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gi|17568305|ref|NP_509836.1|      --------------------------MKLKLTVLLILVHASASYKPPA------IEVEDYQVQEHDSIGKFVELEEHTR--LILKCSAHHNGDLKYNFPSMEGNVGYDENNFK------KRMEEYYDDAFGDKVLTLNDVRESDTGTYSC   110
gi|17568311|ref|NP_509835.1|      --------------------------MRVSLTEFLVLAQVVTTLQPIT------IKVDFHEVKHHESIGDYVELVEGKNRDISLTCYGQHK-NLKIEPPKREE----HAGFPE------IGIRTSAEWKKNEYWFLLKNVRQCDTGSYYC   107
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gi|17563712|ref|NP_506728.1|      ------------------------------------------------------------------------------------------------------------------------------------------------------
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gi|114649218|ref|XP_509605.2|     ------------------------------MVSYWDTG---VLLCALLSCLILTGSSSGSKLKDPELSLKGTQHVMQAGQTLHLQCRGEAAHKWSLPEMVSKE--SERLSITK-SACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPT   114
gi|73993482|ref|XP_534520.2|      ------------------------------MVSCRDTG---VLLCALLGGLLLTGSSSGSKLKGPELSLKGTQHVMQAGQTLYLKCRGEAAHSWSLPETVRKE--SKRLSITK-SACGRNGKQFCSTLTLNMAQANHTGFYSCKYLSIPA   114
gi|194671875|ref|XP_001249769.2| -----------MPATQVTENQVPRLCLAAFRFTREDTKKRPAQDCRGRAFRTWRRSSSGSILRHPELSLKGTRHVMQAGQTLNLKCRGGAAHAWYLPEAVNRENQSGKLNITK-SACGKNLKKFCSTLTLNAAQANHTGFYSCRYLSAPA   138
gi|34328180|ref|NP_034358.2|      ------------------------------MVSCWDTA---VLPYALLGCLLLTGYGSGSKLKVPELSLKGTQHVMQAGQTLFLKCRGEAAHSWSLPTTVSQE--DKRLSITPPSACGRDNRQFCSTLTLDTAQANHTGLYTCRYLPTST   115
gi|11276093|ref|NP_062179.1|      ------------------------------MVSCWDTA---VLPCALLGCLLLTGYCSGSKLKGPELSLKGTQHVMQAGQTLFLKCRGEAAHSWSLPTTVSQE--DKKLSVTR-SACGRNNRQFCSTLTLNMAQANHTGLYSCRYLPKST   114
gi|45383624|ref|NP_989583.1|      ------------------------------MPRQLLSG-----TVLLGAAFLLAGSTSGSKLKVPVLSVNGRQHVVQAGQTLNLTCRGEMLHSWSLPEALSKD--SKRLNVTK-YACGRNGTQFCSTLTLSRTQANDTGRYSCRYPTSPV   112
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gi|25146689|ref|NP_741035.1|      ------------------------------------------------------------------------------------------------------------------------------------------------------
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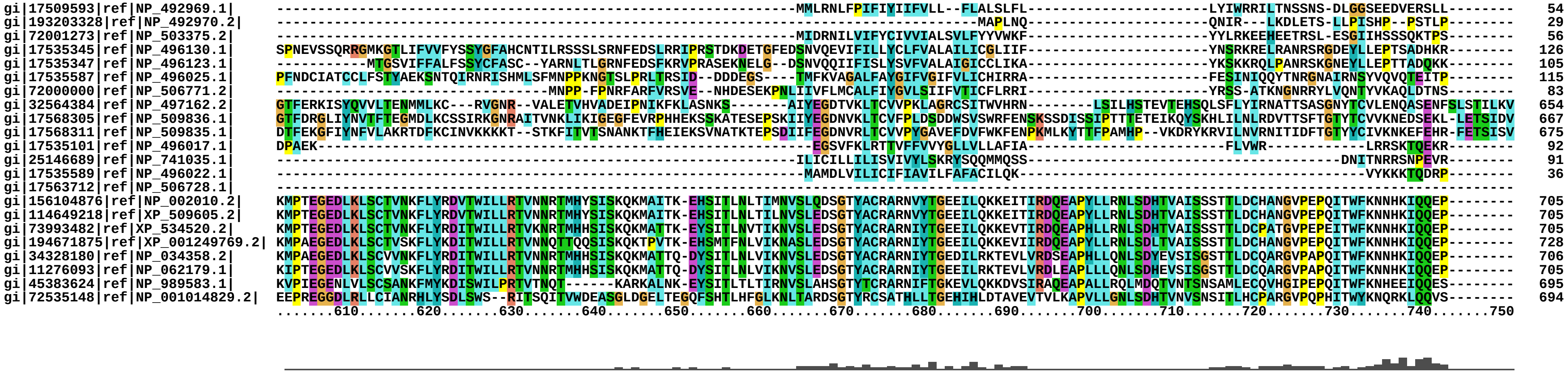

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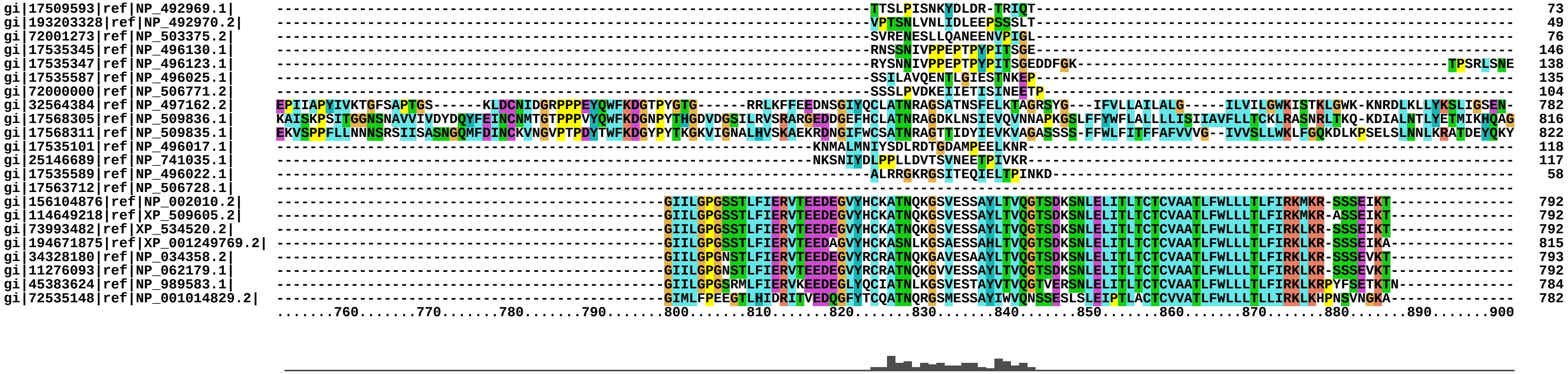

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gi|72001273|ref|NP_503375.2|         ------------------------------------------------------------------------SVRENESLLQANEENVPIGL----------------------------------------------------------    76
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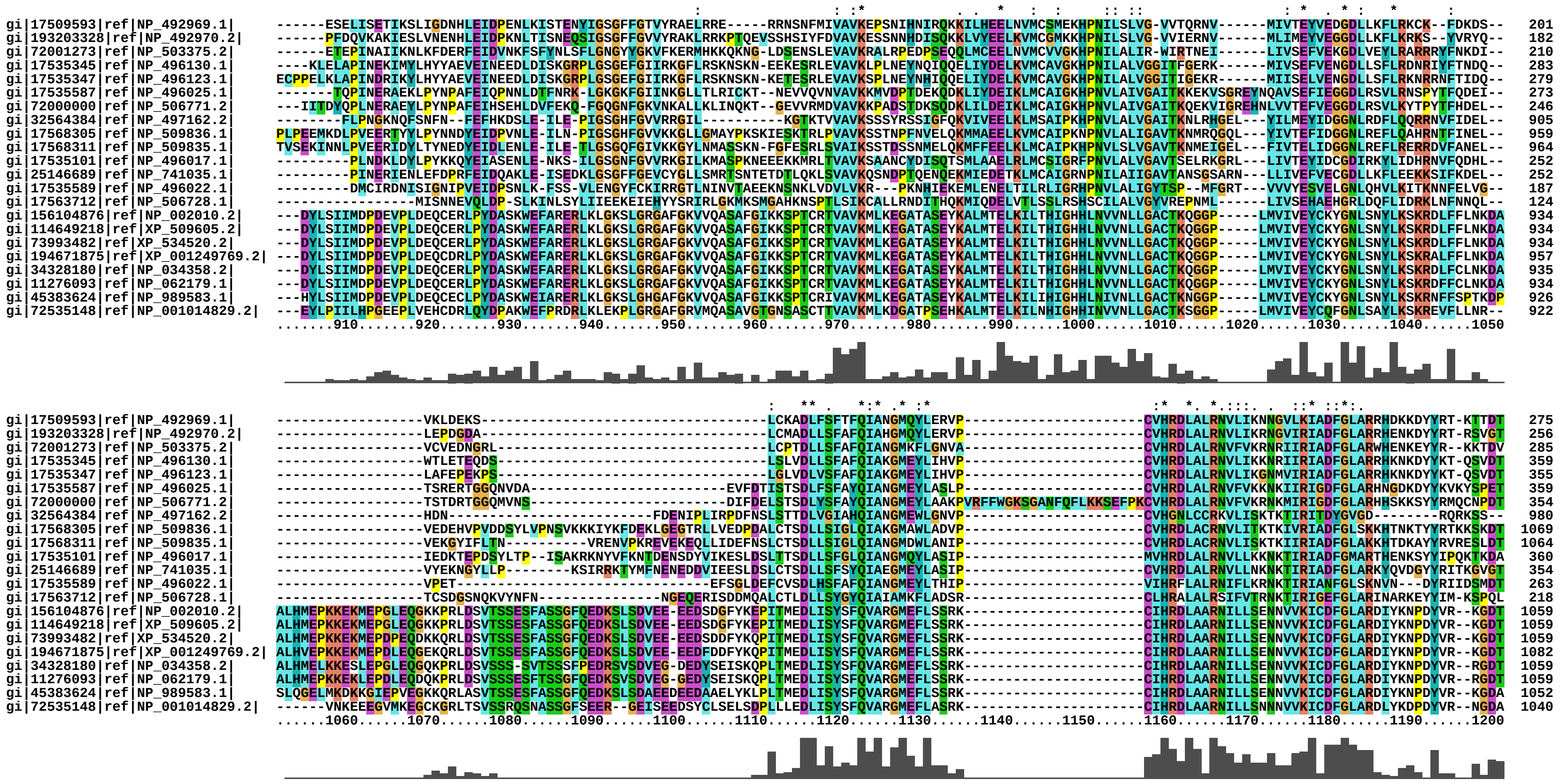

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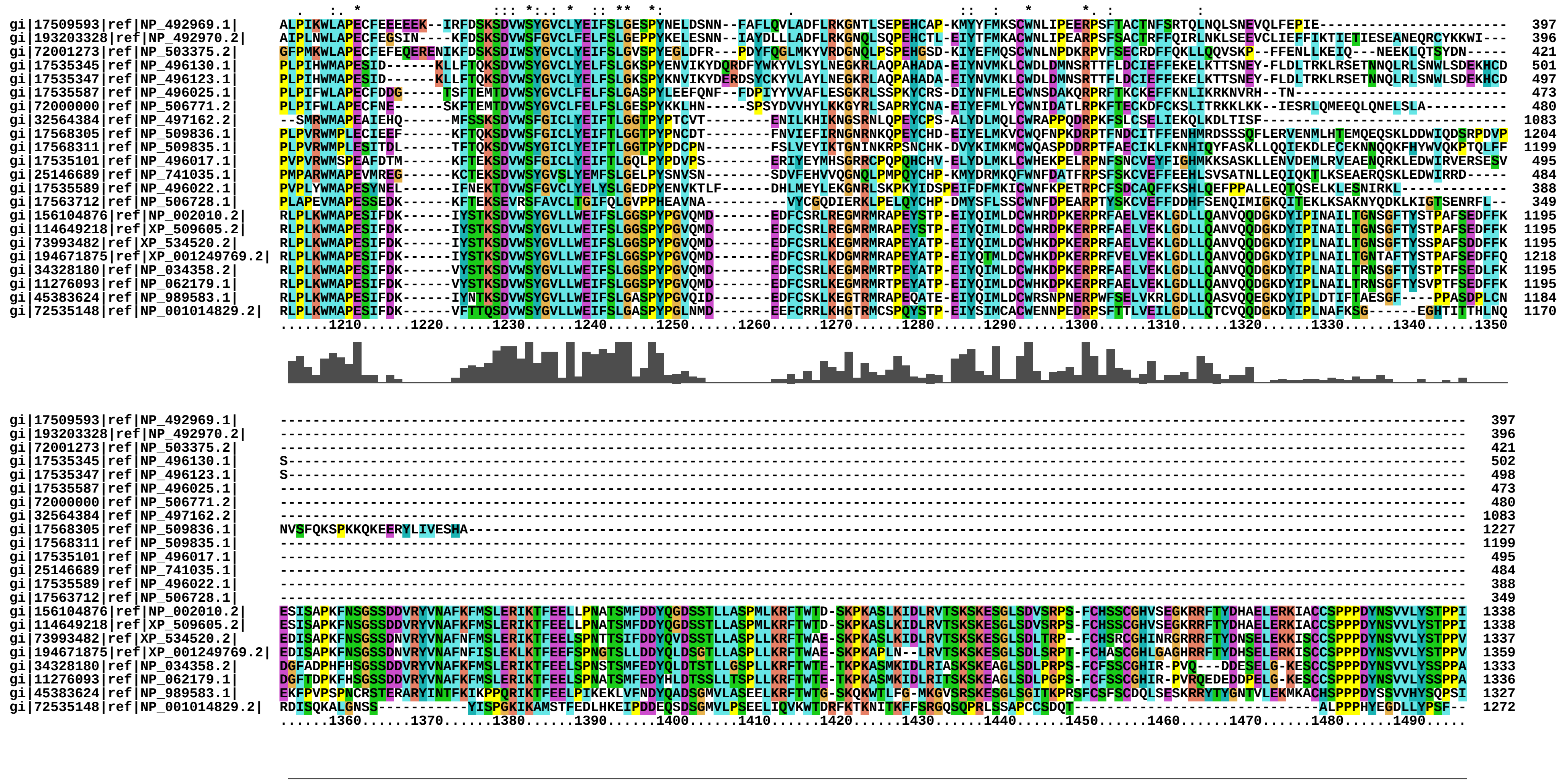

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gi|17535347|ref|NP_496123.1|     S------------------------------------------------------------------------------------------------------------------------------------------------   498
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gi|17535101|ref|NP_496017.1|     -------------------------------------------------------------------------------------------------------------------------------------------------   495
gi|25146689|ref|NP_741035.1|     -------------------------------------------------------------------------------------------------------------------------------------------------   484
gi|17535589|ref|NP_496022.1|     -------------------------------------------------------------------------------------------------------------------------------------------------   388
gi|17563712|ref|NP_506728.1|     -------------------------------------------------------------------------------------------------------------------------------------------------   349
gi|156104876|ref|NP_002010.2|    ESISAPKFNSGSSDDVRYVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPMLKRFTWTD-SKPKASLKIDLRVTSKSKESGLSDVSRPS-FCHSSCGHVSEGKRRFTYDHAELERKIACCSPPPDYNSVVLYSTPPI  1338
gi|114649218|ref|XP_509605.2|    ESISAPKFNSGSSDDVRYVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPMLKRFTWTD-SKPKASLKIDLRVTSKSKESGLSDVSRPS-FCHSSCGHVSEGKRRFTYDHAELERKIACCSPPPDYNSVVLYSTPPI  1338
gi|73993482|ref|XP_534520.2|     EDISAPKFNSGSSDNVRYVNAFNFMSLERIKTFEELSPNTTSIFDDYQVDSSTLLASPLLKRFTWAE-SKPKASLKIDLRVTSKSKESGLSDLTRP--FCHSRCGHINRGRRRFTYDNSELEKKISCCSPPPDYNSVVLYSTPPV  1337
gi|194671875|ref|XP_001249769.2| EDISAPKFNSGSSDNVRYVNAFNFISLEKLKTFEEFSPNGTSLLDDYQLDSGTLLASPLLKRFTWAE-SKPKAPLN--LRVTSKSKESGLSDLSRPT-FCHASCGHLGAGHRRFTYDHSELERKISCCSPPPDYNSVVLYSTPPV  1359
gi|34328180|ref|NP_034358.2|     DGFADPHFHSGSSDDVRYVNAFKFMSLERIKTFEELSPNSTSMFEDYQLDTSTLLGSPLLKRFTWTE-TKPKASMKIDLRIASKSKEAGLSDLPRPS-FCFSSCGHIR-PVQ---DDESELG-KESCCSPPPDYNSVVLYSSPPA  1333
gi|11276093|ref|NP_062179.1|     DGFTDPKFHSGSSDDVRYVNAFKFMSLERIKTFEELSPNATSMFEDYHLDTSSLLTSPLLKRFTWTE-TKPKASMKIDLRITSKSKEAGLSDLPGPS-FCFSSCGHIR-PVRQEDEDDPELG-KESCCSPPPDYNSVVLYSSPPA  1336
gi|45383624|ref|NP_989583.1|     EKFPVPSPNCRSTERARYINTFKIKPPQRIKTFEELPIKEKLVFNDYQADSGMVLASEELKRFTWTG-SKQKWTLFG-MKGVSRSKESGLSGITKPRSFCSFSCDQLSESKRRYTYGNTVLEKMKACHSPPPDYSSVVHYSQPSI  1327
gi|72535148|ref|NP_001014829.2|  RDISQKALGNSS-----------YISPGKIKAMSTFEDLHKEIPDDEQSDSGMVLPSEELIQVKWTDRFKTKNITKFFSRGQSQPRLSSAPCCSDQT------------------------------ALPPPHYEGDLLYPSF--  1272
                                 ......1360......1370......1380......1390......1400......1410......1420......1430......1440......1450......1460......1470......1480......1490.....
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