

>TNKS1[H.sapiens][NP\_003738.2]

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>TNKS2[H.sapiens][AAK13463.1]

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>TNKS1[M.musculus][EDL35446.1]

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>TNKS2[M.musculus][NP\_001157107.1]

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>TNKS1[G.gallus][NP\_989671.1]

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>TNKS1[X.laevis][XP\_018099068.1]  
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>TNKS1[S.salar][XP\_014017013.1]  
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AASSIDNLAGPLNELGAAGTSGVADGATGSDRKEGELVMDLNMNISQFLKSLGLEHLRDI FEREQISLDVLADMGHEELKEIGI  
NAYGHRHKLIKIGVERLLGGQQGANPYLTFFHCANQGTVLIDLAPDDKEGQSVVEEEMQSTIREHRDGGNAGGVFSRYNIIKIQKV  
VNKKLRERYTHRQKEISDENHNHNHNERMLFHGSPFINAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPT  
HKDRSCYLCHRQMLFCRVTLGKSFLQFSAMKMAHAPPGHHSVIGRPSVNGLAYAEYVIYRGEQAYPEYLITYQILKPESTATS  
AAGEDQKS

>TNKS2[S.salar][XP\_014034742.1]  
MASVARFWGSANTNSKLYIYENTTPLMSTRQCSRVLGLGGVFPVGVDTPRSSEPNIREFEACRNGDVERVRRLVRPENVNSRDT  
AGRKSTPLHFAAGFGRDGVVDYLLQNGANVHARDEGGLVSLHNACSFHGHSEVVNLLLRHGADANSRDNWSYTPLHEAAIKGKS  
EVCIVLLQHGAEPTIRNTDGRTALDLAEASTKAVLTGEYRKDDLLESARSGNEDKLMAALLTPLNVNCHASDGRKSSPLHLAAG  
YNRVKTVQLLLKHGADVHAKDKGDLVPLHNACSYGHYEVTDLIVKQGACVNAMDWQFTPLHEAASKNRVDVCSLLVSYGADP  
TFLNCHNQSAIDLSPTPQLKERLAYEFRGHALLQAAREADLRLKKHLSLETITFKHPLTHETALHCAATSPYPKRKQVCELL  
LRKGANVNEKTKDFLTPLHLASEKSHNDIEVLVKHEAKVNALDNLGQ TALHRAAHCGHLQTCRLLLKAGCDPLVMSLQGFSP  
SQMGNESVQEILHEGTLIGNSDVDWQLEASKSGDLEIVKKLCTMQNVNCRDVEGRQSTPLHFAAGYNRVSVVEYLLHHGADV  
HAKDKGGLVPLHNACSYGHYEVAELLVIHGAVVNIADLWKFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGSTPLDLVKDG  
DTDMQDLLRGDAALLDAAKKGCLARVEKLCSPDNVNCRDAQGRHSTLLHLAAGYNNLEVAEYLLQHGAEVNSQDKGGLIPLHN

AASYGHVDVAALLIKYDACVNATDKWAFTPLHEAAQKGRQTQLCALLLAHGADPALRNQEGQSPLDLVTVDVDRALLTAAMPSPS  
ALPGCYKPVVISMSSPVGVVPPSLASASTPLSTLASRNSLDNQATASTCTAFPELPALLGPGSGAVGTDNKEVPGVDLSIGQF  
LNNLGLEHLLLEIFEREQITLDVLVEMGHKELKEIGINAYGHRHKIKGVERLISGPQSLNPYLTNTANS GTILIDLVSDDKE  
FQLVEEELQSTIREHRDGGLAGGVFNRYNIVKIQKVCNKKLWERYTHRREKVESEENHNHNSNERMLFHGSPFVNAI IHKGFDER  
HAYIGMFGAGIYFAENSSKSNQYVYIGGGTGCKHLKDRSCYVCQRHLLFCRVTLGKSFLQFSAMKMAHSPFGHHSVTGRPS  
VNGLSLAEYVIYRGEQAYPEYLITYQILKPDASVDG

>TNKS[P.marinus][XP\_032806710.1]

MAARRAHLASPPSSSSSLSPSSGSLDTTTAAAAAAAATTTAAAAAATTTAAAMTTTAAVSATSSPSTTAAAAAAVAAAAATGSG  
PGSGQDSSADGGDAGKELFEACRNGDVGRVKRLVSPNLVNARDTTGRKSTPLHFAAGFGRKDVVEHLLQNGANVHARDDDGGLI  
PLHNACSFGHAENVNLLLRQGADPNARDNWNYPPLHEAAIKGKIDVCIVLLQHGADPGIRNTDGKTALDLAEPTAKAVLTGEY  
KKDELEEAARSGNEEKLMALLTPLNVNCHASDGRKSTPLHLAAGYNRVIRIVQLLLQHGADVHAKDKGGLVPLHNACSYGHYEV  
TELLVKHGASVNAMD LWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHSKSAIDLAPTSELKERLVYEFRGHSLQAAREA  
DVTRVKKHLGLDIINFKHPQTHETALHCAVASPYPKRKQVSELLLRKGANVNEKTKDLLTPLHVASDKAHNDVIDVLLKHGAK  
INVTDSLQGTSLHRAAHAGHLTTTCRLLLSHGCDPNLPSLQGFATAAQLGNESVQQILHESLTPVRNSDVEHQLLEAAKAGDLDT  
VKQLCTTQTVCNCRDMEGRHSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAEELLVKRGAVNVNADL  
WKFTPLHEAAAKGKYEICKLLLKHGADPTKKNRDGNTPLDLVKEGDTDIQDLLRGDAALLDAAKKGCLARVQKLCSEGENVNC  
DSQGRNSTPLHLAAGYNNLEVAEYLLLEHGADVNAQDKGGLIPLHNAASYGHVDIAALLIKYSACVNATDKWAFTPLHEAAQK  
RTQLCALLLAHGADPSMKNQEGQTPLDLATADDVRALLIDAMPPEALPVTHKPPSIPTIAATSAAATAALALGPTPALASLAP  
SPVPSGASASGAGGVPLLASPSSTPASLSAASSMDSLTGACGVAPSPVPAGAIAGAAGDGTLLGACGVSADGATGPADKPD  
RSADFEIPGLDMNINMFLKGLGLDHLRDI FEKEQITLDVLADMGHEELKEIGINAYGHRHKIKGVERLLGAQQGGLAYPGAN  
PYLSYHTTAQGTLLIDLPPDDKEYQSVEDEMQSTIREHKDGGQAGGVFNRYNVIKIQKVRNKKLWERYTHRREKVEEENHNHH  
NERMLFHGSPFINAI INKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGCPVHKDRSCYICQRQMLFCRVTLGKSF  
LQFSAMKMAHSPFGHHSVIGRPSVNGLAFAEYVIYRGEQAYPEYLITYQILKPECTPDLTSAAGQKS

>TNKS[B.belcheri][XP\_019641281.1]

MAGRAMLSSDRIHCDESSGCRELFEACRNGDVARVKKLITPQNVNARDTAGRKSTPLHFAAGFGRKDVVEHLLQNGANVHAR  
DDGGLIPLHNACSFHAEVVTLLLRNGADPNARDNWNYPPLHEAAIKGKIDVCIVLLQNGADPSIRNTDGKTALDLAEPSAKT  
VLTGDYKKDELLEAARSGNEDKLMALLTPLNVNCHASDGRKSTPLHLAAGYNRVIRIVQLLI QHGADVHAKDKGGLVPLHNAC  
YGHFEVTELLLKHGASVNAMD LWQFTPLHEAASKSRIEVCSSLLLSHGADPTLLNCHSKSAIDVASTPELQEKLSYEFKGHCLL  
DGARQTDMAKVKKHLQLDIVNFKHPYTHDTALHCAALSPYPKRRQITELLIRKGANLNDKNKEFLTPLHVASDKYIDVMEVL  
LKHGAKVNALDSLQGTALHRGAHCHGVQACRLLLSFGVDPISIVSLQGVATAAQMATEAVQQMLHEDPPSGPADECDQLEAAKA  
GDLEAVKVLCPNPTVCNCRDVNCRHSTPLHFAAGYNRVAVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVCELLLKHGAVV  
NVADLWKFTPLHEAAAKGKYEICKLLLKHGADPNKKNRDNTPLDLVRDGDTDI QDLLRGDAALLDAAKGNLARVQKLATPE  
NINCRDTQGRNSTPLHLAAGYNNVEVAEFLENGADVNAQDKGGLIPLHNASSYGHVEIAQLLIKYGTCVNATDRWNFTPLHE  
AAQKGRQTQLCALLLAHGADPTMKNQEGQTPLDLATAEDVRALLVDAMPQSLPAAITAATVKAASPISSPSTTPSSTPGVLST  
ASSMDHLVGAVGGAGQGDGAIDRSAGEGESLLDMTISSEFLQQLGLNLQDLDFNKEQITLDILGEMGHEELKEIGVNAYGHRHK  
LIKGVERILGGTGHTLPIYLTALGSHGTILTDLSDDKEYQSVEEVQSTIRQHKDQGGAGGIFNRYNVIKIQKVRNKRLED  
RYVHRREKVESEENHNQSNERMLFHGSPFINAI INKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGCP IHKDRSCY  
ICQRQMLFCRVTLGKAFLQFSAMKMAHAPPGHHSVIGRPSVGGLNFAEYVIYRGEQAFPEYLITYQIVKPEAPAAPSPDQK

>TNKS[D.melanogaster][NP\_651410.1]

MANSSRSRAILSVNLDVAMANDPLRELFEACKTGEIAKVKKLITPQTVNARDTAGRKSTPLHFAAGYGRREVVEFLLNSGASI  
QACDEGLHPLHNCCSFGHAENVRLLLKAGASPNTTDWNYPPLHEAASKGKVDVCLALLQHGANTIRNSEQKTPLELAD  
TRPVLTGEYRKDELLEAARSGAEDRLLALLTPLNVNCHASDGRNSTPLHLAAGYNRIGIVEILLANGADVHAKDKGGLVPLHN  
ACSYGHFDVTKLLIQAGANVNANDLWAFPLHEAASKSRVEVCSLLLSRGADPTLLNCHSKSAIDAAPTREL RERIAFEYKGH  
CLLDACRKCDVSRAKKLVC AEIVNFVHPYTGDTPLHLAVVSPDGKRKQLMELLTRKGSLLNEKNKAFLTPLHLAAELLHYDAM  
EVLLKQGAQVNALDSLQGTPLHRCARDEQAVRLLLSYAADTNIVSLEGLTAAQLASDSVLKLLKNPPDSETHLLEAAKAGDL  
TVRRIVLNNPISVNCRDLDGRHSTPLHFAAGFNRPVQVFLLEHGAEVYAADKGGLVPLHNACSYGHYEVTELLVKHGANNV  
SDLWKFTPLHEAAAKGYDICKLLLKHGADPMKKNRDGTADLVKESDHDVAELLRGPSSALLDAAKGNLARVQRLVTPESI  
NCRDAQGRNSTPLHLAAGYNNFECAEYLLENGADVNAQDKGGLIPLHNASSYGHLDIAALLIKHKT VVNATDKWGFTPLHEAA  
QKGRQTQCSLLLAHGADAYMKNQEGQTPIELATADDVKCLLDAMATSLSQQALSASTQSLTSSSPAPDATAAAAPGTSSSSS  
SAILSPTTETVLLPTGASMILSVPVPLPLSSSTRISPAQGAEEANGAEGSSDDLLPADTITNVSGFLSSQQLHHLIELFERE  
QITLDILAEMGHDDLKQVGVSAYGFRHKILKGIAQLRSTTGIGNNVNLC TLLVDLLPDDKEFVAVEEEMQATIREHRDNGQAG  
GYFTRYNIIRVQKVQNRKLWERYAHRREQEIAEENFLQSNERMLFHGSPFINAIVQRGFDERHAYIGMFGAGIYFAEHSSKSN  
QYVYIGGGIGCPSHKDKSCYVCPRLLLCRVALGKSFLQYSAMKMAHAPPGHHSVVGSRPSAGGLHFAEYVVYRGEQSYPEYL  
ITYQIVKPDDSSSGTETDR

>TNKS[N.vectensis][XP\_032220531.1]

MPCQAKMASKKLASNPTFLSDPDVCEGGRELFEACRNGDVSKVRKLVNNSNVNVRD TAGRKSSPLHFAAGFGRKEVVEYLLQ  
CGADVHAMDDGGLIPLHNACSFHAEVVRILLSHGADANARDNWNYPPLHEAAVKGKVDVCVLLQHGADPNIRNTDGKTALD  
VAEAAAKLVLTGDYKDELLEGARSGNEEKLM SLLTPLNVNCHASDGRKSTPLHLAAGYNRVGVVQLLLKHGADVHAKDKGGL  
VPLHNACSYGHFEVTELLIKHGASVNAMD LWQFTPLHEAASKARVEVCALLLHGADPTLLNCHSKSAIDAAPTKE LQEKLLS  
EFKGHQLLEAAKGCDTAKIKKLIT TETINFQHPLTLDTPLHVAVASSSPKKKGV IETLLKKGADPNLQNKSSYAPLHVAAEKG  
LFEAMELLLKHGAKVNAIDSAGQTALHVAAIAGQVQACRVLMNGADPTCQTFQGYTAFEVAPEPVQKVLHVNEESPSPVSDA  
EKQLEAAKTGDL ETVKNLCTAQTVNCRDL DGRCTPLHFAAGYNRVRVVEYLLNGADVHAKDKGGLVPLHNACSYGHYEV  
ELLVKHGAIVNVADLWKFTPLHEAAAKGKYEICQLLLKHGADPQKKNRDGYTPLDLVKEGSDVADLLRGDAALLDAAKGNL  
IRITKLATPENINCRDTQGRNSTPLHLAAGYNHLEVAEYLLLEHGADVNAQDKGGLIPLHNASSYGHVDIAALLIRYNTDVNAT

DRWLFTPLHEAAQKGRTQLCALLLAHGAEPMSKNQEGQSPVDLATAEDVKCLLGDAMLSTQTTSVSTAPVAKVPAPVTATAGA  
ATPATGPISGMAPLSQANSSLLANSPAGHGDGAFSNRSVSEAQGEAVRSISAVHPGLDVDVGQFLDGLQLNNLKEIFEREQIS  
WDVLVDMGHEELKEIGIHAYGHRHKILKAVKEKISGMGLGLGPFSTSQVQGSVIQELSMVDKDFASVADEMQSTIVEHRDSGT  
AGGVFTSYTILKIERVVNTKLWEKYVYRRREIADSNHNHANERMFLFHGSPFINAIVQKGFQQRHAYIGGMFGAGIYFAENSSK  
SNQYVYGIGGGSGCPTHKDRSCYSCERQLLLCRVALGKPFYQFSAVKMAHAPPGHNSVIGRPSGGLSFAEYVIYRGEQAYPE  
YLITYKINKPDT

>TNKS[A.queenslandica][XP\_019848937.1]

MDTRDHQAKIPGDSRQTSQSIEEGESADKNTGDLARLFEACKNGDIDTVQNLIQQRQSSANERDLHGRKSTPLHFAAGFGRRD  
IVKFLIEKGAHVDFRDEGGIPLHNCSFGHVDVVQLLLSNGANPN AQDNWKFSPLEAAIKGKADV CIVLLQH GADSSLLNT  
DRKAPIDLANGQAREVLLGTYRQDELEAAKVGDEQLMQILTPLNVNCHASDGRRSTPLHLAAGYNRTSIVQLLLKQGADVH  
AKDKGGLVPLHNACSYGHYEVAELLLKYGASINVTDLWQFTPLQEAASKGRSDVCSLLLAHGANPSIANCHGKTAFNLAPSEE  
FRKKLDSEYRGYQLLAAEDGGIILLKKLLSSQLLKFQHHQTLDTLLHKAVLSKSSNRQSVIDALLKRGINLNIGNKENMTPL  
ICAAKKGILEVVEQLVQRGANINHQDINGMTSLHWAVQNEHAQICRYLLSSGANPSIVNNQGQTIYQLKTSDTIQLILKNEPP  
VSQFEIEQQLLAARNSDLEILKKICTPQNVNCRDTKGRMSTPLHFAAGYNRVTVVEFLLENGADVHAKDKGGLVPLHNACSY  
GHYEVAELLVKYKANVNAMD LWKFTPLHEAAAKEKYDICKLLLKNGANVH SKNRDNLTPIDL VKDPKSDLADLLRGE PAL LDA  
AKKGEIERVKKLLTEDNVNCRDEYGRNSTPLHLAAGYNHLDVVEYLL ENKADVNAKDKGGLVPLHNASSYGHVDVASLLIRYN  
SVINATDRWNFTPLHEAAQKGRTQVCSLLI IHGADVLYKNQEGQIPLDLATADDVIALQDAMMKDIPLTIPPAEKEAKSNIV  
NKGLTAAGASLLASELV LGDGVDDKNGMVTQQRGGPAGVG DGS DKGFMSYRGGGDAPPWHNVTVKDILTELELGH LVELFER  
EQITIDILIEMN GDDLQSIGITAFGVRHRL LKRIREL VQGNNEEYPVGVT TTKPTQGTQLIELSSDDKEFIDTADLMQSTICE  
HRDDGKAGGVFDSYEILKIERIVNTKV WERYKYRRKEVAESNNNCANELM L F HGSPFVPYIVHNGFDERHAYIGGMFGAGIYF  
AEHSSKSNQYVYGIGGGNGCPEHKNRSCYTCLR KLLL CRVVLGKPV EQYTAVRIA HAPPGHHSVIGRPSAGGLNYPEYVIYRG  
EQAYPEYIITFRIKKPSATDSMSSSSSLDMSNNT

TNKS [A.queenslandica] [XP_019848937.1]	-----	0
TNKS [D.melanogaster] [NP_651410.1]	-----	0
TNKS [N.vectensis] [XP_032220531.1]	-----	0
TNKS [P.marinus] [XP_032806710.1]	-----	0
TNKS [B.belcheri] [XP_019641281.1]	-----	0
TNKS1 [S.salar] [XP_014017013.1]	--MAVSRSSQQQQGN-----LLS	17
TNKS1 [X.laevius] [XP_018099068.1]	--MAAPSRSSQQQ-----QVPTAAAGQSSQPPSASPPLSP-----SSRRA-----ASCLSPPC	46
TNKS1 [G.gallus] [NP_989671.1]	--MAAPRR-----SQ-HHHHHGPPPPPGPASPPAASPPRSPSLAPAEIG-PA	46
TNKS1 [H.sapiens] [NP_003738.2]	--MAASRRSQHHHHHHQQQLQPAPGASAPPPPPPLSPGLAPGTTT-ASPTASGLAPFA	57
TNKS1 [P.abeli] [XP_024106876.1]	--MAASRRSQHHHHHHQQQLQPAPGASAPPPPPPLSPGLAPGTTT-ASPTASGLAPFA	57
TNKS1 [M.musculus] [EDL35446.1]	GKMAASRRSQHHHHHHQQQLQPAPGASAPPPPPPLSPGLAPGPTT-ASPTAGGLAPFA	59
TNKS2 [S.salar] [XP_014034742.1]	-----	0
TNKS2 [X.laevius] [XP_018082988.1]	-----	0
TNKS2 [G.gallus] [NP_989672.1]	-----	0
TNKS2 [M.musculus] [NP_001157107.1]	-----	0
TNKS2 [H.sapiens] [AAK13463.1]	-----	0
TNKS2 [P.abeli] [XP_024109627.1]	-----	0
TNKS [A.queenslandica] [XP_019848937.1]	-----	0
TNKS [D.melanogaster] [NP_651410.1]	-----	0
TNKS [N.vectensis] [XP_032220531.1]	-----	0
TNKS [P.marinus] [XP_032806710.1]	-----MAARRAHLASPSSSSSLSPSSGSLDTTTAAAA-----AAAA	36
TNKS [B.belcheri] [XP_019641281.1]	-----	0
TNKS1 [S.salar] [XP_014017013.1]	PPRNGSLSVSPPGSPSLNL-----VTATLVPPDGERGCSTGMEN-PL-ASPDQTS	66
TNKS1 [X.laevius] [XP_018099068.1]	SPETNALSLSREGPDSEPEGEAASQPGITPRPLSPPPGEAANI-----	89
TNKS1 [G.gallus] [NP_989671.1]	AQRHS-----LAGPECEA-----PPDAERPAPAE-----	70
TNKS1 [H.sapiens] [NP_003738.2]	SPRHG-----LALPEGDGSRDPPDRPRSPDPVDGTSCCSTTSTICTVAAAPVVPVAV	108
TNKS1 [P.abeli] [XP_024106876.1]	SPRHG-----LALPEGDGSRDPPDRPRSPDPVDGTSCCSTTSTICTVTAAPVVPVAV	108
TNKS1 [M.musculus] [EDL35446.1]	SPRHG-----LALPEGDGSRDPPDRPRSPDPVDGAVCTVA-----APAAVPA	102
TNKS2 [S.salar] [XP_014034742.1]	-----	0
TNKS2 [X.laevius] [XP_018082988.1]	-----	0
TNKS2 [G.gallus] [NP_989672.1]	-----	0
TNKS2 [M.musculus] [NP_001157107.1]	-----	0
TNKS2 [H.sapiens] [AAK13463.1]	-----	0
TNKS2 [P.abeli] [XP_024109627.1]	-----	0
TNKS [A.queenslandica] [XP_019848937.1]	-----MDTRDHQAKIPGDSR-----Q	16
TNKS [D.melanogaster] [NP_651410.1]	-----MANS-----SR	6
TNKS [N.vectensis] [XP_032220531.1]	-----MPCQAKMASK	10
TNKS [P.marinus] [XP_032806710.1]	TTTAAAAA-----TTTAAAMTTTAAVSATSSPST-----TAAAAAATAAAAA	80
TNKS [B.belcheri] [XP_019641281.1]	-----MAGRAMLSS	10
TNKS1 [S.salar] [XP_014017013.1]	ALSSGSSTSP-----TTTTSGGSSSVSSP	91
TNKS1 [X.laevius] [XP_018099068.1]	--LSPTSSLPPAPSPSSGSSSSS-----SPSSNSLCTGGSPAESPESGIVIGVSSV	139
TNKS1 [G.gallus] [NP_989671.1]	--CSEGAAPGPPPGSGSSGSSASSSSSS-----SSTSSSVASSPAESPE-----	114
TNKS1 [H.sapiens] [NP_003738.2]	STSSAAGVAPNPAGS---GSNNPSSSSSSPSSSSSSPSSPGSSLAESPAAAGVSSSTAPL	165
TNKS1 [P.abeli] [XP_024106876.1]	STSSAAGVAPNPAGS---GSNNPSSSSSSPSSSSSSPSSPGSSLAESPAAAGVSSSTAPL	165
TNKS1 [M.musculus] [EDL35446.1]	--SAAVGVAFTPAGGGGGGNNSSASSASTPSSSSSPSSPGSSLAESPAAAGVSSSTAPL	160
TNKS2 [S.salar] [XP_014034742.1]	-----MA-SVARFWSANTNSKLYI-----YENTTPLMSTRQCSRVL	36
TNKS2 [X.laevius] [XP_018082988.1]	-----MSGRRCAGAS	10
TNKS2 [G.gallus] [NP_989672.1]	-----MAARRCAGGA	10
TNKS2 [M.musculus] [NP_001157107.1]	-----MSGRRCAGGG	10
TNKS2 [H.sapiens] [AAK13463.1]	-----MSGRRCAGGG	10
TNKS2 [P.abeli] [XP_024109627.1]	-----MSGRRCAGGG	10
TNKS [A.queenslandica] [XP_019848937.1]	TSQSIEEGESADKNTGDLARLFEACKNGDIDTVQNLIQQRQSSANERDLHGRKSTPLHFA	76
TNKS [D.melanogaster] [NP_651410.1]	SRAILSVNLDVAMANDPLRELFEACKTGEIAKVKKLIT-P-QTVNARDTAGRKSTPLHFA	64
TNKS [N.vectensis] [XP_032220531.1]	KLASNPFTFLSDPDVCEGRELFEACRNGDVSRVKRLVTNN-SNVNVRDTAGRKSSPLHFA	69
TNKS [P.marinus] [XP_032806710.1]	GGSPGSGQDSSADGGDAGKELFEACRNGDVGRVKRLVS-P-LNVNARDTTGRKSTPLHFA	138
TNKS [B.belcheri] [XP_019641281.1]	-----DRIHCDSSGCRELFEACRNGDVSRVKRLIT-P-QNVNARDTAGRKSTPLHFA	61
TNKS1 [S.salar] [XP_014017013.1]	GGSGTTPGDD-SGIGGAFRELFEACRNGDVSRVKRLVD-S-VNVNAKDMAGRKSTPLHFA	148
TNKS1 [X.laevius] [XP_018099068.1]	GI---GPGDPLSAVSGAFRELFEACRNGDVSRVKRLLE-P-ANVNAKDMAGRKSTPLHFA	194
TNKS1 [G.gallus] [NP_989671.1]	-----AAGPSGAFRELLEACRNGDVTRVKRLVD-A-GNVNAKDMAGRKSTPLHFA	162
TNKS1 [H.sapiens] [NP_003738.2]	GPGAAGPGTGVPVAVSGALRELLEACRNGDVSRVKRLVD-A-ANVNAKDMAGRKSTPLHFA	223
TNKS1 [P.abeli] [XP_024106876.1]	GPGAAGPGTGVPVAVSGALRELLEACRNGDVSRVKRLVD-A-ANVNAKDMAGRKSSPLHFA	223
TNKS1 [M.musculus] [EDL35446.1]	GAGAAGLPGVPVAVSGALRELLEACRNGDVSRVKRLVD-A-ANVNAKDMAGRKSSPLHFA	218
TNKS2 [S.salar] [XP_014034742.1]	GLGGVFPVGDTPRSGEPNREIFEACRNGDVERVRLVR-P-ENVNSRDTAGRKSTPLHFA	94
TNKS2 [X.laevius] [XP_018082988.1]	GSAASHGN---IGAGGEPARELFEACRNGDVERVRLVN-S-DNVNSRDTAGRKSTPLHFA	66
TNKS2 [G.gallus] [NP_989672.1]	AALAEAPG---CGSAVEPARELFEACRNGDVERVRLVR-P-ENVNSRDTAGRKSSPLHFA	66
TNKS2 [M.musculus] [NP_001157107.1]	AACAS-AG---AEAVEPSARELFEACRNGDVERVRLVT-P-EKVNSRDTAGRKSTPLHFA	65
TNKS2 [H.sapiens] [AAK13463.1]	AACAS-AA---AEAVEPAARELFEACRNGDVERVRLVT-P-EKVNSRDTAGRKSTPLHFA	65
TNKS2 [P.abeli] [XP_024109627.1]	AACAS-AA---AEAMEPAARELFEACRNGDVERVRLVT-P-EKVNSRDTAGRKSTPLHFA	65
TNKS [A.queenslandica] [XP_019848937.1]	AGFGRRDIVKFLIEKGAHVDFRDEGLIPLHNCSFQHVDVQVLLSNGANPNADNWK	136
TNKS [D.melanogaster] [NP_651410.1]	AGYGRREVVEFLNSGASIQACDEGLHPLHNCCSFGHAEVVRLLLKAGASPTTNDNWN	124
TNKS [N.vectensis] [XP_032220531.1]	AGFGRKEVVEYLLQCGADVHAMDDGGLIPLHNACSFHAEVVRIILLSHGADANARDNWN	129
TNKS [P.marinus] [XP_032806710.1]	AGFGRKDVVEHLLQNGANVHARDGGGLIPLHNACSFHAEVVNLLLRQGDADPNARDNWN	198
TNKS [B.belcheri] [XP_019641281.1]	AGFGRKDVVEHLLQNGANVHARDGGGLIPLHNACSFHAEVVTLRLRNGADPNARDNWN	121
TNKS1 [S.salar] [XP_014017013.1]	AGFGRKDVVDHLLQTGANVHARDGGGLIPLHNACSFHAEVVSLLLCQGDADPNARDNWN	208
TNKS1 [X.laevius] [XP_018099068.1]	AGFGRKDVVEHLLQTGANVHARDGGGLIPLHNACSFHAEVVTLRLCQGDADPNARDNWN	254
TNKS1 [G.gallus] [NP_989671.1]	AGFGRKDVVEHLLQTGANVHARDGGGLIPLHNACSFHAEVVSLLLCQGDADPNARDNWN	222
TNKS1 [H.sapiens] [NP_003738.2]	AGFGRKDVVEHLLQMGANVHARDGGGLIPLHNACSFHAEVVSLLLCQGDADPNARDNWN	283
TNKS1 [P.abeli] [XP_024106876.1]	AGFGRKDVVEHLLQMGANVHARDGGGLIPLHNACSFHAEVVSLLLCQGDADPNARDNWN	283
TNKS1 [M.musculus] [EDL35446.1]	AGFGRKDVVEHLLQMGANVHARDGGGLIPLHNACSFHAEVVSLLLCQGDADPNARDNWN	278
TNKS2 [S.salar] [XP_014034742.1]	AGFGRDQVVDYLLQNGANVHARDGGGLVSLHNACSFHGEVNVNLLLRHGADANSRDNWSY	154
TNKS2 [X.laevius] [XP_018082988.1]	AGFGRKDVVEHLLQSGANVHARDGGGLIPLHNACSFHAEVVSLLLRHGADPNARDNWN	126
TNKS2 [G.gallus] [NP_989672.1]	AGFGRKDVVEYLLQSGANVHARDGGGLIPLHNACSFHAEVVNLLLRHGADPNARDNWN	126
TNKS2 [M.musculus] [NP_001157107.1]	AGFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHAEVVNLLLRHGADPNARDNWN	125
TNKS2 [H.sapiens] [AAK13463.1]	AGFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHAEVVNLLLRHGADPNARDNWN	125
TNKS2 [P.abeli] [XP_024109627.1]	AGFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHAEVVNLLLRHGADPNARDNWN	125
TNKS [A.queenslandica] [XP_019848937.1]	SPLHEAAIKGKADVIVLLQHGADSSLLNTDRKAPIDLANGQAREVLLGTYRQDELLEAA	196
TNKS [D.melanogaster] [NP_651410.1]	TPLHEAASGKGVDCVCLALLQGHANHTIRNSEQKTPLELADEATRPVLTGEYRKDELLEAA	184
TNKS [N.vectensis] [XP_032220531.1]	TPLHEAAVKGKGVDCVCLALLQHGADPNIRNTDGKTALDVAEAAKLVLTGDYKKDELLEGA	189
TNKS [P.marinus] [XP_032806710.1]	TPLHEAAIKGKIDVIVLLQHGADPGIRNTDGKTALDLAEPTAKAVLTGEYKKDELLEAA	258
TNKS [B.belcheri] [XP_019641281.1]	TPLHEAAIKGKIDVIVLLQHGADPNIRNTDGKTALDLAEPTAKAVLTGDYKKDELLEAA	181
TNKS1 [S.salar] [XP_014017013.1]	TPLHEAAIKGKIDVIVLLQHGADPNIRNTDGKSALDLADPSAKAVLTGEYKKDELLEAA	268
TNKS1 [X.laevius] [XP_018099068.1]	TPLHEASIKGKIDVIVLLQHGADPNIRNTDGKSALDLADPSKAVLTGEYKKDELLEAA	314

TNKS1[G.allus][NP_989671.1]	TPLHEAAIKGKIDVCIIVLLQHGADPNIRNTDGSALDLADPSAEAVLTGEYKKDELLEAA	282
TNKS1[H.sapiens][NP_003738.2]	TPLHEAAIKGKIDVCIIVLLQHGADPNIRNTDGSALDLADPSAKAVLTGEYKKDELLEAA	343
TNKS1[P.abelii][XP_024106876.1]	TPLHEAAIKGKIDVCIIVLLQHGADPNIRNTDGSALDLADPSAKAVLTGEYKKDELLEAA	343
TNKS1[M.musculus][EDL35446.1]	TPLHEAAIKGKIDVCIIVLLQHGADPNIRNTDGSALDLADPSAKAVLTGEYKKDELLEAA	338
TNKS2[S.salar][XP_014034742.1]	TPLHEAAIKGSEVCIVILQHGAEPITRNTDGRALTDLAESTKAVLTGEYKKDELLEAA	214
TNKS2[X.laevis][XP_018082988.1]	TPLHEAAIKGKIDVCIIVLLQHGADPNIRNTDGRALTDLSDPSAKAVLTGEYKKDELLESA	186
TNKS2[G.gallus][NP_989672.1]	TPLHEAAIKGKTDCVIVILQHGAETPIRTNDGRALTDLADPSAKAVLTGEYKKDELLESA	186
TNKS2[M.musculus][NP_001157107.1]	TPLHEAAIKGKIDVCIIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGDYKKDELLESA	185
TNKS2[H.sapiens][AAK13463.1]	TPLHEAAIKGKIDVCIIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKKDELLESA	185
TNKS2[P.abelii][XP_024109627.1]	TPLHEAAIKGKIDVCIIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKKDELLESA	185
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TNKS[A.queenslandica][XP_019848937.1]	KVGDEQLLMQIILTPLNVNCHASDGRSRSTPLHLAGYNRTSIVQLLLKQGADVHAHKDKGGL	256
TNKS[D.melanogaster][NP_651410.1]	RSGAEDRLALLTPLNVNCHASDGRSRSTPLHLAGYNRTSIVQLLLKQGADVHAHKDKGGL	244
TNKS[N.vectensis][XP_032220531.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVGVQLLLKHGADVHAHKDKGGL	249
TNKS[P.marinus][XP_032806710.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGGL	318
TNKS[B.belcheri][XP_019641281.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGGL	241
TNKS1[S.salar][XP_014017013.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGGL	374
TNKS1[X.laevis][XP_018099068.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGGL	374
TNKS1[G.gallus][NP_989671.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGGL	374
TNKS1[H.sapiens][NP_003738.2]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGGL	402
TNKS1[P.abelii][XP_024106876.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGGL	343
TNKS1[M.musculus][EDL35446.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGGL	403
TNKS2[S.salar][XP_014034742.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSSPLHLAGYNRVKTVQLLLKHGADVHAHKDKGL	274
TNKS2[X.laevis][XP_018082988.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGL	246
TNKS2[G.gallus][NP_989672.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGL	246
TNKS2[M.musculus][NP_001157107.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGL	245
TNKS2[H.sapiens][AAK13463.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGL	245
TNKS2[P.abelii][XP_024109627.1]	RSGNEEKLMSLLTPLNVNCHASDGRKSTPLHLAGYNRVRIVQLLLKHGADVHAHKDKGL	245
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TNKS[A.queenslandica][XP_019848937.1]	VPLHNACSYGHYVEAELLKYGASINVTLDWQFTPLQEAAASKRGSDVCSLLSHGANPFI	316
TNKS[D.melanogaster][NP_651410.1]	VPLHNACSYGHFVDTKLLIQAGANVNADLWQFTPLHEAASKRVNVCSSLLSHGADPTL	304
TNKS[N.vectensis][XP_032220531.1]	VPLHNACSYGHFEVTPELLKHGASVNAMDLDWQFTPLHEAASKARVVCALLLGHGADPTL	309
TNKS[P.marinus][XP_032806710.1]	VPLHNACSYGHYEVTPELLKHGASVNAMDLDWQFTPLHEAASKNRVVCSSLISYGADPTL	378
TNKS[B.belcheri][XP_019641281.1]	VPLHNACSYGHFEVTPELLKHGASVNAMDLDWQFTPLHEAASKRSIEVCSSLISHGADPTL	301
TNKS1[S.salar][XP_014017013.1]	VPLHNACSYGHFEVTPELLKHGASVNAMDLDWQFTPLHEAASKNRVVCSSLLSHGADPTL	388
TNKS1[X.laevis][XP_018099068.1]	VPLHNACSYGHFEVTESLLKHGACVNAMDLDWQFTPLHEAASKNRVVCSSLLSHGADPTL	434
TNKS1[G.gallus][NP_989671.1]	VPLHNACSYGHYEVTPELLKHGACVNAMDLDWQFTPLHEAASKNRVVCSSLLSHGADPTL	402
TNKS1[H.sapiens][NP_003738.2]	VPLHNACSYGHYEVTPELLKHGACVNAMDLDWQFTPLHEAASKNRVVCSSLLSHGADPTL	463
TNKS1[P.abelii][XP_024106876.1]	VPLHNACSYGHYEVTPELLKHGACVNAMDLDWQFTPLHEAASKNRVVCSSLLSHGADPTL	463
TNKS1[M.musculus][EDL35446.1]	VPLHNACSYGHYEVTPELLKHGACVNAMDLDWQFTPLHEAASKNRVVCSSLLSHGADPTL	458
TNKS2[S.salar][XP_014034742.1]	VPLHNACSYGHYEVTDIIVKGACVNAMDLDWQFTPLHEAASKNRVVCSSLISYGADPTL	334
TNKS2[X.laevis][XP_018082988.1]	VPLHNACSYGHYEVTPELLKHGASVNAMDLDWQFTSLEAASKNRVVCSSLISYGADPTM	306
TNKS2[G.gallus][NP_989672.1]	VPLHNACSYGHYEVTPELLKHGACVNAMDLDWQFTPLHEAASKNRVVCSSLISYGADPTL	306
TNKS2[M.musculus][NP_001157107.1]	VPLHNACSYGHYEVTPELLKHGACVNAMDLDWQFTPLHEAASKNRVVCSSLISYGADPTL	305
TNKS2[H.sapiens][AAK13463.1]	VPLHNACSYGHYEVTPELLKHGACVNAMDLDWQFTPLHEAASKNRVVCSSLISYGADPTL	305
TNKS2[P.abelii][XP_024109627.1]	VPLHNACSYGHYEVTPELLKHGACVNAMDLDWQFTPLHEAASKNRVVCSSLISYGADPTL	305
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TNKS[A.queenslandica][XP_019848937.1]	ANCHGTAFNLAPSEEFRRKKLDSERYGQQLLAAREADGGIIILLKLLSSQLLKFPQHQTLD	376
TNKS[D.melanogaster][NP_651410.1]	LNCNKSATDAAPTRELRLERIAFYFKGHCLLDACRKCDVSRAKVLCAEVNFVHPYTGD	364
TNKS[N.vectensis][XP_032220531.1]	LNCNKSATDAAPTKEQLKELLESFFKGHQILEAAKGCDATAIKKLLITTETINFQHLPTLD	369
TNKS[P.marinus][XP_032806710.1]	LNCNKSATDLAPTSSELKERLVIEFFKGHSLLQAAREADLVTRVKHLLGLDINFKHPQTHE	438
TNKS[B.belcheri][XP_019641281.1]	LNCNKSATDVASTPELQEKLSIEFFKGHSLLDGARQDTMAKVKKHLLQDIVNFKPQTHD	361
TNKS1[S.salar][XP_014017013.1]	LNCNKSATDMAPTPELKERLTIEFFKGHSLLQAAREADLAKVKKTLALEIFSKHPQTNTE	441
TNKS1[X.laevis][XP_018099068.1]	VNCHGKSATDMAPTPELKERLTIEFFKGHSLLQAAREADLAKVKKTLALEIFNKQPQSHE	494
TNKS1[G.gallus][NP_989671.1]	VNCHGKSATDMAPTPELRELRITIEFFKGHSLLQAAREADLAKVKKTLALEIFNKQPQSHE	462
TNKS1[H.sapiens][NP_003738.2]	VNCHGKSATDMAPTPELRELRITIEFFKGHSLLQAAREADLAKVKKTLALEIFNKQPQSHE	523
TNKS1[P.abelii][XP_024106876.1]	VNCHGKSATDMAPTPELRELRITIEFFKGHSLLQAAREADLAKVKKTLALEIFNKQPQSHE	523
TNKS1[M.musculus][EDL35446.1]	VNCHGKSATDMAPTPELRELRITIEFFKGHSLLQAAREADLAKVKKTLALEIFNKQPQSHE	5

TNKS2 [M.musculus] [NP_001157107.1]	VNALDSLQGTSLHRAAHCGLQTCRLLSSYGCDPNIISLQGFALTQMGNNVQQLLQEG-	484
TNKS2 [H.sapiens] [AAK13463.1]	VNALDNLGQTSLSHRAAYCCHLQTCRLLSSYGCDPNIISLQGFALTQMGNNVQQLLQEG-	484
TNKS2 [P.abeli] [XP_024109627.1]	VNALDNLGQTSLSHRAAYCCHLQTCRLLSSYGCDPNIISLQGFALTQMGNNVQQLLQEG- :* * * * * . . * * : . . . : * : : : . . : : *	484
TNKS [A.queenslandica] [XP_019848937.1]	EPVVSQFEIEQQLLEAARNSDLEILKKI--CTPQNVNCRDTKGRMSTPLHFAAGYNRVTV	553
TNKS [D.melanogaster] [NP_651410.1]	-----PDSETHLLEAAKAGDLDTVRRIVLNNPISVNCRLDGRHSTPLHFAAGYNRVTV	535
TNKS [N.vectensis] [XP_032220531.1]	ESPSFVDAEKQLLEAAKTGDLETVKNL--CTAQTVNCRLDGRHSTPLHFAAGYNRVTV	547
TNKS [P.marinus] [XP_032806710.1]	SLPVNSDVEHQQLLEAAKAGDLDTVKQL--CTQTQVNCRDMGRHSTPLHFAAGYNRVSV	615
TNKS [B.belcheri] [XP_019641281.1]	-PPSGPADECDQQLLEAAKAGDLEAVKVL--CNPHTVNCRDVNGRHSSTPLHFAAGYNRVAV	537
TNKS1 [S.salar] [XP_014017013.1]	-VPTNSDSDVYRFLLEAAKAGDLDVQQL--CTPQNVNCRDLEGRHSTPLHFAAGYNRVAV	624
TNKS1 [X.laev] [XP_018099068.1]	-TPVRTSDVDYRLLLEASKAGDLDIVKQL--CSSQNVNCRDLEGRHSTPLHFAAGYNRVSV	670
TNKS1 [G.gallus] [NP_989671.1]	-TPVRTSDVDYRLLLEASKAGDLETVKQL--CSPQNVNCRDLEGRHSTPLHFAAGYNRVSV	638
TNKS1 [H.sapiens] [NP_003738.2]	-TPRTSDVDYRLLLEASKAGDLETVKQL--CSSQNVNCRDLEGRHSTPLHFAAGYNRVSV	699
TNKS1 [P.abeli] [XP_024106876.1]	-TPRTSDVDYRLLLEASKAGDLETVKQL--CSPQNVNCRDLEGRHSTPLHFAAGYNRVSV	699
TNKS1 [M.musculus] [EDL35446.1]	-TPMRTSDVDYRLLLEASKAGDLETVKQL--CSPQNVNCRDLEGRHSTPLHFAAGYNRVSV	694
TNKS2 [S.salar] [XP_014034742.1]	-TLGNSDSDVQQLLEASKSGDLEIVKVL--CTMQNVNCRDVEGRQSTPLHFAAGYNRVSV	570
TNKS2 [X.laev] [XP_018082988.1]	-LPFSNSDADSQLLEAAKAGDLDVVKVL--CTSQSVNCRDVEGRQSTPLHFAAGYNRVAV	542
TNKS2 [G.gallus] [NP_989672.1]	-IPLGNSDADRQLLEAAKAGDVTVKKL--CTVQSVNCRDIEGRQSTPLHFAAGYNRVSV	542
TNKS2 [M.musculus] [NP_001157107.1]	-ASLGHSEADRQLLEAAKAGDVTVKKL--CTVQSVNCRDIEGRQSTPLHFAAGYNRVSV	541
TNKS2 [H.sapiens] [AAK13463.1]	-ISLGNSEADRQLLEAAKAGDVTVKKL--CTVQSVNCRDIEGRQSTPLHFAAGYNRVSV	541
TNKS2 [P.abeli] [XP_024109627.1]	-ISLGNSEADRQLLEAAKAGDVTVKKL--CTVQSVNCRDIEGRQSTPLHFAAGYNRVSV : : : : : * : : : : . : : : : * : : : : * : : : : *	541
TNKS [A.queenslandica] [XP_019848937.1]	VEFLLENGADVHAKDKGGLVPLHNACSYGHYEVAELLVKYKANVNAMDWKFTPLHEAAA	613
TNKS [D.melanogaster] [NP_651410.1]	VQFLLHEGAEVVAADKGGVPLHNACSYGHYEVTCELLVKHGAVNVNADLWKFTPLHEAAA	595
TNKS [N.vectensis] [XP_032220531.1]	VEYLLLNGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAIVNVADLWKFTPLHEAAA	607
TNKS [P.marinus] [XP_032806710.1]	VEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKRGAVNVNADLWKFTPLHEAAA	675
TNKS [B.belcheri] [XP_019641281.1]	VEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVCCELLVKHGAVNVNADLWKFTPLHEAAA	597
TNKS1 [S.salar] [XP_014017013.1]	VEYLLHHGADVHAKDKGGLVPLHNACSYGHYEVAELLVVRHGASVNVNADLWKFTPLHEAAA	684
TNKS1 [X.laev] [XP_018099068.1]	VEYLLHHGADVHAKDKGGLVPLHNACSYGHYEVAELLVVRHGASVNVNADLWKFTPLHEAAA	730
TNKS1 [G.gallus] [NP_989671.1]	VEYLLHHGADVHAKDKGGLVPLHNACSYGHYEVAELLVVRHGASVNVNADLWKFTPLHEAAA	698
TNKS1 [H.sapiens] [NP_003738.2]	VEYLLHHGADVHAKDKGGLVPLHNACSYGHYEVAELLVVRHGASVNVNADLWKFTPLHEAAA	759
TNKS1 [P.abeli] [XP_024106876.1]	VEYLLHHGADVHAKDKGGLVPLHNACSYGHYEVAELLVVRHGASVNVNADLWKFTPLHEAAA	759
TNKS1 [M.musculus] [EDL35446.1]	VEYLLHHGADVHAKDKGGLVPLHNACSYGHYEVAELLVVRHGASVNVNADLWKFTPLHEAAA	754
TNKS2 [S.salar] [XP_014034742.1]	VEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVHGAVNVNADLWKFTPLHEAAA	630
TNKS2 [X.laev] [XP_018082988.1]	VEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVTCELLVKHGAVNVNADLWKFTPLHEAAA	602
TNKS2 [G.gallus] [NP_989672.1]	VEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVNVNADLWKFTPLHEAAA	602
TNKS2 [M.musculus] [NP_001157107.1]	VEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVNVNADLWKFTPLHEAAA	601
TNKS2 [H.sapiens] [AAK13463.1]	VEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVNVNADLWKFTPLHEAAA	601
TNKS2 [P.abeli] [XP_024109627.1]	VEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVNVNADLWKFTPLHEAAA * : : : : * : : : : * : : : : * : : : : * : : : : * : : : : *	601
TNKS [A.queenslandica] [XP_019848937.1]	KEKYDICKLLKNGANVHSKNRDNLPTIDLVDKPKSADLALLRGEFALLDAAKKGEIERV	673
TNKS [D.melanogaster] [NP_651410.1]	RGKYDICKLLKKGADPMKKNRDGATPADLVKESDHDVAELLRGPALLDAAKKGNLAVR	655
TNKS [N.vectensis] [XP_032220531.1]	RGKYEICQLLLKKGADPQKNRDGDTPLDLVKEGSDVADLLRGDAALLDAAKKGNLIRI	667
TNKS [P.marinus] [XP_032806710.1]	RGKYEICKLLKKGADPTKKNRDGNTPLDLVKEGDTDIQDLLRGDAALLDAAKKGNLAVR	735
TNKS [B.belcheri] [XP_019641281.1]	RGKYEICKLLKKGADPMKKNRDGNTPLDLVRDGDGTDIQDLLRGDAALLDAAKKGNLAVR	657
TNKS1 [S.salar] [XP_014017013.1]	RGKYEICKLLKKGADPTKKNRDGNMPLDMVKDGDGTDIQDLLRGDAALLDAAKKGNLAVR	744
TNKS1 [X.laev] [XP_018099068.1]	RGKYEICKLLKKGADPTKKNRDGNTPLDLVKDGDGTDIQDLLRGDAALLDAAKKGNLAVR	790
TNKS1 [G.gallus] [NP_989671.1]	RGKYEICKLLKKGADPTKKNRDGNTPLDLVKEGDTDIQDLLRGDAALLDAAKKGNLAVR	758
TNKS1 [H.sapiens] [NP_003738.2]	RGKYEICKLLKKGADPTKKNRDGNTPLDLVKEGDTDIQDLLRGDAALLDAAKKGNLAVR	819
TNKS1 [P.abeli] [XP_024106876.1]	RGKYEICKLLKKGADPTKKNRDGNTPLDLVKEGDTDIQDLLRGDAALLDAAKKGNLAVR	819
TNKS1 [M.musculus] [EDL35446.1]	RGKYEICKLLKKGADPTKKNRDGNTPLDLVKEGDTDIQDLLRGDAALLDAAKKGNLAVR	814
TNKS2 [S.salar] [XP_014034742.1]	RGKYEICKLLQHGADPTKKNRDGSTPLDLVKDGDGTMDQDLLRGDAALLDAAKKGNLAVR	690
TNKS2 [X.laev] [XP_018082988.1]	RGKYEICKLLKKGADSTKKNRDGNTPLDLVKDGDGTDIQDLLRGDAALLDAAKKGNLAVR	662
TNKS2 [G.gallus] [NP_989672.1]	RGKYEICKLLQHGADPPKKNRDGNTPLDLVKDGDGTDIQDLLRGDAALLDAAKKGNLAVR	662
TNKS2 [M.musculus] [NP_001157107.1]	RGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGDGTDIQDLLRGDAALLDAAKKGNLAVR	661
TNKS2 [H.sapiens] [AAK13463.1]	RGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGDGTDIQDLLRGDAALLDAAKKGNLAVR	661
TNKS2 [P.abeli] [XP_024109627.1]	RGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGDGTDIQDLLRGDAALLDAAKKGNLAVR * * : : : * : : : * : : : * : : : * : : : * : : : * : : : *	661
TNKS [A.queenslandica] [XP_019848937.1]	KKLLTEDNVNCRDEYGRNSTPLHLAAGYNNHLDVVEYLLNKAADVNAQDKGGLVPLHNASS	733
TNKS [D.melanogaster] [NP_651410.1]	QRLVTPESINCRDAQGRNSTPLHLAAGYNNFCAEYLLENGADVNAQDKGGLVPLHNASS	715
TNKS [N.vectensis] [XP_032220531.1]	TKLATPENINCRDTQGRNSTPLHLAAGYNNHLEVAEYLLHAGADVNAQDKGGLVPLHNASS	727
TNKS [P.marinus] [XP_032806710.1]	QKLCSENVNCRDSQGRNSTPLHLAAGYNNLEVAEYLLHAGADVNAQDKGGLVPLHNASS	795
TNKS [B.belcheri] [XP_019641281.1]	QKLATPENINCRDTQGRNSTPLHLAAGYNNVLEVAEYLLHAGADVNAQDKGGLVPLHNASS	717
TNKS1 [S.salar] [XP_014017013.1]	QKLCSPENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLHAGADVNAQDKGGLVPLHNASS	804
TNKS1 [X.laev] [XP_018099068.1]	QKLCTQENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLHAGADVNAQDKGGLVPLHNASS	850
TNKS1 [G.gallus] [NP_989671.1]	QKLCTPENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLHAGADVNAQDKGGLVPLHNASS	818
TNKS1 [H.sapiens] [NP_003738.2]	QKLCTPENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLHAGADVNAQDKGGLVPLHNASS	879
TNKS1 [P.abeli] [XP_024106876.1]	QKLCTPENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLHAGADVNAQDKGGLVPLHNASS	879
TNKS1 [M.musculus] [EDL35446.1]	QKLCTPENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLHAGADVNAQDKGGLVPLHNASS	874
TNKS2 [S.salar] [XP_014034742.1]	EKLCPDNVNCRDAQGRHSTPLHLAAGYNNLEVAEYLLQHGAEVNSQDKGGLVPLHNASS	750
TNKS2 [X.laev] [XP_018082988.1]	KKLCTPENVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLVPLHNASS	722
TNKS2 [G.gallus] [NP_989672.1]	KKLCPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLVPLHNASS	722
TNKS2 [M.musculus] [NP_001157107.1]	KKLSSPDVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLVPLHNASS	721
TNKS2 [H.sapiens] [AAK13463.1]	KKLSSPDVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLVPLHNASS	721
TNKS2 [P.abeli] [XP_024109627.1]	KKLSSPDVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLVPLHNASS * : : : : * : : : * : : : * : : : * : : : * : : : * : : : *	721
TNKS [A.queenslandica] [XP_019848937.1]	YGHVDVASLLIRYNSVINATDRWNFTPLHEAAQKGRQTQVCSLLIHGADVYLLKNQEGQIP	793
TNKS [D.melanogaster] [NP_651410.1]	YGHLDIAALLIKHKTTVNATDKWFTPLHEAAQKGRQTQLCSLLLAHGADAYMKNQEGQTP	775
TNKS [N.vectensis] [XP_032220531.1]	YGHVDIAALLIRYNTVNATDRWFTPLHEAAQKGRQTQLCALLEAHGADPMSKNQEGQSP	787
TNKS [P.marinus] [XP_032806710.1]	YGHVDIAALLIKYSAVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPMSKNQEGQTP	855
TNKS [B.belcheri] [XP_019641281.1]	YGHVEIAALLIKYGTVCVNATDRWNFTPLHEAAQKGRQTQLCALLEAHGADPTMKNQEGQTP	777
TNKS1 [S.salar] [XP_014017013.1]	YGHVDIAALLIKFNTCVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPTMKNQEGQTA	864
TNKS1 [X.laev] [XP_018099068.1]	YGHVDIAALLIKYNTCVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPTMKNQESQTP	910
TNKS1 [G.gallus] [NP_989671.1]	YGHVDIAALLIKYNTCVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPTMKNQEGQTP	878
TNKS1 [H.sapiens] [NP_003738.2]	YGHVDIAALLIKYNTCVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPTMKNQEGQTP	939
TNKS1 [P.abeli] [XP_024106876.1]	YGHVDIAALLIKYNTCVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPTMKNQEGQTP	939
TNKS1 [M.musculus] [EDL35446.1]	YGHVDIAALLIKYNTCVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPTMKNQEGQTP	934
TNKS2 [S.salar] [XP_014034742.1]	YGHVDVAALLIKYDACVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPALRNQEGQSP	810
TNKS2 [X.laev] [XP_018082988.1]	YGHVDVAALLIKYNACVNANDKWFTPLHEAAQKGRQTQLCALLEAHGADPALRNQEGQAP	782
TNKS2 [G.gallus] [NP_989672.1]	YGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPTLKNQEGQTP	782
TNKS2 [M.musculus] [NP_001157107.1]	YGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPTLKNQEGQTP	781
TNKS2 [H.sapiens] [AAK13463.1]	YGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPTLKNQEGQTP	781
TNKS2 [P.abeli] [XP_024109627.1]	YGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRQTQLCALLEAHGADPTLKNQEGQTP * : : : : * : : : * : : : * : : : * : : : * : : : * : : : *	781
TNKS [A.queenslandica] [XP_019848937.1]	LDLATADDVIALLDAMMKDIPLT-IPPAEKAESNIVN-----KG-----	833
TNKS [D.melanogaster] [NP_651410.1]	IELATADDVKCLLDAMATSLSQQALSASTQSLTSSSPAPDATAAAGFTSSSSSSSAILS	835



TNKS[N.vectensis][XP_032220531.1]	VDLATAEDVKCLLGDMAMSLTQTTSVSTAPVAKVPAPVTAT-AGAA-----	831
TNKS[P.marinus][XP_032806710.1]	LDLATADDVRALLIDAMPPPEALPVTHKPPSIPTIAATSAA-ATAALALGPTPALA--SLA	912
TNKS[B.belcheri][XP_019641281.1]	LDLATAEDVRALLIDVAMPPOQSLPAAIATATVKAASP-----	913
TNKS1[S.salar][XP_014017013.1]	LDLATADDIRALLMDAMPDPDALPSCFKPQATVVVSAGS-----	901
TNKS1[X.laevius][XP_018099068.1]	LDLATADDIRALLIDAMPPPEALPSCFKPQATVVSA-S-----	946
TNKS1[G.gallus][NP_989671.1]	LDLATADDIRALLIDAMPPPEALPTCFKLQATVVSA-S-----	914
TNKS1[H.sapiens][NP_003738.2]	LDLATADDIRALLIDAMPPPEALPTCFKPQATVVSA-S-----	975
TNKS1[P.abelii][XP_024106876.1]	LDLATADDIRALLIDAMPPPEALPTCFKPQATVVSA-S-----	975
TNKS1[M.musculus][EDL35446.1]	LDLATADDIRALLIDAMPPPEALPTCFKPQATVVSA-S-----	970
TNKS2[S.salar][XP_014034742.1]	LDLVTVDVVRALLTAAMPSPALPGCYKQVIVSMSSPV-----	847
TNKS2[X.laevius][XP_018082988.1]	LDLVTADDVRALLTAAMPPEALPTFYKQQLNVPQPS-----	819
TNKS2[G.gallus][NP_989672.1]	LDLVTADDVSALLTAAMPSPALPSCYKQVIVSVQTA-----	819
TNKS2[M.musculus][NP_001157107.1]	LDLVSADDVSALLTAAMPSPALPTCYKQVIVSGVRGP-----	818
TNKS2[H.sapiens][AAK13463.1]	LDLVSADDVSALLTAAMPSPALPSCYKQVIVLNGVRSP-----	818
TNKS2[P.abelii][XP_024109627.1]	LDLVSADDVSALLTAAMPSPALPSCYKQVIVLNGVRSP-----	818
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TNKS[A.queenslandica][XP_019848937.1]	-----LTAAGASLL-----ASELVLDGVDKNGMVTQ----QRGGPAGV	869
TNKS[D.melanogaster][NP_651410.1]	PTTETVLLPTGASML-----SVP--VPLPLSSSTRISP-----AQG--	870
TNKS[N.vectensis][XP_032220531.1]	-----TPATGPISGMAPLSQANSS-----LLANSFAGHG--	860
TNKS[P.marinus][XP_032806710.1]	P-----SPVPSGASAGAGGVPLLASPSSTPASLSAASSMDSLTGACGVAPSPVPAIGA	968
TNKS[B.belcheri][XP_019641281.1]	-----ISSPSTTPSSTPGVLTASSMDHLVGA-----V-GG	843
TNKS1[S.salar][XP_014017013.1]	-----V-----ISPASTPSCLSAASSIDNLAG-----PLNELGAA-GT	933
TNKS1[X.laevius][XP_018099068.1]	-----I-----ISPSTPSCLSAASSIDNLTG-----PLAELAVG-GV	978
TNKS1[G.gallus][NP_989671.1]	-----L-----ISPASTPSCLSAASSIDNLTG-----PLAELAVG-GA	946
TNKS1[H.sapiens][NP_003738.2]	-----L-----ISPASTPSCLSAASSIDNLTG-----PLAELAVG-GA	1007
TNKS1[P.abelii][XP_024106876.1]	-----L-----ISPASTPSCLSAASSIDNLTG-----PLAELAVG-GA	1007
TNKS1[M.musculus][EDL35446.1]	-----L-----ISPASTPSCLSAASSIDNLTG-----PLTDLAVG-GA	1002
TNKS2[S.salar][XP_014034742.1]	-----GVVPPPSLGSSTPLSTLASRSLDNQATSTCTAFPELAL---	889
TNKS2[X.laevius][XP_018082988.1]	-----TTAAALSSVPLSS--PTLSAASSLDNL-----ASSFSETTSV-S	857
TNKS2[G.gallus][NP_989672.1]	-----SSTADPLSSVPSPP--SSLSAASSLDNL-----SGSFSELSPV-VG	857
TNKS2[M.musculus][NP_001157107.1]	-----GATADALSSGSPSP--SSLSAASSLDNL-----SGSFSELSAV-VS	856
TNKS2[H.sapiens][AAK13463.1]	-----GATADALSSGSPSP--SSLSAASSLDNL-----SGSFSELSAV-VS	856
TNKS2[P.abelii][XP_024109627.1]	-----GAPADALSSGSPSP--SSLSAASSLDNL-----SGSFSELSAV-VS	856
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TNKS[A.queenslandica][XP_019848937.1]	GDGSDKGFMSYR-----GGGDAPPVHNWTVKDLITELGHLVELFER	913
TNKS[D.melanogaster][NP_651410.1]	-----AEANGAEAGSSS-----DD-LLPADTITNVSGFLSSQQLHLLIELFER	912
TNKS[N.vectensis][XP_032220531.1]	-----DGAFSNRS-VSE---AQ---GEAVRSISAVHPLGLVDVQFLDGLQLNNLKEIFER	909
TNKS[P.marinus][XP_032806710.1]	GAAGDGTLLGACGVSAADGATGPADKPDARSADFEIPLDMNINMFLKGLDHLRDIPEK	1028
TNKS[B.belcheri][XP_019641281.1]	-----AGQGDGAIDR-----SAVEG-ESLDMTISISSFQQLGLNQLLDIFNK	884
TNKS1[S.salar][XP_014017013.1]	-----SGVADGATGS-----DRKEGELVMLDMNISQFLKSLGLEHLRDIPEK	975
TNKS1[X.laevius][XP_018099068.1]	-----SNAGDGAAGT-----ERKEGEVTVLDININQFLKSLGLEHLRDIPEK	1020
TNKS1[G.gallus][NP_989671.1]	-----SNTGDGAAGT-----ERKEGEVSGLDMNITQFLKSLGLEHLRDIPEK	988
TNKS1[H.sapiens][NP_003738.2]	-----SNAGDGAAGT-----ERKEGEVAGLDMNISQFLKSLGLEHLRDIPEK	1049
TNKS1[P.abelii][XP_024106876.1]	-----SNAGDGAAGT-----ERKEGEIAGLDMNISQFLKSLGLEHLRDIPEK	1049
TNKS1[M.musculus][EDL35446.1]	-----SNAGDGAAGA-----ERKEGEVAGLDMNISQFLKSLGLEHLRDIPEK	1044
TNKS2[S.salar][XP_014034742.1]	-----LGPSGAVGT-----DN--KEVPGVDLSIGQFLNNLGLEHLLIEFER	928
TNKS2[X.laevius][XP_018082988.1]	-----GGAEGASGL-----DK--KDEGVLDNINQFLRNLGLEHLLIDVFER	895
TNKS2[G.gallus][NP_989672.1]	-----TNSAEGATVL-----EK--KEVSGVDFSINQVFNRLGLEHLLIDVFER	897
TNKS2[M.musculus][NP_001157107.1]	-----SSAEGATGL-----QR--KEDSGIDFSITQFIRNLGLEHLLIDVFER	896
TNKS2[H.sapiens][AAK13463.1]	-----SSGTEGASSL-----EK--KEVPGVDFSITQFVFNRLGLEHLLIDVFER	896
TNKS2[P.abelii][XP_024109627.1]	-----SSGTEGTSLL-----EK--KEVPGVDFSITQFLRNLGLEHLLIDVFER	896
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TNKS[A.queenslandica][XP_019848937.1]	EQITIDILIEMGDDQLQSIGITAFGVHRHLLKRIRELVOGNNEEY--P---VGVTTTKPT	968
TNKS[D.melanogaster][NP_651410.1]	EQITLDILAEMGHDDLKQGVSAVGRHKLKLGIAQLRSTTIG-----NNVN	960
TNKS[N.vectensis][XP_032220531.1]	EQISWDVLVDMGHEELKEIGINAYGHRHKLKAVKEKISGMGLG----LGPFSST--SQV	962
TNKS[P.marinus][XP_032806710.1]	EQITLDVLADMGHEELKEIGINAYGHRHKLKIGVERLLGAQQGGLAYPGANPYLSYHTTA	1088
TNKS[B.belcheri][XP_019641281.1]	EQITLDILGEMGHEELKEIGINAYGHRHKLKIGVERLLGGTGT-----TLNPLYTLPALGS	939
TNKS1[S.salar][XP_014017013.1]	EQITLDVLADMGHEELKEIGINAYGHRHKLKIGVERLLGGQ-----GANPLYTFHCAN	1029
TNKS1[X.laevius][XP_018099068.1]	EQITLDVLADMGHEELKEIGINAYGHRHKLKIGVERLLGGQ-----GTNPLYTFHCVS	1074
TNKS1[G.gallus][NP_989671.1]	EQITLDVLADMGHEELKEIGINAYGHRHKLKIGVERLLGGQ-----GTNPLYTFHCVS	1042
TNKS1[H.sapiens][NP_003738.2]	EQITLDVLADMGHEELKEIGINAYGHRHKLKIGVERLLGGQ-----GTNPLYTFHCVN	1103
TNKS1[P.abelii][XP_024106876.1]	EQITLDVLADMGHEELKEIGINAYGHRHKLKIGVERLLGGQ-----GTNPLYTFHCVN	1103
TNKS1[M.musculus][EDL35446.1]	EQITLDVLADMGHEELKEIGINAYGHRHKLKIGVERLLGGQ-----GTNPLYTFHCVN	1098
TNKS2[S.salar][XP_014034742.1]	EQITLDVLVEMGHKEELKEIGINAYGHRHKLKIGVERLLISGPQ-----SLNPLYTLNTAN	982
TNKS2[X.laevius][XP_018082988.1]	EQITLDVLVEMGHKEELKEIGINAYGHRHKLKIGVERLLISGQH-----GLNPLYTLNTNS	949
TNKS2[G.gallus][NP_989672.1]	EQITLDVLVEMGHKEELKEIGINAYGHRHKLKIGVERLLISGQ-----GLNPLYTLNTSS	951
TNKS2[M.musculus][NP_001157107.1]	EQITLDVLVEMGHKEELKEIGINAYGHRHKLKIGVERLLISGQ-----GLNPLYTLNTSSG	950
TNKS2[H.sapiens][AAK13463.1]	EQITLDVLVEMGHKEELKEIGINAYGHRHKLKIGVERLLISGQ-----GLNPLYTLNTSG	950
TNKS2[P.abelii][XP_024109627.1]	EQITLDVLVEMGHKEELKEIGINAYGHRHKLKIGVERLLISGQ-----GLNPLYTLNTSG	950
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TNKS[A.queenslandica][XP_019848937.1]	QGTQLIELSSDDKEFIDTADLMQSTICEHRDDGKAGGVFDSYEILKIERIVNTKWERYK	1028
TNKS[D.melanogaster][NP_651410.1]	LCTLLVDLLPDDKEFVAVEEEMQATIREHRDNGQAGGYFTRYNIIRVQKVNKRLWERYA	1020
TNKS[N.vectensis][XP_032220531.1]	QGSVIQELSMVDKDFASVADQMSTIREHRDNGAGGVFTSYTILKIERIVNTKLWERYV	1022
TNKS[P.marinus][XP_032806710.1]	QGTLLIDLPPDDKEYQSVDEEMQSTIREHKDGGQAGGVFNRYNVIKIQKVNKRLWERYT	1148
TNKS[B.belcheri][XP_019641281.1]	HGTILTDLSPDDKEYQSVDEEVQSTIREHKDGGQAGGVFNRYNVIKIQKVNKRLWERYV	999
TNKS1[S.salar][XP_014017013.1]	QGTVLIDLAPDDKEQSVDEEEMQSTIREHRDGGNAGGVFSRYNIKIQKVVNKLRLERYT	1089
TNKS1[X.laevius][XP_018099068.1]	QGTVLDDLADDDKEYQSVDEEEMQNSIREHRDGGNAGGVFNRYNVIKIQKVVNKLRLERFC	1134
TNKS1[G.gallus][NP_989671.1]	QGTILLDLAPDDKEYQSVDEEEMQSTIREHRDGGNAGGVFNRYNVIKIQKVVNKLRLERFC	1102
TNKS1[H.sapiens][NP_003738.2]	QGTILLDLAPDDKEYQSVDEEEMQSTIREHRDGGNAGGVFNRYNVIKIQKVVNKLRLERFC	1163
TNKS1[P.abelii][XP_024106876.1]	QGTILLDLAPDDKEYQSVDEEEMQSTIREHRDGGNAGGVFNRYNVIKIQKVVNKLRLERFC	1163
TNKS1[M.musculus][EDL35446.1]	QGTILLDLAPDDKEYQSVDEEEMQSTIREHRDGGNAGGVFNRYNVIKIQKVVNKLRLERFC	1158
TNKS2[S.salar][XP_014034742.1]	SGTILLDLVSDDDKEFQVVEELQSTIREHRDGGLAGGVFNRYNVIKIQKVCNKLWERYT	1042
TNKS2[X.laevius][XP_018082988.1]	SGTILLDLAPDDKEFQVVEEEMQSTIREHRDGGHAGGVFTKYNIILKIQKVCNKLWERYT	1009
TNKS2[G.gallus][NP_989672.1]	SGTILLDLSSDDKEFQSVDEEEMQSTVREHRDGGHAGGVFNRYNVIKIQKVCNKLWERYT	1011
TNKS2[M.musculus][NP_001157107.1]	SGTILLDLSPDDKEFQSVDEEEMQSTVREHRDGGHAGGVFNRYNVIKIQKVCNKLWERYT	1010
TNKS2[H.sapiens][AAK13463.1]	SGTILLDLSPDDKEFQSVDEEEMQSTVREHRDGGHAGGVFNRYNVIKIQKVCNKLWERYT	1010
TNKS2[P.abelii][XP_024109627.1]	SGTILLDLSPDDKEFQSVDEEEMQSTVREHRDGGHAGGVFNRYNVIKIQKVCNKLWERYT	1010
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TNKS[A.queenslandica][XP_019848937.1]	YRRKEVAESNNNCANELMLFHGSPFVPIYVHNGFDERHAYIGGMFGAGIYFAEHSKSNQ	1088
TNKS[D.melanogaster][NP_651410.1]	HRRQEIAEENFLQSNRMLFHGSPFINAIVQRGFDERHAYIGGMFGAGIYFAEHSKSNQ	1080
TNKS[N.vectensis][XP_032220531.1]	YRRREIADSNHNHNERMLFHGSPFINAIVQKQDQQRHAYIGGMFGAGIYFAENS KSNQ	1082
TNKS[P.marinus][XP_032806710.1]	HRRKEVTEENHNHNERMLFHGSPFINAIIKNGFDERHAYIGGMFGAGIYFAENS KSNQ	1208
TNKS[B.belcheri][XP_019641281.1]	HRRKEVSEENHNQSNRMLFHGSPFINAIIKNGFDERHAYIGGMFGAGIYFAENS KSNQ	1059
TNKS1[S.salar][XP_014017013.1]	HRQKEISDENHNHNERMLFHGSPFINAIIKNGFDERHAYIGGMFGAGIYFAENS KSNQ	1149
TNKS1[X.laevius][XP_018099068.1]	HRQKEVSEENHNHNERMLFHGSPFINAIIKNGFDERHAYIGGMFGAGIYFAENS KSNQ	1194
TNKS1[G.gallus][NP_989671.1]	HRQKEVSEENHNHNERMLFHGSPFINAIIKNGFDERHAYIGGMFGAGIYFAENS KSNQ	1162
TNKS1[H.sapiens][NP_003738.2]	HRQKEVSEENHNHNERMLFHGSPFINAIIKNGFDERHAYIGGMFGAGIYFAENS KSNQ	1223

TNKS1 [P. abelii] [XP_024106876.1]	HRQKEVSEENNHNHNERMLFHGSPFFNAI IHKGFDERHAYI IGMGFGAGIYFAENSSKSNQ	1223
TNKS1 [M. musculus] [EDL35446.1]	HRQKEVSEENNHNHNERMLFHGSPFFNAI IHKGFDERHAYI IGMGFGAGIYFAENSSKSNQ	1218
TNKS2 [S. salar] [XP_014034742.1]	HRKKEVSEENNHNHNERMLFHGSPFFNAI IHKGFDERHAYI IGMGFGAGIYFAENSSKSNQ	1102
TNKS2 [X. laevis] [XP_018082988.1]	HRQKEVTEENNHNHNERMLFHGSPFFNAI IHKGFDERHAYI IGMGFGAGIYFAENSSKSNQ	1069
TNKS2 [G. gallus] [NP_989672.1]	HRKKEVSEENNHNHNERMLFHGSPFFNAI IHKGFDERHAYI IGMGFGAGIYFAENSSKSNQ	1071
TNKS2 [M. musculus] [NP_001157107.1]	HRKKEVSEENNHNHNERMLFHGSPFFNAI IHKGFDERHAYI IGMGFGAGIYFAENSSKSNQ	1070
TNKS2 [H. sapiens] [AAK13463.1]	HRKKEVSEENNHNHNERMLFHGSPFFNAI IHKGFDERHAYI IGMGFGAGIYFAENSSKSNQ	1070
TNKS2 [P. abelii] [XP_024109627.1]	HRKKEVSEENNHNHNERMLFHGSPFFNAI IHKGFDERHAYI IGMGFGAGIYFAENSSKSNQ	1070
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TNKS [A. queenslandica] [XP_019848937.1]	VYVIGGGNGCPEHKNRSCYICLRKLLLCRVVLGKFPVQYTVAVTAHAPGGHSHVIGRPS	1148
TNKS [D. melanogaster] [NP_651410.1]	VYVIGGGGICGCPSHKDKSCYVCPRQLLLCRVALGKSFLOYSAMKMAHAPPGGHSHVIGRPS	1140
TNKS [N. vectensis] [XP_032220531.1]	VYVIGGGGCGCPTHKDRSCYICRQMLLLCRVALGKFPFQFSYAVKMAHAPPGGHSHVIGRPS	1142
TNKS [P. marinus] [XP_032806710.1]	VYVIGGGTGCPVHKDRSCYICQRQMLFCRVTLGKSFLOFSAMKMAHSPGGHSHVIGRPS	1268
TNKS [B. belcheri] [XP_019641281.1]	VYVIGGGTGCPICHKDRSCYICQRQMLFCRVTLGKSFLOFSAMKMAHAPPGGHSHVIGRPS	1119
TNKS1 [S. salar] [XP_014017013.1]	VYVIGGGTGCPCTHKDRSCYICHRQMLFCRVTLGKSFLOFSAMKMAHAPPGGHSHVIGRPS	1209
TNKS1 [X. laevis] [XP_018099068.1]	VYVIGGGTGCPCTHKDRSCYICHRQMLFCRVTLGKSFLOFSAMKMAHAPPGGHSHVIGRPS	1254
TNKS1 [G. gallus] [NP_989671.1]	VYVIGGGTGCPCTHKDRSCYICHRQMLFCRVTLGKSFLOFSAMKMAHAPPGGHSHVIGRPS	1222
TNKS1 [H. sapiens] [NP_003738.2]	VYVIGGGTGCPCTHKDRSCYICHRQMLFCRVTLGKSFLOFSAMKMAHAPPGGHSHVIGRPS	1283
TNKS1 [P. abelii] [XP_024106876.1]	VYVIGGGTGCPCTHKDRSCYICHRQMLFCRVTLGKSFLOFSAMKMAHAPPGGHSHVIGRPS	1283
TNKS1 [M. musculus] [EDL35446.1]	VYVIGGGTGCPCTHKDRSCYICHRQMLFCRVTLGKSFLOFSAMKMAHAPPGGHSHVIGRPS	1278
TNKS2 [S. salar] [XP_014034742.1]	VYVIGGGTGCPCLHKDRSCYVCRRHLLFCRVTLGKSFLOFSAMKMAHSPGGHSHVIGRPS	1162
TNKS2 [X. laevis] [XP_018082988.1]	VYVIGGGTGCPICHKDRSCYICVRHQLLFCRVTLGKSFLOFSAMKMAHSPGGHSHVIGRPS	1129
TNKS2 [G. gallus] [NP_989672.1]	VYVIGGGTGCPICHKDRSCYICVRHQLLFCRVTLGKSFLOFSAMKMAHSPGGHSHVIGRPS	1131
TNKS2 [M. musculus] [NP_001157107.1]	VYVIGGGTGCPICHKDRSCYICVRHQLLFCRVTLGKSFLOFSAMKMAHSPGGHSHVIGRPS	1130
TNKS2 [H. sapiens] [AAK13463.1]	VYVIGGGTGCPVHKDRSCYICVRHQLLFCRVTLGKSFLOFSAMKMAHSPGGHSHVIGRPS	1130
TNKS2 [P. abelii] [XP_024109627.1]	VYVIGGGTGCPVHKDRSCYICVRHQLLFCRVTLGKSFLOFSAMKMAHSPGGHSHVIGRPS	1130
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TNKS [A. queenslandica] [XP_019848937.1]	AGGLNYPPEYVIYRGEQAYPEYIITFRIKKPSATDSMSSSSSLDMSNNNT	1196
TNKS [D. melanogaster] [NP_651410.1]	AGGLHNFAYVYRGEQSPYELITYQIVKPDSSSGTEDTR----	1181
TNKS [N. vectensis] [XP_032220531.1]	SGGLSFAEYVIYRGEQAYPEYLITYKINKPDT-----	1174
TNKS [P. marinus] [XP_032806710.1]	VNGLAFAYEYVIYRGEQAYPEYLITYQILKPECTPDLTSAAGQKS----	1312
TNKS [B. belcheri] [XP_019641281.1]	VNGLNFAEYVIYRGEQAFPEYLITYQIVKPEAPSPADQK-----	1162
TNKS1 [S. salar] [XP_014017013.1]	VNGLAYAEYVIYRGEQAYPEYLITYQILKPESATSAAGBDQKS----	1253
TNKS1 [X. laevis] [XP_018099068.1]	VNGLAYAEYVIYRGEQAYPEYLITYQIMKPEAPSTLQAATAEQKT----	1298
TNKS1 [G. gallus] [NP_989671.1]	VNGLAYAEYVIYRGEQAYPEYLITYQIVKPEAPSTGTAAEQKT----	1266
TNKS1 [H. sapiens] [NP_003738.2]	VNGLAYAEYVIYRGEQAYPEYLITYQIMKPEAPSTATAAEQKT----	1327
TNKS1 [P. abelii] [XP_024106876.1]	VNGLAYAEYVIYRGEQAYPEYLITYQIMKPEAPSTATAAEQKT----	1327
TNKS1 [M. musculus] [EDL35446.1]	VNGLAYAEYVIYRGEQAYPEYLITYQIMKPEAPSTATAAEQKT----	1322
TNKS2 [S. salar] [XP_014034742.1]	VNGLSLAEYVIYRGEQAYPEYLITYQILKPDASVDG-----	1198
TNKS2 [X. laevis] [XP_018082988.1]	VNGLALAEYVIYRGEQAYPEYLITYQIMKPEAVAEG-----	1165
TNKS2 [G. gallus] [NP_989672.1]	VNGLALAEYVIYRGEQAYPEYLITYQIVKPEATTEA-----	1167
TNKS2 [M. musculus] [NP_001157107.1]	VNGLALAEYVIYRGEQAYPEYLITYQIVIRPEGMVDG-----	1166
TNKS2 [H. sapiens] [AAK13463.1]	VNGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG-----	1166
TNKS2 [P. abelii] [XP_024109627.1]	VNGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG-----	1166
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