S1 Dataset. Alignment of Lost City MutY homologs.

Chemical motifs are highlighted in columns. Alignment was generated by *Promals3D* [88], guided by the structure of *Gs* MutY. It was necessary to align sequences in the first block including up to N146 separately from the second block and third block because otherwise the Cterminal domain residues were aligned inconsistently. The homologs flagged with dark red highlighting were eliminated because of missing chemical motifs. The homolog flagged with light pink highlighting required manual adjustment so as to align the H-x-FSH motif. The representative LCHF MutYs have the following contig ids: *Marinosulfonomonas* MutY, c_000001803648; *Rhodobacteraceae* MutY, c_000002747260; *Thiotrichaceae* MutY, c_000000598175; *Flavobacteriaceae* MutY, c_000001535696.

Conservation: sp P17802 MUTY ECOL	28	9 5 579 67999 5 5 65 7 55 6 9 989 KTPYKVWLSEVMLQQTQVATVIP-YFERFMARFPTVTDLANAPLDEVLHLWTGLG			140
sp_P83847_MUTY_GEOS c_000003652391_2	34 37	RDPYKVWVS <mark>E</mark> VMLQ <mark>O</mark> TRVETVIP-YFEQFIDRFPTLEALADADEDEVLKAWEGLG PDPYTVWLS <mark>E</mark> VMLQ <mark>O</mark> TTVAAVTG-YFRRFTTRWPTVQALAAADDGDVMGAWAGLG			146 149
c_000003032391_2 c_000000031207_6	26	EDPYAIWLSEVMLQQTRVTTVIP-YWHRFLEKYPDPKSLARAPLEQVLELWAGLG			138
c_000000430975_4 c 000001007148 4	38 35	PNVYHVWLSEIMLQQTKVATVLS-YYLNFLHKWPTLNDLATATRQNVLQAWAGLG RDPYVVWVREIMLQQTTVTAVVP-YLDRFLKRFPTVESLAGAKSAEVLRVWEGLG			150 147
c_000001092848_3	48	PDPYRVWLS <mark>E</mark> IMLQ <mark>Q</mark> TTVGAVKP-YCERFLERWPTVEALARADLQEVMKAWAGLG	<mark>Y</mark> YSRARNLKKCAEEVAHRHGGVFPDTEAGLKALPGIGD	<mark>Y</mark> TAAAVAAIAFGRRAAVV <mark>D</mark> G <mark>N</mark>	160
c_000001151029_1 c_000001797282_1	1 58	WLSEIMLQOTKVATVLS-YYSNFLHKWPTLADLAMATRHNVLQAWAGLG PDPYRVWLSEVMLQOTTIAAVRP-YFERFLTRFPDIFALAEAPEEAVMSAWAGLG			107 169
c_000001803648_25	40	PDPYRIWMS <mark>E</mark> VMLQ <mark>Q</mark> TTVAAVAK-YFHAFTTRWPTIIALASANDDDVMGQWAGLG	<mark>Y</mark> YARARNLLKCARVVVADYGGNFPDTRDELLKLPGIGP	<mark>Y</mark> TAAAIASIAFGRSETVM <mark>D</mark> A <mark>N</mark>	152
c_000002078955_4 c_000002106160_4	40 28	AEPYRVWMSEVMLQQTTVAAVAK-YFHAFTKRWPTVDALAAAKDQDVMGQWAGLG KEPYKIWLSETMLQQTQVKTVIP-FYNSWIEKYPDFESVAGARLDSLLKSWEGLG			152 140
c_000003607531_2	38	KVPYKIWLS <mark>E</mark> IMLQ <mark>Q</mark> TTVTTVGP-YFQHFLKTWPTIDELANASLDDVLKVWQGLG	<mark>Y</mark> YSRARNLHKCAKLICNNFDGRFPNTEEQLEQLPGIGP	<mark>Y</mark> TAAAILAIAFDKPAIVV <mark>D</mark> G <mark>N</mark>	150
c_000003872363_4 c 000004820107 1	36 43	PDPYHIWLSEVMLQQTTVAAVVK-YFNTFTKRWPNIQALATAQDADVMAEWAGLG PNPYYVWLSEIMLQQTTVVTVGP-YFTKFVERWPAIHDLAKADRDDVMHEWAGLG			148 155
c_000005774797_1	29 40	PNPYHVLLS <mark>E</mark> FMLQ <mark>Q</mark> TTVATVKT-YFEQFTKKWPSVEHFSHATDDEIMAQWAGLG	<mark>Y</mark> YARARNLVKTIHTIHNQGHFPASAYELQKLPGIGP	<mark>Y</mark> TSAAIAAIAFNEPILPR <mark>D</mark> G <mark>N</mark>	139 152
c_000005867021_3 c_000004546210_2	31	PDPYRIWLSEVMLQOTTVVAVAK-YFHVFTKRWPNITALANAKDEDVMGEWAGLG PSKYKTWISEIMLQOTQVNTVEP-YFHRFMERFPTVEELASSSPDEVLQIWSGLG			143
c_000004551008_5 c_000002511148_4	31 26	PSKYKTWISEIMLQ <mark>O</mark> TQVATVEP-YFIQFIQRFPEVTELASSSLDEVLQLWSGLG KTPYRVWVSEIMLQOTQVSTAIP-YFEKFIKEIPDVKSLSEASLDLVLSLWSGLG			143 138
c_000002511148_4 c_000000577378_2	14	KTPYRVWVSEIMLQQTQVSTVIP-YFKKFVREIPNIKSLSEASLDLVLSLWSGLG			126
c_000000598175_2 c_000000754627_3	37 34	INPYRVWVSEIMLQQTQVKTVIP-YFEKFMATFPDVQTLAHADQDLVLKHWSGLG KTPYKVWVSEVMLQQTQVVTVIP-YFEKFMQSFPDIIALANADEDQVLHHWTGLG			149 146
c_000000811118_1	25	KDPYKVWISEIMLQQTQVTTVIP-YFNKFISEYPTIKTLASTSLDEVLSLWSGLG	<mark>Y</mark> YTRARNIHKTAKILKKDFDCKLPNEIEALMSLPGIGF	<mark>S</mark> TAGAILSLGFEQSGVIL <mark>D</mark> G <mark>N</mark>	137
c_000000899687_2 c_000001176522_24	29 50	NDPYSIWVSEIMLQQTQVKTVIP-YYERWIKTLPTIDKLANAPEQKILKLWEGLG RTPYRVWVAEVMLQQTQVKTVVP-YFERFMEAFPAVDVLADAEMDAVLSQWAGLG			141 160
c_000001345122_1	4	ISPYRVWVS <mark>E</mark> IMLQ <mark>Q</mark> TQVKTVIP-YYQRFMKSFPSIEQLASATQDEVLAHWAGLG	<mark>Y</mark> YARGRNLHKSAQIIQTEYYGKFPQIFDDIIALPGIGK	<mark>S</mark> TAGAIMSIALKQRMPIL <mark>D</mark> G <mark>N</mark>	116
c_000001515736_6 c 000001682161 6	18 25	RDPYRVWLSEIMLQOTQVSTVLG-YYQRFLDAFPDVASLAGAPQDAVLALWSGLG PTPYRTWVSEIMLQOTQVKTVIP-YYLRFMESFPTIQSLAKASQEQVLAHWAGLG			130 137
c_000001923643_29	28	RDPYRVWLS <mark>E</mark> IMLQ <mark>Q</mark> TQVSTVLG-YYQRFLDAFPDVASLAAAPQDAVLALWSGLG	<mark>Y</mark> YSRARNLHRCAQAVVQEWGGAFPRRAEDLATLPGIGR	<mark>S</mark> TAGAIASFCFSERVPIL <mark>D</mark> A <mark>N</mark>	140
c_000002030994_5 c 000002038721 4	26 28	INPYRVWVSEIMLQQTQVKTVIP-YYEKFMTSFPDVQTLASADQDTVLKHWSGLG KSPYHIWISEIMLQQTQVKTVIP-YFHKFINSFPSIKSLAKSDLDKVLANWSGLG			138 140
c_000002523527_15 c_000002608528_2	43 26	RDPYRIWLS <mark>E</mark> IMLQ <mark>Q</mark> TQVAAVIE-YFQRFVAALPTVAALAAASADEVMALWAGLG	<mark>Y</mark> YSRARNLHRCAKTVVDEHAGVFPTDPEVLVTLPGIGR	<mark>S</mark> TAAAIAAFSAGVRSPIL <mark>D</mark> G <mark>N</mark>	155 138
c_000002961510_2	29	INPYRVWVSEIMLQOTQVKTVIP-YYQKFMTTFPDVQTLANADQDLVLKHWSGLG KDPYSIWVSEIMLQOTQVKTVIP-YYERWIKTLPTIGKLANAPEQKILKLWEGLG			141
c_000002979152_8 c 000003248034 1	34 46	RTSYRVWUSEIMLQOTQVVTVIP-YYERFMQSFPAVEGLAKATQNEVLDHWTGLG KNPYHIWLSEVMLQOTRVTTVVP-YYERFLDRFPTLESLATASEQSVLQAWSGLG			146 158
c_000003294679_3	31	KTPYSIWUSEIMLOOTQVKTVIP-YFKKFIVSFPTLRVLAQASLDDVLHHWSGLG			143
c 000003333364 1 c 000003402697 5	28 28	YDPYEVWISEVILQQTQMERGVA-YIERFLERFPTMESLAAAEEDEVLKVWEGLG REPYYVWVSEIMSQQTQIDRVADQFFPRFIETFPTVEALAAADWETVYPCWDGLG			140 141
c_000003492925_4	25	DDPYHIYLS <mark>E</mark> VMLQ <mark>Q</mark> TQVKTVLERYYFPFLKKFPTLKALGDANLDDVLKMWEGLG	<mark>Y</mark> YSRAKNLHKTAGLIEVLPSDIDELIRLPGIGK	<mark>N</mark> TAHAVATFVYKKPVPIM <mark>E</mark> A <mark>N</mark>	133
c_000003766664_5 c 000003948186 72	41 28	PTPYKVWVSEIMLQOTRVETVIP-YFQRFLSSFPDVHALAAASLDEVLSRWSGLG ITPYRVWLSEIMLQOTQVATVIS-YFERFVQTFPDVGALARAPLDEVLHLWTGLG			153 140
c_000005057120_4	28	ITPYRIWLS <mark>E</mark> VMLQ <mark>Q</mark> TQVATVIP-YFNQFIDYFPDIHKLATAEDDAVLHLWSGLG	<mark>Y</mark> YARARNLHKTAKILSKN-KGIFPDDLDSLMELPGIGR	<mark>s</mark> tagailsiafnnsypil <mark>d</mark> g <mark>n</mark>	139
c_000005590109_5 c_000006063368_2	28 26	ISPYRVWLSEVMLQQTQVTTVIP-YFNHFIQKFPDVHQLANAPLDSVLHLWSGLG KSPYKVWISEIMLQQTQVTTVIP-YFNKFLLRFPNIEKLAESELDEVMSYWSGLG			139 138
c_000000467631_2	7	STPYQTWLS <mark>E</mark> IMLQ <mark>Q</mark> TQVTTVIP-YFNRFIQTFPNIATLADAPLDAVLQHWAGLG	<mark>Y</mark> YARARNLHKTA-IIINKNGGVFPDDVDGLLELPGIGR	<mark>S</mark> TAGAILSIAFNKSHPIL <mark>D</mark> G <mark>N</mark>	118
c_000000788235_1 c 000001187176 11	27 28	ITPYRVWISEIMLQOTQVATVIP-YYQRFITSFPDVTTLANADEDLVLQHWAGLG MTPYRVWVSEIMLQOTQVATVIP-YYERFMAALPDVHALAAAPADEVLHLWTGLG			139 140
c_000001660697_64	28	GDAYRTWLS <mark>E</mark> IMLQ <mark>Q</mark> TQVSAVLG-YYARFIERFPTVQALAAAPADDVMAAWAGLG	<mark>Y</mark> YTRARNLHRCAQIVVAEHGGIFPRDPEVLASLPGIGR	<mark>S</mark> TAAAIAAFSYGVRAAIL <mark>D</mark> G <mark>N</mark>	140
c_000003378864_2 c_000003910742_3	39 28	RDPYAIWLSEIMLQOTQVETVLP-YYDRFLTAFPTIADLAAAPLGRVLKMWEGLG PTPYRVWISEIMLQOTQVVTVIP-YYQNFMDSFPDVRTLAHAEEDLVLQHWAGLG			151 140
c_000004116181_2 c_000006223903_1	1 29	VWVSEIMLQQTQVATVVP-YFNRFMAQFPDVKTLAQTSLDAVLQHWAGLG RNPYRIWISEIMLQQTQVTTVIP-YYERFMARFPHIVTLASAKLDTVLAEWTGLG			106 141
c_000001029068_2	2	-NYYYWLSEVILOOTQVIIVIF-IIERFMARFFHIVILASARIDIVLAEWIGLG -NYYYWLSEVVLQ <mark>Q</mark> TQVASAVG-YFSNFIKRFPTIGALSAASEDDVLSAWSGLG			113
c_000001128125_11 c 000001595844 4	36 27	ISPYRVWVSEIMLQQTQVATVIP-YFKRFMLSFPNVEVLAKATQDEVLSHWAGLG SDAYAIWLSEIILQQTRVAQGMP-YYIRFLEAFPTVFDLAKADEQEVMRLWQGLG			148 139
c_000001719155_2	31	rdpyrilvs <mark>e</mark> fmlq <mark>q</mark> tqvktvip-yferwiksfptlqklaearestvlkhweglg	<mark>Y</mark> YSRARNLRKAAQKIQQEYSGKVPESMNEIMKLPGVGR	<mark>Y</mark> TAGAVLSIAFGQKVPVL <mark>D</mark> G <mark>N</mark>	143
c_000002363038_6 c_000002561400_1	36 1	INPYRVWVSEIMLQQTQVVTVIP-YFERFMQRFPEVSDLAAASQDEVLSHWAGLG EIMLQQTQVATVIP-YFERFMQRFPKVADLACADQEEVLTYWAGLG			148 104
c_000002566035_2	28	VSPYKVWVS <mark>E</mark> IMLQ <mark>Q</mark> TQVITVIP-YFKRFMKRFPDVQTLANSSLDEVLHYWTGLG	<mark>Y</mark> YARARNLYKTAKIITKEYQGNFPLSLNEIMSLPGIGR	STAGAVLSLSYDKCFPIL <mark>D</mark> G <mark>N</mark>	140
c_000002598045_3 c_000004188575_41	26 28	ITPYKVWVSEIMLQQTQVVTAIP-YFKKFIQEFPTVKSLSKATPDQVLKLWSGLG PTPYQVWVSEIMLQQTQVATVIP-YYQRFMIRFPDNATLAAASQDDVLSYWTGLG			138 140
c_000000240049_1	26	KSLYRVWVS <mark>E</mark> IMLQ <mark>Q</mark> TQVTTVIP-YFARFMLQFNDIEALSNATQDDVLLYWAGLG	<mark>Y</mark> YSRARNLHKAAQIIQQQHGGCFPRQYNDVLALPGIGP	<mark>S</mark> TAGAILAQSQGQRHAIL <mark>D</mark> G <mark>N</mark>	138
c_000002139456_2 c_000003535614_2	26 28	KSLYRVWVSEVMLQ <mark>O</mark> TQVATVIP-YFARFMQQFSDIEALSNATQDEVLLYWAGLG RSLYRVWVS <mark>E</mark> IMLQ <mark>O</mark> TQVATVIP-YYQRFMQRFKNIAALAEATQDDVLLHWAGLG			138 140
c 000002657784 4 c 000003800129 15	25 30	KTPYKVWIS <mark>E</mark> IMLQ <mark>O</mark> TQVVTVIP-FYSAFINRFPNIQELATSSEEEVMSFWSGLG TTPYRVWIS <mark>E</mark> MMLQ <mark>O</mark> TQVNTAKD-YFLNFIEQYPDLESIKNASEEEILILWKGLG	<mark>y</mark> ysrarniyktaqılqkkfesklpsslsqlislpgigp	<mark>S</mark> TAGAILSLGYKKRAPIL <mark>D</mark> A <mark>N</mark>	137 142
c_000003716781_1	17	DDAYSVWISESMLQQTRVETVIP-YFERFLKRFPTVEALAEADIDEVLARWSGLG			129
c_000001556689_3 c_000001834452_1	18 1	RDPYAILVSEIMLQOTRVETVIN-RYGSFLERFPTIADLAIASLDDVLAEWSGLG WISEIMLQOTRVEVVVP-YFEAFIKRFPSIEVLANAQEEEVLSYWAGLG			130 107
c_000004255004_2	35	RDPYAIWVSETMLQQTRVATVLP-YYYRFMKAFPSVEALDQAPLDAVRNVWSGLG	<mark>Y</mark> YQRAANLKKAASVLMNRHNGKLPADYQTLLGLPGVGQ	<mark>Y</mark> TAGAVLSIAFDRRYPAP <mark>D</mark> G <mark>N</mark>	147
c_000000605438_3 c_000000581237_15	31 31	QSAYEIYLS <mark>E</mark> IMLQQTQVKTVLERFYFQFLEKFPTLKAVANAPVDDILKAWEGLG QSAYEIYLS <mark>E</mark> IMLQQTQVKTVLERFYFQFLDKFPTLKDVANAPVDDVLKAWEGLG			140 140
c 000002529579 2	31 1	QNSYKIYLS <mark>E</mark> IMLQ <mark>Q</mark> TQVKTVLERFYFQFLEKFPTLEAVANAPVDDVLKAWEGLG	<mark>Y</mark> YTRARNLHKTAIATKGVLPKRAEALEKLSGIGK	STAHAVACFAFNEPLPIL <mark>D</mark> A <mark>N</mark>	140
c_000006097838_1 c_000000583727_6	27	RDPYAIWISEVMLQQTQVKTVIP-YWRRWMEQLPDIASLAAADEDTVIKLWEGLG RDPYAIWVSEIMLQQTQVKTVIP-YWQRWMKQLPDIASLAAADEDTVIKLWEGLG			113 139
c_000005807640_2 c_000000134878_1	29 12	RDPYAIWVSEIMLQQTQVKTVIP-YWQRWMQRLPDIASLAAADEDTVIKLWEGLG NDPYKIWISEIMLQQTQVSTVQD-YYLRWIKRFPTIQSVADASIDEVLKHWEGLG			141 123
c_000005136725_3	27	SDPYKIWIS <mark>E</mark> IMLQ <mark>Q</mark> TQVSTVRD-YYIRWIKQFPDIQSVADASIDKVLKYWEGLG	<mark>Y</mark> YSRVRNFHKSCQMLIRNK-QDIPKGLDEFQKLKGVGP	<mark>Y</mark> IASAVQSIAFNIPTGVI <mark>D</mark> G <mark>N</mark>	138
c_000001684786_4 c_000002971826_23	24 34	PEPYRVWVSEIMLQOTRVETVIP-YFERFLDRFPTPAALAEASEDEVLTLWSGLG PEPYRVWVSEIMLQOTRVDTVIP-YFERFLDRFPTLSDLAAASEDEVLTLWSGLG			136 146
c_000002040695_2	37	ANPYFVFIS <mark>E</mark> VMLQ <mark>Q</mark> TTVATVVP-YFKKWIKKWPTLHALAEASLDDVLHTWQGLG	<mark>Y</mark> YRRARNVHRCAQEVVQSYGGLFPQNVSQLRKLPGIGP	<mark>Y</mark> TAGALSAIAFEQNSVAV <mark>D</mark> G <mark>N</mark>	149
c_000003263657_32 c_000005989041_2	41 38	NDPYSVWISEMMLQQTQVTQAEP-YYERFMAQFPSVETLAGATLDDVLKAWEGLG KDPYKIWLSEIMLQQTTVKAVGP-YFQLFLKTWPTIDKLAKATLDDVLRVWQGLG			153 150
c_000002391082_2	36	DNPYHIWIS <mark>E</mark> IMLQ <mark>Q</mark> TRVDQMGA-YFERFVGAFPTVEKLAAASEDQVLKVWEGLG	<mark>Y</mark> YARARNMHKAAVQIAGQLGGCIPDTYAGLIELPGIGE	<mark>Y</mark> TAAAVSSIAFDRDHPVL <mark>D</mark> G <mark>N</mark>	148
c_000003839553_2 c_000003996707_2	43 34	SDPYHIWISEIMLQOTRVDQMGG-YFERFITAFPTLEALAGASGDEVLKVWEGLG GNPYHVWISEIMLQOTRVDQMQP-FFERFTAAFPTVGALAAASQEEVLKAWEGLG			155 145
c 000002044706 1	16 31	DDPYRILVS <mark>E</mark> IMLOOTRVTTVLR-YYPAFLERFPTLADLAAADQEDVLAAWSGLG KREYYTLVSEFMLOOTQVSTVIP-YFKNFIKDIPDLNSLAKINEKKLLKYWEGLG			128 143
c_000006007075_1 c_000002094036_4	7	QKEYYTLVS <mark>E</mark> FMLQ <mark>Q</mark> TKVSTVIP-YFNNFLKNIPNMQSLAKINEKKLLKYWQGLG	<mark>Y</mark> YSRAKNLKKTAKIIVDNYQGKLPSDFEELKKLPGIGD	<mark>Y</mark> TANAISAIVFNKPTIPL <mark>D</mark> G <mark>N</mark>	119
c_000002762689_1 c_000005516980_2	31 31	KKQYYTLVSEFMLQQTQVATVIP-FFNRFIKNIPDLEALANFDNHKLIKLWEGLG KREYYTLVSEFMLQQTQVSTVIP-YFKNFIKNIPNLKMLAKVQNKKLIKLWEGLG			143 143
c_000003920004_1	37	PNPYYVLVS <mark>E</mark> FMLQ <mark>Q</mark> TTVNTVIS-RFKDFIKKWPNLKKLSMINENQILQFWSGLG	<mark>Y</mark> YARAKNLLNSAKIISLKFNNIVPDNYNDLIDLPGVGD	<mark>Y</mark> TAKAVLGIGYNKSVMPV <mark>D</mark> A <mark>N</mark>	149
c_000004008511_2 c_000004481347_1	31 38	PDPYFVFVS <mark>E</mark> YMLQ <mark>Q</mark> TTVGTVKT-RFEEFILKWPSINDLARISEKTILNFWSGLG TNAYYVLVS <mark>E</mark> FMLQ <mark>Q</mark> TTVNTVTK-RFNEFIKLWPSIDKLSRISENRILRFWSGLG			143 150
c_000003787733_3	30	NDLYKIWLS <mark>E</mark> VMLQ <mark>Q</mark> TRVNTVVP-YYLLWVKKYKSIKSVAKADYQNLLKLWEGLG	<mark>Y</mark> YSRCKNFYKSCLIIINDYDGKIPLDYLTFRSLPGVGD	YIASAVLSIGLNQPHAAI <mark>D</mark> S <mark>N</mark>	142
c_000000754657_2 c_000000990943_3	30 30	HDLYKIWISEVMLQQTRVNTVVP-YYLRWVEKYESIKSVAKADELKLLKLWEGLG NDLYKIWISEVMLQQTRVNTVVP-YYLRWVEKYKSIKSVAKADDLKLLKLWEGLG	YYSRCRNFHKACKIIVNDYGGEFPSDYQKFRLLPGVGD	YTASAVFSIGLKQTYAAI <mark>D</mark> G <mark>N</mark>	142 142
c_000004474996_2	29 17	NDLYKIWLSEVMLQQTRVETVIP-YYLKWVEKYKTIKSVAEADGQKLLKLWEGLG	YYSRCRNFHKACKIVVNDFTGEIPSDYQNFRSLPGVGD	YTASAVFSIGLNQTYPAL <mark>D</mark> GN	141 129
c_000001463500_11 c_000001286181_5	24	nnlyhvyls <mark>evmloo</mark> tkyktaip-yykrwlkkyptiesvalsnlddllklweglg ndpykvwys <mark>e</mark> imlo <mark>o</mark> tqystvip-fyenfmksfpdyltlskanldevlnnwaglg	<mark>F</mark> YRRAKNLHQTAKIITDKYHQVFPNNYEDLVALPGIGE	STAGAILALAFNKKGTIL <mark>D</mark> GN	136
c_000001293628_3 c_000001535696_8	30 24	repyrvwvs <mark>e</mark> imlo <mark>o</mark> trvetaip-yynrwmerfptvdalaegheoavlkaweglg rdpykiwls <mark>e</mark> imlootrvaogap-yylkfikhfatvydlakaseeovlklwoglg			142 136
c_000001614067_2	37	SNPYFVYLSEIMLQQTVVKTVIP-YFLKFVRKWPDINALAKAELHEINSYWAGLG	<mark>Y</mark> YSRAKNLHETAKIISNKYDGFLPTDKNSLMALPGIGE	YTSSAIMAIAFDRKSNVV <mark>D</mark> G <mark>N</mark>	149
c_000001765289_1 c 000001961666 1	3 18	DDPYKIWLSEIMLQOTQVKTVVP-YYNRWIKRYPSIKSVALADLGAVLKMWEGLG VDAYKVWVSEIMLQOTTVNAVIS-RYKKFISRFTNVKVLAKAPLEEVLEEWAGLG			115 130
c_000002018097_4	25	NEPYNIWLSEVMLQQTQVKTVVP-YYTKWIKKFPTLKSVAESDLNSLLKLWEGLG	YYSRCRNFHKATQIVVEKYKSVVPNDYKLFRQLPGVGD	YIASAVLSIAYNKKYPAV <mark>D</mark> AN	137
c_000002843512_36 c_000002930199_1	26 22	DDPYHIYLS <mark>E</mark> VML <mark>QO</mark> TQLKTVLERYYFPFLKRFPTLKTLGETPLDDVLKMWEGLG NNPYKIWIS <mark>E</mark> IILQ <mark>O</mark> TQIQTGIR-YYHKFIRHFPDINSLALAEEVDVLNVWQGLG	YYNKAKNLHKTATLIEELPSNIDELIKLPGIGK <mark>Y</mark> YNRVLNMLYSAKIIVKQHKSTFPTKYDELIKLKGIGP	TAHAVATFAYKKPVPIMEAN TAAAISSICKNEKRAVL <mark>D</mark> GN	134 134
c_000003033795_2 c_000003888107_2	22 23	RTPYRVWVSEIMLOOTQVNTVIP-YYKKWIKKYPTLKSFKESNFDDVIKIWEGLG HDPYKIWISEIMLOOTQVSTVIP-YYNKWINKFPNATKLSKANYNDVLKLWEGLG	<mark>Y</mark> YSRCHNMFNAAKLINSTFPNNYDDLINLPGIGD	YTAKTILAIAFKKNFVGI <mark>D</mark> TN	130 131
c_000003888107_2 c_000004013286_6	44	hdpykiwiseimlootovstvip-yynkwinkfpnatklskanyndvlklweglg Rdpyaiwvs <mark>e</mark> imlo <mark>o</mark> tovntvvp-fferfiesfptveklaaateaavlkrweglg			131 156

c_000004852258_1 c_000005254087_1			18 144
c_000005603677_1	29	QDPYKIWLAEIIMQQTRLEQGLP-YYERFIAAYPSIKELAETEEQKLMKLWQGLGYYARARNLQATAKRIVAEYAGIFPDNYKAILDLKGVGEYTAAAIASFAYDLPYAVV <mark>D</mark> GN 1	41
c_000003283462_3 c_000002687221_1	17 31	· · · · · · · · · · · · · · · · · · ·	.29 .43
c_000003347358_19	57	deayyiyls <mark>e</mark> vmlq <mark>q</mark> tqvktvleryyipfierfptlkhlgeapldvlkmweglg <mark>y</mark> ynraknlhktatlvdqlpsnideliklpgigk <mark>y</mark> tahavatfafhqpvpim <mark>e</mark> an 1	.65
c_000002701031_2 c_000000582753_3	24 32		.36 .44
c_000001713769_5	24	NDPYSVWLS <mark>E</mark> IILQ <mark>Q</mark> TRIAQGLP-YYLKFINKYPTINSLAKANENDILILWQGLG <mark>Y</mark> YSRARNLLKTAKFIVDERNGKFPTTYIELIKLKGIGE <mark>Y</mark> TAGAISSICFNERRAVL <mark>D</mark> GN 1	36
c_000004369364_1 c_000006057486_30			.39 .40
c_000005494072_10	24	KDPYKIWLS <mark>E</mark> IILQ <mark>Q</mark> TKIEQGLP-YYMSFVENYPNIETLAIADEQEVLKLWQGLG <mark>Y</mark> YSRARNLHFTAKSIVKNHNGKFPDNYNELLKLKGVGD <mark>Y</mark> TASAISSICFDEKCAVV <mark>O</mark> GN 1	36
c_000001742634_3 c_000002826998_2			.39 .39
c_000003159439_6	24	SNPYHIWIS <mark>E</mark> IILQQTRVDQGLD-YYKRFIATFPTINNLAKAKEEAVLKLWQGLG <mark>Y</mark> YSRARNLHFSAQYIVNELDGKFPSSYKELLKLKGVGD <mark>Y</mark> TASAIASICYNEVTAVV <mark>O</mark> GN 1	36
c_000004887214_1 c_000005037037_2			.41 .39
c_000001059964_1	19	YEPYQVWIS <mark>E</mark> IMLQ <mark>Q</mark> TQVQTMLP-YYHRWMERLPRLQDVAEASEDLLIKLWEGLG <mark>Y</mark> YRRVHNIKKTAVIICRDYGGTFPGSYRQQIQLPGIGP <mark>Y</mark> TAGAIASIAFNFSEPVL <mark>B</mark> GN 1	31
c_000002498472_1 c 000004615912 3			.40 .29
c_000004766858_2	30	YHPYEIWVS <mark>E</mark> IMLQQTQVKTMLP-FYTRWMSELPTVHSVAAASEEMVLKLWEGLG <mark>Y</mark> YSRARNLQKAARVICDEHGGELPADFDHIRALPGIGP <mark>Y</mark> TAGALASIAFNQPRPVV <mark>DGN</mark> 1	42
c_000002747260_18 c_000005371561_38	36 36	· · · · · · · · · · · · · · · · · · ·	.48 .48
c_000000169465_2		VTPYKVWVS <mark>I</mark> IMLQQTQVTTVIP-YFKRFMASFPTVHDLAKASQDDVLHHWTGLG <mark>Y</mark> YARARNLHKAANTLVEKYNGEFPYSLEEVMDLPGIGR <mark>S</mark> TAGAILSLSRNMRFFILD <mark>GN</mark> 1	44
c_000003254110_11 c_000004750284_20	32 32		.44 .44
c_000000141782_15	37	ATPYRVWIS <mark>E</mark> VMLQ <mark>Q</mark> TQVATVIP-YFERFLQRFPDVATLAAADADSVLHLWSGLG <mark>Y</mark> YARARNLHRAARVVVEAHGGEFPRRFEEVQALPGIGR <mark>S</mark> TAGAILSLGCGQRHAIL <mark>D</mark> GN 1	49
c_000002717847_8 c_000004054799_1			.43 .30
c_000006126673_1	43	PNPYFVWLS <mark>E</mark> IMLQ <mark>Q</mark> TTVSAVIP-YFLKFTQRWPDVWALANADVDDIMSAWAGLG <mark>Y</mark> YARARNMHKCAKTIVSDYDGIFPQEQAVLKTLAGIGD <mark>Y</mark> TSAAITAIVFDKYATVV <mark>D</mark> GN 1	.55
c 000000339186 3 c 000003029168 2	1 32		.12 .44
c_000001863436_1	48	GDPYAIWVS <mark>E</mark> VMLQ <mark>Q</mark> TQVVTVID-YYTRWLARFPDVETLAAAEIDEVLELWAGLG <mark>Y</mark> YRRARLLHRAAQHVVEECGGALPQTAGELEDLPGIGP <mark>Y</mark> TAGAIASIAFGEAAPLV <mark>G</mark> GA 1	.60
c_000002830137_4 c_000004612302_3			.53 .47
c_000001933926_1	21	TDPYRVWLS <mark>E</mark> IMLQQTTVATVTP-YFLRFVERWPTVHDLAAADLDRVLHAWQGLG <mark>Y</mark> YARARNMHACAKRISGDMAGVFFDQENELRRLPGIGP <mark>Y</mark> TAAAIAAIAAIAFDRPATPV <mark>GG</mark> N 1	.33
c_000003136334_1 c 000005849454 9			.45 .42
c_000001169194_1	41	TDPYRILVS <mark>E</mark> IMLQ <mark>Q</mark> TRVETVLR-YYESWLKRFPTLGALASANSREVLKAWEGLG <mark>Y</mark> YRRARNLHSAARRIRELPGGHFPTSYRDLRKLPGVGQ <mark>Y</mark> TAGAVASIGFGEIVPAV <mark>E</mark> GN 1	.53
c 000002786947 2 c 000001279808 52			.53 .41
c_000000358065_2	31	QKQYFILIS <mark>E</mark> FMLQ <mark>Q</mark> TQVKTVIP-YFENFINKIPNLKSLAKVNNRKLMKCWEGLG <mark>Y</mark> YSRAKNLKKSAKIIIDNYKGRLPNDFEELKKLPGIGD <mark>Y</mark> TASAISAIAFNKPIIPL <mark>D</mark> GN 1	.43
c_000003745941_1 c_000004187032_4	22 31		.32 .43
c_000006067315_3	31	QTEYFTLVS <mark>E</mark> FMLQ <mark>Q</mark> TQVKTVIP-YFNNFINKIPNLKKLANVNETRLMKCWEGLG <mark>Y</mark> YSRARNLKKTAKIIISEFNSNLPNTIEELKNLPGIGD <mark>Y</mark> TSRAVLAIAFNKPIIPL <mark>D</mark> GN 1	.43
c_000005543774_1 c_000006211484_1			.13 .35
c_000002718976_3	32	KKLYYRLLSEFMLQQTQVKTVIP-YFNKFTKKFKTIKALSKSNEREILKMWEGLGYYRRARNLLACSKILVKNYKSRLPRSIIEIKKLPGIGDYTANALLGLVYNEPRIAVDGN 1	44
c_000002992548_1 c_000000456751_1	33 1	~ · · · · · · · · · · · · · · · · · · ·	.45 .09
c_000002655634_1	28	kkeyyvlvs <mark>e</mark> fmlq <mark>o</mark> tqvktvip-yfkkfvtkipnlktlstsnekqvlklweglg <mark>y</mark> yrrvrnlhktakillkqykaklpkkfqeiiklpgvge <mark>y</mark> tanslsalihnkpcipi <mark>g</mark> m 1	40
<pre>c_000004232403_2 6u7t.before.V147.pdb</pre>			.39 .40
Consensus_aa:		.ssY.l@lsElMLQQTpV.hhhs.Y@.p@hpp@PslpsLA.tpbppllphWpGLGYYsRt+Nlhphtp.l.pph.t.hPpshp.lLPGlGTAtAlhtht@spshlDtN	
Conservation:	141	95 9 VKRVIARCYAVSGWPGKKEVENKLWSISEG-VTPAVGVERFNÖAMMDIGAMICTRSKVPKSICPLONGGIAAANNSWALYPGKKPK	225
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS	141 147	VKRVLARCYAVSGWPGKKEVENKLWSLSEQ-VTPAVGVERFNØAMMDLGAMI <mark>C</mark> TRSKPK <mark>G</mark> SL <mark>C</mark> PLQNG <mark>C</mark> IAAANNSWALYPGKKPK VMRVLSRLFLVTDDIAKPSTRKRFEQIVRE-IMAYENPGAFN <mark>E</mark> ALIELGALV <mark>C</mark> TPRRPS <mark>C</mark> LL <mark>C</mark> PVQAY <mark>C</mark> QAFAEGVAEELPVKMKK	225 231
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2	147 150	vkrvlarcyaysgwpgkkevenklwslseg-vtpavgverfwgammlgamic*rskpkcsleplomgilaannswalypgkkpk vmrvlsrlflvytddiakpstrkfegivre-imayenpgafnealielgalvctprrpscllepvgaycqafaegvaeelpvkmkk vervmarifdistfligakpalkaras-ltpkirpggyagavmlgaticTaraptcgveplongcharragtaaelekktpk	231 232
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_000000031207_6 c_000000430975_4	147 150 139 151	VKRVLARCYAYSGWPGKKEVENKLWSLSEQ-VTPAVGVERFØAMMDLGANICTRSKPKCSLEPLONG LAAANNSWALYPGKKPK VMRVLSRLFLVTDDIAKPSTRKRFEQIVRE-IMAYENPGAFNEALIELGALVCTPRPSCLLEPVQAYCQAFAEGVAELPVKMKK VERVMARLFDISTFLE	231 232 223 233
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_00000362391_2 c_000000031207_6 c_000000430975_4 c_000001007148_4	147 150 139 151 148	VKRVLARCYAVSGWPGKKEVENKLWSLSEQ-VTPAVGWERFNÖAMMDLGAMICTRSKPKCSLC-PLQNGGLAAANNSWALYPGKKPK VMRVLSRIFLIVTDIA	231 232 223 233 231
sp_P17802_MUTY_ECOL sp_F83847_MUTY_GEOS c_0000003552391_2 c_000000031207_6 c_000000031207_5_4 c_000001007148_4 c_000001092848_3 c_000001151029_1	147 150 139 151 148 161 108	VKRVLARCYAVSGWPGKRSTEKUENKLWSLSEQ-VTPAVGVERFØAMMDLGAMICTRSKPKCSLE PLONG LAAANNSMALYPGKKPK VMRVLSRLFLVTDDIAKPSTRKFEGQIVRE-IMA	231 232 223 233 231 243 190
sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_000000031207_6 c_000000430975_4 c_000001097148_4 c_000001097148_4 c_000001199202_1 c_000001797282_1	147 150 139 151 148 161 108 170	VKRVLARCYAYSGWPG	231 232 223 233 231 243 190 252
sp_P17802_MUTY_ECOL sp_F83847_MUTY_GEOS c_0000003552391_2 c_000000031207_6 c_000000031207_5_4 c_000001007148_4 c_000001092848_3 c_000001151029_1	147 150 139 151 148 161 108	VKRVLARCYAVSGWPG	231 232 223 233 231 243 190 252 235 235
sp_17802_MUTY_ECOL sp_P83847_MUTY_GBOS c_000003652391_2 c_000000312077_6 c_00000033975_4 c_000001007148_4 c_0000010972848_3 c_000001151029_1 c_000001797282_1 c_000001803648_25 c_000002078955_4 c_000002078955_4	147 150 139 151 148 161 108 170 153 153	VKRVLARCYAYSGWPG	231 232 223 233 231 243 190 252 235 235 223
sp_P17802_MUTY_ECOL sp_P83847 MUTY_GEOS c_000003652391_2 c_000000312077 6 c_0000000312077 6 c_000001007148 4 c_000001097148 3 c_000001151029 1 c_000001797282_1 c_00000197368 25 c_000002078955_4 c_000002106160 4 c_000003607531_2 c_000003872363_4	147 150 139 151 148 161 108 170 153 153	VKRVLARCYAYSGWPG — KREVENKLWSL — SEQ-VTP — AVGVERFØAMMDLGANICTRSKPKCS — LE PLONG LAAANNSWALYPGKKPK — VWRVLSRLFLVTDDIA — KESTRKFEGI — VRE - IMA — YENPGAFNEALIELGALVCTPRPSCL — LE PVQAYE QAFAEGVAELPVKMKK — VERVMARLEDISTFLD — GARPALKAR — AAS - LTP — KLEPGDYAQAVMDLGATITARAPTIG — - V-UPLKDC HARRAGTAAELPKTFK — VERVLSRYLKIDGNPK — SGTARKRIQQA — ADD — ALD — GENFGDHNOALMDLGRSITCTPRSPDC — RE PLASG GARAGGEPTRWFTRROK — VERVUSRIFQITQFIF PER PLASK — SKREGUNQAIMDLGSIVOTPRSPDC — RE PLASG GARAGGEPTRWFTRROK — VERVUSRIFQITQFIF PER PLASK — SKREGUNQAIMDLGSIVOTPRSPKRCK — VCPLHDIGLANISGTPSDFPKRTPR — TARFYARLLALRSDLH — SGEGRRQLWSL — AER-IVP — RDRPGEFNQALIDLGATVGCV - TPRCQ — EC PVGSS GRSLELGEVERIPARASK — VERVUSRIFQITQPIP — LSRFTLRQL — AAG - LTP — SKREGUNQAMMDLGSIVCTPRNFRCS — VC PLQAFGARGAAQESFPYKASK — VERVUSRIFQITQPIP — LSRFTLRQL — AAG - LTP — SKREGUNQAMMDLGSIVCTPRNFRCS — VC PVGHIGLANISGTPSDFFKRTPR — VERVLSRANVEAPLP — GSRPEIRL — TOA - LVP — PDRFGGFAQALMDLGATICTPKRPACA — LC PLOMAFGARAGGSFPFKIKV — VERVLSRANVEAPLP — SKREGUNAAMMDLGSIVCTPRNFRCS — VC PWRSTAGLAGGNGSFPFRIKV — VERVMARMEDHSSLP — SAKELLAC — AAA - LTP — DFRAGDYAAANMDLGSIVCTPRNFRCA — VC PWRSTAGLAGGNGSFPFRIKV — VERVMARMEDHSSLP — SAKELLAC — AAA - LTP — DFRAGDYAAAVMDLGATICTPKRPACA — LC PWRSTAGLAGGNGSFPFRIKV — VERVMARMEDHSSLP — NAKPULSTAGAAQESFPKFTR — VERVMARMEDHSSLP — NAKPULSTAGAAQESFPKFTR — VRINKMYCKTEK — VERVMARMEDHSSLP — NAKPULSTAGAAQESFPKFTR — VRINKMYCKTEK — NAKPULSTAGAAQESFPKFTR — VRINKMYCKTEK — TNIKKMYCKTEK — TNIKKMYCKTEK — RSPRGGPNAAMMLGATICTPKRPRC — NC PLKLSGGTLSGSPESYSPKFR — VERVMARMEDHSSLV — LEPETYAGALAPGAANT — VERVMARMEDHSSLV — LEPETYAGALAPGAATA — PREPGGPNAAMMLGATUCTRPRRPCC — NC PLKLSGGTLSGSPESYSPKFR — VERVMARMEDHSSLV — NAKPULSTAGAAA — LPP — DFRAGGYAAVMDLGATUCTRPRRPCC — NC PLKLSGGTLSGSPESYSPKFR — VERVMARMEDHSSLV — LPP — LPRCLAGAAA — LPP — DFRAGGYAAVMDLGATUCTRPRRPCC — NC PLKLSGGTLSGSPESYSPKFR — VERVMARMEDHSSLV — NAKPULSTAGAAA — LPP — DFRAGGYAAVMDLGATUCTRPRRPCC — NC PLKLSGGGTLSGSPESYSPKFR — VERVMARMEDHSSVV — VERVMARMEDHSSVV — LPRCLAGAAA — LPP — DFRAGGYAAVMDLGATUCTRPRRPCC — NC P	231 232 223 233 231 243 190 252 235 235 223 236 231
sp_P17802_MUTY_ECOL sp_P83847 MUTY_GEOS c_000003552391_2 c_000000312077 6 c_000000439975_4 c_00001092848_3 c_00001191282_1 c_000001797282_1 c_000001797282_1 c_000002078955_4 c_000002078955_4 c_000002078955_4 c_000003807531_2 c_000003872363_4 c_000004820107_1	147 150 139 151 148 161 108 170 153 153 141 151 149 156	VKRVLARCYAVSGWPG	231 232 223 233 231 243 190 252 235 235 223 236 231 240
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sp_ P17802_MUTY_ECOL sp_ P83847 MUTY_ECON c_00003652391_2 c_0000003552391_2 c_00000031207_6 c_00000192463_3 c_00001922463_3 c_0000197282_1 c_0000197282_1 c_0000197282_1 c_0000197282_1 c_00002106160_4 c_00003607531_2 c_000002807531_2 c_000003872363_4 c_00000482017_1 c_000005867021_3 c_00000482017_1 c_000005867021_3 c_00000587021_3 c_00000587021_3 c_00000577378_2 c_00000551148_4 c_00000577378_2 c_0000059175_2 c_000001754627_3 c_0000059175_2 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_00000175522_1 c_00000175522_1 c_00000175522_2 c_00000175522_2 c_00000175522_1 c_00000175522_2 c_00000175522_2 c_00000175522_2 c_00000175522_3 c_00000175522_2 c_00000175522_2 c_00000175522_2 c_00000175522_3 c_00000175522_2 c_00000175522_3 c_000000175522_3 c_000000175522_3 c_000000175522_3 c_000000175522_3 c_000000175522_3 c_0000000175522_3 c_000000175522_3 c_00000175522_3 c_0000000175522_3 c_00000175522_3 c_00000175522_3 c_00000175522_3 c_000000175522_3 c_00000175522_3 c_000	147 150 139 151 148 161 153 153 141 155 161 144 139 156 153 154 155 155 155 155 155 155 155 155 155	VREVIABLE LITDID A: MESTERREGO VEF - MAYOVERPRAMALICIANI TRISPECS - LEPLONG LAANINSMALTPGKER - VERVABALIDIDATE - VERTERREGO VEFIND CHARRACTABLINGKE - VERVABALIDISTPLP - GARPALKAR - AAS - LTP - KLREGOVA ANDOLGATI TRARPFOG - VEPIND CHARRACTABLIRERY WE VERVASHIVATIONER - GARPALKAR - AAS - LTP - KLREGOVA ANDOLGATI TRARPFOG - VEPIND CHARRACTABLIRERY WE VERVASHIVATIONER - GARPALKAR - ADD - ALD - GENEROINE ALD GENEROINE ALD GENEROINE ALD GENEROINE ALD CHARRACTABLIRERY WE VERVASHIVATIONER - LISEPTLEGO - AAD - LTP - SERREGOVA ALDOLGSIVETERPEPOG - VEPIND CHARRACTABLIRERY WE VERVASHIVATION - VEPIND CHARRACTAR	231 232 233 233 243 252 231 190 252 235 235 232 236 231 222 235 223 223 223 223 221 222 223 223 223 223
sp_ P17802_MUTY_ECOL sp_ P83847 MUTY_ECON c_00003652391_2 c_0000003552391_2 c_00000031207_6 c_00000192246_3 c_00000197248_4 c_00000197248_1 c_0000197248_1 c_0000197248_1 c_0000197248_1 c_00000197248_1 c_00000278955_4 c_00002078955_4 c_000002106160_4 c_00003872363_1 c_00003872363_1 c_00003872363_1 c_00003872363_1 c_00003872363_1 c_000004820107_1 c_00005567021_3 c_000005774797_1 c_00005567021_3 c_000005774797_1 c_000005774797_1 c_00000577378_2 c_00000577378_2 c_000001754627_2 c_000001754627_3 c_0000018718_1 c_0000018718_1 c_0000018718_1 c_0000018718_6 c_0000018718_6 c_0000018718_6 c_000001823643_2 c_000001823643_2 c_00000232857_1 c_00000232857_1 c_00000232857_1 c_00000232857_1 c_00000232857_1 c_00000232857_1 c_00000232863_2 c_00000329467_3 c_000000329467_3 c_00000329467_3 c_00000329467_3 c_00000329467_3 c_00000329467_3 c_00000329467_3 c	147 150 151 148 161 153 153 153 153 151 149 153 144 139 141 131 138 142 147 131 138 142 143 144 144 141 142 144 144 144 144	VREVIARCYATORIAS. — SEQ. VTP — AVGVERTNAMBLIGHT TRISPE'S. — LPIQNG LAANINSMALTPGREW. VREVARALIDIDIDA — KEPTERREĞQ VEF. VAR. — TENERGANALLICHAY TERREĞG. — VOYAN QAFAEVAELIVYMKK. VERVARALIDISTPLP. — GARPALKAR. AASLTP — KLREGO'AANVOLGATI TARAPT'G. VEPLINC GHARRAGTAALIKERTB'R. VERVYSKIPQITQPIP — LSRPILIQL. AAGLTP — SERREĞU'RA ANDLOSIV TERREÇG. — VEPLINC GHARRAGTAALIKERTB'R. VERVYSKIPQITQPIP — LSRPILIQL. AAGLTP — BORDEĞE'RA LIDLGSIV TERREÇG. — VEPLINC GHARRAGTAALIKERTB'R. VERVYSKIPQITQPIP — LSRPILIQL. AAGLTP — BORDEĞE'RA LIDLGSIV TERREÇG. — VEPLINC GHARRAGTARGESFEVRASK. VERVYTKLERATGTELP. — AAREQO'RKA. VAALVP — BERGGE'RA LIDLGSIV TERREÇG. — LPQAF CARGANAQESFEVRASK. VERVYTKLERATGTELP. — AAREQO'RKA. VAALVP — BERGGE'RA LINGLGAT'U TERREÇG. — LPQAF CARGANAQESFEVRASK. VERVYTKLERATGTELP. — GARPEG'RA ANDLATI TO TERREÇG. — LPQAF CARGANAQESFEVRASK. VERVYTKLERATGTELP. — GSRPETIERL. — TQALVP — DERREĞG'RA ANDLOGAT'U TERREĞG. — LPQAF CARGANAQESFEVRASK. VERVYTKLERATGTELP. — GSRPETIERL. — TQALVP — DERREĞG'RA ANDLOGAT'U TERREĞG. — LPQAF CARGANALIKETE'R. VERVYARALINI HEPLP. — SARFELLAR. — AAALTP — DERREĞG'RA ANDLOGAT'Ü TERREĞG. — LPQAF CARGANALIKETE'R. VERVYARALINI HEPLP. — AANFELTAK. — AAALTP — DERREĞG'RA ANDLOGAT'Ü TERREĞG. — LEVEL'A CANALLIKETE'R. VERVYARALINITE'REPL. — BARE TILECAAM. — LAP. — TTT — GORREĞG'RA ANDLOGAT'Ü TERREĞG. — LEVEL'A CANALLIKETE'R. VERVYARALINITE'REPL. — BARE TILECAAM. — LAP. — TTT — GORREĞG'RA ANDLOGAT'Ü TERREĞG. — LEVEL'A LALDEĞGANALLIKETE'R. VERVYARALINITE'REPL. — BARE TILECAAM. — LAP. — TTT — GORREĞG'RA ANDLOGAT'Ü TERREĞG. — LEVEL'A LALDEĞGANALLIKER'REPLE'VARQU'Ü TERREĞG'Ü TERREĞG'Ü TERREĞG'Ü TERREĞĞĞĞÜ TÜ TERREĞĞĞÜ TERREĞĞĞÜ TERREĞĞĞĞÜ TERREĞĞĞĞÜ TERREĞĞĞĞĞÜ TERREĞĞĞĞĞÜ TERREĞĞĞĞÜ TERREĞĞĞĞÜ TERREĞĞĞĞÜ TERREĞĞĞĞÜ TERREĞĞĞĞÜ TERREĞĞĞĞĞÜ TERREĞĞĞĞÜ TERREĞĞĞÜ TERREĞĞÜ TERREĞĞÜ TERREĞĞÜ TERREĞĞÜ TERREĞĞĞÜ TERREĞĞĞÜ TERREĞĞĞÜ TERREĞĞÜ T	231 232 232 233 243 252 231 190 252 235 235 236 231 222 228 223 223 223 224 221 222 223 224 221 222 224 222 223 223 224 221 222 223 224 221 222 223 223 224 221 222 223 223 223 223 223 223 223 223
sp_ P17802_MUTY_ECOL sp_ P83847 MUTY_ECON c_00003652391_2 c_0000003552391_2 c_00000031207_6 c_00000013207_6 c_000001092846_3 c_000001972882_1 c_00000197282_1 c_00000197282_1 c_00000197282_1 c_000001805731_2 c_00000287363_4 c_00003872363_4 c_00003872363_4 c_00004820107_1 c_00003872363_4 c_00004820107_1 c_000058707378_2 c_0000058707378_2 c_0000058707378_2 c_0000017652_2 c_0000017662_1 c_00000177497_1 c_000000177497_1 c_00000177497_1 c_00000177497_1 c_00000177497_1 c_00000177497_1 c_00000177497_1 c_00000177497_1 c_000003401749_1 c_00000340174_1 c_00000340174_1 c_000003378864_2 c_000003478235_1 c_000001187176_1 c_000003378864_2 c_000003378864_2 c_000003378864_2 c_000003378864_2 c_000003378864_2 c_0000003378864_2 c_000003378864_2 c_0000001187176_11	147 150 139 151 148 161 153 153 153 151 149 153 144 139 141 152 138 142 143 144 139 141 151 153 144 144 139 141 141 142 143 144 141 142 144 141 142 144 141 141 142 144 144	VERVILARCIAYSOMPG - KREVERKINSL - SEQ-VFP - AVGVERFNAMEDICANI CPRSFRESC - L. PUGA CARAGNARELYDGKKER - VERVILARCHYDDIA - KPSFREREGIL - L. VERLAGARA LILICALVE CHARACTURE AND LATE OF THE MERCHANDER CONTROL OF THE MERCANDER CONTROL OF THE MERCHANDER CONTROL OF THE MERCHANDER CONTRO	231 223 233 243 245 235 236 231 222 247 201 222 2247 201 222 224 223 225 228 223 225 228 223 225 225 228 225 225 225 225 225 225 225
sp_P17802_MUTY_ECOL sp_P83847 MUTY_ECOS c_00003652391_2 c_000000452937_6 c_000000430975_4 c_000001092484_3 c_00001197282_1 c_00000197282_1 c_0000197282_1 c_0000197282_1 c_0000197282_1 c_00000197282_1 c_000002078955_4 c_00002106160_4 c_00003607531_2 c_000004820107_1 c_00005867021_3 c_00004820107_1 c_00005867021_3 c_00004546210_2 c_00004551008_5 c_000002511148_4 c_0000059175_2 c_0000059175_2 c_0000059175_2 c_000001118_1 c_0000059175_2 c_000001176522_1 c_0000001176522_1 c_000001176522_1 c_0000001176522_1 c_000001176522_1 c_0000001176522_1 c_000001176522_1 c_00000117652_1 c_000001176522_1 c_000001176522_1 c_00000117652_1 c_00000117652_1 c_00000117652_1 c_00000117652_1 c_00000117652	147 150 151 148 161 153 153 153 153 153 153 153 15	VENURALCHAYSONFG - KREVERKINSL - SQ-VPP - AVGVERFNAMEDICANI (FRSFRESC - LEVAC CARAGEMENT LYRE IN VENURAL ILICALLY FERRESC - LEVAC CARAGEMENT LYRE IN VENURAL FOR THE STREET - CAREALKAR - ANS-LIF - KLREGGYA AVEDICATI (FRARPEG) - VERLOC GLARAGE FIRSTER - VERLOC GLARAGE FIRS	231 243 223 1190 252 235 236 228 223 228 223 226 227 229 222 225 226 227 227 227 227 227 227 227 227 227
sp_ P17802_MUTY_ECOL sp_ P83847 MUTY_ECON c_00003652391_2 c_0000003552391_2 c_00000031207_6 c_00000013207_6 c_000001092846_3 c_000001972882_1 c_00000197282_1 c_00000197282_1 c_00000197282_1 c_000001805731_2 c_00000287363_4 c_00003872363_4 c_00003872363_4 c_00004820107_1 c_00003872363_4 c_00004820107_1 c_000058707378_2 c_0000058707378_2 c_0000058707378_2 c_0000017652_2 c_0000017662_1 c_00000177497_1 c_000000177497_1 c_00000177497_1 c_00000177497_1 c_00000177497_1 c_00000177497_1 c_00000177497_1 c_00000177497_1 c_000003401749_1 c_00000340174_1 c_00000340174_1 c_000003378864_2 c_000003478235_1 c_000001187176_1 c_000003378864_2 c_000003378864_2 c_000003378864_2 c_000003378864_2 c_000003378864_2 c_0000003378864_2 c_000003378864_2 c_0000001187176_11	147 150 139 151 148 161 153 153 153 151 149 153 144 139 141 152 138 142 143 144 139 141 151 153 144 144 139 141 141 142 143 144 141 142 144 141 142 144 141 141 142 144 144	VERVILARCIAYSOMPG - KREVERKINSL - SEQ-VFF - AVGVERFNAMEDICANI TERSEPSES - L. PUGNOZ CARAGOMERE LYPTOKK - VERVILARCH TO THE CONTROLL OF THE CON	231 223 233 243 245 235 236 231 222 247 201 222 2247 201 222 224 223 225 228 223 225 228 223 225 225 228 225 225 225 225 225 225 225

c_000001595844_4	140	VFRVLARYTANFIDIG	TPAGKKEFTLL	ANQ-LLD	KKQPGKFN	AIMDLGALV <mark>C</mark> KPTNPD <mark>C</mark> S	N <mark>C</mark> PLQIK <mark>C</mark> QAFSQDTIAQLPVKEKK 224
c_000001719155_2 c_000002363038_6	144 149	VKRVLSRLFLLKENGE	TRKSENILWET	MQQ-LLP	ETGAGNFN	AIMELGATV <mark>C</mark> LPKNPL <mark>C</mark> L:	LCPLKRNCQAQKSGKQNLYPPRKRA 228 LCPVKTDCRALKTDQVASFPNSKPK 233
c_000002561400_1	105	VKRVLTRFFGVHGWPG	EKQVENRLWHR	ADE-LTP	SVRFADYT	AIMDLGATL <mark>C</mark> KRSKPN <mark>C</mark> I'	r <mark>C</mark> PVHSG <mark>C</mark> QALKKGEVHLLPSFKPK 189
c_000002566035_2 c_000002598045_3	141 139						CPLTLTCFAREMGKQHDFPGKKPT 225 CPVNQDCSAFKEGLVDTLPLKVKR 223
c_000004188575_41	141	VKRVLARFYAIASWPG	NKATEQQMWQQ	ADN-LLP	DQRIAAYI	AQMDLGATL <mark>C</mark> TRSKPN <mark>C</mark> D	CCPLQSNCQAYARGTPTDFPIAKPK 225
c_000000240049_1 c_000002139456_2	139 139						VCPLSEDCLAYQQQRVADFPGKKPK 223 GCPLSEDCLAHQQQTVADFPGKKPK 223
c_000003535614_2	141	VKRVLARYQAIEGWPG	KPAIEKQLWVF	AER-YTP	TEELADYT	AIMDLGATL <mark>C</mark> TRASPK <mark>C</mark> G	SCPLNNGCKALANNCVAALPTRKPK 225
c_000002657784_4 c 000003800129 15	138 143						ICPVSRDCIAFNKKLIQVLPRKKLT 222 CPLGRWCLSKKNGSFYTYKKKK 220
c_000003716781_1	130	VRRVLARWFAVEGVV	-TKAEPRREIEGL	AAA-LVG	GVNDPGSWN	ALMELGATV <mark>C</mark> LPKDPR <mark>C</mark> D:	SCPVMTECRARARGLERAVPELPVR 215
c_000001556689_3 c_000001834452_1	131 108						CPCSSYCEAHELGIEEQIPPRRSK 215 CPISEKCVARATNRVTEIPKKAKR 195
c_000004255004_2	148	ARRVYARLLSLTN	LRAINET	AEQ-MVS	HSRPGDFN	AVMELGATV <mark>C</mark> LPGKPR <mark>C</mark> E	R <mark>C</mark> PLAYR <mark>C</mark> QARSVGAFKLQLRRPTR 225
c_000000605438_3 c_000000581237_15	141 141						CPFVSLCQGKDEPLLYPTKKKK 218 CPFEPLCQGKESPLLYPEKKVK 218
c_000002529579_2	141	VKRILYRFFAVKEA	NEKKLWEM	AYD-LYD	KENAYIYN	TMMDIGSLI <mark>C</mark> THKNPL <mark>C</mark> T	QCPFVSLCQGKDEPLLYPTKKKK 218
c_000006097838_1 c_000000583727_6	114 140						CPLKGHCIARKQNKVNRIPVSAKR 207 CPLKGRCTARKQNKVETIPALAKR 233
c_000005807640_2	142	VARVLTRLLGIEESPK	ARPVADRLWSV	ADE-LVNHAVTL	RKPSQQNASAFN	AMMELGALV <mark>C</mark> TPRNPL <mark>C</mark> G	O <mark>C</mark> PLKGR <mark>C</mark> IARKQNKVETIPALAKR 235
c_000000134878_1 c_000005136725_3	124 139						CPIHNGCKALKLGIQSDLPIKIKK 206 CPIQYGCKALKLGIQADLPVKIKK 221
c_000001684786_4	137	VERVMTRILRLAENPR	QVSTKKRLKEI	AGG-WMP	ADKASSFN	AMMELGALI <mark>C</mark> SPVSPD <mark>C</mark> P	S <mark>C</mark> PVREV <mark>C</mark> AAAEQGDPENFPRLPPK 221
c_000002971826_23 c_000002040695_2	147 150						ACPIHDACAAAEHGDPENFPKLPPR 231 LCPIKTLCKSAHHNTVHLFPHKTKK 232
c 000003263657 32	154	VIRVLSRLYRIHEDAT	KGPAKRRFQEL	ADG-LLQ	KGQAADFN	AMMELGATV <mark>C</mark> LPQKPR <mark>C</mark> T	VCPVQCHCRAFHELSDPSGLPYKPP 238
c_000005989041_2 c 000002391082 2	151 149						LCPWKKCCIANQRNFVDQVPQKVSK 236 CCPVGQWCRAQAELDDPSALPYKVP 233
c_000003839553_2	156	VIRVLCRHLRIEGDPR	RAQIKAELIAA	VEA-LLA	RGQAGDFN	AMMELGARI <mark>C</mark> TPRKPL <mark>C</mark> E	r <mark>c</mark> pvgat <mark>c</mark> raraelddptalpykap 240
c_000003996707_2 c_000002044706_1	146 129	VTRVLCRLLRLEGDPR VIRVLTRLFRIPGDPG	KAAVKTELIAA TAAVSRRLWQL	GER-LLA ATD-VLP	RGRAGDFN	AMMELGARI <mark>C</mark> KPTSPACG(ALMDLGATVCKPIAPLCE(CAVVEMCRAHAELDDPAQLPTKVR 230 CPLAGLCAVRAAGNAEDFPNAGRR 213
c_000006007075_1	144	VERIIKRILNLKTEKE	ISKENIIKK	KKI-LGM	SDRSSDYA	ALMELGALV <mark>C</mark> KPKNPY <mark>C</mark> K	K <mark>C</mark> PITKN <mark>C</mark> LSYKKKDFEIISKN 223
c_000002094036_4 c_000002762689_1	120 144						KCPITKNCLSYKKKDFKIKPKN 199 CPISNKCIALKKKDFLLTKIK 223
c_000005516980_2	144	IERVLKRYLYLKKENE	IQKENLIEK	KSV-FGL	SQRSSDYA	ALMELGALI <mark>C</mark> KPSNPL <mark>C</mark> N	CPISKKCKSFRKKDFNLIKNT 223
c_000003920004_1 c_000004008511_2	150 144	IKRMLARLYGLDQSIN IERILVRLYGLKLPII	LINKKITSL KIKNDLRKK	SKF-YES SDN-FIS	KKQSSNLI	AFMDYGSIICVPRNPKCG: AFMDFGSLICTPRNPD <mark>C</mark> V	I <mark>C</mark> IISRE <mark>C</mark> IANQRKISNIIPKKIKS 232 N <mark>C</mark> LIQKN <mark>C</mark> NAFNYNLQDIIPVKLKS 226
c_000004481347_1	151	IKRIIARLYGIKTSLL	LNKKTIEDI	ASK-YQS	SNKASDLI	SFMDYGSVI <mark>C</mark> LPRNPK <mark>C</mark> D	E <mark>C</mark> LIEKF <mark>C</mark> EARKKNIQHLIPFKNLS 233
c_000003787733_3 c_000000754657_2	143 143	VRRVMARILRIKHITK	RNKKRIHNT	LIE-WMD	PERPGDING	ALMDLANKICKVDHAQCN	rcpidkycmaekmsipesyptklnk 225 scpideicmankmsipesyptrikk 225
c_000000990943_3	143	VRRVMARVLRIKNITN	RNKKRINNT	LIK-WMD	PVRPGDIN	ALMDLANSI <mark>C</mark> RVDHAH <mark>C</mark> S	I <mark>C</mark> PIDEI <mark>C</mark> MAEKMPIPESYPIKVKK 225
c_000004474996_2 c_000001463500_11	142 130						r <mark>C</mark> PIDEI <mark>C</mark> MANNMSIPESYPAKLEK 224 I <mark>C</mark> PVSQF <mark>C</mark> KAKKTLLPFGYPIKINK 212
c_000001286181_5 c_000001293628_3	137 143	VKRVVSRYLNVENNPR	ELKKSIKPF	LYQ-NSP	KANYQSFG	GMMDLGSLI <mark>C</mark> VKEKPK <mark>C</mark> D:	LCPIQKTCLSFKKQDFIKTKKNT 217
c 000001535696 8	137						VCPLTKQCRAETEGTQELRPAPKRR 222 SCPLSDSCVALQENKIDTLPVKLKK 221
c_000001614067_2	150	VERVFSRFYAVEKPIK	ESKIFIKNI	AEK-HLP	DNRHGDYA	ALMDLGSLI <mark>C</mark> IPKSPR <mark>C</mark> KI	MCPLLAICDVGGTTSAKQYPIKLPK 232
c_000001765289_1 c_000001961666_1	116 131						KCPLSFGCKA-FKTNKPDYYPKPAA 197 LCPLKLNCKGYISNQIKVSVKNKKL 212
c_000002018097_4	138 135	LKRVISRYLGIKKLTR	RNTLRIHNQ	LNK-MLT	NGRPGDIN	ALMDVGSLI <mark>C</mark> KPNDVI <mark>C</mark> I	K <mark>C</mark> PLINK <mark>C</mark> KGYSYGNPIMYPDKNKR 220
c_000002843512_36 c_000002930199_1	135	VYRLISRLYNINTAIN	TNKGREEFQSI	ANN-LLP	NKNTGLYN	AIMDFGSIQ <mark>C</mark> KKYNPK <mark>C</mark> N:	ICPLQKECQSAILGIVNERPVKTLS 219
c_000003033795_2 c_000003888107_2	131 132						CPLKKICKAYTSSSPILYPTPKVP 213 VCPINDSCRAFLSLNPVDYPAPIKP 214
c_000003888107_2 c_000004013286_6	157						QCPIKEWCRAFQEGLQEELPFTPIQ 241
c_000004852258_1 c_000005254087_1	119 145	HSRIIARVLGVKNQTS VVRVI.SRI.TDFAEDVT	RNLNRINNY	LKK-LVR	EGNPGEIN	ALMDMGSNI <mark>C</mark> KSNKVI <mark>C</mark> V ATMELGOTICT.PTKTDCV	VCPFHFSCKAFQSGHPLSYPKKILP 201 ACPLTAVCLARQRGTQMERPVRPPR 229
c_000005603677_1	142	VYRVLSRYFGQALPID	SSAGKKWFKAK	AQA-LLW	EDDPANYN	AMMDFGALH <mark>C</mark> RPKNPS <mark>C</mark> GI	CPLAKNCQAKANKQQLELPKKGKK 226
c_000003283462_3 c_000002687221_1	130 144						RCPLKLFCKAGNTLNPEKYPRPLSK 212 ICPVNTYCYSYVNNTVDKFPTKIKK 226
c_000003347358_19	166	VKRILCRLEKLRTP	SDTELWDI	AYT-LVD	KINPFDYN	AMMDIGATV <mark>C</mark> IPKKPQ <mark>C</mark> D:	I <mark>C</mark> PLNDI <mark>C</mark> KGQEEPTLYPTKKRR 243
c_000002701031_2 c_000000582753_3	137 145	VIRVLSRYFGIQTPFD VYRFISRLYGVSTPIN	SSDGKKEFQLL SGKANKEFKVI	AEE-LLI LNA-IID	KEKAGENN	AIMEFGALQCTPKSPNCN	VCPLQNTCFAFNNNLILELPKKAKK 221 SCTFSEICFAYKNNVIKDLPVKLKA 229
c_000001713769_5	137	VYRVIARFYGIDVPVN	NHLGKKFYMDY	AQK-LAP	KKSCGDYN	GIMDFGSLI <mark>C</mark> KPKAPL <mark>C</mark> DI	K <mark>C</mark> MLAKD <mark>C</mark> IASKMKNVNYFPVRLKK 221
c_000004369364_1 c_000006057486_30	140 141						OCPLHSDCLAFAQDIISSLPVKAKK 224 OCPLNDSCFALQNNQIKTLPIKTNK 225
c_000005494072_10	137	VYRVLSRYFGIEYAIN	SSKGIKKFKTL	AQS-LLL	NENFGLHN	AIMDFGATI <mark>C</mark> TPKKAK <mark>C</mark> D	S <mark>C</mark> IFCES <mark>C</mark> SALQHNKVSELPVKTPK 221
c_000001742634_3 c_000002826998_2	140 140						CIFNDSCIALQKNKITELPTKTNK 224 CFLKKKCQALQENKISKLPVKSKK 224
c_000003159439_6	137	VYRVLARYFGIRTSTN	STKGIKEFKQL	AQE-LID	TKDPATFN	AIMEFGAIQ <mark>C</mark> KPKNPN <mark>C</mark> N	N <mark>C</mark> PLNTS <mark>C</mark> IALQKKLITILPIKDKK 221
c_000004887214_1 c_000005037037_2	142 140	VIRVLSRFFGIENTFQ	TVKEKKEFQEI	ADV-LIS	KKSAADYN	AIMDFGAQI <mark>C</mark> TPKNYQ <mark>C</mark> E	KCPISANCFAYKNKQQNNLPLKKKK 224
c_000001059964_1	132	MIRVISRMMNNQEEPR	LAKTRKRLWQL	ARE-WIP	EGEARRFN	AMMEIGALI <mark>C</mark> LPSNPK <mark>C</mark> L:	LCPMNNHCRALQKGTVSLIPLKPPK 216 SCPLVTHCLALKYDLVPERPVPKKS 225
c_000002498472_1 c_000004615912_3	141 130						LCPLSKKCIALKEELVTTLPIKSKK 214
c_000004766858_2 c_000002747260_18	143 149	IERVLCRIEDIGEPPK	STPVQKQLWSL	AAE-WIP	HGHAREFN	GLMELGATL <mark>C</mark> TPRNPS <mark>C</mark> L	LCPANAWCVAFHTGRTDTIPAPRVR 227 ICPVMTGCTARAAGAQADLPRKTPK 231
c_000005371561_38	149	VERVMARLFDIHEPLP	AAKPVLKAQ	AAA-LTP	ATRPGDHA	AVMDLGATI <mark>C</mark> TPRNPA <mark>C</mark> G:	I <mark>C</mark> PLRAP <mark>C</mark> AARAAGTQADLPRKTPK 231
c_000000169465_2 c 000003254110 11	145 145						ECPLQADCIAYAQGAQADYPGKKPK 233 ECPLQPDCIAYAQGAQTDYPGKKPK 233
c_000004750284_20	145	VKRVLARYYAIEGWPG	QKAVENALWDV	AEK-NTP	QNRCANYT	VMMDLGAMV <mark>C</mark> TRSKPK <mark>C</mark> D	E <mark>C</mark> PLQRD <mark>C</mark> VAFAQGKQTDYPGKKPK 229
c_000000141782_15 c_000002717847_8	150 144	VKRVLARYHAVAGWPG VKRVLARLFLOOEF	ETAVSRRLWAL KEGLFWNL	AER-YTP SAO-CLD	DNRTADYN	AMMDLGATVCVRRRPRCG GIMDIGATLCTPKAPLCP	VCPLADGCRARREGNPEAYPGSRPR 234 ECPLNKNCLAFKENDFQLPSSKKPI 223
c_000004054799_1	131	VKRVLGRYKKISFKT	ENEKQKKLWLI	SEE-LTP	NKESFEYT	GIMDLGATH <mark>C</mark> SKSRPR <mark>C</mark> D:	LCPVSNDCDSAFKEVSNKVSLRKAI 214
c_000006126673_1 c_000000339186_3	156 113						SCPLKEGCTAYSLGQAEEYPKRQKK 240 ACPVARSCTARRERATEIIPAKGEP 198
c_000003029168_2	145	VARVVSRLFALEGDLK	DTALQKKLWEI	TED-LVP	NKRPGDFN	AMMELGAII <mark>C</mark> STDSPR <mark>C</mark> T	LCPLAKPCHARVTGEPWRFPSESVT 229
c_000001863436_1 c_000002830137_4	161 154	VARVLARLFAVDGDPR TTRVLSRLLAFHGDPS	SGDNQRRFWRL ORVGOOLLWAF	AGA-LID AES-LLP	RGRPGDFN	SLMELGATVCTPQGPSCL: SLMELGSEICIPRKPNCE:	LCPVREYCQAFATGDPTRYPAVAKR 245 RCPVRMLCAAHRQGEQLSIPISRRR 238
c_000004612302_3	148	TARLFSRLLALSVDPS	SSEGRGRLWSL	AER-VVP	RTRAGEFN	ALIDLGATV <mark>C</mark> GV-EPR <mark>C</mark> Q1	ECPVRSSCRSLEQGVVDRVPVRSPR 231
c_000001933926_1 c_000003136334_1	134 146	VERVTARLHRISKPLP	AAKPEIAEV GAKKYLKEK	AQR-LTP AAE-LTP	RQRAGDFA SERSGDYA	ALMDLGATVCRPRRPNCG AVMDLGATVCTPRKPNCP	ACPWNASCLAHAAGIQETLPRKLPK 216 LCPWSYICKAYLAGDAEKFPKRVPK 228
c_000005849454_9	143	VKRVAARWAGLELAADDLALE	EKAARALGEAWMT	DLP-LGK	LSAPGELN	GLMELGATV <mark>C</mark> SPRNAD <mark>C</mark> G	ACPLASGCVALADGMVDVLPLPKRA 233
c_000001169194_1 c_000002786947_2	154 154						OCPVQLWCTAHEQGTQALSPAGVRR 233 OCPVQRWCTAHEQGTQALSPAGIRR 233
c_000001279808_52	142	ISKIITVLWPN	KGTVKV	AES-LVA	AANSGYIWN	AMMDLASSLRAGNEIE	-AELGSTYFADVEVRDQFKPKRKKPSRTAK 219
c_000000358065_2 c_000003745941_1	144 133						NCPITKNCLSFKKKDFEIKKKN 223 ICPFNSVCLGRNHQPER-LPIKAAK 217
c_000004187032_4	144	IERVLKRYLHLKKDNE	IQKNNLIKK	KSI-FGI	SSRASDYA	ALMELGAMICKPKNPECS	ACPILKSCKSYKKKDFDLAKIR 223
c_000006067315_3 c_000005543774_1	144 114	VKRVLLRLFNLETKD		PAN-LFK	TKRNGDLA	ALMEFGAII <mark>C</mark> KPKDPL <mark>C</mark> Y	KCLLKKNCLYYKSESKI-RFNKKIK 185
c_000006211484_1 c_000002718976_3	136 145	VKRVLFRLDNININD		AVN-LFK	TQRNGDLA	ALMEFGALV <mark>C</mark> RPKDPR <mark>C</mark> H	ckikkm <mark>c</mark> ayfkskski-kfnrkik 207 r <mark>c</mark> clnkt <mark>c</mark> kyfksskki-kniknkm 226
c_000002992548_1	146	IKRVFSRLFNANL	EKNEKRIKRI	TKE-QLY	TDRCGDLA	ALMEFGAVI <mark>C</mark> KPSNPM <mark>C</mark> N:	I <mark>C</mark> NLKAN <mark>C</mark> YFFKNKTSV-LVNKKRR 225
c_000000456751_1 c 000002655634 1	110 141						I <mark>C</mark> HLQKY <mark>C</mark> KFFNSENYI-SLNKKFS 191 I <mark>C</mark> NLKKY <mark>C</mark> KFFNGENYT-LPNKKFF 222
c_000004232403_2	140	HRRVISRILGIKNLSR	HNKNRINNY	LKQ-LVA	IDRPGEIN	AIMDIGSII <mark>C</mark> KPKEVF <mark>C</mark> D	FCPVQFSCKACVSSKPLEYPNKIYN 222
6u7t.after.N146.pdb Consensus_aa:	141	VMRVLSRLFLVTDDIA	KPSTRKRFEQI	VRE-IMA	YENPGAFN	ALIELGALV <mark>C</mark> TPRRPS <mark>C</mark> L:	LCPLC.thP

-A	WLAQRQIA		QFADEESLRQ	YCFP	EVLLAQRPPS-GLWGG	-LLLQ	RTGYF	QTLPE	226	P17802_MUTY_ECOL
-v	MVGEQYGLQV	KEKLEQ	SCETDGADG	LWEFP	RVLIRKRDST-GLLAN	-AVLAD	VPLAV	TAVKQ	232	P83847_MUTY_GEOS
-A	DQPPFA	DADKMIG	TSDWNDAPG	MLGWP	AWLLERRPDK-GLLGG	-YLARD	RYGIV	QPKPT	233 224	00003652391_2 00000031207_6
-A	SIHAQAPIP	SRH	GSLWKASPL	MTEIP	AISLRORPEN-GIFGG	-YWIER	RYGVV	RKKQR	234	00000430975 4
-v	SEVADWGCD	RFDERLIE	ALSRDRALARS	MWGFP	RLLLIQHPDG-ERWGG	-VVMR	VFELL	RDVTD	232	00001007148_4
		GEDGP							244	00001092848_3
-A	SIHAQAPIP	SRH VAAAL	GSLWQAAPL	MIEID	AIVLKQKPEN-GIFGG		RYGVV	TKKKK	191 253	00001151029_1 00001797282 1
		VARALI							236	00001737202_1
-A	ENPPVS		GAEWGAKAV	MLGWP	AWLLERRPDK-GLLGG	-YIARR	RYGIA	PVKPI	236	00002078955_4
-v	LLKNKFKLEV	PHPQLEE	GGRTLTKNN	WELP	SFLIIKRAGY-KHLNN	-GVIW	QNVLT	QSLPW	224	00002106160_4
-T	EICEAAPFK	SPK	STVWLERSL	MEET P	SLFLKKKPEN-GLLGG	-YTARR	RYGTA	RVKAV	237 232	00003607531_2 00003872363 4
-Q	IKLP(TTEWDIRP	MLGLP	NILFIRRPEN-EMLGG	-FWISD	KRGHV	KPKPQ	241	00004820107 1
-L	PI1	FQP	TSDWSTSPV	MALP	NIGFVRRDKD-ALLGG	NYIYN	WNAFA	RSKKK	223	00005774797_1
									236	00005867021_3
-T	WCEQQFTNN		ÖIÖTYDD BK	WSFP	KT ET EKEKKEK-GIWGG	-TMILE	ESMYF	KKKKL	229 229	00004546210_2 00004551008_5
-c	ELSRRFKTD(EAEKKNELEL	WAFI	EVLLEKRKPK-GIWGG	-LLPQG	KKVVW	KSKPT	224	00004551000_5
-c	ELSRRFKTD(EAEKKNELEL	WTFI	EVLLEKRKPK-GIWGG	-LLPQG	KKVVW	KSKPT	212	00000577378_2
-I	WLKSNYGKL		QFEKRAFAEE	WCFP	EVFMQKRPPV-GIWGS	-VILKN	KQAIM	KVMPE	235	00000598175_2
	FLAQQGLK		EFNEYSELET	WITE	KVLMEKKPNS-GIWGG	-TIIK	KSCHQ	KAVPK	232 223	00000754627_3 00000811118 1
		PEECLKR							227	00000899687 2
									248	00001176522_24
LK	FLDGNEMVATLE		EFDSVQEIDL	LWSLP	QVALVKRPEK-GIWGG	-LILVT	KEKFF	KIIPT	202	00001345122_1
3T	YAQAAWSQDG		VFEDYAALQS	YSPP	RVWLQKRPQA-GIWAG	-LLAVD	ESWWL	IKRSS	220 223	00001515736_6
RS	FITDNNVKCLL		EFDEVALLEN	VADD	RVWI.ERRPOO-GIWAG	-LVLLT	KEKWF	KTIPT	230	00001682161_6 00001923643 29
-ь	WLDDSFGMS1		QFDKTALAEE	WCFP	EVLMQKRPPV-GIWGG	-LILQN	KHTVM	KEMPE	224	00002030994 5
-L	FNL1		EANSLNYEK	WLFP	KVLLKRNVNK-GIWQN	-LLIA	KNINW	SQKKE	226	00002038721_4
-P	LELARAYGSI	SEAAEESA	EMPVDTVPFD	LWSLP	DVLVQLRPSS-GIWGG	-LIVRH	RSTVM	AAIPE	251	00002523527_15
		PEECLKR							224 227	00002608528_2 00002961510_2
		PEECLRR							232	00002981510_2
-L	ARWSI	ADL	EVEGPFLNQ	WELP	QILMKQRSVNARLMPG	-IACE	VMTSV	RKKKR	247	00003248034_1
-P	WYQSRFGAYI		EISKDCSVSD	WSFP	RIYLERRPSS-GVWGG	-LFLRF	KTTNM	KTNPL	229	00003294679_3
-v	EFQEELEWDV	PAQCVVR	GGTVEKGET	WEFP	YIFIQKRPED-GVWPG	-GVLV	VDVAS	KPAVP	225	00003333364 1
-v	ETĀFEAGID/	FRECVKR	GGRKEKGEN	WEFP WGFF	KLSLTORKG-KSFEG	-WI'AA	IEVGI	WANKHR	220 212	00003402697_5 00003492925_4
-A	LVKETVGLT	KAGVGR	LKEVDETPS	WEVE	AVLLTQRPEK-GLFGG	-VIRD	IALVAC	RPPKK	239	00003492925_4
-v	YCEQELQIAV		ELATGQNAIT	LWSLP	EVWLEKRPAQ-GIWGG	-LLIEN	RHTQM	NNIPT	226	00003948186_72
-М	WCLEN-DIAN		EFQSFAEIKS	WSFP	QFLLEKRPAS-GIWGG	-LMLQD	KQLIF	KVLAV	225	00005057120_4
-I	CFLEK-GIP		EYESLANIQS	WSFP	RILLEQRPKT-GIWGG	-LMCQD	KKITF	KSLPV	225 224	00005590109_5 00006063368 2
-D	ECKSIFQIK		EREREEMLAN	WST.P	T.VT.T.EKRPAT-GIWEG	-TTF12	KNTMF	KTKTT	204	00006063366_2
-L	WYEOYFSTH1		OFDTYLOAOO	WSLP	EIFIIKRPPS-GIWGG	-LLLIN	KKAVF	KTLPE	225	00000788235_1
-A	LVIAQ-GWQ <i>I</i>		QLDSREQLDA	WCPP	DIWLQRRPDS-GLWGG	PLLVN	RQCLM	KRIPV	226	00001187176_11
TV	LDADTVRQAALAYGT\		LVGEMDDALDAHP	LWSLP:	TVLLQRRPQR-GIWGG	-VIALH	RAATM	KAIPE	231	00001660697_64
		IEETVRREI							238	00003378864_2 00003910742 3
									192	00003310712_3
									226	00006223903_1
-A	KTAHNFHPQ		ECSATDKAIT	WSFV	GVYLQKRPAK-GIWGG	-LIFDN	KTTAM	KPKPV	199	00001029068_2
-E	SIESQTTV1	DNEVKIV	EFDSLQGFKE	VEED	DAATUKBARK-DIMUG	-FTFFW	KKAFF	KDKPV	234 225	00001128125_11 00001595844 4
-I	EIKEELGVT	PEQCLHR	GGKFESGES	WEFP	RIYIQKRKAE-GLMGG	-GVLF	IAVSA	APSTK	229	00001719155_2
DΑ	FLNGEIHRHDA		EFDSYDRAVD	WSLP	QVFLYKRPQK-GIWAG	-LLQKN	KQKWL	KNKPV	234	00002363038_6
-L	YLQTQTPGI		EFCSVTDAKT	LWSFP	QIRLIKRPQK-GIWAG	vvQLN	KQAWF	KEKPV	190	00002561400_1
-I	MIKRKYGFN		EFSSPLRIEE	WCFP	EILLEQRPSS-GIWGG	-AIMEN	RDTVF	AVIPK	226 224	00002566035_2
									224	00002598045_3 00004188575_41
									224	00000240049 1
-v	SVERNWQLNV		ELTLDESIAE	MWSLP	YYLMEKRPSS-GIWGG	-LIIRN	REKRL	KILPV	224	00002139456_2
-v	EVKNTWQIIV		ELALEAPIIT	LWSLP	AYLMEKRPPT-GIWGG	-LIIRN	QQKRL	KILPI	226	00003535614_2
-ĸ	ECLTMFEKRI		ESENIQDLGK	WSFL	KVLLKKRNNL-GVWKG	-LVVMN	KTVFW	KÖKbe	223 221	00002657784_4 00003800129 15
		PAELELEL	TREVAAAELRLF	WELP	RVLLRRRDEG-GRMAG	-FLVH	VELEM	PTPID	216	00003716781 1
-v		LTEKPASSHSRAQEAKLSR							216	00001556689_3
-G	AWREFQPQR	PDL	SVPYDQKEE	LWEPP	GVLLEERKSGWNQG	-GVAS	VHLLY	INWKE	196	00001834452_1
		IDETL	TPENLPAEL	WELP	RILLHRRPDK-GILAS	-TLAK	VQWPL	TKA	226	00004255004_2
-c			QEEDFEF	WGFK	KYALAQNEEKLLSG	-11YA	KKKAL	IKKDI	219 219	00000605438_3 00000581237 15
-I.	J		OEEDFEL	WGFK	KYALAONEERLLSG	-VIYH	RKRTL	IKKPI	219	00000501257_15
-Q	LASTKLALG(VQPAD	NWLVDDTQ	WEFP	NVFVQRRPSG-EVNSG	-FIIA	RRFIG	APVSK	208	00006097838_1
-Q	LAKRELKLG	LKPAA	NWQVNDAE	WEFP	KVFVQRRPSG-EVNAG	-FLIA	RRFIG	AATTN	234	00000583727_6
		ATADQ								00005807640_2 00000134878 1
		IESAIKR IKSAIKR								00000134878_1 00005136725_3
-I	RLGQALETD	GGIAA	LSLPGD	WLFP	RCLLERSESF-DFLEG	-GIIR	VELEA	RKTIA	222	00003130725_5
-I	RLRKRLATS	GGIAA	LARPDS	LWSFP	RYLLERNEDL-DYLEG	-GIIR	VELEA	RKTVA	232	00002971826_23
-K		EAH LTEGVTR	TQSWVHKKT	WRPL	VSVLLEKEHG-PLLEG	-FFLVHIPS	RWGHF	TKKPC	233	00002040695_2
		SPE								00003263657_32 00005989041 2
		LQQCLQR								00003989041_2
-I	EIREELGIE	LEECLVR	GGKQEEGET	WEFP	QLLIAQRPAE-VMLGG	-GVIS	HYQVAA	KKKKP	241	00003839553_2
		LQECLRR								00003996707_2
		RLASTLCG-								00002044706_1 00006007075_1
-D	I		MREITYP	LIFP	QILLIKNDKF-KFLKN	-TLYK	KFYLA	KKIIN	200	00008007075_1
			MOELSKP	SIFP	KYLLIKNTKF-NFLKN	-KVYK	KYYLL	KKNNN	224	00002762689_1
			MEELFQP	LRIFP	RYLLIKNTKF-NFLKN	-KVYK	KYFIL	KKNIN	224	00005516980_2
		LLVRD								00003920004_1
		SLVTD								00004008511_2 00004481347 1
-I	QISKDFNIY	PIGALRR	SAEIQFNET	WEFP	KFLITKRPEN-ALLGE	-GIIW	KEIVA	KIIPH	226	00003787733 3
-I	QIKEKWDID	PVGALRR	GGEIASSET	LWEFP	KFLITKREEN-ALLGG	-GIIW	KEIVA	KVIPH	226	00000754657_2
-I	KIKEECDID	PIEALRR	GGEFESNET	LWELP	KFLITKRSEN-ALLRG	-GIIW	KDIVT	KVIPH	226	00000990943_3
		PIGALRR							225	00004474996_2
-k	1TW9TWLL	DDIQLFN	KRELFOT	MALD	ELTIMEKENN-SMTCC	-FIYO	ESFHW	SIKNI	213 218	00001463500_11 00001286181_5
-R	DLGVQLSAR	GELR-VGDSLHGRCSARLE	AVEMEAEERNPWGGE	WEFP	ELLMVRRPPD-GLLGG	-LVTLN	ASYAV	PRVRE	223	00001286181_5
PQ	RLCEVMHLADDP(LEEVKK	LIETKREID	LWQFP	KTLLNQRKGK-DIWQN	-IIPIAEAD	RYFNY	TKVRN	222	00001535696_8
GM	FNKKKPNFLGN	RFKKSPK	SIGWYEESN	MDVLP	AVLFETNKSS-GLLAN	-FYLQN	RYGLF	KEKEE	233	00001614067_2
		LEAALKR								00001765289_1
		DDYVK								00001961666_1 00002018097 4
	TWUNDEPS	KIKALKT	AIEVPL	WGFF	KLSLTQRTGKFLHC	-MLYF	REONT	VVPT	213	00002018097_4
	HQYFKPFK	REKIMA	LIESKEKLN	YELP	QFLIQQRGTN-DIWKK	-LFIK	RYFNY	RKPKI	220	00002930199_1
-	DIFFEDERAL M. 1	ATOATTR	GGKIEKKET	WEFP	KILITKRQNK-NFLPG	-SVVE	YDIAV	KKIPI	214	00003033795_2
-v	EVKEETNLT	RKKAVIR							215	00003888107 2

Conception 1	c 000004852258 1	202	KTIPTKTIAAALVNHGDNIFITKRPLK-GLLGGLWELPNIELVNGEIPEDLLKIKFADQFGI	LTI 264
Comment Comm	c_000005254087_1	230	krtphydvvagiiwqngvspgeggrfliaqrpln-gllgg <mark>l</mark> wef <mark>p</mark> ggkqepdetlpqalereireemdn	MMI 299
Content				
Commonweight Comm	c_000002687221_1		VSRPHHNVAVGLIWKDNRILISKRNAS-GLLGGLWEFPGGKIRSGESGSSCVVRKTQEILN	VLV 289
Concession Con			VVPTREENILVRVYDDKLSLTQREGKELHGEWGFESVEVPH	284 ИSТ 281
CONSIDERATION 12	c_000000582753_3	230	rkstnryftyyyisdsnhlyikkrvgk-giwes <mark>l</mark> yef <mark>p</mark> lsenliafenevldkQifknsin	NDF 291
CONSISTING 1				
CONSIDERATION 12				
CONCESSION C. C. C. C. C. C. C. C	c_000005494072_10		ikikkryfnylvvlskknkitlnkrink-giwon <mark>l</mark> fef <mark>p</mark> lietvetitiktlveheylekiinkko	QLVD 289
Conception Con			INIKK	TTIN 292
Commonweight Comm			IKIKKRYFNYLVIINSQNKIALQRRKHK-DIWKGLYEFPLIETLTAIDIEQLLETEEFHQIINED(QAI 288
Control 1 20 20 20 20 20 20 20	c_000004887214_1	227	LKIKKRYFNYLILKTKNEETLVKQRKGK-GIWQNLYEFPLLETEKEINYLELIDHSIFKKMIEEN	NFD 293
Conception Con			VKVKE	VRF 287
GOODSTILLE 18 221				
CONSTRUCTION CONS			IRKKKRYFHYFISHFEGKILLRKRIQK-DIWQN <mark>L</mark> YEF <mark>P</mark> MLETKDEELKISRVQKTQLWQQLFi	HGNEKVKVL 284
COMMINISTRATION SERVICE				
CONCENTION 15 25 25 25 25 25 25 25	c_000005371561_38		KPKPTRRGIAYLGRRADGAWLLERRPEK-GLLGGMLGWPGSDWAESPPEASPPC	CPG 286
CONSIDERATION 213 CONTROL CO			KALPEKSTYMMVAQFNSQVYLEQRPST-GLWGGLYGFIEVSSIEEGIEQLAKRG:	ISV 289
CONSIDERATION 213 CONTROL CO			KALPERATMWAQFNSQVIEQRET-GMGETGETEVSIEEGIE	VNV 285
CONSIDERATION 213 CONTROL CO	c_000000141782_15		rekplratrmllivdggrvllerrpps-giwgg <mark>l</mark> wcp <mark>p</mark> ecppevdves	LEV 291
\$6,00006126731 210			KKDVYLEFSLYKDGPKYFLAQTEAL-GFWKKLWMPPVKIVN	263
CONSTRUCTION 150				
CONSIDERATION 1	c_000000339186_3		IRYEDKQIDVYLITRGPRYLVQQRPEG-GVNAGFWEFPNSDSGNKYSAPKAPK	247
Concentration Concentratio			VPLQSREE-VGIVIWAGKPYNADSLIFIVQRPPT-GLWAGLWEFPHDEQTTDEP	PTM 298
\$ 0.0000137314 1 22			TQTEHVVEAAVVIRRGSRVLLRRHEDR-ERWAGLWDFPRFPFDPDATNNGHQQLVDKSRELTGI	FEI 303
		232	VRTTDLYQLLLVIRRDDRLLLIQHPER-ERWGGMWGFPALSRTGPLLKSRIDELQIASEAAEWGC	CDV 297
CONSTRUCTION CONTRIBUTION CONT				
CONCESTATION 234	c_000005849454_9	234	kkwvdlemvflvhrvgvrvglqkrtsgwspg <mark>l</mark> yep <mark>p</mark> saicesfataneAssahestahslarehr	A 299
	c_000001169194_1		VPAREISFLLVILQTEEGEVMLVQRPPE-GLLAG <mark>M</mark> WAF <mark>P</mark> EQELAKPLDCAATSRDRAIELAMS1	LGAEVV 301
CONSIDERATION CONSIDERATIO			KKTTKRRKHRTEVGIACIWREGKYLVOARPKG-KSFEGSWEFPGGKREKGESFRGCVKREIEEEVGI	LNV 287
COURSEPTION 260 COUNTY	c_000000358065_2	224	KKIINKFYLATLYKHDDQVLLIKNDKF-KFLKN <mark>L</mark> LIFPMKEISQS	C 268
COURSEPTION 260 COUNTY			KIKQETIDRAWVEQGGKLLLHRANDKS-RRLSGTLELPTLDVMGYSATALMK	268
COORDITIONS 186			KFNKIKYFEANIYQNQNKYLLIKNSKF-KFLNN <mark>L</mark> LIFPMKEVEKN	к 26
COMMONSTRIPS 3	c_000005543774_1		IESKTYDIFCYLRKNKKQIALTKNNDL-GFLKKFNLPEIKATSKK	N 230
CONDESSIONAL 1 226				
CONSIDERATION 1923			kkeqkynvycylkkkkkeialtknkhl-sflsn <mark>f</mark> nip <mark>e</mark> tkietsnnkk	N 273
Concernation:			IKEKKINIYCYLNRYKKEIALTKNKNL-SFLNNFKMPEIOMVVANNNLK	к 240
Conservation: ### Conservation:			TKEKKFNVYCYLMKYKREIALAKNRNI-GFLYBKMPEIQMEVTNNNLK	R 271 FTT 285
Conservation: ### Conservation:			TAVKQVPLAVAVLADDEGRVLIRKRDST-GLIANLWEFPSCETDGADG	283
COURT COUR	Conservation:		6	
COURT COUR	sp_P17802_MUTY_ECOL		6 DNLTQLTAFRETESHFHLDIVPMWLPVSSFTG	APV 350 ASGVRRPD- 360
COURT COUR	sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2	295 287	6 DNLTQLTAFR TFSH FHLDIVPMWLFVSSFTG	APV 350 ASGVRPD- 360
CONDUISIONS 1	sp_P17802_MUTY_ECOL sp_P83847_MUTY_GEOS c_000003652391_2 c_000000031207_6	295 287 287	6 DNLTQLTAFRETEN FHLDIVPMWLFVSSFTG	APV 35(ASGVRRPD- 366 338 LLEVFR 352
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C 00000260528 2 282 DEAIKLSEINT SEFH LHIPPLINM -ETPLK -IGVMENDD - KWYSLSSLKKYP FPAANVKIVYKIT -EK 356 C 000002979152 8 290 PSLQAYARIE ESFH - LSAKVLRIEL - DSDKR - LGYMERTNA - LWYMMHKDHPGG - FPAANVKIVYKIT -EK 356 C 00000248034] 3 302 KHRKLICKER ST FR - VYDSIYPAIL - EGE - LFPPE - CRUPCPRILATIP - LTTVTRKALAVLS - PNSDMDDQN 372 C 000003294679 3 286 KHRKLKCHR ST FR - VYLTAFLIRF - GEPPECW - PPEVLHDATEG - WWYSFAELDRIT - FPAGHRKLLEGG - NG C 000003402647 9 3 286 AASETIAVIRG ST EF - VYLTAFLIRF - GEPPECW - PPEVLHDATEG - WWYSFAELDRIT - FPAGHRKLLDGMS - ROHRYMUV - 356 C 000003402697 5 288 SWPHYFELIRE E TE - LLIKPHRCJI - QAGEP - SPQEEQBI - KWYSPDDFGDID - FIKINHKALDKIK - EMKY - 356 C 000003402697 5 288 SWPHYFELIRE E TE - LICKVYVYDE - LDAEQN - SYFTSSKIQKLA - ISKVDDKILKLYL - DTIQTY - 316 C 000003402697 5 288 SWPHYFELIRE E TE - LICKVYVYDE - LDAEQN - SYFTSSKIQKLA - ISKVDDKILKLYL - DTIQTY - 316 C 000003402697 5 302 C 00000559109 5 302 C 0000059109 5 302 C 0000059109 5 302 C 0000059109 5 302 C 0000059109 5 302 C 00000063368 2 302 C 302	sp_ P17802_MUTY_ECOL sp_ P83847_MUTY_GEOS c_00003652391_2 c_00000031207_6 c_00000031207_6 c_000001092148_4 c_00000192248_3 c_000001151029_1 c_000001797282_1 c_000001979282_1 c_000002078955_4 c_000002106160_4 c_000003807631_2 c_000003872363_4 c_000003872363_4 c_000003872363_6 c_00000587072_3 c_0000058707373_2 c_00000555108_5 c_000005551148_4 c_000005573738_2 c_0000005573738_2 c_000000558175_2 c_00000058175_2 c_00000058175_2 c_0000001573738_2 c_0000001573738_2 c_0000001573738_2 c_0000001573738_2 c_0000001573738_2 c_000000588175_2 c_0000001573738_2 c_0000001573736_6 c_000001573736_6 c_000001573736_6 c_000001573736_6 c_000001573736_6 c_0000001573736_6 c_0000001573736_6 c_0000001573736_6 c_0000001573736_6 c_0000001573736_6 c_0000001573736_6 c_0000001573736_6 c_0000001573736_6 c_00000000030994_5	295 287 294 298 303 251 313 290 287 297 286 292 287 287 287 287 287 287 287 287 287 28	ELTEPIVSER AFSILV WQLTVFFGRL VHGG PVEEFY RLAFEDELKAYA FPVSHQRWREYK EW WRTHGREW TFPIFH LILRIRVAREL PDDI TPAUG ELLSKHARFARSD LPTV ELLGKHARFARSD LPTV ELLGKHARFARSD LPTV LPTV PEGT LELSKHARFARSD LPTV LPTV PEGT FWCKEEVKAQA LPSLHHKINTHMY KA EW WIDELATTP LSVAGRRVATRVE RIJ PWEEP GTVT TFFIFT LALSYYRARV ADMP APAGS BEFT EWVGIDELATTP LSVAGRRVATRVE RIJ PWEEP GTVT TFFIFT LALSYYRARV ADMP APAGS WWCAPGLLAGEA LPTVMKKVVEAA1 SGI WKROPGLIVG STFIFD LELKI ALATTP APAGT RFTFRALDEP LPGIMKRVLAHAF DPI WODDFGAEW STFIFT LRILSLRVATI GNK APAGT RFTFRALDEP LPGIMKRVLAHAF DPI WODDFGAEW STFIFT LRILSLRVATI GNK PPATG DPI SKNAFDPET LPTVMKRVARTAR TRIJ WOVLNAEW TFFIFT LRILSLRVATI GNK PPATG DPI SKNAFDPET LPTVMKRVARTAR TRIJ WOVLNAEW TFFIFT LRILSLRVATI GNK PPATG DPI SKNAFDPET LPTVMKRVARTAR TRIJ WOVLNAEW TFFIFT LRILSLRVATI GNK PPATG DPI SKNAFDPET LPTVMKRVARTAR TRIJ WOVLNAEW TFFIFT LRILSLRVAT MONTH QISGG LWDRDRILDEPA LPTVMKRVARTAR TRIJ WOVLNAEW TFFIFT LRILSLRVAV WDQT QISGG LWDRDRILDEPA LPTVMKRXWARPAS RKI DWHLGAEW STFIFD LIL SEWGNIGOTR IFFITD LILSLRIVVA KNV TPYVG MFIFSNKFDPDD LPTVMRKAHALAD AAI SERGTHLSW STFIFD LIL SEWGNIGOTR IFFITD LILWDYBERPK SFFIFT LILHDYWAWATV NEN SPDVG KFIADDCFDPAD LPTVMRKAHKLAL GSI LWVDSWEPFK SFFIFT LYTHPIQIRM DGOFM NTAHTERT QSFELMQLOSIG LSAPVKGLVNNLLY LNINKKLGKW SFFI YN LEAIPYLAKL ESNK KYKNS VWUDYKNVESLG LPAPIKKTINQLT KP-LNINKLGKW SFFI YN LEAIPYLAKL ESNK KYKNS VWUDYKNVESLG LPAPIKKTINQLT KP-LNINKLGKW SFFI KYS SFFI YN LEAIPYLAKL ESNK KYKNS VWUDYKNVESLG LPAPIKKTINQLT KP-LNINKLGKW SFFI KYS SFFI KYS LYTHPIQURM DGOFM NTAHTERT QSFFLANGLOSIG LSAPVKGLVNLLY LYDEDSSFFI HIS NK LYTHPIQURM DGOFM NTAHTERT QSFFLANGLOSIG LPAPIKKTINQLT	361
C 00000279152 8 290 PSLQAYABILEESSEH-LISAKVLRIBL-DSDKKLGYMEETNALGYMEETNALMYNMHKDHGG-FPAPIKKLISRNL-L-L-356 C 000003246034 1 302 KHYKLICKER ST FRL-VDVSITYALL EGE-LPEFF CHVPGRALATIP-LTYTREALAVLS-PNSSDENDEN 372 C 000003333364 1 288 AASSETAVIR GT FR-VTLTAFILER GEPPEGWPEPULDATEGWVSFABLDRYT-FPAGHRKLLOMS-ROMBYAWIL 366 C 000003333364 1 288 SVRPHFYELLEE TE-LLLRFHRCQIQAGEPSPQEEQEIKNVSPDDFGDID-FIKTNHKALDKIK-EMRY	sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_000003652391_20 c_00000031207_6 c_00000031207_6 c_000001091248_4 c_000001091248_3 c_000001191292_1 c_00001797282_1 c_00001803648_25 c_00000278955_4 c_00000278955_4 c_00000278955_4 c_000003670531_2 c_000003670531_2 c_000004820107_1 c_0000057774797_1 c_00005774797_1 c_0000587021_3 c_00004546210_2 c_000005571148_4 c_00000577378_2 c_000000587021_3 c_00000181118_1 c_00000577378_2 c_000000181118_1 c_000000577378_2 c_00000181118_1 c_00000181118_1 c_00000181118_1 c_00000181118_1 c_00000181116_1 c_00000181116_1 c_0000018116_1 c_000001816_1 c_0000018116_1 c_000001816_1 c_00000	295 287 294 298 303 251 313 290 287 286 292 276 287 287 287 287 287 287 287 287 287 287	ELTEPIVSEE AFSILV WOLTVFORL VHGG PVEEFY RLAPEDELKAYA FPVSHQRVWREYK EWI WARTLRGEWY TTPIF H LILRIRVALEL PDDI	364
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C 000003294679 3 286 LKISBNITLOEKSEFD—LKIHLFRAEP—DIAIK — NIANDBS—LMYKBDSQTRIG—LAAPVKKLLETQF—NIQ— 353 C 000003333364 1 288 AASETIAVIR GT FR—VLITAFLLEF — GEPPEGW—PEVPLHDATES—VWYSFAELDTT—FRAERKILDOMS—RDMRYALV—366 C 00003402697 5 288 SVRPHFYELLEF = TE—LLLRFRHCQI—QAGEP——SPQEEQEI —KWVSPDDFGDID—FLKTNHRALDKLK—EMRY—356 C 00003492925 4 253 CASEYIGEVT AIT FK—LICKYVYDE———LDAEQN—SYFTSKIÇKLA—ISKVDKNILKLY—CHTQTY—316 C 000003492925 4 253 CASEYIGEVT AIT FK—LICKYVYDE———LDAEQN—SYFTSKIÇKLA—ISKVDKNILKLY—CHTQTY—316 C 000003492925 4 253 CASEYIGEVT AIT FK—LICKYVYDE———LDAEQN—SYFTSKIÇKLA—ISKVDKNILKLY—CHTQTY—316 C 000003492925 4 253 CASEYIGEVT AIT FK—LICKYVYDE———MDIAVFALSV—KGREPS—PALSTITGG—MMIHSPEALEDIG—VGRVTHKILEAA—THEISQGE—378 C 000003492925 4 280 SCYGLIERGRIT SIFH—LLITPHINES—SQQTT—HVMEDQQ—LMYMMRYBASVG—LAAPVKKLLEQTS—NQ—350 C 00000557120 4 280 SVYQHIERGRIT SIFH—LLITPHINES—SQQTT—HVMEDQQ—LMYMMRYBASVG—LAAPVKKLLEQTS—NQ—350 C 0000063590109 5 282 KLIKQLDEQRIT SIFH—LDYTAVLWXT—EMRIN—NWESNOS—WYKSTQLKFLG—LEPPIKKLLQNQN—NREV C 000000467631 2 281 PSILQTKKVKIS SIFFN—LEAPTIVKNI—EMPIN——WHADAS—WYKSTQLKFLG—LPFIKKLLQNQY—346 C 000000467631 2 261 TSKKQLDGQRIT SIFH—LDYTPIEVNI—EMPIN—NWESNOS—WYKSTQLKFLG—LFPIKKLLQNQY—324 C 000000467631 2 261 TSKKQLDGQRIT SIFH—LDYTPIEVNI—EMPIN—NWESNOS—WYKSTGLING—EFPAINTINKIN—EDP—3350 C 00000160697 61 283 AEPEALSUR T SIFH—LDYTPIEVNI—EMPIN—NWESNOS—WYKSEQINSIG—LATPIKKLQNQ——324 C 00000160697 64 297 SDVEAAGALT TIEFF—LHMILLHADI—TKP——ATLDDW—RWYLREPSRIG—LAPPKKLLQRA—LNTQAERTSP—356 C 000003378864 2 301 EVGPLVTQVKR AIS FRITHARYKCLLEG—TPH —PKVAVES—RWYLNEDLOGA—FPRANKRUEVLEQPSAMPEVT—375 C 0000003278874 3 284 ENTEKSTILS IS SIFR—LHMILLHADI—TKP——PKVAVES—NWYLNEDLOGA—FPRANKRUEVLEQPSAMPEVT—375 C 000000223903 1 284 LFESNANVLR SIFFI—LATTPCRALEGG—TPH—PKVAVES—NWYLNEDLOGA—FPRANKRUEVLEQPSAMPEVT—375 C 000000223903 1 284 LFESNANVLR SIFFI—LATTPCRALEGG—TPH—PKVAVES—NWYLNEDLOGA—FPRANKRUEVLEQPSAMPEVT—375 C 000000223903 1 284 LFESNANVLR SIFFI—LATTPCRALEGG—TPH—PKVAVES—NWYLNEDLOGA—FPRANKRUEVLEQPSAMPEVT—332 C 000000223903 1 284 LFESNANVLR SIFFI—LATTPCRALEGG—TPH—PKV	sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_0000031207_6 c_00000031207_6 c_000000131207_6 c_00000192148_4 c_00000192148_4 c_00000192848_3 c_00001151029_1 c_000001797282_1 c_00000278955_4 c_00000278955_4 c_000002807531_2 c_00000287353_1 c_000003872363_4 c_000003872363_1 c_000003872363_1 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000005511148_4 c_000005571378_2 c_000005511148_4 c_000000551118_1 c_00000058175_2 c_00000151118_1 c_000001511	295 287 287 287 298 303 32 3287 297 286 292 276 299 290 287 7 286 292 276 293 287 287 282 222 276 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 274 290 283 287 287 287 287 287 287 287 287 287 287	ELTEPIVSER AFSILV WQLTVFFGRL VHGG PVEEFY RLAPEDELKAYA FPVSHQRWREYK EW WRTHGREW TFIF H LILRIRVAREL PDDI	364
C 000003402697	sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_000003652391_2 c_00000031207_6 c_00000013207_6 c_000001092484_3 c_000001151029_1 c_000001797282_1 c_000001797282_1 c_00000278955_4 c_00000278955_4 c_00000278955_4 c_00000278955_4 c_000003607531_2 c_000003607531_2 c_000004820107_1 c_000005867021_3 c_000005867021_3 c_000005517378_2 c_000005511148_4 c_00000577378_2 c_0000059867021_3 c_00000598175_2 c_0000011118_1 c_0000098967_2 c_000001118_1 c_000001135122_1 c_000001135122_1 c_0000011515736_6 c_0000011515736_6 c_000001203694_5 c_00000238721_4 c_00000238721_4 c_00000238721_1 c_00000238721_1 c_00000238721_1 c_000000238721_1 c_000000238721_1 c_000000238721_1 c_000000238721_1 c_000000238721_1 c_00000238721_1 c_000000238721_1 c_000000238721_1 c_000000238721_1 c_000000238721_1 c_000000238721_1 c_00000029915_2 c_0000029915_10_2 c_0000029915_8	295 287 287 287 298 303 32 298 292 296 290 290 287 728 282 2276 292 283 287 284 290 287 388 282 276 6 282 276 6 282 276 6 302 300 290 300 290 300 2	ELTEPIVSER AFSILV — WQLTVFFGRL — VHGG — FVEEFY — RLAPEDELKAYA — FPVSHQRVWREYK — EW WRTHGREW T TFIF H — LILRINARE — PDDI	361 362 363 364 365 367 367 367 367 367 367 367
□ 000003492925 4 253 CASEYIGEVIA TEFK - LICKVYVYDE - LIDAGN - SYFTSSKIQKLA - ISKVIDNILKLYL - DTIQTY - 316 316 000003766664 5 302 RIEGQCSSVR VITERD - MDIAVFALSV - KGREPS - PALSTYTGG - MWIHSPEALEDLG - VGRVTRKILEAAA - THEISGGER - 378 378 000003766664 5 302 RIEGQCSSVR VITERD - MDIAVFALSV - KGREPS - PALSTYTGG - MWIHSPEALEDLG - VGRVTRKILEAAA - THEISGGER - 378 378 0000035057120 4 284 DSCTELAPRENT SIFH - LLTTPLHIKS - SQOTT - HVMEDQQQ - LWYMRKPASVG - LAAPVKKLLRGTS - MQ - 350 00000557120 4 282 QSVQHIEGQRT TSIFH - LDYTAVLVKT - ERRIN - NVMESNOS - VWYKSDKINALG - LPFITKKLLQNY - 346 350 00000663368 2 282 QSLIKQLDGRT TSSIFH - LDYTGINVKI - ERRIN - WWISHON - WWISTQLKFIG - LPFITKKLLQNY - 346 342 000006676312 2 261 TSKKQLDGGR TSSIFH - LBATPYLVKI - KEKK - SIKNT - WWISTQLKFIG - LPFITKKLLQNQ - 324 340 000000768235 1 283 PSATTESHFS TS SFR - LEAIPYLVKI - ERPIN - NVMEANQS - WWYKSEQINSLG - LAPTKRLLQNQ - 324 324 0 00000187176 11 283 AEPEALSSLENT SIFH - LDQFLUKV - DAPOR - VTESGQ - WWYNLEPSRIG - LAPVKKLLQRAE - LNTQADERTSP - 356 360 000003378864 2 297 DVEAAGALT TITTFF - LIMHLHADI - TKP - ATILDDW - RWYLAQLBVSC - LPAPVKLALGRAE - LNTQADERTSP - MOUNTAIN - PROVINCE - PROV	sp_17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_000003652391_2 c_00000031207_6 c_0000001207_6 c_000001092148_4 c_000001151029_1 c_00001197282_1 c_00001979282_1 c_000002078955_4 c_000002078955_4 c_000002106160_4 c_000003807531_2 c_000002807531_2 c_000004820107_1 c_000005867021_3 c_000004870107_1 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_00000137497_1 c_000005867021_3 c_00000137497_1 c_000005867021_3 c_00000137497_1 c_000001374627_1 c_000002508528_2 c_000002508528_2 c_000002508528_2 c_000002508510_2 c_000002508528_2 c_000002508528_2 c_000002508528_2 c_0000002508528_2 c_000002508528_2 c_000002508510_2 c_000002508528_2 c_000002508528_2 c_000002508528_2 c_0000002508528_2 c_000002508528_2 c_000002508528_2 c_000002508528_2 c_000003250879152_8 c_000003250879152_8 c_000003250879152_8 c_000003250879152_8 c_000003250879152_8	295 287 287 287 287 287 294 290 287 287 282 270 303 287 287 287 287 287 287 287 290 287 287 287 287 287 287 287 287 287 287	ELTEPIVSER AFSILV WOLTVFORL VHGG PVEEPY RLAPEDELKAYA FPVSHQRWRRYK EWI BWRTLRGEWY TFIF H LILRIRVALEL PDDI	361 361 362 363 364 367 367 368 368 368 368 368 378 368 36
c_00000344816 72 28 DSCTELAPRRITSSFH-LLITPLHIRS—SQOTT HYMEDQQQ LMYMNRFRASVG-LABFVKRLIRGTS-NQ 350 c_00000559109 5 28 KLIKQLDEQR T SSYH-LDYTGINKYI EMPIN NVMENDS VMYKSTQLKFLG-LEPTIKKLQNQY 346 c_00000663366 2 28 PSILQIKKVKISSS SFH-LEAPTIVKII KEKK SIKNT VMYDSKNIESLG-LEPTIKKLQNQY 346 c_00000467631_2 261 TSKKQLDGQR T SSYH-LDYTPIEVKI EMPIN NVMEANQS VMYKSEQINSLG-LATPIKKLQNQ 324 c_00000187176_11 283 APPEALSPLENT SIFF LQQTLLITQ STPIK RVWEGTPS LMYNSTTFMGG-FPAPIKTI INKIN-EDF 350 c_00000187076_6 297 SDVEAAGALTIT TIFF LDGPLIVEV DAFDR VTESGQ WYNLEEPSRIG-LAAPVKLLQRAE-INTQAERTN 363 c_00000310742_3 284 ENTEKETILS TISTER—LIMBILHADI TTP PKVAVES RWYNLEEPSRIG-LAAPVKLLQRAE-INTQAERTN 363 c_000004116181_2 249 KTSELVELTIR TISTER—LIMBILHADI TTP PKVAVES RWYNLEEPSRIG-LAAPVKLLQFAE-PKNATKULEGPFAE 363 c_000002223903_1 284 LFESANSVLR SEFRI	sp_ P17802_MUTY_ECOL p_ P3847_MUTY_ECOS c_00003652391_2 c_000000352307_6 c_00000031207_6 c_00000031207_6 c_00000109148_4 c_00000109148_4 c_000001992848_3 c_00001197282_1 c_00001803648_25 c_0000027895_4 c_0000027895_4 c_00000387531_2 c_00000387531_2 c_000004820107_1 c_00000587021_3 c_000004820107_1 c_00000587021_3 c_000004551008_5 c_00000587021_3 c_00000811118_4 c_00000577378_2 c_000000573738_2 c_00000181118_1 c_00000573738_2 c_00000181118_1 c_00000573738_2 c_00000181118_1 c_00000573738_2 c_000000573738_2 c_00000573738_2	295 287 287 287 298 303 323 287 297 287 287 297 287 287 289 280 290 290 387 287 287 287 287 287 287 287 287 287 2	ELTEPTVSEE AFSILV WQLTVFFGRL VHGG PVEEFY RLAPEDELKAYA FPVSHQRVWREYK EW WRRTLRGEWR TTPIF H LILRIRVAREL PDDI	361 362 363 364 365 367 367 367 367 367 367 367
00000663368 2 282 PSIJQIKKVIKSSSFR-LEAIPYLVKI-KEKK- SIKNT -WVDSKNIESIG-IPSPVKKTIKEIR-VP 344 000000467631 2 261 TSKKQLDOGR T SSYH-LDYPTEKVIEMPIN -NVMEANGS-WYKNSEQINSIG-LATPIKELDON- 324 00000187176 11 283 PSATTESHFS-TSFFR-LDQPTLLITQ-STPIK -VTESGQ-WYNILEFSRIG-LAPVKKLLQRAE-LNTQADERTSP 350 00000187176 21 283 ABPEALSFLENTSFFR-LDIGPLLVEV-DAPDR -VTESGQ-WYNILEFSRIG-LAPVKKLLQRAE-LNTQADERTSP 356 000003378864 2 297 SDVEAAGALTITTFFR-LHMILHADI-TKP -ATLDDDW RWVPLAQLANSVC-LPAPVKLALETU-OPSIL- 363 000003378864 2 301 EVGFLVTQVR-ASSFRITLHAYHCKILIGG-TPPI -PKVAVES -RWVPLIQLBOYG-FPADREVTP	sp_ P17802_MUTY_ECOL p_ P3847_MUTY_ECOS c_000003652391_2 c_000000352391_2 c_00000031207_6 c_00000031207_6 c_000001092484_3 c_00000119170282_1 c_0000119170282_1 c_00001977282_1 c_000002106160_4 c_000002106160_4 c_00000367531_2 c_000002106160_4 c_000003872363_4 c_000004820107_1 c_0000057774797_1 c_0000587021_3 c_000004850107_1 c_000055774797_1 c_00005867021_3 c_000005511148_4 c_00000577378_2 c_0000011118_1 c_00000577378_2 c_0000011118_1 c_00000577378_2 c_0000011118_1 c_00000577378_2 c_0000011118_1 c_00000577378_2 c_00000011118_1 c_00000577378_2 c_000000577378_2 c_0000000577378_2 c_000000577378_2 c_0000000577378_2 c_00000577378_2 c_000005747977_2 c_000005747977_2 c_000005747977_2 c_000005747977_2 c_000005747977_2 c_000005747977_2	295 287 287 287 298 303 32 3287 297 287 287 297 287 287 297 287 287 287 287 287 287 287 287 287 28	ELTEPTYSTE AFSILV WQLTVFFGRL VHGG PVEEFY RLAPEDELKAYA FPVSHQRVWRSYK EW BURTLRGEVY TTPI H- LILRINVALEL PDDI	361
00000663368 2 282 PSIJQIKKVIKSSSFR-LEAIPYLVKI-KEKK- SIKNT -WVDSKNIESIG-IPSPVKKTIKEIR-VP 344 000000467631 2 261 TSKKQLDOGR T SSYH-LDYPTEKVIEMPIN -NVMEANGS-WYKNSEQINSIG-LATPIKELDON- 324 00000187176 11 283 PSATTESHFS-TSFFR-LDQPTLLITQ-STPIK -VTESGQ-WYNILEFSRIG-LAPVKKLLQRAE-LNTQADERTSP 350 00000187176 21 283 ABPEALSFLENTSFFR-LDIGPLLVEV-DAPDR -VTESGQ-WYNILEFSRIG-LAPVKKLLQRAE-LNTQADERTSP 356 000003378864 2 297 SDVEAAGALTITTFFR-LHMILHADI-TKP -ATLDDDW RWVPLAQLANSVC-LPAPVKLALETU-OPSIL- 363 000003378864 2 301 EVGFLVTQVR-ASSFRITLHAYHCKILIGG-TPPI -PKVAVES -RWVPLIQLBOYG-FPADREVTP	sp_ P17802_MUTY_ECOL sp_ P83847 MUTY_GEOS c_00003652391_2 c_00000031207-6 c_00000031207-6 c_000001097148_4 c_00000197248_3 c_00001151029_1 c_00001797282_1 c_00001797282_1 c_000002708955_4 c_000002708955_4 c_0000028067531_2 c_000003872363_4 c_000003872363_4 c_000003872363_6 c_000004820107_1 c_0000058707771_2 c_0000058707771_2 c_0000058707777_1 c_000058707777_1 c_000005870777_1 c_000005774797_1 c_000005774797_1 c_000005774797_1 c_0000058707378_2 c_000001585102_1 c_00000157622_1 c_000001754621_0_2 c_0000001754621_0_2 c_000001754621_0_2 c_000001754621_0_2 c_000001754621_0_2 c_000001754621_0_2 c_000001754621_0_2 c_000001754621_0_2 c_000001754621_0_2 c_000001754621_0_2 c_000001754621_0_2 c_00000001754664_1_2 c_00000329467_0_3 c_00000329467_0_3 c_000003492925_4 c_000003492925_4 c_0000034066664_5	295 287 287 287 287 287 298 303 32 298 298 298 299 290 290 287 287 287 287 289 262 279 283 316 282 276 68 282 282 288 283 316 288 288 253 33 289 290 290 287 287 287 287 287 287 287 287 287 287	ELTEPIVSE AFSILV - WOLTVFORL - VHGG - FVEEPY - RLAPEDELKAYA - FFVSHQRWREYK - EW DWRTHGROW TFIF H- LILRINVAREL - PDDI	ASGVRRPD 364
00000663368 2 282 PSIJQIKKVIKSSSFR-LEAIPYLVKI-KEKK- SIKNT -WVDSKNIESIG-IPSPVKKTIKEIR-VP 344 000000467631 2 261 TSKKQLDOGR T SSYH-LDYPTEKUK. -ENFORMAN -WYSKEQINSIG-LATPIKELDON. 324 00000187176 11 283 PSATTESHFS-TSFFR-LDQPTLLITQ-STPIK -VTESGQ-WYYNLEFSRIG-LAPVKKLLQRAE-LNTQADERTS 350 000001606097 64 297 SDVEAAGALTITTFFR-LHMILHADI TKP -ATLDDDW -RWYLAQLANSVC-LPAPVKLALETU-OPSIL 363 000003378864 2 301 EVGFLYTQVR AFSFRITLHAYHCRILIGG-TPPI -PKVAVES -RWYLINGLOPA-FFRANKRVLEVLEQPRAMEVTP- 375 000000310742 3 284 ENFEKETKLS-TS SFR-LQYTTLVVRT-DNPLN -FVWAVES -LWYNESTKTGG-FPAPIEKTETIL-T- 344 00000032161618 2 249 KTSEVLPTLR-TTSEFH-LQYTTLVVRT-DNPLN -FVWEGTPS-LWYNSCHYGLG-FPAPIEKTETIL-T- 320 000000321000 281 LFSAANSVLR-STIFF-LAITPQPARA-PKRLT -RWGSTGL -WYKREPF- -WYKREPF- 2000000223903 1 284 LFSAANSVLR-STIFF-LAITPQPARA-PKRLT -RWGSTGL -WYKREPF- -WYKREPF- 2000000229062 2 257 QVKKKLLLINS -WYKREPF- -WYKREPF-	sp_ P17802_MUTY_ECOL p_ P3847_MUTY_ECOS c_00003652391_2 c_0000003652391_2 c_00000031207_6 c_0000003575_4 c_00001092484_3 c_0000119248_3 c_00001197282_1 c_00001977282_1 c_00001977282_1 c_0000027895_5_4 c_000027895_5_4 c_0000027895_5_4 c_0000027895_5_4 c_0000027895_6_2 c_000003872363_2 c_000004820107_1 c_00000587021_3 c_00004820107_1 c_00005867021_3 c_00006857021_3 c_000008567021_3 c_000008567021_3 c_000008567021_3 c_000008567021_3 c_000008577378_2 c_000008567021_3 c_000008577378_2 c_000008577378_2 c_0000001745627_3 c_000008577378_2 c_0000008577378_2 c_000000757378_2 c_000000237457_2 c_00000237457_3 c_00000337457_3 c_00000337457_3 c_00000337457_3 c_00000345925_4 c_00000345925_5_4 c_00000345935_7 c_00000345935_7 c_00000345935_6_7 c_000000000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_000000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_000000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_0000000345935_6_7 c_00000345935_6_7 c_00000345935_6_7 c_00000345035_6_	295 287 287 294 303 313 313 32 32 287 297 297 297 297 297 297 297 297 297 29	ELTEPIVSE AFSILV - WOLTVFORL - VHGG - FVEEPY - RLAPEDELKAYA - FFVSHQRWREYK - EW DWRTHGROW TFIF H- LILRINVAREL - PDDI	ASGVRRPD 364
C 00000188235 1 283 PSATTESSFS_TTSFFR-LQACTLITQSTPIKRVMECTFSLMYNSNTTFMGG-FFAPIKTINKIN-EDF350	sp_ P17802_MUTY_ECOL p P83847 MUTY_ECOS c_00003652391_2 c_000003652391_2 c_000000312077_6 c_000001092148_4 c_000001092148_4 c_000001151029_1 c_000001797282_1 c_00000197282_1 c_00000278955_4 c_00000278955_4 c_00000278955_4 c_000002106160_4 c_000003607531_2 c_000004820107_1 c_000005867021_3 c_000004820107_1 c_000005867021_3 c_000005571378_2 c_000005591148_4 c_0000055917378_2 c_000000898175_2 c_00000898175_2 c_00000898175_2 c_0000011118_1 c_0000098987_2 c_000001118_1 c_000001116522_04 c_00001345122_1 c_000001345122_1 c_000001345120_1 c_000001345122_1 c_000001345122_1 c_000001345122_1 c_000001345122_1 c_000001345122_1 c_000001345122_1 c_000001345122_1 c_00000324679_3 c_00000238791_5 c_00000238791_5 c_000003248034_1 c_0000033948186_72 c_000003948186_72 c_0000005595100_5	295 287 287 298 303 323 257 287 297 298 287 297 298 287 297 297 297 297 297 297 297 297 297 29	ELTEPTYSEE AFSILVWQLTYFGGELWIGG	ASGVRRPD 364
C_00000187176_11 283 AEPEALSPLRITSSFH-LDIOPLLVEV-DAPOR	sp_ P17802_MUTY_ECOL sp_ P83847 MUTY_GEOS c_00003652391_2 c_0000031207_6 c_00000011207_6 c_0000011207_8 c_00000192148_4 c_00000192148_4 c_00000192248_3 c_00001197282_1 c_00001797282_1 c_00000278955_4 c_00000278955_4 c_000002807531_2 c_000003872363_4 c_000003872363_4 c_000003872363_6 c_000002871277_7 c_00005867021_3 c_000005867021_3 c_00000587120_3 c_00000587120_3 c_00000151118_4 c_00000598175_2 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_000001754627_3 c_00000175522_6 c_000002387256_6 c_000002387256_6 c_00000238725_1 c_00000238725_1 c_00000223872_1 c_00000338834_1 c_0000338886_7_2 c_000003886_7_2 c_000003886_7_2 c_0000003886_7_2 c_000003886_7_2 c_00000585712_0_4 c_00000555712_0_4 c_00000555712_0_4 c_00000555712_0_4 c_00000555712_0_4 c_000005555112_0_5 c_0000065336_2	295 287 287 287 298 303 32 328 292 296 290 290 287 287 282 222 276 6 282 276 282 282 282 288 288 288 288 288 288 28	ELTEPTYSEE AFSILVWQLTVFGGEL	ASGVRRPD 364
C 000003378864 2 301 EVGPLYTOVRA & SERITLHAYHCRILEG TPH PKVAVES RWYEINGLDGFA-FFKANKRVLEVLEGPEAMEETTP 375 375 C 000003910742 3 284 ENTEKETKLS TT SEFR LHIHALLING TPPIK RVWEGTPS LHYNRSKFTGG FPAPIEKLFTRIL-T 349 36 C 000004116181 2 249 KTSEVLEPILS TT SEFR LQYTTLVVRT DNPIN FVMEVDGA WYNRAEQIPGLG LPAPVKRLDMLIINEDNND 320 32 C 0000010229083 1 284 LFESAMSVLRS THEF LAITPGPARA PRRIT RRMGSTGL LMYRPGEPF LMYRPGEPF 332 32 C 000001029068 2 257 QVRKKLPLIN RS STHYY LTI 20 257	sp_ P17802_MUTY_ECOL p= P3847 MUTY_ECOS c= 00003652391_2 c= 000000652391_2 c= 000000031207-6 c= 0000001097148_4 c= 000001197282_1 c= 00000197282_1 c= 00000197282_1 c= 00000197282_1 c= 000001803648_2 c= 000002106160_4 c= 000003807531_2 c= 000002106160_4 c= 000003807531_2 c= 000002106160_4 c= 000003872363_4 c= 00000482017_1 c= 00000487017_1 c= 000005867021_3 c= 00000487017_7 c= 000005867021_3 c= 000005867021_3 c= 000005867021_3 c= 000005867021_3 c= 000005867021_3 c= 00000598175_2 c= 000000598175_2 c= 000000988175_2 c= 000000988175_2 c= 000000131612_1 c= 00000089817_2 c= 000001345122_1 c= 00000146646_1 c= 000001466646_1 c= 0000004666466_1 c= 0000004666646_1 c= 0000004666646_1 c= 00000046666466_1 c	295 287 287 287 298 303 32 298 298 298 299 290 287 287 284 290 290 287 284 292 292 284 292 282 282 282 282 282 282 282 282 282	ELTEPTYSFELATSILV—WQLTVFFGRI.—VGIGG—PVEEFY—RLAPEDELKAYA—FFVSGQRWREYK—EM DWRTHGRUNT TIFFH—LILTRIVAEL PDDI — TPAVC FILLARARPRSD—LPTV ELICHADRFQA TYR—LILTRIVAEL PDDI — TPAVC FILLARARPRSD—LPTV ELICHADRFQA TYR—LELKIMTINS —EVT — PEGG — FFVGREWKQA—LPALHRISTAARA—ELI DWRCHGRUY'S ST HFD—LELKIMTINS —EVT — PEGG — FFVGREWKQA—LPALHRISTAARA—ELI DWRCHGRUY'S ST HFD—LELKIMTINS —EVT — PEGG — FFVGREWKQA—LPALHRISTAARA—ELI DWRCHGRUY'S ST HFD—LELKIMTINS —EVT — PEGG — FFVGREWKQA—LPALHRISTAARA—ELI DWRCHGRUY'S ST HFD—LELKIMT — APAGG — RETURNING THE PLANGRYNATRVE—ENI DWRCHGRUY'S ST HFD—LELKI — APAGG —RETRABLODEP—LPGIMRKVLAHA—PDF DWODPGAEVR S THE —LRISING — CANA — KPTAG — HFIADADEDET —LPTVWRKAYRIA—TV DWQUINAEVR THE HE—LRISING — TO COMPANIAN — FFVANHILLEN — PPATG — PRANHILLEN — PPATG — PRANHILLEN — PPATG — PRANHILLEN — PPATG — PPATG — PPATGROWER — PPAT	ASGVERED 361
C 000003910742 3 284 ENTEKETKLSTTSFFRLHIHALLIRQTPPIK	sp_ P17802_MUTY_ECOL p P83847 MUTY_ECOS c_00003652391_2 c_000003652391_2 c_00000031207-6 c_000001092148_4 c_000001092148_4 c_000001151029_1 c_00001197282_1 c_00001979282_1 c_000002078955_4 c_000002078955_4 c_000002078955_4 c_000003807531_2 c_000003872363_4 c_000003872363_1 c_00000454021_1 c_000005774797_1 c_000005870797_1 c_000005870797_1 c_000005870797_1 c_000005774797_1 c_000001574797_1 c_00000157470_1 c_00000157470_1 c_00000157470_1 c_00000157470_1 c_00000157470_1 c_00000157470_1 c_00000157470_1 c_000000467631_2 c_0000001671767_1	295 287 287 298 303 323 282 290 290 302 287 287 288 282 290 302 280 302 282 282 282 282 282 282 282 282 282 2	DIRTLEGEVIT TO FFR - LILTRIVAEL - PODI - TPAVG - FLAPEDELKAYA - FFVSSIQKVMPEYKEWD DWRTLEGEVIT TO FFA - LILTRIVAEL - PODI - TPAVG - FILABORP A TRK - LILTRIVAEL - PODI - TPAVG - FILABORP A TRK - LILTRIVAEL - PODI - TPAVG - FILABORP A TRK - LILTRIVAEL - PODI - TPAVG - FILABORP A TRK - LILTRIVAEL - PODI - TPAVG - FILABORP A TRK - LILTRIVAEL - PODI - TPAVG - FILABORP A TRK - LILTRIVAEL - PODI - TPAVG - FILABORP A TRK - LILTRIVAEL - PODI - TPAVG - FROM - FR	ASGVRRPD 364
C_000004116181_2 249 KTSEVLPPILRITSSFHLQYTTLVVRTDMPLN	sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_000003652391_2 c_000000352391_2 c_000000352391_2 c_000000352391_2 c_000000352391_2 c_000001092484_3 c_00001092484_3 c_00001197282_1 c_00001797282_1 c_00001797282_1 c_000002106160_4 c_0000036731_2 c_0000036731_2 c_000004820107_1 c_0000587021_3 c_00004820107_1 c_0000587021_3 c_00004851008_5 c_00002511148_4 c_00000577378_2 c_000005511148_4 c_00000577378_2 c_00000811118_1 c_00000577378_2 c_0000011118_1 c_00000577378_2 c_0000011118_1 c_00000577378_2 c_000000577378_2 c_000002038721_4 c_000002038721_4 c_000002038721_4 c_000002038721_4 c_000002038721_4 c_000002038721_4 c_000002038721_5 c_000003333364_1 c_00003333364_1 c_00003333364_1 c_000003333364_1 c_00003333364_1 c_00003333364_1 c_00003333364_1 c_000003333364_1 c_00003333364_1 c_000003333364_1 c_0000003333364_1 c_000003333364_1 c_0000003333364_1 c_000003333364_1 c_000003333364_1 c_000003333364_1 c_000003360666_1 c_00000368235_1 c_0000066836_2 c_0000066836_2 c_0000066836_2 c_0000066836_2 c_0000066836_2 c_0000066836_2 c_000000066836_2 c_0000066836_2 c_0000000688285_1 c_0	295 287 287 297 296 297 297 297 297 297 297 297 297 297 297	ELTEPTYSFE A.B. ILV - WQLTVYFEGEL - VHGG - PVEEPY - RLAPEDELRAYA - FYSHGRWHEEVK - EMU DWRTHEGEVY TO HH - LILIRIRVAEL - PDDI - TFAVG - FLISHAFFED - LPTV ELIGHADEFG ALT NK - LETIFLIVYRY - QGE - IFAGV - ETIPIDGGEN - LPALHRKSIAARA - ELI DWREHEGGY SET BT - LELKIMTINS - EVT - PECT - FWCREEVKAGA - LPALHRKSIAARA - ELI DWREHEGGY ST TO SET BT - LELKIMTINS - RSSSW - BGDVTA - EWWGIDELATRP - LSVAGRRVATRVE - RI PWEEC - GTV TX FIT - LALSVYRAW - ADAP - APAGS - WWCAEGLGEA - LPTVHKRVEVAGAI - SGE DWKROPGGLVY SET BT - LELKIT MRKRLEGIVE GO FF - LELKITYFVARV - ALATP - APAGT - RFTPRSALDDEP - LPGLMRKVLAHAF - DPI DWQDPGAEVVS SET BT - LRLSIKVATI - GGK - KPTAG - HFIADAFDPET - LPTVWRKAYKIAGA - TOP DWQDYLAARVY TO FF - LRLSIKVATI - GGK - KPTAG - HFIADAFDPET - LPTVWRKAYKIAGA - TOP UWQYLAARVY TO FF - LRLSIKVATI - GGK - PPEVRFF - RWIRLINGINGYA - PFRANKLIFINAD - E- WGWKIAGTVA AN FQ - LOLGVYRVAVV - MDQT - QISGG - IWWDEBLDEFA - LPTVWRKAYKIAGA - TOP UWGYLAGVY TO FF - LRLSIKVATI - KRV - IPTVG - MFIPSDKFDPDD - LPTVWRKAHALAD - AAI SEKQTNISLYS SET BT - LILI SEKNGIGGIR I WI ID - L UNIVICAGEVY TO FF - LRLAWIYVATV - NEN - SPDVG - KFIADDCFDPAD - LPTVWRKAHALAD - AAI SEKQTNISLYS SET BT - LILI SEKNGIGGIR I WI ID - L UNIVICAGEVY TO FF - LRLAWIYVATV - NEN - SPDVG - KFIADDCFDPAD - LPTVWRKAHALAD - AAI SEKQTNISLYS SET BT - LILI SEKNGIGGIR I WI ID - L UNIVICAGEVY TO FF - LRAWIYVATV - NEN - SPDVG - KFIADDCFDPAD - LPTVWRKAHALAL - GSI LWVDSWEPFR SEN BD - LYTHPIQIRM - DGGPM - MTANYSKIT - QSFSINQLOSIG - ISAPVKGIVNKLY - LWVDFWEEPR SEN BD - LYTHPIQIRM - DGGPM - MTANYSKIT - QSFSINQLOSIG - ISAPVKGIVNKLY - LWNDFWEEPR SEN BD - LYTHPIQIEM - DGGPM - MTANYSKIT - QSFSINQLOSIG - ISAPVKGIVNKLY - LWNDFWEEPR SEN BD - LYTHPIQIEM - DGGPM - MTANYSKIT - QSFSINQLOSIG - ISAPVKGIVNKLY - LWNDFWEEPR SEN BD - LYTHPIQIEM - DGGPM - MTANYSKIT - QSFSINQLOSIG - ISAPVKGIVNKLY - LWNDFWEEPR SEN BD - LYTHPIQUE - CSKK - KYKNS - WWDYNVSSIG - ISAPVKGIVNKLY - LWNDFWEEPR SEN BD - LYTHPIQUE - CSKK - KYKNS - WWDYNVSSIG - ISAPVKGIVNKLY - LWNDFWEEPR SEN BD - LYTHPIQUE - CSKK - KYKNS - WWDYNVSSIG - ISAPVKGIVNKL	361 361 362 363 364 374 374 374 374 375 375 375 37
c_000001029068_2 257	sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_000000352391_2 c_00000031297_6 c_0000003575_4 c_00001092484_3 c_00001197282_1 c_0000197282_1 c_0000197282_1 c_0000197282_1 c_000027895_5_4 c_000027895_5_4 c_000027895_5_4 c_000027895_6_2 c_00000387236_3_2 c_000004820107_1 c_0000587021_3 c_00004820107_1 c_00005867021_3 c_0000687021_3 c_00006857031_2 c_000005867021_3 c_00000887021_3 c_00000887021_3 c_00000887021_3 c_00000887021_3 c_00000887021_3 c_00000887021_3 c_00000887021_3 c_00000887021_3 c_000000877378_2 c_000001374527_3 c_0000089587_2 c_000001374527_3 c_0000089587_2 c_000001345122_1 c_000001345122_1 c_000001345122_1 c_00000253527_1 c_00000253527_1 c_00000238721_4 c_00001238731_5_8 c_00000238731_5_8 c_00000238731_7_8 c_00000238731_7_8 c_00000238731_1 c_00000339346_7_3 c_00000339346_7_3 c_00000339346_7_3 c_00000339346_7_3 c_00000349235_7_1 c_00000349235_7_1 c_00000349235_7_1 c_00000349235_7_1 c_00000349235_7_1 c_00000349235_7_1 c_000000467631_2 c_00000349235_1 c_00000349235_1 c_00000349235_1 c_000000467631_2 c_00000349235_1 c_00000349235_1 c_00000349235_1 c_000000349235_1 c_00000349235_1 c_00	295 287 287 294 303 313 32 32 32 32 32 32 32 32 32 32 32 32 32	ELTEPTYSFE A.B. ILV WQLTVYFEGEL VHGG PVEEPY RLAPEDELRAYA - FYSHGRWHEEVKEMU DWRTHEGGY TY FH LILRIRVARL PDDI TPAVG FLISHAFFSD LPYV LLIGHDAFF, ALT RK LEITELVYRY QGE IPAGV FITPIDGGRM LPALHRKSIAAAR ELI DWREHEGGY SET BTD LEIKIMTINS EVT PECT FWCREEVERQA LPALHRKSIAAAR ELI DWREHEGGY SET BTD LEIKIMTINS RASSW BEGVYTA EWUGIDELATRP LSVAGRRVATRVE RI WEEC-GTVT TY FIT LALSVYRAW ADAP APAGS WWCABGLGEA LPYVMRKWYEAIA SGE DWREPGGGIVY SET BTD LEIKI ADAP APAGS WWCABGGA LPYVMRKWYEAIA SGE DWREPGGGIVY SET BTD LEIKI ADAP APAGS RFIPRSALDDEP LPGLMRKVLBAHF DPI DWQDPGAEVUS SET BT LRLSIRVATI GRK PPATA RFIPRSALDDEP LPGLMRKVLBAHF DPI DWQDPGAEVUS SET BT LRLSIRVATI GRK PPATA PPAT	ASGVRRPD 364
	sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_00000031207-6 c_00000031207-6 c_000001092148_4 c_00000199248_3 c_000001151029_1 c_00001797282_1 c_00001797282_1 c_00000278955_4 c_00000278955_4 c_0000028067531_2 c_000003872363_4 c_000003872363_4 c_00003872363_4 c_00004820107_1 c_000005877777_1 c_00005870701 c_00005877777_1 c_00005870777_1 c_00000587077_1 c_000005774797_1 c_0000587077_1 c_0000058707_1 c_000005774797_1 c_0000058717_5 c_00000157652_1 c_00000157652_1 c_00000175652_1 c_00000175652_1 c_00000175652_1 c_0000018515736_6 c_0000018515736_6 c_0000018515736_6 c_0000018515736_6 c_0000018515736_6 c_0000018515736_6 c_0000018515736_6 c_0000018523643_2 c_0000018515736_6 c_0000018523643_2 c_00000238721_4 c_00000238721_4 c_00000338721_6 c_00000338721_4 c_00000338726664_5 c_000003294679_3 c_000003294679_3 c_000003492925_4 c_0000033948186_72 c_000003492925_4 c_00000349295_7_5 c_00000349295_7_5 c_00000349295_7_5 c_00000349295_7_1 c_00000349295_7_5 c_00000349295_7_1 c_00000349295_7_5 c_00000349295_7_1 c_00000349295_7_5 c_00000349295_7_1 c_00000349295_7_1 c_00000349295_7_5 c_00000349295_7_1 c_000000486_1 c_00000486_1 c_00000486_1 c_00000486_1 c_00000486_1 c_0000486_1 c_00000486_1 c_0000486_1 c_000486_1 c_000486_1 c_000486_1 c_000486_1 c_000486_1 c_000486_1 c_000486_1 c_	295 287 287 298 303 32 298 292 276 6 282 222 286 282 282 284 282 282 284 283 287 301 284 284 284 284 284 284 284 284 284 285 286 286 286 286 286 286 286 286 286 286	ELTEPTVSFE A.B. ILV. — WQLTVYFEGEL — VHGG — PVEEPY — RLAPEDELRAYA — FYSHGRWHEEVK — EM DWRTHEGEVY TY HH — LILRERVAEL — PDDI — TPAVG — FLISHERPED — LPTV — LILGERDER ALT RK — LETIPLYVRY — QGE — IPAGV — ETIPLOGGR — TPALHRKSIAAR— ELL DWKRHEGGV SY ST HD — LELKIMTINS — EVT — PEGT — FWCREREVERQA — LPSLWRKHRIMHY — RESSW — EGVTA — EWGIDELATRP — LSVAGRKVARVE — RI PWEPC—GTV TO HT — LALSVYRAKV — ADMP — APAGS — WWGADELATRP — LSVAGRKVARVE — RI DWKPHGGGV SY ST HD — LELKIY — ADMP — APAGS — WWGADELATRP — LSVAGRKVARVE — RI DWGC — GTV TO — LELKIY — APAGT — RFIPSALDDEP — LPGIARRYLARRA — TRI DWQCARAVY S THE H — LALSIKVATI — GKK — PFATG — HFIADADEPDET — LPTVMRKAYKIAR — TRI DWQCARAVY S THE H — LALSIKVATI — GKK — PFATG — HFIADADEPDET — LPTVMRKAYKIAR — TRI DWQCARAVY S THE H — LALSIKVATI — GKK — PFATG — HFIADADEPDET — LPTVMRKAYKIAR — TRI DWQCARAVY S THE H — LALSIKVATI — GKK — PFATG — HFIADADEPDET — LPTVMRKAYKIAR — TRI DWQCARAVY S THE H — LALSIKVATI — GKK — PFATG — HFIADADEPDET — LPTVMRKAYKIAR — TRI DWQCARAVY S THE H — LALSIKVATI — GKK — PFATG — HFIADADEPDET — LPTVMRKAYKIAR — TRI DWQCARAVY S THE H — LALSIKVATI — TRI STANDAY — TRI ST	361 361 362 363 364 367 367 367 368 368 368 368 368
	sp_P17802_MUTY_ECOL sp_P83847_MUTY_ECOS c_00003652391_2 c_0000003552391_2 c_00000031207_6 c_000000131207_6 c_000001092484_3 c_00001197282_1 c_00001797282_1 c_00001797282_1 c_00000278955_4 c_0000278955_4 c_00002106160_4 c_00003607531_2 c_000003607531_2 c_000004820107_1 c_000005867021_3 c_000004820107_1 c_00005867021_3 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000005867021_3 c_000008867021_3 c_0000089687_2 c_0000011118_1 c_00000989687_2 c_000001118_1 c_00000989687_2 c_000001116522_24 c_00001345122_1 c_000001345122_1 c_000001345123_1 c_0000034515136_1 c_000001345123_1 c_0000034513_1 c_	295 287 297 298 287 297 298 287 297 298 287 297 298 287 297 297 297 297 297 297 297 297 297 29	ELTETUSFER AND LY—WQLTVPFORL—VIGG——PVEETY—RLAFEDELKAYA—FPUSHQRVMERUX—EMBORITAGENET THE HILLIRIVABLE PDDI—TPANG—FILSKHARA—FPUSHQRVMERUX—EMBORITAGENET THE PLITITION OF FLICKHARD FOR THE SHARM SELECTION OF THE	ASGVRRPD 364

_000001595844_4	288	NIKNKLGPVTQL <mark>LT</mark>	HQKVIGQFFDITL	VGE	KDLDI	APISKVDLQVFPFPKMMMMYINRIMA
_000001719155_2	292 293	HIDEKLMTVKHSYT	RFRVILHVFLCRV	LSGRV	SPTHCEEW	DWVKTEELDRYPFPAANVKIIKSLRKNQGRS
_000002363038_6 _000002561400_1	293	EGLIEWDDFRHTES	HYHLDIYPLIFDE	QASTDIEIGQP RGAPKNTAKI	ISEPGGVYDAEOG	QWFDINRLKSGEIGVPVPIRKMISSL
000002566035 2	284					KWIHPKTNPNLGLPAPVLSMLIDLNNTKRAVLNES-
000002598045_3	282					VWVNFKNVESLGLPAPVKKTINQITMP
000004188575_41	280 282					IWYKIEDALTLGLPAPVKKTLLTLSKG
000000240049_1 000002139456 2	282					QWHADITQLALAAPISAIFRENNSLK QWHADITQLALAAPISAIFRENNSLK
000003535614 2	284					QWQVDISKLALAAPVSAIFNAK
000002657784_4	281					VWVDKKGLKALGIPTPVKNIFEVLKLNDQTS
000003800129_15	263	NNNREIKHGLS	HRELHLEFLVTSG		TPKGG	KWINKNEFNNLPTPKPISDKLEQYAKSFL
000003716781_1 000001556689 3	273 294	LQREEVGELRHSIT	KHRIRARVLRAVP	GRDE	DECIEVEDUNIDOS	AWFERSEIEALGVTGMTSKALTLGRARSR
000001336669_3	254	KLGEMMGSARHTIT	RHRIOARVHOVEG	GGQTIMAGA	W	GWFTIEEVMTLALAASARKTLTTLLDIDLTTAHNPG NGKGAVDPSSVPLSSLGRKVLSIAGVLGGLLLLSPD
000004255004_2	275					RWVSLANLHAYPLSSLSTKALSAARQHLPTTRKLGG
000000605438_3	263	ENMTGLGEFKQH <mark>YT</mark>	HFTLDARVVLLKD		KKQE	NYFTVEEIHDLALSGADRKALALLEKYLQ
000000581237_15	263 263	KDMIKLGEFKOHYT	HFTLEASVVLVQN		KEQE	RYFRINEIHALALSGADRKGLALIEKHLA
000002529579_2 000006097838 1	268	VEPESICIINHSIT	CYRNRLEMFVIFR	TRKPL	LAKLKG	NYFTIDEIHDLALSGADRKALALLEKYLQ KWVPLAKLDEIPLTTAHRKAANQFAG
000000583727_6	294	AKFQPLCNINHSIT	RYRNRLEMIVAEP	KRKPR	LAKLKG	EWLPLAKLAELPLTAAHRKASDYFLKTANSR
000005807640_2	295	AELEPLCTINHSIT	RYRNRLEMFVIEP	ARKPR	LAKLNG	EWIPLAKLDELPFTTSHHKAANQFC
000000134878_1	270					KWIHTSKLHSYAF
000005136725_3 000001684786 4	285 280					RWVKTSRLHSYAFPKASIKLFNAIKSIE RWALPEELGSVL-PVSSLCLKIADRLS
000002971826_23	290					RWGRADELGNVL-PVSSLCLKIADRLS
000002040695_2	291					QWVLLNQMNDYPLSSLTKKSLAFLVKNLELEKEQAF
000003263657_32	303	KTDLVLPTVLHVFT	HFKITLYGFGCTF	IKGAA	KALTCHDA	RWVSQTQLADFAFSRAHNRLIDIMKKEAAKGQVEME
000005989041_2	297					IWVDRNRLDDFALPNIMKKVLAFALRHNQHFSREFF
000002391082_2 000003839553 2	298 305	EVGARLTSVDHAYS	HESITLHALEARY	LRGEP	QAIGCADW	KWIVPDELDDYALPRADRLIVEFLRQDGRQLGLFDS
000003839553_2 000003996707_2	295	EVGGLLAKVDHOES	HFSITLNLFEAMY	RGGEP	EAVECDDW	RWIDPAELDDLPMPRADRRALEELS-EEEGQRVPVLMA
000003996707_2	271	LVVTSEHRFS	HRHWTTRVYRA	RVEDE	CSGPADASHWSEGL	RWTCAGDLGKLAVPEASRKTLRPCLRASRGSLPG
000006007075_1	268	KNLQKTLN <mark>F</mark> K <mark>MS</mark>	NMNMNIVIKIMKI	ssn	ISDS	SWIKETKFNHYTFPTFTKKIFNSLENYL
000002094036_4	245	SLLKSKNKLN <mark>L</mark> K <mark>MS</mark>	MMNMNICIDFVKI	KKK	PKNG	LWIESSKLENCMIPTFTKKIFASVKNNL
000002762689_1	268	LSSTDIVNFKMS	NMNMNIKIEHKNK	VGS	LPTS	HWIDPKKLKNYTLPTFTKKIVRYLESNK
000005516980_2 000003920004 1	268 293	NENENENENE	HEDMNIKIQYSKN	NTV		YWVDQKKLNNYMLPTFTKKVVKYLENNK
000003920004_1 000004008511 2	293	NKLKLKGFVDYSFS	HFDLETEVFFTKV	KKDY	FANO	KWIKKNNIKISGLPTVMKKIIEVAL
000004481347_1	294	VKYKRIGKITYSFS	HFDLDIGIYKSKV	VKKK	FKNF	NWIKSNKIDTSGMPTVMKEIVKKSLKI
000003787733_3	289	NIGKKIGHVK <mark>H</mark> A <mark>YS</mark>	HFRITLTLYQCKT	NRSVK	NIYKEY	KWIIPTEVNNYPFPKSNHKLFK
000000754657_2	289	NIKKKVGNVK <mark>H</mark> AYS	HFKITLTLYRCQS	QGSVK	SNNKEY	RWITPAEIKYFPFPKSNHKLFDVLNSNGWNV
000000990943_3	289					RWITPIEVNNYPFPKSNHKLFTILNSDGWNV
000004474996_2 000001463500 11	288 276					RWITPSEIQYFPFSKSNHKLFNLLNSNGWNV
000001483300_11	263	ONTNET PSEKHSTS	HKDFHISPRIINI	PDDME	TDDKKT	CWIRPKDINNYAFSKSNHKLFKILNTNGWTI IWIEKNKIAKLGAPKPVLDIVKKILNQNDKGLL
000001293628 3	302	VRFSPLPEVRHTFT	HLKAVYRPMLVIG	TRCEG	SNPDSEH	KWVLPDQVEDLPLFVAQRRILDLAWAALEGC GSILLSEIENYPVPVLIANFINTFKNSYFWPNNSIF RFVQKTNINELALPSLIKKILNALKNNEILDF
000001535696_8	292	VLRYNHKIIV <mark>H</mark> K <mark>LS</mark>	HQQLHTHFWIVVI	SNELD		GSILLSEIENYPVPVLIANFINTFKNSYFWPNNSIF
000001614067_2	298	KWKILDQNLNHIFT	HFKLNCSLAIATI	NDENAL	VNDLSKSSY	RFVQKTNINELALPSLIKKILNALKNNEILDF
000001765289_1	262	SIKKRIGAVDHAYS	HFSITFHGYHCIE	NGEK		
000001961666_1 000002018097 4	274 284	NRILSKNVVRHEFS	HFKLELEVYYIET	RFP	QITHG	EWLKTKQAGKQLPSVMKKVLDNI
000002018097_4	254	CASKYIGEVTHAYT	HFKLIIOVYVYDE		LDAEKN	SYFSSQEIQKLAISKVDDKILNLFLNSIECD
000002930199 1	281	SNIKNKYTIEHNLS	HQKLKISFWDVDA	KNIN	TQKGF	EKITLDNISNYPFAKPLEKYFQTQHLIT
000003033795_2	277	SNPIFLGNIT <mark>H</mark> K <mark>YS</mark>	HFGVNISFFISFP	KSIKS	FNSSQEY	RWIRIKNILNYPLPKANHKMLDILKKL
000003888107_2	278	KNPNYLGQIK <mark>H</mark> QYS	HFKVLISLFLADV	NDISS	LKPNQNY	KWTTRKQLDKFALPKANYKMLEILDKLN
000004013286_6	307 265	QIGNKIGQIRYVVI	RFRTTVDCYEAHF	SNIGKPNRSKNDIS	SVNTLQKEQQEAGSLWHM	QWATRKQIDSFPMSVPARRVIRLLADFD
000004852258_1 000005254087_1	300	RTDRFLTSIKHAYT	HFRHNVLLINCQA	KDQP LRGEP	OHIGVADH	KWVSFSDLDQYAFSKANHKLFKLVELRND AWVTLADLDKYA
000005603677 1	290					ELVDAQSWPNYPLPRLIAQYWEKKQLAFF
000003283462 3	276					RWITPGEIGDYPFPRANHKLFNQLENFYSNG
000002687221_1	290	APVAFVKQIK <mark>H</mark> A <mark>YS</mark>	HFSITVDAYSCTF	RGGRP	RALGCADY	RWIYPHETGKYAFHSAGHKLFDKILETAS
000003347358_19	285	CASEYIGKVT <mark>H</mark> AYT	HFKLICKVYVYYE		NHPEEA	DYFSEEEIQKIAISKVDEKIVNLYGNFLKYD
000002701031_2	286					KYISKKELKNYPISRLLEKYLENIGMI
000000582753_3 000001713769_5	292 288	TILENGGDITHKI C	HKLINVERMITENT	FDA1	RLENI	IKVEKEDFESYPIHRLMEKMMEQVGK NSIKFSDVNKYPVPRLIEKFLDKFNYKHF
000001713703_3	288	KIKHKSAPSKOLLT	HQKIIGIF			
000006057486_30	292					NTVNWQNLSNFALPTLIQNFVDDFKK
000005494072_10	290					NTISIDELKKYPVPVLIDNFIKDFEM
000001742634_3	293	PYLFNEKTVI H KLS	HQHIYTKFWIVKL	DVNLE		QTIPLNSIEKYPVSTLIQNFIKEFNF
000002826998_2 000003159439_6	290 289	QIKKISLPFRONLT	HKKIIATFFEIDF	MDKFS	NKNNNY	IKIERKNLSKFAFPKIIDLYLKDNSLNLAMK
000003159439_6 000004887214 1	289 294	LOLLTPKVVVHKT	HOHIAIKEMEIEA	PTFRS		NSILIEDLEKYPVPKLIQNFIEKFDNIKLNPATKATISWOELLKLPFPIVIFKFIREFLETSMPNFDTPI
000004887214_1	288	KVKKRSKNFTORLT	HQKLNAIFIEIDL	KTK	INKOF	INTDINNLSKFAFP
000001059964_1	280	QLGKEIHTLEHRYT	SFRTRVSFFTATV	HVLPE	ssqkrv	ATISWQELLKLPFPIVIFKFIREFLETSMPNFDTPI INTDINNLSKFAFP
000002498472_1	289	EIVEKITNTVHHYT	RYKVTLHCFLLRL	KKGSDT	DPVLHAAQDF	NWVPFKALQEYAFPAGHRKLITYL
000004615912_3	285	QTKKYQQELT	'HQKISAYFWEIN	LNVAP	VNIYDF	ILIDSKNLAKFAFPKIIALYLENNSLNL
000004766858_2 000002747260_18	292	PWRDDCAFUDETER	HEHATLHCRLCTV	AEIPS	VLPDNA	QWLTLGEISALALPRVFQRLRKRLLDEVSA QFIPHHAFRPGQLPTVMRKAYDLASATFLGN
000002747260_18	287	NWRTVPGEVRHTET	HFHLVLELRRADL	PEDC	TTMRG	OFLAPGGFRPSDLPTAMRKAFDLARDG
000003371301_30	290	DETRTLEGFRHTFS	HFHLDITPVVAVV	NSAPS	KRVAETAF	RWFSLNEPIEVGLAAPTTKIIQQLMR
000003254110 11	290	EETKTLETFRHTFS	HFHLDITPVVAVV	NSPPT	KRVADTAF	RWFSLGEPIEVGLAAPTTKIIKQLIG
000004750284_20		EEIQQLDEFRHTFS	HFHLDITPLIAVV	NSTPQ	KRVAENES	RWFLLDEPIEVGLAAPTTKIIKTLAK
000000141782_15	292	TRPOAWPGLRHTFT	HrQLDIQPVRLRL	TAAPA	RLMDGDRH	VWYNVESPDARGLAAPVARLLQGLALEDTRA
000002717847_8 000004054799 1	264 260	NAANKHALS	HINIHEKEKQIAN	DKKCD	GMKG	
000004054799_1 000006126673 1	302	KPYKOLPFIMHVET	HFSLKLYLCKTSE	FICDN	VPEEH	LISNL
000000339186 3	248	-NGQPFASARHSIT	RYRIQLNAHLIHA		KRGKG	MWCTSDEIRSLPFSSAHLKLIGKLPHRLDK LWVRLDGLHKHPFSSPQHEIIKTLDKEAALQLAGLV
000003029168_2	299	QKLTKLVTIT <mark>Y</mark> T <mark>V</mark> M	RTRTTLHVFEGML	DLETS	TMQEASSR	LWVRLDGLHKHPFSSPQHEIIKTLDKEAALQLAGLV
000001863436_1	316	TPRVELGEVVHHFS	HIRMTITAEHRVA	SSEQVRL	RSDDEVGQEA	RWVSAVELVDLPMSAAMRKIEGLYRELGSGAI
000002830137_4	304	EPVRQLTTIQHGVT	FFQITLQCHLAQC	VSGRK	RGPHL	SWRMPHELEHLPLSVTARKIGRLVAKLAD
000004612302_3 000001933926_1	298 277	PARET DCZANDROBA	HEHLELOTMONTED	KAGIW		EWVEIDELTARPLSVAARRVADGVQAGQRCGGASG-
000001933926_1	289	DWQMLSGKVRHTFT	HFHLEL			
000005849454_9		KLGAYOGOVERTTT	HHRIRAHVYAAEG			APTHLEDPTOVPLTGLARKVLDRITSA
000001169194 1	302	GVASALAEVQ <mark>H</mark> RFT	'HLQARYRPWVVPV	AKL	LNGEGN	VWMTPGEPVDFPIPVAQHKVLDALAECGATLGSSES MWMTPGEPVDFPIPAAQHKVLDALAECRATPDSLES
000002786947_2	302	GHASALAEIQHR <mark>FT</mark>	HLQARYRPWVVPV	AKL	LTGEGS	MWMTPGEPVDFPIPAAQHKVLDALAECRATPDSLES
000001279808 52	288	SVRSHFYEELHEFE	RTELLLRFHRCQI	QAGEP	QALENQEL	KWVSPDEFDSVGFLKTNIKALEKLKSMRV
000000358065_2 000003745941 1	269 269	DCMTDTIMBURC	MSOTTEDING	KKK	LKNG	LWVEKTKLENHMIPTFTKKIFASVKHNL EWIDLEQIKKVTLSGPHKRWINEILTDFNKQK
000003745941_1 000004187032_4	269 268	KNENENENEVA	NWNWNIKIOAIKA	NSEA	DHAEM	EWIDLEQIKKVTLSGPHKRWINEILTDFNKQK
000004187032_4	269	FNTSLNKKIN <mark>I</mark> KMS	NMDMKIILNKKNK	LIK	IKNS	YLVDKKNIKDLILPSFTKKIFNSVSNYL
000005543774_1	231	KNWKFLCNYKNSIS	NKKLNLNLYYKFS	SRI	PSKY	NWYSL-KKNKEFIPTFTKKIFKQITHLY
	253					
	273	QNWIFLKNYK <mark>N</mark> S <mark>IS</mark>	NLKLNINLYYKFS	KKI	PRSF	nwysl-nknner1psftk
000002718976_3		MODERNI CHIMINE	NTV MITHER TOWNS	KNK	DKKV	MWYPIDRRSNEFIPSFTK
000002718976 <u>3</u> 000002992548_1	274	NGWIILCNIKNNIS	MIKMNINLFIKFI	10010	FILLE	
000006211484_1 000002718976_3 000002992548_1 000000456751_1	241	RGWYYLCSYKNNIS	NIKMNIDLFYKFT	KKI	PKKF	NWYSIDRSNQEFIPSFTKKIFKKIAKVYS
000002718976 <u>3</u> 000002992548_1	241 272	REWNYLCNYKNNIS	NIKMNINLFYKFT	KNK	PKKF	NWYSIDRSNQEFIPSFTKKIFKKIAKVYS DWYSVDKSSQEFMPSFTKKII