

**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 C-terminal 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: 9 5 57 67999 5 5 65 7 55 6 9 98989 9 5 8 65969 67 66 5 859

sp P17802 MUTY ECOL 28 KTPYKVVWSVLMQITQVATVTP-YFFERMARFPTVTLDAALPDEVLHWLTGVLGYARARNLHAAQQAVALTHGKGFTPEEFEEAALPGVGRGTAGAGLSLSLGHFPFLIG 1400

sp P83847 MUTY GEOS 37 RDPYKVVWSVLMQITRVEVTTP-YFEQIFDRFPTLEALAADEDEVLKAWEGVLGYSRVNRNLHAAVEKVTYRKGKGVDPDDPGLGKLPGLGVTAGVALLSLAYGFPFPAVIG 146

0.000003652391 2 37 PDPYKVVWSVLMQITAAVAVTP-YFFRRFTTQVLAALAAADGVDMGAWAGLGYARARNLHAAKVCVCTHAGAFITPTVYAGLIALPGIGFTAGVALLSIADFAREVAVVIG 149

0.000000031207 6 26 EDPYALIVWSVLMQITRTVTTP-VYHFLFKRFPDKSLARLQGVLEWAGLGYSRGRNLHAAQVTVLNDHGGIFPTFDELKLGKLPGLGFTAAALCSIAYGEPFLAVIG 138

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0.00001007148 4 35 RDPYVWVWSVLMQITTAATVTP-YLDRFLKRPFTVEALSAGAEVLNVEWGLGYSRARNLSHAKGLVEWEGQWRNTATEITQSLPGVGTAGVALLSIADFAREVAVVIG 147

0.00001092848 3 48 PDPYRVWSVLMQITTVGAVTP-CECFERLFRFPTVEALARDLVEKMAWAGLGYSRARNLHAAQAEVAHRHGGVPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 160

0.00001151029 1 1 -----WISVLMQITQVATVTP-YYSNLFHKGPTLADLAMAHTHRAVQLQAWAGLGYARARNLHAAQCAVMEKYGFTFPFKTEKLEKLPGLGHGTAAALVAIHAQGSVAVIG 167

0.00001179282 1 58 PDPYVWSVLMQITTTAAVTP-YFFRFTTRFPDIFALAAPEHVAWSAWAGLGYSRARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 169

0.00001180648 25 40 RDPYKVVWSVLMQITTAATAVTP-YPHAFITRFPPTLILALASANDDDVMGAWAGLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 152

0.00001206161 4 28 EDPYKVVWSVLMQITTVAVTP-YFNSWKLEFPTVSGVAGARLSDLSWAGLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 150

0.00003607531 2 36 KPYKVVWSVLMQITQVTVTP-YFQHLKCTVPTIDELANASLDDVLKAWGVLGYSRARNLHAAKLCINDFGRFPNTFTEQLEQLPGIGGTAAALVAIHAQGRRAAVVIG 148

0.00003872363 4 36 PDPYVWSVLMQITTTAAVTP-YFNTFTKRWNPALATAQADDAWAEWAGLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 148

0.00004820107 4 34 PNFYVWSVLMQITQVTVTP-YFTFKVERWAPHDHSHADRDVHEWAGLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 155

0.00005774797 1 29 PNHYVWSVLMQITTTVATVTP-YFNTFKVERWAPHDHSHADRDVHEWAGLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 155

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0.00004546210 3 31 PSKYKTVWSVLMQITQVNTVTP-YFHRMFERPTTEALANASDEVLKAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 143

0.00004551008 5 34 PSKYKTVWSVLMQITQVATVTP-YFQIFQRPFTVEALSILDLKAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 152

0.00002511148 4 26 KPYRVWWSVLMQITQVSTAIP-YEFKIFIEIDPVKLSLSDLDVLKAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 138

0.00000577378 2 14 KPYRVWWSVLMQITQVSTVTP-YFQKFIIEIDPVKLSLSDLDVLKAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 126

0.00000598175 3 37 INPYRVWWSVLMQITQVSTVTP-YFQKFIIEIDPVKLSLSDLDVLKAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 149

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0.00001515736 6 18 RDPYRVWSVLMQITQVSTVTP-YQYRMKSPSTEQIATASQDEVLHAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 116

0.00001682161 2 25 PTPYRVWSVLMQITQVSTVTP-YQYRMKSPSTEQIATASQDEVLHAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 137

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0.00002038721 4 40 KSPYHIVWSVLMQITQVATVTP-YFHKIFNSFPKLSLAKSDLDVLKAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 143

0.00002523527 15 43 RDPYRVWSVLMQITQVAAVTP-YFQYFVAALPTAALAAASDEVLHAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 155

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0.00002979152 3 34 RPYRVWWSVLMQITQVSTVTP-YFERWIKITFTGLKLANAPQKILKAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 146

0.00003249034 1 46 KSPYHIVWSVLMQITQVSTVTP-YFERWIKITFTGLKLANAPQKILKAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 148

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0.00003766664 5 41 PTPYRVWSVLMQITQVSTVTP-YQYRMKSPSTEQIATASQDEVLHAWGVLGYARARNLHAAQCAVMAAGRFFPTFDEAGLKGALPGIGDTAAALVAIHAQGRRAAVVIG 153

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Conservation: 95 9 75 87 85 9 5 9 8 9 5  
sp\_P17802\_MUTY\_ECOL 141 VKRVLRYAVSGWPG---KKEVENKLSL---SEQ-VTP-----AVGVERFNMAMDLGAMICTRSKPKCS---LCPQNGCILAANNWSWALYVGRKKPK--- 225  
sp\_P38447\_MUTY\_GEOS 142 VMKRLSLFLVTDIDIA---KPSSTRKFEQI---VRS-IMA-----KRNPAFNAELIELGALVCTPRRPSCL---LCPQVQAYCAAFAGVAELVPKMK--- 231  
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c 000000430975 4 151 VERVSRIFPTQPIPLP---LSRPTLRQLA---AAG-LTP-----SKRPGDYAAVMDLGSIVCTPKSPKCM---VCPIDCLANISCTPRPKTP--- 222  
c 000001007148 4 148 TARYFARLIALRSIDLH---SGEGKQKMSL---AER-LTP-----KPRGDYAAVMDLGSIVCTPKSPKCM---VCPIDCLANISCTPRPKTP--- 231  
c 000001092848 3 161 VERVITRLRAIGTPLP---AAKPOVRKA---VAA-LTP-----AERPGDYAAVMDLGATICTPRRPSCL---LCPQVQAYCAAFAGVAELVPKMK--- 243  
c 000001151029 1 108 VERVSRIFPTQPIPLP---LSRPTLRQLA---AAG-LTP-----SKRPGDYAAVMDLGSIVCTPRNPKCN---VCPIDCLANISCTPRPKTP--- 190  
c 000001797282 1 170 VERVLSRAYAEAPLIP---GSRPEIRLL---TQA-LTP-----PDRPGDYAAVMDLGATICTPRKPCA---LCPWMRRCARSLRGTAQSPRKTIP--- 252  
c 000001803648 25 153 IERVMARMDIHSLPL---SAKPELLAC---AAS-LTP-----DPRGDYAAVMDLGATICTPKSASCG---VCPWFSFALRINGTAQVSLPKTKTP--- 235  
c 000002078955 4 153 VERMARMLRHHTPLP---AAKPELFSE---ATA-LTP-----DLRAGDYAAVMDLGATICTPKSPKTCG---VCPWFSFALRINGTAQVSLPKTKTP--- 235  
c 000002106160 4 141 VNRMARMLRLRLRFTTP---YNNKRVLSL---LIR-WLD-----LRPGDYAAVMDLGSIVCTPKSPKCM---VCPIDCLANISCTPRPKTP--- 222  
c 000003360753 1 2 151 VERVITRVFGIFKPLP---EAPRIIKDCAAK---LAT-KTP-----RGRPGDYAAVMDLGATICTPRKPKLCLD---LCPWERYKILANQNFVDVPRKAPK--- 236  
c 000003872363 4 149 VERMARMLFNVTPLP---AAKPELTAH---AAA-LTP-----VDRAGDYAAVMDLGATICTPKSPGCG---ICPCTEYALPEGDAANLPLRPK--- 231  
c 000004820107 1 156 IERIMARLYAITEPLP---DSKANLNLAA---GLS-EER-----KDRPGDYAAVMDLGATICTPKSPKCS---LCPVNDSCITAKRQGTAEISLPIKIKQ--- 222  
c 000005774797 1 140 VERVITRVFGIFKPLP---EAPRIIKDCAAK---LAT-KTP-----RGRPGDYAAVMDLGATICTPKSPKCM---VCPIDCLANISCTPRPKTP--- 222  
c 000005867021 3 153 VERMARMLRHHTPLP---AAKPELTAH---AAA-LTP-----VDRAGDYAAVMDLGATICTPKSPGCG---ICPCTEYALPEGDAANLPLRPK--- 231  
c 000004546210 2 144 VKRVLRSFFGKMGWSG---ESKVSKEMLWL---SAK-SLP-----VDNFEIYTGIMDLGATVCLPKNPNCN---NCPINVKYSYLINQVLVDSKPKLA--- 228  
c 000004551008 5 144 VKRVLRSFFGKMGWSG---ESKVSKEMLWL---SAK-SLP-----VDNFEIYTGIMDLGATVCLPKNPNCN---NCPINVKYSYLINQVLVDSKPKLA--- 228  
c 000002511148 4 139 VKRVLRYAIEGKLEK---TSKKRKLWQV---SEG-LLP-----DNKIEVYTAIMDLGATVCTKSNFVCLN---LCPIDNCAARRAGTAELVPKMK--- 211  
c 000000577378 2 127 VKRVLRYAIEGKLEK---TSKKRKLWQV---SEG-LLP-----DNKIEVYTAIMDLGATVCTKSNFVCLN---LCPIDNCAARRAGTAELVPKMK--- 211  
c 000000598175 2 150 VKRVLTRVFGVMDGPG---KADVLKWLML---AEQ-TTP-----ASRNADYTAIMDLGATICTRSKPRCE---DCLPDKADLAFQGGNQTYPTPKSPK--- 234  
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c 000001345122 1 117 VKRVLTRVFGVMDGPG---KADVLKWLML---AEQ-TTP-----ASRNADYTAIMDLGATICTRSKPRCE---DCLPDKADLAFQGGNQTYPTPKSPK--- 234  
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c 000003492925 4 134 ISKIITVLMWPG---QTVTEV---ANE-LVS-----LSQSGYANNAMDLASSIRAGNPVE---GALGETYFSDAICRLFKPKRKKPEKKIK 219  
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c 000003948186 72 140 VIKVLSRLCLAEKLEP---SDKLRLRI---AYN-LVP-----KRNFDYTAIMDLGATICTRSKPKCL---VCPIDNCAARRAGTAELVPKMK--- 211  
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c 000001595844 4 240 VFRVLARYTANFIDIG --TPAGKKEFTLL-- ANQ-LLD-- KKQPKGFNAIMDLGALVCKPTNPDGS-- NCPQIKCQAFSQDITIAQLPVKEKK-- 224  
c 000001719155 2 244 VKRVLRSRLFLKENGEE --TRKSENILWET-- MQQ-LLP-- ETGAGNFNAIMDLGATVCLPKNPICL-- LCPLEKRNQAYQKQGVNLYPPKRA-- 228  
c 000002363038 6 246 VKRVLRSRYFALEGWPG --EKRVENQMMGL-- ADN-LTP-- ETDADYTTAIMDLGATLCKRSKPNCN-- LCPVKTCRALTKDQVASFNPSPK-- 233  
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c 000002566035 2 241 VKRVLTRYHGIKGWPG --EKKIENKLWSL-- AEL-YTP-- RGLTKYTTAIMDLGATVCTRRKPCD-- ICPLTLTCTFAREMGQHDFFGPKGP-- 225  
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c 000002657784 4 240 VKRVLARYKKEGDLIS --KALNITKLWRI-- SES-LTP-- EERVDLYTAIMDLGALVCTKSSPKR-- ICVPSRDCIAPFNKILQVLRPKLT-- 222  
c 000003800129 15 243 VKRVLGRLYNQESY --QKKFWEFL-- SKK-ILD-- KSNFLPQCGIMDYGATCTHINPCD-- ECPLEGRWCLKSGNSFYVYKKK-- 210  
c 000003716781 1 240 VKRVLARHFAVEGVV --TKAEPRREIEGL-- AAA-LVG-- GVNDSGWNALMELGATVCLPKDPRD-- SCVMTCECARARGARVETPLPVR-- 225  
c 000001556689 3 241 VARIMCRALAGIADDTT --RSKVRQRLAEM-- AAD-AIE-- CHPPGTFFNAIMELGARVCTPRSPRD-- CQCPSSCECAHELGIEEQIYPPRKS-- 215  
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c 0000044255004 2 246 ARRVYRLRLSLITN --LRANINET-- AEQ-MVS-- HSRPQDFNAIMELGATVCLPGKPRCE-- RCPPLAYRCQARSVGAFFQLRLPRTK-- 225  
c 000000605438 3 241 VKRILYRFFFAVKEA --NDKGLWEM-- AED-LYD-- KDNAYITNMDIGSALCTHGNPLCT-- CQPFVSLCQKGEPL-- LYPTKGGK-- 218  
c 000000581237 15 241 VKRILYRFFAMTSC --NDKGLWEM-- SYE-LYD-- RENSIYITNMDIGSALCTHGNPACD-- VCPFEPLCQKGEPL-- LYPEKVKK-- 218  
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c 000000536725 3 241 VNRRVSRFLYQDPPS --KNKKMEKFP-- MSI-IIN-- DNRPGDINAMDLGRVYCKPSTPLCD-- ECPITNGCKALKLIGQSDPLPIKIK-- 221  
c 000001684786 4 240 VERNVTRKILRLAENPR --QVSTKGRKLEI-- AGG-WMP-- ADKASSFNAIMELGALICSVPSPDCP-- SCVPREVCARAEQDGPENFPLPKP-- 221  
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c 000002040695 2 240 IARVSRVRLVQPSGKE --ALTPSILRQP-- ISL-FLP-- RGRASDYNAMDELGALICRPNFQCS-- LCPITKTLCKSAHNTVPLPHKTK-- 232  
c 000003263657 32 240 VTRVLSRLYRHEHAT --KGPARKRFPFL-- ADG-LIQ-- KQQAADFNAMDELGATVCLPKPRCT-- VCPVCHRCARFHELSDPGSLPYKP-- 238  
c 000005989041 2 240 IERVITRIFGICTPFP --EAKTIVDCAAK-- LAP-KIT-- KGRGDFYTAIMDLGALVCRPKPLCD-- LCPMKCKILANQRNFVDQPVQKSK-- 236  
c 000002391082 2 249 VTRVLCRLRIEEDPR --RTAIEAELIAA-- GEA-LIA-- RGEAGDFNAIMELGARVCTPRNPICP-- TCPVQWQCAQAEGLDPSALPYKVP-- 233  
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c 000006007075 1 240 VERIIRKILNTEKE --ISKENILKE-- KKI-LGM-- SDRSSDYAALMELGALVCKPKNPYCK-- KCPITNCKSAHNTVPLPHKTK-- 223  
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c 00000498472 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000004615912 3 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000004766858 2 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000002747260 18 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000005371561 38 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 00000169465 2 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000003254110 11 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000004750284 20 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000000141782 15 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000002717847 8 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000004405479 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000006126673 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000000339186 3 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000003029168 2 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000001863436 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000002830137 4 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000004612302 3 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000001933926 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000003136344 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000005849454 9 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000001169194 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000002786947 2 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000001279808 52 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000000358065 2 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000003745941 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000004187032 4 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000006067315 3 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000005543774 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000006211484 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000002718976 3 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000002992548 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000004656751 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 00000265634 1 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
c 000004232403 2 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
6u7t.after.N146.pdb 240 VTRVLSRLILRLNPT --YNNRRIRNR-- LTK-WMD-- PERPGDINAMDLANKICRVDHAYCN-- TCPIDRVCMARKMIPESYPTIKNK-- 225  
Consensus\_aa: 1.RVhsRhh.lp.....ppph.h.....s.....hhs.....ppsp@QhM-lGthlC..ppP.C.....CP1...C.t.....hP..... 225

## Conservation:

sp_P17802 MUTY_ECOL	226	--- QTLFE ---	RTGYF ---	LLIQ ---	HEDEVLLAQRPPS -	GLWGGLYCFE -	QFADEESLRQ ---	WLAQRQIA ---	A	281	
sp_P83847 MUTY_GEOS	232	--- TAVKQ ---	VPLAV ---	AVLAD ---	DEGRVLLIRKRST -	GLLANIMEFF -	SCETDGADG ---	KEKLEQ ---	V	294	
c_000003652391_2	233	--- QPKPT ---	RYGIV ---	YLARD ---	AHGAWLLERRPDK -	GLLGGMLGWF -	TSNDNDAPG ---	DQPPFA ---	A	286	
c_000000031207_6	234	--- RTEEQ ---	QWMAA ---	AVVW ---	CGDQVVLWIGDG -	ELIAGHRGT -	LARLSGSGGL ---	DADKMIG ---	GA	286	
c_000000430975_4	224	--- RKQQR ---	RYGVV ---	YWIER ---	RDGALISLRQRPEN -	FIQGGMTET -	GSLLWASPL ---	SRH ---	A	293	
c_000001007148_4	232	--- RDVID ---	VFELL ---	VVMR ---	RGRKLLILQHPPD -	ERWGGWGEFF -	ALSRDALARS ---	RFDERLIE ---	V	297	
c_000001092848_3	244	--- AAKPS ---	RKGA --	FVAVR ---	ADDAVLLRRRPPD -	GLLGGMEFF -	TSGWSAGSD ---	SASAFP ---	A	302	
c_000001151029_1	191	--- TKRKL ---	RYGVV ---	YWIER ---	RDGAVILRQRPEN -	GIQGGMTET -	GSLLWAAFL ---	SRH ---	A	250	
c_000001179782_1	253	--- AKGAL ---	RKGA --	FVAVR ---	SGDEAVILRTRPDE -	GLLGGMALEF -	GSAWEPVDY ---	VAAAL ---	A	312	
c_000001803646_25	236	--- PVKPT ---	RYGIA ---	YIARR ---	PDGAWLLERRPDK -	GLLGGMLGWF -	GAQWQDAV ---	DKPPVS ---	A	289	
c_000002078955_4	236	--- PVKPT ---	RYGIA ---	YIARR ---	PDGAWLLERRPDK -	GLLGGMLGWF -	GAQWQDAV ---	ENPPVS ---	A	289	
c_000002106160_4	224	--- QSLFW ---	QNVLT ---	GVIV ---	KRDSFLIIKRAYG -	KHLNNIMWLE -	GGRTLTKNN ---	PHPOLLE ---	V	286	
c_000003607531_2	237	--- VKKAV ---	RKGVV ---	FLAAL ---	SDGSLFLRRRPPD -	GLLGGMEFF -	STWLLERSL ---	SPK ---	T	296	
c_000003872363_4	232	--- PAKVI ---	RYGTA ---	YIARR ---	HDGAWLLERRPDK -	GLLGGMLGWF -	GSEWGEEAV ---	ENPPVS ---	A	285	
c_000004820107_1	241	--- KPKPK ---	RKGRV ---	FWISD ---	DSGNILFIRRRPEN -	EMLGGMLGLE -	TTEWDIRP ---	IKLP ---	Q	291	
c_000005774797_1	223	--- RSKKK ---	WNAFA ---	YVIYN ---	ADGNIGFVRDDK -	ALLGGWALEF -	TSDWSTSPV ---	FQP ---	P	275	
c_000005867021_3	236	--- PVKPT ---	RYGIA ---	YIARR ---	PDGAWLLERRPDK -	GLLGGMLGWF -	GAQWQDAV ---	EKPPIV ---	A	289	
c_000004546210_2	229	--- KKKRT ---	ESMYF ---	LMIVF ---	DGKGLFLEKRRPK -	GIWGGIWSFF -	QIQLADDPQI ---	WCEQOFTNN ---	I	286	
c_000004551008_5	229	--- KKKRT ---	ESTYF ---	LMIVF ---	DGKGLFLEKRRPK -	GIWGGIWSFF -	QIQLADDPKT ---	WCEQOFTNN ---	I	286	
c_000002511148_4	224	--- KSKPT ---	KKVVV ---	LLPQG ---	PSGEVLLERKRPK -	GIWGGIWAFT ---	EAKKNELEL ---	ELSRKPTNK ---	I	281	
c_000000577378_2	232	--- KSKPT ---	KKVVV ---	LLPQG ---	PSGEVLLERKRPK -	GIWGGIWAFT ---	EAKKNELEL ---	ELSRKPTNK ---	I	281	
c_000000598175_2	215	--- KVMPE ---	KQAIM ---	VILKN ---	SKQEVFMQRPVP -	GIWGGIWSFF -	QFKRAFABE ---	WKSNSYKLI ---	I	292	
c_000000754627_3	232	--- KAVKE ---	KSCDW ---	LIIK ---	HNDKVLMEKRPNS -	GIWGGIWSFF -	EFNYSLELT ---	FLAQQGLK ---	A	286	
c_000000811118_1	223	--- KEKIE ---	KKIDW ---	LIIK ---	TGNKVLKRRKPK -	GIWGGIWSFF -	EKDFSSKKI ---	SKI ---	L	273	
c_000000896887_2	227	--- ISSKK ---	IEVSA ---	GIII ---	KMKKVYIQRKVN -	GLMGIMWLEF -	GGKREQES ---	EIKEELRVN ---	V	289	
c_000001176522_24	248	--- KVMPE ---	KKVCW ---	QVSLI ---	QGCWVLVQNPAP -	GLMGIMWLEF -	EGNR ---	FLDGNEMVAT ---	I	261	
c_000001345127_1	202	--- KIIPT ---	KEKFT ---	LIIVT ---	EARFVALLRRPDK -	GIWGGIWSFF -	EFISVQIDIL ---	FLDGNEMVAT ---	I	261	
c_000001515736_6	220	--- IKRSS ---	ESNWL ---	LIAVD ---	ARRKVLQKQPSA -	GIWAGIWSFF -	VTEHYAALQS ---	YAOAANSQD ---	GT	278	
c_000001682161_6	223	--- KTIPT ---	KERWF ---	LVLIT ---	KEGNIGLTKRPAP -	GIWGGIWSFF -	EFDEVKILLEN ---	FLTDNNVKCL ---	L	282	
c_000001923643_29	230	--- LKRSR ---	EAWWL ---	LIAVD ---	QGGVWLERRPDK -	GIWAGIWSFF -	VFNREALEQ ---	AAARHWAA ---	RS	288	
c_000002030994_5	224	--- KEMPE ---	KHTVM ---	LIIQN ---	DQGEVLMQRPVP -	GIWGGIWSFF -	QFKTALAE ---	WLDTSFGMS ---	L	281	
c_000002038721_4	226	--- SKQKE ---	KNNIN ---	LLIA ---	SKDKVLLKRRNPK -	GIWGGIWSFF -	EANSIYNEK ---	FNIL ---	L	275	
c_000002523527_15	251	--- AALPE ---	RSTVM ---	LIVRH ---	GRDVLLQRPAP -	GLMGIMWLEF -	EMPVDTVPD ---	SEAAEESA ---	P	315	
c_000002608528_2	224	--- KVMPE ---	KQTMV ---	LIIQN ---	KGQEVFMQRPAP -	GIWGGIWSFF -	QFDNHNVLV ---	WLDNNYVS ---	F	281	
c_000002961510_2	227	--- VFSKK ---	IEVSA ---	GIII ---	KMKKVYIQRKVN -	GLMGIMWLEF -	GGKREQES ---	EIKEELRVN ---	V	289	
c_000002979152_8	232	--- KDKRI ---	KQSMV ---	LYVSN ---	ENADVLLERRST -	GIWGGIWSFF -	EFETNVKAND ---	WLVTKTFALE ---	S	289	
c_000003248015_3	247	--- RKKGR ---	KQSMV ---	LYVSN ---	ENADVLLERRST -	GIWGGIWSFF -	EFETNVKAND ---	WLVTKTFALE ---	S	289	
c_000003294679_3	229	--- KTNPL ---	KTNLM ---	LFLRF ---	EDRIYLLERRPDK -	GIWGGIWSFF -	EISKDCSVSD ---	WYQSRFGAY ---	P	285	
c_000003333364_1	225	--- KPAVP ---	VDVAS ---	GVIV ---	HDGYIFIQKRPD -	GVWPGIWSFF -	GGTVEKGET ---	PAQCVRV ---	V	287	
c_000003402697_5	212	--- TEKPKRKRH ---	IEVGI ---	ACTIV ---	REGKYLQARPKG -	KSFEGSWEFF -	GGKREKGEN ---	FRECVKR ---	V	287	
c_000003492925_4	212	--- VVPT ---	REENT ---	MLYV ---	YNDKLSLTQRTG -	KFLHGLWGEF -	NTEMPL ---	ETQEEVGD ---	V	252	
c_000003766664_5	229	--- RPPKK ---	IALLVAC ---	VIRO ---	EQGAVLLTQRPKE -	GLFGIMWLEF -	LKEVDETPS ---	KAGVGR ---	V	301	
c_000003948186_72	236	--- NNPTT ---	RHTVM ---	LIIEN ---	TAGEVLLERKPAQ -	GIWGGIWSFF -	ELATGQNAIT ---	YCEQELQIA ---	V	283	
c_000005057120_4	225	--- KVLAV ---	QGLIF ---	LMLQD ---	QGVVFLLEKRPAS -	GIWGGIWSFF -	EFQSFAEIKS ---	WCLEN ---	D	281	
c_000005590109_5	225	--- KSLPV ---	KSTIV ---	LMLQD ---	QGVVFLLEKRPAS -	GIWGGIWSFF -	EFQSFAEIKS ---	WCLEN ---	D	281	
c_000006063368_2	224	--- KKKRT ---	KHVVH ---	LITVS ---	HKGKVLQKRLAK -	GLMGIMWLEF -	EKEKEMLEK ---	ECKSTFOIK ---	D	281	
c_000000467631_2	204	--- KTLFV ---	KNIME ---	LMLKD ---	ELGLVLLERKPPS -	GIWGGIWSFF -	EFETLSLEIQS ---	FQCOQ ---	N	260	
c_000000788235_1	225	--- KTLFE ---	KKAVF ---	LLLIN ---	INHEIFITIKRPPS -	GIWGGIWSFF -	QFDTYLQACQ ---	WYEQFSTH ---	L	282	
c_000001187176_11	226	--- KRIPV ---	RQCLM ---	PLIVN ---	PQGDVILQRRPDS -	GIWGGIWSFF -	QLDSREQLDA ---	LIVAQ ---	GW	282	
c_000001660697_64	231	--- KALPE ---	RAATM ---	VIALH ---	GETVTLQRRPQR -	GIWGGIWSFF -	LVGMSDDALDAH ---	LADATVQAALAYGV ---	V	296	
c_000003378864_2	238	--- KPVFH ---	HHIGV ---	GVIVK ---	DDQVLLQRRPPE -	GLLGGIWEFF -	GGKQEPAT ---	TEETVREIREELGV ---	V	300	
c_000003910742_3	226	--- KVIPE ---	KNAVW ---	LMLIN ---	NKDEVEFMQRPAP -	GIWGGIWSFF -	QFDDYDQACA ---	WHNNYFGFP ---	C	283	
c_000004116181_2	226	--- KQKAT ---	RTCVF ---	LILVN ---	AKQELLQKRPSP -	GIWGGIWSFF -	EVEDTIEAII ---	WCSKR ---	K	248	
c_000006223903_1	192	--- RFRFR ---	REVVW ---	IMIKD ---	SRDRVLLERRASS -	GIWGGIWSFF -	ECFVEALEP ---	WCRMRFGAG ---	I	283	
c_000001029068_2	199	--- KKKPV ---	KTTAM ---	LIFDN ---	KGQGVYLLKRPAP -	GIWGGIWSFF -	ECSATDKAIT ---	KTANHHFQ ---	A	256	
c_000001128125_11	234	--- KDKPV ---	KRAFF ---	LLILL ---	SERQVLLERKPPQ -	GVWAGIWSFF -	EFDSLQGTKE ---	SIESQGT ---	I	290	
c_000001595844_4	225	--- IKRKT ---	RYFYF ---	FVFER ---	KGSDDYIKRRTK -	DIWQSYIEFF ---	NIESKPTLN ---	FQEKYPRIK ---	F	287	
c_000001719155_2	229	--- APSTK ---	IAVSA ---	GVIV ---	RNNRYITQKRKA -	GLMGIMWLEF -	GGKFSGES ---	PEQCLHR ---	I	291	
c_000002363038_6	234	--- KKKPV ---	KQKWL ---	LILQN ---	SAEQVFLYKRPQ -	GIWAGIWSFF -	EFDSYDRAVD ---	FLNGEIRH ---	DA	292	
c_000002561400_1	190	--- KKKPV ---	KQAWF ---	VQQLN ---	AKQVILYKRPQ -	GIWAGIWSFF -	EFCSVTDAKT ---	YLQQTGPG ---	L	246	
c_000002566035_2	226	--- AVTPE ---	RDTYF ---	AIMEN ---	NNGEILLERQPS -	GIWGGIWSFF -	EFSSFLRIE ---	MIKRYKGFN ---	I	283	
c_000002598045_3	226	--- KSKLT ---	KKVLV ---	LLPQG ---	PSGEVLLERKRPK -	GIWGGIWSFF -	ETERKAELEL ---	ALSRNFDNS ---	I	281	
c_000004188575_41	226	--- KQSHW ---	KQSHW ---	LIIIT ---	DDRVVLLSKRPK -	GIWGGIWSFF -	SFDTHYL ---	EKLHNTL ---	K	279	
c_000000420049_1	224	--- KILPV ---	REKRL ---	LIIIRN ---	KQGHVLLERKPPS -	GIWGGIWSFF -	ELTLDKSLAE ---	SIERNNWLS ---	V	281	
c_000002139456_2	224	--- KILPV ---	REKRL ---	LIIIRN ---	KQGHVLLERKPPS -	GIWGGIWSFF -	ELTLDKSLAE ---	SIERNNWLS ---	V	281	
c_00000353614_2	226	--- KILPI ---	QOKRL ---	LIIIRN ---	EQGAVYLLERKPP -	GIWGGIWSFF -	ELALEAPIIT ---	EVKNTWQII ---	V	283	
c_000002657784_4	223	--- KKKPF ---	KTFVW ---	LIVMN ---	KMGKVLKRRNPL -	GVWKGIMWLEF -	ESENIDQLGK ---	ECLTMFEKR ---	K	280	
c_000003800129_15	211	--- TPKIK ---	VFLNY ---	EIYK ---	RDGCTVIMKRMPL -	GVWNEIWMPE ---	YKIVE ---	ECLTMFEKR ---	K	280	
c_000003716781_1	216	--- TPTID ---	VELEM ---	FLVH ---	DHGRVLLERRDEG -	GVWAGIWELE ---	TREVAALRLIF ---	PAELELEL ---	---	272	
c_000001556689_3	216	--- LVKA ---	VTEYA ---	AVIE ---	DNGRLLILFRQRP -	SIVSDMEFF ---	TLDRLADTSRSSLTEKPASSHRAEAKLSR ---	YIKEQLGWS ---	V	293	
c_000001834452_1	196	--- INWKE ---	HYLLA ---	GVAS ---	CPSGVLLERKPE -	GVWQGLWGEF ---	SVFYDQKEE ---	PDL ---	AWREFQPKR ---	G	253
c_000004255004_2	226	--- TKA ---	VQWFL ---	TLAK ---	WRSRILLRRRPDK -	GLASIMWLEF ---	TPENLPAEL ---	IDETL ---	---	274	
c_000000605438_3	219	--- IKKPI ---	RKRAL ---	LIYA ---	KNDKYALAQNEE ---	RLLSGLWGPF ---	QEEDEF ---	QEEDEF ---	I	262	
c_000000581237_15	219	--- IKKPI ---	RKRTL ---	LIYH ---	KNDKYALAQNEE ---	RLLSGLWGPF ---	QEEDEF ---	QEEDEF ---	S	262	
c_000002529579_2	219	--- IKKPI ---	RKRTL ---	LIYH ---	KANDYALAQNEE ---	RLLSGLWGPF ---	QEEDEF ---	QEEDEF ---	L	262	
c_000006097838_1	208	--- APVSK ---	RFRFG ---	FIIA ---	WHGNVFMQRPSP -	EVNAGSWEFF ---	NWLVDDTQ ---	LASTKIALG ---	Q	267	
c_000000583727_6	234	--- AATIN ---	RRFPG ---	FLIA ---	WHGNVFMQRPSP -	EVNAGSWEFF ---	NWLVDDTQ ---	LASTKIALG ---	Q	267	
c_000005807640_2	207	--- AATIK ---	RRFPG ---	FLIT ---	WHGNVFMQRPSP -	EVNAGSWEFF ---	NWLVDDTQ ---	LASTKIALG ---	Q	267	
c_00000134878_1	207	--- ETKRH ---	YDVAV ---	GIIV ---	DKKGLLITKRAKE ---	GLLGGIWEFF ---	GGKIKRNEK ---	TESAIRK ---	I	269	
c_000005136725_3	222	--- HTRFH ---	YDVAV ---	GIIV ---	DKKGLLITKRAKE ---	GLLGGIWEFF ---	GGKIKRNEK ---	TESAIRK ---	I	269	
c_000001684786_4	222	--- RKTIA ---	VELEA ---	GIIR ---	RGRKLLERNEDL ---	DYLEGLWGEF ---	LARPS ---	GOIAA ---	I	279	
c_000002971826_23	232	--- RKTVA ---	VELEA ---	GIIR ---	RGRKLLERNEDL ---	DYLEGLWGEF ---	LARPS ---	GOIAA ---	I	289	
c_000002040695_2	233	--- TKKPC ---	RMGHF ---	FFLVHIPPSSGFPVSLIEKHE -	PLIEGLWLEF ---	---	TQSWVHKHT ---	EAH ---	---	290	
c_000003263657_32	239	--- KKKPF ---	BHDHV ---	GVIV ---	LDKFLIILQRPD -	GLLGGIWEFF ---	GGRRESSES ---	LEHGVTR ---	---	302	
c_000005989041_2	237	--- KVKPV ---	RKGVV ---	FLAAL ---	SDGSLFLRRRPPD -	GLLGGMEFF ---	STWLLERSL ---	SPK ---	---	296	
c_000002391082_2	234	--- KKKPV ---	HYQVA ---	GVIC ---	KGRDILLAQRPAS -	GLMGIMWLEF ---	GGKQEEGT ---	LQCCIQR ---	---	297	
c_000003839553_2	241	--- KKKPV ---	HYQVA ---	GVIS ---	KGRQILLAQRPAP -	VMLGGIWEFF ---	GGKQEEGT ---	LEECILV ---	---	304	
c_000003996707_2	231	--- KPTRP ---	HYEVTA ---	GVIV ---	KGSKLLVLRPSPD -	GLMGIMWLEF ---	GGKREPES ---	LQECILR ---	---	294	
c_000002044706_1	214	--- TKVTF ---	VQVVA ---	LFLAK ---	QDGSFLLVRRPAP -	GLAGIWELE ---	GRELGDGAPE ---	RLASTLIG ---	---	270	
c_000006007075_1	224	--- KKKID ---	KYFLI ---	KIYK ---	KNKKILLIRNTKF -	NFLKNLRIFF ---	MEETPK ---	MEETPK ---	---	267	
c_000002094036_4	200	--- KKKIN ---	KYFLA ---	TLVK ---	NQNKILLIRNTKF -	NFLKNLRIFF ---	MEETPK ---	MEETPK ---	---	244	
c_000002762689_1	224	--- KKKNN ---	KYLLA ---	KVYK ---	DKNKYLLIRNTKF -	NFLKNLRIFF ---	MEETPK ---	MEETPK ---	---	267	
c_000005516980_2	234	--- KKKNN ---	KYFLA ---	KVYK ---	DKNKYLLIRNTKF -	NFLKNLRIFF ---	MEETPK ---	MEETPK ---	---	267	
c_000003920004_1	233	--- KKSRR ---	KYTRAL ---	IILN ---	GSEELIVRRRASK -	GMLPSMLEV ---	NNDVMTKK ---	LLIVRD ---	---	292	
c_000004008511_2	227	--- KSTKR ---	KYSRAY ---	IFYN ---	EKNEILLIRKRPK -	GMLASMLEF ---	NNDVMTKK ---	SIVTD ---	---	286	
c_000004481347_1	234	--- LEQKK ---	KPTRAY ---	ITMN ---	KKNELVLRRRASK -	GMLASMLEF ---	NNDVMTKK ---	DVYKDL ---	---	293	
c_000003787733_3	226	--- KILPH ---	KEIVA ---	GIIV ---	QKQKFLITKRPEN -	ALLGELWEFF ---	SAEQIFNET ---	PIGALRR ---	---	288	
c_00000754657_2	226	--- KILPH ---	KEIVA ---	GIIV ---	QKQKFLITKRPEN -	ALLGELWEFF ---	SAEQIFNET ---	PIGALRR ---	---	288	
c_000000909043_3	216	--- KILPH ---	KIDVT ---	GIIV ---	RGRKLLITKRPEN -	ALLGELWELE ---	QKREFSNET ---	PIGALRR ---	---	288	
c_000004474996_2	225	--- KILPH ---	KEIVA ---	GMIC ---	QKQKFLITKRPEN -	ALLGELWEFF ---	GWEIVSSET ---	PIGALRR ---	---	287	
c_000001463500_11	213	--- SIKNI ---	KHFA ---	ALIV ---	YMKFLIMKRPEN -	SMLGIMWLEF ---	NTQIDKIS ---	DDIQLFN ---	---	275	
c_000001286181_5	218	--- VTKTO ---	ESFHW ---	FIYQ ---	KNNKVMLCNRPD -	GIWPNLVWFF ---	KRELFTQ ---	---	---	262	
c_000001293628_3	223	--- PVKRE ---	ASYAV ---	LIVTN ---	PVGEVLLERRPDK -	GLLGGIWEFF ---	AVEMEAEERNPWGELR -	VGDLSHGRCARLE ---	---	301	
c_000001535696_8	232	--- TKVRN ---	RYFNY ---	ITPIAEADDGSRKTLINQKRGK -	DIWQNLWQFF ---	---	LIEETKREID ---	LEEVKE ---	---	291	
c_000001614067_2	233	--- KEKEE ---	RYGLF ---	FYQLN ---	KDGAFLVETNKS -						



c 000004852258 1 202 --- KTIPT --- KTIAA --- ALVN --- HGDNIFITKRLPK - GLLGGLWELF --- NIELVNGEI --- PEDLLKI --- KFADQFGLT --- I 264  
c 000005254087 1 230 --- KRTHYDVVAGIWNQNG --- VSPG --- EGGRFILIAQRLPN - GLLGGLWELF --- GGRQEPDET --- LPQALER --- EIREEMDM --- I 299  
c 000005603677 1 222 --- LKIKK --- RYFFY --- FVWRG --- TNGGYLRKRQEK - DIWQGLYEFY --- MIELDKPLK --- TSELKT --- LWAHWELIE --- L 289  
c 000003283462 3 213 --- KNIPH --- YDVVV --- GMIW --- KEGRFILIKRQENQ - KHLGGLWELF --- GKIKENNER --- SELALIR --- EIKECDFE --- V 275  
c 000002687221 1 227 --- VSRPH --- HNVAV --- GLIW --- KDRRLIKRQENAS - GLLGGLWELF --- GKIRSGES --- GSSCVVR --- KTQELINVL --- V 289  
c 000003347358 19 244 --- VVPT --- REENI --- LVVR --- YDDKLSLTQREK - KFLHGLWGEF --- SVEVPH --- --- --- 284  
c 000002701031 2 222 --- LKIKK --- RYFFY --- LIIN --- ENEKILIKRQEK - GIWGLYQYF --- LIENSVKKE --- RDIENSKS --- WKGLFKHNS --- I 285  
c 00000582753 3 230 --- RKSTN --- RYFFY --- YIIS --- DSNHLYIKRQEK - GIWGLYQYF --- LSENLIAPF --- NEVLQK --- QIFKNSIND --- F 291  
c 000001713769 5 222 --- NAKPI --- IHFNV --- LVIL --- DSDHMLCMRRIKN - GIWGLYQYF --- MIESKELIN --- KTQVLSN --- EIFKSIAPIS --- NSD 287  
c 000004369364 1 226 --- IKKPT --- RYFFY --- LVVR --- EKDLFLIKRQYK - DIWQGLYEFY --- NIEGMEIN --- ESEIREA --- IQKQFNKL --- V 287  
c 000006057486 30 226 --- LKIKK --- RHFNF --- VVI - N --- NNQHTYTHQRKDN - DIWQGLYQYF --- LIESKHEDTN --- KVIKSSIF --- QOFFKANSY --- T 291  
c 000005494072 10 222 --- LKIKK --- RYFFY --- LVVL --- KXKXITLANKRINK - GIWGLYQYF --- LIETVETITIK --- TLVEHEYL --- EKINKKQL --- VD 289  
c 000001742634 3 225 --- IKIKK --- RYFFY --- LILLIT --- KDNKITLKRINK - DIWGLYEFY --- LIETKTEINEN --- KLIVNDFF --- QKILINDTT --- IN 292  
c 000002826998 2 225 --- IKKKT --- RYFFY --- LVLPN --- GKNITVQKRRTK - DIWQGLYEFY --- LIETDKIIS --- QKELMKS --- ELWKEVSDF --- DF 289  
c 000003159439 6 222 --- IKIKK --- RYFFY --- LVLIN --- SGNKIALQRKHK - DIWQGLYEFY --- LIETLTAIDIE --- QLTETEFP --- HQINEDQA --- I 288  
c 000004487214 1 227 --- LKIKK --- RYFFY --- LILKT --- KNEETILVKRQK - GIWGLYEFY --- LIETEKEINYL --- ELIDHSIF --- KMIENNFN --- D 293  
c 000005037037 2 225 --- VKVKE --- RYFFY --- LVLIN --- IDNTTYIEQRQNN - DIWGLYQYF --- MIETQQLIN --- KPKELEK --- LITNKINVR --- F 287  
c 000001509964 1 217 --- KVKKI --- LYRGC --- AVIL --- FQDGLILCKRQNP - GLLEGWELF --- SVELGKGDN --- LRKALQE --- HLLEELGCP --- F 279  
c 000002498472 1 226 --- KKIIP --- IDMAT --- GILI --- HNGMLFTQKRPD - DVWGLWELF --- GGRMELKET --- PEQTVVR --- EFLEETEFP --- V 288  
c 000004615912 3 215 --- IRKKK --- RYFFY --- FISHP --- EGKILLRKRQK - DIWQGLYEFY --- MLETDEELK --- ISRVQKT --- QWQQLFHGNEKVRVL 284  
c 000004766858 2 228 --- PEITR --- IEKLT --- ALVQ --- NGDCWLVRKRP - GMLGGLWELF --- TWELPSNSN --- AAAMLQ --- QLEDYQVA --- A 291  
c 000002747260 18 232 --- KPKPT --- RHGIA --- YLGRR --- ADGAWLLERRPEK - GLLGGLWELF --- GGDWAETAT --- EAPPID --- A 285  
c 000005371561 38 232 --- KPKPT --- RHGIA --- YLGRR --- ADGAWLLERRPEK - GLLGGLWELF --- GSDWAESP --- EASPECP --- G 286  
c 00000169465 2 234 --- KALPE --- KSTYM --- MVAQ --- FNSQVILEQRSP - GLWGLYQYF --- EVSSIEEGIE --- QIAKRGIS --- V 289  
c 000003254110 11 234 --- KALPE --- KATFM --- MVAQ --- FNSQVILEQRSP - GLWGLYQYF --- EVSSIEEGIE --- QIAKRGIS --- V 289  
c 000004750284 20 230 --- RVTFV --- RQTYM --- LIPI --- FGQVILEQRSP - GIWGLYQYF --- EAQSAEIGIS --- LLAQRGIE --- V 285  
c 000001417182 15 235 --- REKFL --- RQTYM --- LILVD --- GGRVILLERPPS - GIWGLYQYF --- ECPFEVDVES --- YCRHELGE --- V 291  
c 000002717847 9 224 --- KKD --- VILEF --- SLVK --- DGQVFLAQTEAL - GFWKLLWELF --- YKIVN --- --- --- 263  
c 000004054739 1 215 --- QKPT --- VKLN --- FILPH --- TKONELMHKKQAS - EYKESLWELF --- DGDVEKIK --- --- --- G 259  
c 000006126673 1 241 --- KARFQ --- RYGVV --- YWISD --- DGNLILHKKRPEK - GLYGLYQYF --- TSSWETDIE --- TVEH --- PIFISEQIK --- P 301  
c 00000339186 3 199 --- IRYED --- KQIDV --- YLIT --- RGRPYLVQRP - GVNAGWELF --- NSDSGNKYS --- AFK --- --- 247  
c 000003029168 2 230 --- VPLQREE --- VGIWVAG --- KPYN --- ADSLIFIVQRP - GTWAGWELF --- HDEQTTDEP --- HMAAAR --- IAEATVGP --- M 298  
c 000001863436 1 246 --- ARQKP --- VVAARTAVTSWGGA --- EGRRFILMVKRPAD - GLLGGLWELF --- TVEAAGDVA --- PTAQAVS --- RLRLARTGSP --- V 315  
c 000002830137 4 230 --- TQTEH --- VVEAA --- LVIR --- RGRSVLLRHRERD - ERWAGLWELF --- RFFDPDATN --- NGHQQLVD --- KSELRTGE --- I 303  
c 000004612302 3 232 --- VRTED --- LYQLL --- LVIR --- RDRRLILQHPEK - ERWAGLWELF --- ALSRTGPLKS --- RIDELQIA --- SEAEWGCDD --- V 297  
c 000001933926 1 217 --- VARET --- RHGVV --- FWATR --- GDCGVLLRRRPEH - GLLGGLWELF --- STEWRECPW --- RIRSAV --- KAAPFA --- A 276  
c 000003136334 1 229 --- KRKPT --- RYATV --- FWLLD --- GRGNVLLRRRREK - GLLGGLWELF --- STDWLENT --- PTKENS --- MFAPAA --- V 288  
c 000005849454 9 234 --- KQWVD --- LEMVT --- LVHR --- VGVKVLQKRTS --- GWSGLYEFY --- SAICESFATANE --- ASSAESTAH --- SLAREHR --- A 299  
c 000001169194 1 234 --- VPARE --- ISFLI --- VILQT --- EEEGVMLVQRP - GLLAGWELF --- EQELAKPLD --- CAATSRD --- RAEILAMSILGA --- EVV 301  
c 000002786947 2 234 --- APARE --- IFFLI --- VILQT --- EEEGVMLVQRP - GLLAGWELF --- EQELAKPLD --- CSTTRD --- RAIGLAMTLGA --- EVV 301  
c 000001279808 52 234 --- KKTITKRRHR --- IEVGI --- ACTW --- REGKYLQVARKP - KSPFGSWELF --- GGRKREKES --- FRGCVKR --- EIEEEVGLN --- V 287  
c 00000358065 2 224 --- KKIIN --- KFYLA --- TLVK --- HDOQVILLKNDPK - KFLKNNLWELF --- MKEISQS --- SAT --- AIMK --- C 268  
c 000003745941 1 218 --- KIKQE --- TIDRA --- WVEQ --- GGRKLLHRANDKS - RRLSGLEL --- TLDVMG --- --- --- 268  
c 000004187032 4 224 --- KKNKE --- KYFIL --- KVIK --- KQKQVILLVNTKP - NPLKNNLWELF --- MEELSKP --- --- --- 267  
c 000006067315 3 224 --- KFNKI --- KYFEA --- NIYQ --- KQKQVILLKNNK - KFLKNNLWELF --- MEELSKP --- --- --- 268  
c 000005543774 1 208 --- IQSKN --- YDIFC --- YLQK --- NKQKIALTKNDL - GFLKNNLWELF --- IKTATSK --- --- --- N 230  
c 000006211484 1 208 --- IQSKN --- YDIFC --- YLQK --- NKQKIALTKNDL - GFLKNNLWELF --- IKTATSK --- --- --- N 252  
c 000002718976 3 227 --- IKSKN --- YDIFC --- YI - N --- TKQKIALTKNNQI - SFLKNNLWELF --- IKTATSK --- --- --- N 272  
c 000002992548 1 226 --- KKEQK --- YNVVC --- YLQK --- KKEKIALTKNNQI - SFLKNNLWELF --- IKTATSK --- --- --- N 273  
c 00000456751 1 222 --- IKKKE --- INIYC --- YLNR --- YKKEIALTKNNQI - SFLKNNLWELF --- IKTATSK --- --- --- K 240  
c 00000265634 1 193 --- TKEKK --- FNVVC --- YLNR --- YKKEIALTKNNQI - SFLKNNLWELF --- IKTATSK --- --- --- R 271  
c 000004232403 2 227 --- KKIPT --- RNILAA --- ALIE --- YGDIYILSKRP - GQGLWELF --- NIELKNGKS --- PEKSLKE --- SINNHGYFT --- I 285  
6u7t.after.N146.pdb 226 --- TAVQ --- VPLAV --- AVIAD --- DEGRVILRKDST - GLIANNWELF --- SCETDGDG --- KEKLEQ --- MVGEQ --- 283  
Consensus\_aa: . . . . . h . . . . . hh . . . . . phh . . . . . shh . . . . . h . . . . . p . . . . . p . . . . .

Conservation: 6  
sp\_P17802 MUTY\_ECOL 282 DNLITQLTAFRITSHF --- LDIVPMMLPV --- SSFTG --- CMDEGNA --- LWYNLAQPPSPVG --- LAAPVERILLQQLR --- TGAAPV --- 350  
sp\_P83847 MUTY\_GEOS 295 ELTPTVIFSFIAFSLV --- WQLTVFPGRL --- VHGG --- PVEEY --- RLAPPEDELKAYA --- FVSHQRVWREYK --- EWASGVRRPD --- 366  
c 000003652391 2 287 DMKTLRGVETITSHF --- LILIRVIAEL --- PDDI --- TPAVG --- FLISKHAFRPSD --- LPTV --- TQFDGDANG --- 338  
c 000000031207 6 287 ELIGHADRFQDAITSHF --- LFTHPLVYKY --- QGE --- IPAGV --- ETIPIIDGDR --- LAPALHRKSIAAAR --- ELLIEVFR --- 352  
c 000000430975 4 287 DWKPHGRVYFSTSHF --- LELIKMTIN --- EVTI --- DEGT --- FWCRRKEVKAQA --- LPSLHKIMTHY --- KA --- 354  
c 000001007148 4 288 EFYQWMEVFGQSHF --- LHLQIVAMW --- RSGSW --- EGQTA --- EWGIDELATRP --- LSVAGRRVATVRE --- RILRHNGAQA --- 370  
c 000001092848 3 303 PWEFC --- GTVITITSHF --- LALSIVYARV --- ADMP --- APAGS --- WWCAPGLLAGEA --- LPTVMKVVAAI --- SCATHARRPTG --- 373  
c 000001151029 1 251 DMKPGQGLVYFSTSHF --- LELKI --- --- --- --- --- --- --- --- 272  
c 000001797282 1 313 RWRKLRLVLRGCTSHF --- LELTVFVARV --- ALATP --- APAGT --- RFTPRSALDDEP --- LPLGLMRKVLAFH --- DPKPEPEKPR --- 385  
c 000001803648 25 290 DWQDPGAEVRSITSHF --- LRLSLRISV --- GNA --- KPTAG --- HFTADADFPEP --- LPTVMKRYARIAR --- TQFDGDANG --- 358  
c 000002078955 4 290 DWQQLVNAEVRITSHF --- LRLSLRVATI --- GNM --- PPATG --- DFLSKNAFDEP --- LPTVMKRYARIAR --- TQFDGDANG --- 355  
c 000002106160 4 287 TIKNKIGELIRVSHF --- ITLSGFHCLR --- INGSK --- PEVNRFP --- RWIRLNEINQYA --- FPKANHLKLNMQ --- E --- 351  
c 000003607531 2 297 QWVLIAGTVNIAITSHF --- LQLQVRVAV --- NQDT --- QISGG --- IWDVDRILDEFA --- LPLNLMKGVAFAS --- KRIQPLRLDC --- 368  
c 000003872363 4 286 DWQRLDAQVRITSHF --- LRLSLRVVA --- KNV --- IPTVG --- MFIPSDKDFD --- LPTVMKRYARIAR --- AAFDGH --- 351  
c 000004820107 1 276 ESEQTNLSVKSITSHF --- LIL --- --- --- --- --- --- --- --- 311  
c 000005774797 1 276 SEWKGIGQIRITSHF --- L --- --- --- --- --- --- --- --- 293  
c 000005867021 3 287 DWHVLGAERITSHF --- LRLMVHVAIV --- NEN --- SPDVG --- KFIADDCDFD --- LPTVMKRYARIAR --- GSFVGD --- 355  
c 000004546210 2 287 LWDVSWEPFKASITSHF --- LYIHPQIRIM --- DGQFM --- NTAYSKT --- QSFSLNQLDLSG --- LSAPVGLVNNLY --- TQFDGDANG --- 351  
c 000004551008 5 287 LWDVSWEPFKASITSHF --- LYIHPQIRIM --- DGQFM --- NTAHTPKT --- QSFSLNQLDLSG --- LSAPVGLVNNLY --- TQFDGDANG --- 351  
c 000002511148 4 282 LNIKLSKRVKASITSHF --- LEAIPYLAKE --- ENSK --- KYKNS --- VWDYKNNVESL --- LAPVKKITINQIT --- KP --- 344  
c 000000577378 2 270 LNIKLSKRVKASITSHF --- LEAIPYLAKE --- GSKN --- KYKNS --- VWDYKNNVESL --- LAPVKKITINQIT --- KP --- 332  
c 00000598175 2 293 QESIALAAEIKITSHF --- LYIQLPLIN --- EPTIE --- LGVMEDNES --- LWYNITTEFNGG --- LAAPVQTLINQIT --- NIEKEIENGIN --- 369  
c 00000754627 3 287 SDLANVAPITVSHF --- LILRNLHLM --- EKALPD --- VWRDQL --- VWPDLQSGITNG --- LAAPVQTLINQIT --- AIV --- 353  
c 000000811118 1 274 PVREDPSFPEHLSKK --- LLSIVKRLTI --- KNRD --- LSLDRQL --- NWVLSDSVWNG --- LKPVKDLKXID --- --- 338  
c 00000089687 2 290 VSLNKVMTIKITSHF --- VLTIVFNCKL --- QKQKI --- RPDGCEQW --- KWSLSLKKYK --- FPAANVKIVKYL --- EK --- 356  
c 000001176522 24 289 --- GEALSAPRITSHF --- LDITPYLWHT --- HSDD --- MPQOAG --- QWPLAQAALQEN --- IPAANVKIVLEVI --- EYEQNR --- 354  
c 000001345122 1 262 EQAVI --- KITIYSHY --- LRMKPM --- --- --- --- --- --- --- --- 281  
c 000001515736 6 279 RSWQDLPGFLVITSHF --- LHLHPLVIV --- DQAYA --- ALVSEADES --- CWADAAMAEGL --- LAPAPKILLDAEL --- A --- 345  
c 000001682161 6 283 DSVELIKQLKITSHF --- LMMNPMVLQI --- ERE --- AIEEV --- SWFELENLNGV --- LPTPIKILLRESF --- A --- 343  
c 000001923643 29 289 ADWTELEPAFLVITSHF --- LHLHPLVIV --- HGSGP --- DAAMADGQS --- CWADARAWADM --- LAPVVKILLDAQF --- AG --- 356  
c 000002030994 5 282 SEADKLSKIKITSHF --- LHIQPLINT --- ETPLK --- MGVMEDHDS --- LWYNITTEFNGG --- LAAPVQTLINQIT --- DIVKGTQNDIN --- 358  
c 000002038721 4 276 EKEKSLPLVNLSHQK --- LSIPTFKYFL --- KNRD --- LPIDRRGF --- VVWNNKESVWNG --- IPKPVKILLNHL --- E --- 340  
c 000002523527 15 316 ARAYLAGELITVITSHF --- LLIRAIRVDL --- DTVAL --- EGDAAS --- RWLSLDDLDMLG --- TPAPVKILLDAQF --- RFLG --- 383  
c 000002608528 2 282 DEAKLSKIKITSHF --- LHIHPLINM --- ETPLK --- IGVMEDHD --- --- --- --- --- 321  
c 000002961510 2 290 ISLNKVMITIKITSHF --- VTLNVFNCEL --- QKQKI --- RPDGCEQW --- KWSLSLKKYK --- FPAANVKIVKYL --- EK --- 356  
c 000002979152 8 290 PSLQAYAEIEEITSHF --- LSAKVLRIEL --- DSDKR --- LGVMEETNA --- LWYNMHKDNPGG --- FPAPIKILLRNL --- L --- 356  
c 000003248034 1 302 KHPKILCKFRASITSHF --- YDVSITYAIL --- EGE --- LPEFP --- CWWPQKILATIP --- LITVTRKALAVLS --- PNSSDRNDEQN --- 372  
c 000003294679 3 286 LKISRWKTLQKRSITSHF --- LKIHLEKAE --- DIAIK --- NIANDSA --- LWYKSDSQTRIG --- LAAPVKKILETQF --- NIQ --- 353  
c 000003333364 1 288 AASETIAVIRIGITSHF --- VTLTAFLKRP --- GEPFEGW --- PEPVLHATGE --- WWSFPAELDRY --- FPAHRRKLDQMS --- DRMKYAMIV --- 366  
c 00000340297 5 288 SVRPHYFELAEITSHF --- LLLIRPHQKI --- QAGEP --- SPOQEQI --- KWSFDDGDID --- FLKTNHRLKDLK --- EMRV --- 356  
c 000003492925 4 253 CASEYIEGFAITSHF --- LKIVKPYVE --- LLAQEN --- LWYKSDSQTRIG --- LAAPVKKILETQF --- NIQ --- 353  
c 000003766664 5 302 RIEQCSVSRVYITSHF --- MDIANVALSV --- KGRFES --- PALSPYTG --- SVTFSKTIQKLA --- ISKVDKILLNLY --- DTQITQ --- 316  
c 000003948186 72 284 DSCTEALAPRITSHF --- LLITPLHIKS --- SQOTT --- HVMEDQOQ --- LWYNMHKPVASV --- LAAPVKKILETQF --- NIQ --- 350  
c 000005057120 4 282 QSVQIEKQRITSHF --- LDYTAIVLKT --- ENRIN --- NVMESNGS --- KWSLSLKKYK --- FPAANVKIVKYL --- EK --- 356  
c 000005590109 5 282 KLIKQLEQRIITSHF --- LDYTGIMVKI --- ENPIN --- IVMEANQS --- VVWYKSTQLKFLG --- LPTPIKILLQNY --- 346  
c 000006063368 2 282 PSLIQIKVKISITSHF --- LEAIPYLAKE --- KEKK --- SIKNT --- VVWDSKNIESLG --- ITPSVKKTIEIR --- VP --- 344  
c 00000647631 2 261 TSKQQLDQRIITSHF --- LDYTPIEVKI --- ENPIN --- NVMEANQS --- VVWYKSTQLKFLG --- LPTPIKILLQNY --- 324  
c 000007788235 1 283 PSATTESHFSITSHF --- LQAQTLITQ --- STPIK --- RVMEGTPS --- LWYNNTTTFMG --- LAPVKKITINQIT --- ED --- 350  
c 000001187176 11 283 AEPEALSPLRITSHF --- LDIPQLVIRV --- DAPDR --- VTESQ --- VVWYKSTQLKFLG --- LPTPIKILLQNY --- 324  
c 000001660697 64 297 SDVEAGALITITSHF --- LHMHLHADI --- TKP --- ATLDLDD --- RWVPLQALNSVG --- LAPVKKILETQF --- NIQ --- 363  
c 000003378864 2 301 EVGPLVITVQRIITSHF --- LTHAYHCLRLG --- TPH --- PKVAVES --- RWVPLQALNSVG --- LAPVKKILETQF --- NIQ --- 375  
c 000003910742 3 284 ENTEKETKLSITSHF --- LHIHALLIRQ --- TTPIK --- RVMEGTPS --- LWYNNTTTFMG --- LAPVKKITINQIT --- ED --- 349  
c 000004116181 2 249 KTSVELPLRITSHF --- LQYTTLVVKT --- DNPLN --- FVMEVDQA --- VVWYKSTQLKFLG --- LAPVKKILETQF --- NIQ --- 332  
c 000006223903 1 284 LFESANVLRISITSHF --- LAITPQPARA --- PKRLT --- RRMQSTGL --- LWYKPEGFP --- --- --- 320  
c 000001029068 2 257 QVRKLLPLINASTSHF --- LTI --- --- --- --- --- --- --- --- 376  
c 000001128125 11 291 ESILVWNYFRTITSHF --- LDYPLVRLD --- EGESVPVFTIG --- KQNNDEKASAEM --- NWIELDRINKGEVGP --- VVWYKSTQLKFLG --- 374

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c 000002566035 2  
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