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gi|15237411|ref|NP_199440.1|      ----------------------------------------------------------------------------------------MDVPEETRLRHKRDFIQFLDS-----------MYME   150
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gi|145613273|ref|XP_363833.2|     ----------------------------------------------------------------------------------------------------------------------------   150
gi|32416474|ref|XP_328715.1|      ----------------------------------------------------------------------------------------MDYNALRDEAVRDRVRQAQEFLDP--HDQHQR----SYRP   150
gi|19075295|ref|NP_587795.1|      ----------------------------------------------------------------------------------------MTELLADEVFKDRVRIFQEYLEHDTDDANVT----LYQE   150
gi|50309887|ref|XP_454957.1|      ----------------------------------------------------------------------------------------MSDAMNQTSDAVFTDRMRRFQEFLDTHSHYTREIRSILEFNS   150
gi|45198873|ref|NP_985902.1|      ----------------------------------------------------------------------------------------MELPLNEAHDALFSDRVRRFQEFLDSHDAYADEIRAILVHNG   150
gi|6320803|ref|NP_010882.1|       ----------------------------------------------------------------------------------MEGSTGFDGDATTFFAPDAVFGDRVRRFQEFLDTFTSYRDSVRSIQVYNS   150
gi|24639835|ref|NP_511048.2|      ----------------------------------------------------------------------------------------MAHEGEQFIKDIQREYVDFLDDEEDQG-------IYAG   150
gi|58396614|ref|XP_322026.2|      ----------------------------------------------------------------------------------------MAED-DQRLASIQNEYLNFLDDEEDQG-------TYTA   150
gi|6631095|ref|NP_002379.2|       ----------------------------------------------------------------------------------------MAG-TVVLDDVELREAQRDYLDFLDDEEDQG-------IYQS   150
gi|114607814|ref|XP_001151750.1|  ----------------------------------------------------------------------------------------MAG-TVVLDDVELREAQRDYLDFLDDEEDQG-------IYQS   150
gi|73973306|ref|XP_538960.2|      MGKTTTPRMQRAPRLARRPNDQPPRVSSLPHWSAFLFVRGQKHRAPEVLFPATARPGSGNAEEEQALDWMLAILALWWREKSASFRAGAGPCGDPRRGAGGGGSVAAGMAG-TVVLDDVELREAQRDYLDFLDDEEDQG-------IYQS   150
gi|33859484|ref|NP_032589.1|      ----------------------------------------------------------------------------------------MAG-TVVLDDVELREAQRDYLDFLDDEEDQG-------IYQN   150
gi|109485811|ref|XP_236988.4|     ----------------------------------------------------------------------------------------MAG-TVVLDDVELREAQRDYLDFLDDEEDQG-------IYQN   150
gi|61888858|ref|NP_001013604.1|   ----------------------------------------------------------------------------------------MAG-TVVLDDVELREAQRDYLDFLDDEEDQG-------IYQS   150
gi|57530231|ref|NP_001006421.1|   ----------------------------------------------------------------------------------------MAAPAGGLGDAELREAQRDYLDFLDDEEDQG-------VYHG   150
gi|47086897|ref|NP_997732.1|      ----------------------------------------------------------------------------------------MAA--EVVDDQEMREAQRDYLDFLDDDQDQG-------IYQS   150
gi|124506457|ref|XP_001351826.1|  ---------------------------------------MESLSIEKNSTPFGRSEYRTFNSELNYTLMDSSLNHSSILDNSMKIEKDSRDKRLQKLNQNIVSEYESGRQSVVFTQQKYKQLLEGFLLFVQTNKYIHQKITELRTEAI   150
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gi|115464471|ref|NP_001055835.1|  AVRDMVQNK-------------------------------RHRLIIGMDDLRNHSL---DLARRVIRSPAEYMQPASDAVTEVARNLDPKFLKE-------GQRVLVGFSGPFGFHRVTPRDLMSSFIGTMVCVEGIVTKCSLVRPKV   300
gi|145613273|ref|XP_363833.2|     ----------------------------------------------------------------------------------------------------------------------------   300
gi|32416474|ref|XP_328715.1|      DIVLMLQKN-----------------------------QRRLVVNIDHVRDHSS---EVAEGLLTDPFNWTLAFNHALKTIVSTVPQARPDQ----IDPDVLYYCAWAGSFGLHTCNPRTLSSQHLNNMVSIEGIVTRTSLIRPKV   300
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gi|50309887|ref|XP_454957.1|      NVVKEKKTD-------------DDYLNTADKDTMDHDTNQLPLRITVSLDDLREFDK---TFWTGLLQVPSFFLPPAERAVSETAMALDDSPLGFRGFQNDPSRQWRLSFKGSFGPNSLSPRTLNSTHLNKLISVEGIVTRTSLVRPKL   300
gi|45198873|ref|NP_985902.1|      --LNAERGD-------------GAWDKKSGP-----AGASLPRRLTVSLDDIREFDR---AYWTGLLVQPAYFLPAAERAVTDLAAVLEDTRVAR---AAGPSSEWRLSFRGAFGAHALSPRTLMATHLNQLVSIEGIVTRTSIVRPKL   300
gi|6320803|ref|NP_010882.1|       NNAANYNDDQDDADERDLLGDDDGDDLEKEKKAASSTSLNILPHRIIISLDDLREFDR---SFWSGILVEPAYFIPPAEKALTDLADSMDDVPHPN-ASAVSSRHPWKLSFKGSFGAHALSPRTLTAQHLNKLVSVEGIVTKTSLVRPKL   300
gi|24639835|ref|NP_511048.2|      HVKDMIAEK-----------------------------SKRLIVNVNDLKRKNP---QRALGLLSNAADEQLAFGRALKEYASTVDPGYAKM-------HEDLFVGFEGCFGNRHVTPRSLTSIYLGNMVCVEGIVTKVSLIRPKV   300
gi|58396614|ref|XP_322026.2|      HVRKMINDK-----------------------------SKRLVVNIDIRRKNP---GRALALLNSAFDEQLAFSRALKDYVSTIDMSYAKT-------QEDFHVAFEGSFGNKHVTPRSLTSRFLGNLVCVEGIVTKVSLIRPKV   300
gi|6631095|ref|NP_002379.2|       KVRELISDN---------------------------QYRLIVNVNDLRRKNE---KRANRLLNNAFEELVAFQRALKDFVASIDATYAKQ-------YEEFYVGLEGSFGSKHVSPRTLTSCFLSCVVCVEGIVTKCSLVRPKV   300
gi|114607814|ref|XP_001151750.1|  KVRELISDN---------------------------QYRLIVNVNDLRRKNE---KRANRLLNNAFEELVAFQRALKDFVASIDATYAKQ-------YEEFYVGLEGSFGSKHVSPRTLTSCFLSCVVCVEGIVTKCSLVRPKV   300
gi|73973306|ref|XP_538960.2|      KVRELISDN---------------------------QYRLIVNVNDLRRKNE---KRANRLLSNAFEELVAFQRALKDFVASIDATYAKQ-------YEEFYIGLEGSFGSKHVSPRTLTSCFLSCVVCVEGIVTKCSLVRPKV   300
gi|33859484|ref|NP_032589.1|      KVRELISDN---------------------------QYRLIVSVNDLRRKNE---KRANRLLNNAFEELVAFQRALKDFVASIDATYAKQ-------YEEFYIGLEGSFGSKHVSPRTLTSCFLSCVVCVEGIVTKCSLVRPKV   300
gi|109485811|ref|XP_236988.4|     KVRELISDN---------------------------QYRLIVNVNDLRRKNE---KRANRLLNNAFEELVAFQRALKDFVASIDATYAKQ-------YEEFYIGLEGSFGSKHVSPRTLTSCFLSCVVCVEGIVTKCSLVRPKV   300
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gi|57530231|ref|NP_001006421.1|   KVRDMISDN---------------------------QYRLLVNINDLRRRNE---KRANRLLSNAFEELIAFQRALKDFVASVDATYAKQ-------YEDFYIGLEGSFGSKHVSPRTLTACFLSCIVCVEGIVTKCSLIRPKV   300
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gi|124506457|ref|XP_001351826.1|  DEYNRMQNKNIPN-------------------------IIIHQRLICNINNFQTGNEQFELLAKCLIKEPYLALPAYQAAIKELWKSEDSKVDID---------PPKIGICGWLGRHHVTPRGLQSSMINKLVAVEGVVNKCSTVQPKL   300
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gi|115464471|ref|NP_001055835.1|  VKSVHYCPATGGT-----------LSREYRDITSFVG--LPTGSVYPTRDENGNLLVTEYGMCEYKDHQTLSMQEVPENSAPGQLPRTVDIIVEDDLVDSCKPGDRVSIVGVYKALPGKSKGSVSGV----------FRTVLIANNVSLM   450
gi|145613273|ref|XP_363833.2|     ----------------------------------------------------------------------------------------------------------------------------   450
gi|32416474|ref|XP_328715.1|      VKSVHYSEAKKTF-----------HYREYRDQTMTNG-IVTN-SVYPREDEEGNPLETEYGFSTYRDHQTISIQEMPERAPAGQLPRGVDVILDDDLVDRVKPGDRIQLVGIFRTLGNRNTNHNSAL----------FKTVILANNIVLL   450
gi|19075295|ref|NP_587795.1|      IKSVHYCEATKRH-----------HFKQYADATMNGG-LSFQSTVYPTQDENGNPLSIEFGFSTFRDHQSISLQEMPERAPPGQLPRSIDILLDDDLVDTVKPGDRVNIVGQYRSMGSKTSGNTSAT----------FRTVLLANNVVLL   450
gi|50309887|ref|XP_454957.1|      LRSVHYAQTTGHH-----------HYRDYRDATTTLTTSVPTPAIYPEEDQEGNKLVTEYGFCHYMDHQRITVQEMPEKAPPGQLPRSIDVILDDDLVDKTKPGDRINIVGVYKSLGAGGLTGGSNNNDKGNGALSGFRTVVIGNTVYPL   450
gi|45198873|ref|NP_985902.1|      LRSVHLSKNTGAH-----------YYRDYRDATTTLVTEVPTPAIYPEADPEGNPLNTEYGYSTYMDHQRVTVQEMPEKAPPGQLPRSVDVILDDDLVDKTKPGDRVNIVGVFKSIGAGGMSGGSSS-DHGNNGLAGFKTLIIGNTVYPL   450
gi|6320803|ref|NP_010882.1|       IRSVHYAAKTGRF-----------HYRDYTDATTTLTTRIPTPAIYPTEDTEGNKLTTEYGYSTFIDHQRITVQEMPEMAPAGQLPRSIDVILDDDLVDKTKPGDRVNVVGVFKSLGAGGMNQSNSN------TLIGFKTLILGNTVYPL   450
gi|24639835|ref|NP_511048.2|      VRSVHYCPNTRKV-----------MERKYTDLTSFEA--VPSGAAYPTKDEDGNLLETEYGLSVYKDHQTLTIQEMPEKAPAGQLPRSVDIVCDDDLVDRCKPGDRVQIVGSYRCLPGKRGGYTSGT----------FRTVLLANNISLL   450
gi|58396614|ref|XP_322026.2|      VKSVHYCPATKKV-----------MERRYTDLTSFEA--VPSSAVYPTKDDDGNLLETEFGLSVYKDHQTLSIQEMPEKAPAGQLPRSVDVVCDDDLVDRCKPGDRVQIVGNYRCLPGKQGGYTTGT----------FRTILIANNISQL   450
gi|6631095|ref|NP_002379.2|       VRSVHYCPATKKT-----------IERRYSDLTTLVA--FPSSSVYPTKDEENNPLETEYGLSVYKDHQTITIQEMPEKAPAGQLPRSVDVILDDDLVDKAKPGDRVQVVGTYRCLPGKKGGYTSGT----------FRTVLIACNVKQM   450
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gi|33859484|ref|NP_032589.1|      VRSVHYCPATKKT-----------IERRYSDLTTLVA--FPSSSVYPTKDEENNPLETEYGLSVYKDHQTITIQEMPEKAPAGQLPRSVDVILDDDLVDKVKPGDRIQVVGTYRCLPGKKGCYTSGT----------FRTVLIACNVKQM   450
gi|109485811|ref|XP_236988.4|     VRSVHYCPATKKT-----------IERRYSDLTTLVA--FPSSSVYPTKDEENNPLETEYGLSVYKDHQTITIQEMPEKAPAGQLPRSVDVILDDDLVDKVKPGDRIQVVGTYRCLPGKKGGYTSGT----------FRTVLIACNVKQM   450
gi|61888858|ref|NP_001013604.1|   VRSVHYCPATKKT-----------IERRYSDLTSLVA--FPSSSVYPTKDEENNPLETEYGLSVYKDHQITIQEMPEKAPAGQLPRSVDVILDDDLVDRVKPGDRVQVVGTYRCLPGKKGGYTSGT----------FRTVLIACNVKQM   450
gi|57530231|ref|NP_001006421.1|   VRSVHYCPATKKT-----------IERRYTDLTSLDA--FPSSTVYPTKDEENNPLETEYGLSVYKDHQTISIQEMPEKAPAGQLPRSVDVILDDDLVDKVKPGDRIQVVGTYRCLPGKKGGYTSGT----------FRTILIACHIKQM   450
gi|47086897|ref|NP_997732.1|      VRSVHYCPATKKT-----------MERKYTDLTSLDA--FPSSAIYPTKDEENNPLETEFGLSVYKDHQTITIQEMPEKAPAGQLPRSVDIILDNDLVDAVKPGDRTQVIGTYRCLPGKKGGFTSGT----------FRTIMIACHVKQM   450
gi|124506457|ref|XP_001351826.1|  VQSVYIGEAVHDMNADAKTSEKTVHLRPHYDITDFDKTAKDSGRPPASDPEGRIMHKHEIGLCKYKNHQKFVIQETPEDAPTGQMPRWVEVIVEDDLCDIVKCGDRVRWGVYRANCGQANSTNSGLG----------RSFLIANNVLVK   450
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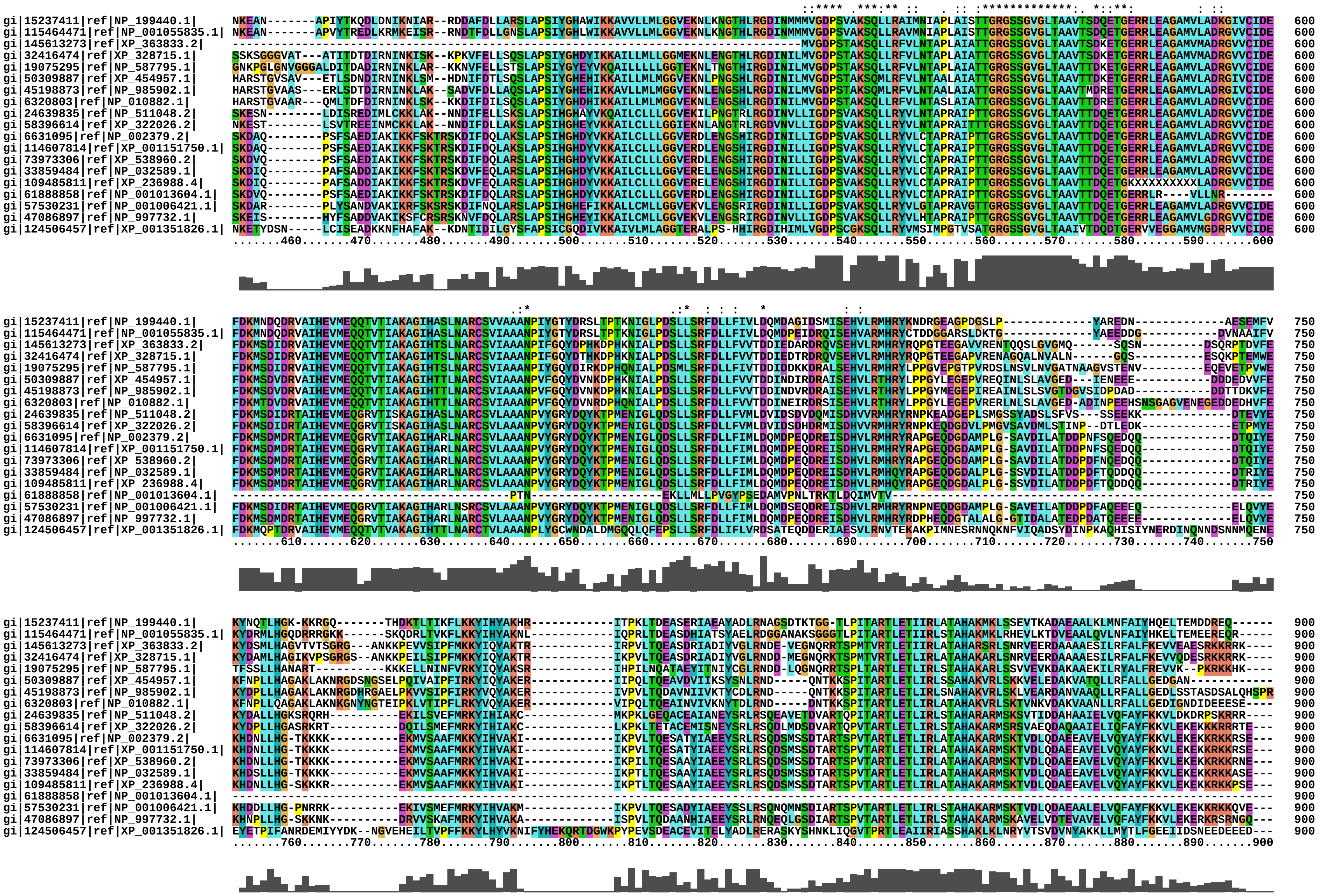

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                                                                                                                   ::**** .***:** ::   . :: :*************:. *::**:         : ::
gi|15237411|ref|NP_199440.1|     NKEAN-------APIYTKQDLDNIKNIAR--RDDAFDLLARSLAPSIYGHAWIKKAVVLLMLGGVEKNLKNGTHLRGDINMMMVGDPSVAKSQLLRAIMNIAPLAISTTGRGSSGVGLTAAVTSDQETGERRLEAGAMVLADKGIVCIDE   600
gi|115464471|ref|NP_001055835.1| NKEAN-------APVYTREDLKRMKEISR--RNDTFDLLGNSLAPSIYGHLWIKKAVVLLMLGGVEKNLKNGTHLRGDINMMMVGDPSVAKSQLLRAVMNIAPLAISTTGRGSSGVGLTAAVTSDQETGERRLEAGAMVLADRGVVCIDE   600
gi|145613273|ref|XP_363833.2|    ----------------------------------------------------------------------------------MVGDPSTAKSQLLRFVLNTAPLAIATTGRGSSGVGLTAAVTSDKETGERRLEAGAMVMADRGVVCIDE   600
gi|32416474|ref|XP_328715.1|     SSKSGGGVAT---ATITDTDIRNINKISK--KPKVFELLSQSLAPSIYGHDYIKKAILLMLLGGMEKNLENGTHLRGDINILMVGDPSTAKSQLLRFVLNTAPLAIATTGRGSSGVGLTAAVTSDKETGERRLEAGAMVMADRGVVCIDE   600
gi|19075295|ref|NP_587795.1|     GNKPGLGNVGGGALDITDADIRNINKLAR--KKNVFELLSTSLAPSIYGYEYVKQAILLLLLGGTEKNLTNGTHIRGDINILMVGDPSTAKSQLLRFVLNTAPLAIATTGRGSSGVGLTAAVTTDKETGERRLEAGAMVLADRGVVCIDE   600
gi|50309887|ref|XP_454957.1|     HARSTGVSAV---ETLSDNDIRNINKLSM--HDNIFDTLSQSLAPSIYGHEHIKKAILLMLMGGVEKNLPNGSHLRGDINILMVGDPSTAKSQMLRFVLNTAALAIATTGRGSSGVGLTAAVTTDKETGERRLEAGAMVLADRGIVCIDE   600
gi|45198873|ref|NP_985902.1|     HARSTGVAAS---ERLSDTDIRNINKLAK--SADVFDLLAQSLAPSIYGHEHIKKAVLLMLMGGVEKNLENGSHLRGDINILMVGDPSTAKSQMLRFVLNTAALAIATTGRGSSGVGLTAAVTMDRETGERRLEAGAMVLADRGIVCIDE   600
gi|6320803|ref|NP_010882.1|      HARSTGVAAR---QMLTDFDIRNINKLSK--KKDIFDILSQSLAPSIYGHDHIKKAILLMLMGGVEKNLENGSHLRGDINILMVGDPSTAKSQLLRFVLNTASLAIATTGRGSSGVGLTAAVTTDRETGERRLEAGAMVLADRGVVCIDE   600
gi|24639835|ref|NP_511048.2|     SKESN--------LDISREDIMLCKKLAK--NNDIFELLSKSLAPSIHGHAYVKQAILCLLLGGVEKILPNGTRLRGDINVLLIGDPSVAKSQLLRYVLNTAPRAIPTTGRGSSGVGLTAAVTTDQETGERRLEAGAMVLADRGVVCIDE   600
gi|58396614|ref|XP_322026.2|     NKEST--------LSVTREEINMCKKLAK--NNDIFDLLAKSLAPSIHGHEYVKKAILCLLLGGIEKNLANGTRLRGDVNVLLIGDPSVAKSQLLRYVLNTAPRAITTTGRGSSGVGLTAAVTTDQETGERRLEAGAMVLADRGVVCIDE   600
gi|6631095|ref|NP_002379.2|      SKDAQ--------PSFSAEDIAKIKKFSKTRSKDIFDQLAKSLAPSIHGHDYVKKAILCLLLGGVERDLENGSHIRGDINILLIGDPSVAKSQLLRYVLCTAPRAIPTTGRGSSGVGLTAAVTTDQETGERRLEAGAMVLADRGVVCIDE   600
gi|114607814|ref|XP_001151750.1| SKDAQ--------PSFSAEDIAKIKKFSKTRSKDIFDQLAKSLAPSIHGHDYVKKAILCLLLGGVERDLENGSHIRGDINILLIGDPSVAKSQLLRYVLCTAPRAIPTTGRGSSGVGLTAAVTTDQETGERRLEAGAMVLADRGVVCIDE   600
gi|73973306|ref|XP_538960.2|     SKDVQ--------PSFSAEDIAKIKKFSKTRSKDIFDQLARSLAPSIHGHDYVKKAILCLLLGGVERDLENGSHIRGDINILLIGDPSVAKSQLLRYVLCTAPRAIPTTGRGSSGVGLTAAVTTDQETGERRLEAGAMVLADRGVVCIDE   600
gi|33859484|ref|NP_032589.1|     SKDIQ--------PAFSADDIAKIKKFSKTRSKDVFEQLARSLAPSIHGHDYVKKAILCLLLGGVERELENGSHIRGDINILLIGDPSVAKSQLLRYVLCTAPRAIPTTGRGSSGVGLTAAVTTDQETGERRLEAGAMVLADRGVVCIDE   600
gi|109485811|ref|XP_236988.4|    SKDIQ--------PAFSADDIAKIKKFSKTRSKDVFEQLARSLAPSIHGHDYVKKAILCLLLGGVERELENGSHIRGDINILLIGDPSVAKSQLLRYVLCTAPRAIPTTGRGSSGVGLTAAVTTDQETGKXXXXXXXXXLADRGVVCIDE   600
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gi|57530231|ref|NP_001006421.1|  SKDAR--------PLYSANDVAKIKRFSKSRSKDIFNQLARSLAPSIHGHEFIKKALLCMLLGGVEKVLENGSRIRGDINILLIGDPSVAKSQLLRYVLGTAPRAVGTTGRGSSGVGLTAAVTTDQETGERRLEAGAMVLADRGVVCIDE   600
gi|47086897|ref|NP_997732.1|     SKEIS--------HYFSADDVAKIKSFCRSRSKNVFDQLARSLAPSIHGHEYIKKAILCMLLGGVEKVLENGSRIRGDINVLLIGDPSVAKSQLLRYVLHTAPRAIPTTGRGSSGVGLTAAVTTDQETGERRLEAGAMVLGDRGVVCIDE   600
gi|124506457|ref|XP_001351826.1| NKETYDSN-----LCISEADKKNFHAFAK--KDNTIDILGYSFAPSICGQDIVKKAIVLMLAGGTERALPS-HHIRGDIHIMLVGDPSCGKSQLLRYVMSIMPGTVSATGRGSSGVGLTAAIVTDQDTGERVVEGGAMVMGDRRVVCIDE   600
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                                                                         .:*                    .:*  : : :   *           : :
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gi|115464471|ref|NP_001055835.1| FDKMNDQDRVAIHEVMEQQTVTIAKAGIHASLNARCSVIAAANPIYGTYDRSLTPTKNIGLPDSLLSRFDLLFIVLDQMDPEIDRQISEHVARMHRYCTDDGGARSLDKTG-------------YAEEDDG-----------DVNAAIFV   750
gi|145613273|ref|XP_363833.2|    FDKMSDIDRVAIHEVMEQQTVTIAKAGIHTSLNARCSVIAAANPIFGQYDPHKDPHKNIALPDSLLSRFDLLFVVTDDIEDARDRQVSEHVLRMHRYRQPGTEEGAVVRENTQQSLGVGMQ------SQSN---------DSQRPTDVFE   750
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gi|50309887|ref|XP_454957.1|     FDKMSDVDRVAIHEVMEQQTVTIAKAGIHTTLNARCSVIAAANPVFGQYDVNKDPHKNIALPDSLLSRFDLLFVVTDDINDIRDRAISEHVLRTHRYLPPGYLEGEPVREQINLSLAVGED---IENEEE-----------DDDEDVVFE   750
gi|45198873|ref|NP_985902.1|     FDKMSDVDRVAIHEVMEQQTVTIAKAGIHTTLNARCSVIAAANPVFGQYDVNKDPHKNIALPDSLLSRFDLLFVVTDDINDVRDRAISEHVLRTHRYLPPGYMEGEPIREAINLSLSVGTDGVSIDPDAD-----------DDTTDKVFE   750
gi|6320803|ref|NP_010882.1|      FDKMTDVDRVAIHEVMEQQTVTIAKAGIHTTLNARCSVIAAANPVFGQYDVNRDPHQNIALPDSLLSRFDLLFVVTDDINEIRDRSISEHVLRTHRYLPPGYLEGEPVRERLNLSLAVGED-ADINPEEHSNSGAGVENEGEDDEDHVFE   750
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gi|61888858|ref|NP_001013604.1|  ----------------------------------------PTN-------------------EKLLMLLPVGYPSEDAMVPNLTRKTLDQIMVTV-------------------------------------------------------   750
gi|57530231|ref|NP_001006421.1|  FDKMSDIDRTAIHEVMEQGRVTIAKAGIHARLNSRCSVLAAANPVYGRYDQYKTPMENIGLQDSLLSRFDLLFIMLDQMDSEQDREISDHVLRMHRYRNPNEQDGDAMPLG-SAVEILATDDPDFAQEEEQ-------------ELQVYE   750
gi|47086897|ref|NP_997732.1|     FDKMSDMDRTAIHEVMEQGRVTIAKAGIHARLNARCSVLAAANPVYGRYDQYKTPMENIGLQDSLLSRFDLLFIMLDQMDPEQDREISDHVLRMHRYRDPHEQDGTALALG-GTIDALATEDPDATQEEEE-------------ELQVYE   750
gi|124506457|ref|XP_001351826.1| FDKMQPTDRVAIHEVMEQQTVTVAKAGIHTTLNARCTVLAAANPLYGCWNDALDMGQQLQFEPSLLSRFDLIFLVRDSATEQDDERIAESVLRNVTEKAKPIMNESRNNQKNFVIQADSYDINPKAQHISIYNERDINQNNDSNNMQENE   750
                                 .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750

gi|15237411|ref|NP_199440.1|     KYNQTLHGK-KKRGQ-------THDKTLTIKFLKKYIHYAKHR------------ITPKLTDEASERIAEAYADLRNAGSDTKTGG-TLPITARTLETIIRLATAHAKMKLSSEVTKADAEALKLMNFAIYHQELTEMDDREQ-------   900
gi|115464471|ref|NP_001055835.1| KYDRMLHGQDRRRGKK------SKQDRLTVKFLKKYIHYAKNL------------IQPRLTDEASDHIATSYAELRDGGANAKSGGGTLPITARTLETIIRLSTAHAKMKLRHEVLKTDVEAALQVLNFAIYHKELTEMEEREQR-----   900
gi|145613273|ref|XP_363833.2|    KYDSMLHAGVTVTSGRG---ANKKPEVVSIPFMKKYIQYAKTR------------IRPVLTQEASDRIADIYVGLRNDE-VEGNQRRTSPMTVRTLETIIRLATAHARSRLSNRVEERDAAAAESILRFALFKEVVEAESRKKRRK----   900
gi|32416474|ref|XP_328715.1|     KYDAMLHAGIKVPSGRGS--ANKKPEILSIPFMKKYIQYAKTR------------IKPVLTQEASDRIADIYVGLRNDD-MEGNQRKTSPMTVRTLETLIRLATAHAKARLSNRVEERDAAAAESILRFALFKEVVQDESRKKRRK----   900
gi|19075295|ref|NP_587795.1|     TFSSLLHANART----------KKKELLNINFVRKYIQYAKSR------------IHPILNQATAEYITNIYCGLRNDD-LQGNQRRTSPLTARTLETLIRLSTAHAKARLSSVVEVKDAKAAEKILRYALFREVVK--PKRKKHK----   900
gi|50309887|ref|XP_454957.1|     KFNPLLHAGAKLAKNRGDSNGSELPQIVAIPFIRKYIQYAKER------------IIPQLTQEAVDVIIKSYSNLRND-----QNTKKSPITARTLETLIRLSSAHAKVRLSKKVELEDAKVATQLLRFALLGEDGAN------------   900
gi|45198873|ref|NP_985902.1|     KYDPLLHAGAKLAKNRGDHRGAELPKVVSIPFIRKYVQYAKER------------IVPVLTQDAVNIIVKTYCDLRND-----QNTKKSPITARTLETLIRLSNAHAKVRLSKLVEARDANVAAQLLRFALLGEDLSSTASDSALQHSPR   900
gi|6320803|ref|NP_010882.1|      KFNPLLQAGAKLAKNKGNYNGTEIPKLVTIPFLRKYVQYAKER------------VIPQLTQEAINVIVKNYTDLRND-----DNTKKSPITARTLETLIRLATAHAKVRLSKTVNKVDAKVAANLLRFALLGEDIGNDIDEEESE----   900
gi|24639835|ref|NP_511048.2|     KYDALLHGKSRQRH----------EKILSVEFMRKYIHIAKC-------------MKPKLGEQACEAIANEYSRLRSQEAVETDVARTQPITARTLETLIRLSTAHARARMSKSVTIDDAHAAIELVQFAYFKKVLDKDRPSKRRR----   900
gi|58396614|ref|XP_322026.2|     KYDPLLHGASRKRT----------DQILSMEFMRKYIHIAKC-------------LKPKLTETACEMISNEYSRLRSQDLMDSDVARTQPVTARTLETLIRLSTAHAKARMSRSVAEQDAQAAIELIQFAYFKKVLEKEKKKRRRTE---   900
gi|6631095|ref|NP_002379.2|      KHDNLLHG-TKKKK----------EKMVSAAFMKKYIHVAKI-------------IKPVLTQESATYIAEEYSRLRSQDSMSSDTARTSPVTARTLETLIRLATAHAKARMSKTVDLQDAEEAVELVQYAYFKKVLEKEKKRKKRSE---   900
gi|114607814|ref|XP_001151750.1| KHDNLLHG-TKKKK----------EKMVSAAFMKKYIHVAKI-------------IKPVLTQESATYIAEEYSRLRSQDSMSSDTARTSPVTARTLETLIRLATAHAKARMSKTVDLQDAEEAVELVQYAYFKKVLEKEKKRKKRSE---   900
gi|73973306|ref|XP_538960.2|     KHDNLLHG-TKKKK----------EKMVSAAFMRKYIHVAKI-------------IKPILTQESAAYIAEEYSRLRSQDSMSSDTARTSPVTARTLETLIRLATAHAKARMSKTVDLQDAEEAVELVQYAYFKKVLEKEKKRKKRNE---   900
gi|33859484|ref|NP_032589.1|     KHDSLLHG-TKKKK----------EKMVSAAFMKKYIHVAKI-------------IKPTLTQESAAYIAEEYSRLRSQDSMSSDTARTSPVTARTLETLIRLATAHAKARMSKTVDLQDAEEAVELVQYAYFKKVLEKEKKRKKASE---   900
gi|109485811|ref|XP_236988.4|    KHDNLLHG-SKKKR----------EKMVSAAFMKKYIHVAKI-------------IKPTLTQESAAYIAEEYSRLRSQDSMSSDTARTSPVTARTLETLIRLATAHAKARMSKTVDLQDAEEAVELVQYAYFKKVLEKEKKRKKPSE---   900
gi|61888858|ref|NP_001013604.1|  ------------------------------------------------------------------------------------------------------------------------------------------------------   900
gi|57530231|ref|NP_001006421.1|  KHDDLLHG-PNRRK----------EKIVSMEFMRKYIHVAKM-------------IKPVLTQESADYIAEEYSSLRSQNQMNSDIARTSPVTARTLETLIRLSTAHAKARMSKTVDLQDAEAALELVQFAYFKKVLEKEKKRKKQVE---   900
gi|47086897|ref|NP_997732.1|     KHNPLLHG-SKKNK----------DRVVSKAFMRKYIHVAKA-------------ISPVLTQDAANHIAEEYSRLRNQEQLGSDIARTSPVTARTLETLIRLSTAHAKARMSKAVELVDTEVAVELVQFAYFKKVLEKERKRSRNGQ---   900
gi|124506457|ref|XP_001351826.1| EYETPIFANRDEMIYYDK--NGVEHEILTVPFFKKYLHYVKNIFYHEKQRTDGWKPYPEVSDEACEVITELYADLRERASKYSHNKLIQGVTPRTLEAIIRIASSHAKLKLNRYVTSVDVNYAKKLLMYTLFGEEIIDSNEEDEEED---   900
                                 .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900
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gi|15237411|ref|NP_199440.1|      ----------------EERQREQAEQERTPSGRRGNQ------RRNNEDGAENDTANVDSETADPMEVDEP-------------------------------------------------------SVEQFSG-----------  1050
gi|115464471|ref|NP_001055835.1| ----------------EMEMKQQADHDAGASGGNADE------HRSSGN--------------DPMDVDVG-------------------------------------------------------------NASNDQ------------  1050
gi|145613273|ref|XP_363833.2|    ----TQNVEYAS--SSEDDSSDEDDD--GDLRSTARASTSRSARGTARTRRG--AVNANGRR----ADTSGAPVDADDDDEDQEPE----ASAPRRSNRSGRGAVAS-----SSQSQSQVSYASSVPASQLETQEEDDEDAEADGLA---  1050
gi|32416474|ref|XP_328715.1|      ----TRPAEGEDGMSSDSDDSDDDDDDVATQTTTARSSAARASRASRASQRASRRTPANGASSSSAANANGTPREEEETQGAEEEEEDIYDATPRRSTRSARTTGDSQPSFASSLPASQLRSTRSQRSSRRTAQNQDDEEELASGAANLN  1050
gi|19075295|ref|NP_587795.1|      ----KQRLEAGEEFDSEDDNSDDMDIEESEEEMDTNMVIDSGSRRVTRSQNATSQSQESGSE-------IGSSIAG----------------------TAGSYNVGT-----SNTQLSWPSTHSTLPATSRELASSDRNINTGTSVA---  1050
gi|50309887|ref|XP_454957.1|      -------FDEQEFAEGRTTEKS------PRKKPRASPRKKRGAVYKEVDSEDAE-EDQEMAETQPDPADGLEST---MVRLAPEQE-----EDLQRRLEQNLRVSPRRQLSVERRVLSQSDHQQQVLHHSSQSSTGPLETGSQLEPS---  1050
gi|45198873|ref|NP_985902.1|      KRQRTRMYTEEEPAPALQQSHSGADADATSSSIVATPIRAR-NLPRDIDPDASDAEDDGDAVYLPDSITSLTP----MTRLPHDEE-----LDLQRRMERGLRVSPR---LASRRILSDSENLPAHPPTSAASMRQHLQQ-AAHSPS---  1050
gi|6320803|ref|NP_010882.1|       -------YEEALSKRSPQKSPKKRQRVRQPASNSGSPIKSTPRRSTASSVNATPSSARRILRFQDDEQNAGEDDNDIMSPLPADEE-----AELQRRLQLGLRVSPR-----RREHLHAPEEGSSGPLTEVGTPRLPNVS-SAGQDD---  1050
gi|24639835|ref|NP_511048.2|      -----------------NSGSDAEDDNGEASSQRS-----PSRRSKRTRTATVGADSDEEDIEPPQPDAGDL-------------------------------------TRRETRRSLPARSVAMLMASPSSEEQSVATSTTE---  1050
gi|58396614|ref|XP_322026.2|      ----------------NDDSQDEMEDDEEEAAVQEETAASQGTRRSKRTRVEHH-DDSDHEELLTSPPDRGDL-------------------------------------TRRTTITS-PRVAESATMDTEEAAESSVVA-------  1050
gi|6631095|ref|NP_002379.2|       ----------------DESETEDEEEKSQE-DQEQKR-----KRRKTRQPDAKDGDSYDPYDFSDTEEEMP-----------------------------------QVHTPKTADSQE-------TKESQKV-----------  1050
gi|114607814|ref|XP_001151750.1| ----------------DESETEDEEEKSQE-DQEQKR-----KRRKTRQPDAKDGDSYDPYDFSDTEEEMP-----------------------------------QVHTPKTADSQE-------TKESQKV-----------  1050
gi|73973306|ref|XP_538960.2|     ----------------DESETDDEEEKSQE-DQEQKS-----KRRKTRHPDAKDGGSYDPYDFSDTEEEMP-----------------------------------QVHTPKTADSQE-------TKESQKV-----------  1050
gi|33859484|ref|NP_032589.1|     ----------------DESDLEDEEEKSQE-DTEQKR-----KRRKT---HAKDGESYDPYDFSEAETQMP-----------------------------------QVHTPKTDDSQEKTDDSQETQDSQKV-----------  1050
gi|109485811|ref|XP_236988.4|    ----------------DESDLEDEEEKSQEEDTEQTR-----KRRKT---QAKDGESYDPYDFSEAEREMP-----------------------------------QVHTPKTDDSQEKTDESQETQESQKV-----------  1050
gi|61888858|ref|NP_001013604.1|  ------------------------------------------------------------------------------------------------------------------------------------------  1050
gi|57530231|ref|NP_001006421.1|  ----------------DDSETEKEEEEEETQPEKEGR-----KQRRKKARTEGEEESYDPYDFSDAEQEMPEV-----------------------------------QAHTPKTPESSA-------TGEAKKP-----------  1050
gi|47086897|ref|NP_997732.1|     ----------------QDAASEDEEEEEDE--AQDTP-----RPPRKRRRGSQGSESYDPYDF-DTETDIPQI-----------------------------------QSPAPARQGDEE-------PDQNGHT-----------  1050
gi|124506457|ref|XP_001351826.1| ----------------EEEEEEEEEEDELEEDEEDDDDEEEKLKKKRRQRQKRASRKRSGEKKDLASNKKKKK-----------------------------------KSEQPNENGNENYMIDDLPSNKSNDT-----------  1050
                                  .......910.......920.......930.......940.......950.......960.......970.......980.......990......1000......1010......1020......1030......1040......1050
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gi|15237411|ref|NP_199440.1|      ------------------------------------TVSAARIETFERVFGQHMR--THRLDDISIADIETVVNNNG-----VGASRYSADEIMALLEKLQDDNKVMISDGKVHII-  1167
gi|115464471|ref|NP_001055835.1| ------------------------------------DVPAERIEAFEAILGQHVL--ANHLDQISIDEIEQTVNR-------EAAAPYNRRQVEFILERMQDANRIMIRDGIVRII-  1167
gi|145613273|ref|XP_363833.2|    ---DEAAALNIGQDDGPE-------------------ITASRLGAFRQALGQLQSTDLFEDDTASLDNVVTAVNAKI-GSRSGG--AFSKDEAVKALRKMDEANQVM----------  1167
gi|32416474|ref|XP_328715.1|      VDEDEDEEMDVDGEAAPENQEEEEEEEEEEEDEEPAPISEHRLDVFRRALGPLLNSGLFEDDAADVDELIKAVNEKIPGGRRGGEQKFEKEEALQALREMTERNQLMYTDGQLVYKI  1167
gi|19075295|ref|NP_587795.1|      ----SEVSASVSEQSTVS-------------------LPREKMSVFMARLASLTKSELFSEECASLEDVLESINNIE---DDVG---FSREEAIVALKEMDAQNKIMFSDN-VVYRI  1167
gi|50309887|ref|XP_454957.1|      --HMTLDFMSIEEMDQGS-------------------ISTGRLSSLSGIVARLMQSDIFEEESYPVAALFERINEQVP--EEEK---FTVDEYVAGLRIMSDRNNLMVADGKVWRV-  1167
gi|45198873|ref|NP_985902.1|      --RAPDESATVEHIEPGS-------------------ISPGRLSIISGIIARLMQTDLFEDEHYPIIALLEKVNEELP--EEDK---FSMEEYLAGLNIMSDRNNLMIAEDKVWRV-  1167
gi|6320803|ref|NP_010882.1|       --EQQQSVISFDNVEPGT-------------------ISTGRLSLISGIIARLMQTEIFEEESYPVASLFERINEELP--EEEK---FSAQEYLAGLKIMSDRNNLMVADDKVWRV-  1167
gi|24639835|ref|NP_511048.2|      ---------------------------------PAIISDARLGEFKNNLQRLFR--EAREQSLALARITTAINVGS-------QEPFTAGEIEAAVHRMTEDNQIMVADDIVFLI-  1167
gi|58396614|ref|XP_322026.2|      ------------------------------------ISEARLKLFRQGVFMAFK--HFHDQSVSLARLTTHINENSG------DEAFTPGEITAAVNQMTESNNIMVHDDMVFLI-  1167
gi|6631095|ref|NP_002379.2|       ----------------------------------ELSESRLKAFKVALLDVFR--EAHAQSIGMNRLTESINRDS-------EEPFSSVEIQAALSKMQDDNQVMVSEGIIFLI-  1167
gi|114607814|ref|XP_001151750.1| ----------------------------------ELSESRLKAFKVALLDVFR--EAHAQSIGMNRLTESINRDS-------EEPFSSVEIQAALSKMQDDNQVMVSEGIIFLI-  1167
gi|73973306|ref|XP_538960.2|     ----------------------------------ELSESRLKEFKVALLDVFR--EAHAQSVGMNRLTESINRDK-------EEPFSSAEIQAALSKMQDDNQVMVSEGIIFLI-  1167
gi|33859484|ref|NP_032589.1|     ----------------------------------ELSEPRLKAFKAALLEVFQ--EAHEQSVGMLHLTESINRNR-------EEPFSSEEIQACLSRMQDDNQVMVSEGIVFLI-  1167
gi|109485811|ref|XP_236988.4|    ----------------------------------ELSESRLKAFKAALLEVFQ--EAHAQSVGMIHLTESINRNK-------EEPFSSEEIQASLSRMQDDNQVMVSEGIVFLI-  1167
gi|61888858|ref|NP_001013604.1|  ------------------------------------------------------------------------------------------------------------------------  1167
gi|57530231|ref|NP_001006421.1|  ----------------------------------ELADPRLKAFKAALLEVFK--SSHAQSVGLKNVMESINRDN-------PEPFSLAGVKVALAHMQDDNQIMVSDDIIFLI-  1167
gi|47086897|ref|NP_997732.1|     ----------------------------------ELSEDRFKEFKAALHKVFR--SSHAQSVGLIALMESINKSC-------PSAFNETDFRAALARMQDDNQVMLADDIIFLI-  1167
gi|124506457|ref|XP_001351826.1| ----------------------------------LDIKEIERLIVENVTLNDPGDGLKDVELLDLIILGNKDKMP--ELSKLDINQLRQIINSLNDMDGAPIYYVKKDKIVYKC  1167
                                  ......1060......1070......1080......1090......1100......1110......1120......1130......1140......1150......1160.......
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