```
gi|112380630|ref|NP_036266.2|     MSR-----VAKYRRQVSEDPDIDSLLETLSPEEMEELEKELDVV-DPDGS-----VPVGLRQRNQTEKQSTGVYNREAMLNFCEKETKK-LMQREMSMDESKQVETKTDAKNGEERGRDASKKALGPRRDSDLGKEPKRGGLKKSFS---   150
gi|114571799|ref|XP_001148071.1|  MSR-----VAKYRRQVSEDPDIDSLLETLSPEEMEELEKELDVV-DPDGS-----VPVGLRQRNQTEKQSTGVYNREAMLNFCEKETKK-LMQREMSMDESKQVETKTDAKNGEERGRDASKKALGPRRDSDLGKEPKRGGLKKSFS---   150
gi|139948705|ref|NP_001077184.1|  MSK-----VAKYRRQVSEDPDIDSLLSTLSPEEMEELEKELDVV-DPDGS-----VPVGLRQRNQTEKPSTGAYNREAMLSFCEKETKK-LIQREASVDEGKQVETKTDAKKGEDKGRDAGKKPLGPRRDSDLGKEPKKGSMKKSIS---   150
gi|134948541|ref|NP_444336.2|     MSK-----VAKYRRQVSEDPDIDSLLSTLSPEEMEELEKELDVV-DPDGS-----IPVGLRQRNQTDKQPSGSFNREAMLNFCEKESKK-LIQREMSVDESKQVGRKTDAKNGEEKDSDASRKAPGPRQDSDLGKEPKKGVLKKSFS---   150
gi|109497910|ref|XP_222660.4|     MSK-----VAKYRRQVSEDPDIDSLLSTLSPEEMEELEKELDVV-DPDGS-----IPVGLRQRNQTDKQPSGSFNREAMLNFCEKESKK-IIQREMSVDESKQVGRKTDAKNGEDKGSNASRKALGPRQDSDVGKEPKKGVLKKSFS---   150
gi|118108885|ref|XP_426094.2|     ------------------------------------------------------------------------------------------------------   150
gi|189525220|ref|XP_001335496.2|  MSRRKVKGLTKTGRQVSEDPELDSLLSNLSTAEMEELEKEVSVVPPDPPSEIIVVDQTDLKPSAPVRKESQLSSQTDDFKSQPKKESRKQEYLRKMGLSQEKNISASDSRDGGLQRTSSTSSFPKRDSRLEDRTRRVTEGTRDEKFGPSA   150
                                  1.......10........20........30........40........50........60........70........80........90........100.......110.......120.......130.......140.......150

gi|112380630|ref|NP_036266.2|     ---------RDRDEAGGKSGEKPKEEKIIRGIDKGRVRAAVDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDK--KREEMKEVAKKEDDEKVKG------ERRNTDTRKEGEKMKRAGGNTDMKKEDEKVKRGTGNTDTKKDD   300
gi|114571799|ref|XP_001148071.1|  ---------RDRDEADGKSGEKPKEEKIIRGIDKGRVRAAVDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDK--KREEMKEVAKKEDDEKVKG------ERRNTDTRKEGEKMKRAGGNTDMKKEDEKVKRGTGNTDTKKED   300
gi|139948705|ref|NP_001077184.1|  ---------RDKDEADGRSAERPKEEKLVRGLEKGRVRAVVDKKEAGKEG-----PAAPRKDEEKQ---RN--VSRDKGK--KGEQPEAASKTAAPEKAKG------PRTGEDTRAEAQESK--GGRRDR--------------AARPED   300
gi|134948541|ref|NP_444336.2|     ---------RDREEADGRGGEKPKEEKVIRGIDKGRVRAAVDRKESGKDGREERAAAARK-EEEKTGSVKNAGLSRDKDK--KKEEVKEPSKKEE-VKLTA------ESRNTVGRREDGRLK--ESSKE-NKKPEDEGIGSGGRDWRKED   300
gi|109497910|ref|XP_222660.4|     ---------RDREEADSRGSEKPKEEKVIRGIDKGRVRAAVDRKEAGKDGREERAAATTKKEEEKTGSVRNAGLSRDKDK--KREEVKEPSKKEE-VKLTA------ENRSTVGRQEDGKQK--ESREDRDKKPEVKGIGCGSRDSRKED   300
gi|118108885|ref|XP_426094.2|     ------------------------------------------------------------------------------------------------------   300
gi|189525220|ref|XP_001335496.2|  VSKRDEEIEKKNETKDQNDGSRLRDRREMRESSSSKTKELISKLQEKKEDSKEKNKKEDRGKRESGESRAKEMISRIQEKEEKEREKKEEIRKREETKSKGYISRLEENQNQVHEDKTKEENKHRDEKQIRSSEKVKETTALSENKEKES   300
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                                                                  .                 :*:     *:*** :*:*: **. :*::*****: *..: *::*:***: ** :* *:*** *******:***  *: ** :**:***** :*.**
gi|112380630|ref|NP_036266.2|     EKVKKNEPLHEKEAKD-------------DSKTKTPEKQTPSGPTKPSEGPAKVEEEAAP--SIFDEPLERVKNNDPEMTEVNVNNSDCITNEILVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKANKTITSLNLDSNHITGKG   450
gi|114571799|ref|XP_001148071.1|  EKVKKNELLHEKEAKD-------------DSKTKTPEKQMPSGPTKPSEGPAKVEEEAAP--SIFDEPLERVKNNDPEMTEVNVNNSDCITNEILVRFTEALEFNTVVKVFALANTRADDHVAFAIAIMLKANKTITSLNLDSNHITGKG   450
gi|139948705|ref|NP_001077184.1|  EKARKEEPHEAKAPRE-------------DSKTPVPEKPTPGAPAKPADGPAKAEEEATP--SIFDEPLERVKSNDPEVTEVNVNNSDCITTEILVRFAEALEFNTAVKVFALANTRADDHVAFAIAIMLKANKTITSLNLDSNHITSKG   450
gi|134948541|ref|NP_444336.2|     EKVKKEENQPDKEVRE-------------ESKTKAPEKQAPSCPNKPSDGQARAEEEAAP--SIFDEPLEKVKNNDPEMTEVNVNNSDCITNEILVRFTEALEFNTVVKVFALANTRADDHVAFAIAIMLKANKTITSLNLDSNHITGKG   450
gi|109497910|ref|XP_222660.4|     EKVKKEETQPDKGVRE-------------EGKTR--EKQPPSGPSKPSDGQARAEEEAAP--SIFDEPLEKVKNNDPEMTEVNVNNSDCITNEILVRFTEALEFNTVVKVFALANTRADDHVAFAIAIMLKANKTITSLNLDSNHITGKG   450
gi|118108885|ref|XP_426094.2|     ----------------------------------------SAPEQP-------KEDEAS--SIFDELIEKVKNNDADVTEVNVNNSDCINNETLVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKSNKVLTSINLDSNHITGKG   450
gi|189525220|ref|XP_001335496.2|  ENVKRLQECNAKSSDKGRGDVQKHNENVNEVHKPKEEKIENCVSDTILKGKTKEEEEDDESASMFDEDLEKVRRNDPGMTDLNVNNSEVIKTKTLIQFSEALKNNTHIKAFSLANCRADDHVAYAIADTLRNNKSITSINLDSNLLTSKG   450
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                  *:::::** :*.:************ ***:***::*:**********************:**:******:*********: **      .    *  * **:
gi|112380630|ref|NP_036266.2|     ILAIFRALLQNNTLTELRFHNQRHICGGKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKQRQKRLQEQRQAQEAKGEK----KDLLEVPKAGAVAKGSPKPSPQPSPKPSPKNSPKK---------GGAPAAPPPPP--   600
gi|114571799|ref|XP_001148071.1|  ILAIFRALLQNNTLTELRFHNQRHICGGKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKQRQKRLQEQRQAQEAKEEK----KDLLEVPKAGAVAKGSPKPSPQPSPKPSPKNSPKK---------GGAPAAPPPPP--   600
gi|139948705|ref|NP_001077184.1|  ILAIFRALLQNSSLTELRFHNQRHICGGKTEMEMAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDRQRQKRLQEQRQAQEAQAQEAQAGKALLEVPQARPPARGSPRPSLQPPPKAAPKNSPGK---------GGAPAVPPPPP--   600
gi|134948541|ref|NP_444336.2|     ILAIFRALLQNNTLTELRFHNQRHICGGKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKQRQKRLQEQKQAQEASGEK----KDRLEVPKVGALAKGSPKPSPQPSPKPAPKNSPKK---------AGVPAAPPPPP--   600
gi|109497910|ref|XP_222660.4|     ILAIFRALLQNNTLTELRFHNQRHICGGKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKQRQKRLQEQKQAQEASGEK----KDRLEVPKVGALPKGSPKPSPQPSPKSAPKNSPKK---------AVGPAXXASPS--   600
gi|118108885|ref|XP_426094.2|     ILAIFRALLQNDTLTELRFHNQRHICGGKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDRQRQKRLQEQKLAQER-GEK----KDLLEVPK-------------------------------------------   600
gi|189525220|ref|XP_001335496.2|  IMSLIQALQHNSTLTELRFHNQRHIIGGKSEMEMTKILKENTTLLKLGYHFELAGPRMTMTNILSRNMDRQRQKRLQEQKQAQAQGAGDK---KDSLGVPKP-SFGKGSPRASPIPSPIPSPAPSPKLTHKKRVSGLVGGPPPPPPPPGG   600
                                  .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

gi|112380630|ref|NP_036266.2|     PPLAPPLIME--NLKNSLSPATQRKMGDKV-LPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ-------------------------------   696
gi|114571799|ref|XP_001148071.1|  PPLAPPLIME--NLKNSLSPATQRKMGDKV-LPAQEKNSRDQLLAAIRSSNLKQLKKWKCPNCFSRTRLQGTICQCHDCSGLTSQGYTDPAHPIPG   696
gi|139948705|ref|NP_001077184.1|  PPLAPPLIME--NLRNSLSPATQRKMGDKA-LPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ-------------------------------   696
gi|134948541|ref|NP_444336.2|     PPLAPPLIME--NLKNSLSPATQRKMGDKV-LPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ-------------------------------   696
gi|109497910|ref|XP_222660.4|     PSTGPTPYHG--EPKELTLTSHPEEDGRQS-APCPGEELTX---PTPSCHPFQQPXAAEEGRGAQAASI---------------------------   696
gi|118108885|ref|XP_426094.2|     ------------------------------------------------------------------------------------------------   696
gi|189525220|ref|XP_001335496.2|  PPPPPPPMLDGDFLKNSLTPVSQRKLDDRSGGRGAAQNTRDQLLASIRNSNVKQLKKVAVPKLLQ-------------------------------   696
                                  .......610.......620.......630.......640.......650.......660.......670.......680.......690......
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