

Seryl-tRNA synthase

Sequences :

>NP_006504.2 serine--tRNA ligase, cytoplasmic isoform a [Homo sapiens]
MVLDDLFRVDKGGDPALIRETQEKRFKDPGLVDQLVKADSEWRRRCFRADNLNKLNLCSKTIGERMKK
KEPVGDDSEVPENLVSFDDLADALANLKVSQLKKVRLLLIDEAILKCDAERIKLEAERFENLREIGNLLH
PSVPISNDEEDVNKVERIWDGCTVRRKYSHVDLVVMVDGFEGEKGAVVAGSRGYFLKGVLVFLQALIQY
ALRTLGSRGYIPIYTPFFMRKEVMQEVQALSQFDEELYKVIKGSGSEKSDDNSYDEKYLIIATSEQPIAALH
RDEWLRPEDLPIKYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKIEQFVYSSPHDNKSWEMFEEMITTAEE
FYQSLGIPYHIVNIVSGSLNHAASKKLLDEAWFPGSGAFRELVSCSNCTDYQARRLRIRYGTQTKMMMDKV
EFVHMLNATMCATTRTICAILENYQTEKGITVPEKLKEFMPGLQELIPFVKPAPIEQEPSKKQKKQHGE
SKKKAARVDLTLENRLQNMEVTA

>NP_001125910.1 serine--tRNA ligase, cytoplasmic [Pongo abelii]
MVLDDLFRVDKGGDPALIRETQEKRFKDPGLVDQLVKADSEWRRRCFRADNLNKLNLCSKTIGERMKK
KEPVGDDSEVPENLVSFDDLADALANLKVSQLKKVRLLLIDEAILKCDAERIKLEAERFENLREIGNLLH
PSVPISNDEEDVNKVERIWDGCTVRRKYSHVDLVVMVDGFEGEKGAVVAGSRGYFLKGVLVFLQALIQY
ALRTLGSRGYIPIYTPFFMRKEVMQEVQALSQFDEELYKVIKGSGSEKSDDNSYDEKYLIIATSEQPIAALH
RDEWLRPEDLPIKYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKIEQFVYSSPHDNKSWEMFEEMITTAEE
FYQSLGIPYHIVNIVSGSLNHAASKKLLDEAWFPGSGAFRELVSCSNCTDYQARRLRIRYGTQTKMMMDKV
EFVHMLNATMCATTRTICAILENYQTEKGITVPEKLKEFMPGLQELIPFVKPAPIEQEPSKKQKKQHGE
SKKKAARVDLTLENRLQNMEVTA

>NP_001191908.1 serine--tRNA ligase, cytoplasmic isoform 2 [Mus musculus]
MVLDDLFRVDKGGDPALIRETQEKRFKDPGLVDQLVKADSEWRRRCFRADNLNKLNLCSKTIGERMKK
KEAVGDDSEVPENLVNFDLLADALAALKVSQLKKVRLLLIDEAILKQCDGERVKLEAERFENLREIGNLLH
PSVPISNDEEDADNKNVERIWDGCTVRRKYSHVDLVVMVDGFEGEKGAVVAGSRGYFLKGPLVFLQALIQY
ALRTLGSRGYIPIYTPFFMRKEVMQEVQALSQFDEELYKVIKGSGSEKSDDNSYDEKYLIIATSEQPIAALH
RDEWLRPEDLPIKYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKIEQFVYSSPHDNKSWEMFEDIATAEE
FYQSLGIPYHIVNIVSGSLNHAASKKLLDEAWFPGSGAFRELVSCSNCTDYQARRLRIRYGTQTKMMMDKV
EFVHMLNATMCATTRTICAILENYQAEKGIAVPEKLKEFMPGLQELIPFVKPAPIEQEPSKKQKKQHGE
SKKKAKEVPLENLQSQMEVTA

>NP_001026563.1 serine--tRNA ligase, cytoplasmic [Gallus gallus]
MVLDDLFRADKGGDPAAVREMRQKRKFDPALVDALVRADGAWRRRCFRADNLNKLNLCSKTIGDKMKK
KEPVGDDSEVPESAQNLDLTDADVLGGLQVSQLKKVRLLLIDEAILCEDAERVRLAERFESLREIGNLLH
PSVPISNDEEDADNKNVERIWDGDCSRKKYSHVDLVVMVDGFEGEKGAVVAGSRGYFLKGPLVFLQALIQY
ALQSLRAKGYTPVYTPFFMRKEVMQEVQALSQFDEELYKVIKGSGSEKSDDNSYDEKYLIIATSEQPIAALH
RDEWLRPEDLPIKYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKIEQFVYASPHDNKSWEMFEDIATAEE
FYQSLGIPYHIVNIVSGSLNHAASKKLLDEAWFPGSGAFRELVSCSNCTDYQARRLRIRFGQTKMMMDKV
EFVHMLNATMCATTRTICAILENYQTEEGIVVPELRDPMPPDLRQIIRFVKPAPIEQELSKKQKKQHQEG
GRKKAAGGERVLEEQMNMVSSA

>XP_018104878.1 serine--tRNA ligase, cytoplasmic [Xenopus laevis]
MVLDDLFRFREDKGGNPVLVRETQKRKFDPLVDLTLLNSDTAWRRSRFPADNLNKLNLCSKTIGERMKK
KEPLGDSDDLVPENIQLDQLTAEVLALSVTQIKRLVRLIDEAIIAATDAERIKLEAERFESLREIGNLLHP
TVPIISNDEEDADNKNVERTWGDCEIQKKYSHVDLVVMVDGFEGEKGAVVAGSRGYFLKGPLVFLQALIQFA
LHTLSEKGYTPVYTPFFMRKEVMQEVQALSQFDEELYKVIKGSGSEKSDDNSYDEKYLIIATSEQPIAALH
DEWLKPEDLPYRIVGISTCFRQEVGSHGRDTRGIFRVHQFEKIEQFVYASPHDNKSWEMFEDIATAEP
YQMLGIPYRIVNIVSGSLNHAASKKLLDEAWFPGSGAFRELVSCSNCTDYQARRLRIRYGTQTKMMMDKV
FVHMLNATMCATTRAICAILENYQTEEGIIIVPEKLRFMPPLGLDKIIFVKPAPIDQELTKKQKQQQEK
GKKTENGLDQTESMKVHSA

>XP_013991973.1 serine--tRNA ligase, cytoplasmic-like [Salmo salar]
MVLDDLFRADKGGDPEVIRETQKRKFDVSLVDKLVDHADTEWRKCRFTADNLNKAKNLCSKTIGERMKK
KEPIGDEDDLDDAQNLALADTDLAPLTVTQIKKVRLLIDEAVAQKSDSERVKLEERFQYLRIGNLLH
PSVPISNDEEDADNKNVERTWGDCTVQKKYSHVDLVVMVDGYDGEKGAIVAGSRGYFLKGPLVFLQALINY
ALRMLHKNYQMLYTPFFMRKEVMQEVQALSQFDEELYKVIKGSGSEKSDTAIDEKYLIIATSEQPIAFL
RDEWLKPEELPIRYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKIEQFVFASPHDNKSWEMDEMIGTAAE
FYQTGLPIYRIVNIVSGALNHAASKKLLDEAWFPGSAAFRELVSCSNCLDYQARRLRIRYGTQTKMMMDKA
DYVHMLNATMCATTRVMCAILETYQTEEGIIPEVLRNFMPPGMTEMLKFKVPAPIDVEMSKKQKKQQDG
GKKKQSGDQLQNQVDNMSVHDS

>XP_032819422.1 serine--tRNA ligase, cytoplasmic [Petrotyzoon marinus]
MVLDDLFRADKGGDPTVRVRENQARRFKDVCLVDTLVQADTQWRACRYRADNLNKLNLCSKTIGDRMKK
KEDPQGBETLPEGTGFLDELADTDLAALSVAQIKVLRLLQIDNAILALCDTERLRLAERVLDLSREVGNILH
PSVPISNDEEDADNKNVERTWGDCTVQKKYSHVDLVVMVDGFEGEKAIVSGSRGYFLKGPLVFLQALIQAL
ALQRLYSQGYTFLYTPFFMRKEVMQEVQALSQFDEELYKVIKGSGSEHADDSSYDEKYLIIATSEQPIAAFH
RDEWLKPEQLPMRYAGLSSCFRQEVGSHGRDTRGIFRVHQFEKIEQFYVYSPHDNKSWEMFDEMVKTAEG
FYQELGIPYRIVNIVSGALNHAASKKLLDEAWFPGSAAFRELVSCSNCTDYQARRLRVRYGTQTKMMMDKA
EFVHMLNATMCATTRTICAILETYQTETGVVVPEALRFMPMPGLKEELKFKVKSAPIDQEQIKKQKRGKGD
GLAANLGNMAVNS

>XP_019634257.1 PREDICTED: serine--tRNA ligase, cytoplasmic-like [Branchiostoma belcheri]
MVLDDLFRVDRGGDPNKIRENQSKRYKDVTLVDNVVQADEQWRKLRYQADTLNRLNLCSKTIGERMKK
KEPVGEESESPTEDELEKLTPEALQAMTVNQIKQIRTII DKSILENTAGRAEVEKLRQENLKEIGNILH
ADVPISNDEEDDNRTERTNGDCTVRRKYSHVDLITMIDGYDGERGAVTAGSRGYMKGIATVFLQALIQY
ALRLIYEKGYTALYTPFFMKNKGMSEVAQALSQFDEELYKVIKGSGEKDDQTEDVKYLIIATSEQPIAAFH
RDEWMKPEDLPIKYAGISTCFRQEVGSHGRDTRGIFRVHQFEKVEQVFLSKPDDSWGLFHEMIGNAEFYY
KTLGIPYRIVNIVSGALNNAAMKYDLLEAWFPGSGAFRELVSCSNCLDYQARRLLVRYGTQTKMNEKPEF
VHMLNATMCATTRVICAILENHQTEEGIVIPEVLRQYMPGGTEFITFVKPAPIEEQATKKKKAGKKKEKV
KPTQDGEAEKVTEQVQNMVAVNEG

>NP_001259982.1 Seryl-tRNA synthetase, isoform B [Drosophila melanogaster]
MVLDDLFRSDKGGNPDLVRENQKKRFKDVAVETVIAKDTWRQCRHRADNLNKLNVCSKVIGERMKK
KEPVGAMSEDLPADVTKDLTIEAIVETQLPLTVNQIKQLRVLLDDAMTENQKSLAEAQTRNTLSREVGNH
LHESVPVSNDEEDENRVERTFGDCEKRGKYSHVDLIVMIDGMNAEKAIVSGRGYFLTGAAVFLQALIQ
HALHLLYARDYVPLYTPFFMRKEVMQEVQALSQFDEELYKVIKGSGSEKAEVGI DEKYLIIATSEQPIAAY
HREWLPESSLPIKYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKVEQFVLTS PHDNKSWEMMDMIGNAE
QFCQSLGIPYRIVNIVSGALNHAASKKLLDEAWFGSGAYRELVSCSNCLDYQARRLLVRFQGTQKKNAA
VDYVHMLNATMCAATRVICAILETHQTEGTIKVPEPLKYMPAKFQDEIPFVKPAPIDLLEAAAEKQKQK
KEKTKKDPAAQ

>XP_001639063.2 serine--tRNA ligase, cytoplasmic [Nematostella vectensis]
MKFFSPSLQLRTVRISFVFRILSSSSSKMVLDDLRYADKGGNPDKIRENQSKRYSDVTLVDKVV EAD
TQWRKFRFSKDNWNKLNLCSKQIGDKMKKKEPVGDDTLPEKVELDGLLELTAEMLQQLTVTQIKIIVRTL
VDNMAKKNEEVARLEKLRNEKLFVGNILHDSVRI SNDEENPVDRIVGDCSVRRKYSHVDLVHMDVGV
DIDRGSVVGASRGYFLKGPLVFLHEHALIQHATRMLYGKGFIPLSTPFFMRKEVMQEVQALSQFDEELYKV
VGGADEAGYEKYLIATSEQPIAAFHGRGEWMDKNDLPKKYAGFSTCFRQEAGAHGRDTRGIFRVHQFEK
IEQFVICS PHDNI SWEIFDEMI GNAE EFHKS LGIPYRIVS IVSGALNNAAAKLLDEAWFPASGAFREL
VSCSNCTDYQARRLVRFQGTQKMGVSTEXVHMLNATMCAVSRVICAILENNQTEEGVVMQALPHLYLPQD
LHFLKFKVPAPIDDKPEQKKQKKGKNKANNE SVGCL ESKLEDVNL

>XP_047126420.1 serine--tRNA ligase, cytoplasmic [Hydra vulgaris]
MLQCHQLKRLHQPNNSLKKLRFSTSSSLKMVLDELFRSDKGCCPEKIRENQSKRFKDVTLVDKVV EADEK

WRKLRFAQDNWNKLNLCSTIGLKMKNKEPEGESDLLPDSLSNIEELQALNPDTLEKFTVLQIKRIRGL
IDDIYNKCESERVGCEKVRHECLFEVGNWLHDSVVVSNDEEENEIVRVVGDCTTKKKFSHVDLLAMIDGV
DYERGANVAGNRGYFLKGPVLLQQALINLALQTLVSGSYTPIYTPFFMRKEVMQEVQLSQFDEELYKV
VGKGSERDDDTAVEEKYL IATSEQPIAAFHREGWMSTSDLPKKYAGISSCFRQEVGCHGRDTRGIFRVHQ
FEKVEQFVICSPHDNESWKHLDEMVNNAEKFYQALNIPYRIVGIVSGALNNAAKKLDLEAWFFGSGAFR
ELCSCSNCTDYQARRLLVRYGQTKMNDKTEFCHMLNATMCASTRVICCILENNQTEEGITVPELLRPFM
GNVEFIKYVKTAPIEGNKDVKGKSNKKKPEKIEENLKNLDVKE

>XP_003383114.1 PREDICTED: serine--tRNA ligase, cytoplasmic-like isoform X2 [Amphimedon queenslandica]
MPLDLLLFRADQGGNPDIMRDMQKKRFKDVIVHVKVVMEDTQWRKLRFESDNWNKLNHCSTIGEXMKK
KEPIGESADVPESLVTKLDSITPDEIKSLTVTQIKRLQQLIEASDKNSTKRKELEETRSFHLAQIGNSL
HPSVPI SDNEDNNRVERTFGDASIRKKYSHMDLVVMVDGVDMQRGTTVAGNRCYYLKGPLVFLEQALIQF
ALSTLSEKSFVPLYTPFFMKKEVMQEV AHLSDYEEMLYKVIKSSSEIVDDSNVEEKYL IATSEQPIAAFH
RGDWLDPQTLPLKYAGLSSCFRQEVDSHGRDTRGIFRVHQFQKVEQFCLTSPHDDVSWKMFDEMISNAEF
FYQQLGIPYRVVNIIVSGELNLAAMKYDLEGLFPGSGAYRELVCSNCLDYQVRRLQVRFLTKKMNAQA
DYVHMLNATMCATTRTICAILENNQTEEGVVVPEILRQYMPFAYKEFIKFVQAAPIHEPITKKQENQMAQ
MEKDNEAQS

Alignment

XP_047126420.1[H.vulgaris]	---MLQCHQLKRLHQPNNSLKKLRFSTSSLMKVLDELFRSDKGCCPEKIRENQSKRFF	56
XP_003383114.1[A.queenslandica]	-----MPLDLLLFRADQGGNPDLMRDMQKKRFF	28
XP_001639063.2[N.vectensis]	MKFFSPSLHQLRTVRI--SFVFRRLSSSSSKMVLDDLRYADKGGNPDKIRENQSKRYS	58
XP_019634257.1[B.belcheri]	-----MVLDDLFRVDRGGDPNKIRENQSKRYK	28
NP_001259982.1[D.melanogaster]	-----MVLDDLFRSDKGGNPDLVRENQKKRFF	28
XP_013991973.1[S.salar]	-----MVLDDQFRADKGGDPVIRETQKRKFF	28
XP_032819422.1[P.marinus]	-----MVLDDLFRADKGGDPTRVRENQARRFF	28
XP_018104878.1[X.laevis]	-----MVLDDLFRFDKGGNPELVIRETQKRKFF	28
NP_001026563.1[G.gallus]	-----MVLDDLFRADKGGDPAAVREMQRKFF	28
NP_001191908.1[M.musculus]	-----MVLDDLFRVDKGGDPALIRETQEKRRFF	28
NP_006504.2[H.sapiens]	-----MVLDDLFRVDKGGDPALIRETQEKRRFF	28
NP_001125910.1[P.abelii]	-----MVLDDLFRVDKGGDPALIRETQEKRRFF	28
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XP_047126420.1[H.vulgaris]	DVTLVDKVVAEDEKWRKLRFAQDNWNKLNKLSKTIGLKMKNKEPEGESD-LLPDSLNI	115
XP_003383114.1[A.queenslandica]	DVIHVDKVVEMDTQWRKLRFSEDNWNKLNKNSKTIGEKMKKKEPIGESA-DVPES--LV	85
XP_001639063.2[N.vectensis]	DVTLVDKVV EADTQWRKFRFSKDNWNKLNKLSKTIQIDKMKKKEPVGDDE-TLPKE--VL	115
XP_019634257.1[B.belcheri]	DVTLVDNVVQADEQWRKLRVQADTLNRLKNLCSKTIGEKMKKKEPVGEESSESPTE----	84
NP_001259982.1[D.melanogaster]	DVALVETVIAKDETEWRQCRHRADNLNKVNKNSCVIGEKMKKKEPVGAMESDLPAD-VT	86
XP_013991973.1[S.salar]	DVSLVDKLVHADTEWRKCRFTADNLNAKLNCSKTIQGEKMKKKEPIGEDD-SLP-D--DA	84
XP_032819422.1[P.marinus]	DVCLVDTLVQADTQWRACRYRADNLNKLNLCSKTIQIDKMKKKEPDGQDE-TLP-E--GT	84
XP_018104878.1[X.laevis]	DPGLVDTLLNSDTAWRKSRFAQDNLNKQNLNCSKTIQGEKMKKKEPLGDS-D-VLP-E--NI	84
NP_001026563.1[G.gallus]	DFALVDALVRADGAWRRCRFRADNLNKLNLCSKTIQIDKMKKKEPVGSDE-SVP-E--SA	84
NP_001191908.1[M.musculus]	DFGLVDQLVKADSEWRRCRFRADNLNKLNLCSKTIQGEKMKKKEPVGDDE-SVP-E--NV	84
NP_006504.2[H.sapiens]	DFGLVDQLVKADSEWRRCRFRADNLNKLNLCSKTIQGEKMKKKEPVGDDE-SVP-E--NV	84
NP_001125910.1[P.abelii]	DFGLVDQLVKADSEWRRCRFRADNLNKLNLCSKTIQGEKMKKKEPVGDDE-SVP-E--NV	84
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XP_047126420.1[H.vulgaris]	EELQALNPDTLEKFTVLQIKRIRGLIDDIYNKCESERVGCEKVRHECLFEVGNMLHDSVV	175
XP_003383114.1[A.queenslandica]	TKLDSITPDEIKSLTVTIQIKRLQQLIEEASDNCKTKRKELEETSRFLHAQIGNSLHPSVP	145
XP_001639063.2[N.vectensis]	DGLEELTAEMLQQLTVTIQIKVIRTVDDGMAKNEEVARLEKLRNEKLFEVGNILHDSVR	175
XP_019634257.1[B.belcheri]	DELEKLTPEALQAMTVNQIKIRTIIDKSLIENAGRAEVEKLRNKELEIGNILHADVP	144
NP_001259982.1[D.melanogaster]	KDLTEIVAETLQPLTVNQIKQLRVLIDDAMTENQKSLEAEQTRNTSLREVGNLHESVP	146
XP_013991973.1[S.salar]	QNLEALTADTLAPLTVTIQIKKVRLLVDEAVQSDSERVKLEERFYQLREIGNLHPSVP	144
XP_032819422.1[P.marinus]	PGLDELTAADTLAALSVAQIKRLRLQIDNAIALCDETERLKEAVRLDLSREVGNLHPSVP	144
XP_018104878.1[X.laevis]	-QLDQLTAEVLALSVTQIKRLRVLIDEAIAATDAERIKLEAERFESLREIGNLHPTVP	143
NP_001026563.1[G.gallus]	QNDELTAADVLGGVQSQIKKVRLLIDEAILECDAERVKLEAERFESLREIGNLHPSVP	144
NP_001191908.1[M.musculus]	LNFDLLTADALAALKVYSQIKKVRLLIDEAIIQKCDGERVKLEAERFENLREIGNLHPSVP	144
NP_006504.2[H.sapiens]	LSFDDLTADALANLKVSQIKKVRLLIDEAIIKCDKAERIKLEAERFENLREIGNLHPSVP	144
NP_001125910.1[P.abelii]	LSFDDLTADALANLKVSQIKKVRLLIDEAIIKCDKAERIKLEAERFENLREIGNLHPSVP	144
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XP_047126420.1[H.vulgaris]	VSNDDE-ENIEIVRVGDCTTKKKFSHVDLLAMIDGVDYERGANVAGNRGYFLKPGVLLIQ	234
XP_003383114.1[A.queenslandica]	ISDNED-NNRVERTFGDASIRKKYSHMDLVVMVGDVDMQRTTVAGNRCYFLKGPLVFLE	204
XP_001639063.2[N.vectensis]	ISNDED-ENPDRIVGDCSVRKKYSHVDLVHMDVGDVIDRGSVVAGSRGYFLKGPLVFLE	234
XP_019634257.1[B.belcheri]	ISNDEDEDNRTERTGDCTVRKKYSHVDLITIMIDGYGERGAVTAGSRGYMKGIAVFLE	204
NP_001259982.1[D.melanogaster]	VSNDDE-ENRVERTFGDCEKRGKYSHVDLIVMIDGMNAEKAIVSGRGYFLTGAAVFLE	205
XP_013991973.1[S.salar]	ISNDEADNKVERTGDCTVQKKYSHVDLVVMIDGYGEKGAIVAGSRGYFLKGPLVFLE	204
XP_032819422.1[P.marinus]	VSNDDEADNKVERTGDCTVRKKYSHVDLVVMVDGYGEKGAIVSGRAYFLKGPLVFLE	204
XP_018104878.1[X.laevis]	ISNDEDDNKVERTGDCIEQKKYSHVDLVVMVDGFEKGAIVAGSRGYFLKGPLVFLE	203
NP_001026563.1[G.gallus]	ISNDEADNKVIRIWDGDCSRKKYSHVDLVVMVDGYGEKGAIVAGSRGYFLKGPLVFLE	204
NP_001191908.1[M.musculus]	ISNDEADNKVIRIWDGCTVRKKYSHVDLVVMVDGFEKGAIVAGSRGYFLKGPLVFLE	204
NP_006504.2[H.sapiens]	ISNDEDDNKVIRIWDGCTVRKKYSHVDLVVMVDGFEKGAIVAGSRGYFLKGPLVFLE	204
NP_001125910.1[P.abelii]	ISNDEDDNKVIRIWDGCTVRKKYSHVDLVVMVDGFEKGAIVAGSRGYFLKGPLVFLE	204
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XP_047126420.1[H.vulgaris]	QALINLALQTLVSGSYTPIYTPFFMRKEVMQVEAQLSQFDEELYKVVKGKSERDDDTAVE	294
XP_003383114.1[A.queenslandica]	QALIQFALSTLSEKSFVPLTPFFMRKEVMQVEAHLSDIEEMLYKVIKGSSEIVDSDSNE	264
XP_001639063.2[N.vectensis]	HALIQHATRLMYKGFPLSTPFFMRKEVMQVEAQLSQFDEELYKVVKGKAD---EAGYE	291
XP_019634257.1[B.belcheri]	QALIQYALRLILEKGYTALYTPFFMRKVMQVEAQLSQFDEELYKVIKGSSEKDDQDTE	264
NP_001259982.1[D.melanogaster]	QALIQHALHLLIYARDYVPLYTPFFMRKEVMQVEAQLSQFDEELYKVIKGSSEKAEVGD	265
XP_013991973.1[S.salar]	QALINYALRMLHSKNYQMLYTPFFMRKEVMQVEAQLSQFDEELYKVIKGSSEKSEDTAID	264
XP_032819422.1[P.marinus]	QALIQALQLRLYSQGYTPLYTPFFMRKEVMQVEAQLSQFDEELYKVIKGSSEHADDSVD	264
XP_018104878.1[X.laevis]	QALIQFALHTLSEKGYTPIYTPFFMRKEVMQVEAQLSQFDEELYKVIKGSSEKSDDSVD	263
NP_001026563.1[G.gallus]	QALIQYALQSLRAKGYTPVYTPFFMRKEVMQVEAQLSQFDEELYKVIKGSSEKAESSVD	264
NP_001191908.1[M.musculus]	QALIQYALRTLGSRGYTPYTPFFMRKEVMQVEAQLSQFDEELYKVIKGSSEKSDDSYD	264
NP_006504.2[H.sapiens]	QALIQYALRTLGSRGYPIYTPFFMRKEVMQVEAQLSQFDEELYKVIKGSSEKSDDSYD	264
NP_001125910.1[P.abelii]	QALIQYALRTLGSRGYPIYTPFFMRKEVMQVEAQLSQFDEELYKVIKGSSEKSDDSYD	264
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XP_047126420.1[H.vulgaris]	EKYLIIATSEQPIAAFHRGEMWSTDLPKKYAGISSCFRQEVGCHGRDTRGIFRVHQFEKV	354
XP_003383114.1[A.queenslandica]	EKYLIIATSEQPIAAFHRGDWLDPQTLPLKYAGLSSCFRQEVDSHGRDTRGIFRVHQFQKV	324
XP_001639063.2[N.vectensis]	EKYLIIATSEQPIAAFHRGEMWMDNDLPKKYAGFSTCFRQEAGAGHRDTRGIFRVHQFEKI	351
XP_019634257.1[B.belcheri]	VKYLIIATSEQPIAAFHRDEWMPEDLPKYAGISTCFRQEVGSHGRDTRGIFRVHQFEKV	324
NP_001259982.1[D.melanogaster]	EKYLIIATSEQPIAAFHRDEWLPESSLPFIKYGALSTCFRQEVGSHGRDTRGIFRVHQFEKV	325
XP_013991973.1[S.salar]	EKYLIIATSEQPIAALHRDEWLPEELPIRYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKI	324
XP_032819422.1[P.marinus]	EKYLIIATSEQPIAALHRDEWLPEELPIRYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKI	324
XP_018104878.1[X.laevis]	EKYLIIATSEQPIAALHRDEWLKPEDLPVRYAGISTCFRQEVGSHGRDTRGIFRVHQFEKI	323
NP_001026563.1[G.gallus]	EKYLIIATSEQPIAALHRDEWLKPEDLPKYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKI	324
NP_001191908.1[M.musculus]	EKYLIIATSEQPIAALHRDEWLRPEDLPKYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKI	324
NP_006504.2[H.sapiens]	EKYLIIATSEQPIAALHRDEWLRPEDLPKYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKI	324
NP_001125910.1[P.abelii]	EKYLIIATSEQPIAALHRDEWLRPEDLPKYAGLSTCFRQEVGSHGRDTRGIFRVHQFEKI	324
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XP_047126420.1[H.vulgaris]	EQFVICSPHDNCSWKHLDEMVNNAEKFYQALNIPIYRIVGIVSGALNNAAKKLDLEAWFP	414
XP_003383114.1[A.queenslandica]	EQFCLTSPHDDVSKWMPDEMI SNAEFFYQQLGIPYRVNIVSGELNLAAMKYDLEGLFP	384
XP_001639063.2[N.vectensis]	EQFVICSPHDNISWEIFDEMI SNAEFHKS LGIPYRIVIVSGALNNAAKKLDLEAWFP	411
XP_019634257.1[B.belcheri]	EQFVLSPKDD--SWGLFHEMIGNAEEFYKTLGIPYRIVNIVSGALNNAAMKYDLEAWFP	382
NP_001259982.1[D.melanogaster]	EQFVLTSPHDNKSWEMMDEMI SNAEFQCS LGIPYRVNIVSGALNHAASKKLDLEAWFG	385
XP_013991973.1[S.salar]	EQFVFASPHDNKSWEMMDEMI SNAEEFYQTLGIPYRIVNIVSGALNHAASKKLDLEAWFP	384
XP_032819422.1[P.marinus]	EQFVYTSPHDNKSWEMFDEMVKTAEGFYQELGIPYRIVNIVSGALNHAASKKLDLEAWFP	384
XP_018104878.1[X.laevis]	EQFTYASPHDNKSWEMFEEMITAEFSFYQMLGIPYRIVNIVSGALNHAASKKLDLEAWFP	383
NP_001026563.1[G.gallus]	EQFVYASPHDNKSWEMFDEMIATAEEFYQSLGIPYHIVNIVSGALNHAASKKLDLEAWFP	384
NP_001191908.1[M.musculus]	EQFVYASPHDNKSWEMFDEMITAEFYQSLGIPYHIVNIVSGALNHAASKKLDLEAWFP	384
NP_006504.2[H.sapiens]	EQFVYASPHDNKSWEMFDEMITAEFYQSLGIPYHIVNIVSGALNHAASKKLDLEAWFP	384
NP_001125910.1[P.abelii]	EQFVYASPHDNKSWEMFDEMITAEFYQSLGIPYHIVNIVSGALNHAASKKLDLEAWFP	384
	*** . * * * * : * * : * * * * : * * * * : * * * * : * * * * *	
XP_047126420.1[H.vulgaris]	GSAGFRELVSCSNCTDYQARRLLVRYGQTKKMDKTEFCHMLNATMCASTRVICILENN	474
XP_003383114.1[A.queenslandica]	GSAGYRELVSCSNCLDYQARRLQVRFLTKKMDKQADYVHMLNATMCATTRTICAILENN	444
XP_001639063.2[N.vectensis]	ASGAFRELVSCSNCTDYQARRLQVRFGQTKKMGVSTEVYHMLNATMCASVRVICAILENN	471
XP_019634257.1[B.belcheri]	GSAGFRELVSCSNCLDYQARRLLVRYGQTKKMKNEPEFVHMLNATMCATTRVICAILENN	442
NP_001259982.1[D.melanogaster]	GSAGYRELVSCSNCLDYQARRLLVRYGQTKKMDKADYVHMLNATMCATTRVICAILETH	445
XP_013991973.1[S.salar]	GSAAFRELVSCSNCLDYQARRLRIRYGGTKKMDKADYVHMLNATMCATTRVMCAILETY	444
XP_032819422.1[P.marinus]	GSAAFRELVSCSNCTDYQARRLRIRYGGTKKMDKAEFVHMLNATMCATTRTICAILETY	444
XP_018104878.1[X.laevis]	GSAGFRELVSCSNCTDYQARRLRIRYGGTKKMDKDFVHMLNATMCATTRAICAILENY	443
NP_001026563.1[G.gallus]	GSAGFRELVSCSNCTDYQARRLRIRFGQTKKMDKDFVHMLNATMCATTRTICAILENY	444
NP_001191908.1[M.musculus]	GSAGFRELVSCSNCTDYQARRLRIRYGGTKKMDKDFVHMLNATMCATTRTICAILENY	444
NP_006504.2[H.sapiens]	GSAGFRELVSCSNCTDYQARRLRIRYGGTKKMDKDFVHMLNATMCATTRTICAILENY	444
NP_001125910.1[P.abelii]	GSAGFRELVSCSNCTDYQARRLRIRYGGTKKMDKDFVHMLNATMCATTRTICAILENY	444

	..*:*:** ***:** :*:* *** :	:***** :*:****.	
XP_047126420.1[H.vulgaris]	QTEGGIIVPELLRPFMGN---VEFIFYKVKTAPIEGNKDVGKSNKKPK-----EK		521
XP_00383114.1[A.quenslandica]	QTEGGVVVPEILRQYMPAYKEFIKFQVAAPHEIPTIKQNMAGMEKDNEAQS----		499
XP_001639063.2[N.vectensis]	QTEGGVVMPPALHLYLPQLD--HLFKVFKVPADDDKPEQQKKQKKKGKNKANNE----SVGC		527
XP_019634257.1[B.belcherii]	QTEGGIIVPELVSTYKPMYGG--TEFITTVKPPIEEQATKKKKAGKKGKVPTQDGPEAEK		501
NP_001259982.1[D.melanogaster]	QTETGIKVPKLFPKMYPKAFQDEIPFVKPAPIDLLEAAAEQGKGGKEKTQDKPA--G---		500
XP_013991973.1[S.salar]	QTEGGIIIEVLNIRMPFMGMTEMLIKFVKPAPIDVEMSKSQKKQKQ---dgggkkqqs-G-DQ		501
XP_032819422.1[P.marinus]	QTETGVVPELRPFMPPLGKEELKFVKSPAPIDQEGLIKQRKKQ---GDG-----		498
XP_018104878.1[X.laevis]	QTEGGIIVPEKLRSFMPPLGKLDIKFVKPAPIDQELLTKQKKQKQ---EGGKKTE---NGC		491
NP_001026563.1[G.gallus]	QTEGGIIVPEKLRFMPPLQDLIIIFRVKPAPIEGLSLKQKKQKQ---EGGKKKA--GERV		501
XP_032819422.1[P.marinus]	QHEGKIIVPEKLRFMPPLQDLIIIFRVKPAPIDEPSKKQKKQH---EGSKKHA---KEVP		499
NP_006504.2[H.sapiens]	QTEGKITVTPEKLKEFMPGLQELIIPFVKPAPIEQEPSKKQKKQH---EGSKKAAA--RDVT		501
NP_00125910.1[P.abelii]	QTEGKITVTPEKLKEFMPGLQELIIPFVKPAPIEQEPSKKQKKQH---EGSKKAAA--RDVT		501
	** *: *:* :* : :	: *:* :***:	
XP_047126420.1[H.vulgaris]	IENLNKLNLDVKE-	533	
XP_00383114.1[A.quenslandica]	-----	499	
XP_001639063.2[N.vectensis]	LESKLEDVNL---	537	
XP_019634257.1[B.belcherii]	VTEQVQNMAVNEG	514	
NP_001259982.1[D.melanogaster]	-----	501	
XP_013991973.1[S.salar]	LQNNQDNMSVHDS	513	
XP_032819422.1[P.marinus]	LAANLNQNSVHDS	504	
XP_018104878.1[X.laevis]	LDTQMSMKVHSA	511	
NP_001026563.1[G.gallus]	LEENQNNMGVSSA	512	
NP_001191908.1[M.musculus]	LLENQLSMVEITDA	514	
NP_006504.2[H.sapiens]	LENRLQNMVEITDA	514	
NP_00125910.1[P.abelii]	LENRLQNMVEITDA	514	

Percent identity matrix:

```
#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: XP_047126420.1[H.vulgaris] 100.00 61.35 65.20 67.94 63.19 65.60 66.67 65.73 66.00 66.20 65.80 65.80
2: XP_003383114.1[A.queenslandica] 61.35 100.00 61.46 62.75 61.32 63.71 63.88 65.38 64.31 63.56 63.10 63.10
3: XP_001639063.2[N.vectensis] 65.20 61.46 100.00 66.14 65.18 65.21 67.34 64.34 67.46 66.27 66.27 66.27
4: XP_019634257.1[B.belcheri] 67.94 62.75 66.14 100.00 66.53 68.70 67.94 67.39 69.55 69.82 69.74 69.74
5: NP_001259982.1[D.melanogaster] 63.19 61.32 65.18 66.53 100.00 68.61 68.98 69.03 70.02 68.69 69.01 69.01
6: XP_013991973.1[S.salar] 65.60 63.71 65.21 68.70 68.61 100.00 75.79 77.25 78.95 79.45 78.17 78.17
7: XP_032819422.1[P.marinus] 66.67 63.88 67.34 67.94 68.98 75.79 100.00 75.94 79.17 77.78 76.98 76.98
8: XP_018104878.1[X.laevis] 65.73 65.38 64.34 67.39 69.03 77.25 75.94 100.00 81.60 81.96 81.41 81.41
9: NP_001026563.1[G.gallus] 66.00 64.31 67.46 69.55 70.02 78.95 79.17 81.60 100.00 86.72 85.80 85.80
10: NP_001191908.1[M.musculus] 66.20 63.56 66.27 69.82 68.69 79.45 77.78 81.96 86.72 100.00 95.90 95.70
11: NP_006504.2[H.sapiens] 65.80 63.10 66.27 69.74 69.01 78.17 76.98 81.41 85.80 95.90 100.00 99.81
12: NP_001125910.1[P.abelii] 65.80 63.10 66.27 69.74 69.01 78.17 76.98 81.41 85.80 95.70 99.81 100.00
```