CLUSTAL 2.0.11 MULTIPLE SEQUENCE ALIGNMENT

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                                                      : : * .*:* :       *  . : ::  :.          .. .*  .:* *:* *   .* * :   : : *:
gi|110347451|ref|NP_000433.3|   ---------------MQPRWAQGATMWLGVLLTLLLCS---SLEGQENSFTINSVDMKSLPDWTVQNGKNLTLQCFADVSTTSHVKPQHQMLFYKDDVLFYNISSMKSTESYFIPEVRIYDSGTYKCTVIVNNKEKTTAEYQLLVEGVPS   132
gi|114670032|ref|XP_511582.2|   ---------------MQPRWAQGATMWLGVLLPLLLCS---SLEGQENSFTINSVDMKSLPDWTVQNGKNLTLQCFADVSTTSHVKPQHQMLFYKDDVLFYNISSMKSTESYFIPEVRIYDSGTYKCTVIVNNKEKTTAEYQLLVEGVPS   132
gi|73965385|ref|XP_853419.1|    ---------------MQLEWTQEGKMWLGALLILLLCP---SLEGQENSFTINDIHMEILPGEEVQNGENMTLQCIVDISTTSHIKPQHWVLFYKDDVLFHNVSSVENTESYFIPRARVYDAGTYKCTVILNNKKKTSLEYQVWVKGVSD   132
gi|27807033|ref|NP_776996.1|    ---------------MQLRWTQRGMMWLGALLTLLLCS---SLKGQENSFTINSIHMQILPHSTVQNGENLTLQCLVDSTTSRVKPLHQVLFYKDDVLHHNVSSRRNTESYLIPHVRVCDSGRYKCNVILNNKEKTTPEYEVWVKGVSD   132
gi|74024907|ref|NP_032842.2|    ---------------MLLALGLTLVLYA---SLQAEENSFTINSIHMESLPSWEVMNGQQLTLECLVDISTTSKSRSQHRVLFYKDDAMVYNVTSREHTESYVIPQARVFHSGKYKCTVMLNNKEKTTIEYEVKVHGVSK   122
gi|118099748|ref|XP_001234536.1|                                                                           MSIICHADISKSTDFNLQHNITIFKDGKLVFMSVSGKGDARYEVPMARSSHTGDYQCAVEAGGKIKHSDSLHVWVTGMTK    80
gi|189517404|ref|XP_697859.3|   MPLYTKKGVSACVFSERSESASRSPVRMGAGLLWLGLAGLWQALGTRAAITIDQVRLTVHPGNEVVSGTNLILRCEADVSHSLSRPPTHSFSFLHNGQVVYSKNISASVVERTFSPARVSNSGQYECTVRIEDKAKTSNRQTLRITGLQT   150
                                1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140......150
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                                *  :   ...   .:*   :     *.  **   .: * ::       *      :  :.:.            *    :.  *                * : . * . : ** :  ..*        *::: :: *:
gi|110347451|ref|NP_000433.3|   PRVTLDKKEAIQGGIVRVNCSVPEEKAPIHFTIEKLELNEKMVKLKREKNSRDQNFVILEFPVEEQDRVLSFRCQARIISGIHMQTSESTKSELVTVTESFSTPKFHISPTGMIMEGAQLHIKCTIQVTHLAQEFPEIIIQKDKAIVAHN   282
gi|114670032|ref|XP_511582.2|   PRVTLDKKEAIQGGIVRVNCSVPEEKAPIHFTIEKLELNEKMVKLKREKNSRDQNFVILEFPVEEQDRILFFRCQARIISGIHMQTSESTKSELVTVTESFSTPKFHISPTGMIMEGAQLHIKCTIQVTHLAQEFPEIIIQKDKAIVAHN   282
gi|73965385|ref|XP_853419.1|    PIVTLDKKEAIEGGVVKVNCSVPEEKPPIHFTIEKLKLDTKGFKQKREKTSPNRNFMMLEFTVEEQDVIFFQCQARIISGTHMETSRAIKSELVTVTESFSNPKFHVSPEGVITEGDQLYIRCTIQVTHLVQAFPEIIIQKDKAIVAHK   282
gi|27807033|ref|NP_776996.1|    PRVTLDKKEVIEGGVVVVNCSVPEEKAPVHFTIEKFELNIRGAKKKREKTSQNQNFVTLEFTVEEQDRTIRFQCQAKIFSGSNVESSRPIQSDLVTVRESFSNPKFHIIPEGKVMEGDDLQVKCTVQVTHQAQSFPEIIIQKDREIVAHN   282
gi|74024907|ref|NP_032842.2|    PKVTLDKKEVTEGGVVTVNCSLQEEKPPIFFKIEKLEVGTKFVKRRIDKTS-NENFVLMEFPIEAQDHVLVFRCQAGILSGFKLQESEPIRSEYVTVQESFSTPKFEIKPPGMIIEGDQLHIRCIVQVTHLVQEFTEIIIQKDKAIVATS   271
gi|118099748|ref|XP_001234536.1| PILIAEEKEVFEGEVVKLRCELPEEVPPLYFVFQKMKVNS------TPKQKLQEELYRNFSVVEFPVDEGDDILQFDCFGQRRVRFEFETSLISNKTLITVKEPFIKPTLHIKPSSNITEGKBIRFECSTVVAKMRD--IEIILLRNKTILSSV   226
gi|189517404|ref|XP_697859.3|   PTMKVKSDIVSEGEDIIATCSAAERTGTLMFLFYE-------DNQEVKSEVSNTNTISITLTMKKLTDIYLECAYMVVRHPTAGFSNNSNTVKVFVRDLKELIPQISFSPSASVVEGERVAIKCEVQD----RSALEMFLTKDGTILHR-   288
                                .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                .     **   .   * .*.* **.*  .*         : :* **.:* *  *  * .* **            .:.  : .       :        .  .: * * * *   : * *           .* * : .    ::
gi|110347451|ref|NP_000433.3|   RHGNKAVYSVMAMVEHSGNYTCKVESSRISKVSSIVVNITELFSKPELESSSFTHLDQGERLNLSCSIPGAP------PANFTIQKED----TIVSQTQDFTKIASKSDSGTYICTAGIDKVVKKSNTVQIVVCEMLSQPRISYDA-QFEV   421
gi|114670032|ref|XP_511582.2|   RHGNKAVYSVMAMVEHSGNYTCKVESSRISKVSSIVVNITELFSKPELESSSFTHLDQGERLNLSCSIPGAP------PANFTIQKED----TIVSQTQDFTKIASKSDSGTYICTAGIDKVVKKSNTVQIVVCEMLSQPRISYDA-QFEV   421
gi|73965385|ref|XP_853419.1|    RHGNEATYSVMAMAEHNGNYTCKVEASRISKVSSIVVNITELFSKPKLESSITRLDQGESLNLWCSIPEAP------PANFTIQKEN----TIVSQSQNFTKIASATDSGTYTCNASMGKKVVKKSRAVQIVTVCEMLSKPRIFYDS-SBEV   421
gi|27807033|ref|NP_776996.1|    SLSSBEAVYSVMATTEHNGNYTCKVESNRISKVSSVVVNVTELFSKPKLESSSRLDQGEDLNLLCSIPGAP------PANFTIQKGG----MTVSQTQNFTKRVSEWDSGLYTCVAGVGFVKRSNTVQITVCEMLSKPSIFHDS-RSEV   421
gi|74024907|ref|NP_032842.2|    KQSSEAVYSVMAMVEYSGHYTCKVESNRISKASSIMVNITELFPKPKLEFSSSRLDQGELLDLSCSVSGTP------VANFTIQKEE----TVLSQYQNFSKIAEESDSGEYSCTAGIGKVVKRSGLVPIQVCEMLSKPSIFHDA-KSEI   410
gi|118099748|ref|XP_001234536.1| RDQITLKYSAVATLEGSKTTHNVVTELFPKPILTASMNELDEHKELTLSCSIKDFQ------NASFSILRKHSSRDILLRNSRNLTMRASVNDTGSYICKAEVNRIVKESKPVTIRVYAPVSMPSISVFSGLPEV   370
gi|189517404|ref|XP_697859.3|   -FHISFTYSLTVREEDSGDYVCKTEKGSVQKKVENRLSVTALFTRPILTMSPYEVFEGEFFKLNCSSSVISNKISKEDIKYVLLKDG----QRISTNPIFRKSASLVNNGKYSCWAMARGVNKTSLPHLLKAKVPVSVPVLSAVG----KV   430
                                .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440......450
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                                :   *:.: : *       **  **  : :  .
gi|110347451|ref|NP_000433.3|   IKGQTIEVRCESISGTLPISYQLLKTSKVLENSTKNSNDPAVFKDNPT---EDVEYQCVADNCHSHAKMLSEVLRVKVIAPVDEVQISLSSKVVESGEDIVLQCAVNEGSGPITYKFYREKEGKPFYQMTSNATQAFWTKQKASKEQEG   568
gi|114670032|ref|XP_511582.2|   IKGQTIEVRCESISGTLPISYQLLKTSKVLENSTKNSNDPAVFKDNPT---EDVEYQCVADNCHSHAKMLSEVLRVKVIAPVDEVQISILSSKVVESGEDIVLQCAVNEGSGPITYKFYREKEGKPFYQMTSNATQAFWTKQKASKEQEG   568
gi|73965385|ref|XP_853419.1|    IKGQTIAVSCQSINGTTPISYHLLKTSNILESRDMSSNEPAVFKDNPT---KDTEYQCIVDNCHSHSEMVSEVLRVKVIAPVDEQVKLSILMNAEVFEFGKDIELLCSVNEATGPITYKFYKEAGS-LLYQITSNETHAVWVKSKASKEDEG   567
gi|27807033|ref|NP_776996.1|    IKGQTIEVSCQSVNGTAPIFYQLSNTSKPVANQSVGSNKPAIFRVKPT---DEVBYCCSADNCHSHSKMFSEVLRVKVIAPVDEAQLVVLK-GEVEPGEPIVFYCSVNEGSFPITYKFYKESKPFYQDTINATQIMWHKTTASKEYEG   567
gi|74024907|ref|NP_032842.2|    IKGHAIGISCQSENGTAPITYHLMKAKSDFQTLEVTSNDPATFTDKPT---RDMEYQCADNCHSHPAVFSEILRVRVIAPVDEVVISILSSNEVQSGSEMVLRCSVKEGTSPITFQFYKEKEDRPFHQAVVNDTQAFWHNKQASKKQEG   557
gi|118099748|ref|XP_001234536.1| VLGRPLNLTCCLMMGTPPITFTFYKGNKNKKKIAK-                                                                                                                  405
gi|189517404|ref|XP_697859.3|   IVGRPFKVLCEAKNGTLPITYTLLKDHTPVDSRVVNGTERAIFTITSIRFPGEIDSFTCQAYNGPRFIRTSDALTAPVIVPVSEPMLKPQETTVTE-GSDLVLTCSVQEGGYPITFTWHNKLLLLYSRQEVQSSKGSHIVKMITRDQRG   579
                                .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590......600
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gi|110347451|ref|NP_000433.3|   EYYCTAFNRANHASSVPRSKILTVRVILAPWKKGLIAVVIIGVIIALLIIAAKCYFLR-----KAKAKQMPVEMSRPAVP-------LLNSNNEK-MSDPNMEANSHYGHNDDVRNHAMKPINDNKEPLNSDVQYTEVQVSSAE-SHKDL   704
gi|114670032|ref|XP_511582.2|   EYYCTAFNRANHASSVPRSKILTVRVILAPWKKGLIAVVIIGVIIALLIIAAKCYFLR-----KAKAKQMPVEMSRPAVP-------LLNSNNEK-MSDPNMEANSHYGHNDDVGNHAMKPINDNKEPLNSDVQYTEVQVSSAE-SHKDL   704
gi|73965385|ref|XP_853419.1|    QYYCTASNRANRLKSSPQSNVLTVRVFLAAWIKGLIAVVVIGVIGVLILGARCYILK-----KAKAKQTPVEMSRPAVP-------LLNSTNEKMLSDPDVDVGNHAMKPLTENKEPLTLDVEYTEVEVTSPE-PYQGL   704
gi|27807033|ref|NP_776996.1|    QYYCTASNRANLSKHVIQSNTLTVRVYLP-LEKGLIAVVVIGVIIVTLVLGAKCYFLR-----KAKAKQMPVEMSRPAAP-------LLNSNNEKTLSDAGTEADRHYGYNEDVGNHAMKPLNENKEPLTLDVEYTEVEVTSPE-PHQGL   703
gi|74024907|ref|NP_032842.2|    QYYCTASNRASSMRTSPRSSTLAVRVFLAPWKKGLIAVVIGVIATLIVAAKCYFLR-----KAKAKQKPVEMSRPAAP-------LLNSNSEK-ISEPSVEANSHYGYDDVSGNDAVKPINQNKDPQNMDVEYTEVEVSSLE-PHQAL   693
gi|118099748|ref|XP_001234536.1|                                                                                                                                                     405
gi|189517404|ref|XP_697859.3|   DYHCEASNQALETK---QSKPARIGVSLALWKKALIGVLCILLLVAIVVVLTVFFKKTSHPRRKRQATELSVKPSRPKSGDPMRMSLTLDIEDNTVLNGTPCVMGRNVWSENASGSDSDDHTDEESELVQPEQADPSREIPMPKNAEDEY   726
                                .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740......750
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gi|110347451|ref|NP_000433.3|    GKKD--TETVYSEVRKAVPDAVESRYSRTEGSLDGT---    738
gi|114670032|ref|XP_511582.2|    GKKD--TETVYSEVRKAVPDAVESRYSRTEGSLDGT---    738
gi|73965385|ref|XP_853419.1|     ETKG--TETVYSEIRKANPDFMENRYSRTEGSLDGT---    738
gi|27807033|ref|NP_776996.1|     GTKGTETETVYSEIRKADPDFVENRYSRTEGSLDGS---   739
gi|74024907|ref|NP_032842.2|     GTRA--TETVYSEIRKVDP---------KNGRLP-----   716
gi|118099748|ref|XP_001234536.1| -------------------------------------    405
gi|189517404|ref|XP_697859.3|    IIQHTEVQVSTPGVPEQAEGQAALEYVQLNNSEQETHDT   765
                                 .......760.......770.......780.........
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