

Myssoensis.XP\_021350409.1\_elongation\_factor\_2like  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel\_  
Myssoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r  
Hsapies.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ribo  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri  
Aplanci.LOC110989613\_116\_kDa\_U5\_small\_nuclear\_ribo  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281  
Myssoensis.XP\_021349219.1\_elongation\_factor\_2like  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2  
Myssoensis.XP\_021362159.1\_elongation\_factor\_2like  
Lanatina.XP\_013394736.1\_elongation\_factor\_2  
Cintestinalis.LOC100177993\_elongation\_factor\_2like  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo  
Hsapies.NP\_001952.1\_elongation\_factor\_2  
Bbelcheri.LOC109464429\_elongation\_factor\_2like  
Aplanci.LOC110987647\_elongation\_factor\_2like  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel\_  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G  
Hsapies.NP\_078856.4\_elongation\_factor-like\_GTPase  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase\_  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPa  
Myssoensis.XP\_021362732.1\_elongation\_factorlike\_G  
  
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Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r  
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Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281  
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Lanatina.XP\_013394736.1\_elongation\_factor\_2  
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Bbelcheri.LOC109464429\_elongation\_factor\_2like  
Aplanci.LOC110987647\_elongation\_factor\_2like  
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Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438  
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Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT  
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Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel\_  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G  
Hsapies.NP\_078856.4\_elongation\_factor-like\_GTPase  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase\_  
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Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu  
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Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel\_  
Myssoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r  
Hsapies.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ribo  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri  
Aplanci.LOC110989613\_116\_kDa\_U5\_small\_nuclear\_ribo  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281  
Myssoensis.XP\_021349219.1\_elongation\_factor\_2like  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2  
Myssoensis.XP\_021362159.1\_elongation\_factor\_2like  
Lanatina.XP\_013394736.1\_elongation\_factor\_2  
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Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo  
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Bbelcheri.LOC109464429\_elongation\_factor\_2like  
Aplanci.LOC110987647\_elongation\_factor\_2like  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438  
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Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel\_  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G

Hsapiens.NP\_078856.4\_elongation\_factor-like\_GTPase -----MVNLSLDKMIQ  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas -----MRTVTPGQLAQ  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase -----MKGVDAEQLSR  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPa -----MKSSTQKLAIE  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G -----MRTTTPEKLVQ  
  
200a 220a 240a 260a 280a  
Myessoensis.XP\_021350409.1\_elongation\_factor\_2like VMKIPESVRNVAVIGGTD-----GMVPLMNLNKKRGAENLTAEESGRCKRYVD-----PMAANLTC  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu LMDCPLEIRSVAFCGHLHH-----GKTSFVDCLEIQTHPDIRAKEDKDRLRYTDYKLEVERGLSVKSTPMT  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 LMDSPELVRNVACGHLHH-----GKTTFCDALIEQTHPYLASTENKELRYTDYKLEVERGLSVKSTPMT  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel LMDTPPLIRNVVALVGHLLH-----GKTTFVDCLEIQTHPYQFETMEERQRLRYTDYKLEVERGLSVKSTPMT  
Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea LMDTPDLIRNVVTLGHLHH-----GKTSFVDCVLSQTHPEIDGTDKDLRYTDYKLEVERGLSVKSTPMT  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea MMDSPELIRNISIIGHLLH-----GKTNFVDCLEMQTHPDIAKHEEKDLRYTDYKLEVERGLSVKSTPMT  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r LMDNPDILIRNVALCGHLHH-----GKTSFVDCVLSQTHPEMEIEEGKDLRYTDYKLEVERGLSVKSTPMT  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r LMDNPDILIRNVALCGHLHH-----GKTSFVDCVLSQTHPEMEIEEGKDLRYTDYKLEVERGLSVKSTPMT  
Hsapiens.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ribo LMDNSELIRNVVTLGHLHH-----GKTCFVDCLEIQTHPEIRKRYDQLCYTDYKLEVERGLSVKSTPMT  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri LMDNPELIRNVVLAAGHLHH-----GKTTFVDCLEMQTHPDIFTKEDQRLRYTDYKLEVERGLSVKSTPMT  
Aplanci.LOC110989613\_116\_kDa\_U5\_small\_nuclear\_ribo MMDNAELIRNVVLAAGHLHH-----GKTSFVDCLEMQTHPELRVKEDGSIRYTDYKLEVERGLSVKSTPMT  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 TMSKPHNIRNMCVIAHVDH-----GKSTLTDLAVLVKAGI-ITEQQAGQRRFTDSLEAEQKGIITIKSSAVS  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 LINKPNTIRNICILGQMSN-----GKSTLIN-LFQNGQIP-----FNNGQ-----TIRSKFYL  
Myessoensis.XP\_021349219.1\_elongation\_factor\_2like AMDHRTGVNRNAVIAHVDH-----GKTLTDSLAKAGV-INTDQAGDKCAMDKRDEQLKGIITIKSTAIS  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 LMAKNKINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Myessoensis.XP\_021362159.1\_elongation\_factor\_2like IMDNKLINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Lanatina.XP\_013394736.1\_elongation\_factor\_2 IMDHKMINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Cintestinalis.LOC100177993\_elongation\_factor\_2like IMDKKSINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo IMDKKINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Hsapiens.NP\_001952.1\_elongation\_factor\_2 IMDKKANIRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Bbelcheri.LOC109464429\_elongation\_factor\_2like VMDKKINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Aplanci.LOC110987647\_elongation\_factor\_2like IMDKKANIRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507 LMDKKINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438 LMDKKINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati LMDKKINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT LMDKKINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661 LMDKKINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel LMDKKINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G LMDKKINRNMVIAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Hsapiens.NP\_078856.4\_elongation\_factor-like\_GTPase LQKNTANIRNICVLAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas LQGNQPNVNRNICVLAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase LQENATANIRNICVLAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPa LQRNPANIRNICVLAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G LQRNPANIRNICVLAHVDH-----GKSTLTDSLVSAGI-IAESRAGDARFTDKRDEQRCITIKSTAIS  
  
300a 320a 340a 360a 380a  
Myessoensis.XP\_021350409.1\_elongation\_factor\_2like LYHTCAPADLPGE-----AVEGNK-----DFVINILDPGSGVDFSAEVDTLTIRMMDGAVVMDICIS-----GVTLDTKLVLQKSIERRVKPVL  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu LVL-----SDLNK-----SYLLNIFDTPGHVNFSDVTAARLDCDAVCFVDDH-----GVLMTDLIRIKHALQERLPLIL  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 ILI-----PDLKDK-----NFLNINILDPGHVNFSDVTAARLDCDAVCFVDDH-----GVLMTDLIRIKHALQERLPLIL  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel LVL-----QDVQKQ-----SYLLNIFDTPGHVNFSDVTAAMRMSDGVVLFIDAAE-----GVLMTDLIRIKHALQERLPLIL  
Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea LVL-----PDSKKK-----SFLVNVFDPGHVNFSDVTAAFRISDGVVVFDAAE-----GVLMTDLIRIKHALQERLPLIL  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea LIL-----PDTGKG-----SYLFNIMDSPGHVNFSDVTAAMRLSDGVVLFIDAE-----GVLMTDLIRIKHALQERLPLIL  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r LLL-----QDTRTK-----SYLVNVFDPGHVNFSDVTAAFRMCDAVIFIDAAE-----GVLMTDLIRIKHALQERLPLIL  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r LLL-----QDTRTK-----SYLVNVFDPGHVNFSDVTAAFRMCDAVIFIDAAE-----GVLMTDLIRIKHALQERLPLIL  
Hsapiens.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ribo VVL-----PDTGKG-----SYLFNIMDTPGHVNFSDVTAAGRLISDGVVLFIDAAE-----GVLMTDLIRIKHALQERLPLIL  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri LVL-----PDSRKG-----SYLVNIDSPGHVNFSDVTAAGRLISDGVVLFIDAAE-----GVLMTDLIRIKHALQERLPLIL  
Aplanci.LOC110989613\_116\_kDa\_U5\_small\_nuclear\_ribo LVM-----PDSRKG-----HFLNIMDTPGHVNFSDVTAAYRLSDGVVIFIDAAE-----GVLMTDLIRIKHALQERLPLIL  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 MYELDDQILGD-----LKRQDN-----GFLVNLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 FRYK-----SEDEQ-----DFLINLIDTPGHVNFSDVTSVLRICDGAFLIIDCIS-----GVCVQTEVLRQAIAERIKPVL  
Myessoensis.XP\_021349219.1\_elongation\_factor\_2like LLYEVDPKLPAG-----SETGLK-----CEVLNIDSPGHVNFSDVTAALRVADGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 LYNELNADQLQYVRKQVPSDVSQKAECCGFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Myessoensis.XP\_021362159.1\_elongation\_factor\_2like LLYELAMEDMYKQYKQYGENEERKN-----CFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Lanatina.XP\_013394736.1\_elongation\_factor\_2 LLYELPEKKDKIMFQ-----KYNEEK-----GFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Cintestinalis.LOC100177993\_elongation\_factor\_2like MYELSDRDMQWVE-----GQKHGN-----GFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo MYELSDKDKMQWVE-----GQKHGN-----GFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Hsapiens.NP\_001952.1\_elongation\_factor\_2 LLYELSENDLNFK-----QSKDGN-----GFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Bbelcheri.LOC109464429\_elongation\_factor\_2like LLYELPAKDFVFKQE-----REPBIT-----HFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Aplanci.LOC110987647\_elongation\_factor\_2like MYELSEADMSYIT-----QEKDGN-----GFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507 LLYELPAKDFVFKQE-----REPBIT-----HFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438 LLYELPAKDFVFKQE-----REPBIT-----HFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati LLYELPAKDFVFKQE-----REPBIT-----HFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT MYFEVEEKOLVFTHPE-----DQREKKE-----GFLINLIDSPGHVNFSDVTAALRVTDGALVVDVDS-----GVCVQTEVLRQAIAERIKPVL  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661 LLYEQAE-----EMAGNE-----DYLVLNIDSPGHVNFSDVSTAVRLCDGAILVVDVDE-----GVCPTQAVLRQAIAERIKPVL  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G LRY-----ALAAGE-----EYLINLIDSPGHVNFSGEVCTAVRLCDGAILVVDVDE-----GVCPTQAVLRQAIAERIKPVL  
Hsapiens.NP\_078856.4\_elongation\_factor-like\_GTPase LHY-----ATGNE-----EYLINLIDSPGHVNFSDVSTAVRICDGCILVVDVDE-----GVCPTQAVLRQAIAERIKPVL  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas LQF-----QKES-----DYLVLNIDSPGHVNFSDVSTAVRLCDGAILVVDVDE-----GVCPTQAVLRQAIAERIKPVL  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase LRF-----SQDQ-----DYLINLIDSPGHVNFSGEVCTAVRLCDGAILVVDVDE-----GVCPTQAVLRQAIAERIKPVL  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPa LHF-----AQSGE-----EYLINLIDSPGHVNFSDVSTAVRLCDGAILVVDVDE-----GVCPTQAVLRQAIAERIKPVL  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G LAV-----QRDAQ-----EYLVLNIDSPGHVNFSDVSTAVRLCDGAILVVDVDE-----GVCPTQAVLRQAIAERIKPVL  
  
400a 420a 440a 460a 480a  
Myessoensis.XP\_021350409.1\_elongation\_factor\_2like FVNNIDRAIMEHKLQEDLYQTHSVVAAAGKGMAT-----YSD-ESGPMGS-VQ-FSPVKGNVLFSGS  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu CLNKIDRLVLELKLPPNDAYYKIKNIIDEVNSLIST-----FSEGAGVSLPEP-QHIVSPPLGNVCFAS  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 CINKIDRLMLELKLPPQDAYYFKLKHIDEVNGLIST-----YSEDE-----NT-ASYVSPPLGNVCFAS  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel CINKIDRLILELKLPPQDAYYFKLKHIVEVNGLIST-----YGA-----PDDN-LI-VSPILGNVCFAS  
Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea CINKVDRLILELKLPPDAYYFKLRLHIEEVNALLSV-----YAED-----EN-KI-VSPILGNVCFAS  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea CINKIDRLILELKLPPADAYYFKLRLHIDEVNNLLST-----YSDTENIPN-----VSPILGNVCFAS  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r CINKIDRLILELKLPPDAYYFKLRLHIDEVNGLIST-----FADEE-----ED-MS-VSPILGNVCFAS  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r CINKIDRLILELKLPPDAYYFKLRLHIDEVNGLIST-----FADEE-----ED-MS-VSPILGNVCFAS  
Hsapiens.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ribo CINKIDRLILELKLPPDAYYFKLRLHIDEVNGLIST-----YSTD-----EN-LI-VSPILGNVCFAS  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ribo CINKIDRLMLELKLPPDAYYFKLRLHIDEVNGLISTSV-----YSEES-----EP-VV-VSPILGNVCFAS  
Aplanci.LOC110989613\_116\_kDa\_U5\_small\_nuclear\_ribo CINKIDRLVLELKLPPADAYYKLRNITEINGLMSV-----YSDA-----EP-MM-VSPILGNVCFAS  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 IINKVDRCILQKQVEPEELQKLSGIIARCNLIAT-----YSTD-----EP-MM-VSPILGNVCFAS  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 FLNKDFEIFLNLQIYEEDYIQHOFIRKNNISI-----GD-LQ-THPVKGVTSFSGS  
Myessoensis.XP\_021349219.1\_elongation\_factor\_2like MLNKIDRCVMEVQDHEELQVSLCRTQIVSVNVAVDM-----YG-----QPDVMKG-LT-LDPSLGVNAFVC  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 FMNKIDKALSTMQDQESLYQHLRSRVNNVNIAT-----FSE-HDGMGD-VT-VNPGMGTVGFGS  
Myessoensis.XP\_021362159.1\_elongation\_factor\_2like FMNKMIDLALLTLQVQDEELQYQNFQIRIVSVNVNVM-----VSS-EDSPLG-VI-IDPSQGVTVGFGS  
Lanatina.XP\_013394736.1\_elongation\_factor\_2 FMNKMIDLALLTLRLDREAMYTFQRTIESVNVNIVT-----YAS-EDGMGD-FT-VEPTKGVTVGFGS  
Cintestinalis.LOC100177993\_elongation\_factor\_2like FMNKMIDRALLELQLEKEDLYQTFQRIVESVNVNIVT-----YAV-EDGMGMN-IM-IDPQKGVTVGFGS  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo FMNKMIDRALLELQLEKEDLYQTFQRIVESVNVNIVT-----YAV-EDGMGMN-IM-IDPQKGVTVGFGS  
Hsapiens.NP\_001952.1\_elongation\_factor\_2 FMNKMIDRALLELQLEPELYQTFQRIVESVNVNIVT-----YAV-EDGMGMN-IM-IDPQKGVTVGFGS  
Bbelcheri.LOC109464429\_elongation\_factor\_2like FMNKMIDRALLELQLEMEDLYNNFSRVENNVNIVT-----YSD-EDGMGMN-IM-VYEPKGVTVGFGS  
Aplanci.LOC110987647\_elongation\_factor\_2like FMNKMIDRALLELQLEMEDLYQTFQRIVESVNVNIVT-----YAD-ESGPMGD-IQ-VDPCKGVTVGFGS  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507 FMNKMIDRALLELQLEDELYQTFQRIVESVNVNIVT-----YGD-DSGPMGE-LQ-VDPCKGVTVGFGA

Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438 FMNMKDRALLELQQLQEDLFQTFQRIVENVNVIAT-----YGD-DSGPMGE-LQ-VDPTKGTGVGFGA  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati FMNMKDRALLELQDAEELVYQTFQRIVENVNVIAT-----YND-DGGPMGE-VR-VDPKSGSVGFGS  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT VLNKFDRLFLQLGLSPQVYDRILRVLEQINSVLAEMFTADVMQQTGWGEAD-----GDSVRQSAEGTYTWTSGLEATDDSD-HVYFSPDKANVLFTS  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661 VLNKIDRLIILEKMTPLAEYLHIRGILENINAVVAEQFTSLLEKSVQDEANEIEKKETNNDIVDDGDD-----DWA-----RNEA-QMCFSPHYNNVLFCS  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel VLNKIDRLIILEKQMDPLDAYFHLCQVLEQVNAVLSGISFASDILAKEDITKDD-----NYESALEEVDSDS-ELYFSPSSGNVIFCS  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G VLNKIDRLITEKFTPEEAHLHQQVLEQVNAVTSGLSYSAEVLEKIGQTESS-----QVETENGEEVVYDSSGIADTDDSD-KLYFSPSHGNVVFAS  
Hsapies.NP\_078856.4\_elongation\_factor-like\_GTPase VINKIDRLIVELKFTPQEAYSHLNKILEQINALTGTLFTSKVLEERAERETE-----SQVNPSEQGEQ-VYDWTSGLEDTDDSD-HLYFSPQEGNVVFTS  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas VLNKVDRLITEKNSPMEAHVLQVQLEQVNSIMGNLSTDMVMKGTJEDTSD-----NAVKEPTVATEDHVFDYSLELHDTHDDSD-NLYFSPQEGNVVFTS  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase VLNKIDRLISELYKTPQEAHLRLQVLEQVNAVGNLFASGVLEQATQONTERTVQSNDSERCQTNEEKVYVWSDSGLEETDDSD-NIYFSPDQGNVIFAS  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPa VLNKIDRLVSEWKFPTLETYLHQLQVLEQVNAVITGELFTSGVFKESSQAE-----NQKEVKVTNGDQ-VYEWSSALDDTDDSD-DLYFSPDQGNVIFAS  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G VLNKIDRLIMELKMDPLAEAFHLLQVLEQVNLVTNELFTTEIMAKTSSTQTDG-----AGGEKEKSAVSNDDTQADDEERNITFFSPTQGNVIFAS  
500a 520a 540a 560a 580a  
Myessoensis.XP\_021350409.1\_elongation\_factor\_2like ASQSWGVT-----LGEIAAKQAQELK-----VAPSVLLSKLWGNDFYNSSQK-----KWNKNEP-----SKDYIRAFNLEVLDPILFKLFE  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu SYRRCFT-----LESFAKIYDTDFAD-----SIDYKSAKRLWGDQYFSSETR-----TFKSKP-----PTASSLSRSEVFEILEPIYKIFA  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 SYRRCFT-----LKSFAKIYADTHGG-----TFDQAFSKRLWGLDYDPKTR-----TFGKGK-----PTAQTSGRSFNKFIILEPIYKILA  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel SLYGFCFT-----LKSFAKIYADTYEG-----VAYLDFAKRLWGDYFNSKTR-----KFSKKQ-----PHNSAQSRSEVFEILEPIYKILA  
Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea SYRRCFT-----LASFAKIYGETYGG-----INEKEFARRLWGDYFNSKTR-----KFTKPK-----PHSTQARSEVFEILEPIYKILFS  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea SQYAFCT-----LMSFANLYVKQFG-----EVDPKQFARRLWGDYFNSKTR-----RFSKKP-----PHNTAQSRSEVFEILEPIYKILFS  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r SYRRCFT-----LSSFAKIYSDTYGG-----INTYEFARRLWGDYFNSKTR-----KFSKKP-----ANSTQSRSSEVFEILEPIYKILFS  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r SYRRCFT-----LSSFAKIYSDTYGG-----INTYEFARRLWGDYFNSKTR-----KFSKKP-----ANSTQSRSSEVFEILEPIYKILFS  
Hsapies.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ri SQYSCFT-----LGSFAKIYADTFGD-----INTQEFARRLWGDYFNSKTR-----KFTTKA-----PTSSSQRSSEVFEILEPIYKILA  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri SQYRCFT-----LQSFASKIYEDTYGG-----FSAKELSRRLWGDYFNSKSR-----KFTSKP-----PMSTQSRSSEVFEILEPIYKIFA  
Aplanci.LOC10989613\_116\_kDa\_U5\_small\_nuclear\_ri SQYSCFT-----LQSFASKIYSDTYGG-----IDHQEFARRLWGDYFNSKTR-----KFTTKS-----PVSTAQSRSEVFEILEPIYKILFA  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 KGHGWFT-----IPQFATPLAEKTK-----ATKEKYMRLWGDYFNSKTR-----KWLSEYEQSRSSSDAKRGSFTQILQPLYQLIN  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 CLHGWFT-----LKEFADYISIKFG-----IDNNKLMLEYLWDDHYSFENN-----QWSENK-----TEGYHRGFCQFLDPLFKIYQ  
Myessoensis.XP\_021349219.1\_elongation\_factor\_2like GLHGWFT-----LVNFAFADYIAKFG-----LSEKLMRLWGEHYNNFNG-----TWNRIG-----GDGYVRGFCQFLDPLFKIYQ  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 GLQSWFT-----LHTMAFYAKRTFG-----MDADKLPLRLWGDYFNSKTR-----KWRKSK-----TDPKDVAFVHFLDPLFKIYQ  
Myessoensis.XP\_021362159.1\_elongation\_factor\_2like GLHGWFT-----LKDFAVRYETKFK-----MNQELMKLWGNDFNNAEAK-----KWRKSK-----TDPKDVAFVHFLDPLFKIYQ  
Lanatina.XP\_013394736.1\_elongation\_factor\_2 GLHGWFT-----LKMFAADYATKFK-----VPAAKLMKRLWGDYFNSKTR-----KWKAKN-----DKSGQRGFTLYLPLTYNNVFN  
Cintestinalis.LOC100177993\_elongation\_factor\_2like GLHGWFT-----LKQFAEMYAEKFK-----VPLPKLMNRLWGDYFNSKTR-----KWKSKT-----SPENERGFTFALPTIKYKVD  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo GLHGWFT-----LKQFAEMYSEKFK-----VPLPKLMNRLWGDYFNSKTR-----KWKSKT-----SPESDRGFTFALPTIKYKVD  
Hsapies.NP\_001952.1\_elongation\_factor\_2 GLHGWFT-----LKQFAEMYVAKFAKGEGLGPAERAKKVEDMMKLWGDYFNSKTR-----KFSKATSPEGKLPRTFCQLDPLFKVFD  
Bbelcheri.LOC109464429\_elongation\_factor\_2like GLHGWFT-----LKQFGLYSNRKFK-----IELSKMKMLWGDYFNSKTR-----KWKATP-----GGGYIRGFCQFLDPLFKVFD  
Aplanci.LOC10987647\_elongation\_factor\_2like GLHGWFT-----LKQFAEMYSNKFK-----IEPAKLMKRLWGDYFNSKTR-----KWKNTG-----GGGYIRGFCQFLDPLFKIYKFS  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507 GLHGWFT-----LKEFAEMYASKFK-----IEVDKLMKRLWGDYFNSKTR-----KWSKSG-----GGGYVRGFCQFLDPLFKVFD  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438 GLHGWFT-----LKEFAEMYASKFK-----IEVDKLMKRLWGDYFNSKTR-----KWSKSG-----GGGYVRGFCQFLDPLFKVFD  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati GLHGWFT-----LKQFSEMYSEKFK-----IDVVKLMNRLWGENFENAKTK-----KWKQKQ-----EADNKRSEFCMYLIDPLFKVFD  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT AVDGGWFT-----ISDFGPAAYERNM-----LPRKGLLKLWGDYFNSKTR-----SPSGDGLPRVPHKA-----RANKKPFVFLQVILIDHLLHIYK  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661 ALDGGWFT-----IHHFADLYAKKLS-----IKREVLKMLWGDYFNSKTR-----RVFKGA-----QSKGQKPFVFLQVILENLSVSYE  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel AYDGAFT-----VDFPAAMYAKRLE-----MSRKOLENLWGDYFNSKTR-----EALPGA-----QEKAKPFVFLQVILENLSVSYD  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G AADGGWFT-----LQIHFARISSTKLG-----IREKVLNRLWGDYFNSKTR-----KILPGA-----QAKGKKTFLVQVILENLSVSYD  
Hsapies.NP\_078856.4\_elongation\_factor-like\_GTPase AIDGGWFT-----LEHFAQYASKLN-----IKREVLKMLWGDYFNSKTR-----KIMKGD-----QAKGKPFVFLQVILENLSVSYD  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas AIDGGWFT-----LEHFAQYASKLN-----IKEDILQVLWGDYFNSKTR-----RVMKGA-----QAKGKPFVFLQVILENLSVSYD  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase AIDGGWFT-----IGHFAELYSVKLG-----INAGVLKTLWGDYFNSKTR-----RIRKGA-----QAKGKPFVFLQVILENLSVSYE  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPa AYDGGWFT-----LHNFADMFSSKLG-----IKREVLKTLWGDYFNSKTR-----RIMKGA-----QSKVKPFVFLQVILENLSVSYE  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G 600a 620a 640a 660a 680a  
Myessoensis.XP\_021350409.1\_elongation\_factor\_2like ASGN-----VQGSALPDLIENLGVMQSLDNNET-----NTRTNVQEMMQWLPISNSLLTMIIVHLPSPQTS-QRYRSSELLVSR-----KT-DAVGT  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu QTAG-----DVDTCPLRCLSELGILSKSEFKL-----NVRPLLRIFSRFFGDFSGFVSMCVHVPSPVAS-AKNTISHTYSG-----PL-DSAIT  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 HVVG-----DVDIALSGVLDGLRITKTELK-----NVRPLLRVLCARFGEFGEFTDMLIQTIPSPAN-AHKSVDIHLTYG-----SK-QEDIV  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel QVVG-----DVDITLSDTLAEGLNLYRVSKEMKS-----NIRPLLRVLCNRFMGDCSGFVDMCVHLPSPADN-AKKNVIEHVTY-----PG-EGDIY  
Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea QVVG-----DVDDECLPRVLDGLGILSTKEERKL-----NIRPLLRVLCRRFFGDFTFGVDMCVHLPSPADN-AKKNVIEHVTY-----SS-DSDLA  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea QVVG-----DADSTLPRVLDGLGILSTKEEMKM-----NIRPLLRVLCRRFNGFSGFVDMCVHLPSPADN-AKKNVIEHVTY-----PQDDTEL  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r MTVG-----DVDLNLQVCEELGILSTKEERKL-----NIRPLLRVLCRRFFGDFSGFVDMCVHLPSPADN-AKKNVIEHVTY-----PL-DTELA  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r MTVG-----DVDLNLQVCEELGILSTKEERKL-----NIRPLLRVLCRRFFGDFSGFVDMCVHLPSPADN-AKKNVIEHVTY-----PL-DTELA  
Hsapies.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ri QVVG-----DVDTSLPRVLDGLGILSTKEERKL-----NIRPLLRVLCRRFFGDFTFGVDMCVHLPSPADN-AKKNVIEHVTY-----GV-DSDLG  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri QVVG-----DVDSTLPRVLDGLGILSTKEEMKM-----NIRPLLRVLCRRFFGDFTFGVDMCAEHKSPYAA-AKKNVIEHVTY-----PQ-DDQVA  
Aplanci.LOC10989613\_116\_kDa\_U5\_small\_nuclear\_ri QVVG-----DVDSTLPRVLDGLGILSTKEEMKM-----NIRPLLRVLCRRFFGDFTFGVDMCVHLPSPADN-AKKNVIEHVTY-----PQ-DSDLG  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 ACAD-----LMNEEVLTLISKIDVLPDKLSDASIDSKTISNVNMRKWLPAEAMHLHILVHLPSPVQA-QVYRIQHLTYG-----PQ-DDQVA  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 IKN-----YKDELERLMQNLNNDKELSEK-----GDNELLLIMQWLAIIDILSKMIILHLPSPVIA-QVYRIQHLTYG-----PM-DDDAA  
Myessoensis.XP\_021349219.1\_elongation\_factor\_2like TLKT-----KEKEEVFLTKDKNLISGESEAE-----SGKPLMRKVMQKWLPAEALHLEMFVAHLPSPVIA-QVYRIQHLTYG-----PM-DDDAA  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 AVQD-----EKDPMQKMLTAIDVKLSTEEHQ-----PAKVLKTMHKLWGLPAGDCLLEMICHLSPSPVIA-QVYRIQHLTYG-----PK-DEEAA  
Cintestinalis.LOC100177993\_elongation\_factor\_2like TCMK-----GEHSEKILKLMGMVKLSTDEKDL-----REKNLLKVMKRWMPAGDALLQMIIVHLPSPVIA-QVYRIQHLTYG-----PT-DEEVA  
Lanatina.XP\_013394736.1\_elongation\_factor\_2 KCDVGLNLENENVEPTVLIEIKEMGVKLSTAEKEL-----KDKPLLVKVMRWMPAGDALLQMIIVHLPSPVIA-QVYRIQHLTYG-----PP-DDKVA  
Cintestinalis.LOC100177993\_elongation\_factor\_2like AIMN-----NKTTEIGKLMKCNVVKLGDDKDK-----VEKQLLKAFMTWLPAGDTLLQMIITHLSPVIA-QVYRIQHLTYG-----PA-DEEVA  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo AIMN-----FKKEETAKLIEKDKLSTDEKDK-----EGKPLLVKVMRWMPAGDALLQMIITHLSPVIA-QVYRIQHLTYG-----PH-DDDAA  
Bbelcheri.LOC109464429\_elongation\_factor\_2like AIMN-----FKKDDTAKVLEIKVQKLTKEEKL-----EGKPLLVKVMRWMPAGDALLQMIITHLSPVIA-QVYRIQHLTYG-----PH-DDDAA  
Aplanci.LOC10987647\_elongation\_factor\_2like AIMN-----FKKDDTAKVLEIKVQKLTKEEKL-----EGKPLLVKVMRWMPAGDALLQMIITHLSPVIA-QVYRIQHLTYG-----PH-DDDAA  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507 AIMD-----CKKDEYLALDLKINKLQGDGRDKLEGGKPLLLKVMQWLPAGDVLLTMIATHLSPVIA-QVYRIQHLTYG-----PQ-DDDAP  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438 AIMD-----CKKDEYLALDLKINKLQGDGRDKLEGGKPLLLKVMQWLPAGDVLLTMIATHLSPVIA-QVYRIQHLTYG-----PQ-DDDAP  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati AIMN-----YKKEEIGTLLEKILKIDSEKDK-----DGKALLTVMRTWLPAGEALLQMIATHLSPVIA-QVYRIQHLTYG-----PH-DDDAA  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT TIIV-----DNMRDMAPHIAERLGLKESRLHQ-----SVDNRTLVRSILSTQWLPGLAIFRTIVDTCPSPLAASRERAGYMLFGESSVTQFVSGEDAVT  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel TIIT-----KRDNEKLEKIVASIGAKLIPDIGH-----SDPCVPLHLLFNQWLPVASAFVDMVVTQLNPKAL-NPTDKIEQMKCNKRRFDTLIPETQRLK  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G ITAI-----KRDKDKPLGAEIAGLGLKATRDRL-----TDPKQIKAVLQWLPIDKSVLHMVQHVPVPHKI-SDERAQRLYLPANVLISSLPPELEIK  
Hsapies.NP\_078856.4\_elongation\_factor-like\_GTPase AVYI-----RDKRSEKIKTSLNINISARVVRGKSEPKTYLQICQWLPVLAELVSSVCQYLPSPDI-SGERVEGLMCGSTRFSAHLSKSDK  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas AVLV-----KDKDKIDKIVTSLGLKIGAREARH-----SDPKVQINACISQWLPISHAVALMVQKLPSPDI-TAERVELMCTGQTFDSFPPEQALK  
Aplanci.LOC10988091\_elongation\_factorlike\_GTPase AVLV-----RDKKEKVERIKVSLNIVTISARDARH-----NDPRVLQVQWLPVLAELVAMTVDQLPSPIQI-SPEKVEGLMCTGQTFDSFPPEQALK  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPa TILV-----KRDKDKMLKIDSINLKIARDLRH-----NDPKVHLQICQWLPVLAELVAMTVDQLPSPIQI-SPEKVEGLMCTGQTFDSFPPEQALK  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G AVTV-----KDKDKEMIKIKTSLNINISARVVRGKSEPKTYLQICQWLPVLAELVAMTVDQLPSPIQI-SPEKVEGLMCTGQTFDSFPPEQALK  
SVSV-----NRDAEMTEKIKVSLGLKISPRDMRH-----NDPRMKLQICQWLPVLAELVAMTVDQLPSPIQI-SPEKVEGLMCTGQTFDSFPPEQALK  
700a 720a 740a 760a 780a  
Myessoensis.XP\_021350409.1\_elongation\_factor\_2like -----SAVTKCDP-----SGP-LIMYVTKWY-----  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu -----RMIACRA-----ESPHLMVHTTKLY-----  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 -----TDMKNCP-----NAP-VIHTTKNY-----  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel -----RDMISCNQ-----YGT-LMVHSSKMV-----  
Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea -----EVMCTCDP-----DSP-LMVHTTKLY-----  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea -----QAMYTCDP-----DGP-LMVHTTKMY-----  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r -----DSMTQCDP-----DGP-LMIHTTKLY-----  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r -----DSMTQCDP-----DGP-LMIHTTKLY-----  
Hsapies.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ri -----EAMSDCDP-----DGP-LMCHTTKMY-----  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri -----DAMLECDP-----EGP-LMLHTTKMY-----  
Aplanci.LOC10989613\_116\_kDa\_U5\_small\_nuclear\_ri -----DTMIECDP-----EGP-LMLHTTKMY-----  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 -----CAMKACDP-----KGD-VMYISKKI-----  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 -----SYMKECDP-----DGP-LMYISKKI-----  
Myessoensis.XP\_021349219.1\_elongation\_factor\_2like -----VAMKHCP-----NGP-LMYISKKI-----  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 -----IGIMNCDP-----NAC-LMYISKKI-----  
Myessoensis.XP\_021362159.1\_elongation\_factor\_2like -----IAMKNCDP-----KGP-LMYISKKI-----  
Lanatina.XP\_013394736.1\_elongation\_factor\_2 -----QAMKECDP-----KGE-LMYISKKI-----

Cintestinalis.LOC100177993\_elongation\_factor\_2like-----TAIMNCDP--KGP-LMMYVSKMV-----  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo-----TAIINCA--KGP-LMMYVSKMV-----  
Hsapie...NP\_001952.1\_elongation\_factor\_2-----MGIKSCDP--KGP-LMMYISKMV-----  
Bbelcheri.LOC109464429\_elongation\_factor\_2like-----LGIKNCNP--DGP-LMMYVSKMV-----  
Aplanci.LOC110987647\_elongation\_factor\_2like-----LGIKNCNP--NGP-LMMYISKMV-----  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507-----LGIKSCDP--TAP-LMMYISKMV-----  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438-----LGIKSCDP--TAP-LMMYISKMV-----  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati-----IAVKS...DGP-LMMYISKMV-----  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT\_SDGSNAGQSILREV...SCRDNGTEEDYEDESAAPPAIDALEACSSNADAP-VIIFVSKVFWADKLKNAFSTIVFPKNVPKSVQPPKSVQFPAPRFATP  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661-----QAFIDCSDDDQAP-VIVCVSKLF-----SVHNSALSONRQKPLTAEDIAQRREFLKQKQL  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel-----ESFTSCDA-NSSN-VIAFVSKMT-----PVHITHLPQNRPKRLTDQEVQRRDEVRRIIE  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G-----QDFLSCGS-DSST-TIVLVSKMV-----AVDSKMLPQNKRQPLTVEIEVKRRRELVRQKHA  
Hsapie...NP\_078856.4\_elongation\_factor-like\_GTPase-----AAFMKCGSED...TAP-VIIFVSKMF-----AVDAKALPQNRPPLTQEEIAQRREARQRHA  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas-----QDFIMCSAEDSAP-VIVFISKMF-----SVDPKVLPHNRPPLTQEEIEKKRELARQRHQ  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase-----SALVFCPT--P-I-----KPLTEELQRRREARQRHQ  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPa-----EDFLSCSPGEDKP-VIVFISKMF-----PFDQCCLPQNKRQPLT...EADLAQRRLVARQRHA  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G-----DAFISCS...TSDNSP-VILFVSKMF-----PVERKMLPQFKORPLSEAEIQRRRQARQRHL  
800a-----820a-----840a-----860a-----880a-----  
Myessoensis.XP\_021350409.1\_elongation\_factor\_2like-----TLYAIGRVFSGSIVSGSEIK-----  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu-----PDEDA-----V-----  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250-----STSDV-----T-----  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel-----PNDDC-----T-----  
Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea-----PTQDA-----T-----  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea-----STEDG-----V-----  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r-----PTEDA-----T-----  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r-----PTEDA-----T-----  
Hsapie...NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ribo-----STDDG-----V-----  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri-----PTEDA-----T-----  
Aplanci.LOC10989613\_116\_kDa\_U5\_small\_nuclear\_ribo-----STEDG-----V-----  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657-----PAQDG-----S-----  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281-----PQSDT-----N-----  
Myessoensis.XP\_021349219.1\_elongation\_factor\_2like-----PTSDK-----G-----  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2-----PTSDK-----G-----  
Myessoensis.XP\_021362159.1\_elongation\_factor\_2like-----PTTDK-----G-----  
Lanatina.XP\_013394736.1\_elongation\_factor\_2-----PTSDK-----G-----  
Cintestinalis.LOC100177993\_elongation\_factor\_2like-----PTSDK-----G-----  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo-----PTSDK-----G-----  
Hsapie...NP\_001952.1\_elongation\_factor\_2-----PTSDK-----G-----  
Bbelcheri.LOC109464429\_elongation\_factor\_2like-----PTSDK-----G-----  
Aplanci.LOC110987647\_elongation\_factor\_2like-----PTTDK-----G-----  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507-----PTSDK-----G-----  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438-----PTSDK-----G-----  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati-----PTSDK-----G-----  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT\_GRIVVHNDV-----ETAIK-----  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661-----NKTTP-----NEEYG-----  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel-----ERKQKS-----EQAEL-----  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G-----ERKLAETNSSNHKEDQP-----  
Hsapie...NP\_078856.4\_elongation\_factor-like\_GTPase-----EKLAAGQQA...LEPTQD-----  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas-----EKLAALTSQTQEPQEQ-----  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase-----QRVANQQQDAR-PDSQL-----  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPa-----QRLAAQSDGTQ-EAAVS-----  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G-----EKM...SGPTDVVNEKTDEEVTISQSGT...VTNSGTASAVNGGAGSVEANGIAMEIKATKKEAEEEAFTVFVAFARISGTVKKGQKLYLPGKHPDSQVEEG  
900a-----920a-----940a-----960a-----980a-----  
Myessoensis.XP\_021350409.1\_elongation\_factor\_2like-----ESQ-----  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu-----DEEDS-----  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250-----DPEDS-----  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel-----DEEDS-----  
Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea-----DEEDS-----  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea-----DEEDS-----  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r-----DEEDS-----  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r-----DEEDS-----  
Hsapie...NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ribo-----DEEDS-----  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri-----DEEDS-----  
Aplanci.LOC10989613\_116\_kDa\_U5\_small\_nuclear\_ribo-----DEEDS-----  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657-----SNTDL-----  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281-----KKDDL-----  
Myessoensis.XP\_021349219.1\_elongation\_factor\_2like-----NNKSADL-----  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2-----KKDDC-----  
Myessoensis.XP\_021362159.1\_elongation\_factor\_2like-----KKDDL-----  
Lanatina.XP\_013394736.1\_elongation\_factor\_2-----KKEDL-----  
Cintestinalis.LOC100177993\_elongation\_factor\_2like-----KKEDL-----  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo-----LDAPFLTNSLIYI-----  
Hsapie...NP\_001952.1\_elongation\_factor\_2-----KKEDL-----  
Bbelcheri.LOC109464429\_elongation\_factor\_2like-----KKEDL-----  
Aplanci.LOC110987647\_elongation\_factor\_2like-----KKEDL-----  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507-----KKDDL-----  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438-----KKDDL-----  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati-----KKEDL-----  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT\_LLDPANADLP...LGPLRIPEEDDLTSLVQARHRSSSCSSISSNLGAFSAGSVGDSGHDDQVLRHVYVGIT-DVVQFCGGQNNAFHLKDPSCPIDLS  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661-----DLNELSVRS-----ISHVV-----  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel-----K-----EGEAPYA-----  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G-----EDSELEEA-----INSNPHI-----  
Hsapie...NP\_078856.4\_elongation\_factor-like\_GTPase-----VPLGFSAPPDG-----LPQVPHM-----  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas-----QLSDAPDG-----LSQLKHV-----  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase-----DEGVMSFVES-----EVS...SSV-----  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPa-----EIEGEGTSD...LTSVSELTSGHHI-----  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G-----AVRVGGSVDD-----LGTHDHI-----  
1000a-----1020a-----1040a-----1060a-----1080a-----  
Myessoensis.XP\_021350409.1\_elongation\_factor\_2like-----CGNLCAIRGVE--QMIAKMGVVTSH-----SSPVVFTDIR--HSVSPVQLDIDQKN--PGDANPLLIEIKRLMKLHPVLECSIAASG  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu-----AGNWVLIEGVD--QAIVKTSTITSAHSD-----SEAFIFHPLT--FNTISVIVKIAVEPVN--PSELPMKLDGLRKVNKSVPLLT...KVEESG  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250-----AGNWVLIEGVD--QSIK...TATIVDSGLVRGRTHATNIDDDVQIFRPLK--FNTTSVIVKIAVEPVN--PSELPMKLDGLRKVNKSVPLLT...KVEESG  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel-----AGNWVLIEGID--QCIVKTSTIVDINV--EDLVIFRPLK--FNTQSIKIAVEPVN--PSELPMKLDGLRKVNKSVPLLT...KVEESG  
Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea-----AGNWVLIEGID--QPIVKTATITDVSGH--NEVHIFRPLK--FNTNSVMKIAVEPVN--PSELPMKLDGLRKVNKSVPLLT...KVEESG  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea-----AGNWVLIEGVD--EPIVKTSTITQARGN--EAAHIFRPLK--FNTSSSVKIAVEPVN--PSELPMKLDGLRKVNKSVPLLT...KVEESG  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r-----AGNWVLIEGID--QPIVKTSTITTEATGN--EAAFIFRPLK--FNTSSSVKIAVEPVN--PSELPMKLDGLRKVNKSVPLLT...KVEESG  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r-----AGNWVLIEGID--QPIVKTSTITTEATGN--EAAFIFRPLK--FNTSSSVKIAVEPVN--PSELPMKLDGLRKVNKSVPLLT...KVEESG  
Hsapie...NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ribo-----AGNWVLIEGVD--QPIVKTATITTEPRGN--EAAQIFRPLK--FNTTSVIVKIAVEPVN--PSELPMKLDGLRKVNKSVPLLT...KVEESG  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri-----AGNWVLIEGVD--QPIVKTSTITTEARGN--DEAVIFRSLK--FNTSSSVKIAVEPVN--PSELPMKLDGLRKVNKSVPLLT...KVEESG  
Aplanci.LOC110989613\_116\_kDa\_U5\_small\_nuclear\_ribo-----AGNWVLIEGVD--EPIVKTSTITTESRGL--DEVVIFRPLK--FNTSSSVKIAVEPVN--PSELPMKLDGLRKVNKSVPLLT...KVEESG

Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 AGNVVALTGID--KCLLKTATITTN-----AEAHNFRVMK----FVSFPPVVRVAVDKD---PADHAKLVGDLKKLVQADSLVQLVNLN-G

Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 CGNICGLIGID--RYLKNGTITTY-----ENAYLIRMKK----FHVSPPLVRVAVEPTN---VEDLPKLEKLYLNQDPIVECTWEESG

Myessoensis.XP\_021349219.1\_elongation\_factor\_2like CGNTVGLVGLD--KYLKSGSTVSTY-----QAHNMVAVMR----FVSFPPVVRVAVDPVN---AAELPKLLEGLQRLTKSDPMVQCITEN-G

Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 CGNICGLVGLD--QFLVKTGTITTF-----SGAHNMQRMK----FVSFPPVVRVAVDCKN---PSDLPKLVEGLKRLAKSDPMVLIIQTEESG

Myessoensis.XP\_021362159.1\_elongation\_factor\_2like CGNICGLVGLD--QFLVKTGTITTF-----EGAHNLKQMK----FVSFPPVVRVAVECTN---PSLPLKLVGELKRLAKSDPMVQCTTEESG

Lanatina.XP\_013394736.1\_elongation\_factor\_2 CGNICGLVGLD--QFLVKTGTITTF-----DQAHNMKMKK----FVSFPPVVRVAVEAKN---PAELPKLVEGLKRLAKSDPMVLCIEESG

Cintestinalis.LOC100177993\_elongation\_factor\_2like CGNICGLVGLD--NFLVKTGTLTTS-----DQAHNMKQMK----FVSFPPVVRVAVEAKN---PSDLPKLVEGLKRLAKSDPMVLCQIEESG

Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo CGNICGLVGLD--NFLVKTGTLTTS-----DQAHNMKQMK----FVSFPPVVRVAVEAKN---PSDLPKLVEGLKRLAKSDPMVLCIEESG

Hsapiens.NP\_001952.1\_elongation\_factor\_2 CGNIVGLVGLD--QFLVKTGTITTF-----EHAHNMRVMK----FVSFPPVVRVAVEAKN---PADLPKLVEGLKRLAKSDPMVQCIIEESG

Bbelcheri.LOC109464429\_elongation\_factor\_2like CGNIVGLVGLD--QYLVTGTLTSTF-----EHAHNLRVMK----FVSFPPVVRVAVEPKN---PSLPLKLVGELKRLAKSDPMVQCIIEESG

Aplanci.LOC110987647\_elongation\_factor\_2like CGNIVGLVGLD--QYLVTGTISTY-----DNAHNMKVMK----FVSFPPVVRVAVEAKD---PSQLPKLVEGLKRLAKSDPMVQCIIEESG

Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507 CGNICGLVGLD--QYLKTGTITTF-----ENAHNLRVMK----FVSFPPVVRVAVEPRN---PADLPKLVEGLKRLAKSDPMVQCIIEESG

Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438 CGNICGLVGLD--QYLKTGTITTF-----ENAHNLRVMK----FVSFPPVVRVAVEPRN---PADLPKLVEGLKRLAKSDPMVQCIIEESG

Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati SGNICGLVGLD--QFLVKTGTITTF-----KDAHNMKVMK----FVSFPPVVRVAVEPKN---PADLPKLVEGLKRLAKSDPMVQCIIEESG

Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT AGNVVLMGASVITSLPKSLGVSSLRV-----ATSEARRVLP LAGLAIWHGAPVVSIAIEPASATDPNDMVRLENGRLRLERSDPCAEITFSKPG

Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661 AGNIVAIGQLD--SLVLKSATLSTD-----IFCPSFTGLH---FEVSPIVRVAIETKN---PSQMQLRHHGKMLLNQADPIVECTLKDTG

Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel Cintestinalis.LOC100175902\_elongation\_factorlike\_G SGCIGIGGLE---EVVLNSATLCSS-----MACPPFNALT---VDVAPIRVRVAYESYL---LSEMSCLVEGLKRLNQAQPCVQVMVQETG

Hsapiens.NP\_078856.4\_elongation\_factor-like\_GTPase FGMVLIGIGGLQ--DFVLKSATLCSL-----PSCPPFIPLN---FEATPIRVRVAVEPKH---PSEMPQLVGMKMLLNQAQPCVQILIQETG

Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas AGNLTIGIGGLQ--AHVLKSATVSTT-----IACPAFSPTVY---LDAAPIRVRVAVEPKH---AGDMSALMQGLKRLNQAQSSSVELVQESG

Aplanci.LOC110988091\_elongation\_factorlike\_GTPase AGNVLIGIGGLE---ELVLKSATVSTT-----VACPAFTSMT---FAAAPIRVRVAVEPKH---LADMPSLVGMKMLLNQAQPCVVEILVQETG

Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPA AGNVLIGIGGLE---EHVLKSGTSLST-----VACPAFTAMY---FEAAPIRVKVALEPVH---PADMPKLHVGMKMLLNQAQPCVVEILIQETG

Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G AGNLTIGIGGLE---DHILKSGTSTST-----VMCPAFDFY---LDASPIRVRVALEPKH---AGDMVHLVRGMKMLLNQAQPCVQVLVQETG

1100a 1120a 1140a 1160a 1180a

Myessoensis.XP\_021350409.1\_elongation\_factor\_2like LHILGTSTSEHMLRCKSYLEK---QMVLPKPTKLVHAYRETV-----TEEPEML

Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu ERIRGTGELYLDYDCVMHDLRLKLYS-DIEVKVADPVVAFCETV-----VETSSLK

Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 EHILGTGELYLDYDCVMHDLRLMYS-EIDIKVADPVVTFCETV-----VETSSLK

Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel EHVLGTGELYLDYDCVMHDLRLMYS-EIDIKVADPVVAFCETV-----VETSSLK

Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea EHILGTGELYLDYDCVMHDLRLMYS-EIDIKVADPVVTFCETV-----VETSSLK

Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea EHVLGTGELYLDYDCVMHDLRLMYA-EIDIKVADPVVAFCETV-----VDTSSLK

Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r EHIVLTGELYLDYDCVMHDLRLKLYS-EIDIKVADPVVTFCETV-----VETSSLK

Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r EHIVLTGELYLDYDCVMHDLRLKLYS-EIDIKVADPVVTFCETV-----VETSSLK

Hsapiens.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ri EHVLGTGELYLDYDCVMHDLRLMYS-EIDIKVADPVVTFCETV-----VETSSLK

Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri EHVMGTGELYLDYDCVMHDLRLMYS-EIDIKVADPVVAFCETV-----VETSSLK

Aplanci.LOC110989613\_116\_kDa\_U5\_small\_nuclear\_ri EHVLGTGELYLDYDCVMHDLRLMYS-EIDIKVADPVVAFCETV-----VETSSLK

Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 QVIAAAGELHLEICLDLEEDHA-RCPLKVATPIVYRETI-----IAESRQT

Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 EHIVKATSEYHLQHCLTKFFKN---SIKVSDDPIISYCETV-----SQSDRL

Myessoensis.XP\_021349219.1\_elongation\_factor\_2like QHIVAGAGEMHLDICLDLENDHA-CIPIKRSEPVVTYKEGV-----TQSRDRV

Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 EHIIAGAGELHLEICLDLEEDHA-CIPIKKSEPPVVSYRETV-----TEVSSVQ

Myessoensis.XP\_021362159.1\_elongation\_factor\_2like EHIIAGAGELHLEICLDLEEDHA-GISIKKSDPVVSYRETV-----GEISSHV

Lanatina.XP\_013394736.1\_elongation\_factor\_2 EHIIAGAGELHLEICLDLEEDHA-SIPLKVTPPVVSYRETV-----AEMSKMT

Cintestinalis.LOC100177993\_elongation\_factor\_2like EHIVAGAGELHLEIACSTLFCNVCN-VFLIQKSDPVVSYRETV-----FEASSQT

Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo EHIVAGAGELHLEICLDLEEDHA-QIPIKKSDPVVSYRETV-----NEASDRM

Hsapiens.NP\_001952.1\_elongation\_factor\_2 EHIIAGAGELHLEICLDLEEDHA-CIPIKKSDPVVSYRETV-----SEENSVL

Bbelcheri.LOC109464429\_elongation\_factor\_2like EHIVAGAGELHLEICLDLEEDHA-AIPIKKSDPVVSYRETV-----EESDIDM

Aplanci.LOC110987647\_elongation\_factor\_2like EHIVAGAGELHLEICLDLEEDHA-CIPIKKSDPVVSRESV-----SMESKQT

Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507 EHIVAGAGELHLEICLDLEEDHA-CIPIKVSDPVVSYRETV-----SEESDIM

Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438 EHIVAGAGELHLEICLDLEEDHA-CIPIKVSDPVVSYRETV-----SEESDIM

Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati EHIIAGAGELHLEICLDLEEDHA-CIPLKKSDDPVVSYRETV-----SEESDQM

Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT EYLLHAAGEIMHMQCLEDLTTFYAPDLLEHLSPPFVPPRETIVTEACPPASYPVFPDSLAFAKAQLERLEKEHLYDDARENCVRLCTSNEEEEAFLOQQS

Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661 EYILSTAGEVHLQRICDLDLTKRIA-RIEIIVSAPIIPFRETI-----IPPPKVDVFNESLANHQH---QMKSN---KITKE---RPWQ

Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel EHVIITLGEVHVEKCVHDLLEQSYA-KIKVNSKPIVSPFRETI-----VPAATVDMVNEAIVKT-----AEDKD

Cintestinalis.LOC100175902\_elongation\_factorlike\_G EHVI IAAGEVHLQRICDLDLKNRFA-KIEIKSSAIPVFPRETV-----IPRPKVDVNLNETIQDK---DIMQKNWLKDKESGGGNLTKESEK

Hsapiens.NP\_078856.4\_elongation\_factor-like\_GTPase EHVLVTAGEVHLQRICDLDLKERFA-KIHIVSSEPIIPFRETI-----TKPKKVDVNEIEGHQKQ---VAVH---QMKEDQSKSIPGEG

Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas EHVLVTAGEVHLQRICDLDLTKRFA-KIELNVSDPMVPFRETI-----IPPPKVDVNEVIDHDNTN---RITKS---GKEAT---DE-K

Aplanci.LOC110988091\_elongation\_factorlike\_GTPase EHVI VAAGEVHLERCLDLDLDRFA-KIEIIVNSPPIVFPRETI-----IVPPKVDVNEVIDDINQ---IQRT---SNISE---FESE

Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPA EHVI MAAGEVHLQRICDLDLIRERYS-KIELNVSAIPVFPRETI-----VPPTVDRVNEAITNEKQV---SMAIQ---ENSDE---EDIE

Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G EHVIITAGEVHLQRICDLDLRYRYA-KIGLHASSPIVFPRETI-----INPPKVDVNEAVQDQPI---KTARA---KEFED---DE-E

1200a 1220a 1240a 1260a 1280a

Myessoensis.XP\_021350409.1\_elongation\_factor\_2like -----CTAVCPNN-----KKNEISIKT---KPLPNGLCECIEEGF

Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu -----CFSESNNK-----KNKITMIA---EPLDKGLAEDIENK-V

Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 -----CFAETPNK-----KNKITMIA---EPLKGLAEDIQEV-V

Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel -----CFAETPNK-----KNKITMIS---EPLKGLAEDIENG-T

Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea -----CFAETPNK-----R

Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea -----CFAETPNR-----KNKITMIA---EPLKGLAEDIENE-V

Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r -----CFAETPNK-----KSEMSLRSMQPPNRNRTGE

Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r -----CFAETPNK-----KNKITMIA---EPLKGLAEDIENE-V

Hsapiens.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ri -----CFAETPNK-----KNKITMIA---EPLKGLAEDIENE-V

Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri -----CFAETPNK-----KNKITMIA---EPLKGLAEDIENE-V

Aplanci.LOC110989613\_116\_kDa\_U5\_small\_nuclear\_ri -----CFAETPNK-----KNKITMIA---EPLKGLAEDIENE-V

Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 -----AFTKTTNK-----HNKFFMRA---LPLEEGLAEAIESG-R

Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 -----CLSKSPNK-----HSRIYMTA---QPLPGLAEDIEND-R

Myessoensis.XP\_021349219.1\_elongation\_factor\_2like -----CLAKSFNK-----LCRLMNTA---EPLLETLCEDIDEG-K

Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 -----ALSKSPNK-----HNRLLFRA---EPLGEELTKIEDDN-V

Myessoensis.XP\_021362159.1\_elongation\_factor\_2like -----CLSKSPNK-----HNRILYMK---QPLSSDCAVDIDDG-K

Lanatina.XP\_013394736.1\_elongation\_factor\_2like -----CLSKSPNK-----HNRILYMTA---QPMPDGLPKDIDDG-K

Cintestinalis.LOC100177993\_elongation\_factor\_2like -----CLSKSHNK-----HNRILYMTA---EPLPDGLPEKIDEGDK

Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo -----CLSKSPNK-----HNRILFMTA---QPLPEGLSEKIDEGDK

Hsapiens.NP\_001952.1\_elongation\_factor\_2like -----CLSKSPNK-----HNRILYMK---RFPFDGLAEDIDKG-E

Bbelcheri.LOC109464429\_elongation\_factor\_2like -----CLSKSPNK-----HNRILFMKA---RPLTEGIAEDIDRG-D

Aplanci.LOC110987647\_elongation\_factor\_2like -----CLSKSPNK-----HNRILFMRC---LPPFDGLSEDIEKD-E

Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507 -----CLSKSPNK-----HNRILFLKA---RPMPDGLAEDIDKG-E

Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438 -----CLSKSPNK-----HNRILFLKA---RPMPDGLAEDIDKG-E

Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati -----CLSKSPNK-----HNRLLMKA---LPMPDGLPEDIDNG-D

Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT L-----QQTCTMETSPTRYLPLGMLQLPHSKSRTRVFRVFTA---HPVENLLTWLETRAAAYMHLLMRVAVKHKS

Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661 L-----LEDGLIELSTQNG-----QCQVQIRA---VPLPAGITCLDENTS---LLVAIEQAQ-----GRDDRK

Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel L-----VSKKIAVQTLNK-----LGTLLKIVA---VPLPAEAVELLETHSE---FFKEALAIIP-----RNQLLSEKWTALIA

Cintestinalis.LOC100175902\_elongation\_factorlike\_G L-----LNNAKSKKGIIVMTEPNK-----QSTLVVRA---VSLPPDVIKLLENGD---LLKVLSSMEAFKFDLWFHRRRLSTGNSISSQGE

Hsapiens.NP\_078856.4\_elongation\_factor-like\_GTPase V-----DSDGLITITTPNK-----LTLISVRA---MPLPEEVTOILEENDS---LIRSMELT-----SS-----LNEGE

Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPas L-----KWGGPVLVQTPNK-----LCSLKVSA---MPLPEDI SNLDNNAD---LLRTLDD-----KMTKSSGDISRHOA

Aplanci.LOC110988091\_elongation\_factorlike\_GTPase I-----SKDGSLDLTKSNK-----LSSCFRLA---RPLPEEVTKLLEVNNE---LIRILDQTS-----VAVLSRR---TNEQD

Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPA L-----IPEGLVETLTPNR-----MCTIRLRA---IPLPYEVAKIIDDHAE---LIRILKQYS-----MARVEK-----ETDQA

Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G V-----IETGLVEMYTTNQ-----KCCIRIRA---VSLPDAVTDLLEQNVN---LLKTLHGLN---RAKVVYQNSKVKDGTGV

1300a 1320a 1340a 1360a 1380a

Myessoensis.XP\_021350409.1\_elongation\_factor\_2like -----ISADQDPEARAEYALKNFG-----YDVS-----EADRLWSFGGSSGNNLLYY-----

Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu -----VRIDWPKQKQLEFFLKKYE-----WDLL-----AARSIAWFGPDSTGPNILVDDTLP-----

Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 -----VHIGWNKKRISDFQNRVE-----WDIL-----AARSIAWFGPDINGPNILDDTLS-----

Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel -----VCINWNKKRIGEFFQVNYD-----WDLL-----AARSIAWFGPDSTGPNILVDDTLP-----

Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea -----

Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea-----VQIGWNRKRLGEFFQTKYD-----WDLL-----AARSIWAFGPDAAAGPNILVDDTLP-----  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclea\_r-----VDRLFPQPG-----WHTLLSWHPVWVSHITLWRFPP-----  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclea\_r-----VQITWPRKRLGEFFQTKYD-----WDLL-----AARSIWAFGPDATGPNILVDDTLP-----  
Hsapies.NP\_004238.3\_116\_kDa\_U5\_small\_nuclea\_ribo-----VQITWNRKRLGEFFQTKYD-----WDLL-----AARSIWAFGPDATGPNILVDDTLP-----  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclea\_ri-----VRITWNRKRLGEFFQTKYD-----WDLL-----AARSIWAFGPDNTGPNILVDDTLP-----  
Aplanci.LOC110989613\_116\_kDa\_U5\_small\_nuclea\_ribo-----VQINWNRKRLGEFFQTKYD-----WDLL-----AARSIWAFGPDATGPNILVDDTLP-----  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657-----ISSKQDPKVRSKILVEEFG-----WDLP-----STKKIWAFGPHDNGPNILVD-----  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281-----IIFNQDIKTRTQVLYVESYN-----FDVT-----DARKIWCFGPNENGPNMLID-----  
Myessoensis.XP\_021349219.1\_elongation\_factor\_2like-----VKATQDVVRERAQYLAANYG-----FDNQ-----EARKIWCFGPNNGPNMLVD-----  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2-----VTAKQDPKARGRILTENYG-----WDAT-----DARKIWCFGPDRTGPNVVD-----  
Myessoensis.XP\_021362159.1\_elongation\_factor\_2like-----IAPRQDFKERGKYLTETHN-----FDPT-----EARKIWSFGPEGTGNPLVD-----  
Lanatina.XP\_013394736.1\_elongation\_factor\_2-----VTPRQDPKERGKYLDATYD-----WDVN-----EARKIWSFGPEGTGNPMVID-----  
Cintestinalis.LOC100177993\_elongation\_factor\_2like-----IFPRQDAKLGRVLDNFG-----FVVN-----EARKIWCFGPEGTGNLLID-----  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo-----IFPRQDAKLGRVLDNFD-----FDVN-----EARKIWCFGPEGTGNLLID-----  
Hsapies.NP\_001952.1\_elongation\_factor\_2-----VSAQELKQARYLAEKYE-----WDVA-----EARKIWCFGPDGTGPNILTD-----  
Bbelcheri.LOC109464429\_elongation\_factor\_2like-----INARDDIKTRARKLADYD-----WDVT-----EARKIWCFGPDNGPNMLVD-----  
Aplanci.LOC110987647\_elongation\_factor\_2like-----ITSRTEPKARGFLADKYD-----YEVN-----EARKIWCFGPEGTGNLLID-----  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507-----VTPRQEFKARARYLNEKYD-----YDVN-----EARKIWCFGPEGTGNLLMD-----  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438-----VTPRQEFKARARYLNEKYD-----YDVN-----EARKIWCFGPEGTGNLLMD-----  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati-----QLNDQTLNETIKQLREKLNEEFIAANDK-----YDVT-----EARKIWCFGPDGTGPNFIID-----  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT-----SSSRALTLCKRFEFEESQDLDAVPEACYFLEWH-S-----LKGRLLCLGPGQVQVGNLLSLRLRSNF-----  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661-----SIKVLTAALKDLQ-----LFLGSLTSL-----PE-E-----LVNRIWALGPNRCGTNILLN-LSD-----  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel-----QNDQTLNETIKQLREKLNEEFIAANDK-----YDVT-----EARKIWCFGPDGTGPNFIID-----  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G-----EDGAEIPSLNNVTISVKNIIKNVLFQ-----KWS-N-----AVEHIWAFGPRNGPNILNKEDD-----  
Hsapies.NP\_078856.4\_elongation\_factor-like\_GTPase-----MIHQKTQEKIWEFKGKLEHQLT-----GRR-----WR-N-----IVDQIWSFGPRKCGPNILVNKSED-----  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPase-----KVTAEITNRLTELKSTLEAKFAQAGKH-----YR-G-----AIDQIWSFGPRKCGPNILNVRVAG-----  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase-----SLTAEITLAQLREFQNTLDAFAFANAGKK-----WR-G-----AADRIWSFGPRKCGPNILNLCIDG-----  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPA-----AER-----WN-G-----VNNRIVSFGPRKCGPNILNRIPE-----  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G-----KDK-----GVKDTVLEALSHFKSSLKAFTEEGKT-----WT-D-----VDINIWAFGPRKCGPNILNVRVAG-----  
1400a 1420a 1440a 1460a 1480a  
Myessoensis.XP\_021350409.1\_elongation\_factor\_2like-----ISKQV-----RDQGHIKDSIISGFQWAAREGILCEESMRGVRIEVRAY-----WQL-----  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclea\_ribonu-----SEVDKGL-----LGS-----VRDYIVQGFQWGTREGPLCDEP IRNVKFKILD-----ALI-----  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250-----HEVNKTL-----LTSEPVKESIVQGFQWATREGPLCDEP IRNVKFKILD-----ASI-----  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel-----SEVDKNL-----LTA-----VKDSIVQGFQWGTREGPLCDEP IRNVKFKILD-----GVI-----  
Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea-----SEVDKSL-----LGS-----VKDSIVQGFQWGSREGPLCDEP IRNVKFKILD-----AVI-----  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea-----L-----LTV-----CLQCIL-----YWLGEVML-KTLOSQAHHCTQ-----SKL-----  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclea\_r-----SEVDKGL-----LNS-----VKDSIVQGFQWGTREGPLCDEP IRNVKFKILD-----AVI-----  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclea\_r-----SEVDKAL-----LGS-----VKDSIVQGFQWGTREGPLCDELIRNVKFKILD-----AVV-----  
Hsapies.NP\_004238.3\_116\_kDa\_U5\_small\_nuclea\_ribo-----SEVDKGL-----LNS-----VKDSIVQGFQWGTREGPLCDEP IRNVKFKILD-----AVI-----  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclea\_ri-----SEVDKAL-----LNS-----VKDSIVQGFQWGTREGPLCDEP IRNVKFKILD-----AVI-----  
Aplanci.LOC110989613\_116\_kDa\_U5\_small\_nuclea\_ribo-----SEVDKGL-----LNS-----VKDSIVQGFQWGTREGPLCDEP IRNVKFKILD-----AVI-----  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657-----ATKSV-----DGLSNIQDAVVAQFOWTTOGCVASENLRGVRIELLD-----AEI-----  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281-----CTKGV-----QYLSEFKDFLLKMFQFTTKNGILIEENLRNIRFDIHD-----ITH-----  
Myessoensis.XP\_021349219.1\_elongation\_factor\_2like-----AKSV-----QYLDQIRIVRAGFQWSTEGVCEENMRGVQFNQD-----AHI-----  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2-----VTKGV-----QYLMIDKDSVVAQFQVMTDGLCDENMRGIRFNIED-----VVL-----  
Myessoensis.XP\_021362159.1\_elongation\_factor\_2like-----VTKGV-----QYLAELKDSVVVGFQWATKEGVLCDEENVRGVRFDIHD-----VTL-----  
Lanatina.XP\_013394736.1\_elongation\_factor\_2-----VTKGV-----QYLINEIKESVAGFQWATKEGVLCDEENMRGVRFNCD-----VTL-----  
Cintestinalis.LOC100177993\_elongation\_factor\_2like-----CTKAV-----QYLSQIKDSVVAGFQWASKEGVLCDEENMRGIRFNIDH-----VTL-----  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo-----CTKAV-----QYLINEIKDSVVAGFQWASKEGVLCDEENMRGIRFNIDH-----VTL-----  
Hsapies.NP\_001952.1\_elongation\_factor\_2-----ITKGV-----QYLINEIKDSVVAGFQWATKEGALCEENMRGVRFDIHD-----VTL-----  
Bbelcheri.LOC109464429\_elongation\_factor\_2like-----CTKGV-----QYLINEIKDSVVAGFQWASKEGVLCDEENMRGIRVFIHD-----VTL-----  
Aplanci.LOC110987647\_elongation\_factor\_2like-----CTKGV-----QYLINEIKDSVVAGFQWATKEGVLCDEENVRGVRFNIDH-----VTL-----  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507-----CTKGV-----QYLINEIKDSIAGFQWATKEGVLAENVRGVRFDIHD-----VTL-----  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438-----CTKGV-----QYLINEIKDSIAGFQWATKEGVLAENVRGVRFDIHD-----VTL-----  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati-----CTKSV-----QYLINEIKDSVVAGFQWASKEGILADENLRGVRFNIYD-----VTL-----  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT-----FRLDTAWGKPMSPWSDAAGQPGADAVPTGEVGGGAVHIFPL-----SYGKAILRGFQVATEQGLCAEPMRGVAFVLEDIYAEDRIQLTPRILTSADLLAKE-----  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661-----HRGSTIWANVLNNEEKITNS-----LMKDDYDLSIVNGFQLATAGSGICEEP LMVGFI IER-----LTI-----  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel-----YEQPDFWSSHAKSDTDRSKTD-----PRK-DFNSSLVNGFQITISVAGLCEEPMGVCFAVLE-----WSI-----  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G-----YRRPSIWTVCVG-----NVDIDIG-----SYR-ECDSHISIGFQLATLSGPLCEEPMGVCFAVLE-----WKV-----  
Hsapies.NP\_078856.4\_elongation\_factor-like\_GTPase-----FQN-SVWTGPAD-----KASKEAS-----YR- DLGNSIVSGFQLATLSGPMCEEP LMGVCFVLEK-----WDL-----  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPase-----YQRPSVWDSIDK-----GEVKSAA-----QFR-PFDHAIGSGFQLATLAGLCEEP LMGVCFVLEE-----WTMHGQLSEK-----  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase-----YNRPAIWHCLD-----EEKDRAG-----EIR-DFDSSVSGFQLATFAGLCEEPMGVCII IEN-----WTMEHSNSD-----  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPA-----YDRPSIWSCLSTIE-DQVAKVG-----KIR-EYDSNIVSGFQLATLQGMCEEPMGVCFSVEK-----WEM-----  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G-----YDRPSVW-----DIQSGSEG-----LLR-DFDSNIVSGFQLATLAGLCEEP LRGVCFVIEK-----WEYLDMSYAK-----  
1500a 1520a 1540a 1560a 1580a  
Myessoensis.XP\_021350409.1\_elongation\_factor\_2like-----ADD-----SGEAHQGS-----  
Egranulosus.XP\_024347861.1\_U5\_small\_nuclea\_ribonu-----AQEP IHRGG-----ANEALHRGG-----  
Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250-----ANEALHRGG-----ANEPLHRGG-----  
Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel-----ANEPLHRGG-----AGEPLHRGG-----  
Myessoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea-----AGEPLHRGG-----AGEPLHRGG-----  
Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea-----AGEPLHRGG-----AGEPLHRGG-----  
Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclea\_r-----AGEPLHRGG-----AGEPLHRGG-----  
Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclea\_r-----AGEPLHRGG-----AGEPLHRGG-----  
Hsapies.NP\_004238.3\_116\_kDa\_U5\_small\_nuclea\_ribo-----AGEPLHRGG-----AGEPLHRGG-----  
Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclea\_ri-----AGEPLHRGG-----AGEPLHRGG-----  
Aplanci.LOC110989613\_116\_kDa\_U5\_small\_nuclea\_ribo-----AGEPLHRGG-----AGEPLHRGG-----  
Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657-----HRDSAHRPP-----TPDAIHRGG-----  
Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281-----TPDAIHRGG-----HSDPAHRGG-----  
Myessoensis.XP\_021349219.1\_elongation\_factor\_2like-----HSDPAHRGG-----HADA IHRGG-----  
Egranulosus.XP\_024354781.1\_Elongation\_factor\_2-----HADA IHRGG-----HADA IHRGG-----  
Myessoensis.XP\_021362159.1\_elongation\_factor\_2like-----HADA IHRGG-----HADA IHRGG-----  
Lanatina.XP\_013394736.1\_elongation\_factor\_2-----HADA IHRGG-----HADA IHRGG-----  
Cintestinalis.LOC100177993\_elongation\_factor\_2like-----HADA IHRGG-----HADA IHRGG-----  
Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo-----HADA IHRGG-----HADA IHRGG-----  
Hsapies.NP\_001952.1\_elongation\_factor\_2-----HADA IHRGG-----HADA IHRGG-----  
Bbelcheri.LOC109464429\_elongation\_factor\_2like-----HADA IHRGG-----HADA IHRGG-----  
Aplanci.LOC110987647\_elongation\_factor\_2like-----HADA IHRGG-----HADA IHRGG-----  
Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507-----HADA IHRGG-----HADA IHRGG-----  
Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438-----HADA IHRGG-----HADA IHRGG-----  
Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati-----HADA IHRGG-----HADA IHRGG-----  
Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT-----ATHEVAAELKKANEPAPPEVGEAAVESDPIALAAKRAQAAIKRRQKADFISSMSWLNLRDDDDNANNEDGEDGCDLDDGDWYNDNDNDQNLESEVEE-----  
Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661-----NTIVSN-----QESSETVDNTDNDTDLA-----TNTTAVTPNPDIEISLIETLSVT-----  
Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel-----QSEGEDL-----  
Cintestinalis.LOC100175902\_elongation\_factorlike\_G-----SAPPV-----SSQEHKTEKEQVITFA-----DDLTPVQSNQ-----  
Hsapies.NP\_078856.4\_elongation\_factor-like\_GTPase-----SKFEQ-----GASDLAKEGQEE-NEFC-----SGNGENQELQDGCSEAFEKRTS-----  
Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPase-----RTTKNNDALTNDSFNAVS-----REETETEGESVSSEHS-----DASDTVTGMSPCSHSVSPREHR-----  
Aplanci.LOC110988091\_elongation\_factorlike\_GTPase-----RFFGASQTSSEILNVANES-----RLSSNKSSRSSENFCSI-----DAEVSTTSVSRSDELQEP IKGK-----  
Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPA-----HSEPQ-----LPSTLDEEEDENGELQP-----NQLKNNSTAKPKPDASLEPG-----  
Myessoensis.XP\_021362732.1\_elongation\_factorlike\_G-----LARISESDD-----KLTDLSSSVK-NL I1-----EEVDKCMDSKDEDSCEEV-----

1600a 1620a 1640a 1660a 1680a

Mysoensis.XP\_021350409.1\_elongation\_factor\_2like Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel\_ Mysoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r Hsapies.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ri Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri Aplanci.LOC10989613\_116\_kDa\_U5\_small\_nuclear\_ri Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 Mysoensis.XP\_021349219.1\_elongation\_factor\_2like Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 Mysoensis.XP\_021362159.1\_elongation\_factor\_2like Lanatina.XP\_013394736.1\_elongation\_factor\_2 Cintestinalis.LOC100177993\_elongation\_factor\_2like Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo Hsapies.NP\_001952.1\_elongation\_factor\_2 Bbelcheri.LOC109464429\_elongation\_factor\_2like Aplanci.LOC10987647\_elongation\_factor\_2like Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507 Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438 Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661 Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel Cintestinalis.LOC100175902\_elongation\_factorlike\_G Hsapies.NP\_078856.4\_elongation\_factor-like\_GTPase Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPase Aplanci.LOC10988091\_elongation\_factorlike\_GTPase Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPase Mysoensis.XP\_021362732.1\_elongation\_factorlike\_G

1700a 1720a 1740a 1760a 1780a

Mysoensis.XP\_021350409.1\_elongation\_factor\_2like Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel\_ Mysoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r Hsapies.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ri Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri Aplanci.LOC10989613\_116\_kDa\_U5\_small\_nuclear\_ri Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 Mysoensis.XP\_021349219.1\_elongation\_factor\_2like Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 Mysoensis.XP\_021362159.1\_elongation\_factor\_2like Lanatina.XP\_013394736.1\_elongation\_factor\_2 Cintestinalis.LOC100177993\_elongation\_factor\_2like Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo Hsapies.NP\_001952.1\_elongation\_factor\_2 Bbelcheri.LOC109464429\_elongation\_factor\_2like Aplanci.LOC10987647\_elongation\_factor\_2like Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507 Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438 Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661 Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel Cintestinalis.LOC100175902\_elongation\_factorlike\_G Hsapies.NP\_078856.4\_elongation\_factor-like\_GTPase Bbelcheri.LOC109463052\_elongation\_factorlike\_GTPase Aplanci.LOC10988091\_elongation\_factorlike\_GTPase Lanatina.XP\_013413557.1\_elongation\_factorlike\_GTPase Mysoensis.XP\_021362732.1\_elongation\_factorlike\_G

1800a 1820a 1840a 1860a 1880a

Mysoensis.XP\_021350409.1\_elongation\_factor\_2like Egranulosus.XP\_024347861.1\_U5\_small\_nuclear\_ribonu Avaga.UJR09000.1\_hypothetical\_protein\_I4U23\_013250 Dmelanogaster.CG4849\_uncharacterized\_protein\_Dmel\_ Mysoensis.XP\_021345506.1\_116\_kDa\_U5\_small\_nuclea Cintestinalis.LOC100175824\_116\_kDa\_U5\_small\_nuclea Lanatina.XP\_013419342.1\_116\_kDa\_U5\_small\_nuclear\_r Lanatina.XP\_023933490.1\_116\_kDa\_U5\_small\_nuclear\_r Hsapies.NP\_004238.3\_116\_kDa\_U5\_small\_nuclear\_ri Bbelcheri.LOC109461499\_116\_kDa\_U5\_small\_nuclear\_ri Aplanci.LOC10989613\_116\_kDa\_U5\_small\_nuclear\_ri Avaga.UJR26319.1\_hypothetical\_protein\_I4U23\_007657 Avaga.UJR19151.1\_hypothetical\_protein\_I4U23\_022281 Mysoensis.XP\_021349219.1\_elongation\_factor\_2like Egranulosus.XP\_024354781.1\_Elongation\_factor\_2 Mysoensis.XP\_021362159.1\_elongation\_factor\_2like Lanatina.XP\_013394736.1\_elongation\_factor\_2 Cintestinalis.LOC100177993\_elongation\_factor\_2like Cintestinalis.LOC100178953\_LOW\_QUALITY\_PROTEIN\_elo Hsapies.NP\_001952.1\_elongation\_factor\_2 Bbelcheri.LOC109464429\_elongation\_factor\_2like Aplanci.LOC10987647\_elongation\_factor\_2like Avaga.UJR10301.1\_hypothetical\_protein\_I4U23\_014507 Avaga.UJR35689.1\_hypothetical\_protein\_I4U23\_028438 Dmelanogaster.eEF2\_eukaryotic\_translation\_elongati Egranulosus.XP\_024355481.1\_Elongation\_factor\_Tu\_GT Avaga.UJR28421.1\_hypothetical\_protein\_I4U23\_009661 Dmelanogaster.CG33158\_uncharacterized\_protein\_Dmel

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Cintestinalis.LOC100175902_elongation_factorlike_G -----
Hsapiens.NP_078856.4_elongation_factor-like_GTPase -----EEY--LHFGEKADSENQARKYMNAVRKRKGLYVEE-KIVEHAEKQRTLSSKNK-----
Bbelcheri.LOC109463052_elongation_factorlike_GTPas -----EEL--MHFGEKADSENQGRLYMNSVRRRKGLYVDE-KIVEHAEKQRTLSSKNK-----
Aplanci.LOC110988091_elongation_factorlike_GTPase_ -----EEL--LHFGEKAENENQALKYMNGVRRRKGLYIDK-KTVEHAEKQRTLSSKNK-----
Lanatina.XP_013413557.1_elongation_factorlike_GTPa -----EEY--MHFGEKADSENRRARIYMDNVRRRKGLKVDE-RIVEFAEKQRTLSSKKK-----
Myessoensis.XP_021362732.1_elongation_factorlike_G -----EEY--LHFGEKADSDNKARQYVNAVRKRKGLKVDE-KIVEHAEKQRTLTRNK-----
                                     1900â          1920â          1940â          1960â          1980â

Number of sequences: 34
Alignment width: 1984
Sequence type: aa
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