CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT

File: Z: eta gamma evolution eta sequences astapa-fa-caeel-drome-humanGb15.ps

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    GBB-entamoeba ----------------------------------------LSLTYMAEDLQAKIIQTRKEIDQIKEETRANREAKEDTTMKKFT--SEIPGISRSDHVKFKRGLRGHISKIYAMHWASDSTHLVSASQDGLMLTWDGQTTNKIHCIRIRS   108
       GBB-diatom -----------------------------------------------------------------------------------------------------RTLKGHFGKVYAMHWNSDSQTLVSASQDGKLIIWNAFTTNKVQAIPLRS    49
   plant_ancestor --------------------------------------------MSVAELKERXAXATXEVNXLREXLRQRRXXLLDTDVARFSXAQGXTPVSFT-DLVCXRTLQGHTGKVYSLDWXXEXXRIVSASQDGRLIVWNALTSQKTHAIKLXC   105
   fungi_ancestor -----------------------------------------------------IAAARREAEXLKEXIXXKKDXLADTTLRAMA--XDIXXLX---VMKPXRTLKGHLAKIYAMHWASDXRHLVSASQDGKLIXWDAYTTNKVHAIPLRS    92
P17343|GBB1_CAEEL --------------------------------------------------MSELDQLRQEAEQLKSQIREARKSANDTTLATVA--SNLEPIGRI-QMRTRRTLRGHLAKIYAMHWASDSRNLVSASQDGKLIVWDSYTTNKVHAIPLRS    97
Q20636|GBB2_CAEEL -------------------------------------MPENSQPTTTEKGSEYLEQLANEAEELRKKLDQERHKLNDIPIQQAA--ERLDVMGAL-GVKQRRILKGHVGKVLCMDWSLDKRHIVSSSQDGKVIVWDGFTTNKEHALTMPT   110
P26308|GBB1_DROME --------------------------------------------------MNELDSLRQEAESLKNAIRDARKAACDTSLLQAA--TSLEPIGRI-QMRTRRTLRGHLAKIYAMHWGNDSRNLVSASQDGKLIVWDSHTTNKVHAIPLRS    97
Q9W3J1|GBB5_DROME -----------------------------------MSEAAVPASNANANATEKMASLVREAENLKTKLEEERQKLNDVNLSNIA--ERLEQIAYV-NIKPRKVLKGHQAKVLCTDWSPDKRHIISSSQDGRLIIWDAFTTNKEHAVTMPT   112
P62873|GBB1_HUMAN --------------------------------------------------MSELDQLRQEAEQLKNQIRDARKACADATLSQIT--NNIDPVGRI-QMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSYTTNKVHAIPLRS    97
P62879|GBB2_HUMAN --------------------------------------------------MSELEQLRQEAEQLRNQIRDARKACGDSTLTQIT--AGLDPVGRI-QMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSYTTNKVHAIPLRS    97
P16520|GBB3_HUMAN --------------------------------------------------MGEMEQLRQEAEQLKKQIADARKACADVTLAELV--SGLEVVGRV-QMRTRRTLRGHLAKIYAMHWATDSKLLVSASQDGKLIVWDSYTTNKVHAIPLRS    97
Q9HAV0|GBB4_HUMAN --------------------------------------------------MSELEQLRQEAEQLRNQIQDARKACNDATLVQIT--SNMDSVGRI-QMRTRRTLRGHLAKIYAMHWGYDSRLLVSASQDGKLIIWDSYTTNKMHAIPLRS    97
O14775|GBB5_HUMAN MCDQTFLVNVFGSCDKCFKQRALRPVFKKSQQLSYCSTCAEIMATEGLHENETLASLKSEAESLKGKLEEERAKLHDVELHQVA--ERVEALGQF-VMKTRRTLKGHGNKVLCMDWCKDKRRIVSSSQDGKVIVWDSFTTNKEHAVTMPC   147
            ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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    GBB-entamoeba SWVMTCAYAPS-MKFVACGGLDNIVSIYSIAPKSSSSEPLNNTTAELAGHVGYISCMRYV--DENRILTSSGDSTCCLWDVEQSAKIMDFK-----DHQADVMCVSVSPD--QNTFVSGACDSMAKLWDIR-MENCVATFTGHDADINAI   247
       GBB-diatom SWVMTCAFEQSKGNLIACGGLDNVCSIYNTQQAS---TSNARASKELVAHDGYLSCCRFV--DEGHVVTSSGDSTCIYWDVNSGEVLKTFS-----DHKSDVMSVAISPE-NNNIFVSGSVDTTAKVWDIR-NGKCVQTHIGHEADINSV   187
   plant_ancestor AWVMTCAFSPX-GNSVACGGLDNVCSIFNLSSXADK-DGNLPVSXXLXGHXGYLSSCXYVPXXEXHXVTSSGDXTCXLWDVXTGLXXSVFGGEFQSGHTADVMSVSISSS-NPNXFXSGSCDTTAKLWDXRXASRAVRTFXGHEGDVNTV   252
   fungi_ancestor SWVMTCAYAPS-GNFVACGGLDNICSIYNLRXG------XXRVARELSGHSGYLSCCRFI--XDRQILTSSGDMTCMLWDIEXGXKVMEFX-----DHXGDVMSLSXXPN--XNVFVSGACDATAKXWDIR-TGKXVQTFXGHESDINAV   225
P17343|GBB1_CAEEL SWVMTCAYAPS-GSFVACGGLDNICSIYSLKTR----EGNVRVSRELPGHTGYLSCCRFL--DDNQIVTSSGDMTCALWDIETGQQCTAFT-----GHTGDVMSLSLSPD--FRTFISGACDASAKLWDIR-DGMCKQTFPGHESDINAV   232
Q20636|GBB2_CAEEL TWVMACAFSPS-SQMIACGGLDNKCSVVPLSFE----DDIIQKKRQVATHTSYMSCCTFLR-SDNLILTGSGDSTCAIWDVESGQLIQNFH-----GHTGDVFAIDVPKCDTGNTFISAGADKHSLVWDIR-SGQCVQSFEGHEADINTV   248
P26308|GBB1_DROME SWVMTCAYAPS-GSYVACGGLDNMCSIYNLKTR----EGNVRVSRELPGHGGYLSCCRFL--DDNQIVTSSGDMSCGLWDIETGLQVTSFL-----GHTGDVMALSLAPQ--CKTFVSGACDASAKLWDIR-EGVCKQTFPGHESDINAV   232
Q9W3J1|GBB5_DROME TWIMACAYAPS-GNFVACGGLDNKVTVYPITSD----EEMAAKKRTVGTHTSYMSCCIYPN-SDQQILTGSGDSTCALWDVESGQLLQSFH-----GHSGDVMAIDLAPNETGNTFVSGSCDRMAFIWDMR-SGHVVQSFEGHQSDVNSV   250
P62873|GBB1_HUMAN SWVMTCAYAPS-GNYVACGGLDNICSIYNLKTR----EGNVRVSRELAGHTGYLSCCRFL--DDNQIVTSSGDTTCALWDIETGQQTTTFT-----GHTGDVMSLSLAPD--TRLFVSGACDASAKLWDVR-EGMCRQTFTGHESDINAI   232
P62879|GBB2_HUMAN SWVMTCAYAPS-GNFVACGGLDNICSIYSLKTR----EGNVRVSRELPGHTGYLSCCRFL--DDNQIITSSGDTTCALWDIETGQQTVGFA-----GHSGDVMSLSLAPD--GRTFVSGACDASIKLWDVR-DSMCRQTFIGHESDINAV   232
P16520|GBB3_HUMAN SWVMTCAYAPS-GNFVACGGLDNMCSIYNLKSR----EGNVKVSRELSAHTGYLSCCRFL--DDNNIVTSSGDTTCALWDIETGQQKTVFV-----GHTGDCMSLAVSPD--FNLFISGACDASAKLWDVR-EGTCRQTFTGHESDINAI   232
Q9HAV0|GBB4_HUMAN SWVMTCAYAPS-GNYVACGGLDNICSIYNLKTR----EGNVRVSRELPGHTGYLSCCRFL--DDSQIVTSSGDTTCALWDIETAQQTTTFT-----GHSGDVMSLSLSPD--MRTFVSGACDASSKLWDIR-DGMCRQSFTGHVSDINAV   232
O14775|GBB5_HUMAN TWVMACAYAPS-GCAIACGGLDNKCSVYPLTFDKN--ENMAAKKKSVAMHTNYLSACSFTN-SDMQILTASGDGTCALWDVESGQLLQSFH-----GHGADVLCLDLAPSETGNTFVSGGCDKKAMVWDMR-SGQCVQAFETHESDINSV   287
            ruler .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                   :.* *  : :**** :*:*:* *:  ::  :                                 ** :              *:*::* :  . :* *..:.***  : :*
    GBB-entamoeba AFHPSGNAFITGSDDFSCKLFDIRADRELMNYSS-ESMQHGVTSVAISSTGRYLFCGYDDLGCLWWDVLKG----DYITKLTGHENRVSCLGVSPDGYALCTGSWDSTLRIWAN-----   356
       GBB-diatom AFFPDGHAFGTGSDDASCRLFDMRSYGEVNKFKS-DKITCGITSVAFSRSGRLMFGGYDDFNTYVWDTLSDAD-QCAFALPTPHENRVSCLGVNKNGDALCTGSWDTNLKIWA------   298
   plant_ancestor KFFPDGXRFGTGSDDGSCRLFDIRTGHELQVYQXXGDGXXXVTSVAFSRSGRLLFAGYSNGNCYVWDTLLAXVVLNLGXLQXXHENRVSCLGLSADGDALCTGSWDXNLKIWAFGGXRX   371
   fungi_ancestor QFFPXGNAFATGSDDASCRLFDXRADRELNXYS-------------------------------VWDTLKG----ERVGILX-HENRVSCLGVSXDGMALCTGSWDSTL-VWA------   301
P17343|GBB1_CAEEL AFFPSGNAFATGSDDATCRLFDIRADQELAMYSH-DNIICGITSVAFSKSGRLLFAGYDDFNCNVWDSMRQ----ERAGVLAGHDNRVSCLGVTEDGMAVCTGSWDSFLKIWN------   340
Q20636|GBB2_CAEEL RFHPNGDAFATGSDDATCRLFDLRADRQVCVYEK-ESILFPVNGVDFSLSGRILFAGYGDYRVGVWDSLKC----ARHSVLYGHENRISCLRTSPDGTAVCSASWDCTIRIWA------   356
P26308|GBB1_DROME TFFPNGQAFATGSDDATCRLFDIRADQELAMYSH-DNIICGITSVAFSKSGRLLLAGYDDFNCNVWDTMKA----ERSGILAGHDNRVSCLGVTENGMAVATGSWDSFLRVWN------   340
Q9W3J1|GBB5_DROME KFHPCGDAIATGSDDSSCRLYDMRADREVAVFAK-ESIIFGVNSVDFSVSGRLLFAGYNDYTVNLWDTLKS----ERVCLLYGHENKVSCVQVSPDGTALSTGSWDYTIRVWA------   358
P62873|GBB1_HUMAN CFFPNGNAFATGSDDATCRLFDLRADQELMTYSH-DNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKA----DRAGVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN------   340
P62879|GBB2_HUMAN AFFPNGYAFTTGSDDATCRLFDLRADQELLMYSH-DNIICGITSVAFSRSGRLLLAGYDDFNCNIWDAMKG----DRAGVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN------   340
P16520|GBB3_HUMAN CFFPNGEAICTGSDDASCRLFDLRADQELICFSH-ESIICGITSVAFSLSGRLLFAGYDDFNCNVWDSMKS----ERVGILSGHDNRVSCLGVTADGMAVATGSWDSFLKIWN------   340
Q9HAV0|GBB4_HUMAN SFFPNGYAFATGSDDATCRLFDLRADQELLLYSH-DNIICGITSVAFSKSGRLLLAGYDDFNCNVWDTLKG----DRAGVLAGHDNRVSCLGVTDDGMAVATGSWDSFLRIWN------   340
O14775|GBB5_HUMAN RYYPSGDAFASGSDDATCRLYDLRADREVAIYSK-ESIIFGASSVDFSLSGRLLFAGYNDYTINVWDVLKG----SRVSILFGHENRVSTLRVSPDGTAFCSGSWDHTLRVWA------   395
            ruler .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.........
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