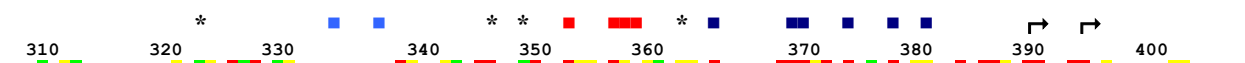


230 240 250 260 270 280 290 300

eIF5_YEAST EWAVDMSEEAIRARAKELE-----VNSLSTQLDEYGEWILLEQAGEDKE-NLPSDVELYKKAEDVLDNDPKTGCVLQAQ---CLFDEEDVNN--EIAEH
eIF5_CANGL EWAVDMSEEAIRARAKELQ--VANGA-----VDTELTKLEEYGEWIIINEAGEDKS-NLPSDVELYKKAIVEDVLDSPDKIACVLAQ---CITFEDIVN--EISEH
eIF5_CANAL EWAVDMSQEAIARAKARELE-----GLSLQNNKDFEFGEWLLKESNGSKD-DLPSDVELYKRVIELEIADTPELTVQLVLAQ---VLFDDDIIN--QIPEH
eIF5_KLULA DWAVDMSEEAIRARAKELQGEADK-----ETGFEKSLKEEFGEWLHE-----E-ELPTDIELYKKAIAEELLEDDPKVAAVLVAQ---VLDEEDIVS--DISEP
eIF5_EREGO DWAVDVSEEAIVARALELQGEDG-----NVSKFSTLDFEFGEWVLAG-GSDDD-ELPNDAIVYKKAIELELLQEPKIACVLAQ---ALFDENIVD--QISTH
eIF5_DEBHA DWAVDMSEEAIEARARELE-GLS-----LNEDQKFNQFGEWLLDESKDSKD-DLPSDIDILYKRVIELEILENPELTVQLVLAQ---VLFDDDIIE--QIEEH
eIF5_YARLI TWTVDTSEAAVAAVQREVEQGVA-GI-----ALEENDYTFIPEGWCSL-----GEPDVELYKKAIELEIGSDSKTVOVLAQ---TIEDDKIVK--QDEH
eIF5_SCHPO DWAVDTSEEAIVARAVQLEGNMKDSLTLSDLRGDEEEAESSRDQFGEWLED-----NYPGVSVDVEIYKMKKEENIHHKSAIVVLAQ---CIITSPVVG--EIEKH
eIF5_ASPNI NNNVVDVSEEAIVARAKELPDDLKRALALDEGD-DEGADGTPTAYDELGSGWLDLTATEKGGISKVEDVEIYLKAKELGLETCHKHTLAVLAQ---TIIDETAK--QVDGR
eIF5_NEUCR EWAVDMSEEAIVARAVQNLPGEFKQKLVNGEEDDEEGGNTVYDQLGTWVDEDAKAGGINNVDDVEIYLKAKELGIDAKHTTAVVLAQ---CLFDENIVA--QIPGR
eIF5_GIBZE EWAVDMSEEAIVAKAQSILPGEFKAALNIGDDDEDEGGGPTIYDELGDWISQSAEKEGGIDKVESIDIVYKAKELGIEGKHTVLAQ---TIIDKNIVA--QISKR
eIF5_USTMA DWSVDTSEAAVAAVSKALGSEVSSVLVGDGDD--EDEDDESPIYAQFQQLQANRKGQEGREKTPAEVYKKAQFEGIEKHKHTVQLVLAQ---ALTDTEAPK--EIEKY
eIF5_CAEEL DWEPEFVPEPNGMLSAGMGK-----LVLDKD--LEKSEEQRDLMLHTFLKAKEEDRISDAKGTALRDEAERLELKQKASILLANV-----LDDDKIVSDKQINTH
eIF5_CAEER DWEPEFVPEPNGMLSAGMGK-----LVLDKD--LEKSKERQLDMLHDFLVKAKDEGRISDAKGTALRDEAERLELKQKASILLANV-----LDDDKIVSDKQINTH
eIF5_DROME GWSVDVSKAEIRARAKELQDLTDGAGK-MTISDD--YDKTEKERIDIFYELVKDKRDKKQLDDVQTHKELVIEAERLIDINKAPVLVAE-----LETENIHK--DVQKN
eIF5_ANOGA SMTVDTSEEAIVARAVQDLTDGAKN-MTVSDD--FDKTEKERIDIFYELVKDKRDKKQLDDVQTHKELVIEAERLIDINKAPVLVAE-----LETENIHK--DVQKN
eIF5_TETNI DWAEETTEEAQRRRMEETSDHAKN-LTLSDD--LEKPLEERVDFYFNFKVQRKENGITID--GADKEILAEERLIDVKAMGPLILSEI-----LENESIRE--QIKKY
eIF5_DANRE DWAEETTEEAQRRRMEETSEHAKG-LTLTED--LEKSLERVNIYFNFKVKKKDSGTID--SADKDI LAEERLIDVKAMGPLILSEI-----LEDENIRD--QIKKY
eIF5_XENLA DWGEDTTAEAQRRRMEETSDHAKN-LTLSDD--LEKPFVEYRNLDFVFKKKEEGVID--FCDDKILAEERLIDVKAMGPLVLSVEI-----LDDDKIRD--QIKKY
eIF5_GALGA DWGEDTTAEAQRRRMEETSDHAKN-LTLSDD--LERTVEERVNLLDFVFKKKEEGVID--SSDKDI LAEERLIDVKAMGPLVLSVEI-----LDEKIRE--QIRKY
eIF5_MOUSE DWGEDTTAEAQRRRMEETSDHAKG-LTLSDD--LERTVEERVNLLDFVFKKKEEGVID--SSDKDI LAEERLIDVKAMGPLVLSVEI-----LDEKIRE--QIKKY
eIF5_HUMAN DWGEDTTAEAQRRRMEETSDHAKV-LTLSDD--LERTIEERVNLLDFVFKKKEEGVID--SSDKDI LAEERLIDVKAMGPLVLSVEI-----LENEKIRE--QIKKY



eIF2Be_YEAST DFEKEGLATVERAMENNHD-----LDTALLELTLRSMNV-----TYHEVRIATITALLRRVYHFIAQT--LGRKDAVVK--VFNQW
eIF2Be_CANGL DFLVFGLATVERAIEENDHD-----LDTALLELTLRSMNV-----TYHEVRIATATALLRRVYHFITQT--LGRKEAVFK--VFGQW
eIF2Be_DEBHA DFEKELATVDRSMENNHD-----LDTALLELTLRSMNV-----TYHEVRLATSKALLHKTTHFITDTT--LDVKEATEK--IENKN
eIF2Be_SCHPO DFNKEAQSLSRRAEFENNHQ-----IDIAALELTLRSMANNA-----NYHEVRSATVALLARRMHLDV--SKEALAK--VMTWR
eIF2Be_USTMA EFRSAAIASLRAEFENHT-----VDDAAIELTLRSMANV-----PLKEVRKVTVEIILHKDCPEQ--PKQMLK--VLDKW
eIF2Be_ARATH YFEKEVEGTVLRVAEENIK-----PDLVLTMEINSGRLSFMN-----ESADCAGATFFSMIKLALDTPHNSGS--EYKNAAS--ITTKW
eIF2Be_DROME SFPGRSDLSLTRGFREKSN-----VDFVLEINSGRLSAYNM-----SLKEVNFNVKVAEIMGQSIIVEPANDN--WLVAINA--AFKQL
eIF2Be_GALGA VFQNEVLTGLQGRGEEENIS-----CQNLVLEINSLKWAYNI-----SLNEMMQVLSKVVLEFPLQQLDANLDSQNFSAIILP--LAKNW
eIF2Be_RABIT VFQNEVLTGLQGRGKEENIS-----CQNLVLEINSLKWAYNI-----SLKEVMQVLSHVVLEFPLQQMDSPLEANRYCALLLP--LAKNW
eIF2Be_HUMAN VFQNEVLTGLQGRGKEENIS-----CQNLVLEINSLKWAYNV-----SLKEVMQVLSHVVLEFPLQQMDSPLSSRYCALLLP--LAKNW



310 320 330 340 350 360 370 380 390 400

eIF5_YEAST NAFITKLLV-TPEYEKNFMGGIERFLGLEH---KDLIPLTKIILVQLVNNIIISSEELMRFGTNS---SKKFPKPEVSKKVRRAAKPFIITWLETARSDDEEDDE*
eIF5_CANGL SAFTTKKLVFV-NADYEKNLGGIERFLGLEH---KELIPLTKIILVQLVNNIIISSEELMRFGTNS---SKKFPKPDVSKKVRRAAKPFIITWLENASDEESDEE*
eIF5_CANAL VGLITKINGDEEFKALGLSERLFFGLEK---PNLIPQIPIKILHGFVDRDLISEEVLKIKGSKV---SKKYPKPDVSKKVRRAAKPFIITWLETARSDDEEDDE*
eIF5_KLULA TAFITQKLLV-DEDFEKNFLGGIERFLGLDH---QELIPLTKIILVQLVNNIIISSEELMRFGTNC---SKKFPKPDVSKKVRRAAKPFIITWLETARSDDEEDDE*
eIF5_EREGO AALAQKLFV-SDDFEKQLGLSERLFLGLDH---PDLIPLTKIILVQLVNNIIISSEELMRFGTNC---SKKFPKPEVSKKVRRAAKPFIITWLENASDEESD*
eIF5_DEBHA LGLLAKLIDHSDSFEKSLGLSERLFLGLEN---QALISALPKIILVITMDKOLISEEVIISGSKV---SKKYPKPDVSKKVRRAAKPFIITWLETARSDDEEDDE*
eIF5_YARLI KGLITKIVA-SDEHEKALGGIERLVLGLTH---PDLIPLTKIILVQLVNNIIISSEELMRFGTNC---SKRYVDRKSKKVRRAAKPFIITWLETARSDDEEDDE*
eIF5_SCHPO GALFKKICT-TDKHERALLGGIERLFLGLDH---LVHIDVVKIILVQLVNNIIISSEELMRFGTNC---SKKYVSRKSKKVRRAAKPFIITWLENASDEESDEE*
eIF5_ASPNI APLAKKIT-T-SERHEKALGGIERLFLGKEH---PELLISQVAVILGMYQNDLVSEETLKAQCSKA---SKKYVDIQSRKVRRAAKPFIITWLETARSDDEEDDE*
eIF5_NEUCR APMKRVVT-SERHEKALGGIERLFLADLG---KESDKIVKILQLYVHHDLCSSEVITKNGSKA---SKKYVDGTSKVRRAAKPFIITWLETARSDDEEDDE*
eIF5_GIBZE ASMKQVVT-SERHERALLGGIERLVLGGADHPMPQSVIKIILQLYVHHDLCSSEVITKNGSKA---SKKYVDISTSKVRRAAKPFIITWLETARSDDEEDDE*
eIF5_USTMA GAVLVKVVGDSEKHKQAMGGFERLAGVQC---PTLVNGVFKIIMALYQIDVLDLDFVKNNGTHV---SKKYVSDISKVRRAAKPFIITWLETARSDDEEDDE*
eIF5_CAEEL RNLILRLTLNDKKAQRYLLGVEQVIHKHE---AELLTKSAHIKSLYDVEDEEDSLISNGERP---SKKYVSKSFAKIIENSQVILNWLKREAEETFEESDDEI*
eIF5_CAEER RNLILRLVMDLTKKAQRYLLRGIEQVIHRYE---DDLTKSAHIKSLYDADICEEVLISNGERP---SKKYVSKSFAKIIENSQVILNWLKREAEETFEESDDEI*
eIF5_DROME RPLILRLTLNPKAQRYYLIGSVEQVVELHK---GILMSKVAIGIKFLYDLILDEAVILVIAQKV---SKRHVSKNIAAEIHERAKPFIITWLENASDEESDEE*
eIF5_ANOGA RNLILRLTHEDKKAQRYLLIGSLEQVLSLHA---DKMLKVFGLKFLDVLDEKVIDLVSQRK---SKKYVSKETAQIHERAKPFIITWLETARSDDEEDDE*
eIF5_TETNI KRHLRLCHNNKKAQRYLLGGFECVVKLHQ---VQLLPRVVIILKLDADLLEEDVITFAEAKAV---SKKYVSKELAKEIHAKEPFIITWLETARSDDEEDDE*
eIF5_DANRE KRHLRLCHNNKKAQRYLLGGFECVVKLHQ---TQLLPRVVIILKLDADLLEEDVITFAEAKAV---SKKYVSKELAKEIHAKEPFIITWLETARSDDEEDDE*
eIF5_XENLA RRHLRLCHNNKKAQRYLLHGFECVIDMHQ---SHLSKIPHIKEMMDADLLEEVILSWEAKP---SKKYVSKELAKDIRAKPFIITWLETARSDDEEDDE*
eIF5_GALGA RRHLRLCHNNKKAQRYLLHGFECVVMAMHQ---SLLSKIPHIKEMMDADLLEEVILSWEAKP---SKKYVSKELAKDIRAKPFIITWLETARSDDEEDDE*
eIF5_MOUSE RRHLRLCHNNKKAQRYLLHGLECVVMAMHQ---AQLISKIPHIKEMMDADLLEEVILSWEAKP---SKKYVSKELAKEIRKAEPFIITWLETARSDDEEDDE*
eIF5_HUMAN RRHLRLCHNNKKAQRYLLHGLECVVMAMHQ---AQLISKIPHIKEMMDADLLEEVILSWEAKP---SKKYVSKELAKEIRKAEPFIITWLETARSDDEEDDE*

eIF2Be_YEAST GLLFKRQVDFEEYIDLNLIMEKIVEQSF---DKPDILFSAIVSLDNDIIEEDVLYKWDNV-----STDPRYDEVKLLVYKVVLELQNDDESEEE*
eIF2Be_CANGL GALLNROVFEPEEYIDLNLIMEIAEQKF---EKPEFLESAINTLDNDIIEEDSYEWDNV-----SQDSKYDQVKTITAKWVDWRNRAEESDDE*
eIF2Be_DEBHA GLLFKRQVDFEEYVDLILIQDVCNSVDK---SYNGRILEMANIYNQDIVEEENLYKWDSE-----SSTANDELVQVRLITKGVVDLWLEAESEESD*
eIF2Be_SCHPO GLLLAKLIFSHEEQVDNVLITLQKCVRLS-----MTRHFTQLIGYFVLEAEENAEQEYSDP-----RSSEGAALRDAGGQVVDLWLEAESEESGE*
eIF2Be_USTMA CPLISVVA--VDDQIEALAVQHCARTEG---YFKLPLPLKPKVNDVISENIVGWNKSPLSRESSEAVGGEKGNLRAAEVIRYILESQSDDEEDDE*
eIF2Be_ARATH KDLLGFYAKKIDIEQVIMKFEEMCQESH---ELGPLETQIHLVLDKVDVLEQADLIRVIEEEK---AGADEADKYLQCDFTFIQWLKREAEESDDEEDDE*
eIF2Be_DROME CFVYSNYIKSDESDMMLKALELDYEENHL---VRGKISQVHYLVLDKDFVLSAIAQAYLAQ-----DEEHAHLRQSLAKLVAIDLQSSKEDDDEDD*
eIF2Be_GALGA TPLIKNYIKRSSDHLNALFAIEEFLEHDS---LCTSIKAVIMTFFVQLEILEEDVILNWFSLR---DTSDKGQLRKNQRLQRFIOWLKEAEESDGD*
eIF2Be_RABIT SPVFRNYIKRAADHLEALAAIEEFLEHEA---LGTCAKVMGMGFVQLEILAEETILSIFGQR---DVTDKGRQLRKNQRLQRFIOWLKEAEESDDE*
eIF2Be_HUMAN SPVFRNYIKRAADHLEALAAIEDFELEHA---LGISMAKVMGMGFVQLEILAEETILSIFGQR---DITDKGQLRKNQRLQRFIOWLKEAEESDDE*