Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu		
		EKEDHSHAMQLLEKTDEAFSVVLHDDKKYYPSAMEVYGPDV
		SNVDQTSDMEDDRDEAEGEDISVDVSNLSTAVVLHEDKKYYPSALELYGPDV
Dmelanogaster.CG4849_uncharacterized_protein_Dmel_		
		YGADEDEDMDADDADDVA-EMQVVLHEDKKYYPTAEEVYGPEV
		EEEEEREEMEQDTHVTGTEVVLHEDKKYYPSHEEVYGPTV
		EADEEEMDMDRDDDQDIN-DMQVVLHEDKKYYPTPEEVYGPEV EADEEEMDMDRDDDQDIN-DMQVVLHEDKKYYPTPEEVYGPEV
		EMDDDDDDDDDVGDHDDDHPGMEVVLHEDKKYYPTAEEVYGPEV
Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ri		DYGEDEDDADEAMDQDVEPSMAVVLHEDKKYYPSAEEVYGADV
Aplanci.LOC110989613_116_kDa_U5_small_nuclear_ribo		EIEEDEDEQVEAGDISQAVVLHEDKKYYPTAEEVYGPDV
Avaga.UJR26319.1_hypothetical_protein_I4U23_007657	MDADITUE GNI IGI BEDODOEDEBSEBGI EI Q	DIEDDEDEÇVERODI SQRVVBNEDKKIII IABEVIGIDV
Avaga.UJR19151.1_hypothetical_protein_I4U23_022281		
Myessoensis.XP_021349219.1_elongation_factor_2like		
Egranulosus.XP_024354781.1_Elongation_factor_2	MMVVMQGGHTAELLSYVRLLPPAYSPRIYVVASNDNLSDQKASELENT	HQNNDFLVEKLPRAREVGQSYFTSIFTTCYASIIATLLVLKHRPRLVLCNGP
Myessoensis.XP_021362159.1_elongation_factor_2like		
Lanatina.XP_013394736.1_elongation_factor_2		
Cintestinalis.LOC100177993_elongation_factor_2like		
Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo		
Hsapiens.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		
Hsapiens.NP_078856.4_elongation_factor-like_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPas		
Aplanci.LOC110988091_elongation_factorlike_GTPase_		
Lanatina.XP_013413557.1_elongation_factorlike_GTPase_		MUVIUKADK
Myessoensis.XP_021362732.1_elongation_factorlike_G		PingNgn1nk
	Dâ 20â 40â	60â 80â
Myessoensis.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_		
Myessoensis.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	ETIVHEEDTQPLTEPIIAPVKRTKFQVA	
Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_ribo	ETIVQEEDTQPLTEPIIKPVKTKKFTLM	
Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ri	ETIVHEEDTQPLTEPIIKPVKRNKFAHI	
Aplanci.LOC110989613_116_kDa_U5_small_nuclear_ribo	ETIIHEEDTQPLTDPIIAPVKQKKFTMT	
Avaga.UJR26319.1_hypothetical_protein_I4U23_007657		
Avaga.UJR19151.1_hypothetical_protein_I4U23_022281		
Myessoensis.XP_021349219.1_elongation_factor_2like		
Egranulosus.XP_024354781.1_Elongation_factor_2	GTCVPVCLAAWVVHSFMRGSKAVVFVESVCRTRYLSLSGRLLYHLHLA	LVVVQWPHLVKNKNSCLRAIKDDAVTGSGQPSPVNAPARGHLLSRRVVIRGQ
Myessoensis.XP_021362159.1_elongation_factor_2like		
Lanatina.XP_013394736.1_elongation_factor_2		
Cintestinalis.LOC100177993_elongation_factor_2like Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo		
Hsapiens.NP_001952.1_elongation_factor_2		
Bbelcheri.LOC109464429_elongation_factor_2like		
Aplanci.LOC110987647_elongation_factor_2like		
Aplanci.LOC110987647_elongation_factor_2like Avaga.UJR10301.1_hypothetical_protein_I4U23_014507		
Aplanci.LOC110987647_elongation_factor_2like Avaga.UJR10301.1_hypothetical_protein_I4U23_014507 Avaga.UJR35689.1_hypothetical_protein_I4U23_028438		
Aplanci.LOC110987647_elongation_factor_2like Avaga.UJR10301.1_hypothetical_protein_I4U23_014507 Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_eukaryotic_translation_elongati		
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		
Aplanci.LOC110987647_elongation_factor_2like Avaga.UJR10301.1_hypothetical_protein_I4U23_014507 Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_eukaryotic_translation_elongati		
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		
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Hsapiens.NP_078856.4_elongation_factor-like_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPas				MPTVTPCOT A
Aplanci.LOC110988091 elongation factorlike GTPase				MKGVDAEQLS
Lanatina.XP 013413557.1 elongation factorlike GTPa				MKSKSTQKLA
Myessoensis.XP_021362732.1_elongation_factorlike_G	2202	2400	260â	MRTTTPEKLV
200 Myessoensis.XP_021350409.1_elongation_factor_2like	VMKIPESVRNVAVIGGTDS		GMVPLMNGLNRKAGPNL	TAEESGRCRKYDVDPMAANLT
Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu	LMDCPELIRSVAFCGHLHH		GKTSFVDCLIEQTHPDI	RAKEDKDLRYTDYLKLEVERGLSVKSTPM
Avada ILTR09000 1 hypothetical protein T4H23 013250	T.MDSPET.VRNVATCGHT.HH		GKTTFCDAI.TEOTHPYI.	ASTENKELRYTHTLETEGERGVSTKSTPF
Dmelanogaster.CG4849_uncharacterized_protein_Dmel_	LMDTPPLIRNVALVGHLHH		GKTTFVDCLIRQTHPQF	ETMEERQLRYTDTLFTEQERGCSIKATPV
Myessoensis.XP_021345506.1_116_kDa_U5_small_nuclea Cintestinalis.LOC100175824_116_kDa_U5_small_nuclea	LMDTPDLIRNVTLCGHLHH		GKTSFVDCLVSQTHPEI	DGTDDKDIRYTDTLFTEQERGVSIKASPV
Lanatina XP 013419342 1 116 kDa H5 small nuclear r	T.MDNPDT.TRNVAT.CGHT.HH		GKTSFVDSI.VEOTHPEM	ETEEGKDI.RYTDTI.FTEOERGI.STKSI.PV
Lanatina.XP 023933490.1 116 kDa U5 small nuclear r	I.MDNPDI.TRNVAI.CGHI.HH		GKTSFVDSLVEOTHPEM	ETEEGKDLRYTDTLFTEOERGLSTKSLPV
Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_ribo	LMDNSELIRNVTLCGHLHH		GKTCFVDCLIEQTHPEI	RKRYDQDLCYTDILFTEQERGVGIKSTPV
Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ri	LMDNPELIRNVVLAGHLHH		GKTTFVDCLMEQTHPDI	FTKEDRQLRYTDTLFTEQERGVSIKSQPV
Aplanci.LOC110989613_116_kDa_U5_small_nuclear_ribo	MMDNAELIRNVTLAGHLHN		GKTSFVDCLMEQTHPEL	RVKEDGSIRYTDTLFTEQERGVSIKAQPV
Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_022281	T THE THE THE TANK TH		GKSTLTDALVYKAGI-I	TEQQAGQRRFIDSLEAEQERGIIIRSSAV
Myessoensis.XP_021349219.1_elongation_factor_2like	AMDHRTGVRNI.AVIAHVDH		GKTTLTDSLLAKAGV-T	NTDOAGDKCAMDTRKDEOLKGITIKSTAI
Egranulosus.XP_024354781.1_Elongation_factor_2	LMAKNKNIRNMSVIAHVDH		GKSTLTDSLVSKAGI-I	AESRAGDARFTDTRKDEQDRCITIKSTAI
Myessoensis.XP_021362159.1_elongation_factor_2like	IMDNKLNIRNMSVIAHVDH		GKSTLTDSLVSKAGI-I	AGSKAGEARFTDTRKDEQERCITIKSTAI
Lanatina.XP_013394736.1_elongation_factor_2	IMDHKMNIRNMSVIAHVDH		GKSTLTDSLVSKAGI-I	ASAKAGETRFTDTRKDEQERCITIKSTAI
Cintestinalis.LOC100177993_elongation_factor_2like Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo	IMDKKSNIRNMSVIAHVDH		GKSTLTDSLVSKAGI-I	AGSKAGEARFTDTRKDEQDRCITIKSTAI
Hsapiens.NP_001952.1_elongation_factor_2	IMDKKINIKNMSVIAHVDH		GKSTLTDSLVSKAGI-M	ASARAGETRFTDTRKDEQDRC111KS1A1 ASARAGETRFTDTRKDEQERC1T1KSTA1
Bbelcheri.LOC109464429_elongation_factor_2like	VMDKKKNTRNMSVTAHVDH		GKSTLTDSLVSKAGI-I	ASQKAGETRFTDTRKDEQERCITIKSTAI
Aplanci.LOC110987647_elongation_factor_2like	IMDKKANIRNMSVIAHVDH		GKSTLTDSLVSKAGI-I	ASQRAGEARFTDTRKDEQERCITIKSTAI
Avaga.UJR10301.1_hypothetical_protein_I4U23_014507	LMDKKKNIRNMSVIAHVDH		GKSTLTDSLVCKAGI-I	ASQKAGEMRFTDTRKDEQERCITIKSTAI
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438	LMDKKKNIRNMSVIAHVDH		GKSTLTDSLVCKAGI-I	ASQKAGEMRFTDTRKDEQERCITIKSTAI
Dmelanogaster.eEF2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Elongation_factor_Tu_GT				
Egranulosus.xP_U24355481.1_Elongation_factor_fu_G1 Avaga.UJR28421.1_hypothetical_protein_I4U23_009661	LOENTELIRNICTIAHUDH	valibrkrkgvfik1SF1	GKTTI.ADDI.T.ASNGT-T	STRLAGKLRLMDSI.EAEOVRGITMKSSAV
Dmelanogaster.CG33158 uncharacterized protein Dmel	LORRROOVRNICILAHVDH		GKTTLADSLVASNGI-I	SQRMAGKLRYLDNRSDEQERGITMKSSSI
Cintestinalis.LOC100175902_elongation_factorlike_G	LQKNSQNIRNICILAHVDH		GKTTLADALIASNGI-I	SKRMAGKLRYMDSRDDEQLRGITMKSSAI
Hsapiens.NP_078856.4_elongation_factor-like_GTPase	LQKNTANIRNICVLAHVDH		GKTTLADCLISSNGI-I	SSRLAGKLRYMDSREDEQIRGITMKSSAI
Bbelcheri.LOC109463052_elongation_factorlike_GTPas Aplanci.LOC110988091_elongation_factorlike_GTPase_	LQGNPQNVRNICILAHVDH		GKTTLADVLVASNGV-I	SKRLAGKLRYLDSRADEQIRGITMKSSAI
Aplanci.LOCI10988091_elongation_factorlike_GTPase_ Lanatina.XP_013413557.1_elongation_factorlike_GTPa	LOBNDANIBNICII AUVDH		GKTTMADALLSSNG1-1	SSRMAGKLRYMDSRQDEQLRGITMKSSAI
Myessoensis.XP_021362732.1_elongation_factorlike_G	LOKNPSNIRNICILAHVDH		GKIILADVLVASNGI-I	SORMAGKI.RYMDSREDEQVRGIIMKSSAI SORMAGKI.RYMDSREDEOTRGITMKSSAI
300		340â	360â	380â
Myessoensis.XP_021350409.1_elongation_factor_2like	LYHTCAPADLPGMEAVEGN	TDFVINILDTPGSVDFSAEVD	TTLRMMDGAVVMVDCIS	GVTLDTKLVLKQSIRERVKPV
Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu				
Avaga.UJR09000.1_hypothetical_protein_I4U23_013250				
Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nuclea				
Cintestinalis.LOC100175824_116_kDa_U5_small_nuclea	I.TIPDTKC	KSFLVNVFDIFGHVNFSDEVI	AAFRISDGVVVFVDAAE	GVMLNTEGLIKHALGERLSVT
Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r				
Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r				
Hsapiens.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_14U23_022281				
Myessoensis.XP_021349219.1_elongation_factor_2like				
Egranulosus.XP_024354781.1_Elongation_factor_2				FEAIVSLVGVCVQTETVLRQAIAERIKPI
Myessoensis.XP_021362159.1_elongation_factor_2like				
Lanatina.XP_013394736.1_elongation_factor_2 Cintestinalis.LOC100177993_elongation_factor_21ike	LYYELPEKDKDIMFQKYNEE	KGFLINLIDSPGHVDFSSEVI	AALRVIDGALVVVDCVS	GVCVQTETVLRQAIAERIKPV
Cintestinalis.LOC100177993_e10ngation_lactor_zirke Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo	MYYELSDKDMOWVEGKKEC	NGFLINLIDSPGHVDFSSEVI	AALRVIDGALVVVDCVS	GVCVQTETVLRQAISERIRFI
Hsapiens.NP_001952.1_elongation_factor_2				GVCVQTETVLRQAIAERIKPV
Bbelcheri.LOC109464429_elongation_factor_2like	LFYELAEKDMDFVPSEGKESNTE	RGFLINLIDSPGHVDFSSEVT	AALRVTDGALVVVDCVS	GVCVQTETVLRQAISERIKPV
Aplanci.LOC110987647_elongation_factor_2like				GVCVQTETVLRQAIAERIKPV
Avaga.UJR10301.1_hypothetical_protein_I4U23_014507	LYYELPAKDFVFIKQEREPEI	THFLINLIDSPGHVDFSSEVT	AALRVTDGALVVVDCVS	GVCVQTETVLRQAIAERIKPI
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_eukaryotic_translation_elongati	LYYELPAKDFVF1KQEREPE1	THFLINLIDSPGHVDFSSEVI	AALRVIDGALVVVDCVS	GVCVQTETVLRQATAERIKPI
Egranulosus.XP_024355481.1_Elongation_factor_Tu_GT	T.FYNPTI.KI.SRHTSPOAAADDE	NGF LINLIDSPGHVDF SSEVI	TAVRICDCAMIVVDVAE	GVCVQTETVLRQATAERIKFT
Avaga.UJR28421.1 hypothetical protein I4U23 009661	LVHEKED	KKYLINLIDTPGHVDFSSEVS	TAVRLCDGAIILVDVVE	GVCPQTLAALRQAWLEHLRII
Dmelanogaster.CG33158_uncharacterized_protein_Dmel	LYYQEAEEMAGN	PDYLINLIDSPGHVDFSSEVS	TAVRLCDGAIVVVDVVE	GVGPQTRACLRQIYEEQLKPV
Cintestinalis.LOC100175902_elongation_factorlike_G				
<pre>Hsapiens.NP_078856.4_elongation_factor-like_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPas</pre>				
Bbelcheri.LOC109463052_elongation_factorlike_GTPas Aplanci.LOC110988091_elongation_factorlike_GTPase_	I.RFQKES	DDAI'LMI'LDSECHADESSEAS	TATRI.CDGAT.WWW.TWF=	GVCPOTHVVI.DOAMIEHTTEO
Lanatina.XP_013413557.1_elongation_factorlike_GTPa				
Myessoensis.XP_021362732.1_elongation_factorlike_G		QEYLVNLIDSPGHVDFSSEVS	TAVRLCDGAVVVVDVVE	
400		440â	460â	480â
Myessoensis.XP_021350409.1_elongation_factor_2like				
Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1 hypothetical protein I4U23 013250	CINKIDRIWIEI'KI DDOUVAALAIKI KU	ITTDEVNSLIST		r Segagy Slep-yhty SPLLGNVCFA
Dmelanogaster.CG4849_uncharacterized_protein_Dmel_				
Myessoensis.XP_021345506.1_116_kDa_U5_small_nuclea	CINKVDRLILELKLPPTDAYFKLRH	IILEEVNALISV		YAEDEEN-KI-VSPLLGNVCFA
Cintestinalis.LOC100175824_116_kDa_U5_small_nuclea	CINKIDRLILELKLPPADAYFKLRH	IIVDEVNNLLRT		YSDTENIPNVSPLNGNVCFA
Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r	CINKIDRLILELKLPPTDAYYKLRH	IIVDEVNGLIST		FADEEED-MS-VSPLKGNVCFA
Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r	CINKIDRLILELKLPPTDAYYKLRH	IIVDEVNGLIST		
<pre>Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ri</pre>	CINKIDRIMI.EI.KI.DDTDAYYKLRH	IIVDEVNGLISM		ISTDEN-LI-LSPLLGNVCFS
Aplanci.LOC110989613 116 kDa U5 small nuclear ribo	CINKIDRLVLELKLPPADAYYKLRN	IIITEINGLMSV		YSDEAEP-MM-VSPLLGNVCFA
Avaga.UJR26319.1_hypothetical_protein_I4U23_007657	IINKVDRCILEQKVEPEELYQKLSG	GIIARCNALIAT		YRSTDDAIYSD-EH-FNPKIGNVAFA
	FLNKFDEIFLNLQIEYEDIYQHFQR	IIKNINSI		GD-LQ-IHPVKGTVSFG
Avaga.UJR19151.1_hypothetical_protein_I4U23_022281	MLNKLDRCVMEVQLDHEELYRSLCR	TIQSVNNAVDM		YGQPDVMGK-LT-LDPSLGNVAFG
Avaga.UJR19151.1_hypothetical_protein_I4U23_022281 Myessoensis.XP_021349219.1_elongation_factor_2like		VVENVNVIIAQ		FSE-HDGPMGD-VT-VNPGNGTVGFG
Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_024354781.1_Elongation_factor_2	FMNKLDKALSTMGQDPESLYQHLSR	TTDMUMUTUMM		
Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_024354781.1_Elongation_factor_2 Myessoensis.XP_021362159.1_elongation_factor_2like	FMNKMDLALLTLQVDQESLYQNFQR	RIIENVNVIVNM		
Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_024354781.1_Elongation_factor_2 Myessoensis.XP_021362159.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2	FMNKMDLALLTLQVDQESLYQNFQR FMNKMDLGLLTLRLDREAMYTEFQR	RIIENVNVIVNMRTIESVNVIIST		YAS-EDGPMGD-FT-VEPTKGTVGFG
Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_024354781.1_Elongation_factor_2 Myessoensis.XP_021362159.1_elongation_factor_2like	FMNKMDLALLTLQVDQESLYQNFQR FMNKMDLGLLTLRLDREAMYTEFQR FMNKMDRALLELQLEKEDLYQTFQR FMNKMDRALLELQLEKEDLYQTFQR	RIIENVNVIVNMRIIESVNVIISTRIVESVNVIVATRIVESVNVIVATRIVESVNVIVAT		YAS-EDGPMGD-FT-VEPTKGTVGFGYAV-EDGPMGN-IM-IDPQKGTVGFGYAV-EDGPMGN-IM-IDPQKGTVGFG
Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_024354781Elongation_factor_2 Myessoensis.XP_021362159.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2 Cintestinalis.LOC10017993_elongation_factor_2like Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo Hsapiens.NP_001952.1_elongation_factor_2	FMNKMDLALLTLQVDQESLYQNFQR FMNKMDLGLLTLRLDREAMYTEFQR FMNKMDRALLELQLEKEDLYQTFQR FMNKMDRALLELQLEKEDLYQTFQR MMNKMDRALLELQLEPEELYQTFQR	RIIENVNVIVNM		YAS-EDGPMGD-FT-VEPTKGTVGFGYAV-EDGPMGN-IM-IDPQKGTVGFGYAV-EDGPMGN-IM-IDPQKGTVGFGYGEGESGPMGN-IM-IDPVLGTVGFG
Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_024354781.1_Elongation_factor_2 Myessoensis.XP_021362159.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2 Cintestinalis.LOC100177993_elongation_factor_2like Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo	FMNKMDLALLTLQVDQESLYQNFQR FMNKMDLGLLTLRLDREAMYTEFQR FMNKMDRALLELQLEKEDLYQTFQR FMNKMDRALLELQLEKEDLYQTFQR MMNKMDRALLELQLEFEELYQTFGR FMNKMDRALLELQLEMEDLYNNFSR	IIIENVNVIVNM		YAS-EDGPMGD-FT-VEPTKGTVGFGYAV-EDGPMGN-IM-IDPQKGTVGFGYAV-EDGPMGN-IM-IDPQKGTVGFG

```
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 FMNKMDRALLELQLQQEDLFQTFQRIVENVNVIIAT-
Dmelanogaster.eEF2_eukaryotic_translation_elongati FMNKMDRALLELQLDAEELYQTFQRIVENVNVIIAT----
Egranulosus.XP_024355481.1_Elongation_factor_Tu_GT VLNKFPRLFLQLGLSF1QVYDRILRULEQINSVLAEMFTI
Avaga.UJRS42421.1_hypothetical_protein_14U23_009661 VLNKIDRLIIGLKMFPLEAYLHIRGLLENINAVVAEQFTS
Dmelanogaster.CG33158_uncharacterized_protein_Dmel VLNKLDRLILEKQMDPLDAYFHLCQVLEQVNAVLGSIFAS
                                                                                                                                                                                                                                                                            --YND-DGGPMGE-VR-VDPSKGSVGFGS
                                                                                                               VI.NKFDRI.FI.OI.GI.SPIOVYDRII.RVI.EOINSVI.AEMFTADVMOOTHGWEAD------GDSVROSAEGTYTWSTGI.EATDDS-HVYFSPDKANVI.FTS
                                                                                                               VLNKIDRLIGLEMPTLEASYLHIRGILENINAVVAEQIINOVALABHI IAUVMQVINGMEAD------GUSVKQSAEGIIINSIGLEAIDUS-NYIISFURANVUH IS
VLNKIDRLIGLEMMPTLEASYLHIRGILENINAVVAEQFISTELLEKSVDQEANEEIKKETNNDIVDDGDD--DWA----RNEA-QWCFSPHYNNUFAS
VLNKLDRLILEKQMDPLDAYFHLCQVLEQVNAVIGSIFASDILAKEDITKKD-----------NESALEEVDDS-ELYFSPSSGNVIFCS
VLNKIDRLITELKFTPEEAHLHLQQVLEQVNAVTGSLYSAEVLEKIGQTESS------QVETENGEEVVYDWSSGIADTDDS-KLYFSPSHGNVVFAS
Cintestinalis.LOC100175902_elongation_factorlike_G
Hsapiens.NP 078856.4 elongation factor-like GTPase
                                                                                                               VINKIDRLIVELKFTPQEAYSHLKNILEQINALTGTLFTSKVLEERAERETE----SQVNPNSEQGEQ-VYDWSTGLEDTDDS-HLYFSPEQGNVVFTS
Bbelcheri.LOC109463052_elongation_factorlike_GTBas VLNKVDRLITELKNSPMEAHLVLQVLEQVNSIMGNLFSTDVMKKGTTEDST----NAVKEPTVATEBHVFPYSLELDHTDDS-NLIFSEQGNVVFAS
Aplanci.LOC110988091_elongation_factorlike_GTBase_VLNKIDRLISELKYTPQEAHLRLQQVLEQVNAVVGNLFASGVLEQATQQNTERTVQSNDSERCQTMEEKVVYDMSDGLEETDDS-N1YFSPDQGNVFAS
Lanatina.KP_013413557.l_elongation_factorlike_GTPa VLNKIDRLISELKYTPQEAHLRLQQVLEQVNAVVGNLFASGVLEQATQQNTERTVQSNDSERCQTMEEKVVYDMSDGLEETDDS-N1YFSPDQGNVFAS
Myessoensis.XP_021362732.l_elongation_factorlike_GTPa VLNKIDRLIMELKMDPLEAFFHLQVLLEQVNLVTNELFTTEIMAKTSSQTDG------AGQEKEKSKAVSNDWTIQADDEDEERNIFFSPTQGNVVFAS
                                                                                                                                                                                                              560â 580â
--VAPSVLLSKLWGDNFYNSSQK----KWKNEP----SKDYIRAFNLFVLDPIFKLFE
                                                                                                                                                     520â
                                                                                                                                                                                                540â
                                                                                                         500â
Myessoensis.XP_021350409.1_elongation_factor_2like ASQSWGVT--
Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu SYYRFCFT--
Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 SYYRFCFT--
                                                                                                                                                     -I.GETAAKOAEKI.K----
                                                                                                                                                       -LESFAKIYTDTFAD----
-LKSFAKIYADTHGG----
                                                                                                                                                                                                              SIDYKSFAKRLWGDQYFSSETR----TFKSKP---PTASSLRSFVEFILEPIYKIFA
TFDFQAFSKRLWGDLYYDPKTR----TFGKKG---PTAQTSRSFVQFILEPLYKILA
Dmelanogaster.CG4849 uncharacterized protein Dmel SLYGFCFT-
                                                                                                                                                      -LKSFAKLYADTYEG-----
                                                                                                                                                                                                              -VAYLDFAKRLWGDMYFNSKTR----KFSKKQ---PHNSAQRSFVEFILEPMYKLIA
Wyessoensis.XP_021345506.1_116_kDa_U5_small_nuclea SYYRFCFT-Cintestinalis.LOC100175824_116_kDa_U5_small_nuclea SYYRFCFT-Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r SYYRFCFT-Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r SYYRFCFT-
                                                                                                                                                                                                             -- INEKEFARRIWGDMYFNSKTR----KFTKKP---PHTNAQRSFIEFVLEPLYKLFS
-- EVDPKQFARRIWGDVYFNQKTR----RFSKKP---PHTNAQRSFIEFVLEPLYKIFS
-- INTYEFARRIWGDIYFNSKTR----KFSKKP---ANSTSQRSFVEFILEPLYKIFS
                                                                                                                                                       -I.ASFAKTYGETYGG-----
                                                                                                                                                      -LASFAKITGETTGG------
-LNSFANLYVKQFGN------
-LSSFAKIYSDTYGG-----
                                                                                                                                                      -LSSFAKIYSDTYGG-----
                                                                                                                                                                                                             --INTYEFARRLWGDIYFNSKTR----KFSKKP---ANSTSQRSFVEFILEPLYKIFS
Hsapiens.NP_004238.3_116_kba_U5_small_nuclear_ribo SQYSICFT------
Bbelcheri.LOC109461499_116_kba_U5_small_nuclear_ri SQYRFCFT------
Aplanci.LOC110989613_116_kba_U5_small_nuclear_ribo SQYSMCFT-------
Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 GKHGWAFT-------
                                                                                                                                                      -LGSFAKIYADTFGD-----
                                                                                                                                                                                                                -INYOEFAKRLWGDIYFNPKTR-
                                                                                                                                                                                                                                                                      -KFTKKA---PTSSSORSFVEFILEPLYKILA
                                                                                                                                                                                                                                                                      -RFTKKP---PMSTSQRSFVEFILEPLYKIFA
-KFTKKS---PVSTAQRSFVEFILEPLYKIFA
-KWLSYEQSRSSDDAKRGFTQFILQPLYQILN
                                                                                                                                                       LOSESKIYEDTYGG---
                                                                                                                                                                                                                -FSAKELSRRLWGDIYFNSKSR
                                                                                                                                                       LASFAKIYADSYGG--
IPQFATFLAEKTK---
                                                                                                                                                                                                                -IDHQEFAKRLWGDIYFNPKIR
-ATKEKYMDRLWGESYYSSSSK
Avaga.UJR19151.1_hypothetical_protein_14U23_022281 CLHGWAFT--
Myessoensis.XP_021349219.1_elongation_factor_2like GLHRWGFT--
Egranulosus.XP_0243547811.1_Elongation_factor_2 GLGSWAFT--
Myessoensis.XP_021362159.1_elongation_factor_2like GLHGWAFT--
                                                                                                                                                      -LKEFADIYSIKFG-----
                                                                                                                                                                                                               -IDNNKLMEYLWDDHFYSFENN-
                                                                                                                                                                                                                                                                      -QWSENK----TEGYHRGFCQFILDPLFKIYQ
                                                                                                                                                       -I.VNFARI.YAAKFG-----
                                                                                                                                                                                                               -I.SEEKI.MRRI.WGEHYYNPGTR
                                                                                                                                                                                                                                                                       TWNRIG---GDGYVRGFNKFILEPLYTML
                                                                                                                                                      -MDADKLLPRLWGDNFFNAAEK
-MNQEKLMKKLWGNNFFDEGAK
                                                                                                                                                                                                                                                                      -KWRKSK---TDPKDVRAFVHFILDPITKIFR
-KWIKES----DGKAVRGFVKYILDPIYLVFN
                                                                                                                                                                                                                                                                      -KWAKNN---DDKSGORGFTLYVLTPIYNVFN
 Lanatina.XP 013394736.1 elongation factor 2
                                                                                                               GLHGWAFT-
                                                                                                                                                      -LKMFADMYATKFK------VPAAKLMKRLWGDOFFNPKTK-
Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo GLHGWAFF------
Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo GLHGWAFS-----
Hsapiens.NP_001952.1_elongation_factor_2
GLHGWAFF------
Hsapiens.NP_001952.1_elongation_factor_2
                                                                                                                                                      -LKOFAEMYAEKFK-------VPLPKLMNRLWGDNYFNPAMK-
                                                                                                                                                                                                                                                                      -KWSKTK----SPENERGFNTFALTPIYKVFD
                                                                                                                                                      - VFDE KENNIKERE KOMENTER BESTELLENGENE FOR BESTELLENGE FOR BESTEL
                                                                                                                                                                                                                                                                       -KWAKSK----SPESDRGFNTFVLTPIYKVFD
-KFSKSATSPEGKKLPRTFCQLILDPIFKVFD
                                                                                                                                                                                                                                                                      -KMVKCK-
Bbelcheri.LOC109464429_elongation_factor_2like
                                                                                                                GLHGWAFT-
                                                                                                                                                                                                                                                                      -KWAKTP----GEGYIRGFNKFVLDPIYKVFD
Boeleneri.LUC10946442_elongation_ractor_flike
Aplanci.LUC110987647_elongation_factor_flike
GLHGWAFT----
Avaga.UJR10301.1_hypothetical_protein_I4U23_014507 GLHGWAFT----
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 GLHGWAFT----
Bmelanogaster.eEFf_eukaryotic_translation_elongati GHGWAFT----
Egranulosus.XP_024355481.1_Elongation_factor_Tu_GT AVDGWGFR----
                                                                                                                                                      -LKQFAEIYSNKFK----
                                                                                                                                                                                                                -IEPAKLMKRLWGDQFFNAKEK-
                                                                                                                                                                                                                                                                      -KWNKTG----GDGYVRGFNQFVLDPIYKIFS
                                                                                                                                                                                                                                                                    ---KWSKSG----GEGYVRGFCQFVLDPIFKVFR
---KWSKSG----GEGYVRGFCQFVLDPIFKVFR
---KWQKQK----EADNKRSFCMYILDPIYKVFD
                                                                                                                                                      -I.KEFAEMYASKFK---
                                                                                                                                                                                                                TEVDKIMKRIWGDNFFSPSEK---
                                                                                                                                                      -LKEFAEMYASKFK--
-LKQFSEMYSEKFK--
                                                                                                                                                                                                                -IEVDKLMKRLWGDNFFSPSEK---
-IDVVKLMNRLWGENFFNAKTK---
                                                                                                                                                                                                                -LPKKGLLKALWGDYYFTSSPDGGLPRVKPHA---RAKNKKPVFVQLIIDHLHHIYK
                                                                                                                                                      -ISDFGDFWAERMN-
-IKREVLMKTLWGDFYFDRKSK----RVFKGA---OSKGOKPMFVOFILENIWSVYE
                                                                                                                                                                                                                -MSRKDLENVLWGDFYYNSKKK---
-IREKVLNRTLWGDYYVNNKAK---
                                                                                                                                                                                                                                                                                          -QEKAKKPMFVQFVLENIWSLYD
-QAKGKKTLFVQFILENLWSIYD
                                                                                                                                                                                                                                                                      -EALPGA-
Hsapiens.NP_078856.4_elongation_factor-like_GTPase AIDGWGFG---
Bbelcheri.LOC109463052_elongation_factorlike_GTPas AIDGWGFR---
                                                                                                                                                  ---IEHFARIYSQKIG-
                                                                                                                                                                                                                -IKKEVLMKTLWGDYYINMKAK--
                                                                                                                                                                                                                                                                    --KIMKGD-
                                                                                                                                                                                                                                                                                          -QAKGKKPLFVQLILENIWSLYD
                                                                                                                                                      -LEHFAKOYASKLN----
                                                                                                                                                                                                                -IKEDILOKVLWGDFYVHSKTK----RVMKGA---OAKGKKPLFVOFVLENVWAVYD
Aplanci.LOC110988091_elongation_factorlike_GTPase_AIDGWGRG-
Lanatina.XP_013413557.1_elongation_factorlike_GTPa ALDGWAFS-
Myessoensis.XP_021362732.1_elongation_factorlike_G AYDGWGFT-
                                                                                                                                                                                                              -TDHFATMYAAKI.G-----
                                                                                                                                                      - IGHFAELYSVKLG-
- LNHFADMFSKKLG-
                                                                                                                                                                                                640â
                                                                                                         600â
                                                                                                                                                     620â
                                                                                                                                                                                                                                            660â
                                                                                                                                                                                                                                                                                        680â
Myessoensis.XP_021350409.1_elongation_factor_2like ASGN--
Egranulosus.XP_024347861._U5_small_nuclear_ribonu QTAG--
Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 HVVG--
                                                                                                                                                                                                  -NTRTNVOEMMCOWLPISNSLLTMIVIHLPSPOTS-ORYRSELLVSR-
                                                                                                                                        VOGSALPDLIENLGVOMSLDNNET-
                                                                                                                                                                                                                                                                                                                        -KT-DAVGT
                                                                                                                                                                                                  -NYRPLERIFFORSEGFVSMCVKHVPSPVAS-ARVRISHTYSG-----
-NVRPLERIFSRFFGDFSGFVSMCVKHVPSPVAS-ARVRISHTYSG-----
-NYRPLERLVCARFFGEFKGFTDMIIQHIPSPIAN-AHSKIEHLYTG-----
-NIRPLERLVCNRFMGDCSGFVDMCVEHIKSPLEN-AKRKVDHIYTG-----
                                                                                                                                       -DVDTCLPRLCSELGIHLSKSEFKL-
-DVDIALSGVLDELGIRLTKTELKL-
Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ QVVG-
                                                                                                                                        -DVDTTLSDTLAELNVRVSKEEMKS-
                                                                                                                                                                                                                                                                                                                         -PK-EGDIY
Myessoensis.XP 021345506.1 116 kDa U5 small nuclea OVVG-
                                                                                                                                        -DVDECLPRLCDELGISLTKEERKL-
                                                                                                                                                                                                   NIRPLLRIVCRRFFGDFTGFVDMCVEHLPSPADN-AKNKIEHVYTG
                                                                                                                                                                                                                                                                                                                         -SS-DSDLA
Nyessoensis.Xr_021939001:110_Mba_U5_small_nuclea QVVG--
Cintestinalis.L0C100175824_116_kba_U5_small_nuclea QVVG--
Lanatina.XP_013419342.1_116_kba_U5_small_nuclear_r MTVG--
Lanatina.XP_023933490.1_116_kba_U5_small_nuclear_r MTVG--
                                                                                                                                                                                                  -NIRPLLRIVCSRFMGHPSGFVEMCVEHIPSANNA-ARNKVMHTYTG-
-NIRPLLRIVLSRFMGHPSGFVEMCVQHVPSPGDH-AKSKVEHTYTG-
-NIRPLLRIVLRRFFGDFSGFVDMCVQHVPSPGDH-AKSKVEHTYTG-
-NIRPLLRIVLRRFFGDFSGFVDMCVQHVPSPGDH-AKSKVEHTYTG-
                                                                                                                                       -DADSTIPRVIDELGVYLSKEEMKM-
                                                                                                                                                                                                                                                                                                                        -PQDDTELV
                                                                                                                                        -DVDLNLPQVCEELGISLTKEERKL
-DVDLNLPQVCEELGISLTKEERKL
                                                                                                                                                                                                                                                                                                                         -PL-DTELA
-PL-DTELA
Hsapiens.NP 004238.3 116 kDa U5 small nuclear ribo QVVG--
                                                                                                                                       -DVDTSLPRTLDELGIHLTKEELKL-
                                                                                                                                                                                                  -NIRPLLRLVCKKFFGEFTGFVDMCVQHIPSPKVG-AKPKIEHTYTG-
                                                                                                                                                                                                                                                                                                                         -GV-DSDLG
Bbelcheri. LOC109461499_116_kba_U5_small_nuclear_ri QVVG--
Aplanci.LOC110989613_116_kba_U5_small_nuclear_ribo QVVG--
Avaga.UJR26319.1. hypothetical_protein_14U23_00757 ACAD--
Avaga.UJR19151.1_hypothetical_protein_14U23_022281 IIKN--
                                                                                                                                         DVDSTLPRALEELGVHLIKEEMKM--NIRPLLKLICRFFGDFTGFVDMCAEHIKSPYAA-ARTKVEHTYTG-
DVDSTLPGVLDELGIHLTKEEMKM--NIKPLLKLUCSKFFGDFTGFVDMCVDHVPSPVAA-AKMKIEHLYTG-
LNMEEVETLLSKIDVKLTFDKLDASILDSKITISNVMKRWLPASEAMLHLVLHLESPYQA-QVYKIQHLGY
YKKDELERLMNQLNINNDKELSEK---GDENLLKLIMKQWLAIDNILSKMIIHLPSPIIA-QKYRTEILYQG-
                                                                                                                                        -DVDSTLPRALEELGVHLTKEEMKM-
                                                                                                                                                                                                                                                                                                                        -PL-ENELG
                                                                                                                                        -DVDSTLPGVLDELGIHLTKEEMKM-
                                                                                                                                                                                                                                                                                                                         -PV-DSDLA
                                                                                                                                                                                                                                                                                                                          PQ-DDQVA
                                                                                                                                                                                                                                                                                                                                 -DEMS
Myessoensis.XP_021349219.1_elongation_factor_2like
Egranulosus.XP_024354781.1_Elongation_factor_2
Myessoensis.XP_021362159.1_elongation_factor_2like
Lanatina.XP_013394736.1_elongation_factor_2
                                                                                                               TLKT-
                                                                                                                                        KEKEEVFKLTDKLNIHLSGEERAE-
                                                                                                                                                                                                   SGKPLMRKVMOKWLPVADALLEMFVAHLPSPLTA-OKYRTDLLYEG
                                                                                                                                                                                                                                                                                                                         -PM-DDDAA
                                                                                                               AVQD -----EDKPMIQKMLTAIDVKLSTEEHDQ-
TCMK-----GEHSKALTLVEKMGVKLTSDEKDL-
KCVDGLNLENENVETPVLELIEKMGVKLSAEEKEL-
                                                                                                                                                                                                  -PAKVLLKTIMHKWLPAGDCLLEMICIHLPSPFVS-QRYRMEMLYEG-
                                                                                                                                                                                                                                                                                                                         -PK-DDEAA
                                                                                                                                                                                                   REKNILKVVMRKWMPAGDALLQMIVIHLPSPVTA-QYYRTDTIYEG
-KDKPLLKAVMRKWLPAGDALLQMICVHLPSPVTS-QKYRTELLYEG
Lanatina.KP_013394736.l_elongation_factor_2 KCVDGL
Cintestinalis.LOC100177993_elongation_factor_2like AIMN--
Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo AIMN--
Hsapiens.NP_001952.l_elongation_factor_2
Belcheri.LOC10946429_elongation_factor_2like AIMN--
Aplanci.LOC110987647_elongation_factor_2like AIMN--
                                                                                                                                     --NKTEEIGKLMEKCNVKLKGDDKDK--
                                                                                                                                                                                                  -VEKQLLKGFMRTWLPAGDTLLQMITIHLPSPVVA-QKYRSELLYEG-
                                                                                                                                                                                                                                                                                                                        -PA-DDEVA
                                                                                                                                                                                                 --VEKQLIKAFMRTWLPAGGTILOMITIHLPSPVVA-QKYRSELLYEG-

--BGKPLIKAVMRKWLPAGDALLOMITIHLPSPVTA-QKYRCELLYEG-

-EGKPLIKVAMRKWLPAGBALLQMICTHLPSPVTA-QKYRMELLYEG-

--BGKPLIKKEVMRKWLPAGBALLOMITIHLPSPVTS-QKYRMELLYEG-
                                                                                                                                        NKTEEIGKIMEKONVKIKGDDKDK--
                                                                                                                                                                                                                                                                                                                        -PA-DDEVA
                                                                                                                                        FKKEETAKLIEKLDIKLDSEDKDK-
                                                                                                                                                                                                                                                                                                                         -PP-DDEAR
                                                                                                                                        FKKDDTAKVLEKLQVKLTTEEKGL--
FKKDETAKLLEKLKIKLTGESKDK--
                                                                                                                                                                                                                                                                                                                          PH-EDEA
                                                                                                                                                                                                                                                                                                                         -PH-DDPCA
Apianci.LOCI1098/64/_eiongation_tactor_Z11ke AINN-
Avaga.UUR10301.1_hypothetical_protein_I4023_014507 AIMD-
Avaga.UUR35689.1_hypothetical_protein_I4023_028438 AIMD-
Dmelanogaster.eEF2_eukaryotic_translation_elongati AIMN-
Egranulosus.XP_024355481.1_Elongation_factor_Tu_GT TIIV-
                                                                                                                                        CKKDEYLALLDKLNIKLOGDDRDKLEEGGKPLLKLVMKOWLPAGDVLLTMIAIHLPSPVVA-OKYRAELLYEG-
                                                                                                                                                                                                                                                                                                                         -PO-DDEAF
                                                                                                                                     Avaga.UJR28421.1_hypothetical_protein_IdU23_009661 TIIT--
Dmelanogaster.CG33158_uncharacterized_protein_Dmel IIAI--
Cintestinalis.LOC100175902_elongation_factorlike_G AVVI--
Hsapiens.NP_078856.4_elongation_factor-like_GTPase AVLK--
                                                                                                                                     -RRDNEKLEKIVASIGAKLIPRDIGH--SDPCVPLHLLFNQWLPVASAVFDMVVTQLPNPKAL-NTDKIEQLMCNKSRRFDTLLPETQRLK
                                                                                                                                     -RKDKDKHPGIAEKLCIKLATRDLRI—TIPPKLQIKAVLGGWLPIDKSVLHMVIQHVPPPHKI-SDERAGRLYPANVDLSSIPPETIELK
RRDKERSEKITKSIALNISARDVRVGKSEPKTYLQAICGGWLPLAEAVLSSVCQYLPSPSDI-SGERVEGIMCGSTRSFSALHSKSQDLK
-RKDKDKDIKUTVISLGKLKGAREARI-SDEVQUINAICSGWLPISHAVLAWVCQKLPSPLDI-TIAERVERICKGSGTESFPETQALK
-RRDKEKVEKIVKSLNVTISGARAFAH--NDPRVLLQAVCGGWLPISHAVLAWVCQKLPSPLDI-TAERVERICKGSGTFDSFPETQALK
Bbelcheri.LOC109463052_elongation_factorlike_GTPas AVLV-
                                                                                                                                     KROKOKHIKIIOSINIKITAARDIRH--NDPKVHLQAICAQWILPISQAVISMVCQKLPSPINI-DAVRIEKUMCAGGRRFNTLPPQSQLIK
RKOKEMIEKIVKSININIPPRDSRH--TDARVHLQAIVSQWLPLSKAVLDVVCSHLPSPKDF-LPERVEKIMCGGARRYDSLPSQTQQIK
NRDAEMTEKIVKSLGLKISPRDMRH--NDPRWKLQAIMGQWLSVSRAVLDVVVEKLPSPLEI-SEDRVEKIMCSQSQNFLSFPKATQEIK
Aplanci.LOC110988091_elongation_factorlike_GTPase_ TILV--
Lanatina.XP 013413557.1 elongation factorlike GTPa AVTV--
 Myessoensis.XP_021362732.1_elongation_factorlike_G SVSV-
                                                                                                          700â
                                                                                                                                                                                                  740â 760â
-SAVKTCDP--SGP-LIMYVTKWY---
Myessoensis.XP_021350409.1_elongation_factor_2like --
Gyranulosus.XP_024347861.1_U5_small_nuclear_ribonu -----
Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 -----
Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ -----
                                                                                                                                                                                                  -RDMIACRA--ESPHLMVHTTKLY------
                                                                                                                                                                                                   Myessoensis.XP_021345506.1_116_kDa_U5_small_nuclea -----
Cintestinalis.LOC100175824_116_kDa_U5_small_nuclea ----
                                                                                                                                                                                                   -EVMCTCDP--DSP-LMVHTTKLF-
                                                                                                                                                                                                   -QAMYTCDP--DGP-LMVHTCKMY-----
Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r

Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r

Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_ribo

Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ri
                                                                                                                                                                                                   -DSMTOCDP--DGP-I.MIHTTKI.Y-----
                                                                                                                                                                                                   -DSMTQCDP--DGP-LMIHTTKLY---
                                                                                                                                                                                                   -EAMSDCDP--DGP-LMCHTTKMY-----
                                                                                                                                                                                                   -DAMLECDP--EGP-LMLHTTKMY------
Avaga.UJR19151.1_hypothetical_protein_I4U23_022281
                                                                                                                                                                                                  -DTMTECDP--EGP-LMLHTTKMY------

      Myessoensis.XP_021349219.1_elongation_factor_2like

      Egranulosus.XP_024354781.1_Elongation_factor_2

      Myessoensis.XP_021362159.1_elongation_factor_2like

      Lanatina.XP_013394736.1_elongation_factor_2

                                                                                                                                                                                                   VAMKHCNP--NGP-LMLYVSKMV----
                                                                                                                                                                                                  -IGIMNCDP--NAC-LMMYVSKMV-----
                                                                                                                                                                                                   -TAMKNCDP--KGP-I.MMYVSKMV------
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Column C	G'		TITINIOND WOD IN	W. Carlotte
Received 1.000 1	Cintestinalis.LOC100177993_elongation_factor_Zlike Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo		KGP-LMM KGP-LMM	YVSKMV
April Control Contro			MGIKSCDPKGP-LMM	YISKMV
August Disputch Control Cont				
The Company	Avaga.UJR10301.1 hypothetical protein I4U23 014507		LGIKSCDPTAP-LMM	YISKMV
Spreamingst No. 2013-2011_1 Impact on Assert Park Society	Avaga.UJR35689.1_hypothetical_protein_I4U23_028438		LGIKSCDPTAP-LMM	YISKMV
August 1984 1,	Egranulosus.XP_024355481.1_Elongation_factor_Tu_GT	SDGSNAGQSILREVVYSCRNDGTEEDY	EEDESAAFPAIDALEACSSNADAP-VII	FVSKVFWADKLKNAFSTIVFPKNVPKSVQPPKSVQFPSAPRFATP
Calcast 1.15 D. COLO TROPS A STORY TO A STORY	Avaga.UJR28421.1 hypothetical protein I4U23 009661		QAFIDCSSDDQAP-VIV	CVSKLFSVHNSALSQNRQKPLTAEDIAQRREFLKQKQL
Respond Company Comp	Dmelanogaster.CG33158_uncharacterized_protein_Dmel Cintestinalis.LOC100175902 elongation factorlike G		ESFTSCDA-NSSN-VIA ODFLSCGS-DSST-TIV	.VSKMTPVHITHLPQNRPKRLTDQEVQQRRDEVRRRIE
Aghana (1.00109809). a long time fairs of law CONTROL (1.000000). A CONTROL (1.0000000). A CONTROL (1.00000000). A CONTROL (1.00000000). A CONTROL (1.000000000000000000000000000000000000	Hsapiens.NP_078856.4_elongation_factor-like_GTPase		AAFMKCGSEDTAP-VII	FVSKMFAVDAKALPQNKPRPLTQEEIAQRRERARQRHA
Landing P. 1941 1977	Bbelcheri.LOC109463052_elongation_factorlike_GTPas		QDFLMCSAEDSAP-VIV	FISKMFSVDPKVLPHNRPRPLTQEEIEKKRELARQRHQ
Speciments 20, 201300003 decognic d	Lanatina.XP_013413557.1_elongation_factorlike_GTPa		EDFLSCSPGEDKP-VIV	FISKMFPFDRQCLPQNKQRPLTEADLAQRRLVARQRHA
Speciments 20, 201300003 decognic d	Myessoensis.XP_021362732.1_elongation_factorlike_G	0203	DAFISCSTSDNSP-VIL	FVSKMFPVERKMLPQFKQRPLSEAEIQQRRQQARQRHL
August 1995 Depot Depot	Myessoensis.XP_021350409.1_elongation_factor_2like	QIGET	N	TLYAIGRVFSGSIVSGSEIK
December 1, 1989 The Proposition of the Control	Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu	PDEDA	V	SFHAFGRVLSGRLEAGQDVRVLGEAYSLN
	Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849 uncharacterized protein Dmel	STSDV	T	SFHVLGRIFCGTLKTGQDVRILGENYSLK
Land In 20, 20141944 118 And 15 and 1 packed 1	Myessoensis.XP_021345506.1_116_kDa_U5_small_nuclea	PTQDA	T	SFHVYGRVISGTLYANQEVKILGENYSLQ
Land In. D. 201313090.1 11 A. No. 19. Seal 1, pucker_ito	Cintestinalis.LOC100175824_116_kDa_U5_small_nuclea	STEDG	V	SFRVFGRVISGTVRAGDMVKVLGENYTLD
Black 1.0019461 (99.118, Nb. 08. mail _meilar_ri	Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r	PTEDA	T	AFHVLGRVMSGTLYANQDVKILGENYSLQ
Aplanet 1.0011099803 11, 12, 10, 10, 301 11, 10, 10, 10, 10, 10, 10, 10, 10, 10,				
Page 1.	Aplanci.LOC1109461499_116_kDa_U5_small_nuclear_ri	STEDA		GFLVFGRVMSGTIHANQDIRVLGESYTLD
Ngessionsis.W_D0134511.i.elongation_factor_jike	Avaga.UJR26319.1_hypothetical_protein_I4U23_007657	PAQDG	S	RFLCFGRIFSGTIVSGTNVRILGPDFQPG
Paramicons No. 92 02351610.1_Paramicon Enter 2 PTON	Avaga.UJR19151.1_hypothetical_protein_I4U23_022281	PTSDK	N	RFYAVGRIFSGIVRTNQTVRIMGPNFILG
Nyseconsis. Nr. 02136193. clospicion_factor_1186		PTSDK	G	RFTALGRVFSGTIATGQKVRIMGPNYVHG
Cincrestinalis_IOCIO0179993_clongation_factor_like	Myessoensis.XP_021362159.1_elongation_factor_2like	PTTDK	G	RFYAFGRVFSGCIATGOKARIMGPNYIOG
Characterials:.0C10017993_Log.Contry_FOOTEN_c1 Asspace.NPL_0013_Log.Control_rator_2 Proceedings	Lanatina.XP_013394/36.1_elongation_factor_2 Cintestinalis.LOC100177993 elongation factor 2like	PTSDK	G	RFYAFGRVFSGTTATGMKARIMGPNFKPG
Bedient.i.Oc10946412_stongstion_factor_2like	Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo	PTSDK	G	RFFAFGRVFAGTVATIMVARMSLEOVTPW
Aplanci, I.O. 1.0997667 elongation_factor_211ks PTDN		PTSDK	G	RFYAFGRVFSGLVSTGLKVRIMGPNYTPG
ANGE UNBASSES, L. PYDENELICAL PROTEIN, ETCOS. 1 (1021) 28438 PTOSK	Aplanci.LOC110987647 elongation factor 2like	PTTDK	G	RFYAFGRVFSGKVASGQKVRIMGPHYVPG
Deal angosater.ceft2_euksyotic_translation_elongsti	Avaga.UJR10301.1_hypothetical_protein_I4U23_014507	PTSDK	G	RFYAFGRVFSGVVQTGQKARIMGPNYVPG
Egrandious x, 20, 20, 25, 25, 28, 11, Elongation_factor_Tu_GT GRIVFHROW-TAIR Mayas_UN_20, 20, 20, 20, 20, 20, 20, 20, 20, 20,	Avaga.UJR35689.1_hypothetical_protein_14U23_U28438 Dmelanogaster.eEF2 eukarvotic translation elongati	PTSDK	G	RFYAFGRVFSGVVQTGQKARIMGPNYVPG
Deal anguaster. C033158_uncharacterized_protein_Deal ERROGO	Egranulosus.XP_024355481.1_Elongation_factor_Tu_GT	GRIVVHHDNVETAIK	NPANSPFSDT	EFVALSRIYSGRVKIGQRLFVLGPKFDGSNIPKC
Cintestinalis. Colon/1902_elongation_factorilke_GTBase ERRIADTRSSNINEDDP				
Beacheri.LOC109463092_elongation_factorlike_GTPace_				
Aplanci. LOCI10988091_elongation_factorlike_GTPack_ANNOCOMA_PDSQLENMISSESTLECKROSSGSSTELLARAFFSGRIEGOSTLENGOSTLYNANTHENDERMALAR Myessoensis_XP_021345557_lelongation_factorlike_GEMORETONOCOMPRESSSTEWARDSESSPSEEMANDERSCENTSTONOCOMPRESSSTEWARDSESSPSEEMANDERSCENTSTONOCOMPRESSSTEWARDSESSPSEEMANDERSCENTSTONOCOMPRESSSTEWARDSESSPSEEMANDERSCENTSTONOCOMPRESSSTEWARDSE				
Lanatian.XP_013413557.lelongation_factorlike_0ffwgGMTVMCMTKEMSCETTSCGSTVTWGGGMTVMCGGMTVMCGGMTVMCGGMTVMCMTKEMSCETTSCGSTVTWGGGMTVMCGGMTVMCMTKEMSCETTSCGSTVTWGGGMTVMCGGMTVMCMTKEMSCETTSCGSTVTWGGGMTVMCMTKEMSCAMSCAMSWGGGAPENNIAMTMC				
Myessoensis.XP_021350409.1_elongstion_factor_2like			ENMIEPSENGVMLPSESILEG	KKGDEGE-IFLAFAKVFSGKIHKGQKLYVLNPKHDPMKALAK
Myessoenisis.NP_021335049.1_elongation_factor_2like		QRLAAQSDGTQ-EAAVS	SEVAVQPEKQESEPFEKEAGE	NEIEEEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSRVLE-
Debugs	Myessoensis.XP_021362732.1_elongation_factorlike_G	QRLAAQSDGTQ-EAAVS EKMSGPTDVVNEKTKDEEVTTSQGSTV	SEVAVQPEKQESEPFEKEAGE FSNGTASAVNGGGAPSVEANGIAMEIKA	NEIEEEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSRVLE- IKKEAEEEAPTVFVAFARIYSGTVKKGQKLYVLGPKHDPSQVEEG
Delangaster. CG4849_uncharacterized_protein_Dmel_	Myessoensis.XP_021362732.1_elongation_factorlike_G 90 Myessoensis.XP_021350409.1_elongation_factor_2like	QRLAAQSDGTQ-EAAVS EKMSGPTDVVNEKTKDEEVTTSQGSTV 0â 920â ESQ	SEVAVQPEKQESEPFEKEAGE ISNGTASAVNGGGAPSVEANGIAMEIKA 940â	NEIEEEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSRVLE- TKKEAEEEAPTVFVAFARIYSGTVKKGGKLYVLGPKHDPSQVEEG 960â 980â RKTKIS-ETSIVIGDKICPVPEVI
Cintestinalis.LOCIO0175824_116, kDa_U5_small_nuclear	Myessoensis.XP_021362732.1_elongation_factorlike_G 90 Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu	QRLAAQSDGTQ-EAAVS	SEVAVQPEKQESEPFEKEAGEI TSNGTASAVNGGGAPSVEANGIAMEIKA 940â	WEIEBEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSRVLE- KKEAEBEAPTVFVAFARIYSGTVKKGQKLYVLGPKHDPSQVEG 960å 980å
Lanatian x P	Myessoensis.XP_021362732.1_elongation_factorlike_G 90 Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 Dmelanoqaster.GG4849 uncharacterized protein Dmel	QRLAAQSDGTQ-EAAVS	-SEVAVQPEKQESEPFEKEAGEI ISNGTASAVNGGGAPSVEANGIAMEIKA 940â	NEIEEEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSRVLE- TKKEAEEEAPTVFVAFARIYSGTVKKGQKLYVLGPKHDPSQVEEG 960å 980åRKTKIS-ETSIVIGDKICPVPEVIRPAVAG-RLWIFCGRYRIEUNRVP
Heaplens.NP_004238.3 116, kbm_015_small_nuclear_rit	Myessoensis.XP_021362732.1_elongation_factorlike_G 90 Myessoensis.XP_021350409.1_elongation_factor_21ibe Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UUR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nuclea	QRLAQSDGTQ-EAAVS	-SEVAVQPEKQESEPFEKEAGE FSNGTASAVNGGGAPSVEANGIAMEIKA 940å	NEIEEEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSQVLEG 1KKEAEEEAPTVFVAFARIYSGTVKKGQKLYVLGPKHDPSQVEG 960â 980â
Bebleheri.LOC.10946i499_116_kDa_U5_small_nuclear_ri	Myessoensis.XP_021362732.1_elongation_factorlike_G 9	ORLAAQSDGTQ-EAAVS	-SEVAVQPEKOESE	KEIEEEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSQVLEG JKKBAEEEAPTVFVAFARIYSGTVKKGQKLYVLGPKHDPSQVEG 980â ————————————————————————————————————
Aplanci.LOC110989613, 21, bypothetical_protein_14023, 007657 SSTDL	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.GG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat cintestinalis.IOC100175824_116_kDa_U5_small_nuclear_r Lanatina.XP_0213419342.116_kDa_U5_small_nuclear_r Lanatina.XP_02134193490.1_116_kDa_U5_small_nuclear_r	QRLAAQSDGTQ-EAAVS	SEVAVQPEKQESEPFEKEAGE FSNGTASAVNGGGAPSVEANGIAMEIKA 940ā	KEIEBEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSQRULE JKKEAEBEAPTVFVAFARIYSGTVKKGQKLYVLGPKHDPSQVEG 960å 980å
AVAGA_UJR1915.1. hypothetical_protein_I4U23_022281	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.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_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleac_intestinalis.LoClo0175824_116_kDa_U5_small_nucleac_Inatina.XP_013419342.1_116_kDa_U5_small_nuclear_r Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r Hsapiens.NP_0042383.3 116_kDa_U5_small_nuclear_r Hsapiens.NP_0042383.3 116_kDa_U5_small_nuclear_r	QRLAAQSDGTQ-EAAVS	-SEVAVQPEKQESEPFEKEAGE FSNGTASAVNGGGAPSVEANGIAMEIKA 940â	NEIEBERSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSQVEEG 1KKEAEBEAPTVFVAFARIYSGTVKKGQKLYVLGPKHDPSQVEEG 960â 980â
Myessoensis NP_021349219.1_elongation_factor_2	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UUR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_l16_kDa_U5_small_nucleat Cintestinalis.LoC100175824_l16_kDa_U5_small_nucleat Lanatina.XP_0213419342.1_l16_kDa_U5_small_nuclear_r Lanatina.XP_02343490.1_l16_kDa_U5_small_nuclear_r Hsapiens.NP_004238.3_l16_kDa_U5_small_nuclear_ribo Bbelcheri.LoC109461499_l16_kDa_U5_small_nuclear_ribo	QRLAQSDGTQ-EAVS	SEVAVQPEKQESEPFEKEAGEI FSNGTASAVNGGGAPSVEANGIAMEIKA 940ā	NEIEEEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSQVLEG 1KKEAEEEAPTVFVAFARIYSGTVKKGQKLYVLGPKHDPSQVEG 960å 980å
Myessoensis.XP_021362159.1_elongation_factor_21	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.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_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat cintestinalis.LoC100175822_116_kDa_U5_small_nuclear_r Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_rib Bbelcheri.LoC109461499_116_kDa_U5_small_nuclear_rib Aplanci.LoC110989613_116_kDa_U5_small_nuclear_rif Aplanci.LoC110989613_116_kDa_U5_small_nuclear_rif Aplanci.LoC110989613_116_kDa_U5_small_nuclear_rif Aplanci.LoC110989613_116_kDa_U5_small_nuclear_rif Aplanci.LoC110989613_116_kDa_U5_small_nuclear_rif Aplanci.LoC11091618_DeloC110818618	ORLAQSDGTQ-EAVS	-SEVAVQPEKQESE	KEIEEEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSQVLEG 960â 980â
Cantastinalis, LOC10017993.elongation_factor_21ike	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hppothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat cintestinalis.IOC100175824_116_kDa_U5_small_nucleat Lanatina.XP_0213419342.1_116_kDa_U5_small_nuclear_r Lanatina.XP_0213419342.1_116_kDa_U5_small_nuclear_r Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribo Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR29151.1 hypothetical_protein_I4U23_0072281	ORLAQSDGTQ-EAVS	-SEVAVQPEKQESE	KEIEEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSRVLE 1608 9808
Haspiens.NP_001952.1_elongation_factor_2	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hppothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat Cintestinalis.LoC0100175822_116_kDa_U5_small_nucleat Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r Hsapiens.NP_004238.3.116_kDa_U5_small_nuclear_ribo Bbelcheri.LoC109461499_116_kDa_U5_small_nuclear_ribo Bbelcheri.LoC109461499_16_kDa_U5_small_nuclear_ribo Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_022281 Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_024354781.1_Elongation_factor_2	ORLAQSDGTQ-EAVS	-SEVAVQPEKQESE	KEIEBEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSQVLEG 960â 980â
Haspiens.NP_001952.1_elongation_factor_2	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hppothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat Cintestinalis.LoC0100175822_116_kDa_U5_small_nucleat Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r Hsapiens.NP_004238.3.116_kDa_U5_small_nuclear_ribo Bbelcheri.LoC109461499_116_kDa_U5_small_nuclear_ribo Bbelcheri.LoC109461499_16_kDa_U5_small_nuclear_ribo Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_022281 Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_024354781.1_Elongation_factor_2	ORLAQSDGTQ-EAVS	-SEVAVQPEKQESE	KEIEBEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSQVLEG 960â 980â
Bebelcheri_LOC109876442_elongation_factor_2like	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.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_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleac cintestinalis.IOC100175824_116_kDa_U5_small_nucleac Lanatina.XP_0213349349.1_116_kDa_U5_small_nuclear_r Hanatina.XP_023933490.1_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribo Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR29151.1_hypothetical_protein_I4U23_0076257 Avaga.UJR19151.1_hypothetical_protein_I4U23_0076257 Avaga.UJR19151.1_hypothetical_protein_I4U23_0076257 Avaga.UJR19151.1_hypothetical_protein_I4U23_0076257 Avaga.UJR19151.1_hypothetical_protein_I4U23_0076257 Avaga.UJR19151.1_hypothetical_protein_I4U23_0076257 Avaga.UJR19151.1_hypothetical_protein_I4U23_0076257 Avaga.UJR39151.1_bypothetical_protein_I4U23_0076257 Avaga.UJR39151.1_bypo	QRLAQSDGTQ-EAVS	SEVAVQPEKQESE	
Avaga_UJR10301.1_hypothetical_protein_I4U23_028438	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UUR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat Gintestinalis.LOC100175824_116_kDa_U5_small_nucleat Lanatina.XP_0213419342.1_116_kDa_U5_small_nuclear_r Lanatina.XP_021349349.1_116_kDa_U5_small_nuclear_r: Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC1019861499_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC10198613_116_kDa_U5_small_nuclear_ribo Avaga.UUR26319.1_hypothetical_protein_I4U23_007657 Avaga.UUR26319.1_hypothetical_protein_I4U23_022281 Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_0213325159.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Cintestinalis.LOC100177993_elongation_factor_2like Cintestinalis.LOC100177993_elongation_factor_2like Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo	QRLAQSDGTQ-EAVS	SEVAVQPEKQESE	
Avaga_UJR35689.1_hypothetical_protein_I4U23_028438	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.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_ Myessoensis.XP_021345506.1_l16_kDa_U5_small_nucleat Cintestinalis.LoCl001075822_l16_kDa_U5_small_nucleat Lanatina.XP_013419342.1_l16_kDa_U5_small_nuclear_r Lanatina.XP_023933490.1_l16_kDa_U5_small_nuclear_rib Bbelcheri.LOCl109461499_l16_kDa_U5_small_nuclear_rib DBbelcheri.LOCl109461499_l16_kDa_U5_small_nuclear_rib Aylanci.LOCl10989613_l16_kDa_U5_small_nuclear_rib Ayaga.UJR26319.1_hypothetical_protein_I4U23_002281 Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_024354781.1_Blongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Cintestinalis.LOCl00177893_elongation_factor_2like Cintestinalis.LOCl00177993_elongation_factor_2like Cintestinalis.LOCl00177993_elongation_factor_2like Cintestinalis.LOCl00177993_elongation_factor_2	QRLAQSDGTQ—EAVS— EKMSQPTDVVNEKTKDEEVTTSQGSTV 0A 920A	SEVAVQPEKQESE———PFEKEAGE FSNGTASAVNGGGAPSVEANGIAMEIKA 940å	KEIEEEKSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSQRVLE 960å 980å
Dmelanogaster.eFF2_eukaryotic_translation_elongati	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UUR09000.1_hppothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_i16_kDa_U5_small_nucleat Gintestinalis.LoCl00175824_i16_kDa_U5_small_nucleat Lanatina.XP_013419342.1_i16_kDa_U5_small_nuclear_r Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_ribo Bbelcheri.LoCl109861499_l16_kDa_U5_small_nuclear_ribo Avaga.UUR26319.1_hypothetical_protein_I4U23_007657 Avaga.UUR26319.1_hypothetical_protein_I4U23_02261 Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_021354781.1_Elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Cintestinalis.LoCl00177993_elongation_factor_2like Cintestinalis.LoCl00177993_elongation_factor_2like Cintestinalis.LoCl00177993_elongation_factor_2like Lanatinalis.LoCl00178953_LDW_QUALTY_PROTEIN_elo Hsapiens.NP_001952.1_elongation_factor_2	ORLAQSDGTQ-EAVS	SEVAVQPEKQESE———PFEKEAGE ISNGTASAVNGGGAPSVEANGIAMEIKA 9408	
Avaga_UJR28421.1_hypothetical_protein_I4U23_009661 DLBLSVRSISHHV	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.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_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleac cintestinalis.LOC100175824_116_kDa_U5_small_nucleac Lanatina.XP_0213349340.1_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribo Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR2919.1_elongation_factor_21ike Egranulosus.XP_021349219.1_elongation_factor_21ike Lanatina.XP_0213394736.1_elongation_factor_21ike Lanatina.XP_0213362159.1_elongation_factor_21ike Lanatina.XP_013394736.1_elongation_factor_21ike Lanatina.XP_001394736.9_elongation_factor_21ike Lanatina.XP_001394736.1_elongation_factor_21ike Lanatina.XP_0013644049_elongation_factor_21ike Cintestinalis.LOC100179939_alongation_factor_21ike Aplanci.LOC1109864429_elongation_factor_21ike Aplanci.LOC110987647_elongation_factor_21ike Avaga.UJR10301.1_hypothetical_protein_I4U23_015014507	QRLAQSDGTQ-EAVS	-SEVAVQPEKQESE	
Dmelanogaster_CG33158_uncharacterized_protein_Dmel K	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hppothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat Gintestinalis.LoC0100175824_116_kDa_U5_small_nucleat Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_ribo Bbelcheri.LoC1109861499_116_kDa_U5_small_nuclear_ribo Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_002631 Myessoensis.XP_0213613918.1_elongation_factor_2like Egranulosus.XP_021362159.1_elongation_factor_2like Egranulosus.XP_021362159.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Cintestinalis.LoC100177993_elongation_factor_2like Lanatinalis.LoC100178953_LOW_QUMLTLY_PROTEIN_elo Hsapiens.NP_001952.1_elongation_factor_2like Epranulosus.XP_001964429_elongation_factor_2like Aplanci.LoC110987647_elongation_factor_2like Aplanci.LoC110987647_elongation_factor_2like Aplanci.LoC110987647_elongation_factor_2like Aplanci.LoC110987647_elongation_factor_2like Aplanci.LoC110987647_elongation_factor_12like Avaga.UJR10301.1_hypothetical_protein_I4U23_014507 Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEFZ_eukaryotic_translation_elongati	QRLAQSDGTQ—EAVS———————————————————————————————————	-SEVAVQPEKQESEPFEKEAGE ISNGTASAVNGGGAPSVEANGIAMEIKA 9404	
Hsapiens.NP_078856.4_elongation_factorlike_GTPase VPLGFSAPPDG	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR369000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.GG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat Cintestinalis.LOC100175824_116_kDa_U5_small_nucleat Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r Lanatina.XP_0213493490.1_116_kDa_U5_small_nuclear_r Haspiens.NP_004238.3_116_kDa_U5_small_nuclear_r Haspiens.NP_004238.3_116_kDa_U5_small_nuclear_r Haplanci.LOC110989613_116_kDa_U5_small_nuclear_r Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_bloogation_factor_2like Egranulosus.XP_021349219.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Cintestinalis.LOC1001778953_loNg_UJALITY_PROTEIN_elo Hsapiens.NP_001952.1_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_2like Aplanci.UGC110987647_elongation_factor_2like Aplanci.UGC134569.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_eukaryotic_translation_elongatic Egranulosus.XP_024354541.1_Elongation_factor_TU_GT Egranulosus.XP_0243555481.1_Elongation_factor_TU_GT Egranulosus.XP_024355481.1_Elongation_factor_TU_GT Egranulosus.XP_024355481.1_Elongation_factor_TU_GT Egranulosus.XP_024355481.1_Elongation_factor_TU_GT Egranulosus.XP_024355481.1_Elongation_factor_TU_GT Egranulosus.XP_0243555481.1_Elongation_factor_TU_GT Egranulosus.XP_024355481.1_Elongation_factor_TU_GT Egranulosus.XP_024355481.1_Elongation_factor_TU_GT	QRLAQSDGTQ—EAVS—— EKMSQPTDVVNEKTKDEEVTTSQGSTV 08 9203	SEVAVQPEKQESE———PFEKEAGE FSNGTASAVNGGGAPSVEANGIAMEIKA 940å	
Bebcheri LOC109463052_elongation_factorlike_GTPas = -DLSDAPGDLSQLKHV	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.GG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleac cintestinalis.LOC100175824_116_kDa_U5_small_nucleac Lanatina.XP_0213349340.1_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC109443940.1_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribo Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_0076257 Myessoensis.XP_021349219.1_elongation_factor_21ike Egranulosus.XP_021362159.1_elongation_factor_21ike Lanatina.XP_013394736.1_elongation_factor_21ike Lanatina.XP_001362159.1_elongation_factor_21ike Lanatina.XP_001362159.1_elongation_factor_21ike Lanatina.XP_001364429_elongation_factor_21ike Cintestinalis.LOC100177993_elongation_factor_21ike Aplanci.LOC110987647_elongation_factor_21ike Aplanci.LOC110987647_elongation_factor_21ike Aplanci.LOC110987647_elongation_factor_21ike Aplanci.LOC110987647_elongation_factor_14U23_028438 Dmelanogaster.EgF2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Elongation_factor_14U23_028438 Dmelanogaster.EgF2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Elongation_factor_LOT_DGT Avaga.UJR28421.1_hypothetical_protein_I4U23_029661 Dmelanogaster.Egf2_18358_uncharacterized_protein_Dmel	QRLAQSDGTQ—EAVS—— EKMSGPTDVVNEKTKDEEVTTSQGSTV 20 20 20 20 20 20 20 20 20 20 20 20 20	SEVAVQPEKQESE———PFEKEAGE FSNGTASAVNGGGAPSVEANGIAMEIKA 940A	
Aplanci.LOC110988091_elongation_factorlike_GTPaseDEGWMSFFVESEVSGSSV	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UUR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat Cintestinalis.LOC100175824_116_kDa_U5_small_nucleat Lanatina.XP_021349342.1_116_kDa_U5_small_nuclear_ribons Lanatina.XP_021349342.1_116_kDa_U5_small_nuclear_ribons Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribons Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribons Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribons Avaga.UUR26319.1_hypothetical_protein_I4U23_007657 Avaga.UUR26319.1_hypothetical_protein_I4U23_022281 Myessoensis.XP_0213349219.1_elongation_factor_21ike Egranulosus.XP_0213394736.1_elongation_factor_21ike Lanatina.XP_013394736.1_elongation_factor_21ike Cintestinalis.LOC100178953_LOW_OUALITY_PROTEIN_elo Hsapiens.NP_001952.1_elongation_factor_21ike Aplanci.LOC110987647_elongation_factor_21ike Aplanci.LOC110987647_elongation_factor_21ike Avaga.UUR10301.1_hypothetical_protein_I4U23_014507 Avaga.UUR28421.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_eukaryotic_translation_elongatier Egranulosus.XP_024355481.1_Elongation_factor_1_G Avaga.UUR28421.1_hypothetical_protein_I4U23_009661 Dmelanogaster.GG33158_uncharacterized_protein_Dmel Cintestinalis.LOC100775902_elongation_factor_Dmel Cintestinalis.LOC100775902_elongation_factor_I6con_Cintestinalis.LOC100775902_elongation_factor_Dcator_I6con_Dmel Cintestinalis.LOC100775902_elongation_factor_Drator_I6con_Dmel Cintestinalis.LOC100775902_elongation_factor_Drator_I6con_Dmel Cintestinalis.LOC100775902_elongation_factor_Drator_I6con_Dmel Cintestinalis.LOC100775902_elongation_factor_Drator_I6con_Dmel Cintestinalis.LOC100775902_elongation_factor_Drator_I6con_Dmel Cintestinalis.LOC100775902_elongation_factor_Drator_I6con_Cintestinalis.LOC100775902_elongation_factor_Drator_I6con_Cintestinalis.LOC100775902_elongation_factor_Drator_I6con_Cintestinal	ORLAQSDGTQ-EAVS	SEVAVQPEKQESE———PFEKEAGE ISNGTASAVNGGGAPSVEANGIAMEIKA 940å	
Myessoensis.XP_021362732.1_elongation_factorlike_G -AVRVGQSVDDLGTHDHI	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.GG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat cintestinalis.IoC100175824_116_kDa_U5_small_nucleat Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r Lanatina.XP_021343490.1_116_kDa_U5_small_nuclear_r Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_r Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribo Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR2919.1_elongation_factor_21ike Egranulosus.XP_021349219.1_elongation_factor_21ike Egranulosus.XP_021354781.1_Blongation_factor_21ike Lanatina.XP_013394736.1_elongation_factor_21ike Cintestinalis.LOC100177993_elongation_factor_21ike Cintestinalis.UG100177993_elongation_factor_21ike Avaga.UJR10301.1_hypothetical_protein_I4U23_0028438 Dmelanogaster.GG33158_uncharacterized_protein_I4U23_028438 Dmelanogaster.EEFZ_eukaryotic_translation_elongati Egranulosus.XP_024355481.Elongation_factor_1UGA Avaga.UJR28421.1_hypothetical_protein_I4U23_028438 Dmelanogaster.EG33158_uncharacterized_protein_Dmel Cintestinalis.LOC100175992_elongation_factor_11ke_GRPass Bbelcheri.LOC10948055_elongation_factor-like_GRBas Bbelcheri.LOC10948055_elongation_factor-like_GRBas Bbelcheri.LOC10948055_elongation_factor-like_GRBas Bbelcheri.LOC10948055_elongation_factor-like_GRBas Bbelcheri.LOC10948055_elongation_factor-like_GRBas Bbelcheri.LOC10948055_elongation_factor-like_GRBas	QRLAQSDGTQ-EAVS	SEVAVQPEKQESE———PFEKEAGE FSNGTASAVNGGGAPSVEANGIAMEIKA 940A	
Myessoensis.XP_021350409.1_elongation_factor_2like CGNLCAIRGVE-QMAKKGVVTSHSPEVVFTDIRHSVSPVVQLDIQKNPGDAPNLLIEIKRLMKLHPVLECSIAASG Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu ACNWVLIEGVD-QAIVKTSTITSAHSD	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UUR20900.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat Gintestinalis.LoC100175824_116_kDa_U5_small_nucleat Lanatina.XP_0213349349.1_116_kDa_U5_small_nuclear_ribo Egranulosus.XP_02343490.1_116_kDa_U5_small_nuclear_ribo Ebelcheri.LoC109461499_116_kDa_U5_small_nuclear_ribo Ebelcheri.LoC109461499_116_kDa_U5_small_nuclear_ribo Avaga.UUR26319.1_hypothetical_protein_I4U23_007657 Avaga.UUR26319.1_hypothetical_protein_I4U23_022281 Myessoensis.XP_021349219.1_elongation_factor_21ike Egranulosus.XP_021349219.1_elongation_factor_21ike Egranulosus.XP_021362159.1_elongation_factor_21ike Cintestinalis.LoC100177993_elongation_factor_21ike Lanatina.XP_01392.1_elongation_factor_21ike Lanatina.SP_01395.1_elongation_factor_21ike Aplanci.LoC1109887647_elongation_factor_21ike Aplanci.LoC1109887647_elongation_factor_21ike Aplanci.LoC1109887647_elongation_factor_14U23_014507 Avaga.UUR28421.1_hypothetical_protein_I4U23_014507 Avaga.UUR285689.1_hypothetical_protein_I4U23_014507 Avaga.UUR28421.1_hypothetical_protein_I4U23_00861 Dmelanogaster.CG33158_uncharacterized_protein_Dmel Cintestinalis.LoC100175902_elongation_factor-Iike_G Hsapiens.NP_078856.4_elongation_factor-like_G Hsaplens.NP_078856.4_elongation_factor-like_G Hsaplens.NP_078856.9_elongation_factor-like_G Hsaplens.NP_078856.9_elongation_factor-like_G Hsaplens.NP_078856.9_elongation_factor-like_G Hsaplens.NP_078856.9_elongation	QRLAQSDGTQ—EAVS———————————————————————————————————	SEVAVQPEKQESE———PFEKEAGE ISNGTASAVNGGGAPSVEANGIAMEIKA 940å	REIEERSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSRVLE S608
Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu AGMV/LIEGVDQAIVKTSTITSAHSD	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.GG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleac Cintestinalis.IOC100175824_116_kDa_U5_small_nucleac Cintestinalis.IOC100175824_116_kDa_U5_small_nuclear_ribo Egranulosus.XP_021349340.1_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribo Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_0076278 Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_024354781.1_Elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Cintestinalis.LOC100177993_elongation_factor_2like Cintestinalis.UOC100177993_elongation_factor_2like Aplanci.LOC1109864429_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_12like Aplanci.LOC110987647_elongation_factor_2like Dmelanogaster.Ceff2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Elongation_factor_11ke_C Avaga.UJR35689.1_hypothetical_protein_I4U23_009661 Dmelanogaster.Ceff2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Elongation_factor_11ke_G Esapiens.NP_078856.4_elongation_factor-like_GTPase Bbelcheri.LOC109464052_elongation_factor-like_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPase Aplanci.LOC1109869119575.1_elongation_factorlike_GTPase Aplanci.LOC1109869719575.1_elongation_factorlike_GTPase Aplanci.LOC1109463052_elongation_factorlike_GTPase Aplanci.LOC1109463052_elongation_factorlike_GTPase Aplanci.LOC1109463052_elongation_factorlike_GTPase Aplanci.LOC1109463052_elongation_factorlike_GTPase Aplanci.LOC1109463055_elongation_factorlike_GTPase	QRLAQSDGTQ-EAVS	SEVAVQPEKQESE———PFEKEAGE ISNGTASAVNGGGAPSVEANGIAMEIKA 9403	
Avaga_UUR09000.1_hypothetical_protein_I4U23_013250 AGMW/LIEGUDQSILKTATIVONSGLVRGRRTHATNIDDVQIFRPLKFNTTSVIKIAVEPVNPSELPKMLDGLRKVNKSYPLLNTKVEESG Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ AGNWVLIEGIDQCIVKTSTIVDINVP	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UUR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat Cintestinalis.LoC100175824_116_kDa_U5_small_nucleat Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_ribons Elongain.NP_004238.3_116_kDa_U5_small_nuclear_ribons Bbelcheri.LoC109461499_116_kDa_U5_small_nuclear_ribons Bbelcheri.LoC109461499_116_kDa_U5_small_nuclear_ribons Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR26319.1_hypothetical_protein_I4U23_002281 Myessoensis.XP_021349219.1_elongation_factor_2like Egranulosus.XP_021362159.1_elongation_factor_2like Egranulosus.XP_021362159.1_elongation_factor_2like Cintestinalis.LoC100177993_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Aplanci.LoC1109887647_elongation_factor_2like Aplanci.LoC1109887647_elongation_factor_2like Aplanci.LoC1109887647_elongation_factor_2like Avaga.UJR10301.1_hypothetical_protein_I4U23_014507 Avaga.UJR28421.1_hypothetical_protein_I4U23_014507 Avaga.UJR28421.1_hypothetical_protein_I4U23_014507 Avaga.UJR28421.1_hypothetical_protein_I4U23_00461 Dmelanogaster.cEF2_eukaryotic_translation_elongati Egranulosus.XP_024355481.Elongation_factor_Tu_GT Avaga.UJR28421.1_hypothetical_protein_I4U23_00461 Dmelanogaster.CG33158_uncharacterized_protein_Dmel Cintestinalis.LoC100175902_elongation_factor_Tu_GT Brayen.NP_078856.4_elongation_factor_Tike_GTPase Bbelcheri.LoC109463052_elongation_factorlike_GTPase Bbelcheri.LoC109463052_elongation_factorlike_GTPase Lanatina.XP_013413557.1_elongation_factorlike_GTPase Lanatina.XP_013413557.1_elongation_factorlike_GTPase Lanatina.XP_013413557.1_elongation_factorlike_GTPase Lanatina.XP_013413557.1_elongation_factorlike_GTPase Lanatina.XP_013413557.1_elongation_factorlike_GTPase	QRLAQSDGTQ—EAVS———————————————————————————————————	-SEVAVQPEKQESEPFEKEAGE ISNGTASAVNGGGAPSVEANGIAMEIKA 940A 940A 	REIEERSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSRVLE S608
Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ AGNWVLIEGIDQCIVKTSTIVDINVP	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.GG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat cintestinalis.IOC100175824_116_kDa_U5_small_nucleat Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r Lanatina.XP_021334940.1_116_kDa_U5_small_nuclear_r Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_r Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_ribo Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribo Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_bologation_factor_2like Egranulosus.XP_021362159.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Cintestinalis.LOC100177992_elongation_factor_2like Avaga.UJR10301.1_hypothetical_protein_I4U23_028438 Dmelanogaster.G33158_uncharacterized_protein_l0123_028438 Dmelanogaster.G33158_uncharacterized_protein_l01257 Avaga.UJR28421.1_hypothetical_protein_I4U23_028438 Dmelanogaster.G33158_uncharacterized_protein_Dmel Cintestinalis.LOC100175902_elongation_factor_Tu_GT Avaga.UJR28421.1_hypothetical_protein_I4U23_009661 Bnelanogaster.G33158_uncharacterized_protein_Dmel Cintestinalis.LOC100175902_elongation_factorlike_GTPase Aplanci.LOC110988091_elongation_factorlike_GTPase Aplanci.LOC110988091_elongation_factorlike_GTPase Aplanci.XP_01313557.1_elongation_factorlike_GTPase Aplanci.XP_01313557.1_elongation_factorlike_GTPase Aplanci.XP_01313557.1_elongation_factorlike_GTPase Aplanci.XP_0131557.1_elongation_factorlike_GTPase Aplanci.XP_0131557.1_elongation_factorlike_GTPase Aplanci.XP_0131557.1_elongation_factorlike_GTPase Aplanci.XP_0131557.1_elongation_factorlike_GTPase Aplanci.XP_0131557.1_elongation_factorlike_GTPase Aplanci.XP_013155	ORLAAQSDGTQ-EAVS	SEVAVQPEKQESE———PFEKEAGE FSNGTASAVNGGGAPSVEANGIAMEIKA 9404 9404 //QARHRSSSCSSISSNLSGAFSAGSVGD.	REIEERSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSRVLEF S608
Cintestinalis.LOC100175824_116_kDa_U5_small_nuclea AGNWVLMEGVDEPIVKTSTITQARGNEEAHIFKPLKFNTSSVVKIAVEPVNPSELPKMLDGLRKVNKSYPLLTTKVEESG Lanatina.KP_013419342.1_116_kDa_U5_small_nuclear_r AGNWVLIEGIDQPIVKTSTITEATGNEEAFIFRPLKFNTSSVIKIAVEPVNPSELPKMLDGLRKISKSYPLVTTKVEESG Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r AGNWVLIEGIDQPIVKTSTITEATGN	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UUR90900.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_l16_kDa_U5_small_nucleat Cintestinalis.LoC100175824_l16_kDa_U5_small_nucleat Lanatina.XP_0213349349.1_l16_kDa_U5_small_nuclear_ribon Elongation_IAMP_013419342.1_l16_kDa_U5_small_nuclear_ribon Bbelcheri.LoC109461499_l16_kDa_U5_small_nuclear_ribon Bbelcheri.LoC109461499_l16_kDa_U5_small_nuclear_ribon Bbelcheri.LoC109461499_l16_kDa_U5_small_nuclear_ribon Avaga.UUR26319.1_hypothetical_protein_I4U23_007657 Avaga.UUR26319.1_hypothetical_protein_I4U23_022281 Myessoensis.XP_0213349219.1_elongation_factor_21ike Egranulosus.XP_024354781.1_Blongation_factor_21ike Egranulosus.XP_013394736.1_elongation_factor_21ike Lanatina.XP_013394736.1_elongation_factor_21ike Avaga.UUR26319.1_hypothetical_protein_I4U23_014507 Avaga.UUR35689.1_bnypothetical_protein_I4U23_014507 Avaga.UUR35689.1_hypothetical_protein_I4U23_014507 Avaga.UUR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_eukaryotic_translation_elongatic Egranulosus.XP_024355481.1_Elongation_factor_Iu_EGRavaga.UUR28421.1_hypothetical_protein_I4U23_009661 Dmelanogaster.CG33158_uncharacterized_protein_Dmel Cintestinalis.LoC100175902_elongation_factorlike_GTPase Bbelcheri.LoC109463052_elongation_factorlike_GTPase Lanatina.XP_013413557.1_elongation_factorlike_GTPase Lanat	QRLAAQSDGTQ-EAVS	SEVAVQPEKQESE———PFEKEAGE ISNGTASAVNGGGAPSVEANGIAMEIKA 9408 VQARHRSSSCSSISSNLSGAFSAGSVGD. 10408 10408 10408 10408	REIEERSDQ-VFLAFARYYSGTVKKGQKLYVLGPKHDPSRVLE S608
Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r AGNWVLIEGIDQPIVKTSTITEATGNEEAFIFRPLKFNTSSVIKIAVEPVNPSELPKMLDGLRKISKSYPLVTTKVEESG Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r AGNWVLIEGIDQPIVKTSTITEATGN	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UUR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat Cintestinalis.IOC100175824_116_kDa_U5_small_nucleat Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_ribon Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribon Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribon Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribon Avaga.UUR26319.1_hypothetical_protein_I4U23_007657 Avaga.UUR19151.1_hypothetical_protein_I4U23_007657 Avaga.UUR19151.1_hypothetical_protein_I4U23_007657 Avaga.UUR19151.1_hypothetical_protein_I4U23_007657 Avaga.UUR19151.1_hypothetical_protein_I4U23_007657 Avaga.UUR19151.1_bologation_factor_2like Egranulosus.XP_02134781.1_Elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2like Cintestinalis.IOC1001778953_longation_factor_2like Cintestinalis.IOC1001778953_longation_factor_2like Aplanci.LOC110987647_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_12like Aplanci.SOC100178953_longation_factor_1016401640164016401640164016401640164016	QRLAQSDGTQ-EAVS	SEVAVQPEKQESE———PFEKEAGE FSNGTASAVNGGGAPSVEANGIAMEIKA 940A 940A VQARHRSSSCSSISSNLSGAFSAGSVGD. 1040A 1040A 1040A 1040A 1058 1	
Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_ribo AGNWVLIEGVDQPIVKTATITEPRGNEEAQIFRPLKFNTTSVIKIAVEPVNPSELPKMLDGLRKVNKSYPSLTTKVEESG Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ri AGNWVLIEGVDQPIVKTSTITEARGNDEAYIFRSLKFNTSSVIKIAVEPVNPSELPKMLDGLRKVNKSYPLLTTKVEESG	Myessoensis.XP_021362732.1_elongation_factorlike_G gnanulosus.XP_0224347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nuclear_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleae_ Cintestinalis.LOC100175824_116_kDa_U5_small_nucleae_ Cintestinalis.IOC100175824_116_kDa_U5_small_nuclear_ Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_ribon Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribon Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribon Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_007657 Cintestinalis.LOC100177993_elongation_factor_21ike Egranulosus.XP_0223454781.1_Blongation_factor_22ike Lanatina.XP_03394736.1_elongation_factor_22ike Cintestinalis.LOC100177993_elongation_factor_21ike Cintestinalis.LOC100177993_elongation_factor_22ike Aplanci.LOC1109864429_elongation_factor_21ike Avaga.UJR10301.1_hypothetical_protein_I4U23_007867 Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.EG7_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Blongation_factor_11ike_GTPase_ Aplanci.LOC1109863052_elongation_factor_like_GTPase_ Bbelcheri.LOC109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC110988091_elongation_factorlike_GTPase_ Bbelcheri.LOC1109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC1109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC1109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC1109463052_elongation_factorlike_GTPase_ Bbelcher	QRLAAQSDGTQ—EAAVS——————————————————————————————————	-SEVAVQPEKQESEPFEKEAGE FSNGTASAVNGGGAPSVEANGIAMEIKA 9404 //QARHRSSSCSSISSNLSGAFSAGSVGD. 10404 10404SEPAFIFHPLTFN LVRGRRTHATNIDDVQIFRPLKFN P	REIEERSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSRVLE S608
Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ri AGNWVLIEGVDQPIVKTSTITEARGN	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UUR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleat_ Cintestinalis.LOCI00175824_116_kDa_U5_small_nucleat_ Lanatina.XP_0213349342.1_116_kDa_U5_small_nuclear_ribon Boelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribon Ebelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribon Ebelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribon Avaga.UUR26319.1_hypothetical_protein_I4U23_007657 Avaga.UUR26319.1_hypothetical_protein_I4U23_002281 Myessoensis.XP_0213349219.1_elongation_factor_2like Egranulosus.XP_024354781.1_Elongation_factor_2like Egranulosus.XP_021362159.1_elongation_factor_2like Cintestinalis.LOC100177993_elongation_factor_2like Cintestinalis.LOC100178935_LOW_QUALITY_PROTEIN_elo Hsapiens.NP_001952.1_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_2like Aplanci.UOC110987647_elongation_factor_2like Aplanci.UOC110987647_elongation_factor_2like Aplanci.UOC110987647_elongation_factor_2like Aplanci.UOC1094355481.1_Elongation_factor_1007 Avaga.UUR35689.1_hypothetical_protein_I4U23_014507 Avaga.UUR35689.1_hypothetical_protein_I4U23_0028438 Dmelanogaster.CG33158_uncharacterized_protein_Dmel_ Cintestinalis.LOC100175902_elongation_factor1ike_GTPas Elanatina.XP_013413557.1_elongation_factor1ike_GTPas Elanatina.XP_013413557.1_elongation_factor1ike_GTPas Lanatina.XP_013413557.1_elongation_factor1ike_GTPas Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Dmelanogaster.G4849_uncharacterized_protein_Dmel_ Dmelanogaster.G4849_uncharacterized_protein_Dmel_ Dmelanogaster.G4849_uncharacterized_protein_Dmel_ Dmelanogaster.G4849_uncharacterized_protein_Dmel_ Dmelanogaster.G54849_uncharacterized_protein_Dmel_ Dmelanogaster.G54849_uncharacterized_protein_Dmel_ Dmelanogaster.G54849_uncharacterized_protein_Dmel_ Myessoensis.XP_02135566.1_116_kDa_U5_small_nuclear_ribonu Avaga.U	QRLAAQSDGTQ-EAAVS	SEVAVQPEKQESE———FFEKEAGE ISNGTASAVNGGGAPSVEANGIAMEIKA 9408 VQARHRSSSCSSISSNLSGAFSAGSVGD. 10408 SEPAFIFHPLT——FN LVRGRRTHAINIDDVQIFRPLK——FN 2	WEIEERSDQ-VFLAFARYYSGTVKKGQKLYVLGPKHDPSRVLE 9808
	Myessoensis.XP_021362732.1_elongation_factorlike_G Myessoensis.XP_021350409.1_elongation_factor_2like Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu Avaga.UJR309000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleae Cintestinalis.IOC100175824_116_kDa_U5_small_nucleae Cintestinalis.IOC100175824_116_kDa_U5_small_nucleae. Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_ribon Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribon Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribon Avaga.UJR26319.1_hypothetical_protein_I4U23_007657 Avaga.UJR2919.1_elongation_factor_21ike Egranulosus.XP_024345781.1_Blongation_factor_21ike Egranulosus.XP_024345781.1_Blongation_factor_21ike Lanatina.XP_03394736.1_elongation_factor_21ike Lanatina.XP_03394736.1_elongation_factor_21ike Cintestinalis.LOC100177993_elongation_factor_21ike Cintestinalis.UOC100177993_elongation_factor_21ike Avaga.UJR35689.1_hypothetical_protein_I4U23_007667 Avaga.UJR35689.1_hypothetical_protein_I4U23_008643 Dmelanogaster.eEf2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Elongation_factor_21ike Avaga.UJR35689.1_hypothetical_protein_I4U23_008643 Dmelanogaster.eEf2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Elongation_factor_TU_GT Avaga.UJR35689.1_hypothetical_protein_I4U23_008643 Dmelanogaster.eEf2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Elongation_factor_Tu_GT Avaga.UJR35689.1_hypothetical_protein_I4U23_008643 Elanatina.XP_031433557.1_elongation_factor_like_GTPase Bbelcheri.LOC109463052_elongation_factor_like_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTP	QRLAQSDGTQ-EAVS		REIEERSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSQVEG 9808
	Myessoensis.XP_021362732.1_elongation_factorlike_G gnanulosus.XP_0224347861.1_U5_small_nuclear_ribonu Avaga.UJR09000.1_hypothetical_protein_I4U23_013250 Dmelanogaster.CG4849_uncharacterized_protein_Dmel_ Myessoensis.XP_021345506.1_116_kDa_U5_small_nucleac_ Gintestinalis.IOC100175824_116_kDa_U5_small_nucleac_ Gintestinalis.IOC100175824_116_kDa_U5_small_nucleac_ Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_ribonu Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribonu Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ribonu Avaga.UJR19151.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_007657 Avaga.UJR19151.1_hypothetical_protein_I4U23_007657 Cintestinalis.IOC100177993_elongation_factor_21ike Egranulosus.XP_0223454781.1_Blongation_factor_22 Myessoensis.XP_02136219.1_elongation_factor_21ike Lanatina.XP_013394736.1_elongation_factor_22 Myessoensis.XP_02136219.1_elongation_factor_21ike Cintestinalis.IOC100177993_elongation_factor_21ike Cintestinalis.IOC100177993_elongation_factor_21ike Cintestinalis.IOC109464429_elongation_factor_21ike Aplanci.LOC110987647_elongation_factor_21ike Aplanci.LOC110987647_elongation_factor_21ike Aplanci.LOC110987647_elongation_factor_21ike Aplanci.LOC110987647_elongation_factor_11ike_GTPase_ Bbelcheri.LOC109463052_elongation_factor_11ike_GTPase_ Dmelanogaster.CG33158_uncharacterized_protein_Dmel Cintestinalis.LOC100178902_elongation_factor_11ike_GTPase_ Bbelcheri.LOC109463052_elongation_factor_11ike_GTPase_ Bbelcheri.LOC109463052_elongation_factorlike_GTPase_ Bbelcheri.LOC109463052_elong	QRLAAQSDGTQ-EAAVS		REIEERSDQ-VFLAFARVYSGTVKKGQKLYVLGPKHDPSQVEG 9808

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Avaga.UJR26319.1_hypothetical_protein_14U23_007657 AGNVVALTGID--KCLLKTATITTN----------AEAHNFRVMK----FSVSPVVRVAVDVKD---PADHAKLVDGLKKLVQADSLVQVLNEN-GAVaga.UJR19151.1_hypothetical_protein_14U23_022281 CGNICGLIGID--RYLIKNGTITTY-------------ENAYLIRKMK----FHVSPLVRVAVEPTN----VEDLPKLIEKLKYLNQLDPIVECTWEESGAVAGA.
Myessoensis.XP_021349219.1_elongation_factor_2like CGNTVGLIVGLD-KYLIKSGTVSTY------QHAHNMAVMR---
Egranulosus.XP_024354781.1_Elongation_factor_2 CGNICGLVGVD-QFLVKTGTITTF------SGAHNMRQMK---
Myessoensis.XP_021362159.1_elongation_factor_2like CGNICGLVGVD-QFLVKTGTLTTF------------EGAHNLKQMK---
                                                                                                              -FSVSPVVRVAVDPVN---AAELPKLLEGLORLTKSDPMVOCITEN-G
                                                                                                               FSVSPVVRVAVDCKN---PSDLPKLVEGLKRLAKSDPMVLIQTEESG
                                                      CGNICGLVGVD-QFLVKTGTLTTF-----CGNICGLVGVD-QFLVKTGTLTTF-----
                                                                                                               FSVSPVVRVAVEAKN---PAELPKLVEGLKRLAKSDPMVLCCIEESG
Lanatina.XP_013394736.1_elongation_factor_2
Cintestinalis.LOC100177993_elongation_factor_2like
                                                                                               -DQAHNMKMMK
                                                      CGNICGLVGVD--NFLVKTGTLTTS-----
                                                                                              --DQAHNMKQMK-
                                                                                                              -FSVSPVVRVAVEAKN---PSDLPKLVEGLKRLAKSDPMVLCQIEESG
Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo
Hsapiens.NP_001952.1_elongation_factor_2
Bbelcheri.LOC109464429_elongation_factor_21ike
                                                      CGNICGLVGVD--NFLVKTGTLTTS-----DOAHNMKOMK-
                                                                                                              -FSVSPVVRVAVEAKN---PSDLPKLVEGLKRLAKSDPMVLCHTEESG
                                                      -FSVSPVVKVAVEAKN---FSULPKIVEGLKKLAKSDPMVLCHLEESG
-FSVSPVVRVAVEAKN---PADLPKLVEGLKRLAKSDPMVQCIIEESG
-FSVSPVVRVAVEPKN---PSELPKLVEGLKRLAKSDPMVQCIIEESG
-FSVSPVVRVAVEAKD---PSQLPKLVEGLKRLSKSDPMVQCIIEESG
Aplanci.LOC110987647_elongation_factor_2like
-FSVSPVVRVAVEPRN---PADI.PKI.VEGI.KRI.AKSDPMVOCITEESG
                                                                                                              -FSVSPVVRVAVEPRN---PADLPKLVEGLKRLAKSDPMVQCIIEESG
                                                                                             ---KDAHMKVMK----FSVSPVVRVAVEPKN---PADLPKLVPGLKRLAKSDPMVQCIIEESG
-ATSEARRVLPLAGLAIWHGAPVVSLAIEPASATDPNDMVRLENGLRLLERSDPCAELTFSPKG
Avaga.UJR28421.1 hypothetical protein I4U23 009661 AGNIVAIGQLD--SLVLKSATLSTD------IFCPSFTGLH----FEVSPIVRVAIETKN---PSQMKQLRHGMKLLNQADPLVECTLKDTG
Dmelanogaster.CG33158_uncharacterized_protein_Dmel
Cintestinalis.LOC100175902_elongation_factorlike_G
Hsapiens.NP_078856.4_elongation_factor-like_GTPase
                                                                                                              -VMATPILRVAIEFVQ---PQDMPKLVKGLKLLNQADACVQVSVAPTG
-VDVAPIIRVAVESYL---LSEMSCLVEGLKLLNQADPCVQVMVQETG
-FEATPIVRVAVEPKH---PSEMPQLVKGMKLLNQADPCVQILIQETG
                                                      AGNIVGIGGLE-SHIVKTATLSSS-----LDCTSESELS-
-LDAAPIVRVAVEPKH---AGDMSALMQGLRLLNQADSSVEVLVQESG
Aplanci.LOC110988091_elongation_factorlike_GTBase_ AGNVLGIGGLE-ELVLKSATVSST------VACPAFTSMT-
Lanatina.XP_013413557.1_elongation_factorlike_GTPa AGNVLGIGGLE-EHVLKSGTLSST-------VACPAFTAMY-
Myessoensis.XP_021362732.1_elongation_factorlike_G AGNILGIGGLE-DHILKSGTVSST-------WMCPAFTDFY-
                                                                                                              -FAAAPIVRVAVEPKH---LADMPSLVMGMKLLNOADPCVEVLVOETG
                                                                                                            1100â 1120â 1140â 1140â Myessoensis.XP_021350409.1_elongation_factor_2like LHILTGTSEHLMLRCKSYLEK----QMVLKPTKLHVAYRETV
Egranulosus. XP_024347861.1_U5_small_nuclear_ribonu_ERITRGTGELYLDCVMHDLRRLYS-DIEVKYADPVVAFCETV---
Avaga_UJR09000.1_hypothetical_protein_I4023_013250_EHITLGTGELYLDCVMHDLRRMYS-EIEIKVADPVVTFCETV----
Dmelanogaster.CG4849_uncharacterized_protein_Dmel__EHVILGTGELYLDCVMHDLRRMYS-EIDIKVADPVVAFCETV----
Weyssoensis.XP_021345506.1_116_kba_U5_small_nuclea_EHITLGTGELYLDCVMHDLRKMYS-EIDIKVADPVVSFCETV----
                                                                                                            VETSSI.K-----
                                                                                                            Cintestinalis.LOC100175824 116 kDa U5 small nuclea EHVVLGTGELYLDCVMHDLRRMYA-EIDIKVADPVVAFCETV---
                                                                                                            -VDTSSLK-----
Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r EHIVLGTGELYLDCVMHDLRKLYS-EIDIKVADPVVTFCETV--
Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r EHIVLGTGELYLDCVMHDLRKLYS-EIDIKVADPVVTFCETV--
Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_ribo EHVILGTGELYLDCVMHDLRKLYS-EIDIKVADPVVTFCETV--
                                                                                                            WETSSI K
Bbelcheri.LOC109461499 116 kDa U5 small nuclear ri EHVIMGTGELYLDCVMHDLRKMYS-EIDIKVADPVVAFCETV--
                                                                                                            -VETSSLK-----
Aplanci.LOC110988613_116_kDa_U5_small_nuclear_ribo_EHVVLGTGELYLDCVHHDLKKMYS-EIDIKVADFVVAFCETV---
Avaga.UJR26319.1_hypothetical_protein_I4U23_02281_EHIVKAISEYHLQHCLKTFKEN-----SIKVSDPJISYCETV---
Avaga.UJR19151.1_hypothetical_protein_I4U23_022281_EHIVKAISEYHLQHCLKTFKEN-----SIKVSDPJISYCETV---
Myessoensis.XP_021349219.1_elongation_factor_2like_QHIVAGAGEMHLDICLKDLENDHA-CIPIKRSEFVVTYKEGV---
                                                                                                            VETSSI.K-----
                                                                                                            Egranulosus.XP_024354781.1_Elongation_factor_2
Myessoensis.XP_021362159.1_elongation_factor_2like
Lanatina.XP_013394736.1_elongation_factor_2
                                                      EHIIAGAGELHLEICLKDLEEDHA-CIPIKKSEPVVSYRETV----
                                                      EHIIAGAGELHLEICLKDLEEDHA-GISIKKSDPVVSYRETV-
EHIIAGAGELHLEICLKDLEEEHA-SIPLKVTPPVVSYRETV-
FEASSQT-----
-SEESNVI.-----
                                                                                                            -SEESDIM------
                                                                                                            -SEESDIM-----
                                                                                                            SEESDOM-----VPFDSLAFAKAQLERELKEKHLVYDDARENCVRLCTSNEEEEAFLQQQS
                                                      EYLLHAAGEIHMQKCLEDLTTYFAPDLELHTSPFLVPFRETVTEACPPAS
                                                                                                            -IPPPKVDFLNESLANQHQ-----QMKSN----KTTKE----RPPW
-VPAATVDMVNEAIVKT------AEDKD------
Dmelanogaster.CG33158 uncharacterized protein Dmel EHVITTLGEVHVEKCVHDLEOSYA-KIKVNVSKPIVSFRETI-
Cintestinalis.LOC100175902_elongation_factorlike_G EHVITAAGEVHLQRCLDDLKERFA-KIHISVSEPIIPFRETU----
Hsapiens.NP_078856.4_elongation_factor-like_GTPase_EHVLVTAGEVHLQRCLDDLKERFA-KIHISVSEPIIPFRETI----
Bbelcheri.LOC109463052_elongation_factorlike_GTPas_EHVLVTAGEVHLQRCLDDLTQRFA-KIELNVSDPMVPFRETI----
                                                                                                            -IPRPKVDVLNELIETQDK-----DIMQKWNLKDKESGDGNLTKESEK
                                                                                                           Myessoensis.XP_021362732.1_elongation_factorlike_G V----IETGLVEMYTTNQ--------KCCIRIRA--VSLPDAVTDLLEQNVN-----LKTLHGLN-------RAKVYGQNSKVKDTGV
1360â
                                                                                                                                       1380â
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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					
Hsapiens.NP_004238.3_116_kDa_U5_small_nuclear_ribo					
Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ri		VRITWNRKRLGEFFQTKYD	WDLL	AARSIWAFG	PDNTGPNILVDDTLP
Aplanci.LOC110989613_116_kDa_U5_small_nuclear_ribo		VQINWNRKRLGEFFQTKYD	WDLL	AARSIWAFG	PDATGPNILVDDTLP
Avaga.UJR26319.1_hypothetical_protein_I4U23_007657					
Avaga.UJR19151.1 hypothetical protein I4U23 022281					
Myessoensis.XP_021349219.1_elongation_factor_2like		VKATQDVRERAQYLAANYG			
		VTAKQDPKARGRILTENYG			
Egranulosus.XP_024354781.1_Elongation_factor_2					
Myessoensis.XP_021362159.1_elongation_factor_2like		IAPRQDFKERGKYLTETHN			
Lanatina.XP_013394736.1_elongation_factor_2		VTPRQDPKERGRYLADTYD			
Cintestinalis.LOC100177993_elongation_factor_2like		IFPRQDAKLRGRYLADNFG	FVVN	EARKIWCFG	PEGTGANLLID
Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo		IFPRQDAKLRGRYLADNFD	FDVN	EARKIWCFG	PEGTGANLLID
Hsapiens.NP_001952.1_elongation_factor_2		VSARQELKQRARYLAEKYE	WDVA	EARKIWCFG	PDGTGPNILTD
Bbelcheri.LOC109464429_elongation_factor_2like		INARDDIKTRARKLADDYG	WDVT	EARKIWCFG	PDTNGPNMLVD
Aplanci.LOC110987647_elongation_factor_2like		ITSRTEPKARGRFLADKYD			
Avaga.UJR10301.1_hypothetical_protein_I4U23_014507					
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438		VTPRQEFKARARYLNEKYD			
Dmelanogaster.eEF2_eukaryotic_translation_elongati		VSAKDEFKARARYLSEKYD			
Egranulosus.XP_024355481.1_Elongation_factor_Tu_GT		SSSRRALTCLKRFEEEFSAQLDAVPPEAC			
Avaga.UJR28421.1_hypothetical_protein_I4U23_009661					
Dmelanogaster.CG33158_uncharacterized_protein_Dmel		SIKVKLIAALKDLQLFGLSTLS	PE-E	LVNRIWALG	PRNCGTNILLN-LSD
Cintestinalis.LOC100175902_elongation_factorlike_G	EDGAEIPSLENNVTSVKNIIKNVLF	QLKIKPETLEEIKKLKSDLETAFENAGRR	KWS-N	AVEHIWAFG	PRGNGPNILLNKEDD
Hsapiens.NP_078856.4_elongation_factor-like_GTPase	NTH	MIHQKTQEKIWEFKGKLEQHLTGRR	WR-N	IVDQIWSFG	PRKCGPNILVNKSED
Bbelcheri.LOC109463052_elongation_factorlike_GTPas					
Aplanci.LOC110988091_elongation_factorlike_GTPase_					
Lanatina.XP_013413557.1_elongation_factorlike_GTPa					
Myessoensis.XP_021362732.1_elongation_factorlike_G	ADA	CUNDALIDATION CONTRACTOR CONTRA	WT-D	VIDNIWARC	DEDUCDANT TABLEC
Myessoensis.xr_U21362/32.i_elongacion_lactorlike_G					
			1460â	1480â	
Myessoensis.XP_021350409.1_elongation_factor_2like	ISKQV	RDQGH1KDS11SGFQWA	AREGILCEESMRG	/RIEVRYAK	WQL
Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu					
Avaga.UJR09000.1_hypothetical_protein_I4U23_013250					
Dmelanogaster.CG4849_uncharacterized_protein_Dmel_	SEVDKNL	LTAVKDSIVQGFQWG	TREGPLCEEPIRN	VKFKILD	GVI
Myessoensis.XP_021345506.1_116_kDa_U5_small_nuclea					
Cintestinalis.LOC100175824_116_kDa_U5_small_nuclea		I.GSVKDSTVOGFOW	SREGPLODEPIRM	/KFKTI.D	AVT
Lanatina.XP 013419342.1 116 kDa U5 small nuclear r	T	TVCIOCIIV	II CECVMI -KTI OS	AHHCTO	SK1
Lanatina.XP_023933490.1_116_kDa_U5_small_nuclear_r					
Hsapiens.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	SEVDKAL	LNSVKDSIVQGFQWC	TREGPLCDEPIRN	VKFKILD	AVI
Avaga.UJR26319.1_hypothetical_protein_I4U23_007657	ATKSV	DGLSNIQDAVVAAFQWT	TQEGVVASENLRG	VRIELLD	AEI
Avaga.UJR19151.1_hypothetical_protein_I4U23_022281	CTKGV	QYLSEFKDFFLKMFQF7	TKNGILIEENLRN:	IRFDIHD	ITH
Myessoensis.XP_021349219.1_elongation_factor_2like	ASKSV	OYLODIRDIVRAGEOWS	TEEGVLCEENMRG	JOFNIOD	AHI
Egranulosus.XP_024354781.1_Elongation_factor_2		QYLNDIKDSVVAAFQFV			
Myessoensis.XP_021362159.1_elongation_factor_2like		QYLAEIKDSVVAAFQF			
Lanatina.XP_013394736.1_elongation_factor_2		QYLNEIKESVVAGFQWA			
Cintestinalis.LOC100177993_elongation_factor_2like		QYLSQIKDSVVAGFQWA			
Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo					
Hsapiens.NP_001952.1_elongation_factor_2	ITKGV	QYLNEIKDSVVAGFQWA	TKEGALCEENMRG	VRFDVHD	VTL
Bbelcheri.LOC109464429_elongation_factor_2like		QYLNEIKDSVVAGFQWA			
Aplanci.LOC110987647_elongation_factor_2like		QYLNEIKDSVVAGFQWA			
Avaga.UJR10301.1_hypothetical_protein_I4U23_014507					
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438	CTKGV	QYLNEIKDSCIAGFQWA	TKEGVLAEENVRG	VRFDIHD	VTL
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_eukaryotic_translation_elongati	CTKGV	QYLNEIKDSCIAGFQWF	TKEGVLAEENVRG SKEGILADENLRG	VRFDIHD VRFNIYD	VTL
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Elongation_factor_Tu_GT	CTKGVCTKSV FRLDTAWGKPMSPWSDAAQGPGADA	QYLNEIKDSCIAGFQWF QYLNEIKDSVVAGFQWF VPTGEVGGGGAVHIPFL-SYGKAILRGFQVF	TKEGVLAEENVRG SKEGILADENLRG TEQGPLCAEPMRG	/RFDIHD /RFNIYD /AFVLEDIYAED	VTL VTL RIQLPTPRILTSADLLAKE
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_09661	CTKGVCTKSV FRLDTAWGKPMSPWSDAAQGPGADA' HRGSTIWANVLNNEEKITTNSS	QYLNEIKDSCIAGFQWA QYLNEIKDSVVAGFQWA VPTGEVGGGGAVHIPFL-SYGKAILRGFQVA LMKDDYDLSIVNGFQLA	TKEGVLAEENVRG SKEGILADENLRG TEQGPLCAEPMRG TAKGSLCEEPLMG	/RFDIHD /RFNIYD /AFVLEDIYAED: /GFIIER	VTL VTL RIQLPTPRILTSADLLAKE LTI
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_09661 Dmelanogaster.CG33158_uncharacterized_protein_Dmel		QYLNEIKDSCIAGFQWA QYLNEIKDSVVAGFQWA VPTGEVGGGAVHIPFL-SYGKAILRGFQVA 	TKEGVLAEENVRGY SKEGILADENLRGY TEQGPLCAEPMRGY TAKGSLCEEPLMGY SVAGPLCEEPMQGY	VRFDIHD VRFNIYD VAFVLEDIYAED VGFIIER VCFAVLE	VTL VTL RIQLPTPRILTSADLLAKE LTI
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			TKEGVLAEENVRGY SKEGILADENLRGY TEQGPLCAEPMRGY TAKGSLCEEPLMGY SVAGPLCEEPMQGY TLSGPLCEEPMYG	/RFDIHD //RFNIYD //AFVLEDIYAED: //GFIIER //CFAVLE ICFVIEE	VTL PTL RIQLPTPRILTSADLLAKE
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_09661 Dmelanogaster.CG33158_uncharacterized_protein_Dmel			TKEGVLAEENVRGY SKEGILADENLRGY TEQGPLCAEPMRGY TAKGSLCEEPLMGY SVAGPLCEEPMQGY TLSGPLCEEPMYG	/RFDIHD //RFNIYD //AFVLEDIYAED: //GFIIER //CFAVLE ICFVIEE	VTL PTL RIQLPTPRILTSADLLAKE
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Blongation_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			ATKEGVLAEENVRGY ASKEGILADENLRGY ATEQGPLCAEPMRGY ATAKGSLCEEPLMGY CSVAGPLCEEPMQGY ATLSGPLCEEPMYG ATLSGPMCEEPLMGY	VRFDIHD VRFNIYD VAFVLEDIYAED: VGFIIER VCFAVLE ICFVIEE VCFVLEK	VTL PTL RIQLPTPRILTSADLLAKE
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Blongation_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 Bbelcheri.LOC109463052_elongation_factorlike_GTPase	-CTKGVCTKSV- FRLDTAWGKPMSPWSDAAQGFGADA HRGSTIWANVLNNEERITTNSS YEQPPPWSSHAKSDTD1RSKTD YRRPSIWTCVGDNVD1DIG- FQN-SVWTGPADKASKEAS YQRPSVWDSIDKGEVKSAA	QYLNEIKDSCIAGFOW. QYLNEIKDSVVAGFOW. VPTGEVGGGGAVHIPPI-SYGKALLRGFQVI- LMKDDYDLSIVNGFOLI- PRK-DFNSSLVNGFOLI- SYR-ECHBIISGFOLI- RYR-DLGNSIVSGFOLI-	ATKEGVLAEENVRGY ASKEGILADENLRGY ATEQGPLCAEPMRGY ATAKGSLCEEPLMGY SVAGPLCEEPMQGY ATLSGPLCEEPMYGT ATLSGPMCEEPLMGY ATLSGPMCEEPLMGY ATLSGPMCEEPLMGY ATLAGPLCEEPLMGY	VRFDIHD VRFNIYD VAFVLEDIYAED: VGFIIER VCFAVLE ICFVIEE VCFVLEK VCFMVEE	
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_eukaryotic_translation_elongati Egranulosus.XP_024355481.1_Blongation_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 Bbelcheri.LOC109463052_elongation_factorlike_GTPase Aplanci.LOC110988091_elongation_factorlike_GTPase			TKEGVLAEENVRGY SKEGILADENLRGY STEQGPLCAEPMRGY STAKGSLCEEPLMGY SVAGPLCEEPMYGGY TLSGPLCEEPLMGY TLSGPMCEEPLMGY STLAGPLCEEPLMGY STAGPLCEEPMGY STAGPLCEEPMGY	VRFDIHD VRFNIYD VAFVLEDIYAED VGFIIER VCFAVLE VCFVLEK VCFWLEK VCFMVEE VCIIIEN	VTL- VTL- RIQLPTPRILTSADLLAKE LTI- WSI- WKV- WDL- WDL- WTMHGQLSEK
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438 Dmelanogaster.eEF2_ewkaryotic_translation_elongati Egranulosus.XP_024355481.1_Elongation_factor_Tu_GT Avaga.UJR28421.1_hypothetical_protein_I4U23_009661 Dmelanogaster.GG33158_uncharacterized_protein_Dmel Cintestinalis.LOC100175902_elongation_factorlike_GTBase Bbelcheri.LOC109463052_elongation_factorlike_GTPase Aplanci.LOC110988091_elongation_factorlike_GTPase Lanatina.XP_013413557.1_elongation_factorlike_GTBase_ Lanatina.XP_013413557.1_elongation_factorlike_GTBase_	-CTKGVCTKSV	OYINBIKDSCIAGFOW OYINBIKDSVVAGFOW VPTGEVGGGGAVHIPFL-SYGKAILRGFQVF LWKDDYDLSIVNGFQLI PRK-DFNSSLVNGFQLI SYR-BCDHSIISGFQLI RYR-DLGNSIVSGFQLI QFR-PFDHAIGSGFQLI EIR-PFDSNIVSGFQLI KIR-BYDSNIVSGFQLI	ITKEGVLAEENVRG' ISKEG I LADENLRG' ITEQGPLCAEPMRG' ITAKGSLGEEPLMG' ISVAGPLCEEPMQG' ITLSGPLCEEPMYG: ITLSGPLCEEPLMG' ITLAGPLCEEPLMG' ITLAGPLCEEPLMG' ITFAGPLCEEPMMG' ITFAGPLGEEPMMG' ITLQGPMCEEPMMG'	VRFDIHD VRFNIYD VAFVLEDIYAED! VGFIER VCFAVLE VCFVLEK VCFVLEK VCFWEE VCFVEK VCIIIEN VCFSVEK	VTL
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 Hsapiens.NP_078856.4_elongation_factor-like_GTPass_Bbelcheri.LOC109463052_elongation_factor-like_GTPass_Aplanci.LOC110988091_elongation_factorlike_GTPass_Lanatina.XP_031413557.1_elongation_factor-like_GTPass_Myessoensis.XP_021362732.1_elongation_factorlike_GTPass_Myessoensis.XP_02136	-CTKGV- CTKSV- FRLDTAWGKPMSPWSDAAQGFGADA HRGSTIWANVLNNEERITTNSS YRRPSIWTCVGDNVDIDIG- FQM-SVWTGPADKASKEAS YNRPAIWHCLDSEEKDRAG- YNRPAIWHCLDSEEKDRAG- YDRPSVWSDQVAKVG YDRPSVWSDQOSEG	QYLNEIKDSCIAGFQW. QYLNEIKDSVVAGFQW. VPTGEVGGGGAVHIPFL-SYGKALLRGFQV	ITKEGVLAEENVRG' ISKEGILADENLRG' ITEGGPLCAEPMRG' ITAKGSLCEEPLMG' SVAGPLCEEPMGG' ITLSGPLCEEPMYG' ITLSGPLCEEPMYG' ITLAGPLCEEPLMG' ITLAGPLCEEPLMG' ITLAGPLCEEPLMG' ITLAGPLCEEPMG' ITLAGPLCEEPMG' ITLAGPLCEEPMG' ITLAGPLCEEPMG' ITLAGPLCEEPMG' ITLAGPLCEEPMG' ITLAGPLCEEPMG'	VRFDIHD VRFNIYD VRFNIYD VRFVIEDIYAED VGFIIER VCFAVLE VCFVIEK VCFWEE VCFIIEN VCFSVEK VCFVIEK	- VTL
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 Hsapiens.NP_078856.4_elongation_factor-like_GTPase Bbelcheri.LOC109463052_elongation_factorlike_GTPas Aplanci.LOC110988091_elongation_factorlike_GTPase_Lanatina.XP_013413557.1_elongation_factorlike_GTPa Myessoensis.XP_021362732.1_elongation_factorlike_GTPa	-CTKGVCTKSV FRLDTAWGKPMSPWSDAAQGFGADA' HRGSTIWANVLNNEEKITTNSS YEQPDFWSSHAKSDTDIRSKTD YRRPSIWTCVGDNVOIDIG FQN-SWWTGPADKASKEAS YQRPSVWDSIDKGEVKSAA YNRPAIWHCLDSEEKDRAG YDRPSIWSCLESIE-DQVAKVG YDRPSVWDIGSEG Jâ	OYLNEIKDSCIAGFQW	ITEGVLAEENVRGI SKEGILADENLRGY ITEQGPLCAEPMRGY ITAKGSLCEEPLMGGY ITLSGPLCEEPMGGY ITLSGPLCEEPMGGY ITLSGPLCEEPLMGY ITLSGPLCEEPLMGY ITLSGPLCEEPLMGY ITLAGPLCEEPLMGY ITLGGPMGEEPLMGY ITLGGPMGEEPLMGY ITLGGPLCEEPLRGY 1560å	VRFDIHD VRFNIYD VAFVLEDIYAED! VGFIIER VCFAVLE VCFVUEE VCFWUEE VCFWUEE VCFSVEK VCFSVEK VCFVUEK VCFVUEK	VTL VTL VTL RIQLPTPRILTSADLLAKE LTI WSI WKV WKV WDL WTMHQQLSEK WTMEHSNSC WEM WEM WEM WEYLDMSYAK
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 Hsapiens.NP_078856.4_elongation_factorlike_GTFass Ebbelcheri.LOC109463052_elongation_factorlike_GTFass Aplanci.LOC110988091_elongation_factorlike_GTPass Lanatina.XP_013413557.1_elongation_factorlike_GTPas Myessoensis.XP_021362732.1_elongation_factorlike_G 150 Myessoensis.XP_021350409.1_elongation_factor2 2like	-CTKGVCTKSVCTKSV- FRLDTAWGKPMSPWSDAAQGFGADA HRGSTIWANVLNNEERITTNSSYREPSIWTCVGDNVDIDIG- FQN-SVWTGFADKASKEAS- YQRPSVWSIDIKGEVKSAA YNRPAIWHCLDSEEKDRAGYDRPSIWSCLESIE-DQVAKVG YDRPSIWSCLESIE-DQVAKVGDIQGSEG à 1520à	QYLNEIKDSCIAGFQW QYLNEIKDSVVAGFQW VPTGEVGGGGAVHIPFI-SYGKALLRGFQVI	ITKEGVLAEENVRG' ISKEGILADENLRG' ITEGGPLCAEPMRG' ITAKGSLCEEPLMG' SVAGPLCEEPMGG' ITLSGPLCEEPMGG' ITLSGPLCEEPLMG' ITLAGPLCEEPLMG' ITLAGPLCEEPLMG' ITLAGPLCEEPLMG' ITLAGPLCEEPLMG' ITLAGPLCEEPLMG' ITLAGPLCEEPLRG' 1560â	/RFDIHD //RFNIYD //RFNIYD //RFVLEDIYAED: //GFIIER //CFAVLE //CFVLEK //CFWUEE //CFIIEN //CFVIEK //CFVIEK //CFVIEK	
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	GQIIPTARRVAY	
Avaga.UJR09000.1_hypothetical_protein_I4U23_013250	GQLIPTARRVAY	SSFLLAT-PRLMEPYNFVEVIAPADCVSAVYTVLGRRRGHVTLDAP
Dmelanogaster.CG4849_uncharacterized_protein_Dmel_	GQIIPTARRVAY	SAFLMAT-PRLMEPYLFVEVQAPADCVSAVYTVLARRRGHVTQDAP
Myessoensis.XP_U2I3455U6.1_116_kDa_U5_small_nuclea Cintestinalis.LOC100175824_116_kDa_U5_small_nuclea	GQIIPTSRRVAY	SAFLMAT-PRLMEPYMFVEVIAPADCVSAVYTVLARRRGHVTQDAP
Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r	RQTGPTHR	DRLSVCLYSITGRLYLETP
	GQIIPTARRVAY	
	GQIIFIARKVVI	
Aplanci.LOC110989613_116_kDa_U5_small_nuclear_ribo	GQIIPTARRVAY	SAFLMAT-PRLMEPYYFVEVQAPADCVSAVYTVLARRRGHVTQDAP
Avaga.UJR26319.1_hypothetical_protein_I4U23_007657	DQIIPAIRRCLI	ASLHMAQ-PRLLEPIFLVDIECPTRMIGKVYSTLNKRRGQISEENE
Avaga.UJR19151.1_hypothetical_protein_14U23_U22281 Myessoensis.XP 021349219.1 elongation factor 2like	GQILPTIRRVMY	ASMLTAQ-PRLYQPIYLSEIQCSDVNIPYVYGVLNRYHGIISEQCN ASVLTAA-PRIMEPVYKVEIKAPKYVLGGVVSVLTKRRGOIVDOEE
Egranulosus.XP_024354781.1_Elongation_factor_2	GQIIPTARRCFY	GACLTAS-PAILEPVYVCEIQTPEDALGGIYSTLNKKRGIIFSEEN
Myessoensis.XP_021362159.1_elongation_factor_2like	GQIIGTARRVMY	ASALTAT-PNIMEPIYLVEIEVPENAIGGVFSTLNKRRGEILQQSP
Lanatina.XP_013394736.1_elongation_factor_2	GQIIPTTRRVLY	'ASVLTAR-PKLMEPVYLVEIQAPESVVGNIYGVLNKRRGTVNEATT 'ACOLTAS-DDILEDMYLVOLOCDEOVVGGVVGVLNKDDGOVNOTVD
	GQIIFIARRVLI	
Hsapiens.NP_001952.1_elongation_factor_2	GQIIPTARRCLY	ASVLTAQ-PRLMEPIYLVEIQCPEQVVGGIYGVLNRKRGHVFEESQ
Bbelcheri.LOC109464429_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_2like	GQIIPTARRCLY	
	GQIIFIIRKULI	
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438	GQIIPTCRRVLY	AGMLTAK-PRLYEPVYLCEVQCPEVAVGGIYGVLNRRRGHVFEEHQ
	GQIIPTTRRCLY	
	DEEANSEVEEEHAAKSEKKLTLREHFYWQRRSDNDWLSDVTPGLLTPAMARACT SDESSTLQSQQKPRRVIDKSKIVFTQGPLS-GQIVSTVRDGCF	
	NSRGPFS-GQVLTAAKEVCF	
Cintestinalis.LOC100175902_elongation_factorlike_G	LGPLS-GQLISTSKESCF	RSFQAQP-QRLMAAMYTCNIQATG
	QKGESPLTDCYGPFS-GQLIATMKEACF LSQGVDEDSESSGDDSDRETAESDFMNR-HGPFT-GQLISTMKEACF	
	SPSPLVLAKSPTSDSSSPLVGSPDVSSPWPHFAGRGYGPMS-GQIISTVKEGCF	
Lanatina.XP_013413557.1_elongation_factorlike_GTPa	TEKSVQFKRDVYGPVS-GQIMSTVKDGLF	KAFQSQP-QRLMVAMYTCVIRATAEVLGKVYAVLGRRHGRVTFEDM
Myessoensis.XP_021362732.1_elongation_factorlike_G 1700	RDVIKPQRKREYGPFS-GQIISCVIAGCF	RKAFQTQP-QRLMVAMYKCNIQANSDVLGKLYGVLGKRNGSILEGDM 1760â 1780â
	-LGRTPMSVVCCFLPGEKCLGISGELGSSAKRVEVAFDHWELMNSDPL-	
Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu	-ISGSPLYIIKAFLPVIDSFGFETDLRTHSQGQAF-CMSV-FNHWQMVPGDPL-	
	-VPGSPLYSLKAFLPAIDSMGFETDLRTHTQGQAF-CMSV-FHHWQIVPGDPL-	
	-VSGSPIYTIKAFIPAIDSFGFETDLRTHTQGQAF-CLSV-FHHWQIVPGDPL-	
Cintestinalis.LOC100175824_116_kDa_U5_small_nuclea	-VPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-GLSV-FHHWQIVPGDPL-	
Lanatina.XP_013419342.1_116_kDa_U5_small_nuclear_r	WTRVSFVPW-SPSL-PLLWPGNS	
Lanatina.XP_U2393349U.l_II6_kDa_U5_small_nuclear_r Hsaniens NP 004238 3 116 kDa_U5_small_nuclear_ribo	-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-CLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-SLSV-FHHWQIVPGDPL-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTIKAFIPAIDSFGFTDLRTHTQGAF-IPGSPLYTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	
Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ri	-IPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-CLSV-FHHWQIVPGDPL-	
Aplanci.LOC110989613_116_kDa_U5_small_nuclear_ribo	-VPGSPLYTIKAFIPAIDSFGFETDLRTHTQGQAF-CLSV-FHHWQIVPGDPL-	
	$- LQGTTLTR IKAYLPVNESFGYTEELRHATSGTAF - PQCQ - FDHWAILPGEPF - LIKPSHLIIKAYLPVCESFSFNNILQSN KII - SQCL - FDHWELINEDPL - FDHWELINEDPL] - FDHWELINEDPL - FDHWELINEDPL - FDHWELINEDPL - \mathsf{FDHWE$	
Myessoensis.XP 021349219.1 elongation factor 2like	-DVGTPMVTLKAFLPVNESFGFTEMLRGETGGQAF-PQLV-FDHWQVLPGDPL-	
Egranulosus.XP_024354781.1_Elongation_factor_2	-TPGTPIYIVKAYLPVNESFGFTAELRAATSGKAF-PQCQ-FDHWQLYPGNPL-	
	AQPGRPTCTIKAYLPVNESFGFTAHLRSNTGGQAF-PQCV-FDHWKIMTGDVH-	
Lanatina.XP_013394736.1_elongation_factor_2	-DRGVQ-YTVKAFLPVNESFGFVSHIRQETGGQAF-PQCV-FDHWDLLPGDVT- -NLGTPILTVNAYLPVNESFGFTADLRSNTGGQAF-PQCV-FDHWQVFNGDPL-	
	-NPGTPILTVNAYLPVNESFGFTADLRSNTGGOAF-POCV-FDHWOVFNGDPL-	
Hsapiens.NP_001952.1_elongation_factor_2	-VAGTPMFVVKAYLPVNESFGFTADLRSNTGGQAF-PQCV-FDHWQILPGDPF-	
Bbelcheri.LOC109464429_elongation_factor_2like Aplanci.LOC110987647_elongation_factor_2like	- VVGTPMFIVKAYLPVNESFGFTADLRSNTGGQAF-PQCV-FDHWQILPGDPY-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVKAYLPVNESFGFTADLRSQTGGQAF-PQCV-FDHWQILPGDPS-VPGTPMFMVTAT-VPGTPMFMTAT-VPGTPMFMTAT-VPGTPMFMTAT-VPGTPMFMTAT-VPGTPMFMTAT-VPGTPMTAT	
Avaga.UJR10301.1_hypothetical_protein_I4U23_014507	-VTGTPMFIVKAYLPVNESFGFTADLRSNTGGQAF-PQCV-FDHWQVMNQDPF-	
Avaga.UJR35689.1_hypothetical_protein_I4U23_028438	-VTGTPMFIVKAYLPVNESFGFTADLRSNTGGQAF-PQCV-FDHWQVMNQDPF-	
	-VVGTPMFVVKAYLPVNESFGFTADLRSNTGGQAF-PQCV-FDHWQVLPGDPS-	
Avaga.UJR28421.1_hypothetical_protein_I4U23_009661	-REGEECFVTHARLPVVESFGLTNDLRKRTSGLVSLPQLR-PGGWEVLEVDPLÇ-KEGTSTFIIKAELPVAESFGFAEEMRKKASGLAS-PQISGKTYWEIIELDPF-	;RDASGHIAILGEIHIKVWQRQQEAIKRLRLSERNIVVIADIIISPL
	$- {\tt TQGSGNFAVTCLLPVIESFNFAQEMRKQTSGLAC} - {\tt PQLM-FSHWEVIDIDPF-PQLM-PSHWEVIDIDPF-PQLM-FSHWEVIDPF-PQLM-FSHWEVIDIDPF-PQLM-FSHWEVIDIDPF-PQLM-FSHWEVIDPF-PQLM-FSHWEVIDPF-PQLM-FSHWEVIDIDPF-PQLM-F$	WLPTTE
Cintestinalis.LOC100175902_elongation_factorlike_G	WEGTENBETTWAN DUA EGEGEA DETENBEGANA DON DON DON	MIDTE
	-KEGTDMFIIKAVLPVAESFGFADEIRKRTSGLAS-PQLV-FSHWEIIPSDPF-NESLSVFSIQAALPVAESFGFAEEIRKKTSGLAS-PQLV-FSHWEVVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKKTSGLAS-PQLV-FSHWEVVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKKTSGLAS-PQLV-FSHWEVVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKKTSGLAS-PQLV-FSHWEVVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFSIQAALPVAESFGFAEEIRKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFTAEFGFAEEIRKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFTAEFGFAEEIRKTSGLAS-PQLV-FSHWEVNSDPF-NESLSVFTAEFGFAEETGFAEFGFAEETGFAEFGFAEFGFAEFGFA	
Aplanci.LOC110988091_elongation_factorlike_GTPase_	-REGSPVFDITATLPVAESFGFAEEIRKRTSGLAS-PQLF-FSHWQVVLSDPF-	WEPSTE
Lanatina.XP_013413557.1_elongation_factorlike_GTPa	-MEGSQIFSITAVLPVVESFGFAEEIRKRTSGLAS-PQLQ-FSHWEVVDLDPY-	WVPTTE
Myessoensis.XP_021362732.1_elongation_factorlike_G 180	-TEGSQTFNVVATLPVVESFGFAENIRKKTSGLAS-PQLV-FSHWQVLDVDPF- Dâ 1820â 1840â	WVPTTE 1860â 1880â
	SAAALVAMETRARKGI	
Egranulosus.XP_024347861.1_U5_small_nuclear_ribonu	DRTIQIQPLVAQPATHLAREFMIKTRRKGI	NEDV-SINKYFDDPMLLEFAKQDVMLSYAL
Avaga.UJR09000.1_hypothetical_protein_I4U23_013250	DKSIVIRPLEAQPANHLAREFMIKTRRRKGI	SEDV-SINKFFDDPMLLELARQDVLLNYPI
Myessoensis.XP_021345506.1_116_kDa_U5_small_nuclea	DROTTIN BEL QQASIBARE MIRINGRO	
Cintestinalis.LOC100175824_116_kDa_U5_small_nuclea	DKSVVIRPLEPQPATHLAREFMVKTRRRKGI	SEDV-SISKFFDDPMLLELARQDVMFNYPI
	VLVKMSASTNF	
	DKS111RPLEPQPATALAREFM1K1RRKKG1	
Bbelcheri.LOC109461499_116_kDa_U5_small_nuclear_ri	DKSIVIRPLEPQPATHLAREFMIKTRRKGI	SEDV-SINKFFDDPMLLELARQDVMLNYPM
	TKCGQIVSEIRQRKSI	
	SNIRRIIHNIRKFKGI	
Myessoensis.XP_021349219.1_elongation_factor_2like	SKAGTVVRAIRQRKGI	NPLIPALDNFLDRL
Egranulosus.XP_024354781.1_Elongation_factor_2	SKPGALVAGIRKRKGK	TECHNOLOGIA
Myessoensis.XP_021362159.1_elongation_factor_2like Lanatina.XP_013394736.1_elongation_factor_2	SNSGKIVVATRKRKGI	KEGLPKLDDYLDKL
Cintestinalis.LOC100177993_elongation_factor_2like	SKPFTVVSATRKRKGI	SENVPSLDKFLDKL
Cintestinalis.LOC100178953_LOW_QUALITY_PROTEIN_elo	SKPFAVVSATRKRKGI	NETVPLLEKFYDKL
Hsapiens.NP_001952.1_elongation_factor_2 Bbelcheri.LOC109464429_elongation_factor_2like	SRPSQVVAETRKRKGI	
Aplanci.LOC110987647_elongation_factor_2like	SKPGVVVIEIRKRKGI	
Avaga.UJR10301.1_hypothetical_protein_I4U23_014507	SKIRQIIYDIRKRKGI	KEGIPPLDDYYDKL
	SKIRQIIYDIRKRKGI	
	SKPYAIVQDTRKRKGI SGPGIAVRPASPNSSSTSDSEVDEDLAQAESNNQLTRLRTYLRDVRKRKGI	
Avaga.UJR28421.1_hypothetical_protein_I4U23_009661	EEFLHFGEKADFENRAKKYMNDVRRRKGI	RVEE-KIVEHAEKQRTLKRNK
Dmelanogaster.CG33158_uncharacterized_protein_Dmel	EELMHFGEKADSANRAKVYMDSVRRRKGI	FVDE-QVVEHAEKQRTLSKNK

Cintestinalis.LOC100175902 elongation factorlike G -				
Hsapiens.NP 078856.4 elongation factor-like GTPase -		LHFGEKADSENOARKYMNAVRI	ADACT MINE ATTEMPENO	OTI CENIE
	ELI	LHF GEKADSENQARKIMNAVKI	VKVGTIAEF-VIAEUÕI	KITSKNK
Bbelcheri.LOC109463052_elongation_factorlike_GTPas -	EEL	MHFGEKADSENQGRLYMNSVRI	RRKGLYVDE-KIVEHAEKQI	RTLSKNK
Aplanci.LOC110988091_elongation_factorlike_GTPase	EEL	LHFGEKAENENQALKYMNGVRI	RRKGLYIDK-KTVEHAEKQI	RTLSKNK
Lanatina.XP 013413557.1 elongation factorlike GTPa -	EEY	MHFGEKADSENRARIYMDNVRI	BRKGI.KVDE-BIVEFAEKO	RTI.SKKK
Myessoensis.XP_021362732.1_elongation_factorlike_G -	EEY	LHFGEKADSDNKARQYVNAVRI	KRKGLKVDE-KIVEHAEKQI	RTLTRNK
1900â	à 1920â	1940â	1960â	1980â

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