

A

>6AR1 (Group II Intron)
NQGAPGIDG-VSTDQQLRDYIR-----AHWSTIHAQLLAG---TYRPA----PVRREIIPKPG-----GGTQRLGIPTVVDRLI
QQAILQELTPIFDP-----DFSSSSFGFRPGRNAHDAVRQA---QGYIQ-----EGYRYVVDMDLEKFFDRVNHDL
MSRVARKVKDKRVLKLRAYLQA-----GVM-----IEGVKVQTEEGTPQGGPLSPLLANILLDDLDKELEK
RG-----LKFCRYADDCNIYVKSRLRAGQVRKQSIQRFLKTLKLVNEE-----KSAVDRPW-----
-----KRAFLGFSFTPERKARI---RLAPRSIQRL---KQIRQLTNPN-ISMPERIHRVN
QYVMGWIGYFRL-----VETPSVLQT-----IEGWIRRR-----LRLCQWL
>SLACS
RGAAPGLDG-WTRELLYPLTLD---PALKMEIAAVVKDIINADVSMVEVGRRLQ-ATSLTVLRKPN-----GKYRPIGAESVWAKLA
SHIAISRVMKTAEKK---FSGIQ-FGVGG-----HIE---EAIKAK---IRKDF-----ATKGLAMLDRGNAYNAISRRAI
LEAVYGDSTWSPLRWLVSLLLTG-----TGEVGFYENG-----KLCHTWESTRGVRQGMVLGPLLFSIGTLATLRLRLQQ
TFP-----EAQFTAYLDDVTVAAP-PEELKNVCAATAEAM-EALGIVNNAD-----KTEVLELT---GDTGF---
-----GTAV---KRVREFLERTWP--DPMS---EEIREGVKEMMETDRLFKAIVELP-LYNRTRWRILA
MSAMPRTITFLLRNH---DMQHTHRVASW-----FDERTTQV-----MEHILGQ
>CRE1
RGTAAPGLDG-WTRELLPLAEDPALLHEITSVVSIMQGGKVA---EVVARRLR-SSAVTPIPKDE-----AGTKIRPIVPESAWLKLA
SLVAMAEIPSSFKET---FKGWQ-YGVWG-----DVA---KAVAK---IRRDS-----EEHEYLVALDGVNAYNTMSRAHI
LQAVYAEQRLKPIWGVVVKVALGG-----PGFLGVYRDG-----CLKGNLWSTKGIRQGMVLGPLYATGMAAAGIPVRQ
RIP-----GVPVTAYIDDITLAASGAEGA-RAAEAYADAL-ETVGVVVTNAR-----KSMVVGPE---GTRVG---
-----IGG---VDLPV---VAEARILGAHFRARGTPEARTIEWLQAAVEKW---RPIHQKLRQDI-IPKNIAMMTTR
ISLGSKMTFLLQTH---SPQELETAKT-----ADDEVEQT-----LQHLMGQ
>CRE2
RAAAPGLDG-WTRELLVPITED---KGLLTELTAIVQDMLVG---NVHPSFAT-RIRACILHPFR---KEAGSAKVRPITPESALMKLA
AHIALDSVEKSFST---FKGWQ-YGVWG-----DSTEA---VKRIR---EAYAE-----ASSDTLVALDATNAYNMSRRHI
LEAAYAQPPELRFQFVGNLSLGA-----AGELALYENG-----AKIHALKSTEGVRQGMVLSPLLFANAMSGIIRPLME
MHP-----RVKVVAYLDDVTLIGP-HAAVQDFLAEAGPQL-SRVGFDINPA-----KSHHLAKL---EVPEA---
-----LSV---SGR---TIPIA---QGVVRILGAGFRGDTASVE---EWWWEKTKTH---DHYFEKLQSEW-LPRLARLQLLR
GSTVPRNLNHLRTH---KPEELNRSTTW-----FDERVMET-----ALNIANI
>GAU97528_Ramazottius_
VDSAAAGPDR-VLVRVIKQEAUME---VLAVIAAVLLEMNATKE---HPLPSVLQ-LALTVLIIHKG---DVTGDNNYRPIISCSARRVL
ERVVDRHLRRYGS-----VSRFR-QGFTSAPGTHVNASIL---GSVSK---KAQAE-----QSTVVVVLLDIKQAFEGILHVHL
KKTILRASPLPTLVRNLLSLQGS-----NRTQLQVGG-----QRSSAIPVKKGVFGVPLSPMLYNMSTDYVTRNMT
APIAAEYGFPL---CEGEQPVTFGLGFADDSTVVGKSREEAIQLTEMAIGLF-KEIGLEVSPT-----KSKAIVVE---NG-----
-----VMSEVPLYL---SSG---AVIEATKKGEKVRYLGATVTDQLDF-----DQGEVIKQL---TDQVDRLVHFADHLADQKLNLLN
QWLLPSIIYPLQTA---PNTILKVFLQT-----VDKIVKST-----VREILQL
>BLAG 1
ADTAPGPDH-VLVRALKDATC-----YEIIAKIATTMLQH---SFVPECLQ-KARTVLIYKGG---DDKDLGNWRPITICSVVRRI
ERILDARLRALVN-----LCENQ-RGFTNSPGTLINTSIL---ESILV---AAKSK-----KKDCTIVFLDISKAFDNVGNHHL
QNSLSALRIPFKLSSLLILQQRG-----NKTQIETGR-----CRTKPIDIKRGIMQGSPLSPILYNISTDHILDELSN
QELQDEYGFSLV---SPGLSNITALGFADDTLIAAKSMNSARILVELAMSRF-KEIGLDINTD-----KCRCISII---KG-----
-----CVRYNPLNL---TSG---QTIASITPDENIKYLGVSYNATIL---DAANSIEEL---KNKLDRLASTPLLPQHOKYTVLC
SFICPTLIYKFQTT---PLKKLPAKFLSD-----ADVLIKT---LKEVLQL
>BLAG 5
VDTAPGPDH-VLMRVLKDDAA-----TGVLSLLATRLMRT---GHVPPCLL-IARSILIHKSG---DVNDITNYRPIITICSVVRVI
ERTLDRRLKEYVS-----FNRHQ-RGFTSSPGTLMNTSL---RSILT---SAKTK-----KCNATLVFLDIRKAFDNVGHHL
QKTLESPLIPSLLSNLNLNLEN---NHTRFEINH-----HKTNLVPLARGVMQGSPLSPTLYNLSTDHILNELSE
DGVAKAYGYQL---VPGLPVTVLGFADDTVIVANSTTSALELTKMAIERF-RSIGLEINFS-----KSVAINIS---CGK-----
-----LNPYNSLLV---AEN---ATIPCLGPNEFVRYLGVNFADACLF-----DSQVTNLNDL---KNKLDLLISSPLLNPDQKFCILN
SSICPSLIYTFQTT---PLNKIPNKFIEA-----ADKIIKSG-----LKEILQL
>BLAG 2
VDTAPGPDH-VLVRVIRNEIV-----YEILAIATRLMSS---GIVPRCFK-TARTVLIHKAA---DVNILSNWRPITICSVLRRI
ERVLDKHLRTFVS-----FNEHQ-RGFTTNSGTLINTSIL---RKVLK---TTKDN-----KEDVTVVFLDISKAFDNIGHKHL
DLTLSAEPKPAKLKDLINLQIN-----NTTNIQTSL-----GQTKAINLRGVMQGSPLSPTLYNLATDFIDELTE
LSLLQYQYKSI---SPQLSSLSIMGFADDTLLMGKNSETTLELHIALQRF-QEIGLQVNPQ-----KCTGISIK---RG-----
-----KLVEEVHLI---NEK---FTIKTINNQEVRYLGAFFQDNALF-----DKDSTIKQL---HKKLELASSPLLSKSDQKFLVN
TAICPTLIYRFQTT---DLQTIPLQLFHT-----ADKLVRST-----LKDILQL
>BLAG 4
TDSAPGPDH-ILVRTKLTEC-----SPVIAVILKIMLQW---GMVPDRMR-GARTILIYKGG---ERCSVSSWRPISVCSVIRRI
ERALDSVLRQYLT-----LNNNQ-RGFVSQLGTSINTSLV---DGCLK---KAKLE-----QRNVSIVMLDVAQAFDSVGLDHL
EKCLDSQFLPTSCTLIKTITRG-----NFTRIHNKG-----QISEPIELKRGVFGQGSPLSPILFNLSIDFIIKELSE
KQITDKYGFKI---SNLHDLSVAAFADDLVVGQNMHAARELVMMTKYLL-QQIGLQNLIA-----KVSINIE---HG-----
-----KLQDKELLL---YSG---YAIRGITKEEKIKYLGVSFNDEIIF-----DRESFITS---RNDLQILVSTPMLRPDQKLNIVN
QYIWPKFIIYALQMV---PVHKLPLTFLED-----VDKLIRSA-----VKEMLLL
>BLAG 3
IDTSAGIDH-VLVRTIKELKT-----SKLLCLLTNAMLKF---KICPGILK-TARTVLLFKGG---DETKLSNWRPISIFSICRI
EKVINRRLKSYIE-----LSPHQ-RGFINVPGTHINTSII---NGCLT---RAKKE-----KRNCCIAFLDISKAYDNVGHVH
KRCLLRTNMPNNLRDLVLNLLQG-----NKIQIESGF-----QKTKPIQVQKGVAQGSPLSPGLFNALDDTLKELAD
PNVREVFQFSL---HPDLEKVSGLAFADNIALISKDEASLQTLINMTVFNL-DAIGLKVNPK-----KCLMLINK-----
-----NGFLEQGGIL---VGG---QTLEFIKPGEIYKYLGVTFDEIVL---DKSTLIKNF---ENDLNSLTVSNLLTPDQKLNIVN
QYIWSMLIYPLQCT---PLDKIPSSFLQD-----IDKLLRSS-----IKEIIGL
>BLAG 6
LDTAPGPDH-VLFKVVKELKC-----MKIISIIANIMLSW---NYVPNSFQ-SGRTILIFKSG---DPNSLKNWRPITIFSILRRI
ERALERKIRPFVE-----LSTCQ-RGFISTPGTFINSSI---NSCLQ---KSKKE-----KGDCCITFLDVSKAFDSIGHKHI
EMSLNSTSIPSQKSLVLSLVKN-----NSVGIELDA-----TTRTKPINIEKGVAQGSPLSPLLFNLSIDFIIYRNLND
FQNASQYGYRL---TEEVNDLIALSFADDIALISNNETSAVFMIERNVQCL-TEIGLNLNAS-----KSKIIINIK---KG-----
-----KLMNTTWT---LND---IKINSIQAEETIKYLGVTYNDEIILD---KCSIIITNLN---RSISKLITSSL-LKPDQKLNILN
QYIWPFTLIYPLQCA---PLCKLQLGFLQD-----IDKIVKNA-----VKEIVGL
>R2_PS
SKTAKGVDG-VGLEELKRVR-----RTLFIINLGLW---THVPESLY-KGRITLIPKKS---LPFLAGDFRPICVLPVVVRL
HRLILAKRLAIVQ-----HTEFQ-AGFQSGRSTSENIFLL---RTILE---SLPAG-----KESMYIALLDFRKAFFDSVGHVH
CGLLRDLGLPERLTGYVESIYRS-----VHLTGLGD-----WVFQGRGVQLGDPISPFLFNLMIDYILSGTQA
GVGVG-----VGERIVSSLAYADDLALLASSRRGLNANLESLARA-RSVNLAALGIN---KCATIGKR---WLGREKK---
-----MILDREFFL---LEG---VAIPVYRWNNIYKYLGIETSPGAA-----ARWSVTGL---RNRLSKLESAC-LKPQQRMHLLR
CYLLPGLYYGLIH-----QGISVGLLRS-----ADKQVRAA-----ARKILHL

>RaR2
NNTAAGPDG-IQPKSWNRISL-----KYKTLIYNLLLY--EKVPHKLK-VSRTVFIPKKD--GSSDPGEFRPLTICSVVLRGF
NKILVQRLVSLYK-----YDERQ-TAYLPIDGVGTNIHVL---AAILN---DSNTK-----LSELHVALLDITKAFNRLHHTSI
IKSLVGKGFYPYGFITFIRMYTG-----LQTMQFEG-----HCKMTQVNRGVYQGDPLSGPIFLLAIEKGLQALDK
EVGYD-----IGDVRVNAGAYADDTDLVAGTRLGLQDNINRFSSTI-KQVGLEVNPR-----KSMTSLV---PSGKEKK-
-----MKVETGKPF--AND---VPLKELSINDFWRYLGISYTNEG-----PERLSLTI---EQDLERLTKAP-LKPQQRIHMLN
AYVIPKYQDKLVL-----SKTTAKGLKR-----TDRQIRQY-----VRRWLKL
>R8Hm-A
KDSASGPDG-LLLQDVRRLLGP-----LLLCNIFNMWYL---HGIPVEEN-RCRTILLYKSG--DRHLASNYRPVTIGNMLNRLY
AKIWDKRIRKNVR-----LHVRQ-KAFIPVDGCFENVKTI---QCVLQ---SYRKR-----KLEHNVPFIDLAKAFDITLHDSI
RKALWRKGVPSPGVVDSLYAG-----AVTSISVGK-----TKTRSICINSGVKQGCPLSPLLFNLILDELAERIA
TGCGLD-----LDGHVLSMAFADDYVLLAKDSVEMNELIRVCSTFF-KEKGLSVNPG-----KCQSLRVL---PVKEKKRS
M-KVLVRPHRWRIK--DQD---VDIPSMTYDSLGLYGVSIDPTGK-----IALPIEEW---KNWMTKLKECK-LKPEQKVKLK
EVVCSRNVYVLRM-----SECGISELRS-----WTRFVRNW-----AKNIIHL
>R8Hm-B
KDSASGPDG-LLLQDVKKASP-----RQLCIIFNMWYL---HGIPVVEN-RCRTILLHKG--EKHLTSNYRPVTIGNMLNRYV
AKIWDRRIRKNLQ-----LHVRQ-KAFVPLDGCFCENVKTI---QCILQ---SYRRS-----RREHNVPFVDLAKAFDITLHDSI
EKALLRKGI PRSVIKVVDLYAG-----AVTSITVGK-----TKTRPICINSGVKQGCPLSPLLFNLVIDELAERLEA
TGCGLD-----LEGHVLSMAFADDYVLLAKDSVEMNVLNMCNTFF-EEKGLAVNPA-----KCQSLRVL---PVK-GKRS
M-KVLTRTRHWKIN--NQD---VEIPSMTYESVGKYLGVMDPAGK-----IALPIEEW---KLWLTRLRECK-LKPDQKVVLK
EVVCARANYVLRM-----SGCGICELRK-----WSRFVRGW-----VKSIIHF
>R24_MR
KQSASGPDK-ITRDDLRKANL-----ADVGLLNIVFGL---CRTPTLLR-HNRTVLIPKKG--DLSLTSNWRPITVSSIFSRLL
HKILASRLSNNIK-----LHHAQ-RGFTPCDGMSSSTIL---DAIVR---EHRTN-----GKPLYVLSIDLTAKAFDIHP IAI
ENSLINKGVQHTVYIMSTYKD-----VDTTIECHG-----ERSSPIRMCRGVRQGDTSPLMFNIAIDDLVTSINT
TDGVQ-----LGNSKIGCLLFADDIIFVSNTVHGINEHLRRLRAFL-EGTHMEVNPS-----KCRALQLA---RVPGTRK-
-----VVVDTKPKFS--IDG---ASVPTLRVLEQLKYLGHGYSQSGM-----LAPSPSNL---ESMLERLRRAA-LRPWQKLYILN
RYLIPRLIHCCQS-----SSITAGRLEY-----MDRLIRKF-----IKKTLHL
>R2-1_MR
KESAPGIDG-ITREHLRSMR-----PDLYALLNIIWGM---KCLPPVLR-SNRTSLIPKSG--NTRELKQWRPIMVSSRVLRL
NKVIVSRLENEIK-----LNYHQ-RGFTKIDGVMANNTIL---QTAIR---TMRNS-----SKPFIILSIDLAKAFDRSVISVI
IDALWRRGVDEHTICYIEANYRN-----ITTTIECHG-----KRSRPINVDRGVKQGDPI SGFLFNVVLDGLLQKLHD
QTGIQ-----INGTNIAALAFADDIVLMAPTMMIRSHRIVESYF-RRHGFEVNVE-----KCATFQYI---PVPGTRK-
-----LVVETKPLFK--ING---TDVPTLNVSSQLKYLGLQYGRGA-----TCPTPSKT---EEMLSRLGKSP-LKPWQKLVNLQ
RYLIPRLHHGMQM-----MDVNKKLTY-----LDGCIVKF-----VKETLHL
>R2Sm-A
HGTAAGIDR-LTSYDLMRFGK-----NGLAGYLNMLLAL---AYLPTNLS-TARVTFVPKSS---SPVSPEDFRPISVAPVATRCL
HKILAKRWMPLFP-----QERLQ-FAFLNRDGCFAVNLL---HSVIR---HVHTR-----HAGASFALLDISRAFDTVSHDSI
IRAAKRYGAPELLCRLNYYR-----STSCVN-----RTELHPTCGVKQGDPLSPLLFIMVLDDELLEGLDP
MTHLT-----VDGESLNYIAYADDLVVPAPNAELLQRLDRISLLL-HEAGWSINPE-----KSRTLDLI---SGHGSK--
-----ITALSQTEFT--IAG---MRIPPLSAADTFDYLGIKS NFKGR-----CPVAHIDL---NNYLTEISCAP-LKPQQRMKILK
DNLLPRLLYPLTT-----GIVHLKTLKS-----MDRNIHTA-----IRKWRL
>R2NS-1_CSi
GNSSPGLDK-LTPRMLRRFNA-----NVLAGYFNLLLS---GGCPHLC-RARITLVPKVP--NPTSPDQLRPI SVSSILVRCF
HKVLADRWSRRLQ-----LPSLQ-FAFLHRDGCLEATSL---HALLR---HSSAT-----ASNLSLAFVDISKAFDSVSHDTI
VRSAAEAFGAPSPLVRYIAQSYEN-----AVAVFP-----SSEVHCHRGVRQGDPLSPLLFIMAMDEVGLGSM
QLGYQ-----FHDTLVDGFADFVWVCAESQARLKEKLEAAAVEL-GRAGMKINAR-----KTKAMVIC---GDRKHR--
-----ATAVSVEPFC--FAE---ELITPLGPTDTVTYLGIPFTFKGK-----GVFNHRQHL---LKLDEVTRAP-LKPHORMEITR
NYLIPRLTYSLVL-----QVHRNTLKR-----LDNYIRQS-----IRGWLRL
>R2Ci-B
TPSAPGPDK-LTLDGVKRIPI-----AELVSHYNLWLYA---GYQPEGLR-EGITTILIPKIK--GTRDPAKLRPITVSSIFICRIF
HRCLAQRMETSLP-----LGERQ-KAFRKVDGICHNIWSL---RSLIH---NSKDN-----LKELNITFLDVRKAFDSISHKSL
GIAAARLGLPPPLITYISNLYPN-----CSTKLKVN---KISKPIEVRRGVRQGDPLSPLLFNAVMDWALSELDP
RVGVQ-----IGEQRINHAFADDIILVSSTKIGMVSSINTLSRHL-AKSGLEISAG-----KEGKSASMAIVVDGKKKM-
-----WTVDPPLPRFK--VNS---QKIPALSITQYKYLGINIDAQGA-----RNDAAIRL---TEGLAELSRAP-LKPQQRLYLLR
VHLLPKLQHGLVL-----SSCAKRALTY-----LDKSVRSA-----IRRWLTL
>R2Nvec-A
KKSASGPDG-VPAAALQTMGA-----ASLAAHFNWLWLA---GTQPKRLT-ECRTIFVPKEV--NTHLPLHHRPITIGSVVRLF
HQTLGKPM EAVLP-----LGSQ-RGFRKGDGICQNIWLL---HTLIR---RSTD L-----LRPLKLVFLDVKKAFDSVSHESL
LIAAKRLGVPGLLTYINELYSR-----SETVFEVG-----ESSGVKVSQGVKQGDPLSSTLFNCVIDWAVSDLD
HIGVL-----LGESRVSLAYADDLVLLSETEAALTSQLNSIEKSL-AHCGLKLSTG-----DSGKSASLNIVIDGAKR-
-----WVWNPTPFLR--ASG---GEIRSLVANETYKYLGINIGAQGV-----KAAEYNAF---KEALDNLSRAP-LKPQQRLFLK
TYLLPQLHHSVLV-----SRTTGKLLNS-----LDALVRKA-----VRGWLKL
>R2-1_MDe
ADSAAQPDG-ITVNVNIGMDI-----RLRLFLNMIMKR---GRLDDDLK-SARTVLIPKKG--GNIRPENTRPLSITSVVLRLH
HKILAKRLKSLQT-----FSDSQ-KAFIDCDGTQENLAIL---NTLTL---DARKN-----LKSIHIATLDRKAFDSVSHKTI
IDSITGMGCPKMFIDYVTDLYLN-----ARTVFQYNG-----SSTFLDIKRGVLQGDPLSPLLFNLVMDRAIVKLSA
NIGYT-----YNGAIINCIAYTDDIILIAETKCGLSLIDALTSEL-ASFGLQTNIG-----KSSTISLV---PSGRQKK-
-----IKVITEPSSL--VSG---QFLSAIGVMDVWRYLGVDFRCNV-----LNGSEYGI---DANLRKLDRAP-LKPQQRLKMLC
VAIIPRYLHSLVL-----GRVNKTKLAG-----FDNLIRKY-----VRKWLYL
>R2A_Nv1
KRTAAGPDG-MTTTAWN SIDE-----CIKSLFNMI MYH---GQCPRRYL-DSRTVLIPKEP--GTMDPACFRPLSIASVALRHF
HRILANRIGEHGL-----LDTRQ-RAFIVADGVAENTSLL---SAMIK---EARMK-----IKGLYIAILDVKKAFDSVEHRSI
LDALRRKKLPLEMRNYIMWYRN-----SKTRLEVVK-----TKGRWIRPARGVRQGDPLSPLLFNCVMDAVLRLPE
NTGFL-----MGAEKIGALVFADDLVLLAETREGLQASLSRIEAGL-QEQGLEMMPR-----KCHTLALV---PSGKEKK-
-----IKVETHKFFT--VGN---QEITQLGHADQWKYLG VVYNSYG-----PIQVKINI---AGDLQRVTAAP-LKPQQRMAILG
MFLIPRFIHLVL-----GRTSNADVRK-----GDKIIRKT-----VRGWLRL
>R2-1_TCas
QISAPGSDQ-IPVAAVKTMSE-----LELAILFNII LFR---NVQPSAWG-VLRTTLVPKDG---DLRNPANWRPITISSALQRL
HRVLAARLSKLV-----LSSSQ-RGFTTIDGTLANALIL---HEYLQ---YRRQT-----GRTYXVSLDVRKAFD TVSHCSV
SRALGRFGIPSVIREYILATFGA-----QTTIKCS-----VTRTPRMLRGVRQGDPLSPVLFNLMVDELEKVE
KYEGGSL-----QSGERCAIMAFADDLILIAADRQDVPAMPDDVSTFL-ERRGMSV NPA-----KCRAL IAG---AVSGR---
-----SVVRTGSSYK--IHN---TPIPNVDALDAFYKLGLEFGHKGV-----ERPTIHNL---SVLNNLRRAP-LKPDQKCLFIR
QYVIPRLLYGMQN-----PQVTSRVLRE-----ADRLIRRH-----LKTYHYHL
>R2LcA
SSTAPGVGD-FSAKQLRSMSP-----RVLNKILNLLLS---ENLPNSFK-MHKTVLIPKID--DPKSPGDFRPITISPVLARLL
NKILAAARLSKLV-----ISQRQ-KAFLPVDGCGENIFLL---DYILR---SSKKS-----SKSVAMAVLDVKKAFDSVSHHSI
LRALNEAKCPINFINFVRNSYDG-----CTTKLTCCG-----TSFPDSVRMNRGVKQGDPLSPVLFNLIIDSARIKLPD
SIGYVI-----RDGLKINCLAYADDLILVASSRAGLKTLLNIVA EHL-SLRGLDLNAA-----KCHGLSII---ASGAKT-
-----TVSAAADSLD--LDG---QPIKNLGVLDWTYLGIPFSLHGR-----AEKVSPDL---TNLLNKLQKAP-LKLQKLYAVR
NFVIPRALHGLIL-----SKTNLKE LNT-----LDRAIRVF-----LRTL LYL

>R2L1
PSTAPGVDG-FSAQQLRSMTP-----RVLNKKILNLLLLC---ENLPNSFK-MHKTVLIPKIV---DPKSPGDFRPITISPVLARHL
NKILAARLSKLV-----ISQRQ-KAFLPVXGCGENIFLL---DYILX---NSKKK-----SKSVMAVLVDVKXAFDSVSHHSI
LRALNEAKCPVNLXNFVRNSYDG-----CTTKLTCGG-----TSSPDSVRMNRGVKQXXPLSPVLFNLIIIDS AIRKLPD
SIXYLI-----RDGLINCLAYADDLILVASTRAGLKTLNIIVAEHL-SLRGLDLNAA-----KCHGLSII---ASGKAKT-
-----TVVXALESLD-LDG---QPIKNLRVLDTWYLGIPFSLHGR-----AXKFSPDL---SNLLNKLQKAP-LKIQKLYAVR
NFIIIPRALHGLIL-----SRTNLKELNT-----LDRAIRVF-----IRTLHL
>R2La
SSTSPGPDG-VTARMLRSIPA-----RVLNKKLLNLLLF--EDLPAVFK-CHRTVLIPKID--NPTSPGEFRPITISSIVVRQL
NKIIAARVSEGV-----INPRQ-KAFRQIDGCAENVFLL---DFILR---DAKTK-----IKSLSLATVDIKKAFDSVSHHSI
FRAIRGARPENLVNYIQNSYSG-----CTTQISVGG-----SISASKIPMNRGVKQGDPLSPVLFNLVINEIIRKLPA
SIGYPI-----NSELINCIAIYADDLILVTNTREGLKLLGLLNEEL-PKRGLELNAS-----KCFGLSLT---ALGKLLK-
-----THLCTSDQLD-LHG---TLIKNLTAESWVYLGVPFISHGR-----SKSFSPDL---EALLNKLQKSP-LKLQKLFALR
VYLIPRLLHGLVL-----SRVAIGELKI-----MDKLILKH-----LRVWLRL
>R2Lc-B
TSTSPGPDG-VTARMLRSIPA-----RVLNKKLLNLLLF--EDLPAVFK-CHRTVLIPKVD--NPALPGEFRPITISSIIVRQL
NKIIAARVSEGV-----INPRQ-KAFRQIDGCAENVFLL---DFILR---DAKTK-----IKSLSLATVDIKKAFDSVSHHSI
FRAIRGARPENLVNYIQNSYSG-----CTTQISVGG-----SISTTKILMNRGVKQGDPLSPVLFNLVINEIIRKLPA
SIGYPI-----NSELINCIAIYADDLILVANTREGLKLLNLLNEEL-PKRGLELNAS-----KCFGLSLT---ALGKLLK-
-----THLCTSDQLD-LHG---TLIKNLTAESWVYLGVPFISHGR-----SKSFSPDL---EALLNKLQKSP-LKLQKLFALR
VYLIPRLLHGLVL-----SRVAIGELKI-----MDKLILKH-----LRVWLRL
>R2NS-1_SMed
LKTSSGPDN-ISTEVLREIPV-----LVLVKLFNLIILL---SHLPSEFK-SSRTTLIPKVE---TPKDPGDYRPISVSSVVRAL
NKILASRVSNNGK-----GAHAQ-KGFKALDGCLENTVLL---NCILG---DAKIN-----NKSIALSFIDMKKAFDSVNHDSI
LRAATIAGYPKLLGLGYIKESYNG-----ADTEVEK-----IKATFKRGVKQGDPLSPVLFNNIVELAIIKKAHE
SGIGYR-----MNGTVFPIIMAYADDIILLSEKEGLQDLDIVLTEL-RHNGLEANAD-----KCASI IAK---KDGKQK-
-----KWVSSDSVL---AAG---KTMPCMNANSMYKYLGIYFGPLGI-----TTERLTKIY---SDQLYNIGIAP-LKPQQRLMIN
DFLLPGILHEAVL-----GNTNVGELKD-----LDMKTRVA-----IRKWLHL
>R2-1_PPap
PGSAAGIDR-ISVQQFQRCVP-----HVRVLLFNVLVV---GHLPGRMS-CARTVFLPKVE---GSSDPKDYRPISITSVITRQF
HKILAARLTSMHA-----WDERQ-AGFLPVDGCGENLAIL---NELIR---FSRVN-----RRELHLASLDISKAFDMVPRQAI
INSVAQLGAPQNLVEYLKGLYAN-----NQTTLEYGG-----SELYCRVKRGVRQGDPLSPVLFNLVMEALVRLDK
KLSFS-----LYGVSUNGLAYADDVILVASTSGGLQKNTESFLGAL-REIGLDLNLIA-----KCKSLSLK---PSGRDKR-
-----CKVLSSESLS-IGG---TSVPQVDLVGFWRYLGIWFSGPRV-----VSPEQLSM---GVYLERISKAP-LKPQQRIRILV
DYLLPKYTHGSVL-----GRYTRKTYKA-----MDAQIRSY-----VRKWLHL
>R2-2_Tcas
NGAAPGPDG-IAVSVWNKLP-----EAAALLFNVLVLLG---RCLPAELT-RTRTVFIPKTD---APRTPADYRPIISIASVVARHF
HRVLSARVQRI PDLF---TKYQR-GFLSGVDGIADNLSVL---DTMLT---MSRR-----CKHLHLAALDVSKAFDTVSHFAI
VRACRSIFG-----SAETVLEEG-----GRRHFVQVRXGVQXDPLSPVLFNLVLDRAKRLST
DVGFRL-----TDATKVITALAFADDVVLCAATTARGLQTNLDVLEAEL-RLAGLLNPN-----KCQALSLV---ASGRDHK-
-----VKLVTKPTFFK---VGQ---NTIHQVDASSIWKYLGIQFRSGSM-----CGCGSEGV---AAGLKRITCAP-LKPQQRMHLR
VFFLPKFYHAWTF-----GRLNAGVLRR-----LDVVVVRTS-----VRTWLRL
>R2-1_PBa
NGTAPGLDG-ITPRAWNAVVP-----GLRALVFNLLLLA---ETAPLSIT-TTRTVFLEKGGM-SDRPGPSEYRPLSIGSVIIRHL
HKILAKRLAALDI-----FDARQ-RGFRPVDGVCENITVL---SSVLG---DARR-----CKSLHVACVDLSKAFDTVSHAAI
HRTLEELGLPREFRDYVRAIYAE-----ARTVLQPTG-----RQMSPIHVGRGVQGDPLSPVLFNLVVDRAIGLSE
DVGYR-----LESRLINALGYADDIVLLSSTKIGLQENLTRLHAFA-LQNGLTINAN-----KTGVLSMV---ASGRDKK-
-----VKIDMTPYFT---VGG---ALIPQRSVDVWYTLGGMYPQAR-----EYASVPPL---ANSIRHITKAP-LKPQQRLRLR
DCLLPRYHRLI-----GTITSKILKE-----MDVLLRAA-----VRRWLRL
>R28_MR
PQSAPGPDG-IGVRQWRAVPP-----SVRALLYNIVLAT---GGFSPALL-TSRTVFVPKKSG--DPDSPGDYRPISVTSVVVRQL
HKILANRLRASGL-----VDL-RQRCFDDGCGENIAAL---AAVIH---DSRSH-----LRELHVASLDIAKAFDSVSHQAI
ARVLTTLGVPCELVSVYTTMYAR-----SSTMFEVGR-----QRSELPVGRGVQGDPLSPILFCLVVDLSILRTVPP
DVGYD-----LGSRRLNALAYADDFLLFAASVWGMQKTLGLVEQRA-GEYGLTFNAQ-----KCSVLSLV---PSGDKK-
-----MKVITPTPLFH-LGRQ---AFIPQITTAEWRYLGVDFRSTG-----PKKSRI DL---TTYLDRIGKAP-LKPQQRLKLLR
CFLLPRLYHVLVL-----GRTTLGALRA-----LDVLTRAA-----VRKWLRL
>R2-7_MR
LDTAVGPDG-VTARQWRAVLP-----AVRALLYNIILKR---GSFPASML-ESRTVFPLPKKQ---HSVNPADFRPISIASVVVRQL
HKILANRLRRTNL-----VDE-RQRCMDGCAENITVL---ASLLD---DARHG-----LKLHLVSLDCAKAFDSVSHHAI
DATLKECGLPAGFVQYISRTYSD-----SSTRLEVR-----NRSEPIKTNRGVQGDPLSTLIFCLCFDRVARTLSP
HIGYD-----LNNTRISTLLYADDAFLVSTTAPGMNILLRSVEESA-GEVGLSFNTS-----KCSALSLI---PSGKEKK-
-----MKVGTPTPTFFK---TSQ---GFIQTITPSQEWRYLGVDFOYSG-----PKKASRSL---KIELERISKAP-LKPQQRLRLR
VYLLPRYHHLVL-----SRTTLGHLRG-----LDLQVRAA-----VRRWLSL
>R2-1_IS
VNSAAGPDG-FSARLLKSVA-----LLLRVMVNLLLV---RRVPAALR-DARTTFIPKVP---DAVDPSQFRPITVASVLVRQL
HKILANRLRAEIP-----LNFQ-RQFQVVDGCAENIWL---STALN---EART-----RRPLHMASVDLTKAFDRVTTDAI
LRGARRAGLSGEFIGYKELYTT-----SRTLLQFQG-----ESLLVEPTTGVRQGDPLSPILFNLVLDEYLSLSDP
DISFV-----SGDLRLDAMAFADDLIVFASTPAGLQDRDLALVEFF-DPRGLRVNVK-----KSF TSLQ---PGRDKK-
-----KVVCQDQFT---IGG---TPLPASKVATPWRYLGMTFTPQGS-----INKGTSEQL---DLLLTRTSKAP-LKPQQRLVLRL
NYLLPRLYHRLVL-----GPWSAALLLK-----MDTTIRGA-----IRRWMDL
>R2-1_Rmi
SSSAAGPDG-FAARELRKVPP-----VILQVLLNLLLLL---KRLPLFLT-QARTIFIPKVP---GASTASQHRPISISHVLLRL
HKIYFRLLADLD-----LDLQ-RAFLPVDGCAENILL---ATIID---EARKS-----LRPLSLASLDIAKAFDRVVLPAI
LRALRRKGISEDFISYIEDFYQN-----AVTVLTFGG-----KSLVVHPTVGVRQGDPLSPVLFNLVIDEFLAELDP
QLAFT-----SEGKVSAMAFADDIILTATHWGLKQQIDRLNSFL-GARGLKINAA-----KSTTLVIE---PSGWQKR-
-----SKIRTDIDFF---VNG---ERLATTNCTSTWRYLGVHGVKGL-----EKGLVRRQL---AILLERVSKAP-LKPQQRLVLRL
FYLLPRLYHRLVL-----GPISAKTLLT-----IDRVVRS-----VRRWLAL
>R2_FA
MTTSPGPDG-ITVRQLYLVE-----QLLVRIILNLLMAC---GKMPDSFL-ESKTTLIPKPP---NSTEPGDFRPITVQSVLVRQL
NKILAARVAQHPI-----LDERQ-RGFRPVDGVAHNIFEL---DMILR---CHRSE-----FRDLRLASLDIAKAFDSITHNTI
EDTMEVRGFPKPMINYIMACYRR-----SKTRFTFNG-----WISDVTKPTCGVKQGDPLSPILFNLVMDRMIRKLKPK
EVGVN-----VGSKHYNGLTFADDLLLFATTPPEGLQSSDIIHVLFL-LECGLLINKQ-----KSFVLTVK---AYPKLKK-
-----TAVIVTEKYM---LDR---HILPAIDREKLFHYLGVPFTAEGR-----CRDDTIAHL---KRKIDVLTKAP-LKPQQRLFALR
VVILPSCYHILTL-----GGSNLSLLKK-----IDLMVRAA-----GRKWCC
>R2-5_MR
MTTAPGPDG-LTARQIRAVPL-----EVLVRIFNIFLVC---GRLPKHLL-ESRTILIPKDK---NASEPGDFRPITISSVMTRTY
HKVIARRFAGSIE-----LDKRQ-KAFXPDVGCAENIFDL---DMVLR---YHRES-----FKSIFMASTDVAKAFDSVSHRAM
YDTLRSKGVPAPLVEYVRDYER-----STTRLTSGD-----WQSDLIRCGVKQGDPLPPIIFNMIDRLKLKLP
EIGVD-----VGESHFNALAFADDLLFMASSTKGLQTCLDLASEYL-LKCGLRVNAX-----KSFTVALR---NVPHVKK-
-----SXVDGKVRFR---CLG---HEMPSLKTREDQWRYLGVPFTPEGR-----SSARADEQL---KQTLGKLTSAF-LKPQQRLFALR
VVVLXGLHHLLSL-----GNVTLSLLRK-----VDKLVRAA-----VRKWLDL

>R2_Dan
LSSSPGPDG-ITPKTARSVPE-----GIMLRIMNLILWC--GNLPYSIR-LARTIFIPKKA--TANQPQDYRPISVPSVIVRQL
NAILASRLSAAIN-----WDTRQ-RGFLPTDGCADNTTIV--DLVLR-----EHHKR-----FKSCYIGTLDVSKAFDAVAHEAV
YNTLASYGAPKGFINYLRKAYEG-----GGTMLAGNG-----WVSEAFIPARGVKQGDPLSPILFNLVIDRLLRSLPS
EIGAK-----VGNAMTNAAAFADDIVLFAETPMGLQKLLDTTVCFL-SSVGLTLNTD-----KCFTVSIK---GQAKQK--
-----CTVVERRSFL--IGG---RECPSLKRTDEWKYLGKFTAEGR-----ARYDPAEDL---GPKLLRLTRAP-LKPQQKLFALR
TVLIPQLYHKLTL-----GSVTIGVLKK-----FDKLVRYT-----ARKWLGL
>R2_DS1
LSSSPGPDG-ITPKSAREVPS-----GIMLRIMNLILWC--GNLPHSIR-LARTVFIKTV---TAKRPQDFRPISVPSVLVRQL
NAILATRLNSSIN-----WDPRQ-RGFLPTDGCADNATIV--DLVLR---HSHKH-----FRSCYIANLDVSKAFDSLSHASI
YDTLRAYGAPKGFVDYVQNTYEG-----GGTSLNGDG-----WSSEEFVPARGVKQGDPLSPILFNLVMDRLLRNLPS
EIGAK-----VGNAITNAAAFADDLVLFAETRMGLQVLDDKTDLFL-SLVGLKLNAD-----KCFTVGIK---GQPKQK--
-----CTVLEAQSFY--VGS---REIPSLKRTDEWKYLGINFATGR-----VRCNPAEDI---GPKLQRLTKAP-LKPQQRMFALR
TVLIPQLYHKLAL-----GSVAIGVLRK-----TDKLIRY---VRRWLNL
>R2B_DM
LTSSPGPDG-ITSQTSAPI-----GIMLRIVNLILWC--GDLVPFPR-MARTIFIPKTV---RANRPQDFRPISVPSIVVRQL
NAILASRLTAAVS-----WDPRQ-RGFLPTDGCADNATIV--DLVLR---DHHKR-----YASCYIATLDVSKAFDSVAHDAV
FNTVTAYGAPKSFVDYVRRYSG-----GGTYFNNGD-----WRSEEFVPARGVKQGDPLSPVLFNLIIDRLLRSLPK
DIGVH-----VGNAKVNACAFADDLMLFASTPKGLQELNLTTVKFL-SSVGLTLNAD-----KCFTISIK---GQPKQK--
-----VTVVEQRTFC--IG---RARVQLKRSEEWKYLGIHFTADGR-----ARYNPSEDI---GPKLERLMQSP-LKPQQKLFALR
TVLVLPQLYHKLTL-----GSVALGVLRK-----CDKLVRSF-----ARKLLGL
>R2_DPe
LTKSPGPDG-ITPRTVRSIPS-----GVMLRIMNLILWC--GKLPVSIR-QARTIFIPKVG--NASRPQDFRPI TVQSVVMVRIL
NAILASRLTSSVD-----WDPRQ-RGFLPTDGCADNTTIV--DLILR---DHHKR-----CKSLYIATLDISKAFDSVSHAAY
SATLTAYGAPKEFVDYVQNSYEV-----CGTTLNGDG-----WRSEEFIPARGVVRQGDPLSPIIFNLIIDQLLRSPYN
EIGAT-----IGDHTTNAAAFADDIVLFAETRLGLQTMLDTTVDL-SSVGLTLNSD-----KCFTVGIK---GQPKQK--
-----CTVVIPEFTR--IGS---RSCPALKRTDEWKYLGITFTTAQGR-----TRYSPADDL---GPKLLRLTRSP-LKPQQKLFALR
TVLIPQLYHKLTL-----GSVMIGVLRK-----CDILVRST-----VRKWLGL
>R2_BM
WRTSPGPDG-IRSGQWRAVP-----HLKAEMFNAMMAR---GEIPEILR-QCRTVFVPKVE---RPGGPGEYRPIASIASIPLRHF
HSILARRLLACCP-----PDARQ-RGFICADGTLENSAVL---DAVLG---DSRKK-----LRECHVAVLDFAKAFDTPVSHAL
VELLRLRGMPEQFCGYIAHLYDT-----ASTTLAVNN-----EMSSPVKVGVRQGDPLSPILFNVVMDLILASLPE
RVGYR-----LEMEIVSALAYADDLVLLAGSKVGMQESISAVDCVG-RQMGLRLNCR-----KSAVLSMI---PDGHRKK--
-----HHYLTERTFN--IGG---KPLRQVSCVERWRYLGVDFEASG-----CVTLEHSI---SSALNNISRAP-LKPQQRLEILR
AHLIPRFQHG FVL-----GNISDDRLRM-----LDVQIRKA-----VGQWLRL
>R2C_Ngi
QNTAAGIDG-LTVGDLKGVSR-----EMLARIFNLFMWC--GKLPHELC-ASRTILLPKPK---GAKVPGEFRPITVTSVLIRTF
HKVLAERLKVVP-----LDPRQ-RGFRESDGCAENVMLL---DMTIR---YHHER-----RRKMFLALLDMAKAFDSVSFESM
REVLTTKGIPTPFIEYFMTHLED-----SFTVLQHGN-----WQSGKIHPTCGVKQGDPLSPPIFNFIIMDEMLKRLPK
EIGVN-----LDGLFVNAMAFADDLSLVANTEQGLQILIDEATSFL-GLCGLRANPN-----KCVTLAIK---TIPKEKK--
-----TAIDPSSHFR--IGN---AVIPSLKRTDEWVYLGKIFNSNGR-----LISDAKPKL---IKDLELTKAP-LKPQQRLWALK
VIVIPGILYRGTL-----GSSTAGYLR-----LDCVIRAY-----VRRWLRL
>R2_AM
SSGATGPDG-FSVRSLKCTPS-----RVLAKVFNLFLE--EKLPAFLM-TSRTVLVPKVK---EPKAPTDYRPISVSSTLVRLF
HKILARRLTLASG-----LDSRQ-RGFVPVDGCAENLVVL---ESAIR---SAKNY-----KRSLFVASMIDIKNAFGSVAHEAI
FEALSKSGAPDSFVTYVRNCYDG-----FASVVKLG-----RDTAQTTVRQGVQGDPLSPILFNLVIDQIIRSLPE
TVGVQL-----DANTKLNSMAFADDLILLSSSEAGMRMLGVLAGVS-SKFGLIFHPG-----KCKYLAMI---WAGKQKK--
-----MKIATDLSFE--IGG---GFMTVPVGTETWKYLGAYLGQIG-----IQPARLSL---QTFLERIAKSP-LKPQQKLYLIR
VHLLPKLIYPLVM-----APIRASMLNK-----LDRMVRVA-----LTGKDGI
>R2Ci-D
VASASGPDG-VSVSGMTKIGA-----RVLCMFLNVWQFT---GRTPRWTK-ENRTTLIAKSAS--AAEDVGDWRPITIGSHVVRLY
AKLLSRRLGSCVQ-----LNLQ-RAFRDVQGAENVMLL---SGMIR---DAKAR-----SRDLNLVFLDLAKAFDTPVSHSI
VKALRRQVPEKFVRVYQDLYDG-----AVTTVSVGG-----RATPQLVVRKGVKQGCPLSPLLFNLVLDELIDELSS
SFGYTL-----DDGSKLSVMAFADDLVLSSGSLAGRLKLIETTQQL-LRCGMGLNVQ-----NCTSLGWK---SMVGKQ--
-----VRLRTEPFVR--VGD---SELACLGPNSTCRYLGIHFGMVGS-----CRIRREI---RESLLRLASSA-LKPEQKVFMRL
SFLIPRWYSVTL-----TRTVSFLSW-----IDRVVRMR-----VRAILHA
>R2-1_BTe
KKAAGPDG-LQRDHLTIPGL-----PIIMAKIYNILVYC---SYFPSAWK-ENRTTLIPKINK--PCSLVENWRPITISPIGRIF
SSIIDGRIRRGTV-----LNMQR-KGFTSENGCKINIELL---NSALN---YSKR-----NSGGIFTIVDISKFDTVPFSAI
KPCLAKKGPALIVDLIDEMYKN-----VKTTIKTKD-----GGVEIMIRRGVKQGDPLSPLLFNLCLPLELEIEE
QASGINV-----SEHRKVSVLAFADDIVLLGADAREAQHQINVLTDYL-QSLMMNLSIE-----KCQTFEVV---AKKD--
-----TWFIKEPGLK--IGN---QIMPTVPDEAFKYLGAIGPWKGV-----HCGVIVPEL---LSVVKVRKLS-LKPGQKVELLT
KYIFPRYIYHLLV-----SPPSDTVLKL-----LDSEVRQE-----VKTILHL
>R2-2_MR
PKSAAGPDG-LMKRDVIKSGH-----LYILYPMFNLIVAA--GRQPDARW-KNITKLLNKEGK--DPSLPGSYRPIITISPLFSRIF
WGLIDQQLRLRIN-----ITPRQ-KGFVPEMGCFLNVNLL---NEIIR---IAKR-----KQGIVITQVDISRAFDTVPFSAI
LNALNAKGLPKVQVQIMDSYSN-----ISTQIQYS-----STFDISIKRGVKQGDPLSPILFNIIVMESLILKLES
MPGFKI-----NDRTNLSLAFADDLMLFADNVEDARAQNLNLCQFL-DSVDMDISID-----KCAAFQII---TSKD--
-----SWYIIDPHLT--VAQ---GSIAFLGPDTPLSYLGAKISPVWVG---KTDYSIQGL---KACVGRVQSLA-LKPHQKVELMA
RHIIPHYLYGLIL-----SIPSISVIRQ-----LDQCVRVA-----VKEYLHL
>R2_KF
KDYAPGPDG-VTKLKVQSMGA-----YPSLLAKVYNLMLT--GYFSSCWK-EHKTSLIPKDRG--SPMDVSNWRPITIGSLLSRIY
TGLIERRLRTVSD-----IHQRQ-VGFMPVNGCAANLFIF--DECIR---QAKK-----EGTIVGSLIDVAKAFDTPVPHAI
LRLSSQGVDEHTMAHIRMYSG-----IRTRINGKG-----SDIPLVRGVKQGDPLSPMLFNMVMDPLIRDLQR
KGFR-----IGGHEIGALAFADDIVLLADSIDGAQDHVDQVGRYM-NKLGMTLNPR-----KSSSFLT---AMRK--
-----TWICRDPLGS--IGE---TKVPGARPSALKYLGVNYTLSEGL-----ESGALIDKL---MQAVNRARGLA-LKPLQKVNLI
ERIIKFLYGIIL-----GGPSLTRLHA-----ADKCVRMA-----VKEILHL
>R2B_Nv1
NDSAAGPDG-VTKDDLGRGV-----SIALSKLFNSILLA--GYYPKAWR-ENRTTLIPKPEK--DPADVKNWRPITISSMVSRYV
SGLLDQVRRAVIK-----CQDRQ-KGFTTEENGCFNSIQLL---DDAVS---NAK-----KAGGVITILDVSKAFDTPVPHAI
QGCKLEKGIPEYVAAYISSMYRD-----CSTAIRTS-----GDVKIGMKRGVKQGDPLSPILFNLVLEPLERLQ
TSGVE-----IEGMNLSCAAFADDIVCFANTAPEAGRQLRMVADYL-GRLDMSLSVS-----KCIAVEV---PHRK--
-----TWYTKNPGLE--VNG---NAVPSISPSETFKYLGAKVSPWKGL---LEGFESDAF---REVISRVRQLP-LKPMQKVDLLQ
MYIFPRYTYGLIT-----SPPAKAVLKT-----IDRIIRTR-----IKEILHL
>R2Ame1
SDTAAGADQ- IKKFHLRKKGA-----LHVFAKL CNLLMLH---RIYPAQWK-TNRTTLIPKPGK--SAAEVENWRPITIGSLLGRIY
SAMIDRKLRSIK-----QHIRQ-KGFTQEDGCKNNIAIL---SSALT---KMKE-----DSGGIITIIDISKAFDTPVPHGEI
SQSLMKNKGVSPICEYIQKMYIG-----CKTIIYCRD-----KKTLPVDILRGVKQGDPLSPLLFNLIIDPIIGTLDE
TTEGK-----LENENISVLAFAADDLVLAKDKETADKQNRLINEYL-DDLKMKVSAE-----KCTTFEIK---RQNK--
-----TWFLGDPQLT--LGQ---QRIPYADPEAAIKYLGTFNFPWRG-----LCKTSIKEI---IDAARTVKQLK-LKPHQKINLIR
TYLLPRYIHLKVA-----NPPPLGTLDL-----IDKELKTI-----IKEILHL

>R2_Rm_Ribo
NASAPGPDG-VKKCHVATRAK-----QAVLSALFNTVLLT--GILPAEWS-TNRTTMIPKEGK--DASLLANWRPLTISSVLSRIF
WGCVDTMRMRVVR-----LTPRQ-KGFVAEAGCFNNVLL-----DSVLR-----HAKC-----GGGVAVVQLDISKAFDTPHCTI
ATALLNKGLPPFLANLVSRAVVG-----QRTHLNVRG-----EKVEVRNPLVIVKQGDPLSPMLFNLIMEPMINELES
KPGYRI-----DEETQISSLVFADDLILLASDAPKAQVLLSTVHRYL-CNLGMSLAAS-----KSFAFQVT---RTQDSWCL
VDPLGLKLSKGDEERC---HNL---EGIPFAGVPDRRLRYLGVSVSPWFGI-----DIRETRANL-----TEVLHKLCLRLA-LKPWQKHLLI
THLVPHYLPPELVA-----AAPALTTLRE-----LDQELRVV-----VKKIFHL
>R2_Bg_Ribo
STTAPGPDG-INIQAVRSAPA-----QAVLSTFYSLILL--GRPPAAWR-ENRSVLIPKEGY--DVRLISNYRPLTIGSILSRIF
WGIIDRRRLRELLK-----IHRYQ-KGFTTEPGCYQNVRIF-----SEVLR---QAKS-----ARGLVAVQLDISKAFDTPHAAI
ATVLRQKGLPPYFADMVRRSYEG-----AYTSIRVRD-----HRIQLELKRGVKQGDPLSPMLFNLIMEPLLNKLES
LGGVTL-----ADGSQLACLAFADDLILLADNRERARELLETVEEFL-DGLGMKIWAP-----KSAFEIV---PTKDS---
-----WCVVDPGLRL--RQG---GAITYAGPDHSLKYLGVKVPWVG---DVSDLRTHF---SKTLEDTRKLP-LKPHQKLHLLK
TYLIPHFTHRLVS-----SLPSIAELRA-----LDLEIRGC-----VKQILHL
>R2_RU
PSSAPGLDG-VGKIHLVGKGI-----TLVLAKLYNLLFLT--GGYPECWK-RNRTVFIPIKIGK--DLSEVGGWRPLTIGSLLARMY
SAFLERRIRRVTS-----LSSSQ-RGFTNIQGCCHVNLTL--KEGIR---QAKV-----KNGGVIVSVDIEKAFDTPHSAVI
FSRLASQGVPLLRKIIISNMYK-----VYTVIEGQ-----CIPIKRGVKQGDPLSPMLFNLIAIDPVLRSLEE
FQGGPL-----LGNSAIKILAFDDDIILGASSAGQAQQMVMDLIGL-TSCGLGVSHR-----KCGFQIV---NKNK---
-----TWAIVDPMIT--LNG---SSLPFGSPEDRLPYLGVDTNPWDRK-----SRDAGQRL---ISAAGRGSQLS-LKPQQKINLIT
TFLLPKFLYLILIE-----DPPSPAYLKS-----IDHDLRQI-----YKNILHL
>R2_RL
PSSAPGLDG-VRKIHLVGKGI-----TLVLVKLYNLLFLT--GGYPECWK-RNRTVFIPIKIGK--DLSEVGGWRPLTIGSLLARMY
SAFLERRIRRVTS-----LSLSQ-RGFTNIQGCCHVNLTL--KEGIR---QAKV-----KNGGVIVSVDIEKAFDTPHSAVI
FSRLASQGVPLLRKIIISNMYK-----VYTVIEGQ-----CIPIKRGVKQGDPLSPMLFNLIAIDPVLRSLEE
FQGGPL-----LGNSAIKILAFADDIILGASSAGQAQQMVMDLIGL-TSCGLGVSHR-----KCGFQIV---NKNK---
-----TWTIVDPMIT--LNG---SSLPFGSPEDRLPYLGVDTNPWDRK-----SRDAGQRL---ISAAGRGSQLS-LKPQQKINLIT
AFLLPKFLYLILIE-----DPPSPAYLKS-----IDHDLRQI-----YKNILHL
>R2Dr
NASTPGPDG-VGKRDISNWDP-----ECETTLQLFNMWFT--GVIPSRLK-KSRTVLLPKSSDPGAEMEIGNWRPITIGSMVLRIF
TRVINTRLTBACP-----LHPRQ-RGFRSPGCSSENLEVL---ECLLR---HSKEK-----RSQ LAVVFVDFAQAFDTPVSHHEM
LSVLEQMNVDPHMVNLIREIYTN-----SCTSVELGR-----KEGPDIPVRVGVKQGDPLSPMLFNLALDPLIQSLER
TGKGCE-----AEGHKVTALAFADDLALVAGSWEGMAHNALVDFEC-LTTGLTVQPK-----KCHSFMVR---PCRG---
-----FTVNDPCPWV--LGG---KALQLTNIENSIKYLGVKNPWAGI-----EKPDLTVAL---DRWCKRIGKSL-LKPSQKVYILN
QFAIPRLFYLAH-----GGAGDVMLQN-----LDGTIRKA-----VKKWLHL
>R2-1_GA
NRSSPGPDG-ITKVALSKWD-----EGIKLAHMYSTWLVS--AGIPKVF-KCRTTLIPKTGDVSLHGDVGQWRPITIASVLRLY
SRILTERMTVACP-----SHPRQ-RGFIASPGCSSENMLL---EGCMS---LSKAG-----NGSLAVVFVDFAQAFDTPVSHHEM
LSVLVQKGLDQHVMVELIKDSYEN-----SVTKVHCQE-----GCSTDIAMKVGKQGDSPMLFNLALDPLIQQLER
EAGLGF-----VNGKSITAMAFADDLAIIVSDSWEGMRANDILVDFC-ELTGMRTQPS-----KCHGFLIE---KSGRS--
-----YKVNRCPEWL--LND---TALHMGPKESIKYLGQVNPWTGI-----FAEDTVAKL---RQWVVAISKTP-LRPLDKVSLLC
QFAVPRVIFVADH-----CMLSAKALTE-----MDRSIRQA-----VKRWLHL
>R2-1_Ssa
NNTAAGPDG-ITKPALLEWD-----TGAKLAAIFSIWLTS--GTLPGPFK-KCRTTLIPKTDDPILLTQVAGWRPLTIGSVVLRLY
SRILTHRLERACP-----INPRQ-RGFISSPGCSSENLMIL---GGLIK---RSWAK-----GERLAVVLVDFAFAFDTSVSHSHI
LETLRQGLDEHIIGIVGDSYTD-----VTTITIVSG-----EQSPPIDMRVGVKQGDPMSPMLFNLALDPMIDTLER
YGLGYR-----MGEQQTALAFADDLVLVSDSWEGMACNIRILEEFC-RLTGLRIQPR-----KCHGFLIQ---KIQRA---
-----RSVNLCKPWI--VCG---EELHMGPEESVSYLGKMPSPWHGI-----MEPDQVERL---CNWISSIGRSP-LKPSQKVRMLN
VYAAPRMTYQADH-----GGLGPIVLNV-----LDGMIRKA-----VKVWLHL
>R201-A
NGTAPGPD-ISKALLDWD-----RGEQLARLYTTWLIG--GVIPRVFK-ECRTKLLPKSSDPVELQDIGGWRPVTIGSMVTRLF
SRILTMLTRACP-----INPRQ-RGFIASPGCSSENMLL---DEIVR---RSRRD-----GGPLAVVFVDFAFAFDTSVSHSHI
LCVLEEGGLDRHVIGLIRNSYVD-----CVTRVGCVE-----GMTPPPIQMKVGKQGDPMSPMLFNLALDPLIKLET
AGTGLK-----WGDLSIATLAFADDLVLVSDSEEGMGRSLGILEKFC-QLTGLRVQPR-----KCHGFFMD---KG-----
-----VVNCGGTWE--ICG---SPIHMIPPGESVRYLGQVGPGRGV-----MEPDLIPTV---HTWIERITEAP-LKPSQRMVRVN
SFALPRIIYQADL-----RKVTVTKLAQ-----IDGIVRKA-----VKKWLHL
>R2-1_Gav
SKSAPGPDK-LTLRDLRRAD-----EGDALAELFSLWLIT--GTVPDGLK-ECRSVLIPKTVDRKLGQGNWRPITIGSIVLRIF
SRVLITARLAAACP-----INPRQ-RGFIAPGCAENLKL---ELLRL---KRKR-----RQPLGVVFVDLARAFAFDTSVSHSHI
SWVLKAGVDEHIVNLIEDSYQK-----VTTRVQVFN-----GVTPPISIKTVGVKQGDPMSPMLFNLALDPLIKLET
DGQGVK-----VGSASLTTLAFADDLVLVSDSWEGMLKNISILEDFC-NLTGLRVQPK-----KCQGFFLN---PTCDS---
-----FTVNNCEAWK--IAG---REITMLGPGESTRYLGLNVGPWVGI-----DKPDLGTQL---SSWLERIGTAP-LKPMQKLSLLV
QYAIPLNLYQADY-----AGIGRVALEA-----LDSMNRK-----VKEWFHL
>R2-1_ZA
KGSAPGPDG-IALGDIKMDP-----GYSRTAELFNLWLTA--GDIPDMVR-GCRTVLIPKSTTPERLKDINNWRPITIGSILLRIF
SRIIITARMTKACP-----LNPRQ-RGFIAPGCAENLKL---QSIIR---TAKNE-----HKPLGVVFVDIAKAFDTSVSHQHI
IHVLQQRVRDPHIVGLVNNMYKD-----ISTYVTTKK-----NHTDKIQIRVGVKQGDPLSPMLFNLALDPLCKLEE
SGKGFH-----RGQSSITAMAFADDLVLVSDSWENMNKNISILETFC-NLTGLKTQGQ-----KCHGFYIK---PTKDS---
-----YTINNCPAWT--ING---TPLNMNPGESEKYLGLQIDPWTG---AKYDLSTKL---KIWLESIDRAP-LKPLQKLDILK
TYTIPRLTYLADH-----SEMKAGALEA-----LDQQIRTA-----VKDWLHL
>R2-1_TG
KGSAPGPDG-ITLGDVVKMDP-----EFSRTMEIFNLWLT--GKIPDMVR-GCRTVLIPKSSKPDRLKDINNWRPITIGSILLRIF
SRIVTARLSKACP-----LNPRQ-RGFIRAAGCSSENKL---QTIIW---SAKRE-----HRPLGVVFVDIAKAFDTSVSHQHI
IHALQQREVDPHIVGLVSNMYEN-----ISTYITTKR-----NHTDKIQIRVGVKQGDPMSPMLFNLALDPLCKLEE
SGKGYH-----RGQSSITAMAFADDLVLVSDSWENMNNTNISILETFC-NLTGLKTQGQ-----KCHGFYIK---PTKDS---
-----YTINDCAAWT--ING---TPLNMIDPGSEKYLGLQFDPWIGI-----ARSGLSTKL---DFWLQRIDQAP-LKPLQKTDILK
TYTIPRLIYIADH-----SEVKTALLET-----LDQKIRTA-----VKEWLHL
>R2-1_Gfo
KGSAPGPDG-IALGDIRKMDP-----EYTRTAELFNLWLTS--GEIPDMVR-GCRTVLIPKSSKPERLKDINNWRPITIGSILLRIF
SRIIITARLTACAP-----LNPRQ-RSFIISAAGCSSENKL---QTIIR---TAKNE-----HRPLGVVFVDIAKAFDTSVSHQHI
IHVLQRRVRDPHIIIGLVKNMYKD-----ISTVIITKK-----NTYTDKIQIQVGVKQGDPLSPMLFNLALDPLCKLEE
HGKGFH-----RGQSSITAMAFADDLVLVSDSWEDMNANIKILETFC-DLTGLKTQGQ-----KCHGFYIK---PTKDS---
-----YTVNNCAAWT--ING---TPLNMNPGESEKYLGLQFDPWVGI-----AKTSLPEKL---DFWLERIDRAP-LKPFQKLDILK
TYTIPRLTYVADH-----SEMKAGALEA-----LDRTIRSA-----VKDWLHL
>R2NS1_CGi
KDSAAGPDE-IELKTVMAKDP-----KGXILVNLFSFLYR---KKVPEIFK-GNRSILLPKGND--GLEDVNNWRPLTISSSVLRIF
TSLLARVRVLDSCA-----LNPRQ-RGLIAAGCSSENSFL---SEMIN---HAKKE-----RRQLCVTFDLAKAFDTSVSHKH
IAGLRRFGSPHEFIDIVADLYNG-----ASTVFQTD-----GQTGEIPMTRGVKQGDPLSPMLFNLALDPLLEVIGR
QNNGY-KFGP-----EESDRIESLCYADDNALMTESPDENMENLALVEKFC-CETGMRLNIK-----KSATFCIT---PCGSRSY-
-----TWNTTKTKVA--IKG---ERVPIPPDGCMKYLGSKMSPVWTK-----IRKDIVAQL---EGMVESIGGAH-LKPRQKLVLLN
HYALVRLTYALTQ-----DAYPXXVLGK-----LDLIVRAA-----IRRWAKL

>NeSL-1_TV
HLSAHGLDG-IPNSVYMLFPVS-----AAKFLSILFRSIIIS--GHIPDCWK-LSKTVMLFKKD---DPSLAKNWRPISLGITSCTYRIF
MTLVNKAQMIPM-----PHAMQ-KGFVRGATLSEHIAVA---NEVLC-----QSTRT-----QSEMFQTAIDFTNAFGTVPHQLI
FDSLEAKKVPDSIINLLKDLKYG-----ARTAIYTRH-----AHSEIVPVRGVIQGCPLSPILFNCCLDPLLYAVQR
RHPEDGYRFQD---KAGQYSIAIQAYADDVLVISPTHEGMQRILNTVDEFQ-KIAKLKVAPQ-----KCVTLAKT---STA-----
-----IQPFR---IGP---DEIPIKTSMDNITYLGIPISGTTKTSRF---AAATGILEKV---KAQIRVVVFASH-LALSQKIIALR
VFILPQLDFYMFH-----NVFRVNDLKA-----TDQMIRGL-----IDKEAPT
>Utopia-1_ACa
NGSAPGIDG-IPYEAYKRTKL-----DATLAHVFEVVRNL--ARLPARWD-VARTVLLYKKG---DPNDTGNWRPISLQVTIYKIF
TAALSKRLISWAGKHNT--FSASQ-KGFLPAEGCHEHAFVL---RSVLD---DARRH-----KQNVYLAWYDLRNFAGSVSHDLI
AWCAAMLGLPRYLRLDAIGAIRH-----SALFVQVGD-----QETTVIPMRGCVKQGCPLSPILFNLCVPEPALRCLRR
TTGYKPY-----GTSITVEGQAYADDLLTAAPSAYHAARQVATIEWA-NWAGVSFVVQALSLDAPAGKCAALAIN---FEGG----
-----LMHSDIPALK--VQG---AAIPAMSRNNVRYLGVHVGLTDALG---QANELLEKA---SRDARTICASG-LEFPWQKVVAIK
TFILSRLPFFHHN-----GKIQRGRCQQ-----FDRELREN-----LRAALRL
>Utopia-1_LV
TNSAPGKDR-LEYRHRRADG-----SFSISEAIFNKCLAE--GRIPAPWK-TASTILLHKAG---PTDDPANFRPIALQSLCYKLF
MAVLADRLTKWACENQY--LSPEQ-KSARPCGECFEHSFLL---SAALK---DCRRN-----QKTICIGWLDLRNAGFSIPHVI
KIVLSSSLGVDSLVTTLLMDAYNG-----ASTSFTLTG-----GQTDTPVIRSGVKQGCPCMSPIILFNLAIELIIRAVKK
NASDNHLGVT---VQGNKLSILAYADDLVLLSRDTGLQSLQVAGSSA-STLQMOKFKPQ-----KCATLTLDD---CKR-----
-----GTNVQRSAHH--IQG---AAIPSLTEERYRYLGVPIGLPRLT---SLQESSRKL---SSDIETISSSL-LAPWQKLDAIK
TFVIPILQYTLRA-----TEYLSKDLKP-----LRAAIKH-----VKKICHL
>Utopia-1_CF1
TNSAPGPDG-ITYRDLRGADP-----GARLLAALFNACYRL--EAVPASWK-TSNTVLVYKKG---DRDSLENWRPLALGDTAPKLF
AAILADRLMTWAVTNNK--LCPAQ-KGFLRDEGCEYHNFVL---QEILT---DARRT-----RRQAVVAWLDSLNAFGSVPHAAI
RRALVRSGVPGGLVNVWNSMYDG-----CSTRVRTAE-----GYTTPVLIRSGVRQGCPLSPIVFDLAIDSVLRAYTA
VDAGFD-----LLGSRHSVVAYADDIALVADSPGMRRLLAVAEGAA-SSVGLRFPNA-----KCATLHLA---AGS-----
-----GGRVLPPTTFV--IQG---QPVHHLSSGEPYRHLGVPTGSSVDQ-----TPPATIGGL---LEDLRAVDQSL-LAPWQKLEVVA
TNILPRLDFLLRG-----ATVGKPLKA-----ADLQVRM-----AKSWLNL
>Utopia-1_AEc
NNSAPGPDG-VSVYRDLRGADR-----GARLLTALYNICLRL--EAVPASWK-TSNTVLIHKKG---DRGMLENWRPLALGDTVPKLF
AAILADRLTDWAVTRGK--LCSAQ-KGFLRDEGCEYHNFVL---QEVLT---HAKRS-----KRQAVVAWLDSLNAFGSIPHATI
RRALIRSAVPRGLIAIWDSMYDG-----CTTRVRTAE-----GHTAPIRIRSGVRQGCPLSPIIFNLAIIDSVVRVAAE
XNDGYS-----LHGNTWSALAYADDIALLAQTPEGMERMLASVEAEA-ASVGLRFPNA-----KCATLHVH---AGN-----
-----GGRVLPSTFQ--IQG---ETINPLAQGESYTHLGVPTGFSVDQ-----TPYAAVGDI---VSDLRAVDRSL-LAPWQKIEMLG
TFILSRLDFLLRG-----ARVFKGPLTA-----VDLNIIRH-----VKSXLNL
>Utopia-1_CMy
KNTAPGKDG-IPYSLKKRDP-----GCLVLATLFNQCKRF--CRTPSSWK-KAMTVLVYKKG---ERDDPSNWRPISLCSTMYKLY
ASCLASRITWESVSGGA--ISSIQ-KGFMSCEGCEYHNFVL---QTIE---TARRA-----RRQCAVAWLDLANAFGSMPPHHI
FATLQEFMGPENFLRVIREVYEG-----CSTTIRSVE-----GETAEIPIRSGVKQGCPLSPIIFNLAMEPLLRAISN
GTDGFN-----LHGERVSVLAYADDLVLTADDPESLQGMLDATSRRA-DWMGLRFPNAK-----KCATLHID---GSK-----
-----RDSVQTTGFQ--IQG---EPVPLAEGQAYQHLGTPTGFRVRQ-----TPEDTIQEI---LQDAAKIDASL-LAPWQKINALN
TFLIPRISFVLRG-----SAVAKVPLNK-----ADKIVRQL-----VKKWFL
>Utopia1B_CPB
KNTAPGKDG-IRYHLLKKRDP-----GCLVLAALIFTCKQF--HRVPRSWK-KSMTVLIHKKG---ERDDPGNWRPISLCSTIYKLY
ASCLAARITDWSVCGGA--VSSVQ-KGFMSCEGCEYHNFL---QTAIQ---EARRS-----KRQCAVAWLDLTNAFGSIPHHHI
FATLGEFGMPETFIQLLRDLYKD-----CTTIRATD-----GETDAIPIRRGVKQGCPLSPIIFNLAMEPLIRAIS
GPTGFD-----LHGKKISILAYADDLALVADSSSLQOMLDVTSQAA-EWMGLRFPNK-----KCASLHVD---GGA-----
-----RALVRPSRFL--IQG---EPMASLEEGEVYQHLGTPTGVRVRQ-----TPEDTIAEI---LRDAAQIDSSL-LAPWQKINALN
TFLIPRISFVLRG-----SAVAKVPLNK-----ADSTIRQL-----VKKWLYL
>Utopia-1_ENe
LRSAGPDG-IRFSVYKQFADV-----LIPAMSAIYNACSKH--RQVPRKWK-ESVTVLIPKGG---DPKSVKNWRPINLQDCIYKLY
AALWAQKIAAWAKSGV--ASKSQ-KGFMPVNGCHEHLFLA---QSLN---STRRS-----KKPLYMTYYDLQNAFGSISHQLI
HVVLQAQRLPKHAQEVIMDLQYQ-----ASFCLITKE-----GCTGRIVNQRGVKQGCPLSPILFNLAIEPLQLRLAA
CNEGLELRITD--GKPVQKVSHMAYADDLKTVAATRVGISKLHQVVEDFL-QWTGLKANPS-----KCATLGLK---VQKA-----
-----KQVPDPVKLT--LHY---EVLPPVVLGEAYKYLGIKDALESPVQQ---SQILRAMSRI---KKDLNKLRLSE-LLPWQKLDALR
TFVMSRLDYLRH-----CYPYKQLVA-----FDVYVRAA-----LKAFAKL
>R5-2_SM
DNTSPGIDG-IQYKDLALLDP-----EGILLSFLFNKIIS--KIIPTSWK-TFKTILIPKPKDKTDNYDKVSSWRPIALLSVIYKVF
ASILTTRLTWSWICNDI--LHIGQ-KGGSVHEGCVHEHNSIL---SSALE---HSKYS-----KNSPLAIAWLDIKDAFGSVPHDYL
WSVLKTIQVSEEFITIVKLYTD-----TQSFYSCGP-----IVTPNLSIKKGVKQGCPLSMILFSAINPVEAISR
SCIEPFM-----IGDSPVQVLAYADDIALVANNVENLQKIVDVAVEAA-TEIGFEYRPE-----KCGYMQLP---RVN-----
-----INGEIL--INE---KEIKKLSKEFYQYLGVPVGEDNDQ---SPYAILDKV---VSDTKKIADSG-LFGWQKLKAYK
IFIHSRLTFAFRT-----REIKTMALSA-----SQGNTNSCGNNSSKLRGHLRRLNL
>R5
SKSAAGLDW-ITYEDIKLGDP-----SGEILQPIFEYIVQN--NICPSEK-ASRTIMIPKPGK--SDYSDPSSWRPITITSAYVRL
MKYLTWELYNWILLNQM--LSRSQ-KSLGKPEGCHDHANML--NMLIQ---DVRRTQNTSPNINKNKRLYIVFLDFTNAFGSVPLDTL
MYVPQRFGLGTSALTLIKLYLD-----NYTNVTCGE-----SKIENVKLNKGVKQGCPLSMILFNFINIIIRAIEA
MPDVHGYP-----LGMDIRILAYADDIALISDSHKDLQEMVYKAEYIG-RILGLLFNPS-----KCALMDIP---HDK-----
-----KRTPPI--VNG---EMIKCVGKADPYKYLGTFRSFRKL-----DIKELLQMM---MDETKLITESN-LHPHQKIHAYE
TFIHSQLPFHLRH-----SRIPFSDFITNRKTNKTTNNSNSEKSIQKAYDPE--SGQLFLNTFAL
>R5-1_SM
THSAPGSDK-ITFSDWRRLDP-----DFEFLAALFNNILRT--GKSPNKWK-TFRTKLIIPGKEHSPHEVSSWRPLAILDTAYRFF
ATILNRRLLSWIAKRN--LCSNQ-KAVGIPDGCAEHNTVI---SLAKE---WAVIN-----GKDINIVWLDLADAFGSVPHDLI
WHSLSRLKLKNKTINLIKDMYND-----CYTVYECG-----KHTKTIKVNNGVKQGCPCMSMTLFSLTINFILQNILK
EYPLI-----IHNHNISIMAYADDLVLIADTREKMRKMIKDITKYT-DSATLKFRPS-----KCGYFQLK---RNH-----
-----NDPPIT--LYD---EQIPIIDENHLYKYLGVDFGQKGKH-----NIDTILNTA---LDDTTKILSSD-LHPAQKLQAYK
TFIHSRLIFPFRN-----CNINHMTLDT-----NRNRTVQH-----REKQLGF
>LIN9_SM
TDSAPGEDN-IPLRQWIIWNN-----DGVLFDMFNYIKRT--HDIPDMWK-NYTTTLLIKPGKSQESNIPANWRPISILPSTYRIF
MKVLNKRVLWEANRGL--ISKWQ-KAVDKANGCDEHSYIQAALIEKAN--RSYK-----NEQCHLAFDLADAFGSIPFQVI
WHTLKNMGMDDEETINLLKEYKD-----CSTKYKCGK-----NESEKIKITKGVQGCPLSMTLFSLCQYLIQGIAE
KKKGAT-----IAGQEVCLAYADDLVIVANTAKDMQMLTTIENLA-KQADLIFKPA-----KCGYRDP---RDK-----
-----KSMK--IYG---KEISIVDEKNVYTYLGVRIQDTKKK---DLNVRFEV---KKKTTAIFKSK-LRSDQKLEAYN
IFCQSKFVYILQG-----EDIAKTKIET-----YDEIKKM-----IKEDILK
>R4_Hme1
NWKAPGTDN-IHNYWYKLTCT-----HSLLLKHINQFIQSP---CTLPLFIT-NGITYMLPKGL---DPTNPANYRPITCLQTIYKII
TACITDIIYKHIDQNNI--LAEQQ-KGCRKNSQCKEQTLTI---DAIV---MKQAH-----NKNXNTMYIDYRKAFDSVPHSWL
LYILKKYKIHPIILITFLSSVMLS-----WKTRLKLNNN---ETLITDWIKIQRGIFQGDALSPLWFLCALNPLSELLNN
TNTGFKLKH---NTYHIIISLMYDDIKLYASNKELKILADLTQSFS-TDIRMEFGIE-----KCKVHSIK---RGKS-----
-----QONTYIL--NTG---EQIESMDENSTYKYLGFQQAQIQK---QTKIELTNKF---KFRLNQILRSQ-LNSRNIIKAIN
TYAIPILTYSFAI-----INWSQTDLSN-----LQRIINTH-----MTTHRKH

```

>R4-2_AS
PFKAAGPDG-IHAYWKKHLP-----AGKLLGNIIVWLVT--GKVSCRWLMRGRTVLLPKKG---DLRLPQNYRPITCLNTCYKLL
TATIAKALLRHLDKGEA--IPQQQ-RALRKKEWGCTHAILL---DRAVA----TDATTQ-----KGRPLSIAWLDPKKAFDLSHSHYI
RWILESNNVPKTTATTFFKLMAG-----WETRYELKYKTRGCMISIQRSQPVKIVNGIFQGDALSPLLFIILSVSPISFALEN
KAKPYRSSVQ--LSGKGFSLGHQFYVDDDKIYAPNRRRELNVALVAKNIS-TAIGLDLNV-----KCAQAHYT---PNVQ-----
-----QLEVTFLADEEP--LMELPVLGLRQSYRYLIGIDQKFLATKN----ALQRFEEESL----FNRSALFRSD-LTWQRQMSNAFQ
SIALGGLRYGFLN-----TNGAGQKLSE-----ALKHARDI-----DVRIRSL
>R4_AL
PWKAPGPDG-LHAHWKALPS-----AKRLLGELVVDLWLT--GKVTGWMCRGRTILIPKKG---DRGDPSNYRPITCLNTCYKVL
TSVMNSVILSHLSRGEA--LPMNQ-RAMRKREWGCTHAMVL---DRAMV---MDAMAQ-----KKHLSVAWLDIRKAYDSVSHEYI
RWAINSVNIPRSVQLTLKRLMSD-----WETRFESTQCR----PKLRSDKMKVNLNGIFQGDLSPTLFLVLCIAPISYALNK
GVGQCQSSSGW--SAGYGFEIGHQFYMDLKLARTPAMLDLQVQVSEVS-EAMGLHLNLS-----KCAKAHYA---PHGA----
-----GGAQEAVEGAEGSRKGEIPIGLRSTYKYLGVQRLPMEV----ALKEFEDKF----MDRAETIFASE-LTWGQMATAYN
TIAIAGLRVYYSN-----TNGASPKLLE-----ALKRAATL-----DTRIRDL
>R4-5_BX
PNKAAGPDG-LPGCVWKCLPNA-----SNWLCTWLIIKKLACS--RIDTPRWLS-EGRVVLMMKKG---DPNDPANYRPIACLNTCYKLM
TSVIERAIREQVTACTP-LIPSEQ-VANRKGVGCTHASIV---DRLVTGTAAMSKGQ-----NADLRVLFYDCKKAFDVSVRDHM
FRVLDVAGVDRKIYYLLKSTMN-----WTVRYELRRSG----RVERSAPLRVKRGLLQGDLSPTWFLCLCIAPISHALRL
RNPGPCIRQVAGHSDGGQVHVSHLFYMDDLKVYCTGEAAQVRAERLVPFL-SQIGLCVNES-----KSAAGAAGP---SR-----
-----TLR---SSLPLLGVDQKYKYLGIESGFVANEA---SAYSRMQTTI---LAKVQSILDVEGHTVQGRRRIAIR
TVAFPGAALFLGNIILGDKQPNSAKADMLK-----LDMVIREK-----IRRKGLL
>HERO-1_BF
AGSAPGPNQ-VSYQIYKCPK-----VVRLLWKLFRVAWK--QCIPSAWR-RAGGVLPKKE---VSTDIKQFRNISLLNVEGKLF
FSILTKRMITYLLANNYIDTEVQK-AGVPGFPGCIEHASTI---WQQIQ---MARRQ-----KEDLHVVDLDTNAYGAVPHSVI
HYALNFWFVPTIRMTIQNYFQD-----FRVSVTTTPQ-----FTTGWQOLEKGIAMGCTISPLFLVLGFEIFLIGARQ
VAGGIKLP-----SGQRLPPLRAIMDDVTSILRSAPCTRRVLQLEELT-DWARMRFKPS-----KSRSLSLR---KGK-----
-----SSNRVFS---INN---QDIPTIQ-QEPVKSLGRLYTSDIADT---KRQQLVKQA---VEGLRAIDKCE-LPGKLVKWLQ
SVLIPRLKWPMMK-----YDIPLSTADQ-----VEGKANSF-----VRKWLGV
>HEROTn
NNSAPGPNQ-VPYLVIYKCPK-----LLARLWKILRVIWRR---GKVAHQWR-WAEGVVPKKE---KSTLIEQFRTISLLNVEGKIF
FSILSHRLSDFLKNQYIDSSVQK-GGIPGVPGCLEHCGVV---TQLIR---EAREG-----RGLAVLWLDLANAYGAIPHKLIV
EMALARHHVPCSIKTLIMDYDS-----FHLRFVTSG-----SVTSEWHRLEKGIITGCTISVIFALAMNMLAKSAEP
ECRGPITK-----SGIRQPPIRAFMDDLTVTTTSVPGCRWILQGLERLM-TWARMRFKPG-----KSRSLVLK---AGK-----
-----VTRDFRFY---LGG---QDIPSVS-EKPVKSLGKMFDSGLKYA---FSIRETNDQL---GHWLTLVDKSG-LPGKFKAWVYQ
HGILPRILWPLL---YEFPISTVEG-----LERRVSSC-----LRRWLGL
>HERO-1_SP
NASSPGQNG-IPYKMYKCPK-----LLKIIWKLMLDVWRT--KYIPVQWR-VAEGVYIPKSAT-PNEKTIITDFRPIALLNVEAKMF
FAIPAKRLETYMRKNGYLDTTVQK-GGVGGHPGVWEHVATL---WEVIK---DAKTS-----QKNLVAIWLDLANAFGSVPAAI
AFALKWYHLPESLVSLMNNYVVG-----LYARFSVKD-----WNSEWQKFSVGIFMGCTLSPILFVITFNLLNDFLKS
TPAKQYHLK-----RDFNVPMKEYMDDITITASVESAGSILSKVNDPM-DWSKMRIPV-----KSRSLVVH---GGK-----
-----VKHIEPFA---VDG---QTIPGVH-NKPVKFLGLRIDGNLKN---VARQDMVSL---GRWLHTIDKCV-LTGVMKWCWYQ
YLIVPRMQWKLMI-----YDVPVSQVEK-----METLVSKK-----LRRWLGA
>HERO-1_HR
AKATPCPLDQISVIALKRCPI-----LRTYLHKLIVKCWNA--GTIPLCWR-KALTILIHKKG---DANDPANFRPITLQPVLKIF
STLIKRLNHLNQLQNNFISTNIQK-GFYPTLDGLAEHTQML---SHLMK---DAKRY-----QRSIIALLDLRANAFGEVNHQLI
NSILLYHHVPQLFRNLILSIYS---YAISVSIND-----QLTPLLVRKGVLGQDPCSPLLFNLCFNPLMKILEG
DEPKQCGYLWG--PTSDVRARSWLQFADDTAIIAHNSESQAKLIDLNLAWC-RWSDMQMRVD-----KCCVFGMM---KKDG----
-----SYDQFLPRLT--IDN---IPIPPVELGSGFYKLGKIYDAELKDT---KAKEEMVSKL---TRLKRTTDLK-VSTQMKLQVLR
RFIPSQLKFELRS-----YNLSLTWIKNN-----LDNMVTEA-----VRDWLTM
>HERO3_BF
ATSAPGPDG-IMYGLKHLPA-----CHLFLSTLFSKLLES---GDPPTSWS-SGNVSLIHKDG---SPEAAENFRMICTLSCVSKIF
HQLLSERWAKYMTCSNLD-IDPETQKAPLTGINGCUEHVQVM---REILA---HAKKN-----RRTVHITWFDLADAFGSVEHCLI
YYQMERNNGFPPIITTYIKNLYSR-----LKGKVKGPG-----WESDPFPFGRGVFGQDNLSPIIFLTVFPQPLQLHLKG
VEQQHGYN-----LNDKHYVTLPFADDFCLITTNKRQHQKLITQISSNT-KSMNLKLPK-----KCKSMSIV---SGK-----
-----PSDISFT--IDG---DPVKT--KDAPEKFLGGYITFLSATK---ETYDILAKTI---ETTVENINKSA-IRNEYKLRVYM
EYAFPSWRYMLMV-----HDLTDTQLQK-----LDSHTKA-----IKTWLRM
>R4-4_Sra
NWKCPGENG-IPIFLIKKLPS-----AKTFVKKWMKGVVEN--RIPITEYDI-KGNAYAIFKKG---DKNIESNYRFINALNSHYKLL
MKYLNKCVREWCNSN---ISDNQ-FSGKQGYDGALDIGIT---NRLIQ---EM-----GQFAQGWDYMQKAYDSVDHSRL
KMIINSVKEIPKPIRNLCKLPKMYKFSVNVCSPNRDENGKIIKE-----KKKSWITMKRGIYQGCSLAPWFLCLCLAPLQWKMKQ
IIDPIDL-----YGQKKIDILLFMDDIKGFGKNKNELDKITNLIINY-KEIGLTINKD-----KTEYS-----
-----IPDEEKIIQYKYMGVYENKKTACDE--INAEQLLMKL---DEKMDKIFNSK-LNVKNIKAIN
GCVIPTCTYLFSSH-----EFS-DEERIQ-----LARNVDIR-----IRSYMNT

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B

Conservation:		14649373	411	132	21		12	322	22	1	1
6ar1_chainD_p001	1	ALLERILARDNLTALKRVEANQ	GAPGIDG-VST	QDLRDYIR-----	AHWSTIHAQLLAG---	TYR	57				
SLACS	1	-----	RGAPGLDG-WT	RELLYPLTD---	PALKMIEIAAVVKDIINADVS	MEV	44				
CRE1	1	-----	RGTAPGLDG-WT	RELLPLAEDPALLHEITS	VSVSDIMQGKVA---	EVV	44				
CRE2	1	-----	RAAAPGLDG-WT	RELLVPITED---	KGLLTELTAIVQDMLVG---	NVH	41				
GAU97528_Ramazzottius_	1	-----	VDSAAGPDR-VL	VRVIKQEAUME---	VLAVIAAVLLEMNATKE---	HPL	42				
Blag_1	1	-----	ADTAPGPDH-VL	VRALKDATC-----	YEIIAKIATTMLQH---	SFV	37				
Blag_5	1	-----	VDTAPGPDH-VL	MVRVKDDAA---	TGVLSLLATRLMRT---	GHV	37				
Blag_2	1	-----	VDTAPGPDH-VL	VRVIRNEIV-----	YEILAIATRLMSS---	GIV	37				
Blag_4	1	-----	TDSAPGPDH-IL	VRTLKLTEC-----	SPVIAVILKIMLQW---	GMV	37				
Blag_3	1	-----	IDTSAGIDH-VL	VRTIKELKT-----	SKLLCLLTNAMLKF---	KIC	37				
Blag_6	1	-----	LDTAPGPDH-VL	FKVVKELC-----	MKIISIIANIMLSW---	NYV	37				
R2_PS	1	-----	SKTAKGVDG-VG	LEELKRVPR-----	RTLFNINLGLW---	THV	34				
RaR2	1	-----	NNTAAGPDG-IQ	PKSWNRISL-----	KYKTLIYNLLLYY---	EKV	36				
R8HmA	1	-----	KDSASGPDG-LL	LQDVRRLLGP-----	LLLCNIFNMWYL---	HGI	35				
R8HmB	1	-----	KDASGPDG-LL	LQDVKKASP-----	RQLCIFNMWYL---	HGI	35				
R24_MR	1	-----	KQSASGPDK-IT	RDDLKANKL-----	ADVVGLLNIVFGL---	CRT	36				
R21_MR	1	-----	KESAPGIDG-IT	REHLRSMR-----	PDLYALNIIWGM---	KCL	36				
R2SmA	1	-----	HGTAGGIDR-LT	SYDLMRFGK-----	NGLAGYLNMLLAL---	AYL	36				
R2NS1_CSi	1	-----	GNSSPGLDK-LT	PRMLRRFNA-----	NVLAGYFNLLLLS---	GGC	36				
R2CiB	1	-----	TPSAPGPDK-LT	LDGVKRIPI-----	AELVSHYNLWLYA---	GYQ	36				
R2NvecA	1	-----	KKSASGPDG-VP	CAALQTMGA-----	ASLAHPNLWLLA---	GTQ	36				

R21_MDe	1	-----ADSAAGPDG-ITVVNWIGMDI-----	RLRLFLFLNMIMKR--	GRL	36
R2A_NVi	1	-----KRTAAGPDG-MTTAWNSIDE-----	CKSLFNMMIMYH--	QQC	35
R21_TCAs	1	-----QISAPGSDQ-IPVAAVKTMSE-----	LELAILEFNIIILFR--	NVQ	36
R2LcA	1	-----SSTAPGVGDG-FSAKQLRSMSP-----	RVLNKLNLNLLLLS--	ENL	36
R2Ll	1	-----PSTAPGVGDG-FSAKQLRSMTP-----	RVLNKLNLNLLLLC--	ENL	36
R2La	1	-----SSTSPGPDG-VTARMLRSIPA-----	RVLNKLNLNLLLLFI--	EDL	36
R2LcB	1	-----TSTSPGPDG-VTARMLRSIPA-----	RVLNKLNLNLLLLFI--	EDL	36
R2NS1_SMed	1	-----LKTSSGPDN-ISTEVLEIIPV-----	LVLVKLFNLIILL--	SHL	36
R21_PPap	1	-----PGSAAIDR-ISVQQFORCPV-----	HVRVLLFNVLVLLV--	GHL	36
R22_TCAs	1	-----NGAAPGPDG-IAVSVWNKLPP-----	EAALLFNVLVLLG--	RCL	36
R21_PBa	1	-----NGTAPGLDG-ITPRAWNAVVP-----	GLRALVFNLLLLLA--	ETA	36
R28_MR	1	-----PQSAPGPDG-IGVRQWRAVPP-----	SVRALLYNIIVLAT--	GGF	36
R27_MR	1	-----LDTAVGPDG-VTARQWRAVLP-----	AVRALLYNIILKR--	GSF	36
R21_IS	1	-----VNSAAGPDG-FSARLLKSVPA-----	LLLRVMVNLVLLV--	RRV	36
R21_RMl	1	-----SSSAAAGPDG-FAARELRKVPP-----	VILQVLLNLLLLLL--	KRL	36
R2_FA	1	-----MTTSPGPDG-ITVRQLYLVP-----	QLLVRIINLMLMAC--	GKM	36
R25_MR	1	-----MTTAPGPDG-LTARQIRAVPL-----	EVLVRIFNIFLVC--	GRL	36
R2_Dan	1	-----LSSSPGPDG-ITPKTARSVPE-----	GIMLRIMNLILWC--	GNL	36
R2_DSi	1	-----LSSSPGPDG-ITPKSAREVPS-----	GIMLRIMNLILWC--	GNL	36
R2B_DM	1	-----LTSSPGPDG-ITSQTARSIP-----	GIMLRIVNLILWC--	GDL	36
R2_DPe	1	-----LTKSPGPDG-ITPRTVRSIPS-----	GVMLRIMNLILWC--	GKL	36
R2_BM	1	-----WRTSPGPDG-IRSGQWRAVPP-----	HLKAEMFNAMMAR--	GEI	36
R2C_NGi	1	-----QNTAAGIDG-LTVGDLKGVSR-----	EMLARIFNLFMWC--	GKL	36
R2_AM	1	-----SSGATGPDG-FSVRSCLKCTPS-----	RVLAKVFNLFLL--	EKL	36
R2CiD	1	-----VASAGPDG-VSVSGMTKIGA-----	RVLCMLFNVLVQFT--	GRT	36
R21_BTe	1	-----KKAAGPDG-LQRDHLTIPIGL-----	PIIMAKIYNILVYC--	SYF	37
R22_MR	1	-----PKSAAAGPDG-LMKRDVIGKSH-----	LYILYPMFNLIIVAA--	GRQ	37
R2_KF	1	-----KDYAPGPDG-VTKLKVQSMGA-----	YPSLLAKVYNLVMLT--	GYF	38
R2B_NVi	1	-----NDSAAGPDG-VTKDDLGRGV-----	SIALSKLFNSILLA--	GYI	37
R2Amel	1	-----SDTAAGADQ-IKKFHLRKKGA-----	LHVFAKLCNLLMLH--	RIY	37
R2_Rm_ribo	1	-----NASAPGPDG-VKKCHVATRAK-----	QAVLSALFNLTLLT--	GIL	37
R2_Bg_ribo	1	-----STTAPGPDG-INIQAVRSAPA-----	QAVLSTFYSLILLL--	GRP	37
R2_RU	1	-----PSSAPGLDG-VGKIHLVGKGI-----	TLVLAKLYNLLFLT--	GGY	37
R2_RL	1	-----PSSAPGLDG-VRKIHLVGKGI-----	TLVLAKLYNLLFLT--	GGY	37
R2Dr	1	-----NASTPGPDG-VGKRDISNWD-----	ECETLTQLFNMMWFT--	GVI	38
R21_GA	1	-----NRSSPGPDG-ITKVALSKWD-----	EGIKLAHMYSTWLVS--	AGI	38
R21_SSa	1	-----NNTAAGPDG-ITKPALLEWD-----	TGAKLAAIFSIWLT--	GTL	38
R20IA	1	-----NGTAPGPDG-ISKALLDWD-----	RGEQLARLYTTWLIG--	GVI	38
R21_Gav	1	-----SKSAPGPDG-LTLRDLRRAD-----	EGDALAELFSLWLIT--	GTV	38
R21_ZA	1	-----KGSAPGPDG-IALGDIKKMD-----	GYSRTAELFNWLTA--	GDI	38
R21_TG	1	-----KGSAPGPDG-ITLGDVVKMD-----	EFSTRTEIFNLWLT--	GKI	38
R21_GFo	1	-----KGSAPGPDG-IALGDIRKMD-----	EYTRTAELFNWLTS--	GEI	38
R2NS1_CGi	1	-----KDSAAGPDE-IELKTVMAKD-----	KGXILVNLFNNSFLYR--	KKV	38
NeSL1_TV	1	-----HLSAHGLDG-IPNSVYMLFPVS-----	AAKFLSILFRSIIIS--	GHI	39
Utopial_ACa	1	-----NGSAPGIDG-IPYEAYKRTKL-----	DATLAHVFEVVRNLN--	ARL	37
Utopial_LV	1	-----TNSAPGKDR-LEYRHIRRAD-----	SFSISEAIFNKCLAE--	GRI	38
Utopial_CF1	1	-----TNSAPGPDG-ITYRDLRGAD-----	GARLLAALFNACVRL--	EAV	38
Utopial_AEc	1	-----NNSAPGPDG-VSYRDLRGADR-----	GARLLTALYNICLRL--	EAV	38
Utopial_CMy	1	-----KNTAPGKDG-IPYSLKKRDP-----	GCLVLATLFPNQCKRF--	CRT	38
UtopialB_CPB	1	-----KNTAPGKDG-IRYHLLKKRDP-----	GCLVLAALFTKCKQF--	HRV	38
Utopial_ENe	1	-----LRSAPGPDG-IRFSVYKQFADV-----	LIPAMSAIYNACSKH--	RQV	39
R52_SM	1	-----DNTSPGIDG-IQYKDLALLD-----	EGILLSFLFNKIISS--	KII	38
R5	1	-----SKSAAGLDW-ITYEDIKLGDP-----	SGEILQPIFEYIVQN--	NIC	38
R51_SM	1	-----THSAPGSDK-ITFSDWRRLD-----	DFEFLAALFNNILRT--	GKS	38
LIN9_SM	1	-----TDSAPGEDN-IPLRQWIIWN-----	DGVLPDMFNKIKRT--	HDI	37
R4_Hme1	1	-----NWKAPGTDN-IHNYWYKLTCT-----	HSLLLKHIHQFTQSP--	CTL	39
R42_AS	1	-----PFKAAGPDG-IHAYWWKHLPS-----	AGKLLGNIIVEVLVT--	GKV	38
R4_AL	1	-----PWKAPGPDG-LHAHWWKALPS-----	AKRLLGELVDVWLTT--	GKV	38
R45_BX	1	-----PNKAAGPDG-LPGCVWKCLPNA-----	SNWLCTWLKKLKACS--	RIDT	40
HERO1_BF	1	-----AGSAPGPNP-VSYQIYKKCPK-----	VVRLWKLFVRVAKK--	QCI	38
HEROTn	1	-----NNSAPGPNP-VPYLVIYKRCPK-----	LLARLWKILRVIVRR--	GKV	38
HERO1_HP	1	-----NNSAPGQNG-IPYKMYKKCP-----	LLKIWKMLLDVWRT--	KYI	38
HERO1_SR	1	-----AKATPCPLDQISVIALKRCPI-----	LRTYLHKLIVKCNNA--	GTI	39
HERO3_BF	1	-----ATSAPGPDG-IMYGHLKHLPA-----	CHLFLSTLFSKLLS--	GDP	38
R44_SRa	1	-----NWKCPGENG-IPIFLIKKLPS-----	AKTFVKKWMKGVVEN--	RPI	39
Consensus_aa:	sAsG.D...l...h..hs.....h..lhp.hh.....h			
Consensus_ss:		hhhhhhhhhh	hhhhhhhhhhhhhh		

Conservation:	5	22	2244363911	11	1323396734242117242234213411	11	5	3531
6arl_chainD_p001	58	PA----	PVRRVEIPKPG-----	GGTRQLGIP	TVDRLIQQAILQELTP	IFDP----	DFSSSSFGFR	110
SLACS	45	GRRLQ-	ATSLTVLRKPN-----	GKYRPIGAES	VWAKLASHIAISR	VMKTAEEK-----	FSGIQ-FGVG	100
CRE1	45	ARRLR-	SSAVTPIPKDE-----	AGTKIRPI	VPESAWLKLASLVAMAE	IPSSFKET----	FKGWQ-YGVW	102
CRE2	42	PSFAT-	RIRACILHPPFR-----	KEAGSAKVR	PITPESALMKLAHIALDS	VEKSFSTR-----	FKGWQ-YGVW	102
GAU97528_Ramazzottius	43	PSVLQ-	LALTVLIHKGG----	DVTDGNNYRPI	SICSARRRVLERVVDRH	LRRYGS-----	VSRFR-QGFT	101
Blag_1	38	PECLQ-	KARTVLIYKGG-----	DDKDLGNWR	PITICSVVRRRIERILDA	RLRALVN-----	LCENQ-RGFT	96
Blag_2	38	PPCLL-	IARSILHKSG-----	DVNDITNYRPI	TICSVVRRVIERTLDRRL	KEYVS-----	FNRHQ-RGFT	96
Blag_2	38	PRCFK-	TARTVLIHKAA-----	DVNILSNWRPI	TICSVLRRVIERVLDKHL	RTFVS-----	FNEHQ-RGFT	96
Blag_4	38	PDRMR-	GARTILIYKKG-----	ERCSVSSWRP	ISVCSVIRRLIERALDS	VLRLQYLT-----	LNNNQ-RGFV	97
Blag_3	38	PGILK-	TARTVLLFKGG-----	DETKLSNWRP	SIFSVCIRIIEKVINRLK	SYIE-----	LSPHQ-RGFI	96
Blag_6	38	PNSFQ-	SGRTILIFKSG-----	DPNSLKNWRPI	TIFSILRRIIERALERK	IRPFVE-----	LSTCQ-RGFI	96
R2_PS	35	PESLY-	KGRITLIPKKS-----	LPELAGDFRP	ICVLPVVVRLHLRILAK	RLAIVQ-----	HTEFQ-AGFQ	92
RaR2	37	PHKLK-	VSRVFIPIKKKD-----	GSSDPGEFRPLT	ICSVVLGRGNKILVQRL	LVSLYK-----	YDERQ-TAYL	96
R8HmA	36	PVEEN-	RCRITILYKSG-----	DRHLASNYRPV	TIGNMLNRLYAKIWDK	RIRKNVR-----	LHVRQ-KAFI	94
R8HmB	36	PVVEN-	RCRTILLHKGG-----	EKHLTSNYRPV	TIGNMLNRVYAKIWDK	RIRKNLQ-----	LHVRQ-KAFV	94
R24_MR	37	PTLLR-	HNRTVLIPIKKG-----	DLSLTSNWRP	ITVSSIFSRLHLKILAS	RLSNNIK-----	LHHAQ-RGFT	95
R21_MR	37	PVLR-	SNRTSLIPKSG-----	NTRCLKWRP	IMVSSRVLRLLNKVIVS	RLNEIK-----	LNYSQ-RGFT	95
R2SmA	37	PTNLS-	TARVTFVPKSS-----	SPVSPEDFRPI	SVAPVATRCLHKILAK	RWMLFP-----	QERLQ-FAFL	95
R2NS1_CSi	37	PHLC-	RARITLVPKVP-----	NPTSPDQLRPI	SVSSILVRCFHKVLADR	WSRRLQ-----	LPSLQ-FAFL	95
R2CiB	37	PEGLR-	EGITTLIPKIK-----	GTRDPAKLRPIT	VSSSFCIRIFHRCCLAQ	RMETSLP-----	LGERQ-KAFR	95
R2NvecA	37	PKRLT-	ECRTIFVPKEV-----	NTHLPLHHRPIT	IGSVVVRFLHQILGK	PMEAVLP-----	LGSQ-RGFR	95

R21_MDe
R2A_NVi
R21_TCAs
R2LcA
R2Ll
R2La
R2LcB
R2NS1_SMed
R21_PPap
R22_TCAs
R21_PBa
R28_MR
R27_MR
R21_IS
R21_RM1
R2_FA
R25_MR
R2_Dan
R2_DSi
R2B_DM
R2_DPe
R2_BM
R2C_NGi
R2_AM
R2CiD
R21_BTe
R22_MR
R2_KF
R2B_NVi
R2Amel
R2_Rm_ribo
R2_Bg_ribo
R2_RU
R2L
R2Dr
R21_GA
R21_SSa
R201A
R21_Gav
R21_ZA
R21_TG
R21_GFo
R2NS1_CGi
NeSL1_TV
Utopial_ACa
Utopial_LV
Utopial_CFl
Utopial_AeC
Utopial_CMy
UtopialB_CPB
Utopial_ENe
R52_SM
R5
R51_SM
LIN9_SM
R4_Hmel
R42_AS
R4_AL
R45_BX
HERO1_BF
HEROTn
HERO1_SP
HERO1_HR
HERO3_BF
R44_SRa
Consensus_aa:
Consensus_ss:

37 DDDLK-SARTVLI PKGK---GNIRPEN TRPLSITSVVLRHLHLKILAKRLKSLQT-----FSDSQ-KAFI 95
36 PRRYL-DSRTVLI PKEP---GTMDPACFRPLS IASVALRHFRHILANRIGEHGL-----LDTRQ-RAFI 94
37 PSAWG-VLRITVL PKDG---DLRNPANWRPITISSALQRLHLHRVLAARLSKLVS-----LSSSQ-RGFT 95
37 PNSFK-MHKTVLIPKID---DPKSPGDFRPIITISPVLARLNLNKILAAARLSKLVP-----ISQRQ-KAFL 95
37 PNSFK-MHKTVLIPKIV---DPKSPGDFRPIITISPVLARHLNLKILAAARLSKLVP-----ISQRQ-KAFL 95
37 PAVFK-CHRTVLIPKID---NPTSPGEFRPITISSIVVRQLNKIIAARVSEGV-----INPRQ-KAFR 95
37 PAVFK-CHRTVLIPKVD---NPALPGEFRPITISSIIVRQLNKIIAARVSEGV-----INPRQ-KAFR 95
37 PSEFK-NSRTTILPKVE---TPKDPGYRPI SVSSVFVRALNKILASRVSNNGK-----GAHAQ-KGFK 95
37 PGRMS-CARTVFLPKVE---GSSDPKDYRPI SITSVITRQPHKILAAARLTSMHA-----WDERQ-AGFL 95
37 PAELT-RTRTVFI PKTD---APRTPADYRPI S IASVVARHFRHVL SARVQRIPDLF---TKYQR-GFLS 97
37 PLSIT-TTRTVFLEKGGM-SDRPGPSEYRPLS IGSVIRHLHLKILAKRLAALDI-----FDARQ-RGFR 97
37 SPALL-TSRTVVFV PKKSG---DPDSPG DYRPI SVVVRQLHLKILANRLRASGL-----VDL-RQRC 94
37 PASML-ESRTVFLPKKQ---HSVNPADFRPI S IASVVRQLHLKILAMRLRRTNL-----VDE-RQRC 93
37 PAALR-DARTTFI PKVP---DAVDPQFRPITVASVLQRLHLHLKILAKRLAALDI-----LNFARQ-RAFQ 95
37 PLFLT-QARTIFI PKVP---GASTASQHRPI S ISHVLLRLLHLKILYFRLLADLD-----LDLQ-RAFL 95
37 PDSFL-ESKTTLI PKKP---NSTEPGDFRPI TVQSVLVRQLNKILAAARVAQHIP-----LDERQ-RGFR 95
37 PKHLL-ESRTILIPKKD---NASEPGDFRPIITISVMTRTYHKVIARRFAGSIE-----LDKRQ-KAFX 95
37 PYSIR-LARTIFI PKKA---TANQPQDYRPI SVSPSVVRQLNAILASRLSAIN-----WDTRQ-RGFL 95
37 PHSIR-LARTVFI PKTV---TAKRPQDFRPI SVSPSVLVRQLNAILATRLNSIN-----WDPRQ-RGFL 95
37 PVPFR-MARTIFI PKTV---RANRPQDFRPI SVSPSVVRQLNAILASRLTAAVS-----WDPRQ-RGFL 95
37 PVSIR-QARTIFI PKVP---NASRPQDFRPI TVQSVMVRLNAILASRLTSSVD-----WDPRQ-RGFL 95
37 EILLR-CRTVVFV PKVE---RPGGPGEYRPI S IASILPLRHFSILARLLACCP-----PDARQ-RGFI 95
37 PEHLR-ASRTILL PKKP---GAKVPGEFRPI TVTTSVLIRTFHKVLAERLKVVP-----LDPRQ-RGFR 94
37 PAFML-TSRTVVL PKVP---EPKAPT DYRPI SVSSTVLRLFKHLARLLTASG-----LDLRQ-RGFI 95
37 PRWTK-ENRTTILIAKSA---AAEDVGDWRPI ITIGSHVVRLYAKLLSRLRGSCVQ-----LNLQ-RAFR 96
37 PSAWK-ENRTTILIPKINK---PCSLVENWRPITISPIGRIFSSIIDGRIRRGTV-----LNMQR-KGFT 97
37 PDARW-KNITKLLNKEGK---DPSLPGSYRPI ITISPLFSRIFWGILDQQLRLIRIN-----ITPRQ-KGFI 97
37 SSCWK-EHKTSLIPKDRG---SPMDVSNWRPITIGSLLSRIYTGILERRLRITVSD-----IHQRQ-VGFM 98
37 KAWR-ENRTTILPKPEK---DPADVKNWRPITISSMVSRYVSGLLDQVRVAVIK-----QCDRQ-KGFT 97
37 PAQWK-TNRTTILIPKPKG---SAEEVENWRPITIGSLLGRIYSAMIDRLKRSKIK-----QHIRQ-KGFT 97
37 PAEWS-TNRTTILPKKEG---DASLLANWRPLTIGSLVSRIFWGCVDTRMRVRV-----LTPRQ-KGFI 97
37 PAARW-ENRSVLIPKEGY---DVLISNYRPLTIGSILSRIFWGIIDRLRELLK-----IHRYQ-KGFT 97
37 PECWK-RNRTVFI PKIGK---DLSEVGWRPLTIGSLLARMYSAFLERRIRRVTS-----LSSSQ-RGFT 97
37 PECWK-RNRTVFI PKIGK---DLSEVGWRPLTIGSLLARMYSAFLERRIRRVTS-----LSSSQ-RGFT 97
37 SRLK-KSRTVLLPKSSDPGAEMEIGNWRPITIGSMVLRLFTRVINTRLTEACP-----LHPRQ-RGFR 100
37 PKVFK-KCRTTILIPKTDGVS LHGDVVGQWRPI ITIASVLRLYSRILTERMTVACP-----SHPRQ-RGFI 100
37 GPFK-KCRTTILIPKTDGVS LHGDVVGQWRPI ITIASVLRLYSRILTERMTVACP-----SHPRQ-RGFI 100
37 PRVFK-ECRTKLLPKSSDPVLELDIGGWRPITIGSMVTRLFSRILTMRLTRACP-----INPRQ-RGFI 101
37 PDGLK-ECRSVLIPKTVDRKLGQGNWRPITIGSIVLRLFSRVLTARLAAACP-----INPRQ-RGFI 100
37 DMVR-GCRTVLIPIKSTTPERLKDINNWRPITIGSILLRLFSRIITARMTKACP-----LNPRQ-RGFI 100
37 DMVR-GCRTVLIPIKSSKPRDLKDINNWRPITIGSILLRLFSRIITARLTKACP-----LNPRQ-RGFI 100
37 DMVR-GCRTVLIPIKSSKPRDLKDINNWRPITIGSILLRLFSRIITARLTKACP-----LNPRQ-RSFI 100
37 EIFK-GNRSILLPKGND---GLEDVNNWRPLTIGSVLRLYTSLARVLDSCA-----LNPRQ-RGLI 98
37 PDCWK-LSKTVMLFKKD---DPSLAKNWRPIGITSCTYRIFMTLVNKLQMPIPM-----PHAMQ-KGFV 98
37 PARWD-VARTVLLYKKG---DPNDTGNWRPISLQVTIYKIFTAALSKRLISWAGKHNT---FASAQ-KGFL 100
37 PAPWK-TASTILLHKAG---PTDDPANFRPIALQSCLYKLFMAVLADRLTKWACENQY---LSPEQ-KSAR 101
37 PASWK-TSNTVLLVYKKG---DRDSLENWRPLALGDTAPKLFALADRLTDMTEWAVTNNK---LCPAQ-KGFL 101
37 PASWK-TSNTVLIHKKG---DRGMLENWRPLALGDTVPKLFALADRLTDMTEWAVTNNK---LCPAQ-KGFL 101
37 PSSWK-KAMTVLVYKKG---ERDDPSNWRPISLCSITMYKLYASCLASRI TEWSVSGGA---LTSIQ-KGFM 101
37 PRSWK-KSMTVLIHKKG---ERDDPGNWRPISLCSITMYKLYASCLASRI TEWSVSGGA---LTSIQ-KGFM 101
37 PRKWK-ESVTVLIPKGG---DPKSVKNWRPILNQCIDIYKLYAALWAQKIAAWAKSGV---ASKSQ-KGFM 102
37 PWSWK-TFKTILIPKPKDPTDN YDKVSSWRPIALLSVIYKVFASILTRLTSTNNDI---LHIGQ-KGGS 104
37 PSEK-ASRTIMIPKPKG---SDYSDPSSWRPITISAVYRLLMKYL TWELYNWILLNQ---LSRSQ-KSLG 103
37 PNKWK-TFRTKLIIKPKGEHSPHEVSSWRPILALDITAYRFFATILNRLLSWIAKRLN---LCSNQ-KAVG 104
37 PDMWK-NYTTTILLHKAG---DNDPANFRPIALQSCLYKLFMAVLADRLTKWACENQY---LSPEQ-KSAR 101
37 PLFIT-NGITYMLPKGL---DPTNPANYRPIITCLQTIYKIITACITDI IYKHIDQNNI---LAEQQ-KGCR 102
37 SCRWMRGRTVLLPKKG---DLRLPQNYRPIITCLNTCYKLLTATIAKALLRHLDKGEA---IPQQ-RAIR 102
37 TTGWMCRGRTTILIPKKG---DRGDPNRYRPIITCLNTCYKLVTSVMNSVILSHSRGEA---LPMNQ-RAMR 102
37 PRWLS-EGRVVLLMKKG---DPNDPANRYPIITCLNTCYKLVTSVMNSVILSHSRGEA---LPMNQ-RAMR 102
37 PSARW-RAGGVLI PKEK---VSTDIKQFRNISLLNVEGKLFSSILTCKRMITYLLANNYIDTEVQK-AGVP 103
37 AHQWR-WAEGVWVPKEE---KSTLIEQFRITISLLNVEGKLFSSILTCKRMITYLLANNYIDTEVQK-AGVP 103
37 PVQWR-VAEGVYIPKSAIT-PNEKITITDFRPIALNVEAKMFPAIPAKRLETYMRKNGVLTITVQK-GGVG 105
37 PLCWR-KALTILIHKKG---DANDPANFRPIITCLQVLYKIFSTLKNRHLNFI LQNNFISTNIQ-KGYF 104
37 PTSWS-SGNVSLIHKDG---SPEAAENFRMICTLSCVSKIFHQILSERWAKYMTCNLD-IDPETQKAFIT 103
37 TEYDI-KGNAYAI PKKG---DKNIESNYRFINALNSHYKLLMKLVKCVREWCNLD-IDPETQKAFIT 103
P..hp..sphhhll.K....p.p...p@RPIs1.shh..hh..hspcl1..h.....h...Q..th.
hhh eeeee hhhhhhhhhhhhhhhhhhhhh

Conservation: 2541252 34 11241 22 1 12121331493358763524 25 24 21

6arl_chainD_p001 111 PGRNAHDAVRQA---QGYIQ-----EGYRYVVDMDLEKFFDRVNHDIILMSRVARKVK 159
SLACS 101 G-----HIE---EAIK---IRKDF-----ATKGSALMDGRNAYNAISRAALEAVYGDST 146
CRE1 103 G-----DVA---KAVAK---IRRDS-----EEHEYLVALDGVNAYNTMSRAHILQAVYAEQR 148
CRE2 103 G-----DSTE---VKIR---EAYAE-----ASSDVLVALDATNAYNRMSRRHILEAAYQPE 150
GAU97528_Ramazottius_ 102 SAPGTHVNASIL---GSVSK---KAQAE-----QSTVVVVLIDIKQAFEGILHVHLKDLTLRASPL 155
Blag_1 97 NSPGTLINTSIL---ESILV---AAKSK-----KKDCTIVFLDISKAFDNVGHNLQNSLSALRI 150
Blag_5 97 SSPGTLMTSLL---RSILT---SAKTK-----KCNATLVFLDIRKAFDNVGHNLQNSLSALRI 150
Blag_2 97 NNSGTLINTSIL---RKVLK---TKDN-----KEDVTVFLDISKAFDNVGHNLQNSLSALRI 150
Blag_4 98 SQLGTSINTSLV---DGCLK---KAKLE-----QRNVSVIMLDVAQAFDSVGLDHLEKCLDSQFL 151
Blag_3 97 NVPGTHINTSII---NGCLT---RAKKE-----KRNCCTIAFLDISKAYDNVGHHEHVKRCLLRTNM 150
Blag_6 97 STPGTTFNSSLI---NSCLQ---KSKE-----KGCCTITFLVDISKAFDSVGHNLQNSLSALRI 150
R2_PS 93 SGRSTSENIFLL---RTILE---SLPAG-----KESMYIALLDLFRKAFDSVNHVTLVCGLLRDLGL 146
RaR2 97 PIDGVGNTIHVL---AAILN---DSNTK-----LSELHVALLDITKAFNRLHHTSIKISLVGKGF 150
R8HmA 95 PVDGCFENVKTI---CQVLQ---SYRRK-----KLEHNVVFLIDAKAFDPTVLHDSIRKALWRKGV 148
R8HmB 95 PLDGCFFENVKTI---QCILQ---SYRRS-----RREHNVVFLIDAKAFDPTVLHDSIRKALWRKGV 148
R24_MR 96 PCDGIMSSSTIL---DAIVR---EHRTN-----GKPLYVLSIDLTKAFDKIHPAIIENSINKGV 149
R21_MR 96 KIDGVMANNTIL---QTAIR---TMRNS-----SKPFIISIDLAKAFDRVSIVSIIDALWRRGV 149
R2SmA 96 NRDCGCEAVNLL---HSVIR---HVHTR-----HAGASFALLDISRAFDTVSHDSIRAAKRYGA 149
R2NS1_CSi 96 HRDGCLEATSLL---HALLR---HSSAT-----ASNLSLAFVDISKAFDSVSHDTIVRSAAEFGA 149
R2CiB 96 KVDGICHNIWSL---RSLIH---NSKDN-----LKELNITFLDVRKAFDSISHKSGIAAARLGL 149
R2NvecA 96 KGDGICQNIWLL---HTLIR---RSTD L-----LRPLKLVFLDVKKAFDSVSHESLLIAAKRLGV 149

R21_Mde	96	DCDGTQENLAIL	---NTLLT----	DARKN-----	LKS	THIATLTLDR	KA	FDSVS	HKTI	IDSIT	GMGC	149		
R2A_Nvi	95	VADGVAENTSLL	---SAMK---	EARMK-----	IKGLY	IAILL	DVKK	A	FDSVE	HRS	ILDALRR	KKL	148	
R21_TCas	96	EIDGTLANALIL	---HEYLQ---	YRRQT-----	GRTY	XVVLVD	VRKAF	DTVS	HCSV	SVALGR	FGI	149		
R2LcA	96	PVDGCGENIFLL	---DYILR---	SSKKS-----	SKS	VAMAVL	DVKK	A	FDSVS	HSH	ILRALNE	AKC	149	
R2Ll	96	PVXGCGENIFLL	---DYILX---	NSKKK-----	SKSV	MAVL	DVKK	A	FDSVS	HSH	ILRALNE	AKC	149	
R2La	96	QIDGCAENVFLL	---DFILR---	DAKTK-----	IKSL	SLAT	VDIK	A	FDSVS	HSH	SIFRAIR	GARC	149	
R2LcB	96	QIDGCAENVFLL	---DFILR---	DAKTK-----	IKSL	SLAT	VDIK	A	FDSVS	HSH	SIFRAIR	GARC	149	
R2NS1_SMed	96	ALDGCLENTVLL	---NCILG---	DAKIN-----	NK	SIALSF	LD	IMKFA	FDSVN	HDS	ILRAATI	IAGY	149	
R21_PPap	96	PVDGCGENLAIL	---NELIR---	FSRVN-----	RREL	HLASL	DIS	KA	FDMV	PPQA	INSVAQ	LGA	149	
R22_TCas	98	GVDGIADNLSVL	---DTMLT---	MSRRC-----	CKHL	HLAAL	DVSK	A	FDTVS	HFAI	IVRAC	SIFG	151	
R21_PBa	98	PVDGVCENITVL	---SSVLG---	DARRR-----	CKSL	HVAC	VDLS	KA	FDTVS	HAAI	HRTLE	EELGL	151	
R28_MR	95	FDDGCGENIAAL	---AAVIH---	DSRSH-----	LREL	HVASL	DI	AKA	FDSVS	HQAI	ARVLT	TLGV	149	
R27_MR	94	MDDGCAENITVL	---ASLLD---	DARHG-----	LKE	HLIVSL	DCA	A	FDSV	HHA	IDATL	KCEGL	147	
R21_IS	96	PVDGCAENIWLL	---STALN---	EARTR-----	RRPL	HMAS	VDLT	KA	FDRVT	TDAIL	LRGAR	RAGL	149	
R21_Rmi	96	PVDGCAENILLL	---ATIID---	EARKS-----	LRPL	SLASL	DI	AKA	FDRVL	PAI	LALRR	KGI	149	
R2_FA	96	PVDGVAHNIFEL	---DMILR---	CHRSE-----	FRDL	LRASL	DI	AKA	FDS	INT	HIEDT	MEV	RGF	149
R25_MR	96	PVDGCAENIFDL	---DMVLR---	YHRES-----	FKSI	FMAST	DVA	KA	FDSV	SHRAMY	DTLR	SKGV	149	
R2_Dan	96	PTDGCADNTTIV	---DLVLR---	EHHKR-----	FK	SCYIGT	LDV	SKA	FDAVA	HEAVY	TNLAS	YGA	149	
R2_DSi	96	PTDGCADNATIV	---DLVLR---	HSHKH-----	FRSCY	IANL	DVSKA	FDSLS	HS	IYD	TLRAY	GA	149	
R2B_DM	96	PTDGCADNATIV	---DLVLR---	DHHKR-----	YASCY	IATL	DVSKA	FDSVA	HDAV	FNVT	YTAY	GA	149	
R2_DPe	96	PTDGCADNTTIV	---DLILR---	DHHKR-----	CKSLY	THATL	DIS	A	FDSV	SHAAVS	ATLT	AYGA	149	
R2_BM	96	CADGTLSENSAVL	---DAVLG---	DSRKK-----	LRECH	VAVL	DFA	KA	FDTVS	HEAL	VELL	LRGM	149	
R2C_Ngi	95	ESDGCENVMML	---DMTIR---	YHHER-----	RRKM	FLLAL	DM	A	FDSV	SFESM	REVL	TTKGI	148	
R2_AM	96	PVDGCAENLVLL	---ESAIR---	SAKNY-----	KRSL	FVASM	DI	KA	FDSVA	HEA	IFEAL	SKGA	149	
R2Cid	97	DVQGCENVMML	---SGMIR---	DAKAR-----	SRDL	NLV	FLDL	PA	FDSV	HSSIV	KALRR	QGV	150	
R21_BTe	98	SENGCKINIELL	---NSALN---	YSKR-----	NSGG	IPTIV	D	ISKV	FDPV	HAAL	KPCL	AKKGV	150	
R22_MR	98	PEMGCFLNVNLL	---NEIIR---	IAKR-----	KQGI	VITQ	VDIS	KA	FDTVP	SFAIL	NALNA	KGL	150	
R2_KF	99	PVNGCAANLFI	---DECIR---	QAKK-----	EGT	IVGSL	DI	KA	FDTVP	HEA	ILRAL	SSQV	151	
R2B_Nvi	98	EENGCFPSNIQLL	---DDAVS---	NAK-----	KAGG	VITIL	D	VS	KA	FDPV	HAVIQ	GCLE	KKGI	149
R2Amel	98	QEDGCKNNIAIL	---SSALT---	KMKE-----	DSGG	IITIL	D	ISKAF	FDPV	HCEI	ISQ	LMNKV	150	
R2_Rn_ribo	98	AEAGCFNNVLL	---DSVLR---	HAKC-----	GGGV	VAVQ	LD	IS	KA	FDTVP	PGT	IATALL	RKGL	150
R2_Bg_ribo	98	TEPGCYQNVRI	---SEVLR---	QAKS-----	ARGL	VAVQ	LD	IS	KA	FDTVP	HAAI	ATVLR	RQGL	150
R2_RU	98	NIQGGCHVNLTL	---KEGIR---	QAKV-----	KNGG	VIVSD	I	IE	KA	FDTIP	HSVIF	SR	LASQGV	150
R2_RL	98	NIQGGCHVNLTL	---KEGIR---	QAKV-----	KNGG	VIVSD	I	IE	KA	FDTIP	HSVIF	SR	LASQGV	150
R2Dr	101	RSFGCSENLEVL	---ECLLR---	HSKEK-----	RSQ	LAVV	FVD	FA	QA	FDTVS	HEHML	SVLE	QMN	154
R21_GA	101	ASPGCSENLMML	---EGCMS---	LSKAG-----	NGSL	LAVV	FVD	FA	QA	FDTVS	HEHML	SVL	VQKGL	154
R21_SSa	101													

R21_MDe	150	PKMFIDYVTDLYLN-----ARTVFQYNG-----SSTFLDIKRGVLQGDPLSPLLFNL	196
R2A_NVi	149	PLEMRNYIMWVYRN-----SKTRLEVVK-----TKGRWIRPARGVRQGDPLSPLLFNC	196
R21_TCAs	150	PSVIREYILATFGA-----QTTIKCGS-----VTRPRIMRLRGVRQGDPLSPVLFNL	196
R2LcA	150	PINFINFVRNSYDG-----CTTKLTCGG-----TSFPDSVRMNRGVKQGDPLSPVLFNL	198
R2Ll	150	PVNLXNFVRNSYDG-----CTTKLTCGG-----TSSPDSVRMNRGVKQXXPLSPVLFNL	198
R2La	150	PENLVNYIQNSYSG-----CTTQISVGG-----SISASKIPMNRGVKQGDPLSPVLFNL	198
R2LcB	150	PENLVNYIQNSYSG-----CTTQISVGG-----SISTTKILMNRGVKQGDPLSPVLFNL	198
R2NS1_SMed	150	PKLLLGIKESYNG-----ADTEVEK-----IKATFKRGVQGDPLSPVLFNN	192
R21_PPap	150	PQNLVEYLKGLYAN-----NQTTLEYGG-----SELYCRVKRGVRQGDPLSPLLFNL	196
R22_TCAs	152	-----SAETVLEEG-----GRRHFVQVRXGVRQXDPLSPLLFNL	185
R21_PBa	152	PREFRDYVRAIYAE-----ARTVLQPTG-----RQRMSPIHVGRGVQGDPLSPLLFNL	200
R28_MR	149	PCELVSYVTTMYAR-----SSTMFEVRG-----QRSELPFVGRGVQGDPLSPILFCL	196
R27_MR	148	PAGFVQYISRTYSYD-----SSTRLEVGR-----NRSEP1KTNRGVRQGDPLSLIFCL	195
R21_IS	150	SGEFIGYLKELYTT-----SRTLLQFQG-----ESLLVEPTTGVVRQGDPLSPILFNL	196
R21_RM1	150	SEDFISYIEDFYQN-----AVTVLTFGG-----KSLVVHPTVGVRQGDPLSPLLFNL	196
R2_FA	150	PKPMINYIMACYRR-----SKTRFTFNG-----WISDTVKPTCGVRQGDPLSPILFNL	197
R25_MR	150	PAPLVEYVRDVER-----STTRLTGSD-----WQSDLIRCGVKQGDPLPPIIFNM	195
R2_Dan	150	PKGFINYLKAYEG-----GGTMLAGNG-----WVSEAFIPARGVKQGDPLSPILFNL	197
R2_DSi	150	PKGFVDYVQNTYEG-----GGTSLNGDG-----WSSEEFVPARGVKQGDPLSPILFNL	197
R2B_DM	150	PKSFVDYVRRWYSG-----GGTYFNGGD-----WRSEEFVPARGVKQGDPLSPVLFNL	197
R2_DPe	150	PKEFVDYVQNSYEV-----CGTTLNGDG-----WRSEEFIPARGVKQGDPLSPILFNL	197
R2_BM	150	PEQFCGYIAHLYDT-----ASTTLAVNN-----EMSSPVKVGKRGVRQGDPLSPILFNV	197
R2C_NGi	149	PTPFIEYFMTHLED-----SFTVLQHG-----WQSGKIHPTCGVKQGDPLSPPIFNF	196
R2_AM	150	PDSFVTYVRNCYDG-----FASVVKLG-----RDTAQTTVRQGVVQGDPLSPILFNL	196
R2CiD	151	PEKFVRIVQDLYDG-----AVTTVSVGG-----RATPQLVVKRGVKQGDPLSPLLFNL	198
R21_BTe	151	PALIVDLIDEMYKN-----VKTTIKTKD-----GGVEIMIRRGVKQGDPLSPLLFNL	197
R22_MR	151	PKVVVQLIMDSYNS-----ISTQIQYQS-----STFDISIKRGVKQGDPLSPILFNI	197
R2_KF	152	DEHTMAHIRMYSYG-----IRTRINGKG-----SDIPLVGRGVKQGDPLSPMLFNM	196
R2B_NVi	150	PETVAAYISSMYRD-----CSTAIRTRS-----GDVKIGMKRGVKQGDPLSPILFNL	196
R2Amel	151	PSPICEYIQKMYIG-----CKTIIYCRD-----KKTLPVILRGVKQGDPLSPLLFNL	198
R2_Rm_ribo	151	PPFLANLVSRAYVG-----QRTHLNVRG-----EKVEVRNPLVIVRGQGDPLSPMLFNL	198
R2_Bg_ribo	151	PPYFADMVRRSYEG-----AYTSIRVRD-----HRIQLELRGVKQGDPLSPILFNM	197
R2_RU	151	PPLLRKIIISNMKYD-----VYTVIEGQ-----CIPIKRGVKQGDPLSPLLFNI	193
R2_LR	151	PPLLRKIIISNMKYD-----VYTVIEGQ-----CIPIKRGVKQGDPLSPLLFNI	193
R2Dr	155	DPHMVNLIIRIYTN-----SCTSVELGR-----KEGPDIPVRVGKQGDPLSPLLFNL	202
R21_GA	155	DQHMVELIKDSYEN-----SVTKVHCQE-----GCSTD1AMKVGKQGDSPMLFNL	202
R21_SSa	155	DEHIIIGVGDSTDT-----VTTTITVSG-----EQSPPIDMRVGKQGDPLSPMLFNL	202
R2O1A	156	DRHVIGLIRNSYVD-----CVTRVGCVE-----GMTTPIQMKVGKQGDPMSPMLFNL	203
R21_Gav	155	DEHIVNLIEDSYQK-----VTTTRVQFN-----GVTTPPISIKTGKQGDPMSPMLFNI	202
R21_ZA	155	DPHIVGLVNMYKD-----ISTYVTTKK-----NTHTDKIQIRGVKQGDPLSPLLFNL	203
R21_TG	155	DPHIVGLVSNMYEN-----ISTYITTKR-----NTHTDKIQIRGVKQGDPMSPMLFNL	203
R21_GFo	155	DPHIIGLVKNMYKD-----ISTVITTKK-----NTYTDKIQIQGVKQGDPLSPLLFNL	203
R2NS1_CGi	153	PEHFDIVADLYNG-----ASTVFQTD-----GQTGEIPMTRGVKQGDPLSPLLFNI	200
NeSL1_TV	153	PDSIINLLKDLKYG-----ARTAIYTRH-----AHSEIVPVRRGVIGQCCLSPILFNC	200
Utopial_ACa	155	PRYLRLDAIGAIRYH-----SALFVQVGD-----QETTGVIPIRMCGVKQGCPLSPLLFNL	203
Utopial_LV	156	PDLSLVTLLMDAYNG-----ASTSFTLTG-----GQTDTPVIRSGVKQGCPLSPILFNL	203
Utopial_CF1	156	PGGLVNVWNSMYDG-----CSTRVRTAE-----GYTTPVLIRSGVRQGCPLSPIVFDL	203
Utopial_AEc	156	PRGLIAIWDSMYDG-----CTTRVRTAE-----GHTAPIPIRSGVRQGCPLSPILFNL	203
Utopial_CMy	156	PENFLRVIREVYEG-----CSTTIRSV-----GETAEPIIRSGVKQGCPLSPILFNL	203
UtopialB_CPB	156	PETFIQILRLDYKD-----CTTTIRATD-----GETDAIPIRRGVKQGCPLSPILFNL	203
Utopial_ENe	156	PKHAQEVIMDLYQG-----ASFCLTKE-----GCTGRIVNQRGVKQGCPLSPILFNL	204
R52_SM	160	SEEFITIVKLLYTD-----TQSFYSYCGP-----IVTPNLSIKKGVKQGCPLSPMLFSI	207
R5	167	GTSALTILKNLYLD-----NYTNVTCGE-----SKIENVKLNKGVKQGCPLSMLLFNI	214
R51_SM	159	KNKTINLIKDMYND-----CYTVYECGE-----KHTKTIKVNNGVKQGCPLSMTLFSL	206
LIN9_SM	161	DEETINLLKEIYKD-----CSTKYKCGK-----NESEKIKITKGVKQGCPLSMTLFSL	208
R4_Hmel	156	HPLLITLSSVMLS-----WKTRLKLINNN-----ETLITDWIKIQRGIFQGDALSPILFNL	207
R42_AS	159	KTITATFFKLMDAG-----WETRYELKYKTKRGCMISIQRSQPVKIVNGIFQGDALSPILFNL	215
R4_AL	159	PRSVQLTLKRLMSD-----WETRFESTQCR-----PKLRSDMKMVLNIFQGDALSPILFNL	215
R45_BX	163	DRKIYYLLKSFMTMN-----WTVRYELRRSG-----RVERSAPIRLVRKGLLQGDALSPILFNL	214
HERO1_BF	158	PETIRYTMQNYFQD-----FRVSVTTPQ-----FTTGWQQLLEKGIAMGCTISPLFVL	205
HEROTn	158	PCSIKTLIMDYYS-----FHLRFVTSG-----SVTSEWHRLEKGIITGCTISVILFAL	206
HERO1_HP	160	PESLVSIMNNYYVG-----LYARFSVKD-----WNSEWQKFSVGIFPMGCTLSPILFVI	207
HERO1_SR	159	QPLFRNLISYSS-----YAISVSIND-----QLTPLVVRKGLVQGDPLSPILFNL	206
HERO3_BF	158	PPIITTYIKNLYSR-----LKGKVKGPG-----WESDPPFFGRGVFQGDNLSPILFLT	205
R44_Sra	151	IPKPIRNLCKLPKMYKFSVNCSPNDRENGKIIKE-----KKKSWTIMKRGIVQGCCLAPLWFLCL	211
Consensus_aa:		s..h..hl..hh.s.....h.h.....s..h.hppG1.QGssLSPHFs1	
Consensus_ss:		hhhhhhhheeeeee	eehhhhhh
Conservation:		244 32 411 1 21 2112275993242414 131 12113 2 1 14513	
6ar1_chainD_p001	202	LLDDLDKELEKRG-----LKFCRYADDNCNIYVKSIRAGQRVKQSIQRFLKTLKLV	253
SLACS	196	GTLATLRLRLQQTFF-----EAQFTAYLDDVTVAAP-----PEELKNVCAATAEAM-----EALGIVN	247
CRE1	198	GMAAAIGPVRQRIP-----GVPVTAYIDDTLAAASGAEGA-----RAAEAYADAL-----ETVGVVT	249
CRE2	200	AMSGIIRPLMEMHP-----RVKVVAYLDDVTLIGP-----HAAVQDFLAEAGPQL-----SRVGFDI	251
GAU97528_Ramazottius	204	STDYVTRNMTEAPIAAEYGFPL-----CEGEQPVTFGLFADDSTVVGKSRREEAIQLEMAIGLF-----KEIGLEV	269
Blag_1	199	STDHILDELSNQELQDEYGFSSV-----SPGLSNITAGLFADDTLIAAKSMNSARILVELAMSRF-----KEIGLDI	264
Blag_5	199	STDHILNELSEDEGVAKAYGYQL-----VPGLKPVTVLGFADDTVIVANS-----TTSALETLMKAIERF-----RSIGLEI	264
Blag_2	199	ATDFIFDELTELSSLQQYGKSI-----SPQLSSLSIMGFADDTLLMGKNS-----ETTLELHIALQRF-----QEIGLQV	264
Blag_4	200	SIDFIIKELSEKQITDKYGFKI-----SNNLDHLSVAAFADDLVVIGQN-----MHAARELVMMTKYLL-----QQIGLQL	265
Blag_3	200	ALDDTLKELADPNVREVFGLSL-----HPDLEKVSGLAFADNIALISKDEASIQTLINMTVFNL-----DAIGLKV	264
Blag_6	199	SIDFIYRNLDNFQNASQGYRL-----TEEVNDLIALSFADDIALISNN-----TSAVFMIERVYNQCL-----TEIGLNL	265
R2_PS	190	MIDYILSGTQAGVGVG-----VGERLVSSLAYADDLALLASSRRGLNANLESVLARA-----RSVNILAL	248
RaR2	198	AIEKGLQALDKVEGYD-----IGDVRVNAGAYADDTDLVAGTRLGLQDNLNRRSSSTI-----KQVGLLEV	256
R8HmA	197	ILDELAERIEATGCGLD-----LDGHVLSMAFADDYVLLAKDSVEMNELIRVCSSTFF-----KEKGLSV	256
R8HmB	197	VIDELAERLEATGCGLD-----LEGHVLISSMAFADDYVLLAKDSVEMNVLNMVNCNTFF-----EKGGLAV	256
R24_MR	198	AIDDLVTSINTTDGVQ-----LGNSKIGCLLFADDIIFVSNTVHGINEHLRLRLAFL-----EGTHMEV	256
R21_MR	198	VLDGLLQKLDHDTGIQ-----INGTNIAALAFADDIVLMAPTMIMRSHIRIVESYF-----RRHGFV	256
R2SmA	193	VLDLLEGLDPMTHLT-----VDGESLNYIAYADDLVVFPAPNAELQKRLKLDRLSLLL-----HEAGWSI	251
R2NS1_CSi	193	AMDEVGLSLMPQLGYQ-----FHDTLVDFGAFADDDWVVCASQARLKEKLEAAAVEL-----GRAGMKI	251
R2CiB	198	VMDWALSELDPRVGVQ-----IGEQRINHLAFADDILVSSSTKIGMVSSINTLSRHL-----AKSGLEI	256
R2NvecA	198	VIDWAVSDLDPHIGVL-----LGESRVSLFAYADDVLVLLSETEAALTSQLNSTIEKSL-----AHCGLKL	256

R21_MDe	197	VMDRAIVKLSANIGYT-----YNGAI	INCIA	YTD	II	LIAETKCGLQSLIDALTSEL	-AS	FGLQT	255																																																								
R2A_NVi	197	VMDAVLRRLLPENTGFL-----MGAEK	I	GALV	FADD	LVL	LAET	REG	QASLSRIEAGL	-QE	QGLEM	255																																																					
R21_TCAs	197	VMDELLLEKVNKEYEGGSL-----QSGER	CAIMAF	ADD	LIL	LADRDQDVP	PAMFDDV	STFL	-ERR	GMSV	257																																																						
R2LcA	199	IIDS	AI	RKLP	DSIGYVI	-----RDGLK	INCLAY	ADD	LIL	VASSRAGLKTLLN	IVAEHL	-SLR	GLDL	258																																																			
R2L1	199	IIDS	AI	RKLP	DSIXYLI	-----RDGLK	INCLAY	ADD	LIL	VASTRAGLKTLLN	IVAEHL	-SLR	GLDL	258																																																			
R2La	199	VINEI	IRKLP	PASIGYPI	-----NSEL	SINCIAY	ADD	LIL	VNTREG	LKLLGLL	NEEL	-PKR	GLEL	258																																																			
R2LcB	199	VINEI	IRKLP	PASIGYPI	-----NSEL	SINCIAY	ADD	LIL	VANTREG	LKLLNLL	NEEL	-PKR	GLEL	258																																																			
R2NS1_SMed	193	IVELA	IKKAYE	SGIGYR	-----MNGT	VFP	IMAY	ADD	LIL	SESGEGQLDL	IVLT	TEL	-RHNG	LEA	252																																																		
R21_PPap	197	VMES	ALVRL	DKKLSFS	-----LYGV	SVNGLAY	ADD	VIL	VAST	SGGLQKNT	ESFL	GAL	-REI	GLDL	255																																																		
R22_TCAs	186	VLD	RALKRL	STDV	GFRL	-----T	DAT	KVTALAF	ADD	VVL	CATT	ARG	LQTN	LDVLE	AEL	-RLAG	LLLL	245																																															
R21_PBa	201	VVDR	ALGIL	SEDV	GYR	-----L	ESRL	INALGY	ADD	IVLL	SSTK	I	GLQEN	LTRL	LHA	AAF	-LQN	GLTI	259																																														
R28_MR	197	VVDS	ILRT	VPPD	VGYD	-----L	GGS	RLNALAY	ADD	FLL	FAAS	VWG	MQEST	LGLVE	QRA	-GEY	GLTF	255																																															
R27_MR	196	CFDR	VARTL	SPHIGYD	-----L	NNTRI	STLLY	ADDA	FLVSTT	APGMN	ILLRS	VEESA	-GE	VGL	SF	254																																																	
R21_IS	197	VLDE	YLS	SLDP	DIS	FFV	-----S	GD	RLRD	AMAF	ADD	LIV	FAST	PAG	LQDR	LDAL	VEFF	-DPR	GLRV	255																																													
R21_RM1	197	VIDE	FLAEL	DPQL	LAFT	-----S	EGMK	VSA	MAF	ADD	ILT	TAT	HWGL	KQQL	IDRLN	SFL	-GARG	LKI	255																																														
R2_FA	198	VMDR	MIRKL	PKPE	GVN	-----V	GSKHYN	GLTF	ADDD	LLL	FATT	PEGL	QSS	DI	IVHL	FL	-LEC	G	LLI	256																																													
R25_MR	196	IIDR	LLKL	IPPE	IGVD	-----V	GESH	FNALAF	ADDD	LLF	MAST	T	KGL	QT	CLD	LASE	YEL	-LKC	GLRV	254																																													
R2_Dan	198	VIDR	LLRSL	P	SEIGAK	-----V	GNAIT	NAAAF	ADD	IVL	FAET	PMGL	QK	LD	TTV	CF	-SSV	GLTL	256																																														
R2_DSi	198	VMDR	LLRNL	P	SEIGAK	-----V	GNAIT	NAAAF	ADD	LVL	FAET	RMQ	QVLL	DKT	LD	FL	-SLV	GLKL	256																																														
R2B_DM	198	IIDR	LLRSL	PKD	IGVH	-----V	GNAK	VNACAF	ADD	LML	FAST	P	KGL	QEL	LNTT	V	KFL	-SSV	GLTL	256																																													
R2_DPe	198	IIDQ	LLRSY	PNE	IGAT	-----I	GDHT	TNAAAF	ADD	IVL	FAET	RL	GL	Q	TM	LD	TTV	DFL	-SSV	GLTL	256																																												
R2_BM	198	VMD	LILAS	LPER	VGYR	-----L	EMEL	V	SALAY	ADD	LVL	L	AGS	IDG	AQD	HDV	Q	GRY	M	-RQM	GLRL	256																																											
R2C_NGi	197	IMDE	MLKRL	PKPE	IGVN	-----L	DGL	FVN	AMAF	ADD	LSL	VAN	TE	QGL	QIL	IDE	ATS	SFL	-GLC	GLRA	255																																												
R2_AM	197	VIDQ	IIRSL	P	ETVGV	QL	-----D	ANT	KLNS	MAF	ADD	LIL	SSS	EAG	MRR	ML	GVL	AGVS	-SKF	GLFI	256																																												
R2CiD	199	VLD	ELIDEL	SSS	FGYTL	-----D	GS	KL	SVMAF	ADD	VLS	SGS	L	AG	RLK	LETT	I	VH	FL	-LRC	G	MGL	258																																										
R21_BTe	198	CLEP	LEEIEE	EQAS	GINV	-----S	HRK	VSVLAF	ADD	IVLL	GAD	ARE	AHQ	Q	IN	VT	DYL	-QSL	MMNL	258																																													
R22_MR	198	VMS	LI	LKLES	MPG	FKI	-----N	DR	TNLS	SLAF	ADD	LMF	LAD	N	VED	ARA	Q	LN	L	CQ	FL	-DSV	MDMI	257																																									
R2_KF	197	VMD	PI	IRD	LQ	RKGR	-----I	GHE	I	ALAF	ADD	IVL	L	ADS	IDG	AQD	HDV	Q	GRY	M	-NKL	G	MTL	254																																									
R2B_NVi	197	VLEP	LLER	LQET	SGVE	-----I	EGM	NLS	CAAF	ADD	IVC	F	ANT	A	PE	AGR	Q	LR	M	VAD	YL	-GR	L	MSL	255																																								
R2Amel	199	IIDP	I	IGTL	DETT	EGIK	-----L	ENEN	I	SVLAF	ADD	LVL	L	AKD	KET	AD	K	Q	N	L	RI	NE	YL	-D	LM	KMV	258																																						
R2_Rm_ribo	199	IMEP	MINE	LES	KPGYR	-----D	ETQ	I	SSLV	FADD	LIL	L	AD	PA	K	Q	IN	VT	DYL	-C	N	L	G	MSL	258																																								
R2_Bg_ribo	198	IMEP	LLNK	LES	LG	V	TL	-----A	DGS	QLAC	LAF	ADD	LIL	L	AD	N	R	E	R	E	L	L	T	E	E	F	L	-D	L	G	M	K	I	257																															
R2_RU	194	AIDP	V	LR	S	LEEF	Q	GG	LP	-----L	GNS	A	K	I	L	A	F	DD	I	L	G	A	S	A	G	A	Q	Q	M	V	D	M	L	G	I	G	L	-T	S	C	G	L	G	V	253																				
R2Dr	203	ALD	P	L	I	Q	S	L	E	R	T	G	K	C	E	-----A	B	E	G	H	K	V	T	A	L	A	F	ADD	L	A	L	V	A	G	S	W	E	G	M	A	H	N	L	A	L	V	D	E	F	C	-L	T	T	G	L	T	V	262							
R21_GA	203	ALD	P	L	I	Q	S	L	E	R	E	G	R	G	F	P	-----V	G	N	K	S	I	T	A	M	A	F	ADD	L	A	I	V	S	D	S	W	E	G	M	R	A	N	L	D	I	L	V	D	F	C	-E	L	T	G	M	R	T	262							
R21_SSa	203	ALD	P	M	I	D	T	L	E	R	Y	G	L	G	Y	R	-----M	G	E	Q	I	T	A	L	A	F	ADD	L	V	L	V	S	D	S	W	E	G	M	A	C	N	I	R	L	E	E	F	C	-R	L	T	G	L	R	I	262									
R2O1A	204	AMDP	L	I	H	K	L	E	T	A	G	T	G	L	K	-----W	G	D	L	S	I	A	T	L	A	F	ADD	L	V	L	V	S	D	S	E	E	G	M	C	R	S	L	G	I	L	E	K	F	C	-Q	L	T	G	L	R	V	263								
R21_Gav	203	AMD	P	L	I	A	K	L	E	T	D	G	Q	G	V	-----V	G	S	A	S	L	T	T	L	A	F	ADD	L	V	L	L	S	D	S	W	E	G	M	L	K	N	I	S	I	L	E	D	F	C	-N	L	T	G	L	R	V	262								
R21_ZA	203	AMD	P	L	L	K	L	E	S	S	G	K	F	H	-----R	G	Q	S	S	I	T	A	M	A	F	ADD	L	V	L	L	S	D	S	W	E	G	M	A	C	N	I	R	L	E	E	F	C	-R	L	T	G	L	R	V	263										
R21_TG	204	AMD	P	L	L	C	K	L	E	S	S	G	K	Y	H	-----R	G	Q	S	S	I	T	A	M	A	F	ADD	L	V	L	L	S	D	S	W	E	N	M	N	T	N	I	S	I	L	E	T	F	C	-N	L	T	G	L	R	V	263								
R21_GFo	204	AMD	P	L	L	C	K	L	E	H	G	K	F	H	-----R	G	Q	S	K	I	T	A	M	A	F	ADD	L	V	L	L	S	D	S	W	E	D	M	N	A	N	I	K	I	L	E	T	F	C	-D	L	T	G	L	R	V	263									
R2NS1_CGi	201	AMD	P	L	L	E	I	G	R	Q	N	G	Y	-K	F	G	P	-----E	E	S	D	R	I	E	S	L	C	Y	A	D	D	N	A	L	M	T	E	S	P	D	M	N	E	N	A	L	V	E	K	F	C	-C	E	T	G	M	R	L	263						
NeSL1_TV	201	CLD	P	L	L	Y	A	V	Q	R	R	H	F	E	D	Y	R	F	Q	D	-----K	A	G	Q	Y	S	I	A	I	Q	A	Y	A	D	D	V	L	V	I	S	P	T	H	E	G	M	Q	R	I	L	N	T	V	D	E	F	Q	-K	I	A	K	L	K	V	266
Utopial_ACa	204	CVEP	A	L	R	C	L	R	R	T	T	G	Y	K	F	Y	-----G	T	S	I	T	V	E	G	Q	A	Y	A	D	D	L	L	T	A	P	S	A	Y	H	A	A	R	Q	V	A	T	I	E	E	W	A	-N	W	A	G	V	S	F	264						
Utopial_LV	204	AIE	L	I	I	R	A	V	K	N	A	S	D	N	H	L	G	V	T	-----V	Q	G	K	N	L	S	I	L	A	Y	A	D	D	L	V	L	S	R	D	T	E	G	L	Q	S	L	L	V	A	G	S	S	A	-S	T	L	Q	M	Q	F	267				
Utopial_CF1	204	AID	S	V	L	R	A	V	T	A	V	D	A	G	F	D	-----L	L	G	S	R	H	S	V	V	A	Y	A	D	D	I	A	L	V	A	D	S	P	E	G	M	R	R	L	L	A	V	A	E	G	A	-S	S	V	G	L	R	F	263						
Utopial_AEc	204	AID	S	V	R	V	A	A	E	X	N	D	G	S	Y	-----L	H	G	N	T	W	S	A	L	A	Y	A	D	D	I	A	L	L	A	Q	T	P	E	G	M	R	M	L	A	S	V	E	A	E	A	-A	S	V	G	L	R	F	263							
Utopial_CMy	204	AMEP	L	L	R	A	I	S	N	G	T	D	G	F	N	-----L	H	G	E	R	V	S	V	L	A	Y	A	D	D	L	V	L	T	A	D	D	P	E	S	L	Q	G	M	L	D	A	T	S	R	A	A	-D	W	M	G	L	R	F	263						
UtopialB_CPB	204	AMEP	L	I	R	A	I	S	S	G	P	T	G	F	D	-----L	H	G	K	I	S	I	L	A	Y	A	D	D	L	A	L	V	A	D	S	S	E	S	L	Q	M	L	D	V	T	S	Q	A	A	-E	W	M	G	L	R	F	263								
Utopial_ENe	205	AIEP	L	L	Q	R	L	A	A	C	N	E	G	L	R	T	T	D	-----G	K	P	Q	V	K	V	S	H	M	A	Y	A	D	D	L	K	T	V	A	A	T	R	V	G	I	S	K	L	H	Q	V	E	D	F	L	-Q	W	T	G	L	K	A	270			
R52_SM	208	AINP	V	L	E	A	I	S	R	S	C	I	E	P	M	-----I	G	D	S	P	V	Q	L	A	Y	A	D	D	I	A	L	V	A	N	N	V	E	N	I	Q	K	I	V	D	V	A	E	A	-T	E	I	G	F	E	Y	268									
R5	215	F	I	N	I	I	R	A	I	E	A	M	P	D	V	H	G	Y	P	-----L	G	D	M	D	I	R	I	L	A	Y	A	D	D	I	A	L	I	S	D	S	H	K	D	I	Q	E	M	V	Y	K	A	E	Y	I	G	-R	I	L	G	L	L	F	276		
R51_SM	207	T	I	N	F	I	L	Q	N	I	L	K	E	Y	P	L	I	-----I	H	N	H	N	I	S	I	M	A	Y	A	D	D	L	V	L	I	A	D	T	R	E	K	M	R	K	M	I	K	D	I	T	K	Y	-D	S	A	T	L	K	F	265					
LI	209	C	I	Q	I	Y	L	I	Q	I	A	E	K	K	G	A	T	-----I	A	G	E	V	C	I	L	A	Y	A	D	D	L	V	I	V	A	N	T	A	K	D	M	Q	M	L	L	T	T	I	E	N	L	A	-Q	Q	A	D	L	I	F	268					
R4_Hmel	208	ALN	P	L	S	E	L	L	N	N	T	N	T	G	F	L	K	H	N	-----N	T	Y	H	I	I	S	H	L	M	Y	M	D	D	I	K	L	Y	A	S	N	N	K	E	L	K	I	A	D	L	V	A	S	-T	D	I	R	M	E	F	271					
R42_AS	216	S	V	S	P	I	S	A	L	E	N	K	A	K	P	Y	R	S	S	V	Q	-----L	S	G	K	G	F	S	L	G	H	Q	F	Y	V	D	D	L	K	I	Y	A	P	N	R	E	L	V	N	A	L	V	A	K	N	S	-T	A	I	G	L	D	L	282	
R4_AL	211	C	I	A	P	I																																																											

R21_MDe 256 NIG-----K**SSTIS**LV--PSGRQKK-----IKVITEPS**F**L--VSG---QFLSAIGVMDVWRYLYG 302
R2A_NVi 256 MPR-----K**CHT**LALV--PSGKEKK-----IKVETHK**P**FT--VGN---**Q**ET**Q**LGHADQWKYLYG 302
R21_TCAs 258 NPA-----K**CRA**LIAI--AVSGR-----**S**V**V**RTGSS**Y**K--IHN---**T**PIPNVDALDA**F**KYLYG 302
R2LcA 259 NAA-----K**CH**GLSII--ASGKAKT-----TYVSAAD**S**LD--LDG---QPIKNLGVLDTW**T**YLYG 305
R2Ll 259 NAA-----K**CH**GLSII--ASGKAKT-----TYVXALES**L**D--LDG---QPIKNLRLVLDTW**T**YLYG 305
R2La 259 NAS-----K**CF**GLSLT--ALGKLKK-----THLCTSDQ**L**D--LHG---TLIKNLTA**E**ESWVYLYG 305
R2LcB 259 NAS-----K**CF**GLSLT--ALGKLKK-----THLCTSDQ**L**D--LHG---TLIKNLTA**E**ESWVYLYG 305
R2NS1_SMed 253 NAD-----K**CAS**I**I**AK--KDGQKQ-----KWVISSDS**V**L--AAG---K**T**MP**CM**NANSM**Y**KYLYG 298
R21_PPap 256 **N**LA-----K**CK**SLSLK--PSGRDKR-----CKVLS**E**S**Q**LS--IGG---**T**SV**P**QVDLV**G****F**WRYLYG 302
R22_TCAs 246 **N**PN-----K**Q**AL**S**LV--ASGR**D**HK--VKLVTKPT**F**K--V**G**Q---N**T**I**H**QVDASSI**W**KYLYG 292
R21_PBa 260 **N**AN-----K**T**GVLSMV--ASGRDKK-----VKIDMT**P**Y**F**T--V**G**G---**A**LIP**Q**RS**P**VD**T**WYLYG 306
R28_MR 256 **N**AQ-----K**CS**VLSLV--PSGDKDK-----MKVIT**P**L**F**H--LGRQ---A**F**IP**Q**IT**T**AE**W**RYLYG 303
R27_MR 255 **N**TS-----K**C**SALSLI--PSGKEKK-----MKVGT**T**PT**F**K--**T**SQ---G**F**IT**Q**IT**P**S**Q**EWRYLYG 301
R21_IS 256 **N**VK-----K**S**FTLSLQ--PGRDKK-----KV**V**CD**Q**I**F**T--**I**G**G**---**T**PL**P**ASKVAT**P**WRYLYG 301
R21_RMl 256 **N**AA-----K**S**TT**L**IV--PSGWQKR-----SKIR**T**DI**D****F**F--V**N**G---E**R**L**A**TT**N**CT**T**STWRYLYG 302
R2_FA 257 **N**KQ-----K**S**FVLTVK--AYPKLKK-----TAVIVTE**K**Y**M**--L**D**R---HIL**P**AID**R**EKL**F**HYLYG 303
R25_MR 255 **N**AX-----K**S**FT**V**ALR--NVPHVKK-----SXVDGKV**R**FR--C**L**G---H**E**MPS**L**TRED**Q**WRYLYG 301
R2_Dan 257 **N**TD-----K**C**FT**V**SIK--GQAKQK-----CTV**V**ERR**S****F**L--**I**G**G**---R**E**CP**S**L**K**RTDEW**K**YLYG 302
R2_DSi 257 **N**AD-----K**C**FT**V**GIK--GQPKQK-----CTVLEA**Q**S**F**Y--V**G**S---R**E**IP**S**L**K**RTDEW**K**YLYG 302
R2B_DM 257 **N**AD-----K**C**FT**T**SIK--GQPKQK-----VT**V**VE**Q**RT**F**C--**I**G---R**A**RV**Q**L**K**RS**E**EW**K**YLYG 301
R2_DPe 257 **N**SD-----K**C**FT**V**GIK--GQPKQK-----CTV**V**IP**E**T**F**R--**I**G**S**---R**S**CP**A**L**K**RTDEW**K**YLYG 302
R2_BM 257 **N**CR-----K**S**SS**F**LIT--PDGHRKK-----HHY**L**T**E**RT**F**N--**I**G**G**---K**P**L**R****Q**V**S**C**V**ER**W**RYLYG 303
R2C_NGi 256 **N**PN-----K**C**VT**L**AIK--TIPKEKK-----**T**AID**P**SS**H**FR--**I**G**N**---A**V**IP**S**L**K**RTDEW**V**YLYG 302
R2_AM 257 **H**PG-----K**C**TY**L**AMI--WAGQKQK-----MK**I**A**T**DL**S****F**E--**I**G**G**---G**F**MT**P**V**G**VT**E**TW**K**YLYG 303
R2CiD 259 **N**VQ-----K**N**CT**S**LGW**K**--SMVGGK**Q**--V**L**RL**R**TE**P****F**V--V**G**D---S**E**L**A**CL**G**PN**S**T**C**RYLYG 305
R21_BTe 259 **S**IE-----K**Q**CT**F**EVV--AKKD-----TW**F**IK**E**PK**L**K--**I**G**N**---Q**I**MP**T**VD**P**DEA**F**KYLYG 302
R22_MR 258 **S**ID-----K**CA**A**F**Q**I**I--TSKD-----S**W**Y**I**ID**P****H**L**T**--V**A**Q---G**S**I**A****F**L**G**PD**T****P**LSYLYG 301
R2_KF 255 **N**PR-----K**S**SS**F**LIT--AMRK-----TWIC**R**DP**L**S--**I**G**E**---T**K**V**P**GAR**P**SSA**L**KYLYG 298
R2B_NVi 256 **S**VS-----K**C**IA**V**EYV--PHRK-----TWY**T**K**N**P**G**L**E**--V**N**G---N**A**VP**S**IS**P**SE**T****F**KYLYG 299
R2Amel 259 **S**AE-----K**C**TT**F**EIK--RQNK-----TW**F**LGD**P****Q**L**T**--L**G**Q---Q**R**IPYAD**P**EAA**I**KYLYG 302
R2_Rm_ribo 259 **A**AS-----K**S**FA**F**Q**I**T--RTQDSWCLVD**P**GL**K**LS**K**GDE**E**RC--**H**N**L**---E**G**IP**F**AG**V**DR**L**RYLYG 311
R2_Bg_ribo 258 **W**AP-----K**S**VAF**E**IV--PTKDS-----W**C**VVD**P**GL**R**L--R**Q**G---G**A**IT**Y**AG**P**D**H**SL**K**YLYG 302
R2_RU 254 **S**HR-----K**CF**G**F**Q**I**V--NKNK-----TW**A**IVDP**M**IT--L**N**G---S**S**LP**F**SG**P**ED**R**LPYLYG 297
R2_RL 254 **S**HR-----K**CF**G**F**Q**I**V--NKNK-----TW**T**IVDP**M**IT--L**N**G---S**S**LP**F**SG**P**ED**R**LPYLYG 297
R2Dr 263 **Q**PK-----K**CH**S**F**MVR--PCRG**A**-----F**T**VND**C**PP**V**W--L**G**G---K**A**L**Q**L**T**NI**E**NS**I**KYLYG 307
R21_GA 263 **Q**PS-----K**CH**G**F**LIE--KSGSR**S**-----Y**K**VNR**C**E**P**W**L**--L**N**D---T**A**L**H**MV**G**PK**E**SI**K**YLYG 308
R21_SSa 263 **Q**PR-----K**CH**G**F**L**Q**--K**I**QRA-----R**S**VNL**C**K**P**W**I**--V**G**C---E**E**L**H**MV**G**PE**E**SV**S**YLYG 307
R20LA 264 **Q**PR-----K**CH**G**F**FMD--K**G**-----V**V**NG**C**G**T**W**E**--**I**C**G**---S**P**I**H**MI**P**GES**V**RYLYG 304
R21_Gav 263 **Q**PK-----K**C**Q**G**F**F**LN--P**T**CDS-----F**T**VNN**C**E**A**W**K**--**I**A**G**---R**E**IT**M**L**G**PG**E**STRYLYG 307
R21_ZA 264 **Q**GQ-----K**CH**G**F**YIK--PTKDS-----Y**T**INN**C**PA**W**T--**I**N**G**---T**P**LN**M**IN**P**GESE**K**YLYG 308
R21_TG 264 **Q**GQ-----K**CH**G**F**YIK--PTKDS-----Y**T**IND**C**A**W**T--**I**N**G**---T**P**LN**M**ID**P**GESE**K**YLYG 308
R21_GFo 264 **Q**GQ-----K**CH**G**F**YIK--PTKDS-----Y**T**VNN**C**A**W**T--**I**N**G**---T**P**LN**M**IN**P**GESE**K**YLYG 308
R2NS1_CGi 264 **N**IK-----K**S**AT**P**CI**T**--PCGSR**S**Y-----T**V**NT**T**K**T**K**V**A--**I**K**G**---E**R**VP**V**IP**D**PG**C**M**K**YLYG 310
NeSLl_TV 267 **A**PQ-----K**C**VT**L**AKT--S**T**A-----I**Q**PF**R**--**I**G**P**---D**E**IP**I**K**T**SMD**N**ITYLYG 304
Utopial_ACa 265 **V**VQ**A**LSLDAPAG**K**CA**A**L**A**IN--F**E**GG-----L**M**H**S**ID**P****A**L**K**--V**Q**G---A**A**IP**A**MSR**N**NV**Y**RYLYG 317
Utopial_LV 268 **K**PQ-----K**C**AT**L**TL**D**--C**K**R-----G**T**N**V**R**Q**SA**H**H--**I**Q**G**---A**A**IP**S**L**T**E**E**ER**Y**RYLYG 310
Utopial_CFl 264 **N**PA-----K**C**AT**L**H**L**A--A**G**S-----G**G**R**V**L**P**TT**F**V--**I**Q**G**---Q**P**V**H**L**S**SG**E****P**Y**R**H**L**G 306
Utopial_AEc 264 **N**PA-----K**C**AT**L**H**V**G--A**G**N-----G**G**R**V**L**P**TS**F**Q--**I**Q**G**---E**T**IN**P**LA**Q**GES**Y**TH**L**G 306
Utopial_CMy 264 **N**AK-----K**C**AT**L**HID--G**S**K-----R**D**S**V**QT**T**G**F**Q--**I**Q**G**---E**P**V**I**PLA**G**Q**A**Y**H**L**G** 306
UtopialB_CPB 264 **N**PK-----K**C**AS**L**HVD--G**G**A-----R**A**L**V**RP**S**R**F**L--**I**Q**G**---E**P**MA**S**L**E**E**G**E**V**Y**Q**H**L**G 306
Utopial_ENe 271 **N**PS-----K**C**AT**L**GL**K**--V**Q**K**A**-----K**Q**V**P**DP**V**K**L**T--L**H**Y---E**V**LP**V**V**L**KG**E**A**Y**KYLYG 314
R52_SM 269 **R**PE-----K**C**G**Y**Q**L**P--R**V**N-----I**N**GE**I**L--**I**N**E**---K**E**IK**L**LS**K**E**F**Y**Q**Y**L**G 307
R5 277 **N**PS-----K**C**AL**M**D**I**P--H**D**K-----K**R**TP**P**I**L**--V**N**G---E**M**IK**C**V**G**K**A**D**P****Y**KYLYG 316
R51_SM 266 **R**PS-----K**C**G**Y**F**Q**LK--R**N**H-----N**D**PP**I**T--L**Y**D---E**Q**IP**I**D**E**N**H**L**Y**KYLYG 304
LIN9_SM 269 **K**PA-----K**C**G**Y**RD**P**--R**D**K-----K**S**MM**K**--**I**Y**G**---K**E**IS**V**DE**K**N**Y**TYLYG 306
R4_Hmel 272 **G**IE-----K**CK**V**H**SIK--R**G**KS-----Q**Q**NT**Y**I**L**--N**T**G---E**Q**IE**S**MD**E**N**S**T**Y**KYLYG 312
R42_AS 283 **N**VE-----K**CA**Q**A**H**T**--P**N**V**Q**-----Q**L**E**V**E**T**L**A**DE**E**P--L**M**EL**P**V**L**GL**R**Q**S**Y**R**YLYG 326
R4_AL 278 **N**LS-----K**CA**K**A**HYA--P**H**G**A**-----G**G**AQ**E**AVEG**A**EGSR**K**E**I**P**I**L**G**RA**S**T**Y**KYLYG 323
R45_BX 284 **N**ES-----K**S**A**A**A**G**P--S**R**-----T**L**R---S**S**LP**L**L**G**V**K**D**Q****Y**KYLYG 315
HERO1_BF 268 **K**PS-----K**S**RS**L**SLR--K**G**K-----S**S**NR**V****F**S--**I**N**N**---Q**D**IP**T**IQ--Q**E**P**V**KS**L**G 306
HEROTn 269 **K**PG-----K**S**RS**L**VLK--A**G**K-----V**T**DR**F**RY--L**G**G---T**Q**IP**S**V**S**--E**K**P**V**KS**L**G 308
HERO1_SP 272 **K**PV-----K**S**RS**L**V**V**H--G**G**K-----V**K**HIE**P****F**A--V**D**G---Q**T**IP**G**V**H**--N**K**P**V**K**F**L**G** 311
HERO1_HR 274 **R**VD-----K**CC**V**G**MM--K**K**D**G**-----S**Y**D**Q**L**P**RL**T**--**I**D**N**---I**P**IP**P**V**L**GS**G****F**KYLYG 317
HERO3_BF 268 **K**PR-----K**CK**SMS**I**V--S**G**K-----P**S**DIS**F**T--**I**D**G**---D**P**V**K**T**T**--K**D**A**P**E**K**FL**G** 306
R44_Sra 273 **N**KD-----K**T**E**Y**S-----I**P**DE**E**K**I**IQ**Y**KY**M**G 294
Consensus_aa: p.....**K**t..s.h.....h.....h.....l..h...p.h**c**Y**L**G
Consensus_ss: eeeee ee e eeeee

Conservation: 2 22 11 1 2 3114 131 7221452 342 24252314 311
6arl_chainD_p001 271 **F**S**F**T**P**ER**K**A**R**I---R**L**A**P**RS**I**Q**R**L---K**Q**R**I**R**Q**L**T**N**P**N--ISMP**E**RI**H**R**V**N**Q**Y**V**M**G**W**I**G**F**Y**R**L----- 325
SLACS 276 **R**T**W**P--D**P**M**S**---E**E**IRE**G**EV**E**KK**A**M**E**T**D**RL**F**K**A**IV**E**L**P**--L**Y**N**R**T**R**W**R**I**L**A**M**S**A**M**P**R**I**T**F**LL**R**N**H**----- 333
CRE1 282 **A**H**F**R**A**RG**T****P**E**A**RT**I**E**W**L**Q**A**A**VE**K**W---R**P**I**H**Q**K**L**R**Q**D**I--I**P**K**N**I**A**M**M**M**T**RIS**L**G**S**K**M**T**F**L**Q**T**H**----- 341
CRE2 287 **A**G**F**R**G**D**T**A**S**V**E**---E**W**V**W**E**K**T**K**T**H**---D**H**Y**F**E**K**L**Q**S**E**W--L**P**RL**A**R**L**Q**L**L**R**G**S**T**V**PR**L**N**H**LL**R**T**H**----- 343
GAU97528_Ramazzottius_ 311 **A**T**V**T**D**Q**L**D**F**---D**Q**E**V**IK**Q**L---T**D**Q**V**D**R**L**V**H**F**A**H**L**H**A**D**Q**K**L**N**L**N**Q**W**L**P**S**I**I**Y**PL**Q**T**A**---P 366
Blag_1 306 **V**S**Y**N**A**T**I**L---D**A**ANS**I**E**E**L---K**N**K**L**D**R**L**A**ST**P**LL**Q**PH**Q**K**Y**T**V**L**C**S**F**IC**P**T**L**I**Y****F**Q**T**T---P 360
Blag_5 306 **V**N**F**AD**A**CL**F**---D**S**Q**V**T**L**N**D**L---K**N**K**L**D**L**L**I**S**S**PL**L**N**P**D**Q**K**F**C**I**L**N**SS**I**CP**S**L**I**Y**T**F**Q**T**T**---P 362
Blag_2 306 **A**P**F**Q**D**N**A**L**F**---D**K**D**S**T**I**K**Q**L---H**K**K**L**E**L**L**A**SS**P**L**K**S**D**Q**K**F**L**V**L**N**T**A**I**C**P**T**L**I**Y**R**F**Q**T**T---D 361
Blag_4 307 **V**S**F**N**D**E**I**I**F**---D**R**ES**F**IT**S**L---R**N**D**L**Q**I**L**V**ST**P**M**L**R**P**D**Q**K**L**N**I**V**N**Q**Y**I**W**K**P**F**I**Y**A**L**Q**M**V**---P 362
Blag_3 305 **V**T**F**E**D**E**I**V**L**---D**K**ST**L**L**K**N**F**---E**N**D**L**N**S**L**T**V**S**N**L**L**T****P**D**Q**K**L**N**I**V**N**Q**Y**I**W**S**M**L**I**Y**P**L**Q**C**T**---P 360
Blag_6 307 **V**T**Y**N**D**E**I**L**D**---K**S**C**I**I**T**N**L**N---R**S**IS**K**L**I**T**S**S**L**--L**K**P**D**Q**K**L**N**I**L**Q**Y**I**W**P**T**L**I**Y**P**L**Q**C**A**---P 362
R2_PS 295 **I**ET**S**P**G**A**A**-----A**R**WS**V**T**G**L---R**N**RL**S**K**L**E**S**A**C**--L**K**P**Q**Q**R**M**H**LL**R**C**Y**LL**P**G**L**Y**Y**G**L**I**H**----- 345
RaR2 304 **I**S**Y**T**N**E**G**-----P**E**RL**S**L**T**I---E**Q**D**L**ER**L**T**K**A**P**--L**K**P**Q**Q**R**I**H**M**L**N**A**Y**I**P**K**Y**Q**D**K**L**V**L----- 353
R8HmA 309 **V**S**I**D**P**T**G**K-----T**A**LP**I**EE**W**---K**N**W**M**T**K**L**K**E**C**K--L**K**P**E**Q**K**V**K**I**L**KE**V**V**C**S**R**V**Y**V**L**R**M**----- 359
R8HmB 308 **V**MID**P**AG**K**-----T**A**LP**I**EE**W**---K**L**W**L**T**R**L**R**E**C**K--L**K**P**D**Q**K**V**K**V**L**KE**V**V**C**A**R**A**N**Y**V**L**R**M----- 358
R24_MR 304 **H**G**Y**S**Q**S**G**M-----L**A**PS**P**SN**L**---E**S**M**L**ER**L**RR**A**A--L**R**P**W**Q**K**L**Y**I**L**N**R**Y**L**IP**R**L**I**H**C**Q**S**----- 354
R21_MR 304 **L**Q**Y**G**F**R**G**A-----T**C**PT**P**SK**T**---E**E**MLS**R**L**G**K**S**P--L**K**P**W**Q**K**L**N**V**L**Q**R**Y**L**IP**R**L**H**G**M**Q**M**----- 354
R2SmA 298 **I**K**S**N**F**K**G**R-----C**P**VA**H**IDL**L**---N**N**Y**L**T**E**IS**C**A**P**--L**K**P**Q**Q**R**M**K**L**K**D**N**L**L**P**R**L**L**Y**P**L**T**L----- 349
R2NS1_CSi 298 **I**P**F**T**F**K**G**K-----G**V**F**N**H**R**Q**H**L---L**K**L**L**D**E**V**T**R**A**P--L**K**P**H**Q**R**M**E**IT**R**N**Y**L**I**PR**L**T**Y**SL**V**L----- 349
R2CiB 307 **I**NIDA**Q**G**A**-----R**N**DA**A**RI**L**---T**E**GL**A**E**L**S**R**A**P**--L**K**P**Q**Q**R**L**Y**L**L**R**V**H**L**L**P**K**I**Q**H**GL**V**L----- 357
R2NvecA 307 **I**NIGA**Q**G**V**-----K**A**A**E**Y**N**A**F**---K**E**AL**D**N**L**S**R**A**P**--L**K**P**Q**Q**R**L**P**LL**K**T**Y**LL**P**Q**L**H**H**SL**V**L----- 357

R21_MDe	303	VDFRCNV-----	LNSEYGI--	DANLRKLDRA	LKPPQRLKMLCVAIIPRYLHSLVL	352
R2A_Nvi	303	VVYNSYG-----	PIQVKINI--	AGDLQRVTAAP	LKPQQRMAILGMFLIPRIHKLVL	352
R21_TCAs	303	LEFGHKGV-----	ERPTIHNL--	SVWLNLRRA	LKPPQKCLFIRQYVIPRLLYGMQN	353
R2LcA	306	IPFSHLGR-----	AEKVSPDL--	TNLLNKLQKAP	LKLQKQKYAVRNFVIPRALHGLIL	356
R2Ll	306	IPFSHLGR-----	AXKFSDDL--	SNLLNKLQKAP	LKIQQKLYAVRNFVIPRALHGLIL	356
R2La	306	VPFSHIGR-----	SKSFSDDL--	EALLNKLQKSP	LKLQKQLFALRVYLIPRLLHGLVL	356
R2LcB	306	VPFSHIGR-----	SKSFSDDL--	EALLNKLQKSP	LKLQKQLFALRVYLIPRLLHGLVL	356
R2NS1_SMed	299	IYFGPLGI-----	TTERLTKIY--	SDQLYNIGIAP	LKPQQRLEMINDFLLPGLLHEAVL	350
R21_PPap	303	IWFSGPRV-----	VSPEQLSM--	GVYLERISKAP	LKPQQRIRILVDYLLPKYTHGSVL	353
R22_TCAs	293	IQFRGSGM-----	CGCGSEGV--	AAGLKRTICAP	LKPQQRMHLLRVFFLPKFYHAWTF	343
R21_PBa	307	GMYQGAR-----	EYASVPPL--	ANSIRHITKAP	LKPQQRLLRLRDCLLPRIYHKLVI	356
R28_MR	304	VDFRSTG-----	PKKSRIIDL--	TTYLDRIKAP	LKPQQRLLKLLRCFLLPRIYHVLVL	353
R27_MR	302	VDFQYSG-----	PKKASRSL--	KIELERISKAP	LKPQQRLLILRVLYLLPRYHHHLVL	351
R21_IS	302	MTFTPQGS-----	INKGTSERL--	DLLLTRTSKAP	LKPQQRLLVLRNLYLLPRIYHRLVL	353
R21_RMi	303	VHFGVKGL-----	EKGLVRRLQ--	AILLERVSKAP	LKPQQRLLVLRFYLLPRIYHRLVL	354
R2_FA	304	VPFTAAGR-----	CRDDTIAHL--	KRKIDVLTAP	LKPQQRLLFALRVVLLPSCYHLLTL	355
R25_MR	302	VPFTPEGR-----	SSARADEQL--	KQTLGKLTAP	LKPQQRLLFALRVVLLXGLHLLSL	353
R2_Dan	303	IKFTAEG-----	ARYDPAEDL--	GPKLRLRLTRAP	LKPQQRLLFALRTVLIPQLYHKLTL	354
R2_DSi	303	INFATAGR-----	VRCNPAEDI--	GPKLQRLTKAP	LKPQQRMFALRTVLIPQLYHKLTL	354
R2B_DM	302	IHFTADGR-----	ARYNPSEDI--	GPKLERLMQSP	LKPQQRLLFALRTVLIPQLYHKLTL	353
R2_DPe	303	ITFTAQGR-----	TRYSPADDL--	GPKLRLRLTRSP	LKPQQRLLFALRTVLIPQLYHKLTL	354
R2_BM	304	VDFEASG-----	CVTLHSHI--	SSALNNISRAP	LKPQQRLLILRAHLIPRFYHGVVL	353
R2C_NGi	303	IKFNSNGR-----	LISDAKPKL--	IKDLELLTKAP	LKPQQRLLWALKVIVIPGILYRGTL	354
R2_AM	304	AYLGQIG-----	IQPARLSL--	QTFLERIAKSP	LKPQQRLLYLRVHLLPKLIYPLVM	353
R2CiD	306	IHFQMVGS-----	CRIRREI--	RESLLRLASSA	LKPQQRVLMRSFLIPRWYSVTL	356
R21_BTe	303	AKIGPWKGV-----	HCGVIVPEL--	LSVVKVRVKLS	LKPQQRVLLTKYIFPRYIYHLLV	355
R22_MR	302	AKISPWVGV-----	KTDYSIQGL--	KACVGRVQSLA	LKPQQRVLMARHIIPHYLYGLIL	354
R2_KF	299	VNYTLSEGL-----	ESGALIDKL--	MQAVNRARGLA	LKPQQRVLLILRIIPKFLYGLIL	351
R2B_NVi	300	AKVSPWKGL-----	LEGFESDAF--	REVISRVQRLP	LKPMQKVDLLQMYIFPRYTYGLIT	352
R2Amel	303	TNPNPWGI-----	LCKTSIKET--	IDAARTVKQLK	LKPQQRVLLIRTYLIPRYIHKLVA	354
R2_Rm_ribo	312	VSVSPWFGI-----	DETRERANL--	TEVHLKLCRLA	LKPQQRVLLHLYLIPRYHLLVA	364
R2_Bg_ribo	303	VKVSPWVGV-----	DVSDLRTHF--	SKTLEDTRKLP	LKPQQRVLLHLYLIPRYHLLVS	355
R2_RU	298	VDNPNWDRK-----	SRYDAGQRL--	ISAAKRGSQLS	LKPQQRVLLHLYLIPRYHLLVS	350
R2_RL	298	VDNPNWDRK-----	SRYDAGQRL--	ISAAKRGSQLS	LKPQQRVLLHLYLIPRYHLLVS	350
R2Dr	308	VKNPNWAGI-----	EKPDLTVAL--	DRWCKRIGKSL	LKPQQRVLLHLYLIPRYHLLVS	360
R21_GA	309	VQVNPWTGI-----	FAEDTVAKL--	RQWVVAISKTP	LRPLDKVSLLCQFAVPRYFVADH	361
R21_SSa	308	MKVSPWHGI-----	MEPDVPERL--	CNWIISIGRSP	LKPQQRVLLHLYLIPRYHLLVS	360
R201A	305	VQVGPGRGV-----	MEPDLIPTV--	HTWIERITEAP	LKPQQRVLLHLYLIPRYHLLVS	357
R21_Gav	308	LNVPWVGI-----	DKPDLGTQL--	SSWLERIGTAP	LKPQQRVLLHLYLIPRYHLLVS	360
R21_ZA	309	LQIDPWTVG-----	AKYDLSTKL--	KIWLESIDRAP	LKPQQRVLLHLYLIPRYHLLVS	361
R21_TG	309	LQFDPWIGI-----	ARSGLSTKL--	DFWLQRIDQAP	LKPQQRVLLHLYLIPRYHLLVS	361
R21_GFo	309	LQFDPWVGI-----	AKTSLPEKL--	DFWLERIDRAP	LKPQQRVLLHLYLIPRYHLLVS	361
R2NS1_CGi	311	SKMSPWVTK-----	IRKDIVAQL--	EGMVESIGGAH	LKPQQRVLLHLYLIPRYHLLVS	363
NeSLl_TV	305	IPISGTKTSRF-----	AAATGILEKV--	KAQIRVVFASH	LALSQKIIALRVFLLPQLDFYMFH	360
Utopial_ACa	318	VHVGTLTALG-----	QANELLEKA--	SRDARTICASG	LEPWQKVVAIKTFILSRLPFFHFN	371
Utopial_LV	311	VPIGLPRLT-----	SLQESSRKL--	SSDIETISSSL	LAPWQKLDALKTFFVILQYTLRA	363
Utopial_CF1	307	VPTGSSVDQ-----	TPFATIGGL--	LEDLRAVDQSL	LAPWQKLEVVATNLLPRLDLFLRG	359
Utopial_AEc	307	VPTGFSVDQ-----	TPYAAVGDI--	VSDLRAVDRSL	LAPWQKLEIEMLTGTFILSRDLFLRG	359
Utopial_CMy	307	TPTGFRVRQ-----	TPEDTIQET--	LQDAAKIDASL	LAPWQKLEIEMLTGTFILSRDLFLRG	359
UtopialB_CPB	307	TPTGFRVRQ-----	TPEDTIAEI--	LRDAAQIDSSL	LAPWQKLEIEMLTGTFILSRDLFLRG	359
Utopial_ENe	315	IKDALESPVQ-----	SQILRAMSRI--	KKDLNKLRLSE	LLPWQKLDALRTFVMSRLDYLRH	370
R52_SM	308	VPVGEDNDQ-----	SPYALIDKV--	VSDTKKIADSG	LFQWQKLAAYKIFIHSLRTFAFRT	360
R5	317	TFRSWFRKL-----	DIKELLQMM--	MDETCLITESN	LHPQKQIHAYETFIHSQLPFFHLRH	369
R51_SM	305	VDFGQKGKH-----	NIDTILNTA--	LDDTTKILSSD	LHPAQKLAQYKTFIHSRLIFPFRN	357
LIN9_SM	307	VRIQDTKKK-----	DLNVRFEEV--	KKKTTAIFKSK	LRSDQKLAAYKIFIHSLRTFAFRT	359
R4_Hmel	313	FQQAQKIQKK-----	QTKIELTNKF--	KFRNLQILRSQ	LNSRNIKAINTYAIPIITYSFAI	367
R42_AS	327	IDQKFLATKN-----	ALQRFESL--	FNRAAIFRSD	LTWRQMSNAFQSIAGGLRYGFLN	380
R4_AL	324	VEQRLLPMEV-----	ALKEFEDKF--	MDRAETIFASE	LTWGQMATAYNITIAIAGLRYYSN	377
R45_BX	316	IESGFVANE-----	SAYSRMQTTI--	LAKVQSILDV	EGHTVQRRRIARTVAPGGAFFILGNI	377
HERO1_BF	307	RLYTILKVFLO-----	KRGQELVKQA--	VEGLRAIDKCE	LPGKLVKVCQSVLIPRLKWPMMKM	361
HEROTn	309	KMFDDGSLKY-----	FSIRETNDQL--	GHWLTLDVDSG	LPGKFKAWVYQHGILPRILWPLLV	363
HERO1_SP	312	RLIDGNLKD-----	VARQDMVSL--	GRWLHTIDKCV	LTGVMKCIYQYLVIPRMQWKLMI	366
HERO1_HR	318	KIYDGLKDT-----	KAKEEMVSKL--	TRLLKRTTDLK	VSTQMKLVQLRRFIPSQLKFELRS	372
HERO3_BF	307	GYITFLSKTK-----	ETYDILAKTI--	ETTVENINKSA	IRNEYKLRYVMEYAFPSWRYMLMV	361
R44_Sra	295	VYENNKATAC-----	INAEQLMLKL--	DEKMDKIFNSK	LVNKNIIKAINGCVIPTCTYLFSH	350
Consensus_aa:		h.h.s.....p.h.....	hp.l.ps..Lps..p+h.hlp.hhhsp.h@.h.....			
Consensus_ss:		eee	hhhhhhhh	hhhhhhhh	hhhhhhhhhhhhhhhhhhhhhh	

Conservation:	11 1 31	141 421	3312213		
6arl_chainD_p001	326	--VETPSVLQT-----	IEGWIRRR-----	LRLCQWLQWKRVRTRIRELRALGLKETA	370
SLACS	334	DMQHTHRVASW-----	FDERTTQV-----	MEHILGQ-----	359
CRE1	342	SPQELETAAKT-----	ADDEVEQT-----	LQHLMGQ-----	367
CRE2	344	KPEELNRSTTW-----	FDERVMET-----	ALNIAINI-----	369
GAU97528_Ramazzottius	367	TNTILKVFLO-----	VDKIVKST-----	VREILQL-----	392
Blag_1	361	LKKLPKAKFLSD-----	ADVLIKT-----	LKEVLQL-----	386
Blag_5	363	LNKIPNKFIEA-----	ADKIIKSG-----	LKEILQL-----	388
Blag_2	362	LQTIPLQFLHT-----	ADKLVRST-----	LKDILQL-----	387
Blag_4	363	VHKLPPLTFLED-----	VDKLIRSA-----	VKEMLLL-----	388
Blag_3	361	LDKIPSSFLQD-----	IDKLLRSS-----	IKELIGL-----	386
Blag_6	363	LCKLQLGFLQD-----	IDKIVKNA-----	VKEIVGL-----	388
R2_PS	346	-QGISVGLLRS-----	ADKQVRAA-----	ARKILHL-----	370
RaR2	354	-SKTTAKGLKR-----	TDQRIRQY-----	VRRWLKL-----	378
R8HmA	360	-SECGISELRS-----	WTRFVRNW-----	AKNI IHL-----	384
R8HmB	359	-SGGICELRK-----	WSRFVRGW-----	VKSIIHF-----	383
R24_MR	355	-SSITAGRLEY-----	MDRLIRKF-----	IKKTLHL-----	379
R21_MR	355	-MDVNKKKLT-----	LDGCIKVF-----	VKETLHL-----	379
R2SmA	350	-GIVHLKTLKS-----	MDRNIHTA-----	IRKWLRL-----	374
R2NS1_CSi	350	-GQVHRNTLKR-----	LDNYIRQS-----	IRGWLRL-----	374
R2CiB	358	-SSCAKRALTY-----	LDKSVRSA-----	IRRWLTL-----	382
R2NvecA	358	-SRTTGKLLNS-----	LDALVRKA-----	VRGWLKL-----	382

R21_MDe	353	-GRVNKTKLAG	-----FDNLIRKY	-----VRKWL	YL-----	377
R2A_NVi	353	-GRTSNADVRR	-----GDKIIRKT	-----VRGWL	RL-----	377
R21_TCAs	354	-PQVTSRVLRE	-----ADRLIRRH	-----LKTY	YHL-----	378
R2LcA	357	-SKTNLKELNT	-----LDRAIRVF	-----LRTL	LYL-----	381
R2Ll	357	-SRTNLKELNT	-----LDRAIRVF	-----IRTL	LHL-----	381
R2La	357	-SRVAIGELKI	-----MDKLILKH	-----LRVWL	RL-----	381
R2LcB	357	-SRVAIGELKI	-----MDKLILKH	-----LRVWL	RL-----	381
R2NS1_SMed	351	-GNTNVGELKD	-----LDKMT RVA	-----IRKWL	HL-----	375
R21_PPap	354	-GRYTRKTYKA	-----MDAQIRSY	-----VRKWL	HL-----	378
R22_TCAs	344	-GRLNAGVLR	-----LDVVVRTS	-----VRTWL	RL-----	368
R21_PBa	357	-GTITSKILKE	-----MDVLLRAA	-----VRRWL	RL-----	381
R28_MR	354	-GRITLGGALRA	-----LDVLTAA	-----VRKWL	RL-----	378
R27_MR	352	-SRTTLGHLRG	-----LDLQVRAA	-----VRRWL	SL-----	376
R21_IS	354	-GPWSAALLLK	-----MDTTIRGA	-----IRRWM	DL-----	378
R21_RMi	355	-GPISAKTLLT	-----IDRVV RSA	-----VRRWL	LAL-----	379
R2_FA	356	-GGSNLSLLKK	-----IDL MVRAA	-----GRKWC	CL-----	380
R25_MR	354	-GNVTLSLLRK	-----VDKL VRAA	-----VRKWL	DL-----	378
R2_Dan	355	-GSVTIGVLKK	-----FDKLVR YT	-----ARKWL	GL-----	379
R2_DSi	355	-GSVAIGVLRK	-----TDKLIRY	-----VRRWL	NL-----	379
R2B_DM	354	-GSVALGVLRK	-----CDKLVR SF	-----ARKLL	GL-----	378
R2_DPe	355	-GSVMIGVLRK	-----CDILVR ST	-----VRKWL	GL-----	379
R2_BM	354	-GNISDDR LRM	-----LDVQIRKA	-----VGQWL	RL-----	378
R2C_NGi	355	-GSSTAGYLR	-----LDCVIRAY	-----VRRWL	RL-----	379
R2_AM	354	-APIRASMLNK	-----LDRMVRVA	-----LTGKD	GI-----	378
R2CiD	357	-TRVTVSFLSW	-----IDRVV MR	-----VRAIL	HA-----	381
R21_BTe	356	-SPPSDTVLKL	-----LDSEVRQE	-----VKTIL	HL-----	380
R22_MR	355	-SIPSI SVIRQ	-----LDQCVRVA	-----VKEYL	HL-----	379
R2_KF	352	-GGPSLTR LHA	-----ADKCVRMA	-----VKEIL	HL-----	376
R2B_NVi	353	-SPPAKAVLKT	-----IDRIIRTR	-----IKEIL	HL-----	377
R2Amel	355	-NPPPLGTLDL	-----IDKELKT I	-----IKEIL	HL-----	379
R2_Rm_ribo	365	-AAPALTTLRE	-----LDQELRVV	-----VKKIF	HL-----	389
R2_Bg_ribo	356	-SLPSIAELRA	-----LDLEIRGC	-----VKQIL	HL-----	380
R2_RU	351	-DPPSPAYLKS	-----IDHDLRQI	-----YKNIL	HL-----	375
R2_RL	351	-DPPSPAYLKS	-----IDHDLRQI	-----YKNIL	HL-----	375
R2Dr	361	-GGAGDVMLQN	-----LDGTIRKA	-----VKKWL	HL-----	385
R21_GA	362	-CMLSAKALTE	-----MDRSIRQA	-----VKRWL	HL-----	386
R21_SSa	361	-GGLGPIVLNV	-----LDGMIRKA	-----VKVWL	HL-----	385
R2Ola	358	-RKVTVTKLAQ	-----IDGIVRKA	-----VKKWL	HL-----	382
R21_Gav	361	-AGIGRVALEA	-----LDSMNRK	-----VKEWF	HL-----	385
R21_ZA	362	-SEMKA GALEA	-----LDQQIRTA	-----VKDWL	HL-----	386
R21_TG	362	-SEVKTALLET	-----LDQKIRTA	-----VKEWL	HL-----	386
R21_GFo	362	-SEMKA GALEA	-----LDRTIRSA	-----VKDWL	HL-----	386
R2NS1_CGi	364	-DAYPXXVLGK	-----LDLIVRAA	-----IRRWA	KL-----	388
NeSL1_TV	361	-NVFRVNDLKA	-----TDQMIRGL	-----IDKEA	PT-----	385
Utopial_ACa	372	-GKIQRGRCQQ	-----FDRELREN	-----LRAAL	RL-----	396
Utopial_LV	364	-TEYLKSDLKP	-----LRAAI IKH	-----VKKIC	HL-----	388
Utopial_CFl	360	-ATVGKKPLKA	-----ADLQVRRM	-----AKSWL	NL-----	384
Utopial_AEc	360	-ARVFKGPLTA	-----VDLNIRRH	-----VKSWL	NL-----	384
Utopial_CMy	360	-SAVAKVPLNK	-----ADKIVRQL	-----VKKWL	FL-----	384
UtopialB_CPB	360	-SAVAKVPLNK	-----ADSTIRQL	-----VKKWL	YL-----	384
Utopial_ENe	371	-CYPYKQQLVA	-----FDVYVRAA	-----LKAAF	KL-----	395
R52_SM	361	-REIKTMALSA	-----SQGNTNSCGN	NSSKLRGHLR	IRLNL-----	395
R5	370	-SRIPFSDFITNRKT	TKNTTNSNDSEKSIQKAYDPE	--SGQLFLNT	FAL-----	415
R51_SM	358	-CNINHMTLDT	-----NRNRTVQH	-----REKQL	GF-----	382
LIN9_SM	360	-EDIAKTKIET	-----YDEEIKKM	-----IKEDIL	K-----	384
R4_Hme1	368	-INWSQTDLN	-----LQRIINTH	-----MTTHR	KH-----	392
R42_AS	381	-TNGAGQKLSE	-----ALKHARDI	-----DVRIR	SL-----	405
R4_AL	378	-TNGASPKLLE	-----ALKRAATL	-----DTRIR	DL-----	402
R45_BX	378	QPNSAKADMLK	-----LDMVIREK	-----IRRKGL	L-----	403
HERO1_BF	362	-YDIPLSTADQ	-----VEGKANSF	-----VRKWL	GV-----	386
HEROTn	364	-YEFPISTVEG	-----LERRVSSC	-----LRRWL	GL-----	388
HERO1_SP	367	-YDVPVSQVEK	-----METLVSKK	-----LRRWL	GA-----	391
HERO1_HR	373	YNLSLTWIKNN	-----LDNMVTEA	-----VRDWL	TM-----	398
HERO3_BF	362	-HDLTDTQLQK	-----LDSIHTKA	-----IKTWL	RL-----	386
R44_SRa	351	-EFS-DEERIQ	-----LARNVDIR	-----IRSYM	NT-----	374
Consensus_aa:	lp.....	h-...lp.h.....	l+phh.h.....		
Consensus_ss:		hhhhhh	hhhhhhhh	hhhhh		

Supplementary Figure 6

Alignment of amino acid sequences used to construct a phylogenetic tree. PROMALS3D (PROfile Multiple Alignment with predicted Local Structures and 3D constraints) software was used. The resulting alignments in FASTA format and with the predicted secondary structures are shown in Figures A and B, respectively.