

gi | 6678291 | ref | NP_033380.1 | -----NTRAPRCPAVRSLLRSHRYREVWPLATFVRRLLGLGEGR--RLVOPGDPKIYRITLVAQCLVCMHWGQSPPPADLFSHVOVSLKELVARVVORLCE-----RNERNVLAFGFELLNARGGPPMAFTSS 118
gi | 55741827 | ref | NP_445875.1 | -----MPRAPRCPAVRSLLRSHRYREVWPLATFVRRLLGLGEGS--RLVOPGDPKVFRTLVAQCLVCPVWGSQPPADLFSHVOVSLKELVARVVORLCE-----RGERNVLAFGFALLNARGGPPMAFTSS 118
gi | 109633031 | ref | NP_937983.2 | -----MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLLGPPGQW--RLVORGDPAAFRALVAQCLVCPVWDARPPPAAPSFROVSLCKELVARVLRORLCE-----RGAKNVLAFGFALLDARGGPPMAFTSS 118
gi | 114598857 | ref | XP_001141663.1 | -----MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLLGPPGQW--RLVORGDPAAFRALVAQCLVCPVWDARPPPAAPSFROVSLCKELVARVLRORLCE-----RGAKNVLAFGFALLDARGGPPMAFTSS 118
gi | 74003121 | ref | XP_851664.1 | -----MPRAPRCRAVRALLRGRYREVLPPLATFVRRLLGPPGPR--LLVRRGDPAAFRALVAQCLVCPVWDARPPPAAPCFROVSLCKELVARVVORLCE-----RGARNVLAFGFALLDARGGPPMAFTSS 118
gi | 114053049 | ref | NP_001039707.1 | -----MPRAPRCRAVRALLRGRYREVLPPLATFVRRLLRPPGQW--RLVRRGDPAAFRALVAQCLVCPVWDARPPPAAPCFROVSLCKELVARVVORLCE-----RGARNVLAFGFALLDARGGPPMAFTSS 118
gi | 71896531 | ref | NP_001026178.1 | MBERGAGPGVGRRLRNVAAREEPPAAVLGALRCYAAEAPLEAFVRRLEQGGTGEVLEVRGDDAQCYRTFVSGCVVCPYGARAIPEPICFQGLSSQSEVIRIVRORLCE-----KKGKLNLAIFYGSLLENSCHGPPVLPSSC 137
gi | 139947514 | ref | NP_001077335.1 | -----MSGQSTDGGEFFVLEILLRSLYPVVQTLKEEFDDGLQFPDGRKFFVLEETDARFKKLLSGLLVCAVY----PPQLRVPALQLSLLVPLVLAFTLNLHKR-----KKLRNVLGFGYQSLDFTSSDFRPHGD 121
gi | 15237420 | ref | NP_197187.1 | -----MPKPRRHRVPEILWRLFGNRRARNLNDATVDLIPNRNITQPQCRCRCQGLCGSSDKPAFLLRSDDPPIHYRKLHLRHFVVLHQPPPLDFFPTE-----WWSQREIVERIIEEMQSG-CDCCQNVICAR 122
gi | 115488246 | ref | NP_001066610.1 | -----MPRRRRRRRAAPGGQVPEELRLAYGARALTGRAVFSLLSPSR--HCSPCPACRGRVAGSGLACRRWSEHLRSDGPVAYRRLITRAVCAIAADDLSAPPPRYTPGNSGHSQARLVREMMKSIIVADQSHGTKNVLNCG 137



gi | 6678291 | ref | NP_033380.1 | VRSYLPNTVIEITLRSVGAWMLLLSRVGGDLLVYLLAHCALYLLVPPSCAYOVCGSPPLYQICATIDWIPSVSASYRPT-----RPVGRNFTNLRFLQOIK-SSSRQEAPKPLALPSRGTKRRLSLT 237
gi | 55741827 | ref | NP_445875.1 | VHSYLPNSVTESELCSVGAWMLLLSRVGGDLLVYLLSHCALYLLVPPSCAYOVCGSPPLYQICATIDTWSVPAGYRPT-----RPVGGNFTNLGSAHQIK-NSGHQEAPKQALPSRGTKRRLSLT 237
gi | 109633031 | ref | NP_937983.2 | VRSYLPNTVTDALRGSVGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYOVCGPPPLYQLG-----AATQARPPP-----HASGPRN-----RLGCERAWNHSVREAGVPLGLPAPGARRRGGSA 228
gi | 114598857 | ref | XP_001141663.1 | VRSYLPNTVTDALRGSVGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYOVCGPPPLYQLG-----AATQARPPP-----HASGPRN-----RLGCERAWNHSVREAGVPLGLPAPGARRRGGSA 228
gi | 74003121 | ref | XP_851664.1 | VRSYLPNTVTEILRGSVGAWGLLLRRVGGDVLVHLLARCALYLLVAPSCAYOVCGPPPLYDLCA-----PASLPLPAP-----GLPGLGAGAGASADLRPTROAONSQARRRGGSA 228
gi | 114053049 | ref | NP_001039707.1 | VRSYLPNTVTEILRGSVGAWGLLLRRVGGDVLVHLLARCALYLLVAPSCAYOVCGPPPLYDLCA-----AAAAARRPT-----ROVGGTRAGFGLRFPASSNGGGEAEGLEAARQAGARRRGGSA 232
gi | 71896531 | ref | NP_001026178.1 | IYSYLSNVTETIIRISGLWEILLRIGDDVMYLLIEHCALFMLVPPNCYOVCGQPIYELISRNVGGSPFGRVRRYSRFKHNLLDLYVRKRLVFRHRLKSKQWVKCRPRRRSHRIQSLRSQYPSAKVNFQAGQISTV 287
gi | 139947514 | ref | NP_001077335.1 | VS-----QTAASISTSEVWKRNQRIGTEVTRYLQDCAVFTVPPSCVLOVCGEPVYDILLMPSRWSGFFLNSNDNE-----RISGAMRKFPAVQKTVAISKRRTRDNEKIVSKRRRVRKETVNN 236
gi | 15237420 | ref | NP_197187.1 | YDKYDQSPILELLTSSWEFLFKRVRGHVDMVYLLQQTSIFLPLLLGKKHQVSGPPLCKTKRRLLSVHENKRRKDDN-----VQPPTKROWLSSAVDDCPKDDSAITPTVGEDVDQHKREKKT 241
gi | 115488246 | ref | NP_001066610.1 | LHEGGQSTICISDLVSSSSWITLLHRIGDILLMICYLLRCSIFLPLVKKNDYVSGVPLNVVLRNPFASITVARKRQPQTKAKCHTCYLWKSANMAEN-----LEITCHDSSNSGVNSSFSSSTCKIVTQSCETCGSIRRAESKDPSE 279



gi | 6678291 | ref | NP_033380.1 | ST-----SVPSAKKARCY-----PVPRVEEGPHROVL-----PTPSGKS-----WVPSPARSPPEVPTAEKDLSSKGVSDLSLSG----- 302
gi | 55741827 | ref | NP_445875.1 | ST-----NVPsAKKARFE-----PALRVDKGPHROVV-----PTPSGKT-----WAPSPAAAPKVPAAKNLSLKGKASDPSLSG----- 302
gi | 109633031 | ref | NP_937983.2 | SR-----SLPLPKRPRRG-----AAPEPERTPVGQGS-----WAHPGTRGSDRGCVVSPARPAEATSLLEGALSG-----TRHSHPs----- 298
gi | 114598857 | ref | XP_001141663.1 | SR-----SLPLPKRPRRG-----AAPEPERTPVGQGS-----WAHPGTRGSDRGCVVSPARPAEATSLLEGALSG-----TRHSHPs----- 298
gi | 74003121 | ref | XP_851664.1 | GS-----GVPLAKRPRRS-----VAS-----EPERGAH-----RSFP-----RAQPPVSEAPVTF-AVAAS-----PAAWEG----- 282
gi | 114053049 | ref | NP_001039707.1 | RG-----RLPPAKRPRRG-----LEPG-----RDLEGGVA-----RSPP-----RVVPTRDAAEAARKRQDVPQ-----PCRLFPQ----- 289
gi | 71896531 | ref | NP_001026178.1 | IARLEKQCSSLCLPARAPSLKRRKRDGEVETIARVKVMKEKTEEQACIIVPDVQSSQRHGTSWVHAPRAYGLIKEIYISERSNSEMSGPSVRRSHPKGRPVADKSSFPQGVGNKRIKIGAEKRAESNRRTGEMINPTIKPFR 437
gi | 139947514 | ref | NP_001077335.1 | NNG-----NYSRLCFAIKKR-----AIDNEENISLKR-----MEETDVAKIRNENHESQFAISKKRARDNEENISLKRQRMEEIDQ----- 312
gi | 15237420 | ref | NP_197187.1 | KR-----SRIYLKRRRQ-----RKVN-----FKKVDNAPCITPSTNGKVTGNDMMNLITG----- 289
gi | 115488246 | ref | NP_001066610.1 | CNCXKFPDGRSGECCNICYTHNTRKRRKRLYSWQRSSKKKQVCSVDESSAEWSKLNQSNFNMSNGPSENLAGKMNDAQSVELVDVNTSLARSNDDSSSEIRVIV-----AIIISSEKSPCVFID 399



gi | 6678291 | ref | NP_033380.1 | -----SVCKCHKPSSITSLSPPRQNAFQL--RPFITRHFLYSRGQGERLNPSSFLLSNLQPNLIGARRLVEIIFLGRSPT-----SGPLCRTHRLSRRYWQMRPLFQQLLVNHACQVVRLLRSH 417
gi | 55741827 | ref | NP_445875.1 | -----SVCKCHKPSSITSLSPPRQDAEKL--RPFITRHFLYSRGGQBELNPSFLLNSLPPSLIGARRLVEIIFLGRSPT-----SGPFCRTRRLPRRYWQMRPLFQQLLMNHAKCQVVRFLRSH 417
gi | 109633031 | ref | NP_937983.2 | -----VGRQHHAGPPSISRPPRPWDPCP--PVYAEKHFYLSG--DKEQLRPSFLLSSLRPSLIGARRLVEIIFLGRSPT-----PGTFRRLPRLPQRYWQMRPLFELLGNHACQVYVLLKTH 412
gi | 114598857 | ref | XP_001141663.1 | -----VGRQHHAGPPSISRPPRPWDPCP--PVYAEKHFYLSG--DKEQLRPSFLLSSLRPSLIGARRLVEIIFLGRSPT-----PGTFRRLPRLPQRYWQMRPLFELLGNHACQVYVLLKTH 412
gi | 74003121 | ref | XP_851664.1 | -----GPGTRPTTAWHSPGQGVPHD--PAHPETKRFLYCSG--GRRLRPSFLLSALRPSLIGARRLVEIIFLGRSPT-----PGTFRRLPRLPQRYWQMRPLFELLGNHACQVYVLLKTH 396
gi | 114053049 | ref | NP_001039707.1 | -----GERGVG--SASWRLSP--SEGEPGA--GACAEIKRFLYCSG--GGEQLRPSFLLSALRPSLIGARRLVEIIFLGRSPT-----PGTFRRLPRLPQRYWQMRPLFELLGNHACQVYVLLKTH 400
gi | 71896531 | ref | NP_001026178.1 | GIERRINPTHKPELNSVQTEPMGASGDRKQENPPAHLAKQLPNTLSRS--TVYFKRFLYLSRS--YQBYFPSFLLSRLQCGAGGRLLIIFLQSNPLKEQQNOSLFPQOKWRKRLPKRYWQMRPLFQKLVKNHEKCPVLFRLRN 584
gi | 139947514 | ref | NP_001077335.1 | -----VAKIRNENHGSQWPKPADQRPSPS--QCSIRVLSMLYNGRMKNFLNKRKILKGVGGARRMQGEDLVRMIFLQESND-----SKPKLPRKRFAMVPLFRLRRLQHRKCPVRLFLQRK 424
gi | 15237420 | ref | NP_197187.1 | -----INGSLTDFWQKA--KQVKNKRFKFLGSETYSVIPPNIILKILRPNCS--DSKLLMNHIFGEVNVWSVTP-----SHGKNCPSGSIKLYSLKSLKLNKILKKS--SHLKMLLDKH 396
gi | 115488246 | ref | NP_001066610.1 | RGSQGLSCHYLSLSEVQVQSLCPVGVSSYLHLNSCSICIFNLSNASKSLDLSLIRNIGIFVNRRTYSVFHCKHLSKRR--RPDALSLVKHIFGINSQCA--LLKLNCHSTYTRKSNCLCCWLPKTSKLNKILRNSKRCQVKKLFLKH 545



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gi|6678291|ref|NP_033380.1| CRFRITANQ-----QVTDALNLSPPH-----LMDLLRLHSSPWVYGFRLRACLKVVSVASLWGTTRHNERFFKLNKFFISLGGYKLSLQELMWMKMKVEDCHWLRSPPG 515
gi|55741827|ref|NP_445875.1| CRFRITANQ-----RVDMADTSPSH-----LISLLRLHSSPWVYGFRLRACLRELVPAGLWGTTRHNERFFLNKFFISLGGYAKLSLQELMWRVKVEDCHWLRSPPG 515
gi|109633031|ref|NP_937983.2| CPLRAAVT-----PAAGVCAREKPKQGSVAAPPEEEDTPRR-----LVOLLROHSSPWVYGFVRACLRRLVPPGLWGSRRHNERFFLNKFFISLGGYAKLSLQELTWKMSVRDCAWLRRSPG 525
gi|114598857|ref|XP_001141663.1| CPLRAAVT-----PAAGVCAREKPKQGSVAAPPEEEDTPRR-----LVOLLROHSSPWVYGFVRACLRRLVPPGLWGSRRHNERFFLNKFFISLGGYAKLSLQELTWKMSVRDCAWLRRSPG 525
gi|74003121|ref|XP_851664.1| CPLRAMAAKESGNCANRGGVIGICPLERP-----VAAPQEQ-----LDSTR-----LVOLLROHSSPWVYAFVRACLCWLVPITGLWGSRRHNERFFLNKFFISLGGYAKLSLQELTWKMKVRDCWVWLGNGPG 514
gi|114053049|ref|NP_001039707.1| CPLPASAPRAGPDHCKPGVGGCPSERP-----AAAPQEQ-----ANSGR-----LVOLLROHSSPWVYGLLRACLRRLVPAAGLWGSRRHNERFFLNKFFISLGGYAKLSLQELTWKMKVQDCAWLRRSPG 518
gi|71896531|ref|NP_001026178.1| CPVLLSEACLKKELELQQAALPGEAKVHKHLEHGKESTEGTAPNSFLAPPVSLACGQPERGQHPAEGSDPLLRLELROHSSPWVYGFVRECLRLVPAELWGSRRHNERFFLNKFFISLGGYAKLSLQELTMWKRVDCAWVLRKAG 734
gi|139947514|ref|NP_001077335.1| CAGNPDVVKD-----MESLTKSHSRYRVLVRECLRHIIIPHLWGCQEQ-----LHFLSNVKNFLLLGKFERLILVGLMWRMKVQACHWLGPKKR 511
gi|15237420|ref|NP_197187.1| CPVLLQEDALKSCTISQSSRRQKADKLPKSSSSSITGKPKCPS-----VEERKLCNDQVSVFIWAICRYIVPESLLGTHQMRVLRKNIWAFVRRRNEKCHVNFHLKVKPSDFPFARKEL 517
gi|115488246|ref|NP_001066610.1| CSVKCKVAP-----DVTIKNDGKAHYPPGKAAAYDVR-----SFSRLEAYSTHQVAVSVVAVLKRIYVPEKLLGNSFGKRSRLRTNWKVPIKLRRETFEQLSDCIGDLKVSHTYVLSNIEF 654
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

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gi|6678291|ref|NP_033380.1| KDRVPAAEHR-----LRERILATFLFWLMDTYVOLLRSFFYITESTFQKNRLLFFYRKSVWSKLOSIGVROHLERVLRELSEQEVRRHQDQWVLAAMPICRLRFPKPNGLRPIVNMVSMGTRALG---RRKQACHFTQRLKI 650
gi|55741827|ref|NP_445875.1| KDTVPAAEHR-----LRERILAMFLFWLMDTYVOLLRSFFYITESTFQKNRLLFFYRKSVWSKLOSIGIROQLERVQLRELSEQEVKHHQDQWVLAAMPICRLRFPKLNGLRPIVNMVSMGMDTRAFG---KKKQTOCFTQSLKI 650
gi|109633031|ref|NP_937983.2| VGCVPAAEHR-----LREIILAKFLHWLMSVYVVELLRSFFYVTEITTFQKNRLLFFYRKSVWSKLOSIGIROHLKRVQLRELSEAEVRRHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFR---REKRAERLTSRVKA 660
gi|114598857|ref|XP_001141663.1| VGSVPAAEHR-----LREIILAKFLHWLMSVYVVELLRSFFYVTEITTFQKNRLLFFYRKSVWSKLOSIGIROHLKRVQLRELSEAEVRRHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFR---REKRAERLTSRVKA 660
gi|74003121|ref|XP_851664.1| ACCVPAAEHR-----RREIILARFLCWLMTGYVVELLRSFFYVTEITTFQKNRLLFFYRKSVWSKLOSIGIROHLKRVQLRELSEAEVRRHREARPAALLTSRLRFPKPSGLRPIVNMVYVVGARTFR---RDKKVOHLTSQTKI 649
gi|114053049|ref|NP_001039707.1| ARCVPAAEHR-----QREAVLGRFLHWLMTGYVVELLRSFFYVTEITTFQKNRLLFFYRKSVWSKLOSIGIROHLKRVQLRELSEAEVRRHREARPAALLTSRLRFPKPSGLRPIVNMVYVVGARTFR---RDKKVOHLTSQTKI 653
gi|71896531|ref|NP_001026178.1| NRSVPAYEHC-----VREIILAKFLHWLMSVYVVELLRSFFYVTEITTFQKNRLLFFYRKSVWSKLOSIGIROHLKRVQLRELSEAEVRRHREARPAALLTSRLRFPKPSGLRPIVNMVYVVGARTFR---RDKKVOHLTSQTKI 872
gi|139947514|ref|NP_001077335.1| Q---CASEHR-----VREWMLCQCMGWLMSGFVVGVLVRAQFYITESTMGKHTLRFYRGDVSRLQDQAFRAHLCKGQWRPLPSQALKVFN---SAVTSRIRFIPKTSMRPIIRLSGSRD-----TLVYFQCVRV 632
gi|15237420|ref|NP_197187.1| CCMVNGHELOSES-----IRSTQMLCKWISWLFLEIVKLVHFNFYATEOGGRLNIYYRKRSENERLISKEISKALDGYLVVDDAAEES-----SRKLSKFRFLPKANGVVMVLDPS-----SSRSQSLRD 638
gi|115488246|ref|NP_001066610.1| SNCVCSAIIIGKTCGSSSTAEERQKNILHCWISWLFLEIVKLVHFNFYATEOGGRLNIYYRKRSENERLISKEISKALDGYLVVDDAAEES-----SRKLSKFRFLPKANGVVMVLDPS-----SSRSQSLRD 784
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900

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gi|6678291|ref|NP_033380.1| LFSVLNLYERTKHPHLMGSSVGLMNDIYRTWRAFLVLRVARDLQPRMYFVKADVTGAYDAIPQDKLVEIVANIRRSE---STYCIROYAVVVRDSQGVH---KSFRRQVTLSDLOPYMGOFLKHLQSDASALRNSVVIQESISMNETG 795
gi|55741827|ref|NP_445875.1| LFSVLNLYERTKHPNLMGASVLGSDSYRIWRFTVLRVARDLQPRMYFVKADVTGAYDAIPQDKLVEIVANIRRSE---SMYCIROYAVVQKDSQGVH---KSFRRQVTLSDLOPYMGOFLKHLQSDASALRNSVVIQESISMNETG 795
gi|109633031|ref|NP_937983.2| LFSVLNLYERARRPGLLGASVGLGDDIHRARWTFVLRVARDLPPPELYFVKVDVTGAYDITIPQDRLETVIASIIPKQ---NHYLCVRRYAVVQKAAHGHV---KAFKSHVSTLSDLOPYMROFVAHLOET---SPLRDAVVIQESSLNLEAS 802
gi|114598857|ref|XP_001141663.1| LFSVLNLYERARRPGLLGASVGLGDDIHRARWTFVLRVARDLPPPELYFVKVDVTGAYDITIPQDRLETVIASIIPKQ---NHYLCVRRYAVVQKAAHGHV---KAFKSHVSTLSDLOPYMROFVAHLOET---SPLRDAVVIQESSLNLEAS 805
gi|74003121|ref|XP_851664.1| LFSVLNLYERARRPGLLGASVGLGDDIHRARWTFVLRVARDLPPPELYFVKVDVTGAYDITIPQDRLETVIASIIPKQ---NHYLCVRRYAVVQKAAHGHV---KAFKSHVSTLSDLOPYMROFVAHLOET---SPLRDAVVIQESSLNLEAS 792
gi|114053049|ref|NP_001039707.1| LEAVLNLYERARRPGLLGASVGLGDDIHRARWTFVLRVARDLPPPELYFVKVDVTGAYDITIPQDRLETVIASIIPKQ---NHYLCVRRYAVVQKAAHGHV---KAFKSHVSTLSDLOPYMROFVAHLOET---SPLRDAVVIQESSLNLEAS 795
gi|71896531|ref|NP_001026178.1| LFSVLNLYERTVNTSIIGSSVFGRDDIYRKWKEFVTKVFESGGEMPHFYFVKGDVSRAFDTIPHKLVEVISQVLKPSQTVYGIWVAVIMITPTGKAR---KLYKRHVSTFEDFIPDMKQFVSKLOER---ISLRNAIVVEQCLTFENNS 1017
gi|139947514|ref|NP_001077335.1| LQNVLSVCVREAPGPMGSTVWGWQDIHRRLDQFSPQKSSP---RPLYFVKVDVSGAYDSLPHLKLVEVLKEVLPFAEQSFFLRQYSVWSDPTRGRL---KRFCTKAEMSEPLN---MKGQVVDQVQ---GRLHDAILVER---HSSEVRG 771
gi|15237420|ref|NP_197187.1| THAVLKDIQLKEPDLVSSVDFDDDFYRNLCPLYLHLRSGSEGLPPLYFVAVDVFKAQFSDVQGLLHVIQSFLEKDEY---ILNRCRLVCCGKRNSNVN---KILVSDKNSNFSRFTSTVPYN---ALQSIIVDKGENHRVRK 773
gi|115488246|ref|NP_001066610.1| CHLIMKLRDEKPEMFSSVDFVNNVHGNLSQFISKRSLMKLKVYIVVAVDVSRAFDCVSHDMVLMKIMDDAFKQDE---VTVRRCSEVICNRSKNLY---RFDNSASIGNGNSIYDLSIQIS---GGGIFVDQGTICRILK 920
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050

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gi|6678291|ref|NP_033380.1| SSLFDFFLHFLRHSVVKIGDRCYTCQGIPOGSSLSLTLCLSCFCGDMENKLFQAEVQRDG-----LLLRVDDFLLVTPHLDAQKTFLSLTVHGVPEYGCMLNLQKTVVNFVPEPGLGGAAPYQLP---AHCLFP 922
gi|55741827|ref|NP_445875.1| SSLLHFFLRFVRRHSVVKIGDRCYTCQGIPOGSSLSLTLCLSCFCGDMENKLFQAEVQRDG-----LLLRVDDFLLVTPHLAHAKAFSLTVHGVPEYGCMLNLQKTVVNFVPEPGLGGAAPFLQP---AHCLFP 922
gi|109633031|ref|NP_937983.2| SGLFDVFLRFCHHAVRIRGKSVVCGIPIQGSILSTLLCSLFCGDMENKLFQAEVQRDG-----LLLRVDDFLLVTPHLTHAKAFLRLTVRGVPEYGCMLNLQKTVVNFVPEDEALGGTAFVQLP---AHGLFP 929
gi|114598857|ref|XP_001141663.1| SGLFDVFLRFVCRHAVRIRGKSVVCGIPIQGSILSTLLCSLFCGDMENKLFQAEVQRDG-----LLLRVDDFLLVTPHLTHAKAFLRLTVRGVPEYGCMLNLQKTVVNFVPEDEALGGTAFVQLP---AHGLFP 932
gi|74003121|ref|XP_851664.1| SSLFHLFLRLVHNVHVRIGKSVVCGIPIQGSILSTLLCSLFCGDMENKLFQAEVQRDG-----LLLRVDDFLLVTPHLTQAFLRLTVKGVPEYGCMLNLQKTVVNFVPEDEALGGTAFVQLP---AHCLFP 919
gi|114053049|ref|NP_001039707.1| SSLFNLFLHFLVRSVHVRIGKSVVCGIPIQGSILSTLLCSLFCGDMENKLFQAEVQRDG-----VLLRLVDDFLLVTPHLTRARDFRLTVRGVPEYGCMLNLQKTVVNFVPEDEALGGTAFVQLP---AHCLFP 922
gi|71896531|ref|NP_001026178.1| SLLFTFFLQMLHNNILEIGHRYICGSIPIQGSILSTLLCSLFCGDMENKLLCGIKDQ-----VLLRLVDDFLLVTPHLMAQRTFLRLIAAGIPEYGFLLNAKTVVNFVPEDEALGGTAFVQLP---DCRLIS 1143
gi|139947514|ref|NP_001077335.1| GDVFQFFQKMLCSYVHYDQCMFROVCGTPOGSSVSSLLNCLCGVGHMEKALLKDIAGKG-----CLMRLVDDFLLVTPHLTKATEFLTLISLGVDPYGCMLNLQKTVVNFVPEDEALGGTAFVQLP---SCLFLP 897
gi|15237420|ref|NP_197187.1| KDLMWVIMNMLKNMMLQDKSFFVQIAGIPIQGHRLSLCCFYVGHLETLIYVPLEEASKDVSSKECSREBEELIIPISVKKLRFIDDLVYVSTTRDQASFSYHRLKHGFKDNCFMNTEKFCINFEKDEEHRCSNRMVFGDNGVFFVR 923
gi|115488246|ref|NP_001066610.1| EQFHLLYEQIKCNILKIGQKYLQVGLAQGSKLSPNLCLVYGHLETLIYVPLEEASKDVSSKECSREBEELIIPISVKKLRFIDDLVYVSTTRDQASFSYHRLKHGFKDNCFMNTEKFCINFEKDEEHRCSNRMVFGDNGVFFVR 1061
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200

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gi|6678291|ref|NP_033380.1| WCGLLLDQTLEVFCDYSGYAOFSIKISLTFQSVFKAGKTMRNKLLSVLRRLKCHGLFLDLOVNSLQTVCTNIYKIFLLQAYRFHACVILPFDQVRVKNLFFFLGIIISQAACCYAILKVKNPGMTLKAS---GSFPPEAAHWLCYQAF 1068
gi|55741827|ref|NP_445875.1| WCGLLLDTRTLEVFCDYSGYGRFSIKMSLTFQGVSRAGKTMRYKLLSVLRRLKCHGLFLDLOVNSLQTVCTNIYKIFLLQAYRFHACVIRLPPGQHVVRKNHAFFLGIISNLASCCYAILKVKNPVSLRAKG-APGSFPPEATRWCYQAF 1071
gi|109633031|ref|NP_937983.2| WCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRLKFGVLRRLKCHSLFLDLOVNSLQTVCTNIYKIFLLQAYRFHACVILPFPHQVWKNPFFFLRVIISDTASLCYSILKAKNAGMSLGAGK-AAGPLPSEAVWLCHQAF 1078
gi|114598857|ref|XP_001141663.1| WCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRLKFGVLRRLKCHSLFLDLOVNSLQTVCTNIYKIFLLQAYRFHACVILPFPHQVWKNPFFFLRVIISDTASLCYSILKAKNAGMSLGAGK-AAGPLPSEAVWLCHQAF 1081
gi|74003121|ref|XP_851664.1| WCGLLLDTRTLEVSCDYSSYAHTSIRASLTFQGGAKPGRNMRRLKLAVALRLKCHCALFLDLOVNGIHTVYMNVYKIFLLQAYRFHACVILPFPNPPVRKNPFFFLRVIADTASCCYSLLKARNAGLSLGAGK-ASGLFPSEAAARWLCHLHAF 1068
gi|114053049|ref|NP_001039707.1| WCGLLLDTRTLEVHGDSYSSYARTSIRASLTFQGFKPGRNMRRLKLAVALRLKCHGLFLDLOVNSLQTVFTNVYKIFLLQAYRFHACVILPFPSPVRSPPAFFLQVIADTASRGYALLKARNAGASLGAGK-AAGLFPSEAAQWLCHLHAF 1071
gi|71896531|ref|NP_001026178.1| WCGLLLDVTLEVYCDYSSYAFSIRSSLFNSRSRIAGKNMKCKLAVLRLKCHPLLLDLKINSLQTVLNIYKIFLLQAYRFHACVILPFPNPKVRNPPDFFLRIISDTASCCYFILKAKNPGVSLGSKD-ASGMFPSEAAEWLCHYHAF 1292
gi|139947514|ref|NP_001077335.1| WCGLMIHHTLTDVYKDYSRDGLSLRYSLLTGSANSPSTVMK-KLLSVLSIKSFDIFLDRLRNSVEAVYRSYKLLILLQALRFHACVRSPLPGQSVNRNPFFFFLKMIWRMIRVINKLLTHINKGLPVCSDV-SGGVLQSEAVQLLFLCLAF 1045
gi|15237420|ref|NP_197187.1| WTGLLINRDFEYQVDYTRLSGHISSTFSVAWQNKPVNRLRQKLCYFLVPKCHPILFDSNINSGEIVRLNIYQIFLLAAMKFCVYVEVSR--FWKLHPQTLFKFIIIEVVRMFRLLINRVRIRINIGSSFRPVLKLYKEEVIWGLDAY 1071
gi|115488246|ref|NP_001066610.1| WSGLLINCELEIQADYTRLDITIIISTITIVKMHS-S TKYIHSKLCHYMRPKCHPIFYDSNINSPTIRVNIYQAFLLCAMKFCVYIRSVSDANVSKLE--LLQVIKRIFRYMHSLIVRRMQDVELHYNVRPVLKLRKKEIHWLGLTAY 1207
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350

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gi|6678291|ref|NP_033380.1| LLKLAHHSVINKCLLGPLRTAQKLLCRKLPKATMILKAAADPALSTDFQTILD 1122
gi|55741827|ref|NP_445875.1| LLKLAHHSVINKCLLGPLRTAQKQLCRKLPKATMILKTAADPALSTDFQTILD 1125
gi|109633031|ref|NP_937983.2| LLKLTTRHRVTYVPLLSLRTAQTQLSRKLPPTLLALEAAAANPALPSDFKTILD 1132
gi|114598857|ref|XP_001141663.1| LLKLTTRHRVTYVPLLSLRTAQTQLSRKLPPTLLALEAAAANPALPSDFKTILD 1135
gi|74003121|ref|XP_851664.1| LLKLAH-----SAPTGVSGGHSRPRHT----- 1092
gi|114053049|ref|NP_001039707.1| LLKLARHRVTSRLLGALRTARARLHRQLPGPTRAALEAAADPALTADFKTILD 1125
gi|71896531|ref|NP_001026178.1| IVKLSNHRKVIKCLLPLKVKMHLFGKIPRDTMELLKIVTEPSLCQDFKTILD 1346
gi|139947514|ref|NP_001077335.1| EILFRFRRSVHCLIPALHKKRKRALQRELCGITLARVRQASSPRIPLDFSMRV- 1098
gi|15237420|ref|NP_197187.1| IQVLKKKNSRVRMLLIYKLSALS--KHSLSQQLSHELRYATDRSNSSSLWKLNY 1123
gi|115488246|ref|NP_001066610.1| IRVLQQQSRVYKDMITLLTAELG--RYCHLGHECDTLRYAVDSSHSMSMFKFKF 1259
.....1360.....1370.....1380.....1390.....1400....

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