTSMDV
FQGFKIPAGYASTYFVSDTASRLTRIAHPLILITDRKISMIHSLPLLQEISEQNQHLIIFCEDIDPDVLATLVVNKLQGLLQVTVVTIPQLSTT
NQELAEDIALFTGTHICPCQEASHVLAPEMVTLGSCLSIEISESQTTLIGGLHIPEVLTALKTRQLAEEIRTTSCLETKKRLIKSTNRLQSSVAIL
PTDEDNEPLYTLALKIMESALSRGYVPGGGVALFYASLTGTPKDDADENSIAISLLQKACCAPLKLLATNADLDGDAVIAKLSSLGTTSLG
ISVFSREIEDLIAGGILDSLATTSTILAQAALDTAILVLSSKILILENQYEISTL

>core/187/1/Org1_Gene736

MENEILLNIESKEIRYAHKNGQLFDLTIERKKVRQLKGNIIYRGRVTNLRNIQSAFINIDERENGFIHISDILENSKKFEQMFDMDVDALP
EEASEAPLLSSEEAPIEEFLKLDSPVLVQVVKEPIGSKGARLTSNISIPGRYLVLLPNSPHRGVSRKIEDPHMREQLKQLIRSFEMPQDMGL
ICRTASTTASTEALINEAHDLLLTWKILEKFYSTEQPCLLYSETDILKKAVITCIDKNYKRLIDDYATYQKCKHMLKKYSPDASIKIEYYRDS
IPMFERFNIEKIDKATRRKIWLSSGGYLFFDKTEAMHTIDVNSGRSTQLESQVEETLVQINLEAAEEIARQLRLRNVGGLVIIDFIDMKSR

KNQRRVLERLKEHMKYDAARCTILSMSEFGLVEMTRQRNRESLMQTLFTLCPYCSGNAIIKTPESVVIEIERDLKKVINHKEHSHLCLVV
HPEIASYMKQENDDNEMINLAKQLKAKLQINTSDSVHLNHYQFFSLITGESIDL

>core/193/1/Org1_Gene97

MADILVIGANPTGLILANMLIQHGISVKVIDHRASPEDPSFLDCRKLPVILSCSSLELLHNSEMLGDFIQANHKIFGARYHWKKRTLLFKFS
QATDSPVPFSLSTTYQSLEQHLIDEFLKRGVIDWSTRPVTLDNSIFIESTKVSQNFENREIYNPKWIIACEADNNLDIRDLVKSQRLAR
RINREVIFINCDEGEPPFEEDHIHLLPITKNFLNFVFYNPQEKTKQLCLPQGTHSISPKLKQKLLYTYNLVISDENFHIKTSHHAFPPEHGNVL
FLGSLNNTLLLSYLNGINNTNIHAAFNLAWKLLPVLKKAALKHLVITKEQEDGNILPYISPTTEKRAKKLPFSRFYTPALMYYFLKGCRKFNTT
GEEYYPHPHQALKYRSSDIKMSPQDKEIHGPGPGMRAIDARLENGSFLDPLKSSKHLIFFKDIPDLKEALQEEYGEWIEICNVKEPRIL
NLYHANPNLSLFIIRPDRIYGYRTHTFKLHELISYLLRIFASEKTS

>core/200/1/Org1_Gene621

MAASILSQELLDILPYTLKKHCLLPIEESSEAITIAHATATSVIAQDEVKLLIKKPVRFVLKEESEILQRLQQLYSNREGNVSDMLLTMKEED
GTTISEEEDLLETTDIPVVRLLNWILKEAIEERASDIHFEPCEDSMRIRYRIDGVLHDRHSPPSHLRSALTTRLKVLAKMDIAEHRLPQDG
RIKIHIGGQEVDMRVSTVPVIYGERVVLRILDKRNVIDIAGLHMPKGTIELFKDTITAPEGILLVTGPTGSGKTTTLYSVLQELKGPLTNIM
TIEDPPEYKLPGIAQIAVKPKIGLTFARGLRHLLRQDPDILMVGEIRDQETAETAEIAQAALTGHLVVSTLHTNDAISAIPRLDMGIESYLLSA
TLVGVAQRLVRTICPYCKVAYTPENQEKSFSLASLGKDEMPLYRGQGCVHCFRSGYKGRQGIYEFLRPNTLFRSEVASNRPHYILRETA
EQNGFLPILEHGIALAVSGETTLAEVLRVTKRCD

>core/220/1/Org1_Gene305

MDLKELLHGVQAKIYGKVRPLEVRNLTRDSRCVSVGDIFIAHKGQRYDGNDFAVDALANGAIAIASSLYNPFLSVVQIITPNLEELEAELS
AKYYEYPSSKLHTIGVTGTNGKTTVTCLIKALLDSYQKPSGLLGITIEHILGEGVIKDGFTTPTPALLQKYLATMVRQNRDAVVMEVSSIGL
ASGRVAYTNFDTAVLTNITLDHLDHFHGTFFETYVAAKAKLFSLVPPSGMVVINTDSPYASQCIESAKAPVITYGIESAADYRATDIQLSSSG
TKYTLVYGDQKIACSSSFIGKYNVYNLLAAISTVHASLRCDLEDLLEKIGLCQPPPGRDPVLMGPCPVYIDYAHTPDALDNVLTGLHELLP
EGGRLIVVFGCGGDRDRSKRKLMAQVVERYGFAVVTSDNPRSEPPEDIVNEICDGFYSKNYFIEIDRKQAITYALSASDRDIVLIAGKGH
EAYQIFKHQTVAFDDKQTVCEVLASYV

>core/224/1/Org1_Gene792

MLCATVSGPSFCEAKQQILKSLHLVDIIELRDLINELDDQELHTLITTAQNPILTFRQHKEMSTALWIKLYSLAKLEPKWMDIDVSLPKT
ALQTIRKSHPKIKLILSYHTDKNEDLDAIYNEMLATPAEYKIVLSPENSSEALNYIKKARLLPKPSTVLCMGTHGLPSRVLSPLISNAMNYA
AGISAPQVAPGQPKLELLSYNYSKLSEKSHIYGLIGDPVDRSISHLSHNFLLSKLSLNATYIKFPVTIGEVVTFSSAIRDLPFSGLSVTMPLK
TAIFDHVDALDASAQLCESINTLVFRNQKILGYNTDGEGVAKLLQKNISVNNKHIAIVGAGGAAKAIAATLAMQGANLHIFNRTLSSA
AALATCCKGKAYPLGSLENFKTIDIIINCLPPEVTFPWRFPPIVMDINTKPHPSPYLERAQKHGSLIIHGYESMFIEQALLQFALWFPDFLTP
ESCDSEFRNYVKNFMAKV

>core/225/1/Org1_Gene321

MMSRLRFRLAALGIFFILLVPNSVSAKTIVASDKEKVGVLVYDNSVEAFQQILDCIDHANFYVELCPCMTGGRTLKEMVDHLEARMDLV
PELCSYIIQPTFTDAEDQKLLKALKERHPNRFFYVFTGCPPSTSILAPNVIEMHIKLSIIDGKYCILGGTNFEFEMCTPGDEVPEKVDNPR
FVSGVRRPLAFRDQDIMLRSTAFGLQLREEYHKQFAMWDYYAHMWFIDNPEQFAGACPPLTLEQAEETVFPGFDDKHEDLVLDSS
KIRIVLGGPHDKQPNPVTQEYLKLIQGARSSVKLAHMYFIPKDELLNALVDVSHNHGVHLSLITNGCHELSPAITGPYAWGNRINYFALL
YGKRYPLWKKWFCEKLKPYERSIYEFWETQLHKKCMIIDDEIFVIGSYNFGKSDAFDYESIVVIESPEVAAKANKVFNKDIGLSIPVS
HGDIFSWYFHSVHHTLGHQLTYMPA

>core/226/1/Org1_Gene728

MRIVQVAVEFTPIVKVGGLGDAVASLSKELAKQNDVEVLLPHYPLISKFSSSQVLSEFSFYEFGLKQQASASISYSEGLTLTIITLDSQIELF
STTSVYSENNVVRFSFAFAAAAAAYLQEADPADIVHLHDWHVGLLAGLLKNPLNPVHISKIVFTIHNFYRGYCYSTQLLAASQIDDFHLSH
YQLFRDPQTSVLMKGALYCSDYITTSLTYVQEIINDYSDELHDAILARNSVFSGIINGIDEDVWNPKTDPALAVQYDASLLSEPDLFT
KKEENRAVLYEKLGISSDYFPLICVISRIVEEKGPPEFMKEIILHAMEHSYAFILIGTSQNEVLLNEFRNLQDCLASSPNIRLILDFNDPLARLT
AAADMICIPSHREACGLTQLIAMRYGTVPVLRKTGGLADTVIPGVNGFTFFDTNNEFRAMLSNAVTTYRQEPDVWNLIESGMLR
ASGLDAMAKHYVNLYQSLLS

>core/233/1/Org1_Gene824

MDKSTGVPLSPPHSKESEMIVLGCMLTGVHYLNLAANQLYEEDFYLEHKIIFRVLQDAFKQDKPIDVHLAGEELKRHNQITVIGGPSY
LITLAEFAGTAAYLEEYVDIIRSKSILRKMISTAKEIEKRALEQPKNVAEALDEAQNSFFKISQSTSVSQYTLVADKLRGLTTTTDKPYLVQL
QERQELFLQNAQGDNKSFFTGIPTHFIDLDQLIHGFSPSNLMILAAPAMGKTALALNIAENLCFQNRPLIGIFSLEMTVDQLIHRMICS
RSEVDSKKISIGDLSGHDFQRIVSVINEMQEHTLLIDDQPLKVSDLRARARRMKESYDIQFLIIDYLQLLSGSGTLRATESRQTEISEISRM
LKTARELNIPILCLSQLSRKVEDRANHRPMMSDLRESGSIEQSDSLVMFLLRREYYDPNDKPGTAEIIAKNRHGSIGSVPLVFEKELAR
FRNYSAFECIS

>core/234/1/Org1_Gene566

MKITVNRGLDLSLQGSPKESGFYNKIDPEFVSIDLRFQPLSLKLVQGDVCSGAPIAEYKHPNTYITSHVSGVVTAIRRGNKRSLLD
VIIKKTGPSTSTEYTYDLQTLRSDLSEIFKENGLFALIKQRPFDIPAIPQTTPRDVFINLADNRPFTPSPKHLALFSSREEGFYVFGVRAI
AKLFGLRPHIVFRDRLTLPTQELKTIAHLHTVSGPFPSGSPSIHHSVAPITNEKEVVFTLSFQDVLTHGLFLKGRILHEQVTALAGTALKSS
LRRYVITTKGASFSSLINLNDISDNDTLISGDPLTGRLCKKEEEPFLGFRDHSISVLHNPTKRELFSLRIGFNKPTFTKTYLSGFFKKKRTYTN
PDTNLHGETRPIIDTDIYDKVMPMRIPVVPLIKAVITKNFDLANELGFLEVCGEDFALPTLIDPSKTEMLTIVKESLIEYAKESGILTPHQD

>core/236/1/Org1_Gene452

MKEERSSEILPRVKETKKHAYVSMQEKSCVGECAVVAESEEAESVTVTKIAKLQRMGIEELNILARQYGVKNIGSLTKSQVVFIVKAKS
ERPDELLIGEGVLEVLDPDGFGLRSPTYNYLPSAEDIYVSPAQIRRFDLKKGDTIIGTIRSPKEKEKYFALLKVDKINGSTPDKAKERVLFENL
TPLYPNQIRVMMEMGKDHLAERVLDTAPIGKGQRGLIVAPPRSGKTIVLQSIHAIAVNNPDIVLIVLLIDERPEEVTDMIRQVRGEVVA
STFDEQPERHIQVAEMVIEKARRLVEHGNDVVILLDSITRLARAYNTVQPHSGKILTGGVDASALHKPKRFFGAARNIEGGGSLTILATAL
IDTGSRMDEVIFEEFKGTGNMELVLDRLSDRRTYPADLIKSGTRKEELLYHPSELERVYLFRQAIADLTIDAMHLLGRLKKTNSNAEF
LLSLKE

>core/245/1/Org1_Gene417

MQIAQVFGCGRNGEVKVSAGAKNAATKLLVASLLSDQKCTLRNVPDIGDVSLTVELCKSLGAHVSWDKETEVLEIYTPEIQCTRPPTFS
NVNRIPILLGALLGRCEGVYVPTVGGDAIGERTLNHFHFEGLKQLGVQISSDSSGYAKAPRGLKGNYIHLPPYSGATENLILAAIAHK
GRTVIKNVALEAEILDVLFLQKAGADITTDNDRTIDIFGTGGLGSVDHTILPDKIEAASFGMAAVVSGGRVFVRNAKQELLIPFLKMLRS
IGGGFLVSESGIEFFQERPLVGGVVLETDVHPGFLTDWQQPFAVLLSQAQGSVIHETVHENRLGYLHGLQHMGAECQLFHQCLSTKA
CRYAIGNFPHSAVIHGATPLWASHLVIPDLRAGFAYVMAALIAEGGGSIIENTHLLDRGYTNWVGKLRSLGAKIQIFDMEQEELTTSPTS
LALRDASL

>core/255/1/Org1_Gene311

MLTCNECTTWEQFLNYVKTRCSKTAFFENWISPIQVLEETQEKIRLEVPNIFVQNYLLDNYKRDLCFVPLDVHGEPALFVVAEHKKPSA
PVASQKESNEGISEVFEETKDFELKLNLSYRFDNFIEGSPSNQFVKSAAVGIAGKPGRSYNPLFIHGGVGLGKTHLLHAVGHYVREHHKNL
RIHCITTEAFINDLVYHLKSKSVDKMKNFYRSLDLLLVDDIQFLQNRQNFEEFCNTFETLINLSKQIVITSDKPPSQLKLSERIIARMEWGL
VAHVGPIDLETRVAILQHKAQKGLLIPNEMAFYIADHIYGNVRQLEGAINKLTAYCRLFGKSLTETTVRETLKELFRSPTKQKISVETILKS
VATVFQVKLNDLKGNSRSKDLVLARQIAMYLAKTLITDSLVAIGAAFVKTHSTVLYACKTIEHKLQNDETLKRQVNLCKNHIVG

>core/257/1/Org1_Gene578

MSEPRFVCLSLGSLGNRFKNLQIARTLLGEQAVLGLRSSVILETEALLPGSPPEWDLPYFNSVLVGETTSLRELLVTIKQIEKVVGRAE
ESPPWSPRTIDVDILLYGDESFCCDHTTEITPLSNLLSRPFLIALIASLCPYRRFCTQGSPYHNFTFGELAHHLPSPPGMIRRSLSPTMLMG
VVNVTNDSMSDGGMFLDPEKAVAQAEKLFTEGAAVIDFGAQATNPVKVKQLSVDQEWERLEPVLRLKETWSNRKQYPIISLDTFYP
EILRAMDIYPIQWINDVSGGSQSMAEVARDCELSLVMNHSSSLPVDPKNILSFSVPIGEQLLSWGEKQLKMFSDVGLNANQVIFDPGI
GFGKGAAQSLATLYEIAKFKRLGCPILIGHSRKSFLSLFGNHDPKDRDWETVGLSILLQQQGVDYLRVHNVAAHQKALSVAACEACAPI

>core/262/1/Org1_Gene687

MRAMLLEDWVSLMLSDVSCPKCDKKITGFAIDSQQVQPGDLFFALPGNATDGHQFLKHAATAGAVAAVSHDYQGDSFGLELIRVD
DTKSALQEAGSNQCNLFQGTLVGITGSVGKTTTKEFSKITLSSYKTHASPKSYNSQLTVPLSLLMAEGDEDVMILEMGVSEPGNMQDL
LRIVQPEIAVITHINDQHMHFPQGIQEILKEKSYILQKSKLQLLPKDSPPYLDLRSCSPTAEKFSFSFNDPLADFCYKAISGDSVVIQTPEE
NYCLPIAFSYKPAYTNLLIAVALSWILEVPEEGVIRSLPELKLPPMRFEHSMRNGMQVINDAYNACPEAMIAALDALPLPSDGGKIILIG
HMAELGRYSEEGHALVAEKAASRGDMIFFIGEKWIPVQSVLKSYSCEVSFFSSAQDVKDILKQVARYGDVILLKGSRALALESLLACF

>core/269/1/Org1_Gene648

MPRSLSNEQFSVDLEESPGCIVSALVKVSPEVLNKLKQALKKIKKEITLPGFRKGKAPDDVIASRYPTNVRKELGELVTQDAYHALSTVG
DRRPLSPKAVRSNSITQFDLQEGAKVEFSYEAFFAISDLPWENLSLPQEEAASEISDSIDIEKGLTNIGMFFATKTPVERPSQEGDFISLH
VSKSNDENASSAAIFENKYFKLSEEEEMTDAFKEKFLGISTGHRVVETITSPEIQSFLRGDTLTFTVNAVIEVSIPEIDDEKARQLQAESLDDL
KAKLRIQLEKQAKDKQLQKRFSEAEDALAMLVDFELPTSLEERISLITREKLLNARLIQYCSDEELEKRKSELIKEAEEDATKALKLLFLTHKI
FSDEKLTISREELQYMMDVCSRERFGQQPPKDISNDTLQELVMSARDRLTYSKAIEHVLKKAELLASTPSA

>core/271/1/Org1_Gene642

MWLVLWALAASLAIALVAKGYRRFVYFRRYAVQVIREVRLSMELKEWALAEQQLLPILKKRSYRRQCLFEYMRILRKMQRFESEKLLA
EAKKLGLRGPYFFLEIAYKAYRFGAFKECAQAFASVPQDLFEEEDAACYASALVRLGDLDAACSLIEPWISPLSHQETFTVMGHIYFTSKR
YKDAIDFYNRANALGVCPVEVTYNLAQAYRITSSYAKAGKLFKLLSNPVYKEEALFNIGLCEQKLGRPGKALLIYQSSDLWSRGDALLM
KYAAMAAMDQRDYVLAEPCWELALRCSTFAKDYKCGLGYGFSLCRLRKYGDAERVYCNLIQNFPECLTACKALAWLCGVGYATLLGS
EEGLMYAKKAVELDHSCETLELLSACEARCGNFDAAYEIQSFLSSRDTSLQEKQRRSQILRILRKKLPLNDHHIVEVDALLAA

>core/272/1/Org1_Gene449

MIENDFPEASNFESSHFYRDKVGVILCGGEGKRLSPLTNCRCCKPTVSFGGRYKLIDIPISHAISAGFSKIFVIGQYLTYTLLQQHLFKTYFYH
GVLQDQIHLLAPEARQGDQIWYQGTADAIKRNLLYFEDTEIEYFLILSGDQLYNMDFRSIVDTAIRTHVDMVLVAQPIPEKDAYRMGVL
DIDSEGKLIDFYEKPQEKEVLKRFQLSSEDRIHKLTEDSGDFLGSMGIYLFRRDSLFSLLREEEGNDFGKHLIQAQMKRGQVQTLLYNGY
WADIGTIESYYEANIALTQKPHA EKRLNCYDDNGMIYSKNHHLPGAITDSMISSLLCEGCVINTSHVSRSVLGIRSKIGENSVVDQSII
MGNARYGSPSPSLGIGKDCEIRKAIIDENCCIGNGVKLQNLKGYIKYDSPDKKLFVRDNIIVPQGTHIPDNYIF

>core/274/1/Org1_Gene588

MFQQKQKLSLKYLP SLRMQQGLQMLQSPLTELSSYVVQEIIDNPFFDLSSLEEEEWSPCYRPTNSTFSYLNQTPGPQESLYTRLLPQIEE
AFSTAEERFIAHQIAGNLSDEGLFLRNPEDFAQELELPLEKIHKVWDTIQNLSPEGIASPSLQSYWMKLLRNSSHQQAYSIVRDCYPLMT
NCEFAPIMKKFSLSLSELRNILKKALGSIPWCPAAACTVKPMVSTPLPDIYLFYSSGSWKIEVSTRGLPSIKLNKETFFHYEHLPKKEEQKNLY
QQILSAKWLIKNLKREQTLLQVMETLLPKQEDFLLGKIPAPYPLGIKDLAEDLSFHSTIFRAIENKAVAAPIGIFPLKHLFPRGIHQDSSH
SKENVLQWIRQWIATEQTPLSDSVISDRITAKGIPCARRTVAKYRAQLKILPANKRKKLFYIRSSNSHFRDRQF

>core/279/1/Org1_Gene506

MKRPFPTYLCIIFYGSCASLSLHAGLSFPEVRGATAAVVHADSGKVIFYDKDIDAVIYPASMTKIATALFILKHYPTVLDTLIKVKQDAIASIT
PQAKKQSGYRSPPHWLETDGSTIQLHLREELLGWDLFHALLVCSANDAANVLAMACCGSVEKFMKDLNFFLKEEIGCTHTHFNNPHG
LHHPNHYTTTRDLISIMRCALKEPPFRGVISTTSYKIGATNLHGERILSPTNKLLLPGSTYHYPPALGGKTGTTKTAGKNLIMAAEKNRLL
VTIATGYSGPVSDLYQDVIALCETVFNEPLLKELVPPSDCLQLEIANLGKLSCLPEGLYYDFYASEDREPLSVSFIAHADAFPIEQGDLLG
HWVFYDDEGKKISSQPFYAPCRFERTIKPWKLYMKRVFTSYRTYMSITMLLMYFRIRKHKRYKNLKHYSKI

>core/281/1/Org1_Gene133

MFSRWITLFLLFISLTGCSYSSKHKQSLIPIHDDPVAFSPEQAKRAMDLSIAQLLFDGLTRETHRESNDLELAIASRYTVSEDFCSYTFFIK
DSALWSDGTPITSEDIRNAWEYAQENSPHIQIFQGLNFSTPSSNAITHLDSNPDPFKLLAFPAFAIFKPENPKLFGPYTLVEYFPGHNI
HLKKNPNYYDYHCVSINSIKLLIIPDIYTAIHLLNRGKVDWVGQPWHQGIPWELHKQSQYHYTYTPVEGAFWLCLNTKSPHLNDLQNR
HRLATCIDKRSIIEEALQGTQQPAETLSRGAPQPNQYKKQKPLTPQEKLVLTYPSDILRCQRIAEILKEQWKAAGIDLILEGLEVHLFVNKR
KVQDYAIATQTGVAYYPGANLISEEDKLLQNFEIPIYYLSYDYLTDQDFIEGVIYNASGAVDLKYTYFP

>core/282/1/Org1_Gene229

MNKNLVAIFDYMEKEKGIQRSTIIGAIESALKIAAKKTLRDDANISVNINSRTGDIEVFCEKEIVEICQNPSKEIPLDKAREYDPDCQIGQY
MDVPFVSDNFGRIAHAARQIIGQKLRHAERDVIYEEYRHRVNETLSGVVKRFAKGSNLIIDLKGVEAILPTRFYFYPKTEKHKIGDKIYALLY
EVQSENGGAEVILSRSHAEFVKQLFIQEVPELEEGSVEIVKIAREAGYRTKLAVRSSDPKTDVPVGAFVGMGRGSRVKNIIRELNDEKIDIV
NYSVPSTELLQNLLYPYIEIQKIAILEDKVIIVVNDADYATVIGKRGINARLISHILDYELEVQRMSEYNKLEIQRLQLAEFDSPHLDQPLE
MEGISKLVIQNLEHAGYDTIRRVLLASANDLASVPGISLELAYKILEQVSKYGESKVDKPEIED

>core/290/1/Org1_Gene742

MVCENNILSGRGLELLKKKSNITLTPTIYSVSNHNIKLDKDFSPHALSVIKTLRKAGYIAYIVGGCIRDLLLNTTPKDFDISTSAKP EEIKAIFKN
CILVGKRFRLAHIRFSKQIIEVSTFRSGSTDEDVLITKDNLWGTPEEDVLRDFTINGLFYDPEHEEIIDYTGGVNDLRNRYLRTIGDPFTRF
KQDPVRMLRLLKILSRSPFTVETQTQEALICRQELIKSSQARVFEELIKMLNSGAAKNFFQLLIENHLEILFPYMDKAFRLNRALEEQTA
TYLKALDDKILKKEAEYDRHQLMAIFLPLVNFNVRYKHQKHPYLSLTSVFDYIKNFLEQFFADSFTSCSKNFILTALILQMQRILTPLIPT
KKALFFNKLLHHTRFLEALSLEIRSIVYPKLDKVVYVAWIRHHQTLKCKKDSHSQK

>core/295/1/Org1_Gene909

MKKT MVIDTSVFIYDPEALFSFENTRIIPFPVIEELEAFGKFRDESAKNASRALSNIRLLENAKTKVTDGVLLPSGSELRIEVAPLSNDDRR
GKLLTLELLKIIAKREPMVFVTKSLGRRVRAEALQIESRDYESKRFSFRSLYRGFRELQVSQEDIENFYKNGYLDPLDVVPSPNEYFFMSA
GENHFALGRYYVSEGKIIALKAMDKSVWGKPLNTEQRCALDLLRDDVKLVTLIGQAGSGKTILALAAAMHKVFDKETYNKVLVSRPIV
PMGRDIGFLPGLKEDKLMHWMQPIYDNMEVLFSINQMGNSSALQALMDAKKLEMEALTYIRGRSLPKAFIIIDEAQNLTPHEIKTIIS
RAGKGTKIVLTGDPTQIDSLYFDENSNGLTYLVGKFHHLALYGHMFMTTRTERSELAAAAATIL

>core/305/1/Org1_Gene60

MIKFLSQLFIRHWPRKVVSLSGFIIWILVGQSVTITRTLTVNPPVRIVDLHPDQTVLGLQKSGFLNKKVSLTITGNKNTVQDLRPSNLEVVI
SAANHTESWIATIDKHNLSVDHEINIRKDIHSVDANDIFVRLTQYVTEDILLTITKPIGSPPKGYEYLDVWP KYLNQKVSGPKEYINALKE
QGLELTFNLNKISFEELERNRIAQGSHEIIFPIPKEWKKILIPFENTFMDLNDPQADFLRLFLKRECIPLNLNLPVFLFFPVTFIQTMNPLE
YSLDPVPPIILNHGIHQINIPLYVKDVSQFLDVVKNNMVLTIMPSPQDPSSINWAIEFLDEKTLNTFLQTIIAQEHGILHDIALIDEAGI
RHRFREYLRKLALFTADGEPLNLIAEIKNNKVVIQTKTKETTKLYKKEW

>core/307/1/Org1_Gene146

MSSAIARDCFPSPSPQPSSTLGVHPPKYKSLILSVSLIVLGVLLLCVGMILLVNNAIFSFSVLTVGLGGAGVFLGSLLLLGLIFFVSYHRKLSEA
TRSLEQKITLEYQPWADLRKELNEVQEWSNFLDEWEDFKEVVAQHKSQFATFEGDLLFGREVEKYETIWKELDGRDVALLTELKNI
WGPLEFLRKKGDRLQCEIDKLRKEVMKVGKSGKLACELTKFKSALKDVKIEQECYRDKRKVEKLEVFPEGYRRELLEVLKTRLSVEKEIQL
FEEVVSAAFEELASLHRTVFSEELQEALDKAKAELDIQVRKSVVEDLSCEPTLIQYHLLRLYEYVQCRIVEQFLTQTFSSSEQEKVLEEYAL
KARIRKTLRVKLDQVRANVAFVASTDILLSESESLDGNDSVFEDAHDFFLD

>core/309/1/Org1_Gene668

MIETREEVGSANFVSLERAIEDLRAGKFVIVVDEASREDEGLIAGEKITVEKMTFLLQHTTGVVCAALSQERLLSLDLPPMVKDNRCRF
KTPFTVSVDAAHGVTTGVSAADRTKVQQLADPKSKPEDFISPGHFFPLASSPGGVLRAGHTESTVDLMELAGLQPCGVLAELVNED
YSMMRLPQILEFARKHNIVIPVTSIIAHRMLSDRLVSKISSARLPTIYGDFTHVYESLLEGMQHLALVKGNVAGKSNVLRVHSECVTG
DILGSKRCDCEQLSSAMSIAEKGTVLVYLRGQEGRGIGLGHKVRAYALQDNGYDITVDANLAMGFPVDSREYGIGAQLVDLKLTTI
KLITHNPQKYFGLQGFGLSITERVPLPVRISEDNEQYLRTKQERMGHWLDLPCCNNRVQ

>core/312/1/Org1_Gene689

MCQRILILGTGITGKSVARFLYQQGHYLIGADNSLESLSVDHLHLDRLMGASEFPENIDLVRSPGIKPYHPWVEQAVSLKIPVVTDIQV
ALKTPEFQRYPSFGITGSNGKTTTTLFLTHLLNTLGIPAIAMGNIGLPILDHMGQPGVRVVEISSFQLATQEEHIPALSGSVFLNFSRNHLD
YHRNLDAYFDAKLRIQKCLRQDKTFWVWEECSLGNSYQIYSEEIEILDKGDALKPIYLHNRDNYCAAYALANEVGWVSPEGFLKAIRTF
EKPAHRLEYLGKKDGVHYINDSKATTVTAVEKALMAVGKDVIVILGGKDKGGDFPALASVLSQTTKHVIAMGECRQTIADALSEKIPLTL
SKDLQEAVSIAQTIAQEGDTVLLSPGCASFDQFQSFKERGAYFKLLIREMQAVR

>core/318/1/Org1_Gene874

MKKNASHKTNDKKSLSIWSIGGSIFAMFFGAGNIVFPLALGYHYNAHPWSAYFGMMLTAVCVPLLGLVSM LFYSGDYQKFFFSIGRIP
GMIFITAIILLIGPFGGIPRAIAVSHATLISLSEHKSAFIPSLPIFSAICCVLIYFCKLSRLIQWLGSVFFPIMLVTLWVVIIRSFMIPTHPMVQ
EFIPNARQAWLAGFIEGFNTMDLLAAFFFCIVLISLRQLVAEEKHPTEEEEPLSFQGISKKNKRSLALGFFLAAILLGMTYLG FVLSAARHA
GLLVNVSKGHILGRISAIALGPNSILAGVSVFIACLTTEIALVGIVADFLARVVSFKKLNYSASAVICTLIPTYLISILNFETISHLLLPLLQLSYPAL
IVLACGNIAYKLWNFRYSPVLFYLTLSLTIVLKLVN

>core/322/1/Org1_Gene751

MNLPVSLACLLLSGCVFFLGVFVSSSLYARKKRAFLEKIQKLEHENQLLQTSNLNLSRHQEQIIEFDSNRLALSSHKLIKDMKEEAQNYFGD
TSKSFQSILSPIQTTLTTFKQSLETFETKHAEDRGRLKEQISQLLAVEKKLEHETHVLTDLKHHPGSRGRWGEIQLERILELAGMLKYCDYDS
QTTSAQGAFRADIIIRLPQDRCLIIDAKAPISDSYFSVEEIDKGDLDVKIKEHIKTLKSKSYWEKFHQSPYVILFLPGESLFNDAILAPELM
EIGASSNVILSSPLTLLALLKTIAYMWKQENLQKQIQEVSLLGKELHRRRLQVVFTHFQKIGKNLNQTVQSYNDMTSSFQYRVLPTRLRFE
GLETSSSHQIEEPTPIESLATSFPHTCDIDTNLAVIESLEKQD

>core/323/1/Org1_Gene828

MKTAFHSCYSWFCWLFSLVLFVGGIAGGEPLCPDCKYETKSVLRSDQLPDHLWNYENDCYLTGYVQSLLDMHFLDSRTQVVIEKNRA
YLFSLPVDSSLSEAITNFVRDLPPFICAVEICERPYGECITRSSAERPLLPEKTLGMPIFCGKEGVWLPQNTILFSPLIADPRQVTNSAGIRFN
EKVVGNRVGATIFGGDFILLRLFDVSRFHVDCDFGIQGGVFSVFDLDHPESCMVNSDFFVAGLWSGAIDKWSFRFLWHLSSHLGDEF
ILTHPNFPRFNLSDEGVDLFISFRYTPQIRLYGGCGYIVSRDLTFPERPFYCEWGAELRPFGLREGNLHAQPIFAMHFRCWEEQKFGLDQ
SYILGMEWAKFQEIGRKIRAVLEYHQGFSKEGQFIREPCNYYGFRITYGF

>core/326/1/Org1_Gene145

MVVVALFILGIFFLSGSLAFLVHTSCGVLLGAALPILCIGLVLLAVALIVFLCHKHKTRQDLDDYDQDLDSLVIHKKEIPNDISELRTFEKLQ
NLFQFHTKDFSDLSQELQGKFINCMEKWLTLEDEVTKFLIVRDRFLETRRNFTTFGEQVKGIQSNIFDLHEEKSSLYLELYRLRKDLQVLL
NFFLLPPGILKVDYDEIEAIKGLFIRLTSRLDKLDVKAQERKKFINEMSREFKEVEKAFDIVDRATKKLMDRAKKESPARLFMGRTESLLEM
KKNEEALKNQGLDPENLSHPELSPYQQLLILNYLNSEIVLHHYEFISGTVTSGLTLEECENRMRAASTGLNALLVRKLQFRGAIKSAYFE
KLTEIEKELRSLQDVIKSLELELIHKIKDIVTEET

>core/336/1/Org1_Gene359

MLSVTIVLVGLEMARSKVSKRDSKILDILFATTELYLKTGQPVGSKTLKESFCSDLSTATIRNYFAELEAEGFLKKNHTSGGRIPTDLALRHY
VDHQEECPAEISAPIFDKISQLPSESERNIIKDLQKATELLGEILDLPFFSSPRFENDSVTNIQITQVDKQRAVTILSTEFQQIFTDTLWLPE
ACDTLSIKRIEFLQNYIRKLPTNEELSKKEEHLMSLYNEVVVRYLTRYCNFSEEDLYQTGMSKLLKYEAFKDPEVLALGLSLFENRRQMC
ELLNIGMHKGRATAFIGKELSDILGTSNPGCSVITIPYYMNRSPLGALGILGPINLPYKEALPLLKLFANKINETLTQSFKFKLSFRRPLTSN
CKLSNEPILRTEYSSIKLLPSKETL

>core/337/1/Org1_Gene354

MRRNPHFSLLKPQYLFSEISKLAQFRKENPEISVIDLSIGD TTQPLCRSITQAIKEFCVSQEKQETYRGYGPETGLEKLRTKIAS E VYENRIS
PEEIFISDGAKPDIFRLFSFFGSEKTLGLQDPVYPAYRDIAHITGIRDIIPLACRKETGFIPELPNQSLDILCLCYPNNPTGTVLTFQQLQAL
VNYANQHGTVLIFDAAYSASFVSDPSLPKSIFEIPEAKYCAIEINSFSKSLGFTGMRLAWNVIPKELTYDNNNEPMINDWKRLFATTFN GAS
LLMQEAGYYGLDLFPTPPAISLYLTNAQKLKKSLETAGFSVHGGDHAPYLWVELPEGISDEEAFDFFLHQYHIAVTPGHGFGSCGQGFV
RFSALTQPQNIALACDRLCTASLKETMVLA

>core/345/1/Org1_Gene16

MDYYSILGISKTASAEIKKAYRKLA VKYHPDKNPGDAAAEKRFKEVSEAYEVLSDPQKRDSYDRFGKDGPFAGAGGFGGAGGMGNM
EDALRTFMGAFGGEGFGGGSFFDGLFGGLGEAFGM RSDPAGARQGASKKVHINLTFEAAHGV E KELVVSGYKSCETCSGQGAVNPQ
GIKSCERCKGSGQVVQSRGFFSMAS TCPECGGEGRIITDPCSSCRGQGRVKDKRSVHVHIPAGVDSGMRLKMEGYGDAGQNGAPSG
DLYVFIDVESHPVFERRGDDLILELP IGFVDAALGMKKEIPTLLKTEGSCRLTVPEGIQSGTILKVRNQGFNPVHGKGRGDLLVRISVETPQ
NLSEEQKELLRTFASTEKAENFPKKRSFLDKIKGFFSDFTV

>core/350/1/Org1_Gene992

MMKQGVGQDAKELYTFLSRGNEHYQ PCLWFSLEEEELGFLF DAKMLCAPLSE DHYCHSYLVDLVDQHLKD LILSMFLDPQNI SAGELLK
VSINVGDSFSPLQQKDFLSMVL RDETGNV VVVVFKGVLSLPATQVCKLVEELNSKDYSYLNIFSCHGDSSPQLLFRKELEGTSGRYFTVIC
ALYLGD TDMRSLQLASERIMVSREFDLV DAYAARCKLLKIDHTNWRPGTFSRHAD FADAVDVSAGFNSREFKLITQANQGILESGELPL
PSKTFWEGFLAFCDRVTVTRHFIPMLDAAIKQAVWTHKHPSLIDKECEALDLKTQCLPSIVSYLEYVTNSHEKTSKGPFIQKEI IADCSPLK
EALFPGSDEDVPSTSEDP SDDHPSDLEDS

>core/351/1/Org1_Gene509

MGTPISGNDGDRNTISDPLEESAAEEGDS DLED RVSESATQVIETIADTGIPEATPSEG TNSDLNSDLVDRVEYEARGSLTTMLARIRKA
VSQIWMHVKTKRHPKEQGVRS LGDIPCDLLKATRLPKETAEP PFYFALETALASCRSFFFHVFLRLFTLLRRQHPEAPLDLCGTDPI SPEA
AVAFALILRSCCKWVATDAVQEGLPLEVIEEAGMYNAFSL EATTTVEEVSKRSEL LYS DKRIDGLANVRGITKIITSPYLGAGQCVSVVD
NLKTYDLGRNYTQVLACASQIDEFADKGENEALVMKDILYLVRQDRSKELGDFLMMWSEEHASEVNYDVVLAILEVNLPILEEDYRSH
PLAYQKKLNYVICQFFCSERLTSIEPKD

>core/353/1/Org1_Gene431

MAIKNILVVDDEPLLRDFLSELLTSQGFIPDTAENLRNALQMIRSRDYDLVISDMSMPDGSGLDLIKQSSPHTPVLVVTAYGSIENAV
EAMHQGAFNYLTKPFSSSEALFAFISKAEEELKNLVHENLFLHSQTTPDSSHPLIAESKAMKDLLAIAKKAASSSANIFIHGESGCGKEVLSFFI
HHNSPRANHPYIKVNCAAIPTLLESELFGEKGAF TGATTKKAGRFELAHKGTLLLDEITEVPVNLQAKLLRAIQEKEIEHLGGTKTLSVD
VRILATSNRKLKEAIDDKSFRQDLYYRLNVIPLHLPPLRDRQDDILPLANYFLNKFCRMNNTPLKTLSPKAQELLNYPWPGNIRELSNVL
ERVVILENTSLLTEDMLALA

>core/357/1/Org1_Gene660

MEKPQNRKAPRIFWLNNQVAIPPSERVKESYALHSDIFSLPPGSALKLAEKTEESIRQLVGLKDSHIFRVPHPHVVHIVLAALVENLSM
FQGRNHIIIPAHDDQQLLINSRCRHQGLGTTYDWVTVNHEGRIVEEQLIETLSPRSLLFSLSAAHGLTGVIQPLDPLLSLCKDRRILLHLDIS
DILGRAPLTPEILNADIITFSSAALGGMGSIGGIFIRKSLERVFSSWFPHTSASLCFSAVAAMQTACEERISALPLFTFHTSNLCKKLIQELQ
SVLPSIQLAFSEVQNRLPNIVVAAIPDIPAESLAFHLHQGGIYPSLGYERFQPLAQVLQNCGISPFLCHSALHFSALTERSKDLEFSKLARAM
HDAIKHLTPLLGSSS

>core/366/1/Org1_Gene924

MKHLAVLGSTGSIGRQTLEIVRRYPSEFKIISMASYGNNLRLFFQQLEEFAPLAAAVYNEEVYNEACQRFPHMQFFLGQEGTLQLCIMD
TVTTVVAASSGIEALPAILESMKKGKALALANKEILVCAGELVSKTAKENGIVLPIDSEHNALYQCLEGRITIEGIKKILTASGGPLLNSLE
ELSCVTQDVLNHPiWNMGSKVTVDSSTLVNKGLEIEAYWLFLENIEILAVIHPQSLIHGMVEFLDGSVISIMNPPDMLFPIQYALTAP
ERFASPRDGMDFSKKQTLFFPVDDEERFPSIRLAQQVLEKQGSSGSFFNAANEVLVRRFLCEEISWCDILRKLTTLMECHKVYACHSLED
ILEVDGEARALAEI

>core/370/1/Org1_Gene92

MNTSLKRPLKSHFDVVGSLRPEHLKKTRESLKEGSISLDQLMQIEDIAIQDLIKKQKAAGLSFITDGEFRRATWHYDFMWGFHGVGH
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RKVIRDLYDAGCRYLQLDDCTRGGLVDPRVCSWYGIDEKGLQDLIQYLLINNLVIADRPDDLVLVNLHVCRGNYSKFFASGSYDFIAK
PLFEQTNVDGYYLEFDHERSGDFSPLTFISGEKTVCGLVTSKTPTLENKDEVIARIHQAADYPLERLSLSPQCGFASCEIGNKLTEEEQW
AKVALVKEISEEVWK

>core/371/1/Org1_Gene465

MSDNAHNLLYDKFELPEAVKMLPVEGLPIDKHARFIAEPLERGMGHTLGNALRRALLIGLEAPAIISFAMTGVLHEYMAIEGVIEDVTNI
ILNLKGALLKKYPMQDSSLGRTTQVLKASISIDASDLAAANGQKEVTLQDLLQEGDFAVNPQVIFTVTQPIQLEVVLRIFAQGRGYTPS
ERIVLEDKGVYEIVLDAAFSPVTLVNYFVEDTRVGQDQDFDRLVLIVETDGRVTPKEALAFSTQILTKHFSIFENMDEKKIVFEEAISIEKEN
KDDILHKLILGINEIELSVRSTNCLSNANIETIGELVIMPEPRLLQFRNFGKKSLEIKNKLKEMKLELGMDLTQFGVGLDNVKEKMKWYA
EKIRAKNTKG

>core/377/1/Org1_Gene532

MAVAADSSASWLKSRNNFLSSLGKTEEQVAAPEFPKELCQHKIREKFRLEDVQVSIKFRGSITAVEATKEFGVHLLIQPMVVQPWEVEN
LLFLTSEEDLQELMVAVFDDASLASIFYEKDKLLGFHYFVAEACKLFEELQWVPSLSAKVGGDAIFTATSLQGSFQVVDISLRDGNV
RCRLLLPEDTFQSCQKFFSGLHDESDLHNIDQTQQISLSVEVGYSQLTQEEWHQVVPGSFIMLDSCLYDPETEESGALLTVQKHQFFGG
RFLTPSSGEFKITSYPNLTHEDPPLPENPQASAAPLPGYSRLVVEVARYSLAVSEFIKLNLSILSLGNHPAYGVDIILDGAKVGRGEIIALG
DVLGIRVLEV

>core/380/1/Org1_Gene891

MMLVYCFDPSVPTSPEHRLMAALDRWFFLGGHRVRILTLEGNHYRAFQENMSISTVEKILKLISYLLIPIVLIALLIRCFLHSRFGKNWKCD
SLSDARVPHDVQPFNDFQLFNNQERLNIWKNRRYVSGIDVLMVPVDYLRQFPGFKEIPEAIRCENYVSDGQFSEESKTSYLRAMLTDI
VGYLSDLDETYWTNVILKIRAMCITFESFPGKEADPNYSRVTTHYFDESWKALARHVLGEGNMVNRLDEALIRTEKPGKEGECITKQFL
KDYCKKHLEVMSCPDFIESLVDEKIREFRCP SILNSAVCDVIDRKCQEHLKAIINEANRRLPGMKNSSFTMRGNQVLFYTIFSPPKLPPA
ASSVYF

>core/381/1/Org1_Gene370

MTTCLPQPPKTSPLYSIFEKLDAQERLSSDALHLLLLTNKEDQRTLWNFADQVRKQRVGDTVYYSSTLYLYPTNFCDFSCFKCSFYAKP
GDPKGWLYSPD DLLQQIQNIKTPIEVHIVGGCFPSCNLQYSDLFTKIKEYDPQIHIKALTAIEYAYLSDLDNLSIRDVLLTLKDAGLDSIP
GGGAELVDKIRNFLAPKRLSSSDFLNIHKMAHQLGIHSNITMLCYHKEGPEDLVTHMVKVRDLQDETQGFKNFILLKFAQENNVLGKR
LRKSGQGHAIPKSLMAVARIFLDNFSNMKALWNYLGIEAALDLLSCGANDLSSTHMGEKVFQMASSKEPIKMDAEGMAALITQQG
RTPCLTNSSHV

>core/385/1/Org1_Gene34

MAVEGRVNSSQALNQDCQEVLANKQSKGLLRCRILSIVVAVITFIAGVVLIALTASILTSVPYLALGVFLLIVTLGCIIFALCSEKIKKVPPTP
ISHKEEIIAWFEERKNIDMEKEKEDPEHFGRTATDIPMRSALDQFNHSCHHIHESPALTETYSHQDVLLFKDWCPVTLPDVTSEEEVLI
RSVVGSYLLMEACVPKVSMLIDELHNKLSKSPSERECLFIDKKTQKASFLFTQKDLATFFLAYTRVNDGHLAPFRAGAKWILIHVRLRR
QHNQNDFFTPGHSCYYARLAFNQTRQRLYHQLFNVEKLRSIYANMDKDPLCHPWAFIPIYDLLKTEDHGDGFLEQQEDREYPSRAAQD
QFWG

>core/387/1/Org1_Gene888

MKFVVSRLNELGNLIKKIQSVVPQNTPIPVLTHTVLIETYNDELVFTATDLTVSTRCVTKAKVYEKGAISIPSKRFFQLVKELTEANLEISSAG
EMAQITSGSSCFRLLSMEKEDFPMLPDIQNALRFSLPAEQLKTMQRTSFAVSREESRYVLTGVLLAIANGVATIVGTDGKRLAKIDAEV
TLDKSFSGEYIPIKAVEEIIKMCSDGEATIFLDQDKIAVECDNTLLITKLSGEFPDFSPVISTESNVKLDLHREELITLLKQVALFTNESSHS
VKFSFLPGELTLTANCTKVGEGKVSMAVNYSGELLEIAFNPFFFLDILKHSKDELVSLGISDSYNPGIITDSASGLFVIMPMRLHDD

>core/396/1/Org1_Gene810

MKLYQTLRGIVLVSTGCIFLGMHGGYAAEVPVTSSGYENLLESKEQDPSGLAIHDRILFKVDEENVVTALDVIHKLNLLFYNSYPHLIDSF
PARSQYYTAMWPVVLESVIDEFLMVADAKAKRIATDPTAVNQEIEMFGRDLSPLYAHFEMSPNDIFNVIDRTLTAQRVMGMMVRS
KVMLKVTPGKIREYYRKLKEEASRKVIWKYRVLTIKANTESLASQIADKVRARLNEAKTWDKDRLTALVISQGGQLVCSEEFSSRENSELSQ
SHKQELDLIGYPKELCGLPKAHKSGYKLYMLLDKTSGSIEPLDVMESEKIKQHLFALEAESVEKQYKDRLRKRYGYDASMIAKLLSEEAPPLF
SLL

>core/397/1/Org1_Gene437

MAFKRKTRWLWQVLILSVGLNMLFLLFYSAIFRKDIYKLHLFSGPLIAKSSRKVYLSDFLNEISQASLDDLISLFKDERYMYGRPIKLWA
LSVAIASHHIDITPVLSKPLTYTELKSSVRWLLPNIDLKDFPVILDYLRCHKYPYTSKGLFLIEKMOVQEGWVDEDCLYHFCSTPEFLYLRT
LLVGADVQASSVASLARMVIRCGSERFFHFCNEESRTSMISATQRQKVLKSYLDCEESLAALLLVHDSVVLHEFCDEDLEKVIRLMPQ
ESPYSQNFFSRLQHSPRRELACMSTQRVEAPRVQEDQDEEYVVQDGDLSWLIAKRFGIPMDKIIQKNGLNHHRLFPKGVLKLPKQSQ

>core/400/1/Org1_Gene73

MKIDILSLFPGYFDGPLQTSILGRAIKQRLLDVQLTNLRDFGLGKWKQVDDTPFSGGGMMLMAEPVTSAIRSVRKENSKVIYLSPPQGALL
TAEKSRELAASHLILLCGHYEGIDERAIESEVDEEISIGDYVLTNGGIAALVLIDAVSRFIPGVLGNGQESAERDSLLEGLGPQYTRPREF
EGKEVPEVLLQGDHKAISQWRLEQSERRTYERRPDLYLNYLYKRSIDHKFDEETTTNRDHFCDKISVVLEVNLKRAKNFYCKVFGLDA

MSCENKFCLPHEGKTIFWLREVQAEKKNIVTSLSLDCACEEDFCYLLRRWELFGGKLEKQADEHAVWALAQDLGDHAWIFSWHR
MK

>core/402/1/Org1_Gene217

MSEAPVYTLKQLAELLQVEVQGNIETPISGVEDISQAQPHHIAFLDNEKYSSFLKNTKAGAILSRSQAMQHAHLKKNFLITNESPSLTFQ
KCIELFIEPVTSGFPGIHPTAVIHPTARIEKNVTIEPYVVISQHAHIGSDTYIGAGSVIGAHSVLGANCLHPKVIRERVLMGNRVVVQPG
AVLGSCGFGYITNAFGHHKPLKHLGYVIVGDDVEIGANTTIDRGRFKNTVIHEGTKIDNQVQVAHHVEIGKHSIIVAQAGIAGSTKIGEH
VIIGGQTGITGHISIAHDVIMIAQTGVTKSITSPGIYGGAPARPYQETHRLIAKIRNLPKTEERLSKLEKQVRDLSTPSLAEIPSEI

>core/406/1/Org1_Gene692

MMKKIRKVALAVGGSGGHIVPALSVKEAFSREGIDVLLLGKGLKNHPSLQQGISYREIPSGLPTVLNPIKIMSRTLSCSGYLKARKELKIF
DPDLVIGFGSYHSLPVLLAGLSHKIPLFLHEQNLVPGKVNQLFSRYARGIGVNFSPVTKHFRCPAEVFLPKRSFSLGSPMMKRCTNHTP
TICVVGGSQGAQILNTCVPQALVKLVNKYPNMYVHHIVGPKSDVMKVQHVVYNRGEVLCCVKPFEEQLLDVLLAADLVISRAGATILEEI
LWAKVPGILIPYPGAYGHQEVNAKFFVDVLEGGTMILEKELTEKLLVEKVTFALDSHNREKQRNSLAAYSQQRSTKTFHAFICECL

>core/412/1/Org1_Gene961

MNLPDRKKALEAAVAYIEKQFGAGSIMSLGRHSATHEISTIKTGALSLDLALGIHGVPKGRVIEIFGPRESSGKTTLATHIVANAQKMGGV
AAYIDAEHALDPSYASLIGVNIDDLMISQPDCEGALSIAELLARSGAVDVIVIDSVAALVPKSELEGDIGDVHVGLQARMMSQALRKLT
ATLSRSQTCAVFINQIREKIGVSFGNPETTTGGRALKFYSSIRLDIRRIGSIKGSNSDIGNRIKVKVAKNKLAPPFRIADEFDILFNEGISSAG
CILDHAVEYNIIKKGSWFNYQEKKLGQGREFVREELKRNRKLFKEIEKRIYDVIAANKTPSVHANETPQEVPAQTVEA

>core/413/1/Org1_Gene697

MNLCKRISFEEGLELFVSSPIERLQERADAIKERYPSNEVTYVLDANPNYTNICKIDCTFCAYRKPKSPDAYLLSFDEVRSLLQRYVSSGV
KTVLLQGGVHPGLGIDYLEELVRITVQEFPSIHPHFFSAVEIEHACRVSGISIEQLQLRLWDAGQRTIPGGGAELSERVRKIISPKKMQPG
GWINLHKLALHMGFRRTATMMFGHVENPEDILHLQTLRDAQDSCPGFYFIPWSYKPGNTALRRNVPQQASIETYRILALGRIFLDN
FDHVAASWFGEGKSLGAKALHYGADDFGGVILDES VH KATGWSIQSSEEEICNIIRSEGFIPTVERNTFYQHISCTVSSL

>core/414/1/Org1_Gene703

MKYSLNFKKIDYERVIEVTCSEKVRHLHAIHQTAVGPALGGVRASLYSSFEDACTDALRLARGMTYKAIISNTGTGGGKSVIILPQDA
PSLTEDMLRAFGQAVNALEGTYICAEDLGVSINDISIVAEETPYVCGIADVSGDPSIYTAHGGFLCIKETAKYLWGSSSLRGKKIAIQGIGS
VGRRLQSLFFEGAELYVADVLERAVQDAARLYGATIVPTEEIHALECDIFSPCARGNVIRKDNLADLNCKAIVGVANNQLEDSSAGMM
LHERGILYGPDYLVNAGGLLNVAAAIEGRVYAPKEVLLKVEELPIVLSKLYNQSKTTGKDLVALSDSFVEDKLLAYTS

>core/419/1/Org1_Gene789

MRIAVLGAGYAGLSVTWHLLLHSQGTATIDLFDPIPLGEGASGMSSGLLHAFTGKKALKPPLADQGINATHALITEASKALNPVIVISQG
ILRPAIDEDQAQLFTERVEEFKEVEWWEKARCEISIPSMVIPPNLGALFIKSGVTLNNDLYIQGLADACMKLGTQFYDELIEDLADIEEFY
DHIIVTPGANASILPELKDMPVNKVKGQLEISWPKDLAMLSFSINAHKYMVANTQKNTCILGATFEHNQPEETPDPAIAYQEIMPPVL
SLFPGLKDAQVLHCYAGMRSSSKSRLPVISRIREKLWFLGGLGSKGLLYHGITGDMLAQAVLRKSTAYIAKEFLFTI

>core/420/1/Org1_Gene715

MILLQNIKRCSLKQLKVLATLLLSLSLPTLEAAENRSDSIVWHLDYQEALQKSKEAELPLLVI FSGSDWNGPCMKIRKEVLESPEFIKRVQ
GKFVCVEVEYLKHRPQVENIRQQNLALKSKFKINELPCMILLSHEEREIYRIGSFNETGSNLGDSLCHIVESDSSLRRAFPMMTSLSEL
QRYRLAEELSHKEFLKHALELGVRSDDYFFLSEKFRLLVEVGKMDSEECQRIKKRLLNKDPKNEKQTHFTVALIEFQELAKRSRAGVRQ
DASQVIAPLESYISQFGQQDKDNLWRVEMMIAQFYLDSDQWHHALQHAEVAFEAAPNEVRSHISRSLYIRHQS

>core/422/1/Org1_Gene218

MDVSRKINRHTQFYVDSIDGVIKNFDHKPSEDKSRDHEELEEKLLTITKRIVASAEFQNRKTD SKNYLKKTQWL PFKNEELETKELF
AMLTSMDDKIAQLFFYSPGCSSDWVEFTEVICH LND SIGLGGVLLCCGLFEQQCEHVVTVNKKLDLPLL GTTVVNSLRYYLT YRNISLLN
CQSMSELGKELGDVLKQHGVAF TLIFKEIVDIDLNNYVKLIQGLKRSGNIQARIYDNDVPTLP SVSSSPIALRYSLANTIRGLALHVD FSSLK
FISPSILSNT EHTAKALNSGGECFIFSNLDEFNLGMKIVMQLLRTGKISPEILNKNIMKILMIKRRVRSLYI

>core/428/1/Org1_Gene748

MMEVYSFSPSVRTSFQHRVMAALDNWFFLGRRLLKVSLDSCNSGQACEEYVPISTTEKVLKILSYLLIPIV IALLIRYLLHSNFTAKVSQ
KPWLKTLQLGIDIKSFILPGSHVNTMDSATLFKAIRLEGKRVDVEYHRLHSSDKVVFYIPAQKLPDDLRLTHWLPEKETRKTEYVRHMLA
HVMGYLTSQGKERLQQVVQDSRSSTSLGAEKVLQYRFIDHPQSQGEFQRLNENITTKGSEDKEVVQSDLFDMAFQCWWPQFISVIO
SPTFSEELVHEMSQKLDLDCIYPEDDEFEQKFLNTLLKAVLHHGFEGISVASMGVIFLICPDSLALQIPFLRNQK

>core/435/1/Org1_Gene659

MFFQNLAKKLTALGISPLGCLLIGGVVSCAILFGRSSNPSLAPTQVKTEKTSGNWLKLTQMGNPKLIESLTKKEQLEKDLTSFHPIASAKV
AIALSTEDDVMSPHLHSVILTLRKEESLTPSLLFSITDYLCSSLPGLKREHISLSDNLGNLYIPESITVNSLFIHTLENYLGKIFPKEHFALAYHAK
AEKPTLQLTLNENYIAHLTKEESEKIVAHTKHYLYQNYDDSYDIVIETLPFARLQNKKSFPKVLIGSMILVISLMIVALASFYLARHAYERV
SPEPRKIKRGINISKLEIIQKESPEKIALILSYLDPKKA EALLNRLPEDLKHQVLKYKL

>core/437/1/Org1_Gene355

MTILRKLSQYLFFFSLFCSFIYVATCGSQPDSVSSPKIAIFLSFPHPLEDCSKSCIETLKDFENLPEIVVLNAEDSIVKARKIARSLHTDKNVV
AIVTLGTIATKVM SHIETQKPVIYAAVPDRESLTPKNTMNIYGVNDTLDINQYCFAIQAVATNAQSIVYLKPSEFPFSDLQKEIVKKLHAS
GIEVIEISITSSTFKTRIRQAIDKRPSAIFPLSPLSHKEGT AFLQEILKEKIPITDDTSLISEGACIACSVDYKKSGKQIAKIVHHLLYNNHDVDS
LRKIIAQRLSPTTTTFNEDIKYLGIKLHKTERNQFLSFKSKLEKSEKGNVAVS

>core/445/1/Org1_Gene562

MSYSLRNKKTICVYIIIALGILSFRSIPQEVYDKIRSSFVSLHVKFFPKIKQAPSSHLANLELENLVLKERVASLEEKLYEVSNHTPPLFPEIL
TPYFHKLV EGVVYRDYTHWSSSCWVNVGKTHGIKKNSPVLSGNVLVGLVDYVGEHQSRIRLITDVGMKPSVVAMRGDIQSWWIKH
SLRELIRQVEQISHAYILEKDKYEKISQLQELDSLQGEGENQALLRGILSGVGALWKEGSLCLEGEGFYFSEGKTLLPGDILVTTGLDGVF
PPGLLVARVTKVKAPRDGACTFKIEAQSL EEEKLMELDQLFILPPLEFNPNDRPDIFGLLWD

>core/448/1/Org1_Gene214

MWFSVNKNKKAIIWATGSYLPEKVL SNADLEKMVDTSDEWIVTRTGIKERRIAGPQEYTSLMGAIAAEKAIANAGLSKDQIDCIIFSTA
APDYIFPSSGALAQAHLGIEDVPTFDCQAACTGYLYGLSVAKAYVESGTYNHVLLIAADKLSSFVDYTD RNTCVLFGDGGAACVIGESRP
GSLEINRLSLGADGKLGELSLPAGGSRC PASKETLQSGKHFIAMEGKEVFKHAVRRMETA AKHSIALAGIQEEDIDWFVPHQANERIID
ALAKRFEIDESRVFKSVHKYGNTAASSVGIALDELVHTESIKLDDYLLLVAFGGGLSWGAVVLKQV

>core/455/1/Org1_Gene625

MQPFIFTLLCLTSLVSLVAFDAANARKRCACAQTIERGENFFSIKRSACAEIEYQEKSRRHASAIERISKDKGKVT PKQIAKVATKKKQRYRL
LQVPFSRPPNNSRYNLYALLSEPPECYSDTASWYAIFIRLLRRAYVDTGNVPPGSEYAIANALISNKQEILERGAQLGPDVIETLTLPEEQA
EIFYKMLKGSSNSQSLLNFLHYEEKSLGHCKLNLIFMDPLLEAVLDHPDAYRETSLLRDGIWEAVKRQEHAIQEHGQAAALELFKTRTD
FRLELRDKMQLLSRYDLLPLLNKKMFDYTLGSAGDYFLVDPDTKAISRCRCPSKSIKL

>core/457/1/Org1_Gene803

MRIAVLGVTGLVGQKFVALLHKWYRDWVIAEVVASNSKYGQSYGDACIWQEPIGMPPEMVRDLPIRKIEEVQSDIVVSFLPSSAESM
EAYCLSQGKVVFSNASTYRMHSSVPIIPEVNSDHFQLLEEQPYPGKIITSPNCCVSGITLALAPLRKFSLDHVHIVTLQSASGAGYPGVPS
LDLLANTVPHIVGEEEEKILRETVKILGSSKQPLPCKLSVTVHRVPVAYGHTLSLHVTFSKDVDLDEILYSYQEKNEFPNTYQLYDNPWSP
QARKHLSHDDMRVHLGPITYGGDFRTIKMNVLIHNLVRGAAGTLLASMENYFFDYLKREMCLR

>core/460/1/Org1_Gene567

MSSLTLSRRPRRNRKTAAIRDLLAETHLSPKDLIAPFFVKYGNNIKEEIPSLPGVFRWSLDLLLKEIERLCTYGLRAVMLFPIIPDDLKDAYG
SYSSNPKNILCHSIHEIKNAFPHLCLISDIALDPYTTHGHDGIFLNGEVLNDESVRIFGNIATLHAEMGADIVAPSDMMMDGRIGYIRSKLD
QSGYSKTSIMSYSVKYASCLYSPFRDALSSHVTSGDKKQYQMNPKNVLEALLESSLDEEEGADILMVKPAGLYLDVIYRIRQNTCLPLAA
YQVSGEYAMILSAFQQGWLDKETLFHESLIAIKRAGADMIISYSAPFILELLHQGFEE

>core/463/1/Org1_Gene735

MQFSRYLRYAFDNQYLPEPLYQKFSVFHQNYIDAATKKAADQAEVLCCLQWVKVIEDLKNPFIFPPYHKKIRAPIDLFRLSIDFFSLVIDD
KNSRILNLHRLKEIEEYIARGDNVVLNANHQTCDPQLMYALGKTHPELMENMIFVAGDRVTS DPLARPFSMGCDLLCIYSKRHIATP
PELREEKLLHNQKSMQILKTLLNEGKFIYVAPAGGRDRKNAEGRYPSEFSPESIEVFRLLAKASNQTTHFYFPALKTYDILPPPPKIENAI
GEQRAIFFAPVFFNFGAELFFDALCSKEELIHCDKHAQRTLRAEKVFSIVKNLYEEL

>core/464/1/Org1_Gene800

MREETVSWSLEDIREIYHTPVFELIHKANAILRSNFLHSELQTCYLISIKTGGCVEDCAYCAQSSRYHHTVTPPEPMMKIVDVVERAKRAVE
LGATRVCLGAAWRNAKDDRYFDRVLAMVKSITDLGAEVCCALGMLSEEQAKKLYDAGLYAYNHNLDSPEFYETIITRSYEDRLNTLD
VVNKSISTCCGGIVGMGESEEDRIKLLHVLATRDHIPESVPVNLLWPIDGTPLQDQPPISFWEVLRTIATARVVFPRSMVRLAAGRAFL
TVEQQTLCLAGANSIFYGDKLLTVENNDIDEDAEMIKLLGLIPRPSFGIERGNPCYANNS

>core/465/1/Org1_Gene343

MIDIMQHFKPYTMVPGQKLPIPGSLLYAQVFPTLWRLFSSKHEILNEQTLQVQGPLKRFAVFQDLHRGGLAVTSERYKYYLLPSGECTQ
SIKGLPSAAQAGPLLSLGVHKKHADWQKVRCRRDLKEILPLWFRFAAMAPKGSYRDLETTAIGSLVKTAHQRVLHRETTEIAPALLSIAL
AGFSECFLPRSYDEEFQGILPQDGDPEGGVPFELLSYSGMIQDIFLRHQGQLVEILPALPPEFPCGRLIHVALPNLGTLSIVWTKKTIRQV
ELHAEYSGEVFLKFCSSLCSARLREWSERRLSGSKRLSLGETLEIKAGTTYLWDCFBK

>core/467/1/Org1_Gene376

MPSPMISTDVCQDILGKQKEAVDFFFQAFQPKAMQLAEKILGHSGWVFFSGVGKSGCVARKLVATLQSLSERALFFSPVDLLHGDLG
LVSPGDIVCLFSKSGETQELLDTPHLKSRRAILVAITSMYPYSNLAALSDLVVLPSVAELDPFNLIPTNSTTCQMIFGDFLAMLLFHSRGV
SLSTYGKNHPSGQVGMKANGKVKDFMFPKTEVPFCHLGDKVSFSLEVFSAYGCGVCIVDPQFRLMGIFTDGDLLRRSLASYGGEVLSL
SLEKVMTANPRCITEDSDIAIALQLMESSSPVAVLPVLDNEENRHVTGLLHMHTLAKAGLL

>core/472/1/Org1_Gene250

MDAKMGYIFKVMRWIFCFVACGITFGCTNSGFQNANSRPCILSMNRMHDCVERVVGNRLATAVLIKSLDPHAYEMVKGDKDIA
GSAVIFCNGLGLEHTLSLRKHLENNPNSVKLGERLIARGAFVPLEEDGICDPHIWMDLSIWKEAVIEITEVLIEKFPEWSAEFKANSEELV
CEMSILDSWAKQCLSTIPENLRYLVSGHNAFSYFTRRYLATPEEVASGAWRSRCISPEGLSPEAQISVRDIMAVVDYINEHDVSVVPED
TLNQDALKKIVSSLKKSHLVRLAQKPLYSDNVDDNYFSTFKHNVCLITEELGGVALECCR

>core/476/1/Org1_Gene190

MTIDMHCDLLSHPHFCRKDPAVRCSPEQLLSGGVRQQVCAIFVPHSRGEPNCDKQNSLFFSLPNQYPDIGLLSYEEEEENGSSSQKKSLS
LIRSIENASALGDDTAPLGTLLAKLIHLTKQGPLAYLGIVWKGDNRFGGGTEAPKRLSNDGKVLDDIMYELGVPIDLSHCSDKLAEDILDY
TADKLPNLAVIASHSNFRSVLDHRRNLVDAHAKIVRRKGVIGLNLVRSYVGDSLGDLEKHVLHAENLGILSSIVLGSDFFYANEDENFFF
NECSSAEHPVLNQLIHRIFSKGKAESILSSRAEKFLKQVIVEQVNPKITDVKL

>core/479/1/Org1_Gene302

MELLPHEKQVVEYEKAIAEFKEKNKNSLLSSSEIQKLEKRLDKLKEKIYSDLTPWERVQICRHPSRPRTVNYIEGMCEEVELCGDRTFR
DDPAVVGGFVKIQGQRFVLIGQEKGCDTASRLHRNFGMLCPEGFRKALRLGKLAKEFGLPVVFLVDTPGAYPGLTAEERGQGWAIK

NLFELSRLATPVIIVVIGEGCSGGALGMAVGDSVAMLEHSYYSVISPEGCASILWKDPKKNSEAASMLKMHGENLKQFGIIDTVIKEPIG
GAHHPALVYSNVREFIIQEWLRLKDLAIEELLEKRYEKFRSIGLYETTSSESGPEA

>core/489/1/Org1_Gene462

MRLLSILKLHLFSLRSSSSLSPHYHSCSRSMHLHLLCRWKDADIMEWQQICNILSGVCSRMSGKLVSLQKETQDSCHQEHERIHLQYRE
QLSALEEEYRRREEAKNQDLEKLQQENTWLQNRLAEKLQQIRHQSDIIDEIKKELLQSVQRTEISEGRRLCYEHKIKQLEEQLQRYVSQH
GAPSIEEEDKSSAAYAEINRLKKSLLDLQQEKDIYIKTYHSEIAKLREKLQRQEGAQTSSEVCSIEKLTEVQTDLAEKKAIALLDIVEDQY
CQLRDLHKEKGMAMPSNTKLDHLKGLLGKEPESEVDVVFSESKSLGS

>core/490/1/Org1_Gene738

MEVQIGIDLMGGDHSPLVVWQVLVDVLKSQSSTIPFAFTLFASEEIRKQIQEEFISDLPQEKFPKIISAENFVAMEDSPLAAIRKKSSSMA
LGLDYLQEDKLDAFISTGNTGALVTLARAKIPLFAVSRPALLVCVPTMRGHAVILDVGANISVKPEEMVGFARMGLAYRQCLGDSKIP
TIGLLNIGSEERKGTEAHRQTFRMLRETGGEAFLGNIESGAVFDGAADIVVTDGFTGNIFLKTAEGVFEFLQRILGDKLEADIQRRLDYTF
YPGSVVCGLSKLVKCHGKACGSSLFHGILGSINLAQARLCKRILSNLI

>core/491/1/Org1_Gene424

MLISISLATLPILAFSWASFIEPNWLRRTTAIPWRLPKKHAHLHGLRIAQISDLHFHKRVPEKFLNKVSKSIKNFSPDLIVFCGDLLCRARLED
KERLETFLNTLEAPLGVFAILGNHDYSSYSRNTKGEITCIPEEKSRPIQRAIIAVMQGLFSSPSYRYDPNLTPQEPHPDLLKLLKNTPLTLLH
NTTHVIPNTLNIVGLGDLFARQFHPEQAQFKNYDPSLPGLLLSHNPDGITRLQQYPGDFVLSGSHSGPQVTLSPWPKFARKFFERLSGLEN
PYLARGYFVTKEGKQLYVNRGLGGLKRIRFCSPPEICYITCSYD

>core/492/1/Org1_Gene765

MVLSSDLLRDDKQLDLFFASLDVKKRYLLALSGGSDSLFLFYLLKERGVSTAVHIDHGWRSTSAQEAKELEELCAREGVFPVLYTLTAAE
QGDKDLENQARKKRYAFLYESYRQLDAGGIFLAHHANDQAETVLKRLLES AHLTNLKAMAERSYVEDVLLLRPLLHIPKSSLKEALDARG
ISYLQDPSNEDERYLRARMRKKLFPWLEEVFGKNITFPLTLGEESAELSEYLEKQAQPFSAATHQDSQGELPCPDCLIQQAFLCKWV
MKKFFNAGIAVSRHFLQMVDHLSRSSCATLRMRNKIVIIKPGVVVID

>core/493/1/Org1_Gene502

MKFLLYVPLLLVLVSTGCDAPVSFEPFSGKLSTQRFEPQHSAEEYFSQQQEFLKKGNFRKALLCFGIITHHFPRDILRNQAQYLIGVCYFT
QDHPDLADKAFASYLQLPDAEYSEELFQMKYIAAQRFAQGKRKRICRLEGFPKLMNADEDALRIYDEILTAFPSKDLGAQALYSKAALLI
VKNDLTEATKTLKKLTLQFPLHLSSEAFVRLSEIYLQQAkkePHNLQYLHFAKLNEEAMKKQHPNHPLNEVVSANVGAMREHYARGLY
ATGRFYEKKKKAEAAANIYYRTAITNYPDTLLVAKCQKRLDRISKHTS

>core/494/1/Org1_Gene357

MNRRKARWVVALFAMTALISVGCCPWSQAKSRCIDKYIPVVRLLLEVCGLPEAENVEDLIESSAWVLTPEERFSGELVSICQVKDEH
AFYNDLSLLHMTQAVPSYSATYDCAVVFGGPLPALRQRLDFLVREWQRGVRFKKIVFLCGERGRYQSIEEQEHFFDSRYNPFPTTEENW
ESGNRVTPSSEEEIAKFVWMQMMLLPRAWRDSTSGVRVTFLAKPEENRVVANRKDTLLLFRSYQEAFPGRVLFVSSQPFIGLDACRVG
QFFKGESYDLAPGFAQGVLYHWAPRICLHTLAEWLKETNGCLNISEGCFG

>core/495/1/Org1_Gene848

MRKVAFLVSCFLSVAIGASAAPVRVPGFPQIPEDLVQIKTEVCPKQEVCLAVTIKDDHNLIGVLHLPNTPTPEGGFPTVVLFHGFRGTK
FGGLTGAYRKLGRKFAAAGIATLRVDMAGCGDSEGVAEEVPIETYLRDAQTILETVQEHPDLNAYRLGISGFSLGCHIAFELAKIYNPRDL
NIKALSVWAPIADGGILLKELYENFSKHGEGDIISVGKDFGFGPPPIIVCSGDVDLLIRIQDHVTANSLPTKPYILHQQGIDDTLVSRQQQT
LFKNTAPGRMTFISYPNTGHNLATAPDLDMILDQIVSHFQRTL

>core/497/1/Org1_Gene142

MLVELEALKREFAHLKDQKPTSDQEITSLYQCLDHLEFVLLGLGQDKFLKATEDEDVLFESQKAIDAWNALLTKARDVLGLGDIGAIYQTI
EFLGAYLSKVNRRAFCIASEIHFLKTAIRDLNAYYLLDFRWPLCKIEEFVDWGNDCVEIAKRKLCTFEKETKELNESLLREEHAMEKCSIQD
LQRKLSDIIIELHDVSLFCFSKTPSQEEYQKDCLYQSRLRYLLLLYEYTLCKTSTDFQEQARAKEEFIREKFSLLELEKGIKQTKLEFAIAKSK
LERGCLVMRKYEAAAKHSLDSMFEEETVKSPRKDE

>core/498/1/Org1_Gene277

MTLPMQKSLTSFDDFSQAYAEKVPAIALIGSALEDDKDALIELLVSESFKELGGQGLMPATLMSWTETFALFQEHETLGIIHAEKFPLAT
KEFLSRYARNPQPHLTILIFTTKQECFRELSKALPSALSLSLFGWPADRQKRIIRLLLQRAERVGISCSQSLASLFLRALASTSLPDILSEFDK
LLCSVGKKTSLDHSDIKELVVKKEKASLWKFRDSLLKRDPEVGHQQLHFLLDGEDPLGIITFLRTQCLYGLRSIEEGSKENKHRMFVLYG
KERLHQALNSLFYAETLIKNNVQDPIVAVETLVIRMVNL

>core/500/1/Org1_Gene246

MAMLPKFFLVLLCLGLSCSQKTTTIEGEQMTIFYRIVLGTSLSAKEKASLSQQIDRCFHKIDSIYNNWNPYSELSIINRAPADVPITLSVEL
SEFLDQVDTLYKLSEGRFDPTVGPLKTLWLLHLKSQTLPPKDVWEQHYKDMGWQHLEFQSNTKTLIKKNPHVQIDLCGVVKGYAVDC
LNEICNTFCPNNYVEWGGEIKTSGHHPSGRPWRIFSEAAGTILDIDDMAIATSGNHIQKWCVEGKIYTHILDTRTGKPLELSSYPIQSVS
VVHPSCAYADAIATVLMTFDSKIEAKQWAEHHILTYINDGASS

>core/502/1/Org1_Gene9

MIASIYSFLDYLMVKASASPHTLRNYCLDLNGLKIFLEERGNLAPSSPLQLATEKRKVSELPFSLFTKEHVRMYIAKLIENGKAKRTIKRCLS
SIKSFAHYCVIQKILLENPAETIHGPRLPKELPSPMTYAQVEVLMATPDISKYHGLRDRCLMELFYSSGLRISEIVAVNKQDFDLSTHLIRIR
GKGKKERIIPVTSNAIQWIIQIYLNHPDRKRLEKDPQAIFLNRFGRRISTRSIDRSFQEYLRRSGLSGHITPHTIRHTIATHWLESGMDLKTI
QALLGHSSLETTTVYTQVSVKLLKKQTHQEAPHA

>core/504/1/Org1_Gene780

MRKLILCNPRGFCSGVVRAIQVVEVALEKWGAPIYVKHEIVHNRHVNALRAKGAIFVEELVDVPEGERVISAHGIPPSVRAEAKARKL
IDIDATCGLVTKVHSAAKLYASKGYKIILIGHKKHVEVIGIVGEVPEHITVVEKVADVEALPFSSDTPLFYITQTTLSDDDVQEISSALLKRYPS
IITLPSSSICYATTNRQKALRSVLSRVNYVVVVDVNSSNSNRLREVALRRGVPADLINNPEDIDTNIVNHSGDIAMTAGASTPEDVVQA
CIRKLSSLIPGLQVENDIFAVEDVVFQLPKELRCS

>core/509/1/Org1_Gene28

MRLFSYDKPKIKVQKIKADGFSGWLKCNHCHEMIHANELGQNYNCCPKCSYHYRITAIERVKLLADKDSWRPLYTDLKSQDPLEFIDTD
TYANRLEKARKNTTESEGVIVGICTIGLHPVALAVMDNFNFMAGSMGAVVGEKLTRLIEEAIETRLPVIIVSASGGARMQESVFSLMQM
VKTSAALAKLHEAGLPYISVLNPTSGGVTASFAALGDIIIAEPKALICFAGPRVVAQVIGEDLPEGAQKSEFLLEHGMIDKIVERKELKTTL
QTLLDYFLAQEYTGGSKAPRDLSKRLKEIFLLTDDSE

>core/516/1/Org1_Gene786

MTMPSTQFHTTILEQFSLFLSVDRGLCQQSIAAYRQDISSFLTISAISSPQDISQNSVYIFAEELYRRKEAETTLARRLIALKVFFLFLKDQQL
LPYPPIIEHPKIWKRLPSVLTPQEVDALLAVPLQMEKNPRHLAFRDTAILHTLYSTGVRVSELCDLRLGHVSDDCIRVTGKGSKTRLVPLG
SRAREAIDAYLCPFRDQYQKKNPHEDHLFLSTRGHKLERSCVWRRIHNYAKQVTSKPVSPHSLRHAFATHLLDNKADLRVIQEMLGHA
RIASTEYVYTHVAADSLIEKFLAHHPRNL

>core/519/1/Org1_Gene192

MHLEENQGWEEALLRKVYHQEVPPAILLHGFTLPVLQDKAEQLASEILLSSSPGSEHKVSQKIHPDIYQFFPEGKGRlhsIDLPRGIKKQI
YISPFANYKIYIIEADRMTLAAISAFKVFEEPPKHAVIILTAKVQRLPKTIISRLSIFIERGEKILCSKETFSYLFYQAQCEIPVTEVSQIIKE
SSETDKQVLRDKVQRFMEVLLLELYRDRYTLNLGLKASALNYPEHVKEILQLPLPLDKVLLIVESACRSLNNSSSAASVLEWVAIQVLSLQY
KEKELVSVSPGQDLSN

>core/526/1/Org1_Gene685

MQEKPRHVHRIIHISDVHFHVLVPVNPVHCFNKRLKGLLRKVFGVLVHFQATTIGQRFKVVRSLGADSVCTGDFSLTAMDGEFLLAKHF
VETLAKHSSVYLLPGNHVDVYTLKSLAQQTfYTHFPNDQLQQNKVSFHKITDHWLILLDCSCLNGWFSANGVVHLAQISAIETFLLSLS
PEENVIIANHYPLLSSQNPSHDLINNTHLQNVLKYPKVRLYLHGHEHQAAYVNCADTSPSYILNSGSISLPTNSRFHVIDLYPEKYQVHT
MILKNLLDFDAPLEIANEATWDCQKL

>core/527/1/Org1_Gene297

MEKLLVTDIDGTITHQSHHLDKKVYERLYALHQAGWKFLFLTGRYYKYAARLFSDFDAPYLLGCQNGASVWSSTSSNLLYSKSLPSDLLC
ILQDCMEGATALFSVESGAPYGDHYRFSPPTPIAQDLHEYVDPRYFPNAKEREILFETRSLKDDYAFPSFAAAKVFLRDEVIRIQKELER
QEALTSVATMTLMRWPFDFRYAILFLTDKSVSKGKALDRVVNilyDGKKPFVMASGDDANDLDLIERGDFKIVMSSAPEEMHVVHADP
LAPPADKNGILSAWEAGVRYDDLMSL

>core/530/1/Org1_Gene683

MSKHTSESRIAQDMLERYSGSSVKQFCPYLLLTNFSYIQTFAKLHGVPVFEGSMFSAAHAPHLKTSILDFKLGSPGAALTIDLCsFLPDL
KAALMLGMCGGLRSHYQVGDFVPVASIRGEGTSDAYFPPEVPALANFVVQKATTEVLEDKKANYHIGITHTTNIRFWEFNKKFRKKL
YETKAQSAEMECATLFAAGYRRNLPIGALLISDLPLRKEGIKTSSGNFIFNTYTEDHILTGQEVIENTLEKVMLKRAASDHKKDQQYRGL
PHMEVGEADDTMASGSETSDSDY

>core/531/1/Org1_Gene556

MKVLPPPSIPLLGAHTSTAGGLKNAIYEGRDIGASTVQIFTANQRQWQRRALKEEVIEDFKAALKETDLSYIMSHAGYLINPGAPDPVIL
EKSRIQIYQEILDCITLGISFVNFHPGAALKSSKEDCMNKIVSSFSQSAPLFDSSPPLVVLETTAGQGTLIGSNFEELGYLVQNLKNQIPIGV
CVDTCHIFAAGYDITSPQGWEDVLNEFDEYVGLSYLRAFHLNDSMFPLGANKDRHAPLGEGYIGKESFKFLMTDERTRKIPKYLETPGG
PENWQKEIGELLKFSKNRDS

>core/546/1/Org1_Gene516

MTEEISKDTIIEVAIDDIRVSPFQPRRVFSNEELQELIASIKAVGLIHPPVVREICTGDRVLYYELIAGERRWRAMQLAGATTIPVILKHVIA
DGTAAEATLIENIQRVNLNPIEMAEAFKRLIHVFGLTQDKVAYKVGKKRSTVANYLRLLALSQTIQESLLQGQITLGHAKVILTLEDPIPREK
LNEIIIQEH LAVREAELIAKQLISEEGSSI ELKPTPLDMAESSKQHEELQQLSDLCGYKVQIKTRGSKATVSFHLQNTQDLQKLEAWLSSH
GTLSESLS

>core/549/1/Org1_Gene347

MHEVLILTFTYPLPRTLKQHPDEVHTVPISPNSLFGEGSPILIAGPCTLESYEHTVSSALTVKEAGAQVFRGSIRKPRTSPFSFQGWKEECV
LWHKEAQSIHGLPTETEVLDVRDVEITAEHVDILRIGAKNMHNTPLLQEVSKSHRPIILKRSPAATLEEWLCAA EYILASSPSCPGVILCER
GIRTFEHSTRYTLDLNTVALLKEISSLPVIVDPSHAAGKRSLVPLASAGLSVGADGLMIEVHAHPEKALCDAKQKITPEELHLFAKKHFCP
SESRAHAIS

>core/558/1/Org1_Gene487

MLERTQRTLKREVRYSVGVIHLGKSSTLHLQPAQTNTGIVFQRQSASGNYENVPALLDHVYTTGRSTTLRGS AVIATVEHLM AALRSN
NIDNLIQC SGEEIPIGDGSSNVFVELIDQAGICEQEDKVS IARLTRPVYYQH QDIFLA AFPSDELKISYTLHYPQSSTIGTQYKSLVINEESFR
QEIAPCRTFALYNELCFLMEKGLIGGGCLDN AVVFKDDGIISRGQLRFADEPVRHKILD LIGDLSLVGRP FVAHV LAVSGHSSNIAFGKK
ILEALEL

>core/564/1/Org1_Gene390

MHKVIVFIFLTLYSLKSYGNDVIDKPHVLVSIAPYKFLVEQIAEETCFVYAIVTNHYDPHTYELPPQQIKELRQGD LWFRIGEAF EKT CERN
LTCQQVDLSQNVSLIQGKPCCNQH TTNYDHTWLS PKNLKVQVETIVTTLSKKYPQHATLYQSNGEKLLLALDQLNEEILTITSKAKQRH

ILVSHGAFGYFCRDYNFSQHTIEKSSHVEPSPKDVARVFRDIEQYKISSVILLEYSGRRSSAMLADRFHMHTVNLDPYAENVLVNLKTIAT
TFSSL

>core/565/1/Org1_Gene950

MYFTRDPIIETVITSREGYKLSVRNTKHFSQDPFMVEAIEVISLGNICFFRNCDHSPFLVPAGDYEVM EVRDTKINLKAVGLDRGVKIAG
GREALIKLTSTPLPVIDEKPLADSPEEGTEPTSPSKKEKKEARKDSFKGEKWKEKKLSRRRNHKEIAEVTGASQEILDTVKEELWEESQE
NEIVEQKKFSLLPPPAAKLISEVISQTVVDPVVTSA DLNESLQALVRESSDLINALLSADDAIHFPETEEPT SASFEESSAMFFPETSSATEEE

>core/569/1/Org1_Gene631

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GSIAPHRCAPFGAFYLLDMLS KIRPCGITEEIFLPASSANAILYYTGPVKIALINCLGLYSIAKELKHILDKVVI ERVKNALSPTEKLFLTYCQ
SHPMKHLETTN FLSSWTTDAELRQFVHKQGLEFLGKALTKENASFLWYFLRRLDVGRAYIVEQTLKTWYDHPYVDYFKSRLEQCMKVL
VK

>core/570/1/Org1_Gene380

MDYKLLDSGDGNKLECFGPVTLIRPSSIAVWP KSRPELWSQAQLQYVREGERGAWKNFKRLPEEWEVAFSDVRCLLKRTPF GHLGVF
PEHMGFWPALKQAIEKHKERQVLNLFAYTGAGSIFA AKCGARVTHVDASQA AVRWAQRNVEKNAFPERRIFWVIEDVISFLKKEIRR
NKKYQVILLDPPSYGRGPDGEVFKIDKDLFLLSLCSKLLADDASYFLLTSHTPGHTPEFLRAIARRSVPTLVSEAWSCGESFCGEGVGALP
SGSFVQWIA

>core/571/1/Org1_Gene104

MITGVVLEKHEQRTMFSLTLLNNFTTFGLLHTPLHYNPPYPIVILLHGLASDKTGSKRSHVRLAQELTRLGIAALRVDLLGHGDCEGELM
DFSLENYKQNIREIIEYTHSLLHIDQERLAIFGSSLGGTLALQTL PFFNKIKALAVWAPTISGELMAAEAQKNAPEVITMSQKGAITYAGM
TLNPDFYTQFLKIDIVKELMPSARNLPPILYMQGEQDLLVSINHRTL FTEAFANQDKPITILTPDVDHAFPPFAESSALSDLTQWLKRELTS
GE

>core/572/1/Org1_Gene551

MLLGFLCDCPCASWQCAAVANCYDSVFMSRPEHKPNIPYITKATRRGLRMKTLAYLASLKDARQLAYDFLKDPGSLARLAKALIAPKEA
LQEGNLFFYGCSNIEDILEEMRRPHRILLGFSYCQKPKACPEGRFNDACRYDPSHPTCASCSIGTMMRLNARRYTTVIIPTFIDIAKHLHT
LKKRYPGYQILFAVTACELSLKMF GDYASVMNLKGVGIRLTGRICNTFKAFKLAERGVKPGVTILEEDGFEVLARILTEYSSAPFPRDFCEI
H

>core/575/1/Org1_Gene283

MKLLKNVLLGLFFSMSISGFSEVKVSDTFVKQDTVVEPKIRVLLSNESTTALIEAKGPYRIYGDNVLLDTAIQGQRCVVHALYEGIRWGEF
YPGLQCLKIEPVDDTASLFFNGIQYQGSLYVHRKDNHCIMVSNEVTIEDYLKSVLSIKYLEELDKEALSACIILERTALYEKLLARNPQNF
W
HVKAEEEGYAGFGVTKQFYGVVEEAIDWTARLVVDSPQGLIIDAQGLLQSNVDRLAIEGFNARQILEKFYKD VDFVVI ESWNEELDGEIR

>core/576/1/Org1_Gene197

MKKKLSLLVGLIFVLSSCHKEDAQNKIRIVASPTPHAELLESQEEAKDLGIKLKILPVDDYRIPNRLLLDKQVDANYFQHQAFLDDECERY
DCKGELVVIKLVHLEPQAIYSKKHSSLERLKSQKKLTIAIPVDRTNAQRALHLEECGLIVCKGPANLNMTAKDVC GKENRSINILEVSAPL
LVGSLPDVDAAVIPGNFAIAANLSPKKDSLCLDLSVSKYTNLVVRSEDVGSPKMIKLQKLFQSPSVQHFFDTKYHGNILTM TQDNG

>core/577/1/Org1_Gene344

MVRDIQSESIGKLVFLGTGNPEGIPVPFCSCRVCQNTGIHRLRSSVLIQYQNKTLVIDAGPDFRTQMLVAGVSELDGVFLTHPHYDHIG
GIDDLRAWYIVTQRSPLVLSASTYRFLNKAKEYLFATPNVESSLPAVLEFTILNEDCGQEEFQGIPYTYVSYYQKSCHVTGFRFGNLAYLT
DLCSYDAKIFS YLDNVETLILSAGPSETPIPFQGHKSSHLTVEEAKAFANHAGIKNLIITHISHCLEAERDQHPEVTFAYDGM EVLWTL

>core/582/1/Org1_Gene906

MTQYYFLSSFLPTQLPESVPLFSISDLDDL LYLNLSENDLCNYGLLKRFFDFENFAFFWAGKPIPFSGEVTQENIERMLSSQQWSD DND
FEDFFKDFLMNHKSSQDRLNHFSDLFREFLSYHQTNSSKFLQDYFRFQQQLRVVLAGFRARVLNMDVSYVLRDEDS DPVVLEVLMQ
KDSPNYELPEEFSDLQGVLD DYGLLPHTLNRALALYQFHKLEGFCSDSYFDGNVILARCATYMF AIRNSLASVEKGREIINHIEKAIKW

>core/583/1/Org1_Gene124

MHSKFLSRRKKNSSHKEETSWDCIASSYNKIVQDKGHYYHRETILPQLPSLTGSKSSVLDIGCGQGFLERALPKECRYLGIDISSRLIALA
KKMRSVNSHQFKVADLSKRLEFVEPTLFSHAVAILSLQNMEFPGEAIRNTATLLEPLGQFFIVLNHPCFRIPRASSWHYDENKKAISRHID
RYLSPMKIPIMAHPGQKDSPSTLSFHFPLSYWFKELSSHGFLVSGLEEWTSSTSTGKRAKAENLCRKEFPFLMISCIKIK

>core/585/1/Org1_Gene674

MQGFFPLASGSKGNSAYLGTDSCKILIDLGVSKQVVTRELLSMNIDPEDIQAIFVTHEHSDHISGIKSFVKAYNTPIVCNLETARALCHLLD
SHPEFKIFSTGSSFCFQDLEVQTFNVPHDAVDPVAFIFHYREEKLGFCITDLGWVTSWITHELYDCDYLLIESNHSPELVRQSQRPDVYKK
RVLSKLGHISNQECGQLLQKIITPKLKKLYLAHLSTECNTAELALSTVSESIAITSIAPEIALAQGITSPIYFSRLEVACPR

>core/587/1/Org1_Gene19

MKKPDNDSTFDVRSFFPFDVLCIEQLRKEMSWEVVSAKIPRLPRGWYELMGLSKEDRIDFCLDFWCSVLGIEHKESPSICRFFSLLETIEV
YIYRLEKEPYQLKMFYVFRDGRCGFQGEPPLLDFLGHHRLPPLGDRHYEKFFSIHNGFGKWEDEGIFPMRSLAKVQQKLRQQLVVMN
KMQAEDNCYSLGIFPFYGYEFPAYQSFFFDPEIRRDLPSPNVLLNEESLEHRSLETIELLHLSKSYPPSFLSWLENYLHSEEVYNE

>core/593/1/Org1_Gene371

MSNQLQPCISLGCVSYINSFPLSLQLIKRNDIRCVLAPPADLLNLLIEGKLDVALTSSLGAISHNLGYVPGFGIAANQRILSVNLYAAPTFFN
SPQPRIAATLESRSSIGLLKVLRCRHLWRIPTPHILRFITTKVLRQTPENYDGLLLIGDAALQHPVLPGFVTYDLASGWYDLTKLPFVFALLH
STSWKEHPLPNLAMEEALQQFESSPEEVLKEAHQHTGLPPSLLQEYALCQYRLGEEHYESFEKFREYYGTLYQQARL

>core/600/1/Org1_Gene791

MKTWLFFTFLFSCSSFYASCRYAEVRSIHEVAGDILYDEENFWLILDLDLDTLLQGGEALSHSIWKS KAIQGLQKQGTPEQEAWAVVPF
WIEIQEMGTVQPIESAIFLLIEKIQKQGKTTFVYTERPKTAKDLTKQLHMLNVSLEDTAPQPQAPLPKNLLYTSGLFSGDYHKGPGLDL
FLEICTPLPAKIIYDNQKENVLRIGDLCQKYGIAYFGITYKAQELHPPYFDNIAQVQYNYSKKLLSNEAAALLLRHQMHHE

>core/606/1/Org1_Gene346

MIKQIGRFFRAFIIMPLSLTSCESKIDRNRIWIVGTNATYPPFEYVDAQGEVVGFDIDLAKAISEKLGKQLEVREFAFDALILNLKKHRIDA
ILAGMSITPSRQKEIALLPYYGDEVQELMVVSKRSLETPVLPLTQYSSVAVQTGTTFQEHYLLSQPGICVRSFDSTLEVIMEVRYGKSPVAV
LEPSVGRVVLKDFPNLVATRLELPPECWVLGCGLGVAKDRPEEIQTIQQAITDLKSEGVISLTKKWQLSEVAYE

>core/615/1/Org1_Gene84

MFKLLKNLFLIGCCIVGYFWMRKESIVEQWLSNRLHTQVTVGRVSIRTSGIKIRHICIHNPASERFPYAAEIEYADVRFSSISMLLTQLEI
SELIHGANFTIFPYDSHGKTKNWSLVWKNFHPQKETPSNLWIDRAPVLIRRCFLNTRLYGLRANHKKDIPHLSVPSLEFHSHTSSAKELP
KLSEALPSLLYLAEESLYHLNLPGDIIKPLSQQAHKHFYSSYPQFQDRLNDINTPGTPTEEIIGFIRGLFFH

>core/617/1/Org1_Gene258

MKTQQTQNIIEVWNFYWETQEIEYRDSLIEFYLPVKSVVHRLISGMPSHVKTEDLYASGVEGLVRAVERYNPERSRRFEGYAVFLIKAA
IIDDLRKQDWVPRSVHQKANKLSGAMDSLRQSLGKEPTDELCEYLNISQQELSGWFVSARPALIVSLNEEWPSQSDEGAGMALEERI
PDERAETGYDVVDKQEFSLCLANAIQELEEKERKVMALYYYEELVLKEIGKVLGVSESRSVSIHSKALLKLRAALSAFR

>core/621/1/Org1_Gene613

MKTIAVNSFKGGTAKTSTTLHLGAALAQYHQARVLLIDFDAQANLTSGLGDPDCYDSLAVVLQGEKEIQEVIRPIQDTQLDLIPADTW
LERIEVSGNLAADRYSHERLKYVLGQSVQDKYDYVIDTPPSLCWLTESALIAADYALICATPEFYSVKGLERLAGFIQGISARHPLTILGVALS
FWNCRGKNNSAFAELIHKTTPGKLLNTKIRRDITVSEAAIHGKPVFATSPSARASEDYFNLTKEILLRDI

>core/623/1/Org1_Gene375

MHDALLSILAIQELDIKMIRLMRVKKEHQKELAKVQSLKSDIRRKVQEKELMENLKTQIRDGENRIQEISEQINKLENQQAQVKKMDE
FNALTQEMTTANKERRSLEHQLSDLMDKQAGGEDLIVSLKESLASTENSSSVIEKEIFESIKKINEEGKALLEQRTELKHATNPILLSIYERL
LNNKKDRVVVPIENRVCSGCHIVLTPQHENLVRRKKDRLIFCEHCSRILYWQESQVNAQENSTAKRRRRRAAV

>core/624/1/Org1_Gene165

MKPEESECLCIGVLPARWNSSRYPGKPLAKIHGKSLIQRTYENASQSSLLDKIVVATDDQHIIDHVTDFGGYAVMTSPTCSNGTERTGE
VARKYFPKAEIIVNIQGDEPCLNSEVVDALVQKLRSSPEAEVTPVALTTDREEILTEKKVKCVFDSEGRALYFSRSPIPFILKKATPVYLHIG
VYAFKREALFRYLQHSSTPLSDAEDLEQLRFLEHGGKIHCIVDAKSPSVDYPEDIAKVEQYITCLSNAFY

>core/626/1/Org1_Gene434

MQICVTGVVLRSRPLGKNHTLTTLFTPEGLFTFFAKQGQTLQCDYRETLVPISLGKYTLHRNGSRLPKLTHGDILNAFEAIKQTYALLEAS
GKMIQALLASQWKEKPSHKLFSLFLNHLRIPESSNPEFFAAIFVLKLLQYEGILDTLPCSLCKASLPYACYRYQGHKLCKKHQHKQAISI
EKEEQILQAIHAKQFSELLAIAEFPIAIAEKIFYLFDLQEEKKSERNSSEDYPHEILRLSKVVHPY

>core/628/1/Org1_Gene139

MLMDISHILEDLAYDEGILPREAIEAAIVKQMQITPYLLHILHDATQRVPEIVNDGSYQGHLYAMYLLAQFRESRALPLIILKFAFEDDTPH
AIAGDVLTEDLPRILASVCNDDSLIKELIETPKINPYVAAAISGLVTLVGAGKIPRDKVIRYFAELLYRLEKQPSFAWDNLIAGICTLYPGE
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>core/633/1/Org1_Gene612

MGNLKTLLSRFKNTPTKMEALARKRMEGDPSPLAVRLSNPTLSSKEKEQLRHLLQHYNFREQIEEPDLTQLCTLSAEVKQIHHQSVLL
HGERITKVRDLLKSYREGAFSSWLLTYGNRQTPYNFLVYYELFTLLPEPLKIEMEKMPRQAVYTLASRQGPQEKKEEIRNYRGERKSELL
DRIRKEFPLVETDCRKTSPVKQALAMLTGSGQILTKCTSLSSDEQIILEKLIKLEKVKSNLFPDTKV

>core/635/1/Org1_Gene490

MSLLKDTVFTCLDCENTGLDVKKDRIIEIAAVRFTFDSVISSIEFLINPERVVSAESQRVHHISNAMLRDQPKIAEVFPQIKAFFKEGDYIV
GHSVGFDLQVLAQEMERIGETFLSKYTIIDTLRLAKEYGDSNNLSLAVHFNVPYDGNHRAMKDVEININIFKHLCKRFRFTLEQLKQV
LAKPIKMKYMPGLGKHKGRCFSEIPLAYLQWASKMDFDSDLFSIRHEIKHRQKGTGFSQVNNPFMEL

>core/639/1/Org1_Gene527

MAKQTRRVLFKISGEALSKDSSNRIDEMRLSRLVSELRAVRNNDIEIALVIGGGNLRGLAEQKELQINRVSADQMGM LATLINGMAVA
DALKAEDIPCLLTSTLSCPQLADLYTPQKSIEALDQGKILICTTGAGSPYLTTDTGAALRACELNVDVLIKATMHVDGVYDKDPRLFPDAV
KYDFVSYKDFLSNQLGVMDASAI SLCMDSHIPIRVFSFLQHSLEKALFDPTIGTLVSEDVNHVCSPRH

>core/641/1/Org1_Gene448

MHIYGLADLHLALGVPEKTMEVFGDPWIGYHQKICSEWQAVVHPEDIVLLPGDISWAMN LSEAHKDFAFIGDLPGTKYMIRGNHDY
WSSASTSKILQALPPSLYYLNQGFALLTPHLAVVGVRLWDSPTICVKKENFLTPSTQE QSYTEQDEKIFLRELGR LKRAFAALPKEVTEVIV
MTHYPPISDGTGPGPISEFLEADGRVSLCLFGHIHKVQRPIDGFGNIRGIHYILVAADYVNFVPQEV M

>core/642/1/Org1_Gene580

MKITTVKTPKIYPYDDLYSILESSLPKLNERSIVVITSKIVSLCEGAVVELEKVS KDELIKQEADAYVFVEKYGIYLTKKWGILIPSAGIDESNVE
GYFVLYPRDFLLSVNTLGDWLRNFYHLEHCGIIISDSHTTPLRRGTMGLGLCWNGFFPLYNYVGKPD CFCGRALKMTYSNLLDGLSAAAV
LCMGEGDEQTPIAIIIEAPKITFHSSPTTLQDMSTLAI AEDEDLYGPLLQSMAWETPAPTS

>core/651/1/Org1_Gene322

MKVRIVDSGKSSAASHMAKDRDLLES LQDGELILHLYEWENPCSLTYGHFMRPEKFLLSNYADLGLDAAVRPTGGGFV FHKGDYAFSV
LMSATHPSYSSSVLENYHTVNSFVAKVLEKV FRIQGMLAPEDENSSSRDSGNFCMAKTSKYDVLFGDKKIGGAAQRKVQQGFLHQGS
LFLSGSSSEFYQRFLKPEVLEEII EQIQIHAF FPLGLEAADEV LQEARQQVKEAFIKLFCGEGL

>core/652/1/Org1_Gene835

MTLYLLPNTLGTTRAVETLPSVIGELVHRLDGLIVESDRGGRAFLSLWKIPEVHKFPLAILSKHARLPKAWDFYLEPIVKHGENWGLISDAG
LPCIADPGASLVRRARALGIPVQAFSGPCSITLALMLSGLP SQSFTFLGYLPQSPKERVKS IKAATSKEVSTSVCIETPYRNVYTFESLLDTL
PSYAELCVASDLSGPSELVLTRQVQSWRTTEDLGSVKQSITKVPTIFL FHIPN

>core/654/1/Org1_Gene492

MDISGAVKQKLLQFLGKQKKPELLATYLFYLEQALSLRPVVFVRDKIIFKTPEDAVRILEQDKKIWRETEIQISSEKQVNNENTKRIYICPFT
GKVFADNVYANPQDAIYDWLSSCPQNMEKQGGVRIKRFLVSEDPDVIKEYAVPPKEPIIKTVFASAITGKLFHSLPPLLEDFISSYLRPMT
LEEVQNQTKFQLESSFLSLLQDALVEDKIAAFIESLADDTAFHVVISQWVDTEE

>core/661/1/Org1_Gene571

MIGDKIILFVTEDLSLSSQLKDLASQRSYQILVSPVFPTSFESVAIFCEYLLLPEQIFSPGIFPEEDLIVLFDTFQEEAITKVLNQGATGYLLRP
ITAKVLDAVIRAFLRQHEVLEHSIPDTMTFGDHTFRVLNLVIESPEGSVYLTPEAGILKKLLINRGHLCLRKNLLAEIKGNTKEIARNVDV
HIASLRKKLGPYGSKIVTIRGVGYLFSDDDSIPLQNHNTAHPNEE

>core/662/1/Org1_Gene873

MTKVRLNKFLASAGVASRRKCDEIIFSGSVTVNGRVAEGPFVLVDPEDKVQVGGTSVHLTKKVYFMVHKAIGYLCSEKKFPGTKLVIDL
FAHLPYRVFTVGRLDKETSGLLVTNDGEFANKIIHPSSGITKEYLLKVS RDVSAKDLGKLMEGTFIDGKHVRPVSVTKIRRGTVKIVVSEG
KKHEIRLFADAAGLPILELKRIRIGSLVLGGLRYGEYRELDAELGYMKLSD

>core/665/1/Org1_Gene458

MPTTNCIFDLRGHSILHQLQIEEALLRVANQNFCIINSGAKDSIVLGISRNLNQDVHISRAQADHIPIIRRYSGGGTVFIDSNTLMVSWI
MNSSEASAQPQELLAWTYGIYSPLLPNTFSIRENDYVLGHKKIGGNAQYIQRHRWVHHTTFLWDIDLKLSYYLPIPQQQPTYRNQRS
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>core/667/1/Org1_Gene630

MKFFSLIFKDDDVSPNKKVLSPEAFSAFLDAKELLEKTKADSEAYVAETEQQCAQIRQEAKDQGFKESSESWSKQIAFLEEETKNLRIRVR
EALVPLAIASVRKIIGKELELHPETIVSIISQALKELTQNKHIIISVNP KDLP LVEKSRPELKNIVEYADSLILTAKPDVTPGGCIIETEAGIINAQ
LDVQLDALEKAFSTILKAKNPVDEPSETSSSTDSSSLSDNDQDKKE

>core/668/1/Org1_Gene690

MNRRDMVITAVVVNAILLVALFVTSKRIGVKDYDEGFRNFASSKVTQAVVSEEKVIEKPVVAEVPSRPIAKETLAAQFIESKPVIVTTPPV
PVVSETPEVPTVAVPPQPVRETVKEEQAPYATVVVKKGDFLERIARANHTTVAKLMQINDLTTTQLKIGQVIKVPTSQDVSNEKTPQTQ
TANPENYYIVQEGDSPWTIALRNHIRLDDLLKMNDLDEYKARRLKPGDQLRIR

>core/671/1/Org1_Gene43

MTKHGKRIRGILKNYDFSYSYSLREAIDILKQCPPVRFDQTVDVSIKLGIDPKKSDQQIRGAVFLPNGTGKTLRILVFASGNKVKEAVEAG
ADFMGSDDLVEKIKSGWLEFDVAVATPDMMREVGKLGKVLGPRNLMPTPKTGTVTDDVAKAISELRKKGKIEFKADRAGVCNVGVGK
LSFESSQIKENIEALSSALIKAKPPAAKGQYLVSTISSTMGPGISIDTRELMA

>core/673/1/Org1_Gene164

MLQSCKKALLSIVVSILAFHPIPGMGVEAKSGFLGKVKGWFSKKEIQEEARILPVKDSLWKRYDYTSSSGFSVEFPGEPDHSGQIVEVP
QSEITIRYDTYVTETHPDNTVYVVSWEYPEKVDISRPELNLQEGFSGMMQALPESQVLFMQARQIQGHKALEFWIVCEDVYFRGMLI
SVNHTLYQVFMVYKNKNPQALDKEYEAFSQSFKITKIREPRTIPSSVKKKVSL

>core/676/1/Org1_Gene427

MYLEDYDVFFFDLDGLLDTEPCFYRAFLQACAEFSLEVHWDFSTYYSHHTLGTEIFSKKFIEQYPQAEYMAEIFAKRLQIYYKSLEHAG
PALMPGVEAFIELVLSLNKTFGVVTNSPRDATHTLRTMYPILNKFLFWVTRENYARPKPYGDSYDYAYRTFAREGMKVIGFEDSVKGLR
ALSKIPATLVCINSMAEITPEDYPELKGKEFFSYPSFDVLTEHCSQQKLL

>core/680/1/Org1_Gene432

MRPHRKHVSSKSLALKQSASTHVEITTKAFRLSMLPKQLILEKSDHLPPMETIRVVLTS HKDKLGT EVHV VASHGKEILQTKVHNANPYT
AVINAFKKIRT MANKHSNKRKDR TKHDLGLAAKEERIAIQEEQEDRLSNEWLPVEGLDAWDSLKTLGYVPASAKKKISKKKMSIRMLSQ
DEAIRQLESAAENFLIFLNEQE HKIQCIYKKH DGNVVLIEPSLKP GFCI

>core/685/1/Org1_Gene854

MDLKLDEVASLLDVSEHTVLQWLKEGAIPSYSMNNEYRFSREEIEDWLLHNQALMIQERGEDKEALKDLSLKYSLYKAIHRGGVLCDDV
VHSKEEALQYASKYIAQKFQLDESVLFEMLSHRENLMSTGIGEGIALPHAKDFLINAYYDIVVPMFLAEPYEGALDGKPVGILFFLFACQ
DKSHLNLVNVKIVHLGMSLNARSFFKNYPNKDQLLAYVKEWESQTH

>core/686/1/Org1_Gene948

MILRISTVSLTSCSFSKNSRTCFVTPERITSQKDCPVLLHPKSTTISPPLYDWIPPNREVITAYSFYCRGQGNSIITPEGVLYDCDGLHHSIT
KEEFYIHPRLIEVVRLQLQDHPKVSIIAEAFCCPKHFHFLEASGISLSQLHLQGTAATFALDPPLPMEKLLATIKKLYKKNSDPSLSNFIVTEA
TLTNPELRLTQQDLGSHTTEITVEILDNLQNKETLSSA

>core/688/1/Org1_Gene755

MKPQDLSPFLWKERRPCIQDGVLYVPRHYFEHQNFSTSYHQEFFQNHTSIACELCSGNGDWVVAQAQKDPQVLWIAVEQRFDRVR
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>core/690/1/Org1_Gene581

MTSWIELLDKQIEDQHMLKHEFYQRWSEGKLEKQQLQAYAKDYLLHIKAFPCYLSALHARCDDLQIRRQILENLMDEEAGNPNIHDL
WRQFALSGLGVSEELANHEFSQAAQDMVATFRRLCDMPQLAVGLGALTYEIQIPQVCVEKIRGLKEYFGVSARGYAYFTVHQEADIK
HASEEKEMLQTLVGRENPDVAVLQGSQEVLDLWNLSSFINSTEPSCSK

>core/692/1/Org1_Gene513

MQTLARLFGQSPFAPLQAHLEMVVSCVEYMLPIFTALRDGRYEELLEMALVSDKEYQADCIKNDMRNHLPAGLFMPISRAGILEIISI
QDSIADTAEDVAILLTIRRLNFYPSMETLFFRFLEKNLEAFELTMTLLHEFNQLLESSFGGRKADKARLLVGRVAKSEHESDVLQRELMQI
FFSDDFIPEKEFYLWLQVIRRTAGISDSSEKLAHRINMTLEEK

>core/693/1/Org1_Gene796

MSTTTVKHFIHTASRWEPVLKEIVASNYWHAQWINTLSFLENSGAKKISASEHPTEVKKEVLKHAAEEFRHGHYLKTQISRISSETSLPDYT
SKNLLGGLLTKYYLHLLDLRTCRVLENEYSLSGQTLKTAAYILVTYAIELRASELYPLYHDILKEAQSKITVKSIILEEQGHLEMERELKDLPH
GEELGYACQFEGELCLQFVERLEQMIFDPSSTFTKF

>core/696/1/Org1_Gene823

MGQKGCPIGFRTGVTKKWRSWLWYGKQEFGKFLIEDVRIRQFLRKKPSCQGAAGFVRRMSGKIEVTIQTARPGLVIGKKGAEVDLLK
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HTLRADIDYATACAETTYGIIGIKVWINLGENSSSTTPNNPAAPSAAA

>core/702/1/Org1_Gene798

MQRIIIIGIDTGVGKTIVSAILARALNAEYWKPIQAGNLENSDSNIVHELSGAYCHPEAYRLHKPLSPHKAAQIDNVSIEESHICAPKTTSN
LIETSGGFLSPCTSKRLQGDVFSSWSCSWILVSQAYLGSINHTCLTVEAMRSRNLNILGMVVNGYPEDEEHWLTQEIKLPIIGTLAKEKEI
TKTIISCYAEQWKEVWTSNHQGIQGVSGTPSLNLH

>core/703/1/Org1_Gene301

MNAVNTPKKILCIVADYREISPLIEQLDFTQINEHLYSYRCTDYHLDLYIVHVWGSTAVLNALQSYCQAYTDYDLWINPGFVGACSPCIPL
GQCYTIEKIANLTDTTPVLSEDPPYIFDALPDSPKSSLVTSPVLYHYGFHKTFKLDMEGYAIASQAAEHHIPCSFLKITSDYTPGDGCPF
SRLEEVSQKLTQTLVELLPELMERAIPPKLLPCP

>core/708/1/Org1_Gene414

MIITIDGPSGTGKSTTAKALADHLHFNYCNTGKMYRTLAYARLQSPWATLPLTKFLEPPPSFTFATGQPLESFFNGHLLTSELTTQEVA
NAASELSQLPEVRAFMQDLQRRYAQLGNCVFEGRDMGSKVFPNADLKIFLTSSPEVRAQRRLKDLPEGTLSPQLQAEVVKRDAADA
QRAHDPLVIPENGIVIDSSDLTIRQVLEKILALLFRNEL

>core/709/1/Org1_Gene291

MRKMLVLLASLGLLSPTLSSCTHLGSSGSYHPKLYTSGSKTKGVIAMLPVFHRPGKSLEPLPWNLQGEFTEEISKRFYASEKVFLIKHNAS
PQTVSQFYAPIANRLPETIIEQFLPAEFIVATELLEQKTGKEAGVDSVTASVRVRVFDIRHHKIALIYQEIIECSQLTTLVNDYHRYGWNS
KHFDSTPMGLMHSRLFREVVVARVEGYVCANYS

>core/710/1/Org1_Gene702

MSKKPLYVAHPWHSPTLTQDNYESLCCYIEITPYDSVKFELDKATGLLKVDRPQKFSNFCPLYGLLPQTYCGTASGNYSGEQTRREGIQ
GDKDPLDVCVLTEKNIHHGNILLQARPIGGLRIIDSGEADDKIIAVLEDDLVAEIEDISDCPGTVLDMIQHYFLTYKATPNHLLIKGSPAKIE
IVGIYGKKEAQKVIQLAHEDYLSYIGDTAEVN

>core/720/1/Org1_Gene557

MARYCGPKNRVARRFGANIFGRSRNPLLKKPHPPGQHGMQRKKKSDYGLQLEEKQKLKACYGMIMEKQLVKAFKEVIHKQGNVAQ
MFLERFECRLDNMVYRMGFAKTIFAAQQLVAHGHLVNGRRVDRRSFFLRPGMQISLKEKSKRLQSVKDALESKDESSLPSYISLDKTG
FKGELLVSPEQDQIEAQLPLPINISVVCEFLSHRT

>core/722/1/Org1_Gene52

MSVQVKLTKNsFRLEKQKLARLQTYLPTLKLKKALLQAEVQNAVKDAAECDKDYVQAYERIYAFAEFSIPLCTDCVEKSFEIQSIDNDFE
NIAGVEVPVIREVTLPASYSLLGTPIWLDTMLSASKELVVKVMAEVSKERLKILEEELRAVSIRVNLFEKKLIPETTKILKKIAVFLSDRSIT
DVGQVKMAKKKIELRKARGDECV

>core/723/1/Org1_Gene49

MANLNADGKLKQICDALRLDTLKPAEDEAAALLHNAKEQAKRIIQEAQEEARKILETAEERAHQKIKQGEVALSQAGKRALEALKQAVE
NKIFRESLVEWLEHVTTDPEVSTKLIQALVQALEAQGVSGNLTAYIGKHVSPRAVNELLGKAVTTKLRRKSSVVVGSFVGGVQLKVEEKN
WVLDLSSSALLEIFTRYLQKDFREMIFQGS

>core/724/1/Org1_Gene570

MTYLASSIFSPEDFLYPEIISKAHYTWDILDLMQMLENHVFSGIHGTVESGVTLKNIEKIEAEDAYVESGAYIVGPCILGSQTEVRHGAY
LRGNVITGSRVVGHCTEIKNSYLGHHTKAAHFAYLGDSVLSSEVNLGAGVRCANFRDGRNIYVRSTSDKSKIDTGRRKLGAFLGKG
VAIGCNVVINPGQHILPHTRIRPGQVI

>core/727/1/Org1_Gene460

MYDYIRGTLTYVHTGAIVIECQGIGYHIAITERWAIECIRALHQDFLVFTHVIFRETEHLLYGFHSREERECFRILISFSGIGPKLALAILNALP
LKVLCVVVRSEDIRALASVSGIGKKTAEKLMVELKQKLPDLLPLDSRVETSQTHTTSSCLEEGIQALAALGYSKIAAERMIAEAIKDLPEGSS
LTDILPIALKKNFSGVVKD

>core/730/1/Org1_Gene193

MFIVIEGGEGSGKSSLAKALGDQLVAQDRKVLLTREPGGCLIGERLRDLILEPPHLELSRCCELFLFLGSRAQHIQEVIIIPALRDGYIVICERF
HDSTIVYQGIAEGLGADFVADLCSKVVGPTPFLPNFVLLLDIPADIGLQRKHRQKVFDKFEKKPLSYHNRIREGFLSLASADPSRYLVDA
RESLASLIDKVMLHTQLGLCT

>core/736/1/Org1_Gene453

MLKLLKVSITGDLSSGKTEACQVFQELGAYVVSADEISHSFLIPHTRIGRRVIDLLGSDVVVDGAFDAQIAAKVFYNSVLLQGLEAILHPE
VCRIIEEQYHQSIQDGNYPFVAEVPLLYEIHAKWFDVILVMANEDIRRRERFMKKTGRSSEDFDQRCRFLNVEEKLAQADVVENN
GTKKELHQKIEEYFYALKGAL

>core/740/1/Org1_Gene215

MTRYPDYLSKLIFFLRKLPGIGFKTAEKLA FELISWDSEQLKILGNAFHNVASERSHCPLCFTLKESKEADCHFCREERDNQSLCIVASPKD
VFFLERSKVFKGRYHVLGSLSPITGKHIENERLSILKSRIETLCPKEIILAI DATLEGDATAFLKQELQHFSVNISR LALGLPIGLSFDYVD SG
TLARAFSGRHSY

>core/742/1/Org1_Gene503

MRLFSLGTIYLFSLALSSCCGYSILNSPYHLSSLGKSLLQERIFIAPIKEDPHGQLCSALTYELSKRSFAISGRSSCAGYTLKVELLNGIDKNIG
FTYAPNKLGDKTHRHFIVSNEGRLSLSAKVQLINNDTQEVLDQCVAESVDFDFEPDLGTANAHEFALGQFEMHSEAIKSARRILSIRLA
ETIAQQVYYDLF

>core/743/1/Org1_Gene915

MNWVPKTIDHVDPESEIDIRKVVSCYKLIKEQPEFRSLISELLGVIRCGLRLLKRSKYKEQARTVSEDEDAPLFCLTRSYYQDGYLTPLRAG
PRDLINHYIHLRRRENPKHFFSPKHPCYYARLAFNESVCVYRELFDIERLTMYVEGDYSKEQEKNLQAILSFKTLDEGKDFLIEHKDTDL
IGRGFTDVFCT

>core/744/1/Org1_Gene726

MRIALLSLLMIFPIFGEESRPGSEDGNSNTQEIVGSQDTQVCLYHSYEQGLQASRIEGKPLVIVVLCNSGDDGQACTIGLSETCEEVLS
VLGSIFSELANFVVLVPSGVNPLIYPPIEDPILAEIVKFELFKDESFTGLSIIVVGVTPEGPGDIIEVSPVSLTVEEEETLPSEQTTEVESTSE
LQSEDPAIA

>core/749/1/Org1_Gene312

MFRRTGKGPFEDVQTLYEEETSSPSSYSPYSRSERPETPPSLFDNPKASEARPLNHNLTTEESSLPQWSSTPRTESLLPLEEPETTLGEGVTF
KGELAFERLLRIDGTFEGILVSKGKIIIGPKGVVKADIQLQEAIIEGVVEGNITVSGKVELRGGAIKGDIIQANTLCVDEGVRLGYLAIGIT
DHSERERDL

>core/750/1/Org1_Gene790

MAYGTRYPTLAFHTGGIGESDDGMPPQPFTFCYDSALLQAKIENFNIVPYTSVLPKELFGNIVPVDTCVKSFKHGAVLEVIMAGRGAA
LSDGTHAIATGIGICWGDKNGELIGGWAAEYVEFFPTWINDEIAETHAKMWLKKSLQHELDLRSIAKHSEFQFFHNYINIKQKFGFCL
TALGFLNFENAEPKVN

>core/754/1/Org1_Gene185

MKRYVVGISGASGVILAVKLIKELVNAKHQVEVIISPSGRKTLYYELGCQSFDALFSEENLEYIHTHSIQAIESSLASGSCPVEATIIIPCSMTT
VAAISIGLADNLLRRVADVALKERRPLILVPRETPLHTIHLENLLKLSKSGATIFPPMPMWYFKPQSVEDLENALVGKILAYLNIPSDLTKQ
WSNPE

>core/755/1/Org1_Gene663

MKVIYYEIEEIPSTNTMAKSYMHLWDPYALTVISTKCQTAGTGKFGKSWKSSKGDLLNTFCFFITDLHIDVSRLFRLGTEAVVALCKDLGI
TEAKIKWPNDVLVHGEKLCGVLPETLPVEGLLGVVLGIGLNGNTTKQALKDVGQPATSLQEILGHPIDLETTRELLIHHLLGVLQENLPDS
LATKSNRGN

>core/758/1/Org1_Gene35

MIKKFFIYSLIFSCSFSAPLKGICNEDVSSQSRIEEDPEVLITQLNELIETPIEEGKEIRNELQAISDGQKSSEEIEESCGTSDSEGLSEKTDKES
NEYVLDFFDMSMVQRLEGISKMCQSGQVAQIIDCFNREFDIRNRELELKNRELELREKDLEFKKSILDWNKEKVSRELAFAQREQDIKQTL
LLKK

>core/759/1/Org1_Gene285

MSIKEDKWIREMALNADMIHPFVNGQVNVNEETGEKLISYGLSSYGYDLRLSREFKVFTNVVNSVDPKCFTEDIFISITDDVCIVPPNS
FALARSVEYFRIPRNVLTMCIGKSTYARCGIIVNVTPFEPEWEGHVTIEISNTTLPKAIYANEGIAQVLFFESSTTCEVSYADRKGYQKQ
QGTVPCV

>core/760/1/Org1_Gene684

MVRVSTSEFRVGLRIEIDGQPYLILQNDFVKPGKGQAFNRIKVKNFLTGRVIERTYKSGESVETADIVERSMRLLYTDQEGATFMDDETF
EQEVVFWEKLENIRQWLLEDTIYTLVLYNGDVVAVEPPIFMELISIAETAPGVRGDTASGRVLKPAVTNTGAKIMVPIFIDEGELVKVDTR
TGSYESRVSK

>core/762/1/Org1_Gene987

MMKIPYARLEKGSLLVASPDINQGVFARSVILLCEHSLNGSFGLILNKT LGFEISDDIFTFEKVSNNHNRFCMGGPLQANQMMLLHSCSE
IPEQTL EICPSVYLGGDL PFLQEIASSES GPEINLCFGYSGWQAGQLEKEFLSNDWFLAPGNKD YVFYSEPEDLWALVLKDLGGKYASLS
TVPDNLLL N

>core/766/1/Org1_Gene447

MRILAGKYKGKSLKTF SNPHIRPTSGLVKEAFFSICREDIEGA AFLDLFAGMGAIGFEALS RGAASVVFVDISIKAIQLIHTNSALLGEQLPV
VIFRQDAQSAIQRLIKQKRSFDLIYIDPPYELCNCYVETLLQKIVSGN ILNPEGTLFLENASDEE IACEGLTLRRRRKLGKTYLA EYIVEKDP

>core/768/1/Org1_Gene865

MELVVTSRETGKKSFLKKIRQQGGIPAVVYSAGKSLANITVDALVFKKFLSNLESGALSSTVFSLSYEGRII KALVKDIQYQITTYDVIHLDFE
ELVEDRPVKLNIPIRCINAVDCIGVKLGGS LRQVIRAVRVCKPKDIVPFLELDVRSVGLSQTRKLS DIKIPAGIETITPLKEVAITVSRR

>core/770/1/Org1_Gene121

MVLSSQLSVGMFISTKDGLYKVTSVSKVAGPKGESFIKVALQAADSDVVIERNFKATQEVKEAQFETR TLEYLYLEDES YLFLDLGNYEKL
FIPQEIMKDNFLFLKAGVTVSAMVYDNNVFSVELPHFLELMVSKTDFPGDSL SLSGGVKKALLETGIEVMVPPFVEIGDV IKIDTRTCEYI
QRV

>core/771/1/Org1_Gene360

MTDTPPENEEQHESNVQNENEVEHLQQEIVTLKTELKEKNDKYLMALAESENSRKRLQKERQELMQYALENTLIDFLNPIESMEKALG
FATQMSDDVKNWALGFNMILNQFKQIFEEKGII EYSSIGQKFNPFLHEAVQTEETSEVPEGTILEEFAKGYKIGERPIRVAKVKVAKAPTP
KENKE

>core/772/1/Org1_Gene611

MAAKTKTLELEDNVFLLLEG NLKRIFATPIGYTT FREFQNVVFN CANGQQEIANFFFEMLINGKLTQELAPQQKQAAHS LIAEFMMPIR
VAKDIHERGEFINFITS DMLTQQERCIFLNRLARVDGQEFLLMTDVQNTCHLIRHLLARLLEAQKNPVGEKNLQEI QEEITSLKNHFDELT
KALQ

>core/773/1/Org1_Gene420

MVETVLHNFQRYLSKYLYRVFRFPCRKKTFLLSSHRVLARPSFPVDYCPGKIYDLQEIYEELNAQLFQGALRLQIGWFGRKATRKGKSVVL
GLFHENEQLIRIHRSLDRQEIPRFFMEYLVYHEMVHSVVPREYSLSGRSIFHGKKFKEYEQRFPDYDRAVAWEKANAYLLRGYKKRVGG
GYGRA

>core/776/1/Org1_Gene472

MSRKAREPILLPQGVEVSIQDDKIIVKGPKGSLTQKSVKEVEITLKDNSIFVHAAPHVVDRPSCMQGLYWALISNMVQGVHLGFEKRLE
MIGVGFRASVQGAFLDLSIGVSHPTKIPISTLQVSVEKNTLISVKGLDKQLVGEFAASIRAKRPPEPYKKGIRYENEYVRRKAGKAAKT
GKK

>core/777/1/Org1_Gene41

MYKWYVVQVFTAQEKVKKALEDKFESSGMTDFIQEIILPIENVMEVKKGEHKVVEKYIWPGYLLVKMHLTDESWLYVKSTAGIVEFL
GGGVPVALSEDEVRSILTDIEKKSGVVQKHQFEVGSRVKINDGVFVNFIMGVSEVFHDKGRLSVMVSIFGRETRVDDLEFWQVEEVA
PGQESE

>core/782/1/Org1_Gene474

MSRLKKFYTEEIRKSLFEKFGYANKMQIPVLKKIVLSMGLAEAAKDKNLFQAHLEELTMISGQKPLVTKARNSIAGFKLREGQGIGAKVT
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AQ

>core/786/1/Org1_Gene658

MTTPQSPGSLSQSHLPHPHDPWDTEPTSLPEDPNDKASQELHSLVHLFRKLSIHLSEVEKTVQQLKPDLLELALLICEKFLYKKLENPQE
LALLSTALQRHTTLRSLTPIKVFLHPEDLKLTDWISTHELPMIKHAEFFPDTSCRRSGFKIETPNGILRQEISEELDHLHSVLT

>core/787/1/Org1_Gene407

MACEQHEGCELEEREIEIEDIKSDTKWVSITQAAKLHNVTRQAIYVAIKQKKLKASKETRWEIDIKDLEEYKRNRYSRKKSLEYQGELVFD
NGKGCYSINQVAQILGIPVQKVYYATRTGTIRGERKGAAWVIHVSEIERYKNEYLSKQAAKKLKGAEPKEHQAPNFEPPTEIFPESN

>core/789/1/Org1_Gene794

MTIILCGLPTSGKSSLGKALAKFLNLPFYDLDDLIVSNYSSALYSSSAEIYKAYGDQKFSECEARILETLPPEDALISLGGGTLMYEASYRAIQ
TRGALVFLSVELPLIYERLEKRGLPERLKEAMKTKPLSEILTERIDRMKEIADYIFPVDHVDHSSKSSLEQASQDLITLLKS

>core/791/1/Org1_Gene396

MDRDNEVPLPKPKWIYRTGIGQDSHRFLPESSTKPCILGGIIFDHCPGFQANSDDIIFHAICNAISSVTNKIILGKVADELLQTRGITDSGI
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>core/793/1/Org1_Gene662

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>core/795/1/Org1_Gene991

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FIRQLPQQLHTTVQFIREKIRPESSLQLVTNAQRKTTQDTLKLYEELCDLSQKEFKLQSTLYQKRFELSHKNEKTNQN

>core/800/1/Org1_Gene783

MSHLNYLLEKIAASSKEDFPFPDDLESYLEGYVPDKNIALDITYQKIFKISSEDELEKVYKEGYHAYLDKDYAKSITVFRWLFFNPFVSKFWF
SLGASLHMSEQYSQALHAYGVTAVLRDKDPYPHYAYICYTLTNEHEEAKELEMAWVRAQHKPLYNELKEEILDIRKHK

>core/805/1/Org1_Gene216

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EDLSGEYNAYQSQQYYQSINQSNVKRIQKLIQEVKIAAESVRSKEKLEAILNEEAVLAIAPGTDKTEIIAILNESFKKQN

>core/806/1/Org1_Gene80

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>core/810/1/Org1_Gene732

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>core/815/1/Org1_Gene534

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>core/816/1/Org1_Gene251

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>core/820/1/Org1_Gene281

MSRQNAEENLNFAKELKLPDVAFDQNNTCILFVDGEFSLHLYEEHSDRLYVYAPLLDGLPDNTQRKLALYEKLLGSM LGGQMAGG
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>core/829/1/Org1_Gene299

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>core/831/1/Org1_Gene758

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>core/839/1/Org1_Gene366

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ALRFLENTSPNQEDIYEEISRYLVHSILHMLGYDDTSSEEK RKM RVKENQILCMLRKKHALLTA

>core/842/1/Org1_Gene241

MRIIRFDPYGALSAQSI AKDSRQNSPLVEKISEE IATNEAIRLALLAIGDREQEKKQRHRYKLLGQKQAKVLLSQLRHVHLDFKKLYCDSK
KKEDQE KDEKNKQKRSIKVT KKKKGISLGAAASQAIAAAAEAWVIARNKGVLETASTLFYQKDEEA

>core/843/1/Org1_Gene721

MEKQNLKLDVKEIEFPETVFSRDIETRVIQVIILHCLAKINGVSLLGGNLIDALFGRDIERMKG IYVEQDSKNHLVKVRVEVNVVDYGVSIPE
KTEEIQGCIVSEISEYTGLHVAAVHVIIKGLTQPKDRIDEEIEEEVSVQDLPSPEDFLLENSEG

>core/890/1/Org1_Gene599

MKYRFTEEIEEEPLVNLTP LIDIVFVILMAFIVAVPLIKLDSIALAPGTQE QEVLSSENDSIAVIKVFADHSLTLNEHPITLQELTVRLTLLHKA
YPEKTPLLLQDGETSFRTYQNVKNAIEAAGFHELHVALQN

>core/892/1/Org1_Gene577

MIAIERYQLISKFRMWLFLGCSVEERHFKQPVLSVTFSYNEVPSACLSDKLSDACCYLEVTSLEEIANTKPYALIEHLANELFDSLVISFG
DKASKIDLEVEKERPPVPNLLNPIKFTISKELCPSPVLSA

>core/894/1/Org1_Gene473

MGMTSDSIADLLTRIRNALMAEHLVVDVEHMKMREAIVKILKHKGFFVAHYLVKEENRKRMRVFLQYSDDRKPVIHQLKRVSKPSRRV
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>core/900/1/Org1_Gene292

MRDHAFSKLIGTVRAMVVEGRCPWSLQQSLVSMVEHILGECQEFHEAVLQGKTVQEVGSEAGDVLTLVLILCFLLEREGVLASEDVAN
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>core/903/1/Org1_Gene45

MTTESLETLVEKLSNLTVLELSQLKKLLEEKWDVTASAPVVAVAAGGGGEAPVAAEPTFAVTLEDVPADKKIGVLKVVREVTGLALKEA
KEMTEGLPKTVKEKTSKSDAEDTVKKLQDAGAKASFGL

>core/904/1/Org1_Gene594

MKFTVALFGAEKGSYDTAYFCRSLVDLHNYLGDVSSPGITLAIKTLSDYNVVYFRVREEGYCVDSYFFGLHFLNTQTTLKNIIAIGLPV
GNQHIIASRSLCQKHNSLLLFFDHDLYDLLTFNQPF

>core/906/1/Org1_Gene154

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>core/908/1/Org1_Gene383

MPLSDDEIEQFKRLLMKAKLSHTLEGNAQEVKKPNEATGYSQHQADQGTDTFDRITISLEVTTKEYELLRQINRALEKINESSYGICDV
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>core/912/1/Org1_Gene623

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>core/913/1/Org1_Gene656

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>core/917/1/Org1_Gene226

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>core/918/1/Org1_Gene74

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GKVARARLYYLRGKTGKAAKVKEFVGPRSSKK

>core/922/1/Org1_Gene231

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PELHFYLDLIFSPQDYIENLLWQIQEKEKS

>core/930/1/Org1_Gene368

MSDIQKEEHGSTTIFHLHGKLDGISSPEVQENISQSLAAGSKNIILDCAHLDYMSSAGIRVLLQSYHQVGQHSGKIVLTTVPKTIEQTLVY
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>core/933/1/Org1_Gene286

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>core/936/1/Org1_Gene730

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>core/938/1/Org1_Gene479

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RGGRSPIKRTSHLTVIVGEKER

>core/946/1/Org1_Gene695

MNLSAKEYGDIIVIYLQGS�DAVSVPVQEQYLEQFIQKKHLKIALNFTDVSYISSAGIRLLLSNFKLVQSLGGKMCLCCVKESVTEVMRIAG
LDQLILLCQSEQECLSKL

>core/949/1/Org1_Gene20

MNEPTRTYLESEKDTQDQIEELQATCIVKNAAGIHVRPAGVIVRLFDGEPDVFHTYAGKTINAKSIMSILMLGAPQGGEILVTIRSKEA
HRILQKIQDAFSSGFGEI

>core/954/1/Org1_Gene395

MEPYAVIQTGSQYQVRSGDVIDVELLGEVASDKEVIFQDVLVFDGTKASLGSP TIANAQVKAEYLSHVKG EKVVAYKYKKRKNYHRK
HGHRQKYLRVKIREILI

>core/955/1/Org1_Gene545

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EILTLDLYCAQNI

>core/956/1/Org1_Gene428

MNERTLLLLLKKKGLFLAILDLTQTESSLTTPLEKVLKQKKIFLSCIDRVLDLQIKEFRHAFSSSELPQDIQEELEEIRDVIIRILDTDKRNYAQK
KKEFGIYERP

>core/959/1/Org1_Gene436

MSFKRFLQQIPVRICLLIYLYQWLISPLLGSCCRFFPSCSHYAEQALKSHGFLMGCWLSIKRIGKCGPWHPGGIDMVPKTALQEVLEPY
QEIDGGDSSHSE

>core/965/1/Org1_Gene2

MEQFHLDREEILLAKASALQLSEELIQEYQTSLSAVITSMKEALAIEIDDADSCESLFMHVVNVEDLREDSVTSDFNREEFLRNPESLG
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>core/968/1/Org1_Gene303

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MKRLIETPNKHS

>core/976/1/Org1_Gene77

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WSDVK

>core/978/1/Org1_Gene21

MGSGYAKKKKEAKIMEQQFLEMEASLLEKRYEGQAGNGLVSVVINGKCDLISVKVQPTCLDPEDPEVIEDLFRAAFKLAKEQMDQEM
SLMRSTMPF

>core/979/1/Org1_Gene307

MNKSRLRLCCCLFCGSLFYFYINKQNSLTKLRLEIPCLSVRLRQLEQQNISLRFIDKIERPDHLMEDIAALPEYQYLEYPSEESISLLSYELP

>core/982/1/Org1_Gene451

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>core/988/1/Org1_Gene260

MAKLVITSDDEQQEFELEDNSEIAEPCESMGIPFACTEGVCGTCVIEVLEGRENLSEFTEPEYDFLGEPEDSNERLACQCRIKGGCVKVTF

>core/992/1/Org1_Gene239

MSRKCPLTGKRPRRGYSYTLRGIAKKKKGIGLKVTGKTKRRFFPNMLTKRLWSTEENRFLKLIKISASALRHIDKLGLEKVLERAKSKNF

>core/994/1/Org1_Gene116

MKEYLDFLVQRNVERDPQTKRHCTVSQKFGGESIDAKTTTGQLFHIAGKTEPGHGKLC LGESILKQLLALGIITGYENREREVWVYLD

>core/997/1/Org1_Gene724

MKSEFKLLPFLSVILCCGNLLSSPRRAISVTESIGMSAVKTLVLSEKAHEFLEGIGYGVGASSILRDWQTQQWLEIESLLAQNEVM

>core/998/1/Org1_Gene477

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>core/999/1/Org1_Gene812

MVEIHHKDP SLKKLFALQQSLET LNSLSDIVATYEAMFSLIYEGLNKALRKDQLCYLLSVNSKGELLKSPSGDP IVQTFPIHPHH

>core/1000/1/Org1_Gene538

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>core/1003/1/Org1_Gene40

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>core/1004/1/Org1_Gene539

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>core/1009/1/Org1_Gene211

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>core/1012/1/Org1_Gene547

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>core/1014/1/Org1_Gene590

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>core/1015/1/Org1_Gene769

MKNKIVTLLDQLYEDQESRLQKLGEIVPNLTPEDLLQPMDFPQLEGNPAFRFEEGVLSGIGEVRAAILAALSQEN

>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/1025/1/Org1_Gene951

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>core/1028/1/Org1_Gene498

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>core/1034/1/Org1_Gene348

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>core/1046/1/Org1_Gene953

MSIALNREEVWDNPRHLMFILMQFQQFSGEQDRFGSFLEATIRDRVSFLVLQEKIATLK

>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

MFFIAVRSRGFLDIHGILAARKGKQVVKSTAGAWIGSRGAVFYSLVS

>core/1068/1/Org1_Gene984

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>core/1070/1/Org1_Gene717

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>core/1073/1/Org1_Gene1014

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>core/158/2/Org2_Gene129

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DALRVFNPKTRLFGFIKGPLGLTRGLYKDLDISVIYDYNNMGGFDMLSSSREKIKTEEQKKNILNTVKQLKLDGLLIIGGNNSTDTAMLA
EYFLAHNCKTSVIGVPKTIDGDLKNCWIETSLGFHTSCRTYSEMIGNLAKDALSAKKYHHFIRLMGQQASYTTLECGLQTLPNIALISELIA
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NVRVSKIATEELLAVMVKKEIEKIKPHMEFHSVSHFFGYEARAGFPSNFDNYGIALGIISALFLVRQKTGYMITINNLAQSYTEWQGGGA
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RSL

>core/176/2/Org2_Gene914

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LFTTGSPEDQALVRLFSYYRNHIPAVLASFGLPPPETGGSVFVLLPKQENLLWSQIEVLATRYLKDTFVRNSEWTGSFEMMFYSYNEMCK
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>core/20/4/Org4_Gene980

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IYSINEFIRFLSEFFTSTESSELLGKHAVINLEKETSRLVHNITAMLHTDVFQEALLTRILEAYQLPVPPSILNHLQDLSQTPWVYVSGGTVD
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VLDNVSSYLGISSRITYEKFRSLIETIPKMTLLSSADLRHIYKGLLMQSYQKIYTEEDMYLRLTTAMRHHNLAYPAPLLFADSNWPSIYFG
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>core/67/4/Org4_Gene970

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WWGGCRKAYHTSHAVLQAAFEKDKSKDNLQVKKKHDERMFTFFQKNCREYQKALERLRELQALYPEVSVSLVEAGREENLGSNLE
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SRLESEVSGCREHLREQVKQFETQGLDLIKEELIFVSDVLFKRMVSRVSTVHVPMFEFYEYFELHRLRLRAQWMANAEIYSKVRKAFF
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>core/69/4/Org4_Gene683

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>core/106/4/Org4_Gene361

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YREYKEKYL SQKLD MQILQEVNAEKSEKARLKS LVRDYEKQLEQQDANLKKAKAIWEEELGKQQLKDHEQTQEIKRLNTFMLEYQDG
LRAEQVAEQVRQDLRQLEEKYSHLQEEKQEKEKILEQSVNHFAERFEALQKENVVYKKKLADLEGAAAPTEIREEDGWILAGSASLSQ
KKIRELNEENQELLKLLAFKTRELTQLAADVGAEKEISKLREQIEEQKEELRVLDTMHSEAVKDCEAAQRKCRDLEGLLSPVREDAGMR
FELEIELQRLREENAQLRLEVERLEQEQLQG

>core/208/4/Org4_Gene991

MQRDGRFKWLQDEDTSAHAEQRFRDINGCWEDLKQTIFWVGEHDCMDIETVRKSYMMWLD RYADKFILREKEEKMKRHELPHAT
MVRKASGHAYAKAKAAFEKERSNENQRKVKDIEKWLSKGLAEFRNQESRRARERLRELQTLPGVSVEERVLERQRTKKVNLENLYAD
IEKKYHHCVREQEHWKEVENKEAEFRENREKVLSTEEVLECLQRLEDCLTWSKQLTKAEGSVFEMMFDATEELGNKVLSDV TNRLEI
LCEDA EEMIFRIEEIEMTLRMVELPLLFMKNTFEKASLQYNSCKEMLAKAEPHCKESA IYRSSEERLERLNRDLQTAYTNCHERLQGFSKL
ESEVRTCKDHLREQMKHFEVQGLNFINEELLWVGAEFLTQARLDLVATVPYMEFY LQYHNIKREKVR SQWMAKTERYREIRQAFQGV
MKEDLLAEDTILKEEDYWLLRDDWLLRDERKNRQRR LICNKIAAAQQRVKGF

>core/209/4/Org4_Gene637

MLGILLIASGII FLAVAIPGLSSAVALGLGCGMTALGTVLLITGLVSLIRSEQLALEQVEIKQARTRVNNELDQLSQYVFYTENVLDNLKRW
SYRDLGFVRQAQEEVTNLEQDIEEIFLTRDIRNALDNEEFFMTHAKQCLAQVGESLFQDASIDEFINLAHLSEIRQHLDINDPRWSMIT
KKVKGTVVRFIYVSTMYKQIKSNFEKSDFGQLRKMLLN NYKTIEEVLYQS FQKGYNRAALLSEKTRIHTSSLLHWEKDEDKHLN IKNECA
SRLENFKKFRTLFLGLSEEDVIDFTGASGWDCSKLPRKELPLDGGKKKLRFKRTFADEQVGDWDR TTSLEHMTPQEEDPLDKLMDQVE

QEATSVLKDQDRYWKEIETSEAKFRSLPQEDDFEKQSQIDSYIRLDDHLSVWANQLSAAEDALIEVTDVQEHGNREMLKNIQQGLELI
EDAVKATLPRVDFIQELLEKEELPLVAARMSLENSYLKISS

>core/341/4/Org4_Gene932

MVVSIIYSEILSFSELTSCKHSFPFGPIETASIRIHVFNVVIVCLILGTLFVCLGMVFLGVFSTYLLGMSSMILGLLISIGLALLKFERYGLE
PKELFGVEGGFDKKLPSEIIQMQDQIADLARELDLEQKKDTLIRGFSARLDVLEGSKTEKKQILKIGVPRNLSEIQERAQELNSILEQCKEA
LLFRRKSAQEIFKKLYDRKAAFWRSYREDLWCYSEIHVSKKALSPLYIDGVFEGTAPHFLMEAYAMCRTAKNLRNYVKVCVEDMRMRI
DEEKKRAKQLSVSELLCCCTEIEDLENETNLFTSDSEDLVEEYQIHCIQVMTMLHALWAIYNDEVVCRKPIDTLDRVRARMAVEDCIETFE
ELQMCVVHTKTLELEIAQLYVDILLEA

>core/380/4/Org4_Gene764

MEVYSFHPAVRTSFQHRVMAGLDNWFFLGGYRLKVFLDKNNCGWACQKLVSISKTEKILKILSYLLVPIVLIALLIRCFLHARFKCTWN
RDSLIDSRVPSDVRPFHDFRLFNQERLNIWKNRIYVSGVDVLVASVDYLSQSFSGFNHHPKAIRCENYVRNGQFSEEGKKSYLRGMLT
HIVGYILSVDETYWEDVILKIPAMNILEAAYSRSVSTDPNYQHGGVYFLDKSLQVPARHVLGEGNMLNTAKWMHIRAERPGEKEGEC
IAKQFLKDYCKKHLEVMNCPDFIESLLDEKIREFHCPSVLNSAVCDIIDHKCQEHLLKAIINEANRRRLPGMKNSSFTMCGDQVLFYTVFSP
PKLPPAASSAYF

>core/461/4/Org4_Gene615

MNIYQFSPGVSPNWQASLMARLDSYFCLGGETVTRIISLRPSGLILAKKEKAVVVSIAAKILKILSFILFPLVLTALAIRYLLYNKFNKDLDRAV
FFIPTEITKTEELIIAKNPALVKEAALNVSPFFYSLPKKYQRMKVETPEGKFYKITFSVNLDLLVEDLHLETLDWPTELLKNRPFDFTHPEE
EKLIKDILLKEEGNEYFSLESKKLLARHMMHNIVVLSEEPGRSAFLGRTAFFPNKYPIAKGGVGIPSTTSNLFITWYCFYFYRAATPQSDHP
DGCGFILLERLKLGAEFFYCDLRESNTTGFTLLFEGSNKGVLKNHLFIRDE

>core/462/4/Org4_Gene614

MSNIYSFSPGICPNWQAGLMSKLDLCCFGGETATRIFSMTPSGFSLATEEKVHISTAEEKVILALIFFPIILIALAIRYFLHRKFDRKCFVIP
QDTPKELELILAAANPQLVEKAAREVHPGFFALPTKYQSMYIQTSGQPPKITLSINIDLLLEDLDTDSIPWPKLYLDEDFDFAYYPESKAIID
TVTKLEKNNPGEEFCLESKKILAHYLLEQLFKLETGLNFPTSTIDGGRESFLIKFSHETKKPTVWAFIYFYHHHSNGPKLEKDFKQAGCEVH
NRLLNLGLKYRPQAGAQNDCDGGPYGPRGFLIVWEENYGSVLKDHGFIKDN

>core/473/4/Org4_Gene406

MMTYPVPQNPLLLRILRLMDAFSKSDDERDFYLDRVEGFILYIDLKQEDLNKIYQEELEENAERYCLIPKLTfYEVKKIMETFINEKIYDID
TKEKFLEILQSKNAREQFLEFIYDHEAELEKWQQFYVERSRIIEWLRNNKFHFVFEEIDLFTKNVLEQLKIHLFDAKVGKEITQARQLLS
NKAKIYYsNEALNPRPKRGRPPKQSAKVETETTISSDIYTKVPQAARRFLFLPEITSPSSITfSEKFDTEEEFLANLRGSTRVEDQLNLTNLSE
RFASLKELSAKLGYSLSLSTGDFFGDDEEEEVVTKTKGSKRGRKKSS

>core/556/4/Org4_Gene319

MASIHPTAIIEPGAIGKDVVIEPYVVIKATVTLCDNVVVKSYAYIDGNTTIGKGTIWP SAMIGNKPQDLKYQGEKTYVTIGENCEIREF
AIITSSTFEGTTVSIGNNCLIMPWAHVHVNCTIGNNVVLSNHAQLAGHVQVGDYAILGGMVGVHQFVRIGAHAMVGALSGIRRDVP
PYTIGSGNPYQLAGINKVGLQRRQVPFTTRLALIKAFKKIYRADGCFESLEETLEETLEEYGDIPVKNFIEFCQSPSKRGIER SIDKQALEE
ESADKEGV LIES

>core/743/4/Org4_Gene935

MNWAPKTMDHVDPKSETNIRLVISCYKLIKACQLEFPSLVDEVLLGMKCCAWESFKLV RQYQEQA KTVSAKNAPLFCLTRSYYRDGHL
TPLRAGPRAALS NYLDLRRRENSEKFFNPGHPCYYARLAFNETIQIYRTLFDISKLQIMFESGDYEKGQRENI AVILNFVKTLDDNEKVNFL
LRHNDTRIPGRESATVFCS

>core/865/4/Org4_Gene979

MSNIMGSRRKLKRSFLLIEVLMALSLVCAVLLPCIRFYIAIHRSFEE DIFNLQLPALIDHCFLSVEEKMRQQMAEGTVFTSGKGQTVSLAY
TSQGIGYRIPYGYNVDIRQEV RGDNLKMKVCLADVVELFPDQKQAVSVQRCLCVTL

>core/868/4/Org4_Gene809

MEEFVAYIVKNLVTNPEAVEIR SIEDEDNESIKLEIRVAAEDIGKIIGRRGNTIHALRTLRRVCSRLKKKVQIDLIQPENGTDVIADQDYICD
NDSSNSTEDTFGESDTCCSGHCHYDEDLNQEELDQEEQEEDNMHHSCECSNHH

>core/905/4/Org4_Gene937

MRAGGSLVTTYPKERRRLRSPEQLRVLDDLQSYPNHLHAIELDCDAIPQDLIGATYIITFADFSTYILSLRSYQANSPSDDTWGIWFGSI
DDPVIADRFQAVISFLKDHGFALPSTLAQDPLLCTNK

>core/920/4/Org4_Gene578

MRELNAFELTQPEEYRNRWVLMPCCLKRCRTQHAKVWSYRCVHEASLYEKNCFLLTYDDKHLPQYGSLVKLHLQLFLKRLRDRISP
HKIRYFGCGEYGTKLQRPHYLLIFNYDSLLDG

>core/1056/4/Org4_Gene448

MIDAENQNPKGGSFTSLHTDPKNLFDEEGMPSHLILYSAISITYSSL

>core/19/5/Org5_Gene1037

MESFVSEHPLTLQSMIATILRFWSEQGCVIHQGYDLEVAGAGTFNPATFLRALGPEPYKAAYVEPSRRPQDGRYGVHPNRLQNYHQLQ
VILKVPENFLSLYTESLRAIGLDRDHDIRFIHDDWENPTIGAWGLGWEVWLNGMEITQLTYFQAIGSKPLDTISGEITYGIERIAMYLQ
KKTSIYDVLWNDTLTYGQITQASEKAWSEYNFDYANTEMWFKHFEDFAEEALRTLKNGLSVPAYDFVIKASHAFNILDARGTISVTERT
RYIARIRQLTRLVADSYVEWRASLNYPILLSSTSEPKETSESVVPMISSTEDLLEIGSEELPATFVPIGIQQLESARQVLT DHNIVYEGLE
VLGSPRRLALLVKNVAPEVVQKAFEKKGPMILSLFSPDGDVSPQGQQFFASQGV DISHYQDL SRHASLAIRTVNGSEYLFLLHPEIRLRT
ADILMQELPLLIQRMKFPKMMVWDNSGVEYARPIRWLVALYGEHILPITLGTIIASRNSFGHRQLDPRKISSPQDYVETLRQACVVVS
QKERRMII EQGLRAHSSDTISAIPRLIEEATFLSEHPFVSCGQFSEQFCALPKELLIAEMVNHQKYFPTHETSSGAISNFFIVCDNSPN
DTIIEGNEKALTPRLTDGEFLFKQDLQTPLTTFIEKLKSVTYFEALGSLYDKVERLKAHQRFSTFSSLAASEDLDAIQYCKADLVSAVVNE
FPELQGIMGEYYLKHANLPTASAVAVGEHLRHITMGQKLSTIGTLLSLDRLDNLLACFILGLKPTSSHDPYALRRQSLEVLTLVSASRLPI
DLASLLDRLADHFPSTIEEKVWDKSKTIHEILEFIWGRLKTFMGSLEFRKDEIAAVLIDSATKNPIEILDTAEALQLLKEEHTEKLAVITTTN
RLKKILSSLKLSMTSSPIEVLGDRESNFKQVLDAFPGF PKETSAHAFLEYFLSLADLSNDIQDFLNTVHIANDDGAIRNLRI SLLLTAMDKFS
LHWESVAV

>core/78/5/Org5_Gene341

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RYVEKDFMAMKKFFAHEAYPFTGNPRAWNFINEGLLDYFLTTTRVGEKFLKVVYHPGEKIFSKEKAYQPYRRFDAPFISSEEVWKSSAP
QLLEILKV FQQIENPISKEGFLARAKLFLEERRFPHYVLRQMLEYRRQMFALPPDEALSRGKDLRLFGYQTIQDWFGDAYLSAAVELLIRFI

DEQKKVLPRPSKQEARDDFYDKAKHAYTKISKNKEFSLGFEEFVNSYFQFLEISESEFFNMYRDILLCKRALLLQGGVSFDFQPLTTFFVQ
GKDSIQVEFFRLPKEYSFKTKQELKAFEVYLKLVSLPKSDSLDVPNEILPIATIKAKEPRLVGRRFSIDYKRVALQDLAATVPMVEVLHWQ
QNSEHFQEILQQFPDVETCQSYKDFQHLKPALRDKISLFTRKEILRARPERILQSLQQVPKQSQEVLLSAGKNSALPGISDGQQLAKVLE
NEVLDLYSQDAETYTYIIVNSSFEKEEVLPLYREVLRDLASQLLTSHGHLVDMERLESALRTRYPGEEGASLWQRRLLWKVVENHRLGRH
LEGFSWSLDRSLKTFSRGDKELPQEFDRIFSMKVG DYSSVFMSPNEGPCYYQCLSHLLYDRPASVDKLF LAKSQLDEELLGSYMERFIE
QGVVR

>core/173/5/Org5_Gene103

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DEVPIFATMILT LGKVDRGFSPEEISLIQKLSYPGLSLASLRGSTEIDPNTDLARALVSEFSGDLGKNRADYYSNCLDILALRIHAERQRYL
DQSPCVPGTSEFHKATIEAINTILFYEEAVRYP SKKEMFSDEFSLSSVTDRKFGVCLGVSSLYFSLSQRLDLP LEAVTPPGHIYLR YQGGEV
NIETTAGGRHLPTASYCDCLDLEDLQVRTPEEMIGLTFMNQGSFALQKKKYKEAEEAYKKAQEYLGDEELQELLGFVQILGGKKKEGKS
LIGKSPRASQKGSVAYDY LKGRINIPTLALLFSYPGSNYEEIASYEEELKKAMKSSMPCCEGQRRLASVAFHLGKTAE AVALLEKCVEDIPN
DLSLHLRLCKILCDRHEYTKALKYFIIAERLMEDQGFLKKDNRSFALFYEVKKIISKVAPQKANTLLL MESER

>core/574/5/Org5_Gene71

MLLIYCKKKEIHLQWPQTAKIRFTP KIAMKV KINDQLICIPPFISARWSQIAFIESQEGENKDQGT LRLHLIDGKIISIPNLDQSIIDIAFQEH
LLYLETSQSGKEDSRDDDKLGVGVL MNVLQQITKGNDIQVLPKNLISPLFSGTNPIEAILQHTPEHKDHPDAPTDVLEKMADVIRVLSG
NNATLLPRPEPHCNCMH CQIGRVMNEEDTLAVSDKDLTFR TWDIMQSGDKLYIVTNPLNPSDQFSVYLGPPIGCTCGEPNCEHIKAVL
YT

>core/669/5/Org5_Gene170

MNKKILVLCTAMFFIVCFGLIHKKHTILPPKAHIPTNAKHFTIGNPYAPINITVFEPPSCSACAEFTTEVFLLKKHYIDTGEISFTLIPVCFI
RGSKPAAQALLCIYHHDPRQADIDAYMEYFHRILTYPKEEGSHWATPEVLT KLAEGLKINSGRSVNPKGLEQCIASGQYNEQIKKNNLY
GSQVLGGQLATPTAVVGDYLIEDPTFHEIERAIQHIRQLQAVEGDHDD

>core/794/5/Org5_Gene1063

MSLVSYLSNPQKALVLGSKGFSMDCVDNLKLYIFRLKLP GDTERISYSISPEYIREKGEEELLNSPIEVEGSLGRIDSDQWILSLSLKTQLGLC
CPVCNNFFSHSVCLPDLQRVISHDEVGSGVFDCRPLIRQELLLESDCFEEC SGQGC PERKNILKFLEDRKKHEGN NPFEYL

>core/901/5/Org5_Gene54

MKNKMDYKSQLVFSCPCCKGNVCFSVFNLDVILTCNVCSSTYTFDSVIRNEIRQFVALCKRIHDANSILGNATVSVSVEDNQMDIPFQ
LLFSRFPVVLNLSLDGKKIAIRFLFDALNTSILHQESDLIS

>core/1016/5/Org5_Gene725

MRNMEAKKIKELSKEAQLKKLREKSRVLDEKNKRKAWVAKLVAMPESIREIEKEERVETPQLFQAIAEKILEEGV

>core/1022/5/Org5_Gene818

MWYKSLAGEEKDVSGNECNDYPEVFKDDVSAYVLVTCGQMSSEGKIQVEMTYEGDPAVISYLLTKARDSLDES

>core/1049/5/Org5_Gene865

MRVMRFFCLFFLGFLGSFHCVAEDKGVDLFGVWDDNQITECDDSYMTEGREEVEKVVDA