ervation:	20				65 7 55 6 9 989		969 67 66 5 859
17802_MUTY_ECOL 83847_MUTY_GEOS	28 34	RDPYKVWVS	EVMLQ	TRVETVIP-	-YFEQFIDRFPTLEALADADEDEVLKAWEGLO	YYARARNLHKAAQQVATLHGGKFPETFEEVAALF YYSRVRNLHAAVKEVKTRYGGKVPDDPDEFSRLK	GVGP <mark>Y</mark> TVGAVLSLAYGVPEPAV <mark>D</mark> GN
0003652391_2 0000031207 6	37 26					YYARARNLLKCARVVCETHAGAFPNTYAGLIALF YYSRGRNLHAAACQIVNDHDGIFPRDPELIGKLF	
0000430975_4 0001007148_4	38 35	PNVYHVWLS	EIMLQ	TKVATVLS-	YYLNFLHKWPTLNDLATATRQNVLQAWAGLO	YYARARNLHACAQIVMEKYGGTFPKTEKELLRLF YYSRARNLSRGAKLIVEEWGGQWRNTATELQSLF	GIGH <mark>Y</mark> TAAAIVAIAHGQPSVVV <mark>D</mark> GN
0001092848_3	48 1	PDPYRVWLS	E IMLQ	TTVGAVKP-	YCERFLERWPTVEALARADLQEVMKAWAGLO	YYSRARNLKKCAEEVAHRHGGVFPDTEAGLKALF YYARARNLHACSQIVMEKYGGTFPKTEKELLKLF	GIGD <mark>Y</mark> TAAAVAAIAFGRRAAVV <mark>D</mark> GN
0001151029_1 0001797282_1	58	PDPYRVWLS	EVMLQ	TTIAAVRP-	YFERFLTRFPDIFALAEAPEEAVMSAWAGLO	<mark>Y</mark> YSRARNLHACARTVAA-AGGRFPDTAEGLRKLF	PGIGA <mark>Y</mark> TAGAIAAIAFDRQEAAV <mark>D</mark> GN
0001803648_25 0002078955_4	40 40	AEPYRVWMS	EVMLQ	TTVAAVAK-	YFHAFTKRWPTVDALAAAKDQDVMGQWAGLO	YYARARNLLKCARVVVADYGGNFPDTRDELLKLF YYARARNLLKCARMVVSDYNSEFPETRDELLKLF	PGIGP <mark>Y</mark> TAAAIASIAFGRPECVM <mark>D</mark> GN
0002106160_4 0003607531 2	28 38					YYNRCHNFHKAVKIIVNKYNSSLPINIKDFMVLF YYSRARNLHKCAKLICNNFDGRFPNTEEQLEQLF	
0003872363_4 0004820107_1	36 43	PDPYHIWLS	EVMLQ	TTVAAVVK-	YFNTFTKRWPNIQALATAQDADVMAEWAGLO	YYARARNLIKCARMIVNDHGGVFPNDRAALLALF YYARARNLHKCAQIVSKELNGIFPEEQKDLEKLF	GIGP <mark>Y</mark> TAAAISAIAFGRSACVV <mark>D</mark> GN
0005774797_1	29	PNPYHVLLS	EFMLQ	TTVATVKT-	YFEQFTKKWPSVEHFSHATDDEIMAQWAGLO	<mark>Y</mark> YARARNLVKTIHTIHNQGHFPASAYELQKLF	^P GIGP <mark>Y</mark> TSAAIAAIAFNEPILPR <mark>D</mark> GN
0005867021_3 0004546210_2	40 31	PSKYKTWIS	EIMLQ	TQVNTVEP-	YFHRFMERFPTVEELASSSPDEVLQIWSGLO	YYARARNLLKCARMIVADFGGVFPDTRDDLLKLF YYARARNIHRSAQLIIKQHKGELPSDYESLLHLF	PGIGE <mark>S</mark> TAGAILSLSGIEPKPIL <mark>D</mark> GN
0004551008_5 0002511148_4	31 26	PSKYKTWIS KTPYRVWVS	EIMLQ	TQVATVEP- TQVSTAIP-	-YFIQFIQRFPEVTELASSSLDEVLQLWSGLG -YFEKFIKEIPDVKSLSEASLDLVLSLWSGLG	YYARARNIHRSARIIVNQHHSELPSDYESLLTLF YYARARNLHKSAKIINLEHGGKIPSTRDELMALF	PGIGK S TAGAILSLSGIEPKPIL D AN PGIGR <mark>S</mark> TAGAILALGFNKKAPIL <mark>D</mark> GN
0000577378_2 0000598175_2	14 37					YYARARNLHKSAKIINLDHGGKIPSTGGELMALF YYARARNMHKAAKMICGDFKGQFPDNLEAMQSLS	
0000754627_3 0000811118_1	34 25	KTPYKVWVS	EVMLQ	TQVVTVIP-	YFEKFMQSFPDIIALANADEDQVLHHWTGLG	YARARNIHKAAKIVRDKYQGQFPSTLEEVMDLF YYTRARNIHKTAKILKKDFDCKLPNEIEALMSLF	GIGR <mark>S</mark> TAGAVLSLSLGQHHPIL <mark>D</mark> GN
0000899687_2	29 50	NDPYSIWVS	E IMLQ	TQVKTVIP-	-YYERWIKTLPTIDKLANAPEQKILKLWEGLG	YYSRAKNLKKSAKIICKEMNGKLPNTVKNLQNLF	PGIGR <mark>Y</mark> TAGAISSIAFGLKAPVL <mark>D</mark> GN
0001176522_24 0001345122_1	4	ISPYRVWVS	EIMLQ	TQVKTVIP-	YYQRFMKSFPSIEQLASATQDEVLAHWAGLO	YYARGRNLHKAARQIVAQGGFPETLAGWQALF YYARGRNLHKSAQIIQTEYYGKFPQIFDDIIALF	PGIGK <mark>S</mark> TAGAIMSIALKQRMPIL <mark>D</mark> GN
0001515736_6 0001682161_6	18 25	PTPYRTWVS	E IMLQ	TQVKTVIP-	YYLRFMESFPTIQSLAKASQEQVLAHWAGLO	YYSRARNLHKCAQTVMQQWGGAFPQTAEELATLP YYARGRNLHKTAQTIVEQHKGQFPNRFEEVVALT	GIGR <mark>S</mark> TAGAILSIAMQQRMPIL <mark>D</mark> GN
0001923643_29 0002030994 5	28 26	RDPYRVWLS INPYRVWVS	EIMLQ	TQVSTVLG- TQVKTVIP-	-YYQRFLDAFPDVASLAAAPQDAVLALWSGLG -YYEKFMTSFPDVQTLASADQDTVLKHWSGLG	YYSRARNLHRCAQAVVQEWGGAFPRRAEDLATLF YYARARNMHKAAQMVCDDFAGVFPDNLESMQSLS	PGIGR <mark>S</mark> TAGAIASFCFSERVPIL <mark>DAN</mark> SGIGRSTAAAILSIASNQQEAILDGN
0002038721_4 0002523527_15	28 43	KSPYHIWIS	E IMLQ	TQVKTVIP-	-YFHKFINSFPSIKSLAKSDLDKVLANWSGLO	YYTRAKNIHQASKIIHQKYHGSIPKNYEQLIELF YYSRARNLHRCAKTVVDEHAGVFPTDPEVLVTLF	PGIGE <mark>S</mark> TAGALLTLAFDKPGIIL <mark>D</mark> GN
0002523527_15 0002608528_2 0002961510_2	26 29	INPYRVWVS	E IMLQ	TQVKTVIP-	YYQKFMTTFPDVQTLANADQDLVLKHWSGLO	YARARNMHKAAKMVCDDFSGILPDNLEDMQSLS	GIGR <mark>S</mark> TAAAILSIASNQSQAIL <mark>D</mark> GN
0002979152_8	34	RTSYRVWVS	EIMLQ	TQVVTVIP-	YYERFMQSFPAVEGLAKATQNEVLDHWTGLO	YYSRAKNLKKSAQIICKEMNGELPKTVNDLKNLF YYSRARNLHKAAQFVVEQCNGVLPESLDGLIELF	PGIGR <mark>S</mark> TAAAILSLAGNKSEAIL <mark>D</mark> GN
0003248034_1 0003294679_3	46 31	KTPYSIWVS	E IMLQ	TQVKTVIP-	YFKKFIVSFPTLRVLAQASLDDVLHHWSGLO	YYRRAKYLRASAQQIINKWNGQLPKEYDKLRALF YYARAHNLHKTACLVNEKFSAQLPLDMKELCLLF	PGIGR <mark>S</mark> TAGAILALSCNQKHPIL <mark>D</mark> GN
0003333364 1	28 28	REPYYVWVS	EIMSQ	TQIDRVADQ	PFPRFIETFPTVEALAAADWETVYPCWDGLG	YYARARNLRKGAQHMVEEHGGTFPADVEAARALF YYNRGKNLLKAAKVLVDKHEGELPQTVAGLEALF	PGVGK <mark>Y</mark> TAHAVLAFAFDKKVPAI <mark>D</mark> TN
0003492925_4 0003766664 5	25 41	DDPYHIYLS	EVMLQ	TQVKTVLER	RYYFPFLKKFPTLKALGDANLDDVLKMWEGLG	YYSRAKNLHKTAGLIEVLPSDIDELIRLF YYSRARNLHKASQFVVESWDGIFPSDAKMLEEMF	PGIGK <mark>N</mark> TAHAVATFVYKKPVPIM <mark>E</mark> AN
0003948186_72	28	ITPYRVWLS	E IMLQ	TQVATVIS-	-YFERFVQTFPDVGALARAPLDEVLHLWTGLG	YYARARNLHKAAGLIVDTHGSELPDSVQQLCELF	PGIGR <mark>S</mark> TAGAICAIALRKHAVIM <mark>D</mark> GN
0005057120_4 0005590109_5	28	ISPYRVWLS	EVMLQ	TQVTTVIP-	YFNHFIQKFPDVHQLANAPLDSVLHLWSGLO	YYARARNLHKTAKILSKN-KGIFPDDLDSLMELF YYARARNLHKTAKIISET-DGEFPNDLNLLMQLF	PGIGR <mark>S</mark> TAGAISSIAFNKSQPIL <mark>D</mark> GN
0006063368_2 0000467631_2	26 7	STPYQTWLS	E IMLQ	TQVTTVIP-	YFNRFIQTFPNIATLADAPLDAVLQHWAGLG	YSRARNLYKAALEITCKHKSKLPNSYNELVALF YYARARNLHKTA-IIINKNGGVFPDDVDGLLELF	PGIGR <mark>S</mark> TAGAILSIAFNKSHPIL <mark>D</mark> G <mark>N</mark>
0000788235 <u>1</u> 0001187176 11	27 28	ITPYRVWIS MTPYRVWVS	EIMLQ	TQVATVIP-	-YYQRFITSFPDVTTLANADEDLVLQHWAGLG -YYERFMAALPDVHALAAAPADEVLHLWTGLG	YSRARNLHKAAQQVRDEFSATVPADLDSLQSLV YYSRARNLHRAAKRVVEECAGQFPGDVQGLTDLF	GIGR <mark>S</mark> TAGAILSLAYEQRHAIL <mark>D</mark> GN GIGPSTAGAIASLSMGVRAPILDGN
0001660697_64 0003378864_2	28 39	GDAYRTWLS	E IMLQ	TQVSAVLG-	YYARFIERFPTVQALAAAPADDVMAAWAGLO	YYTRARNLHRCAQIVVAEHGGIFPRDPEVLASLF YYARCRNLHRAAQKIVSDHNGRFPATFEDVLALF	^P GIGR <mark>S</mark> TAAAIAAFSYGVRAAIL <mark>D</mark> GN
0003910742_3	28	PTPYRVWIS	E IMLQ	TQVVTVIP-	-YYQNFMDSFPDVRTLAHAEEDLVLQHWAGLG	<mark>Y</mark> YSRARNLHKSAKLICDEFSGVIPDDIDQIQSLF	GIGR <mark>S</mark> TAGAILSLAYQQQQAIL <mark>D</mark> G <mark>N</mark>
0004116181_2 0006223903_1	1 29	RNPYRIWIS	EIMLQ	TQVTTVIP-	YYERFMARFPHIVTLASAKLDTVLAEWTGLO	YYARARNLHKTAKIIAQQGCFPNTLETLMQLF YYARARHLHQAAGVIVARHGGVFPDQFHDVVALF	PGIGR <mark>S</mark> TAGAILAFSHGQRHAIL <mark>D</mark> G <mark>N</mark>
0001029068_2 0001128125_11	2 36					YYARARNLHKTAQIINRQYSGVFPSTVEQVLALF YYARGRNLHKAARQIVEQHDGIFPSQFDDILALF	
0001595844 <u>4</u> 0001719155 2	27 31					YYSRARNLHFTAQQVANEFGGKFPDNYADLLALK YYSRARNLRKAAQKIQQEYSGKVPESMNEIMKLF	
0002363038_6 0002561400_1	36 1	INPYRVWVS	EIMLQ	TQVVTVIP-	YFERFMQRFPEVSDLAAASQDEVLSHWAGLO	YYARGRNLHKAAQLIVEQHNGVFPKSFDEVLNLF YYARGRNLHKAAQLIVEKHGGQFPSDFEEVLALF	PGIGR <mark>S</mark> TAGAILSISLQQRFPIL <mark>D</mark> GN
0002566035_2	28 26	VSPYKVWVS	E IMLQ	TQVITVIP-	YFKRFMKRFPDVQTLANSSLDEVLHYWTGLO	YYARARNLYKTAKIITKEYQGNFPLSLNEIMSLF YYARARNLHKAAKLICSNHEGKIPSSINELVELF	PGIGR <mark>S</mark> TAGAVLSLSYDKCFPIL <mark>D</mark> GN
0002598045_3 0004188575_41	28	PTPYQVWVS	EIMLQ	TQVATVIP-	YYQRFMIRFPDNATLAAASQDDVLSYWTGLO	<mark>Y</mark> YARARNLHRCAQYVAEIHQGQLPAELDALIALF	PGIGR <mark>S</mark> TAGAIMALAYHQRFSIL <mark>D</mark> GN
0000240049_1 0002139456_2	26 26	KSLYRVWVS	EVMLQ	TQVATVIP-	YFARFMQQFSDIEALSNATQDEVLLYWAGLO	YYSRARNLHKAAQIIQQQHGGCFPRQYNDVLALF YYSRARNLHKAAQIIQQQHGGCFPQQYDDVLALF	PGIGP <mark>S</mark> TAGAILAQALGQRHAIL <mark>D</mark> GN
0003535614_2 0002657784_4	28 25	KTPYKVWIS	EIMLQ	TQVVTVIP-	FYSAFINRFPNIQELATSSEEEVMSFWSGLG	YYSRARNLHKAAQIITASHQGKFPENYHDVLTLF YYSRARNIYKTAQILQKKFESKLPSSLSQLISLF	GIGP <mark>S</mark> TAGAILSLGYKKRAPIL <mark>D</mark> AN
0003800129 <u>1</u> 5 0003716781 1	30 17	TTPYRVWIS	EMMLQ	TQVNTAKD-	YFLNFIEQYPDLESIKNASEEEILILWKGLO	YYRRAKFIYQAKEKIFKDYNGLFPDEFEDIISLF YYSRARRLHAAAREIQDRHDGEFPQTRDEAEDLF	GIGK <mark>S</mark> TAGAILSIAYGKPFPIL <mark>D</mark> AN
0001556689_3 0001834452_1	18		EIMLQ	TRVETVIN-	-RYGSFLERFPTIADLAIASLDDVLAEWSGLO	YYRRPRLLHRLATVVVDTHGGEIPDTLEELLELF YYKRSRLLLKAARVIQSEMDGVLPCDSATLRRLF	PGIGP <mark>Y</mark> TSAAVGSIAFGIPALSI <mark>D</mark> G <mark>N</mark>
0004255004_2	35	RDPYAIWVS	ETMLQ	TRVATVLP-	YYYRFMKAFPSVEALDQAPLDAVRNVWSGLO	<mark>Y</mark> YQRAANLKKAASVLMNRHNGKLPADYQTLLGLF	^P GVGQ <mark>Y</mark> TAGAVLSIAFDRRYPAP <mark>D</mark> GN
0000605438_3 0000581237_15	31 31	QSAYEIYLS	EIMLQ	TQVKTVLER	RFYFQFLDKFPTLKDVANAPVDDVLKAWEGLG	YYTRARNLHKTAIVTKGILPKSAEALEQLS YYTRARNLHKTAVDTKGILPNNAEKLEELS	GIGK <mark>S</mark> TAHAVACFAFDEPLPIL <mark>D</mark> AN
0002529579_2 0006097838_1	31 1	RDPYAIWIS	EVMLQ	TQVKTVIP-	YWRRWMEQLPDIASLAAADEDTVIKLWEGLG	YYTRARNLHKTAIATKGVLPKRAEALEKLS YYSRARNLQKAARLLCEELSGKFPRDLCGVLALF	PGVGR <mark>Y</mark> TAGAICSIAYNQPEPLV <mark>D</mark> G <mark>N</mark>
0000583727_6 0005807640_2	27 29	RDPYAIWVS	EIMLQ	TQVKTVIP-	YWQRWMKQLPDIASLAAADEDTVIKLWEGLO	YYSRGRNLQKAAKRIYDELAGRFPRDLAGMLALF YYSRARNLQKAAKRIRDALSDRFPRDLAGALALF	PGVGR <mark>Y</mark> TAGAICSIAYNQPEPLV <mark>D</mark> GN
0000134878_1 0005136725_3	12 27	NDPYKIWIS	E IMLQ	TQVSTVQD-	YYLRWIKRFPTIQSVADASIDEVLKHWEGLO	YYARARNFYHSCKALSTTT-SCVPKGMDEFQKLK YYSRVRNFHKSCQMLIRNK-QDIPKGLDEFQKLK	GVGP <mark>Y</mark> IGAAVQSIAFNIPAGVV <mark>D</mark> GN
0001684786_4	24	PEPYRVWVS	EIMLQ	TRVETVIP-	YFERFLDRFPTPAALAEASEDEVLTLWSGLG	YYRRARSLLEGAKAVVRDHEGVFPRSYEAALDIF	PGVGP <mark>Y</mark> TAAAILSIAYGEPWPVL <mark>D</mark> GN
0002971826_23 0002040695_2	34 37	ANPYFVFIS	EVMLQ	TTVATVVP-	YFKKWIKKWPTLHALAEASLDDVLHTWQGLG	YYRRARSLLAGAKTVIEHHAGVFPRDYEAALEIF YYRRARNVHRCAQEVVQSYGGLFPQNVSQLRKLF	PGIGP <mark>Y</mark> TAGALSAIAFEQNSVAV <mark>D</mark> GN
0003263657_32 0005989041_2	41 38	KDPYKIWLS	EIMLQ	TTVKAVGP-	YFQLFLKTWPTIDKLAKATLDDVLRVWQGLG	YYARARYLHRAAVQVVDQYGGRIPESLSEISILF YYSRARNMHKCAKLICNNFGGRFPNTEEQLERLF	GIGP <mark>Y</mark> TAAAISAIAFDKPANVV <mark>D</mark> GN
0002391082_2 0003839553_2	36 43	DNPYHIWIS	E IMLQ	TRVDQMGA-	YFERFVGAFPTVEKLAAASEDQVLKVWEGLG	YYARARNMHKAAVQIAGQLGGCIPDTYAGLIELF YYARACNMHKAAKRIAFELEGQIPNTYDGLIDLF	PGIGE <mark>Y</mark> TAAAVSSIAFDRDHPVL <mark>D</mark> GN
0003996707_2 0002044706_1	34 16	GNPYHVWIS	EIMLQ	TRVDQMQP-	FFERFTAAFPTVGALAAASQEEVLKAWEGLG	YYARARNLHRAAQRVV-EAGGNIPDRYEELVGLF FYRRARNLHACARQVVDRYDGEVPRDPEELGSLF	PGIGP <mark>Y</mark> TAAAVSSIAFDRDHPVL <mark>D</mark> G <mark>N</mark>
0006007075_1	31	KREYYTLVS	EFMLQ	TQVSTVIP-	YFKNFIKDIPDLNSLAKINEKKLLKYWEGLO	<mark>Y</mark> YSRVRNLKKTAKIVVSKYKKKLPTTLEELKTLF	PGIGD <mark>Y</mark> TASAILSIAFNKPFIPL <mark>D</mark> GN
0002094036_4 0002762689_1	7 31	KKQYYTLVS	E FMLQ	TQVATVIP-	-FFNRFIKNIPDLEALANFDNHKLIKLWEGLG	YYSRAKNLKKTAKIIVDNYQGKLPSDFEELKKLF YYSRVRNLKKTAQIVVKNFDKKLPRKYLDLKSLF	PGIGD <mark>Y</mark> TASAISAIAFNKRIIPL <mark>D</mark> GN
0005516980 <u>2</u> 0003920004 <u>1</u>	31 37	PNPYYVLVS	EFMLQ	TTVNTVIS-	RFKDFIKKWPNLKKLSMINENQILQFWSGLG	YSRARNLKKTSQVIIKNFKGKVPENFEDLKSLF YYARAKNLLNSAKIISLKFNNIVPDNYNDLIDLF	GVGD <mark>Y</mark> TAKAVLGIGYNKSVMPV <mark>D</mark> AN
0004008511_2 0004481347_1	31 38	PDPYFVFVS	EYMLQ	TTVGTVKT-	-RFEEFILKWPSINDLARISEKTILNFWSGLG	YYSRARNLLKAAKIIKKEFNSKIPNNYDDLINLF YYNRATNLLKTIKIISRDFKFKVPQHYDQLIELF	PGIGD <mark>Y</mark> TTKAILGIAYNKSVMPL <mark>D</mark> VN
0003787733_3	30 30	NDLYKIWLS	EVMLQ	TRVNTVVP-	YYLLWVKKYKSIKSVAKADYQNLLKLWEGLO	YYSRCKNFYKSCLIIINDYDGKIPLDYLTFRSLF YYSRCKNFHKACKIIVNDYDGEVPSDYQKFLLLF	PGVGD <mark>Y</mark> IASAVLSIGLNQPHAAI <mark>D</mark> SN
0000754657_2 0000990943_3	30	NDLYKIWIS	EVMLQ	TRVNTVVP-	YYLRWVEKYKSIKSVAKADDLKLLKLWEGLO	YYSRCRNFHKACKIIVNDYGGEFPSDYQKFRLLF	GVGD <mark>Y</mark> TASAVFSIGLKQTYAAI <mark>D</mark> GN
0004474996_2 0001463500_11	29 17	NNLYHVYLS	EVMLQ	TKVKTAIP-	YYKRWLKKYPTIESVALSNLDDLLKLWEGLG	YYSRCRNFHKACKIVVNDFTGEIPSDYQNFRSLF YYSRCVNFYKACIILYSQYNSQLPNNMTDFLKLF	PGVGN <mark>Y</mark> ISAAVYSIVDKIPAPAV <mark>D</mark> VN
0001286181 <u></u> 5 0001293628_3	24 30	REPYRVWVS	EIMLQ	TRVETAIP-	YYNRWMERFPTVDALAEGHEQAVLKAWEGLG	FYRRAKNLHQTAKIITDKYHQVFPNNYEDLVALF YYSRARNLRRSALIVRERLGGVLPQDSRSLKTLF	PGIGE <mark>Y</mark> SAGAIASIAYGEVVPAV <mark>D</mark> GN
0001535696_8 0001614067_2	24 37	RDPYKIWLS	E IMLQ	TRVAQGAP-	YYLKFIKHFATVYDLAKASEEQVLKLWQGLO	YYSRARHLHATAKTIVNEYGGNFPNTYKELLKLK YYSRAKNLHETAKIISNKYDGFLPTDKNSLMALF	GIGD <mark>Y</mark> TASAIASICFDRPEPVV <mark>D</mark> GN
0001765289_1	3	DDPYKIWLS	E IMLQ	TQVKTVVP-	YYNRWIKRYPSIKSVALADLGAVLKMWEGLO	YYTRCRNFHTAAKIVVKKFNGIIPNNWENFSSLF	PGVGD <mark>Y</mark> TAAAVLSIAFNKPYAVM <mark>D</mark> G <mark>N</mark>
0001961666_1 0002018097_4	18 25	NEPYNIWLS	EVMLQ	TQVKTVVP-	YYTKWIKKFPTLKSVAESDLNSLLKLWEGLO	YYSRARNLHSSAKIIVNKYEGIIPSEENKLINLF YYSRCRNFHKATQIVVEKYKSVVPNDYKLFRQLF	PGVGD <mark>Y</mark> IASAVLSIAYNKKYPAV <mark>D</mark> AN
0002843512_36 0002930199_1	26 22	NNPYKIWIS	EIILQ	TQIQTGIR-	-YYHKFIRHFPDINSLALAEEVDVLNVWQGLG	YNRAKNLHKTATLIEELPSNIDELIKLF YNRVLNMLYSAKIIVKQHKSTFPTKYDELIKLK	GIGP <mark>Y</mark> TAAAISSICKNEKRAVL <mark>D</mark> GN
0003033795 <u>2</u> 0003888107 <u>2</u>	22 23	RTPYRVWVS	EIMLQ	TQVNTVIP-	YYKKWIKKYPTLKSFKESNFDDVIKIWEGLO	YYSRCHNMFNAAKLINSTFPNNYDDLINLF YYSRCKNIYKTSHLVQKNFPDSYSELIKLF	GIGD <mark>Y</mark> TAKTILAIAFKKNFVGI <mark>D</mark> TN
- · · · ·			21				

c_000004013286_6	44	RDPYAIWVSEIMLQQTQVNTVVP-FFERFIESFPTVEKLAAATEAAVLKRWEGLGYYRRARNLHRAAREVTDQYDGQLPRDPATLSRLPGIGQYTAGAILSIAFDCREPIVEA 156	
c_000004852258_1	6	SDPYKIWLS <mark>Z</mark> YMLQ <mark>O</mark> TQVETVIP-YYQKWINHYPTIKSVALENIDNLLKIWEGLG <mark>Y</mark> YSRCRNFHEAIKDIFYNHNGVIPKQIEDFKSLKGVGI <mark>Y</mark> ISGAVMSIAFNQTHIAV <mark>DGN</mark> 118	
c_000005254087_1 c_000005603677_1	32 29	RDPYAVWVAEVMLQTQIATVIP-YYERWLARFPTVQALAEASLDEVLKLWEGLGTYGRARNLHAAVQMVMNEYDGRIPTTAADLLKLKGIGRTANAIASIAYNEAVPVLDGS 144 QDPYKIWLAEIIMQTRLEQGLP-YYERFIAAYPSIKELAETEEQKLMKLWQGLGTYARARNLQATAKRIVAEYAGIFPDNYKAILDLKGVGETAAAIASFAYDLPYAVVDGS 141	
c 000003283462 3	17	TGFYRIWLS IMCOOTOVKRVSI-FYTKWIKRFFTLESVANAKEEHLLKVWEGLGYYNRCRNFYKATKIIIDDYNGKIPNDYQTFRLLPGVGD TASAVLSIAFGMPYPAIDGN 129	
c_000002687221_1	31	SNPYFIWLS <mark>E</mark> VMLQ <mark>Q</mark> TRVSTASP-YYQHWISALPDIHSVAEAPIDNILKLWEGLG <mark>Y</mark> YGRARNFHKACRIIIEKHGGVIPSDPLEFSKLPGVGP <mark>Y</mark> ICAAVMSIAFNLPIPAA <mark>D</mark> GN 143	
c_000003347358_19 c_000002701031_2	57 24	DEAYYIYLSEVMLQQTQVKTVLERYYIPFIERFPTLKHLGEAPLDDVLKMWEGLGYYNRAKNLHKTATLVDQLPSNIDELIKLPGIGKNTAHAVATFAFHQPVPIMEAN SSSYKIWLSEIILQQTRVEQGLP-YFKEFITKFPKIELLAKASEDEVLKLWQGLGYSRARNMRLTAKAIVEKFNGVFPKDYEKILKLKGIGPYTAAAICSFAYNLPYAVVDGN 136	
c_000002701031_2 c_000000582753_3	32	SSYKWIGS ILLQ TKVSQGLP-YRSFIESYPRLEDLAHSSEEKVLKLWQGLGYSRARNLHFTAQVIFNELSNEFPNNYKDLLKLKGVGD TASAIASFAFDEVVPVLLGS 144	
c_000001713769_5	24	NDPYSVWLS <mark>E</mark> IILQ <mark>Q</mark> TRIAQGLP-YYLKFINKYPTINSLAKANENDILILWQGLG <mark>Y</mark> YSRARNLLKTAKFIVDERNGKFPTTYIELIKLKGIGE <mark>Y</mark> TAGAISSICFNERRAVL <mark>DGN</mark> 136	
c_000004369364_1	27	SDPYAIWLS IILQ <mark>O</mark> TRVAQGLP-YYLKFLEAFPTVQDLAQAPEQDIMLLWQGLG <mark>Y</mark> YSRARNLHFTAKQVSDELNGLFPNSYTGLLSLKGVGP <mark>Y</mark> TAAAIASFAYKLPHAVV <mark>IG</mark> N 139	
c_000006057486_30 c_000005494072_10	28 24	KDPYLIWLS IILQTKIAQGTP-YYLKFVEKFGNVSLLAKADEKQVLKLWQGLGTYSRARNLHKTAIYINNNLKGVFPNNYTDLKKLKGIGDTASAIASFCFNLPEATVDGS 140 KDPYKIWLS IILQTKIEQGLP-YYMSFVENYPNIETLAIADEQEVLKLWQGLGTYSRARNLHFTAKSIVKNHNGKFPDNYNELLKLKGVGDTASAISSICFDEKCAVVDGS 136	
c_000001742634_3	27	kkpyfiwls tiil <mark>o</mark> trttoglp-yyiafikhfptifdlaktsetkvlklwoglg <mark>y</mark> ysrarnlhftakyivdnyngkfpenykeliklkgvgd <mark>t</mark> asaiasicynektavv <mark>o</mark> g 139	
c_000002826998_2	27	knpyliwls <mark>e</mark> lilq <mark>o</mark> trveqglp-yflkfkekyptvtdlanaeedeimklweglg <mark>y</mark> ysrarnlhfsakyitaeldgifpkkhteilklkgvgt <mark>y</mark> taaaissfaydlphavl <mark>o</mark> gn 139	
c_000003159439_6 c 000004887214 1	24 29	SNPYHIWIS IIIQ TRVDQGLD-YYKRFIATFPTINNLAKAKEEAVLKLWQGLG YSRARNLHFSAQYIVNELDGKFPSSYKELLKLKGVGD TASAIASICYNEVTAVVDGS 136 REPYKIWLS IIIQ TRVAQGLP-YYQRFIESFPILQNLAAASEQNVLKLWQGLG YSRARNMHFTAQYVVNELGGEFPCSYKELMKLKGVGD TASAVASFCYDEVQPVLDGS 141	
c 000005037037 2	27	KNPYYIMISTILQQTRVEQCTK-YFLAFKKNYLTIFDLAQAKETEVIKLWEGLGYYSRARNLHFTAKYIANDLEGVPPRNYTDLIKLKGYGS TASAIASFAYDIFKAVVDGN 139	
c_000001059964_1	19	YEPYQVWIS <mark>E</mark> IMLQ <mark>O</mark> TQVQTMLP-YYHRWMERLPRLQDVAEASEDLLIKLWEGLG <mark>Y</mark> YRRVHNIKKTAVIICRDYGGTFPGSYRQQIQLPGIGP <mark>Y</mark> TAGAIASIAFNFSEPVL <mark>DGN</mark> 131	
c_000002498472_1 c_000004615912_3	28 17	YSPYQVWISEIMLQQTQMDRVTL-FFTRWMDTFPDVNTLASASETRVLKLWEGLGYYSRARNILKTAQLLVTEYQGQIPDDPKQLLSFPGIGPYTAGAIASISFNHDVPVVDAM 140 KNPYLIWLSEVILQQTRTAQGLP-YYEKFKNRFPTIDLMANAHEDEIMKLWEGLGYYSRARNMHFTAKYITEELGGEFPDTLEGLKKLKGVGPYTAAAIASFAYDLPHAVLDGM 129	
c 000004766858 2	30	MPI LIMLO VILLE TILLE TO THE TILLE T	
c_000002747260_18	36	PDAYAVWLS <mark>E</mark> VMLQ <mark>O</mark> TTVAAVRD-YFRRFTTRWPTVADLAAAEDADVMGEWAGLG <mark>Y</mark> YARARNLLKCARVVVAEHGGHFPDTRDGLLKLPGIGF <mark>Y</mark> TAAAIAAIAFDEPAVVV <mark>O</mark> GN 148	
c_000005371561_38	36	PDPYRVWLS-IMLQ <mark>Y</mark> TTVAAVRD-YFHRFTARWPTVADLAAAEDGDVMGEWAGLG <mark>Y</mark> YARARNLLKCARVVVSEHGGRFPDDPDALLALPGVGPYTAAAIAAIAFIKPETVM <mark>G</mark> S 148	
c_000000169465_2 c 000003254110 11	32 32	VTPYKVWVSEIMLQQTQVTTVIP-YFKRFMASFPTVHDLAKASQDDVLHHWTGLGYYARARNLHKAANTLVEKYNGEFPYSLEEVMDLPGIGRSTAGAILSLSRNMRFPILDGS 144 VTPYKVWVSEIMLQQTQVTTVIP-YFERFMASFPTVHDLAKASQDDVLHHWTGLGYYARARNLHKAANRLVDEYNGEFPFSLEEVMDLPGIGRSTAGAILSLSRNMRFAILDGS 144	
c_000004750284_20	32	VTPYKVWVS <mark>E</mark> IMLOOTQVATVIP-YFNRFMASYPSVFELANASQDDVLHHWTGLG <mark>Y</mark> YARARNLHKAAKTLVEDYEGVFPPTLDEVVSLPGIGR <mark>S</mark> TAGAILSLSRDERYPIL <mark>D</mark> GN 144	
c_000000141782_15	37	atpyrvwis <mark>e</mark> vmlo <mark>o</mark> tqvatvip-yferflqrfpdvatlaaadadsvlhlwsglg <mark>w</mark> yararnlhraarvvveahggefprrfeevqalpgigr <mark>s</mark> tagailslgcgqrhail <mark>b</mark> gn 149	
c_000002717847_8 c_000004054799_1	31 18	ITPYKVWISEMALQQTQVVTAQS-YYSKFLKKYPSLTSMKMATEDDILSLWSGLGYYRRASFIYQAKEKIFLDFNGRFPATYDELITLPGIGRSTAGAILSIAYQKPFPILDAN 143 ISPYRVWISEMALQQTQVKTVIP-YFYKFIKKYPNLGALLQASEDEILAQWSGLGFYRRAKNIYKACRIISEDFNSKLPTNINDLESLPGIGRSTAGAIMSIAFNEGHPILDAN 130	
c_000006126673_1	43	PNPYFVWLS TIMLQQTTVSAVIP-YFLKFTQRWPDVWALANADVDDIMSAWAGIGYYARARNMHKCAKTIVSDYDGIFPQEQAVLKTLAGIGD TSAAITAIVFDKYATVVDGN 155	
c_000000339186_3	1	-DPYSIWVS <mark>E</mark> IMLQ <mark>O</mark> TQVSTVIA-YWERWMRALPTIDKLARAKPTQVLKLWEGLG <mark>Y</mark> YSRARNLQVAAKEIVKNHDGQFPRDRPAIRALPGIGR <mark>Y</mark> TAGAISSIAFGLPEPIV <mark>DG</mark> N 112	
c 000001863436 1	32 48	RDPYAIWISEIMLQTTVESVIP-IYERFMELFFTVDVLAVANPTDVLQAWAGLGYYKRARHLHEAAIEIVNRFGSRIPDHLSDLQSLPGIGRTAGAIASIAFDQCVPVVDTT 144 GDPYAIWVSEVMLQTQVVTVID-YYTRWLARFPDVETLAAAEIDEVLELWAGLGYYRRARLHRAAQHVVEECGGALPQTAGELEDLPGIGPTAGAIASIAFGEAAPLVDG 160	
c 000002830137 4	41	RDLYHIWUS TMLQQTQVATVVP-YFQRFVERFFNITSLAAADEEDVLRIWEGIGYYRRARNLHRAAQQVVQQHHAQFPADFDTLLSLPGIGR TAGAILSIALDQRLPILEAN 153	
c_000004612302_3	35	RDPYAVWIREIMLQQTTVKAVVP-YLERFLDQFPTIEVLAASETDEVLRVWEGLGYYSRARNLHRAARMIVEEWGGQWRETAVELQALPGVGPYTAGAIASFAFDQPAAIVEAN 147	
c_000001933926_1	21 33	TDPYRVWLS_IMLQCTTVATVTP-YFLRFVERWPTVHDLAAADLDRVLHAWQGLGYYARARNMHACAKRISGDMAGVFPDQENELRRLPGIGPYTAAAIAAIAAIAFDRPATPVDGM 133 MDPYRVWLS_IMLOCTTTITVRG-YFEDFVSRWPSIEDLAAAELDAVLHAWQGLGYYARARNLHKCAKLITKEYGGKFPEREEALVKLPGIGPYTAAAIAAIAAIAFGHIATPVDGM 145	
c_000003136334_1 c_000005849454_9	33	MDPYRVWLSEIMLQQTTTITVRG-YFEDFVSRWFSIEDLAAAELDAVLHAWQGLGYYARARNLHKCAKLITKEYGGKFPEREEALVKLPGIGPYTAAAIAAIAFGHIATPVDGN 145 RDPYRTWVSEIMLQQTRVEAVIP-YFEAFLKRFPDVHALATATEEEVLQRWAGLGYYRRAFLHAAAQKVVEDWDGRFPETADTLRAMPGVGAYTSAAIASLAFGEAVPVVDGN 142	
c_000001169194_1	41	TDPYRILVSEIMLOOTRVETVLR-YYESWLKRFPTLGALASANSREVLKAWEGLGYYRRARNLHSAARRIRELPGGHFPTSYRDLRKLPGVGQYTAGAVASIGFGEIVPAVOGN 153	
c_000002786947_2	41	TDPYRILVS IMLQ TRVETVLR-YYESWLKQFFTLGTLASADSTEVLKAWEGLGYYRRAKNLHRAAKHIRNVLGGRFFTSSRDLRQLPGVGQ TAGAVASIGFGEIVPAVIG 153	
c 000001279808_52 c 000000358065 2	28 31	RSPYYVWIS IMSQ TQIDRVAEKFFPRFIATFPTVEALAAASWDEVYPVWEGIG YNRGKNLLKAAQIIVEKHDGEIPQTAVELEALPGVGK TAHAVLAFAFDQKVPAI TI QKQYFILIS FMLQ TQVKTVIP-YFENFINKIPNLKSLAKVNNRKLMKCWEGIG YSRAKNLKKSAKIIIDNYKGRLPNDFEELKKLPGIGD TASAISAIAFNKPIIPL G 143	
c_000003745941_1	22	AALYPTVVS EFMQQTQVKTVLP-YFHRWLKRFPDFKSLAKAKEETVLKHWEGLGYYSRARNLHRLAREILALN-SIPEDPESWQQFKGIGAYTAAAITSISFNHPVACVDGN 132	
c_000004187032_4	31	kkhyytlvs <mark>e</mark> fmlo <mark>g</mark> tqvvtvip-yfdrfinkipnlkklstiqdneliklweglg <mark>y</mark> ysrarnlkktaqiiiskhhgkipnnyedlislpgign <mark>y</mark> tanailaiafnksyipl <mark>dgn</mark> 143	
c_000006067315_3 c_000005543774_1	31 1	QTEYFTLVSEFMLQQTQVKTVIP-YFNNFINKIPNLKKLANVNETRLMKCWEGLGYYSRARNLKKTAKIIISEFNSNLPNTIEELKNLPGIGDYTSRAVLAIAFNKPIIPLDGS 143 KKLYYRILSEFMLQQTQVKTVIP-YFNNFVKKVPSLKALSKSNEKKILKLWEGLGYYSRAKNLHKTSKILVKKYDSQIPDSFEKLKELPGIGDYTANILLALIYNHPRIGIDG 113	
c 000006211484 1	23	KKQYYRIISEMLQQTQVKTVIP-YFNNFVKKIPSLKALSNSDEKTVIKLWEGIGYYARAKNLHKTSKILIKKYNGQIPKSFVKIKELPGIGD TANILLALIYNQPCIALDVN 135	
c_000002718976_3	32	kklyyrlls <mark>e</mark> fmlo <mark>o</mark> tqvktvip-yfnkftkkfktikalsksnereilkmweglg <mark>y</mark> yrrarnllacskilvknyksrlprsiieikklpgigd <mark>y</mark> tanallglvynepriav <mark>o</mark> s 144	
c_000002992548_1 c_000000456751_1	33 1	KEQYYRILS FMLQOTQVKTVIP-YFKNFINKIPNLKVLSSSNEKTILKLWEGIGYYRRAKNLHKTAKILTKNYKGKLPKEFDEIKKLPGVGE TANALLALVYNQPRIPFDG 145YVLVS FMLQOTQVKTVIP-YFTKFVKKIPNLKSLSTSNEKKILKLWEGIGYYRRAKNLHKTAKILIKNCKGKLPKKFAEIKLPGVGE TANSLLALVHNKPSIPIDG 109	
c 000002655634 1	28	KKEYYVLVSEFMLQ TQVKTVIP-YFKKFVTKIPNLKTLSTSNEKQVLKLWEGLGYYRRVRNLHKTAKILLKQYKAKLPKKFQEIIKLFGVGETANSLSALIHNKPCIPILG 140	
c_000004232403_2	27	ndpykiwls <mark>e</mark> vmlq <mark>q</mark> trvetvip-yyntwlenyktiqsvaqanlddlkiwegmg <mark>y</mark> ysrcknfyyaakeiickykgtipnqfdvfkslpgvgd <mark>y</mark> iagavmsiafnqphpsi <mark>dgy</mark> 139	
6u7t.before.V147.pdb Consensus_aa:	28	RDPYKVWVSEVMLQQTRVETVIP-YFEQFIDRFPTLEALADADEDEVLKAWEGLGYSRVRNLHAAVKEVKTRYGGKVPDDPDEFSRLKGVGPYTVGAVLSLAYGVPEPAVDCM 140 .ssy.l@lSelMLQQTpV.hhhs.Y@.p@hpp@PslpsLa.tpbppllphWpGLGYYsRt+Nlhphtp.l.pph.t.hPpshp.l.LPGIGTatalhtht@spshlDtN	
Conservation:		95 9 75 87 85 9 5 9 8 9 5	
Conservation: sp_P17802_MUTY_ECOL	141	vkrvlarcyavsgwpgkkevenklwslseq-vtpavgverfn <mark>o</mark> ammdlgami <mark>c</mark> trskpk <mark>c</mark> sl <mark>c</mark> plqng <mark>c</mark> iaaannswalypgkkpk 22:	5
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS	147	vkrvlarcyavsgwpgkkevenklwslseq-vtpavgverfn q ammdlgami <mark>c</mark> trskpk <mark>c</mark> sl <mark>c</mark> plqng <mark>c</mark> iaaannswalypgkkpk 22. vmrvlsrlflvtddiakpstrkrfeqivre-imayenpgafn <mark>e</mark> alielgalv <mark>c</mark> tprrps <mark>c</mark> ll <mark>c</mark> pvqay <mark>c</mark> qafaegvaeelpvkmkk 23.	1
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2	147 150	vkrvlarcyavsgrpgkkevenklyslseq-vppavgverpngambligamictrskpkgsleplqncctaaannsmalypckkpk 22 vmrvlarchivtddiakpstrkrfeqivre-imayenpgafnealielgalvctprrpscllepvqaycqafaegvaeelpvkmkk 23 vervmarledistplegakpalkaraas-ltp	1
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS	147	VKRVLARCYAVSGØRGKKEVENKLWSLSEQ-VTPAVGVERFNGAMMLGAMI CTRSKPKESLEPLONGCIAAANNSMALYPGKKPK	1 2 3
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00000352391_2 c_000000031207_6 c_000000430975_4 c_000001007148_4	147 150 139 151 148	VKRVLARCYAVSGWFGKKEVENKLWSLSEQ-VTPAVGVERFNĞAMMLIGAMI CTRSKPKESLEPLQNGCIAAANNSMALYPCKKPK	1 2 3 3
sp_P17802 MUTY_ECOL sp_P83847 MUTY_GEOS c_000003652391_2 c_000000031207_6 c_000000430975_4 c_000001007148_4 c_000001092848_3	147 150 139 151 148 161	VKRVLARCXAVSGØPG — KKEVENKUNSL — SEQ-VTP — AVGVERRNÅAMDLGAMLÖTRSKPKËS — LËPLONG TAAANNSMALYPGKKPK — 22 VKRVLSRIELIVIDDIA — KESTRIKFEĞI — VVE IMA — VENNGAFNBALIELGALVYTRERPSCL — VLE PVQAYCQAPEGVAELPLYKMKK — 23 VERVMARLFDISTPLP — GAKPALKAR — AAS-LTP — KLRPGDYAQAVMDLGATI TARAPTG — VCPINDC HARRAGTAAELPKRTFK — 23 VERVUSRYLKIDGNPK —— SGTARRRIQQA — ADD-ALD —— DENRGHNQALMDLGATI CTRRPPCQ — REPLASG CARASGEPTKMPTRQK — 22 VERVVSRIFQITQPIP —— LISRTIEQI —— AAG-LTP —— SKRRGGYAQAIMDLGATI CTRRPKFKN — VCPIHDI CLANISGTPSDFFRTPR — 23 TARYARLLALRSDLH —— SGEGRQUMSL —— AER-TVP —— FORRGEFNQALDLGATUGTVGV — TRRQ —— ECPVRGS CSIELGEVERIPARASR — 23 VERVITRIELAGTSTLP —— AAKPGVKAA — VAA-LVP —— AERFGOFPAGAMDLGATI CTRRPPSG —— ECPVRGS CARAGAGAGESPYKASK — 24 VERVITRIELAGTSTLP —— AAAKPGVKASK — 24	1 2 3 3 1
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00000352391_2 c_000000031207_6 c_000000430975_4 c_000001007148_4	147 150 139 151 148	VKRVLARCYAVSGWPG — KKEVENKUNSL — SEQ-VTP — AVGVERRNÄAMDLGAMI CTRSKPKES — LEPLONG TAAANNSMALYPCKKPK — 22 VKRVLSRLEVITODIA — KPSTRKRFEQI — VYRE IMA — VENNGAPNALIELGALVETREPSCI — LEPVOAYCQAPEGVAEELPVKNKK — 23 VERVUARLEDISTPLP — GAKPALKAR — AAS-LTP — KLRFGDYAQAVMOLGATI CTARAPTG — VCPLNDCGUARRAGTAAELPKRTEK — 23 VERVLSRYLKIDGNPK — SGTARKRIQQA — AAD — AAD — QENPGDHNQ ALMOLGATI CTARAPTG — VCPLNDCGUARRAGTAAELPKRTEK — 22 VERVUSRIPQITOPIP — SFREGUARAGA — AAC — SKRFGDYAQA IMDLGSLUCTPRKPKN — VCPLHDICLANISGTSDFPKRTFR — 23 TARYARLLALRSDLH — SGEGRRQUNSL — AER-TVP — SKRFGDYAQA IMDLGSLUCTPRKPKN — VCPLHDICLANISGTSDFPKRTFR — 23 VERVITRIKALIGTPLP — AAKPOVKA — VAA—LVP — — AERGOFAQAMMOLGSLVCTPRRPSCI — LEPLOAFCAARGAAGASEPYNASK — 24 VERVUSRIFQITOPIP — SARFGDYAQAMMOLGSLVCTPRRPSCI — LEPLOAFCAARGAAGAGESPYNASK — 24 VERVUSRIFQITOPIP — SGRFGITA — AAG-LTP — SKRFGDYAQAMMOLGSLVCTPRRPSCI — LEPLOAFCAARGAAGAGESPYNASK — 24 VERVUSRIFQITOPIP — SGRFGITA — AAG-LTP — SKRFGDYAQAMMOLGSLVCTPRRPSCI — UEPLOAFCAARGAAGAGESPKRIFK — 25 VERVUSRIFQITOPIP — SGRFGITA — AAG-LTP — DRORGOFAQAMMOLGSLVCTPRRPKKN — VCPHHDICLANISGTSDFPKRTFR — 19 VERVLSRAVAVEALP — SGRFGITAL — TOA LVP — DDROGDFAQAMMOLGSLVCTPRRPKK — UEPHWRPCSARSLCTGESSPERKIKV — 25 VERVLSRAVAVEALP — SGRFGITAL — TOA LVP — DDROGDFAQAMMOLGSLVCTPRRPKG — UEPHWRPCSARSLCTGESSPERKIKV — 25 VERVLSRAVAVEALP — SGRFGITAL — TOA LVP — DDROGDFAQAMMOLGSLVCTPRRPKG — UEPHWRPCSARSLCTGESSPERKIKV — 25 VERVLSRAVAVEALP — UEPHWRPCSARSLCTGESSPERKIKV — 25 VERVLSRAVAVEALP — UEPHWRPCSARSLCTGESSPERKIKV — 25 VERVLSRAVEALP — UEPHWRPCSARSLCTGESSPERKIV — 25 VERVLSRAVEALP — UEPHWRP	1 2 3 3 1 3
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_0000000312077_6 c_00000003975_4 c_000001007148_4 c_000001092848_3 c_0000011971282_1 c_000001197282_1 c_000001803648_25	147 150 139 151 148 161 108 170 153	VKRVLARCYAVSGØFG — KKEVENKUNSL — SEQ-VTP — AVGVERFNGAMMLIGAMI CTRSKPKES — LEPLQNGCIAAANNSMALYPGKKPK — 22 VMRVLSRLFLUYTDDIA — KPSTRKRFEQI — VRE IMA — VENIGARDALIELGALVTERPRSCI — LEPVQAV CQAFAEVARELPYKMKK — 23 VERVMARLEDISTPLP — GAKPALKAR — AAS-LTP — KLRPGDYAQAVMDLGATI CTARAPTG — VCPLINDC GARRAGTAAELPKRTPK — 23 VERVLSRYLKIDGNPK — SGTARKRIQQA — ADD-ALD — CENBGDHNQALMDLGRSI CTRSSPDQ — REPLASSCGARASGEPTRWPTRQK — 22 VERVVSRIPGITQPIP — LSRPTINQL — AAG-LTP — SKRFGDYAQAMMLIGASI CTRSSPDG — REPLASSCGARASGEPTRWPTRQK — 23 TARFYARLLALRSDLH — SGEGRRQUNSL — AER- UVP — SKRFGDYAQAMMLIGATI CTPKRPKC — ECPVRGSCRSLELGEVERI PARASR — 23 VERVITRLRALGTPLP — AAKPOVKKA — VAA - LVP — AERPGDFAQAMMLIGATI CTPKRPSCI — LEPLQAFCARGAAQASESFPKKSK — 24 VERVISRATAVEAPLP — SSKPGDYAQAMMLIGATI CTPKRPACA — LCPMMRCCARASCAFFRFR — 19 VERVLSRAVAVEAPLP — SGRPEIRRI — TQA-LVP — PDRRGDFAQAMMLIGATI CTPKRPACA — LCPMMRCCARASLOTGESFPKKIK — 25 IERVMARMIDHISPLP — SSKPEGLIC — AAA - LTP — DFRAGDYAQAMMLIGATI CTPKRPAGA — LCPMMRCCARSLOTGESFPKKIK — 25 IERVMARMIDHISPLP — SSKPELLC — DAA - LTP — DFRAGDYAQAMMLIGATI CTPKRPAGA — LCPMMRCCARRICATION LCPMSTRYCK — 25 IERVMARMIDHISPLP — SSKPELLC — DFRAGDYAQAMMLIGATI CTPKRPAGA — LCPMMRCCARRICATION LCPMSTRYCK — 25	1 2 3 3 1 3 0 2
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_00000031207_6 c_000001031207_6 c_00000107148_4 c_0000011928248_3 c_000001151029_1 c_000001197282_1 c_000001803648_25 c_000002078955_4	147 150 139 151 148 161 108 170 153 153	VKRVLARCYAVSGWPG — KKEVENKUNSL — SEQ-VTP — AVGVERRNÄAMDLGAMI CTRSKPKES — LEPLQNGCIAAANNSMALYPCKKPK — 22 VKRVLSRLEVITDDIA — KESTRKRFEQI — VYRE IMA — YENNGARDALIELGALVETREPSCL — LEPVQAY CQAPEGVAEELPYKNKK — 23 VERVUSKLIVIDGIAP — KESTRATIQA — AAS-LTP — KLREGUYAQAVMOLGATI CTARAPTG — VCPLNOCCHARRACTAAELPKRTEK — 23 VERVUSKLIKOGHPK — SGTARKIQA — AAD — ALD — QENNGGHNQALMOLGSI CTPREPSDC — REPLASGCGARRASCEPTREPTERQK — 22 VERVUSKLIFQITQPIP — SERPTLRQL — AAG-LTP — SKREGUYAQA IMDLGSI CTPREPSC — VCPLHDI CLANISGTPSDFPKRTPR — 23 TARYARLLALRSDLH — SGEGRRQUWSL — ARR-IVP — HORRGEFNQALIDLGATV CGV-TPREPS — UCPLYGSCSASLELGEVER PARASR — 23 VERVITRLERLGTFLP — AARFQVKRA — VAA — LVP — SERRGDYAQAMDLGSI CTPREPS CI — LCPLQAFLARAGAAQESFYNASK — 24 VERVUSKLFQITQPIP — LSRPTLRQL — AAG-LTP — SKREGUYAQAMDLGSI CTPREPS CI — LCPLQAFLARAGAAQESFYNASK — 24 VERVUSKLFQITQPIP — LSRPTLRQL — AAG-LTP — DERGGDFAQAMDLGSI CTPREPS CI — LCPLQAFLARAGAAQESFYNASK — 24 VERVUSKLFQITQPIP — SGRPERTL — TQA-LVP — DERGGDFAQAMDLGSI CTPREPS CI — LCPMRPCFARASLCTGESFPERIKU — 25 IERVMARMDLHSSLP — SSKPELLAC — AAA-LTP — DERGGDFAQAMDLGSI CTPREPACA — LCPMRPCFARASLCTGESFPERIKU — 25 VERVMARMDLHSSLP — SKEPELLAC — AAA-LTP — DERGGDFAQAMDLGSI CTPREPSCG — VCPMSPC ALISTATALIPKKTPK — 23 VERVMARKLHIHTELP — SAKPELLAC — AAA-LTP — DERGGDFAQAMDLGSI CTPREPSCG — VCPMSPC ALISTATALIPKKTPK — 23 VERVMARKLHIHTELP — AAKEPLESK — AATA - LTP — DERAGDYAQAMDLGSI CTPREPSCG — VCPMSPC ALISTATALIPKKTPK — 23 VERVMARKLHIHTELP — AAKEPLESK — AATA - LTP — DERAGDYAQAMDLGSI CTPREPSCG — VCPMSPC ALISTATALIPKKTPK — 23	1 2 3 3 1 3 0 2 5
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_0000000312077_6 c_00000003975_4 c_000001007148_4 c_000001092848_3 c_000001197128_1 c_000001197128_1 c_000001803648_25	147 150 139 151 148 161 108 170 153	VKRVLARCYAVSGØRG	1 2 3 3 1 3 0 2 5 5
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00003652391_2 c_000000031207_6 c_000000031207_6 c_000001007148_4 c_000001092848_3 c_000001151029_1 c_000001797282_1 c_000001803648_25 c_00002106160_4 c_000003607531_2 c_000003872363_4	147 150 139 151 148 161 108 170 153 153 141 151	VKRVLARCXAVSGØRG——KKEVENKUNSL.—SEQ-VTP — AVGVERRNÅAMDLGAML TRSKPKES — LEPLONG TAAANNSMALYPCKKPK — 22 VKRVLSRIJLVITDILA —KESTRKRFEQI — VVEE IMA — VENNGAPNEALIELGALVYTREPESCL — LEPVQAYCAPEACVAELPVKMKK — 23 VERVMARLFDISTPLP — GAKPALKAR —AAS-LTP — KLRPGDYAQAVMDLGATI TARAPT G — VCPLNDC GHARRAGTAAELPKRTFK — 23 VERVUSRYLKIDGNPK — SGTARRRIQQA —ADD-ALD — GENEGHNQALMDLGRSI CTRSPDFOQ — REPLASSCGARASGEPTKMPTRQK — 22 VERVVSRIPGITQPIP — LSRPTIRQL —AAG-LTP — SKRRGDYAQAIMDLGSLVCTPRKPKON — VCPLHDI CLANISGTSDFPRFTFR — 23 TARTYARLLALRSDLH — SGEGRRÜMSL —AER TVP — RORFGEFNQALIDLGATV GV -TPRG — ECPVRSG SIELLGEVERI PARASR — 23 VERVITRLAGIGTPLP — AAAKPQVKA — VAA —LVP — AERFGOPAQAMMDLGATV GV -TPRFQ — ECPVRSG SIELLGEVERI PARASR — 24 VERVVSRIPGITQPIP — LSRPTIRQL —AAG-LTP — SRRGDYAQAMMDLGSLVCTPRKPKS — VCPHHDI CLANISGTSDFPKRTFR — 19 VERVLSRAVAVEADLP — GSRPERIRL — TOA —LVP — PORFGOPAQAMMDLGSLVCTPRKPKS — VCPHHDI CLANISGTSDFPKRTFR — 19 VERVLSRAVAVEADLP — SGRPERIRL — TOA —LVP — PORFGOPAQAMMDLGSLT CTPKSASG — VCPMSFACLARINGTAAVLPKKTFK — 25 IERVMARMID HSSLP — SAKPELLAC —AAA-LTP — DPRGDYAQAMMDLGATI CTPKSASG — VCPMSFACLARINGTAAVLPKKTFK — 23 VERVMARMID HSSLP — SAKPELLAC —AAA-LTP — DRRGDYAQAVMDLGATI CTPKSASG — VCPMSFACLARINGTAAVLPKKTFK — 23 VERVMARMID HSSLP — SAKPELLAC —AAA-LTP — DRRGDYAQAVMDLGATI CTPKSASG — VCPMSFACLARINGTAAVLPKKTFK — 23 VERVMARKLRILRETP — YNKRKVLST — LIR-MLD — SRRGDYAQAVMDLGATI CTPKSPTG — ICPMSCACVALISGTASSPESYFSPKK — 22 VERVITKVFGIFKBLP — EARPI INCAAR — LAP-KTT — SRRGDYAQAVMDLGATVCRRRFRLD — LEPVEKY CLANQONFOQVPRKAFK — 23 VERVMARLHNITLPP — PAAKPLETAM — AAA — LTP — VDRAGDYAQAVMDLGATVCRRRFRLD — LEPVEKY CLANQONFOQVPRKAFK — 23 VERVMARLHNITLPP — PAAKPLETAM — AAA — LTP — VDRAGDYAQAVMDLGATVCRRRFRLD — LEPVEKY CLANQONFOQVPRKAFK — 23 VERVMARLHNITLPP — AAAKPLEFS — LIR-MLD — VDRAGDYAQAVMDLGATVCRRRFRLD — LEPVEKY CLANQONFOQVPRKAFK — 23 VERVMARLHNITLPP — PAAKPLETAM — AAA — LTP — VDRAGDYAQAVMDLGATVCRRRFRLD — LEPVEKY CLANQONFOQVPRKAFK — 23 VERVMARLHNITLPP — AAAKPLETAM — AAA — LTP — VDRAGDYAQAVMDLGATVCRRRFRLD — LEPVEKY CLANQONFOQVPRKAFK — 23	1 2 3 3 1 3 0 2 5 5 3 6
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_000000312077_6 c_000000312077_6 c_000001092848_3 c_000001191282_1 c_00000197282_1 c_00000197282_5 c_000002078955_4 c_000002078955_4 c_00000387531_2 c_00000387531_2 c_00000387531_2	147 150 139 151 148 161 108 170 153 153 141 151 149	VKRVLARCYAVSGØRGG	1 2 3 3 1 3 0 2 5 5 3 6 1 0
sp_P17802_MUTY_ECOL sp_P83847_MUTY_EGDS c_00003652391_2 c_000000031207_6 c_000000031207_6 c_000001007148_4 c_000001092848_3 c_000001151029_1 c_000001797282_1 c_000001803648_25 c_00002106160_4 c_000003607531_2 c_000003872363_4	147 150 139 151 148 161 108 170 153 153 141 151	VERVIARCXAVSGWPG—KEWENKUWSL—SEQ-VTP — AUGUERNNÄAMDLGAMICTESKPKES —LEPLONGCIAAANNSMALYPCKKPK — 22 VARVLSRLEVITDDIA —KESTRKREFQI —VRE IMA —VENGAPNALIELGALVCTREPESCL —LEPVQAYCAPEAGVAELPVKMKK — 23 VERVUARLEDISTELP — GAKPALKAR —AAS-LTP — KLREGDYAQAVMOLGATICTARAPTG — VCPLNDCGIARRAGTAAELPKRTEK — 23 VERVLSRYLKIDGNPK — SGTARKRIQQA —ADD—ALD — QENPGDHNQIMBLGATICTARAPTG — VCPLNDCGIARRAGTAAELPKRTEK — 23 VERVISHPLOTOPIP — SGRETLEQI —AAG-LTP — SKREGDYAQAIMDLGSLVCTPKRPKKN — VCPLHDICLANISGTESDPFKRTFR — 23 TARTYARLLALKSDLH —SGEGRRQUMSL —AER-TVP — RENGEGPAQAIMDLGSLVCTPKRPKKN — VCPLHDICLANISGTESDPFKRTFR — 23 VERVITELRAIGTELP — AAKPOVKA —VAA-LVP — AERFGDYAQAMDLGATVGOV-TPRGO — ECPVRGSCRSLELGEVERIPARASR — 24 VERVUSRIPQITOPIP — LISPTLEQI —AAG-LTP — SKREGDYAQAMDLGSLVCTFREPSCI —LEPLQAFCARGAAAQESFPVKASK — 24 VERVUSRIPQITOPIP — LISPTLEQI —AAG-LTP — SRREGDYAQAMDLGSLVCTFREPSCI —LEPLOPAGRAGAAQESFPKISV — 25 VERVISRAVAVEAPLP — SGREFERL —TQA-LVP — DPRGGDFAQAMDLGSLVCTFREPSCI —LEPMARRESLCTGESFPFKIV — 25 VERVMARMIDHSSLP — SAKPELLAC —AAA-LTP — DPRGGDFAQAMDLGATICTFKSPAGG — VCPMSFACLARINGTAAVLPKKTFK — 23 VERVMARMINHTFLP — AAKPELFSK —AAT LTP — DLRAGDYAQAMDLGATICTFKSPTG — ICPMSCCAVALISSTAAELPKKTFK — 23 VERVMASHLIRLIRETP — YMKKRULST —LIR-WLD — SRREGDPNQALMELGSTVCLPKNPKCE — NCPLKLSCGGTLSGSSESYPSFKKW — 22 VERVITRYPGIFKPLP — EARPIIKOCAAK —LAP-KTT — RGRPGDYAQAMDLGATICTFKSPTG — ICPMSCCAVALISSTAAELPKKTFK — 23 VERVMARLLRUITETP — EARPIIKOCAAK —LAP-KTT — RGRPGDYAQAMDLGATICTFKSPTG — ICPMSCCAVALISSTAAELPKKTFK — 23 VERVMARLLRUITETP — PARKELFS —AAA-LTP — VDRAGDYAQAMDLGATICTFKSPTG — ICPMSCCAVALISSTAAELPKKTFK — 23 VERVMARLLRUITETP — PARKELFS —AAA-LTP — VDRAGDYAQAMDLGATICTFKSPTG — ICPMSCCAVALISSTAAELPKKTFK — 23 VERVMARLLRUITETP — PARKELFS —AAA-LTP — VDRAGDYAQAMDLGATICTFKSPTG — ICPMSCCAVALISSTAAELPKKTFK — 23 VERVMARLLRUITETP — SAKRELTAM —AAA-LTP — VDRAGDYAQAMDLGATICTFKSPTG — ICPMSCCAVALISSTAAELPKTFKTFK — 23 VERVMARLLRUITETP — PARKELFAM —AAA-LTP — VDRAGDYAQAMDLGATICTFKSPTG — ICPMSCCAVALISSTAAELPKTFK — 23 VERVMARLENVITSP — PARKELTAM —AAA-LTP — VDRAGDYAQAMDLGATICTFKSPTG —	1 2 3 3 1 3 0 2 5 5 3 6 1 0 2
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00003652391_2 c_00000031207_6 c_0000001207_6 c_00000109248_3 c_000001151029_1 c_000001197282_1 c_00000197282_1 c_000001803684_25 c_000002106160_4 c_00003607531_2 c_00003807531_2 c_00004820107_1 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000005456210_2	147 150 139 151 148 161 108 170 153 141 151 149 156 140 153 144	VERVIARCXAVSGWPG—KEWENKUWSL—SEQ-VTP — AUGUERTNÄAMDLGAMI CTRSKPKES —LEPLONG TAAANNSMALYPCKKPK — 22 VERVIARCLSHLVITDDIA —KESTERREFQI —VRE IMA —VENGAPRALIELGALVCTREPESCL —LEPVQAYCQAPEGVAELPVYMKKK — 23 VERVUARLEDISTPLP — GAKPALKAR —AAS-LTP — KLRPGDYAQAVMDLGATI CTARAPTG — VCPLNDCGUARRAGTAAELPKRTEK — 23 VERVISRYLKIDGNPK — SGTARKRIQQA —ADD—ALD — QENPGDHNQIAMDLGATI CTARAPTG — VCPLNDCGUARRAGTAAELPKRTEK — 23 VERVISRYLKIDGNPK — SGTARKRIQQA —ADD—ALD — SKRPGDYAQAIMDLGSLVCTPKRPKCN —VCPLHDICLANISGTSDFPKRTFR — 23 TARTYARLLALKSDLH — SGEGRRQUMSL —AER-TVP — SKRPGDYAQAIMDLGSLVCTPKRPKCN —VCPLHDICLANISGTSDFPKRTFR — 23 VERVITRLARIGTPLP — AAAKPOYKA —VAA-LVP — SERFGDYAQAMDLGATV GOV-TPRPG — ECPVGSGSSLELGEVERIPARASR — 24 VERVUSRIPQITOPIP — LISPTLIQU —AAG-LTP — SERFGDYAQAMDLGSLVCTFRRPKSCI — LEPLQAFCAARGAAQESFPVIASK — 24 VERVUSRIPQITOPIP — LISPTLIQU —AAG-LTP — SERFGDYAQAMDLGSLVCTFRRPKSCI — LEPLQAFCAARGAAQESFPVIASK — 25 VERVIARAVAVEAPLP — SGRPEIRL —TQA-LVP — DDRFGDFAQAMDLGSLVCTFRRPKSCI — LEPWARPCARSLCTGESFPRKIKV — 25 VERVMARMIDHSPLP — SGRPEIRL —TQA-LVP — DDRFGDFAQAMDLGSLTCTFKSPAGA — LEPWARPCARSLCTGESFPRKIKV — 25 VERVMARMINHTPLP — SAKPELLAC —AAA-LTP — DDRFGDFAQAMDLGATT CTFKSPAGA — LEPWASCAGAURSTRYKTKT — 23 VERVMARLINHTPLP — AAKPELFSK —ATA —TPP — DLRAGDYAQAMDLGATT CTFKSPTG — LEPWASCAGAULSGTAELFKTKTK — 23 VERVMARLINHTPLP — PARKPELFSK —ATA —TPP — DLRAGDYAQAMDLGATT CTFKSPTG — LEPWASCAGAULSGTAELFKTKTK — 23 VERVMARLINHTPLP — PARKPELFSK —ATA —TPP — DLRAGDYAQAMDLGATT CTFKSPTG — LEPWASCAGAGSESYPEFKTK — 22 VERVITRVFGIFKPLP — PARKPELFSK —ATA —TPP — UDRAGDYAQAMDLGATT CTFKSPTG — LEPWASCAGAGSESYPEFKTK — 23 VERVMARLINHTSLP — PARKPELFSK —ATA —TPP — UDRAGDYAQAMDLGATT CTFKSPTG — LEPWASCAGAGAGAGESPESYPEFKT — 23 VERVMARLENVITFLP — SAKPELTAH — AAA—LTP — UDRAGDYAQAMDLGATT CTFKSPTG — LEPWASCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	1 2 3 3 1 3 0 2 5 5 5 3 6 1 0 2 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00003652391_2 c_00000031207_6 c_00000030975_4 c_00001007148_4 c_000001092848_3 c_000001151029_1 c_00001797282_1 c_000001797282_1 c_000001803648_25 c_000002106160_4 c_000003607531_2 c_000003872363_4 c_000004820107_1 c_000005774797_1 c_00000587021_3 c_000004551008_5	147 150 139 151 148 161 108 170 153 141 151 149 156 140 144	VERVIARCXAVSGRPG—KEEVENKINSL—SEQ-VTP — AVGVERFN AMMDLGATICTRSKPKES — LEPLONG TAAANNSMALYPCKKPK — 22 VERVLSRIJLIVTDDIA —KESTERREFQI —VRE—IMA —VENDGAPRALILELGALVCTREPSCL —LEPVQAYCQAPEGVAELPYVENKKK — 23 VERVMARLFDISTPLP —GAKPALKAR —AAS-LTP — KLRPGDYAQAVMDLGATICTARAPTCG —VCPLNDCCHARRAGTAAELPKRTPK — 23 VERVUSRYLKIDGNPK —SGTARKRIQQA —ADD-ALD — OENBGDHNQALMDLGASICTRSPPCQ — RCPLASGCGARASGEPTRMPTRQK — 22 VERVVSRIPGITQPIP —LSRPTLEQL —AAG-LTP —SKRFGDYAQAIMDLGSICTRSPPCQ — RCPLASGCGARASGEPTRMPTRQK — 22 VERVVSRIPGITQPIP —SARFUNGAL —AER-IVP —RORPGEFNQALIDLGATVCGV-TPRCQ — ECPVRGSCRSLELGEVERIPARASR — 23 VERVITRLBAIGTPLP —AAAKPUYKA —VAA-LVP — BERGGDPAQAMMDLGATVCFNPFKC — VCPHHDICLANISOTSDEPKRTPR — 24 VERVVSRIPGITQPIP — LSRPTLRQL —AAG-LTP — SKRFGDYAQAMMDLGATVCFNPFKC — VCPHHDICLANISOTSDEPKRTPR — 19 VERVUSRIPGITQPIP — LSRPTLRQL —AAG-LTP — SKRFGDYAQAMMDLGSLVCTPRNPKC — VCPHHDICLANISOTSDEPKRTPR — 19 VERVLSRAYAVEADLP — GSRPEIRL —TQA-LVP — PDRFGDFAQALMDLGATICTFKRPAC — LCPMRPCCARSLGTQESFPKKIV — 25 IERVMARMENDIHSPLP — SAKPELLAC —AAA-LTP — DFRAGDYAQAMMDLGATICTFKSPTCG — LCPMSFACLARINGTAAVLPFKTFK — 23 VERVMARLHNIHTPLP — AAKPELFSK —ATA-LTP — DIRAGDYAQAMMDLGATICTFKSPTCG — LCPMSFACLARINGTAAVLPFKTFK — 23 VERVMARLHNIHTPLP — YNKKNVLST —LIR-WLD —SRSRGDFNQALMEGSTVCRFRFLD — LCPMSFACLARINGTAAVLPFKTFK — 22 VERVITRVSGIFKPLP —EARPIKOCAK —LAP-KTT — RORPGDYAQAVMDLGATICTFKSPTCG — LCPMSFACLARINGTAAVLPFKYFK — 23 VERVMARLHNIHTPLP — AAKPELTAM —AAA —LTP — VURRGDYAQAVMDLGATICTFKSPTCG — LCPMSFCACVALISGTASEPSFSPKK — 22 VERVMARLHNIHTPLP — PAKPELTAM —AAA —LTP — VURRGDYAQAVMDLGATICTFTSPEG — LCPCTSYCAALPEGAGAGAGACCARPSPFKK — 23 VERVMARLHNIHTPLP — PAKPELTAM — AAA —LTP — VURRGDYAQAVMDLGATICTFTSPEG — LCPCTSYCAALPEGAGAGACACACACACACACACACACACACACACACACAC	1 1 2 3 3 3 1 1 3 0 0 2 2 5 5 5 3 6 1 0 2 5 6 1 0 2 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_000000352291_2 c_00000031207_6 c_000001007148_4 c_000001092848_3 c_000001197282_1 c_000019797282_1 c_000019707825_1 c_000001803648_25 c_000002106160_4 c_000003807531_2 c_000003872363_4 c_00000480107_1 c_00000587021_3 c_00000454010_2 c_000004551005_5 c_000002577378_2	147 150 139 151 148 161 108 170 153 141 151 149 156 140 153 144 144 139	VERVIARCXAYSGRPG — KKEVENKURSL — SEQ-VTP — AVGVERFN AMMOLGAM CTRSKPKES — LEPLONG TAAANNSMALYPCKKPK — 22 VARVLSRIJLVITDIA — KESTERRFEQI — VVEE IMA — VENDGAPRALILELGALVYTREPESCL — LEPVQAYCAPEGVAELPYVMKKK — 23 VERVMARLFDISTPLP — GAKPALKAR — AAS-LTP — KLRPGDYAQAVMDLGATI CTARAPT G — VCPINDC CHARRAGTAAELPKRTFK — 23 VERVUSRYLKIDGNPK — SGTARRRIQQA — ADD-ALD — OENBGDHNQALMDLGRSI CTRFSPCO — REPLASG CARASGEPTRMPTRQK — 22 VERVVSRIPGITQPIP — LSRPTIRQL — AAG-LTP — SKRRGDYAQAMMOLGATI CTARAPT G — VCPINDC CHARRAGTAAELPKRTFR — 23 TARFYARLLALRSDLH — SGEGRRQUMSL — AER-TUP — SKRRGDYAQAMMOLGATV GV-TPRFQ — ECPVRGS CSIELGEVERI PARASR — 23 TARFYARLLALRSDLH — SGEGRRQUMSL — AER-TUP — BERRGDFAQAMMOLGATV GV-TPRFQ — ECPVRGS CSIELGEVERI PARASR — 23 VERVITRIKALGTOFLP — AAAKPOVKA — VAA-LUP — SERRGDYAQAMMOLGAT VGV-TPRFPSCI — LEPLQAFCARGAAAQESFPVKASK — 24 VERVUSRIFDITQPIP — LSRPTIRQL — AAG-LTP — SERRGDYAQAMMOLGSLV CTRRPPSCI — LEPLQAFCARGAAAQESFPVKASK — 24 VERVUSRIFDITQPIP — LSRPTIRQL — AAAG-LTP — SRRGDYAQAMMOLGSLV CTRRPPSCI — LEPLOAFCARGAAAQESFPVKASK — 25 VERVURANWAMDLHSSLP — SGREDERIL — TOA-LVP — DPRGDGPAQAMMOLGSLV CTRRPPSCI — LEPMRPC FARRS LOTGESFPERIL — 70A-LVP — DPRGDGPAQAMMOLGSLV CTRRPPSCI — LEPMRPC FARRS LOTGESFPERIL — 70A-LVP — DPRGDGPAQAMMOLGSLV CTRRPPSC — LEPMRPC FARRS LOTGESFPERIL — 25 VERVMARMIDHSSLP — SAKPELLAC — AAA-LTP — DPRGDYAQAMMOLGATI CTPKSASG — VCPMSFACLARINGTAAVLPKKTFK — 23 VERVMARMIDHSSLP — SAKPELLAC — AAA-LTP — DRRGDYAQAVMOLGATI CTPKSASG — VCPMSFACLARINGTAAVLPKKTFK — 22 VERVMARLNITHTP — FARRELTAM — AAA-LTP — VURRGDYAQAVMOLGATI CTPKSPC — NCPLKLSGGGTLSGSPESYFSFFEK — 22 VERVMARLVITLEP — DAAKPELTAM — AAA-LTP — VURRGDYAQAVMOLGATI CTPKSPCG — ICPTSCAACALDEGAANDLFRPFK — 23 VERVMARLVITLEPL — DSKANLKNIAA — GLS EER — KORRGDYAQAVMOLGATI CTPTSFKGS — LEPCTSCAACALDEGAANDLFRPFK — 23 VERVMARLVITLEPL — DSKANLKNIAA — GLS EER — KORRGDYAQAMMOLGATI CTPTSFKGS — LEPCTSCAACHLEPKKKFK — 24 VERVUASHVITLEPL — DSKANLKNIAA — GLS EER — KORRGDYAQAMMOLGATI CTPTSFKGS — LEPCTSCAACHLEPKKFK — 22 VERVMARLVITLEPL — DSKANLKNIAA — GLS EER — KORRGDYAQAMMOLGATI CTSTS	1 2 3 3 3 1 3 0 2 5 5 5 3 6 1 0 2 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_000003652391_2 c_00000031207_6 c_0000001027_6 c_00000109248_3 c_000001197282_1 c_00000197282_1 c_00000197282_1 c_00000197282_1 c_0000027895_5_4 c_000002106160_4 c_00003807531_2 c_00003872363_4 c_00003872363_4 c_000005867021_3 c_000045462107_1 c_00005867021_3 c_00000585172_3 c_000005857378_2 c_00000058175_2	147 150 139 151 148 161 108 170 153 141 151 149 156 140 153 144 144 139 127	VERVIARCYAVSGRPG — KKEVENKUNSI. — SEQ-VTP — AVGGERFNÄAMDIGAMI CTRSKPKES — LEPLONG TAAANNSMALYPCKKEK — 22 VARVISRIFLUTDILA — KESTERREFQI — VYEE IMA — YENNGAPRALIELGALVTREPSCL — LEPVOAY CAPEGAVEALELPKYNKKK — 23 VERVUARLIVIDDILA — KESTERREFQI — VYEE IMA — YENNGAPRALIELGALVTREPSCL — LEPVOAY CAPEGAVEALELPKYNKKK — 23 VERVUARLIVIDOIA — CAKPALKAR — AAS-LTP — KLREGUYAQAVMOLGATI CTARAPTG — VÇPLINOC HARRACTAABLIPKRTEK — 23 VERVUSRYLKIJGNPK — SGTARKRIQA — AAD — ALD — GENGGYNQAIMOLGATI CTARAPTG — VCPLINOC HARRACTAABLIPKRTEK — 23 TARFYARLLALRISDLE — SGEGRRQUMSI. — ARE-TVP — KORRGEDYNQAIMOLGATI CTRREPKON — VCPLINI CLANISCTSESPFRRTER — 23 TARFYARLLALRISDLE — SGEGRRQUMSI. — ARE-TVP — KORRGEPNQAI INDIGATV CGV-TPREPSCI — LEPLOAGEVARAGAAQESPFYMASK — 24 VERVUSRIBLITGTOPIP — LISRPTIRQL — AAG-LTP — SKRRGDYAQAMMOLGATI CTRREPSCI — LEPLOAGEVARAGAAQESPFYMASK — 24 VERVUSRIBLITGTOPIP — LISRPTIRQL — AAG-LTP — SKRRGDYAQAMMOLGATI CTRREPSCI — LEPLOAGEVARAGAAQESPFYMASK — 24 VERVUSRIBAVAVEAPLP — GSRPEIRL — TQA-LVP — DERRGDFAQAMMOLGATI CTRREPAGA — LEPHOMPC FARASILOTGESFFREKIV — 25 LERWARMMOLHSSLP — SKRPEIRL — TQA-LVP — DERRGDFAQAMMOLGATI CTRREPAGA — LEPHOMPC FARASILOTGESFFREKIV — 25 LERWARMMOLHSSLP — SAKPELLAC — AAA-LTP — DERRGDYAQAMMOLGATI CTRRESFCG — VCPMSPG CLARINGTAAVLPKKTPK — 23 VARVMASLLBLIRETP — YAKKRULST — LIR-WILD — SRRGDFNQAMMOLGATI CTRRESFCG — VCPMSPG CLARINGTAAVLPKKTPK — 23 VARVMASLLBLIRETP — YAKKRULST — LIR-WILD — SRRGDFNQAMMOLGATI CTRRESFCG — VCPMSPG CALLISCTAAELPKKTPK — 23 VERVMARLENVITELP — AAKPELTAH — AAA-LTP — VDRAGDYAQAVMOLGATI CTRRESFCG — VCPMSPG CALLISCTAAELPKKTPK — 24 VERVITAVLST — LIR-WILD — SRRGDFNQAMMOLGATI CTRRESFCG — VCPMSPG CALLISCTAAELPKKTPK — 24 VERVITAVLST — LIR-WILD — SRRGDFNQAMMOLGATI CTRRESFCG — VCPMSPG CALLISCTAAELPKKTPK — 24 VERVITAVLST — AAKPELTAH — AAA-LTP — VDRAGDYAQAVMOLGATI CTRRESFCG — VCPMSPC CALLISCTAAELPKKTPK — 24 VERVITAVLST — AAKPELTAH — AAA-LTP — VDRAGDYAQAVMOLGATI CTRRESFCG — VCPMSPC CALLISCTAAELPKKTPK — 24 VERVITAVLTEPLP — DSKAALKALLA — CALS-ERE — KORFGGYAQAVMOLGATI CTRRESFCG — VCPMSPC CALLISCTAACH	1 2 3 3 3 1 3 0 2 5 5 5 3 6 1 0 2 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_00000031207_6 c_00000031207_6 c_000001007148_4 c_00000109248_3 c_00001197282_1 c_0000197282_1 c_0000197282_1 c_0000027895_5 d_000002106160_4 c_00000367331_2 c_00000367331_2 c_000004820107_1 c_000004820107_1 c_0000058774797_1 c_0000587021_3 c_00000451008_5 c_00000451108_5 c_00000557378_2 c_00000557378_2 c_00000557378_2 c_00000557378_2 c_00000557378_2 c_00000557378_2 c_00000557378_2	147 150 139 151 148 161 108 170 153 141 151 149 156 140 153 144 144 139	VERVIARCXAYSGRPG — KKEVENKURSL — SEQ-VTP — AUGUERTNÄAMDLGAMI CTRSKPKES — LEPLONG LAAANNSMALYPCKKPK — 22 VERVUSRISHLUTDDIA — KESTERREFQI — VYEE IMA — YENGGAPRALILELGALVCTREPESCL — LEPVQAYCAPEGAPEGVAELPYKMKK — 23 VERVMARLFDISTPLP — GAKPALKAR — AAS-LTP — KLRPGDYAQAVMOLGATI CTARAPTG — VCPLNDCCHARRAGTAAELPKRTEK — 23 VERVUSRIPKINGHEN — SGTARRRIQQA — ADD—ALD — QENEGHNO ALMDLGRSI CTPRSPPDC — REPLAGGCARASGEPTRWFTRGK — 22 VERVVSRIPQITOPIP — SERTINGL — AAG-LTP — SKRRGDYAQAIMDLGSLVCTPRRPKEN — VCPLHDICLANISOTESPPERTTR — 23 TARTYARLLALRSDLH — SGEGRRQUMSL — AER-TVP — SKRRGDYAQAIMDLGSLVCTPRRPKEN — VCPLHDICLANISOTESPPERTTR — 23 TARTYARLLALRSDLH — SGEGRRQUMSL — AER-TVP — SERRGDYAQAIMDLGSLVCTPRRPKEN — VCPLHDICLANISOTESPPERTTR — 24 VERVVSRIPQITOPIP — LARPCVKA — VAA LVP — SERRGDYAQAMMDLGSLVCTPRRPKSC — LEPLQAFCARGAAAQESPYKASK — 24 VERVUSRIPQITOPIP — LSRPTLRQL — AAG-LTP — SERRGDYAQAMMDLGSLVCTPRRPKSC — VCPHNBFC RARSACAAQESPYKASK — 24 VERVUSRIPQITOPIP — LSRPTLRQL — AAA-LTP — DERRGDYAQAMMDLGSLVCTPRRPKSC — VCPHNBFC RARSACATESPERKIKV — 25 IERVMARMIDHSSLP — SKEPELLAC — AAA-LTP — DERRGDYAQAMMDLGSLVCTPRRPKSC — VCPHNBFC RARSALGTGESFPERKIKV — 25 VERVMARHINHTSLP — SAKPELLAC — AAA-LTP — DERRGDYAQAMMDLGSLVCTPRRPKC — VCPHNBFC RARSALGTGESFPERKIKV — 23 VERVMARLHIHTSLP — AAKEELFSK — ATA-LTP — DERRGDYAQAMMDLGSLVCTPRRPKC — NCPHKLSCAGGTLSGSPESYPSPEKK — 23 VERVMARLHIHTSLP — SAKPELLAC — AAA-LTP — DERRGDYAQAMMDLGSLVCTPKSPTG — NCPHKLSCAGGTLSGSPESYPSPEKK — 22 VERVMARLNUTHSPLP — SAKPELIAC — AAA-LTP — VVRKGVYAQAMMDLGSLTCTKSSPGG — NCPHKLSCAGGTLSGSPESYPSPEKK — 23 VERVMARLHNITSLP — SAKPELIAC — AAA-LTP — VVRKGVYAQAMMDLGSLTCTKSSPGG — NCPHKLSCAGGTLSGSPESYPSPEKK — 23 VERVMARLNUTHSPLP — SAKPELIAC — AAA-LTP — VVRKGVYAQAMMDLGSLTCTKSSPGG — NCPHKLSCAGGTLSGSPESYPSPKK — 23 VERVMARLNUTHSPLP — SAKPELIAC — SAKPELIAC — SERRGDYAQAMMDLGSLTCTKSSPGG — NCPHKLSCAGGTLSGSPESYPSPKK — 23 VERVMARLNUTHSPLP — SAKPELIAC — SAKPELIAC — SERRGDYAQAMMDLGSLTCTKSSPGG — NCPHKLSCAGGTLSGSPESYPSPKK — 22 VERVMARLNUTHSPLP — SAKRELIAC — SAKPELIAC — SERRGDYAQAMMDLGSLTCTKSSPGG — NCPHYNKCYSYLNQLUVBETPSKK — 2	1 2 3 3 1 3 0 2 5 5 5 3 6 1 0 2 5 8 8 3 1 4 1 4 1 1 4 1 1 1 4 1 4 1 4 1 4 1 4
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_00000031207_6 c_00000013207_6 c_000001097148_4 c_000001097148_4 c_000001972848_3 c_000001151029_1 c_00000197282_1 c_00000197282_1 c_000002078955_4 c_000002078955_4 c_000002078955_4 c_000003607531_2 c_000003607531_2 c_000004820107_1 c_000005867021_3 c_000005867021_3 c_000005511048_4 c_00000571378_2 c_000005511148_4 c_00000571378_2 c_00000058175_2 c_00000058175_2 c_00000058175_2 c_00000058175_2 c_00000058175_2 c_00000058175_2	147 150 139 151 148 161 108 153 153 141 151 149 156 144 144 139 127 150 147 138	VERVIARCXAYSGRPG — KKEVENKURSL — SEQ-VTP — AUGUERTNÄAMDLGAMI CTRSKPKES — LEPLONG LAAANNSMALYPCKKPK — 22 VARVLSRLEVITDDIA — KESTERREFQI — VYEE IMA — YENGGAPRALILEGALVETREPSCL — LEPVQAYCAPEACVAELPVYMKKK — 23 VERVARALPDISTIP — GAKPALKAR — AAS-LTP — KLREGDYAQAVADLGATI CTARAPTG — VVPLNDCGHARRAGTAAELPKRTEK — 23 VERVISRYLKIDCHYK — SGTARRRIQQA — ADD—ALD — QENERGHNQ ALMDLGATI CTARAPTG — VVPLNDCGHARRAGTAAELPKRTEK — 23 VERVISRIPTIO — — SGRARRIQQA — ADD—ALD — QENERGHNQ ALMDLGATI CTARAPTG — VVPLHDI CLANISGTESDFPKRTFR — 22 VERVISHEQUITO — — SERFILEQI —— AAG-LTP — SKREGDYAQAIMDLGSLVCTPRRPK N — VVPLHDI CLANISGTESDFPKRTFR — 23 TARTYARLLALRSDLH — SGEGRRQUKSL — AER-TVP — FORRGEFNQALIDLGATV GOV-TPRQ — ECPVRGSCRSLELGEVERIPARASR — 23 VERVITELRAGTOTLP — AAKPOVKA — VAA LVP — SERFGDYAQAMMDLGSLVCTRRPFSCI — LEPLQAFCARGAAAQESFPKASK — 24 VERVUSRIFQITOPIP — LISRTINQI — AAG-LTP — SERFGDYAQAMMDLGSLVCTRRPFSCI — LEPLQAFCARGAAAQESFPKASK — 24 VERVUSRIFQITOPIP — LISRTINQI — AAG-LTP — SERFGDYAQAMMDLGSLVCTRRPFSCI — LEPLOAFCARGAAAQESFPKISK — 25 VERVISRIAVAVEAPLP — SGRPEIRIL — TQA-LVP — DPRGGDFAQAMMDLGSLVCTRRPFSCI — LEPHMRPCRARSLCTGESFPFKIKV — 25 VERVMARMINHTSLP — SAKPELLAC — AAA-LTP — DPRGGDFAQAMMDLGSLTCTRKSPAG — VCFMSFACLARINGTAAVLPKKTFK — 23 VERVMARMINHTSLP — SAKPELLAC — AAA-LTP — DLRAGDYAQAMMDLGATI CTRKSPG — VCFMSFACLARINGTAAVLPKKTFK — 23 VERVMARLINHTSLP — YAKKRULST — LIR-WLD — SERFGDPNQALMELGSTVCLPKNPKCE — NCFLKLSCGGTLSCSSPSVPSFKK — 22 VERVITRYFGIFKPLP — EARPIIKDCAAK — LAP-KTT — RGRPGDYAQAMMDLGATI CTRKSPG — LCPMSCCAVALISCTAAELPKKTFK — 23 VERVMARLINNITSLP — SAKRELTAH — AAA-LTP — VURAGDYAQAMMDLGATI CTRKSPG — LCPMSCCAVALISCTAAELPKTFK — 23 VERVMARLINNITSLP — SAKRELTAH — AAA-LTP — VURAGDYAQAMMDLGATI CTRKSPG — LCPMSCCAVALISCTAAELPKTFK — 23 VERVMARLINNITSPL — SAKRELTAH — AAA-LTP — VURAGDYAQAMMDLGATI CTRKSPG — LCPCTEVCAALPEGDAANLPKRPK — 23 VERVMARLINNITSPL — SAKRELTAH — AAA-LTP — VURAGDYAQAMMDLGATI CTRKSPG — LCPCTEVCAALPEGDAANLPKRPK — 24 VERVUSRFFGVGGWS — SEKVSKEUMDL — SAK-SLP — VUNRGGYAQAMMDLGATI CTRKSPG — LCPCTEVCAALPEGDAANLPKRPK — 22 VERVJARFKIEGKLE —	1 2 3 3 1 3 0 2 5 5 5 3 6 1 0 2 5 8 8 3 1 4 1 2 6 1 2 6 1 6 1 2 6 1 2 6 1 2 6 1 2 6 1 2 6 1 2 6 1 2 6 1 2 6 1 2 6 1 2 6 1 2 6 1 2 6 1 2 1 2
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00003652391_2 c_00000031207_6 c_0000003107_148_4 c_000001092848_3 c_00001197282_1 c_00001197282_1 c_00001197282_1 c_00000197282_1 c_000002106166_4 c_000002106166_4 c_000003872363_4 c_000004820107_1 c_000003872363_4 c_000004820107_1 c_000005774797_1 c_00005867021_3 c_000004551008_5 c_000005511148_4 c_00000577378_2 c_00000598175_2 c_00000754627_3 c_00000598175_2 c_00000959887_2 c_000000891118_1 c_000000899887_2 c_0000008917552_2	147 150 139 151 148 161 108 170 153 141 151 149 156 140 153 144 139 127 150 147 138 142 161	VERVIARCXAYSGRPG — KKEVENKUNSL — SEQ-VTP — AVGVERFN AMMDLGAML TESKPKES — LEPLONG TAAANNSMALYPCKKPK — 22 VERVUSRIJLUTDDIA — KESTERREPGI — VPE IMA — YENGGAPRALILEGALV TERPESCL — LEPVOAYCOAPEGVAELPUVMKKK — 23 VERVMARLFDISTPLP — GAKPALKAR — AAS-LTP — KLRPGDYAQAVMDLGATI TARAPT G — VC PINDC CHARRAGTAAELPKRTPK — 23 VERVUSRYLKIDGNPK — SGTARKRIQQA — ADD-ALD — OENBGGHNQALMDLGRSI CTRRSPCQ — REPLASS CGARASGEPTRMPTRQK — 22 VERVVSRIPGITQPIP — LSRPTIRQL — AAG-LTP — SKRRGDYAQAMMDLGATI CTRRSPCQ — REPLASS CGARASGEPTRMPTRQK — 22 VERVVSRIPGITQPIP — SGREGROUNSL — AER-IVP — RORPGEFNQALIDLGATV GGV-TPRGQ — EEPVRGS CSIELGEVERI PARASR — 23 VERVITELRAGIGTLPP — AAAKPOVKA — VAA-LVP — BERGGDYAQAMMDLGATV GGV-TPRGQ — EEPVRGS CSIELGEVERI PARASR — 23 VERVITELRAGIGTLPP — SARFOLVAKA — VAA-LVP — SARRGDYAQAMMDLGATV GGV-TPRGPS — LEPLOAPGCARGAAAQESFPKMSK — 24 VERVUSRIFOITQPIP — LSRPTIRQL — AAG-LTP — SKRRGDYAQAMMDLGSLV CTRRPRSCI — LEPLOAPGCARGAAAQESFPKMSK — 24 VERVUSRIFOITQPIP — SGRPEIRRL — TOA-LVP — DPRGGPAQAMMDLGSLV CTRRPRSCI — LEPHARDE CARRAGAAQESFPKMSK — 25 IERVMARMIDIHSPLP — SAKPELLAC — AAA-LTP — DPRGGPAQAMMDLGSLV CTRRPRSC — VERSFACLARINGTAAVLPKKTFK — 23 VERVMARLHNIHTPLP — SAKPELLAC — AAA-LTP — DFRAGDYAQAWMDLGATI CTPKSPTG — IC PMSCACVALISGTAAELPKKTFK — 23 VERVMARLHNIHTPLP — AAKPELFSK — ATA-LTP — DIRAGGYAQAWMDLGATI CTPKSPTG — IC PMSCACVALISGTAAELPKKTFK — 22 VERVMARLHNIHTPLP — YMKKNVLST — LIR-WILD — SARRGDYAQAWMDLGATI CTPKSPTG — IC PKSCACVALISGTAAELPKKTFK — 23 VERVMARLHNIHTPLP — AAKPELFSK — ATA-LTP — OVRAGDYAQAWMDLGATI CTPTSPKG — IC PCTEYCAALPEGASSESSESYSPERM — 22 VERVMARLHNIHTSLP — PAAKPELTAH — AAA-LTP — VURRGDYAQAWMDLGATI CTPTSPKG — IC PCTEYCAALPEGASSESSESYSPERM — 22 VERVMARLHNIHTSLP — PAAKPELTAH — AAA-LTP — VURRGDYAQAWMDLGATI CTPTSPKG — IC PCTEYCAALPEGAAGAACESPERM — 23 VERVMARLHNIHTSLP — PAAKPELTAH — AAA-LTP — VURRGDYAQAWMDLGATI CTPTSPKG — IC PCTEYCAALPEGAACHLEPKKPKE — 23 VERVMARLHNIHTSLP — PAAKPELTAH — AAA-LTP — PURRGDYAQAWMDLGATI CTPTSPKG — IC PCTEYCAALPEGAACHLEPKKPK — 23 VERVMARLHNIHTSLP — PAAKPELTAH — AAT-LTP — EERGGYAQAWMDLGATI CTRTSPEG — I	1233130255361025883141267
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_00000031207_6 c_00000031207_6 c_00000013207_6 c_000001092846_3 c_000001151029_1 c_00000197282_1 c_00000197282_1 c_000002078955_4 c_000002078955_4 c_000003607531_2 c_0000038072363_4 c_000003872363_4 c_000003872363_1 c_000005774797_1 c_000005867021_3 c_00000577378_2 c_000005751148_4 c_00000577378_2 c_00000598175_2 c_00000598175_2 c_00000598175_2 c_00000089111111_1 c_00000089175_2 c_00000089175_2 c_00000089175_2 c_00000089175_2 c_00000089175_2 c_00000089175_2 c_00000089175_2 c_000000899887_2 c_0000001345122_1	147 150 139 151 148 161 108 153 153 141 151 149 156 144 144 139 127 150 147 138	VERVIARCXAYSGMPG — KKEVENKUNSL — SEQ-VTP — AUGUERTNÄAMDLGATI CTRSKPKES — LEPLONG LAAANNSMALYPCKKEK — 22 VERVUSKIPLIVTDDIA — KESTERREFQI — VYEE IMA — YENGGAPRALILEGALVTPREPSCL — LEPVOAYCGAPEGVAEELPYKNKK — 23 VERVUARLEDISTPLP — GAKPALKAR — AAS-LTP — KLRPGDYAQAVMDLGATI CTARAPTG — VVPLNDCGUARRAGTAAELPKRTEK — 23 VERVUSKIPQITOPIP — GAKPALKAR — AAS-LTP — SKRPGDYAQAVMDLGATI CTARAPTG — VVPLNDCGUARRAGTAAELPKRTEK — 23 VERVUSKIPQITOPIP — GAKPALKAR — AAG-LTP — SKRPGDYAQAMDLGATI CTARAPTG — VVPLHDI LLANISGTPSDFPKRTFR — 23 TARTYARLLAURSDLH — SGEGRRQUNSL — AER-TVP — HORRGEFNQALIDLGATV CGV-TPRPSC — ECPVORSGESLELGEVERIPARASR — 23 VERVITERLAGIGTPLP — AAAKPOVKA — VAA-LVP — BERGGFNQALIDLGATV CGV-TPRPSC — ECPVORSGESLELGEVERIPARASR — 23 VERVITERLAGIGTPLP — SARPGLWAL — AAG-LTP — SKRRGDYAQAMDLGSLV CTRRPPSC I — LDPLOAFCARGAAAQESPYKASK — 24 VERVUSKIFQITOPIP — LSRPTLIQU — AAG-LTP — SKRRGDYAQAMDLGSLV CTRRPPSC I — LDPLOAFCARGAAAQESPYKASK — 24 VERVUSKIFQITOPIP — SKRPEIRL — TOA-LVP — DERRGGFNQALMOLGATI CTRRPPSC I — LCPVARPCARRAGAAQESPYKISK — 25 VERVMARMINHTSPLP — SKRPEIRL — TOA-LVP — DERRGGPAQAMDLGATI CTRKSPAGA — LCPVARPCARRAGAACCESPYKIKV — 25 VERVMARMINHTSPLP — SAKPELLAC — AAA-LTP — DERRGGYAQAVMDLGATI CTRKSPAGA — LCPVARPCARRAGAACACESPYKIKV — 23 VERVMARMINHTSPLP — AAKPELFSK — ATA - LTP — DERRGGYAQAVMDLGATI CTRKSPAG — VCPMSPG CALISTATAVLPKKTPK — 23 VERVMARLINHTSPLP — YAKKRUST — LIR-WLD — SRRPGDPNQALMELGSTV CLEKNPKGE — NCPLULSCGGTLSGSDESYBEPKE — 22 VERVITRVFGIFKDLP — PARPELTAM — AAA-LTP — UDRAGGYAQAVMDLGATI CTRKSPCG — ICPVSCCAVALISTATABLFKTTK — 23 VERVMARLINNITSPLP — AAKPELTAM — AAA-LTP — UDRAGGYAQAVMDLGATI CTRKSPCG — ICPVSCCAVALISTATABLFKTTK — 23 VERVMARLINNITSPLP — SAKPELTAM — AAA-LTP — UDRAGGYAQAVMDLGATI CTRKSPCG — ICPVSCCAVALISTATAVLPKKTEK — 23 VERVMARLINNITSPLP — SAKRELTAM — AAA-LTP — UDRAGGYAQAVMDLGATI CTRKSPCG — ICPVSCCAVALISTATAVLPKYTER — 24 VERVITRVFGIFKDLP — DAKRGDYAQAVMDLGATI CTRKSPCG — ICPVSCCAVALISTATAVLPKYTER — 24 VERVITRVFGIFKDLP — SAKNELTAM — AAA-LTP — UDRAGGYAQAVMDLGATI CTRKSPCG — ICPVSCCAVALISTARGGIAESLPIKKK — 24 VERVITRVFGVYNI	12331302553610258831412671
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_00000031207_6 c_00000031207_6 c_0000001207_6 c_00000192848_3 c_000001151029_1 c_00001197282_1 c_00001803648_25 c_000002106160_4 c_000003803648_25 c_000002803648_25 c_000002803648_25 c_00000380367531_2 c_000003872363_4 c_000003872363_4 c_000003872363_4 c_000004820107_1 c_000005774797_1 c_00000557021_3 c_000005571378_2 c_000005571378_2 c_00000571378_2 c_00000571378_2 c_0000011118_4 c_0000089175_2 c_0000011118_1 c_0000089175_2 c_0000011118_1 c_0000089187_2 c_0000011145122_1 c_0000011515736_6 c_0000011515736_6 c_0000011515736_6 c_00000011515736_6	147 150 139 151 148 170 153 153 153 141 156 153 144 139 127 138 144 139 127 138 141 141 139 127 138 141 141 139 141 141 141 148 148 148 149 149 149 149 149 149 149 149 149 149	VERVIARCYAYSGMPG — KKEVENKUNSI. — SEQ-VTP — AVGUERTNÄAMDIGAMI CTRSKPKES — LEPLONG TAAANNSMALYPCKKEK — 22 VERVIARCHIVTDDIA — KESTERREPGI — VYEE IMA — YENGGAPRALILEGAMY TERPESCL — LEPVOAY CAPAECVABELPYKNKK — 23 VERVUARLEDISTDIP — GAKPALKAR — AAS-LTP — KLREGDYAQAVADIGATI CTARAPTG — VVPLNDCGUARRAGTAABLPKRTEK — 23 VERVUSKIPQITOPIP — GAKPALKAR — AAS-LTP — SKREGDYAQAVADIGATI CTARAPTG — VVPLNDCGUARRAGTAABLPKRTEK — 23 VERVISKIPQITOPIP — JERPTLRQL — AAG-LTP — SKREGDYAQAVADIGATI CTARAPTG — VVPLHDI LLANISGTPSDFPKRTFR — 23 TARTYARLLAURSDIH — SGEGRRQUNSI. — AER-TVP — HORRGEFNQALIDIGATV CGV-TPRPS — VVPLHDI LLANISGTPSDFPKRTFR — 23 TARTYARLLAURSDIH — SGEGRRQUNSI. — AER-TVP — HORRGEFNQALIDIGATV CGV-TPRPS — VVPLHDI LLANISGTPSDFPKRTFR — 23 VERVITRIKALGTPLP — AAAKPQVKA. — VAA-LVP — SERRGDYAQAMDLGSLV-TPRPKS — VVPLHDI LLANISGTPSDFPKRTFR — 24 VERVUSKIFQITOPIP — LSRPTLRQL — AAG-LTP — SKRRGDYAQAMDLGSLV-TPRPKS — VVPHHDI LANISGTPSDFPKRTFR — 19 VERVUSKIFQITOPIP — SKRPEIRL — TOA-LVP — DDRRGDFAQAMDLGSLV-TPRPKR M — VVPHHDI LANISGTPSDFPKRTFR — 19 VERVUSKIFQITOPIP — SKRPEIRL — TOA-LVP — DDRRGDFAQAMDLGSLV-TPRPKR M — VVPHHDI LANISGTPSDFPKRTFR — 19 VERVMARMENHIHTPLP — SAKPELLAC — AAA-LTP — DPRRGDFAQAMDLGATI CTRKSASG — VVPHSFACLARINGTAAVLPKKTFK — 23 VERVMARMINHTSLP — AAKPELFSK — AAT-LTP — DLRAGDYAQAMDLGATI CTRKSASG — VVPHSFACLARINGTAAVLPKKTFK — 23 VERVMARLINLIERTP — YMKKRUST — LIR-WLD — SRRFGDPNQALMELGSTV CLRKPKEE — NCPLKLSCGGTLSGSPESYPEPKE — 22 VERVITRUSGIFFK — PARPLIAC — AAA-LTP — VDRAGDYAQAMDLGATI CTRKSPTG — CPHSCC VALISGTAALBFKKTFK — 23 VERVMARLFNVITPLP — AAKPELFSK — AAT-LTP — VDRAGDYAQAMDLGATI CTRKSPTG — CPHSCC VALISGTAALBFKTFK — 23 VERVMARLFNVITPLP — AAKPELFSK — AAA-LTP — VDRAGDYAQAMDLGATI CTRKSPTG — CPHSCC VALISGTAALBFKTFK — 22 VERVITRUSGIFFK — PARPLIAC — AAA-LTP — VDRAGDYAQAMDLGATI CTRKSPTG — CPHSCC VALISGTAALBFKTFK — 22 VERVITRUSGIFFK — SAKNEKEMDI — SAKNEKYS GURAGAMDLGATI CTRKSPTG — CPHSCC VALISGTAALBFKTFK — 22 VERVITRUSGIFFK — VARAGAMADLGATI CTRKSPTG — CPHSCC VALISGLARHELPVKAQ — 22 VERVITRUSGIFFK — SEKNEKEMDI — SAKNES — DUNNOVYTG GIMLGATI	12333130255361025883141267192
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_0000003552391_2 c_00000031207_6 c_000001007148_4 c_000001092848_3 c_000001197282_1 c_0000197282_1 c_00000197282_1 c_000001803648_25 c_000002106160_4 c_00000387531_2 c_00000387531_2 c_000004820107_1 c_00000587021_3 c_000004820107_1 c_00000587021_3 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000155736_6 c_000001515736_6 c_00000155736_6 c_00000155736_6 c_000001535736_6 c_000001535736_6 c_000001535736_6 c_000001535736_6 c_000001535736_6 c_000001532576_6	147 150 151 148 161 108 170 153 141 151 140 154 144 144 144 144 147 150 147 151 147 151 147 151 147 151 147 151 148 149 151 151 151 151 151 151 151 151 151 15	VERVIARCXAYSGRPG — KKEVENKUNSL — SEQ-VTP — AVGVERFN AMMOLGATI CTRSKPKES — LEPLONG TAAANNSMALYPCKKPK — 22 VERVUSRISHIVTDDIA — KESTERREPGI — VTE IMA — YENGGAPRALILEGAMY TERPESCL — LEPVQAYCAPEGVAELPYKMKK — 23 VERVMARLFDISTPLP — GAKPALKAR — AAS LTP — KLRPGDYAQAVMDLGATI CTARAPT G — VC PLNDC CHARRAGTAAELPKRTPK — 23 VERVUSRYLKIDGNPK — SGTARRRIQQA — ADD—ALD — DENEGHNQALMDLGRSI CTRSPPC Q — REPLASG CARASGEPTKMPTRQK — 22 VERVVSRIPGITQFIP — LISRTIRQL — AAG LTP — SKRRGDYAQAMMDLGATI CTARAPT G — VC PLNDC CHARRAGTAAELPKRTPK — 23 TARTYARLLALRSDLH — SGEGRRQUNSL — AER TUP — FORRGEPNQALIDLGATV GV — TRRG Q — ECPVRGS CSIELGEVERI PARASR — 23 TARTYARLLALRSDLH — SGEGRRQUNSL — AER TUP — BERRGEPNQALIDLGATV GV — TRRG Q — ECPVRGS CSIELGEVERI PARASR — 24 VERVVSRIPGITQPIP — LISRTIRQL — AAG LTP — SERRGDYAQAMMDLGST V CFRPRPSC I — LEPLQAFC AARGAAAQESFYKASK — 24 VERVVSRIPGITQPIP — LISRTIRQL — AAG LTP — SERRGDYAQAMMDLGST V CFRPRPSC I — LEPLQAFC AARGAAAQESFYKASK — 24 VERVVSRIPGITQPIP — LISRTIRQL — AAG LTP — SERRGDYAQAMMDLGST V CFRPRPSC I — LEPLOAFC AARGAAAQESFYKASK — 25 VERVMARMD HSSLP — SGRPERIRL — TOA LVP — DPRGDFAQAMMDLGST V CFRPRPSC I — LEPHMPEC RARSA LOTGESF PERKITV — 25 VERVMARMD HSSLP — SAKPELLAC — AAA - LTP — DPRGDFAQAMMDLGAT CTRKSAS G — VC PRISFACLARINGTAAVLPKKTFK — 23 VERVMARMD HSSLP — SAKPELLAC — AAA - LTP — DPRGDFAQAMMDLGAT CTRKSAS G — VC PRISFACLARINGTAAVLPKKTFK — 23 VERVMARLINITTP — AAKPELFSK — ATA — LTP — DRRGDYAQAVMDLGAT CTRKSAS G — VC PRISFACLARINGTAAVLPKKTFK — 22 VERVMARLVNITTP — EARPLIKOCAAK — ATA — LTP — VURRAGDYAQAVMDLGAT CTRKSPTC DENEKCE — NC PLKLS GGTLSGSPESY FSFKK — 22 VERVMARLVNITTP — SAKRGLIAG — AAA — LTP — VURRAGDYAQAVMDLGAT CTRTSPRC — NC PLKLS GGTLSGSPESY FSFKK — 22 VERVMARLVNITTP — SAKRGLIAG — AAA — LTP — VURRAGDYAQAVMDLGAT CTRTSPRC — NC PLKLS GGTLSGSPESY FSFKK — 22 VERVMARLVNITTP — SAKRGLIAG — LAP — TO	12331302553610258831412671929
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_000003652391_2 c_00000031207_6 c_00000031207_6 c_0000001207_64 c_000001092848_3 c_000001151029_1 c_00000197282_1 c_00000197282_1 c_000001803648_25 c_000002106160_4 c_000003607531_2 c_000003872363_4 c_000003872363_4 c_000003872363_4 c_00000587073797_1 c_000058707085 c_0000058707378_2 c_00000585708_5 c_00000585708_5 c_00000585708_5 c_00000585708_5 c_000001587378_2 c_0000011118_1 c_0000089867_2 c_000001176522_24 c_000001157376_6 c_00000182361_6 c_00000182364_6 c_00000182364_6 c_000000182364_6 c_00000003994_5	147 150 139 151 148 170 153 153 153 141 156 153 144 139 127 138 144 139 127 138 141 141 139 127 138 141 141 139 141 141 141 148 148 148 149 149 149 149 149 149 149 149 149 149	VERVIARCYAYSGRPG — KKEVENKURSL — SEQ-VTP — AVGUERTNÄAMBLIGAMU TESKPKES — LEPLONG TAAANNSMALYPCKYEK — 22 VERVISKPLIVTDDIA — KPSTERREPGI — VYEE IMA — YENGGAPRALILEGAMU TERPESCL — LEPVOAY CAPAECVAEELPYKNKK — 23 VERVUARLED ISTPLP — GAKPALKAR — AAS-LTP — KLREGDYAQAVADLGATI CTARAPTG — VVPLNDCGUARRAGTAAELPKRTEK — 23 VERVUSKIPQITGPIP — SGRARKIQA — ADD — ALD — GENEGHNALINGRSI CTPREPPDC — REPLASG GARASGEPTRWFTRRGK — 22 VERVUSKIPQITGPIP — SGRERGUMSL — AER-TVP — SKREGDYAQAIMDLGSIUCTPREPRC — VVPLHDI LLANISGTPSDFPKRTFR — 23 TARTYARLLAURSDLH — SGEGRRGUMSL — AER-TVP — HERRGEPAQAIMDLGSIUCTPREPRC — VVPLHDI LLANISGTPSDFPKRTFR — 23 TARTYARLLAURSDLH — SGEGRRGUMSL — AER-TVP — HERRGEPAQAIMDLGSIUCTPREPRC — VVPLHDI LLANISGTPSDFPKRTFR — 23 VERVITRIKAHIGTPLP — AAAKPQVKRA — VVAA — VVPH— SERREGDYAQAMMDLGSIUCTPREPSCI — LEPLQAPCARAGAAQESFPVASK — 24 VERVUSKIPQITQPIP — LSRPTLRQL — AAG-LTP — SKRRGDYAQAMMDLGSIUCTPREPSCI — LEPLQAPCARAGAAQESFPVASK — 24 VERVUSKIPQITQPIP — LSRPTLRQL — AAG-LTP — SRRRGDYAQAMMDLGSIUCTPREPSCI — LEPLQAPCARAGAAQESFPVASK — 25 VERVIANDRAUVEAPLP — SGREERELL — TOA LVP — PDREGDFAQAMMDLGSIUCTPREPSCI — LEPVAMPCARASLCTGESFPEKIKV — 25 VERVMARMBHISPLP — SAKPELLAC — AAA-LTP — DPREGDFAQAMMDLGSIUCTPREPACA — LEPWARPCARSLCTGESFPEKIKV — 25 VERVMARMBHISPLP — SAKPELLAC — AAA-LTP — DERAGDYAQAMMDLGATI CTPKSSPTG — LEPWASCIALISGTAAELPKKTPK — 23 VERVMARLINLIERTP — YAKKRUST — LIR-WLD — SRRRGDPNQALMELGSTU CLEKNERGE — NOPILUS CGGTLSGSPESYPEFKIK — 22 VERVITRUSGIFFK — PARPLICACA — LAP-KT — RORGEGIYAQAMMDLGATI CTPKSPTG — LEPWESYC LANLOGATHOUR PKTPK — 23 VERVMARLINLISTEPL — DAKAGDYAQAMADLGATI CTPKSPTG — LEPPENGU CLAULSGTAAELPKKTPK — 23 VERVMARLINNIHSPLP — AAKPELTAH — AAA-LTP — VDRAGDYAQAMMDLGATI CTPKSPTG — LEPPENGU CLAULSGTAAELPKKTPK — 23 VERVMARLINNIHSPLP — AAKPELTAH — AAA-LTP — VDRAGDYAQAMMDLGATI CTPKSPTG — LEPPENGU CLAULSGTAALPKYMPAQ — 22 VERVITRUSGIFFK — SEKNIKEUL — SASTABL — AET-LAH — PERAGGIYAQAMMDLGATI CTPKSPTG — LEPPENGU CLAULSGTAALPKYMPAQ — 22 VERVLASHFYNIDDAIN — RESARLARI — AET-LAH — PERAGGIYAQAMMDLGATI CTPKSPTG — LEPPENGU CLAULSGLENDITIVRAP	123313025536102588314126719293
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_0000003552391_2 c_00000031207_6 c_000001007148_4 c_000001092848_3 c_000001197282_1 c_0000197282_1 c_00000197282_1 c_000001803648_25 c_000002106160_4 c_00000387531_2 c_00000387531_2 c_000004820107_1 c_00000587021_3 c_000004820107_1 c_00000587021_3 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000557338_2 c_00000155736_6 c_000001515736_6 c_00000155736_6 c_00000155736_6 c_000001535736_6 c_000001535736_6 c_000001535736_6 c_000001535736_6 c_000001535736_6 c_000001532576_6	147 150 139 151 148 170 153 153 153 141 149 156 140 147 138 141 117 138 141 138 141 138 141 138	VERVIARCYAVSGRPG—KEWENKUNSL—SEQ-VTP — AUGUERTNÄAMBLIGAMI CTRSKPKES — LEPLONG TAAANNSMALYPCKEKEK — 22 VERVIARCHIVTDDIA —KESTERREFQI — VERE IMA —YENGGAPRALILEGALITERPESCL—LEPVOAYCOAPEGVAEELPKYRKK — 23 VERVMARLEDISTELP — GAKPALKAR — AAS-LTP — KLREGDYAQAVMOLGATI CTARAPTG — VCPLINGC HARRACTAABLPKRTEK — 23 VERVISKILGOMPK — SGTARKRIQA — ADD —ALD — QENPGDHNO ALMOLGATI CTARAPTG — VCPLINGC HARRACTAABLPKRTEK — 23 VERVISKIPOTTOPIP — LSRFTLEQI — AAG-LTP — SKREGDYAQAVMOLGATI CTARAPTG — VCPLING GARRAGEPTREFTER — 23 TARYARLLALRSDLH — SGEGREQUESL — AER-LVP — HORRGEFNQALIDLGATV CGV-TPREFK — VCPLING CHARRACTAABLPKRTEK — 23 VERVITRIKARIGTPLP — AAKPOVKRA — VAA-LVP — HORRGEFNQALIDLGATV CGV-TPREFK — VCPLING LAMISCTSESPFKRTER — 23 VERVITRIKARIGTPLP — LSRFTLEQI — AAG-LTP — SKREGDYAQAVMOLGATI CTRREFSCI — LCPLOAPCARAGAAQESPFVASK — 24 VERVUSRIFQITOPIP — LSRFTLEQI — AAG-LTP — SKREGDYAQAMMOLGATI CTRREFSCI — LCPLOAPCARAGAAQESPFVASK — 24 VERVUSRIFQITOPIP — LSRFTLEQI — AAG-LTP — DERRGDFAQAMMOLGATI CTRREFSCI — LCPHAMPC PARASACAQESPFVASK — 25 VERVIARAVEAPLP — SGREELLAC — AAA-LTP — DERRGDFAQAMMOLGATI CTRESSCG — VCPMSFACLARINGTAAVLPKKTFK — 25 VERVMARMIHITELP — SAKPELLAC — AAA-LTP — DERRGDFAQAVMOLGATI CTRESSTG — VCPMSFACLARINGTAAVLPKKTFK — 23 VERVMARLHIHTELP — SAKPELLAC — AAA-LTP — DERRGDFAQAVMOLGATI CTRESSTG — VCPMSFACLARINGTAAVLPKKTFK — 23 VERVMARLHIHTELP — YAKKRULST — LIR-WLD — SERFGDFNQALMELGSTV CLPKHFKGE — NCPLIKLS CGGTLSGSSESYBSPKEK — 22 VERVITRIVEGIFFKLP — PARKPELFSK — AAT-LTP — DERRGDFAQAVMOLGATI CTRESSTG — VCPMSFACLARINGTAAVLPKKTFK — 23 VERVMARLHNITTELP — AAKPELFAH — AAA-LTP — VURAGDYAQAVMOLGATI CTRESSTG — VCPMSFACLARINGTAAVLPKKTFK — 23 VERVMARLHNITTELP — AAKPELFAH — AAA-LTP — VURAGDYAQAVMOLGATI CTRESSTG — VCPMSFACLARINGTAAVLPKKTFK — 23 VERVMARLHNITTELP — DAKAGDYAQAVADLGATI CTRESSTG — VCPMSFACLARINGTAAVLPKKTFK — 24 VERVITRIVEGIFFK — VARMACHA — AAA-LTP — VURAGDYAQAVMOLGATI CTRESSTG — VCPMSFACLARINGTAALPECKFKTFK — 23 VERVMARLHNITTELP — DAKAGDYAQAVADLGATI CTRESSTG — VCPMSFACLARINGTAACLPKKTFK — 24 VERVLARISPEGIFFK — VARMACHA — AAA-LTP — DERRGD	1233130255361025883141267192935
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_000000355291_2 c_00000031207_6 c_00000031207_6 c_000001097148_4 c_00000109248_3 c_00001197282_1 c_0000197197282_1 c_000001973848_2 c_000002078955_4 c_00002106160_4 c_00003607531_2 c_000003607531_2 c_0000048201077_1 c_0000057737797_1 c_00005867021_3 c_00004546210_2 c_00005511148_4 c_000005737378_2 c_00000551118_1 c_000005737378_2 c_000001754627_3 c_00000175522_24 c_000001754627_3 c_0000001754627_3 c_000001754627_3 c_0000001754627_3 c_000001754627_3 c_00000	147 150 139 151 148 161 108 153 153 151 151 149 127 138 142 143 144 139 127 138 142 131 131 131 131 131 131 131 131 131 13	VERVILARCYAYSGMPG — KKEVENKUMSL — SEQ-VTP — AUGUERTNÄAMBLIGAMU TESKPKES — LE PLONG LAAANNSMALYPCKKEK — 22 VERVUSARLEUTUDDIA — KESTERREFQI — VYEE IMA — YENGGAPRALILEGAMU TERPESCL — LE PVQAY CAPAEGVAEEL PVKMKK — 23 VERVMARLEDISTPLP — GAKPALKAR — AAS LTP — KLRPGDYAQAVADLGATI CTARAPTG — VCPLNDCGHARRAGTAAELPKRTEK — 23 VERVUSRIPKINGHEM — SGTARRRIQQA — ADD—ALD — QENEGHNO ALMDLGRSI CTPREPPD Q — REPLAGG GARRAGEPTREPTREFRE — 22 VERVUSRIPQITOPIP — LISRTIRQL — AAG—LTP — SKRRGDYAQAIMDLGSILVCTPREPREN — VCPLHDIC LANISGTESDPFRETTRE — 23 TARTYARLLALRSDLH — SGEGRRQUMSL — AER TVP — RERGGFAQAIMDLGSILVCTPREPREN — VCPLHDIC LANISGTESDPFRETTRE — 23 VERVITELRALGTELP — AAAROVKA — VAA—LVP — AERRGGPAQAMDLGATI CTREPPSCI — LEPLQAFCARGAAAQESPYMSK — 24 VERVUSRIPQITOPIP — LISRTIRQL — AAG—LTP — SERRGDYAQAMMDLGSILVCTPREPRESCI — LEPLQAFCARGAAAQESPYMSK — 24 VERVUSRIPQITOPIP — LISRTIRQL — AAG—LTP — SERRGDYAQAMMDLGSILVCTPREPRESCI — LEPLQAFCARGAAAQESPYMSK — 25 VERVUSRIPAVEADLP — SGREERIL — TQA—LVP — DERRGGPAQAMMDLGSILVCTPREPREN — VCPHHDIC LANISGTPSDFPRETTRE — 19 VERVUSRIPAVEADLP — SGREERIRL — TQA—LVP — DERRGGDPAQAMMDLGSILVCTPREPREN — VCPHHDIC LANISGTPSDFPRETTRE — 19 VERVMARMIDHESUP — SAKPELLAC — AAA—LTP — DERRGDYAQAMMDLGSILVCTPREPREN — VCPHHDIC LARISGLOTGESFPERKIKV — 25 VERVMARHINHTSUP — AAKEELESK — AAA—LTP — DERRGDYAQAMMDLGSILVCTPREPREN — VCPHHSURSKERSLOTGESFPERKIKV — 23 VERVMARLINHTSUP — AAKEELESK — AAA—LTP — DERRGDYAQAMMDLGSILVCTPREPREN — VCPHHSURSKERSKERS — VCPHSGFTG — VCPHSGFTG — VCPHSGFTG — VCPHSCRSCHARMSTAVERFER —	123313025536102588314126719293503
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECON c_000003652391_2 c_00000031207_6 c_00000031207_6 c_00000031207_6 c_000001007184_3 c_000001197282_1 c_00000197282_1 c_00000197282_1 c_00000278955_4 c_00000278955_4 c_000003872563_4 c_000003872563_4 c_000003872563_4 c_000008773797_1 c_00005774797_1 c_00005774797_1 c_00005573738_2 c_00000551148_4 c_000006958175_2 c_00000598175_2 c_000000598175_2 c_00000013118_1 c_0000099887_2 c_000001315122_1 c_000001515736_6 c_00001230122_1 c_000001582161_6 c_000001582161_6 c_000002523527_15 c_000002523527_15 c_000002523527_15 c_000002525527_15 c_000002525527_15 c_000002525151_0_2	147 150 151 148 161 108 153 153 153 153 151 151 151 151 153 144 139 127 150 147 131 138 142 161 131 138 141 141 153 154 154 155 155 156 157 157 157 157 157 157 157 157 157 157	VERVIARCYAYSGRPG — KKEVENKUNSI. — SEQ-VTP — AUGUERTNÄAMBLIGAMI TESSEPKES — LÉPLONG TAAANNSMALYPCKEKEK — 22 VERVISRILVITODIA — KESTERREFQI — VYEE IMA — YENGGAPRALILEGALITERRESCL — LÉPVOAY CAPREGVABELPYKINKK — 23 VERVUSRYLKIJGRIPK — GAKPALKAR — AAS-LTP — KLREGUYAQAVMOLGATI CTARAPTG — VVPLINDC HARRACTAAELPKRTEK — 23 VERVUSRYLKIJGRIPK — SGTARKRIQA — ADD — ALD — QENFODHNO ALMDLGRSI CTPERSPDE Q — REPLASG GARRASGEPTREPTERQK — 22 VERVUSRYLKIJGRIPK — SGRERGUNSI. — ARE-TVP — KORFGEPYAQATMOLGRSI CTPERSPDE Q — REPLASG GARRASGEPTREPTERQK — 22 VERVUSRIPQITOPIP — LISRFILRQL — AAG-LTP — KORFGEPYAQATMOLGRSI CTPERSPDE Q — REPLASG GARRASGEPTREPTER — 23 YARFYARLLALRSDLH — SGEGRRQUNSI. — ARE-TVP — KORFGEPYAQATMOLGRSI CTPERSPS I — LEPLOAPCARAGAAQESEPYKASK — 24 VERVUSRIPQITOPIP — LISRFILRQL — AAG-LTP — SKRRGDYAQAMMOLGATI CTPERPS I — LEPLOAPCARAGAAQESEPYKASK — 24 VERVUSRIPQITOPIP — LISRFILRQL — AAG-LTP — SKRRGDYAQAMMOLGATI CTPERPS I — LEPLOAPCARAGAAQESEPYKASK — 24 VERVUSRIPQITOPIP — LISRFILRQL — AAG-LTP — DERRGGPAQAMMOLGATI CTPKRSPS I — LEPHOAPCA	1233130255361025883141267192935036
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_000000355291_2 c_00000031207_6 c_00000031207_6 c_000001097148_4 c_00000109248_3 c_00001197282_1 c_0000197197282_1 c_000001973848_2 c_000002078955_4 c_00002106160_4 c_00003607531_2 c_000003607531_2 c_0000048201077_1 c_0000057737797_1 c_00005867021_3 c_00004546210_2 c_00005511148_4 c_000005737378_2 c_00000551118_1 c_000005737378_2 c_000001754627_3 c_00000175522_24 c_000001754627_3 c_0000001754627_3 c_000001754627_3 c_0000001754627_3 c_000001754627_3 c_00000	147 150 139 151 148 161 108 153 153 151 151 149 127 138 142 143 144 139 127 138 142 131 131 131 131 131 131 131 131 131 13	VKRULSRLYAYSOWPO	12331302553610258831412671929350361
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECON c_000003652391_2 c_00000031207_6 c_00000031207_6 c_0000001207_6 c_00000013207_6 c_00000192848_3 c_0000192848_3 c_0000192848_3 c_00000197282_1 c_000001803648_25 c_00000203648_25 c_00000203648_25 c_000002166160_4 c_000003807531_2 c_000003872363_4 c_000003872363_4 c_00000482010_1 c_000005774797_1 c_000005867021_3 c_000005571378_2 c_000005571378_2 c_00000571378_2 c_00000571378_2 c_00000181118_4 c_00000571378_2 c_00000181118_1 c_0000089175_2 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_00000175522_24 c_0000013515736_6 c_000001923643_29 c_00000223827_15 c_00000223827_15 c_00000223827_15 c_00000223827_15 c_00000223827_2 c_00000223827_15 c_00000223827_2 c_00000223827_15 c_00000223827_2 c_00000223827_2 c_00000223827_2 c_0000022361510_2 c_0000022361510_2 c_0000022361510_2 c_0000022361510_2 c_00000232467_3 c_00000324675_3	147 150 139 151 161 108 108 161 170 153 141 151 149 156 140 153 141 139 141 138 141 138 141 139 141 139 141 141 141 141 141 141 141 141 141 14	VKRULSKLINTOLIA KEPTKKREFGI VVE IMA YNDIGAFN BAMBLIGARI TRSKEFGS LE PLANG [AAANNSWALTPGKKEK 22] VKRVLSKLINTOLIA KEPTKKREFGI VVE IMA YNDIGAFN BALIELGALVETERFEGI VVE PLANG (ARKAGUAELPKREFG VVE PLANG CHARKACTARELPKREFG VVE PLANG CHARKACTARELPKREFG VVE PLANG CHARKACTARELPKREFG 23 VERVLSRIKILDONPK SCTRAKRIQA ADA -ALD GENEGONA ANDLIGASI CTERREPOQ VVE PLANG CHARKACTARELPKREFK 23 VERVUSRIFQITQCTP SERPTLRQL AAG-LPP SKREGOYA BALIMLIGASI CTERREPOQ VVE PLANG CHARKACTARELPKREFK 23 VERVUSRIFQITQCTP AAKPQVKKA VAA -LVP SKREGOYA BAMBLIGATIC TERRESCI LE PLQAF CHARGAGARAS CONTROLL ARE IVP RORGER BALILLGATUG V PED-Q EVENGS CRIBLEG VERT LARAS CONTROLL ARE IVP PROFIGER BALILLGATUG V PED-Q EVENGS CRIBLEG VERT LARAS CONTROLL AND STANDARD CONTROL	1233130255361025883141267192935036168
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_0000003552391_2 c_00000031207_6 c_00000031207_6 c_000001097148_4 c_000001992848_3 c_00001197148_2 1 c_00001971492_1 c_00001971492_1 c_000001803648_25 c_000002106160_4 c_00000387531_2 c_00000387531_2 c_000004872017_1 c_00000587731_2 c_000004820107_1 c_0000587021_3 c_00004820107_1 c_00000587021_3 c_00000587021_3 c_00000587021_3 c_00000587021_3 c_00000187021_3 c_000000187021_3 c_000000187021_3 c_000000187021_3 c_000000187021_3 c_000000187021_3 c_000000187021_3 c_000000187021_3 c_000000187021_3 c_00000187022_1 c_00000187022_1 c_00000187022_1 c_00000187022_1 c_00000187022_1 c_000002253527_1 c_000002261510_2 c_000002253527_1 c_000002261510_2 c_000002348034_1	147 150 151 151 161 161 170 153 141 151 151 151 153 144 139 127 150 147 151 111 111 111 111 111 111 111 111 11	VKRVLARCYAVSGWGG	12331302553610258831412671929350361684
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECON c_000003652391_2 c_00000031207_6 c_00000031207_6 c_0000001207_6 c_00000013207_6 c_00000192848_3 c_0000192848_3 c_0000192848_3 c_00000197282_1 c_000001803648_25 c_00000203648_25 c_00000203648_25 c_000002166160_4 c_000003807531_2 c_000003872363_4 c_000003872363_4 c_00000482010_1 c_000005774797_1 c_000005867021_3 c_000005571378_2 c_000005571378_2 c_00000571378_2 c_00000571378_2 c_00000181118_4 c_00000571378_2 c_00000181118_1 c_0000089175_2 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_00000175522_24 c_0000013515736_6 c_000001923643_29 c_00000223827_15 c_00000223827_15 c_00000223827_15 c_00000223827_15 c_00000223827_2 c_00000223827_15 c_00000223827_2 c_00000223827_15 c_00000223827_2 c_00000223827_2 c_00000223827_2 c_0000022361510_2 c_0000022361510_2 c_0000022361510_2 c_0000022361510_2 c_00000232467_3 c_00000324675_3	147 150 139 151 161 108 108 161 170 153 141 151 149 156 140 153 141 139 141 138 141 138 141 139 141 139 141 141 141 141 141 141 141 141 141 14	VERVILARCYAYSOWGG KREVENKLWSL SEQ-VTF ANGUERIN AMMOLGANIT GREKERS L. PLONG LARANNSHALTPGKERR 22 VERVINGRYLLTOTIAL RESTRIKERGG VRE MA YNRIGAINER LILGALV TPRESS L. PLONG CARRACKARE ANGUERING CONTROLL	123313025536102588314126719293503616849
sp_ P17802_MUTY_ECOL sp_ P83847_MUTY_ECOS c_000003652391_2 c_00000031207_6 c_00000031207_6 c_0000001207_64 c_000001092848_3 c_00000192848_3 c_00000192848_3 c_000001972821 c_000002078955_4 c_000002078955_4 c_000002078955_4 c_000003807531_2 c_00003872363_4 c_000003872363_4 c_000003872363_4 c_0000058707777_1 c_00005870707_1 c_00005870707_1 c_000005877378_2 c_00000585175_2 c_00000551148_4 c_00000551148_4 c_00000958175_2 c_00000958175_2 c_000001957378_2 c_000001957378_2 c_000001957378_2 c_000001957378_2 c_0000001957378_2 c_000000195736_6 c_000000195736_6 c_00000195736_6 c_00000195736_6 c_00000239945_1 c_000002238527_1 c_00000223857_1 c_00000223857_1 c_00000223857_1 c_000002238537_1 c_000002238537_1 c_000002324637_3 c_000003333364_1 c_000003333364_1 c_0000033766664_5_5	147 150 151 151 161 161 161 161 161 161 161 161	VKRVLARCYAVSGWFG — KERVENKLWSL — SEQ-VTP — AVGVERFNSAMMOLGANIT TRRESKYKS — L. PLONG (JAANNANSALYPGKKER — 22) VRRVLARCHIVTODIA — KEPSTRKREGGI — VVRE—IMA — YNRGAFNSALIF LAGAVY TRRESKY VRRVLARCHINGSKY — SGYARKIQOA — ADD—ADD—OQENGOMBALMOLGRI TOTRESKY VRRVLARCHINGSKY — SGYARKIQOA — ADD—ADD—OQENGOMBALMOLGRI TOTRESKY VRRVLARCHINGSKY — SGYARKIQOA — ADD—ADD—OQENGOMBALMOLGRI TOTRESKY VRRVLARCHINGSKY — SGRORGUNGANS — ARE TUP—— SKREGOVA ATMOLGSIV TORKKKN — VUPLEDI CLANISOTSDEPERTPR — 22 VERVUSRIFQITOPIP — LISRPIRGL — AAG-LTP — SKREGOVA ATMOLGSIV TORKKKN — VUPLEDI CLANISOTSDEPERTPR — 23 VERVITRILAIGSDL — SAKRQOVRRA — VAA-LVP — AREGODFA DAMMOLGATI CTPERRS II — L. PLOAR GARGAGESPUKARK — 24 VERVUSRIFQITOPIP — LISRPIRGL — AAG-LTP — SKREGOVA AMMOLGATI CTPERRS II — L. PLOAR GARGAGESPUKARK — 24 VERVUSRIFQITOPIP — GSRPEIRGL — AAG-LTP — SKREGOVA AMMOLGATI CTPERRS II — L. PLOAR GARGAANGESPUKARK — 24 VERVUSRIFQITOPIP — GSRPEIRGL — TOA LVP — DERFOD AAMMOLGATI CTPERRS II — L. PLOAR GARGAGESPUKARK — 25 IERVARANIHITELP — GSRPEIRGL — TOA LVP — DERFOD AAMMOLGATI CTPERRS II — L. PURGE GARGAGESPUKARK — 25 VERVARANIHITELP — SAKPELLAC — AAA LTP — DERFOD AAMMOLGATI CTPERAG G — VERSTALLAINGTAAVERKTEK — 23 VREVMARIHITELP — AARPELESK — ATA LTP — DERFOD AAMMOLGATI CTPERAG G — VERSTALLAINGTAAVERKTEK — 23 VREVNARAINHITELP — HARREVIST — LIR-WILD — RERFOD TOA AMMOLGATI CTPERAG G — VERSTALLAINGTAAVERKTEK — 22 VERVITRYCISTRELP — BARPELTAH — AAA LTP — VORAGOVA AVMOLGATI CTPERS G — IC WESC GATLSSESSESYESPERKE — 22 VERVITARVITRIPLP — AARPELTAH — AAA LTP — VORAGOVA AVMOLGATI CTPERS G — IC CTCT VAALECA CALLAINGTAAVERKTEK — 23 VERVARAINHITELP — DERSCHALAIN — REPEGOVA AMMOLGATI CTPERS G — IC CTCT VAALECA CALLAINGTAAVERKTEK — 23 VERVARAINHITELP — DERFOD AAM LGATI CTRES G — IC CTCT VAALECA CALLAINGTAAVERKTEK — 24 VERVARAINHITELP — DERFOD AAM LGATI CTRES G — IC CTCT VAALECA CALLAINGTAAVERKTEK — 22 VERVARAINHITHELP — AARPELTAH — AAA LTP — PERFOD AAM LGATI CTRES G — IC CTCT VAALECA CALLAINGTAA CALLAINGTA CALLAINGTAA CALLAINGTAA CALLAINGTAA CALLAINGTAA CALLAINGTAA CAL	12331302553610258831412671929350361684918
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECON c_00003652391_2 c_000003652391_2 c_00000031207_6 c_00000031207_6 c_00000107148_4 c_00000107148_4 c_000001792848_3 c_00001151029_1 c_00000179282_1 c_000002078955_4 c_00002106160_4 c_00003607531_2 c_000003607531_2 c_000004820107_1 c_000005773797_1 c_000005867021_3 c_00004546210_2 c_0000657037497_1 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000008967021_3 c_000008967021_3 c_000008967021_3 c_000001746621_0 c_000001746221_0 c_00000174622_0 c_000001746221_0 c_0000001746221_0 c_000001746221_0 c_00000174621_0 c_000001746221_0 c_00000174	147 150 139 151 161 170 153 153 153 141 153 144 144 144 144 145 161 115 161 171 181 181 181 181 181 181 181 181 18	VRRVILARCYAVSGWFG — KREVENKINSL — SEQ-VTP — AVGVERFNAMMOLGANI TRERSKYKS — LEPLONG (LAANNSWALTPCKKER — 22) VRRVLARCH/VIDDIA — KPSTRKREGI — VRE THAM — YNDRGAFNALICALLAU TRERSCY — LEPLONG CAPAGEAVERLEVMIKK — 23) VERWARRIFDISTELP — GARFALKAR — AAS-LTP — KIREGUYAAAWMOLGATI CTARAFT G — VEPLONG CHARRACTAAELEKRTER — 23 VERVISHIGORPK — SEGTARKIJOOA — ADD—ADD—OORDONG ALMOLGASI TRERSKYKS — VEPLONG CHARRACTAAELEKRTER — 22 VERVUSRIFDITOPLP — LISRPTIROL — AAG-LTP — SKREGOVAAAMMOLGASI TEPRER KN — VEPLOLG LANISCTSPSPEKETR — 23 VERVISHIJALISSUH — SEGGERGLUSME — AGE-TUP — SKREGOVAAAMMOLGASI TEPRER KN — VEPLOLG LANISCTSPSPEKETR — 23 VERVISHIJALISSUH — SAKPELLGU — AAG-LTP — SKREGOVAAAMMOLGASI TEPRER SI — LEPLOAF CAARGAAAGESFVKASK — 24 VERVVSRIFDITOPLP — LISRPTIROL — AAG-LTP — SKREGOVAAAMMOLGASI TEPRER SI — LEPLOAF CAARGAAAGESFVKASK — 24 VERVVSRIFDITOPLP — SAKPELLG — AAG-LTP — SKREGOVAAAMMOLGASI TEPRER SI — LEPLOAF CAARGAAAGESFVKASK — 24 VERVVSRIFDITOPLP — SAKPELLG — AAA-LTP — DEPREGOVAAAMMOLGASI TEPRER CHEVEL LANISCTSPSPEKER — 23 VERVMARIHISTELP — SAKPELLG — AAA-LTP — DEPREGOVAAAMMOLGASI TEPRER CHEVEL LERINGTAAULEKTER — 23 VERVMARIHISTELP — MIKKENSI — LIR — LID — SKREGOVAAAMMOLGASI TEPRES TI — LEPKSCA VALISCTAAELEKTTER — 22 VERVMARIHISTELP — MIKKENSI — LIR — LID — SKREGOVAAAMMOLGASI TEPRES TI — LEPKSCA VALISCTAAELEKTTER — 22 VERVMARIFYNITELP — DERAGINAAMMOLGASI TEPRES TI — LEPKSCA VALISCTAAELEKTTER — 23 VERVMARIFYNITELP — DERAGINAAMMOLGASI TEPRES TI — VERSCA VALISCTAAELEKTTER — 23 VERVMARIFYNITELP — DERAGINAAMMOLGASI TEPRES TI — VERSCA VALISCTAAELEKTTER — 22 VERVMARIFYNITELP — DERAGINAAMMOLGASI TEPRES TI — VERSCA VALISCTAAELEKTTER — 22 VERVMARIFYNITELP — DERAGINAAMMOLGASI TEPRES TI — VERSCA VALISCTAAELEKTER — 23 VERVMARIFYNITELP — DERAGINAAMMOLGASI TEPRES TI — VERSCA VALISCTAAELEKTTER — 22 VERVMARIFYNITELP — DERAGINAAMMOLGAS TEPRES TI — VERSCA VALISCTAAELEKTER — 23 VERVMARIFYNITELE — SKYNEKLUB — AAA - LIP — VERGGOVAAMMOLGASI TEPRES TI — VERGGOVAAMMOLGAS TEPRES TI — VERGGOVAAMMOLGAS TEPRES TI — VERGGOVAAMMOLGAS TEPRES TI — VERGGOVA	123313025536102588314126719293503616849185
sp_ P17802_MUTY_ECOL sp_ P83847 MUTY_ECON c	147 150 151 151 161 161 161 161 161 161 161 161	VRKYLARCYANSGRIGG—KKEVENKLINSL—SEQ-VTP——AUGUERINGAMMOLGAMIC TERREPG.—LEPYQAYGOARBGGVAELEPKRIKKS.—23 VERWARLEPISTELP—GAKRALKARA—AAS-LTP—KLREGOYAAAWMOLGATIC TARREPG.—VEPLINGCHARRAGTARALEPKRIPR.—23 VERWARLERISTELP—GAKRALKARA—AAS-LTP—KLREGOYAAAWMOLGATIC TARREPTOG—VEPLINGCHARRAGTARALEPKRIPR.—23 VERVISTEKILGORIPR—SCATRRINGQQA—ADD—ALD—GORDORINGALMOLGSILV TERREPTOG—VEPLINGCHARRAGTARALEPKRIPR.—22 VERVYSRIFGITQFIP—LERPTIRGL—AAG-LTP—SKREGOYAAAMMOLGATIC TERREPG.—VEPLINGCHARRAGTARALEPKRIPR.—23 VERVITRILRALGSILH—SGEGRRQUINGL—AAG-LTP—SKREGOYAAAMMOLGATIC TERREPG.—VEPLINGGAGAAAGAAGSEFYRKARSK—24 VERVYSRIFGITQFIP—LERPTIRGL—AAG-LTP—SKREGOYAAAMMOLGATIC TERREPG.—VEPHING ICANTISCTESDEFKRIPR.—23 VERVYSRIFGITQFIP—LERPTIRGL—AAG-LTP—SKREGOYAAAMMOLGATIC TERREPG.—VEPHING ICANTISCTESDEFKRIPR.—25 VERVYARSHANAVERALLP—GGREETRAL—TQA-LVP—PORRGOFAAAMMOLGATIC TERREPG.—VEPHING ICANTISCTESDEFKRIPR.—25 VERVYARSHANAWERALLP—SAKEELLAC—AAA-LTP—DERAGOYAAAWMOLGATIC TERREPG.—UEPHINGARGAAGAAGSEFYRKIKV—25 VERVYARSHANAWERALLP—SAKEELLAC—AAA-LTP—DERAGOYAAAWMOLGATIC TERREPG.—UEPHINGARGAAGAAGASEFYRKIKV—25 VERVYARSHANAWERALLP—SAKEELLAC—AAA-LTP—DERAGOYAAAWMOLGATIC TERREPG.—UEPHINGARGAAGAAGASEFFRENTY—25 VERVYARSHANAWERALLP—AAKEELFSK—TAA-LTP—DERAGOYAAAWMOLGATIC TERREPG.—UEPHINGARGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	1233130255361025883141267192935036168491854
sp_ P17802_MUTY_ECOL sp_ P83847 MUTY_ECON c	147 150 151 148 161 151 153 153 153 153 153 141 151 141 156 140 144 139 141 141 138 141 141 138 141 141 141 141 141 141 141 141 141 14	VREVISERITUTDIA - KEEVERKLIMSI SEQ. VTP - AUGUSERINGAMMOLGAMIC TERSPES - LÉPLQNOGI LAANNINALIFORKRYE - 22 VERWARLEDISTELP - GAKRALKAAR - AAS - LTP - KLREGOYA AVMOLGATI CTARRPS L. LEPVQAYO AFREGOYAELE PRETREM - 23 VERVARRILTORINE - SCARRICQOA - ADD - ALD - QENDERNO ALMOLGATI CTARRPDE Q. VERLINGCHARRAGTARELERETPE - 23 VERVISERILGORIFE - SCARRICQOA - ADD - ALD - QENDERNO ALMOLGSIVE TERRSPED - VERLINGCHARRAGTARELERETPE - 23 VERVISERILGORIFE - SCEGERGUMEN - AER - LTP - SKREGOYA ADMOLGATY COT-PREQ - GEPVERS CRELICEVER TERRARS - 23 VERVITELRALGEDLE - SCEGERGUMEN - AER - LTP - SKREGOYA ADMOLGATI CTERREPS I - LEPTQAFGARGARGAS SEFTRARS - 24 VERVYSER TOTOPI P - LERETLEQL - AAG - LTP - SKREGOYA ADMOLGATI CTERREPS I - LEPTQAFGARGARGA SEFTRARS - 24 VERVYSER TOTOPI P - LERETLEQL - AAG - LTP - SKREGOYA ADMOLGATI CTERREPS I - LEPTQAFGARGARGA SEFTRARS - 24 VERVYSER TOTOPI P - SKREGOYA ADMOLGATI CTERREPS I - LEPTQAFGARGARGA SEFTRARS - 24 VERVYSER TOTOPI P - SKREGOYA ADMOLGATI CTERREPS I - LEPTQAFGARGA SEFTRARS - 25 VERVYMARIHITIST - SAKCELLAC - AAA - LTP - DERAGOYA ADMOLGATI CTERREPS - LEPTGAFGARGA SEFTRARS - 25 VERVYMARIHITIST - AAKELFER - ATA - LTP - DERAGOYA ADMOLGATI CTERREP - COMPRISE AND ATMOLGATIC TERREPS - VERYSEAL GARGE SEFTRAR - LEPTGAFGARGA SEFTRAR	123313025536102588314126719293503616849185443
sp_ P17802_MUTY_ECOL sp_ P83847 MUTY_ECON c_000003652391_2 2 c_00000031207_6 c_00000031207_6 c_0000001207_64 c_00000192846_3 c_00000192846_3 c_00000192846_3 c_00000197282_1 c_00000180197282_1 c_00000180197282_1 c_000002078955_4 c_000002078955_4 c_000002078955_4 c_000002078955_4 c_000002078955_4 c_000003872363_4 c_000004820107_1 c_00000587021_3 c_000004820107_1 c_00000587021_3 c_00000587021_3 c_00000587021_3 c_0000059175_2 c_0000059175_2 c_0000059175_2 c_00000959175_2 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_00000175522_1 c_000000175522_1 c_0000000175522_1 c_000000175522_1 c_0000000175522_1 c_000000175522_1 c_00000017522_1 c_000000175522_1 c_000000175522_1 c_000000175522_1 c_00000000175522_1 c_000000175522_1 c_000000175522_1 c_000000175522_1 c_000000175522_1 c_000000175522_1 c_000000175522_1 c_000000017552_1 c_0000000017552_1 c_0000000000001752_2_1 c_0000000000000000000	147 150 151 148 161 153 153 153 153 153 141 151 156 161 140 147 138 144 144 139 141 156 161 113 153 141 141 153 153 154 154 155 155 155 155 155 155 155 155	NGRUJARCYANSGMIPG — KGEVERNIANSI.— SSQVIT — AUGUERN MADDIGAMI CTREKTERS — L. EPVOAN COARBORGELPYINGKER. 23. VERWARRIFUTDO LA KETRERFEGI — VERTERRES — L. EPVOAN COARBORGELPYINGKER. 23. VERWARRIFUTDO STAPE — SCRAFFILOR — AND -ALD — CORRESPINA ALDIGATI CTRARPTO — VERLOG CHARRAGTIAELPERTER. 23. VERWINSHIFT, CORRESPINA — AND -ALD — CORRESPINA ALDIGATI CTRARPTO — VERLOG CHARRAGTIAELPERTER. 23. TARFFARLIARDH — SGEGRROUMSI. — ARGLIF — SERGEOTAD ALDIGATI CTRARPTO — VERLOG CHARRAGTIAELPERTER. 23. TARFFARLIARDH — SGEGRROUMSI. — ARGLIF — SERGEOTAD ALDIGATI CTRARPS — VERLOG CHARRAGTIAELPERTER. 24. VERWINSHIFT, CORP. — ALGLIF — SERGEOTAD ALDIGATI CTRARPS — VERLOG CHARRAGTIAELPERTER. 25. VERWITKHER CORP. — ALGLIF — SERGEOTAD AND LIGHT CTRARPS — VERLOG CHARRAGTIAELPERTER. 26. VERWINSHIFT, CORP. — ALGLIF — SERGEOTAD AND LIGHT CTRARPS — VERLOG CHARRAGTIAELPERTER. 27. VERWINSHIFT, CORP. — ALGLIF — SERGEOTAD AND LIGHT CTRARPS — VERLOG CHARRAGTIAELPERTER. 28. VERWINSHIFT, CORP. — ALGLIF — SERGEOTAD AND LIGHT CTRARPS — VERLOG CHARRAGTIAELPERTER. 29. VERWINSHIFT, CORP. — ALGLIF — SERGEOTAD AND LIGHT CTRARPS — L. DEPLOAD CHARRAGTIAELPERTER. 29. VERWINSHIFT, CORP. — ALGLIF — DEPLOAD AND LIGHT CTRARPS — L. DEPLOAD CHARRAGTIAELPERTER. 29. VERWINSHIFT, CORP. — ALGLIF — DEPLOAD AND LIGHT CTRARPS — L. DEPLOAD CHARRAGTIAELPERTER. 29. VERWINSHIFT, CORP. — ALGLIF — DEPLOAD AND LIGHT CTRARPS — L. DEPLOAD CHARRAGTIAELPERTER. 29. VERWINSHIFT, CORP. — ALGLIF — DEPLOAD AND LIGHT CTRARPS — L. DEPLOAD CHARRAGTIAELPERTER. 29. VERWINSHIFT, CORP. — ALGLIF — DEPLOAD AND LIGHT CTRARPS — L. DEPLOAD CHARRAGTIAELPERTER. 29. VERWINSHIFT, CORP. — ALGLIF — VERLOG AND LIGHT CTRARPS — L. DEPLOAD AND LIGHT — L. DEPLOAD AND LIGHT CTRARPS — L. DEPLOAD AND LIGHT — L. DEPLOAD AN	1233130255361025883141267192935036168491854433
sp_ P17802_MUTY_ECOL sp_ P83847 MUTY_ECON c	147 150 151 148 161 151 153 153 153 153 153 141 151 156 140 144 139 141 141 138 142 147 156 147 157 158 144 144 145 147 147 159 147 147 147 147 147 147 147 147 147 147	NEWIZARCHANSOMPO - MENTENERISI - SEQVIT - AUGUSTRA MANDIGAMI CTREERES - L. EPUDAC GARARGATAELIPIGENE . 22 VERWARKIPUTDIA K. PETREREFGI - VRE-TUM TYRRES L. L. EPVDAC COARSEALEPHYDRES . 23 VERWARKIPUTDIA COARSEALER . AS A-LIF - KLREGOYADANDIGATI CTRAEPTO - VELEDIC GARRAGATAELIPIGENE . 23 VERWARKIPUTGORPH - SCRARREGODA - ADD - ALD - QUENCEDRE ALDIGISSI CTREEPTO - VELEDIC GARRAGATAELIPIRETE . 23 VERWINSHIPUTGORPH - SCRARREGODA - ADD - ALD - CORDER ALDIGISSI CTREEPTO - VELEDIC GARRAGATAELIPIRETE . 23 VERWINSHIPUTGORPH - SERGERGUMSI . ARR- LIV - RERECEPTO ALDIGISI VETREREC - VELEDIC GLAND CORRESPONDER . 22 VERWINSHIPUTGORPH - SERGERGUMSI . ARR- LIV - RERECEPTO ALDIGISTI CTREEPS L - L. ELGAR CARRAGAAGES FYRASK . 24 VERWINSHIPUTGORPH - SARPELLAC - AAG- LIV - SERGEOYADANDIGSTI CTREEPS L - L. ELGAR CARRAGAAGES FYRASK . 24 VERWINSHIPUTGORPH - SCREPTURI . AAG- LIV - SERGEOYADANDIGSTI CTREEPS L - L. ELGAR CARRAGAAGES FYRASK . 24 VERWINSHIPUTGORPH - SCREPTURI . AAG- LIV - DERECEPTO ADMIGISTI CTREEPS L - L. ELGAR CARRAGAAGES FYRASK . 24 VERWINSHIPUTGORPH - SCREPTURI . AAG- LIV - DERECEPTA AND LIGHT CTREEPS L - L. ELGAR CARRAGAAGES FYRASK . 24 VERWARKEN HERSTE . ATA- LIV - DERECEPTA AND LIGHT CTREEPS L - L. ELGAR CARRAGAAGES FYRASK . 24 VERWARKEN HERSTE . ATA- LIV - DERECEPTA AND LIGHT CTREEPS L - L. ELGAR CARRAGAAGES FYRASK . 22 VERWARKEN HERSTE . ATA- LIV - DERECEPTA AND LIGHT CTREEPS L - L. ELGAR CARRAGAAGES FYRASK . 22 VERWARKEN HITTER L - AAR LIV - DERECEPTA AND LIGHT CTREEPS L - L. ELGAR CARRAGAAGES FYRASK . 22 VERWARKEN HITTER L - BANGER CARRAGAAGES FYRASK . 22 VERWARKEN HITTER L - AAR LIV - VURBER CARRAGAAGES FYRASK . 22 VERWARKEN HITTER L - DERECEPTA AND LIVE CARRAGAAGES FYRASK . 22 VERWARKEN HITTER L - AAG- LIV - VURBER CARRAGAAGES FYRASK . 22 VERWARKEN HITTER L - DERECH CARRAGAAGES FYRASK . 22 VERWARKEN HITTER L - DERECH CARRAGAAGES FYRASK . 22 VERWARKEN HITTER L - DERECH CARRAGAAGES FYRASK . 22 VERWARKEN HITTER L - DERECH CARRAGAAGES FYRASK . 22 VERWARKEN HITTER L - DERECH CARRAGAAGES FYRASK . 22 VERWARKEN HITTER	12331302553610258831412671929350361684918544334
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_0000003552391_2 c_00000031207_6 c_000000107148_4 c_000001092848_3 c_00001092848_3 c_00001197282_1 c_0000197282_1 c_00002106160_4 c_0000367531_2 c_00000367531_2 c_00000367531_2 c_00000367531_2 c_00000367531_2 c_000004820107_1 c_00005867021_3 c_00004820107_1 c_00005867021_3 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000008967021_3 c_000008967021_3 c_0000011118_1 c_000009517536_6 c_00000176522_24 c_0000176522_24 c_0000176522_24 c_000002038721_4 c_0000182161_6 c_00003238371_4 c_00003238371_4 c_00003238361_1 c_00003492925_4 c_00003492925_4 c_00003492925_4 c_00003492925_1 c_000003492925_1 c_00000349235_1 c_00000182335_1 c_00000182335_1 c_00000182335_1 c_00000182335_1 c_00000182335_1 c_00000182335_1 c_00000182335_1 c_00000182335_1 c_00000182335_1	147 150 151 148 161 151 153 153 153 153 141 151 156 140 140 147 150 141 141 141 141 141 141 141 141 141 14	NEWIZARCYANSONICO - RECVENIUSIL - SEQ - VIT - ANGVERPROMODICANI CTRESPES - LE PYQAY QAPAGAZELIFYORCE 23 VERWARRIPUTDIA - KPETRORFEGI - VRE - IMA	1233130255361025883141267192935036168491854433450
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_000003652391_2 c_00000031207_6 c_0000001207_6 c_0000001207_6 c_0000001923648_3 c_00000192848_3 c_0000192848_3 c_00000192848_3 c_00000192848_3 c_00000192848_3 c_000001807531_2 c_000028067531_2 c_00003872363_4 c_00003872363_4 c_00003872363_4 c_00003872363_4 c_00000587012_3 c_00000587012_3 c_00000587012_3 c_00000587012_3 c_0000018737378_2 c_00000587012_3 c_0000018737378_2 c_00000018737378_2 c_00000018737378_2 c_00000018737378_2 c_00000018737378_2 c_00000018737378_2 c_00000018737378_2 c_00000018737378_2 c_000000187366_6 c_00000187366_6 c_00000187366_6 c_00000033833364_1 c_000003294679_3 c_000003378866_2 c_000000187176_11 c_00000187176_11 c_00000187176_11 c_0000018738864_2	147 150 151 151 151 151 151 151 151 151 151	VRIVISLADITODIA — KREVERKINSI — SEQ-VTP — AUVUERPMANDIGAMICTRERENES — LEPLONG LAAANISVALTYGKERK — 22 VERVASALTUTODIA — KERTERREGI — VERTAMAT — YERNEAN PERALIELGALU VERPERSEL — LEVANGO APAREVASELLYMENK — 22 VERVASSILUTIONEN — SCRAFRICAGA — ALD — LID — CERTOGINA AVBIGATICTARAPTIG — VEPLING GRAFALTARE LYMENK — 22 VERVASSILUTIONEN — SCRAFRICAGA — ALD — LID — CERTOGINA AVBIGATICTARAPTIG — VEPLING GRAFAGALELYMENK — 22 VERVASSILUTIONEN — SCRAFRICAGA — ALD — LID — SERGEOTA AVBIGATIC — VEPLING CHARACTARE LYMENTER — 22 VERVASSILUTIONEN — SCREER — ALD — LID — SERGEOTA AVBIGATIC — VEPLING CHARACTARE PROPERTY — 23 TARFYARLIAR SOLID — ALGERITAGI — ALGE — TYP — REPGEOTA AVBIGATIC TERESE — LEPLOLA PARAGAAGES FILLE — VERVASSILUTION — ARE — VEPLING CHARACTARE — VERVASSILUTION — ARE — VEPLING CHARACTARE — VERVASSILUTION — ARE — VEPLING CHARACTARE — VERVASSILUTION — ARE — VERVASSILUTION — ARE — VERVASSILUTION — PERCENDA AVBIGATIC — TERESE — LEPLOLA PARAGAAGES FIVAGA — 24 VERVASSALUTION — CERTIFICA — ALGE — TYP — PERCENDA AVBIGATIC — TERESE — LEPLOLA PARAGAAGES FIVAGAS — 24 VERVASALUTION — CERTIFICA — ALGE — TYP — PERCENDA AVBIGATIC — TERESE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERCENDA — ALGE — TYP — PERCENDA AVBIGATIC — TERESE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERCENDA — ALGE — TYP — VERVAS AVBIGATIC — PERCENDA — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERCENDA — ALGE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERCENDA — ALGE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERCENDA — ALGE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERCENDA — ALGE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERCENDA — ALGE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERCENDA — ALGE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERCENDA — ALGE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — ALGE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERCENDA — ALGE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERCENDA — ALGE — LEPLOLA PARAGAAGES FIVAGAS — 25 VERVASALUTION — PERC	1233130255361025883141267192935036168491854433450
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECON c_00003652391_2 c_000000352971_2 c_00000031207_6 c_0000001207_6 c_0000019248_3 c_00000119248_3 c_00001197282_1 c_0000197282_1 c_00002106160_4 c_00003607531_2 c_00002106160_4 c_00003807351_2 c_000004820107_1 c_000005774797_1 c_00005867021_3 c_00004820107_1 c_00005867021_3 c_00005867021_3 c_000005867021_3 c_00000887021_3 c_00000899887_2 c_0000011181_1 c_00000899887_2 c_000001145122_1 c_000001145122_1 c_00001145122_1 c_00001145122_1 c_000001145122_1 c_000001145122_1 c_000001145122_1 c_000001203871_3 c_00000238721_4 c_0000012038721_4 c_00000238721_4 c_00000238721_5 c_00000238721_5 c_00000238721_5 c_00000238721_5 c_00000238721_6 c_000003394086_7 c_000003394086_7 c_000003394086_7 c_0000033948186_7 c_000003492925_4 c_00000187171_6_1 c_000001866897_64 c_000003910742_3	147 150 151 148 161 151 153 153 153 141 151 151 153 144 139 142 143 153 144 139 141 151 131 138 141 141 139 141 141 141 141 141 141 141 141 141 14	VRIVISLANCYANGAMEGO - KREVENKINSI - SEG-VTP - AUVUERPRAMEDIGAMICTRERENES - LEPLONG LANAINSMALTPGREEK 22 VERVANSLINDIDIA - KSPERRENEGI - VER-IMA - YENGANTAELIELGALUVER SEGULVANK - 22 VERVANSLINDIONE - SCHARRENGAN - AND -LID - KERGOTYA ONDOLGATI CTARAPTIG - VEPINDC GHARRACTABELTYMEK - 22 VERVANSLINDIONE - SCHARRENGAN - AND -LID - CENTOGINA JANUGASI CTARAPTIG - VEPINDC GHARRACTABELTYMEK - 22 VERVANSLINDIONE - SCHARRENGAN - AND -LID - SERGEOTYA OLD LIDGISIVET PREFERO - VEPINDC GHARRACTABEL PREFEROR - 22 VERVANSLINDIONE - SCHARRENGAN - AND -LID - SERGEOTYA OLD LIDGISIVET PREFERO - VEPINDE CHAIRSOTERS FREEDE FRANKER - 23 TARYTAHLAIRABULH - SCENGRIQUESI - AND -LID - SERGEOTYA OLD LIDGISIVET PREFERO - VEPINDE CHAIRSOTERS FILLICE PREFERO - VERNING CHAIR	123313025536102588314126719293503616849185443345075
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_000003652391_2 c_00000031207_6 c_0000001207_6 c_0000001207_6 c_0000001923648_3 c_00000192848_3 c_0000192848_3 c_00000192848_3 c_00000192848_3 c_00000192848_3 c_000001807531_2 c_000028067531_2 c_00003872363_4 c_00003872363_4 c_00003872363_4 c_00003872363_4 c_00000587012_3 c_00000587012_3 c_00000587012_3 c_00000587012_3 c_0000018737378_2 c_00000587012_3 c_0000018737378_2 c_00000018737378_2 c_00000018737378_2 c_00000018737378_2 c_00000018737378_2 c_00000018737378_2 c_00000018737378_2 c_00000018737378_2 c_000000187366_6 c_00000187366_6 c_00000187366_6 c_00000033833364_1 c_000003294679_3 c_000003378866_2 c_000000187176_11 c_00000187176_11 c_00000187176_11 c_0000018738864_2	147 150 151 151 151 151 151 151 151 151 151	VERVISERATION DILLA MESTERREPGI - LEVEN GARAGNERIS SEQ - VIP - AVVERFRED MAD LEGANI TERREPGI - LEVEN GARAGNERIS PERVISER. 22 VERVARALFOISTELD - GARPALIRA AAS - LIP - KLREGOYA OLVELAGET TARAPPI CO - VELAGO CHARRAGTARLERRITER. 23 VERVARALFOISTELD - GARPALIRA AAS - LIP - KLREGOYA OLVELAGET TARAPPI CO - VELAGO CHARRAGTARLERRITER. 24 VERVASHIFUTODI - SIRPITAGI - AAG - LIP - SERGOYA OLVELAGET TARAPPI CO - VELAGO CHARRAGTARLERRITER. 25 VERVASHIFUTODI - SIRPITAGI - AAG - LIP - SERGOYA OLVELAGET TERREPGI CO - VELAGO CHARRAGTER TERREPGI CO - VERNARIA OLD CHARRAGTER TERREPGI	12331302553610258831412671929350361684918544334507515
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_000003652391_2 c_00000031207_6 c_00000031207_6 c_00000031207_6 c_0000001092148_3 c_000001092248_3 c_000001197282_1 c_00000197282_1 c_000002078955_4 c_000002078955_4 c_000002078955_4 c_000003872363_4 c_000003872363_4 c_000003872363_4 c_000003872363_4 c_000005870721_2 c_000005870721_3 c_00000587021_3 c_00000587021_3 c_00000587021_3 c_00000587021_3 c_0000058175_2 c_00000598175_2 c_00000598175_2 c_00000598175_2 c_000001176522_2 c_000001176522_2 c_000001176522_2 c_00000199687_2 c_000000199687_2 c_000001996967_2 c_000001996967_2 c_0000001996967_2 c_0000001996967_2 c_0000001996967_2 c_0000001996967_2 c_0000001996967_2 c_00000019969664_5 c_00000399868_2 c_00000399886_2 c_00000399886_2 c_00000399886_2 c_00000399886_2 c_00000399886_2 c_00000039886_2 c_0000039886_2 c_0000039886_2 c_0000003986_64_2 c_0000003986_2	147 150 151 148 161 151 153 153 153 153 153 144 139 150 153 144 139 141 151 138 142 143 144 139 141 141 142 147 147 147 147 148 149 149 149 149 149 149 149 149 149 149	VRIVISARIJANCYASGREGO - KREVENKINSI - SEQ-VTP - AUVERPREAMBLIGIAMITERSERVES - LEPLONGI LAANNSMALTPGKERKE 22 VERVANSKALTUTOLIA - KSPERKREGO - VERSTREKREGO -	12331302553610258831412671929350361684918544334507515

c_000001128125_11	149	VKRVLSRYFGIHGWPGEKKIEADLWHKADL-LTPPKRFADYTGAIMDLGATTCKRSKPLCGVCPVQKSCVALKREETHSIPASKPK 2	233
c_000001595844_4	140	VFRVLARYTANFIDIGTPAGKKEFTLLANQ-LLDKKQPGKFN <mark>Q</mark> AIMDLGALV <mark>C</mark> KPTNPD <mark>C</mark> SN <mark>C</mark> PLQIK <mark>C</mark> QAFSQDTIAQLPVKEKK 2	224
c_000001719155_2 c_000002363038_6	144 149		228
c_000002561400_1	105	VKRVLTRFFGVHGWPGEKQVENRLWHRADE-LTPSVRFADYT <mark>Q</mark> AIMDLGATL <mark>C</mark> KRSKPN <mark>C</mark> IT <mark>C</mark> PVHSG <mark>C</mark> QALKKGEVHLLPSFKPK 1	189
c_000002566035_2 c_000002598045_3	141 139		225
c_000004188575_41	141	VKRVLARFYAIASWPGNKATEQQMWQQADN-LLPDQRIAAYI <mark>Q</mark> AQMDLGATL <mark>C</mark> TRSKPN <mark>C</mark> DC <mark>C</mark> PLQSN <mark>C</mark> QAYARGTPTDFPIAKPK 2	225
c_000000240049_1 c_000002139456_2	139 139		223
c_000003535614_2	141	VKRVLARYQAIEGWPGKPAIEKQLWVFAER-YTPTEELADYT <mark>Q</mark> AIMDLGATL <mark>C</mark> TRASPK <mark>C</mark> GS <mark>C</mark> PLNNG <mark>C</mark> KALANNCVAALPTRKPK 2	225
c_000002657784_4 c_000003800129_15	138 143		222
c_000003716781_1	130	vrrvlarwfavegvvtkaeprreieglaaa-lvggvndpgswn <mark>g</mark> almelgatv <mark>c</mark> lpkdpr <mark>c</mark> ds <mark>c</mark> pvmte <mark>c</mark> rarargleravpelpvr 2	215
c_000001556689_3 c_000001834452_1	131 108		215 L95
c_000004255004_2	148	arrvyarllsltnr <mark>c</mark> playr <mark>c</mark> qarsvgafklqlrrptr 2	225
c_000000605438_3 c_000000581237_15	141 141	and the control of th	218 218
c_000002529579_2	141	VKRILYRFFAVKEANEKKLWEMAYD-LYDKENAYIYN <mark>Q</mark> TMMDIGSLI <mark>C</mark> THKNPL <mark>C</mark> TQ <mark>C</mark> PFVSL <mark>C</mark> QGKDEPLLYPTKKKK 2	218
c_000006097838_1 c_000000583727_6	114 140		207
c_000005807640_2	142	varvltrllgieespkarpvadrlwsvade-lvnhavtlrkpsqqnasafn <mark>q</mark> ammelgalv <mark>c</mark> tprnpl <mark>c</mark> gd <mark>c</mark> plkgr <mark>c</mark> iarkqnkvetipalakr 2	235
c_000000134878_1 c_000005136725_3	124 139		206 221
c_000001684786_4	137	vervmtrilrlaenprgvstkkrlkeiagg-wmpadkassfn <mark>g</mark> ammelgali <mark>c</mark> spvspd <mark>c</mark> ps <mark>c</mark> pvrev <mark>c</mark> aaaeqgdpenfprlppk 2	221
c_000002971826_23 c_000002040695_2	147 150	and the control of th	231
c_000002040695_2 c_000003263657_32	154	VIRVLSRLYRIHEDATKGPAKRRFQELADG-LLQKGQAADFN <mark>Q</mark> AMMELGATV <mark>C</mark> LPQKPR <mark>C</mark> TV <mark>C</mark> PVQCH <mark>C</mark> RAFHELSDPSGLPYKPP 2	238
c_000005989041_2 c_000002391082_2	151 149	IERVITRIFGICTPFPEAKTIVKDCAAKLAP-KTTRGRPGDYAGAVMDLGAIVCRPKKPLCDLCPWKKCCIANQRNFVDQVPQKVSK 2 VTRVLCRLLRIEEDPRTCPVGQWCRAQAELDDPSALPYKVP 2	236
c_000002591002_2 c_000003839553_2	156		240
c_000003996707_2 c_000002044706_1	146 129		230
c 000002044706_1	144		223
c_000002094036_4	120		199
c_000002762689_1 c_000005516980_2	144 144		223
c_000003920004_1	150	ikrmlarlygldqsinLinkkitslskf-yeskQssnli <mark>q</mark> afmdygsii <mark>c</mark> vprnpk <mark>c</mark> gi <mark>c</mark> iisre <mark>c</mark> ianqrkisniipkkiks 2	232
c_000004008511_2 c_000004481347_1	144 151		226 233
c_000003787733_3	143	VKRVMARILKIKHITKRNNRRIRNRLIK-WMDPERPGDIN <mark>G</mark> ALMDLANKI <mark>C</mark> RVDHAY <mark>C</mark> NT <mark>C</mark> PIDKV <mark>C</mark> MAEKMSIPESYPTKLNK 2	225
c_000000754657_2 c_000000990943_3	143 143	and the control of th	225
c_000004474996_2	142	VIRVMARLLRIKNITKRNKNRIYNTLIK-WMDKERPGDIN <mark>G</mark> ALMDLANKI <mark>C</mark> CVDHAL <mark>C</mark> ST <mark>C</mark> PIDEI <mark>C</mark> MANNMSIPESYPAKLEK 2	224
c_000001463500_11 c_000001286181_5	130 137	and the control of th	212 217
c_000001293628_3	143		222
c_000001535696_8 c_000001614067_2	137 150		221
c_000001765289_1	116	AKRVMSRILGIKNLTSWNLSRINKTLSN-IIPEHTPGNFN <mark>O</mark> SVMELGATL <mark>C</mark> RPRSPS <mark>C</mark> NK <mark>C</mark> PLSFG <mark>C</mark> KA-FKTNKPDYYPKPAA 1	L97
c_000001961666_1	131 138		212
c_000002018097_4 c_000002843512_36	135		212
c_000002930199_1	135	VYRLISRLYNINTAINTNKGREEFQSIANN-LLPNKNTGLYN <mark>Q</mark> AIMDFGSIQ <mark>C</mark> KKYNPK <mark>C</mark> NI <mark>C</mark> PLQKE <mark>C</mark> QSAILGIVNERPVKTLS 2	219
c_000003033795_2 c_000003888107_2	131 132		213 214
c_000004013286_6	157	SRRVLSRVFAIKGDLSRQPMKHLLWDLAKF-VLPEKNVGDFN <mark>Q</mark> AMMELGSQC <mark>C</mark> QKQYPR <mark>C</mark> MQ <mark>C</mark> PIKEW <mark>C</mark> RAFQEGLQEELPFTPIQ 2	241
c_000004852258_1 c_000005254087_1	119 145		201 229
c_000005603677_1	142	VYRVLSRYFGQALPIDSSAGKKWFKAKAQA-LLWEDDPANYN <mark>G</mark> AMMDFGALH <mark>C</mark> RPKNPS <mark>C</mark> GD <mark>C</mark> PLAKN <mark>C</mark> QAKANKQQLELPKKGKK 2	226
c_000003283462_3 c 000002687221 1	130 144		212
c_000003347358_19	166	VKRILCRLEKLRTPSDTELWDIAYT-LVDKINPFDYN <mark>Q</mark> AMMDIGATV <mark>C</mark> IPKKPQ <mark>C</mark> DI <mark>C</mark> PLNDI <mark>C</mark> KGQEEPTLYPTKKRR 2	243
c_000002701031_2 c_000000582753_3	137 145		221
c_000001713769_5	137	vyrviarfygidvpvnnhlgkkfymdyaqk-lapkkscgdyn <mark>g</mark> gimdfgsli <mark>c</mark> kpkapl <mark>c</mark> dk <mark>c</mark> mlakd <mark>c</mark> iaskmknvnyffvrlkk 2	221
c_000004369364_1 c 000006057486 30	140 141		224
c_000005494072_10	137	VYRVLSRYFGIEYAINSKGIKKFKTLAQS-LLLNENFGLHN <mark>Q</mark> AIMDFGATI <mark>C</mark> TPKKAK <mark>C</mark> DS <mark>C</mark> IFCES <mark>C</mark> SALQHNKVSELPVKTPK 2	221
c_000001742634_3 c_000002826998_2	140 140	VYRVLARYFGIKTAINSTNGIKEFKLLAQQ-LLPNNKIGAYN <mark>G</mark> AIMDFGATI <mark>C</mark> TPKKPK <mark>C</mark> DI <mark>C</mark> IFNDS <mark>C</mark> IALQKNKITELPTKTNK 2	224
c_000003159439_6	137	VYRVLARYFGIRTSTNSTKGIKEFKQLAQE-LIDTKDPATFNQAIMEFGAIQCKPKNPNCNNCPLNTSCIALQKKLITILPIKDKK 2	221
c_000004887214_1 c_000005037037_2	142 140		226
c_000003037037_2 c_000001059964_1	132		216
c_000002498472_1	141		225
c_000004615912_3 c_000004766858_2	130 143		214 227
c_000002747260_18	149		231
c_000005371561_38 c_000000169465_2	149 145		233
c_000003254110_11	145	VKRVLARYYAISGWPGQKKVENQLWEVAEK-NTPTNPEGGRCANYT <mark>Q</mark> VMMDLGAMI <mark>C</mark> TRSKPK <mark>C</mark> DE <mark>C</mark> PLQPD <mark>C</mark> IAYAQGAQTDYPGKKPK 2	233
c_000004750284_20 c_000000141782_15	145 150	VKRVLARYHAVAGWPGETAVSRRLWALAER-YTPDNRTADYN <mark>O</mark> AMMDLGATV <mark>C</mark> VRRRPR <mark>C</mark> GV <mark>C</mark> PLADG <mark>C</mark> RARREGNPEAYPGSRPR 2	229 234
c_000002717847_8	144		223
c_000004054799_1 c_000006126673_1	131 156		214 240
c_000000339186_3	113		198
c 000003029168_2 c 000001863436 1	145 161		229 245
c_000002830137_4	154	TTRVLSRLLAFHGDPSQRVGQQLLWAFAES-LLPRKRVGEFNQSLMELGSEICIPRKPNCERCPVRMLCAAHRQGEQLSIPISRRR 2	238
c_000004612302_3 c_000001933926_1	148 134		231 216
c_000003136334_1	146	VERVTARLHRISKPLPGAKKYLKEKAAE-LTPSERSGDYACAVMDLGATVCTPRKPNCPLCPWSYICKAYLAGDAEKFPKRVPK 2	228
c_000005849454_9 c 000001169194 1	143 154		233
c_000002786947_2	154	VRRVLARLFDKHEPGVRWLNHTAAS-LVDKDRPGDWNGALMELGAMICAPKNPRCEDCPVQRWCTAHEQGTQALSPAGIRR 2	233
c 000001279808 52 c 000000358065 2	142 144		219
c_000003745941_1	133	VIRILCRLTADNTVYTDNTQAMKVFTPLAEV-LLDTKTPGQHN <mark>E</mark> AMMEFGAMV <mark>C</mark> SKVNPT <mark>C</mark> DI <mark>C</mark> PFNSV <mark>C</mark> LGRNHQPER-LPIKAAK 2	217
c_000004187032_4 c_000006067315_3	144 144		223
c_000005543774_1	114	VKRVLLRLFNLETKDCLLKKNCLLYYKSESKI-RFNKKIK 1	L85
c_000006211484_1 c_000002718976_3	136 145		207
c_000002992548_1	146	IKRVFSRLFNANLEKNEKRIKRITKE-QLYTDRCGDLAEALMEFGAVICKPSNPMCNICNLKANCYFFKNKTSV-LVNKKRR 2	225
c_000000456751_1 c_000002655634_1	110 141	VKRVFSRLLLINTSNQNIDNEIKKITYK-LPKIDRNADFAEALMEFGALVCKPQNPLCKICHLQKYCKFFNSENYI-SLNKKFS 1 VKRFFSRLFLIDVSSQNFENEIKKITNK-LPKVNRNADLAEALMEFGALVCKPKNPLCKICNLKKYCKFFNGENYT-LPNKKFF 2	191
c_000004232403_2	140	hrrvisrilgiknlsrhnknrinnylkq-lvaidrpgein <mark>q</mark> aimdigsii <mark>c</mark> kpkevf <mark>c</mark> df <mark>c</mark> pvqfs <mark>c</mark> kacvsskpleypnkiyn 2	222
6u7t.after.N146.pdb Consensus_aa:	141	VMRVLSRLFLVTDDIAKPSTRKRFEQIVRE-IMAYENPGAFNEALIELGALVCTPRRPSCLLCPVQAYCQAFAEGVAEELPVKMKK 2 1.RVhsRhh.lpppsplesQAhM-lGthlC.ppP.CCP1C.thP	225

sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c 000003652391 2	226	OTLPE							
c 000003652391 2	232						KEKLEQMVGEQYGLQ		
c_000000031207_6	233 224	QPKPT	-RYGIV	YLARD	-AHGAWLLERRPDK-GLLGG <mark>M</mark> LGW	PTSDWNDAPG	DQPPFA	A	A 21
c_000000430975_4	234	RKKQR	-RYGVV	YWIER	-RDGAISLRQRPEN-GIFGGMTEI	PGSLWKASPL	DADKMIGKEFKRLGLD	A	A 2
c_000001007148_4 c_000001092848_3	232 244	RDVTD	VFELL	VVMR	-RGKRLLLIQHPDG-ERWGG <mark>M</mark> WGF	PALSRDRALARS	RFDERLIESEVADWGCD	v	7 2
c_000001151029_1	191	TKKRK	RYGVV	YWIER	-RDGAIVLRQRPEN-GIFGGMTEI	PGSLWQAAPL	SRHSIHAQAPIP	A	A 25
c_000001797282_1 c_000001803648_25	253 236	PVKPT	RRGAA	FVAIR YIARR	SGDEAVLLRTRPPE-GLLGNMAEP -GDGAWLLERRPDK-GLLGGMLGW	PGSAWEPDYD PGAQWGDQAV	LDAPLD	A A	A 3
c_000002078955_4 c_000002106160_4	236 224						ENPPVSPHPQLEELLKNKFKLE		
c_000003607531_2	237	KVKAV	-RKGVV	FLALM	-SDGSLFLRRRPEN-GLLGGMMEF	STVWLERSL	SPKEICEAAPFK	т	r 2
c_000003872363_4 c 000004820107 1	232 241	PAKPI	-RYGTA	YIARR FWISD	-HDGAWLLERRPDN-GLLGGMLGW -DSGNILFIRRPEN-EMLGGMLGL	PGSEWGEEAV PTTEWDIRP	ENPPFS	A	A 21
c_000005774797_1	223	RSKKK	WNAFA	YVIYN	-ADGNIGFVRRDKD-ALLGG <mark>M</mark> WAL	PTSDWSTSPV	FQPPI	L	ւ 2՝
c_000005867021_3 c_000004546210_2	236 229	PVKPT	RYGIA	YVARR LMIVF	-PDGAWLLERRPDK-GLLGGMLGW -DGKKLFLEKRKPK-GIWGGLWSF	PGAEWGAQAV PQIQLADDPQI	EKPPIVWCEQQFTNN	A I	A 21
c_000004551008_5 c_000002511148_4	229 224	KKKRT	ESTYF	LMIIF	-DGKKLFLEKRKPK-GIWGG <mark>L</mark> WSF	PQIQLADDPKT	WCEQQFTNK	I	21
c_000000577378_2	212	KSKPT	-KKVVW	LLPQG	-psgevllekrkpk-giwgg <mark>l</mark> wtf	IEAEKKNELEL	ELSRRFKTD	c	2 (
c_000000598175_2 c_000000754627_3	235 232	KVMPE	KQAIM KSCHQ	VILKN LIIK	-SKQEVFMQKRPPV-GIWGSLWCF -HNDKVLMEKRPNS-GIWGGLFGF	PQFEKRAFAEE FEFNEYSELET	WLKSNYGKL	I	- 2
c_000000811118_1 c_000000899687_2	223 227	KEKIE	KKIDW	ILIK	-TKNKVLLKRNKEK-GIWQN <mark>L</mark> WVL	PEKDFFSSKKI	SKI	L	ւ 2՝
c_000001176522_24	248	KVMPV	RKVCW	QVSLS	QGCVWLVQNPAR-GLWGGLWVL	PEGNR	PEECLKREIKEELRVN		- 21
c_000001345122_1 c_000001515736_6	202 220						FLDGNEMVAT		
c_000001682161_6	223	KTIPT	-KERWF	LVLLT	-KEGNIGLIKRPAK-GIWGG <mark>L</mark> WSL	PEFDEVKLLEN	FITDNNVKCL	LK	21
c_000001923643_29 c_000002030994_5	230 224						WLDDSFGMS		
c_000002038721_4	226	SQKKE	-KNINW	LLIA	-SKDKVLLKRNVNK-GIWQN <mark>L</mark> WLF	PEANSLNYEK	FNL	L	. 2
c_000002523527_15 c_000002608528_2	251 224	KVMPE	KQTVM	LILKN	-GKQEVFMQKRPPA-GIWGGLWCF	PQFDNHENVLE	SEAAEESALELARAYGS	F	F 21
c_000002961510_2 c_000002979152_8	227 232	VPSKK	IEVSA	GIII	-KNKKIYIQQRSKN-ALMGGLWEF	PGGKREKGES	PEECLKREIKEELRVN	v	7 21
c_000003248034_1	247	RKKKR	VMTSV	IACE	-QGGQILMKQRSVNARLMPG <mark>F</mark> WEL	PEVEGPFLNQ	ADLARWS	L	30
c_000003294679_3 c_0000033333364_1	229 225						PAQCVVREFQEELEWD		
c_000003402697_5	220	TEKPKKRKHR	IEVGI	ACIW	-REGKYLVQARPKG-KSFEGSWEF	PGGKREKGEN	FRECVKREIQEEVGID	v	7 2
c_000003492925_4 c_000003766664_5	212 239	RPPKK	-REENI	MLYV VIRD	-YNDKLSLTQRKGKFLHGLWGF -EQGAVLLTQRPEK-GLFGGLWEV	ENTEMPL PLKEVDETPS	KAGVGRLVKETVGLT	A	- 2! A 30
c_000003948186_72	226 225	NNIPT	RHTQM	LLIEN	-TAGEVWLEKRPAQ-GIWGGLWSL	PELATGQNAIT	YCEQELQIA	v	7 21
c_000005057120_4 c_000005590109_5	225	KSLPV	-KKITF	LMCQD	-QQGRILLEQRPKT-GIWGG <mark>L</mark> WSF	PEYESLANIQS	CFLEK-GIP	I	21
c_000006063368_2 c_000000467631_2	224 204						ECKSIFQIK FCQQN-NFA		
c_000000788235_1	225	KTLPE	-KKAVF	LLLIN	-INHEIFIIKRPPS-GIWGG <mark>L</mark> WSL	PQFDTYLQAQQ	WYEQYFSTH	L	. 21
c_000001187176_11 c_000001660697_64	226 231	KRIPV	-RQCLM	PLLVN VIALH	-PQGDIWLQRRPDS-GLWGGLWCP GETVLLQRRPQR-GIWGGLWSL	PQLDSREQLDA PLVGEMDDALDAHP	LVIAQ-GWQ LDADTVRQAALA	A AYGTV	A 21
c_000003378864_2	238	KPVPH	HHIGV	GVIWK	DDQVLIQLRPPE-GLLGGLWEF	PGGKQEPAET	IEETVRREIREELGVD	v	7 30
c_000003910742_3 c_000004116181_2	226 192	KKQAT	RTCVF	ILIVN	-AKQEILLQKRSPV-GIWGGLWSL	PEVEDTIEAIH	WHENYFGFP	v	7 2
c_000006223903_1 c_000001029068_2	226 199	RPRPR	REVVM	IMIKD	-SRDRVLLERRASS-GIWGGLWSF	PECPVEEALEP	WCRMRFGAG	I	21
c_000001128125_11	234	KDKPV	-KRAFF	LLLLN	-serqvllrkrpqk-gvwag <mark>l</mark> wsl	EFDSLQGFKE	SIESQTTV	I	2 !
c_000001595844_4 c_000001719155_2	225 229						PEQCLHREIKEELGVT		
c_000002363038_6	234	KNKPV	KQKWL	LLQKN	-SAEQVFLYKRPQK-GIWAG <mark>L</mark> WSL	PEFDSYDRAVD	FLNGEIHRH	DA	A 2
c_000002561400_1 c_000002566035_2	190 226	AVIPK	RDTVF	AIMEN	-NNGEILLEQRPSS-GIWGGLWCF	PEFSSPLRIEE	YLQTQTPG	I	21
c_000002598045_3 c_000004188575_41	224 226	KSKLT	-KKVLW	LLPQG	-PSGEILLEKRKEE-GIWGGLWSF	IETEKKAELEL	ALSRNFDSN	I	21
c_000000240049_1	224	KILPV	REKRL	LIIRN	-KQGHYLMEKRPPS-GIWGG <mark>M</mark> WSL	PELTLDKSIAE	SIERNWQLS	v	7 21
c_000002139456_2 c_000003535614_2	224 226						SVERNWQLN		
c_000002657784_4	223	KQKPF	-KTVFW	LVVMN	-KNGKVLLKKRNNL-GVWKG <mark>L</mark> WSF	LESENIQDLGK	ECLTMFEKR		K 21
c_000003800129_15 c_000003716781_1	221 216						PAELELEL		- 2
c_000001556689_3 c_000001834452_1	216 196						TEKPASSHSRAQEAKLSRYIKEQLGWS		
c_000004255004_2	226	TKA	VQWPL	TLAK	-WRSRILLHRRPDK-GILAS <mark>L</mark> WEL	PTPENLPAEL	IDETL		- 2
c_000000605438_3 c_000000581237_15	219 219				-KNDKYALAQNEERLLSGLWGF -KDDKYALSONSERLLSGLWGF			I s	20
c_000002529579_2	219	IKKPI	-RKRTL	VIYH	-KANKYALAQNEERLLSG <mark>L</mark> WGF	KQEEDFEL		L	. 2
c_000006097838_1 c_000000583727_6	208 234						VQPADLASTKLALG		
c_000005807640_2 c_000000134878_1	236 207	AATTK	RRFIG	FLIT	-WHGKVFVQRRPSG-EVNAGFWEF	PNWEV-DAA	ATADQLAKRELRLG	Q	2 2
c_000005136725_3	222	НТКРН	YDVAV	GIIW	-DKQKLLITKRKEE-GLLGG <mark>L</mark> WEF	GGKMKKNET	EIKEELSIN	I	21
c_000001684786_4 c_000002971826_23							GGIAARLGQALETDGGIAARLRKRLATS		
c_000002040695_2	233	TKKPC	-RWGHF	FFLVHIPS	SGSPVSVLLEKEHG-PLLEG <mark>L</mark> WRP	LTQSWVHKKT	FPY	к	. 2
c_000003263657_32 c_000005989041_2	237	KVKPV	-RKGIV	FLALM	-SDGSLFLRRRPET-GLLGGMMEF	STNWLERRI	LTEGVTRTILESTGLT	s	5 2
c_000002391082_2 c_000003839553_2	234 241	KKQKP	HYQVAC	GVIC	-KGDRLLLAQRPSA-GMLGG <mark>L</mark> WEF	PGGKQEEGET	LQQCLQREIAEELAIE	I	2 !
c_000003996707_2	231	KPTRP	HYEVTA	GVIW	-KGSKLLVAQRPSD-GMLGGLWEF	PGGKREPGES	LQECLRREIREELTID	I	2 2 2
c_000002044706_1 c 000006007075 1	214 224						RLASTLCGEFGLTIRPD		
c_000002094036_4	200	KKIIN	-KFYLA	TLYK	-NQNQILLIKNDKF-KFLKNLLIF	PMREITYP		D	2
c_000002762689_1 c_000005516980_2	224 224	KKNIN	KYFIL	KVYK	-KDQRYLLIKNTKF-NFLKNLRIF	PMEELFQP			- 2
c_000003920004_1 c_000004008511_2	233 227	KKSRMK	KYTRAY	IIIN	-GSEEILVRRRASK-GMLPSMLEV	PNDKWVTEKK	SSVSLFK		- 2
c_000004481347_1	234	LEQKKI	KFTRAY	IIMN	-KKNEVLVNRRKSK-GMLASMLEV	NDEWVDVKK	DVYKDLS		- 2
c_000003787733_3 c_000000754657_2	226 226	KIIPH	-KEIVA	GIIW	-QRDKFLITKRPEN-ALLGELWEF -QREKFLITKREEN-ALLGGLWEF	PSAEIQFNET PGGEIASSET	PIGALRRQISKDFNIYPVGALRRQIKEKWDID	I т	[21 [21
c_000000990943_3	226	KVIPH	KDIVT	GIIW	-rgkkflitkrsen-allrg <mark>l</mark> wel	PGGEFESNET	PIEALRRKIKEECDID	I	21
c_000004474996_2 c_000001463500_11							PIGALRRKIKEEWAID		
c_000001286181_5	218	VTKTQ	-ESFHW	FIYQ	-KNNKVMLCKNPDE-GIWPNLWVF	KRELFQT		ĸ	2 (
c_000001293628_3 c_000001535696_8	222	TKVRN	-RYFNY	IIPIAEAD	DGSRKTLLNQRKGK-DIWQN <mark>L</mark> WQF	LIETKREID	ELR-VGDSLHGRCSARLEDLGVQLSAR	DPQ	2 2
c_000001614067_2 c_000001765289_1		KEKEE	-RYGLF	FYLQN	-KDGAVLFETNKSS-GLLANMDVL	PSIGWYEESN	RFKKSPKFNKKKPNFL	GM	1 2
c_000001961666_1	213	KTIRK	GKCY	IIKRL	-NDSKFLFIRNPAK-GLLGSMLLF	PTYGWLHSDH	DDYVKSMIEKFIKN	I	2
	221						KIKALKTYAKNKLGLS		
c_000002018097_4 c_000002843512_36	213	VVPT	KEÖNI						
	220	RKPKI	-RYFNY	LFIK	-KNQQFLIQQRGTN-DIWKKLYEL	LIESKEKLN	REKIMAHQYFKPFK	I	21

						_		
c_000004013286_6 c 000004852258 1	242 202						KIRQLMVRGVGQQTGVP	
c_000005254087_1	230	KRTPHYDVV	VAGIIWQNGVSPG	EGGRFLIAQRPLN	-GLLGG <mark>L</mark> WEF	PGGKQEPDET	LPQALEREIREEMDMM	I 299
c_000005603677_1 c_000003283462_3	227 213						TSELKTLWAHWELEE	
c_000002687221_1	227	VSRPH	HNVAVGLIW	KDNRILISKRNAS	-GLLGG <mark>L</mark> WEF	PGGKIRSGES	KTQEILNVL	V 289
c_000003347358_19 c_000002701031_2	244 222						DDIENCYC WYVI EVUNC	
c_000002701031_2 c_000000582753_3	230						RDIENSKSWKKLFKHNS QIFKNSIND	
c_000001713769_5	222	NAPKI	IHFNYLVLL	DSDHMICMDRIKN	I-GIWKN <mark>L</mark> FQF <mark>I</mark>	PMIESKKELN	EIFKSIAPISNS	D 287
c_000004369364_1 c_000006057486_30	225 226	IKKRT	RYFYYLVFK RHFNFIVI-	EKDLFLIQKRTQK NNNOHTYIHORKDN	-DIWQSLFEF	PNIEGMEELN PLIESKHEIDTN-	ESEIREAIQKKYPNLK KVIKSSIFQDFFKNNSY	Y 287
c_000005494072_10	222	IKIKK	RYFNYLVVL	SKKNKITLNKRINK	-GIWQNLFEF	PLIETVETITIK-	EKIINKKQLV	D 289
c_000001742634_3	225 225						KLVKNDFFQKLILNDTTI	
c_000002826998_2 c_000003159439_6	225						QKELMKSELWKESVSDFD	
c_000004887214_1	227	LKIKK	RYFNYLILK	TKNEETLVKQRKGK	-GIWQN <mark>L</mark> YEF	PLLETEKEINYL-	KKMIEENNF	D 293
c_000005037037_2 c_000001059964_1	225 217	KKVKE	RFFYFLVLN	IDNTTYIEQRQNN	-DIWKG <mark>L</mark> FQFI	PMIETQQLIN	kpkeleklitnkinvr lrkalqehlleelgkp	F 287
c 000001039904_1 c 000002498472 1	226						PEQTVVREFLEETEFK	
c_000004615912_3	215	IRKKK	RYFHYFISH	FEGKILLRKRIQK	-DIWQNLYEF	PMLETKDEELK	ISRVQKTQLWQQLFHGNEKVKV	L 284
c_000004766858_2 c_000002747260_18	228 232	PEITR	IEKLTALVQ RHGIAYLGR	NGDCWLVRKRPEG RADGAWLLERRPDK	-GLMGGLWEFI	PTWEELPSENS PGGDWAETAT	AAAWLTQQLHEDYGVA	A 291 A 285
c_000005371561_38	232	KPKPT	RRGIAYLGR	RADGAWLLERRPEK	-GLLGG <mark>M</mark> LGW	PGSDWAESPP	EASPPCP	G 286
c_000000169465_2	234						QLAKRGIS	
c_000003254110_11 c_000004750284_20	234 230						QFKKRGVN\QFKKRGVN\	
c_000000141782_15	235	REKPL	RRTRMLLIV	DGGRVLLERRPPS	-GIWGGLWCP	PECPPEVDVES	YCRHELGLE	V 291
c_000002717847_8 c_000004054799_1	224 215	KKD	VYLEFSLYK	DGPKYFLAQTEAL	-GFWKKLWMPI	PKIVN		- 263 G 259
c_000004034733_1	241	KARPQ	RYGYVYWIS	DDDGNILVHKRPEK	-GLLGGLYGL	PTSSWETDIE	TVEHPIFISEQIK	P 301
c_000000339186_3	199	IRYED	KQIDVYLIT	RGPRYLVQQRPEG	-gvnag <mark>f</mark> wefi	PNSDSGNKYS	APK	- 247
c 000001863436 1	230 246							
c_000002830137_4	239	TQTEH	VVEAAVVIR	RGSRVLLRRHEDR	-ERWAG <mark>L</mark> WDF	PRFPFDPDATN	KSRELTGFE	303
c_000004612302_3	232	VRTTD	LYQLLLVIR	RDDRLLLIQHPER	-ERWGG <mark>M</mark> WGF	PALSRTGPLLKS-	RIDELQIASEAAEWGCD	V 297
c_000001933926_1 c_000003136334_1	217 229	KRKPT	RYATVFWLL	DGRGNVLLRRREEK	-GLLGG <mark>M</mark> MEV	PSTDWLEENT		V 288
c_000005849454_9	234	KKWVD	LEMVFLVHR	VGVRVGLQKRTS-	-GWSPGLYEP	PSAICESFATANE	ASSAHESTAHSLAREHR	A 299
c_000001169194_1 c_000002786947_2	234 234	VPARE	ISFLLVILQT	EEGEVMLVQRPPE	-GLLAG <mark>M</mark> WAF	PEQELAKPLD	CAATSRDRAIELAMSLGAEV	V 301
c_000001279808_52_	220						FRGCVKREIEEEVGLN	
c_000000358065_2	224	KKIIN	KFYLATLYK	HDDQVLLIKNDKF	'-KFLKN <mark>L</mark> LIF <mark>I</mark>	PMKEISQS		C 268
c_000003745941_1 c_000004187032_4	218 224						SATALMK	
c_000006067315_3	224							
c_000005543774_1	186	IESKT	YDIFCYLRK	NKKQIALTKNNDL	-GFLKK <mark>F</mark> NLP	EIKATSKK		N 230
c_000006211484_1 c_000002718976_3	208 227	IQSKN	YDIFCYLQK YDIFCYI-N	nkkqialtknndl TKKOIALTKNNOI	-GFLKKFNLP -SFLKDFNIP	KIKETSEK EIKE-TNNVSN		N 252 N 272
c_000002992548_1	226	KKEQK	YNVYCYLKK	KKKEIALTKNKHL	-SFLSN <mark>F</mark> NIP	ETKIETSNNKK		N 273
c_000000456751_1	192 223						·	
c_000002655634_1 c_000004232403_2	223						PEKSLKESINNHYGFT	
6u7t.after.N146.pdb Consensus_aa:	226	TAVKQ	VPLAVAVLA	DDEGRVLIRKRDST	-GLLAN <mark>L</mark> WEF	PSCETDGADG		- 283
Concernation		á	6					
Conservation: sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS	282 295	ELTEPIVSFE <mark>H</mark> AFS	<mark>SH</mark> LVWQLTVFPGRL	VHGG		-PVEEPY	: LWYNLAQPPSVGLAAPVERLLQQLRTGAPV RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD	- 366
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2	295 287	ELTEPIVSFEHAFS DWRTLRGEVRHTFT	<mark>SH</mark> LVWQLTVFPGRL <mark>TH</mark> FHLILRIRVAEL	VHGG PDDI		-PVEEPY TPAVG	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD FLLSKHAFRPSDLPTV	- 366 - 338
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS	295	ELTEPIVSFEHAFS DWRTLRGEVRHTFT ELIGHADRFQHAIT	shlvwoltvfpgrl thfhlilrirvæl tyrklfihplvyry	VHGG PDDI QGE		-PVEEPY TPAVG IPAGV	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD FLLSKHAFRPSDLPTV ETIPIDGGDRLPALHRKSIAAARELLLEVFR	- 366 - 338 - 352
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_000000031207_6 c_000000430975_4 c_000001007148_4	295 287 287 294 298	ELTEPIVSFEHAFS DWRTLRGEVRETFI ELIGHADRFQHAII DWKPHPGRVYHSFI EFQEWMDEFQH	SHLVWQLTVFPGRL THFHLILRIRVAEL TYRKLFIHPLVYRY THFDLELKIMTINS TRFRLHLQPIVAMW	VHGG PDDI QGE		-PVEEPY TPAVG IPAGV PEGT	RLAPEDELKAYAFPVSHQRVMREYKEWASGYRRPD- FLLSKHERFPEDSLPTV	- 366 - 338 - 352 - 354 - 370
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003552391_2 c_000000031207_6 c_0000000330975_4 c_000001007148_4 c_000001092848_3	295 287 287 294	ELTEPIVSFE A FE DWRTLRGEVR T FI ELIGHADRFQ A II DWKPHPGRVY S FI EFQEWMDEFQ GVI PWEPC-GTVT T FI	SHLVWQLTVFPGRL THFHLTLRIRVAEL TYRKLFIHPLVYRY THFDLELKIMTINS TRFRLHLQPIVAMW THFTLALSVYRARV			-PVEEPY	RLAPEDELKAYA FPVSHQRVWREYK EWASGVRRPD- FLLSKHAFRPSD LPTV ETTPTDGGDR LPALHRKSTAARA ELLLEVFR FFWCREEVKAQA LPSLMHKIMTHMY KA	- 366 - 338 - 352 - 354 - 370 G 373
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_000000031207_6 c_000000130975_4 c_000001097148_4 c_000001092848_3 c_000001151029_1 c_000001797282_1	295 287 287 294 298 303 251 313	ELTEPIVSFEHAPS DWRTLRGEVRHTFI ELIGHADREGHAI DWKPHPGRVYHSFI EFQEWMDEFQHGVI PWEPC-GTVTHTFI DWKPQPGLVYHSFI RWKRLPGLVRHGFI	SELVWQLTVFPGRL PFHLILRIRVAEL FYRKLFIHPLVYRY PFFDLELKIMTINS FRFRLHLQPIVAMW PFFTLALSVYRARV TFFDLELKI PFFPLELTVFVARV			-PVEEPY	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FLISKHAFRPSDLPTV ETIPIDGGDRLPALHRKSIAAARELLLEVFR FWCRKEVKAQALPSLMMKIMTHMYKA EWWGIDELARPLSVAGRVATKVERILBHNGAQA- WWCAPGLLAGEALPTVMKKVVEAAISGATKARRPI(-RFTPRSALDDEPLPGLMRKVLAHAFDPKPEPEKKP)	- 366 - 338 - 352 - 354 - 370 G 373 - 272 R 385
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_0000003552391_2 c_000000430975_4 c_000001007148_4 c_000001092484_3 c_00000119102921 c_000001797282_1 c_00000197388_25	295 287 287 294 298 303 251 313 290	ELTEPIVSFE AFS DWRTLRGEVRHTF ELIGHADRFQHAI' DWKPHPGRVYHSF EFQEWMDEFQHGV' PWEPC-GTVTHTF DWKPQPGLVYHSF RWKKLPGLVRHGF DWQDPGAEVRHSF	SHLVWQLTVFPGRL TFHLILRIRVAEL TYRKLFIHPLVYRY TFFDLELKIMTINS TFFRLHLQPIVAMW TFFTLALSVYRARV TFFDLELKI TFFPLELTVFVARV THFDLELLYFVARV THFHLRLSLRISVV			- PVEEPY	RLAPEDELKAYAFPVSHQRVMREYKEWASGVRRD- FLISKHAFRSDLPTV- EETIPIDGGDRLPALHRKSIAAARELLLEVFR FWCKREEVKAQALPSIMHKINTHMY	- 366 - 338 - 352 - 354 - 370 G 373 - 272 R 385 - 358
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003552391_2 c_000000433975_4 c_000001007148_4 c_000001097148_3 c_000001109248_3 c_000001151029_1 c_000001797282_1 c_000002078955_4 c_000002078955_4 c_000002106160_4	295 287 287 294 298 303 251 313 290 290 287	ELTEPIVSEE AS EDWATTLRGEVERT EDWATTLRGEVERT ELIGHADRECHAIT DWKPHPGRVYHSFE ECOMMOTER ETVTT FOR EVERT EV	SHLVWQLTVFPGRL THFHLILRIRVAEL TYRKLFIHPLVYRY THFDLELKIMITINS THFTLALSVYRARV THFDLELKT THFPLELTVFVARV THFPLELTVFVARV THFHLRLSLRVATI SHFGLTILSGHRGH			- PVEEPY	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRD- FLISKHAFRSDLPTV- EETIPIDGGDRLPALHRKSIAAARELLLEVFR FWCREEVKAQALPSLWIKINTHINY	- 366 - 338 - 352 - 354 - 370 G 373 - 272 R 385 - 358 - 355 - 351
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS 00003652391_2 c_000000031207_6 c_000000430975_4 c_000001007148_4 c_000001097148_5 c_000001151029_1 c_000001151029_1 c_00000197282_1 c_000002078955_4 c_000002078955_4 c_000002106160_4 c_000003607531_2	295 287 287 294 298 303 251 313 290 290 287 297	ELTEPIVSFE AF DWRTLRGEVR TF ELIGHADRFQ AI DWKPHEGRYY SF EFQEWMDEFQ GF PWEPC-GTVTTF DWKPQPGLYY SF DWQDPGAEVR SF DWQVLNAEVR TF TIKNKIGEIR RYE QWVKLAGTVN AF	SHLVWQLTVFPGRL TFHLILRIRVAEL TYRKLFIHPLVYRY TFFDLELKIMTINS TFFRLHLQPIVAMW TIFFTLALSVYRARV TIFFDLELKI TFFPLELTVFVARV TIFFHLRLSLRISVV TIFHLRLSLRISVATI SFGITLSGFHCRL THFQLQLQVRVAVV				RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FLISKHAFRSDLPTV	- 366 - 338 - 352 - 354 - 370 G 373 - 272 R 385 - 358 - 355 - 351 C 368
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003552391_2 c_000000433975_4 c_000001007148_4 c_000001097148_3 c_000001109248_3 c_000001151029_1 c_000001797282_1 c_000002078955_4 c_000002078955_4 c_000002106160_4	295 287 287 294 298 303 251 313 290 290 287	ELTEPIVSFE AF BURTLRGEVR TF ELIGHADRFO AL DWKPHPGRVY SF FPCEMMBFO GV PMEPC-GYVT TF DWKPQPGLVY SF RWKRLPGLVR GF DWQDDGAEVR SF TKNKIGELR RY QWVKLAGTVN AF DWQRLDAQVR TF	HIVWOLTVFFGEL TYRKLEIRITVRE ITRKLEIPIDVRY HFDLELKIMTINS HFDLELKYFARV HFDLELKVFVARV HFDLELKISIRISV HFHLELSIRISVI HFHLELSIRISVI HFHLELSIRIVATI HFHLELSIRIVATI HFHLELSIRIVATI HFHLELSIRIVATI HFQLQLQVRVAVV			PVEEPY	RIAPEDELKAYA - FPVSHQRVWREYK - EWASGVRRPD- FLISKHAFRPSD - LPTV - ETIPIDGGDR LPALHRKSIAAAR - ELLLEVFR FWCRKEEVKAQA - LPSLMMKIMTHMY - KA EWG JDELARTP - LSVAGRVATRVE - RILBHNSQA WWCAPGLLAGEA - LPTVMKKVVEAAI SGATKARRPI RFTPRSALDDEP - LPGLMRKVLAHAF DPKPEPEKKPI HFIADAPFDET - LPTVMRKAYRIAR TKFDGDANG DFISKNAFDET - LPTVMRKAYRIAR TKFDGDANG RWIRLNEINGYA - FPKANHKLFNLMQ E IWVDRDRDLEFA - LPNLMKKVWAFAS KRIQPLPRLD METPSDKFDPDD - LPTVMRKAHALAD AAFDHG	- 366 - 338 - 352 - 354 - 370 G 373 - 272 R 385 - 358 - 355 - 351
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00003652391_2 c_00000031207_6 c_00000031207_6 c_00001007148_4 c_000001092848_3 c_000001151029_1 c_000001797282_1 c_000001803648_25 c_00000278955_4 c_00000278955_4 c_000003672363_2 c_000003872363_4 c_000004820107_1 c_000007774797_1	295 287 287 294 298 303 251 313 290 290 287 287 286 292 276	ELTEPIVSFE ABY DWRTLREGVR TF ELIGHADRFO AID DWKPHEGRVY SP EFOEWMDEFO GV PWEPC-GTVT TF DWKPOPGLVY SP RWKRLPGLVY GP DWQDDGABVR SF TIKNKIGEIR RY GWYKLAGTVN AP DWQRLDAQVR TF ESEQTNLSVK SEWKGIGGIR IF	HIVWOLTVFFGEL TRKLELRITVAEL TRKLELRIMTINS HFFDLELKIMTINS HFFLALSVYRAFV HFFLELSLIVATIN HFFLELSLIVATIN HFFLELSLIVATIN HFFLELSLIVATIN HFFLELSLIVATIN HFFLELSLIVATIN HFFLELSLIVATIN HFFTILSGEFICEL HFQLQLQVRVAVV HFFRESLIVATIN HFF			PVEEPY	RIAPEDELKAYAFYVSHQRVWREYKEWASGVRRPD- FLISKHAFRSDLPTV- ETIPIDGGDRLPALHRKSIAAARELLLEVFR FWCREEVKAQALPSIMMKIMTIMYKA EWWGIDELARTPISVAGRVATRYERILBHNGAQA- WWCAPGLIAGEALPTVMKKVVEAAISGATKARRPI RFTPRSALDDEPLPGLMRKVLAHAFDPKPEPEKKPI HFIADAPFDETLPTVMRKAYRIARTKFDGDANG DFISKNAFDETLPTVMRKAYRIARTGPFDNN RWIRINEINQYAFYKANHKIPNIMQE IWVDENGLOEFALPNIMKVWAFASKRIQPILPRID- MFIPSDKFPPDDLPTVMRKAHALADAAFDHG	- 366 - 338 - 352 - 354 - 370 G 373 - 272 R 385 - 358 - 355 - 351 C 361 - 311 - 293
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003552391_2 c_00000031207_6 c_000000430975_4 c_000001007148_4 c_000001092484_3 c_000001992848_3 c_00000197282_1 c_00000197282_1 c_00000197285_4 c_000002078955_4 c_000002078955_4 c_00000387531_2 c_00000387531_2 c_00000387531_2 c_00000387531_2 c_00000387531_2 c_000005774797_1 c_000005774797_1 c_000005867021_3	295 287 287 294 298 303 251 313 290 290 287 297 286 292	ELTEPIVSFE AS ENTINGEVER TF ELIGHADRO, AI DWKPHPGRVY SF EFQEMMDEFO GV PWEPC-GTVT TS DWKPQPGLVY SF RWKRLPGLVY SF RWKRLPGLVY SF DWQUDFASVR SF DWQVLNAEVR TS QWVKIAGTVN AF DWQRLDAQVR TS SEWCIGQIR IS SEWCIGQIR IS SWKCIGQIR IS DWHVLGASVR TF	HIVWOLTVFFGRI FHLILRIVABLI TRKLFIBELVYRK HFDLELKIMTINS HFFLALSVYRAW HFFLALSVYRAW HFFLELLYFVARW HFHLELSIRISVV HFHLELSIRISVV HFHLELSIRISVV HFHLELSIRISVV HFHLELSIRISVV HFHLELSIRISVV HFHLELSIRISVI HFGLQLQVRVAVV HFHRELSIRISVI HFGLGLLWHVATV			PVEEPY	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FLILSKHAFRSDLPTV- EETLPIDGGDRLPALHRKSIAARBLLLEVFR FWCRKEEVKAQALPSLMHKIMTHMYKA EWWGIDELATRPLSVAGRRVATKVEBILRHNGAQA- WWCAFGLIAGEALPTVMKKVVEAAISGATKARRFI RETPRSALDDEPLPGLMRKVLAHAFDPKEPEFKEPI- HFIADADFDETLPTVMKAYILAGTQFDDN DFISKNAFDPETLPTVMKAYRIACTQFDDN EWIRLINEIN/JWAFPKANHKIPNIMQ-E IWVDRDRLDEFALPTVMKKWAFASKRIQPLPRLDG METIFSDKFDPDDLPTVMKKAHALADAAFDHG KETADDCFDPADLPTVMKKAHKLALGSFVGD	- 366 - 338 - 352 - 370 G 373 - 272 R 385 - 358 - 355 - 351 C 368 - 351 - 311 - 293 - 293
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_00000031207_6 c_00000033207_6 c_000001007148_4 c_000001092848_3 c_000001151029_1 c_000001797282_1 c_000001797282_1 c_000002106160_4 c_000003607531_2 c_000003872363_4 c_000004820107_1 c_000003872363_4 c_000004820107_1 c_000005867021_3 c_00000455108_5	295 287 287 294 298 303 251 313 290 290 287 287 286 292 276	ELTEPIVSFE AS ENTITURESEY TE ELIGIADERO, AI DWKPHPGRVY SE EROEMDEFO GVI WEPC-GTVT TE WKRPPGLVY SE RWKRLPGLVY SE RWKRLPGLVR GP DWQDEGASVR SE DWQVLNABVR TE SEWKLIGGUR TE SEWKGIGGUR TE LWVDSWEFFK SE LWVDSWEFFK SE LWVDSWEFFK SE ENTREMENTER ELWYDSWEFFK SE ENTREMENTER ELWYDSWEFFK SE ENTREMENTER ELWYDSWEFFK SE LWYDSWEFFK SE	HIVWOLTVFFGEL FRHLIRIRVAEL FRHLIRIRVAEL FRHLELKIMTINS FFHLELVYRAW HFFLELVYRAW HFHLELSIRISVY HFHLELSIRIVY HFHLRISHIVY HFHLRISHIVY HFHLRISHIVY HFHLRISHIVY HFHLRISHIVY HFHLRISHIVY HFHLRISHIVY HFHLRISHIVY HFHLRISHIVY HFHLRISHIVIY HFHLRISHIVY HFH			PVEEPY	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FLISKHAFRSDLPTV- ETIPIDGGDRLPALHRKSIAARBLLLEVR FWCRKEEVKAQALPSLMHKINTHMY EWWGIDELARRPLSVAGRRVATKVE	- 366 - 338 - 352 - 354 - 370 G 373 - 272 R 385 - 355 - 351 C 368 - 351 - 311 - 293 - 351 - 351 - 351
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00003652391_2 c_00000031207_6 c_00000031207_6 c_000001007148_4 c_000001097248_3 c_000001151029_1 c_000001797282_1 c_000001803648_25 c_000002078955_4 c_000002078955_4 c_000003807531_2 c_000003872363_4 c_000004820107_1 c_00005774797_1 c_000055774797_1 c_000005774797_1 c_00000576456210_2 c_000004551008_5 c_000000551148_4	295 287 287 298 303 251 313 290 287 297 286 292 276 290 287 287	ELTEPIVSFE AB DWRTLRGEVR TF ELIGHADRPQ AI DWKPHEGRVY SF EPQEMMEFQ GV PWEPC-GTVT TF DWKPQPGLVY SF RWKRLPGLVR GF DWQDVLABAVR SF DWQVLNAEVR TF TIKNRIGEIR MY GWYKLAGTVN AF DWQRLDAQVR TF SEEQVILLSVK SF SEWKGIGQIR IF LWVDSWEPFK SE LWVDWEPFK SE LWVDWEFFK SE LWIDWEFFK SE LWIKKLEKVK SF	HIVWOLTVFFGRI THELILRIVARI TERLELRIMTINS HEFDLELRIMTINS HEFDLELRIMTINS HEFDLELRIMTINS HEFDLELRIMTINS HEFDLELRIMTINS HEFDLELRIMTINS HEFDLELRIMTINS HEFDLILRIMT HEFDLICLOVERAV HEFDLICLOVERAV HEFDLILRIMT HEFD			PVEEPY	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FLISKHAFRSDLPTV- ETIPIDGGDRLPALHRKSIAAARELLLEVFR FFUCREEVKAQALPSLMMKIMTHMYKA	- 366 - 338 - 354 - 370 G 373 - 272 R 355 - 351 - 351 - 351 - 351 - 355 - 351 - 351 - 351 - 351 - 351 - 351 - 351
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_00000031207_6 c_00000033207_6 c_000001007148_4 c_000001092848_3 c_000001151029_1 c_000001797282_1 c_000001797282_1 c_000002106160_4 c_000003607531_2 c_000003872363_4 c_000004820107_1 c_000003872363_4 c_000004820107_1 c_000005867021_3 c_00000455108_5	295 287 287 294 298 303 251 313 290 290 287 297 286 292 276 292 276 297	ELTEPIVSFE AB DWRTLRGEVR TE ELIGHADREQ AI DWKPEPGEVY SE EFQEWMEEFG GV PWEFC-GTVT TE DWKPOPGLYY SE RWKRLPGLVR GF RWKRLPGLVR GF RWKRLPGLVR GF RWQVLNAEVR TE TIKNKIGEIR TE DWQVLDAGVR TE LWVDSWEPFG SE LWVDFWEFFG SE LWVDFWEFFK SE LWVDFWEFFK SE LHIKKLGKVK SE SEMKGIGGUR IE LWVDFWEFFK SE LWVDFWEFFK SE LHIKKLGKVK SE SEMKRIGGUR IE LWVDSWEPFK SE LHIKKLGKVK SE LHIKKLGKVK SE SENIKLSKVK SE SEMKRIGGUR IE ROMEN GROWNER LWVDFWEFFK SE LHIKKLGKVK SE LHIKKLGKVK SE SESIALBIK TE SEQ SEIALBIK TE SEQ SEQ SEIALBIK TE SEQ SEIALBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEQ SEQ SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEQ SEQ SEQ SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEQ SEQ SEQ SEQ SEABLBIK TE SEQ SE SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEABLBIK T	HIVWOLTVFFGEL TRKLFIHPLVYRY HFDLELKIMTINS HFFLELCHIMTINS HFFLELSTYPARY HFFLELSTYPARY HFFLELSTYPARY HFHRLSIRISVY HFHRLSIRISVY HFHRLSIRISVY HFHRLSIRISVY HFHRLSIRISVY HFHRLSIRISVY HFHLRSIRISVY HFHLRSIRISVY HFHLRSIRISVY HFHLRSIRISVY HFHLRSIRIVY HFHLRSIRIVY HFHLRSIRIVY HFDLIT			PVEEPY	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FLISKHAFRSDLPTV- ETIPIDGGDRLPALHRKSIAAARELLLEVFR FFUCREEVKAQALPSLMBKIMTHMYKA EWWGIDELAGRLPSLMBKIMTHMYKA EWWGIDELAGRALPTVMKKVVEAAISGATKARRPI(RETPRSALDDEPLPGLMRKVLAHAFDPKPEPEKKPI- HFIADADPDEPLPGLMRKVLAHAFDFKPEDEKKPI- HFIADADPDEPLPGLMRKAYLIAHTKPEGGDANG DFISKNAFDPETLPTVMRKAYRIACTQFDDN RWIRINEINQYAFPKANBKLFNLMQE IWVDDKNLDEFALPSLMKWWAFAS KRIPDEFADLPTVMRKAHALADAAFDHG KFIADDCFDEADLPTVMRKAHALADAAFDHG QSFSLNQLDSIGLSAPVKGLVNKLY QSFSLNQLDSIGLSAPVKGLVNKLY QSFSLNQLSIGLSAPVKGLVNKLY VWDYDKNVESIGLPAPVKKTINQLY VWDVDKNVESIGLPAPVKKTINQLY	- 3666 - 338 - 354 - 357 - 370 G 373 - 358 - 355 - 351
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00003652391_2 c_00000031207_6 c_00000031207_6 c_000001007148_4 c_000001092848_3 c_000001151029_1 c_000001797282_1 c_000001803648_25 c_000002106160_4 c_000003807531_2 c_000003872363_4 c_000004820107_1 c_00000587021_3 c_000005870378_2 c_0000005870378_2 c_0000005870378_2 c_0000005870378_2 c_0000005870378_2 c_0000005870378_2 c_0000005870378_2 c_0000005870378_2	295 287 287 294 298 303 251 313 290 297 287 297 286 292 276 290 287 287 282 270 293 287	ELTEPIVSFE AB DWRTLRGEVR TE ELIGHADREQ AI DWKPEPGEVY SE EFQEWMEEFG GV PWEFC-GTVT TE DWKPOPGLYY SE RWKRLPGLVR GF RWKRLPGLVR GF RWKRLPGLVR GF RWQVLNAEVR TE TIKNKIGEIR TE DWQVLDAGVR TE LWVDSWEPFG SE LWVDFWEFFG SE LWVDFWEFFK SE LWVDFWEFFK SE LHIKKLGKVK SE SEMKGIGGUR IE LWVDFWEFFK SE LWVDFWEFFK SE LHIKKLGKVK SE SEMKRIGGUR IE LWVDSWEPFK SE LHIKKLGKVK SE LHIKKLGKVK SE SENIKLSKVK SE SEMKRIGGUR IE ROMEN GROWNER LWVDFWEFFK SE LHIKKLGKVK SE LHIKKLGKVK SE SESIALBIK TE SEQ SEIALBIK TE SEQ SEQ SEIALBIK TE SEQ SEIALBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEQ SEQ SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEQ SEQ SEQ SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEQ SEQ SEQ SEQ SEQ SEABLBIK TE SEQ SE SEABLBIK TE SEQ SEQ SEABLBIK TE SEQ SEABLBIK T	HIVWOLTVFFGEL TRKLFIHPLVYRY HFDLELKIMTINS HFFLELCHIMTINS HFFLELSTYPARY HFFLELSTYPARY HFFLELSTYPARY HFHRLSIRISVY HFHRLSIRISVY HFHRLSIRISVY HFHRLSIRISVY HFHRLSIRISVY HFHRLSIRISVY HFHLRSIRISVY HFHLRSIRISVY HFHLRSIRISVY HFHLRSIRISVY HFHLRSIRIVY HFHLRSIRIVY HFHLRSIRIVY HFDLIT			PVEEPY	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FLISKHAFRSDLPTV- ETIPIDGGDRLPALHRKSIAAARELLLEVFR FFUCREEVKAQALPSLMBKIMTHMYKA EWWGIDELAGRLPSLMBKIMTHMYKA EWWGIDELAGRALPTVMKKVVEAAISGATKARRPI(RETPRSALDDEPLPGLMRKVLAHAFDPKPEPEKKPI- HFIADADPDEPLPGLMRKVLAHAFDFKPEDEKKPI- HFIADADPDEPLPGLMRKAYLIAHTKPEGGDANG DFISKNAFDPETLPTVMRKAYRIACTQFDDN RWIRINEINQYAFPKANBKLFNLMQE IWVDDKNLDEFALPSLMKWWAFAS KRIPDEFADLPTVMRKAHALADAAFDHG KFIADDCFDEADLPTVMRKAHALADAAFDHG QSFSLNQLDSIGLSAPVKGLVNKLY QSFSLNQLDSIGLSAPVKGLVNKLY QSFSLNQLSIGLSAPVKGLVNKLY VWDYDKNVESIGLPAPVKKTINQLY VWDVDKNVESIGLPAPVKKTINQLY	- 3666 - 338 - 354 - 357 - 370 G 373 - 358 - 355 - 351
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003552391_2 c_00000031207-6 c_000000430975_4 c_000001007148_4 c_000001007148_4 c_000001092848_3 c_000001797282_1 c_000001797282_1 c_000001797282_1 c_000002078955_4 c_0000020166160_4 c_000003807531_2 c_000003872363_4 c_000003872363_4 c_000003872363_4 c_00000587021_3 c_00000587021_3 c_00000587021_3 c_00000571378_2 c_00000571378_2 c_00000571378_2 c_00000571378_2 c_00000571378_2 c_00000571378_2 c_000000598175_2 c_000000598175_2 c_000000598175_2 c_000000598175_2 c_000000598175_2 c_000000598175_2 c_000000598175_2 c_000000598175_2 c_000000598175_2 c_000000598175_2	295 287 287 294 298 303 251 313 290 297 287 297 286 292 276 292 287 287 282 279 282 2793	ELTEPIVSFE AB ELIGHADREQ AP ELIGHADREQ AP DWKPAPEGRVY SP PWEPC-GTVT TE DWKPQPGLVY SP RWKRLPGLVY SP RWKRLPGLVY SP RWKRLPGLVY SP RWCVLINAEVR TE TIRNKIGEIR RY GWVKIAGTVN AP DWQRLDAQVR TE SEEQTILLSVK SP SEWKGIGGIR IP DWHVLGAEVR TE LWVDWEPFK SP LNIKKLSKVK SP LNIKKLSKVK SP LNIKKLSKVK SP LNIKKLSKVK SP LNIKKLSKVK SP LNIKKLSKVK SP SSLINLABIL TE SDLINEVAPFT VP SPUEDFSSFE HIL	HIVWOLTVFFGEL FHLILRIVABL TRKLFIHELVYRE FFFDLELKIMTINS HFFTLALSVYRAWY HFFTLALSVYRAWY HFFTLELKIMT HFFTLELKIMT HFFTLELKIMT HFFTLELKIMT HFFTLELKIMT HFFTLELKIMT HFFTLELKIMT HFFTLELKIMT HFFTLELKIMT HFTT		- NY	PVEEPY TPAVG I PAGV PEGT EGGVTA APAGS APAGT KPTAG PPATG PPATG PPATG PPATG PEVNRPF QISGG I PPVG I PPVG TAYKSKT TAHTPKT KYKNS KY	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FILISHARFSEDLPTV ETTPIDGGDRLPALHRKSIAAARELLLEVFR FWCRKEEVRAQALPSLMHKINTHMY	- 3666 - 352 - 354 - 370 370 38 - 272 8 385 - 351 - 35
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00000352391_2 c_00000031207_6 c_00000033207_6 c_00000033207_6 c_000001097148_4 c_000001097148_4 c_000001197148_2 c_000001197282_1 c_000001197282_1 c_00000197282_1 c_000003807551_6 c_000003807551_2 c_000003807551_2 c_000003807551_2 c_000003807551_2 c_000004820107_1 c_000005774797_1 c_000005774797_1 c_000005867021_3 c_000004551008_5 c_00000575378_2 c_00000575378_2 c_000005754627_3 c_000000811118_1 c_00000089687_2	295 287 287 294 298 303 251 313 290 287 287 286 292 276 287 287 287 287 287 287 282 270 293 287 274	ELTEPIVSFE AB ELIGIADRED AT ELIGIADRED AT ELIGIADRED SO EFOREMBEFO GVI PWEPC-GTVT TE PWEPCFOLTVI SP RWKRLPGLVY SP RWKRLPGLVY SP RWKRLPGLVY SP RWYKLAGTVN AP DWOLNAEVR TE CWVKIAGTVN AP DWORLDACVT SE SEWCIGGIR IP LWVDWEPFK SP LNIKKLSKVK SP LNIKKLSKVK SP LNIKKLGKVK SP LNIKKLGKVK SP CSIALABIK TE SDLINEVAPFT VS SUNEVAPFT VS VSLINEVAMFTE VSLINEVAMFTE VSLINEVAMFTE VSLINEVAMFTE VS VSLINEVAMFTE VSLINEVAM	HIVWOLTVFFGRI FRHLIRIRVAEL ITRKLEHBLUYRK HFDLELKIMTINS HFFLALSVYRAKV HFFLALSVYRAKV HFFLELKIMI HFFLELKIMI HFFLELKIMI HFFLELKIMI HFFLELKIMI HFFLELKIMI HFFLELKIMI HFFLELKIMI HFFLIRISHIMI HFFLIRISHIMI HFFLIRISHIMI HFFLIMIHI HFFLIMIHI HFFLIMIHI HFFLIMIHI HFFLELMIMIHI HFFLIMIHI HFFLIMIHI HFFLIMIHI HFFLIMIHI HFFLIMIHI HFFLIMIHI HFFLIMIHI HFFLIMINHIMI HFFLIMINHIMI HFKKHLIMINHIMI HFKKHLIMINHIMI HFKKHLIMINHIMI HFKKHLIMINHIMI HFKKHLIMINHIMI HFKKHLIMINHIMI HFKKHLIMINHIMI HFKKH HFKKH		NY LGV	PVEEPY - TPAVG - I PAGV - I PAGV - PEGT - EGGVTA - APAGS - APAGT - KPTAG - PPATG - PPATG - PPATG - PPATG - TPYVG - I PYVG - I PYVG - I PYVG - KYKNS - SIDRNIF - PDGCGW - MPQQAG	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FILISHARFSDLPTV EFILISHARFSDLPTV EFITPIDGGDRLPALHRKSIAARBLLLEVFR FWCRKEEVKAQALPSLMHKINTHMYKA EWVGIDELATRPLSVAGRRVATKVERILRHNGAQA- WWCAPGLIAGEALPTVMKKVVEAAISGATKARRFI RFTPRSALDDEPLPTVMKKAYLAHAFDPKPEPEKKPI- HFIADADFDETLPTVMKKAYRIARTKFGGDANG DFISKNAFDPETLPTVMKKAYRIACTQFDDN EHVIRLINEINQVAFPKANHKLPILMQE- IWVDRDRLDEFALPTVMKKWAFASKRIQPLPRLDG METIFSDKFDPDDLPTVMKKAHALADAAFDHG KFIADDCFDPADLPTVMKKAHALADSFYGD GSFSINQLDSIGLSAPVKGLVNDLY GSFSINQLSIGSAPVKGLVNDLY VWDYKNVESLGLPAPVKKTINQLT LWYDYLKNVESLGLPAPVKKTINQLT LWYNTITEFRGGLAAPTKKLVKQITAIV NWWNISDSVMG	- 3666 - 358 - 359 - 359 - 370 - 272 - 355 - 351
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_0000003652391_2 c_00000031207_6 c_000001097148_4 c_00001097248_3 c_00001197282_1 c_00001197282_1 c_000001803648_25 c_000002078955_4 c_000002078955_4 c_000003607531_2 c_000003607531_2 c_000004820107_1 c_00000587021_3 c_000004820107_1 c_00000587021_3 c_000005511148_4 c_00000577378_2 c_00000598175_2 c_00000089175_2 c_000001176522_24 c_000001345122_1	295 287 294 298 303 251 313 290 290 287 297 286 292 276 290 287 282 270 293 287 274 290 289	ELTEPTVSFE AB DWRTLRGEVR TF ELIGHADRPQ AI DWKPHEGEVY SF ETQEWMEEPG GV PWEPC-GTVT TF DWKPQPGLVY SF RWKRLPGLVR GF DWQVLNAEVR TF TIKNKIGEIN GF GWVKLAGTVN AF DWQVLNAEVR TF LWLDSWSFF SEWKGIGGIR IF DWHYLGAEVR TF LWVDSWEPFK SF LWVDFWEFFK SF LWVDFWEFFK SF LHIKKLGKVK SP GSSIALABLK TF SOLINEVAPFT VF PVEEDFSFE HL VSLINEVAFFT TF VSLINEVAFFT TF VSLINEVAFFT TF VEEDAVIA	HIV			PVEEPY	RIAPEDELKAYA—-FYSHQRWREYK—EWASGVRRDD- FLISKHAFRSD—LPTV ETIPIDGGDR——LPALHRKSIAAAR—ELLLEVFR— FFUCRKEVKAQA—LPSLMBKIMTHMY—KA— EWWGIDELARTP—LSVAGRAVATEVE—RILBHRGAQA- WWCAPGLIAGEA—LPTVMKKVVEAAI—SGATKARRFIC RETPRSALDDEP—LPGLMRKVLAHAF—DPKEPEKKPI HFIADADFD DET—LPTVMRKAYRIAC—TQFDDN— RWIRINEINQYA—FPKANBKLFNLMQ—E— LWVDENGLIBEFA—LPHIMKWAPAS—KRIQPLPRLD MFIFSDKFDPDD—LPTVMRKAHALAD—AAFDHG— KFIADDCFDBAD—LPTVMRKAHKLAL—GSFVGD— QSFSLNQLDSLG—LSAPVKGLVNKLY— QSFSLNQLDSLG—LSAPVKGLVNKLY— VWVDYKNVESLG—LPAPVKRTNQLY— VWVDYKNVESLG—LPAPVKRTNQLY— VWVDYKNVESLG—LPAPVKTNQLY— VWVDYKNVESLG—LPAPVKTNQLY— VWVDYKNVESLG—LPAPVKTNQLT—KP— LWWNTROG—LAAPVCTLNITK—NIEKELENDT VWVDISKNENGG—LAAPVCTLNITK—NIEKELENDT VWVDISKNENGG—LAAPVCTLNITK—NIEKELENDT VWVDISKNENGG—LAAPVCTLNITK—NIEKELENDT VWVDISKNENGG—LAAPVKLVKUT—LEK— KWVSLSKLKKYP—FPAANVKIVKYLT—EK— QWLPLAQALEMM—IPAAVKRVLQEVI—EYEQNR—	- 3666 - 352 - 354 - 357 - 358 - 358 - 358 - 358 - 358 - 358 - 351 - 311 - 293 - 351 - 353 - 355 - 354 - 354 - 281
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00003652391_2 c_00000031207_6 c_00000031207_6 c_000001007148_4 c_00000109148_3 c_000001197282_1 c_00001197282_1 c_0000197197282_1 c_000001803648_25 c_000002106160_4 c_000003807531_2 c_000003872363_4 c_000004820107_1 c_000003872363_4 c_00000455108_5 c_000005774797_1 c_00000587021_3 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_00000157532_2 c_0000015531_2 c_0000015531_6_2 0000015531_6_2 0000015531_6_2 0000015531_6_2 0000015531_6_2 0000015531_6_2 0000015531_6_2 0000015531_6_2 0000015531_6_2 00000155536_6_2 00000155536_6_6	295 287 287 294 298 303 251 313 290 287 287 286 292 276 287 287 287 287 287 287 282 270 293 287 274	ELTEPIVSFE AS ELIGIADREVA TE ELIGIADREVA SE ELIGIADREVA SE EPQEMMDEFO GVI PWEPC-GTVT TE ESQUILIST LWUDWEPFK SE LWUDWEPFK SE LMITKLISTVK SE LMITKLISTVK SE LMITKLISTVK SE QESIALABIK TE PVELDFSSFE HL VSLINKVMTIK TI VSLINKVMTIK TE EQAVI	HIVWOLTVFFGRI FHLIRIRVAEL YRKLFIBELVYRK HFDLELKIMTINS RFFLELGPIVANW HFTLALSVYRAKV HFPLELTYFVARW HFPLELSIRVSTI HFPLELGRISVYRAV HFHLRLSIRVSTI HFPLELTYFVARW HFHLRLSIRVSTI HFHLIRIPTIJEN HFH			PVEEPY - TPAVG - IPAGV - IPAGV - PEGT - BEGVTA APAGS - APAGT - KPTAG PPATG - PPATG - PPATG - PPATG - IPTVG - ISGG - IPTVG - SPDVG - TAYKSKT - TAHTPKT - KYKNS - KYKNS - WMEDNES - WMEDNES - WINDKQL - SIDRRIF - PDGCGW - MPQQAG - WSEADES	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FLISKHAFRSDLPTV EFIT PIDGGDR	- 3666 - 352 - 354 - 370 G 373 - 272 R 365 - 355 - 355 - 351 - 351 - 355 - 351 - 355 - 351 - 355
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_00000031207_6 c_00000031207_6 c_000001007148_4 c_00000109148_3 c_000001151029_1 c_00000197282_1 c_000001803648_25 c_000001803648_25 c_000002078955_4 c_000002106160_4 c_000003872363_4 c_000004820107_1 c_00000587021_3 c_000004820107_1 c_00000587021_3 c_00000557378_2 c_000000557378_2 c_00000057378_2 c_0000057378_2 c_000057378_2 c_000057378_2 c_0000057378_2 c_0000057378_	295 287 294 298 303 251 313 290 287 287 287 287 287 287 282 270 283 287 270 293 287 270 293 287 270 293 287 270 293 287 270 289 262 279 288	ELTEPIVSFE AS ELIGIADREVA TE ELIGIADREVA SE ELIGIADREVA SE EPQEMMDEFO GVI PWEPC-GTVT TE PWEPC-GTVT TE PWEPC-GTVT TE PWEPC-GTVT TE RWKRLPGLIVA SE RWKRLPGLIVA SE RWKRLPGLIVA SE RWCLLAGER AS DWQVLDADVA TE ESEQTILSVK SE SEWKGIGGIR TE LWVDSWEPFK SE LMIVENGAEVA TE LWVDSWEPFK SE LMIKKLISKVK SE LMIKKLISKVK SE OSSIALABIK TE PVELDFSSFE HL VSLINVAMIK TE PVELDFSSFE HL SEWGLLPGTL VI SEWGLLPGTL V	HIVWOLTVFFGEL FRHLIRIRVAEL FRHLIRIRVAEL FRHLELKIRTINE FFDLELKIMTINS FFFLELVFYARW FFFLELSIRSVYIRIV FFFLELSIRSVYIRIV FFFLELSIRSVYIRIV FFFLELSIRSVYIRIV FFFLELSIRVYIRIV FFFLELSIRVYIRIV FFFLELSIRVYIRIV FFFLIRIPVILI FFF			PVEEPY - TPAVG - IPAGV - IPAGV - PEGT - PEGT - APAGS - APAGT - KPTAG- PPATG - PPATG - PPATG - PPATG - IPTVG - ISGG - IPTVG - SPDVG - TAYKSKT - TAHTPKT - KYKNS - KYKNS - KYKNS - WEENES	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRD- FLISKHAFRSDLPTV ETT PIDGGDRLPALHRKSIAAR	- 3666 - 3526 - 3536 - 3546 - 3556 -
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00003652391_2 c_000000352391_2 c_00000031207_6 c_000001097148_4 c_000001097148_4 c_00001197282_1 c_00001197282_1 c_000001197282_1 c_000002073895_4 c_000002073895_4 c_000003803648_25 c_000002106160_4 c_00000387263_4 c_00000387263_4 c_00000387263_4 c_000005774797_1 c_000005876021_3 c_000005794797_1 c_000005794797_1 c_00000587622_3 c_00000571378_2 c_00000571378_2 c_000001716522_2 c_000001716522_2 c_0000011118_1 c_00000181118_1 c_00000181118_1 c_00000181118_1 c_00000181166_2 c_00000181118_1 c_00000181166_2 c_0000018116_2 c_00000018116_2 c_0000018116_2 c_0000018116_2 c_0000018116_2 c_0000018116_2 c_0000018116_2 c_0000018116_2 c_0000018116_2 c_0000018116_2 c_0000018116_2 c_00000018116_2 c_0000001816_2 c_00000001816_2 c_0000001816_2 c_0000001816_2 c_0000001816_2 c_0000001816_2 c_0000001816_2 c_000001816_2 c_000001	295 287 294 298 303 251 313 3290 287 297 286 292 276 290 287 287 287 297 287 293 287 274 290 289 262 279 283 289 283	ELTEPIVSFE AB DWRTLRGEVR TP ELIGHADRPQ AI DWKPPGREVY SP EVEWMDEFO GV PWEPC-GTVT TP DWKPQPGLVY SP RWKRLFGLVR GP RWKRLFGLVR GP RWCATLAGEVR SP DWQVLNAZVR TP TIKNKIGEIR RY QWVKIAGTVN AP DWQRLDAQVR TP LWVDSWEPFK SP LWVDSWEFFK SP LWVDSWEFFK SP TP GESLALSAFR TP EQAVI RSWQDLPGFL VI SOVELIKGUK TP SADMISKIK TP	SHLVWOLTVFFGRI FFHLILRIRVAEL TRKLFIHPLVYRY HFFDLELKIMIT HFFDLELKIMIN HFFTLALSVYRAW HFFTLALSVYRAW HFFTLALSVYRAW HFFTLELKIMIN HFFTLELKIMIN HFFTLELSIRISVY HFFTLELSIRISVY HFFTLELSIRISVY HFFTLELSIRISVY HFFTLELSIRISVI HFFTLELSIRISVI HFFTLELSIRISVI HFFTLELSIRISVI HFFTLELSIRIVI HFFTLELSIRIVI HFFTLELSIRIVI HFFTLYHPTOIRM HFTTLYHPTOIRM HFTTLYHPTOIRM HFTTLYHPTOIRM HFTTLYHPTOIRM HFTTLYHPTOIRM HFTTLYHPTOIRM HFTTLYHPTOIRM HFTTLYHPTOIRM HFTTLHIPTUR HTT			PVEEPY	RLAPEDELKAYA - FPVSHQRVWREYK - EWASGVRRDD- FLISKHAFRSD- LPTV ETIPIDGGDR LPALHRKSIAAR ELLLEVFR- FFUCRKEEVKAQA - LPSLMMKIMTHMY - KA- EWWGIDELATRP - LSVAGRKVATKVE - RIJRHNGAQA WWCAPGLIAGEA - LPTVMKKVVEAAI - SGATKARRFI RFTPRSALDDEP - LPGLMRKVLAHAF - DDKEPEPKKPI HFIADADPDET - LPTVMRKAYRIAR - TKFEGGDAN- DFISKNAFDET - LPTVMRKAYRIAC - TQFDDN - RWIRLNEINQYA - FPKANHKLFNIMQ - E- IWVDRÜNLÖBEFA - LPHLMKKWAPAS - KRIQPLPRLDI METISDKFDEDD - LPTVMRKAHALAD - AAFDHG SFSLINQLDSLG - LSAPVKGLVNQLY - VWDYKNVESLG - LPAPVKKTINQLT - KP- LWYNTYENGGG - LAAPVKGLVNQLY - VWYDYKNVESLG - LPAPVKKTINQLT - KP- LWYNTYENGG - LAAPVKGLVNGT - NIEKEIENOT VWYLDGSIEVG - LAAPTKKLVKQIT - AIV WWYNISDSING - TPKPKVDILKKYD - KWYSLSKLKKYP - FPAANVKIVKYLT - EK- QWLPLAQALKMY - TPAAVKRVLQEU - EYEQNR - CWADAAAWAELG - LPAPIKKLINGUT - AIV CWADAAAWAELG - LPAPIKKTINGLT - KP- LWYNTISDSWG - TRAVKVLVKYLT - EK- QWLPLAQALKMY - TPAAVKRVLQEU - EYEQNR - CWADAAAWAELG - LPAPIKKLINGEL - A CWADAAAWAELG - LPAPIKKLINGE - A CWADAAAWAGLG - LPAPIKKLINGEF - A CWADAAAWAGLG - LPAPIKKLINGEF - A CWADAAAWAGNG - LPAPVKKLIDAGF - AG - LWWNYLSDSVG - LVAPUTLINITK - DIVKGYQNDT	- 368
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_00000031207_6 c_00000031207_6 c_000001007148_4 c_00000109148_3 c_000001151029_1 c_00000197282_1 c_000001803648_25 c_000001803648_25 c_000002078955_4 c_000002106160_4 c_000003872363_4 c_000004820107_1 c_00000587021_3 c_000004820107_1 c_00000587021_3 c_00000557378_2 c_000000557378_2 c_00000057378_2 c_0000057378_2 c_000057378_2 c_000057378_2 c_0000057378_2 c_0000057378_	295 287 294 298 303 251 313 290 287 287 287 287 287 287 282 270 283 287 270 293 287 270 293 287 270 293 287 270 293 287 270 289 262 279 288	ELTEPIVSFE AS ENTITLESEVE TE ELIGIADREO, AI DWKPHEREVY SE EPOZEMBEFO GVI PWEPC-GTVT TE DWKPDPGLIVY SE RWKRLPGLIVY SE RWKRLPGLIVY SE RWKRLPGLIVY SE RWKRLPGLIVY SE DWOVLINAEVE TE CWVKIAGTVN AF DWORLDACVE TE SEEQENLESVE SE SEWKGIGGIR IF DWHVLGASVE TE LWVDWEPFK SE LNIKKLSKVK SE LNIKKLSKVK SE LNIKKLSKVK SE CESIALAEIK TE SDLINEVAPFT VE PVEEDFSSE HL VSLINEVAMFT EGAVI	HIVWOLTVFFGEL THELILRIVABL TRKLFIHELVYRE HFDLELKIMTINS HFFLALSVYRAW HFFLALSVYRAW HFFLELKIMTH HFFLELKIMTH HFFLELKIMT HFFLELKIMT HFFLELKIMT HFFLELKIMT HFFLELKIMT HFFLELKIMT HFFLELKIMT HFFLELKIMT HFFLILRIST			PVEEPY TPAVG I PAGV PEGT EGGVTA PEGT EGGVTA APAGS APAGS APAGT KPTAG PPATG NEVAGG I PPVG AVINS	RIAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FILISHARFSDLPTV ETIPIDGGDRLPALHRKSIAAARELLLEVFR FWCRKEEVKAQALPSLMHKKIMTHMY EWVGIDELATRPLSVAGRRVATKVEBIJRHKGAQA- WWCAPGLIAGEALPTVMKKVVEAAISGATKARRFI RFTPRSALDDEPLPGLMRKVLAHAFDPKPEPEKKPI- HFIADADFDETLPTVMKKAYRIAR	- 366 - 368 - 369
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_0000003652391_2 c_00000033075_4 c_000001097148_4 c_000001097148_4 c_000001097148_3 c_00001151029_1 c_000001797282_1 c_00000278955_4 c_00000278955_4 c_00000278955_4 c_000003670531_2 c_000003670531_2 c_000003670531_2 c_000004820107_1 c_000057774797_1 c_00005867021_3 c_00000557021_3 c_00000557021_3 c_00000557021_3 c_00000557021_3 c_000005774797_1 c_000005867021_3 c_00000151118_4 c_0000057738_2 c_00000151118_1 c_0000057738_2 c_00000151118_1 c_0000057738_2 c_00000151118_1 c_0000057738_2 c_000001515736_6 c_000001515736_6 c_000001515736_6 c_000002038721_4 c_000002038721_4 c_000002038721_4 c_000002038721_4 c_00000208528_2	295 287 294 315 290 287 297 287 297 287 297 287 297 287 297 287 287 287 287 287 293 287 274 316 287 287 287 287 287 287 287 287 287 287	ELTEPIVSFE AS ENTERGEVE TE ELIGIADREO, AL ELIGIADREO, AL EPQEMMDEFO, GV PWEPC-GTVT TE ENTERGEVE SE EPQEMMDEFO, GV PWEPC-GTVT TE ENTERGEVE SE LINITALISE ENTERGEVE SE LINITALISE ENTERGEVE SE LINITALISE ENTERGEVE SE ENTERGEVE S	SHUYWOLTVFFGKI YRKLFIBELVYRK LFHLILRENABL HFPLELKIMTINS LFRLHLQPIVAMW HFFLALSVYRAKV HFPLELIVFVAKW HFFLELSIRISVY HFFLELISIRISVY HFFLELISIRISVY HFFLELISIRISVY HFFLELISIRISVY HFFLELISIRISVY HFFLELISIRISVY HFFLELISIRISVY HFFLICISIRISVI HFFLICISIRISVI HFFLICISIRIVA HFF			PVEEPY - TPAVG - IPAGV - IPAGV - PEGT - APAGS - APAGS - APAGT - KPTAG - PPATG - PPATG - PPATG - IPTVG	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRD- FLISKHAFRSDLPTV ETT PIDGGDRLPALHRKSIAAARBLLLEVER- FWCKREEVKAQALPSHMIKINTHMY	- 366 (34) - 352 (35) - 354 (35) - 354 (35) - 355 (35) - 351 (35)
sp_17802_MUTY_ECOL sp_P3847_MUTY_GEOS c_00003652391_2 c_00000031207_6 c_00000031207_6 c_00000031207_6 c_000001097148_4 c_000001097148_4 c_000001197148_2 c_000001197282_1 c_0000197197282_1 c_00000197282_1 c_000002106160_4 c_000002106160_4 c_00000387353_2 c_000004587021_3 c_00000459817_1 c_000005774797_1 c_00005867021_3 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_0000057531_2 c_00000151118_4 c_00000577378_2 c_00000151118_1 c_0000057376_2 c_0000015115736_6 c_00001515736_6 c_00001515736_6 c_00001523643_29 c_00000123643_29 c_00000238721_4 c_000002523527_15 c_00000287511_2 c_0000028721_4 c_000002525151_2 c_00000287511_2 c_00000238721_4 c_000002238721_5 c_000002955151_2 c_000002525151_2	295 287 294 298 303 2511 313 3290 287 297 286 6292 276 290 287 270 283 282 276 336 316 316 316 316 316 316 316 316 31	ELTEPIVSFE AS ELIGIADREN TE ELIGIADREN TE ELIGIADREN SE EPOZEMBEFO GVI PWEPC-GTVT TE ESEQTNIAVE SE SEWCIGGIR IF DWHVLGASVR TE LWVDWEPFK SE LNIVENUSEFFK SE LNIVENUSEFFK SE LNIKKLISVK SE QESIALAEIK TE SDLINEVAFFT TE EQAVIK TE EQAVIK TE ESWOLDFGL VI DEVELIKOLK TE EEKESLPLIV VE BEADKLSKIK TE EEKESLPLIV VE DEAIKLSEIK TE EARAYLAGELT VE DEAIKLSEIK TE EARAYLAGELT VE DEAIKLSEIK TE EARAYLAGELT VE DEAIKLSEIK TE EARAYLAGELT VE DEAIKLSEIK TE ESLENEVITY DEAIKLSEIK TE EISLNEVMTH EEKESLPLIV VE DEAIKLSEIK TE EISLNEVMTH	HIVWOLTVYFEGEL FRHLIRRYWEL FRHLIRRYWEL FRHLELRYFANE FFDLELKIMTINS FFFLELSTYFANE FFFLELSTYFANE FFFLELSTYFANE FFFLELSTYFANE FFFLELSTYFANE FFFLELSTYFANE FFFLELSTYFANE FFFLELSTYVANE FFHLELSTRVATI FFHLELSTRVATI FFHLELSTRVATI FFHLELSTRVATI FFHLELMYHVATV FFHLYINFICIEM SYMLEAPYLANE SYMLEAPYLANE SYMLEAPYLANE SYMLEAPYLANE FFFLTINFHVLIMT QFFVTLTYNFICH FFHLDIPTYWHT SYMLEAPYLANE SYM			PVEEPY - TPAVG - I PAGV - I PAGV - PEGT - EGGVTA - APAGS - APAGT - KPTAG - PPATG - PPATG - PPATG - PPATG - PPATG - TAYKSKT - TAHTPKT - KYKNS - WMEDNES - WNDKQL - SIDWRQL - SIDW	RIAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FILISHAFRSTSDLPTV EFTIPIDGGDRLPALHRKSIAAARBLLLEVFR FWCRKEEVKAQALPSLMHKKINTHMYKA EWVGIDELATRPLSVAGRRVATKVEBILRHNGAQA- WWCAPGLIAGEALPTVMKKVVEAAISGATKARRFI RFTPRSALDDEPLPGLMRKVLAHAFDPKEPEPKKPI HFIADADFDETLPTWMKAYRIARTYFFGGDAN DFISKNAFDEETLPTWMKAYRIACTQFDDM HFIADADFDETLPTWMKAYRIACTQFDDM EWWIRLNEINGVAFPKAHKLFNIMQ EIWVDBRLDEFALPTVMKKWAFASKRIQPLPRLDG MFIFSDKFDPDDLPTVMKKWAFASKRIQPLPRLDG GSFSINQLDSIGLSAPVKGLVNKLY QSFSINQLDSIGLSAPVKGLVNKLY QSFSINQLSIGLSAPVKGLVNKLY UWVDYKNVESIGLPAPIKKTINGLT LWYNITTEFNGGLAAPTKKIVKGITAIV WWVIKNUSSIGLAAPTKKIVKGITAIV WWVIKNSUSHGLPAPIKKINGTT LWWYNISSIKKYPFPAANVKIVKYLTEK CWADAAAWABLGLPAPIKKILDAEL CWADAAAWABLGLPAPIKKILDAEL CWADAAAWABLG LPAPIKKILDAEL CWADAAAWABLG LPAPIKKILDAEL CWADAAAWABLG LPAPIKKILDAEL CWADAAAWABLG LPAPIKKILDAEL CWADAAAWABLG LPAPIKKILDAEL CWADAAAWABLG LAPVYKILDAEL CWAUSARNAMG LPAPIKKILDAEL CWADAARWADG LAPVYKILDAG LAWYNVITSENGG LAPVYKILDAG RFGLF KWYSLSSILKKYP FPAANVKIVKYKIT EK KWYSLSSILKKYP FPAANVKIVKYKIT EK KWYSLSSILKKYP FPAANVKIVKYKIT EK KWYSLSSILKKYP	- 366
sp_17802_MUTY_ECOL sp_P3847_MUTY_GEOS c_00003652391_2 c_00000035277_6 c_00000033075_4 c_000001007148_4 c_0000109248_3 c_00001151029_1 c_0000197197282_1 c_00001803648_25 c_000003803648_25 c_000003807531_2 c_000003807531_2 c_000003872363_4 c_000004820107_1 c_00000587021_3 c_000002577479_7 c_00000587021_3 c_000002577479_7 c_000000587021_3 c_000002577479_7 c_000002577479_7 c_000002577479_7 c_000002577479_7 c_000002577479_7 c_0000002577479_7 c_000002577479_7 c_0000002577479_7 c_000002577479_7 c_0000002577479_7 c_0000002577479_7 c_0000002577479_7 c_0000002577479_7 c_0000002577479_7 c_0000002577479_7 c_0000002577479_7 c_000000000257479_7 c_00000002577479_7 c_0000000000257479_7 c_00000000000000000000000000000000000	295 287 287 284 298 303 325 290 290 290 287 282 270 293 287 282 270 293 302 290 287 284 290 287 284 290 293 287 284 290 293 287 284 290 290 290 287 287 288 288 288 288 288 288 288 288	ELTEPIVSFE AS ELIGIADREVA TE ELIGIADREVA TE ELIGIADREVA SE EPQEMBUEFO GVI PWEPC-GTVT TE PWEPCFOTVT TE ESPOTNIA SEWCILGIR TE PWEPCFOT TE LWUDWEPFK SE LNITALGREVA TE LWUDWEPFK SE LNITALGREVA TE LWUDWEPFK SE LNITALGREVA TE LWUDWEPFK SE LNITALGREVA TE ENDELEFS SE LNITALGREVA SE PWEEDFSSFE VSLINKWINTIK TY FOLONIA SEADKLSKIK TE EAWTIEFF LU SEADKLSKIK TE ERWOLDFOFL VI DEAIKLSEIK TE ERWOLDFOFL VI DEAIKLSEIK TE ELEKESLPLIV DEAIKLSEIK TE ELEKESLPLIV BEARMILGELT VE BEARMILGELT FE SLINKWINTIK TY FSLOAYABLE ES KHEPKELCKFR SI ENDELEFFR SE ENDELEFFR FREMENTER FREMENT	HIVWOLTVYFORL FHLIRRYWEL FRACLEIRLYWRIA FFLELVINTINS FFLELVINTINS FFLELVIYARW HFFLELSIRISVY HFFLELSIRISVY HFFLELSIRISVY HFFLELSIRISVY HFFLELSIRISVY HFFLELSIRISVY HFFLELSIRISVY HFFLELSIRISVY HFFLELSIRISVY HFFLELSIRISVI HFFLELSIRISVI HFFLICHIYHVATV HFFLICHIPIOIRM HFFLIVHPIOIRM HFFLIVHPIOIRM HFFLIVHPIOIRM HFFLIVHPIOIRM HFFLIVHVINTI HFFLIVIYNINTI HFFLIVIYNINTI HFFLIPTYLWHI HFF			PVEEPY - TPAVG - IPAGV - IPAGV - PEGT - BEGVTA APAGS - APAGT - KPTAG - PPATG - PPATG - PPATG - PPATG - PPATG - TAYKSKT - TAHTPKT - KYKNS - WMEDNES - WMEDNES - WID - SIDRIF - PPGCEQW - MADGOGG - WMEHDDS - PIDGGEGW - MEDDS - SIDRIF - PPGCEQW - MEDDS - SIDRIF - PPGCEQW - MEDDS - SIDRIF - PPGCEQW - MEDDS - SIDRIF - PDGCEQW - MEDDGCEQW - MEDD	RIAPEDELKAYAFPVSHQRVWREYKEWASGVRRD- FILISHARFSDLPTV EFITPIDGGDRLPALHRKSIAAARBLLLEVFR FWCRKEEVKAQALPSLMHKINTHMYKA EWWGIDELARRPLSVAGRRVATKVERILRHNGAQA- WWCAFGLIAGEALPTVMKKVVEAAISGATKARRFI RFTPRSALDDEPLPGLMRKVLAHAFDPKPEPEKKPI HFIADADFDETLPTVMRKAYRIARTKFGGDANG DFISKNAFDEETLPTVMRKAYRIACTQFDDM EHVIRLNEINGVAFPKANHKIFNIM,O EIWWDRDRLDEFALPTVMRKAYRIACTQFDDM KWIRLNEINGVAFPKANHKIFNIM,O SUFSINQLOSEGLPTVMRKAHLADAAFDHG KFIADDCFDPADLPTVMRKAHLALGSFVGD GSFSINQLOSIGLSAPVKGLVNKLY GSFSINQLOSIGLSAPVKGLVNKLY GSFSINQLOSIGLSAPVKGLVNLY	- 366
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_000000352391_2 c_00000031207-6 c_00000031207-6 c_000001007148_4 c_00001092848_3 c_00001151029_1 c_00001797282_1 c_000001803648_25 c_00000278955_4 c_00000278955_4 c_000003807531_2 c_000003872363_4 c_000004820107_1 c_000005867021_3 c_000005867021_3 c_00000551118_4 c_00000551118_1 c_00000551118_1 c_00000551118_1 c_00000551118_1 c_00000551118_1 c_0000051118_1 c_0000051118_1 c_0000051118_1 c_0000051118_1 c_0000051116_2 c_0000011515736_6 c_0000011515736_6 c_00000123643_29 c_00000123643_29 c_000002523527_15 c_00000250151_2 c_000002523527_15 c_00000250151_2 c_00000250151_2 c_00000250151_2 c_00000250151_2 c_00000250151_3 c_000000250151_3 c_000003246034_1 c_000003246034_1 c_000003246034_1 c_000003246034_1 c_000003246034_1 c_000003246034_1	295 287 287 294 303 303 290 287 297 286 292 276 287 274 290 287 274 290 287 274 290 287 274 290 289 282 276 293 282 276 293 282 276 293 282 276 293 282 293 282 293 282 293 282 293 282 293 283 289 282 283 284 293 284 293 284 293 284 293 284 293 284 293 284 293 284 293 284 293 284 293 284 293 284 293 284 293 284 293 284 293 284 284 293 284 284 293 284 293 284 284 293 284 284 293 284 284 284 284 284 284 284 284 284 284	ELTEPIVSFE AS ELTEPIVSFE AS ELIGIADREQ AS ELIGIADREQ SI EFQEWMDEFQ GV PWEFC-GTVT TI EWKPGPGLVY SP EWKPGPGLVY SP EWKPGPGLVY SP EWKRALPGLVR GS EWKLAGTVN AP EWCOVINAEVR TS EWKLAGTVN AP ESEQNILSVK SS EWKLGGGIR IP DWHVLGAEVR TS LWVD SWEFFK SP LWINEKLISKVK SS QESIALABIK TS EGAVI ——K TES EGAVI ——K TES EGAVI ——K TES EGAVI ——K TES EWKLIGLIK TS ADWTELPAFL VE EEKESLPLIV NL ARAYLAGELT VI EEKESLPLIV NL E	SHLVWOLTVFFGKL IFHLILRERVAEL IFHLILRERVAEL IFHLILRERVAEL IFFLELLYMING IFFLALSVYRAKV IFFLELLYVYAKW IFFLELSIRISVY IFFLELSIRISVY IFFLELSIRISVY IFFLELSIRISVY IFFLELSIRISVY IFFLELSIRISVY IFFLELSIRIVAT IFFLELSIRIVAT IFFLELSIRIVA IFFLELSIRIVAT IFFLELSIRIVAT IFFLELSIRIVAT IFFLELSIRIVAT IFFLIL			PVEEPY - TPAVG - IPAGV - PEGT - PEGT - APAGS - APAGS - APAGT - KPTAG- PPATG - PPATG - PPATG - PPATG - IPTVG -	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRD- FLISKHAFRSDLPTV ETITIDGGDRLPALHRKSIAAARBLLLEVFR FWCKREEVKAQALPSLMIKINTHMY	- 366
sp_17802_MUTY_ECOL sp_P3847_MUTY_GEOS c_00003652391_2 c_00000035277_6 c_00000033075_4 c_000001007148_4 c_0000109248_3 c_00001151029_1 c_0000197197282_1 c_00001803648_25 c_000003803648_25 c_000003807531_2 c_000003807531_2 c_000003872363_4 c_000004820107_1 c_00000587021_3 c_000002577479_7 c_00000587021_3 c_000002577479_7 c_000000587021_3 c_000002577479_7 c_000002577479_7 c_000002577479_7 c_000002577479_7 c_000002577479_7 c_0000002577479_7 c_000002577479_7 c_0000002577479_7 c_000002577479_7 c_0000002577479_7 c_0000002577479_7 c_0000002577479_7 c_0000002577479_7 c_0000002577479_7 c_0000002577479_7 c_0000002577479_7 c_000000000257479_7 c_00000002577479_7 c_0000000000257479_7 c_00000000000000000000000000000000000	295 287 287 284 298 303 325 290 290 290 287 282 270 293 287 282 270 293 302 290 287 284 290 287 284 290 293 287 284 290 293 287 284 290 290 290 287 287 288 288 288 288 288 288 288 288	ELTEPIVSFE AS ELTEPIVSFE AS ELIGIADREQ AS ELIGIADREQ SI EFQEWMDEFQ GV PWEFC-GTVT TI ENKREGEGV SS ENKREGEGV SS ENKREGEGV SS ENKREGGLVR SS ENKREGGLVR SS ENKREGGL R ENKREGGL R ENKREGGV SS ENKREGGI T ESEQNILSVK SS LWOWNEFR SS LWUDWEFFK SS LWUDWEFFK SS LWUDWEFFK SS LWUDWEFFK SS LWUDWEFFK SS LWILKERVK SS LNIKKLSKVK SS LNIKKLSKVK SS LNIKKLSKVK SS ENKREGGV SS LNIKKLSKVK SS ENKREGGV SS LNIKKLSKVK SS ENKREGGV SS ENKR	SHLVWOLTVFFGRI THELILRIVABLE THELIRRIVABLE THETOYSTYTALL THETOYSTYTALL THETOYSTYTALL THETOYSTYTALL THETOYSTYTALL THETOYSTYTALL THETOYSTYTALL THE			PVEEPY - TPAVG - IPAGV - PEGT - PEGT - APAGS - APAGT - KPTAG PPATG - PPATG - PPATG - PPATG - PPATG - IPTVG	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRD- FLISKHAFRSDLPTV ETTPIDGGDRLPALHRKSIAAARELLLEVFR FWCKTEEVKAQALPSLMKIKITHIMY	- 366, 364, 364, 364, 364, 364, 364, 364,
sp_P17802_MUTY_ECOL sp_P3847_MUTY_GEOS c_00003652391_2 c_0000003652391_2 c_00000031207_6 c_00000030975_4 c_00001097148_4 c_00001097148_4 c_00001197282_1 c_00001797282_1 c_000001803648_25 c_00000278955_4 c_00000278955_4 c_00000367531_2 c_00000367531_2 c_00000367531_2 c_000004820107_1 c_0000587021_3 c_00000587021_3 c_00000598175_2 c_000000598175_2 c_0000001515736_6 c_000001515736_6 c_0000015253527_15 c_000002398721_4 c_000002398721_4 c_000002398721_4 c_000003294679_3 c_000003333364_1 c_00003333364_1	295 287 287 297 298 298 298 298 299 290 287 297 276 299 290 287 297 276 299 290 290 290 290 290 290 290 290 290	ELTEPIVSFE AS ENTERGEVER TE ELIGIADERO AT ELIGIADERO AT ELIGIADERO AT ELIGIADERO AT EROPEMBERO SE EROPEMBERO SE EROPEMBERO SE ENVEROPELIVE SE ENVELOPELIVE SE ENVELOPELIVE SE ENVELOPELIVE SE LININGER TE LINIDGER T	HIVWOLTVFFGEL FRHLIARTWAEL FRHLIARTWAEL FRHLIARTWAEL FRHLELKIMTINS FRFLELKIMTINS FRFLELVFYAMW FFTLALSVYRAKV FFFLELSIRISVY FFFLELSIRISVY FFFLELSIRISVY FFFLELSIRISVY FFFLELSIRISVY FFFLELSIRISVY FFFLELSIRISVY FFFLELSIRISVY FFFLELSIRIVY FFFLIARTWY FFFLIARTHWY FFFVTLAWFLAFTLAFF FFFVILARTHWY FFF			PVEEPY - TPAVG - IPAGV - IPAGV - PEGT - APAGS - APAGT - KPTAG - PPATG - PPATG - PPATG - PPATG - PPATG - TAYKSKT - TAHTPKT - KYKNS - KYKNS - KYKNS - KYKNS - KYKNS - WEDNES - WINDKOL - SIDRRIF - PPGCEQW - MPQOAG - WEEDO - STORRIF - PEGDAAS - WEEDO - WEEDO - WEEDO - WEEDO - WEEDO - TAYKSKT - TAHTPKT - KYKNS - KY	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FLISKHARFSDLPTV ETITJIGGDRLPALHRKSIAAAR	- 366, 364, 364, 364, 364, 364, 364, 364,
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_000000352391_2 c_00000031207_6 c_000001097148_4 c_00001097248_3 c_00001197282_1 c_00001197282_1 c_00000197282_1 c_000002073855_4 c_000002073855_4 c_000002106160_4 c_00000387263_1 c_00000387263_1 c_00000387263_1 c_000005774797_1 c_00005867021_3 c_000005774797_1 c_000005774797_1 c_000005774797_1 c_000005774797_1 c_000005774797_1 c_000005774797_1 c_000005774797_1 c_000005774797_1 c_00000157536_6 c_000001754627_2 c_000001754627_3 c_000001823643_29 c_000001823643_29 c_000001823643_29 c_000001823643_29 c_000001823643_29 c_00000223872_1 c_0000022931510_6 c_0000022931510_6 c_0000022931510_6 c_0000022931510_2 c_0000022931510_2 c_0000022931510_2 c_00000329367_3 c_00000329467_3 c_0000032946664_5	295 287 287 297 286 6 298 299 290 297 287 287 297 287 287 297 286 290 290 287 387 297 297 297 297 297 297 297 297 297 29	ELTEPIVSFE AB ELTEPIVSFE AB ELIGHADRED AT ELIGHADRED AT ELIGHADRED AT ELIGHADRED AT ENEMBER ENEMBER AT ENE	HIVWOLTVYFEGEL THELIELRIVABLE TRKLFIBELVYRAW HFDLELKIMTINS HFFLALSVYRAW HFFLALSVYRAW HFFLELKIMI HFFLELKIMI HFFLELKIMI HFFLELKIMI HFFLELKIMI HFFLELKIMI HFFLELKIMI HFFLIELRIVYAWV HFHLELSIRVYATV HFHLELSIRVYATV HFFLIMI HFF HFF HFF			PVEEPY - TPAVG - I PAGV - I PAGV - PEGT - EGGVTA - APAGS - APAGT - KPTAG - PPATG - PPA	RIAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FILISHAHRSTSDLPTV EFTPIDGGDRLPALHRKSIAARBLLLEVFR FWCRKEEVKAQALPSLMHKKITHMYKA EWVGIDELATRPLSVAGRRVATKVERILRHNGAQA- EWVGIDELATRPLSVAGRRVATKVEBILRHNGAQA- WWCASGLIAGEALPTVMKKVVEAAISGATKARRFI RFTPRSALDDEPLPGLMRKVLAHAFDPKPEPEKKPI HFIADADFDETLPTVMRKAYRIARTYFDGDANO DFISKNAFDEETLPTVMRKAYRIACTQFDDN EIWVDRDRLDEFALPTVMRKAYRIACTQFDDN EIWVDRDRLDEFALPTVMRKAHLALASAFDHG EIWVDRDRLDEFALPTVMRKAHRLALSFFVGD GSFSINQLOSIGLSAPVKGLVNDLY GSFSINQLOSIGLSAPVKGLVNDLY GSFSINQLOSIGLSAPVKGLVNDLY WWDYKNVESIGLPAPIKKTINDLTKP WWDYKNVESIGLPAPIKKTINDLT LWYNITTEFNGGLAAPTKKLYKQITAIV NWWNISDSVSWGLAAPTKKLYKQITAIV NWWNISDSVSWG	- 366
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_000000352391_2 c_00000031207_6 c_000001097248_4 c_000001097248_3 c_00001151029_1 c_00000197282_1 c_00000197282_1 c_000002078955_4 c_000002078955_4 c_000002106160_4 c_000003872263_4 c_000003872263_4 c_000003872263_4 c_0000058702_3 c_0000058702_3 c_0000058702_3 c_0000058702_3 c_0000058702_3 c_0000058702_3 c_00000158175_2 c_0000058175_2 c_00000158175_2 c_00000238721_4 c_00000238721_4 c_00000324603_4_1 c_00000324603_4_1 c_000003492925_4 c_00000349185_7_2 c_00000349185_7_2 c_00000349185_7_2 c_000003557120_4	295 287 287 287 298 303 303 303 303 303 303 303 303 303 30	ELTEPIVSFE AS ENTERGEVER TF ELIGIADRED AT ELIGIADRED AT ELIGIADRED AT ELIGIADRED AT ENTERGEN SE ENTERG	HIVWOLTVYFOGH. FRHLIRRYWEL FRHLIRRYWEL FRHLELRYFAWE FFDLELKIMTINS FFFLELGPIVAWW FFTLALSVYRAKV FFFLELGPIVAWW FFFLELGFIVAWW FFFLELGFIVAWW FFFLELGFIVAWW FFFLELGFIVAWW FFFLELGFIVAWW FFFLIRSFROYI FFFLIRSFROOYI			PVEEPY - TPAVG - IPAGV - IPAGV - PEGT - PEGT - BEGVTA PAGS - APAGS - APAGT - KPTAG - PPATG - PPATG - PPATG - PPATG - PPATG - PPATG - STONG - IPTVG	RIAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FILISKHAFRSDLPTV ETTPIDGGDRLPALHRKSIAAARELLLEVRF FWCKREEVKAQALPSLMHKINTHMYKA EWVGIDELARRLSVAGRRVATKVERILRHNGAQA- WWCAFGLIAGEALPTVMKKVVEAAISGATKARRFI RFTPRSALDDEPLPGLMRKVLAHAFDPKPEPEKKPI HFIADADFDETLPTVMRKAYRIARTKFFGGANG DFISKNAFDEETLPTVMRKAYRIACTQFDDM RWIRLNEINGVAFPKANHKIFNIMQ EIWVDBRLDEFALPTVMRKAYRIACTQFDDM KWIRLNEINGVAFPKANHKIFNIMQ EIWVDBRLDEFALPTVMRKAHLADAAFDHG KFIADDCFDPADLPTVMRKAHLADAAFDHG KFIADDCFDPADLPTVMRKAHLAL-GSFVGD GSFSINQLDSIGLSAPVKGLVNKLY GSFSINQLSIGLSAPVKGLVNKLY WYDYKNYESIGLPAPIKKTINGLTKP VWYDYKNYESIGLPAPIKKTINGLTKP	- 366 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_0000003652391_2 c_00000031207_6 c_0000003975_4 c_00001097148_4 c_00001097148_4 c_00001197282_1 c_00001197282_1 c_000001197282_1 c_0000027895_5_4 c_0000027895_5_4 c_0000027895_1 c_00000367531_2 c_00000367531_2 c_000004820107_1 c_000005774797_1 c_00005867021_3 c_00004851008_5 c_000005511148_4 c_000005747378_2 c_00000181118_1 c_00000598175_2 c_00000181118_1 c_00000989687_2 c_000001118_1 c_000001116522_14 c_0000011515736_6 c_0000011515736_6 c_00000123643_29 c_000001254527_1 c_00000258727_1 c_000003258734_1 c_000003258734_1 c_000003258734_1 c_00000325875_2_6 c_00000325875_2_6 c_00000325875_2_6 c_00000325875_1 c_0000035575_1 c_0000035575_1 c_0000035575_1 c_0000035575_1 c_0000035575_1 c_0000035575_1 c_0000035575_1 c_00000035575_1 c_0000035575_1 c_0000035575_1 c_0000035575_1 c_0000055575_1 c_00000055575_1 c_0000055575_1 c_0000055575_1 c_0000055575_1 c_0000055575_1 c_0000055575_1 c_0000055575_1 c_0000055575_1 c_0000055575_1	295 287 287 298 303 329 290 290 287 287 287 287 287 292 2766 316 313 329 289 282 290 289 282 292 282 282 292 282 282 282 282	ELTEPIVSFE AB ELTEPIVSFE AB ELIGIADREVA TE ELIGIADREVA SE EFQEMMDEFO GV PWEPC-GTVT TE EMEROPECTY SE LINIKALSKVI SE LINIKALSKVI SE LINIKALSKVI SE LINIKALSKVI SE EMEROPETY SE LINIKALSKVI SE EMEROPETY SE LINIKALSKVI SE EMEROPETY SE EMEROPETY SE EMEROPETY SE FORD EMEROPETY SE EMEROPETY S EMEROP	SHUYWOLTVFFGKI FFHLILRIVABLI FFHLILRIVABLI FFHLILRIVABLI FFHLILRIVABLI FFHLILRIPLIVYRI FFHLIRLISTINS FFH			PVEEPY - TPAVG - IPAGV - IPAGV - PEGT - APAGS - APAGS - APAGT - KPTAG - PPATG - PPATG - PPATG - PPATG - IPYG - IPY	RLAPEDELKAYA—-FPVSHQRVWREYK—EWASGVRRD- FLISKHAFRSD—-LPTV ETTPIDGGDR——LPALHRKSIAAAR—ELLLEVER- FWCKREEVKAQA—LPSHMIKINTHMY—YA— EWVGIDELATRP—LSVAGRRVATRVE—RILHHNGAQA WWCAPGLIAGEA—LPJWMKKVVEAAI—SGATKARRFI RFTPRSALDDED—LPJWMKKVLAHAF—DPKPEPEKKPI HHTJADAFDET—LPJWMKKVLAHAF—DPKPEPEKKPI HHTJADAFDET—LPTVMKKYLAHAF—DPKPEPEKKPI HHTJADAFDET—LPTVMKKYLAHAF—DFKPEPEKKPI HHTJADAFDET—LPTVMKKYNIAHAF—TRFGGDANG—ENWIRLNEINGVA—FPKANKKIPLIMQ—E— IWVDBRIDEFA—LPHNMKKVWAFAS—KRIGPLPRLD MFIFSDKFDEDD—LPTVMKRAHKLAL—GSFVGD— QSFSLNQLGSIG—LSAPVKGLVNKLY— QSFSLNQLGSIG—LSAPVKGLVNKLY— QSFSLNQLGSIG—LSAPVKGLVNKLY— VWVDYKNVESIG—LPAPIKKTINQLT—KP— LWYNLTEFRGG—LAAPVKGLVNKLY— WYDYKNVESIG—LPAPIKKTINQLT—KP— LWYNLTEFRGG—LAAPVKGLVNKLY— NWYNLKSUSIG—LYAPVKGLVKTINGLT—KP— LWYNLTEFRGG—LAAPVKGLVNKLY— NWYNLKSUSIG—LYAPVKLVKITI—TAIV— NWYNLSDSVMMG—TPKPVKNINGLT—KP— WWYSLSKIKKYP—FPANKVLVKIT—EK— QWLPLAQALKMN—TPAAVKRVLQEVI—EYEQNR— CWADAANWARLG—LPAPVKKLLDAGP—AG— CWADAANWARLG—LPAPVKKLLDAGP—AG— CWADAANWARLG—LPAPVKKLLDAGP—AG— CWADAANWARLG—LPAPVKKLLDAGP—AG— CWADAANWARLG—LPAPVKKLLDAGP—AFGLF— KWYSLSKIKKYP—FPANNKLIKKLSKIL—EK— LWYNNKESVENG—FPAPVKKLLENGA—RFGLF— KWYSLSKIKKTP—FPANNKLLKKLSKIL—L— KWYNKKESVENG—FPAPVKKLLENGA—RFGLF— KWYSLSKIKTP—FPANNKLLKKLLSKIL—L— KWYNKKESVENG—FPAPVKKLLENGA—RFGLF— KWYSLSKIKTP—FPARHKKLLDAGV—RFGLF— KWYSLSKIKTP—FPARHKKLLDAGN—RDMYJANLV— KWYSLSCHAGP—FPARHKLLDAGN—RDMYJANLV— KWYSTSKIKGM—TFRYKKLLENGH—PTIQTY— WYNKESUKSVENG—FRANKLLENGH—PTIQTY— WYNKESUKSVENG—LAPPUKKLLENGH—PTIQTY— WYNKESUKSUKS—LAPPUKKLLENGH—PTIQTY— WYNKESUKSUKS—LAPPUKKLLENGH—PTIQTY— WYNKESUKSUKS—LAPPUKKLLENGH—PTIQTY— WYNKESUKSUKS—LAPPUKKLLENGH—PTIQKLLQNQN—RIGU— WYNKESUKSUKS—LAPPUKKLLQNQN—RIGU—PTIQTY— WYNKESUKSUKS—LAPPUKKLLQNQN—R	- 366 - 350
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_000000352391_2 c_00000031207_6 c_000001097248_4 c_000001097248_3 c_00001151029_1 c_00000197282_1 c_00000197282_1 c_000002078955_4 c_000002078955_4 c_000002106160_4 c_000003872263_4 c_000003872263_4 c_000003872263_4 c_0000058702_3 c_0000058702_3 c_0000058702_3 c_0000058702_3 c_0000058702_3 c_0000058702_3 c_00000158175_2 c_0000058175_2 c_00000158175_2 c_00000238721_4 c_00000238721_4 c_00000324603_4_1 c_00000324603_4_1 c_000003492925_4 c_00000349185_7_2 c_00000349185_7_2 c_00000349185_7_2 c_000003557120_4	295 287 287 287 298 303 303 303 303 303 303 303 303 303 30	ELTEPIVSFE AB ELTEPIVSFE AB ELIGIADREQ AT ELIGIADREQ AT ELIGIADREQ AT ELIGIADREQ AT ENEMBERGE SI ENEMBERG	HIVWOLTVYFGEL FRHLIRIRVAEL FRHLIRIRVAEL FRHLIRIRVAEL FRHLIRIRVAEL FFDLELKIMTINS FFFLELGPIVABW FFFLELGPIVABW FFFLELGPIVABW FFFLELGPIVABW FFFLELGRISVVAIV FFFLELGRISVVAIV FFFLELGRISVVAIV FFFLIRIRVIVAIV FFFLIRIPVIVAIV FFFLIRIPFILIP F			PVEEPY - TPAVG - IPAGV - IPAGV - PEGT - APAGS - APAGT - KPTAG - PPATG - PPATG - PPATG - PPATG - PPATG - PPATG - TRAVE - QISGG - IPTVG - IPAGE - IPTVG - IPAGE	RIAPEDELKAYAFPVSHQRVWREYKEWASGVRRPD- FILISKHARFSDLPTV ETTITLOGODRLPALHRKSIAAAR	- 366 - 350
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_00000031207_6 c_00000031207_6 c_00000031207_6 c_00000109148_4 c_00000109148_4 c_00000192948_3 c_000001151029_1 c_000001803648_25 c_000002106160_4 c_00003807531_2 c_000003872363_4 c_000003872363_4 c_000004820107_1 c_00000587021_3 c_000004820107_1 c_00000587021_3 c_00000587021_3 c_00000587021_3 c_00000587021_3 c_00000587021_3 c_000001851118_4 c_00000587021_3 c_000001851118_1 c_00000587021_3 c_000001851118_1 c_000001851118_1 c_000001851118_1 c_000000577378_2 c_000001851118_1 c_0000018515736_6 c_0000018515736_6 c_0000018515736_6 c_0000018515736_6 c_0000018515736_6 c_00000185252_24 c_00000185252_14 c_00000185255_1 c_00000233972_1_4 c_000001823643_29 c_000002397915_8 c_000002397915_8 c_000002397915_8 c_000003238643_1 c_000003238643_1 c_000003238643_1 c_000003238643_1 c_000003238643_1 c_000003238643_1 c_000003238643_1 c_000003248034_1 c_00003248034_1 c_000003248034_1 c_000003248036_1 c_000003248034_1 c_00000003248034_1 c_000003248034_1	295 287 287 287 294 490 290 290 297 287 282 292 276 6 292 297 287 287 287 297 287 287 297 287 287 287 287 297 287 287 287 287 287 287 287 287 287 28	ELTEPIVSFE AB ELIGIADREP AT ELIGIADREP AT ELIGIADREP AT ELIGIADREP AT ELIGIADREP AT ELIGIADREP AT ENWEPPECIVY SP ENWEPPECIVY SP ENWERPECIVY SP ESEQTINLSVK SP ESEQTINLSVK SP ESEQTINLSVK SP ESEQTINLSVK SP ENWERPECIV SP LINVDWEFFK SP LINVDWEFFK SP LINVDWEFFK SP LINVDWEFFK SP LINVERSEP SP ENWERPECIV ESEASTATE EQAVI ETERSEPLIV NIL ARAYLAGELT VP ERKESLIV NIL ARAYLAGELT VR	HIVWOLTVFFGEL FRHLIRIRVAEL FRHLIRIRVAEL FRHLIRIRVAEL FRHLIRIRVAEL FFDLELKIMTINS FFFLELGPIVARW FFFLELGPIVARW FFFLELGPIVARW FFFLELGRISTSVV FFFLELGRISTSVV FFFLELGRISTSVV FFFLIRIPGIPA FFFLIRIPG			PVEEPY - TPAVG - IPAGV - IPAGV - PEGT - APAGS - APAGT - KPTAG PPATG - SPDVG - TAYKSKT - TAHTPKT - KYKNS - KYKNS - KYKNS - KYKNS - WEENES - AIEV - AMADGOG - WEENES - WEENES - AIEV - MADGOG - WEENES - LIPEF - IANNES - LIPEF - IANNES - LIPEF - IANNES - LIPEF - IANNES - LIPEF - LIDAEQN - LETTIGG - WEENES - WEENES - SIKNT - TANNES - WEENES - SIKNT - WEENES - WEEN	RLAPEDELKAYA—-FPVSHQRVWREYK—EWASGVRRD- FLISKHARFSD—-LPTV ETTITLOGODR——LPALHRKSIAAAR—ELLLEVRE- FWCKREEVKAQA—-LPSLMHKINTHMY—KA -EWWGIDELARRP—LSVAGRRVATKVE—-RILHHNGAQA -WWCAPGLIAGEA—LPTVMKKVVEAAI—SGATKARRFI -RFTPRSALDDEP—LPGLMRKVLAHAF—DPKPEPEKKPI HFIADADFDET—LPTVMRKAYRIAR—TKFGGDANG— DFISKNAFDPET—LPTVMRKAYRIAC—TQFDDN— HFIADADFDET—LPTVMRKAYRIAC—TQFDDN— HFIFSDKFDPDD—LPTVMRKAHLAD—AAFDHG— KFIADDCFDPAD—LPTVMRKAHLAD—AAFDHG— KFIADDCFDPAD—LPTVMRKAHLAL—GSFVGD— GSFSLNQLDSIG—LSAPVKGLVNLY— QSFSLNQLDSIG—LSAPVKGLVNLY— QSFSLNQLDSIG—LSAPVKGLVNLY— VWDYKNVESIG—LPAPIKKTINQLT—KP— WWDYKNVESIG—LPAPIKKTINQLT—KP— WWDYKNVESIG—LPAPIKKTINQLT—KP— WWDYKNVESIG—LPAPIKKTINQLT—KP— WWDYKNVESIG—LPAPIKKTINQLT—KP— WWDYKNVESIG—LPAPIKKTINQLT—KP— WWDYKNVESIG—LPAPIKKTINQLT—KP— WWDYLNGSIG—LSAPVKGLVNLY— UWPLDGSISUG—SAPVKTINQLT—AIV— NWVNISDSVNMG—IFKPVKDILKKYD— CWADAAAWABLG—LPAPIKKLLDAEL—A——— CWADAARWABLG—LPAPIKKLLDAEL—A——— CWADAAWABLG—LPAPIKKLLDAEL—A———— CWADAAWABLG—LPAPIKKLLDAEL—A———— CWADAAWABLG—LPAPIKKLLDAEL—A———— CWADAAWABLG—LPAPIKKLLDAEL—A————— CWADAAWABLG—LPAPIKKLLDAEL—A————— CWADAAWABLG—LPAPIKKLLDAEL—A—————— CWWOYSKLENGM—IFKUKRLDAEL—A——————— CWWOYSKLENGM—IFKUKRLDAEL—A—————————————————————————————————	- 366 - 350
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_000003652391_2 c_00000031207_6 c_00000031207_6 c_000000107148_4 c_000001092848_3 c_000001151029_1 c_00001797282_1 c_000001797282_1 c_000001803648_25 c_0000027895_5_4 c_0000027895_1 c_000003807531_2 c_000003872363_4 c_00000482017_1 c_000005867921_3 c_00000482017_1 c_000005867921_3 c_000005867921_3 c_0000059117497_1 c_000000591175_2 c_00000011118_1 c_000000991176522_2 c_000001176522_2 c_00000117652_2 c_000001176522_2 c_000001176522_2 c_000001176522_2 c_000001176522_2 c_000001176522_2 c_000001176522_2 c_000001176522_2 c_000000117652_2 c_00000117652_2 c_00000117652_2 c_00000117652_2 c_00000117652_2 c_00000117652_2 c_00000117652_2 c_00000117652_2 c_00000117652_2 c_000000117652_2 c_0000000117652_2 c_000000117652_2 c_0000000117652_2 c_000000117652_2 c_000000117652_2 c_000000117652_2 c_000000117652_2 c_000000117652_2 c_000000117652_2 c_000000117652_2	295 287 298 303 323 295 296 290 290 297 286 282 270 302 227 283 287 294 292 228 22 228 22 284 292 284 282 282 284 282 282 282 282 282 28	ELTEPIVSFE AS ELTEPIVSFE AS ELIGIADREQ AS ELIGIADREQ AS EFQEWMDEFQ GV PWEFC-GTVT TI ENWEQPGLVY SS EWKEQFGLVY SS EWKEQFGLVY SS EWKEQFGLVY SS EWKEQFGLVY SS EWKEQFGLVY SS EWKEGGGLY SS EWKEGGGLY SS EWKEGGGLY SS EWKEGGGIR IF ESEQTILSVK SS EWKEGGGIR IF EWVDSWEPFK SS LINIKKLSKVK SL LINIKKLSKVK SL LINIKKLSKVK SS EKWEGGGLY SS EWKEGGGLY IF EWVDSWEPFK SS LINIKKLSKVK SS EWKEGGLY IF EWVDSWEPFK SS LINIKKLSKVK SS EWKEGGLY IF EWFELST EWFDEFSSFE HU VENEWATH TY FUEEFSSFE HU SEADKLSKIK TS EGAVIK TS ESEASLIK TS ESEASLIC TS ESEKCLEGER TS ESEKCL	SHIVWOLTVYFEGH. FHLIKERVAEL FH			PVEEPY - TPAVG - IPAGV - PEGT - PEGT - APAGS - APAGS - APAGT - KPTAG - PPATG - PPATG - PPATG - PPATG - PPATG - IPVG - IPV	RLAPEDELKAYA—-FPVSHQRVWREYK—EWASGVRRD- FLISKHARFSD—-LPTV ETTPIDGGDR——LPALHRKSIAAAR—ELLLEVFR- FWCKREEVKAQA—LPSHMKIKITHIMY—KA— EWVGIDELATRP—LSVAGRRVATRVE—RILHHNGAQA WWCAPGLIAGEA—LPJVMKKVVEAAI—SGATKARRFI RFTPRSALDDED—LPJVMKKVVEAAI—SGATKARRFI RFTPRSALDDED—LPJVMKKVLAHAF—DPKPEPEKKPI HHIADADFDET—LPTVMRKAYRIAG—TOFFDDN— ENWIRLNEINGVA—FPKANHKLFUNKQ—E— IWVDERDLOBFA—LPTVMRKAYRIAG—RTGPDDN— KFIADDCFDEAD—LPTVMRKAHALAD—AAFDHG— KFIADDCFDEAD—LPTVMRKAHALAL—GSFVGD— GSFSLNQLISG—LSAPVKGLVNKLY QSFSLNQLISG—LSAPVKGLVNKLY QSFSLNQLISG—LSAPVKGLVNKLY VWVDYKNVESIG—LPAPIKKTINQLT—KP— LWYNLTEFRGG—LAAPVKGLVNCLY— WVVDYKNVESIG—LPAPIKKTINQLT—RP— LWYNLTEFRGG—LAAPVKGLVNKLY WYPLDGSIEG—LSAPVKGLVNKLY WYPLDGSIEG—LSAPVKGLVNKLY WYPLDGSIEG—LSAPVKGLVNKLY WWYDKKNYESIG—LPAPIKKTINQLT—KP— LWYNLTEFRGG—LAAPVKGLVNKLY WYPLGSIEG—LAAPVKGLVNLY WYPLGSIEG—LAAPVKGLVNCLY WWYSLKSLKYP—FPAANKVLVKLT—EK— QWLPLAQALKWN—TPAAVKRVLQEVI—EYEQNR— CWADAAAWAELG—LPAPIKKLLDAGF—A CWADAAWAELG—LPAPIKKLLDAGF—A CWADAAWAELG—LPAPIKKLLDAGF—A CWADAAWAELG—LPAPIKKLLDAGF—A CWADARAWADMG—LPAPVKKLLDAGF—AFGLF— KWYSLSKLKYG—FPAPIKKLLBALS—ENSSDRNEGU LWYNNKESYING—IPKVYKLLETGF—NIQ— WWYNKESYING—FPAPIKKLLBALS—PNSSDRNEGU LWYNNKESYING—LAAPVKKLLETGF—NIQ— WWYSKELDHNING—FPAPIKKLLBALS—PNSSDRNEGU LWYNNKESYING—LAAPVKKLLETGF—NIQ— WWYSKELDHNING—FPAPIKKLLBAGN—RNMYAWIV WWYSKEDID—FLKYNIRALDKLK—EMRY— SYFTSSKLQKLA—TSKVDDKILKLYLI—DTIQTY— WWYSKEDIDD—FLKYNIRALDKLK—EMRY— SYFTSSKLQKLA—TSKVDDKILKLLQNS—RNMYAWIV— WWYSKEDIGNIG—LAAPVKKLLETGF—NIQ— LWYNNKESYELG—LPTPIKKLLQNG—RNEV— WWYSKEDLENG—LAAPVKKLLRQTS—NICHTY—WYNKSELGE—LPTPIKKLLQNG—RNEV— WWYNKESUSIG—LAAPVKKLLRQTS—NICHTY—WYNKSELGE—LPPAPIKKLLQNG—LNTNNTHFING—FPAPIKKLLQNG—RNEV— WWYNKESUSIG—LAAPVKKLLRQTS—NICHTY—WYNKSELGE—LPPAPIKKLLQNG—RNEV— WWYNKESUSIG—LAPAPVKKLLRQTS—NICHTY— WWYNKESUSIG—LAPAPKKLLQNG—RNEV— WWYNKESUSIG—LAPAPKKLLQNG—RNEV— WWYNKESUSIG—LAPAPKKLLQNG—RNEV— WWYNKESUSIG—LAPAPKKLLQNG—RNEV— WWYNKESUSIG—LAPAPKKLLQNG—LANTANHILLANLD—LAUPNNKLLEFRG—LAPAPKKLLQNG—LANTANHILLANLD—LAUPNNKLLEFRG—LAPAPKKLLQNG—LANTANHILLANLD—LAUPNNKLLEFRG—LAPAPKKLLQNG—LANTANHILLANLD—LAUPNNKLLEFRG—LAPAPKKLLQNG—LA	- 366, 361, 361, 361, 361, 361, 361, 361,
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_00000031207_6 c_000000031207_6 c_0000001097148_4 c_0000109248_3 c_00001197148_4 c_00001197148_1 c_000011971282_1 c_00001803648_25 c_0000220895_4 c_000002387236_3 c_000004820107_1 c_00000587021_3 c_0000085774797_1 c_00005867021_3 c_00000587021_3 c_000000587021_3 c_000000587021_4 c_000001823643_29 c_00000238971_4 c_00000238971_4 c_00000238971_5 c_00000238971_5 c_00000238971_5 c_00000238971_5 c_00000238971_5 c_00000323871_5	295 287 287 287 294 490 290 290 297 287 282 292 276 6 292 297 287 287 287 297 287 287 297 287 287 287 287 297 287 287 287 287 287 287 287 287 287 28	ELTEPIVSFE AB ELTEPIVSFE AB ELIGIADREQ AT ELIGIADREQ SU EFQEWMDEFQ GV PWEFC-GTVT TI ENGREGERY SP EFQEWMDEFQ GV PWEFC-GTVT TI ENGREGERY SP EFQEWMDEFQ GV EFGERY SP EFQEWMDEFQ GV EFGERY SP EFQEVINAEVE SP EFQEVINAEVE SP EFGERY SP EFGERY SP EFGERY SP EFGERY SP LWYDWEFFX SP EFGERY SP EFGE	SHUYWOLTVYFEGH. FHLIKERVAEL FHYLIKERVAEL FHYLIKERVAEL FFYLIKERVAEL FFYLIKERYAEL FFYLIKERYAEL FFYLIKERYAEL FFYLIKERYAEL FFYLIKERYAEL FFYLIKERYAEL FFYLIKERRYAEL FFYLIKERRYAEL FFYLIKERRYAEL FFYLIKERRYAEL FFYLIKERRYAEL FFYLIKERYAEL FFYLI			PVEEPY - TPAVG - TPAVG - IPAGV - PEGT - PEGT - APAGS - APAGS - APAGT - KPTAG - PPATG - PPATG - PPATG - PPATG - PPATG - PPATG - IPTVG -	RLAPEDELKAYAFPVSHQRVWREYKEWASGVRRD- FLISKHARFSDLPTV ETTPIDGGDRLPALHRKSIAAARELLLEVFR FWCKREEVKAQALPSHMKIKITHIMY	- 366, 364, 364, 364, 364, 364, 364, 364,
sp_17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_00000031207_6 c_00000031207_6 c_00000031207_6 c_00000109148_4 c_00000109148_4 c_00000192948_3 c_00001151029_1 c_000001797282_1 c_000001803648_25 c_00000278955_4 c_00000278955_4 c_000003607531_2 c_000003607531_2 c_000003607531_2 c_000004820107_1 c_000005867021_3 c_000004820107_1 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_0000089687_2 c_0000011118_1 c_000005571378_2 c_0000011118_1 c_00000989687_2 c_0000011118_1 c_0000011118_1 c_0000011118_1 c_0000011118_1 c_00000238721_4 c_0000111515736_6 c_0000111515736_6 c_0000111515736_6 c_00000238721_4 c_00000238721_4 c_00000238721_4 c_00000238721_4 c_00000238721_4 c_00000238721_4 c_00000324679_3 c_00000238721_4 c_00000324679_3 c_000003333364_1 c_000003348186_72 c_00000348186_72 c_00000467631_2 c_00000348186_72 c_00000348186_72 c_00000467631_2 c_000003187176_11 c_000001877176_11 c_000001877176_11 c_000001877176_11 c_000001877176_11	295 287 287 297 297 297 297 297 297 297 297 297 29	ELTEPIVSFE AS ENTITURESEY TY ELIGIADREPO AT ELIGIADREPO SU EPQEMMDEFO GV PWEPC-GTVT TY ENTITURESEY SY EPQEMMDEFO GV PWEPC-GTVT TY ENTITURESEY SY ENTITURESEY SY ENTITURESEY SY ENTITURESEY SY ENTITURESEY SY ESEQUILLYK SY ESEWKGIGQIR TY LINVDSWEPFK SY LINIKLISKVK SY LINIKLISKVK SY QSSIALABIK TY PUEDFSSFE HU VINIKLISKVK SY ESELIKLY SY PUEDFSSFE HU VINIKLISKVK SY PUEDFSSFE HU ESENELLY IN SADNTELPAFL VI SANTELPAFL VI SAN	SILVWOLTVYFGEL FFHLILARRYMEL FFHLILARRYMEL FFHLELRYMEN FFFLELLYFYARW FFFLELLYFYARW FFFLELSARSYN FFFLELSTSYN FFFLELSARSYN FFFLICARSYN FFFLICARSY			PVEEPY - TPAVG - TPAVG - IPAGV - PEGT - PEGT - PEGT - APAGS - APAGS - APAGT - KPTAG - PPATG -	RLAPEDELKAYA—-FPVSHQRVWREYK—EWASGVRRPD- FLISKHARFSD—-LPTV ETITIDGGDR——LPALHRKSIAAR—ELLLEVER- FWCKREEVKAQA—LPSLMHKINTHMY—KA- EWVGIDELATRP—LSVAGRRVATRVE—RILHHNGAQA WWCAPGLIAGEA—LPGIMRKVVLAHAF—DPREPERKP; HFITADADFDET—LPGIMRKVLAHAF—DPREPERKP; HFITADADFDET—LPGIMRKVLAHAF—DPREPERKP; HFITADADFDET—LPTVMRKAYRIAC—TQFDDN— RWIRLNEINGVA—FPKANHKIFDIMQ—E- IWVDERLDEFA—LPTVMRKAYRIAC—TQFDDN— KFIADDCFD—LPTVMRKAHALAD—AAFDHG— KFIADDCFDPAD—LPTVMRKAHALAD—AAFDHG— KFIADDCFDPAD—LPTVMRKAHALAL—GSFVGD— QSFSINQLDSIG—LSAPVKGLVNKLY— QSFSINQLDSIG—LSAPVKGLVNKLY— VWVDVKNVESIG—LPAPIKKTINQLT—KP— LWYNLTEFRGG—LAAPVCTLINITK—NIEREIENGT VWYDLKNVESIG—LPAPIKKTINQLT—RP— VWYDLKNVESIG—LPAPIKKTINQLT—RP— VWYDLKNVESIG—LAAPVCTLINITK—NIEREIENGT VWYPLDGSISUG—LSAPVKRINQLT—AIV— NWWNISDSVBMG—TPKPVKDILKKYD— KWYSISKLKKYP—FPAANWKIVKYLT—ER— QWLPLAQALKMN—IPAAVKRVLQEVI—EYEQNR— CWADAARAMAM—LPAPIKKLIDAEL—A———— CWADAARAMM—LPAPIKKLIDAEL—A———— CWADAARAMM—LPAPIKKLIDAEL—A———— KWYSISKLKKYP—FPAANWKIVKYLT—ER— LWYNNTEFRGG—LAAPVCTLINITK—NICHEIENGF—LAAPVCTLINITK—NICHEIENGF—LAAPVCTLINITK—NICHEIENGF—LAAPVKKLLEQQA—RFGLF— KWYSISKLKWYP—FPAANWKIVKVLT—ER— LWYNNTKESWG—IPKFVKLLDAQE—AG——FGLF— KWYSISKLKWYP—FPAANWKIVKVLT—ER— LWYNNTKESWG—FPAPIKKLLENQA—RFGLF— KWYSISKLKWYP—FPAANWKIVKKLLE—PNSDRNNDEQ; LWYNKGSCTHG—LAAPVKKLLEQQA—RFGLF— KWYSISKLKAYP—FPAANWKLLENGA—NIQ— VWYSKBOLDGG—FPAPIKKLLONGN—NEV— VWYSKBOLDGG—FPAPIKKLLONGN—NEV— VWYSKBOLDGG—FPAPIKKLLONGN—NEV— VWYSKBOLDGG—FPAPIKKLLONGN—NEV— VWYKSGUNALG—LAAPVKKLLEQP—NIQ— VWYKSGUNALG—PRAPUKKLLEQP—NIQ— VWYKSGUNALG—LAAPVKKLLEQP—NIQ— VWYKSGUNALG—LAAPVKKLLEQP—NIQ— VWYKSGUNALG—LAAPVKKLLEQP—NIQ— VWYKSGUNALG—LAAPVKKL	- 366 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_000000352391_2 c_00000031207_6 c_00000013207_6 c_000001092148_4 c_000001197282_1 c_00001197282_1 c_0000197282_1 c_00000197282_1 c_000001803648_2 c_000002106160_4 c_000003872363_4 c_000003872363_4 c_00003872363_4 c_000004820107_1 c_000005774797_1 c_00005877797_1 c_000005870797_1 c_000005870797_1 c_00000577378_2 c_00000577378_2 c_00000579378_2 c_00000176522_2 c_00000176522_2 c_00000176522_1 c_0000017652367_1 c_00000176522_1 c_000001766664_1 c_00000338864_1 c_00000338864_1 c_00000338864_2	295 287 287 287 297 286 298 298 298 299 290 297 287 287 287 287 287 287 287 287 287 28	ELTEPIVSFE AB ELTEPIVSFE AB ENTERGEVE TF ELIGIADEPO AT ELIGIADEPO AT ELIGIADEPO AT ENTERGENE SEPCEMBEFO GV PWEPC-GTVT TF ENWENDEGLIVE SEP ENWENDEGLIVE SEP ENWENDEGLIVE SEP ENWENDEGLIVE SEP ENWENDEGLIVE SEP ENWENTER THE SEP ENWELLAGER TF ENW	SHUYWOLTVYFORM IFHLILARRYMEL IFRALEIBLUYRAW IFDLELKIMTINS IFFLEIGPIVAMW IFFLEIGPIVAMW IFFLEIGPIVAMW IFFLEIGPIVAMW IFFLEIGPIVAMW IFFLEIGPIVAMW IFFLEIGPIVAMW IFFLEIGFICH IFFLEIGRISTOV IFFLEIGFICH IFFLEIGRISTOV IFFLEIGFICH IFFLEIGFICH IFFLEIGFICH IFFLICHIMTHVATV IFFLICHIPTIFI IFFLICHIMTHVATV IFFLICHIPTIFI IF			PVEEPY - TPAVG - IPAGV - IPAGV - IPAGV - PEGT - EGEVTA - APAGS - APAGT - KPTAG - PPATG - STONG - IPTVG - IPAGG - IPTVG - IPAGGG - IPTVG - IPAGGG - IPTVG - IPAGGG - IPAGGG - IPAGGG - IPAGGG - IPAGGG - IPAGGGG - IPAGGGG - IPAGGGG - IPAGGGG - IPAGGGG - IPAGGGGG - IPAGGGGG - IPAGGGGG - IPAGGGGGG - IPAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	RIAPEDELKAYA—-FPVSHQRVWREYK—EWASGVRRPD- FILISKHAFRSD—-LPTV ETITJIGGDR——LPALHRKSIAAR—-ELLLEVPR- FWCKREEVKAQA—-LPSLMHKINTHMY—-KA	- 366
sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_000003652391_2 c_0000003652391_2 c_0000003652391_2 c_0000003652391_2 c_0000003652391_2 c_0000003652391_2 c_0000017148_4 c_0000192848_3 c_00001151029_1 c_000001797282_1 c_000001803648_25 c_00000278955_4 c_00000278955_4 c_00000367531_2 c_00000367531_2 c_000004820107_1 c_000005774797_1 c_000005867021_3 c_00000456210_2 c_000005571278_2 c_000005571278_2 c_000005571278_2 c_000001754627_3 c_000005571278_2 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000002571378_6 c_000001754627_3 c_000001754627_1 c_0000017559010_5 c_0000001754627_1 c_000001754627_1 c_00000001754627_1 c_000001754627_1 c_0000001754627_1 c_000001754627_1 c_0000001754627_1 c_000001754627_1 c_0000001754627_1 c_0000001754627_1 c_0000001754627_1 c_0000001754627_1 c_0000001754627_1 c_00000017	295 287 287 294 298 303 329 290 290 287 727 282 270 293 383 287 270 283 282 276 282 282 282 282 282 282 282 282 282 28	ELTEPIVSFE AB ELTEPIVSFE AB ELIGIADREVA TE ELIGIADREVA SE EFQEMMDEFO GV PWEPC-GTVT TE EMEROPEGIVY SE EMEROPEGIVY SE EMEROPEGIVY SE EMEROPEGIVY SE EMEROPEGIVY SE EMEROPEGIV SE	SHUYWOLTVYFORM IFHLIKRIVAEL IFHLIKRIVAEL IFHLIKRIVAEL IFHLIKRIVAEL IFFLELLIMTINS IFFLELLIMTINS IFFLELLIMTINS IFFLELLIF			PVEEPY - TPAVG - TPAVG - IPAGV - PEGT - PEGT - APAGS - APAGS - APAGS - PPATG - PPATG - PPATG - PPATG - PPATG - PPATG - IPTVG -	RLAPEDELKAYA—-FPVSHQRVWREYK—EWASGVRRPD- FLISKHARFSD—-LPTV ETITIDGGDR——LPALHRKSIAAR—ELLLEVER- FWCKREEVKAQA—LPSLMHKINTHMY—KA- EWVGIDELATRP—LSVAGRRVATRVE—RILHHNGAQA WWCAPGLIAGEA—LPGIMRKVVLAHAF—DPREPERKP; HFITADADFDET—LPGIMRKVLAHAF—DPREPERKP; HFITADADFDET—LPGIMRKVLAHAF—DPREPERKP; HFITADADFDET—LPTVMRKAYRIAC—TQFDDN— RWIRLNEINGVA—FPKANHKIFDIMQ—E- IWVDERLDEFA—LPTVMRKAYRIAC—TQFDDN— KFIADDCFD—LPTVMRKAHALAD—AAFDHG— KFIADDCFDPAD—LPTVMRKAHALAD—AAFDHG— KFIADDCFDPAD—LPTVMRKAHALAL—GSFVGD— QSFSINQLDSIG—LSAPVKGLVNKLY— QSFSINQLDSIG—LSAPVKGLVNKLY— VWVDVKNVESIG—LPAPIKKTINQLT—KP— LWYNLTEFRGG—LAAPVCTLINITK—NIEREIENGT VWYDLKNVESIG—LPAPIKKTINQLT—RP— VWYDLKNVESIG—LPAPIKKTINQLT—RP— VWYDLKNVESIG—LAAPVCTLINITK—NIEREIENGT VWYPLDGSISUG—LSAPVKRINQLT—AIV— NWWNISDSVBMG—TPKPVKDILKKYD— KWYSISKLKKYP—FPAANWKIVKYLT—ER— QWLPLAQALKMN—IPAAVKRVLQEVI—EYEQNR— CWADAARAMAM—LPAPIKKLIDAEL—A———— CWADAARAMM—LPAPIKKLIDAEL—A———— CWADAARAMM—LPAPIKKLIDAEL—A———— KWYSISKLKKYP—FPAANWKIVKYLT—ER— LWYNNTEFRGG—LAAPVCTLINITK—NICHEIENGF—LAAPVCTLINITK—NICHEIENGF—LAAPVCTLINITK—NICHEIENGF—LAAPVKKLLEQQA—RFGLF— KWYSISKLKWYP—FPAANWKIVKVLT—ER— LWYNNTKESWG—IPKFVKLLDAQE—AG——FGLF— KWYSISKLKWYP—FPAANWKIVKVLT—ER— LWYNNTKESWG—FPAPIKKLLENQA—RFGLF— KWYSISKLKWYP—FPAANWKIVKKLLE—PNSDRNNDEQ; LWYNKGSCTHG—LAAPVKKLLEQQA—RFGLF— KWYSISKLKAYP—FPAANWKLLENGA—NIQ— VWYSKBOLDGG—FPAPIKKLLONGN—NEV— VWYSKBOLDGG—FPAPIKKLLONGN—NEV— VWYSKBOLDGG—FPAPIKKLLONGN—NEV— VWYSKBOLDGG—FPAPIKKLLONGN—NEV— VWYKSGUNALG—LAAPVKKLLEQP—NIQ— VWYKSGUNALG—PRAPUKKLLEQP—NIQ— VWYKSGUNALG—LAAPVKKLLEQP—NIQ— VWYKSGUNALG—LAAPVKKLLEQP—NIQ— VWYKSGUNALG—LAAPVKKLLEQP—NIQ— VWYKSGUNALG—LAAPVKKL	- 366 - 354 - 352 - 352 - 354 - 352 - 352 - 354 - 355 - 351 - 354 - 355 - 351 - 354 - 355 - 351 - 354 - 355 - 351 - 354 - 355 - 351 - 354 - 355 - 351 - 354 - 355 - 351 - 354 - 355 - 351 - 354 - 355 - 351 - 354 - 355 - 351 - 354 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351 - 355 - 351

c_000001128125_11	201	FSTVFWNVFDUTE	TUVHINTVDIVVDIN_	-FCFVSDVFTTG	KSONINDEK\$S\$FM	NWTFT DDI NKCEVCVDA DVNKMI EDI SETI DK	374
c_000001595844_4	288	NIKNKLGPVT <mark>Q</mark> L <mark>I</mark>	THQKVIGQFFDITL	VGE	KDLDI	nwieldrlnkgevgvpapvnkmlerlsetldk apiskvdlqvfpfpkmmmyinrima	348
c_000001719155_2 c_000002363038_6	292 293					DWVKTEELDRYPFPAANVKIIKSLRKNQGRSQWFDINRLKSGEIGVPVPIRKMISSL	362 370
c_000002561400_1	247	EGLIEWDDFRHTE	SHYHLDIYPLIFDE	RGAPKNTAKI	ISEPGGVYDAEQG	SWFDIQLLLDGGLAVPAPVNKLIGRLDELVE	327
c_000002566035_2 c_000002598045_3	284 282	KOOKEAKAKAK	THFHLTIRPIHIKI	KKCK	KDYDTKVL	KWIHPKTNPNLGLPAPVLSMLIDLNNTKRAVLNES- VWVNFKNVESLGLPAPVKKTINQITMP	358 344
c_000004188575_41	280	TVSKQPAVFRHIE	THFKLDIHPHLYHA	KQSAA	ENITGQA	IWYKIEDALTLGLPAPVKKTLLTLSKG	
c_000000240049_1 c_000002139456_2	282 282					QWHADITQLALAAPISAIFRENNSLK	347 347
c_000003535614_2	284					QWHADITQLALAAPISAIFRENNSLK QWQVDISKLALAAPVSAIFNAK	345
c_000002657784_4 c_000003800129_15	281 263	KDLKTYPDINHS	SHLNLNAKLFLLKL	NEDIN	YNINKGKY	VWVDKKGLKALGIPTPVKNIFEVLKLNDQTS	351 320
c_000003800129_15 c_000003716781_1	273	T.OREEVGET.RHST	TKHRTRARVT.RAVP	GRDE	I.PECW	kwinknefnnlptpkpisdkleqyaksfl awferseiealgvtgmtskaltlgrarsr	337
c_000001556689_3	294	RLGPKLGEIRHGM	TDRRISCHVYEASL	SGSQTTMAGA	PTGLEKSDHNIPDS	GWFTIEEVMTLALAASARKTLTTLLDIDLTTAHNPG	380
c_000001834452_1 c_000004255004_2	254 275	QQGDPVALIHHAI	TRHRIQARVHQVEG	KIPV		GWFTIEEVMTLALAASARKTLTTLLDIDLTTAHNPGNGKGAVDPSSVPLSSLGRKVLSIAGVLGGLLLLSPDRWVSLANLHAYPLSSLSTKALSAROHLFTTRKLGGNYFTVEEIHDLALSGADRKALALLEKYLQ-	317 346
c_000000605438_3	263	enmtglgefk <mark>o</mark> hy	THFTLDARVVLLKD		KKQE	NYFTVEEIHDLALSGADRKALALLEKYLQ	322
c_000000581237_15 c_000002529579_2	263 263	KDMIKEGEFKOHI	THE T LEASAALAGN		KEQE	RYFRINEIHALALSGADRKGLALIEKHLA NYFTIDEIHDLALSGADRKALALLEKYLQ	322 322
c_000006097838_1	268	VEPESLCIINHSI	TCYRNRLEMFVIFR	TRKPL	LAKLKG	KWVPLAKLDEIPLTTAHRKAANQFAG	331
c_000000583727_6 c_000005807640_2	294 295	AKFQPLCNINHSI AELEPLCTINHSI	TRYRNRLEMIVAEP	KRKPR ARKPR	LAKLKG	EWLPLAKLAELPLTAAHRKASDYFLKTANSR	362 357
c_000000134878_1	270	KPETIIHQVD <mark>H</mark> HY	SHFSVTINAINCKY	NGGDI	KLSGPTDF	EWLPLAKLAELPLTAAHRKASDYFLKTANSREWIPLAKLDELPFTTSHHKAANQFC	322
c_000005136725_3 c_000001684786_4	285 280	KPEKLIHQVDHHY ETGEELKAIKHSI	SHFSVTINAINCYY	NGGKI GSFTI	KLSGPTDF	RWVKTSRLHSYAFPKASIKLFNAIKSIE RWALPEELGSVL-PVSSLCLKIADRLS	352 343
c_000002971826_23	290	EEGAELEAIR <mark>H</mark> SI	TFRRLTLRPRILGA	GSFST	RAKPSF	RWGRADELGNVL-PVSSLCLKIADRLS	353
c_000002040695_2 c_000003263657_32	291 303	ASWTLLGQIQHVE	THETLKLDLWYTIR		KALTCHDA	QWVLLNQMNDYPLSSLTKKSLAFLVKNLELEKEQAR RWVSQTQLADFAFSRAHNRLIDIMKKEAAKGQVEMF	359 378
c_000005989041_2	297	QWVKITGTVTQPF	THFELQLQVRVAVV	ENKP	KSSEG	IWVDRNRLDDFALPNIMKKVLAFALRHNQHFSREFF	368
c_000002391082_2 c_000003839553_2	298 305	EVGARLTSVDHAY	SHFSITLHALEARY	LRGEP	QAIGCADW	KWIVPDELDDYALPRADRLIVEFLRQDGRQLGLFDS	373 331
c_000003996707_2	295	EVGGLLAKVDHGE	SHFSITLNLFEAMY	RGGEP	EAVECDDW	RWIDPAELDDLPMPRADRRALEELS-EEEGORVPVLMA	371
c_000002044706_1	271 268	LVVTSEHRE	SHRHWTTRVYRA	RVEDE	CSGPADASHWSEGL	rwtcagdlgklavpeasrktlrpclrasrgslpg swiketkfnhytfptftkkifnslenyl lwiessklencmiptftkkifasvknnl	353
c_000006007075_1 c_000002094036_4	245	SLLKSKNKLNLK	SNMNMNICIDFVKI	KKK	PKNG	LWIESSKLENCMIPTFTKKIFASVKNNL	306
c_000002762689_1	268 268	LSSTDIVNEKM	SNMNMNIKIEHKNK	VGS	LPTS	HWIDPKKLKNYTLPTFTKKIVRYLESNK	327
c_000005516980_2 c_000003920004_1	268					YWVDQKKLNNYMLPTFTKKVVKYLENNK	327 309
c_000004008511_2	287	NKLKLKGFVDYSF	SHFDLETEVFFTKV	KKDY	FANQ	KWIKKNNIKISGLPTVMKKIIEVAL	346
c_000004481347_1 c_000003787733_3	294 289	NIGKKIGKITYSE	SHFRLDIGIYKSKV	vkkk NRSVK	NIYKEY	NWIKSNKIDTSGMPTVMKEIVKKSLKIKWIIPTEVNNYPFPKSNHKLFK	355
c_000000754657_2	289	NIKKKVGNVK <mark>H</mark> AY	SHFKITLTLYRCQS	QGSVK	SNNKEY	kwiiptevnnypfpksnhklfksngwnv	357
c_000000990943_3 c_000004474996_2	289 288	NIEKEVGYVKHAY NIKNKVGYVKHAY	SHFKITQTLFQCQT	QESVK OESVK	SINKEY	RWITPIEVNNYPFPKSNHKLFTILNSDGWNVRWITPSEIQYFPFSKSNHKLFNLLNSNGWNV	357 356
c_000001463500_11	276	QIQNKICTIK <mark>H</mark> SY	SHFDIRVSLYHCRI	NDINI	KNMKNV	CWIRPKDINNYAFSKSNHKLFKILNTNGWTI	344
c_000001286181_5 c_000001293628_3	263 302	QNINELPSFKHSI VRFSPLPEVRHTE	SHKDFHISPRIINI THLKAVYRPMLVIG	PDDME TRCEG	TDDKKT	IWIEKNKIAKLGAPKPVLDIVKKILNQNDKGLL KWVLPDQVEDLPLPVAQRRILDLAWAALEGC	333 371
c_000001535696_8	292	TIT DVNIUVT TUUVT	CUCC T UBUEWITATIT	CMPT D		COTTTCCTCNVDVDVTTANCTNDCVNCVCWDNNCTD	250
c_000001614067_2 c_000001765289_1	298 262	KWKILDQNLNHIF SIKKRIGAVDHAY	THFKLNCSLAIATI SHFSITFHGYHCIE	NDENAL NGEK	VNDLSKSSY		371 292
c_000001961666_1	274	NRILSKNVVR H EF	SHFKLELEVYYIET	RFP	QITHG	EWLKTKQAGKQLPSVMKKVLDNI	331
c_000002018097_4 c_000002843512_36	284 254	CASKYIGEVTHAY	SHYKLLVTPFECEV	LNA	DSRIG	RWIRVGEIDKYAFSKVNHKLFNAIGIKNY	347 317
c_000002930199_1	281	SMIKMKIIIE	SUČKPKISEMDADW	KMIM	IQKGF	EKIILDNISNIFFAKFLEKIFQIQHLII	344
c_000003033795_2 c_000003888107_2	277 278	SNPIFLGNITHKY	SHFGVNISFFISFP	KSIKS	FNSSQEY	RWIRIKNILNYPLPKANHKMLDILKKLKWTTRKQLDKFALPKANYKMLEILDKLN	342 344
c_000003000107_2 c_000004013286_6	307	QIGNKIGQIR <mark>Y</mark> VV	TRFRTTVDCYEAHF	SNIGKPNRSKNDI	SVNTLQKEQQEAGSLWHM	QWATRKQIDSFPMSVPARRVIRLLADFD	392
c_000004852258_1 c_000005254087_1	265 300	KVGHKLGMINHTE	THFKMNVLLYNCQA	KDQP	LSKNTE	KWVSFSDLDQYAFSKANHKLFKLVELRND	330 351
c_000005603677_1	290	VWALISGQEQQL	SHQKIIARFLWPKQ	PLPQ	ALSADW	AWVTLADLDÖYA ELVDAQSWPNYPLPRLIAQYWEKKQLAFF	355
c_000003283462_3 c 000002687221 1	276 290	VPKKKIESIK H KY	SHFSITLTAFHCKI	KNGAK	VPSKQST	RWITPGEIGDYPFPRANHKLFNQLENFYSNG	345 358
c_000003347358_19	285					RWIYPHETGKYAFHSAGHKLFDKILETAS DYFSEEEIQKIAISKVDEKIVNLYGNFLKYD	348
c_000002701031_2 c_000000582753_3	286 292	QILKISATIK <mark>H</mark> QL	THQTIFARFWHIDT	KIQ	KVENS	KYISKKELKNYPISRLLEKYLENIGMI	347 353
c_000000382733_3 c_000001713769_5	288	IILFNSSPIIHKI	SHKTIYAKFWILPV	NGSNS	KDEN1	IKVEKEDFESYPIHRLMEKMMEQVGK NSIKFSDVNKYPVPRLIEKFLDKFNYKHF	348
c_000004369364_1	288 292	KIKHKSAPSKOLI	THQKIIGIF			NSIKFSDVNKYPVPRLIEKFLDKFNYKHFNTVNWQNLSNFALPTLIQNFVDDFKKNTISIDELKKYPVPVLIDNFIKDFEM	309 349
c_000006057486_30 c_000005494072_10	292	VSLFNPKPIIHKI	SHQHIYTSFWIVNY	NTCSK NGSVS		NTISIDELKKYPVPVLIDNFIKDFEM	347
c_000001742634_3	293	PYLFNEKTVIHKI	SHQHIYTKFWIVKL	DVNLE		QTIPLNSIEKYPVSTLIQNFIKEFNF	350
c_000002826998_2 c_000003159439_6	290 289					INIERANLSKFAFFKIIDLILKDNSLNLAMK	358 354
c_000004887214_1	294	LQLLTPKVVV <mark>H</mark> KI	SHQHLYIKFWEIRV	PTFRS		ATISWQELLKLPFPIVIFKFIREFLETSMPNFDTPL	361
c_000005037037_2 c_000001059964_1	288 280	OLGKEIHTLEHRY	THQKLNAIFIEIDL TSFRTRVSFFTATV	KTK HVLPE	INKQF	INTDINNLSKFAFP	336 326
c_000002498472_1	289	EIVEKITNTVHHY	TRYKVTLHCFLLRL	KKGSDT	DPVLHAAQDF	RFVKTSEVE NWVPFKALQEYAFPAGHRKLITYL ILIDSKNLAKFAFPKITALYLENNSLNL	355
c_000004615912_3 c_000004766858_2	285 292	QTKKYQCEL RIGPELFKMEHDY	THOKISAYFWEIN	LNVAP AEIPS	VNIYDF	ILIDSKNLAKFAFPKIIALYLENNSLNLQWLTLGEISALALPRVFQRLRKRLLDEVSA	345 359
c_000002747260_18	286	PWRDPGAEVRHTE	THFHLRLALRVADL	PASA	TPRTG	QFIPHHAFRPGQLPTVMRKAYDLASATFLGN	352
c_000005371561_38 c_000000169465_2	287 290	NWRTVPGEVRHTE	THFHLVLELRRADL	PEDC	TTMRG	QFLAPGGFRPSDLPTAMRKAFDLARDG RWFSLNEPIEVGLAAPTTKIIQQLMR	349 355
c_000003254110_11	290	EETKTLETFRHTE	SHFHLDITPVVAVV	NSPPT	KRVADTAF	RWFSLGEPIEVGLAAPTTKIIKQLIG	355
c_000004750284_20 c_000000141782_15	286 292	TRPOAWPGT.RETE	SHFHLDITPLIAVV	NSTPQ TAAPA	KRVAENES	RWFLLDEPIEVGLAAPTTKIIKTLAK	351 362
c_000002717847_8	264	KFNAANKHAL	SHRHIHFRFKQIAN	LPT	GMKG	EWFSKKDLANIALPKPISDKLLQDG	319
c_000004054799_1 c_000006126673_1	260 302					LDSN-L	296 362
c_000000339186_3	248	-NGOPFASARHSI	TRYRIOLNAHLIHA		KRGKG	MWCTSDEIRSLPFSSAHLKLLGKLPHRLDK	308
c 000003029168 2 c 000001863436 1	299 316	QKLTKLVTITYTV	MRTRTTLHVFEGML	DLETS	TMQEASSR	LWVRLDGLHKHPFSSPQHEIIKTLDKEAALQLAGLV RWVSAVELVDLPMSAAMRKIEGLYRELGSGAI	374 391
c_000002830137_4	304	EPVROLTTIOHGV	TRFOITLOCHLACC	VSGRK	RGPHL	SWRMPHELEHLPLSVTARKIGRLVAKLAD	369
c_000004612302_3	298 277	EVEEWLQEFRHGV	TRFRLHLQPVVASW	RAGHW	IGPVVA	EWVEIDELTARPLSVAARRVADGVQAGQRCGGASG-	370 309
c_000001933926_1 c_000003136334_1	289	DWOMLSGKVRHTE	THFHLEL				308
c_000005849454_9	300	KLGAYQGQVRHTI	THHRIRAHVYAAEG		0	APTHLEDPTQVPLTGLARKVLDRITSA	354
c_000001169194_1 c_000002786947_2	302 302	GHASALAEIQHRE	THLQARYRPWVVPV	AKL	LTGEGS	MWMTPGEPVDFPIPAAQHKVLDALAECRATPDSLES	373 373
c_000001279808_52	288	SVRSHFYEELHEF	ERTELLLRFHRCQI	QAGEP	QALENQEL	KWVSPDEFDSVGFLKTNHKALEKLKSMRV	356
c_000000358065_2 c_000003745941_1	269 269	RGNTPIVTRKRGI	SNSQITEPIWRLSD	NSEA	DHAEM	EWIDLEQIKKVTLSGPHKRWINEILTDFNKQK	330 336
c_000004187032_4	268	KNFNENFNEK	SNMNMNIKIQYLKN	LKK	FPSS	YWFDKRRLDNYMLPTFTKKVVKYLEKN	326
c_000006067315_3 c_000005543774_1	269 231	FNTSLNKKINIKM KNWKFLCNYKMS	SNKKLNINI.YYKFQ	LIK	IKNS	YLVDKKNIKDLILPSFTKKIFNSVSNYL	330 291
c_000006211484_1	253	KNWRFLCNYKNSI	SNKKLNINLYYKFT	ski	PSEY	NWYSL-NKNNEFIPSFTK	303
c_000002718976_3 c_000002992548_1	273 274	NGWIYLCNYKNNI	SNIKMNINLFYKFI	KNK	рккү	nwysl-kenkefipsftkrifrqvstlf	333 325
c_000000456751_1	241	RGWYYLCSYKNNI	SNIKMNIDLFYKFT	ккі	PKKF	NWYSIDRSNOEFIPSFTKKIFKKIAKVYS	303
c_000002655634_1 c_000004232403_2	272 286	REWNYLCNYKNNT	SNTKMNTNT.FYKFT	KNK	PKKF	DWYSVDKSSQEFMPSFTKKII	326 351
6u7t.after.N146.pdb	284	ELTEPIVSFE H AF	SHLVWQLTVFPGRL	VHGG	PVEEPY	RLAPEDELKAYAFPVSHQRVWREYKEWAS	349
Consensus_aa:						@hpph.phshsp+hhp.h	