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gi|161076460|ref|NP_001097242.1| -MNVESQLKTPPTHIRNLVKHVNKRNFNESSEQINQFVKEHGL-----EADRSSLRHLFSVINFS-DLVPSVTVQLQAKLLGIQLERQLHSSSFVSNICYAFD-----------QFFASNQKSLKPVAVADLVGQVARLTGINKVCECV   131
gi|158299778|ref|XP_319808.4|   ------------------------------------------------------------------------QARLLATELASLTNKPQLVANVCFAVD-----------NPFP-QQKSLKP--TSNLLAQISKTLSCTPIQETA    59
gi|94383743|ref|XP_899766.2|    -MNLDS-LSLALSQISYLVDNLTKKNYRASQQEIQHIVNRHGP-----EADRHLLRCLFSHVDFSGDGKSSGKDFHQTQFLIQECASLITKPNFISTLSYAID-----------NPLH-YQKSLKP--APHLFAQLSKVLKLSKVQEVI   128
gi|109507689|ref|XP_001060702.1| -MNLDS-LSLALSQISYLVDNLTKKNYRASQQEIQHIVNRHGP-----EADRHLLRCLFSHVDFSGDGKSSGKDFHQTQFLIQECASLITKPNFISTLSYAID-----------NPLH-YQKSLKP--APHLFAQLSKVLKLSKVQEVI   128
gi|42716275|ref|NP_057368.3|    -MNLDS-LSLALSQISYLVDNLTKKNYRASQQEIQHIVNRHGP-----EADRHLLRCLFSHVDFSGDGKSSGKDFHQTQFLIQECALLITKPNFISTLSYAID-----------NPLH-YQKSLKP--APHLFAQLSKVLKLSKVQEVI   128
gi|114662880|ref|XP_511007.2|   -MNLDS-LSLALSQISYLVDNLTKKNYRASQQEIQHIVNRHGP-----EADRHLLRCLFSHVDFSGDGKSSGKDFHQTQFLIQECALLITKPNFISTLSYAID-----------NPLH-YQKSLKP--APHLFAQLSKVLKLSKVQEVI   128
gi|119910031|ref|XP_613555.3|   -MNLDS-LSLALSQISYLVDNLTKKNYRASQQEIQHIVNRHGP-----EADRHLLRCLFSHVDFSGDGKSSGKDFHQTQFLIQECASLITKPNFISTLSYAID-----------NPLH-YQKSLKP--APHLFAQLSKVLKLSKVQEVI   128
gi|118096204|ref|XP_414043.2|   -MNLDS-LSLALSQISYLVDNLTKKNYRASQQEIQHIVNRHGP-----EADRHLLRCLFSHVDFSGDGKSSGKDFHQTQFLIQECASLITKPNFISTLSYAID-----------NPLH-YQKSLKP--SPHLFAQLSKVIKLSKVQEVI   128
gi|121582322|ref|NP_001073420.1| -MNLDS-LSLALSQISYLVDNLTKKNYRASQQEIQHIVNRHGP-----EADRHLLRCLFSHVDFSGDGKSSGKDFHQTQFLIQECVSLITKPNFISTLCYAID-----------NPLH-YQKSLKP--SPHLFTQLSKVLKLSKVQEVI   128
gi|212645813|ref|NP_498516.2|   MHSTSGLAPVFRVEENHMIRNRENLERPISKKGTITLLSKMPMGFVLNSCSCAYIDNLLAHSSIHRVKPHSFMIQRLVVICGRSSPSLPNHAANIILSAFNFC-----------QIEAPAKKFLEEDAALSLFHTILSYSTVTQINRSG   138
gi|42561615|ref|NP_171710.3|    ---------MTPSKVAGHTRFLLHSFHDSDVDSIALQLSQFVDFG--VETSIPVLKTCLDCFTARRSHPNSLQLEKVVSLLFKHVLKLSNLATLLPHALNDFELTQESVDDLTTI------------------------------LN   106
gi|115483368|ref|NP_001065354.1| ------------------------------------------------------------------------------------------------------------------------------------------------------
                                1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|161076460|ref|NP_001097242.1| FALALTHSSYTELKHSARNNLKGSLSELIDSYLG-NKGTGP-----------ADSGLREISFDLLQYLLCCLSEY------VQPQVEAQFLIKLREEFPRQAVPLVLA------PFLYGSTTATIAGAGASETDAEAEATTNSNSSS--   254
gi|158299778|ref|XP_319808.4|   LSIALLHSEQPEIVRFAEAHLKNCLTELIESYIDSDSGSNN-----------VEGSLNDVSPEFLQQILSLISYGRHTALGLTDQTYERFRSQLCRDFPRDRVPLILA------PLLY-----------AESSEISAEILKLNTHSI--   178
gi|94383743|ref|XP_899766.2|    FGLALLNSSSPDLRGFAAQFIKQKLPDLLRSYIDADVSGN-----------QEGGFQDIAIEVLHLLLSHLLFGQKGAFGVGQEQIDAFLKTLRRDFPQERCPVVLA------PLLY-----------PEKRDILMDRILPDSGGV--   246
gi|109507689|ref|XP_001060702.1| FGLALLNSSSPDLRGFAAQFIKQKLPDLLRSYIDADVSGN-----------QEGGFQDIAIEVLHLLLSHLLFGQKGAFGVGQEQIDAFLKTLRRDFPQERCPVVLA------PLLY-----------PEKRDILMDRILPDSGGV--   246
gi|42716275|ref|NP_057368.3|    FGLALLNSSSSDLRGFAAQFIKQKLPDLLRSYIDADVSGN-----------QEGGFQDIAIEVLHLLLSHLLFGQKGAFGVGQEQIDAFLKTLRRDFPQERCPVVLA------PLLY-----------PEKRDILMDRILPDSGGV--   246
gi|114662880|ref|XP_511007.2|   FGLALLNSSSSDLRGFAAQFIKQKLPDLLRSYIDADVSGN-----------QEGGFQDIAIEVLHLLLSHLLFGQKGAFGVGQEQIDAFLKTLRRDFPQERCPVVLA------PLLY-----------PEKRDILMDRILPDSGGV--   246
gi|119910031|ref|XP_613555.3|   FGLALLNSSSTDLRGFAAQFIKQKLPDLLRSYIDADVSGN-----------QEGGFQDIAIEVLHLLLSHLLFGQKGAFGVGQEQIDAFLKTLRRDFPQERCPVVLA------PLLY-----------PEKRDILMDRILPDSGGV--   246
gi|118096204|ref|XP_414043.2|   FGLALLNSFSSDLRGFAAQFIKQKLPDLLRSYIDADVSGN-----------QEGGFQDIAIEVLHLLLSHLLFGQKGAFGVGQEQIDAFLKTLRRDFPQERCPVVLA------PLLY-----------PEKRDILMDRILPDSGGI--   246
gi|121582322|ref|NP_001073420.1| LGLALSNSSNADLRGFAAQFVKQKLPDLLRSYVDADLGGN-----------QEGGFQDIAIEVLHLLLSHLLFGQKGSSGVGQEQIDAFLKTLCRDFPQERCPVVLA------PLLY-----------PDKRDILMDRILPDSGDL--   246
gi|212645813|ref|NP_498516.2|   IEILGAQRLTSALCDLIYAYTKTMDDMVASKTLTHLCKKLAGLFDPLVVLPFISKLAKSRRLRHYLQPLFLGHCEYTSDTWGVSPEGAEIYNQIARGNFTTQTLIEIVQ------TFLEKEVKEVIISSTTDPIKLVQYLISCSNPDN--   280
gi|42561615|ref|NP_171710.3|    FSISENIGFALALTDFERLDAKTTGRNLLAQIEQLCANTG----------------QILSSELIHSVLSFLRKSEDLSMHLDSFLQFLSSAQPRDDFSFALTPMLAQQVHEAP-------------VFRSMDFHTDSADNDLDAILA   225
gi|115483368|ref|NP_001065354.1| ------------------------------------------------------------------------------------------------------------------------------------------------------
                                .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|161076460|ref|NP_001097242.1| ---FEADALNEVGIEDIYDHLSEIIFTNQGKNNIMDTSWINLILEIGYEFTSSVEECKNHLCSRERERAELQSKDVAKIVGLMCRRHSSLLDCNVNLPTPANFWPGQGQGGGSNSSGSSQTQITPQQQNPGSSNNNDGSDGNSSSDKKDK   401
gi|158299778|ref|XP_319808.4|   ---LQS-------------------------SIMKTSWTNLVVEVGYSFTATFDDCRNHLLKVGGR--DITPQDVAKIVSSMCLTHESLSESSINLPTPSAFWP-QGSG-----------------DPSGQKGKDGNGGSSAS-----   273
gi|94383743|ref|XP_899766.2|    ---AKT---------------------------MMESSLADFMQEVGYGFCASIEECRNIIMQFGVR--EVTAAQVARVLGMMARTHSGLTDG---IPLQSISAP--GSGIWS-------------------DGKDKSEGAQAH-----   334
gi|109507689|ref|XP_001060702.1| ---AKT---------------------------MMESSLADFMQEVGYGFCASIEECRNIIMQFGVR--EVTAAQVARVLGMMARTHSGLTDG---IPLQSISAP--GSGIWS-------------------DGKDKSEGAQAH-----   334
gi|42716275|ref|NP_057368.3|    ---AKT---------------------------MMESSLADFMQEVGYGFCASIEECRNIIVQFGVR--EVTAAQVARVLGMMARTHSGLTDG---IPLQSISAP--GSGIWS-------------------DGKDKSDGAQAH-----   334
gi|114662880|ref|XP_511007.2|   ---AKT---------------------------MMESSLADFMQEVGYGFCASIEECRNIIVQFGVR--EVTAAQVARVLGMMARTHSGLTDG---IPLQSISAP--GSGIWS-------------------DGKDKSDGAQAH-----   334
gi|119910031|ref|XP_613555.3|   ---AKT---------------------------MMESSLADFMQEVGYGFCASIEECRNIIMQFGVR--EVTAAQVARVLGMMARTHSGLTDG---IPLQSISAP--GSGIWS-------------------DGKDKSDGAQAH-----   334
gi|118096204|ref|XP_414043.2|   ---AKT---------------------------MMESSLADFMQEVGYGFCTSIEECRNIIMQFGVR--EVTAAQVARVLGMMARTHSGLTDG---IPLQSISAP--GSGIWS-------------------DGKDKSDGAQAH-----   334
gi|121582322|ref|NP_001073420.1| ---NKT---------------------------MMESSLADFMQEVGYGFCASLEECRNIILQYGVR--EVTASQVARVLGMMARTHSGLSDG---ISLQTITNPVGGGGIWS-------------------DGKDKSDSSQA------   335
gi|212645813|ref|NP_498516.2|   ---TEIVQALAFLLYSN----TKLLPAGSGGTIDMDVQAADTITTARLGDTKFTQPVKDALLDSGRE---ALLRRMEIYGVSLLSSVENFVTELKQAPIQKKMVTNNSVANAILYMLQYN-----------FDMSRDIENGRQDNSPFWG   409
gi|42561615|ref|NP_171710.3|    EID-----------------------------KEVSVGDLMGELGCGFTADAQQCKEILSSFAPLG----EATISRIVGNVSRTCADLEDNQTTFSTFTVALG----------------------------SCIPTELPTPR-----   306
gi|115483368|ref|NP_001065354.1| ------------------------------------------------------------------------------------------------------------------------------------------------------
                                .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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gi|161076460|ref|NP_001097242.1| KETTEATQTWKPDVFVQALKEVV------PQLNWKDVCMELDHPEFVLKDRIGLELLLTILRLATGSN----IFPHPECIYRHWANTEGQLSLIATMLKNP-DLFSFADFVFSQPALDVLKTAPDADNKEISSWKSLHLVEVLLSIADKG   540
gi|158299778|ref|XP_319808.4|   -----EVTTWKPEVLVQALKEVV------PALNWKEVCVALDHPEFLLKDRAGLSLLLTIVKMGMQASNMGQTFP-VECLYQRWTNVEGQLSIISLILKNS-DLYSFADHIYTSVSLDLLKTPPETDSKEVACWMSLHLVDVLLYIADHA   410
gi|94383743|ref|XP_899766.2|    --------TWNVEVLIDVLKELN------PSLNFKEVTYELDHPGFQIRDSKGLHNVVYGIQRGLGME----VFP-VDFIYRPWKHAEGQLSFIQHSLINP-EVFCFADYPCHTVATDILKAPPEDDNREIATWKSLDLIESLLRLAEVG   464
gi|109507689|ref|XP_001060702.1| --------TWNVEVLIDVLKELN------PSLNFKEVTYELDHPGFQIRDSKGLHNVVYGIQRGLGME----VFP-VDFIYRPWKHAEGQLSFIQHSLINP-EVFCFADYPCHTVATDILKAPPEDDNREIATWKSLDLIESLLRLAEVG   464
gi|42716275|ref|NP_057368.3|    --------TWNVEVLIDVLKELN------PSLNFKEVTYELDHPGFQIRDSKGLHNVVYGIQRGLGME----VFP-VDLIYRPWKHAEGQLSFIQHSLINP-EIFCFADYPCHTVATDILKAPPEDDNREIATWKSLDLIESLLRLAEVG   464
gi|114662880|ref|XP_511007.2|   --------TWNVEVLIDVLKELN------PSLNFKEVTYELDHPGFQIRDSKGLHNVVYGIQRGLGME----VFP-VDLIYRPWKHAEGQLSFIQHSLINP-EIFCFADYPCHTVATDILKAPPEDDNREIATWKSLDLIESLLRLAEVG   464
gi|119910031|ref|XP_613555.3|   --------TWNVEVLIDVLKELN------PSLNFKEVTYELDHPGFQIRDSKGLHNVVYGIQRGLGME----VFP-VDLIYRPWKHAEGQLSFIQHSLINP-EIFCFADYPCHTVATDILKAPPEDDNREIATWKSLDLIESLLRLAEVG   464
gi|118096204|ref|XP_414043.2|   --------TWNVEVLIDVLKELN------PSLDFKVVTYELDHPGFQIRDSKGLHIVVFGIQRGLGME----VFP-VNAIYRPWKHAEGQLSFIQHSLINP-DIFCFADYPCHAVTTDILKAPPEDDNREIATWKSLDLIESLLRLAEVG   464
gi|121582322|ref|NP_001073420.1| ---------WNVEVLIDVVKEVN------PNLNFKEVTYELDHPGFLIRDSKGLQIVVYGIQRGLGME----VFP-VDLIYRPWKHAEGQLSFIQHSLLSP-EVFCFADNPCHTVAIDTLKAPPEDDNREIATWKSLDLVESLLRLSEVG   464
gi|212645813|ref|NP_498516.2|   GSNFVIGITRFVEEQQAAVRDMEGFSDWYPDINWVEVIKEFDSEEFAICRQTIIMFADIFPIMFQPQN-----FP-VSFFLTPWRYYDHQLRLFEFMIEYA-DTS--LSKHMRQHVIYCLTSMHAADSSQLAKILDVAHDIKPTGLSELL   550
gi|42561615|ref|NP_171710.3|    --------SWNVDILVDTIKQLQ-----APGISWRKVIENLDHDGFDIPNMESFSFFMRIYKAACKEP-----FPLDAVCGSVWKNMDGQLSFLKHAISAPPEVFTFMHSPRKLVYIDNMHSQEQQLGLSNHAWLSLDLLDVLCQLAERG   438
gi|115483368|ref|NP_001065354.1| ------------------------------------------------------------------------------------------------------------------------------------------------------
                                .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
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gi|161076460|ref|NP_001097242.1| -YYTQVHELFKFPAQNCPDVLFLALLNTSPPMTPLRQDLFNQLIPTFLG-NHPNSNVILASAWSSN--NFQLRSNIMNAMSEWY-LRGNEFDQVKLSRILDLAQDLKALSALLNARSFLFIIDLACLASRREYLKLEKWLTDKIREHGEP   685
gi|158299778|ref|XP_319808.4|     NLSEKVMKIFKVPGSLCPDVLFLALLQINPPMTTARQELFTNLVPIFLG-NHPNAGTILHHAWNHSTFNVTLRPIILHAMSDWY-MVG-EGDQSRLSRILDVAQDLKALSNLLNIRTYMFIIDLACLA----------------------   535
gi|94383743|ref|XP_899766.2|      -QYEQVKQLFSFPIKHCPDMLVLALLQINTSWHTLRHELISTLMPIFLG-NHPNSAIILHYAWHGQGQSPSIRQLIMHAMAEWY-MRGEQYDQAKLSRILDVAQDLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTDKIREHGEP   611
gi|109507689|ref|XP_001060702.1| -QYEQVKQLFSFPIKHCPDMLVLALLQINTSWHTLRHELISTLMPIFLG-NHPNSAIILHYAWHGQGQSPSIRQLIMHAMAEWY-MRGEQYDQAKLSRILDVAQDLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTDKIREHGEP   611
gi|42716275|ref|NP_057368.3|      -QYEQVKQLFSFPIKHCPDMLVLALLQINTSWHTLRHELISTLMPIFLG-NHPNSAIILHYAWHGQGQSPSIRQLIMHAMAEWY-MRGEQYDQAKLSRILDVAQDLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTDKIREHGEP   611
gi|114662880|ref|XP_511007.2|     -QYEQVKQLFSFPIKHCPDMLVLALLQINTSWHTLRHELISTLMPIFLG-NHPNSAIILHYAWHGQGQSPSIRQLIMHAMAEWY-MRGEQYDQAKLSRILDVAQDLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTDKIREHGEP   611
gi|119910031|ref|XP_613555.3|     -QYEQVKQLFSFPIKHCPDMLVLALLQINTSWHTLRHELISTLMPIFLG-NHPNSAIILHYAWHGQGQSPSIRQLIMHAMAEWY-MRGEQYDQAKLSRILDVAQDLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTDKIREHGEP   611
gi|118096204|ref|XP_414043.2|     -QYEQVKQLFSFPIKHCPDMLVLALLQINTSWHTLRHELISTLMPIFLG-NHPNSAIILHYAWHGQGQSPSIRQLIMHAMAEWY-MRGEQYDQAKLSRILDVAQDLKALSMLLNGTPFAFVIDLAALASRREYLKLDKWLTDKIREHGEP   611
gi|121582322|ref|NP_001073420.1| -HYEQVKQLFSFPIKHCPDMLVLALLQISTSWHTLRHELISTLMPIFLG-NHPNSAIILHYAWHGQGQSPSIRQLIMHSMAEWY-MRGEQYDQAKLSRILDVAQDLKSLSMLLNGTPFAFVIDLAALASRREYLKLDKWLTDKIREHGEP   611
gi|212645813|ref|NP_498516.2|     NQAPKHLAFMVDLACLASKRDYLNLEKWIEDKEKAHGEAMTVAVLQFIQKKYQHAQLVAAIAPKTQATTPGAPSEPLQVLIPFVSKRARKPLRQQFPLVFQVMKENSGRSSSVSSGGHVQQSSGSQPQQQQFGGGSGLPPSGVVPVQQQP   700
gi|42561615|ref|NP_171710.3|      -HAVLVSSLLQYPLTQCPRTLLLGMTHIKTAYNLIQREVVSAILPVIIT--SPQDSGFIHNLWHQNAELVLWGIIDAQHLKADS-----------MLRIIEICHELKILSVVLESVPVSSSIRLAVLASLRGLLDIENWLPNCLYMYKDL   574
gi|115483368|ref|NP_001065354.1| ------------------------------------------------------------------------------------------------------------------------------------------------------
                                  .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750
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gi|161076460|ref|NP_001097242.1| FMQAIIKVLHRRCPQVINAKVPEDQLPPKQAQLLPETVTTMINCLQTCINNCMQPEMVEVIMQMTANVAIMANKARAQQQQQPGLVPPPPPTILRGHRGMDLPGGIVPPPPQQPFSGNLNAQMFGPGMDPLTNMS--NNLAGLNLSGP--   831
gi|158299778|ref|XP_319808.4|     ------------------------------------------------------------------------------------------------------------------------------------------------------
                                  ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|94383743|ref|XP_899766.2|      FIQACMTFLKRRCPSILGGLAPEKD-QPKSAQLPAETLATMLACLQACAG-SVSQELSETILTMVANCSNVMNKARQ----------PPPGVMPKGRPPSASSLDAISPVQIDPLAGMASLSIGGSAAPHTQSMQGFPPNLGSAFSTPQS   749
gi|109507689|ref|XP_001060702.1| FIQACMTFLKRRCPSILGGLAPEKD-QPKSAQLPAETLATMLACLQACAG-SVSQELSETILTMVANCSNVMNKARQ----------PPPGVMPKGRPPSASSLDAISPVQIDPLAGMASLSIGGSAAPHTQSMQGFPPNLGSAFSTPQS   749
gi|42716275|ref|NP_057368.3|      FIQACMTFLKRRCPSILGGLAPEKD-QPKSAQLPPETLATMLACLQACAG-SVSQELSETILTMVANCSNVMNKARQ----------PPPGVMPKGRPPSASSLDAISPVQIDPLAGMTSLSIGGSAAPHTQSMQGFPPNLGSAFSTPQS   749
gi|114662880|ref|XP_511007.2|     FIQACMTFLKRRCPSILGGLAPEKD-QPKSAQLPPETLATMLACLQACAG-SVSQELSETILTMVANCSNVMNKARQ----------PPPGVMPKGRPPSASSLDAISPVQIDPLAGMTSLSIGGSAAPHTQSMQGFPPNLGSAFSTPQS   749
gi|119910031|ref|XP_613555.3|     FIQACMTFLKRRCPSILGGLAPEKD-QPKSAQLPPETLATMLACLQACAG-SVSQELSETILTMVANCSNVMNKARQ----------PPPGVMPKGRPPSASSLDAISPVQIDPLAGMASLSIGGSAAPHTQSMQGFPPNLGSAFSTPQS   749
gi|118096204|ref|XP_414043.2|     FIQACMTFLKRRCPSILGGLAPEKD-QPKSAQLPPETLATMLACLQACAG-SVSQELSETILTMVANCSNVMNKARQ----------PPPGVMPKGRPPSASSLDAISPVQIDPLAGMASLSLGGSAAPHTQSMQGFPPNLGSAFSTPQS   749
gi|121582322|ref|NP_001073420.1| FIQACVTFLKRRCPSIMGGLAPEKD-QPKSAQLPPETLATMLACLQSCAG-SVSQELSETILTMVANCSNVMNKARQ----------PPPGVLPKGRAPSTSSLDAISPVQMDPLSAMGSLSLGVSSTSHTPSMQGFPSLQGSAFSNPQS   749
gi|212645813|ref|NP_498516.2|     QQPPSLQQQHSQQSLPTPPTTSQQQIHVQQSVPGPIQRPAQFAPQPMFPPQAQAQHQHQHMMGQPPPSSQNAQPGMN----------LLMNMSPFASGNNRDLLKVVQPAPPPPSSMSPSTQMMRSLIPPLTQRQ----NSNSGWHAAPA   836
gi|42561615|ref|NP_171710.3|      FAEECLKFVKN-----------------------------------------------------------------------------------------------------------VHFSES   591
gi|115483368|ref|NP_001065354.1| ------------------------------------------------------------------------------------------------------------------------------------------------------
                                  .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900
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gi|161076460|ref|NP_001097242.1| -NGAFNFGNMLTSPSRLMTPGANPYPLNLMQMP-QAPPPPNVGNLGRMLPGGP--------QQQTPTPTPTAP----NPNNPVMADLQIPVSKEVEDEVNSYFQRIYNHQPNPTLSIDEVLDILQRFKESSNRREQEVFLCMLRNLFEEY   967
gi|158299778|ref|XP_319808.4|     GNSAFSFNNIIATPPSPSRLLPSSSPFPMMPLPPGAAAAAQAGTLSRLQQTPN--------DKLGAAAAAGAAGIPTQALAPFTADAPLPVSKEVEDEANSYFQRIYNLPPHPTLSIDEVLDMLQRYKDSPNRHENDVYQCMLRNLFEEY   704
gi|94383743|ref|XP_899766.2|      PAKAFPPLSTPNQTTAFSGIGGLSSQLP-GGLGTGSLTGIGTGALGLPAVNNDPFVQRKLGTSGLNQPTFQQSKMKPSDLSQVWPEANQHFSKEIDDEANSYFQRIYNHPPHPTMSVDEVLEMLQRFKDSTIKREREVFNCMLRNLFEEY   898
gi|109507689|ref|XP_001060702.1| PAKAFPPLSTPNQTTAFSGIGGLSSQLPVGGLGTGSLTGIGTGALGLPAVNSDPFVQRKLGTSGLNQPTFQQSKMKPSDLSQVWPEANQHFSKEIDDEANSYFQRIYNHPPHPTMSVDEVLEMLQRFKDSTIKREREVFNCMLRNLFEEY   899
gi|42716275|ref|NP_057368.3|      PAKAFPPLSTPNQTTAFSGIGGLSSQLPVGGLGTGSLTGIGTGALGLPAVNNDPFVQRKLGTSGLNQPTFQQSKMKPSDLSQVWPEANQHFSKEIDDEANSYFQRIYNHPPHPTMSVDEVLEMLQRFKDSTIKREREVFNCMLRNLFEEY   899
gi|114662880|ref|XP_511007.2|     PAKAFPPLSTPNQTTAFSGIGGLSSQLPVGGLGTGSLTGIGTGALGLPAVNNDPFVQRKLGTSGLNQPTFQQSKMKPSDLSQVWPEANQHFSKEIDDEANSYFQRIYNHPPHPTMSVDEVLEMLQRFKDSTIKREREVFNCMLRNLFEEY   899
gi|119910031|ref|XP_613555.3|     PAKAFPPLSTPNQTTAFSGIGGLSSQLPVGGLGTGSLTGIGTGALGLPAVNSDPFVQRKLGTSGLNQPTFQQSKMKPSDLSQVWPEANQHFSKEIDDEANSYFQRIYNHPPHPTMSVDEVLEMLQRFKDSTIKREREVFNCMLRNLFEEY   899
gi|118096204|ref|XP_414043.2|     PAKAFPPLSTQNQTTGFSGIGGLSSQLPVGGLTTGSLTGIGTGALGLPAVNNDPFVQRKLSTSGLSQPTFQQSKMKPSDLSQVWPEANQNFSKEIDDEANSYFQRIYNHPPHPTMSVDEVLEMLQRFKDSNIKREREVFNCMLRNLFEEY   899
gi|121582322|ref|NP_001073420.1| PAKAFSNLPNPNPSTAFPGINPLSSQLQ-GPLST-SLSGIGSG-LGMPTVSSDVFSARKMSTPGLNPPTFQQT-----DLSQVWPEANQHFSKEIDDEANSYFQRIYNHPPHPTMSVDEVLEMLQRFKDSNIKREREVFNCMLRNLFEEY   891
gi|212645813|ref|NP_498516.2|     PQRPSGPPTPQQQMDFRGQIQEFAPQGPHQLQRSGSVTGRSMGIVGQKTSSNFSVG-----APIPGSAAATAAAAANVQQPMNEDFQSMTFAEDIQEEANSYFEKIYSVNN--AMSVENLIDLLKRFRVSNDRRERLVLACVVKNLFEEY   979
gi|42561615|ref|NP_171710.3|      DDFRAKIFHPSDPLSDLHLEATTSLLKVLKAHDNAITSSQLVEEIEKVN-----------------AAILDCNPKLQNGEAKDSSAPNAYGDDVEAEANAYFHQMF----SSHLSVDAMVQMLSRYKESLVPREKLIFECMIANLFEEY   719
gi|115483368|ref|NP_001065354.1| ------------------------------------------------------------------------------------------------------------------------------------------------MVSNLFEEY     9
                                  .......910.......920.......930.......940.......950.......960.......970.......980.......990......1000......1010......1020......1030......1040......1050
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                                  :** :**: :*: :: : *.:: . :: : : :. ::* *:::*     : :: **  **::   :*    : *: : .  ::      *   :
gi|161076460|ref|NP_001097242.1| RFFCQYPEKELQITAQLFGGIIDRNLVPTFVALGLSLRCVLDALRKPDGSKLYYFGVTALDRFRTRLHTYNKYCEHIRSIPHFSDFPPHLIQYVEYGMH----------------GQEPPPQKLIG--LSNTIPSAISS-----------  1088
gi|158299778|ref|XP_319808.4|     KFFPQYPDKELQTTAQLFGGMVERNLVTTYVALGLALRCVLDALKKPEGTKMYYFGITALDRFKNKLHLYPKYCEYVHSIAHFSEFPAHLIEYIEYGSQ----------------GQEPPNKTLGPGPLPPSILQFMPSGAAGRG-----   833
gi|94383743|ref|XP_899766.2|      RFFPQYPDKELHITACLFGGIIEKGLV-TYMALGLALRYVLEALRKPFGSKMYYFGIAALDRFKNRLKDYPQYCQHLASISHFMQFPHHLQEYIEYGQQ----------------SRDPPVKMQGSITTPGSIALAQAQAQAQV------  1025
gi|109507689|ref|XP_001060702.1| RFFPQYPDKELHITACLFGGIIEKGLV-TYMALGLALRYVLEALRKPFGSKMYYFGIAALDRFKNRLKDYPQYCQHLASISHFMQFPHHLQEYIEYGQQ----------------SRDPPVKMQGSITTPGSIALAQAQAQAQV------  1026
gi|42716275|ref|NP_057368.3|      RFFPQYPDKELHITACLFGGIIEKGLV-TYMALGLALRYVLEALRKPFGSKMYYFGIAALDRFKNRLKDYPQYCQHLASISHFMQFPHHLQEYIEYGQQ----------------SRDPPVKMQGSITTPGSIALAQAQAQAQV------  1026
gi|114662880|ref|XP_511007.2|     RFFPQYPDKELHITACLFGGIIEKGLV-TYMALGLALRYVLEALRKPFGSKMYYFGIAALDRFKNRLKDYPQYCQHLASISHFMQFPHHLQEYIEYGQQ----------------SRDPPVKMQGSITTPGSIALAQAQAQAQV------  1026
gi|119910031|ref|XP_613555.3|     RFFPQYPDKELHITACLFGGIIEKGLV-TYMALGLALRYVLEALRKPFGSKMYYFGIAALDRFKNRLKDYPQYCQHLASISHFMQFPHHLQEYIEYGQQ----------------SRDPPVKMQGSITTPGSIALAQAQAQAQV------  1026
gi|118096204|ref|XP_414043.2|     RFFPQYPDKELHITACLFGGIIEKGLV-TYMALGLALRYVLEALRKPFASKMYYFGIAALDRFKNRLKDYPQYCQHLASISHFIQFPHHLQEYIEYGQQ----------------SRDPPVKMQGSITTPGSIALAQAQAQAQV------  1026
gi|121582322|ref|NP_001073420.1| RFFPQYPDKELHITACLFGGIIEKGLV-TYMALGLALRYVLEALRKPFGSKMYYFGIAALDRFKNRLKDYPQYCQHLASIAHFLQFPHHLQEYIEYGQQ----------------SRDPPVKMQGSITTPGSIALAQAQAQSQ-------  1017
gi|212645813|ref|NP_498516.2|     RFFHEYPERELRTTAAVYGGIIREDII-SNVQFATAVRKVIESLSADPNTMLWTFGIVALQHCRSKLCAYPKVCQMIVSSENFARFPQLLKDYVIAGVK----------------GELPPEG-------------------GRH-----  1087
gi|42561615|ref|NP_171710.3|      RFFPKYPERQLKIASILFGSVIKHQLI-SSLTLGMALRLVLDSLRKPADSKMFLFGSKALEQFVNRLVELPQYCNHILQISHLRSTHPELVTVIEQALSRISSGNLESDAS--VSHPGPSQSFPGNGELSGS---GIGQPALQLSSPLQL   863
gi|115483368|ref|NP_001065354.1| KFFPKYPDTQLKLAAVLMGSLIKHQLV-AHLGLGIALRSVLDALRKSIDSKMFMFGTTALEQFMDRLIEWPQYCNHILQISHLRATHAELVAAIERVLAKISSSQNEPNVGSMLSADQHGSSSIGNMEASEASWQLINPTPTQLERSHQQ   158
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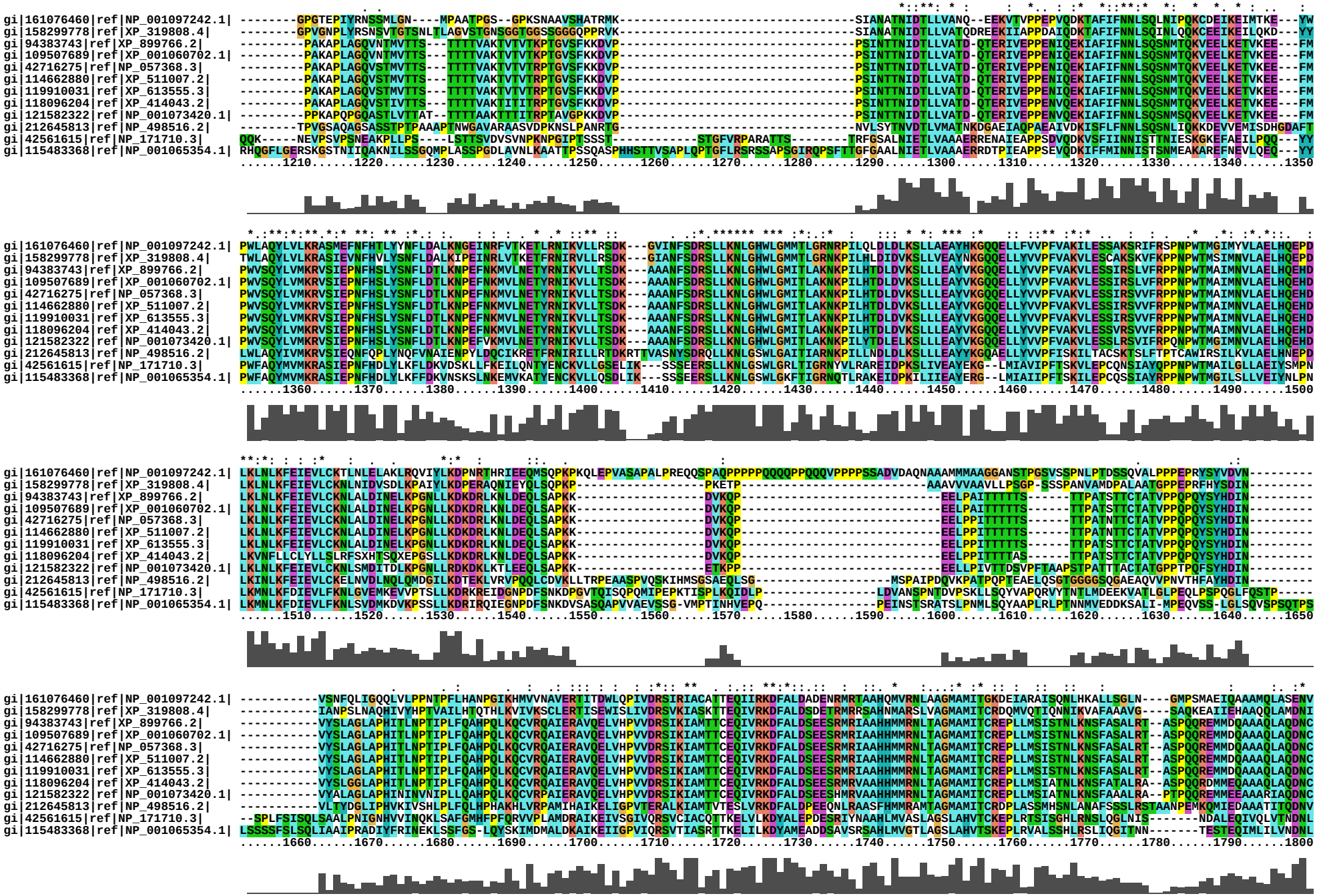
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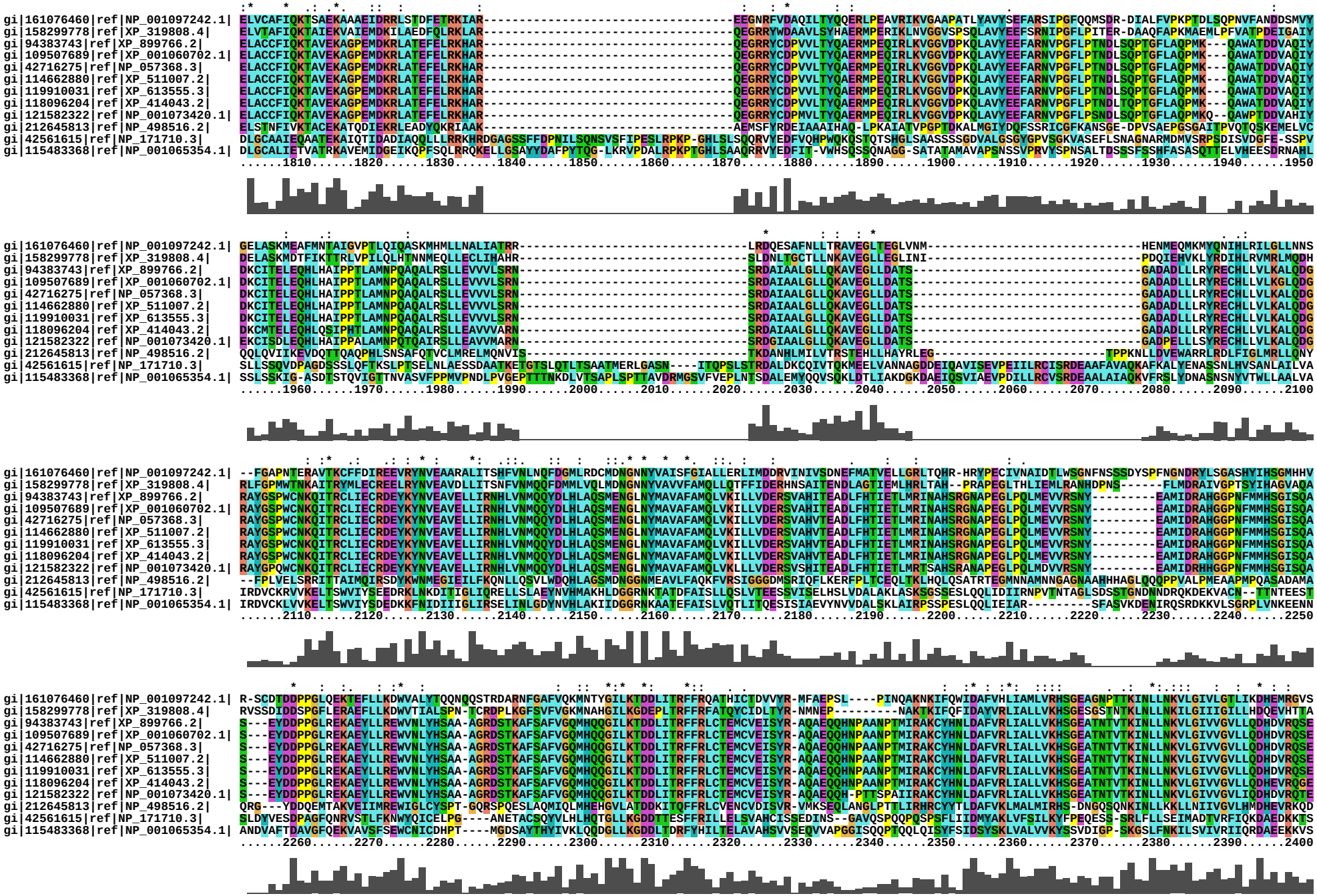
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gi|119910031|ref|XP_613555.3|
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.....1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900.....1910.....1920.....1930.....1940.....1950
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gi|118096204|ref|XP_414043.2|    FQQLPYHRIFIMLLLELN--APEHVLETINFQTLTAFCNTFHILRPTKAPGFVYAWLELISHRIFIARMLAHT------PQQKGWPMYAQLLIDLFKYLAPFLRNVELTKPMQILYKGTLRVLLVLLHDFPEFLCDYHYGFCDVIPPNCI  2126
gi|121582322|ref|NP_001073420.1| FQQLPYHRIFIMLLLELN--APEHVLETINFQTLTAFCNTFHILRPTKAPGFVYAWLELISHRIFIARMLAHT------PQQKGWPMYAQLLIDLFKYLAPFLRNVELNKPMQILYKGTLRVLLVLLHDFPEFLCDYHYGFCDVIPPNCI  2124
gi|212645813|ref|NP_498516.2|    FNAMPYHRILISLFNEITGPDPLKLLEPIAWSILEAFGQTFFALQPRRMPGFAFAWLDIVGHRNVIGRLLANTGIAETVDAVKTAATYTQLIISHLKFLAPFLRNIQLPKSIAILYKGTLRVLLVILHDFPELLCEFHYVICDTIPPNCV  2257
gi|42561615|ref|NP_171710.3|     LNSKPYFRLFINWLLDLC--SLDPGTDGANFQVLTAFANAFHALQPLKIPAFSFAWLELVSHRSFMPKLLTVN-------GQKGWPYVQRLLVDLLQFLEPFLRNAELGGPVHFLYKGTLRVLLVLLHDFPEFLCDYHFTFCDVIPSSCI  2122
gi|115483368|ref|NP_001065354.1| FNPRPYFRLFINLLSELT--TSDLHHDSANFQVLTAFANAFHVLQPLRVPAWSFAWLELVSHRSFMPKLLLCN-------AQKGWPFFQRLLVDLFKFMEPYLRNAELGQPIHLLYKGTLRVLLVLLHDFPEFLCDYHFSFCDVIPPSCI  1446
                                  ......2410......2420......2430......2440......2450......2460......2470......2480......2490......2500......2510......2520......2530......2540......2550
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                                  *:**:***.:**:****** : *:* :* : :    *    .    : . ::  :*.**   :    **.:*   *       .  *.:*.  ::*:** *.* :*:  ::                                  ::*: * :: **
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gi|158299778|ref|XP_319808.4|    QMRNLILSPYPRNMRLPDPFTPNLK-VDMLNDIGGSPRISINYASSIQPVSFKKDLDSYLKA-RAPVTFLSELRSNLQIS----NEVGSRYNIPLMNALVLYVGTQAIAHIRSKNLGPTMS---------TIIHSAHMDIFQNLAVDLDT  2077
gi|94383743|ref|XP_899766.2|     QLRNLILSAFPRNMRLPDPFTPNLK-VDMLSEINIAPRILTNFTG-VMPPQFKKDLDSYLKT-RSPVTFLSDLRSNLQVS----NEPGNRYNLQLINALVLYVGTQAIAHIHNKGSTPSMS---------TITHSAHMDIFQNLAVDLDT  2259
gi|109507689|ref|XP_001060702.1| QLRNLILSAFPRNMRLPDPFTPNLK-VDMLSEINIAPRILTNFTG-VMPPQFKKDLDSYLKT-RSPVTFLSDLRSNLQVS----NEPGNRYNLQLINALVLYVGTQAIAHIHNKGSTPSMS---------TITHSAHMDIFQNLAVDLDT  2260
gi|42716275|ref|NP_057368.3|     QLRNLILSAFPRNMRLPDPFTPNLK-VDMLSEINIAPRILTNFTG-VMPPQFKKDLDSYLKT-RSPVTFLSDLRSNLQVS----NEPGNRYNLQLINALVLYVGTQAIAHIHNKGSTPSMS---------TITHSAHMDIFQNLAVDLDT  2260
gi|114662880|ref|XP_511007.2|    QLRNLILSAFPRNMRLPDPFTPNLK-VDMLSEINIAPRILTNFTG-VMPPQFKKDLDSYLKT-RSPVTFLSDLRSNLQVS----NEPGNRYNLQLINALVLYVGTQAIAHIHNKGSTPSMS---------TITHSAHMDIFQNLAVDLDT  2260
gi|119910031|ref|XP_613555.3|    QLRNLILSAFPRNMRLPDPFTPNLK-VDMLSEINIAPRILTNFTG-VMPPQFKKDLDSYLKT-RSPVTFLSDLRSNLQVS----NEPGNRYNLQLINALVLYVGTQAIAHIHNKGSTPSMS---------TITHSAHMDIFQNLAVDLDT  2260
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gi|121582322|ref|NP_001073420.1| QLRNLILSAFPRNMRLPDPFTPNLK-VDMLSEINIAPRILTNFTG-VMPSQFKKDLDSYLKT-RSPVTFLSELRSNLQVS----NEPGNRYNIQLINALVPYVGTQAIAHIHNKGSTPSMS---------TITHSAHMDIFQNLAVDLDT  2258
gi|212645813|ref|NP_498516.2|    QLRNLILSAYPRQMRLPDPFALNFKQVDTIPEMAVEPKSNLNMAT-IIPDNIRIPLDEYLAN-RISVDFLPNLPTLLQTQ----NQAGTKYNTTVMNALVLYVGIRAIEHLHLRRQRISTL---------NIAHTSYMDIFQNLAIQLDT  2392
gi|42561615|ref|NP_171710.3|     QMRNIILSSFPRNMRLPDPSTPNLK-IDLLPEIVEAPCILSEVDAALKAKQMKNDVDEYLTSRQQNSTFLSELKTKLLLSSSEASSAGTRYSVPLINSLVLYTGMQAIQQLQAGETQAQN-------------VVALQMFKYLSMELDT  2257
gi|115483368|ref|NP_001065354.1| QMRNVILSAFPRNMRLPDPSTPNLK-IDLLAEISIPPRIMSDVDGALKSKQMKTQVDEYLK--RPDGSFLTDLKQKLLLPQNEANIAGTRYNVPLVNSLVLYVGMQAVQQLQLNKMNASASAQQMNQSQLDVQIETATELFRNLVMNSDT  1593
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                                  *****::*.********* ******  .*:** ::  : :******:*:***:. ****************.      .:*  :                  *.       ..*  *
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gi|158299778|ref|XP_319808.4|    EGRYLFLNAIANQLRYPNSHTHYFSCCILYLFAEANSEAIQEQITRVLLERLIVNRPHPWGLLITFIELIKNPI---YKFWDHDFVH-----------------CAPEIERLFESVAKSCMVTS--------------------------  2181
gi|94383743|ref|XP_899766.2|     EGRYLFLNAIANQLRYPNSHTHYFSCTMLYLFAEANTEAIQEQITRVLLERLIVNRPHPWGLLITFIELIKNPA---FKFWNHEFVH-----------------CAPEIEKLFQSVAQCCMGQK--------------------------  2363
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gi|42716275|ref|NP_057368.3|     EGRYLFLNAIANQLRYPNSHTHYFSCTMLYLFAEANTEAIQEQITRVLLERLIVNRPHPWGLLITFIELIKNPA---FKFWNHEFVH-----------------CAPEIEKLFQSVAQCCMGQK--------------------------  2364
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gi|118096204|ref|XP_414043.2|    EGRYLFLNAIANQLRYPNSHTHYFSCTMLYLFAEANTEAIQEQITRVLLERLIVNRPHPWGLLITFIELIKNPA---FKFWNHEFVH-----------------CAPEIEKLFQSVAQCCMGQK--------------------------  2364
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gi|212645813|ref|NP_498516.2|    EGRYLLFNGIANQLRYPNAHTHYFSCVFLYLFKNSTNDTIQEQITRILFERLVALRPHPWGLLITFIELIKNPT---YNFWRYEFTS-----------------CAPEIQRLFQNVANTCVPAQ--------------------------  2496
gi|42561615|ref|NP_171710.3|     EGRYLFLNAIANQLRYPNNHTHYFSFIMLYLFFESDQEIIQEQITRVLLERLIVNRPHPWGLLITFIELIKNPR---YSFWKQAFI-----------------RCAPEIEKLFESVARSCG---------------------------  2358
gi|115483368|ref|NP_001065354.1| EGRYLLLNAIANQLRYPNNHTHYFSFIILYLFSEANQEIVQEQITRVLLERLIVNRPHPWGLLITFIELIKGRRRRPSKWWRQRLTDGGGGDGGDSDGGDVGARCGAARRLRGGGAAALCDGAAAWRRRRGGGGGDVGARCGAARRLRGG  1743
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gi|94383743|ref|XP_899766.2|     QAQQVMEGTGAS------------------  2375
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gi|42716275|ref|NP_057368.3|     QAQQVMEGTGAS------------------  2376
gi|114662880|ref|XP_511007.2|    QAQQVMEGTGAS------------------  2376
gi|119910031|ref|XP_613555.3|    QAQQVMEGTGAS------------------  2376
gi|118096204|ref|XP_414043.2|    QAQQVMEGTGAS------------------  2376
gi|121582322|ref|NP_001073420.1| QAQQVMEGTGAS------------------  2374
gi|212645813|ref|NP_498516.2|    GSQPQAQPDGAPGPLGNNTGAANQQQNPNTN  2527
gi|42561615|ref|NP_171710.3|     GLKPVDEGMVSG----GWVSDNSH-------  2378
gi|115483368|ref|NP_001065354.1| GAAALCDGAVAWRRRRGGVEAAAWWRG----  1770
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