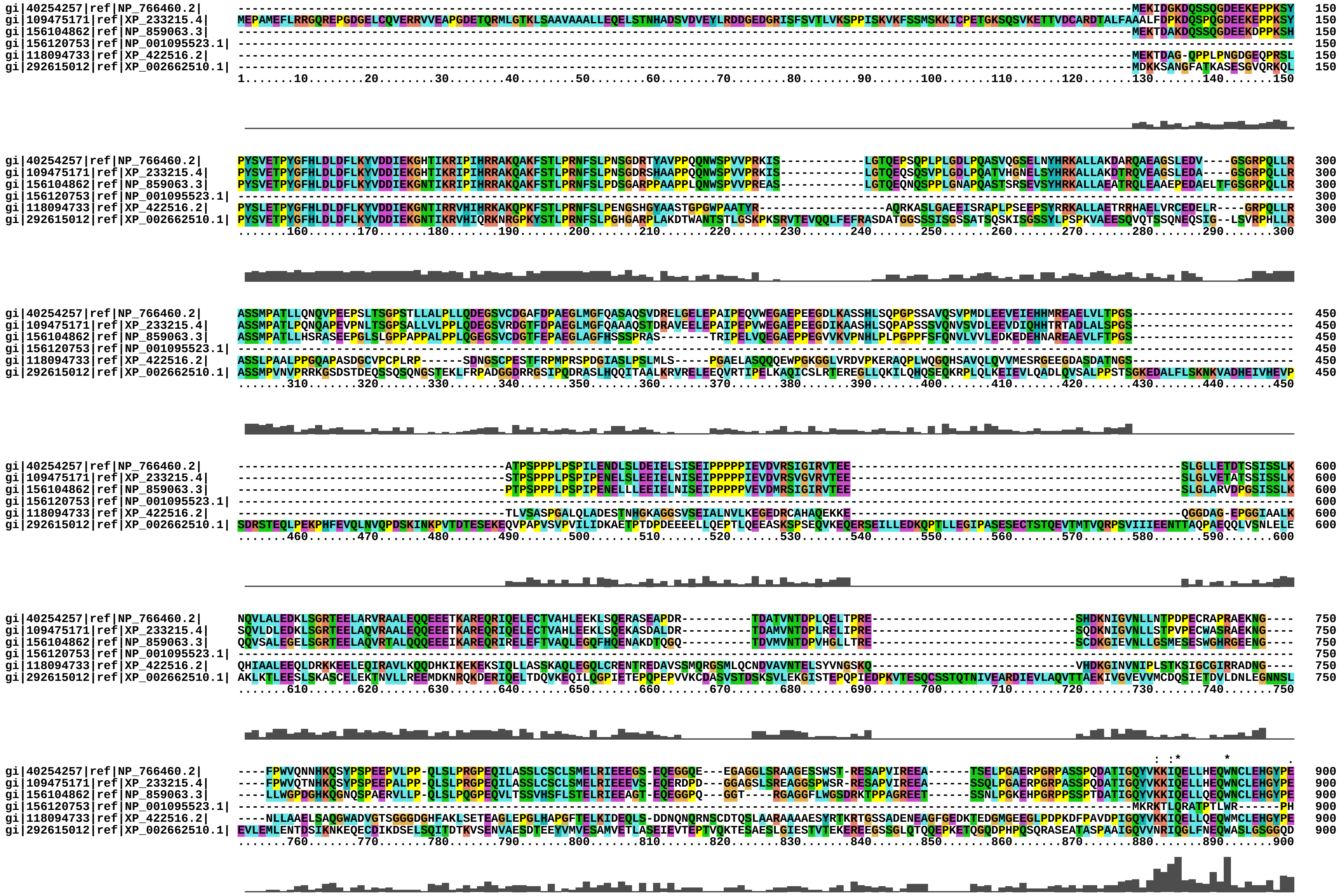

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gi|156104862|ref|NP_859063.3|    -------------------------------------------------------------------------------------------------------------------------------MEKTDAKDQSSQGDEEKDPPKSH   150
gi|156120753|ref|NP_001095523.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|118094733|ref|XP_422516.2|    -------------------------------------------------------------------------------------------------------------------------------MEKTDAG-QPPLPNGDGEQPRSL   150
gi|292615012|ref|XP_002662510.1| -------------------------------------------------------------------------------------------------------------------------------MDKKSANGFATKASESGVQRKQL   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

gi|40254257|ref|NP_766460.2|     PYSVETPYGFHLDLDFLKYVDDIEKGHTIKRIPIHRRAKQAKFSTLPRNFSLPNSGDRTYAVPPQQNWSPVVPRKIS------------LGTQEPSQPLPLGDLPQASVQGSELNYHRKALLAKDARQAEAGSLEDV----GSGRPQLLR   300
gi|109475171|ref|XP_233215.4|    PYSVETPYGFHLDLDFLKYVDDIEKGHTIKRIPIHRRAKQAKFSTLPRNFSLPNSGDRSHAAPPQQNWSPVVPRKIS------------LGTQEQSQSVPLGDLPQATVHGNELSYHRKALLAKDTRQVEAGSLEDA----GSGRPQLLR   300
gi|156104862|ref|NP_859063.3|    PYSVETPYGFHLDLDFLKYVDDIEKGNTIKRIPIHRRAKQAKFSTLPRNFSLPDSGARPPAAPPLQNWSPVVPREAS------------LGTQEQNQSPPLGNAPQASTSRSEVSYHRKALLAEATRQLEAAEPEDAELTFGSGRPQLLR   300
gi|156120753|ref|NP_001095523.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   300
gi|118094733|ref|XP_422516.2|    PYSLETPYGFHLDLDFLKYVDDIEKGNTIRRVHIHRKAKQPKFSTLPRNFSLPENGSHGYAASTGPGWPAATYR------------------AQRKASLGAEEISRAPLPSEEPSYRRKALLAETRRHAELVRCEDELR----GRPQLLR   300
gi|292615012|ref|XP_002662510.1| PYSVETPYGFHLDLDFLKYVDDIEKGNTIKRVHIQRKNRGPKYSTLPRNFSLPGHGARPLAKDTWANTSTLGSKPKSRVTEVQQLFEFRASDATGGSSSISGSSATSQSKISGSSYLPSPKVAEESQVQTSSQNEQSIG--LSVRPHLLR   300
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gi|40254257|ref|NP_766460.2|     ASSMPATLLQNQVPEEPSLTSGPSTLLALPLLQDEGSVCDGAFDPAEGLMGFQASAQSVDRELGELEPAIPEQVWEGAEPEEGDLKASSHLSQPGPSSAVQSVPMDLEEVEIEHHMREAELVLTPGS-----------------------   450
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gi|156120753|ref|NP_001095523.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   450
gi|118094733|ref|XP_422516.2|    ASSLPAALPPGQAPASDGCVPCPLRP------SDNGSCPESTFRPMPRSPDGIASLPSLMLS-----PGAELASQQQEWPGKGGLVRDVPKERAQPLWQGQHSAVQLQVVMESRGEEGDASDATNGS-----------------------   450
gi|292615012|ref|XP_002662510.1| ASSMPVNVPRRKGSDSTDEQSSQSQNGSTEKLFRPADGGDRRGSIPQDRASLHQQITAALKRVRELEEQVRTIPELKAQICSLRTEREGLLQKILQHQSEQKRPLQLKEIEVLQADLQVSALPPSTSGKEDALFLSKNKVADHEIVHEVP   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

gi|40254257|ref|NP_766460.2|     --------------------------------------ATPSPPPLPSPILENDLSLDEIELSISEIPPPPPIEVDVRSIGIRVTEE-----------------------------------------------SLGLLETDTSSISSLK   600
gi|109475171|ref|XP_233215.4|    --------------------------------------STPSPPPLPSPIPENELSLEEIELNISEIPPPPPIEVDVRSVGVRVTEE-----------------------------------------------SLGLVETATSSISSLK   600
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gi|156120753|ref|NP_001095523.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   600
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gi|292615012|ref|XP_002662510.1| SDRSTEQLPEKPHFEVQLNVQPDSKINKPVTDTESEKEQVPAPVSVPVILIDKAETPTDPDEEEELLQEPTLQEEASKSPSEQVKEQERSEILLEDKQPTLLEGIPASESECTSTQEVTMTVQRPSVIIIEENTTAQPAEQQLVSNLELE   600
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gi|40254257|ref|NP_766460.2|     NQVLALEDKLSGRTEELARVRAALEQQEEETKAREQRIQELECTVAHLEEKLSQERASEAPDR----------TDATVNTDPLQELTPRE-----------------------------SHDKNIGVNLLNTPDPECRAPRAEKNG----   750
gi|109475171|ref|XP_233215.4|    SQVLDLEDKLSGRTEELAQVRAALEQQEEETKAREQRIQELECTVAHLEEKLSQEKASDALDR----------TDAMVNTDPLRELIPRE-----------------------------SQDKNIGVNLLSTPVPECWASRAEKNG----   750
gi|156104862|ref|NP_859063.3|    QQVSALEGELSGRTEELAQVRTALQQQEEEIKAREQRIRELEFTVAQLEGQFHQENAKDTQGQ----------TDVMVNTDPVHGLLTRE-----------------------------SCDKGIEVNLLGSMESESWGHRGEENG----   750
gi|156120753|ref|NP_001095523.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   750
gi|118094733|ref|XP_422516.2|    QHIAALEEQLDRKKEELEQIRAVLKQQDHKIKEKEKSIQLLASSKAQLEGQLCRENTREDAVSSMQRGSMLQCNDVAVNTELSYVNGSKQ-----------------------------VHDKGINVNIPLSTKSIGCGIRRADNG----   750
gi|292615012|ref|XP_002662510.1| AKLKTLEESLSKASCELEKTNVLLREEMDKNRQKDERIQELTDQVKEQILQGPIETEPQPEPVVKCDASVSTDSKSVLEKGISTEPQPIEDPKVTESQCSSTQTNIVEARDIEVLAQVTTAEKIVGVEVVMCDQSIETDVLDNLEGNNSL   750
                                 .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750

                                                                                                                                                                   : :*      *        .
gi|40254257|ref|NP_766460.2|     ----FPWVQNNHKQSYPSPEEPVLPP-QLSLPRGPEQILASSLCSCLSMELRIEEEGS-EQEGGQE---EGAGGLSRAAGESSWST-RESAPVIREEA------TSELPGAERPGRPASSPQDATIGQYVKKIQELLHEQWNCLEHGYPE   900
gi|109475171|ref|XP_233215.4|    ----FPWVQTNHKQSYPSPEEPALPP-QLSLPRGPEQILASSLCSCLSMELRIEEEVS-EQERDPD---GGAGSLSREAGGSPWSR-RESAPVIREEA------SSQLPGAERPGRPASSPQDATIGQYVKKIQELLHEQWNCLEHGYPE   900
gi|156104862|ref|NP_859063.3|    ----LLWGPDGHKQGNQSPAERVLLP-QLSLPQGPEQVLTSSVHSFLSTELRIEEAGT-EQEGGPQ---GGT----RGAGGFLWGSDRKTPPAGREET------SSNLPGKEHPGRPPSSPTDATIGQYVKKIQELLQEQWNCLEHGYPE   900
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gi|292615012|ref|XP_002662510.1| EVLEMLENTDSIKNKEQECDIKDSELSQITDTKVSENVAESDTEEYVMVESAMVETLASEIEVTEPTVQKTESAESLGIESTVTEKEREEGSSGLQTQQEPKETQGQDPHPQSQRASEATASPAAIGQVVNRIQGLFNEQWASLGSGGQD   900
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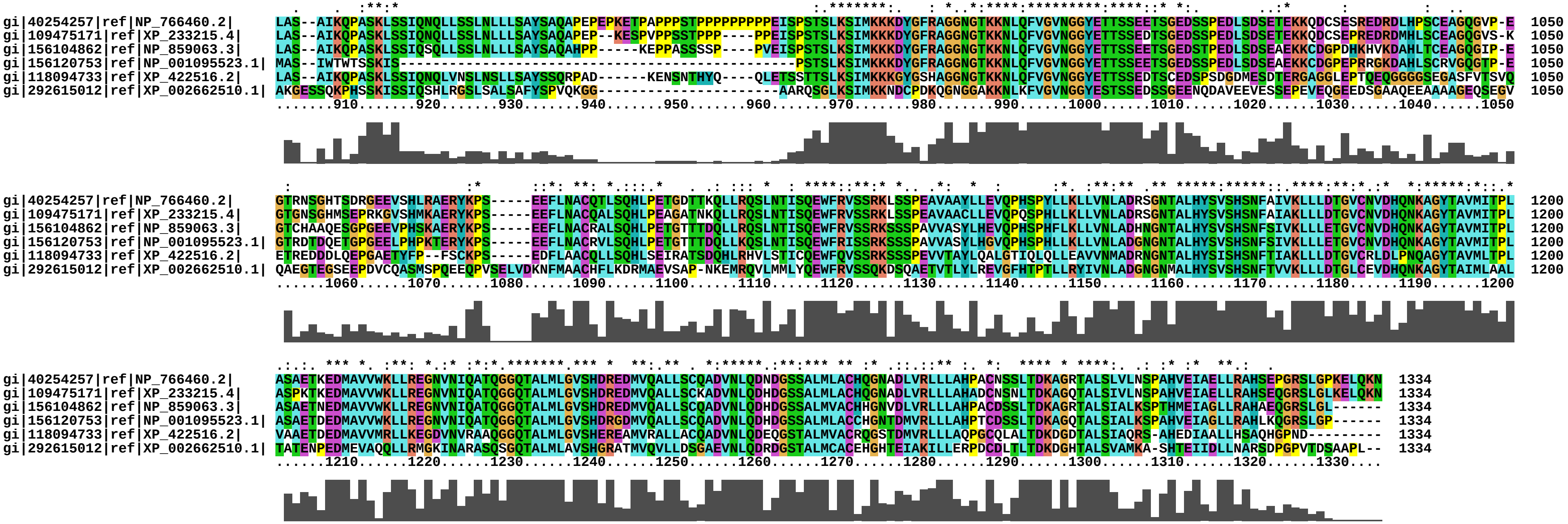

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                                   .    .  :**:*                                                  :.*******:.   : *..*:****:*********:****::* *:.       ..:*      :         : ..
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gi|109475171|ref|XP_233215.4|    LAS--AIKQPASKLSSIQNQLLSSLNLLLSAYSAQAPEP--KESPVPPSSTPPP----PPEISPSTSLKSIMKKKDYGFRAGGNGTKKNLQFVGVNGGYETTSSEDTSGEDSSPEDLSDSETEKKQDCSEPREDRDMHLSCEAGQGVS-K  1050
gi|156104862|ref|NP_859063.3|    LAS--AIKQPASKLSSIQSQLLSSLNLLLSAYSAQAHPP-----KEPPASSSSP----PVEISPSTSLKSIMKKKDYGFRAGGNGTKKNLQFVGVNGGYETTSSEETSGEDSTPEDLSDSEAEKKCDGPDHKHVKDAHLTCEAGQGIP-E  1050
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gi|118094733|ref|XP_422516.2|    LAS--AIKQPASKLSSIQNQLVNSLNSLLSAYSSQRPAD------KENSNTHYQ----QLETSSTTSLKSIMKKKGYGSHAGGNGTKKNLQFVGVNGGYETTSSEDTSCEDSPSDGDMESDTERGAGGLEPTQEQGGGGSEGASFVTSVQ  1050
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                                 .......910.......920.......930.......940.......950.......960.......970.......980.......990......1000......1010......1020......1030......1040......1050

                                  :                     :*      ::*: **: *.:::.*   . .: ::: *  : ****::**:* *.. .*:  *  :      :*. :**:** .** *****:*****::.****:**:*.:*  *:*****:*::.*
gi|40254257|ref|NP_766460.2|     GTRNSGHTSDRGEEVSHLRAERYKPS-----EEFLNACQTLSQHLPETGDTTKQLLRQSLNTISQEWFRVSSRKLSSPEAVAAYLLEVQPHSPYLLKLLVNLADRSGNTALHYSVSHSNFAIVKLLLDTGVCNVDHQNKAGYTAVMITPL  1200
gi|109475171|ref|XP_233215.4|    GTGNSGHMSEPRKGVSHMKAERYKPS-----EEFLNACQALSQHLPEAGATNKQLLRQSLNTISQEWFRVSSRKLSSPEAVAACLLEVQPQSPHLLKLLVNLADRSGNTALHYSVSHSNFAIAKLLLDTGVCNVDHQNKAGYTAVMITPL  1200
gi|156104862|ref|NP_859063.3|    GTCHAAQESGPGEEVPHSKAERYKPS-----EEFLNACRALSQHLPETGTTTDQLLRQSLNTISQEWFRVSSRKSSSPAVVASYLHEVQPHSPHFLKLLVNLADHNGNTALHYSVSHSNFSIVKLLLETGVCNVDHQNKAGYTAVMITPL  1200
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                                 .:.:. *** *. :**: *.:* :*:*.*******.*** *  **:.** . *:*****.:**:*** ** :* .::.::** :. *:  **** * ****:. .: :* :*  **.:  .
gi|40254257|ref|NP_766460.2|     ASAETKEDMAVVWKLLREGNVNIQATQGGQTALMLGVSHDREDMVQALLSCQADVNLQDNDGSSALMLACHQGNADLVRLLLAHPACNSSLTDKAGRTALSLVLNSPAHVEIAELLRAHSEPGRSLGPKELQKN  1334
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gi|156120753|ref|NP_001095523.1| ASAETDEDMAVVWKLLREGNVNIQATQGGQTALMLGVSHDRGDMVQALLSCQADVNLQDHDGSSALMLACCHGNTDMVRLLLAHPTCDSSLTDKAGQTALSIALKSPAHVEIAGLLRAHLKQGRSLGP------  1334
gi|118094733|ref|XP_422516.2|    VAAETDEDMAVVMRLLKEGDVNVRAAQGGQTALMLGVSHEREAMVRALLACQADVNLQDEQGSTALMVACRQGSTDMVRLLLAQPGCQLALTDKDGDTALSIAQRS-AHEDIAALLHSAQHGPND---------  1334
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