

>Smp_315690.2 gene=Smp_315690

MINEPPPGNFYLNPFLLL PNIAGQNLLLFYDYLNVNIRQTDKDTLIFYESVTYGIYFPFVNGIPGTGM
QRVPGLLQDEMARKKSVLSYHYWCWLLQSTPATEHMPSWKQYLCDQLLLNYTFKNVRSIVQSTGGGRF
LTEFGLCLPDGNPESINTVECNALNAADRNFESWTYWDGYELFSNLNVENISLKSFRTYPQSTAGQ
PVQLRFDVDSGVFYAFVPTQKNCTNVNSTLLVAEIFVPMSEIHYPHGVKTRFNPEQLNYEVYENNTNL
IFVYMPYIAGQNLLLFYDYLNVNIRQTDKDTLIFYESVTYGIYFPFVNGIPGTGMQRVPGLLQDEMAR
KKSVL SYHYWCWLLQSTPATEHMPSWKQYLCDQLLLNYTFKNVRSIVQSTGGGRFLTEFGLCLPDGNP
ESINTVECNALNAADRNFESWTYWDGYELFSNLNVENISLKSFRTYPQSTAGQPVQLRFDVDSGVF
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IELIEITIIIPNQ.

>Smp_317470.2 gene=Smp_317470

MINEPPPGNFYLNPFLLL PNIAGQNLLLFYDYLNVNIRQTDKDTLIFYESVTYGIYFPFVNGIPGTGM
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LTEFGLCLPDGNPESINTVECNALNAADRNFESWTYWDGYELFSNLNVENISLKSFRTYPQSTAGQ
PVQLRFDVDSGVFYAFVPTQKNCTNVNSTLLVAEIFVPMSEIHYPHGVKTRFNPEQLNYEVYENNTNL
IFVYMPCTLIKTNIELIEITIIIPNQ.

>Smp_318880.1 gene=Smp_318880

MYKVYGIYLSDDVKRIYYGEYADALLGLLKTEEIPDIYQHSIPLPLPPLLHAIDP.

>Smp_319020.1 gene=Smp_319020

MYNSGSKVTSTCNHSNISALSEYTKMVFLILGIEIAITLLIIIIILSPLETVHKTPNPWTVLPWILMYV
FSYCNLIIIVIC.

>Smp_349630.1 gene=Smp_349630

MRYTILRSLWLSFHLIIIWRYFNCHEVCENPDLLSYDNIIFENDSYRYSLHYHYSMRIRLNQSQLA
FNDSYRNFPFPYFFKPKFSFRFYDTLIDDVYIYYGRILLTSERYYYLGDIEENFAQNIQRSETVVFNE
NELLAVKRN FVITVNDTDVSAKMTSVIQPNGKITLYFDNIPTIEGIEWISKINATFGCGMYFLDHEI
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ENHQSRITEAT.

>Smp_349560.1 gene=Smp_349560

MRIRLNQSQLAFNDSYRNFPFPYFFKPKFSFRFYDTLIGDVYIYYHGRILLTSERYYYLGDIEENFAQNI
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GCGMYFLDHEIPVPKWKIKSGTLVEYEVIGKNCWKFDTSEACQGATTNMRICIWCPKVNKCIESNDND
THGLKVNDCHVENHQSRITEAT.

>Smp_179970.1 gene=Smp_179970

MRYNFSPSLWILIYLFVWNYKRFNCNDICKNPDL EHYENVIFENDTYRYSLHYHYSMRIQRNQPPV
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EKELLGAKWTF SINVGSEVTATMTTLMHPNGKLSFHYDNIPMEIEESRLQSKIVGIIRCEGGLKKPE
ISVPAKWKIKSGSLVEFEVIGEICSQYNTSETCQKATTLTMTCFWCEKGKKCIESNDQNT HGLKVND CR
VEKSDVNDLNSSTTMEHSETTLGITEVQTTKTTEGNKQDKSHWYLYVVIPLVASLFLICIGCIIWRWL
LRRKRSNG.

>Smp_173350.1 gene=Smp_173350

MRYNFSPSQLIIYVIFVWSHKRFNCNDICNNR ALRNYENIIIENDTYRYSLHYHYSMRIRRNQSQPV
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ELLGVKRNFLININDSEVTATMITLLHPNGKVSFYDNIPTDIDGSKLESKIVGTIRCGGVNVDHGIP
VPAKWKIKSGTLVEFESIGEICSQYNTIETCQRSTTLKTTCIWCEKGEKCIESNNPDTHVLKVNDCSVE
KKSDVNDLNSSTTTEHSERTLGITEVQTTKT DENKQHKSHWYLYVVIPLVASLFLICIGCIIWRWL
RRKRSNE.

>Smp_317840.1 gene=Smp_317840

MDKFVAFQVHCICKVWHTCHANNALHLEMLALIWHEDVAWIISSFNSQTLYKDINIETSQHILFFV
K.

>Smp_165590.1 gene=Smp_165590

MSYENIIFENDSYRYSLHYHYSMRIHLNQYQPAFNDSYRNFNFSYFVKPKFSFRFYDSL INEVYIYYH
GRIRLTREGDDYFGDIEHFAQKIRRSETVVFNEKELLAVKRNFLITVKD TDVPAKMTSVIQPNGKITL
YFDNVSCTIS.

>Smp_165600.1 gene=Smp_165600

MTGVIQPNGKISLYFDNIPAEVDESECISKINATLSCSFQGFIDHEIPVPAKWIKSGTLVEYEVIGTL
SFHRNLFETCQRATTTKMTCTWCEKGDKCLESNDEDTHELVNDCRVEVGIC.

>Smp_319240.1 gene=Smp_319240

MAFITPDDIYEIIENMLLYIWPTVQSTSGCQPISTPFLLMQYCDAMSRYSKDPDVRFGFLFSYSAVD
GHTGFNIPRKYSNLSAEDLGSLEDLVFRLTGQRISIFTVQNIKSQDLNLLKPECGLVVFVFIKGN
TEIELKALVMARVEVAKLIDSKGLSIYEPGFHFLWINQFPLFEKNNLGMCKQKRNVCYCSALVLC.

>Smp_319340.2 gene=Smp_319340

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VSSVHCVVDYVVKCVVERFYAYHHLDELCSMLKKSNSNSLSSKRHDSSAQSNRDKILDSSSELGSDRV
LVIEPIIVETLQIITCSELYLRFIQRRIADIKQSNLTEDDFKKKSNEISKFFESSQLVCQVQDLLSK
YLNLEQYYLRVTIMKALSSDEVKSSNVWCFIDDVFFITKKSILRSLSSGNVDTICAMVNHSCSILID
LMVNDFLGNIIRTGFPSGWVQDAYNYVQNSVAVAGSLSSSSSIVNVPTVSSFMIGPNALARYHFLVT
LNSIEASQKNLLSLVNHLESELNLLYQNQEINS.

>Smp_350240.1 gene=Smp_350240

MRYNFSPSLWILIYVIFGRPYKRFNCSDICKNPDLKRYENVIFENDSYRYSLHYNYSMRILRNQPPV
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EKELFGVKRNF SINVGTEVTATMTTLIHTNGKISFYDNIPMEIEESQLQSKIVGSIRCEGEDTEER
EIRVPVDWIKSGTLVEFEAIGEICSQYNTSETCQRSTTLKTTCIWCEKGEKCIESNNPDTHGLKVND
RVETTKTTDENKQHKSHWYLYVVIPLVASLFLICIGCIWRWLLRRKRSDE.

>Smp_243170.1 gene=Smp_243170

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LVGCASKLALQLSGKVEQLDLVKNHVLKCDKLSHIITVRNSAIGVKRCLVDSKLDEAAGYVFTYLEM
ERDIISLISLLSADNPDNNPLTTLDSDRQILVKMAVEKFDEYVSKRDEKNIVYLLKIFFLLGETNEGI
RRFSIYLCYISNKCELLITTNKSSSSQSSEFVSANLITEILLFVADTLKNNSMYVETYCGPGNIFGLV
SSVHCVVDYVVKCVVERFYSHHLDELCSMLKKSNSNSLSSKIHDSAQSNRDKILDSSSELGSDRV
VIEPIIVETLQIITCSELYLRFIQRRIADIKQCNLAEDDFKKKSNEISKFFESSQLVCQVQDLLSKY
LNLEQYYLRVTIMKALSSDEVKSSNVWCFIDDVFFITKKSILRSLSSGNVDTICAMVNHSCSILIDL
MVNDFLGNIIRTGFPSGWVQDAYNYVQNSVAVAGSLSSSSSIVNVSTVSSFMIGPNALARYHFLVT
SIEASQKNLLSLVNHLESELNLLYQNQEINSQKLNMCITELVSISDQLQALLDSAFEHLSTSVIQSQV
KTLLNVFKSLKYDLLEEDLDVFAANDRWIESCIAHTEDFLKPFVLSIENNDRFVLILINEILHQLD
QFIQRKFSRFGAIQLEKEYHNLFAYLTSISYSSLRDYFTRSLQICRLNLDREVEVLYYWNSSNWRL
TAHEVRSSLSLRDFAVNEIRALKIQ.

>Smp_199340.1 gene=Smp_199340

LTLFSLFIPKASVSSLPFVYKSHACGELSTQHINSTVTVCGWLEFCRLSSRFLVLRDDRGLIQIYC
DKNSLKIPQFNSESVLRVTGKVQARPEKDVNKRMPTEIEIEVAESIEILSHSSPLSFLPKDAANVNEM
ERLKRYRIDLRSSNMQRNIRFRSSIIQLMRSFLCQNGFTEIETPYLFKITPGGAREFVVPKFPGLW
YCLPQSPQFKQLLMISGFSKYMQVACFRDETSSDRQPEFTQLDIEMAFITPYDIYEIIENMLLYI
WPTVQSTLGCQPISTPFLRMQYCDAMSRYSKDPDVRFGFLFSYSAVDGHTGFNIPRKYSNLSAEDL
GSLEDLVFRLTGQRISIFTVQNIKSQDLNLLKPECGLVVFVFIKGNTEIELKALGMARVEVAKLID
SKGLSIYEPEFHFLWINQFPLFEKNNLQWQKSVHHPFTAASPETAHFLYTDPSKVIGLHYDLVCNGQE
VGGGSIRVHNPEVQKYIFTEILKENSCEMEYFLTALNSGAPPHGGIALGLDRLIAIFVNAKSIRDVIA
FPAADGKDLLCGTPTMVDDEILSQYCISVSNHSKS.

>Smp_180260.1 gene=Smp_180260

MNDQRSATDKLAYNCPHIIQMKEPSKIVKKVNILEIICDTFSIRGVARMRRGPPFLRGLWFCFVIMT
VGLLLTTYLLVQDYLVDVSVNIHVELDAKSPFALTICHHPFSQNAYHLRRNGDVMSSSIFNKHMR
NLTHKFLMDNDVDAAETLYQYDSLSTYYQNLKAIDAYRLGHDTTAFLNCRMRRVNHTMQIEDNCMHMDG
FQIRKFSHTYFNCHTFEPKTKVEAEDNTIALIVSLGTDPNYNNQEAFLVDLFEMARGLRVVVHEP
GTYPDLEREGLHVETGKLNEINYQPVWLKRLNTPQNPCRAEFIYRNPELASITDYKLPRLTGLCFAYA
YNDLNVSYRYTQSQCILFHQQKDIIEKCRQYIYNPRPQYPSSNLPYCGSILEGDFDILALAKRIQCL
TSGPLNVTVKSQYESTLCHPRCRYTYESTISVTTWRAVDWQLHWRQLNRAFKSMQYDVKINGEDWN
ITQKNELSLANDFQISVNAINDLNLQGDNFAYVVLKRRASDVRVSQEKLVLSISVLLSRIGGLCSLSI
GLTAAFIVELIEFTYRLVTTERSNIIRNKSIENTDSNSVSDGEYKNKLKRSATCI.

>Smp_311250.1 gene=Smp_311250

MYNYSINKPMYFATLIHDELYKELIDVLGIQRFLFRSEIDLHTIDKVYKAKYGIYLSDDVKRIYYGE
YADALLKLLKRRHPRYISTFNTITSITSRD.

>Smp_349570.1 gene=Smp_349570

MRYKFSRSLWILIYLIFFVWPYERFNCNDICKNPDLYHYENVIIENDTYRYSLHYNYSMRIQRNQSQPV
PSERFKNKINDKYTARLQFSSSFYGSHVQIIEFYRDYGEYVYEFWSYIGMMFSYIKNYTKSESRLH
EKELLGVKRNFSINVNGTDVTATMTSLIHPNGKVSLLYDNIPTTEIKVSALRSKILGPIRCEGERENRH
IITVPAKWIKSGTVVEFEAIGEICSQYNTSETCQRATTSKMTCIWCQKGGKCIENNPDPHGLKGND
RVQNNNSVNDVSTLTPVKDIERTLRSTEVQFTEDLIETTEETDEHSNMTALITEENKQHKSHWYLYV
IPLVTSFLVLCIGCIIWRWLLRRKRSDE.

>Smp_350510.1 gene=Smp_350510

LVTSPKMRHTLLRCLSMTFYVIVLWPKFSKSEIDCEDSKLQHRQNVIVQNDYQYSLHYNYSMRIR
CDQLHPVVSNSFIKFSDDQKVNPKFSFKYDSDVYSFHIDKTGAIAFNVGQIFINIPNFHSSDFEILN
DKELVAVKWSFKSNEDGTDGTAKITCLIHANGKISLYFANIPSKIQGNLQIGIIGQIYCKTGKSPR
LNPVPAKWIKSGTLMYEYVIGTMCSTYTTTESCQKEKTSMTCIWCDKANKCIASNDQDTQMLKVNDCH
VETNSKVTDLSTSTPIQQSETTSDVTEVEVEEDLKTNSKVTDLSTSAPIQQSETTSDVTEVEVEEDLK
TNSKVTDLSTSTPIQQSETTSDVTEVEVEEDLKTNSKVTDLSTSTPIQQSETTSDVTEVEVEEDLKT
SEIEDLSTPASIKRSETTSGVTEVQTEGNVKEVSEKTAQQSNLTTKTIEVKNHKKSSWYLYIVIPLV
SLFLIFVGCFIWIWINRKWKITSLSLCHKNFRVNYSF.

>Smp_201260.1 gene=Smp_201260

MLKYHIHTNVFCQALFHLPTDFLELCSIYQAQNLCSCESEHFISFNGVHLKLCRYKSSNFTEVDNC
RDIEHPCDPDGTIV.

>Smp_327340.1 gene=Smp_327340

MEYFLTALNSGAPPHGGIALGLDRLIAIFVNAKSIRDVIAFLKAADGKDLLCGTPTMVDDEILSQ.

>Smp_184350.1 gene=Smp_184350

MDSNVCMIIDFSDLKDLVEKSRNVKADVSEIKDLLARRSEIEHKLKKINSLLIPDFHKLQVNAENSSK
LVGCASKLALQLSGKVEQLDFVKNHVLKCVDKLSHIITVRNSAIGVKRCLVDSKLDEAAGYVFTYLEM
EKDIISLISRLSADNPDPNPLTTLDDSRQILVKMAVEKFDEYVSKRYEKNIVYLLKIFFLLGETNEGI
RRFSIYLCSYISNKCELLITTNKSSSQSSEFVSANLITEILEFVADTLKNNSMHVETCYGPGNIFGLV
SSVHCVVDRYVKCVVERFYSHHLDELCSMLKKSNSNSLSSKRHDSSAQSNRDKILDSSSELGSDRVL
VIEPIIVETLQIITCESELYLRFIQRRIADIKQCNLTEDDFKKKSNEISKFFENSQVLCVQVQDLSKY
LN.

>Smp_349580.1 gene=Smp_349580

MRYNFSPSLWILIYLIFFVWNYKRFNCNDICKNPDLEHYENVIFENDTYRYSLHYYYSMRIQRNQSQPV
PSERFKNMHVVYKARPQFSISFYGSHIREIDFHKRHGDYEFGRSYIGNTYNYIENYKKSEYRVLH
EKELLGAKWTF SINVGSEVTAIMTSLIHPNGKLSFYDNIPTENEEIKLLSGIVGSIRCEGGLKKPE
ISVPAKWIKCGSLVEFEVIGEICSQYNTSETCQNAATTSITTCIWCEKGEKCIENNPDPHDLKVND
VQKKSDVNDVSTSTPIKDIETTLRSTEVQVTENLIETTEERYKHLTTKTTDENKQHKSHWYLYVVIPL
VASLFLICIGCIIWRWLLRRKRSDE.

>Smp_125500.1 gene=Smp_125500

MQEDQPFKVAVVGGGIGGASSAYFLRQIFGNKVSITLFEKSGRIGGRIKTVPCGETCESGASAIHSS
NYYMYSFANQFKIPMVPLRNADQRLLLFEEGYKPVFSNVTQDTLLTPVHLLWRYGFSLLRARLYLMA
RIREFTHIYALQQRGECFASPGLLLEKLSKHFPEMTKCTYAEWMRKEIGLNENYINELGFGILSSNYC
QNSADAHAFVGVISSACTVSDVFTIENGAEQIPQKLVEVALAGNPSGAPKEFIHATVKKITRTDNDRL
CLSYDLANNKTEEGFLDYVILSLPLHQESNISTSHDIKLPSRLYHEMCRTFLSGQINYSLFDLQKRL
LKPNQWATFLPISSYYSNEKHPVRSITRLPFKSESDSLKDGVSIFSEPKYIPDPKTALSKLILKYP
DDHNQIDVVRWLAYPTYHPVNDPYTDLGQFKLASRVYYPNAIESTASCMEMAIIGGRNVALLIANEMK
HLREDQKSMFTRLTNFIKKEAN.

>Smp_214320.2 gene=Smp_214320

MQQLISLCKVMKMMKRPRREIKMLTAGETVIIIIILITANKFETASRSLVDLMGEAEFQRILLT
LPKDEQINMIIQAMDKDSTNCSFPKHLKTRINDYKYAAYKSSIQKFLSLEPYTRARSTTAPHIYHEEC
LRLEKLYFTKWAVHYLSKNAATDITLLQSYENEEYEAKKGDKNADRRRDWSGLLRVRISEKWKRELL
DDVESAYIAETRTKVNVNKEKLKKQLTNTENKIEAQLNIVKELESKAIQATNEHMDNRDDKSLKEQY
EAYSTLAKELRSLVDLMGEAEFQRILLTLLPKDEQINMIIQAMDKDSTNCSCKF.

>Smp_350160.1 gene=Smp_350160

MRYNFSPSLWILVYVIFVWLYKRFNCNDYCERPDLYNYEIVIIENDTYRYSIHYKYSMRIQRNQSQPVPSEHFISKIYDKYDILPGFSFSYYGSHVRRISYHDAELVYDVGYSHIGNIYNYVNNNLETYVIRGKELLGVKRNYSTNVYGTEVTATMTSLIQPNGKVSFYDNIPTIEEYKVRSKIRGLINCEGGRKKHEISVPAKWIKSGSLVVFEAIREICSQYNTNETCQNAEISILTCFWCEKKEKCIISNLQDTHDCRVEKNSNVNDLNIISTTMEHSKTTSGITEVQNRTRTTEENKQHKSHWLYVVIPLVASLFLICIGCIIWRWLLRRKRSNE.

>Smp_350150.1 gene=Smp_350150

MRYNFSPSLWMLIYLIFVWPYKLFNCNDICNNPDLGHHEIVIIENDTYRYSLHYKYSMTIQRNQSQPVSSERFKNKIDGVYRSDPEFSSSFYGSQIHEIAFNVHHHMLVFRGFQIGEINYIENYEKTESRVLDEEELLGVKRDFLINVNGAEVTATMTSLIDSNGKVSLEYDNIPKEIEESQLKSGILGIISCENVVTNHEISVPAKWIKSGTLVVYEAIGKICSQYNTNETCQNAIPNLTCFWCEKKEKCIISNLQDTHDCRVEKTSDVNDLSTSTPIKDIETTLTSTEVQVSENLIETTTDETDKHLKTSVDNLSTSTPIKDIETTLTSTEVQVSENLIIETTTDETDKHFNRTTRTTGENKKHKSHWLYVVISLVASLFLICVGCIIWRWLLRRKRSNE.

>Smp_307880.1 gene=Smp_307880

MCSRFSIVIFFGIVLSLFLQLDVAGNYNLQNAKLFFKNVFNHTAKKLAFINVYKLELTRHSISLEQFNLSSSEVVNYAERIGRIIKAMENSLKTLVSWTEEEVSKYSWNPKLKPDIIKYNDLRELKLGDKRLVDAPGYHFKIMPKNKSGVHLPVEVYNGDSTVFHTLRWTDVLDSIFPTEPNLHFTYFASFTGILRVYPAFPWRQQNVDMFDVRRRSWFIQSSVPKDLFILLDTSGSMTGQSLKANLSAQKLEALDVEDDYFTVAHFPGAKDHVAPMIVTANNESEPICFNSFVQATRNRKLRLFYDLSTLKARGYSDFPASLKFAYEMFRNLTESARGDRGKELRNKILVLLTDNAFVFDESLSQLKQKSNITTFIYSLGEPVGAAYEHKMKACATNDYYQYLPTVGAVSNLMKDFHEKSTQIRFGPNASPLPTEVILHGASDVLHTNQYKGTGLMVSISIPVYNRTEKLQFLGLMGTELPIELMMNGLPQSKLYPTGYAFVNTNGYLVFHPGLIPEYPWLDDSPYLDFLDVEFNVYGSKTLIRKKLIDNARGSEQIIDFIKVSNDVHTYVKPRLYSFTRLSNTDFGVAFVMPTDQQLFLSIPKSIKSKITTDGSGNYMIDDLVLKLIKAKIILPWKALDVYMKINDHVFNLETPNEHMLHRDEDDQINVKTTLVDEKEEEEYEITNRKETVMEDEEEQQQFKASTSLNDEFISMENEFLSSQLNDTFCVNNTNCLIQDSFLRKLIIIRSTLSSSKVNDESENTPDIKNFNGSSSIILTDQIKETTRVLQSSSEITPPSSPRSETSVGVSDIRIDKNRSSIQTVENTRPMDDKPPITTEVNMSVGFESTTIATTATTATSATSALLRSPNDITSQSTLDMTKNEVDVNNDGVGSDRLITEQNNEIRNFLEKIRNINSSQTELLSQILLEIMIAEKDVSESAESIKLNSPIISRTIALNTGLIWTIPINTNEQFYNELKHWPDSPIFQRVYDSFNLIFWVRLRMNEDSTKPIENPVVTEDNSNSLLQSNTKQIIDNDTINITAQTSENQLQITPTTTNSTINSTKEEQNLNQVDGSKNIRNKDEVIDDYKHSHEIDEYFDESPLTNDDDETVENMESMNETIMNSQDNTALPVTIFTSTITITQGPNDYKAGVMGITLEPDYLSEQLNMIPECSVTQSNKLCYLLLEDAAANIIAVNNKLLYYQIGQFLGYIDPDLMNLSLVQNHVYGVLDKDYDFEGTCFPREDMLETTSPGIHPIPSILMYTQSLFNVRVWLDRLTLVGSVSVFITRAFMGMIRIIAVSGDLNDDVDPQNKPYQCIKLIHRYYSNLGELYGTRNPSINVGFNHRIQGFIQCPQQRNWDVSVQSIIGTNLLLLITDPIFAECEKKTHINRLRRDPVKDVGTDVCETSRAPRYRRQSQKWTLPNDKNPPQCSSTDRLKISLYIVISLNIFSFFLSLYY.

>Smp_335930.1 gene=Smp_335930

MILLKLVFYSEARGKVTIDDDTGYFVDSNGFIKLFHGINCVHKVTPFYIPKLLDPHTFKVLRDWGINVIRLGFSWIALKPHENETNLEYIDIIEKIIDNAGLYGVYIIIDLHQDGLSKRLGAIDAVPDWFMDKIKRPPYLFQYPWPLTKYPNESAWFLTYATYESAHAFESIYKNVSGLWNYFAEYWRITTDRFGKKYNVLGYELINEPPPGNFYLNPFLLLPNIAQNLFFFYDYLCLNLWNIFPFVNGIPGTGMQVRPGLLQDEMARKKSVLSYHYWCWLLQSTPATEHMPSWKRYLCDQLLNNTFKNVRSIVQSTGGGRFLTEFGLCLPDGNPESINTVECNVLAADRNFESWTYWDGYELFNLNVENISLKSFSRTYPQSTAGQPQVQLRFDVDSGVFYAFVPTQKNCTNVNSTLLVAEIFVPMIHYPHGMRTRFIPEQLNYKVYENNTNLIFVYMPCTLIKTNIELIEITIIPNQ.

>Smp_346760.1 gene=Smp_346760

MSIHYPHGMRTRFIPEQLYVEYENNTNLMFFYIPCTLINTNIELIEITIIPKQN.

>Smp_192050.1 gene=Smp_192050

MRIRLHQPPAFTDSYPKIYGSYFVTPRFSFRFYDTLIEVCIYSDGNILLTREAYDYFGGIENFAQNVQESETMVSNEEESLAVKRNFLINVNDKDVSAMTSVIQPNGKITLYFDNVSCIS.

>Smp_335780.1 gene=Smp_335780

MRLTRSSKQLERFGDSKNTPVNTLLRLSWIMILLKLVLYSEARGKVTIDDDTGYFVDSNGFIKLFHGINCVHKVTPFYIPKLLDPHTFKVLRDWGINVIRLGFSWITLPHENETNLEYIDTIEKIIDNAGLYGVYIIIDLHQDGLSKRLGAIDAVPDWFMDKIKRPPYLFQYPWPLKKDPSQSAWFLTYATYESAHAFESIY

KNDNTDRFGKKYNVLGYELINEPPPGNFYLNPLLLLPNIAGQNLLLFYDYL MNVIRQTDKDTLIFYES
VTYGIYFPFVNGIPGTGMQRVPGLLQDEMARKKSVLSYHYWCWPLQSTPATEHMPSWKQYLCDQSCDE
RELKWGQSNVFEYKITEHFSKICGPCSRFFIC.

>Smp_335785.1 gene=Smp_335785
MLVLVSVFQNPYMGKYHNDCLWDSVDIWLTD CIMHQ.

>Smp_180620.1 gene=Smp_180620
MFLLI ALMLVLVSVFQNPYMEVHGGGSR LSVGLGGHLADRLHNASVELAKDVNKT LMDKYGRR.

>Smp_328930.1 gene=Smp_328930
MSVVPTIKHFIIINTYVFRDAFKLFDCTNNLTLLRFRPQLITSTTDHITTEGIISQTENVTHPILTVQ
DVYRIGNETKLI.

>Smp_308060.3 gene=Smp_308060
MDSNVC MIDD FSDLKDLVEKSRNVEADVDEIKDLLARRSEIEHKLKKINSLIPDFHKLQVNAENSSK
LVGCASKLALQLSGKVEQLDFVKADIKQCNLTD DFKKSGEISKCFENSQ LVCQVQDLLSKYLNLEQY
YLRVTIMKMCITELKVSISDQLQALLDSAFEHLSTSVIQSEVKTL LN VF KSLKYD.

>Smp_346860.1 gene=Smp_346860
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SVSNLNKS.

>Smp_349650.1 gene=Smp_349650
MSLWILIYLFVWNYKRFNCNDY CERPDLYPYEIVIIENDTYRYSIHYNYSMRIQHNQS QPVPSE RFK
EKVVDIYEARKPFSYSFYGSNVHEILFYNHGDYVDFDGESHIGNIDNYINNYEKSELRLN EEE LLG
VQRNFSINVNGAEFTATMTTLMHPNGKLSFY YDNIPKEIDGSKLQSKIFGIILCKDDTAEHEIRVPVD
WIKSGTLVEFEAIGEICSQYNTSETCQRSITLKTTCIWCEKGEKCIISNLQDTHDCHVEKTS DVNDLS
TSTPIKDIETMLRSTEVQD TDNLIETTEETDNHLKTS DVNDLSTSTPIKDIETMLRSTEVQD TDN LIE
TTEETDNHLMNTIRTMEENKQHKSHWYLYVVIPLVASLL LICIGCIIWRWLLRRKRSNE.

>Smp_349670.1 gene=Smp_349670
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EYKIKHIYAGFPRFSCSYYGKHVEEIHFNENHANYVYQFESLSIGTIFNYIKSYKKSES RVLDEKELL
GVQRNCSIDVNGSEVTATMTTLIHPNGKLSFY YDNIPMEIEESQLQSEIYGFIRCDYVITGHEILVPV
KWKISGTLVEFEAVGEICSQYKTNETCQNATTSNTTCIWYEKGNACIESINADTHGLKVND CSVENMT
TLTTEENKQHKSHWYLYVVIPLVASLL LICIGCIIWRWLLRRKRSNG.

>Smp_192040.1 gene=Smp_192040
MRYNISPSLWILVYVIFVWSYKRFNCNDYCKNPEIVIIENDTYRYSLHYKYSMRIQRNQS QPVP SVRF
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GVQRNCSIDVNGSEVTATMTTLIHPNGKLSFY YDNIPTEIKESDLQSKIYGLKRDNVITGHEILVPVK
WIKSGTLVEFEAVGEICSQYKTNETCQNATTSNTTCIWCEKGNACIESNNADTHGLKVND CSVENMTT
LTTEENKQHKSHWYLYVVIPLVASLL LICIGCIIWRWLLRRKRSNG.

>Smp_329030.1 gene=Smp_329030
MKLSISTSTKTTGGGRFLTELGLCGDDGNPSSVNTLECKAVLDEADKHFESW TYWDGYFIDDAGNPNQ
NQVQS FIRPYPQSTNGRFLKQHFNHKTGEYSFSFITNQTRNQYSEKQNLIAEIYIPLSVHYPNGYSIN
LNPNNLTTEMKGNTLSIYLPTDLRNEHVLVEMKMVRK.

>Smp_335400.1 gene=Smp_335400
MMLDLFNRLFYILLEILRMIFQLHDEPTPQLITSTTDHITTEAIKSQTENVTHPMLAVQDVYKIGNET
KRKLTYCHMINKYQH L FVHH.

>Smp_349690.1 gene=Smp_349690
MRYNFSPSLWILIYLF FLWPYKRFNCNDICKNPDLLNYENVIIENDTYRYSLHYKYSMRIQRDQPQP V
PSE R FKNKV DVIYDHRPQFSFSFYGYHVQKIYFHERLQPIVYVLGGPYHGEIHNYIENNEKFDTAFLD
EEELLGVQRNFSINVNGTEVTATMTSLIHPNGKVSFHYDNIPKEIDGSKLQSKILRVIFCERD HVIPV
PAKWIKSGTLVEYEAIGEICSQYNTKETCLRATTSKTICIWCEKGNACIESNDQNT HGLKVND C RVEK
KSDVNDLNSSTTMEHSETTLGISEVQVTENHIKITEETDQNLNMTTRTTEENKQHKSHWYLYVVIPLV
ASLFLICIGCIIWRWLLRRKRSNE.

>Smp_349730.1 gene=Smp_349730
MMRYNFLPSLWILVYVIFAWPYKRFNCNDICKNPEIVIIENDTYRYSLHYYSMRIQRYQSEAVPSDR
FKNMIDYKYDRRLQFSFSFYGTHVKIYFHKNLQPILHIFGWSYIRNIHNYIKKYTKIETGVLDEKELF
GVKRNFSINVNGSEVTTTTTTLIHSNGKVSFYDYIPKEIEGSQLKSEIFGQLSCKGVVTNHEIPVPA

KWIKSGTLVEFEAIGEICSQYNTKETCLRATTSKTICIWCEKGNACIESNNQNTHTGLKVND CRVEKNS
DVEDLNSSTTMKHSEKTLRITELQVGENLMNTTEETDKHLNMTTRTTEENKQHKSHWYLYVVILLVAS
LFLICIGCIIWRWLLRRKRSNE.

>Smp_349700.1 gene=Smp_349700

MRYNFSPSLWILIYLFLLWPYKRFNCNDICKNPDLLNYENVIIENDTYRYSLHYKYSMRIQRDQPPV
PSERFKNKVDVIYEHSPQLSFSFYGSHVKNIFHRDGVQPIVYVLGGPYHGEIHNYIENNEKFDTAFLD
EDKLLGVQRNFSINVNGTEVTATMTSLIDPNGKVSFHYDNIPNEIDGSKLQSKILRVILCERDHIPIV
PAKWIKSGTLVEFEAIGEICSQYNTKETCLRATTSKTICIWCEKGNACIESNDQNTHTGLKVND CRVEK
KSDVNDLNSSTTMEHSETTLGISEVQVTENHIKITEETDQNLNMTTRTTEENKQHKSHWYLYVVIPLV
ASLFLICIGCIIWRWLLRRKEVMNDH.

>Smp_201340.1 gene=Smp_201340

MNFIFDFSKDVGQQLGQHLCKLDPFQFQRMNMIYKRKPVRQFGEVLESRTSSQLHNILVAMCKYYQSG
IIFFIG.

>Smp_349710.1 gene=Smp_349710

MRYNFSPSLWILIYLIIFLWPYKRFNCNDICKNPDLLNYENVIIENDTYRYSLHYYSMRIQRDQPPV
PSERFNDKIYGRSDHRPQFSFSFYGSHVKEIYFHERHEEDYVVKSGDSVDAFNKLRIGYIFNFIKNT
ESESWFLDEKELLGVQSNSSISVNGAEVTATMTRLIHPNGKVSFYDNIPTKIEESQLQSKILGLINC
EDVVTNHEIPVPAKWIKSGTLVEFEAIGEICSQYNTSETCQNATTANMTCIWCQKGKKCIESNNPDTH
SLKVND CRVEKKSDVNDLSTSTPIKDVETTLRSTKVQNMTRTTEENKQHKSHWYLYVVIPLVASLFL
ICIGCIIWRWLLRRKRSNE.

>Smp_350220.1 gene=Smp_350220

MRYNFSPSLWILIYLIIFLWPYKRFNCNDICKNPDLLNYENVIIESDSYRYSLHYYSMRIQHNQPPV
PSERFKNKIFGESDINPQFSFSYGFHVQKIAFHKDVQPTLYVIVKPYHGSIDNYIENYEKFDTAVLD
EEELLGVQSNFSTNVNGTEVTATMTTLIHSNRMLSFYDYIPTIEIEQSELRSKILGRIRCEGGFREHV
IPVPAKWIKSGTLVEFEAIGEICSQYYTSETCQNATTSNMTCIWCQKGKKCIESNNADTHGLKVND CR
VQKNSDVNDLNSSTTMEHGETTLGITEVQVGENLMKTTGETDKRLNMTTRTTEENKQHKSHWYLYVVI
PLVTSLFLICIVCIIWRWLLRRKRSNE.

>Smp_350230.1 gene=Smp_350230

MRYNFLPSLWILVYVIFAWPYKRFNCNDICKNPEIVIIENDTYRYSLHYYSMRIQRYQSEAVPSDRF
KNMIDYKFDRLQFSFSFYGSHAKEIYFHKNFQPIHLHIFGWSYIRNIHNYIKKYTKIETGVLDEVPKE
IEGSQLKSEIFGQFCKGVITEDEIPVPAKWIKSGTLVEFEAIGEICSQYNTSETCQNATTANMTCI
CEKGNACIESNNQNTHTGLKVND CRVEIEFGCIRFE.

>Smp_329040.1 gene=Smp_329040

MENIKPNLKLIEDLLTDSILFAEELYKAIPTSNIQITTSLLIDFWGDESDQVKNVYKLYSNESI
KSIEERFGKPTEDFLQCVVETRKVKI.

>Smp_329050.1 gene=Smp_329050

MIFQLHDEPTQLITSTTDHITTEAISKQNTENVTHPMLAVQDVYKIGNETKQTTLKIIQNTIYSFTIK
SY.

>Smp_205300.1 gene=Smp_205300

MNFIFDFSKDVGQQLGQHLCKLDPFQFQRMNMIYKRKPVRQFGEVLESRTSSQLHNILVAMYNYSINK
LMYFATFIHDELHKELIDVLDVQRFLFRSEIDLHTIDKAYKA.

>Smp_349720.1 gene=Smp_349720

MRIQRDQPPVPSERFKIKIYFRTDIYPQFSFSYYGSHVKEIHRDGDVDNVYEFGGSRIGNIFNFIK
NYTKSESWFLDEKELLGVQRNSSISVNGAEVTATMTRLIHPNGKVSFYDNIPTKIEESQLQSKILGL
INCEDVVTNHEIPVPAKWIKSGTLVEFEAIGEICSQYNTSETCQNATTANMTCIWCQKGKKCIESNNP
DTHSLKVND CRVEKKSDVNDLSSSTPIKDIETTLRSTKVQNMTRTTEENKQHKSHWYLYVVIPLVAS
LFLICIGCIIWRWLLRRKRSNE.

>Smp_349740.1 gene=Smp_349740

MRYNFSPSLWILVYVIFVWSYKLFSCNDFCNRFVYQYEIVIIENDTYRYSLHYNYSMRIQHNQPPV
PSERFKNKINRRYTARSISFSFYGSQVREIDFHDGNVDNVYEFGGSRIGNIFNFIKNTKSESWFLDE
NELLGVQKNYSTNVNGTEVKATMTSLIHPNGKVSFYDNIPTKEIDGSKLQSKIVGIIHCEDGTAFHEI
RVPKWIESGTLVEFEAIGEICSQYNTNETCQNAKISILTCFWCEKEKKCIISNLQDTHDCHVEKKSD
VNDLSTSTPIKDIETTLRSTKVQNMTRTTEENKQYKSHWYLYVVIPLVASLFLICIGYIIWRWLLRR
KRTNE.

>Smp_347020.1 gene=Smp_347020

MDTHSLYHLVILFEETKQKLSKLSYRSPSLPYPFIIRKSLKKARHSDLNTSDIQGSRQFNQITVETY
TMDTPESWNLDKGEEISFFSGNPTVETTEGIIHIYKNQREVPRCNDIVTSTVLCFFSVPSHVTVKDLL
RFISPMRDVIEELKIVKDSTPNQYMALLKFRTAEDTVHFYDTYNGTSYNTLEQVACQLMYVSHVEITH
PSTGVAFP TKDLREL PSCPCLERLDEPVQGILTTILCNHTFHDGCISQVEDTICPVCRYVQSPPEMLS
DSQCADC DIRENLWICLICGHVGCGRYGQKHAQVHFEETGHTFALELGKTLVWDYADDAYVHRLAVNH
EDGKLVQLGPSSETGNKKLDIISMEFSAILTSQLESQRAYFESQLDLITTQSNMRLEEMESSVESALS
AAQTAEKKLSEVIKENLVISRKL RQATSLAQRLQRDLEEEERALNQSLLINEKTWRERTEQAESEAKTA
RAECRELLLNLELRDKLNELNTINVHSRKRFRKYQTS LHKNIYL.

>Smp_348000.1 gene=Smp_348000

MNKKIILLTIIYVALMIRVPEHLKTRIKHYKDAYFHSSIQKFLSLEPYTRASSTRAPQIYHEECLRLE
KLYFTKWAVHYLSKNGATDITLLQSYENEYEEAAKKGDKNADPRRDWGGQLRASISKKWKEREILDDVE
SAYIAGPRTNVNVNKEELKKQLTNTGNNIEAQLNNVKELESKAIQAANKHMNNRDDKSLEKQHK EAYS
TLGKELRSLVDLMGEAEFQRILLTTLPKDEQIKMIIQAMDKDSTNCS.

>Smp_348010.1 gene=Smp_348010

MNKKIILLTIIYVALMIRVPEHLKTRIKHYKDAYYNSSIQKFLSLEPYTRASSTRAPQIYHEECLRLE
KLYFTKWAVHYLSKNGATDITLLQSYENEYEEAAKKG DENADPRRDWGGRLRASISKKWKEREILDDVE
SAYIAEPRTNVNVNKEELKKQLTNTGNNIEAQLNNVKELESKAIQAANKHMNNRDDKSLEE QAYEAYS
TLGEELRSLVDLMGEAEFQRILLTTLPKDEQIKMIIQAMDKDSTNCS.

>Smp_348030.1 gene=Smp_348030

MNKKIILLTIIYVALMIRDDYALSEPTDDYALSEPTDDYALSEPTDDYALSEPTDDYALSEPTVPEHL
KTRIKHYKDAYYNSSIQKFLSLEPYTRASSTRAPQIYHEECLRLEKLYFTKWAVHYLSKNGASDITLL
QSYENEYEEAAKKG DENADPRRDWGGRLRASISEKWKEREILDDVESAYIAEPRTNVNVNIEELKKQLT
NTGNNIEAQLNNVKELESKAIQAANKHMNNRVLSLEPYTRASSTRAPQIYHEECLRLEKLYFTKWAVH
YLSKNGATDITLLQSYENEYEEAAKKG DENADPRRDWGGRLRASISKKWKEREILDDVESAYIAEPRTN
VNVNKEELKKQLTNTGNNIEAQLNNVKELESKAIQAANKHMNNRDDKSLEE QAYEAYSTLGEELRSLV
DLMGEAEFQRILLTTLPKDEQIKMIIQAMDKDSTNCS.

>Smp_313480.2 gene=Smp_313480

MFPEHLKTRIKHYKDAYYNSSIQKYEEYEEAAKKG DENADPRRDWGGRLRASISEKWKEREILDDVESAY
IAETRTNVNVNIEELKKQLTNTGNNIEAQLNNVKELESKAIQAANKHMNNRDDKSLEE QHYEAYSTLA
KELRSLVDLMGEAEFQRILLTTLPKDEQIKMIIQAMDKDSTNCS.

>Smp_152510.1 gene=Smp_152510

MPDGLSHKILICGDVKGRVSALYSRVSKVINVAGQFDMMFCLGDFFGTETSEIKRMIDGSLAASLPTY
IVSPYTEIAQKYCQAESGCELCNNLT YLGSGKGYTTMSGRLRVVYMAEWELNSDNCNLPSSLLSEALAA
EDNGFLGVDLLLTCQWPKHVNKLTLSEL PDGCQC CIDSSSILISRLAYLTRPRYHFSCNGVYYERSP
YRNHRVLQEKACHTTRFISLADVKNERNQKYLAL KLIPIDKMDHQDLINQPPDVTENPYREFVDHKKH
SLDRETEVQTEQYFYNNMTKEKPGTVAKK DTHQKRKINTNTFEDTDDIKRQLVDKNDTSEESFQEKID
KNRNHAACWFCLGNPQVKKHLIVSIGTQAYVALPRGP IVPDHALILTIGHHQSWMSCPEYVRSEIEEY
KSRLKRM YAAQ GKAMVTFERNLKTQHYQLQVVPVPF SVAAEVKQVFLELSSNTDFSPCELKPVPRRTE
LDEICRVGIPYFFVELPTGEKLFGRIPKDRISSANLQFGRIVLTDPRILNCPEKADWHDC TDEEDEET
DLAKDFRKMFLPFDVNDDDDNNNTE.

>Smp_194130.1 gene=Smp_194130

MRYNFSPSLRILIYLI FVWPYKR FNCNDICNNADLRHHEIVIIENDTYRYS LHYNYSMRIQRNQSQSV
PSEHFYKIYDKYWVYPRFSFSYYGKHVKQIDFHEDHKLYDFGGYHIGTIINYIKNYEKYEAVVLDEKK
LLGVQRNFSINVNGTEVTATMTTLIHPNGMV SFYYDNIPTAIEEIELKSEISITIRCDNGYKYPGIRV
PAKWKISGTLVEFEAIGEICSQYNRSETCQRATTLTMTCFWCEKGGKCIESNDQNTHV LKVNDCSVEK
SDINDLNSSTTMEHIETTLGITEVQVSENLMKTTGETDKDLTTRTTEENKQDKSHCCLYVVIPLVASL
FLICIGCIIWRWLLRRKKSNE.

>Smp_317140.1 gene=Smp_317140

MNETEDLDVFAANDRWIESCIAHTEDFLKPFRSVLSTENNDRLVLILINEILHQLDQFIQRKSFSRFG
AIQLEKEYHNLFAYLTSISYNSLRDYFTRSLQICRLNLDRVEEVHYYWNSSSWRLTAHEVRSILSLR
RDFAVNEIRSLKLQ.

>Smp_309140.1 gene=Smp_309140

MARVEVAKLIDSKGLSIYEPGFHFLWINQFPLFEKNNLGQWKS VHPFTAASPETAHFLYTDPSKVI G

LHHDLCVNGQEVGGGSIRVHNPEVQKYIFTEILKENSCEMEYFLTALNSGAPPHGGIALGLDRLIAIF
VNAKSIRDVIAFPKAPGGKDLLCGTPTMVDDEILSQYCISVSNHNS.

>Smp_350210.1 gene=Smp_350210

MRYNFSPSLWILIYLI FLWPKYKRFKCNVDCERNLYQYEIVIIENDTYRYSIHYKYSMRIQHNQSQPV
SSDRFTNKIDYRYSARPQFSLSYGSRVHEIRFYEHDEGKVYNFRGLYSGSIYNYIKVKSESRVLDE
KELLGVQRNFLMNVNGTEVTTTMTSLIHPSGKISFYDNIPIREIEESQLKSRIFEQISCRVGGFVRFY
SILVPAKWIKSGTLVEFEAIGEICSQYNTNETCQ NATISNLTCFWCEKIEKCIISNLQHTHDCRIEKT
SDVNDLNSSTTTEHGETTSGITEVQVSENLMKTTEETDKQSYMTRTTEENKQHKSHWYLYVVIPIVA
SLFLICIGCIIWRWLLRRKGSDE.

>Smp_349160.1 gene=Smp_349160

MRYNFSPTLWVLIY LISVWPYKRFNCNDICKNSDLRDYEIVIIENDTYRYSLHYNYSMRIQRHQSQP
LGSFKNMVKDIYAGFPRFSFTYYGSNVRQIDFYKVVNADDIVVFGSIHLGDIVNNIQNYTKLESEIL
DEEELLGVKRNFSVNVNGSEVTATMTSLIHPNGKMSLYDNIPTIEIEQNKLRLSIYGRIACENGHRDH
EIPVSAKWIKSGTLVEFEVIGKICSQYNTSERCQ NATTSNMTCIWCEKGNACIESNDQNTHTGMKVKDC
RVEDTSTGNNGRK.

>Smp_349170.1 gene=Smp_349170

MRYNFSPSLWILVYLFFVWQYKRFNCNEICNDPYLRYEYENVIIENDTYLYSHHYKYSMKIQRHQSQP
PSDRFNIKINGIHTVYPQFTCSYHGSHVHKIMFYEDNADDVYEGRSYIGTNHNYLN NYVKLNSAVLD
EEKLIGVKRTFSINVNGAEVEATMTSLIHPNGKVSFYD KIPKKLWKVKLISKLTGIIKCEDGLQKFF
AIHVPEKWIKSGTLVEFQAIGEFCLQYDTSETCQNAKTPTTTCFCCEKIEEKKEEIEYEQDSGRK.

>Smp_349180.1 gene=Smp_349180

MAYTLFIPNSRVITVVTYTKLCFTKIMQMMYMNMEGLTLETNHNYLN NYVKLNSAVLDEEKLIGVKR
TFSINVNGAEVEATMTSLIHPNGKVSFYD KIPKKLWKVKLISKLTGIIKCEDGLQKFFAIHVPEKWI
KSGTLVEFQAIGEFCLQYDTSETCQNAKTPTTTCFCCEKIEEKKEEIEYEQDSGRK.

>Smp_349190.1 gene=Smp_349190

MRYNVSPSLWILIYLI FVWPYKRLNCNDYCKNSDLRHYENVIIENDSYRYSLHYKYSMRIQRYQSQP
PSDRFNNEIDDVYGGTPQFSCRYYGTHVQIDFERHRDDVYKSGELPIGTIFNFIENYKKSESRVLDE
KELLGVKRTFSINVNVSDVTAKMTNLIHPNGKVS LFYDNIPTIEIESKLQSEIYGLIRCEDGLTKHEI
SVPKWIKSGTLVEFEAIGEICSQKYTSETCQRATTSTMTCFWCEKGKACIESNDQNTHTGLKMND CRV
ENMIT.

>Smp_329950.1 gene=Smp_329950

MNIITIIIIIDTFVVFNNDFTEQISFASLCSQNVLVKPSFLNNQNHIIIVIIIIINCTKSILFFHHKFHAH
YSNDA.

>Smp_154590.1 gene=Smp_154590

MRYNFSPSLWILVYLFFVWQYKRFNCNEICNDPYLRYEYENVIIENDTYLYSHHYKYSMKIQRHQSQP
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EEKLIGVKRTFSINVNGAEVEATMTSLIHPNGKVSFYD KIPKKLWKVKLISKLTGIIKCEDGLQKFF
AIHVPEKWIKSGTLVEFQAIGEFCLQYDTSETCQNAKTPTTTCFCCEKIEEKKEEIEYEQDSGRK.

>Smp_201320.1 gene=Smp_201320

MNITSENTVSNLQLTTSVKSLILLVHSFYDHRSAAVVHWIQMFSRSMHQRRAKKVSSVIYSSFLSSEV
QTKSVVR.

>Smp_329960.1 gene=Smp_329960

MNMSSTHSSISSSSLSYLSNENHQCRQHPDHLRNLDDNQLTYIHCGDHVLYFSNLSNQ.

>Smp_349200.1 gene=Smp_349200

MRYNVSPSLWILIYLFVWPYKRFNCNEICNHPNVRNYENVIIENDTYRYSHHYEYSMRIQRHQSQP
PSDRFNIKINGIHTVYPQFTCNHSEYIRKIMFYADDADDVYDFRGYYIGTMINYLVNYMDFDTAVLD
EKKLLGVKRTFSINVDGSEVEATMTSLIYPNGKVSFYD KIPKEIEVSKFQSKIVGSIRCEGGLQKFF
AIHVPEKWIKSGTLVEFQAMG.

>Smp_102020.1 gene=Smp_102020

MRYNVSPCLWILIYLLFVWPYKRFNCNEICNDPYLRYEYENVIIENDTYLYSHHYKYSMRIQRHQSQP
PSDRFNIKINGVHTVYPQFTCSYHGSHVHKIMFYEDNADDVYEGRSYIGTNHNYLN NYVKLKSAVLD
EENLLGVQRNFSINVNGAEVEATMTSLIYPNGKVSFYD KIPMKLWKVKLISKLTGIIKCEDGLQKSF
AIHVPEKWIKSGTLVEFQAIGEFCLQYDASETCQNAKTPTTTCFCCEKIEEKKEKMMNTGTAAENKQ
EK.

>Smp_086630.1 gene=Smp_086630

MRYNVSPSLWILIYLIFFVWPYKRFNCNEICNPNPGVSNYENVIIENDTYRYSHHYEYSMRIQLHQSKPV
PSDRFNIKINGIHTVYPQFTCNYSKYIRKIMFYADDADDVYDFRGYYIGTMINYIVNYMDFDTAVLD
EKKLLGVKRTFRINVDGSEVEATMTSLIHPNGKVSFYDNIPIKEIEESKFQSKIVGSIRCEGGLQKFF
AIPVPAKWIKSGTLVEFQAMGESCSQHYRSEICQNAKTSTTTCFCCEEKKKCMELNNQDTHGLKVDDC
RVENMNTGTAAENTQIEVMNDT.

>Smp_350320.1 gene=Smp_350320

MRYNFSPSLWVLIYLIFFVWHYKRFNCNDICKNSDLRHYEIVIIENDTYRYSLHYNYSMRIQRYQPQP
SSDRFKNKISYIYAGFPRFSFSYYSNVRQIDFYKVVNADDIVVFESIYLGDIINNIQNYTKLESEIL
DEEELLGVKRNFSINAHGSEVTATMTSLIHPNGKMSLYDNIPTIEIEQNKLRLSIYKGICENGHRDH
EIPVPAKWIKSGTLVEFEVIGKICSQYNTSERCQNATTSNMTCIWCEKGNACIESNDQNTGHMKVKDC
RVENTSTETTEENKPKHSYWYLYVVIPLATSLFLICIGYIIWRWLLRG.

>Smp_349210.1 gene=Smp_349210

MRYNFSPSLWIRIYLIFFVWHYKCFNCNDICKTSDFSPYEIVIIENDTYRYSFHYKYSMRIQRYQPQP
SSDRFKKMSTYIYYATPQFSFSFYGFHVEQIDYKYHGENVFQFQKTYIGTIDSYIKEFENSESRVLD
EKELLGVKTNFSINVNGLDVTATMTSLIHPNGKVSFYDNIPTIEIESRLQSEISGLIRCKEGHTRSP
EISVPAKWIKSGTLVEFEAMRDRCLQYNTSETCQNATTSIVRCFWCERERACIESNDQNTHYLKVND
RVEENPDANDLNSSTTMKHSESVVYFEDDCL.

>Smp_349240.1 gene=Smp_349240

MRYNFSPSLWVLIYLIFFVWHYKRFNCNDYCKNSDLSHYEIVIIENDTYRYSLHYKYSMRIQRNQSQP
PSDRFKNKISYIYYGKPQFSCSYGIIHVEQIDFYKYHGENVFEFGGSYIGTIINYIKNYKKSESRLD
EKELLGVKRNISINVDGSDVTATMTSLIHPNGKVSFYDNIPTIEIESRLQSEIYGLIRCEEGLTRSL
EISVPAKWIKSGTLVEFEAIGEICSQYNTSETCQNATTSNMTCIWCEKGRACIESNDQNTHGLKVND
RVEKNPDVNDLNS.

>Smp_093070.1 gene=Smp_093070

MTSLIHPNGKVSFYDNIPTIEIESRLQSEIYGLIRCEDALFNIIFLVQYRIFSITYFSKYQFLTSS
FLTINIW.

>Smp_349250.1 gene=Smp_349250

MRYNFSPSLWIIYLIFFIWPYKRFNCNDICKISDMRHYEKVIIENDSYRYSLHYNYSMRIQRNQSQP
PSDGFKNKISYIYYGTPOFSCNYYGSHVQIQFSEDLDRDYVVALGRSHIGTINNYIEENEKSEAGVL
NEKELLGVQKNFSIKINGSDDVTATMTSLIHPNGKISFYDNIPIKEIEESQLTSKINGIEKCGNGLTKH
EISVPAKWIKSGTLVEFEAIGEICSQYNTSETCQNVTTSNMTCIWCEKGNACIESNDQNTHGLKVND
RVENTSTGIMEENKPKHSYWYLYVVIPLAASFLICIGYIIWRWLLRSKNSGK.

>Smp_317160.1 gene=Smp_317160

MSARQRRPIAQTLSGFDIAIVMLAQMVLQSGIRVISLPQPSDIPPPGTGVFIVGYGRDDNDRDPSRK
NGGILKKGRATIMECRHATNGNPICVKAGQNFQQLPAPGDSGGPLLSPQGPVLGVVSHGVTLPLNLPD
IIVEYASVARMLDFVRSNI.

>Smp_337500.1 gene=Smp_337500

MSARQRRPIAQTLSGFDIAIVMLAQMVLQSGIRVISLPQPSDIPPPGTGVFIVGYGRDDNDRDPSRK
NGGILKKGRATIMECRHATNGNPICVKAGQNFQQLPAPGDSGGPLLSPQGPVLGVVSHGVTLPLNLPD
IIVEYASVARMLDFVRSNI.

>Smp_306680.1 gene=Smp_306680

MSARQRRPIAQTLSGFDIAIVMLAQMVLQSGIRVISLPQPSDIPPPGTGVFIVGYGRDDNDRDPSRK
NGGILKKGRATIMECRHATNGNPICVKAGQNFQQLPAPGDSGGPLLSPQGPVLGVVSHGVTLPLNLPD
IIVEYASVARMLDFVRSNI.

>Smp_317170.1 gene=Smp_317170

MSARQRRPIAQTLSGFDIAIVMLAQMVLQSGIRVISLPQPSDIPPPGTGVFIVGYGRDDNDRDPSRK
NGGILKKGRATIMECRHATNGNPICVKAGQNFQQLPAPGDSGGPLLSPQGPVLGVVSHGVTLPLNLPD
IIVEYASVARMLDFVRSNI.

>Smp_317180.1 gene=Smp_317180

MVNLQSGIRVISLPQPSDIPPPGTGVFIVGYGRDDNDRDPSRKNGGILKKGRATIMECRHATNGNPIC
VKAGQNFQQLPAPGDSGGPLLSPQGPVLGVVSHGVTLPLNLPDIIVEYASVARMLDFVRSNI.

>Smp_330270.1 gene=Smp_330270

MSARQRRPIAQTLSGFDIAIVMLAQMVLQSGIRVISLPQPSDIPPPGTGVFIVGYGRDDNDRDPSRK

NGGILKKGRATIMECRHATNGNPICVKAGQNFQQLPAPGDSGGPLLSPQGPVLGVVSHGVTLNLPDIIVEYASVARMMLDFVRSNI.

>Smp_330280.1 gene=Smp_330280

MSNRWRFVVVVTLFTYCLTFERVSTWLIRSGEPVQHPAEFPFIAFLTERTMCTGSLVSTRAVLTAGHCVCSPLPVIRVSFLTLRNGDQQGIHHQPSGVKVAPGYISCMSARQRRPIAQTLSGFDIAIVMLAQMVNLQSGIRVISLPPQSDIPPPGTGVFIVGYGRDDNDRDPSRKNGGILKKGRATIMECRHATNGNPICVKAGQNFQQLPAPGDSGGPLLSPQGPVLGVVSHGVTLNLPDIIVEYASVARMMLDFVRSNI.

>Smp_330290.1 gene=Smp_330290

MLNGRTFLMVTLFTYCLTFERASTWLVRKGEPVQDRTEFPYIAFVRTERTMCTGSLVSTRAVLTAGHCVCSPMPVVQVSFLTLRNGDQQGIHHQPSGVKVAPEYMPSCASRQRRRIRQTLSGFDIATVMLAQMVNLQSGIRVISLPPQASDIPTPGTDVFIVGYGRDDNDRDPSRRAGGILKKGRATVMECKHSTTGNPICVQAAAYVFGQITAPGDSGGPLLRSPPQGPVLGVVSHGVTLNRLDVLVEYASVARMMLGFVSSNI.

>Smp_336190.1 gene=Smp_336190

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>Smp_330300.1 gene=Smp_330300

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>Smp_330310.1 gene=Smp_330310

MECKHSTTGNPICVQAAAYVFGQITAPGDSGGPLLRSPPQGPVLGVVSHGVTLNRLDVLVEYASVARMMLGFVSSNI.

>Smp_317270.1 gene=Smp_317270

MECKHSTTGNPICVQAAGEPVQQRTEFPFIALMTDASMTGSLVSSRAVLTAGHCVCQTPIVRVSFLLSLSEFDQRTINHRPLEIKVAPEYNPVCQLKRENKRITKSLGGYDMAIITLNLVNLETGVKVISLATELDIPIPESIAVMVGYGQDIRDPDPSGRYGGILKKGSATIMACRHKTFGDPICVKPGPNSKQIAGPGDSGGPLLLTPQGPIVGVASNGVFLPALADLCVEYSSVPRMLKFILPNI.

>Smp_317190.1 gene=Smp_317190

MECKHSTTGNPICVQAAAYVFGQITAPGDSGGPLLRSPPQGPVLGVVSHGVTLNRLDVLVEYASVARMMLGFVSSNI.

>Smp_169280.1 gene=Smp_169280

MDGNPSTLSILSDKYVFLNPNEQFVRIKNYLDIELDNGQGEFCFLELGIGDGQCPLTPQEMNQSVCTAERLADSLSSHILYLRDRWITAGSQSSATTTTQSGSGVDTLTRPSSVDNGHSSPHRHTLTSSSGESKTKGNSVNIDDGIKSKQNSISTDNNKELSSQDKSETNITDTTSTISSSSNSSSATTGCLVKEYLLRRKTASDDFVDVRVAVVGNVDAGKSTLLGVLTHGELDNGRGLARLRLLRHKHEAESGRTSSVAHDILGFNSIGQVVNKPPIHGHNLWSEICEASAKVITFIDLAGHERYLKTTIFGMTGHAPDYVMFMVGANAGVIGMAKEHLGLALALCVPVFVVVTKIDMCPNVLHETMNLFRILKSPGCRKIPALISSTDDVICCATNFTSERMCPIFSVSNVNGTNLDLLKLFLNLLPSRSEPRNLALAHFQIDEIFSVQGVGTVISGTCLSGIILNDILLLGPDLSGQFNPIISIKSIQRKRLSVNYVRGGQTASFALKKLRRNQVRKGMVLLAPESKPKACIEFIAEVLILHHPPTTISVGYQAMVHAGPVRQTATILKLSHERLRTGDKDMVVFRFIKSPEYLYTGLRLIFREGKTKAVGTVKELVPYSASIQQNPRAKLYKRYATSKTNQPMNNTVTDEIKTLNLSNTSSIPKSTEYISTTTNTTTSQPDTELSNIPVSDLLTSNNINAPANSRQRKHYYHRTRKDITE.

>Smp_187410.1 gene=Smp_187410

MTDFVICRIIFFPSQLLCNQTFEITQFLCLSSLDHLLLNYTFKNVRSIVQSTGGGRFLTEFGLCLPDGNPESINTVECNALNAADRNFESWTYWDGYELFSNLNVENISLKSFSRTYPQSTAGQPVQLRFDVDSGVFYAFVPTQKNCTNVNSTLLVAEIFVPMSEIHYPHGVKTRFIPQLSYKVYENNTNLIFVYMPCTLIKTNIELIEITIIPNQ.

>Smp_332150.1 gene=Smp_332150

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>Smp_349140.1 gene=Smp_349140
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>Smp_331110.1 gene=Smp_331110
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TVFYVLEHRAALITLEVAAELILFLTYHLQTIRAVC.
>Smp_179390.1 gene=Smp_179390
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>Smp_179400.1 gene=Smp_179400
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>Smp_333360.1 gene=Smp_333360
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>Smp_331120.1 gene=Smp_331120
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>Smp_315060.1 gene=Smp_315060
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TTVVY.
>Smp_317220.1 gene=Smp_317220
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ECTNGAQQLYENVSGAWNHWGDFWEIIAKHYGKKS NVLGYDLIN EPPPGNFYSNPLRGFPYAGRYNL
LPVYDYLVERIRQYDKSSLIFYEPVTYGIFTPLSTSGWLGTGFRVPGANRDKSAPSKSVLSYHYWCW
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LDEADKHFESWTFWDGYFIDNAGNPIQSAVFHSSLSSVNKWEISQATFQS.
>Smp_317230.1 gene=Smp_317230
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IRPYPQSTNGRFVKQHFNHETGEYSFSFITNQLSNQYSEKQNLIAEIYIPLSVHYPNGYSINLPNNL
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>Smp_349150.1 gene=Smp_349150
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EKELLGVRRHFSIDVNGSDNAHHEIPVPAKVIKRGTLVEFEAIGEICSQYNTIETCQ NATTSNTTCIW
CEKGEKCI ESNNQHTHGLKVND CRAENMTTRTTEENKQHKSHWYLYVVIPLLASLFLICIGCIIWRLL
LRRKRSNK.
>Smp_334670.1 gene=Smp_334670
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AIMSTDVRRTTSLIDFWGDEFDQVENAYKISKM.

>Smp_337100.2 gene=Smp_337100

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VNQPKIVPNNKFCAANDVHNIRNQIKKELYKAISTSNIQITTSLLIDFWGDEFDQVKNVYKLYSNE
WKSIEERFGKPTEDFLQCVVETRKKVQKQETNEDTFGKPIVNMSEVNKTFHYLLKQKNSTNITEQQLS
NLLCKLNPFLQLEALDDMMYQQDLKRTFFFEVIKRRSSGQMHDLNLLSLYTYSVNKPMYFATLFHDVLH
ISVLT AQRLIFRSEVDLQLVCDIYEALYGTYSDDVKQKYFGKQDNALTNLLKSEETTVVY.

>Smp_344740.1 gene=Smp_344740

MNYSMRSTILFIFIWSSVYTEPIPLSKIRLNQDGMFMDHLGFIKLRGFGNNVQKDFPQYQGNAWNITQ
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IDG IPLWLINQFKRPPTIMQEPWPYKPKLPGWDGAYLYT ECTNGAQQLYENVSGAWNHWDGFW
EIIAKQY G KKS NVLGYDLIN EPPPGNFYSNPLRGFPYAGRYNLLPVYDYLIERIRQYDKSTLIF
YEPVTYGI FTP LMSGWSGTGFRVPGANRDKSAPSKSVLSYHYWCWILQNDYQNSTMPFWKVLCD
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DAGNPIRS AVFHS SLSSVNKWEICQATFQS.

>Smp_123070.1 gene=Smp_123070

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SNNE.

>Smp_165000.1 gene=Smp_165000

MFGDRQVSVISPATRDKEVFRWIPCRPGEVKDENSEIVDVISWVSDVREMSENPTLVELLKETDRSS
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VYGETSFELISQMIDTIAVTSDDVFIDLGSGVGQVVLQVCASTDAKFCYGIEKAEYPAHCASRLDSAF
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LEV TASSPSELISVEGRKLSLQSCLSKNETISRQITSGSTAVHRMEKCESQHLQSELKRSHVHHKDNQ
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SNRLN SLENSNDRCDTNVMNEDHPNNVANRRIVRKCRQLSDSSSLNDTNFENSNNQTAVLRKRMQK
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LIKQHHVLEEK IAEFRQISLLSSANQELVRRHHIEAARLLATATAIKSDNSLQNHPTLNKLCISG
IETKVT EINKNG FHYNSDNIPTSTCSELNYQNAVSLNSVVI PPPPSLTKLSHNTLT CNKFGIP
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SVVPFH THNNKADCDHKVITRN SNSHNNNSNNIINNGTNHRIDKHMNI PPPPPLPMHIHSD
VYVDGVLSSANS LDFDNKHNYC NNNTNN NNISSLLPELNRSFITCRTDYDVSLIQSNRYHTK
SMHASLQDLILDEF SRET PCISVSNSCAIAKTN KNRNVYSISDSSYNYQYENNPVPFQHHN
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>Smp_314170.1 gene=Smp_314170

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AVLNAA DRNFESWTYWDGYELFSNLIVENISLKSFSRTYPQSTAGQPVQLRFDVDSGVFYA
FVPTQKNCTNVNSALLVAEIFV PMSIHYPHGVKTRFIPEQLYEVYENNTNLMFFYIPCT
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>Smp_334820.1 gene=Smp_334820

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>Smp_341290.1 gene=Smp_341290

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>Smp_348060.1 gene=Smp_348060

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KNVSGLWNYFAEYWRITTDREFGKKYNVLGYDLINPPPGNFYLNPFLLPNIAQONLLLFYDYLVSVI
RQTDKDTLIFYESVTYGIFFPFVNGIPGTGMQVRPGLLQDETARKKSVLSYHYWCWLESTPATEHMP
SWKRHLCDQLLLNYAFKNVRSIVQSTGGGRFLTEFGLCLPDGNPDSINTVECNVLAADRNFESEWTY
WDGYELFSNLNVENISLKSFSRTYPQSTAGQPVLQFEDVDSGVFYAFIPTQKNCTNVNSALLVAEIF
APMSIHYPHGMRTRFIPEQLSYKVYENNTNLLFVYMPCTLMKTNIELIEITIIPKQN.

>Smp_334830.1 gene=Smp_334830

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AKEHLQEGPYELIKDAKSRTTVNKLKAETSKILHSLKIKLGTPLWFLNPKSCNPRRFYGLLKIHKDS
TPLRPVVDFSNSPTYNLAKYLARILKPHEKLINHGIKNSMEFKNIIDTIDIEEDEVMASFDVSSLFTN
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NLFMH.

>Smp_349080.1 gene=Smp_349080

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KWSFKSNEDDFTAKITCLIIYANGNISLYFEKIPSQIRKKYLQIGITTQIYCKTVGYNTQGVKSPKI
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ETSQETEDLSTPASIKRTETTSKV.

>Smp_182090.1 gene=Smp_182090

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>Smp_316790.1 gene=Smp_316790

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NVSGLWNYFAEYWRITTDREFGKKYNVLGYELINPPPGNFYLNPFLLPNIAQONLLLFYDYLNVIR
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>Smp_316470.1 gene=Smp_316470

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>Smp_316490.1 gene=Smp_316490

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PIKGRGVKPIVNKTAVSEVFYDIMVVLDSDNKDVGOQLGQRLCKLDPFQFQRLNMIYKRKPVRQFGEVL
ESRTSGQLHNILVAMYNYSINKPMYFATLIHDELHKELIDVLGVQRFLFRSEIDLHTIDKMYKAKYG
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>Smp_317400.1 gene=Smp_317400

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>Smp_349090.1 gene=Smp_349090

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GVKRNFSLSVNGAEIPTEIKESDLQSKIYGLIRCDNVSTNHEIPVPAKWIKSGTLVVFEEIGEICSQY
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>Smp_335540.1 gene=Smp_335540

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>Smp_318020.1 gene=Smp_318020

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NPICVKAGQNFQQLPAPGDSGGPLLSPQGPVLGVVSHGVTLNLPDIIVEYASVARMDFVRSNI.

>Smp_318030.1 gene=Smp_318030

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>Smp_318040.1 gene=Smp_318040

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>Smp_318050.1 gene=Smp_318050

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>Smp_318060.1 gene=Smp_318060

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IIVEYASVARMDFVRSNI.

>Smp_318070.1 gene=Smp_318070

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>Smp_318080.1 gene=Smp_318080

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>Smp_318090.1 gene=Smp_318090

MLAQMVNQLQSGITVISLPPQASDIPTPGTGVFIVGYGRDDNDRDPSRKNGGILKKGRATIMECRHATNG
NPICVKAGQNFQQLPAPGDSGGPLLSPQGPVLGVVSHGVTLNLPDIIVEYASVARMDFVRSNI.

>Smp_318100.1 gene=Smp_318100

MLAQMVNQLQSGITVISLPPQASDIPTPGTGVFIVGYGRDDNDRDPSRKNGGILKKGRATIMECRHATNG
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>Smp_349070.1 gene=Smp_349070

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DIHRYHEISVPAKWIESGSLVEFEAIGEICSQYNTTETCQNAATSNMTCFWCQKGKKCIESNDQNTHG
LKVNDCSVEKYSNVNDLNSSTTMEHSETTSGITEVQVSENLMKTTEETDKQSYMTRTTEENKQHKSH
WYLYVVIPLVASLFLICIGCIIWRWLLRRKRSDE.

>Smp_349030.1 gene=Smp_349030

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ERDIISLISRLSADNPDPNNPLTTLDSDRQILVKMAVEKFDEYVSKRDEKNIVYLLKIFFLLGETNEGI
RRFSIYLCSYISNKCELLITTNKSSSQSSEFVSANLITEILEFVADTLKNNSMYVETYCGPGNIFGLV
SSVHCVVDRYVKCVVERFYAYHHLDELCSMLKKSNSNSLSSKRHDSSAQ SINRDKILDSELGSDRVL
VIEPIIVETLQIITCESELYLRFIQRRISADIKQCENLAEDDFKKKSNKISKFFENSQ LVCQVQD LLSKY
LNLEQYYLRVTIMKALSSDEVDSNNVWCFIDDVFFITKKS LIRSLSSGNVDTICAMVNHSCSILIDL
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NSIEASQKNLLSLVNHLESELNLLYQNQEINSQKLD MCITELKVSISDQLQALLDSAFEHLSTSVIQS
QVKTLNLFVFKSLKYDLLEEDLDVFAANDRWIESCIAHTEDFLRPFRSVLSTENNDRFVLILINEILHQ
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>Smp_349040.1 gene=Smp_349040

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WINQFPLFEKNNLGKWSVHHPFTAASPETAHFLYTDPSKVIGLHYDLVCNGQEVGGGSIRVHNPEVQ
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>Smp_349050.1 gene=Smp_349050

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>Smp_303010.1 gene=Smp_303010

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QTDKDTLIFYESVTYGIFFPFVNGIPGTGMQRPVGLLQDEMARKKSVLSYHYCWLESTPATEHMPS
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DGYELFSNLNVENISLKSFSRTYPQSTAGQPQVLEFDVDSGVFYAFIPTQKNCTNVNSALLVAEIFA
PMSIHYPHGMRTRFIPEQLSYKVYENNTNLMFFYIPCNLIITNIELIEITIIPKQN.

>Smp_349850.1 gene=Smp_349850

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>Smp_321730.1 gene=Smp_321730

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>Smp_321740.1 gene=Smp_321740

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>Smp_349100.1 gene=Smp_349100

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PVPAEWIESGTLVEFESIGEICSQYNTSETCQNAATTSNTTCIWCEKWKTCEIKNQDTHGLKVNDCRV
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>Smp_321750.1 gene=Smp_321750

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>Smp_244800.1 gene=Smp_244800

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SSITDIARVTNSPRLPIGTSPSVSQTFWLKDNLFDLLNTTESQSSWFENRGYQDTLALADAPFGYYSIL
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FIYASDKTLYPNPQASAITTNYLKHYFLGRILAKAIFEGVLVDLQFAYFFLAKIVSRSGGGGVGFDY
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KLNKMIYPQVRAFTAGLNDVIPIDWVRLFDAEELQTLISGADMVIDVDDLQHTFYIGNSINYTETLD
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>Smp_167800.1 gene=Smp_167800

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>Smp_306630.1 gene=Smp_306630

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>Smp_052630.1 gene=Smp_052630

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>Smp_329780.1 gene=Smp_329780

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PVPKWKISGTLVEYEVIGKNCWNFNTSETCQRATTSNMTCIWCQKVNKCIESNDNDTHGLKVNDCRV
ENMITEAT.

>Smp_324410.1 gene=Smp_324410

MNCLFLLFLPSLWSVLSTENNDRFVLILINEILHQLDLFIQRKSFSRFGAIQLEKEYHNLFAYLTSIS
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>Smp_349520.1 gene=Smp_349520

MRIQHNQSQPVPSERFKNKIGFSYKVPKFWFSFYGYHVEEVRFYSDLEYIYGTFTQIGNINNYIQNYE
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GGIYRYHEIRVPAKWKISGTLVEFEAIGEICSQYNTIETCPNATIWNCTWCEKGEKCIIMYNNQDT
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>Smp_324420.1 gene=Smp_324420

MFADLCNSSWMYNTDGKVTNINLNGSNISALPEYTKMVFLILGIEIAITLLVIIILSVLEIVHKTPNPW
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>Smp_324450.1 gene=Smp_324450

MTSVSCIYESFYIIFQIDLHTIDKVYKAKYGIYLSDDVKRIYYGEYADALLKLLKKEEIPDIYQHSIP
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>Smp_349530.1 gene=Smp_349530

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PAKWIKSGTLVEFEAIGEICSQYNTSETCPNATIWNNTTCTWCEKGEKCIIMYNNQDTHDCRVEKTS
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CIGCIIWRWLLRRKRSNE.