

>Smp_349250.1 gene=Smp_349250

-----MRYN-

FSPSLWIIIIYLIFIWPKRFNCNDICKISDMRHYEKVIIENDSYRYSLHYNYSMRIQRNQSQPVPSPDG
FKNKISYIYYGTPQFSCNYYGSHVQQIQFSEDLDR-----
DYVFALGRSHIGTINNYIEENEKSEAGVLNEKELLGV
QKNFSIKINGS DVTATMTSLIHPNGKISFYDNIPEIEESQLTSKINGIEKCGN-----GL-
TKHEISVPAKWIKSGT
LVEFEAIGEICSQYNTSETCQNVTTSNMTCIWCEKGNACIE----
SNDQNTHTGLKVND CRVENTS-----

-----T

GIMEENKPKHSYWYLYVVIPLAASFLICIGYIIWRWLLRSKN-----SGK.

>Smp_349740.1 gene=Smp_349740

-----MRYN-

FSPSLWILVYVIFVWSYKLFSCNDFCNRFVIFYQEIVIIENDTYRYSLHYNYSMRIQHNQPQPVPSE
FKNKINRRYTAR-SISFSFYGSQVREIDFHDG-NV-----
DNVYEFGGSRIGNIFNFIKNYTKSESWFLDENELLGV
QKNYSTNVNGTEVKATMTSLIHPNGKVSFYDNIPEIDGSKLQSKIVGIIHCED-----GT-
AFHEIRVPAKWIESGT
LVEFEAIGEICSQYNTNETCQNAKISILTCFWCEKEKKCII---SNLQDTH-----
DCHVEKKS DVNDLSTSTPIKDIET
TLRSTKVQ-----

-----NMTT

RTTEENKQYKSHWYLYVVIPLVASFLICIGYIIWRWLLRRKR-----TNE.

>Smp_349190.1 gene=Smp_349190

-----MRYN-

VSPSLWILIIYLIFVWPYKRLNCNDYCKNSDLRHYENVIIENDSYRYSLHYKYSMRIQRYQSQPVPSPDR
FNNEIDDDVYYGTPQFSCRYYGTHVVQIDFERH--R-----
DDVYKSGELPIGTIFNFIENYKKSESRLDEKELLGV
KRTFSINNVSDVTAKMTNLIHPNGKVSLFYDNIPTIEIESKLQSEIYGLIRCED-----GL-
TKHEISVPAKWIKSGT
LVEFEAIGEICSQKYTSETCQRATTSTMTCFWCEKGKACIE---
SNDQNTHTGLKMND CRVENMI-----

-----T.

>Smp_086630.1 gene=Smp_086630

-----MRYN-

VSPSLWILIIYLFFVWPYKRFNCNEICNNPGVSNYENVIIENDTYRYSHHYEYSMRIQLHQSKPVPSPDR
FNIKINGIHTVYPQFTCNYSKYIRKIMFYAD-DA-----
DDVYDFRGYYIGTMINYIVNYMDFDTAVLDEKKLLGV
KRTFRINVDGSEVEATMTSLIHPNGKVSFYDNIPEIEESKFQSKIVGSIRCEG-----
GLQKFFAIPVPAKWIKSGT
LVEFQAMGESCSQHYSRSEICQNAKTSTTTCFCCEEKKKCMIE---
LNNQDTHGLKVDD CRVENMNTGTA-----

---AENTQIEV-----M-----NDT.

>Smp_192050.1 gene=Smp_192050

MRIRLHQPQPAFTDS

YPK-IYGSYFVTPRFSFRFYDTLIHEVCIYSD-GN-----

ILLTREAYDYFGGIENFAQNVQESETMVSNEEESLAV

KRNFLINVNDKDVSAEMTSVIQPNGKITLYFDNVSCTIS-----

>Smp_350240.1 gene=Smp_350240

-----MRYN-

FSPSLWILIYVIFGRPYKRFNCSDICKNPDLKRYENVIFENDSYRYSLHYNYSMRILRNQPQVPVPSER

FINMINDKYVANAQFSFSFYGYRLEKIRFHEY-PT-----

DHVKYKFGRSQVGNIINHIKNYTKSESRLDEKELFGV

KRNFSINVNGTEVTATMTTLIHTNGKISFYDNIPEIEESQLQSKIVGSIRCEG-----

EDTEEREIRVPVDWIKSGT

LVEFEAIGEICSQYNTSETCQRSTTLKTTCIWCEKGEKCIE---

SNNPDTHGLKVNDCRVETT-----

KTTDENKQHKSHWYLYVVIPLVASLFLICIGCIIWRWLLRRKR-----SDE.

>Smp_349580.1 gene=Smp_349580

-----MRYN-

FSPSLWILIYLFVWNYKRFNCNDICKNPDLHYENVIFENDTYRYSLHYYYSMRIQRNQSQPVPVPSER

FKNMIHVYKARPQFSISFYGSHIREIDFHKR-HG-----

DTAYEFGRSYIGNTYNYIENYKKSEYRVLHEKELLGA

KWTF SINVGSEVTAIMTSLIHPNGKLSFYDNIPTENEEIKLLSGIVGSIRCEG-----GL-

KKPEISVPAKWIKCGS

LVEFEVIGEICSQYNTSETCQNATTSITTTCIWCEKGEKCIE---

SNNPDTHDLKVNDCRVQKSDVNDFSTSTPIKDIET

TLRSTEVQVTENL-----

IETTEERYK--HLTT

KTTDENKQHKSHWYLYVVIPLVASLFLICIGCIIWRWLLRRKR-----SDE.

>Smp_349150.1 gene=Smp_349150

-----MRYN-

FSPSLWILIYLIFFVWPYKRFNCNDYCKRSDLYNYEIVIIENDTYRYSLHYNYSMRIQRNQSQPVLSDS

FKNKIDGRYKVTPRFSCSYGYGVGHINFFEY-QN-----

DNVIEYGGFIGIINYIKNYEKSESRLDEKELLGV

RRHFSIDVNGSDNA-----

HHEIPVPAKWIKRG

LVEFEAIGEICSQYNTIETCQNATTSNTTCIWCEKGEKCIE---

SNNQHTHGLKVNDCAEN-----

-----MTT
RTTEENKQHKSHWYLYVVIPLLASLFLICIGCIIWRLLLLRRKR-----SNK.
>Smp_349570.1 gene=Smp_349570
-----MRYK-
FSRSLWILIYLIFFVWPYERFNCNDICKNPDLHYENVIIENDTYRYSLHYNYSMRIQRNQSQPVP
FKNKINDKYTARLQFSSSFYGSVQIIEFYRD-YG-----
EYVYEFESYIGMMFSYIKNYTKSESRLHEKELLGV
KRNFSINVTGDTATMTSLIHPNGKVSLEYDNIPTEIKVSALRSKILGPIRCEG-----
ERENRHIITVPAKWIKSGT
VVEFEAIGEICSQYNTSETCQRATTSKMTCIWCQKGGKKEIE---
SNNPDTHGLKGNDCRVQNNVNDVSTLTPVKDIER
TLRSTEVQFTEDL-----

IETTEETDEHSNMTA
LITEENKQHKSHWYLYVVIPLVTSFLVCIGCIIWRWLLRRKR-----SDE.
>Smp_349100.1 gene=Smp_349100
-----MRYN-
FSPSLWILIYLIFFVWPYKRFNCNDICNNPDLRHHEIVIIENDTYRYSLHYHYSMRIQRYQSQPVP
FNNKVDVAVYGVYPRFSFSYYGKHVQIDFYKH-R-----
YVYVFEKSQIGNINNYLENYKYESRVLDEKELLGV
QRNFWINVDSEVTATMTTLIHPNGMVSFYYDNIPTEIGESQLKSKIIGKIRCEK-----
RRVMYHAIPVPAEWIESGT
LVEFESIGEICSQYNTSETCQNATTSNTTCIWCEKWKTCIE---
IKNQDTHGLKVNDCRVEKKSDVNDLNSSTTMEHGET
TSGITEVQ--
ESL-----
--

M-----
KTTGETDKH-----L-----VNI.
>Smp_349170.1 gene=Smp_349170
-----MRYN-
FSPSLWILVYLFFVWQYKRFNCNEICNDPYLRYENVIIENDTYLYSHHYKYSMKIQRHQSQPVPSDR
FNIKINGIHTVYPQFTCSYHGSHVHKIMFYED-NA-----
DDVYEGRSYIGTNHNYLNYYVKLNSAVLDEEKLIGV
KRTFSINVNGAEVEATMTSLIHPNGKVSFYYDKIPKKLWKVKLISKLTGIIKCED-----
GLQKFFAIHVPEKWIKSGT
LVEFQAIGEFCLQYDTSETCQNAKTPTTTTFCCEKIEEKKEEIEYEQDS-----

-----GRK.
>Smp_350220.1 gene=Smp_350220
-----MRYN-
FSPSLWILIYLIFFLWPYKRFNCNDICKNPDLLNYENVIIIESDSYRYSLHYHYSMRIQHNQPQPVP
FKNKIFGESDINPQFSFSYYGFBVQKIAFHKD-VQ-----
PTLYVIVKPYHGSIDNYIENYKFDATAVLDEEELLGV
QSNFSTNVNGTEVTATMTTLIHSNRMLSYYDYIPTIEIQSELRSKILGRIRCEG-----GF-
REHVIPVPAKWIKSGT

QRNFSINVNGTEVTATMTTLIHPNGMVSFYYDNIPTAIEEIELKSEISITIRCDN-----GY-
KYPGIRVPAKWIKSGT
LVEFEAIGEICSQYNRSETCQRATTLTMTCFWCEKGGKCIE---SNDQNTHTVLKVNDCSVEK-
SDINDLNSSTTMEHIET
TLGITEVQVSEN-----

MKTGETDK--DLTT
RTTEENKQDKSHCCLYVVIPLVASLFLICIGCIIWRWLLRRKK-----SNE.
>Smp_349670.1 gene=Smp_349670
-----MRYN-FSPSLWILVYVIFVWSYKRFNCNDYCKNP-----
EIVIIENDTYRYSLHYKYSMRIQRNQAQPVPSYS
FEYKIKHIYAGFPRFSCSYYGKHVEEIHFNEN-HA-----
NYVYQFESLSIGTIFNYIKSYKKSESRVLDEKELLGV
QRNCSIDVNGSEVTATMTTLIHPNGKLSFYYDNIPMEIEESQLQSEIYGFIKCDY-----VI-
TGHEILVPVKWIKSGT
LVEFEAVGEICSQYKTNETCQNATTSNTTCIWYEKGNACIE---
SINADTHGLKVNDCSVEN-----

-----MTT
LTTEENKQHKSHWYLYVVIPLVASLLLICIGCIIWRWLLRRKR-----SNG.
>Smp_350320.1 gene=Smp_350320
-----MRYN-
FSPSLWVLIYLIYFVWHYKRFNCNDICKNSDLRHYEIVIIENDTYRYSLHYNYSMRIQRYQPQPVSDDR
FKNKISYIYAGFPRFSFSYGSNVRQIDFYKVVNA-----
DDIVVFESIYLGDIINNIQNYTKLESEILDEEELLGV
KRNFSINAHGSEVTATMTSLIHPNGKMSLYYDNIPTEIEQNKLRSLIYGKIGCEN-----GH-
RDHEIPVPAKWIKSGT
LVEFEVIGKICSQYNTSERCQNATTSNMTCIWCEKGNACIE---
SNDQNTHTGMKVKDCRVENTS-----

-----T
ETTEENKPHKSYWYLYVVIPLATSLFLICIGYIIWRWLLR-----G.
>Smp_349180.1 gene=Smp_349180
-----MAYTLFIPNSRVVITVV---TYTKLCFTKIMQ-----
M-----

MYMMEGLTLETNHNLYNNYVKLNSAVLDEEKLIGV
KRTFSINVNGAEVEATMTSLIHPNGKVSFYYDKIPKKLWKVKLISKLTGIIKCED-----
GLQKFFAIHVPEKWIKSGT
LVEFQAIGEFCLQYDTSETCQNAKTPTTTTFCCEKIEEKKEEIEYEQDS-----

-----GRK.
>Smp_350230.1 gene=Smp_350230
-----MRYN-FLPSLWILVYVIFAWPYKRFNCNDICKNP-----
EIVIIENDTYRYSLHYYSMRIQRYQSEAVPSDR

FKNMIDYKFDRRLQFSFSFYGSHAKEIYFHKNFQ-----
PILHIFGWSYIRNIHNYIKKYTKIETGVLDE-----
-----VPKEIEGSQKSEIFGQFSCKG-----VI-
TEDEIPVPAKWIKSGT
LVEFEAIGEICSQYNTSETCQNATTANMTCIWCEKGNACIE---
SNNQNTHGLKVNDCRVEI-----

-----EFGCIRF-----E.
>Smp_349520.1 gene=Smp_349520

MRIQHNQSQPVPSER
FKNKIGFSYKVYPKFWFSFYGYHVEEVRFYSD-----
LEYIYGTFQIGNINNYIQNYEKYEAVVLNENGLLGV
QRNFSVNVNGSEVTFMTILIHPSGKISFYDNIPTIEIGENQFKTRIVGTIICGG-----IY-
RYHEIRVPAKWIKSGT
LVEFEAIGEICSQYNTIETCPNATIWNNTTCTWCEKGEKCII--MYNNQDTH-----
DCRVEKTSVDNLSSTTTEHGET
TSGITEVQVSENL-----

MKTTEETDK--QSTT
KTTEENKQHKSHWYLYVVIPLVASLFLICIGCIVWRWLLRRKR-----SNK.
>Smp_154590.1 gene=Smp_154590

-----MRYN-
FSPSLWILVYLFFVWQYKRFNCNEICNDPYLRYENVIIENDTYLYSHHYKYSMKIQRHQSQPVPSDR
FNIKINGIHTVYPQFTCSYHGSHVHKIMFYED-NA-----
DDVYEYGRSYIGTNHNYLNNYVKLNSAVLDEEKLIGV
KRTFSINVNGAEVEATMTSLIHPNGKVSFYDNIPTIEIGENQFKTRIVGTIICGG-----
GLQKFFAIHVPEKWIKSGT
LVEFQAIGEFCLQYDTSETCQNAKTPTTTCFCCEKIEEKKEEIEYEQDS-----

-----GRK.
>Smp_349630.1 gene=Smp_349630

-----MRYT-
ILRSLWLSFHLIIIWPYRYFNCHEVCENPDLLSYDNIIFENDSYRYSLHYHYSMRIRLNQSQLAFNDS
YRN-FPPFYFFKPKFSFRFYDTLIDDVYIYYY-GR-----
ILLTSERYYYLGDIENTFAQNIQRSETVVFENELLAV
KRNFVITVNDTDVSAKMTSVIQPNGKITLYFDNIPTIEIGIEWISKINATFGCGM-----YF-
LDHEIPVPAKWIKSGT
LVEYEVIGKNCWNFNTSEACQGATTPNMRCIWCPKVNCIE---
SNDNDTHGLKVNDCHVENHQ-----

-----S
RITE-----AT.
>Smp_349530.1 gene=Smp_349530

-----MRYN-
FLPSLWILVYVIFVWLYKRSNCNDICNNRKLHGHGIVIIENDTYRYSIHFTHLMRIQHNQSQPVPSE
FKNKIDYRYKAYPKFWFSFYGYHVKDIDFYNN-----
HVFVYESNHIGNINNYIRNYKNSESRVLDEKLLGV
QRNFSVNVNGSEVTFMTILIHPSGKISFYDNIPTIEIESQFKTRIVGTINCGG-----NR-
EGHEIRVPAKWIKSGT
LVEFEAIGEICSQYNTSETCPNATIWNNTCTWCEKGEKCII--MYNNQDTH-----
DCRVEKTSVDNLSSTTTEHGET
TSGITEVQVSENL-----

MKTTEETDK--QSTT
KTTEENKQHKSHWYLYVVIPLVASLFLICIGCIIWRWLLRRKR-----SNE.
>Smp_349700.1 gene=Smp_349700
-----MRYN-
FSPSLWILIYLFLLWPYKRFNCNDICKNPDLLNYENVIIENDTYRYSLHYKYSMRIQRDQPQPVPSE
FKNKVDVIYEHSPQLSFSFYGSHVKNIHFRDG-VQ-----
PIVYVLGGPYHGEIHNYIENNEKFDTAFLDEKLLGV
QRNFSINVNGTEVTATMTSLIDPNGKVSFHYDNIPNEIDGSKLQSKILRVILCER-----
DHVIPVPAKWIKSGT
LVEYEAIGEICSQYNTKETCLRATTSTKICIWCEKGNACIE---
SNDQNTHGLKVNDRCRVEKKSDVDNLSSTTMEHSET
TLGISEVQVTENH-----

IKITEETDQNLNMTT
RTTEENKQHKSHWYLYVVIPLVASLFLICIGCIIWRWLLRRKEV-----MNDH.
>Smp_349710.1 gene=Smp_349710
-----MRYN-
FSPSLWILIYLIFFLWPYKRFNCNDICKNPDLLNYENVIIENDTYRYSLHYYYSMRIQRDQPQPVPSE
FNDKIYGRSDHRPQFSFSFYGSHVKEIYFHER-
HEEDYVVKSGDSVDAFNKLRIGYIFNFIKNYTESESWFLDEKELLGV
QSNSSISVNGAEVTATMTRLIHPNGKVSFYDNIPTKIEESQLQSKILGLINCED-----VV-
TNHEIPVPAKWIKSGT
LVEYEAIGEICSQYNTSETCQNATTANMTCIWCQKGGKCIE---
SNNPDTHSLKVNDRCRVEKKSDVDLSTSTPIKDVET
TLRSTKVQ-----

-----NMTT
RTTEENKQHKSHWYLYVVIPLVASLFLICIGCIIWRWLLRRKR-----SNE.
>Smp_349240.1 gene=Smp_349240
-----MRYN-
FSPSLWVLIYLIFFVWHYKRFNCNDYCKNSDSLHYEIVIIENDTYRYSLHYKYSMRIQRNQSQPVPSE
FKNKISYIYYGKPKQFSCSYGIIHVEQIDFYKY-HG-----
ENVFEFGGSYIGTIINYIKNYKSESRLDEKELLGV
KRNISINVDGSDVTATMTSLIHPNGKVSFYDNIPTIEIESRLQSEIYGLIRCEE-----
GLTRSLEISVPAKWIKSGT
LVEFEAIGEICSQYNTSETCQNATTSNMTCIWCEKGRACIE---
SNDQNTHGLKVNDRCRVEKNPDVND-----

-----LNS.
>Smp_102020.1 gene=Smp_102020
-----MRYN-
VSPCLWILIYLLFVWPYKRFNCNEICNDPYLRYEENVIIENDTYLYSHHYKYSMRIQRHQSQPVPSPDR
FNIKINGVHTVYPQFTCSYHGSHVHKIMFYED-NA-----
DDVYEYGRSYIGTNHNYLNYYVKLKSAYLDEENLLGV
QRNFSINVNGAEVEATMTSLIYPNGKVSFYDIPMKLWKVKLISKLTGIIKCED-----
GLQKSFAIHVPEKWIKSGT
LVEFQAIGEFCLQYDASETCQNAKTPTTTTFCCEKIEEKKE----
KMNMT-----

GTAENKQE-----K.
>Smp_349070.1 gene=Smp_349070

MRIQRYQSQAVPSER
FINKINNKY-AHPQFSCSYGSHVQNIHFYED-----
YEFVYGSYQIGSINNYIKNYRKSESRVLDEEELLGV
QRNFSINVNGSEVTATMTNLMHPNGKVSFYDNIPTKIEESKLQSKIDGPRICED-----IH-
RYHEISVPAKWIESGS
LVEFEAIGEICSQYNTTETCQNATTSNMTCFWCQKGKKCIE---
SNDQNTHTGLKVNDCSVEKYSNVNDLNSSTTMEHSET
TSGITEVQVSEN-----

MKTTEETDKQSYMTT
RTTEENKQHKSHWYLYVVIPLVASLFLICIGCIIWRWLLRRKR-----SDE.
>Smp_349720.1 gene=Smp_349720

MRIQRDQPQVPSPER
FKIKIYFRTDIYPQFSFSYGSYSHVKEIHFRDG-DV-----
DNVYEFGGSRIGNIFNFIKNYTKSESWFLDEKELLGV
QRNSSISVNGAEVTATMTRLIHPNGKVSFYDNIPTKIEESQLQSKILGLINCED-----VV-
TNHEIPVPAKWIKSGT
LVEFEAIGEICSQYNTSETCQNATTANMTCIWCQKGKKCIE---
SNNPDTHSLKVNDCRVEKKSVDNLSSTPIKDIET
TLRSTKVQ-----

-----NMTT
RTTEENKQHKSHWYLYVVIPLVASLFLICIGCIIWRWLLRRKR-----SNE.
>Smp_350210.1 gene=Smp_350210
-----MRYN-
FSPSLWILIYLI FLWPYKRFKCNVDCERPPLYQYEIVIIENDTYRYSIHYKYSMRIQHNQSQPVSSDR
FTNKIDYRYSARPQFSLSYGSRVHEIRFYEYH-DE-----GKVYNFRGLYSGSIYNYIKKV-
KSESRVLDEKELLGV
QRNFLMNVNGTEVTTTTMTSLIHPSGKISFYDNIPIREIEESQLKSRIFEQISCRVG-----
GFVRFYSILVPAKWIKSGT
LVEFEAIGEICSQYNTNETCQNATISNLTFCWCEKIEKCII---SNLQHTH-----
DCRIEKTSDVNDLNSSTTTEHGET
TSGITEVQVSEN-----

MKTTEETDKQSYMTT

RTTEENKQHKSHWYLYVVIPIVASLFLICIGCIIWRWLLRRKG-----SDE.

>Smp_165600.1 gene=Smp_165600

-----MTGVIQPNGKISLYFDNIPAEVDESECISKINATLSCSFQ-----GF-

IDHEIPVPAKWIKSGT

LVEYEVIGTLSFHRNLFETCQRATTTKMTCTWCEKGDKCLE---

SNDEDTHELKVND CRVEVGI-----

-----C.

>Smp_349200.1 gene=Smp_349200

-----MRYN-

VSPSLWILIYLFVWPYKRFNCNEICNHPNVRNYENVIIENDTYRYSHHYEYSMRIQRHQSQPVPSDR

FNIKINGIHTVYPQFTCNHSEYIRKIMFYAD-DA-----

DDVYDFRGYYIGTMINYLVNYMDFDTAVLDEKKLLGV

KRTFSINVDGSEVEATMTSLIYPNGKVSFYDKIPKEIEVSKFQSKIVGSIRCEG-----

GLQKFFAIHVPEKWIKSGT

LVEFQAMG.-----

>Smp_350150.1 gene=Smp_350150

-----MRYN-

FSPSLWMLIYLIFVWPYKLFNCNDICNNPDLGHHEIVIIENDTYRYSLHYKYSMTIQRNQSQPVSSER

FKNKIDGVYRSDPEFSSSFYGSQIHEIAFNH-H-----

HMLVFRGFQIGEIINYIENYEKTESRVLDEEELLGV

KRDFLINVNGAEVTATMTSLIDSNGKVSLYYDNIPKEIEESQLKSGILGIISCEN-----VV-

TNHEISVPAKWIKSGT

LVVYEAIGKICSQYNTNETCQNATIPNLTCFWCEKKEKCII---SSNQDTH-----

DCRVEKTSVDNLDSTSTPIKDIET

TLTSTEVQVSENLIETTTDET-----

DKHLKTSVDNLDSTSTPIKDIETTLTSTEVQVSENLIETTTDETDKHFNRTT

RTTGENKKHKSHWYLYVVISLVASLFLICVGCIIWRWLLRRKR-----SNE.

>Smp_179390.1 gene=Smp_179390

-----MTCFWCEKGNACIG---

SNNQDTHGWKVIDCRVKKNLDVNDLSTSTPIKDIET

SLRSTEVQ-----

-----NMTS
RTTEENKQHKSHWYLYVVIPLVASLFLMCIGCIIWRWLLRRKR-----SNE.
>Smp_173350.1 gene=Smp_173350
-----MRYN-
FSPSQLIIIVIFVWSHKRFNCNDICNNRRLRNYENIIENDTYRYSLHYNYSMRIRRNQSQPVPSKR
FKGNVENIYGVYPRFSFSYYGKHVQQIDFHPK-----
DNVYVFEESQIGIIINYMKNYENTESPVVHDKELLGV
KRNFLININDSEVTATMITLLHPNGKVSFYDNIPTDIDGSKLESKIVGTIRCGG-----VN-
VDHGIPVPAKWIKSGT
LVEFESIGEICSQYNTIETCQRSTTLKTTCIWCEKGEKCIE---
SNNPDTHVLKVNDCSVEKKSDVNDLNSSTTTEHSER
TLGITEVQ-----

-----TT
KTTDENKQHKSHWYLYVVIPLVASLFLICIGCIIWRWLLRRKR-----SNE.
>Smp_349080.1 gene=Smp_349080
-----MRHT-
LLRCLSMTFYVVVLWPYTFKSEIDCEDNELQHRQNVIVQNDSYQYSLHYNYSMKITRHQLHPIVSDN
FIK-FSDNQKVYPNFFFKYYDSDVYSFYIDKT-G-----AI---
AFHEGLVFINIPDIYPSDLEILNNEEMVAV
KWSFKSNEDDFTAKITCLIIYANGNISLYFEKIPSQIRKKYLQIGITTQIYCKTVGYNTQGV-
KSPKINVPAKWIKSET
LVEYEVIGTMCQYTTTTCSCQEEKTSDMTCIWCDKANKCIA---
SNDQSTSKSVNDCHVETSQETEDLSTPASIKRTET
T-----

-----SDV.
>Smp_350510.1 gene=Smp_350510
LVTSPKMRHT-
LLRCLSMTFYVIVLWPYKFSKSEIDCEDSKLQHRQNVIVQNDSYQYSLHYNYSMRIRCDQLHPVVSNS
FIK-FSDDQKVNPKFSFKYYDSDVYSFHDIDKT-G-----AI---
AFNVGQIFINIPNFHSSDFEILNDKELVAV
KWSFKSNEDGTDGTAKITCLIHANGKISLYFANIPSKIQGNLQIGIIGQIYCKT-----GV-
KSPRLNVPAKWIKSGT
LMEYEVIGTMCQYTTTTCSCQEEKTSDMTCIWCDKANKCIA---
SNDQDTQMLKVNCHVETNSKVTDLSTSTPIQQSET
TSDVTEVEVEEDLKTNSKVTDLSTSAPIQQSETTSDVTEVEVEEDLKTNSKVTDLSTSTPIQQSETTS
DVTEVEVEEDLK
TNSKVTDLSTSTPIQQSETTSDVTEVEVEEDLKTNSEIEDLSTPASIKRSETTSGVTEVQTEGNVKEV
SEKTAQQSNLTT
KTIEVNHKKSSWYLYIVVIPLVVSFLIFVGCIFIWINRKWKITSLCHKNFVNYSF.
>Smp_349690.1 gene=Smp_349690
-----MRYN-
FSPSLWILIYLFLLWPYKRFNCNDICKNPDLLNYENVIIENDTYRYSLHYKYSMRIQRDQPQPVPSE
FKNKVDVIYDHRPQFSFSFYGYHVQKIYFHER-LQ-----
PIVYVLGGPYHGEIHNYIENNEKFDTAFLDEEELLGV
QRNFSINVNGTEVTATMTSLIHPNGKVSFHYDNIPKEIDGSKLQSKILRVIFCER-----
DHSVIVPAKWIKSGT

LVEYEAIGEICSQYNTKETCLRATTSTKICIWCEKGNACIE---
SNDQNTHGLKVND CRVEKKSDVNDLNSSTTMEHSET
TLGISEVQVTENH-----

IKITEETDQNLNMTT
RTTEENKQHKSHWYLYVVIPLVASLFLICIGCIIWRWLLRRKR-----SNE.

>Smp_349210.1 gene=Smp_349210

-----MRYN-

FSPSLWIRIYLIFVWHYKCFNCNDICKTSDFPSYEIVIIENDTYRYSFHYKYSMRIQRYQPQPVSDDR
FKKMSTYIYYATPQFSFSFYGFHVEQIDIYKY-HG-----

ENVFQFQKTYIGTIDSYIKEFENSESRVLDEKELLGV

KTNFSINVNGLDVTATMTSLIHPNGKVSFYDNIPTIEIESRLQSEISGLIRCKE-----

GHTRSPEISVPAKWIKSGT

LVEFEAMRDRCLQYNTSETCQNATTSIVRCFWCERERACIE---

SNDQNTHYLKVND CRVEENPDANDLNSSTTMKHSES

VVY-----

-----FED-----DCL.

>Smp_349160.1 gene=Smp_349160

-----MRYN-

FSPTLWVLIYLVSWPYKRFNCNDICKNSDLRDYEIVIIENDTYRYSLHYNYSMRIQRHQSQPNLSGS
FKNMVKDIYAGFPRFSFTYYGSNVRQIDFYKVVNA-----

DDIVVFGSIHLGDIVNNIQNYTKLESEILDEEELLGV

KRNFSVNNGSEVTATMTSLIHPNGKMSLYDNIPTIEEQNKLRSLIYGRIACEN-----GH-

RDHEIPVSAKWIKSGT

LVEFEVIGKICSQYNTSERCQNATTSNMTCIWCEKGNACIE---

SNDQNTHGMKVKDCRVEDTS-----

-----T

GN-----N-----GRK.

>Smp_349090.1 gene=Smp_349090

-----MRYN-FSPSLWILVYVIFVWPYKRYNCNDICKNP-----

EIVIIENDTYRYSLHYNYSMRIQRYQSQPAPSES

FKNKINFVYEAPQFSFSYYGSHVQKIYFYES-HR-----

DDVYVFGRSYIGIIYNMKNYKKFESRILNEKELLGV

KRNFSLSVNGAE-----IPTEIKESDLQSKIYGLIRCDN-----VS-

TNHEIPVPAKWIKSGT

LVVFEIEIGEICSQYNTNETCQNAKTSNTTCIWCEKGKKCIE---

SNNQDTHGWKVNDCHVEIEYG-----

-----YRDN-----GRK.

>Smp_165590.1 gene=Smp_165590

-----M-----

SYENIIFENDSYRYSLHYHYSMRIHLNQYQPAFND

YRN-FNFSYFVKPKFSFRFYDSLNEVYIYYH-GR-----

IRLTREGDDYFGDIEHFAQKIRRSETVVFNEKELLAV

[illegible]

FNNKIDFRYEARPQFSISFYGSHVEEIDFHED-DG-----
NTAYEFGRSYIGNTYNYIENYKKSDTAVLEEKELLGA
KWTFSINVNGSEVTATMTTLMHPNGKLSFHYDNIPMEIEESRLQSKIVGIIRCEG-----GL-
KKPEISVPAKWIKSGS
LVEFEVIGEICSQYNTSETCQKATTLTMTCFWCEKGKKCIE---SNDQNTHGLKVND CRVEK-
SDVNDLNSSTTMEHSET
TLGITEVQ-----

-----TT
KTTEGNKQDKSHWYLYVVIPLVASLFLICIGCIIWRWLLRRKR-----SNG.
>Smp_349650.1 gene=Smp_349650

MSLWILIYLFVWNYKRFNCNDYCERPDLYPYEIVIIENDTYRYSIHYNYSMRIQHNQSQVPVPSER
FKEKVVDIYEARPKFSYSFYGSNVHEILFYNH-DG-----
DYVFDGESHIGNIDNYINNYEKSELRVLNEEELLGV
QRNFSINVNGAEFTATMTTLMHPNGKLSFYDNIPKEIDGSKLQSKIFGIILCKD-----DT-
AEHEIRVPVDWIKSGT
LVEFEAIGEICSQYNTSETCQRSITLKTTCIWCEKGEKCII---SNLQDTH-----
DCHVEKTSVNDLSTSTPIKDIET
MLRSTEVQDNDLIETTEET-----

DNHLKTSVNDLSTSTPIKDIETMLRSTEVQDNDLIETTEETDNHLNMTI
RTMEENKQHKSHWYLYVVIPLVASLLLICIGCIIWRWLLRRKR-----SNE.
>Smp_350160.1 gene=Smp_350160
-----MRYN-
FSPSLWILVYVIFVWLYKRFNCNDYCERPDLYNYEIVIIENDTYRYSIHYKYSMRIQRNQSQPVPSEH
FISKIYDKYDILPGFSFYGSYHVRRIQSYHD--A-----
ELVYDVGYSHIGNIYNYVVNNLETYVIRGKELLGV
KRNYSTNVYGTEVTATMTSLIQPNGKVSFYDNIPTEIEEYKVRSKIRGLINCEG-----GR-
KKHEISVPAKWIKSGS
LVVFEAIREICSQYNTNETCQNAEISILTCFWCEKKEKCII---SNLQDTH-----
DCRVEKNSNVNDLNIISTTMEHST
TSGITEVQ-----

-----NRTT
RTTEENKQHKSHWYLYVVIPLVASLFLICIGCIIWRWLLRRKR-----SNE.