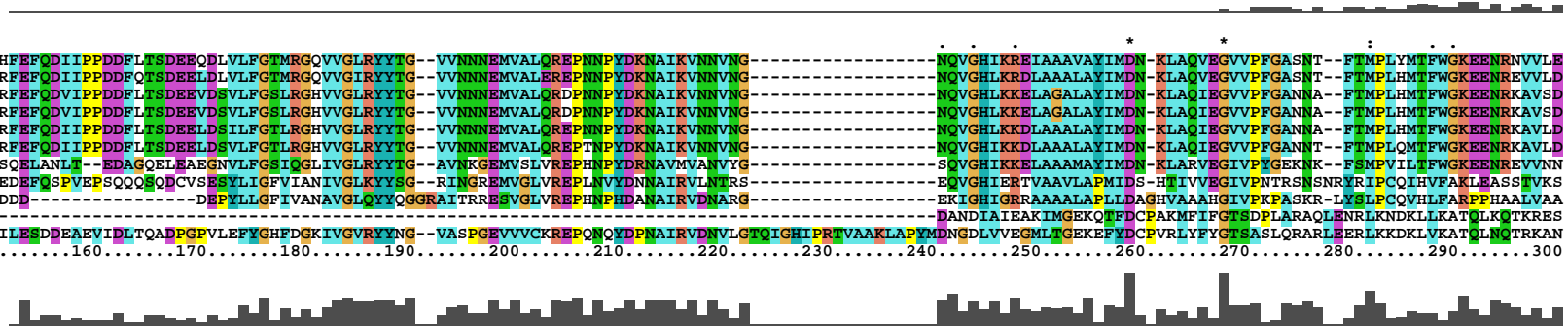
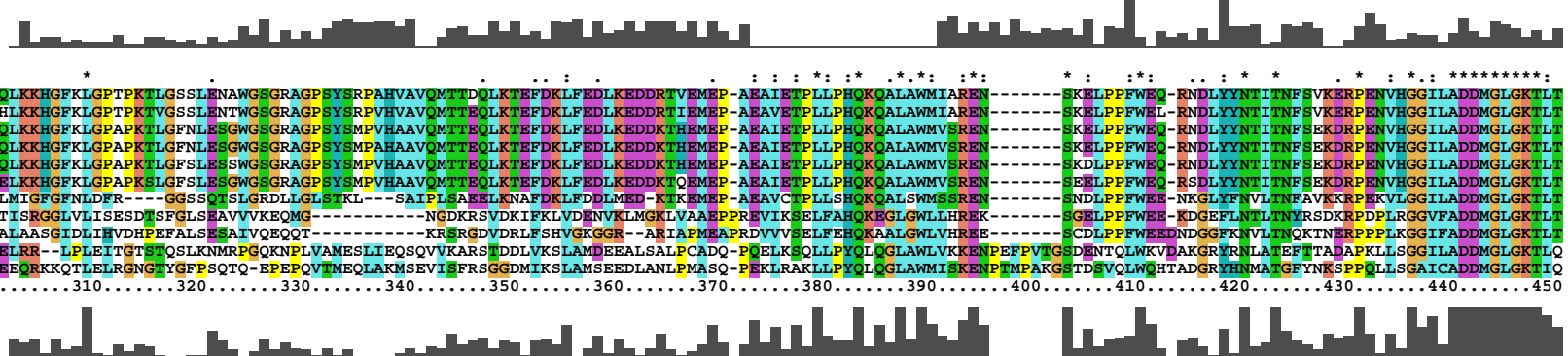


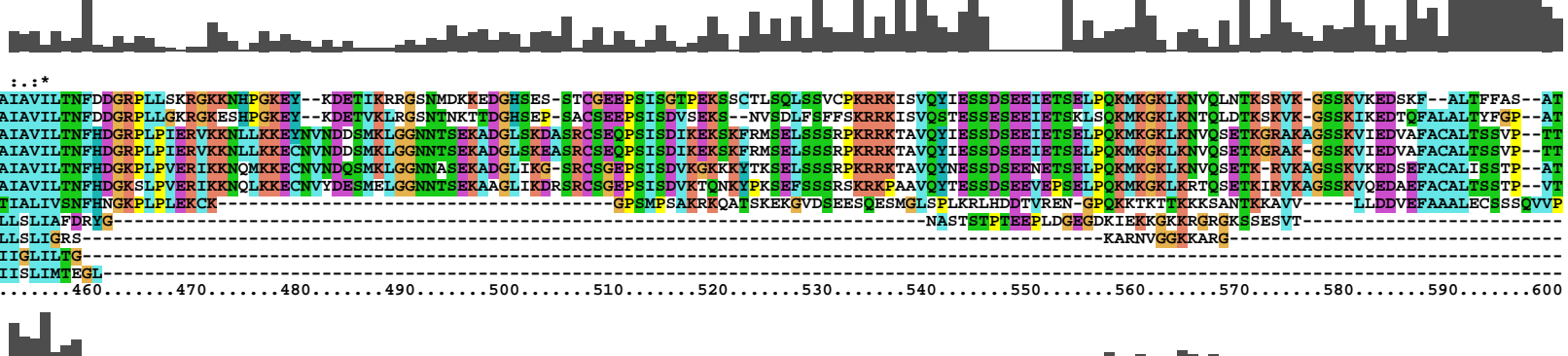
gi | 67763824 | ref | NP_033236.2 |MSYTF-TRGPVVKYSQSVQVGSHEINPRLSYSLFLP 35
 gi | 109464650 | ref | XP_215728.4 | MTLSDVPHSRRFVFPNRSLPTTSELGGILARHTAFEQHKAEPLTLTYFYWLVFDSFFRLGTRSDHRTSLVPHIVAGRSGRRHVSRGACGLLILTCFPAAGPLHLELFLQILSVLFXNRDSVVKYSQSAOYGAHENIPRLSYPPFFP 150
 gi | 21071052 | ref | NP_003062.2 |MSWMF-KRDPVWKYLOTVQYGVHGNPRLSYPTFFP 35
 gi | 114589754 | ref | XP_516811.2 |MSWMF-KRDPVWKYLOTVQYGVHGNPRLSYPTFFP 35
 gi | 73990698 | ref | XP_534300.2 | ---MNCFRFRYSKRVARQAPAEVHRGKPREVTRGLRSGTRAAARAASDEKTRRRLIPARALLLRRSASARCSLA-----VGPAGRSTEAARGLAGAPKPSVSRRLIAMSWMF-KRDPVWKYLOTVQYGAHGNPRLSYPTFFP 134
 gi | 119884988 | ref | XP_588490.3 |MSWMF-KRDPVWKYLOTVQYGVHGNPRLSYPTFFP 35
 gi | 125805885 | ref | XP_693071.2 |MQSSSSLASSTPERAFIDFMDVGS--HMLL 31
 gi | 22326612 | ref | NP_196132.2 |MAQFLRRFSFPMAN 15
 gi | 115473675 | ref | NP_001060436.1 |MASTERRGG--GE 11
 gi | 145603372 | ref | XP_369370.2 |MPK-----SYG-----LHPG-----DTSNNSC 18
 gi | 32416406 | ref | XP_328681.1 |MPKRPYTSVGGAAASDRRDEARRRRLNADSSSGPSSQSQVYVPOSFSTNGLSSSSQTSGRRQLPWPQTIPGTCGAGSRHNTGATSTYSARSLSATPSSQHRPPEVQALHDTLNLWLSQDP 121
 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 67763824 | ref | NP_033236.2 | HPEFQDIIPDDFLTSDEEQLVLFQTRMGQVVGRLRYITG--VVNNNEMVALQREPNNPYDKNAIKVNNVNG.....NOVGHIRKREIAAAVAYIMDN-KLAQVEGVVPPGASNT-FIMPLYMHFWGKEENRNVLVLE 162
 gi | 109464650 | ref | XP_215728.4 | RPEFQDIIPDDFQTSDEELDLVLFQTRMGQVVGIRIYITG--VVNNNEMVALEREPNNPYDKNAIKVNNVNG.....NOVGHILKRDIAAALAYIMDN-KLAQVEGVVPPGASNT-FIMPLHMHFWGKEENRREVLLD 277
 gi | 21071052 | ref | NP_003062.2 | RPEFQDVIPDDFLTSDEEVDVSLFGLRSHVVGRLRYITG--VVNNNEMVALQREPNNPYDKNAIKVNNVNG.....NOVGHILKELAGALAYIMDN-KLAQIEGVVPPGANNNA-FIMPLHMHFWGKEENRKAIVSD 162
 gi | 114589754 | ref | XP_516811.2 | RPEFQDVIPDDFLTSDEEVDVSLFGLRSHVVGRLRYITG--VVNNNEMVALQREPNNPYDKNAIKVNNVNG.....NOVGHILKELAGALAYIMDN-KLAQIEGVVPPGANNNA-FIMPLHMHFWGKEENRKAIVSD 162
 gi | 73990698 | ref | XP_534300.2 | RPEFQDIIPDDFLTSDEELDSILFGLRSHVVGRLRYITG--VVNNNEMVALQREPNNPYDKNAIKVNNVNG.....NOVGHILKDLAALAYIMDN-KLAQIEGVVPPGANNNA-FIMPLHMHFWGKEENRKAIVL 261
 gi | 119884988 | ref | XP_588490.3 | RPEFQDIIPDDFLTSDEELDSILFGLRSHVVGRLRYITG--VVNNNEMVALQREPTNPYDKNAIKVNNVNG.....NOVGHILKDLAALAYIMDN-KLAQIEGVVPPGANNNA-FIMPLQMHFWGKEENRKAIVL 162
 gi | 125805885 | ref | XP_693071.2 | SQELANLH--EDAQEELAEAGNVLFGSIQGLIVGLRYITG--AVNKGEMVSLVREPHNPYDRNAVVMVANVYG.....SIVGHIKKELAAAMAYIMDN-KLARVEGIVPVGKKNK-FIMPVILHFWGKEENREVNN 156
 gi | 22326612 | ref | NP_196132.2 | EDEFQSPVEPSQQQSQDQCVSESYLIGFVIANIVGLKYYSG--RNGREMVLVREPLNVYDNNAIRVLTNRS.....EIVGHIERTVAAVLAIMDS-HITVVEGIVPNTNRSNKNRIRPCQIHVFAKLKASSVTKS 144
 gi | 115473675 | ref | NP_001060436.1 | DDD-----DEPVLGFTVANAVGLQYYQGGRAITRRRESVGLVREPHNPYDANARVNDNARG.....EKIGHIGRAAAALAPLLDAGHVAAGHIVPKPASKR-LYSLPCQVHLFARPPHAALVAA 126
 gi | 145603372 | ref | XP_369370.2 |DANDTALAEKMGKQFDCAKMFIFGTSQDLARQLENLKNDKLKLKATLQKQTKRES 78
 gi | 32416406 | ref | XP_328681.1 | ILESDEAEVIDLQADPGVLEFYGHFDGKLVGVRYVNG--VASPEGVVCCREPPQCYDPNAIRVNDVNLGTQIGHIPRTVAAKLAPVMDNGLVVEGMLTGEKEFYDQVRLYFYGTSAASLQARLBERLKKDKLKKATQKTRKAN 269
160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 67763824 | ref | NP_033236.2 |OLKKGCFKLGPTPKTLGSSLENANGSGRAGPSYSRPAHVAVQMTDQLKTEFDKLFEDLKEDDRIVEMEP-ABEAEITPLLPHQKQALAWMIAREN-----SKELPPFWEQ-RNDLYNTIITNF SVKERPENVHGGILADDMGLGKTLI 303
 gi | 109464650 | ref | XP_215728.4 | HLKKGCFKLGPTPKTVGSSLENTWGSGRAGPSYSRPAHVAVQMTDQLKTEFDKLFEDLKEDDRIVEMEP-ABEAEITPLLPHQKQALAWMIAREN-----SKELPPFWEL-RNDLYNTIITNF SVKERPENVHGGILADDMGLGKTLI 418
 gi | 21071052 | ref | NP_003062.2 |OLKKGCFKLGPAKTLGFNLESQWGSGRAGPSYSMPVHAAVQMTDQLKTEFDKLFEDLKEDDKTHEMPE-ABEAEITPLLPHQKQALAWMVSREN-----SKELPPFWEQ-RNDLYNTIITNF SEKDRPENVHGGILADDMGLGKTLI 303
 gi | 114589754 | ref | XP_516811.2 |OLKKGCFKLGPAKTLGFNLESQWGSGRAGPSYSMPHAAVQMTDQLKTEFDKLFEDLKEDDKTHEMPE-ABEAEITPLLPHQKQALAWMVSREN-----SKELPPFWEQ-RNDLYNTIITNF SEKDRPENVHGGILADDMGLGKTLI 303
 gi | 73990698 | ref | XP_534300.2 |OLKKGCFKLGPAKTLGFNLESQWGSGRAGPSYSMPVHAAVQMTDQLKTEFDKLFEDLKEDDKTHEMPE-ABEAEITPLLPHQKQALAWMVSREN-----SKDLPFFWEQ-RNDLYNTIITNF SEKDRPENVHGGILADDMGLGKTLI 402
 gi | 119884988 | ref | XP_588490.3 |ELKKGCFKLGPAKSLGFNLESQWGSGRAGPSYSMPVHAAVQMTDQLKTEFDKLFEDLKEDDKTHEMPE-ABEAEITPLLPHQKQALAWMVSREN-----SEELPPFWEL-RSDLYNTIITNF SEKDRPENVHGGILADDMGLGKTLI 303
 gi | 125805885 | ref | XP_693071.2 | LMIGFGFNLDPR-----GGSSQISLGRDLLGLSLTKL---SATPLSABELKNAPDKLFDLDMED-KIKEMEP-ABEAVCPPLLPHQKQALAWMVSREN-----SNDLPPFWEE-NKGLYFNVLNFAVKKRPEKVLGGILADDMGLGKTLI 289
 gi | 22326612 | ref | NP_196132.2 | TTSRGGVLVLESDESIFGLSEAVVVKQMG-----NGDKRSVDRIKFLVDENVKMGKLVAAEPPREVIKSELFAHQKEGLGWLLHREK-----SGELPPFWEE-KDGEFNLNITNRSDKRPDLRGGVFADDMGLGKTLI 275
 gi | 115473675 | ref | NP_001060436.1 | ALAASGIDLIVHVDPEFALSESIVVQEQQT-----KRGRGVDRILFVSHVKGKGR--ARIAPMEAPRDVVVSELFEHQKAAALGWLVHREE-----SCDLPFFWEEDNKGFKVLTNOKTNERPPPLKGGIFADDMGLGKTLI 256
 gi | 145603372 | ref | XP_369370.2 |ELRR--LPLEITGTSQSLKNMRPGQKNPLVAMESLIEQSQVVKARSDDLKSLAMDEEALSALPCADQ-PEELKQQLLYQLQGLAWLVKKNPEFVPIGSDENTQWKVDAKGRVNLATEFTADAPKLLSGGILADDMGLGKTLI 225
 gi | 32416406 | ref | XP_328681.1 |EQRKKQTLLELRNGTYGFPSTQV-EPEPQVIMEQLAKMSEVIFRSQGMIRKSLAMSELANLPMASQ-PEKLRAKLLPYQLQGLAWMIKENPTIPARKGSDTSVQLWHTADGRYHMAAGFYNRSPPQLLSGALCADDMGLGKTLI 417
310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 67763824 | ref | NP_033236.2 |AIAVILLNFDDGRPLLSKRGGKHPGKEY--KDEIKRRGSNMDKEDGHSES-STCGEPEISICTPEKSSCTLSQLSSVCPKRRKISVQVIESSDSEIEITSELPOKMGKLNKVLNPKSRVK-GSSKVKEDSKF--ALTFAS--AI 445
 gi | 109464650 | ref | XP_215728.4 |AIAVILLNFDDGRPLLKRGKESHGKEY--KDEIVKLRGNSNKTIDGHSEF-SACEEPIISDVSEKS--NVSDLFFSKRRKISVQSTESSSEIEITSELPOKMGKLNKVLNPKSRVK-GSSKIKEDTFALALTYGFP--AI 560
 gi | 21071052 | ref | NP_003062.2 |AIAVILLNFHDGRPLPVERVKNLLKKEYNVDDSMKLGNNITSEKADGLSKDASRCSQPSISDIKEKSKFRMSLSSSRPKRRRTAVOYIESSDSEIEITSELPOKMGKLNKVLNPKSRVK-GSSKIKEDTFALALTYGFP--AI 451
 gi | 114589754 | ref | XP_516811.2 |AIAVILLNFHDGRPLPVERVKNLLKKECNVDDSMKLGNNITSEKADGLSKDASRCSQPSISDIKEKSKFRMSLSSSRPKRRRTAVOYIESSDSEIEITSELPOKMGKLNKVLNPKSRVK-GSSKIKEDTFALALTYGFP--AI 450
 gi | 73990698 | ref | XP_534300.2 |AIAVILLNFHDGKPLPVERIKKNQMKKCNVDDSMKLGNNITSEKADGLSKDASRCSQPSISDVTKGKKYTKSELSSSRPKRRRTAVOYIESSDSEIEITSELPOKMGKLNKVLNPKSRVK-GSSKIKEDTFALALTYGFP--AI 548
 gi | 119884988 | ref | XP_588490.3 |AIAVILLNFHDGKSLPVERIKKNQMKKCNVYDESMELGGNITSEKAAGLIKDRSRCSQPSISDVTKONKYPKSEFSSSRKRPAAVQYIESSDSEIEITSELPOKMGKLNKVLNPKSRVK-GSSKIKEDTFALALTYGFP--AI 451
 gi | 125805885 | ref | XP_693071.2 |IALIVSNFHNKPLPLEKCK-----GPMPSAKRQQAISKEKQVDEESQESMGLSPLKRLHDDTVREN-GPKKTKTKKKSANPKAVV----LDDVEFAALECSGSSVVE 395
 gi | 22326612 | ref | NP_196132.2 |LLSLIAFDPRY-----LLSLIGRS-----NASTSITPEPLDGEQDKIEKKGKRRGRKSSSVT----- 322
 gi | 115473675 | ref | NP_001060436.1 |ITGLILGL-----KARNVGGKKARG----- 276
 gi | 145603372 | ref | XP_369370.2 |ITSLIMRGL----- 233
 gi | 32416406 | ref | XP_328681.1 | 427
460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 67763824 | ref | NP_033236.2 | **QRKMLKKGMSMMECEACDGERTRATLLIICPLSVLSNWIDQFOGHVKSVDLNFVYVYGPDRIRDSAWLKSODIILTYNLTHTDYGTKDSSPLHSIKWLRVILDEGHAIKRNPAOQTKAVLELEAERRVWLTGTPIONSLKDLWSLLS** 595
gi | 109464650 | ref | XP_215728.4 | **KKKMLKKGTSVMESKKCDTGERTRATLLIICPLSVLSNWIDQFOGHVKSVDLNFVYVYGPDRIRDSAWLKSODIILTYNLTHTDYGTKDSSPLHSIKWLRVILDEGHAIKRNPAOQTKAVLELEAERRVWLTGTPIONSLKDLWSLLS** 710
gi | 21071052 | ref | NP_003062.2 | **KKKMLKKGACAVEGSKKTDVEERPRITLLIICPLSVLSNWIDQFOGHVKSVDLNFVYVYGPDRIRDPALLSKODIVLTYNLTHTDYGTKDSSPLHSIRWLRVILDEGHAIKRNPAOQTKAVLDLESERRVWLTGTPIONSLKDLWSLLS** 601
gi | 114589754 | ref | XP_516811.2 | **KKKMLKKGACAVEGSKKTDVEERPRITLLIICPLSVLSNWIDQFOGHVKSVDLNFVYVYGPDRIRDPALLSKODIVLTYNLTHTDYGTKDSSPLHSIRWLRVILDEGHAIKRNPAOQTKAVLDLESERRVWLTGTPIONSLKDLWSLLS** 600
gi | 73990698 | ref | XP_534300.2 | **KRRMLKKGASAVEGSKKTDIEDRPRITLLIICPLSVLSNWIDQFOGHVKSVDLNFVYVYGPDRIRDPALLSKODIVLTYNLTHTDYGTKDSSPLHSIRWLRVILDEGHAIKRNPAOQTKAVLDLESERRVWLTGTPIONSLKDLWSLLS** 698
gi | 119884988 | ref | XP_588490.3 | **KKKMLKKGASAVEGSKKTDVEDKPRITLLIICPLSVLSNWIDQFOGHVKSVDLNFVYVYGPDRIRDPALLSKODIVLTYNLTHTDYGTKDSSPLHSIRWLRVILDEGHAIKRNPAOQTKAVLDLESERRVWLTGTPIONSLKDLWSLLS** 601
gi | 125805885 | ref | XP_693071.2 | **SKKCVKKSVPSEIETV---AGSVARATLIVLCPVLSNWIDQFOGHVKSVDLNFVYVYGPDRIRDPALLSKODIVLTYNLTHTDYGTKDSSPLHSIRWLRVILDEGHAIKRNPAOQTKAVLDLESERRVWLTGTPIONSLKDLWSLLS** 541
gi | 22326612 | ref | NP_196132.2 | **---RKKLKTDDVVGMMV-----SQKRTLLVCPVPSVISAWITDQHEHIRTDTVTYKVVLYYSGERNRSVLLSQQDVLVTLTSLAFVGNKASPLHKNWELRVILDEGHAIKRNPAOQTKAVLDLESERRVWLTGTPIONSLKDLWSLLS** 462
gi | 115473675 | ref | NP_001060436.1 | **---AKRRKVEEAVE-----ESRPTLVVCPVPSVFSWVTOLEEHKTCGS---LKVLYLHG---ERTKEKKELLYDIVITTYTSLGQLELQE---GSPVKEIEWFRVILDEAHVKNKSAARQTKAVIALNAERRVWLTGTPIONSLKDLWSLLS** 413
gi | 145603372 | ref | XP_369370.2 | **---GGPGLTIVA PMVMSNWSQIENHVVYEDERPSVYIHGGPSRLRDSSEVESYGVVITTYGTMSSSGSKG---PLSKIQWRVVLDEGHAIKRNPAOQTKAVLDLESERRVWLTGTPIONSLKDLWSLLS** 358
gi | 32416406 | ref | XP_328681.1 | **---GTGPTLIVA PMVMSNWSQIENHVVYEDERPSVYIHGGPSRLRDSSEVESYGVVITTYGTMSSSGSKG---ALVKKWRVVLDEGHAIKRNPAOQTKAVLDLESERRVWLTGTPIONSLKDLWSLLS** 548
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi | 67763824 | ref | NP_033236.2 | **FLKLLKP-FIDREWWYRIIQRPVITGDE---GGLRRLQSLIKNITLRRRTKTSKIKGKPVLELPERKVFIOHITLSDBERKIYQSVKNEGRATIGRYFNEG---TVLAHVADVLGILLRLRQICCHTHLLTN---GMSSSGPRSDDTPEELRKM---L** 738
gi | 109464650 | ref | XP_215728.4 | **FLKLLKP-FIDREWWYRIIQRPVITGDE---GGLRRLQSLIKNITLRRRTKTSKIKGKPVLELPERKVFIOHITLSDBERKIYQSVKNEGRATIGRYFNEG---TVLAHVADVLGILLRLRQICCHTHLLTN---GTSSSDPRSDDTPEELRKM---L** 853
gi | 21071052 | ref | NP_003062.2 | **FLKLLKP-FIDREWWYRIIQRPVITGDE---GGLRRLQSLIKNITLRRRTKTSKIKGKPVLELPERKVFIOHITLSDBERKIYQSVKNEGRATIGRYFNEG---TVLAHVADVLGILLRLRQICCHTHLLTN---AVSSNGSPSDDTPEELRKM---L** 744
gi | 114589754 | ref | XP_516811.2 | **FLKLLKP-FIDREWWYRIIQRPVITGDE---GGLRRLQSLIKNITLRRRTKTSKIKGKPVLELPERKVFIOHITLSDBERKIYQSVKNEGRATIGRYFNEG---TVLAHVADVLGILLRLRQICCHTHLLTN---AVSSNGSPSDDTPEELRKM---L** 743
gi | 73990698 | ref | XP_534300.2 | **FLKLLKP-FIDREWWYRIIQRPVITGDE---GGLRRLQSLIKNITLRRRTKTSKIKGKPVLELPERKVFIOHITLSDBERKIYQSVKNEGRATIGRYFNEG---TVLAHVADVLGILLRLRQICCHTHLLTN---AGSSNGSPSDDTPEELRKM---L** 841
gi | 119884988 | ref | XP_588490.3 | **FLKLLKP-FVDREWWYRIIQRPVITGDE---AGLRRRLQSLIKNITLRRRTKTSKIKGKPVLELPERKVFIOHITLSDBERKIYQSVKNEGRATIGRYFNEG---TVLAHVADVLGILLRLRQICCHTHLLTN---AVSSNGSPSDDTPEELRKM---L** 744
gi | 125805885 | ref | XP_693071.2 | **FLKLLKP-FDVEKWSRIIQRPVITGDR---VGLRRLQSLIKNITLRRRTKTSKIKGKPVLELPERKVFIOHITLSDBERKIYQSVKNEGRATIGRYFNEG---TFMANVADVLTILMLRQICCHTHLLTN---VTAADVFG---TFSELRER---L** 681
gi | 22326612 | ref | NP_196132.2 | **FLRFPF-FSIKSVWQSLIQRPVITGDR---KGLSRLQVLMATISLRRTE---KSLIGLPPKTVETCYVELSBERKIYQSVKNEGRATIGRYFNEG---SLMRNVTSLVILRLRQICCHTHLLTN---ELRFT---TSTVSDVDTKPEL** 600
gi | 115473675 | ref | NP_001060436.1 | **FLRFPF-FSIKSVWQSLIQRPVITGDR---KGLSRLQVLMATISLRRTE---KSLIGLPPKTVETCYVELSBERKIYQSVKNEGRATIGRYFNEG---SLMRNVTSLVILRLRQICCHTHLLTN---DLKSWLPSLEEDVSNKPEL** 559
gi | 145603372 | ref | XP_369370.2 | **FLKITGGLESLEVERSVIERGLSYGDS---RAESLLQALMGDLCLRRNKSMK---FVDLKLPPKTVVHRIAFTEAOKKYDALLCEAKGVLDIRKNPKITIQGGFTSVLERLLRLRQICCHTHLLTN---CCKEYKAVLLEGGQVVLTPENRQ** 504
gi | 32416406 | ref | XP_328681.1 | **FLRITGGLEQSEIENTVLIRPLANGEP---KGEALLKSLMGDLCLRRNKDMK---FVDLKLPPKTVVHRIAFTEAOKKYDALLCEAKGVLDIRKNPKITIQGGFTSVLERLLRLRQICCHTHLLTN---CCKEYKAVLLEGGQVVLTPENRQ** 693
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi | 67763824 | ref | NP_033236.2 | **IEKMKLILSSGSDDECAICLDSLTFVPIIHCARHFCKPCICQVQHSEOPHAKCPLCRNDIHEGNLLECPPEELACDTEKKS---SMEWKSSSKINALMHALIELRTRKDPNIKSLVVSQFTTFLSLIETPLKASG---FVFTRLDGSMAOKKRV** 886
gi | 109464650 | ref | XP_215728.4 | **VTKMKLILSSGSDDECAICLDSLTFVPIIHCARHFCKPCICQVQHSEOPHAKCPLCRNSIHGNLLECPPEELACDTEKKS---DMEWTSSSKINALMHALIELRTRKDPNIKSLVVSQFTTFLSLIETPLKASG---FVFTRLDGSMAOKKRV** 1001
gi | 21071052 | ref | NP_003062.2 | **IRKMKLILSSGSDDECAICLDSLTFVPIIHCARHFCKPCICQVQHSEOPHAKCPLCRNDIHEGNLLECPPEELARDSKKS---DMEWTSSSKINALMHALIELRTRKDPNIKSLVVSQFTTFLSLIETPLKASG---FVFTRLDGSMAOKKRV** 892
gi | 114589754 | ref | XP_516811.2 | **IRKMKLILSSGSDDECAICLDSLTFVPIIHCARHFCKPCICQVQHSEOPHAKCPLCRNDIHEGNLLECPPEELARDSKKS---DMEWTSSSKINALMHALIELRTRKDPNIKSLVVSQFTTFLSLIETPLKASG---FVFTRLDGSMAOKKRV** 891
gi | 73990698 | ref | XP_534300.2 | **IRKMKLILSSGSDDECAICLDSLTFVPIIHCARHFCKPCICQVQHSEOPHAKCPLCRNDIHEGNLLECPPEELACDTEKKS---NTEWTSSSKINALMHALIELRTRKDPNIKSLVVSQFTTFLSLIETPLKASG---FVFTRLDGSMAOKKRV** 989
gi | 119884988 | ref | XP_588490.3 | **IKKMKLILSSGSDDECAICLDSLTFVPIIHCARHFCKPCICQVQHSEOPHAKCPLCRNDIHEGNLLECPPEELACNTEKKS---NMEWTSSSKINALMHALIELRTRKDPNIKSLVVSQFTTFLSLIETPLKASG---FVFTRLDGSMAOKKRV** 892
gi | 125805885 | ref | XP_693071.2 | **LQKITLVLSGSDDECAICLDSLRFVPIIHCARHFCKPCICEVIRSEKQAKCPLCRAQIKTKELVEYPGE---QAEIRSDT---GENWRSSSKALALMSNLLKLRNEDPTVKSVMVVSQFTGFLVLEVALREYGF---FSFTRLDGSLIORARAK** 827
gi | 22326612 | ref | NP_196132.2 | **LQKLVAAALQDGEDFDCPCISPPNTIITIRCAHIFCRACILQTLQSKP---LCPCLCRSLQSDLYNAPPPDSSNTDGEDAKSSTKSSKVSALLSLLMASRQENPTKSVVVSQFRKMLLLETPKAAAG---FTILRLDGMIVKRRPQ** 747
gi | 115473675 | ref | NP_001060436.1 | **LKKLASLVDDGDFECPICLAPPAKTVITSCTHIYCOCTIMKILKSSSS---RCPICRRSLCEDLFIAP---EIKHPDESSVNLDRPLSSKQVALLKLLRRS---SEDPKSKSVIFSQRKMLLLETPKAAAG---FNILRLDGSMTAKKRSE** 704
gi | 145603372 | ref | XP_369370.2 | **LLEEARLRLVVEQDDCAVCLDLDVPIIHCARHFCKPCICQVQHSEOPHAKCPLCRNDIHEGNLLECPPEELARDSKKS---CPLCRTELSEDKLVEPAKEDNRSVQVDD---MDESAGSSKNDALLKILGDKLLKSSKSVIIFSQWTSFLNVIQRLLEHTVYGYTRIDGTMKPVARD** 650
gi | 32416406 | ref | XP_328681.1 | **ILQALQLYIESQDEPCIDPLSNPIIHCARHFCKPCIDKVLVQK---CPMCRAPLSEDKLLEPAKES---ATQDEE---LESEKSKAEVALLVLDKESG---KLIIFSQWTSFLNVIQRLLEHTVYGYTRIDGTMKPVARD** 836
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi | 67763824 | ref | NP_033236.2 | **SIICFPONTIAGSPIMLLSLKAGGVGLNLCAASRVFLMDPAWNPAAEDQCFDRCHRLGQKQEVITIKFIVKDSVEENMLKIQNTKRELAAGAFGTKKTNADEMKQAKINEIRTLIDL** 1003
gi | 109464650 | ref | XP_215728.4 | **SIICFPONTIAGSPIMLLSLKAGGVGLNLCAASRVFLMDPAWNPAAEDQCFDRCHRLGQKQEVITIKFIVKDSVEENMLKIQNTKRELAAGAFGTKKTNADEMKQAKINEIRTLIDL** 1118
gi | 21071052 | ref | NP_003062.2 | **SIICFPONTIAGSPIMLLSLKAGGVGLNLCAASRVFLMDPAWNPAAEDQCFDRCHRLGQKQEVITIKFIVKDSVEENMLKIQNTKRELAAGAFGTKKTNADEMKQAKINEIRTLIDL** 1009
gi | 114589754 | ref | XP_516811.2 | **SIICFPONTIAGSPIMLLSLKAGGVGLNLCAASRVFLMDPAWNPAAEDQCFDRCHRLGQKQEVITIKFIVKDSVEENMLKIQNTKRELAAGAFGTKKTNADEMKQAKINEIRTLIDL** 1008
gi | 73990698 | ref | XP_534300.2 | **SIICFPONTIAGSPIMLLSLKAGGVGLNLCAASRVFLMDPAWNPAAEDQCFDRCHRLGQKQEVITIKFIVKDSVEENMLKIQNTKRELAAGAFGTKKTNANEMKQAKINEIRTLIDL** 1106
gi | 119884988 | ref | XP_588490.3 | **SIICFPONTIAGSPIMLLSLKAGGVGLNLCAASRVFLMDPAWNPAAEDQCFDRCHRLGQKQEVITIKFIVKDSVEENMLKIQNTKRELAAGAFGTKKTNASEMKQAKINEIRTLIDL** 1009
gi | 125805885 | ref | XP_693071.2 | **AIEDFQDSTPGSPIMLLSLKAGGVGLNLCAASRVFLMDPAWNPAAEDQCFDRCHRLGSRDVTVIKFIKIVKDSVEENMKIQKQKQELVDKAFGVK---NSQDAKQARIDIRALMEL** 942
gi | 22326612 | ref | NP_196132.2 | **VIGEFQDPELITGPIVLLASLKAAGTGINLTAASRVFLDFPWNVPAVEQAMDRIRHIGQKQKVKIRMIARNSIEERVLEQKKNLANEAFKRRKQ---KDEE---VNVEDVVALMSL** 862
gi | 115473675 | ref | NP_001060436.1 | **VIRQFCVGEDPPIVLLASLKAAGAVNLTAASVYLFDPWNVPGVSEQAMDRIRHIGTKVVKVRLVILKDSIEERMLELQERKKLLISGAFKRRKGGKHEKE---IRVEELQMMGMK** 821
gi | 145603372 | ref | XP_369370.2 | **AMRKLQDTP---DTRILLASLGVCSVGLNLVADTVILADSWWAPAIEDQAVDRVHRLGTRPPTVWRVLMEDTVEERVLVQSEKRDVLSKAFQEKKQ---KTKAKETRMADIMKLLG---** 763
gi | 32416406 | ref | XP_328681.1 | **AIRALDYDP---NTRILLASLGVCSVGLNLVADTVILADSWWAPAIEDQAVDRVHRLGTRPPTVWRVLMEDTVEERVLVQSEKRDVLSKAFQEKKQ---DKKKVETRMADIMKLLS---** 950
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....

