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Conservation:                 9 5 579 67999 5  5    65 7      55     6  9 98989 9   5        5         8       65969 67  66 5            859
sp_P17802_MUTY_ECOL   28  KTPYKVWLSEVMLQQTQVATVIP-YFERFMARFPTVTDLANAPLDEVLHLWTGLGYYARARNLHKAAQQVATLHGGKFPETFEEVAALPGVGRSTAGAILSLSLGKHFPILDGN  140
sp_P83847_MUTY_GEOS   34  RDPYKVWVSEVMLQQTRVETVIP-YFEQFIDRFPTLEALADADEDEVLKAWEGLGYYSRVRNLHAAVKEVKTRYGGKVPDDPDEFSRLKGVGPYTVGAVLSLAYGVPEPAVDGN  146
c_000003652391_2      37  PDPYTVWLSEVMLQQTTVAAVTG-YFRRFTTRWPTVQALAAADDGDVMGAWAGLGYYARARNLLKCARVVCETHAGAFPNTYAGLIALPGIGPYTAAAIAAIAFDRAEVVVDGN  149
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c_000001007148_4      35  RDPYVVWVREIMLQQTTVTAAVVP-YLDRFLKRFPTVESLAGAKSAEVLRVWEGLGYYSRARNLSRGAKLIVEEWGGQWRNTATELQSLPGVGPYTAGAIASFAFDQSAGIVEAN  147
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c_000001797282_1      58  PDPYRVWLSEVMLQQTTIAAVRP-YFERFITRFPDIFAIAEAEAVMSAWAGLGYYARARNLHACARTVAA-AGGRFPDTAEGLRKLPGIGAYTAGAAIASFAFDRQEAAVVDGN  169
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c_000001614067_2      37  SNPYFVYLSEIMLQQTVVKTVIP-YFLKFVRKWPDINALAEEHLKEINSYWAGLGYYSRARNLHKTAKLIISNKYDGFLPTDKNSLMALPGIGEYTSSAIMAIAFDRKSNVVDGN  149
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c_000001961666_1      18  VDAYKVWVSEIMLQQTVTVNAVIS-RYKKFISRFTNVKVLAKEVLEEWAGLGYYSRANLHKYEGIIPSEENKLINLPGIGTYTSGAIRAIAFNRPSLAIDVN  137
c_000002018097_4      25  NEPYNIWLSEVMLQQTVTTVIP-YYTKWIKKFFPTLKSVAESDLNSLLKLWEGLGYYSRCRNFHKATQIVVEKYKSVVPNDYKLFRQLPGVGDYIASAVLSIAYNKKYPAVDAN  137
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6u7t.before.V147.pdb 28  RDPYKVWVSEVMLQQTRVETVIP-YFEQFIDRFPTLEALADADEDEVLKAWEGLGYYSRVRNLHAAVKEVKTRYGGKVPDDPDEFSRLKGVGPYTVGAVLSLAYGVPEPAVDGN  140
Consensus_aa:            .ssY.l@lSElMLQQTpV.hhhs.Y@.p@hppp@PslpsLA.tpbpppllphWpGLGYYsRt+Nlhphtp.l.pph.t.hPpshp.l..LPGlG..TAtAlhtht@sp..shlDtN


Conservation:                  95  9                                                        75 87 85  9   5 9     8    9 5
sp_P17802_MUTY_ECOL 141  VKRVLARCYAVSGWPG------KKEVENKLWSL----SEQ-VTP---------AVGVERFNGAMMDLGAMICTRSKPKCS----LCPLQNGCIAAANNSWALYPGKKPK-----  225
sp_P83847_MUTY_GEOS 147  VMRVLSRLFLVTDDIA------KPSTRKRFEQI----VRE-IMA---------YPNRGAFNEALIELGALVCTPTSPGCL----LCPVQAYCQAFAEGVAEELPVKMKK-----  231
c_000003652391_2    150  VERVMARLFDISTPLP------GAKPALKAR----AAS-LTP---------KLRPGDYAGAVMDLGATICTARAPTCG----VCPLNDCCHARRAGTAAELPKRTPK-----  232
c_000000031207_6    139  VERVSRYLKIDGNPK------SGTARKRIQQA----ADD-ALD---------QENPGDHNQALMDLGRSICTPRSPDCQ----RCPLASGCGARASGEPTRWPTRRQK-----  223
c_000000430975_4    151  VERVVSRIFQITQPIP--------LSRPTLRQL----AAG-LTP---------SKRPGDYAQAIMDLGSLVCTPRKPKCN----VCPLHDICLANISGTPSDFPKRTPR-----  233
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c_000001803648_25   153  IERVMARMHDIHSPLP------SAKPELLAC----AAA-LTP---------DFRAGDYAQAVMDLGATICTPKSASCG----VCPWSFACLARINGTAAVLPKKTPK-----  235
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c_000003607531_2    151  VERVITRVFGIFKPLP------EARPIIKDCAAK----LAP-KTT---------RGRPGDYAQAVMDLGATICTCRPRPLCD----LCPWEKYCIANQQNFVQVPRKAPK-----  236
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c_000005774797_1    140  INRVLSRVYNIDDAIN------RPSARLARI----AET-LAH---------PKRSGDYAQAMMDLGAAICKPKNPNCE----TCPICDQCKAHSLGRTHELPVKAPQ-----  222
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c_000003294679_3    144  VRRVFTRHKAIKGWPG------TTMVQNVLWKI----AED-NTP---------SNRVADYTQAIMDLGATICTRSHPRCE----LCPVNKDCIAHSRGQEAEFPHKNIK-----  228
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c_000003492497_2    142  ISKIITVLWPG--------------QDTVEV---ANE-LVS---------LSQSGYAWNSAMMDLASSLRAGNPVE-------GALGETYFSDEAICRLFKPKRKKPEKKIK  219
c_000003492925_4    134  VKRILCRLHKLKTP-----------SDKELWRI----AYN-LVD---------KKNPFDYNGAMMDIGATLCTPKKPDCE----PLSDICQGGNDPTLYPTKKKR-------  211
c_000003766664_5    154  VIRVLSRLCDLEEEVG------ETKAKERIWDW----AER-LVD---------PQNASAFNQAMMDLGAMLCTPTSPGCD----QCPWREDCRARAAGTVLERPIKKAK-----  238
c_000003948186_72   141  VKRVLSRVRHRVAGWAG------RASVNKELWQL----AER-YTP---------KRRVERYTQAIMDLGATVCVRGQPRCH----ECPVAKHCEALRHDCVQSFPQPKAR-----  225
c_000005057120_4    140  VKRVLTRYFAISGWTG------NSKISNELWEI----SSR-YTP---------KIRVADYTQAMMDLGATLCTRSKPQCT----ICPIQADCLAKKQNKTAELPTPKPA-----  224
c_000005590109_5    140  VRRVLARFHVISGWTG------GTKVSNKLWQL----SSD-YTP---------LLRIADYTQAIMDLGATICIRSKPKCT----QCPINSACLAKIEGKISELPTPKPK-----  224
c_000006063368_2    139  VKRVLTHRKIETDLS------KSSTLKKLWKL----SEL-LLP---------DVRIDTYTQAIMDLGAIVCKKKSPLCE----ICPVNKDCLALKANLVDCLPVKRKI-----  223
c_000000467631_2    119  VKRVLTRYHAIEGWSG------SAKISSELWKI----SAR-YTP---------AERCADYTQAMMDLGATLCTRSKPRCG----ECPISSDCVARIGDKVKLLPTPKPA-----  203
c_000000788235_1    140  VKRVLTRYHAIEGWSG------KGHILKQLWSI----AES-HLP---------DTRYANYTQAMMDLGATICTPKSPGCE----GCPIHADCSAFQAGTPTAYPTPKPK-----  224
c_000001187176_11   141  VKRVLARHAVQGWPG------EKPVHDRLWAI----AEA-HTP---------HSRVAHYTQAMMDLGATLCTRSKPSCL----ICPLQAGCQARMLGEPTAYPQARPR-----  225
c_000001660697_64   141  VKRVFARVFGIDGFPG------DKRVEDTLWRI----AEAVLPP-------ADGIQPYTQGLDMGATVCTRGKPACLTGERACPLESLCEARSTDRVMELPVPRPR-----  230
c_000003378864_2    152  VKRVLSRLYDVSDP-----------VGTAAATRTLWAYSTELLN-------QADDAYTHNQAIMELGATLCTPKKTACT----RCPVSVRCDALARDTVPLRPIKRPR-----  237
c_000003910742_3    141  VKRVLTRYHAWEGWTG------KSQVLKQLWLL----AES-HLP---------ATRYANYTQAMMDLGAIVCSRTKPDCD----HCPLNSNCAALSKGNPTAYPTPKPK-----  225
c_000004116181_1    107  VKRVLFARHAVQGWPG------NASVNKQLWAI----SAR-YTP---------VTRYANYTQAMMDLGATVCTRTRPGCQ----TCPVNENCLARKKSLTEIIPASRPV-----  191
c_000006223903_1    142  VKRVLSRYHAVEGWSG------RAEVARRLWSL----AEA-HTP---------TRRVAAYTQAIMDLGAMVC-RRRPDCA----TCPLAGGCKAHKQNQVHDYPASKPT-----  225
c_000001029068_2    114  VKRVLARYHQVDGHYG------QGKTIKQLWKL----SEK-HTP---------NTRNNDYTQAIMDLGSIVCTRLNPVCD----CCPVALRCLAKKTHTQHLYPASKPK-----  198
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c_000001128125_11   149  VKRVLSRYFGIHGWPG------EKKIEADLWHK----ADL-LTP--------PKRFADYTQAIMDLGATTCKRSKPLCG----VCPVQKSCVALKREETHSIPASKPK-----  233
c_000001595844_4    140  VFRVLARYTANFDIG-------TPAGKKEFTLL----ANQ-LLD--------KKQPGKFNQAIMDLGALVCKPTNPDCS----NCPLQIKCQAFSQDTIAQLPVKEKK-----  224
c_000001719155_2    144  VKRVLSRLFLLKENGE------TRKSENILWET----MQQ-LLP--------ETGAGNFNQAIMDLGATVCLPKNPLCL----LCPLKRNCQAQKSGKQNLYPPRKRA-----  228
c_000002363038_6    149  VKRVLSRYFAIEGWPG------EKRVENQMWGL----ADN-LTP--------ETDFADYTQAIMDLGATLCKRSKPNCN----LCPVKTDCRALKTDQVASFPNSKPK-----  233
c_000002561400_1    105  VKRVLTRFFGVHGWPG------EKQVENRLWEM----ADE-LTP--------SVRFADYTQAIMDLGATVCKRSKPNCI----TCPVHSGCQALKKGEVHLLPSFKPK-----  189
c_000002566035_4    141  VKRVLTRYHGIKGWPG------EKKIENKLWSL----AEL-YTP--------RKLTKQYTQAIMDLGATVCTRRKPDCD----ICPLTLTCFAREMGKQHDFPGKKPT-----  225
c_000002598045_3    139  VKRVLARHFKIEGNLQ------ASSTTKQLWQI----SES-LLP--------GDRIDIYTQAIMDLGATVCTKSNPLCS----NCPVNQDCSAFKEGLVDTLPLKVKR-----  223
c_000004188575_41   141  VKRVLARFYAIASWPG------NKATEQQMWQQ----ADN-LLP--------DQRIAAYIQAQMDLGATLCTRSKPNCD----CCPLQSNCQAYARGTPTTDFPIAKPK-----  225
c_000002400049_1    139  VKRVLARHQAIEGWSG------QSPVSKKLWTI----AEQ-FTP--------ENQLADYTQAIMDLGATVCTRSSAKCG----VCPLSEDCLAYQQQRVADFPGKKPK-----  223
c_000002139456_2    139  VKRVLARYQAVEGWSG------QSQVSKKLWAI----AEQ-LTP--------KEQLADYTQAIMDLGATVCTRSTAKCG----GCPLSEDCLAHQQQTVADFPGKKPK-----  223
c_000003535614_2    141  VKRVLARYEGWPG--------KPAIEKQLWVF----AER-YTP--------TEELADYTQAIMDLGATVCTRASPKCG----VCPLNNGCKALANNCVAALPTRKPK-----  225
c_000002657784_4    138  VKRVLARYKKIEGDLS------KALNIKTLWRI----SES-LTP--------EEKVDLYNQAIMDLGALVCTKSSPKCR----ICPVSRDCIAFNKKLIQVLPRKKLT-----  222
c_000003800129_15   143  VKRVVGRLYNQESY----------QEKKFWEL----SKK-ILD--------KSNPFLFQQGIMDIGATICHIHNPQCD----ECPLGRWCLSKKNGSFYTYKKKK-------  220
c_000003716781_1    130  VRRVLARWFAVEGVV-------TKAEPRREIEGL---AAA-LVG--------GVNDPGSWNQALMELGATVCLPKDPRCD----SCPVMTECRARARGLERAVPELPVR-----  215
c_000001556689_3    131  VARIMCRLAGIADDTR------RSKVRQRLEAM----AAD-AIE--------CHPPGTFNQAIMELGARVCTPRSPRCD----QCPCSSYCEAHELGIEEQIPPRRSK-----  215
c_000001834452_1    108  VCRVAARFLGLKSPLG------SSALRGQARDW----GET-LHAG-------VSAGLAGSLNEGLAMELGATVCRPRAPLCG----TCPISEKCVARATNRVTEIPKKAKR-----  195
c_000004255004_2    148  ARRVYARLLSLTN---------LRAINET-----AEQ-MVS--------HSRPGDFNQAVMELGATVCLPGKPRCE----RCPLAYRCQARSVGAFKLQLRRPTR-----  225
c_000000605438_3    141  VKRILYRFFAVKEA--------NDKKLWEM----AYD-LYD--------KDNAYIYNQTMMDIGSAICTHKNPLCT----QCPFVSLCQGKDEPL--LYPTKKKK-----  218
c_000000581237_15   141  VKRILYRFFAMTSC--------NDKKLWEM----SYE-LYD--------RENSYIYNQTMMDIGSAICTHKNPACD----VCPFEPLCQGKESPL--LYPEKKVK-----  218
c_000002529579_2    141  VKRVLYRFFAVKEA--------NEKKLWEM----AYD-LYD--------RENSYIYNQTMMDIGSLICTHKNPLCT----QCPFVSLCQGKDEPL--LYPTKKKK-----  218
c_000006097838_1    114  VARVLTRLLGIERPSK------QKQVVEQLWSV---TAD-LVKHAVDLQKTSRRNATAFNQAMMELGALICTPRNPLCH----DCPLKGHCIARKQNKVNRIPVSAKR-----  207
c_000000583727_6    140  VARVLTRLLGIEQSPK------DKPVTDRLWSV---ADE-LVKHTVTLQKPRQRNASAFNQAMMELGALVCTPRNPLCG----DCPLKGRCIARKQNKVETIPALAKR-----  233
c_000005807640_2    142  VARVLTRLLGIEESPK------ARPVADRLWSV---ADE-LVNHAVTLRKPSQQNASAFNQAMMELGALVCTPRNPLCG----DCPLKGRCIARKQNKVETIPALAKR-----  235
c_000000134878_1    124  VNRVVSRFYAYQDPPS------KNKKKMEKF----MSL-IIN--------DNRPGDINQAIMDLGRYVCKPSTPLCD----ECPIHNGCKALKLGIQSDLPIKIKK-----  206
c_000005136725_3    139  VNRVVSRFYGYRDPPL------KNKKKIEKF----MNA-IIN--------DKRPGDINQAMMELGALICKPRTPLCD----RCPIQYGCKALKLGIQADLPVKIKK-----  221
c_000001684786_4    137  VERVMTRILRLAENPR------QVSTKKRLKEI---AGG-WMP--------ADKASSFNQAMMELGALICSPVSPDCP----SCPVREVCAAAEQGDPENFPRLPPK-----  221
c_000002971826_23   147  VKRVLTRILRLADNPR------TAATKKYLKEI---AGG-WMP--------RGKASSFNQAMMELGALICVPVSPNCA----ACPIHDACAAAEHGDPENFPKLPPR-----  231
c_000002040695_2    150  IARVFSRVLQYPGSKE------ALTTSLRQP----ISL-FLP--------FKRIGDYTQALMDLGALLCRPCNPQCS----LCPIKTLCKSAHHNTVHLFPHKTKK-----  232
c_000003263657_32   154  VIRVLSRLYRIHEDAT------KGPAKRRFQEL---ADG-LLQ--------KGQAADFNQAMMELGATVCLPGKPRT----VCPVQCHCRAFHELSDPSGLPYKPP-----  238
c_000005989041_2    151  IERVITRIFGICTPFP------EAKTIVKDCAAK---LAP-KTT--------RGRPGDYAQAVMDLGAIVCRPKKPLCD----LCPWKKCCIANQRNFVDQVPQKVSK-----  236
c_000002391082_2    149  VIRVLCRLLRIEEDPR------RTAIEAELIAA---GEA-LLA--------RGEAGDFNQAMMELGARVCTPRNPLCP----TCPVGQWCRAQAELDDPSALPYKVP-----  233
c_000003839553_2    156  VIRVLCRHLRIEGDPR------RAQIKAELIAA---VEA-LLA--------RGQAGDFNQAMMELGARICTPRKPLCE----TCPVGATCRARAELDDPTALPYKAP-----  240
c_000003996707_2    146  VIRVLCRLLRLEGDPR------KAAVKTELIAA---GER-LLA--------RGRAGDFNQAMMELGARICKPTSPACG----QCAVVEMCRAHAELDDPAQLPTKVR-----  230
c_000002044706_1    129  VIRVLTRLFRIPGDPG------TAAVSRRLWQL---ATD-VLP--------QNRPGDINQALMDLGATVCKPIAPLCE----QCPLAGLCAVRAAGNAEDFPNAGRR-----  213
c_000006007075_1    144  VERIIKRILNLKTEKE-------ISKENIIKK----KKI-LGM--------SDRSSDYAQALMEIGALVCKPKNPYCK----KCPITKNCLSYKKKDFEI---ISKN-----  223
c_000002094036_4    120  IERVLKRILNLKSEVK-------TKKENLHKQ----KKV-FGQ--------TNRSNDYVQALMEIGALICKPKIPHCN----KCPITKNCLSYKKKDFKI---KPKN-----  199
c_000002762689_1    144  IERVLKRYLYLKKENE-------INKENLIKK----KKI-FGY--------SNRASDYAQALMELGALICKPNNPHCE----QCPISNKCIALKKKDFLL---TKIK-----  223
c_000005516980_2    144  IERVLKRYLYLKKENE-------IQKENLIEK----KSV-FGL--------SQRSSDYAQALMELGALICVPVSPNCN----QCPISKKCKSFRKKDFNL---IKNT-----  223
c_000003920004_1    150  IKRMLARLYGLDQSIN-------LINKKITSL----SKF-YES--------KKQSSNLIQAFMDYGSIICVPRNPKCG----ICIISRECIANQRKISNIIPKKIKS-----  232
c_000004008511_2    144  IERILVRLYGLKLPII-------KIKNDLRKK----SDN-FIS--------KNSSSDLIQAFMDFGSLICTPRNPDCV----NCLIQKNCNAFNYNLQDIIPVKLKS-----  226
c_000004481347_1    151  IKRIIARLYGIKTSLL-------LNKKTIEDI----ASK-YQS--------SNKASDLIQSFMDYGSVICLPRNPKCD----ECLIEKFCEARKKNIQHLIPFKNLS-----  233
c_000003787733_3    143  VKRVMARILKIKHITK-------RNNRRIRNR----LIK-WMD--------PERPGDINQALMDLANKICRVDHAYCN----TCPIDKVCMAEKMSIPESYPTKLNK-----  225
c_000000754657_2    143  VRRVMSRLLRIKNITK-------RNKKRIHNT----LIE-WMD--------RERPGDINQALMDLANKVCRVDHAQCN----CCPIDEICMANKMSIPESYPTRIKK-----  225
c_000000990943_3    143  VRRVMARVLRIKNITN-------RNKKRINNT----LIK-WMD--------PVRPGDINQALMDLANSICRVDHAHCS----TCPIDEICMAEKMPIPESYPIKVKK-----  225
c_000004474996_2    142  VIRVMARILRIKNITK-------RNKNRIYNT----LIK-WMD--------KERPGDINQALMDLANKICCVDHALCS----TCPIDEICMANNMSIPESYPAKLEK-----  224
c_000001463500_11   130  VTRVLSRILAIRNLTP--------YNRRRIFNV---LEK-FID--------KERPGDVNQALMDLGSSICTPINTECI----ICPVSQFCKAKKTLLPFGYPIKINK-----  212
c_000001286181_5    137  VKRVVSRYLNVENNPR--------ELKKSIKPF---LYQ-NSP--------KANYQSFGQGMMDLGSLICVKEKPKCD----LCPIQKTCLSFKKQDFIKTKKNT------  217
c_000001293628_3    143  VRRVLSRLFDLADDT-----------TDASLRTR--AGE-LVD--------PDRPGDWNQALMDLGATVCTARSPRCS----VCPLTKQCRAETEGTQELRPAPKRR-----  222
c_000001535696_8    137  VYRVLSRYFGVDLPIN--------TTEGVKYYKEL-AFK-VMD--------SQNIRDYNQGIMEFGAIQCAPKNPNCF----SCPLSDSCVALQENKIDTLPVKLKK-----  221
c_000001614067_2    150  VERVFSRFYAVEKPIK--------ESKIFIKNI---AEK-HLP--------DNRHGDYAQALMDLGSLICIPKSPRCK----MCPLLAICDVGGTTSAKQYPIKLPK-----  232
c_000001765289_1    116  AKRVMSRILGIKNL----------TSWNLSRINKT-LSN-IIP--------EHTPGNFNQSVMELGATLCRPRSPSCN----KCPLSFGCKA-FKTNKPDYYPKPAA-----  197
c_000001961666_1    131  VERVITRLFKIDNNK---------KVKNKIKKY---TQS-LIP--------QNKPGDFARALMDLGSLICKRANPTCS----LCPLKLNCKGYISNQIKVSVKNKKL-----  212
c_000002018097_4    138  LKRVISRYLGIKKLTP--------RNTLRIHNQ---LNK-MLT--------NGRPGDINQALMDLGSLICTPKNPDVICI----KCPLINKCKGYSYGNPIMYPDKNKR-----  220
c_000002843512_36   135  VKRILCRLQKLKTP----------TDKELWKI----AYD-LVN--------KKNPFDYNQAMMDIGATLCTPKNPNCE----ACPLSDICQGQSDPALYPTKKKR------  212
c_000002930199_1    135  VYRLISRLYNINTAIN--------TNKGREEFQSI-ANN-LLP--------NNTGLYNQAMDFGSIQCKKYNPKCN----ICPLQKECQSAILGIVNERPVKTLS-----  219
c_000003033795_2    131  LERIGYRILGLKTKTK--------RNKKRVVEY---LEK-NQC--------ANNPGDYNQALMDLGSSLCKASITYCN----QCPLKKICKAYTSSSPILYPTPKVP-----  213
c_000003888107_2    132  LERIGFRLLGLKKRSK--------RNLNRINNI---LEK-IQD--------KNNPGDFNQALMDLGSIQCQSQSVNCR----VCPINDSCRAFLSLNPVDYPAPIKP-----  214
c_000004013286_6    157  SRRVLSRVFAIKGDLS------RQPMKHLLWDL---AKF-VLP--------EKNVGDFNQAMMELGSQCCQKQYPRCM----QCPIKEWCRAFQEGLQEELPFTPIQ-----  241
c_000004852258_1    119  HSRIIARVLGVKNQTS-------RNLNRIKNL----LKK-LVR--------EGNPGEINQALMDLGSKCSNKVICV----NCPFHFSCKAFQSGHPLSYPKKILP-----  201
c_000005254087_1    145  VVRVLSRLTDFAEDVT------TTPAKKQLWQM---AAK-LVP--------ADRPGDYNRAIMELGQTLCLPTKTDCV----ACPLTAVCLARQRGTQMERPVRPPR-----  229
c_000003603677_1    142  VYRVLSRYFGQALPID------SSAGKKWFKAK---AQA-LLW--------EDDPANYNQAMMDFGALHCRPKNPSCG----DCPLAKNCQAKANKQQLELPKKGKK-----  226
c_000003283462_3    130  IKRIMARMLGVKKITN--------FNYKRIKKT---LLN-LIS--------SSRPGDFNQALMDLGSQVCRPNQAHCI----RGCLKLFCKAGNTLNPEKYPRPLSK-----  212
c_000002687221_1    144  AIRVISRMNSIDSPYP--------KSRKKIINF---LSE-HID--------TIRPGYFNQALMDLGRVICTYKSPSCI----ICPVNTYCYSYVNNTVDKFPTKIKK-----  226
c_000003347358_19   166  VKRILCRLEKLRTP----------SDTELWDI----AYT-LVD--------KINPFDYNQAMMDLGTIVCIPKKPQCD----ICPLNDICKGQEEPTLYPTKKRR-----  243
c_000002701031_2    137  VIRVLSRYFGIQTPFD------SSDGKKEFQLL---AEE-LLI--------KEKAGENNQAIMEFGALQCTPKSPNCN----VCPLQNTCFAFNNNLILELPKKAKK-----  221
c_000000582753_3    145  VYRFISRLYGVSTPIN--------SGKANKEFKVI-LNA-IID--------EKNPATFNQAIMDLGSIQCTPKSPNCE----SCTFSEICFAYKNNVIKDLPVKLKA-----  229
c_000001713769_5    137  VYRVIARFYGIDVPVN--------NHLGKKFYMDY-AQK-LAP--------KKSCGDYNQGIMDFGSLICKPKAPLCD----KCMLAKDCIASKMKNVNYFPVRLKK-----  221
c_000004369364_1    140  VYRVLSRYTANFSDIG------TPVGKKEFTLL---ANQ-FLD--------KKQPGRFNQALMDLGSIQCKPVKPICP----DCPLHSDCLAFAQDIISSLPVKAKK-----  224
c_000006057486_30   141  VYRVLSRYFGVSTPIN------SAKGIKEFKQL---AQI-LIN--------PKNPGTHNQSIMEFGALMCKPQKPNCT----NCPLNDSCFALQNNQIKTLPIKTNK-----  225
c_000005494072_10   137  VYRVLSRYFGIEYAIN------SSKGIKKFKTL---AQS-LLL--------NENFGLHNQAIMDFGATICTPKKAKCD----SCIFCESCSALQHNKVSELPVKTPK-----  221
c_000001742634_3    140  VYRVLARYFGIKTAIN------STNGIKEFKLL---AQQ-LLP--------NNKIGAYNQAIMDFGATICTPKKPKCD----ICIFNDSCIALQKNKITELPTKTNK-----  224
c_000002826998_2    140  VYRVLSRYFGIETPMD------TSEGKKQFTHL---ANE-LLL--------KKKPAIYNQAIMDFGATICTPSPDCK----HCFLKKKCQALQENKISKLPVKSKK-----  224
c_000003159439_6    137  VYRVLARYFGIRTSTN------STKGIKEFKQL---AQE-LID--------TKDPATFNQAIMEFGAIQCKPKNPNCN----NCPLNTSCIALQKKLITILPIKDKK-----  221
c_000004887214_1    142  VYRVLSRYFGIRTSIN------TSKAKKEFKCV---AFE-LID--------SKNPGLFNQAIMEFGSLQCTPKNPTCS----ICPLNDTCVALQTNQVEVLPKKQPK-----  226
c_000005037037_2    140  VIRVLSRFFGIENTFQ--------TVKEKKEFQEI-ADV-LIS--------KKSAADYNQAIMDFGAQICTPKNYQCE----KCPISANCFAFNKKQQNNLPLKKKK-----  224
c_000001059964_1    132  MIRVISRMMNNQEEPR------LAKTRKRLWQL---ARE-WIP--------EGEARRFNQAMMEIGALICLPSNPKCL----LCPMNNHCRALQKGTVSLIPLKPPK-----  216
c_000002498472_1    141  VYRVFARIFNIDLIPG------SPEARQLNWEK---AEE-LLP--------KGHARNFNQALMDLGSIQCKPKLPLCT----SCPLVTHCLALKYDLVPERPVPKKS-----  225
c_000004615912_3    130  VYRVLSRFFGIKAAID------ISKNKKIFEVL---AQE-VLD--------ASQAGKYNQAIMDFGATMCKPKSPDCP----LCPLSKKCIALKEELVTTLPIKSKK-----  214
c_000004766858_2    143  IERVLCRIEDIGEPPR------STPVQKQLWSL---AAE-WIP--------HGHAREFNQALMELGATLCTPRNPSCL----LCPANAWCVAFHTGRTDTIPAPRVR-----  227
c_000002747260_18   149  VERVMARLFQIETPLP--------GAKPELTEL---AGR-LTP--------DIRPGDHAQAVMDLGATICTPKSPACG----ICPVMTGCTARAAGAQADLPRKTPK-----  231
c_000005371561_38   149  VERVMARLFDIHEPLP--------AAKPVLKAQ---AAA-LTP--------RNPGDHAQAVMDLGATLCTPRNPSCG----ICPLRAPCAARAAGTQADLPRKTPK-----  231
c_000000169465_2    145  VKRVLARYYSIGGWPG------QKKVENQLWEV---AEK-NTPTN-----SEGGRCANYTQVMMDLGAMICTRSKPKCD----ECPLQADCIAYAQGAQADYPGKKPK-----  233
c_000003254110_11   145  VKRVLARYYAISGWPG------QKKVENQLWEV---AEK-NTPTN-----PEGGRCANYTQVMMDLGAMICTRSKPKCD----ECPLQPDCIAYAQGAQTDYPGKKPK-----  233
c_000004750284_20   145  VKRVLARYYAIEGWPG------QKAVENALWDV---AEK-NTP-------QNRCANYTQVMMDLGAMVCTRSKPKCD----ECPLQRDCVAFAQGKQTDYPGKKPK-----  229
c_000001141782_15   150  VKRVYARYHAVAGWPG------ETAVSRRLWAL---AER-YTP--------DNRTADYNQAIMDLGATVCVRRRPRCG----VCPLADGCRARREGRNPEAYPGSRPR-----  234
c_000002717847_8    144  VKRVLARLFLQQEF-----------KEGLFWNL---SAQ-CLD--------EDDPYSYQQGIMDIGATLCTPKAPLCP----ECPLNKNCLAFKENDFQLPSSKKPI-----  223
c_000004054799_1    131  VKRVLGRYKKISFKT--------ENEKQKKLWLI--SEE-LTP--------NKESFEYTQGIMDLGATHCKSKRPRCD----LCGPVSNDCDSAFKEVSNKVSLRKAI-----  214
c_000006126673_1    156  IERVIARYHAINTPLP--------KAKKEIKERAT-IYT-DNL--------PERPGDYAQALMDLGATICRPKSPLCY----SCPLKEGCTAYSLGQAEEYPKRQKK-----  240
c_000000339186_3    113  VIRVLTRIFGIRKNPK--------DKATREYLWSL-AET-LVA--------KAENSSALNQSLMELGATVCTQRRPDCA----ACFVARSCTARRERATEIIPAKGEP-----  198
c_000003029168_2    145  VARVVSRFALEGDLK------DTALQKKLWEI---TED-LVP--------NKRPGDFNQAMMELGAIICSTDSDPRCT----LCPLAKPCHARVTGEPWRFPSESVT-----  229
c_000001863436_1    161  VARVLARLFAVDGDPR------SGDNQRRFWRL---AGA-LID--------RGRPGDFNQSLMELGAIVCTPGGPSCL----LCFVREYCQAFATGDPTRYPAVAKR-----  245
c_000002830137_4    154  TTRVLSRLLGFNGDPR------QRVGQQLLWAF---AES-LLP--------RKRVGEFNQSLMELGSEICIPRKPNCE----RCPVRMLCAAHRQGEQLSIPISRRR-----  238
c_000004612302_3    148  TARLFSRLLALSVDPS------SSEGRGRLWSL---AER-VVP--------RTRAGEFNQALIDLGATVCGV-EPRCQ----ECPVRSSCRSLEQGVVDRVPVRSPR-----  231
c_000001933926_1    134  IERVMSRLHRLETPLP------AAKPEIAEV----AQR-LTP--------RQRAGDFAQALMDLGATVCRPRRPNCG----ACPWNASCLAHAAGIQETLPRKLPK-----  216
c_000003136334_1    146  VERVTARLHRISKPLP--------GAKKYLKEK---AAE-LTP--------SERSGDYAQAVMDLGATVCTPRKPNCP----LCPWSYICKAYLAGDAEKFPKRVPK-----  228
c_000005849454_9    143  VKRVAARWAGLELAADDLALEKAARALGKAWMT---DLP-LGK--------LSAPGLNEGLMELGATVCSPRNADCG----ACPIASGCVALADGMVDVLPLPKRA-----  233
c_000001169194_1    154  VRRVLARLFDKREP----------RARWLNRT---AAE-LVD--------KDRPGDWNQALMDLGAMICSPKNPRCE----DCPVQLWCTAHEQGTQALSPAGVRR-----  233
c_000002786947_2    154  VRRVLARLFDKREP----------GVRWLNHT---AAS-LVD--------KDRPGDWNQALMDLGAMICSPKNPRCE----DCPQRWCTAHEQGTQALSPAGIRR-----  233
c_000002799919_52   142  ISKIITVLWPN--------------KGTVKV---AES-LVA--------AANSGYIWNSAMMDLASSLRAGNEIE-------AELGSTYFADVEVRDQFKPKRKKPSRTAK  219
c_000000358065_2    144  IERVLKRILNLKTEKE--------TKKENLHKL---KKV-FGI--------TNRSCDYVQALMEIGALLCKPKNPYCE----NCPITKNCLSFKKKDFEI---KKKN-----  223
c_000003745941_1    133  VIRILCRLTADNTVYT------DNTQAMKVFTPL--AEV-LLD--------TKTPGQHNRAMMEFGAMVCSKVNPTCD----ICPFNSVCLGRNHQPER-LPIKAAK-----  217
c_000004187032_4    144  IERVLKRYLHLKKDNE--------IQKNNLIKK---KSI-FGI--------SSRASDYAQALMEIGALICKPNPECS----ACPILKSCKSYKKKDFDL---AKIR-----  223
c_000006067315_3    144  VKRVLKRVFYLKNEKE--------ISKENLINK---KFF-FGK--------SNRSSDYAQALMEIGALICKPANPLCF----ECPISKNCRSFKKNDFEI---TSKN-----  223
c_000005543774_1    114  VKRVLLRLFNLETKD----------------------PAN-LFK--------TKRNGDLARALMEFGALAICKPKDPLCY----KCLLKKNCLYYKSESKI-RFNKKIK-----  185
c_000006211484_1    136  VKRVLFRLDNININD----------------------AVN-LFK--------TQRNGDLARALMEFGALICKPRDRCH----ECKIKKMCAYFKSKSKI-RFNRKIK-----  207
c_000002718976_3    145  VRRVFSRNLNIEENK--------INFDKFIKKN---KKK-FFI--------TKRNDDFVQALMEFGALICKPKDPNCL----TCLNKTCKYFKSSKKI-KNIKNKM-----  226
c_000002992548_1    146  VKRVSRLF--NANL--------EKNEKRIRKI---TKE-QLY--------TDRCGDLARALMEFGAVICKPSNCM----NCLKANCYFFKNKTSV-LVNKKRR-----  225
c_000000456751_1    110  VKRVFSRLLLINTSN---------QNIDNEIKKI--TYK-LPK--------IDRNADFARALMEFGAVLCKPQNPLCK----ICHLQKYCKFFNSENYI-SLNKKFS-----  191
c_000002655634_1    141  VKRFFSRLFLIDVSS---------QNFENEIKKI--TNK-LPK--------VNRNADLARALMEFGAVICKPKNPLCK----NCLKKYCKFFNGENYT-LPNKKFF-----  222
c_000042232403_2    140  HRRVISRILGIKNLSR--------HNKNRINNY---LKQ-LVA--------IDRPGEINQAIMDIGSIICKPKEVFCD----FCPVQFSCKACVSSKPLEYPNKIYN-----  222
6u7t.after.N146.pdb 141  VMRVLSRLFLVTTDDIA------KPSTRKRFEQI--VRE-IMA--------YENPGAFNQALIELGALVCTPRRPSCL----LCFVQAYCQAFAEGVAEELPVKMKK-----  225
Consensus_aa:            l.RVhsRhh.lp.............ppph..h....s...hhs.........ppssp@sQAhM-lGthlC..ppP.C.......CPl...C.t........hP.........
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Conservation:                                                    5   5
sp_P17802_MUTY_ECOL  226  -----QTLPE-------RTGYF----LLLQ-----HEDEVLLAQRPPS-GLWGGLYCFP---QFADEESLRQ--------------------------WLAQRQIA------A  281
sp_P83847_MUTY_GEOS  232  -----TAVKQ-------VPLAV----AVLAD----DEGRVLIRKRDST-GLLANLWEFP---SCETDGADG-------------------KEKLEQ----MVGEQYGLQ------V  294
c_000003652391_2     233  -----QPKPT-------RYGIV----YLARD----AHGAWLLERRPDK-GLLGGMLGWP---TSDWNDAPG--------------------------------DQPPFA------A  286
c_000000031207_6     224  -----RTTEQ-------QWWAA----AVVV-----CGDGVLVWIGDG-ELLAGHRGTP---LARLSGSGL--------------------DADKMIG----KEFKRLGLD-----GA  286
c_000000430975_4     234  -----RKKQR-------RYGVV----YWIER----RDGAISLRQRPEN-GIFGGMTEIP---GSLWKASPL--------------------------SRH----SIHAQAPIP-----A  293
c_000001007148_4     232  -----RDVTD-------VFELL----VVMR-----RGKRLLLIQHPDG-ERWGGMWGFJ---ALSRDRALARS------------------RFDERLIE----SEVADWGCD------V  297
c_000001092848_3     244  -----AAKPS-------RRGAA----FVAVR----GDKKLLRRRPES-GLLGGMSEVP---TSGWSAGSD-------------------GEDGP--------SAASFP------A  302
c_000001151029_1     191  -----TKKRR-------RYGVV----YWIER----RDGAIVLRQRPEN-GIFGGMTEIP---GSLWQAAPL--------------------------SRH----SIHAQAPIP-----A  250
c_000001797282_1     253  -----AKGAL-------RRGAA----FVAIR----SGDEAVLLRTRPPE-GLLGNMAEPP---GSAWEPDYD--------------------VAAAL--------LDAPLD------A  312
c_000001803648_25    236  -----PVKPT-------RYGIA----YIARR----DGAWLLERRPDK-GLLGGMLGWP---GAQWGDQAV--------------------------------DKPPVS------A  289
c_000002078955_4     236  -----PVKPI-------RYGIA----YIARR----TDGAWLLERRPDK-GLLGGMLGWP---GAEWGAKAV--------------------------------ENPPVS------A  289
c_000002106160_4     224  -----QSLPW-------QNVLT----GVIW-----KRDSFLIIKRAGY-KHLNNLWELP---GGRTLTKNN--------------------PHPQLEE----LLKNKFKLE------V  286
c_000003607531_2     237  -----KVKAV-------RKGVV----FLALM----SDGSLFLRRRPEN-GLLGGMMEFP---STVWLERSL--------------------SPK----EICEAAPFK------T  296
c_000003872363_4     232  -----PAKPI-------RYGTA----YIARR----HDGAWLLERRPDK-GLLGGMLGWP---GSEWGEEAV--------------------------------ENPPFS------A  285
c_000004820107_1     241  -----KPKPQ-------KRGHV----FWISD----DSGNILFIRRPEN-EMLGGMLGLP---TTEWDIRP--------------------------------IKLP------Q  291
c_000005774797_1     223  -----RSKKK-------WNAFA----YVIYN----ADGNIGFVRRDKD-ALLGGMWALP---TSDWSTSPV--------------------FQP----------PI------L  275
c_000005867021_3     236  -----PVKPT-------RYGIA----YVARR----PDGAWLLERRPDK-GLLGGMLGWP---GAEWGAQAV--------------------------------EKPPIV------A  289
c_000004546210_2     229  -----KKKRT-------ESMYF----LMIVF----DGKKLFLEKRPKK-GIWGGLWSFP---QIQLADDPQI-------------------------WCEQQFTNN------I  286
c_000004551008_5     229  -----KKKRT-------ESTYF----LMIIF----DGKKLFLEKRPK-GIWGGLWSFP---QIQLADDPKT-------------------------WCEQQFTNK------I  286
c_000002511148_4     224  -----KSKPT-------KKVVW----LLPQG---PSGEVLLEKRPKK-GIWGGLWAFI---EAEKKNELEL-------------------------ELSRRFKTD------C  281
c_000000577378_2     212  -----KSKPT-------KKVVW----LLPQG---PSGEVLLEKRPK-GIWGGLWTFI---EAEKKNELEL-------------------------ELSRRFKTD------C  269
c_000000598175_2     235  -----KVMPE-------KQAIM----VILKN----SKQEVFMQKRPPV-GIWGSLWEFP---QFEKRAFAEE-------------------------WLKSNYGKL------I  292
c_000000754627_3     232  -----KAVPK-------KSCHQ----LIIK-----GKDEVLMEKRPNS-GIWGGLFGFF---EFNEYSELET-------------------------FLAQQGLK-------A  286
c_000000811118_1     223  -----KEKIE-------KKIDW----ILIK-----TKNKVLLKRNKEK-GIWQNLWVLP---EKDFFSSKKI---------------------------SKI------L  273
c_000000899687_2     227  -----ISSKK-------IEVSA----GIII-----KNKKVYIQQRVKN-GLLGGLWSFP---GGKREQGES--------------------PEECLKR----EIKEELRVN------V  286
c_000001176522_24    248  -----KVMPV-------RKVCW----QVSLS-----QGCVWLVQNPAR-GLWGGLWVLP---EGNR---------------------------------------------  288
c_000001345122_1     202  -----KIIPT-------KEKFF----LILVT----EAFQVALVKRPEK-GLWGGLWSLP---EFDSVQEIDL-------------------------FLDGNEMVAT----LK  261
c_000001515736_6     220  -----IKRSS-------ESWWL----LLAVD----ARRRVWLQKRPQA-GIWAGLYSPP---VFEDYAALQS-------------------------YAQAAWSQD-----GT  278
c_000001682161_6     223  -----KTIPT-------KERWF----LVLLT----KEGNIGLIKRPAK-GIWGGLWSLP---EFDEVKLLEN-------------------------FITDNNVKCL----LK  282
c_000001923643_29    230  -----LKRSS-------EAWWL----LIAVD----GQGRVWLERRPQQ-GIWAGLYAPP---VFNEREALEQ-------------------------AAARHWPAA-----RS  288
c_000002030994_5     224  -----KEMPE-------KHTVM----LILQN----KQDEVFMQKRPPV-GIWQNLWCFP---QFDKTALAEE-------------------------WLDDSFGMS-----L  281
c_000002038721_4     226  -----SQKKE-------KNINW----LLIA-----SKDKVLLKRNVNK-GIWQNLWLFP---EANSLNYEK--------------------------FNL------L  275
c_000002523527_15    251  -----AAIPE-------RSTVM----LIVRH----GKDVLVQLRPSS-GIWGGLWSLP---EMPVDTVPFD--------------SEAAEESA----LELARAYGS------P  315
c_000002608528_2     224  -----KVMPE-------KQTVM----LILKN----GKQEVFMQKRPPA-GIWGGLWCFP---QFDNHENVLE-------------------------WLDNNYAVS------F  281
c_000002961510_2     227  -----VPSKK-------IEVSA----GIII-----KNKKIYIQQRSKN-ALMGGLWEFP---GGKREKGES--------------------PEECLKR----EIKEELRVN------V  289
c_000002979152_8     232  -----KDKRI-------KQSVM----LYVSN----ENADVVLERRSST-GLLGGLWSLP---EFETNVKAND-------------------------WLVKTFALE------S  289
c_000003248034_1     247  -----RKKKR-------VMTSV----IACE-----QGGQILMKQRSVNARLMPGFWELP---EVEGPFLNQ---------------------ADL------------ARWS------L  301
c_000003294679_3     282  -----KTNPL-------KTTNM----LFLRF----RDRIYLERRPSS-GVWGGLWSFP---EISKDCSVSD-------------------------WYQSRFGAY------P  285
c_000003333364_1     225  -----KPAVP-------VDVAS----GVLV-----HDGYIFIQKRPED-GVWPGLWEFP---GGTVEKGET--------------------PAQCVVR----EFQEELEWD------V  287
c_000003402697_5     220  TEKPKKRKHR-------IEVGI----ACIW-----REGKYLVQARPKG-KSFEGSWEFP---GGKREKGEN-------------------------FRECVKR----EIQEEVGID------V  287
c_000003492925_4     212  -----VVPT-------REENI----MLYV-----YNDKLSLTQRKG--KFLHGLWGFE---NTEMPL--------------------------------------------  252
c_000003766664_5     239  -----RPPKK-------IALVAC---VIRD-----EQGAVLLTQRPEK-GLFGGLWEVP---LKEVDETPS-------------------------KAGVGR----LVKETVGLT------A  301
c_000003948186_72    226  -----NNIPT-------RHTQM----LLIEN----TAGEVWLEKRPAQ-GIWGGLWSLP---ELATGQNAIT-------------------------YCEQELQIA------V  283
c_000005057120_4     225  -----KVLAV-------KQLIF----LMLQD---QQTQFLLEKRPAS-GIWGGLWSFP---EFQSFAEIKS-------------------------WCLEN-DIA------M  281
c_000005590109_5     225  -----KSLPV-------KKITF----LMCQD---QQGRILLEQRPKT-GIWGGLWSFP---EYESLANIQS-------------------------CFLEK-GIP------I  281
c_000006063368_2     224  -----KTKTT-------KHVHW----LIPYS----RKLRLKRLNK-GLWEGLWVFI---EKEKEEMLKK--------------------------ECKSIFQIK-----D  281
c_000004467631_2     204  -----KTLPV-------KNIMF----LMLKD----ELGLVLLEKRPAT-GIWGGLWSLP---EFETLSEIQS-------------------------FCQQN-NFA------I  260
c_000000788235_1     225  -----KTLPE-------KKAVF----LLLIN----INHEIFIIKRPPS-GIWGGLWSLP---QFDTYLQAQQ-------------------------WYEQYFSTH------L  282
c_000001187176_11    226  -----KRIPV-------RQCLM----PLLVN----PQGDIWLQRRPDS-GLWGGLWEFP---QLDSREQLDA-------------------------LVIAQ-GWQ------A  282
c_000001660697_64    231  -----KAIPE-------RAATM----VIALH----GETVLLQRRPQR-GIWGGLWSLPLVGEMDDALDAHP------------------------LDADTVRQAALAYGTV  296
c_000003378864_2     238  -----KPVPH-------HHIGV----GVIWK----DDQCIYMLQLRPPE-GLLGGLWEFP---GGKQEPAET--------------------IEETVRREIREELGVD---------V  300
c_000003910742_3     226  -----KVIPE-------KNAVM----LMLIN----NKDEVFIMKRPSP-GIWGGLWEFP---QFDDYDQAQA-------------------------WHENYFGFP------C  283
c_000004116181_2     192  -----KKQAT-------RTCVF----ILIVN---AKQELLQKRSPV-GIWGGLWSLP---EVEDTIEAIH-------------------------WCSSR-KIT------V  248
c_000006223903_1     226  -----RPRPR-------REVVM----IMIKD----DRDRVLLERRASS-GIWGGLWCFP---ECPVEEALEP-------------------------WCRMRFGAG------I  283
c_000001029068_2     199  -----KPKPV-------KTTAM----LIFDN---QGGKVYLQKRPAK-GIWGGLWSFV---ECSATDKAIT-------------------------KTAHNFHPQ------A  256
c_000001128125_11    234  -----KDKPV-------KRAFF----LLLLN----SERQVLLRKRKPQK-GVWAGLWSLP---EFDSLQGFKE--------------------------SIESQTTV------I  290
c_000001595844_4     225  -----IKRKT-------RYFYY----FVFR-----KGSDYYIQKRTKK-DIWQSLYEFP---NIESKTPLN-------------------------DNEVKIV----FQEKYPRIK------F  287
c_000001719155_2     229  -----APSTK-------IAVSA----GVLF-----RRNRIYIQKRKAE-GLMGGLWEFP---GGKFESGES--------------------PEQCLHR----EIKEELGVT------I  291
c_000002363038_6     234  -----KNKPV-------KQKWL----LLQKN---SAEQVFLYKRPQK-GIWAGLWSLP---EFDSYDRAVD-------------------------FLNGEIHRH-----DA  292
c_000002561400_1     190  -----KEKPV-------KQAWF----VVQLN----AKNQIRLIKRPQK-GIWAGLWSFT---EFCSVTDAKT--------------------------YLQTQTPG------L  246
c_000002566035_2     226  -----AVIPK-------RDTVF----AIMEN----NNGEILLEQRPSS-GIWGGLWEFP---EFSSPLRIEE-------------------------MIKRKYGFN------I  283
c_000002598045_3     224  -----KSKLT-------KKVLW----LLPQG---PSGEILLEKRKEE-GIWGGLWSFI---ETEKKAELEL-------------------------ALSRNFDSN-----I  281
c_000004188575_41    226  -----KTIPT-------RQSHW----LLILT----DDRRVLLSKRPEK-GIWGGLWCFP---SFDDTHTL--------------------------EQHIDNT------K  279
c_000000240049_1     224  -----KILPV-------REKRL----LIIRN---KQGYVLMEKRPPS-GIWGGMWSLP---ELTLDKSIAE-------------------------SIERNWQLS------V  281
c_000002139456_2     224  -----KILPV-------REKRL----LIIRN---KQGYYLMEKRPSS-GIWGGMWSLP---ELTLDESIAE-------------------------SVERNWQLN------V  281
c_000003535614_2     226  -----KILPI-------QQKRL----LIIRN---KQGAYLMEKRPPT-GIWGGLWEFP---ELALEAPIIT-------------------------EVKNTWQII------V  283
c_000002657784_4     223  -----KQKPF-------KTVFW----LVVMN---KNGKVLLKKRNNL-GVWKGLWSFL---ESENIQDLGK-------------------------ECLTMFEKR------K  280
c_000003800129_15    221  -----TPKKK-------VFLNY----EIYK-----RDGCIYMIKNMDL-GFWNELWMPP---YKIVE-------------------------------------------  262
c_000003716781_1     216  -----PTPID-------VELEM----FLVH-----DHGRVLLRRRDEG-GRMAGLWELP---TREVAAAELRLF----------PAELELEL---------------------  272
c_000001556689_3     216  -----LVKA--------VTEYA----AVIE-----RRDGDKLLFRGQRP-SLVSDMWEFP---TLDSRLADTSSRSLTEKPASSHSRAQEAKLSR----YIKEQLGWS------V  289
c_000001834452_1     196  -----INWKE-------VHLLY----GVAS-----CPSGVLLEERKS-GWNQGLWEFP---SVPYDQKEE--------------------PDL----AWREFQPQR------G  253
c_000004255004_2     226  -------TKA-------VQWPL----TLAK-----WRSRILLHRRPDK-GILASLWELP---TPENLPAEL--------------------IDETL-----------------  274
c_000000605438_3     219  -----IKKPI-------RKRAL----IIYA-----KNDKYALAQNEE-RLLSGLWGFK---QEEDFEF------------------------------------------I  262
c_000000581237_15    219  -----KKKPI-------RKRTL----IIYT----KDDKYALSQNSE-RLLSGLWGFK---QEEEFEF------------------------------------------S  262
c_000002529579_2     219  -----IKKPI-------RKRTL----VIYH----KANKYALAQNEE-RLLSGLWGFK---QEEDFEL------------------------------------------L  262
c_000006097838_1     208  -----APVSK-------RRFIG----FIIA-----WHGNVFVQRPSG-EVNSGFWEFP---NWLVDDTQ--------------------VQPAD----LASTKLALG------Q  267
c_000000583727_6     234  -----AATTN-------RRFIG----FLIA-----WHGKVFVQRRPSG-EVNAGFWEFP---NWQVNDAE--------------------LKPAA----LAKRELKLG-----Q  293
c_000005807640_2     236  -----AATTK-------RRFIG----FLIT-----WHGKVFVQRRPSG-EVNAGFWEFP---NWEV-DAA--------------------ATADQ----LAKRELRLG-----Q  294
c_000000134878_1     207  -----ETKPH-------YDVAV----GIIW-----DKKKLLITKRKEE-GLLGGLWEFP---GGKIKKNEK-------------------------IESAIKR----EIKEELSIN------I  269
c_000005136725_3     222  -----HTKPH-------YDVAV----GIIW-----DKKKLLITKRKEE-GLLGGLWEFP---GGKMKKNET-------------------------IKSAIKR----EIKEELSIN------I  284
c_000001684786_4     222  -----RKTIA-------VELEA----GIIR-----RGKRCLLERSESF-DFLEGLWLFF---LSLPGD-----------------------GGIAA----RLGQALETD------I  279
c_000002971826_23    232  -----RKTVA-------VELEA----GIIR-----RGKRYLLERNEDL-DYLEGLWEFP---LARPDS------------------------GGIAA----RLRKRLATS------I  300
c_000002040695_2     233  -----TKKPC-------RWGHF----FFLVHIPSSGSPVSVLLEKEHG-PLLEGLWRPL---TQSWVHKKT-------------------------EAH----------FPY------K  290
c_000003263657_32    239  -----KKERP-------HHDHVA---GVIK-----LDDKFLIIQRPLD-GLLGGLWEFP---GGRRRESES--------------------LTEGVTR----TILESTGLT------V  302
c_000005989041_2     237  -----KVKPV-------RKGIV----FLALM----SDGSLFLRRRPET-GLLGGMWEFP---STNWLERRI-------------------------SPE----EICEAAPFK------S  296
c_000002391082_2     234  -----KKQKP-------HYQVAC---GVIC-----KGDRLLLAQRPSA-GMLGGLWEFP---GGKQEEGET-------------------------LQQCLQR----EIAEELAIE------I  297
c_000003839553_2     241  -----KKKKP-------HYQVAA---GVIS-----KGRQLLIAQRPAE-VMLGGLWEFP---GGKQEEGET-------------------------LEECLVR----EIREELGIE------I  304
c_000003996707_2     231  -----KPTRP-------HYEVTA---GVIW-----RGKLLVAQRPSD-GMLGGLWEFP---GGKREPGES-------------------------LQECLRR----EIREELTID------I  294
c_000002044706_1     214  -----TKVTF-------VQRVA----LFLEK----QDGSFLLVRRPAD-GLLAGMWELP---GRELGDGEAPE------------------RLASTLCG----EFGLTIRPD------  270
c_000006007075_1     224  -----KKKID-------KYFLI----KIYK-----KNKKILLIRNTKF-NFLKNFKIFP---MEEIPKP-------------------------------------------  267
c_000002094036_4     200  -----KKIIN-------KFYLA----TLYK-----NQNQILLIKNDKF-KFLKNLLIFP---MREITYP-------------------------------------------D  244
c_000002762689_1     224  -----KKNNN-------KYYLL----KVYK-----DKDKILLIKNTKF-NFLKNFSIFP---MQELSKP-------------------------------------------  267
c_000005516980_2     224  -----KKNIN-------KYFIL----KVYK-----KDQRYLLIKNTKF-NFLKNLRIFP---MEELFQP-------------------------------------------  267
c_000003920004_1     233  -----KKSRMK------KYTRAY---IIIN-----GSEEILVRRRASK-GMLPSMLEVP---NDKWVTEKK-------------------------LLVRD-----SSVSLFK------  292
c_000004008511_2     227  -----KSTKRK------KYSRAY---IFYN-----EKNEILIRKRPSK-GMLASMLEIP---NDNWVINKK-------------------------SLVTD-----TIAIKLK------  286
c_000004481347_1     234  -----LEQKKI------KFTRAY---IIMN-----KKNEVLVNRRKSK-GMLASMLEVP---NDEWVDVKK-------------------------KLKRH-----DVYKDLS------  293
c_000003787733_3     226  -----KIIPH-------KEIVA----GIIW-----QRDKFLITKRPEN-ALLGELWEFP---SAEIQFNET-------------------------PIGALRR----QISKDFNIY------I  288
c_000000754657_2     226  -----KVIPH-------KEIVA----GIIW-----QREKFLITKREEN-ALLGGLWEFP---GGEIASSET-------------------------PVGALRR----QIKEKWDID------I  288
c_000000990943_3     226  -----KVIPH-------KDIVT----GIIW-----DKKKFLIKRSEN-ALLRGLWELP---GGEFESNET-------------------------PIEALRR----KIKEECDID------I  288
c_000004474996_2     225  -----KVIPH-------KEFVA----GMIC-----QGNKFLITKRNEN-ALLGGLWEFP---GWEIVSSET-------------------------PIGALRR----KIKEEWAID------I  287
c_000001463500_11    213  -----SIKNI-------KHFIA----AIIW-----YNKEFLIMKPVN-SMLGGLWEFP---NTQIDLKIS-------------------------DDIQLFN----YIKNSLNFT------I  275
c_000001286181_5     218  -----VTKTQ-------ESFHW----FIYQ-----KNNKVMLCKNPDE-GIWPNLWVFP---KRELFQT-------------------------------------------K  262
c_000001293628_3     223  -----PRVRE-------ASYAV----LVTLN----PVGELLMVRRPPD-GLLGGLWEFP---AVEMEAEERNPWGGELR-VGDSLHGRCSARLE----DLGVQLSAR------R  301
c_000001535696_8     222  -----TKVRN-------RYFNY----IIPIAEADDGSRKTLLNQRKGK-DIWQNLWQFP---LIETKREID-------------------------LEEVKK-----RLCEVMHLAD---DPQ  291
c_000001614067_2     233  -----KEKEE-------RYGLF----FYLQN---GLGEDVLFETNKSS-GLLANMDVLP---SIGWYEESN-------------------------RFKKSPK----FNKKKPNFL------GM  297
c_000001765289_1     198  -----KKRKP-------HYTIVA---GIIW-----RDNTFFIQRRPEK-AMLGGLWEFP---GGKVEEGES-------------------------LEAALKR----EIKEECGVV------P  261
c_000001961666_1     213  -----KTIRK-------GKCY----IIKRL---QNLGKFLFIRNPAK-GLLGSMLLFP---TYGWLHSDH-------------------------DDYVK----SMIEKFIKN------I  273
c_000002018097_4     221  -----KPIPT-------KEYVA----VFIS-----YNDHIFINQRSED-GLLGGLWLP---MIEVFENSN-------------------------KIKALKT----YAKNKLGLS------I  283
c_000002843512_36    213  -----VVPT--------REQNI----MLYF-----YNKDKLSLTQRTG--KFLHGLWGFE---AIEVPL-------------------------------------------I  250
c_000002930199_1     220  -----RKPKI-------RYFNY----LFIK-----KNQQFLIQQRGTN-DIWKKLYELP---LIESKEKLN-------------------------REKIMA-----HQYFKPFK------I  283
c_000003033795_2     214  -----KKIPI-------YDIAV----SVVE-----YQNKILITKRQNK-NFLPGLWFP---GGKIEKKET-------------------------ATQAIIR----EVKEETNLT------V  276
c_000003888107_2     215  -----KTIPT-------IKVST----CIIR-----KQNKLLILQRPID-TMLGGLWEFP---GGKIQNNES-------------------------RKKAVIR----EVMEETNLA------I  277
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c_000004013286_6     242  -----PKIQA-------VREVA----VIVR-----KGKRVLVVQRPSD-GRWAGMYDFP---RFECSFRSKE--------------KIRQLMVR----GVGQQTGVP------I  306
c_000004852258_1     202  -----KTIPT-------KTIAA----ALVN-----HGDNIFITKRPLK-GLLGGLWELP---NIELVNGEI--------------PEDLLKI----KFADQFGLT------I  264
c_000005254087_1     230  -----KRTPHYDVVAGIIWQNG---VSPG-----EGGRFLIAQRPLN-GLLGGLWEFP---GGKQEPDET--------------LPQALER----EIREEMDMM------I  299
c_000005603677_1     227  -----LKIKK-------RYFYY---FVWRG-----TNGGYYLRKRQEK-DIWQGLYEFP---MIELDKPLK--------------TSELKT-----LWAHWELEE------L  289
c_000003283462_3     213  -----KNIPH-------YDVVV---GMIW-----KEGRFLIQKRENQ-KHLSGLWELP---GGKIENNER--------------SELALIR----EIKEECDFE------V  275
c_000002687221_1     227  -----VSRPH-------HNVAV---GLIW-----KDNRILISKRNAS-GLLGGLWEFP---GGKIRSGES--------------GSSCVVR----KTQEILNVL------V  289
c_000003347358_19    244  ------VVPT-------REENI---LVRV-----YDDKLSLTQREG-KFLHGLWGFE---SVEVPH--------------------------------------------  284
c_000002701031_2     222  -----LKIRK-------RYFEF---LIIN-----ENEKILIQKREK-GIWKGLYQFP---LIENSVKKSE--------------RDIENSKS----WKKLFKHNS------I  285
c_000000582753_3     230  -----RKSTN-------RYFTY---YYIS-----DSNHLYIKKRVGK-GIWESLYEFP---LSENLIAFE--------------NEVLDK-----QIFKNSIND------F  291
c_000001713769_5     222  -----NAPKI-------IHFNY---LVLL-----DSDHMICMDRIKN-GIWKNLFQFP---MIESKKELN--------------KTQVLSN----EIFKSIAPIS---NSD  287
c_000004369364_1     225  -----IKKRT-------RFFYY---LVFK-----EKDLFLIQKRTQK-DIWQSLFEFP---NIEGMEELN--------------ESEIREA----IQKKYPNLK------Y  287
c_000006057486_30    226  -----IKIKK-------RHFNF---IVI-N----NNQHTYIHQRKDN-DIWKNLYQFP---LIESKHEIDTN-------------KVIKSSIF---QDFFKNNSY------T  291
c_000005494072_10    222  -----IKIKK-------RYFNY---LVVLS----KKNKITLNKRINK-GIWQNLFEFP---LIETVETITIK-----------TLVEHEYL-----EKIINKKQL-----VD  289
c_000001742634_3     225  -----IKIKK-------RFFNY---LILIT----KDNKTIINKRINK-DIWLNLFEFP---LLETKTEINEN-----------KLVKNDFF-----QKLILNDTT-----IN  292
c_000002826998_2     225  -----IKKKT-------RYFNY---LVLNF----GKNTWVQKRTKK-DIWQNLYEFP---LLETDKIIS------------QKELMKS----ELWKESVSDF----DF  289
c_000003159439_6     222  -----IKIKK-------RYFNY---LVIIN----SQNKIALQRRKHK-DIWKGLYEFP---LIETLTAIDIE----------QLLETEEF-----HQIINEDQA-----I  288
c_000004887214_1     227  -----LKIKK-------RYFNY---LILKT----KNEETLVKQRKGK-GIWQNLYEFP---LLETEKEINYL----------ELIDHSIF----KKMIEENNF------D  293
c_000005037037_2     225  -----VKVKE-------RFFYF---LVLN-----IDNTTYIEQRQNN-DIWKGLFQFP---MIETQQLIN-------------KPKELEK----LITNKINVR------F  287
c_000001059964_1     217  -----KKVKI-------LYRGC---AVIL-----FQDGLILCKRNQP-GLLEGLWEFP---SVELGKGDN--------------LRKALQE----HLLEELGKP------F  279
c_000002498472_1     226  -----KKIIP-------IDMAT---GILI-----HNGMLFIQQRLPD-DVWGSLWEFP---GGRMELKET--------------PEQTVVR----EFLEETEFK-----V  288
c_000004615912_3     215  -----IRKKK-------RYFHY---FISHF----EGKILLRKRIQK-DIWQNLYEFP---MLETKDEELK-----------ISRVQKT----QLWQQLFHGNEKVKVL  284
c_000004766858_2     228  -----PEITR-------IEKLT---ALVQ-----NGDCWLVRKRPEG-GLLGGLWEFP---TWEELPSENS-----------AAAWLTQ----QLHEDYGVA------A  291
c_000002747260_18    232  -----KPKPT-------RHGIA---YLGRR----ADGAWLLERRPDK-GLLGGMLGWP---GGDWAETAT--------------------------EAPPID------V  285
c_000005371561_38    232  -----KPKPT-------RRGIA---YLGRR----ADGAWLLERRPEK-GLLGGMLGWP---GGSDWAESPP------------------------EASPPCP------G  286
c_000000169465_2     234  -----KALPE-------KSTYM---MVAQ-----FNSQVYLEQRPST-GLWGGLYGFI---EVSSIEEGIE------------------------QLAKRGIS-----V  289
c_000003254110_11    234  -----KALPE-------KATFM---MVAQ-----FNSQVYLEQRPST-GLWGGLYGFI---EVSSIEEGIE------------------------QFKKRGVN-----V  289
c_000004750284_20    230  -----KVTPV-------RQTYM---LIPM-----FGQQVFLEQRPQS-GIWGGLYGFL---EAQSAEEGIS------------------------LLAQRGIE-----V  285
c_000000141782_15    235  -----REKPL-------RRTRM---LLIVD----GGRVLLERRPPS-GIWGGLWCPP---ECPPEVDVES------------------------YCRHELGLE-----V  291
c_000002717847_8     224  -----KKD---------VYLEF---SLYK-----DGPKYFLAQTEAL-GFWKKLWMPP---VKIVN-----------------------------------------G  263
c_000004054799_1     215  ------QKPT-------VKLN----FILPH----TKNEILMHKKQAS-EYWESLWIPI---DGDEVKIK------------------------------------G  259
c_000006126673_1     241  -----KARPQ-------RYGYV---YWISD----DGNDILVHKRPEK-GLLGGLYGLP---TSSWETDIE-------------TVEH----PIFISEQIK------P  301
c_000000339186_3     199  -----IRYED-------KQIDV---YLIT-----RGPRYLVQQRPEG-GVNAGFWEFP---NSDSGNKYS-------------APK----------------------247
c_000001279808_52    230  -----VPLQSREE-VGIVIWAG---KPYN-----AVLS-DIWGLQVQRPPT-GLWAGLWEFP---HDEQTTDEP-------------HNAAALR----IAEATVGPT-----M  298
c_000001863436_1     246  -----ARQKP-------VAARTAVVTSGGA----EGRRFLMVKRPAD-GLLGGLWEFP---TVEAAGDVA-------------PTAQAVS----RLLARLTGGP---VPA  315
c_000002830137_4     239  -----TQTEH-------VVEAA---VVIR-----RDDRVLLRRHEDR-ERWAGLWDFP---RFPFDPDATN------------NGHQQLVD----KSRELTGFE-----I  303
c_000004612302_3     232  -----VRTTD-------LYQLL---LVIR-----RDDRLLLIQHPER-ERWGGMWGFF---ALSRTGPLLKS-----------RIDELQIA----SEAAEWGCD-----V  297
c_000001933926_1     217  -----VARPT-------RHGVV---FWATR----GDGCVLLRRRPEH-GLLGGMMEFP---STEWRECPW--------------RIRSAV-----KAAPFA------A  276
c_000003136334_1     229  -----KRKPT-------RYATV---FWLLD----GRGNVLLRRREEK-GLLGGMMEVP---STDWLEENT-------------PTKENS------MFAAAA------V  288
c_000005849454_9     234  -----KKWVD-------LEMVF---LVHR-----VGVRVGLQKRTS-GWSPGLYEPP---SAICESFATANE---------ASSAHESTAH----SLAREHR-------A  299
c_000001169194_1     234  -----VPARE-------ISFLL---VILQT----EEGEVMLVQRPPE-GLLAGMWAFP---EQELAKPLD--------------CAATSRD---RAIELAMSLGA---EVV  301
c_000002786947_2     234  -----APARE-------IFFLL---VILQT----EEGEVMLVRRPDK-GLLAGMWAFP---EQELHKPLD--------------CSTTSRD---RAIGLAMTLGA---EVV  301
c_000001279808_52    220  KKTTTKRRKHR-------IEVGI----ACIW----REGKYLVQARPKG-KSFEGSWEFP---GGKREKGES--------------FRGCVKR----EIEEEVGLN------V  287
c_000000358065_2     224  -----KKIIN-------KFYLA---TLYK-----HDDQVLLIKNDKF-KFLKNLLIFF---MKEISQS----------------------------------------C  268
c_000003745941_1     218  -----KIKQE-------TIDRA---WVEQ-----GGKLLLHRANDKS-RRLSGILELP---TLDVMGY----------------------SAT----ALMK--------268
c_000004187032_4     224  -----KKNKE-------KYFIL---KVYK-----KNQKYLLVKNTKF-NFLKNLAIFF---MEELSKP------------------------------------------267
c_000006067315_3     224  -----KFNKI-------KYFEA---NIYQ-----NQNKYLLIKNSKF-KFLNNLLIFF---MKEVEKN-------------------------------------------K  268
c_000005543774_1     186  -----IESKT-------YDIFC---YLRK-----NKKQIALTKNNDL-GFLKKFNLPE---IKATSKK-----------------------------------------N  230
c_000006211484_1     208  -----IQSKN-------YDIFC---YLQK-----NKKQIALTKNNDL-GFLKKFNLPK---IKETSEK-----------------------------------------N  252
c_000002718976_3     227  -----IKSKN-------YDIFC---YI-N-----TKKQIALTKNNQI-SFLKDFNIPE---IKE-TNNVSN------------------------------------N  272
c_000002992548_1     226  -----KKEQK-------YNVYC---YLKK-----KKKEIALTKNKHL-SFLSNFNIPE---TKIETSNNKK-----------------------------------N  273
c_000000456751_1     192  -----IKEKK-------INIYC---YLNR-----YKKEIALTKNKNL-SFLNNFKMPE---IQMVVANNNLK---------------------------------K  240
c_000002655634_1     223  -----TKEKK-------FNVYC---YLNK-----YKREIALAKNRNL-GFLYNFKMPE---IQMEVTNNNLK---------------------------------R  271
c_000004232403_2     223  -----KKIPT-------RNLAA---ALIE-----YGDYILISKRPIN-GQLGGLWKDP---NIELKNGKS---------------PEKSLKE----SINNHYGFT------I  285
6u7t.after.N146.pdb  226  -----TAVKQ-------VPLAV---AVLAD----DEGRVLIRRKRDST-GLLANLWEFP---SCETDGADG-------------KEKLEQ----MVNHGF--------283
Consensus_aa:             ......................h......hh.........phhl.pp....shh.shh.hP.....p......................................p...........


Conservation:                                   6
sp_P17802_MUTY_ECOL  282  DNLTQLTAFRHTFSHFH---LDIVPMWLPV----SSFTG------------------CMDEGNA---------LWYNLAQPPSVG--LAAPVERLLQQLR--TGAPV------  350
sp_P83847_MUTY_GEOS  295  ELTEPIVSFEHAFSHLV---WQLTVFPGRL----VHGG------------------PVEEPY---------RLAPEDELKAYA--FPVSHQRVWREYK--EWASGVRRPD-  366
c_000003652391_2     287  DWRTLRGEVRHTFTHFH---LILRIRVAEL----PDDI------------------TPAVG--------FLLSKHAFRPSD--LPTV--------------  338
c_000000031207_6     287  ELIGHADRFQHAIIYRK---LFIHPLVYRY----QGE--------------------IPAGV--------ETIPIDGGDR---LPALHRKSIAAAR--ELLLEVFR---  352
c_000000430975_4     294  DWKPHPGRVYHSFTHFD---LELKIMTINS----EVT--------------------PEGT--------FWCRKEEVKAQA--LPSLMHKIMTHMY--KA---------  354
c_000001007148_4     298  EFQEWMDEFQHGVTFRF---LHLQPIVAMW----RSGSW------------------EGPVTA--------EWVGIDELATRP--LSVAGRRVATRVE--RILRHNGAQA-  370
c_000001092848_3     303  PWEPC-GTVTHTFTHFT---LALSVYRARV----ADMP------------------APAGS--------WWCAPGLLAGEA--LPTVMKKVVEAAI--SGATKARRPIG  373
c_000001151029_1     251  DWKPQPGLVYHSFTHFD---LELKI--------------------------------------------------------------------------------  272
c_000001797282_1     313  RWKRLPGLVRHGFTHFP---LELTVFVARV----ALATP------------------APAGT--------RFTPRSALDDEP--LPGLMRKVLAHAF--DPKPEPEKKPR  385
c_000001803648_25    290  DWQDPGAEVRHSFTHFH---LRLSLRISVV----GNA--------------------KPTAG--------HFIADADFDPET--LPTVMRKAYRIAR--TKFDGDANG--  358
c_000002078955_4     290  DWQVLNAEVRHTFTHFH---LRLSLRVATI----GNK--------------------PPATG--------DFISKNAFDPET--LPTVMRKAYRLAC--TQFDDN----  355
c_000002106160_4     287  TIKNKIGEIRHRYSHFG---ITLSGFHCRL----INGSK------------------PEVNRPF-------RWIRLNEINQYA--FPKANHKLFNLMQ--E--------  351
c_000003607531_2     297  QWVKIAGTVNHAFTHFQ---LQLQVRVAVV----NDQT------------------QISGG--------IWVDRDRLDEFA--LPNLMKKVWAFAS--KRIQPLPRLDC  368
c_000003872363_4     286  DWQRLDAQVRHTFTHFH---LRLSLRIVVA----KNV--------------------IPTVG--------MFIPSDKFDPDD--LPTVMRKAHALAD--AAFDHG-----  351
c_000004820107_1     292  ESEQTNLSVKHSFTHFD---LIL---------------------------------------------------------------------------------------  311
c_000005774797_1     276  SEWKGIGQIRHIFTHID---L-------------------------------------------------------------------------------------  293
c_000005867021_3     290  DWHVLGAEVRHTFTHFH---LRLMVHVATV----NEN--------------------SPDVG--------KFIADDCFDPAD--LPTVMRKAHKLAL--GSFVGD----  355
c_000004546210_2     287  LWVDSWEPFKHSFSHFD---LYIHPIQIRM----DGQFM------------------NTAYKSKT-------QSFSLNQLDSLG--LSAPVKGLVNKLY-----------  351
c_000004551008_5     287  LWVDPWEPFKHSFSHYD---LYIHPIQIRM----DGQFM------------------NTAHTPKT-------QSFSLNQLGSLG--LSAPVKGLVNQLY-----------  351
c_000002511148_4     282  LNIKKLSKVKHSFSHYN---LEAIPYLAKL----ESNK------------------KYKNS--------VWVDYKNVESLG--LPAPIKKTINQLT--KP--------  344
c_000000577378_2     270  LNIKKLGKVKHSFSHYN---LEAIPYLATL----GSNK------------------KYKNS--------VWVDYKNVESLG--LPAPVKKTINQIT--KP--------  332
c_000000598175_2     293  QESIALAEIKHTFSHFH---LYIQPLIINV----ETPIE------------------LGVMEDNES------LWYNITTEFNGG--LAAPVQTLINITK--NIEKEIENGTN  369
c_000000754627_3     287  SDLNEVAPFTHVFSHFE---LTINPHVLNI----EKAPD------------------VVNDKQL------VWYPLDQSIEVG--LAAPTKKLVKQIT--AIV-------  353
c_000000811118_1     274  PVEEDFSSFEHHLSHKK---LLISVKVLTI----KNKDR------------------LSIDRRIF------NWVNISDSVNMG--IPKPVKDILKKYD-----------  338
c_000000899687_2     290  VSLNKVMTIKHTYTQFR---VTLTVFNCKL----QKKQI------------------RPDGCEQW------KWVSLSLKLKKYP--FPAANVKIVKYLT--EK-------  356
c_000001176522_24    289  --GEALSAFRHTFTHFH---LDITPYLWHT----HSDD------------------MPQQAG--------QWLPLAQALKMN--IPAAVKRVLQEVI--EYEQNR---  354
c_000001345122_1     262  EQAVI----KHTFSHYH---LRMKPMM-----------------------------------------------------------------------------  281
c_000001515736_6     279  RSWQDLPGFLHVLTHKD---LHLHPVLVPV----DQAYA------------------ALVSEADES------CWADAAAWAELG--LPATPIKKLLDAEL--A-------  345
c_000001682161_6     283  DSVEILKQLKHTFSHYH---LMMNPVMLQI----ERE--------------------AIEEV--------SWFELENLNGVG--LPTPIKKILRESF--A--------  343
c_000001923643_29    289  ADWTELPAFLHVLTHRD---LHLHPVRVPV----HGSGP------------------DAAMADGQG------CWADARAWADMG--LPAPVRKLLDAQF--AG------  356
c_000002030994_5     282  SEADKLSKIKHTFSHFH---LHIQPLIINT----ETPLK------------------MGVMEHDDS------LWYNVTTEFNGG--LAAPVQTLLNITK--DIVKGTQNDTN  358
c_000002038721_4     276  EEKESLPLIVHNLSHQK---LSIFTKKYFL----KNKDR------------------LPIDRRGF------VWVNKKESVKMG--IPKPVKTILENHL-----------  340
c_000002523527_15    316  ARAYLAGELTHVFTHFR---LLIRAIRVDL----DTVAL------------------EGDAAS--------RWLSLDDLDMLG--TPAPVRKLLEDQA--RFGLF-----  383
c_000002608528_2     282  DEAIKLSEIKHTFSHFH---LHIHPLIINM----ETPLK------------------IGVMEHDD---------------------------------------------  321
c_000002961510_2     290  ISLNKVMTIKHTYTQFR---VTLTVFNCEL----QKKQI------------------RPDGCEQW------KWVSLSSLKKYP--FPAANVKIVKYLT--EK-------  356
c_000002979152_8     290  PSLQAYAEIEHEFSHFH---LSAKVLRIEL----DSDKR------------------LGVMEETNA------LWYNMHKDNPGG--FPAPIKKLLSRNL--L--------  356
c_000003248034_1     302  KHPKKLCKFRHSITFRL---YDVSIYTAIL----EGE--------------------LPEPF--------CWVPQRKLATIP--LTTVTRKALAVLS--PNSSDRNDEQN  372
c_000003294679_3     286  LKISRWKTLQHKFSHFD---LKIHLFKAEP----DIAIK------------------NIANNDSA------LWYKSDSQTRIG--LAAPVKKLLETQF--NIQ------  353
c_000003333364_1     288  AASETIAVIRHGYTSFM---LTLTVFKKV-----GEPPEGW------------------PEPVLHDATEG-------VWVSFAELDRYT--FPAGHRKLLDQMS--RDMRYAWLV-  366
c_000002786947_2     288  SVRPHFYEELEHEFETE---LLLRFHRCQI----QAGEP------------------SPQEEQEI------KWVSPDDFGDID--FLKTNHKALDKLK--EMRV-----  356
c_000003492925_4     253  CASEYIGEVTHRAYTHFK---LICKVYVYDE------------------------LDAEQN--------SYFTSSKIQKLA--ISKVDDKILKLYL--DTIQTY-----  316
c_000003766664_5     302  RIEGQCSSVRHVLTHRD---MDIAVFALSV----KGREPS------------------PALSTYTGG------MWIHSPEALEDLG--VGRVTRKILEAAA--THEISGQER--  378
c_000003948186_72    284  DSCTELAPRRHTFSHFH---LLITPLHIKS----SQQTT------------------HVMEDQQQ------LWYNMRKPASVG--LAAPVKRLLRQTS--NQ-------  350
c_000005057120_4     282  QSVQHIEKQRHTFSHFH---LDYTAVLVKT----ENRIN------------------NVMESNQS------VWYKSDKINALG--LPAPIKKLLQNQN--RNEV-----  350
c_000005590109_5     282  KLIKQLDEQRHTFSHYH---LDYTGIMVKI----ENPIN------------------IVMEANQS------VWYKSTQLKFLG--LPTPIKKLLQNQY--------  346
c_000006063368_2     282  PSLIQIKKVKHSFSHYH---LEAIPYLVKI----KEKK------------------SIKNT--------VWVDSKNIESLG--IPSPVKTIKEIR--VP-------  344
c_000000467631_2     261  TSKKQLDGQRHTFSHYH---LDYTPIEVKI----ENPIN------------------NVMEANQS------VWYKSEQINSLG--LATPIKRLLQNQ----------  324
c_000000788235_1     283  PSATTESHFSHTFSHFN---LQAQTLLITQ----STPIK------------------IVMEHDD------LWYNSNTTFMGG--FPAPIKTIINKLN--EDF------  350
c_000001187176_11    283  AEPEALSPLRHTFSHFH---LDIQPLLVRV----DAPDR------------------VTESGQ------VWYNLREPSRLG--LAAPVKKLLQRAE--LNTQADERTSP  356
c_000001660697_64    297  SDVEAAGALTHTFSHFH---LHMHLLHADI----TKP--------------------ATLDDW------RWVPLAQLNSVG--LPAPVKLALETLV--QPSLL-----  363
c_000003378864_2     301  EVGPLVTQVRHAYSHFKITLHAYHCRLLRG-----TPH--------------------PKVAVES------RWVPLNGLDQFA--FPKANKRVLEVLEQPPAMPEVTP--  375
c_000003910742_3     284  ENTEKETKLSHTFSHFR---LHIHALLIRQ----DNPLN------------------FVMEVDQA------RWYNRSTKFTGG--FPAPIEKLFTRIL--T-------  349
c_000004116181_1     249  KTSEVLPTLRHTFSHFH---LQYTTLVVRT----DNPLN------------------FVMEVDQA------VWYKAEQIPGLG--LPAPVKRLLDNLI--LNEDNND--  320
c_000006223903_1     284  LFESAWSVLRHSFTHFE---LAITPQPARA----PKRLT------------------RRMQSTGL------LWYKPGEPF-----------------------  332
c_000001029068_2     257  QVRKKLPLINHSFTHYY---LTI----------------------------------------------------------------------------------  276
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c_000001128125_11    291  ESLVEWNYFRETFTHYH---LDIYPLVYRLD--EGEVSPVFTIG--------KSQNNDEKASAEM---------NWIELDRLNKGEVGVPAPVNKMLERLS--ETLDK------  374
c_000001595844_4     288  NIKNKLGPVTQLLTHQK---VIGQFFDITL----VGE----------------------KDLDI---------APISKVDLQVFP--FPKMMMMYINRIM--A----------  348
c_000001719155_2     292  HIDEKLMTVKSYTRFR---VILHVFLCRV----LSGRV----------------SPTHCEEW--------DWVKTEELDRYP--FPAANVKIIKSLR--KNQGRS------  362
c_000002363038_6     293  HSLSEGEPFRASFSHYH---LDIFPLIF-------QASTDYEIGQP---SNRVQETPAEYSVAHH--------QWFDINRLKSGEIGVPVPIRKMISSL--------------  370
c_000002561400_1     247  EGLIEWDDFRRTFSHYH---LDIYPLIFDE----RGAPKNTAKI--------ISEPGGVYDAEQG---------SWFDIQLLLDGGLAVPAPVNKLIGRLD--ELVE-------  327
c_000002566035_2     284  KQQEKEYKPIKBAFTFHFH---LTIRPIHIKI---RIYKD------------------KDYDTKVL--------KWIHPKTNPNLG--LPAPVLSMLIDLN--NTKRAVLNES-  358
c_000002598045_3     282  SNIKKLKKVKBNFSSHFN---LEAIPYLVKV----KKGK------------------KIKNT-------VWVNFKNVESLG--LPAPVKHTINQIT--MP----------  344
c_000004188575_41    280  TVSKQPAVFRHIFTHFK---LDIHPHLYHA----KQSAA-----------------ENITGQA--------IWYKIEDALTLG--LPAPVKKTLLTLS--KG----------  345
c_000000240049_1     282  NSHNDLAAFRRTFSHFH---LDITPCEVDI----TQSAY------------------AIAENDRF---------QWH--ADITQLA--LAAPISAIFRENN--SLK--------  347
c_000002139456_2     282  NSHNDLAAFRRTFSHFH---LEITPCEVDV----AQSAH------------------AIAENDRF---------QWH--ADITQLA--LAAPISAIFRENN--SLK--------  347
c_000003535614_2     284  KKHHDLPVFRRTFSSHFH---LDITPCEIEI----KSISN------------------AIGDDSCY--------QWQ--VDISKLA--LAAPVSAIFNAK--------------  345
c_000002657784_4     281  KDLKTYPDINRSFSSHLN---LNAKLFLLKL----NEDIN------------------YNINKGKY--------VWVDKKGLKALG--IPTPVKNIFEVLK--LNDQTS-----  351
c_000003800129_15    263  ---NNNREIKBGLSHRE---LHLEFLVTSG--------------------------TPKGG---------KWINKNEFNNLP--TPKPISDKLEQYA--KSFL-------  320
c_000003716781_1     273  LQREEVGELRRSITKHR---IRARVLRAVP----GRDE----------------------LPEGW-------AWFERSEIEALG--VTGMTSKALTLGR----ARSR----  337
c_000001556689_3     294  RLGPKLGEIRRGMTFDRR---ISCHVYEASL----SGSQTTMAGA--------PTGLEKSDHNIPDS--------GWFTIEEVMTLA--LAASARKTLTTLL--DIDLTTAHNPG  380
c_000001834452_1     254  KLGEMMGSARRTITRHR---IQARVHQVEG------------------------------W----------NGKGAVDPSSVP--LSSLGRKVLSIAG--VLGGLLLLSPD  317
c_000004255004_2     275  QQGDPVALIHBAITDMR---ITAPVYLLQC----KIPV-----------------------KGPEW-------RWVSLANLHAYP--LSSLSTKALSAAR--QHLPTTRKLGG  346
c_000000605438_3     263  ENMTGLGEFKQHYTHFT---LDARVVLKLD------------------------------KKQE-------NYFTVEEIHDLA--LSGADRKALALLE--KYLQ-------  322
c_000000581237_15    263  KDMIKLGEFKQHYTHFT---LEASVVLVQN------------------------------KEQE-------RYFRINEIHALA--LSGADRKGLALIE--KHLA-------  322
c_000002529579_2     263  NNMTELGEFKQHYTHFT---LDGSVVLVTN------------------------------KKQK-------NYFTIDEIHDLA--LSGADRKALALLE--KYLQ-------  322
c_000006097838_1     268  VEPESLCIINRSITCYR---NRLEMFVIFR----TRKPL-----------------LAKLKG---------KWVPLAKLDEIP--LTTAHRKAANQFA--G----------  331
c_000000583727_6     294  AKFQPLCNINRSITRYR---NRLEMFVAEP----KRKPR-----------------LAKLKG---------EWLPLAKLAELP--LTAAHRKASDYFL--KTANSR-----  362
c_000005807640_2     295  AELEPLCTINRSITRYR---NRLEMFVIEP----ARKPR-----------------LAKLNG---------EWIPLAKLDELP--FTTSHHKAANQFC--------------  357
c_000000134878_1     270  KPETIIHQVDRHYSHFS---VTINAINCKY----NGGDI-----------------KLSGPTDF--------KWIHTSKLHSYA--F----------------------  322
c_000005136725_3     285  KPEKLIHQVDRHYSHFS---VTINAINCYY----NGGKI-----------------KLSGPTDF--------RWVKTSRLHSYA--FPKASIKLFNAIK--SIE-------  352
c_000001684786_4     280  ETGEELKAIKRSITFRR---LTLRPRLLET----GSFTI-----------------RGKPSF---------RWALPEELGSVL--PVSSLCLKIADRLS------------  343
c_000002971826_23    290  EEGAELEAIRRSITFRR---LTLRPRILGA----GSFST-----------------RAKPSF---------RWGRADELGNVL--PVSSLCLKIADRLS------------  353
c_000002040695_2     291  ASWTLLGQIQRVFTHFT---LKLDLWYTIR---------------------------TVKTQG--------QWVLLNQMNDYP--LSSLTKKSLAFLV--KNLELEKEQAR  359
c_000003263657_32    303  KTDLVLPTVLRVFTHFE---ITLYGFGCT----IKGAA-----------------KALTCHDA--------RWVSQTQLADFA--FSRAHNRLDIMK--KEAAKGQVEMF  378
c_000059989041_2     297  QWVKITGTVTQPFTHFE---LQLQVRVAVV----ENKP-----------------KSSEG---------IWVDRNRLDDFA--LPNIMKKVLAFAL--RHNQHFSREFF  368
c_000002391082_2     298  EVGARLTSVDRAYSHFS---ITLHALEARY----LRGEP-----------------QAIGCADW--------KWIVPDELDDYA--LPRADRLIVEFLR--QDGRQLGLFDS  373
c_000003839553_2     305  EAVARLTSVDRAFSHFS---ITLHAIAARY----------------------------EAVECDDW-------RWIDPAELDDLP--MPRADRRALEELS-EEEGQRVPVLMA  331
c_000003996707_2     295  EVGGLLAKVDRGYSHFS---ITLNLFEAMY----RGGEP-----------------EAVECDDW-------RWIDPAELDDLP--MPRADRRALEELS-EEEGQRVPVLMA  371
c_000002044706_1     271  ----LVVTSEHRFSHRH---WTTRVYRA-----RVEDE----------------CSGPADASHWSEGL----RWTCAGDLGKLA--VPEASRKTLRPCLRASRGSLPG----  353
c_000006007075_1     268  --KNLQKTLNFKMSNMN---MNIVIKIMKI----SSN-----------------------ISDS--------SWIKETKFNHYT--FPTFTKKIFNSLE--NYL--------  327
c_000002094036_4     245  SLLKSKNKLNLKMSNMN---MNICIDFVKI----KKK-----------------------PKNG--------LWIESSKLENCM--IPTFTKKIFASVK--NNL--------  306
c_000002762689_1     268  --LSSTDIVNFKMSNMN---MNIKIEHKNK----VGS-----------------------LPTS--------HWIDPKKLKNYT--LPTFTKKIVRYLE--SNK--------  327
c_000005516980_2     268  --KNFNENLNFKMSNMN---MNIKIQYSKN----NIK-----------------------LPSS--------YWVDQKKLNNYM--LPTFTKKVVKYLE--NNK--------  327
c_000003920004_1     293  KKFTKCKPILYSFSHFD-----------------------------------------------------------------------------------------  309
c_000004008511_2     287  NKLKLKGFVDYSFSHFD---LETEVFFTKV----KKDY-----------------------FANQ--------KWIKKNNIKISG--LPTVMKKIIEVAL----------  346
c_000004481347_1     294  VKYKRIGKITYSFSHFD---LDIGIYKSKV----VKKK-----------------------FKNF--------NWIKSNKIDTSG--MPTVMKEIVKKSL--KI--------  355
c_000003787733_3     289  NIGKKIGHVKBAYSHFK---ITLTLYQSKK----QGSV-----------------------NIYKEY------KWIIPTEVNNYP--FPKSNHKLFK--------------  348
c_000000754657_2     289  NIKKKVGNVKBAYSHFK---ITLTLYRCQS----QGSV-----------------------SNNKEY------RWITPAEIKYFP--FPKSNHKLFDVLN--SNGWNV----  357
c_000000990943_3     289  NIEKEVGYVKBAYSHFK---ITQTLFQCQT----QESVK----------------------SINKEY------RWITPIEVNNYP--FPKSNHKLFTILN--SDGWNV----  357
c_000004474996_2     288  NIKNKVGYVKBAYSHFK---ITLTLYQCQT----QESVK----------------------IMNKEY------RWITPSEIQYFP--FSKSNHKLFNLLN--SNGWNV----  356
c_000001463500_11    276  QIQNKICTIKRSYSHFD---NDINI--------------------------------KNMKNV------CWIRPKDINNYA--FSKSNHKLFKILN--TNGWTI-----  344
c_000001286181_5     263  QNINELPSFKRSLSHKD---FHISPRIINI----PDDME-----------------TDDKKT-------IWIEKNKIAKLG--APKPVLDIVKKIL--NQNDKGLL----  333
c_000001293628_3     302  VRFSPLPEVRRTFTHLK---AVYRPMLVIG----TRCEG----------------SNPDSEH------KWVLPDQVEDLP--LPVAQRRILDLAW--AALEGC-----  371
c_000001535696_8     292  VLRYNHKIIVRKLSHQQ---LHTHFWIVVI----SNELD--------------------------------GSILLSEIENYP--VPVLIANFINTFK--NSYFWPNNSIR  359
c_000001614067_2     298  KWKILDQNLNRIFTHFK---LNCSLAIATI----NDENAL----------------VNDLSKSSY------RFVQKTNINELA--LPSSLIKKILNALK--NNEILDF----  371
c_000001765289_1     262  SIKKRIGAVDRAYSHFS---ITFHGYHCIE----NGEK-------------------------------------------------------------------  292
c_000001961666_1     274  NRILSKNVVRREFSHFK---LELEVVYYIET----RFP---------------------QITHG-------EWLKTKQAGKQ--LPSVMKKVLDNI------------  331
c_000002018097_4     284  DILNCFDKVKRSYSHYK---LLVTPFECEV----LNA----------------------DSRIG-------RWIRVGEIDKYA--ISKVDDKILNFL--IKNY------  347
c_000002843512_36    254  CASKYIGEVTBAYTHFK---LIIQVYVYDE--------------------------LDAEKN-------SYFSSQEIQKLA--ISKVDDKILNFL--NSIECD----  317
c_000002930199_1     281  SNIKNKYTIEBNLSHQK---LKISFWDVDA----NNISS--------------------TQKGF--------EKITLDNISNYP--FAKPLEKYFQTQH--LIT-------  344
c_000003033795_2     277  SNPIFLGNITBKYSHFG---VNISFFISFP----KSIKS----------------FNSSQEY------RWIRIKNILNYP--LPKANHKMLDILK--KL--------  342
c_000003888107_2     278  KNPNYLGQIKQYSHFK---VLISLFLADV----NDISS----------------LKPNQNY------KWTTRKQLDKFA--LPKANYKMLEILD--KLN-------  344
c_000004013286_6     307  QIGNKIGQIRVVTRFR---TTVDCYEAHF----SNIGKPNRSKNDISVNTLQKEQQEAGSLWHM--------QWATRKQIDSFP--MSVPARRVIRLLA--DFD-------  392
c_000004852258_1     265  KVGHKLGMINRTFTHFK---MNVLLYNCQA----KDQP-----------------LSKNTE-------KWVSFSDLDQYA--FSKANHKLFKLVE--LRND------  330
c_000005254087_1     300  RTDRFLTSIKBAYTHFR---ITLHAFHATH----LRGEP-----------------QHIGVADH--------AWVTLADLDKYA---------------------  351
c_000005603677_1     290  VWALISGQEQQOLSHQK---IIARFLWPKQ----PLPQ-----------------ALSADW------ELVDAQSWPNYP--LPRLIAQYWEKKQ--LAFF------  355
c_000003283462_3     276  VPKKKIESIKBKYSHFS---ITLTAFHCKI----KNGAK----------------VPSKQST------RWITPGEIGDYP--FPRANHKLFNQLE--NFYSNG----  345
c_000002687221_1     290  APVAFVKQIKBAYSHFS---ITVDAYSCTF----RGGRP----------------RALGCADY------RWIYPHETGKYA--FHSAGHKLFDKIL--ETAS------  358
c_000003347358_19    285  CASEYIGKVTRAYTHFK---LICKVVYYE----------------------------NHPEEA------DYFSEEEIQKIA--ISKVDEKIVNLYG--NFLKYD----  348
c_000002701031_2     286  QILKISATIKBQLTHQT---IFARFWHIDT----KIQ----------------------KVENS-------KYISKKELKNYP--ISRLLEKYLENIG--MI--------  347
c_000000582753_3     292  AIRKVHLKIKBVLSHQN---IYAKLIEVEV----LDVI----------------------RLENY-------IKVEKEDFESYP--IHRLMEKMMEQVG--K--------  353
c_000001713769_5     288  IILFNSSPIIBKLSHKT---IYAKFWILPV----NGSNS----------------------------------NSIKFSDVNKYP--VPRLIEKFLDKFN--YKHF------  348
c_000004369364_1     288  KIKHKSAPSKQLLTHQK---IIGIF---------------------------------------------------------------------------------  309
c_000006057486_30    292  ISKYNQKQIVRKLTHQH---LFTTFWIINT----NTCSK--------------------------------NTVNWQNLSNFA--LPTLIQNFVDDFK--K--------  349
c_000005494072_10    290  VSLFNPKPIIRKLSHQH---LYTSFWIVNY----NGSVS----------------------------------NTISIDELKKYP--VPVLDNFIKDFE--M--------  347
c_000001742634_3     293  PYLFNEKTVIBKLSHQH---IYTKFWIVKL----DVNLE---------------------------------QTIPLNSIEKYP--VSTLIQNFIKEFN--F--------  350
c_000002826998_2     290  QIKKISLPFRQNLTHRK---IIATFFEIDF----MDKFS--------------------NKNNNY------IKIERKNLSKFA--FPKIIDLYLDDNS--LNLAMK----  358
c_000003159439_6     289  TSLSYSDNIKAHKLSHQH---IFSKFWIVET----KQNIL----------------------------------NSILIEDLEKYP--VPKLIQNFIEKFD--NIKLNPATK--  354
c_000004887214_1     294  LQLLTPKVVVRKLSHQH---LYIKFWEIRV----PTFRS---------------------------------ATISWQELLKLP--FPIVIFKFIREFL--ETSMPNFDTPL  361
c_000005037037_2     288  KVKKRSKNFTQRLTHQK---LNAIFIEIDL----KTK---------------------INKQF-------INTDINNLSKFA--FP-------------------  336
c_000001059964_1     280  QLGKEIHTLERRYTSFR---TRVSFFTATV----HVLPE---------------------SSQKRV------RFVKTSEVE-----------------------  326
c_000002498472_1     289  EIVEKITNTVRHYTRYK---VTLHCFLLRL----KKGSDT----------------DPVLHAAQDF------NWVPFKALQEYA--FPAGHRKLITYL------------  355
c_000004615912_3     285  QTKK----XYQQELTHQK---ISAYFWEIN----LNVAP----------------VNIYDF------ILIDSKNLAKFA--FPKIIALYLENNS--LNL--------  345
c_000002766858_2     292  RIGPELFKMERDYTHFH---ATLHCRLCTV----AEIPS---------------VLPDNA------QWLTLGEISALA--LPRVFQRLRKRLL--DEVSA-----  359
c_000002747260_18    286  PWRDPGAEVRRTFTHFH---LRLALRVADL----PASA----------------TPRTG-------QFIPHHAFRPGQ--LPTVMRKAYDLAS--ATFLGN----  352
c_000005371561_38    287  NWRTVPGEVRRTFTHFH---LVLELRRADL----PEDC----------------TTMRG-------QFLAPGGFRPSD--LPTAMRKAFDLAR--DG--------  349
c_000000169465_2     290  DETRTLEGFRRTFSHFH---LDITPVVAVV----NSAPS---------------KRVAETAF------RWFSLNEPIEVG--LAAPTTKIIQQLM--R--------  355
c_000003254110_11    290  EETKTLETFRRTFSHFH---LDITPVVAVV----NSPPT---------------KRVADTAF------RWFSLGEPIEVG--LAAPTTKIIKQLI--G--------  355
c_000004750284_20    286  EEIQQLDEFRRTFSHFH---LDITPLIAVV----NSTPQ---------------KRVAENES------RWFLLDEPIEVG--LAAPTTKIIKTLA--K--------  351
c_000000141782_15    292  TRPQAWPGLRRTFSHFYP---LDIQPVRLRL----TAAPA--------------RLMDGDRH--------VWYNVESPDARG--LAAPVARLLQGLA--LEDTRA-----  351
c_000002717847_8     264  ---KFNAANKBALSRRH---IHFRFKQIAN----LPT--------------------GMKG--------EWFSKKDLANIA--LPKPISDKLLQDG-----------  319
c_000004054799_1     260  NQKYSKIKVNRPLSHLN---LDMKIKTFKI----DKKCD------------------------------LDSN--L---------------------------  296
c_000006126673_1     302  KPYKQLPFIMRVFTHFS---LKLYLCKTSE----FICDN-------------------VPEEH-------KWVFISTLEDIG--FPSVFEKVKKII-----------  362
c_000000339186_3     248  -NGQPFASARRSITRYR---IQLNAHLIHA--------------------------KRGKG-------MWCTSDEIRSLP--FSSAHLKLLGKLP--HRLDK------  308
c_000003029168_2     299  QKLTKLVTITTVMRTR---TTLHVFGMKL----DLETS-----------------TMQEASSR-------LWVRLDGLHKHP--FSSPQHEIIKTLD--KEAALQLAGLV  374
c_000001863436_1     316  TPRVELGEVVRFSHIR---MTITAEHRVA----SSEQVRL----------------RSDDEVGQEA-------RWVSAVELVDLP--MSAAMRKIEGLYR--ELGSGAI----  391
c_000002830137_4     304  EPVRQLTTIQRGVTFFQ---ITLQCHLAQC----VSGRK----------------RGPHL-------SWRMPHELEHLP--LSVTARKIGRLVA--KLAD------  369
c_000004612302_3     298  EVEEWLQEFRRGVTRFR---LHLQPVVASW----RAGHW----------------IGPVVA------EWVEIDELTARP--LSVAARRVADGVQ--AGQRCGGASG-  370
c_000001933926_1     277  AWRELPGAVRRSFTHFH---LELQIMTVET----NEEVEG-------------------------------------------------------------------  309
c_000003136334_1     289  DWQMLSGKVRRTFTHFH---LEL-----------------------------------------------------------------------------------  308
c_000005849454_9     300  KLGAYQGQVRRTITHHR---IRAHVYAAEG--------------------------Q--------APTHLEDPTQVP--LTGLARKVLDRIT--SA-------  354
c_000001169194_1     302  GVASALAEVQRRFTHLQ---ARYRPWVVPV---AKL-----------------LNGEGN-------VWMTPGEPVDFP--IPVAQHKVLDALA--ECGATLGSSES  373
c_000002786947_2     302  GHASALAEIQRRFTHLQ---ARYRPWVVPV---AKL-----------------LTGEGS-------MWMTPGEPVDFP--IPAAQHKVLDALA--ECRATPDSLES  373
c_000000278608_22    288  SVRSHFYEELHEFERTE---LLLRFHRCQI---QAGEP--------------QALENQEL-------KWVSPDEFDSVG--FLKTNHKALEKLK--SMRV-------  356
c_000000358065_2     269  SLSKPDHKLNLKMSNMN---MNISIDFSNN----KKK-------------------LKNG--------LWVEKTKLENHM--IPTFTKKIFASVK--HNL-------  330
c_000003745941_1     269  RGNTPIVTRKRGISNSQ---ITEPIWRLSD----NSEA-----------------DHAEM------EWIDLEQIKKVT--LSGPHKRWINEIL--TDFNKQK---  336
c_000004187032_4     268  --KNFNENFNFKMSNMN---MNIKIQYLKN----LKK-----------------FPSS--------YWFDKRRLDNYM--LPTFTKKVVKYLE--KN-------  326
c_000006067315_3     269  FNTSLNKKINLKMSNMD---MKIILNKKNK----LIK-----------------IKNS--------YLVDKKNIKDLI--LPSFTKKIFNSVS--NYL-------  330
c_000005543774_1     231  KNWKFLCNYKNSISNKK---LNLNLYYKFS----SRI------------------PSKY--------NWYSL-KKNKEF--IPTFTKKIFKQIT--HLY-------  291
c_000006211484_1     253  KNWRFLCNYKNSISNKK---LNLNLYYKFT----SKI------------------PSEY--------NWYSL-NKNNEF--IPSFTK----------------  303
c_000002718976_3     273  QNWIFLKNYKNSISNLK---LNLNLYYKFS----KKI-----------------PRSF--------NWYSL-KENKEF--IPSTFKRIFRQVS--TLF-------  333
c_000002992548_1     274  NGWIYLCNYKNNISNIK---NNINLYFKFI----KNK------------------PKKY--------MWYPIDRRSNEF--IPSFTK----------------  325
c_000000456751_1     241  RGWYYLCSYKNNISNIK---MNIDLFYKFT----KKI-----------------PKKF--------NWYSIDRSNQEF--IPSFTKKIFKKIA--KVYS-----  303
c_000002655634_1     272  REWNYLCNYKNNISNIK---MNIDLFYKFT----KNK------------------PKKF--------DWYSVDKSSQEF--MPSFTKKII------------  326
c_000042232403_2     286  EVGKNIGLIQRTFTHFK---MNITLFCCLL----KYDQ-----------------KIDSSA------KWVRLFELDQYA--FSRGNHKLFQLYQ--KENV-----  351
6u7t.after.N146.pdb  284  ELTEPIVSFEBAFSHLV---WQLTVFPGRL----VHGG--------------------PVEEPY--------RLAPEDELKAYA--FPVSHQRVWREYK--EWAS-------  349
Consensus_aa:             ........hp+.ho+bp...l.hp.h.h...........................................@h..pph.phs..hs...p+hhp.h.............
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