

# TRF1

## Homo sapiens:

>sp|P54274.3|TERF1\_HUMAN RecName: Full=Telomeric repeat-binding factor 1; AltName: Full=Telomeric protein Pin2/TRF1  
MAEDVSSAAPSFPSCATAGSRADPTEEQMAETERNDEEQFECQELLECCQVQVGAPEEEEEEDAGLVAEAEV  
EAVAAGWMLDFLCLSLCRAFRDGRSEDFRRTNSAEAIHGLSSLTACQLRTIYICQFLTRIAAGKTLDA  
QFENDERITPLESALMIWGSIEKEHDKLHEEIQNLIKIQAIACVMENGNFKEAEVFERIFGDPNSYMPFKSK  
KSKLMIISQKDTFHSFFQHFHSYNHMEKIKSYVNYVLSEKSSSTFLMKAAAKVVESKRTRTITSQDKPSG  
NDVEMETEANLDRKSVSDKQSAVTESSEGTVSLLRSHKNLFLSKLQHGTTQQQDLNKKERRVGTLPQSTKK  
KKESRRATESRIPVSKSQPVTPEKHRARKRQAWLWEEDKNLRSGVRKYGEGNWSKILLHYKFNNRTSVML  
KDRWRTMKLKLISDSSED

## Pongo abelii:

>PNJ54419.1 TERF1 isoform 3 [Pongo abelii]  
MAEDVASAAPSFPSCATAGSRADPTEEQMAETERNDEEQFECQELLECCQVQVGAPEEEEEEDAGLVAEAEV  
AAGWMLDFLCLSLCRAFRDGRSEDFRRTNSAEAIHGLSSLTAYQLRTIYICQFLTRIAAGKTLDAQFE  
NDERITPLESALMIWGSIEKEHDKLHEEIQNLIKIQAIACVMENGNFKEAEVFERIFGDPNSYMPFKSK  
LMIISQKDTFHSFFQHFHSYNHMEKIKSYVNYVLSEKSSSTFLMKAAAKVVESKRTRTITSQDKPNGNDV  
EMTETEANLDRKSVSDKQSAVTESSEGTVSLLRSHKNLFLPKLQHGTEQQDLNKKERRVGTLPQSTKKKE  
SRATESRIPVSKSQPVTPEKHRARKRQAWLWEEDKNLRSGVRKYGEGNWSKILLHYKFNNRTSVMLKDR  
WRWTKKLLKICSDSED

## Mus musculus:

>NP\_033378.1 telomeric repeat-binding factor 1 isoform 1 [Mus musculus]  
MAETVSSAARDAPSRGWTDSDSPEQEVEGDAAELLQCQLQGTPREMENAELVAEVEAAGWMLDFLC  
LSLCRAFRDGRSEDFRTRDSAEAIHGLHRLTAYQLKTVYICQFLTRVASGKALDAQFEVDERITPLES  
ALMIWNISIEKEHDKLHDEIKNLIKIQAAVAVCMEIGSFKEAEVFERIFGDPPEFYTPLERKLLKIIISQKDV  
FHSLLQHFHSYSCMMEKIQSYVGDVLSEKSSSTFLMKAATKVVENEKARTQASKDRPDATNTGMDTEVGLNK  
EKSVMGQSTTETETPLDVTVSSIRSHKNALSQLKHRRAPSDFSRNEARTGTLQCETTMERNRRTSGNRNLC  
VSENPQPTDDKSGRRKRQTWLWEEDRLKCGVKKYGEGNWKILLSHYKFNNRTSVMLKDRWRTMKRLKLI  
S

## Gallus gallus:

>NP\_989711.2 telomeric repeat-binding factor 1 [Gallus gallus]  
MSAEGREREGLVPFLPSALAEAAADWVLEFSCCCLCRYFVEECEAEFRWRDVAQAVNSGFSKVTTHQ  
KMVYVLQCLLIRIAEGKRLECHFENDTTISPLESALSFWTLLEREESKLNLTHEEIRRLIQIQVAVVYME  
KGYEKEAAEVLERLFTDSESHKPLRMKLAIAIVKSKDPYVPLLQSFYSYLLLSKVKSYYVKLFLENRTNLF  
LQAATQVSESGGEVRLQNKTLNVKEERENNLEAKQRPAEELRSTTDWLTGDISSRVPPSKKGCRTSS  
VQRLLDKLVNEERGDDLPCSRRRQPWTYEEDKKLKSGVREFGVGNWTKILIHGDFNNRTSVMLKDRWRTL  
CKIK

## Xenopus laevis:

>ABA29525.1 telomeric repeat binding factor 1 [Xenopus laevis]  
MEEETDGPFFDDTAAVATNMWCMDFMFASMCIFYFREDRTEDFQRSTHMLEWLLEGSQKIDAHRRKTIPIAQF  
LMRVAEGKNLDSQFDTDESLTPLETALMAFNQIEEEEDLKHLEIEILLKVQAVVTCMEKGRFKLSAEI  
LDRLPFKESGSKNKLRMKLTMLIEKKDPIHEFLQNFTYAQMKKIKSYIALKMKERPSVFLKAAAKVVEA  
TAKELLDIQSSEDECEQQTNESLENKDDNSSSEYEERDVLSLSNINHVENKDVSSSDYEEATEQLKVCN  
RDINQNELNTNINIQETTEKSTKRHQRLFSIAQRTFWMNPKDCTSKRLLSSINIGKNSKENQENVKDSL  
TEKPLNLSKRRQHMTWEDELLKKGVKRFVGVNWSKILLHYEFNRNTGVMLKDRWRTMKRLKIVDSDCDL

## Salmo salar:

>XP\_014015369.1 PREDICTED: telomeric repeat-binding factor 1 [Salmo salar]  
MEADPNNRKLTITSTTDENVCFSDVATVAKRWMDFSFVSLCQFFKEKGKFEFPNQTISTLETIIDGSPHL  
NTEQKQKRQICGFLARIMHGKHLDSFDRDERLSPLMSAVRVWASQKETVANLSLFQHVNTNLLYVQSVAV  
CLEKGDCGMASSALKWLEEECEIPQNLGIKLSLIVSKRDITYHPFLNFSWNRLLENIQTFLLDRFLEEHP  
DFLLQAATKVVKAQGETGEDSETQEASYTTSRSSEHSKNVQETSVLMRPKKLLSTRNIHPWKPESGKKP  
ALTFMRKRVSTRITYRRALPETTLNNTSLNNTLNATNRKTHGRWPDLDMALKAGVRRHGEKWSRIL  
QEHDFQGRGTGVQLKDRWRVLKKAHVNSS

## Petromyzon marinus:

>XP\_032808952.1 uncharacterized protein LOC116941715 isoform X1 [Petromyzon marinus]  
MAEVRDGLVSEYLSAPLLRERGRDLLFDHLYRLAAAYFELGDYERLSGVYRAASGALQFLREEQPRQVQW  
KLILQIMEMVMRGQFFDPVREGNQMLLEGAVEMVMDLGRECQLEPEVTQEVTRILRLKLLTEARVQVQRNE  
QLQTDLVDVPWYSLDLKLPHILRFIDSVPPSSQASSYVQLLKESLPQETFPANKTNGGKFLHKDHIEAFLS  
IADCREDAENFTFEVLLLTDDVPLSLKLALPAMGAESSPGSELRREDSSVPEGAAANNSVAPARVIVSPQK  
QLSPAKRLMGPETPRHHVPEDSRREEKKVAPLQATPSPFPFPPLSPLLLSDSEBLLPMRIVQSKRSDQS  
TAAACDDAHQMSTTDFIPSTYEEIPPTAPAKDVAGPGSTPPILAIICRKTRSDSPRVVEAAATPRIV  
EDGEVAGSGKPPAATISPAKATCGKWDKGHGHPTRNHVERNGRFPDGFSSABIRRLSLPIMIKDEWSDDE  
DLFGPSKVAGRQSKFGSSARKKKMTTETETQCLKEGVARFVGVNWSKIKRHYLSRTAVQLKDRWRNISK

## Branchiostoma belcheri:

>XP\_019634930.1 PREDICTED: telomeric repeat-binding factor 2-like [Branchiostoma belcheri]  
MIFTCRYEEDGDITALESALPIFDSLVSDFAVPEDQVSEARGLVMTQSVLVCCRGGDFQAAEQVFSRWV  
VPGAATTAKRKKLRKSVQEVMSRGNPDHSLVQVRCSDYDKFLTWMIQFLHLIVDGFSLFLLKAAQKRLRA  
RIDAGDGTAEPEESLSQSESDSDMYETPSENAAPPKEQEEEFVFNPSALLRECFLVMAKEERSGSEWTDV  
NGDYRYNLRGDLAKSREAKTSGAASEKDLEQNREEKTSGSGVRKSPRKHQQAANKSEPTERRSPRKKTS  
ETTGRHEFATHGAVQSRGEKRRKQTDDEENFEKTENRKKTTQTSAPSTDNRNPPGRMQKSGDGTGKDIRYWM  
SDQPSGTSVGRKKVHKQAERTRLVESDESSESEETRKENVQTGSKSKRPDRDRPEYGNQVKETWSSDEETFPA  
PVKKKYIYDSDSDSENFPALPCSAASLVVPRRLVQKREPLDITSGKQVRSRFRWAEYEVENLIKGVQ  
EYGVGHWSEILDNYRFKNRTNVNLKDKRWQLVKSQGVREFP

## Drosophila melanogaster:

No homolog found.

### **Hydra vulgaris:**

>XP\_012558972.1 PREDICTED: putative uncharacterized protein DDB\_G0282499 [Hydra vulgaris]  
MSEQQDTLYNTDFLIMEYFAHKIIKMFLEEYKGCINNNMVHLMNAWKVMVHSSDGIFSDEMRNLYILISL  
IVTCCFSSISQVDQLNLMLEMINTQQQEFQSATEDVSNVCKFLHTKIFLKLLDNGCGKGAKQYLRDHDVL  
CRDSLEQLVSKDSL PENLKPENLKNVCFSYVSEVYKKIPRSRLVLLFDNFMKEKNNTRFKKGKSFLDKVDE  
SDIDISKEVENALPQSQVMTLIPKETDTTYSSSSEPMFNSYQSSTTYVEKESGTFKDSPCIPTKHKHLSND  
SFKEIVDLKYSKNHLKSFYKYGSKYIYNTRSDKVTSNLNSHMIISDFKKSFTFONSKKSDDDMIFDDV  
RSDISDSQTENLGIKCYVDINKVISPKYIEKKANDTQNTYCEQNRSNNDNNETEKNNTSNHSSKLQIGCQ  
NLTELNNENPCSVVSNNISIPGKKKKVVENIHTNNKACHILTNNQINYNKYNLKTKNSDQOTSADSDDI  
YIKTSADLACVKNIDSLREDVTSKDTSIIVTPASLKLLGDEQQNDSKVVFECVCQSSEKKTVSSSVANKK  
SIVNSDESGTSCKWSDDEFVKYNPTVRVPFSKDEEKYIKEGIIKFGIGNWCCKIKRSYPFHPNRTNVSIIK  
DKYRTMKRQGIL

### **Nematostella vectensis:**

No homolog found.

### **Amphimedon queenslandica:**

No homolog found.

## Alignment

XP_012558972.1[H.vulgaris]	-----	0
XP_019634930.1[B.belcheri]	-----	0
XP_032808952.1[P.marinus]	-----	0
XP_014015369.1[S.salar]	-----MEADPNNRTLTI-----	12
ABA29525.1[X.laervis]	-----	0
NP_989711.2[G.gallus]	-----MSE	3
NP_033378.1[M.musculus]	MAETVSSAARDAPSPREGWTDSD-----SPEQEEVGDDAELLQCQLQLGTTPREM	48
P54274.3[H.Sapiens]	MAEDVSSAA---PSPGCAAGGADPTTEQMAETERNDEEQFECQELLECCVQVGAPEEE	57
PNJ54419.1[P.abelii]	MAEDVASAA---PSPGCAAGGADPTTEQMAETERNDEEQFECQELLECCVQVGAPEEE	57
XP_012558972.1[H.vulgaris]	MSEQQDTLYN-----TDFLIMEYFAHKIIMKFL-----EYKGCINNMMVHLMNA	45
XP_019634930.1[B.belcheri]	-----	0
XP_032808952.1[P.marinus]	MAEVRDGLVSEYLSAPLLRERGRDLLFDHLYRLAAAYFELGDYERLSGV-----	49
XP_014015369.1[S.salar]	-----TSTTDENVCFSDVATVAKRWMIDFSFVSLCQFFKEGKFEEFNQTI-----ST	59
ABA29525.1[X.laervis]	MEEETDG-----PPFDDTAAVATNMWCDMFASMCFFYFREDRTDFQRST-----HM	47
NP_989711.2[G.gallus]	AGREREGLVPFLPSALAEAAVADWVLEFSCCCLCRYFVECEAEFRWR-----DV	55
NP_033378.1[M.musculus]	-----ENAEI-----VAEVEAVAAGWMLDFLCLSLCRAFRDGRSEDFRTR-----DS	91
P54274.3[H.Sapiens]	EEEEEDAGL-----VAEAEAVAAGWMLDFLCLSLCRAFRDGRSEDFRTR-----NS	104
PNJ54419.1[P.abelii]	-----EEDAGL-----VAEAEAVAAGWMLDFLCLSLCRAFRDGRSEDFRTR-----NS	101
XP_012558972.1[H.vulgaris]	WKVMVHSSDGIFSDEMRNL-----YILISLIVTCCFSSISQVDQLNMLEMINTQG	96
XP_019634930.1[B.belcheri]	-----MIIFICRYEEDGIDTALESALPIFDSLV	28
XP_032808952.1[P.marinus]	YRAASGALQFLREEQPRQVQMKLIQLMEMVMRGQFFDPVREGNQ-----LEGAVEMVDMLG	107
XP_014015369.1[S.salar]	LETTIDGSPHLNTEQKQKR-----QICQFLARIMHGKHLNDSFDRDERLSPILMSAVRVMSQK	117
ABA29525.1[X.laervis]	LEWLLEGSQKIDAH-RKTI--PIAQFLMRVAEGKNLDSQFDTDESLTPLETALMAFNQIE	104
NP_989711.2[G.gallus]	AQAVNSGFSKVTTQKKMV--YLCQLLIRIAEGKRLECHFENDTITPLESALSFWTLL	113
NP_033378.1[M.musculus]	AEAITHGLHRLTAYQLKTV--YICQFLTRVAGSKALDAQFVERDITPLESALMIWNSIE	149
P54274.3[H.Sapiens]	AEAITHGLSSLTACQLRTI--YICQFLTRIAAGKTLDAQFENDERITPLESALMIWGSIE	162
PNJ54419.1[P.abelii]	AEAITHGLSSLTAYQLRTI--YICQFLTRIAAGKTLDAQFENDERITPLESALMIWGSIE	159
	* :	
XP_012558972.1[H.vulgaris]	QEFQSATEDVSNVCKFLHTKIFLKLNDGCGKGAK-----QYLRDHDVL	140
XP_019634930.1[B.belcheri]	SDPAVPEDQVSEARGLVMTQSVLVC-----CRGG-----DF--QAAEQVFSRVWVP	72
XP_032808952.1[P.marinus]	RECQLEPEVTQEVTRILRLKLLTEA-RVQVQRNEQLQTDLDVPWYSLDLKPHILRFIDSV	166
XP_014015369.1[S.salar]	ETVANL-SLFQHVTNLLYVQSAVVC-----LEKG-----DC--GMASSALKWLEEE	160
ABA29525.1[X.laervis]	EEDD-LKHLHEEIELLLKVQAVVC-----MEKG-----RF--KLSAEILDRLFKE	147
NP_989711.2[G.gallus]	REESKLNTLHEEIRRLLIQIVVAVY-----MEKG-----YY--KEAAEVLERLFTD	157
NP_033378.1[M.musculus]	KEHD--KLHDEIKNLIKQAVAVC-----MEIG-----SF--KEAEVFERIFGD	190
P54274.3[H.Sapiens]	KEHD--KLHEEIQNLIKQAIAVC-----MENG-----NF--KEAEVFERIFGD	203
PNJ54419.1[P.abelii]	KEHD--KLHEEIQNLIKQAIAVC-----MENG-----NF--KEAEVFERIFGD	200
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XP_012558972.1[H.vulgaris]	CRDS---LEQLVSKDSLLENLKPENLKNVCFSYVSEYKKIPRSRLVL---LFDNFMKEK	194
XP_019634930.1[B.belcheri]	GAA-----TTAKRKKL-RSKQVEVMRSGNPDHSLVQVRCSYDKFLTW	114
XP_032808952.1[P.marinus]	PQSSQASSYVQLLKESLPQETPPANKTN-GGKFLH---KDHIEAFL-SIA-DCREDAF	219
XP_014015369.1[S.salar]	C-----EIPQNL-GIKLSLIVSKRDTYHFFLL-NFSWNRLLENI	197
ABA29525.1[X.laervis]	S-----GSNKYL-RMKLTMLIEKKDPYHEFLQ-NFTYAQMMEKI	184
NP_989711.2[G.gallus]	S-----ESHKPL-RMKLAAIVKSKDPYVPLLQ-SFSYSLLSKV	194
NP_033378.1[M.musculus]	P-----EFYTPL-ERKLLKISQKDVFHSFLQ-HFSYSYSCMEKI	227
P54274.3[H.Sapiens]	P-----NSHMPF-KSKLLMISQKDTFHSFPQ-HFSYNHMEKI	240
PNJ54419.1[P.abelii]	P-----NSYMPF-KSKLLMISQKDTFHSFPQ-HFSYNHMEKI	237
	.	
XP_012558972.1[H.vulgaris]	N---NTRFKG--KSFLDKVD---ESDIDIS---KEVENALPQSQVMTLIPKETDIT-YS	241
XP_019634930.1[B.belcheri]	IQLFHLIVDGFSLPFLKAAQVRLARIDAGDGTAEPEESLSQ-----SESDSDMYE	166
XP_032808952.1[P.marinus]	NTEFVLLLTDTVPPSLSLKIALPAMGAAESS--PGSERREDSSVP-----EGAAANNSV	269
XP_014015369.1[S.salar]	QTFLDRLFEEHPSDFLLQAATK--VVKAG--Q--ETGDESETQ-----E--ASYT-	239
ABA29525.1[X.laervis]	KSYIALKMKKEPRSVFLKAAAK--VVEAT--A--KEELDIOGQ-----E--SED-	225
NP_989711.2[G.gallus]	KSVYKFLKENRNTNQLQAATK--QVESE--G--GEVRLVQNK-----T--LNV-	235
NP_033378.1[M.musculus]	QSVYGVDLSEKSSSTFLMKAATK--VVENE--K--ARTQASKDR-----P--DATN-	269
P54274.3[H.Sapiens]	KSVYNYVLSEKSSSTFLMKAANK--VVESK--R--TGTITSQDK-----P--SGND-	282
PNJ54419.1[P.abelii]	KSVYNYVLSEKSSSTFLMKAANK--VVESK--R--TGTITSQDK-----P--NGND-	279
	*	
XP_012558972.1[H.vulgaris]	SSS--EPMPSYQSSTTYVEKESGTFKDSPCIP--TKHKLNSDSFKETVDLKYSKNHLRK	297
XP_019634930.1[B.belcheri]	TPSENEAPPKEQ--EEEFVFNSPAL--LRECFLVMAKEERSGSEWTDVNGDY--RNLRG	220
XP_032808952.1[P.marinus]	APARVISVPQKQ-----LSPAKRLMGPE-----	292
XP_014015369.1[S.salar]	-----TSRS-----	243
ABA29525.1[X.laervis]	-----CEQQ-----	229
NP_989711.2[G.gallus]	-----KEE-----	238
NP_033378.1[M.musculus]	-----TGMD-----	273
P54274.3[H.Sapiens]	-----VEME-----	286
PNJ54419.1[P.abelii]	-----VEME-----	283
	.	
XP_012558972.1[H.vulgaris]	SFKYKGSYKIYNTRSDKKVNTNLNSHMYISDFKKSFTRDNSKKSDDDMIF---DDVRSDI	354
XP_019634930.1[B.belcheri]	DLAKSREAKTSGAAASEKDLQNRKEKTSGSGVRKSP-----RKHQQAANKSEPTERRSPR	275
XP_032808952.1[P.marinus]	-----TPRH---VPEDSREEKEKVAP-----LQATPPSPPPPPP	324
XP_014015369.1[S.salar]	-----SEHS-----K-----VN--QETSV--	255
ABA29525.1[X.laervis]	-----TNESLENKDDNSSS-----EY--EERDVL	252
NP_989711.2[G.gallus]	-----RENNLEAKQR-----P	249
NP_033378.1[M.musculus]	-----TEVGLNKEKSVNGQ-----QSTE-TEPLVDT	298
P54274.3[H.Sapiens]	-----TEANLDRKSVSDK-----QSAV-TESEGT	311
PNJ54419.1[P.abelii]	-----TEANLDRKSVSDK-----QSAV-TESEGT	308
	.	
XP_012558972.1[H.vulgaris]	SDSQTENLGIKCYVDINKVISPKYIEKKNNDTQNIYCEQNRSNNDNNETEKNK-----TS	409
XP_019634930.1[B.belcheri]	KKTSSETTGRHEFATHGAVQSR-----GEKR-----KQOTDEENFEKTENRKKQTQT	322
XP_032808952.1[P.marinus]	LSPL-LLSDSEELLPMRIVQSK-----RSDQSTAEAAACDDAQMSTTDFIPSTY--EEI PP	377
XP_014015369.1[S.salar]	-----	255
ABA29525.1[X.laervis]	LSNI-----NHVENKDVSSSDY--EEATE	274
NP_989711.2[G.gallus]	AEL-----RST--TDWLITGDI--SS--	266
NP_033378.1[M.musculus]	VSLI-----RSH--KNAL-SQL--KH--	314
P54274.3[H.Sapiens]	VSLI-----RSH--KNLFLSKL--QH--	328
PNJ54419.1[P.abelii]	VSLI-----RSH--KNLFLPKL--QH--	325
	.	
XP_012558972.1[H.vulgaris]	NHSSKLQ--IG-QCNLTLSNNEFNCSVVSNNSI-----FGGKK	445
XP_019634930.1[B.belcheri]	SAPSTDNNPGRMOKSGDTGKDIRYWMSTDQPSGVRKKVHKQAEKRTLVESDSSESSE	382
XP_032808952.1[P.marinus]	TAPAKDVAGPGSTP-----PILAIIG--RKRTSDSPRVVEAAATPRLVEDGEVAGPS	429
XP_014015369.1[S.salar]	-----LM	257
ABA29525.1[X.laervis]	QL-----KVCN-----RDIN-----QNELTN-----TTNIQET-TEKSTK	303
NP_989711.2[G.gallus]	-----RVRP--P--S--KKGCR-----	277
NP_033378.1[M.musculus]	-----RRAP--SDFS--RNEART-----GT-----	330
P54274.3[H.Sapiens]	-----GTQQ-----QDLN--KKERRV-----GT-----	344
PNJ54419.1[P.abelii]	-----GTEQ-----QDLN--KKERRV-----GT-----	341
	.	
XP_012558972.1[H.vulgaris]	KVKVENIHTNNKACHILTNQINYNKLNKTKNSDQQTADSDDIYIKTSADLACVKNI-	504

XP_019634930.1[B.belcheri]	ETRKENVITQGS-----KKR-----P-----R-----DRPEY	403
XP_032808952.1[P.marinus]	KPRAATISPAKATCGKWDKGGHGP-----TRNH-----VERNGRFPDGFSSAEIRRLS	478
XP_014015369.1[S.salar]	RPKKKLLS--TRNIHPWKPESGKK-----PALT-----FMRKRIV--STRL--TYRRALP	300
ABA29525.1[X.laavis]	RHQRLFS--IAQRTPNWPKPCT-----SKRL-----LSS-----IN--IGKNSKE	341
NP_989711.2[G.gallus]	-----T-----SSVQRLK	285
NP_033378.1[M.musculus]	-----LQCE-----TIME-----RNR-----RT--SGRNRLC	350
P54274.3[H.Sapiens]	-----PQST-----KSKK-----ES-----RR--ATESRIP	363
PNJ54419.1[P.abelii]	-----LQST-----KSKK-----ES-----RR--ATESRIP	360
XP_012558972.1[H.vulgaris]	-DSLREDVTSKDTSVTPASLKKLLGDEQQNDKVVFEF--VCQSSKEKTVSSSVANKKS	561
XP_019634930.1[B.belcheri]	GNGVKETWSSDEETFPAPVKKKYYIYDS-DSDSSENFPSALPCSA-ASLVVPRRLVQKRE	461
XP_032808952.1[P.marinus]	PLMIKDEWSDEEDLFGP-----SKVAGR--	501
XP_014015369.1[S.salar]	-----ETTLNT-----TSLSNT--	312
ABA29525.1[X.laavis]	-----NQ-----ENVKDS--	349
NP_989711.2[G.gallus]	-----D-----LKNVEE--	292
NP_033378.1[M.musculus]	-----VSENQP--	356
P54274.3[H.Sapiens]	-----VSKSQP--	369
PNJ54419.1[P.abelii]	-----VSKSQL--	366
XP_012558972.1[H.vulgaris]	IVNSDESGTCKWSDDEFVKNYPTVRVPFSKDEEKYIKEGIKKFGIGNWCKIKRSYPFH	621
XP_019634930.1[B.belcheri]	PL-----DITSKGQVRSRFRWAEYEVENLIKGVQEQYGVGHWSEILDNYRFK	507
XP_032808952.1[P.marinus]	-----QSKFGSSARKKKMWTEETETQCLKEGVARFVGNGWSKIKRHYSL-	544
XP_014015369.1[S.salar]	-----TLATNATRKTHGRWPWDLDMALKAGVKRHGEGKWSRILQEHDFQ	356
ABA29525.1[X.laavis]	-----RTEKPLNSKKRQHWTWEEDELLKKGVKRFVGVGNWSKILLHYEFR	393
NP_989711.2[G.gallus]	-----RGDDLPCSRRRQFWTYEEDKKLKSQVREFVCVGNWTKILLHGDFN	336
NP_033378.1[M.musculus]	-----DTDKSGRRKRQTLWNEEDRILKCGVKKYEGGNWAKILLSHYKFN	400
P54274.3[H.Sapiens]	-----VTPEKHRARKRQAWLWEEDKNLRSGVRKYEGGNWSKILLHYKFN	413
PNJ54419.1[P.abelii]	-----VTPEKHRARKRQAWLWEEDKNLRSGVRKYEGGNWSKILLHYKFN	410
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XP_012558972.1[H.vulgaris]	PNRNTNVSIIKDKYRTMKRQGIL----- 642	
XP_019634930.1[B.belcheri]	-NRTNVNLKDKWRQLVKSGTVREFF-- 531	
XP_032808952.1[P.marinus]	-SRTAVQLKDRWRNLISK----- 560	
XP_014015369.1[S.salar]	-GRTGVQLKDRWRVLKKAHKVNSS-- 379	
ABA29525.1[X.laavis]	-NRTGVMLKDRWRTMKRLKIVSDCDL 419	
NP_989711.2[G.gallus]	-NRTSVMLKDRWRTLCKIK----- 354	
NP_033378.1[M.musculus]	-NRTSVMLKDRWRTMKRLKLIS----- 421	
P54274.3[H.Sapiens]	-NRTSVMLKDRWRTMKRLKLISDSSED 439	
PNJ54419.1[P.abelii]	-NRTSVMLKDRWRTMKRLKLICSDSED 436	
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