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gi|24660491|ref|NP_523965.2|      ------------------------------MEMETIEEQSKCEMSITTLPTRICLVGGVGQDADTLQAAES------------------------------FGLPIVTSDTGLDILGES-SDWRTFYVLDDFEGASFEAIHKQKEC--    85
gi|158294792|ref|XP_556459.3|     --------------------------------------MSISTSPSTPEIARICLVGPVAQDAATLAAAQS------------------------------LKLPIVTSDTGAEYIGDDDISIRTVFVLNDFEGPVYDAIYKAKQR--    78
gi|6681261|ref|NP_031926.1|       ------------------------------------------------------------------------------------------------------------------------------------------
gi|62643263|ref|XP_342221.2|     MADDSVLPSPTEITSLADTSVFDSKVTETSKENLCMVSTSNVDE-EMPQVEARVVVVQEAGKQEELLKALK------------------------------EIKVPCVKMDSMEEFGSLDSPEFENIFVVTDFQTSVFNDLYKADCR--   116
gi|21735572|ref|NP_060568.3|      MAENSVLTSTTGRTSLADSSIFDSKVTEISKENLLIGSTSYVEE-EMPQIETRVILVQEAGKQEELIKALK------------------------------DIKVGFVKMESVEEFEGLDSPEFENVFVVTDFQDSVFNDLYKADCR--   116
gi|114590412|ref|XP_516880.2|     MAENSVLTSTTGRTSLADSSIFDSKVTEISKENLLIGSTSYVEE-EMPQIETRVILVQEAAKQEELIKALK------------------------------DIKVGFVKMESVEEFEGLDSPEFENVFVVTDFQDSVFNDLYKADCR--   116
gi|74003651|ref|XP_850841.1|      MADNSLLTSTTGRTSLADSSIFDCKVTEISKENVFIGSASYVEE-EMPQIETRMILVQDAGKQEELIKALK------------------------------EIKVPFVKMESLEEFEGLDSPEFENVFIVTDFQDSVFNELHKMDHR--   116
gi|148236343|ref|NP_001091042.1|  MADDSALASTTGSTSLADSSIFDSKVAETSKENLFIRSTSCVEE-EMPQIETRVILVQESGKQEELIRALKTINIMEVPVIKIKESCPGKSDEKLIKSIVNMEIKLPFVKMESVAEFKSLDSPEFENVFIVMDFQDSVFNELYKADCR--   147
gi|118095280|ref|XP_422790.2|     MADSSTLVSESGRSLLADSSVLDSKVVENSKENVFPGSVVDVEE-EMPQIETRVVLVQEAGKREELLKALE------------------------------EIKVPYIKTNTIEELGDCDSPEFESVFVVTDFQGSIFNNLCKADCR--   116
gi|51468037|ref|NP_001003883.1|   MADSSILTLGPGRSILVDSSVYDSRMAETSKEQYFIGLHSDETEGVLPRVETRVVLVGEACKMAELEKALQ------------------------------DLNTPCIKTDNVCDFGDGENCEFETVFVLKDFQAPEYSFLYKNDSR--   117
gi|17536341|ref|NP_496318.1|      ------------------------------MDVSMLQSPQKRIKTIQKLAVSKKDVHDFKDIFEMLEE------------------------------QKEKRNINIIQYDSLDDLSGDWSEYTFFCGNFDSDLFRTLTKHQETQA    86
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                                                  * .:   ::.   :.    ** *:* *** ::*     . *::.    .   * :    .   . : . *:  .*  *..  * .    .   .::  *:.  : * **   *   *
gi|24660491|ref|NP_523965.2|      --ILGPPALKYAAEMKQTLG--QNSRPIYNYAMRGVVTCFTGIRKKDELTKLVNLIHSMGGCIKKDLN-TKTTHLICNHSGGEKYQYAKTFRLTVVRPAWVFAAWADRNSLEFDATQENFTKTHRLKAFEGQKICFFGFPVEEHQHMVDV   230
gi|158294792|ref|XP_556459.3|     --ILGPPALQQAVRFSEGLV--WNNRPIYNYCMRGVITCFTGIRKKDELTHLVHLIHSMGGSIRKGMD-TKVTHLICNSSGGEKYRYAMTFRLAIIRPNWVLEAWKNRHDPNFSATIETFTKQHRLKAFEGQKVCFFGFPEEEQQHMIDV   223
gi|6681261|ref|NP_031926.1|       ------------------------------MLNLVLCFTGFRKKEELVKLVTLVHHMGGVIRKECN-SKVTHLVANCTQGEKFRVAVSLGTPIMKPEWIYKAWERRNEQCFCAAVDDFRNEFKVPPFQDCILSFLGFSDEEKHSMEEM   117
gi|62643263|ref|XP_342221.2|     --IVGPPVILNCAQMGEPLP--FSCRPLYCTSMLNLVLCFTGFRKKEELVKLVTLVHHMGGVIRKECN-SKVTHLVANCTQGEKFRVAVSLGTPIMRPGWIYEAWERRNEQCFCAADDDFRNEFKVPPFQDCILSFLGFSDEEKHSMEEM   261
gi|21735572|ref|NP_060568.3|      --VIGPPVVLNCSQKGEPLP--FSCRPLYCTSMMNLVLCFTGFRKKEELVRLVTLVHHMGGVIRKDFN-SKVTHLVANCTQGEKFRVAVSLGTPIMKPEWIYKAWERRNEQDFYAAVDDFRNEFKVPPFQDCILSFLGFSDEEKTNMEEM   261
gi|114590412|ref|XP_516880.2|     --VIGPPVVLNCSQKGEPLP--FSCRPLYCTSMMNLVLCFTGFRKKEELVRLVTLVHHMGGVIRKDFN-SKVTHLVANCTQGEKFRVAVSLGTPIMKPEWIYKAWERRNEQDFYAAVDDFRNEFKVPPFQDCILSFLGFSDEEKTNMEEM   261
gi|74003651|ref|XP_850841.1|      --IVGPPVILNCAQKGEPLP--FSCRPLYCTSMMNLVLCFTGFRKKEELVRLVTLVHHMGGVIRKDFN-SKVTHLVANCTQGEKFRIAVSLGTPIMKSEWIYKAWERRNEQDFSASVDDFKNEFKVPPFQDCILSFLGFSDEEKTNMEEM   261
gi|148236343|ref|NP_001091042.1|  --VIGPPVVLNCAEKGEPLP--FSCRPLYCTSMMNLVLCFTGFRKKEELARLVTLVHHMGGVIRKDFN-SKVTHLVANCTQGEKFRVAVSLGTPIMKPEWIHKAWERRNEQDFCASVDDFRNEFKVPPFQDCILSFLGFSDEEKTNMEEM   292
gi|118095280|ref|XP_422790.2|     --VIGPPVVLHCAQKGEPLP--FSCRPLYCASMLNLVLCFTGFRKKDELVKLVTLVHHMGGIIRKDFN-SKVTHLVANSTHGDKFRIAVSLGTPIMKAEWIYKAWEKRNEIDFCAADDDVRNQFKVPPFQDCLLSFLGFSDEEKANMEEM   261
gi|51468037|ref|NP_001003883.1|   --ILGPPAVMHCANKGEPLP--FSSRPLYSMTMLNLSLCFTGFRKKDEVVALVNLVHHMGGTIRKDFDSAKVTHLIARSTHGEKYRLAVCMGTPILTPDWIRKAWEHRDDINFHAGNELFRTEFKVPPFQDCVLSFLGFSEEEKNNMEER   263
gi|17536341|ref|NP_496318.1|      LFIIGASVLKNKLLKNEDLMTLRAARPLYCELMKDVTMKLAAEVPNK--RELVDLVHYMGGSVRKDTV--SRTNVFIAAKVEAKVQSISLVGVPTMRADWVTECWKHRDDSYFDVMEPCFVDKHRLGVFEGLSLFFHGFKQTEIDDMLRS   232
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                     **         .:*::
gi|24660491|ref|NP_523965.2|      LLENGGVCAELDDPECSHVVMPNTGAVFTSTSTSTDTNPSTLINPPESQVPGSSSASQAGEEEQRKAEHLEQAEIKKMEYSHAETDNGMSLDIDQEQKENQGIEDEDDIHFDERLFVEAADIINHGEDQLPESDEEDLEEEQKPKVEEVL   380
gi|158294792|ref|XP_556459.3|     LRTNGGIPTDLEDPECSHVVMPNTGAHLIDATMPLESVSPKKLVTVSPPAAAAVADVPGCESEEPEARELKQQQPQESNAGKEATAALPSLPEENESTEGMAVEPAGSRNDRNGDHMLSIAENDNNQNQFAESSSITRPAVPYIDEGAVP   373
gi|6681261|ref|NP_031926.1|       TEMQGGSYLPVGDERCTHLIVE------------------------------------------------------------------------------------------------------------   139
gi|62643263|ref|XP_342221.2|     TEMQGGTYLPVGDERCTHLIVD------------------------------------------------------------------------------------------------------------   283
gi|21735572|ref|NP_060568.3|      TEMQGGKYLPLGDERCTHLVVE------------------------------------------------------------------------------------------------------------   283
gi|114590412|ref|XP_516880.2|     TEMQGGKYLPLGDERCTHLVVE------------------------------------------------------------------------------------------------------------   283
gi|74003651|ref|XP_850841.1|      TKMQGGNCLPVGDERCTHLVVE------------------------------------------------------------------------------------------------------------   283
gi|148236343|ref|NP_001091042.1|  TKMQGGNCLPVGDERCTHLIVE------------------------------------------------------------------------------------------------------------   314
gi|118095280|ref|XP_422790.2|     TEMQGGCYLPVGDERCTHLVVE------------------------------------------------------------------------------------------------------------   283
gi|51468037|ref|NP_001003883.1|   TQKHGGRFQAVGDERCTHLVVE------------------------------------------------------------------------------------------------------------   285
gi|17536341|ref|NP_496318.1|      LENTGGKLAPS-PTLATHVVYN------------------------------------------------------------------------------------------------------------   253
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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gi|24660491|ref|NP_523965.2|      KEQEVEEDVQASTPKTSKIRTSLKAATPLSSPEMDGIALDFES-----TTQNISPILKAIDECDLETDDLP----PSENDLKRKR--ESFDNVSLMSVDSFALPASTKKPKLIRTGSISRTLRRSVSFVA--EPLMKTLRPRRSSVADAS   517
gi|158294792|ref|XP_556459.3|     EPMPAAATTNTAAPKQDGIVLTSGEANEFLNPNNLSPILKTERGGGSMVDESFRRIVEEKDEDDEDDDTMDDYVIASREAYKRKRQEDSFDDPSLLSVD----ISIASTPKLTRTGSITRGIRRSMSFAAIKTPIKTMLRSRRSSVDPN-   518
gi|6681261|ref|NP_031926.1|       ------------------------------------------------------------------------------------------------------------------------------------------   139
gi|62643263|ref|XP_342221.2|     ------------------------------------------------------------------------------------------------------------------------------------------   283
gi|21735572|ref|NP_060568.3|      ------------------------------------------------------------------------------------------------------------------------------------------   283
gi|114590412|ref|XP_516880.2|     ------------------------------------------------------------------------------------------------------------------------------------------   283
gi|74003651|ref|XP_850841.1|      ------------------------------------------------------------------------------------------------------------------------------------------   283
gi|148236343|ref|NP_001091042.1|  ------------------------------------------------------------------------------------------------------------------------------------------   314
gi|118095280|ref|XP_422790.2|     ------------------------------------------------------------------------------------------------------------------------------------------   283
gi|51468037|ref|NP_001003883.1|   ------------------------------------------------------------------------------------------------------------------------------------------   285
gi|17536341|ref|NP_496318.1|      ------------------------------------------------------------------------------------------------------------------------------------------   253
                                  .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
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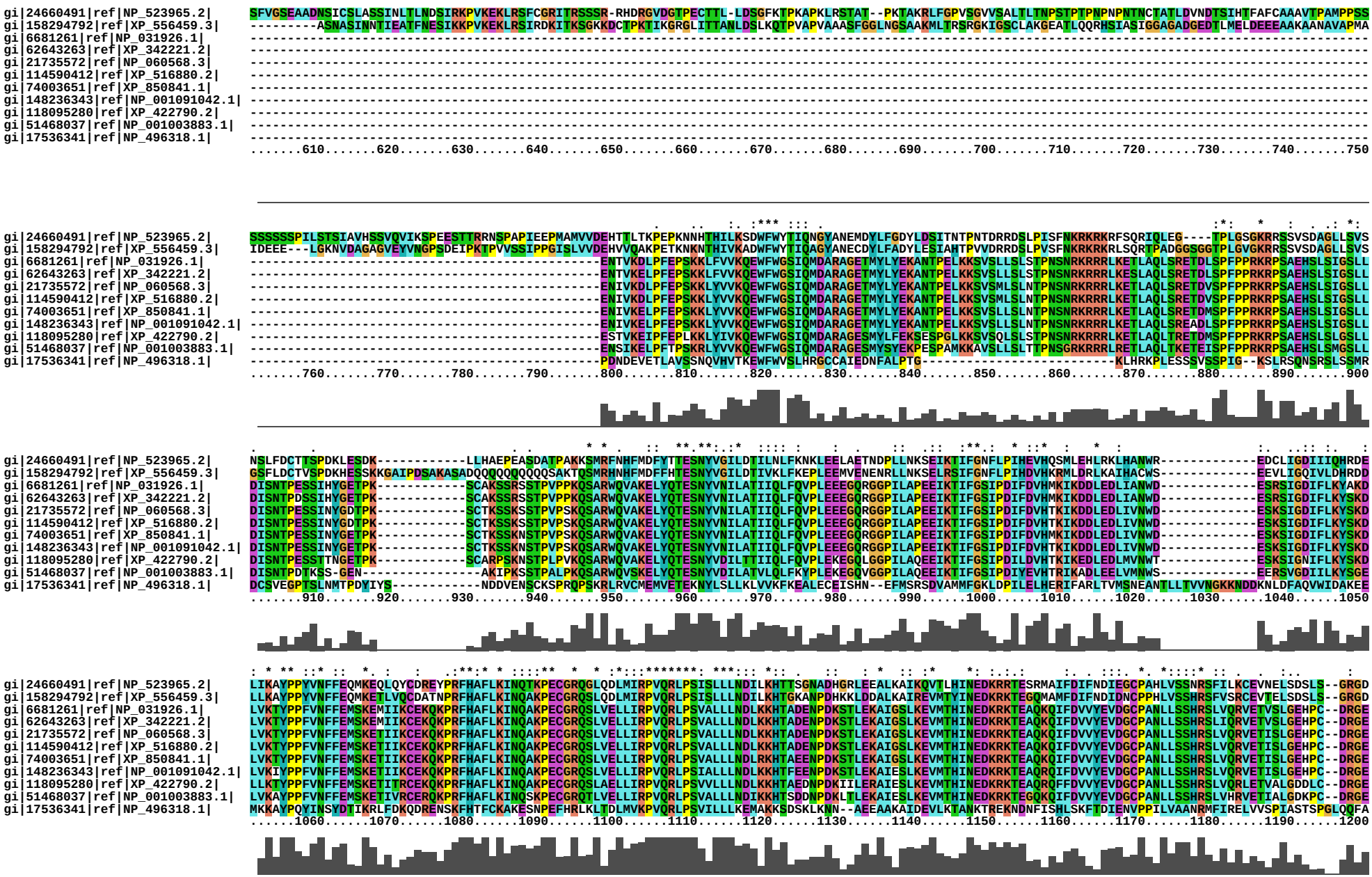
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gi|21735572|ref|NP_060568.3|
gi|114590412|ref|XP_516880.2|
gi|74003651|ref|XP_850841.1|
gi|148236343|ref|NP_001091042.1|
gi|118095280|ref|XP_422790.2|
gi|51468037|ref|NP_001003883.1|
gi|17536341|ref|NP_496318.1|

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                                 : *:** * : : : * .     : .            :::  : *. :: .. *   .                 :  ::                                                  :  .:
gi|24660491|ref|NP_523965.2|     SLVLYLFSDSIELCKRRSKGFNTAKSP------------STAKTHKHLKLISLNTIRLVIDISDSPRAFGL----LLRGDKEK--LYTFTISDEET--------------------------------------DKSVYVKKLCNQI  1173
gi|158294792|ref|XP_556459.3|    PLVLFLFSDTLEVCKKRSRVFNNVKSPNTNSLNLTRSSCATTKPYKHVKLMPLSTVQLVVNIVDSPRAFMLNCRELAQNAKDR--QYSFNIADEEQ--------------------------------------DKLLYLKSLSKQM  1198
gi|6681261|ref|NP_031926.1|      QVTLFLFNDCLEIARKRHKVIGTFRSPH--------DRTRPPASLKHIHLMPLSQIKKVLDIRETEDCHNAFALLVRPPTEQANVLLSFQMTSEEL--------------------------------------PKESWLKMLCRHV   616
gi|62643263|ref|XP_342221.2|     QVTLFLFNDCLEIARKRHKVIGTFRSPH--------DRTRPPASLKHIHLMPLSQIKKVLDIRETEDCHNAFALLVRPPTEQANVLLSFQMTSEEL--------------------------------------PKESWLKMLCRHV   760
gi|21735572|ref|NP_060568.3|     QVTLFLFNDCLEIARKRHKVIGTFRSPH--------GQTRPPASLKHIHLMPLSQIKKVLDIRETEDCHNAFALLVRPPTEQANVLLSFQMTSDEL--------------------------------------PKENWLKMLCRHV   760
gi|114590412|ref|XP_516880.2|    QVTLFLFNDCLEIARKRHKVIGTFRSPH--------GQTRPPASLKHIHLMPLSQIKKVLDIRETEDCHNAFALLVRPPTEQANVLLSFQMTSDEL--------------------------------------PKENWLKMLCRHV   760
gi|74003651|ref|XP_850841.1|     QVTLFLFNDCLEIARKRHKVIGTFRSPP--------GHTRPPASLKHVHLMPLSQIKKVLDIRETEDCHNAFALLVRPPTERANVLLSFQMTSEEL--------------------------------------PKENWLKMLCRHV   760
gi|148236343|ref|NP_001091042.1| QVTLFLFNDCLEIARKRHKVIGTFRSPH--------GQTRPPASLKHIHLMPLSQIKKVLDIRETEDCHNAFALLVRPPTEQANVLLSFQMTSEEL--------------------------------------PKENWLKMLCRHV   791
gi|118095280|ref|XP_422790.2|    QVTLFLFNDCLEIARKRHKVIGAFKSPH--------GHTRPPASLKHVVLMPLSQIKKVLDIRETEDCHKAFALVVRPPTEHNNKLLSFQMTSEEP--------------------------------------PKEDWLKTLCRHV   760
gi|51468037|ref|NP_001003883.1|  HVTLFLFNDCLEIARKRHKVITNFRSPL--------GQTRPPAQLKHITLMPLSQIRRVLDIQDTEECQNAFALVVRPPTEQENLLFSFQLTAEDT--------------------------------------LKTTWLRTLCRQV   757
gi|17536341|ref|NP_496318.1|     KMKLFLFHDVLIITKIRSEKNTMQRLAR--HASFASLHSRQRRPYRYIDQIQLNTMRSAFRIRAPDEIAKCLELQQQNGSTKPNVFVWCLIHRDEQGGDIDTVFESNDDEEVRDFLDDIHVKILSDCGRFFYSSDPSDMNEINDAMVSDM   760
                                 ......1210......1220......1230......1240......1250......1260......1270......1280......1290......1300......1310......1320......1330......1340......1350
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gi|24660491|ref|NP_523965.2|     AAHTCRTDADKLLICRTSQELEVDISDVNVS--------------TLSKAFKLAAKTRLKVGRAFSFNKTPNK----LKRAVSTMMTSPFGSTNSLTPASQLAQMRLASCTNINEVDDEDCASMRSSSPSTQSEML--------VVPPLS  1297
gi|158294792|ref|XP_556459.3|    AENACRTDAGHFLINSTADEVDIDVSDINVG--------------TLSKAFKIASKTRMKVGRVFSFNKTPSK----LKRTVSTMMPSPFGSTQSLTPASQLAQMKLASCTNLNEVCEEGADSNGSSPSSSK------------LVAPMS  1318
gi|6681261|ref|NP_031926.1|      ANTICKADAENLMYVADPESFEVNTKDMDS--------------TLSRASRAIKKTSKKVTRAFSFSKTPKR----ALRMALSSSHSS-EGRSP-PSSGKLAVSRLSSTSSLAGIPSPSLVSLP-----------------------S   721
gi|62643263|ref|XP_342221.2|     ANTICKADAENLMYVTDPESFEVNTKDMDS--------------TLSRASRAIKKTSKKVTRAFSFSKTPKR----ALRMALSSSHSS-EGRSP-PSSGKLAVSRLSSTSSLAGIPSPSLVSLP-----------------------S   865
gi|21735572|ref|NP_060568.3|     ANTICKADAENLIYTADPESFEVNTKDMDS--------------TLSRASRAIKKTSKKVTRAFSFSKTPKR----ALRRALMTSHGSVEGRSP-SSNDKHVMSRLSSTSSLAGIPSPSLVSLP-----------------------S   866
gi|114590412|ref|XP_516880.2|    ANTICKADAENLIYTADPESFEVNTKDMDS--------------TLSRASRAIKKTSKKVTRAFSFSKTPKR----ALRRALMTSHGSVEGRSP-SSNDKHVMSRLSSTSSLAITHSVSTSNVIGFTKHVYVQCLNST----GGRSQYS   886
gi|74003651|ref|XP_850841.1|     ANTICKADAENLIYSADPESFEVNTKDMDS--------------TLSRASRAIKKTSKKVTRAFSFSKTPKR----ALRRALMTSQSSVEGRSP-SSNDKHVMSRLSSTSSLAGIPSPSLISLP-----------------------S   866
gi|148236343|ref|NP_001091042.1| ANTICKADAENLIYTADPESFEVNTKDMDS--------------TLSRASRAIKKTSKKVTRAFSFSKTPKR----ALRRALMASQSSAEGRSP-SSNEKHVMSRLASTSSLAGIPSPSLVSLP-----------------------A   897
gi|118095280|ref|XP_422790.2|    ANTICKADAENLIYAADPDSVEVNTKDMDS--------------TLSRASRAIKKTSKKVTRAFSFSKTPKR----ALRRALMS-HSATEGRSPNSANESYIGSRLNSTSSLAGISSPSLVSLP-----------------------S   866
gi|51468037|ref|NP_001003883.1|  ANTICRADAEDLIQSTDPDSVQVSTKDMDS--------------TLSRASRAIKKTSKKVTRAFSFTKTPKR----VLQRAFMANGTP-DERSP--CPDADRMSRMSSSSTLATVHSPSMINLS-----------------------S   861
gi|17536341|ref|NP_496318.1|     TTRYFRNLCGAKPQYGHGSQMNITVSERSTQNEWSHNESFMPPPQSQSRMRRAFSNAQLTLATTLGFGRNQSRNNLGQINENTTFLQSPRVSCDPAALANMTSVGGLPGCQSESESTPKRGIRSRLTSTTFLGGRHNILGRNTSMRRQAT   910
                                 ......1360......1370......1380......1390......1400......1410......1420......1430......1440......1450......1460......1470......1480......1490......1500
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                                        :
gi|24660491|ref|NP_523965.2|     VQPTRKNK---AVVGRI-----------------------  1311
gi|158294792|ref|XP_556459.3|    VQPTRKNKNPPISIGALRPL--------------------  1338
gi|6681261|ref|NP_031926.1|      FFERRSHTLSRSTTHLI-----------------------   738
gi|62643263|ref|XP_342221.2|     FFERRSHTLSRSTTHLI-----------------------   882
gi|21735572|ref|NP_060568.3|     FFERRSHTLSRSTTHLI-----------------------   883
gi|114590412|ref|XP_516880.2|    WFQSVRHSAFRASFSEILEGNTDFSNFKKVLSKSSLTFVKN   927
gi|74003651|ref|XP_850841.1|     FFERRSHTLSRSTTHLI-----------------------   883
gi|148236343|ref|NP_001091042.1| FFERRSHTLSRSTTHLI-----------------------   914
gi|118095280|ref|XP_422790.2|    IFEKRSHTLSRSTTHLI-----------------------   883
gi|51468037|ref|NP_001003883.1|  AFERKYHTFSRSTTHLI-----------------------   878
gi|17536341|ref|NP_496318.1|     GFAHSEKELPRSKTSSYRVTDI------------------   932
                                 ......1510......1520......1530......1540.
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