

SOX9

Homo sapiens:

>NP_000337.1 transcription factor SOX-9 [Homo sapiens]
MNLDDPFMKMTDEQEKGLSGAPSPMTSEDSAGSPCPSGSGSDTENTRPPQENTFPKGEFDLKKESEEDKFFVCIREAVSQVLKGYDWTLPMPVVRVNGSSKNKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWRLNNESEKRPFV
EEAERLRVQHKKHDPYKYQPRRRKSVKNGQAEAEAEATEQTHISPNALFKALQADSPHSSSGMSEVHSPGEHSGSQSQGPPTPTTPTKTDVQPGKADLKREG**RPLQEGGR**QPPIDF**RDVDIGEL**SSDVISNIETFDVNEFDQYLPNGHGPVPATH
GQVITYTSGYISSTAATPASAGHVWMSKQQAAPPPPPQPPQAPPAQAPPPQQAAPFQQPAAPFQQQAHTLTTLSSEPGSQQRTHIKTEQLSPSHYSEQQHQSFQQIAYSFPNLPHYSPSYPTITRSQYDTDHQNSSSYSHAAGQGTGLYST
FTYMNPAQRPMYTPADIATSGVPSIPQTHSPQHWEQPVYITQLTRP

Pongo abelii:

>XP_009250264.1 transcription factor SOX-9 [Pongo abelii]
MNLDDPFMKMTDEQEKGLSGAPSPMTSEDSAGSPCPSGSGSDTENTRPPQENTFPKGEFDLKKESEEDKFFVCIREAVSQVLKGYDWTLPMPVVRVNGSSKNKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWRLNNESEKRPFV
EEAERLRVQHKKHDPYKYQPRRRKSVKNGQAEAEAEATEQTHISPNALFKALQADSPHSSSGMSEVHSPGEHSGSQSQGPPTPTTPTKTDVQPGKADLKREG**RPLQEGGR**QPPIDF**RDVDIGEL**SSDVISNIETFDVNEFDQYLPNGHGPVPATH
GQVITYTSGYISSTAATPASAGHVWMSKQQAAPPPPPQPPQAPPAQAPPPQQAAPFQQPAAPFQQQAHTLTTLSSEPGSQQRTHIKTEQLSPSHYSEQQHQSFQQIAYSFPNLPHYSPSYPTITRSQYDTDHQNSSSYSHAAGQGTGLYST
FTYMNPAQRPMYTPADIATSGVPSIPQTHSPQHWEQPVYITQLTRP

Mus musculus:

>NP_035578.3 transcription factor SOX-9 [Mus musculus]
MNLDDPFMKMTDEQEKGLSGAPSPMTSEDSAGSPCPSGSGSDTENTRPPQENTFPKGEFDLKKESEEDKFFVCIREAVSQVLKGYDWTLPMPVVRVNGSSKNKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWRLNNESEKRPFV
EEAERLRVQHKKHDPYKYQPRRRKSVKNGQAEAEAEATEQTHISPNALFKALQADSPHSSSGMSEVHSPGEHSGSQSQGPPTPTTPTKTDVQAGKVDLKREG**RPLALGGR**QPPIDF**RDVDIGEL**SSDVISNIETFDVNEFDQYLPNGHGPVPATH
GQVITYTSGYISSTAATPATAGHVWMSKQQAAPPPPPQPPQAPPAQAPPPQQAAPFQQPAAPFQQQAHTLTTLSSEPGSQQRTHIKTEQLSPSHYSEQQHQSFQQIAYSFPNLPHYSPSYPTITRSQYDADHQNSGSYSHAAGQSGSLYSTFT
YMNPAQRPMYTPADIATSGVPSIPQTHSPQHWEQPVYITQLTRP

Gallus gallus:

>NP_989612.1 transcription factor SOX-9 [Gallus gallus]
MNLDDPFMKMTDEQDKCISDAPSPMTSEDSAGSPCPSGSGSDTENTRPPQENTFPKGDQDLKKESEDEKFFVCIREAVSQVLKGYDWTLPMPVVRVNGSSKNKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWRLNNESEKRPFV
EEAERLRVQHKKHDPYKYQPRRRKSVKNGQSEQEESGEQTHISPNALFKALQADSPQSSSSISEVHSPGEHSGSQSQGPPTPTTPTKTDAAQPGKQDLKREG**RPLAGGGR**QPPHIDF**RDVDIGEL**SSDVISNIETFDVNEFDQYLPNGHGPVPA
THGQVITYSGTYGISSSASSPAGAHAWMKQPPQPQPQAPPAQAHTLPALSGEQGPAQQRPHIKTEQLSPSHYSEQQHQSFQQQQQQQQLGYGSFNLQHYSSSYPTITRSQYDYTEHQNSGSYSHAAGQSGGLYSTFTYMNPTQRPMYTP
ADTSGVPSIPQTHSPQHWEQPVYITQLTRP

Xenopus laevis:

>NP_001087942.1 transcription factor Sox-9-B [Xenopus laevis]
MNLDDPFMKMTDEQDKCLSDAPSPMTSEDSAGSPCPSGSGSDTENTRPPQENTFPKGDQEMKKETDEKFFVCIREAVSQVLKGYDWTLPMPVVRVNGSSKNKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWRLNNESEKRPFV
EEAERLRVQHKKHDPYKYQPRRRKSVKNGQSEQDDSAEQTHISPNALFKALQADSPHSTSSMSEVHSPGEHSGSQSQGPPTPTTPTKTDVQPGKADLKREG**RPLQESGR**QPPHIDF**RDVDIGEL**SSSEVISTTETFDVNEFDQYLPNGHGPVGSA
QAPYTGSGYISSTFATSAGGSAMWSKQQQSQQHQSLSTINSEQSQSQQRTHIKTEQLSPSHYSDQQQHQSPQQLNYSFNLQHYSSSYPTITRAQYDYTEHQNSGSYSHAAGQSGGLYSTFTYMNPTQRPMYTPADIATDGVPSIPQTHSPQHW
EQPVYITQLTRP

Salmo salar:

>XP_014034661.1 transcription factor Sox-9-A-like [Salmo salar]
MNLDDPFMKMTDEQDKCLSDAPSPMTSEDSAGSPCPSGSGSDTENTRPSENGLMGPDGPLVEFKKDDDDKFFVCIRDVAVSQVLKGYDWTLPMPVVRVNGSSKNKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWRLNNEGEKR
PFVEEAERLRVQHKKHDPYKYQPRRRKSMKNQSESEEDGSEQTHISPGAIFKALQADSPASSIGEVHSPGEHSGSQSQGPPTPTTPTKTDIAGKVDLKREG**RPLQEGTG**RQLNIDF**RDVDIGEL**SSDVISNIDTDFVNEFDQYLPNGHGPAG
GTAAGQVSYNGTYGISSSAVSQAAGGTAGHSWMTKSSQSQQQHSLTTLGSGEQGNQRTPTTHIKTEQLSPSHYNDQQNSPPQHVTYGSFNLQHYSSSSYPTITRAQYDFDSHQGGTNSYSHAAGQSGGLYSFSSYMSPSQRPMYTPADIATTG
VPSVPQTHSPQQHWQQPVYITQLSRP

Petromyzon marinus:

>XP_032830402.1 transcription factor Sox-9-A [Petromyzon marinus]
MMSDEQHDKXMSDVSPDMSSENCSSVSPADSLAGSDSDQSCGSKRCSDREDGAGASGLLLAAGGGVLDGGVVFLGLRDAGSGKKMEDDDKFPACIREAVSQVLKGYDWTLPMPVVRVNGSSKSKPHVKRPMNAFMVWAQAARRKLADQYPHLH
NAELSKTLGKLWRLNNESEKRPFVEEAERLRVQHKKHDPYKYQPRRRKSGKNGQSESDSGEQTHITTAIYKALQADSPADVHSPGEHSGSQSQGPPTPTTPTKTDVQSNKLDIKREG**RPLQEGGR**QQIDFSNVDIRLSREVINSMESFDVN
EFDQYLPNGHGHGQSVASYGTYGISINGHAWLSKQQQQQQQQQQHTLSSPPPPPFAISSSPQRAHVKTQLSPSHYSDQQQHQSPQQQQQQHQSPQQQQQQQQQQFQAQAQAQQVQQQQQLGGYSPFSIQHYGAAVPAISRQSYADHH
HHHHHHQSSAAAAHYSGHSAGTAGLYSGFSMGPSRQSPYTPITADIATGVPSIPQTHSPSWEQPVYITQLTRP

Branchiostoma belcheri:

>XP_019645392.1 PREDICTED: transcription factor Sox-10-like [Branchiostoma belcheri]
MSETEPTVEVKEEPAEIELSKREREDTDEESSSSGSEDESGPSDRKRHKFPSPQIREAVSNVLKGYDWTLPMPVVRVNGSSKSKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWRLNNEDEKRPFIEEAERLRVQHKKHDPYKY
QPRRRKSNKANQSGDEAGSEASPISANTLFLKALQAESPTGSEPHSPEDLKGPSPHDGSVGVTTPSSQAPPTPTTPTKQDQMGTALKADGMRDPTSNLTAIHRDGPHHHHHPQGHGHPNIDFSNVDIGPLDVMSMESFDFVEFDQYLPNGH
PASASGHHPSHPPTYSYSQMSSAATTTVTSSSSMWAKQNTSPRDNSQEQLRPLVKMEQEHLPPPPPYQTPHPHPASSYNYQPYSSYQHSPPRPQYTDYPPPAHSPQQYFSPHPTSSSIPPPYNYMAPQORSLYPTVAGAPSTWEPYSYQLARP

Drosophila melanogaster:

>CAB63903.1 Sox100B protein [Drosophila melanogaster]
MSDSSSSNCTKDRAPVEALVLANYALKAEQKAQGGGRKEDERITTAVMKVLGYDWNVLQASAKAPSRDKKEHIKRPMAFMVWAQAARRVMSKQYPHLQNSELSKSLGKLWKNLKDSDKKPFMEFAEKLRTMTHKQEHDPDYKYQPRRKKARV
LPSQHSQGDGSGPGEMTLATMGSSSGKPRSSNSNGQRRAGKGNAAADLGSCAATISHANVGSSSDVFSNEAFMKSILNSACAASIMEQSLTLETGLDSCSTASSMSSLTPPATPYNVAPSNAKASAANNPSSLLRLQLEPVANAGDGYGVLLEAG
REYVAIGEVNYQGSQAGSVGAEGGGAGQEMDFLENINGYGGYTSRVSYPAYSYPANGGHFATEEQQQQALQASEALNYKAAADIDPEKIDQYFMDQMLPMTQHHPHHTHPLHPLHHSPPPLNSASLSACSASSSQQFVAEYIEHGLYS
PAASSAQNPNGFGQPYANGAASMTPTLGDPAQQLQSQQQEQQHNPQSQHLLWGTYTVYNNP

Hydra vulgaris:

>XP_002161752.2 PREDICTED: transcription factor SOX-18-like [Hydra vulgaris]
MMAAESTNSFATHVIGNNITHAVSQEQKGEQYOSTTISLSAEAAQCLKNLGBEGILCDDALLRLTMSSTSEHGETEFLDTKNSRVKRPMMNSFMWAQTARKKLAEKYPHLHNAHLSKMLGKLWMLSPDEKQPYVLEASRLDKLKHDEHPEYK
YPRRRPKGLKRGYSTPTTIVISPTTSKPYTIPNSNARIVHAPENENLISRAEAAQIVYATDGMQYIYAVQKSGTPTTMAHHHNGNSVIVSPNTQIPITLVQSTSAPTSNTSYPAYVTVPMPATSTAIFHPAIPVQGVGHTPAFVLRSSYPGNSILSP
SAIPIAYHNIDHRTIESHMQPNQHIKTESTNTIVTKPDGETIVIIQRPIDGHVVPFQLREVPSGATNTITVVPQSQVIQQHIVQTPNNQETKIL

Nematostella vectensis:

>XP_001630037.1 transcription factor SOX-9 [Nematostella vectensis]
MDKKTVEQQVQAVLGLTDGQSVRNHQLNSAIAVNHVLGDYDWSLILPLVVRNGIKTKPHVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWKLNDSEKKPFIEEAERLRIKHKREHPDYKYQPRRKKQKGNNGDAGDATISA
DILLKVLKDGSKLVNPNNGDASASCASPESVSDGEVSSSESCVSPETPTAVPVKNEDVKNEDALSAPQGFPSCKSKDDSNSHAIQVQNGSAHLQQNRRRSFSSFAGDKRRDLSLSCPPIKKRALIPVSSPEVLPTSLDDIFPPSPSPSSDSSIPSHQHREDTLP
LTHFEF
SSYREFMVQLQKLPSSEGFFPNRVAPSATMQQRNQPDNSFFPFSESEVNVCSLAATRQPAFLSPSPSTSGTSSSSNSGRTHTLWK

Amphimedon queenslandica:

>NP_001266245.1 uncharacterized protein LOC100631786 [Amphimedon queenslandica]
MSAGLDQYTVTLQAGSPSCSSLSPPSYQSNLLDVCVDGTATHVHHNGSGRGGNGGSGAGKKEHIKRPMAFMVWAQLERRKMTTEFFDMHNAEISRRLGKLWRLNLSREKQPYIEESERLRIQHMKQYPDYKYRPRRKKGGKKPKPVNNTSYL
GGNDSSGEYYPTTPTTSSSSNCSCGAGIRAPVPTCSIAVQCSMELGEHVIEREPPSSPKQTAETISIQVNGSAHLQQNRRRSFSSFAGDKRRDLSLSCPPIKKRALIPVSSPEVLPTSLDDIFPPSPSPSSDSSIPSHQHREDTLP
LTHFEF
MDPLMPYDPSAVDLALSGSSALSSSSTAASNVLNLNLTFLPLQSSAATSIFSFPNIDSCSTTFDFPELPSDFADIPAGNASEFDTISITLLST

Alignment

XP_002161752.2[H.vulgaris]	-----MMAASETNSNFATHVIQNNNITHAVSQEQRKGEGYSTTISLSEAAQCLKN---	51
NP_0012626245.1[A.queenslandica]	-----MSAGDLQYT-----VILQQAPSPSCSSLSPPSSPY-----	30
CAB63903.1[D.melanogaster]	-----MSDSSSSNCTKDR-----	13
XP_001630037.1[N.vectensis]	-----M-----	1
XP_019645392.1[B.belcheri]	-----MSETETPVEVKEE-----PAEL-----ES--LK--R	22
XP_032830402.1[P.marinus]	-----MMSDE-QHD-----KHMSDVPSFPMSENCVSGSPADSLAGSDSDSCGSGSKRCS	43
XP_014034661.1[S.salar]	MNLLDPFLKMTD-EQD-----KCLSDAPSPMSSEDS-AGSPCPSPGSGSDT-----	48
NP_989612.1[G.gallus]	MNLLDPFMKMTD-EQD-----KCLSDAPSPMTSDEDS-AGSPCPSPGSGSDT-----	43
NP_001087942.1[X.laervis]	MNLLDPFMKMTD-EQD-----KCLSGAPSPMTSEDS-AGSPCPSPGSGSDT-----	43
NP_000337.1[H.sapiens]	MNLLDPFMKMTD-EQE-----KGLSGAPSPMTSEDS-AGSPCPSPGSGSDT-----	43
XP_009250264.1[P.abelii]	MNLLDPFMKMTD-EQE-----KGLSGAPSPMTSEDS-AGSPCPSPGSGSDT-----	43
NP_035578.3[M.musculus]	MNLLDPFMKMTD-EQE-----KGLSGAPSPMTSEDS-AGSPCPSPGSGSDT-----	43
XP_002161752.2[H.vulgaris]	-----LG-----E-----EGILCDDA-----LLRL	66
NP_0012626245.1[A.queenslandica]	-----QSNLLDVCDDGTATHVHH-----	48
CAB63903.1[D.melanogaster]	-----AKPVEALVLANYALK-AEQ-----KEAQGQ-----GGRKEDERITTAVMKVLGY	57
XP_001630037.1[N.vectensis]	D-----KKVTEQQVQAVLGLD-----TDGSQVRNHQLSNAIASAVNHVLDGY	43
XP_019645392.1[B.belcheri]	EREDTDD-----EESSSGSEDDGSGPSDRKRHKFPSPQIREAVSNVLKGY	65
XP_032830402.1[P.marinus]	DREDGAGASGLLLAGGPGVGLDGGVVFGLGRDAGSGKMKDEDDKFPACIREAVSQVLKGY	108
XP_014034661.1[S.salar]	--ENTRPSENGLLMGPDGP-----LVEFFKKDDDKFPVCIRDAVSQVLKGY	87
NP_989612.1[G.gallus]	--ENTRPQENTFPKQDP-----DLKKESEDEKFPVCIREAVSQVLKGY	84
NP_001087942.1[X.laervis]	--ENTRPQENTFPKQDQ-----EMKKEDEDEKFPVCIREAVSQVLKGY	84
NP_000337.1[H.sapiens]	--ENTRPQENTFPKGEPP-----DLKKESEEDKFPVCIREAVSQVLKGY	84
XP_009250264.1[P.abelii]	--ENTRPQENTFPKGEPP-----DLKKESEEDKFPVCIREAVSQVLKGY	84
NP_035578.3[M.musculus]	--ENTRPQENTFPKGEPP-----DLKKESEEDKFPVCIREAVSQVLKGY	84
XP_002161752.2[H.vulgaris]	TMSSTSEHGTEFLDTKNSRVKRPMSFMVWAQTARKKKLAEKYPHLHNAHLSKMLGKLWK	126
NP_0012626245.1[A.queenslandica]	--NGSGRGGNGSGAGKKEHKRPMAFMVWAQLERRKMTTEFPDMHNAEISRRGLKLWR	106
CAB63903.1[D.melanogaster]	DWNLVQASAKAP--SDRKKKEHKRPMAFMVWAQAARRVMSKQYPHLQNSSELSKGLKWK	116
XP_001630037.1[N.vectensis]	DWSLIPLPVRVNGIKTKQKPHVKRPMAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWK	103
XP_019645392.1[B.belcheri]	DWTLVPMPVRVNGSSSKSPHVKKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWR	125
XP_032830402.1[P.marinus]	DWTLVPMPVRVNGSSSKSPHVKKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWR	168
XP_014034661.1[S.salar]	DWTLVPMPVRVNGSSSKNKPHVKKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWR	147
NP_989612.1[G.gallus]	DWTLVPMPVRVNGSSSKNKPHVKKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWR	144
NP_001087942.1[X.laervis]	DWTLVPMPVRVNGSSSKNKPHVKKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWR	144
NP_000337.1[H.sapiens]	DWTLVPMPVRVNGSSSKNKPHVKKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWR	144
XP_009250264.1[P.abelii]	DWTLVPMPVRVNGSSSKNKPHVKKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWR	144
NP_035578.3[M.musculus]	DWTLVPMPVRVNGSSSKNKPHVKKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWR	144
XP_002161752.2[H.vulgaris]	MLSPDEKQPVYLEASRLDKLHKDEHPYKYRPRRRPKGLRGYSTPTMIVSPPTTSKPYT	186
NP_0012626245.1[A.queenslandica]	LLSDREKQPPIEESERLRIQHMKQYPDYKYRPRKKGGKKPKPVNNTSYLGGNDGSGEEY-	165
CAB63903.1[D.melanogaster]	NLKDSDKKPFMEFAEKLRMTHKQEHDPDYKYRPRKKKARVLPSQHS-----GDGSGPGPE	170
XP_001630037.1[N.vectensis]	LLNDEKKKPFIEEAERLRIKHKREHPDYKYRPRKKQKGNNGNDA-----GD-----AT	152
XP_019645392.1[B.belcheri]	MLNDEKRPPIEAAERLRVQHKKDHPDYKYRPRRRKSKNKGQSG-----DEAGSEASP	179
XP_032830402.1[P.marinus]	LLSENEKRPFVEEAERLRVQHKKDHPDYKYRPRRRSKGNKGQSES-----DSSGEQTH	221
XP_014034661.1[S.salar]	LLNEGEKRPFVEEAERLRVQHKKDHPDYKYRPRRRSKMKGQSES-----EDGSEQTH	200
NP_989612.1[G.gallus]	LLNESEKRPFVEEAERLRVQHKKDHPDYKYRPRRRSKVKGQSEQ-----EEGSEQTH	197
NP_001087942.1[X.laervis]	LLNEGEKRPFVEEAERLRVQHKKDHPDYKYRPRRRSKVKGQSEQ-----DDSAEQTH	197
NP_000337.1[H.sapiens]	LLNESEKRPFVEEAERLRVQHKKDHPDYKYRPRRRSKVKGQAEA-----EEATEQTH	197
XP_009250264.1[P.abelii]	LLNESEKRPFVEEAERLRVQHKKDHPDYKYRPRRRSKVKGQAEA-----EEATEQTH	197
NP_035578.3[M.musculus]	LLNESEKRPFVEEAERLRVQHKKDHPDYKYRPRRRSKVKGQAEA-----EEATEQTH	197
XP_002161752.2[H.vulgaris]	IPSN-WARIVHA-PENENLISPRAEAAQIVVATDGMQ-----	221
NP_0012626245.1[A.queenslandica]	-YPT-TM-----PTSSS-NSCSCGAGIRRAPVPTCSIAVQCSMELGEHVIEREPSPK	215
CAB63903.1[D.melanogaster]	MTLSATMGSSGK-PRSSNSNGQRAGKGNAADLGSCAATIS-----HAN-----	214
XP_001630037.1[N.vectensis]	ISADDLLKVLKGDGSKLVPNNGDASA-----SCA-----S-----	181
XP_019645392.1[B.belcheri]	ISANTLFKALQAESPTGSE-----PH-----S-----	201
XP_032830402.1[P.marinus]	ITTNAIYKALQADSPS-----	237
XP_014034661.1[S.salar]	ISPGAIFKALQADS-PAS-----SI-----	220
NP_989612.1[G.gallus]	ISPNAIFKALQADSPQSSS-----SI-----	218
NP_001087942.1[X.laervis]	ISPNAIFKALQADSPHSTS-----SM-----	218
NP_000337.1[H.sapiens]	ISPNAIFKALQADSPHSSS-----GM-----	218
XP_009250264.1[P.abelii]	ISPNAIFKALQADSPHSSS-----GM-----	218
NP_035578.3[M.musculus]	ISPNAIFKALQADSPHSSS-----GM-----	218
XP_002161752.2[H.vulgaris]	---YYAVQKGS-----FTPTMAHHGNS---VIVSPTN---QPI	252
NP_0012626245.1[A.queenslandica]	QTAETISIQVNGSAHLQNNRRSFSSFAGDKRPRDLSLSCPPI-KKRALIP---VSSPPE	271
CAB63903.1[D.melanogaster]	-----VGSSSSDVF-----SNEAFMKSLSNACAASLMESLIETGLDS---PC	254
XP_001630037.1[N.vectensis]	-----PE-SV-----S-----DGEVSSSES	195
XP_019645392.1[B.belcheri]	-----PEDLK-----G-----PSPHDGSVG	216
XP_032830402.1[P.marinus]	-----ADVH-----S-----PGEHS---	247
XP_014034661.1[S.salar]	-----GEVH-----S-----PGEHS---	230
NP_989612.1[G.gallus]	-----SEVH-----S-----PGEHS---	228
NP_001087942.1[X.laervis]	-----SEVH-----S-----PGEHS---	228
NP_000337.1[H.sapiens]	-----SEVH-----S-----PGEHS---	228
XP_009250264.1[P.abelii]	-----SEVH-----S-----PGEHS---	228
NP_035578.3[M.musculus]	-----SEVH-----S-----PGEHS---	228
XP_002161752.2[H.vulgaris]	TLVQSTSAPTSNYPAYVTVPMPATSTAI FHPITAI PVQGVH-TPAFVLRSSYPG-----	304
NP_0012626245.1[A.queenslandica]	VLPTSLDDIFPPSPSSSDSS-----	291
CAB63903.1[D.melanogaster]	STASSMSSLTPPATPYNVAPSNAKA-----SAA-----NNPSLLRLQLSEPVANAGDG	302
XP_001630037.1[N.vectensis]	C--SVSPSPETPTAVPV-----KNEDVKNDEALSAQ---PGF-----	226
XP_019645392.1[B.belcheri]	VTPSSQAPPTPTPTPKQDQM---T-----ALKADGMKRDPTSNTL---TAIHRDGP	263
XP_032830402.1[P.marinus]	--GQSQQPPTPTPTPKTDV-QSNKL-----DLKREG-----	275
XP_014034661.1[S.salar]	--GQSQQPPTPTPTPKTDI-QAGKV-----DLKREG-----	258
NP_989612.1[G.gallus]	--GQSQQPPTPTPTPKTDAQPGQK-----DLKREG-----	257
NP_001087942.1[X.laervis]	--GQSQQPPTPTPTPKTDV-QPKK-----DLKREG-----	256
NP_000337.1[H.sapiens]	--GQSQQPPTPTPTPKTDV-QPKA-----DLKREG-----	256
XP_009250264.1[P.abelii]	--GQSQQPPTPTPTPKTDV-QPKA-----DLKREG-----	256
NP_035578.3[M.musculus]	--GQSQQPPTPTPTPKTDV-QAGKV-----DLKREG-----	256
XP_002161752.2[H.vulgaris]	SNILSPS---AIPAIYHNI DHRTIESHMQPNQHIKTESTNTIVKTPDGETIVIIQRPIDG	361
NP_0012626245.1[A.queenslandica]	--PISHQHRE-----DT-----LPTLHFEFMDPLMPYDP	319
CAB63903.1[D.melanogaster]	YGVVLEAGREY-----VAIGEVNYSQGSAGVQSG-----A-----EGGG	336
XP_001630037.1[N.vectensis]	--P-SCSKDDSDNSHAIDFDVGDLT-----DLM-A-----MGVDSTEFDQYLPITYSQ	271
XP_019645392.1[B.belcheri]	HHHHHPQGHGHPNIDFSNVDIGPL-----DVMS-----MESFDVEEFDQYLPNGH	310
XP_032830402.1[P.marinus]	RPLQEGGRQ Q--IDFSNVDIRELSR-----EVISN-----MESFDVNEFDQYLPNGH	321
XP_014034661.1[S.salar]	RPLQEGTGR QLNIDF RDVDIGEL SS-----DVISH-----IDTFDVNEFDQYLPNGH	306
NP_989612.1[G.gallus]	RPLAQEGGR QPHIDF RDVDIGEL SS-----DVISN-----IETFDVNEFDQYLPNGH	305
NP_001087942.1[X.laervis]	RPLQESGRQ PHIDF RDVDIGEL SS-----EVISt-----IETFDVNEFDQYLPNGH	304
NP_000337.1[H.sapiens]	RPLPQGRQ PP-IDF RDVDIGEL SS-----DVISN-----IETFDVNEFDQYLPNGH	303

XP_009250264.1[P.abelii]	-RFLPEGGRRPP-IDFRDVDIGELSS-----DVISN-----IETFDVNEFDQYLPPNGH	303
NP_035578.3[M.musculus]	-RFLAEGGRPP-IDFRDVDIGELSS-----DVISN-----IETFDVNEFDQYLPPNGH	303
XP_002161752.2[H.vulgaris]	HVVFPQLREVP--SGATNTITVVPQ---SQVIQQHIVQTPNNQE-----TKIL----	404
NP_001266245.1[A.queenslandica]	SAVDLALSGSS-----SALSSSTAAS--NVLSLNTF-----FLQ-----	351
CAB63903.1[D.melanogaster]	AGQEMDFLENIINGYGGYTGSRVSYPAY--SYFANGGHFATEEQQQQALQASEALNYPKPA	395
XP_001630037.1[N.vectensis]	ALLDSLTITKAINT---TQINTQ-----SLSNSRFTTTSQAVQSFPFLPSYREFMVQ-	319
XP_019645392.1[B.belcheri]	PASASGHHSHPPYTSYSQMSSSAT--TVTSSSSWMAKQNTS--PRONSQEQRLPVK-	364
XP_032830402.1[P.marinus]	PGHGQSVAA---SYGGT-----GYSINGHAWLSKQOQQ--QOQQQQQH-----	359
XP_014034661.1[S.salar]	PGAPGTAAGQV--SYNGTYGISSSAVSQAAGGTAGHSWMTKSQSQ-----	349
NP_989612.1[G.gallus]	PGVPATHGQVT--TYSGTYGISSSSASP---AGAGHAMMAKQOQP--PPQPP-----	350
NP_001087942.1[X.laervis]	PGVGS--AQA--PYTGSYGISSTPSAT--TGAGSAMMSKQOQQ--P-----	342
NP_000337.1[H.sapiens]	PGVPATHGQV--TYTGSYGISSTAATP---ASAGHVMSKQOQAP--PPPPQPPQAPPA-	355
XP_009250264.1[P.abelii]	PGVPATHGQV--TYTGSYGISSTAATP---AGAGHVMSKQOQAP--PPPPQPPQAPPA-	355
NP_035578.3[M.musculus]	PGVPATHGQV--TYTGSYGISSTAATP---ATAGHVMSKQOQAP--PPPPQPPQAPQA-	355
XP_002161752.2[H.vulgaris]	-----	404
NP_001266245.1[A.queenslandica]	-----	351
CAB63903.1[D.melanogaster]	ADIDPKEDIQYFMDQMLPMTQHHPHHTPLHHLHHSPLNNSASLSS--ACSSASSQQP	454
XP_001630037.1[N.vectensis]	-----LQKLPESEGSFPPNR-----EHLPPPPPPQYTP-----H-----PP	335
XP_019645392.1[B.belcheri]	-----MEQ-----EHLPPPPPPQYTP-----H-----PP	382
XP_032830402.1[P.marinus]	-----TLSSPPPPPPPAISSPEQRAHVKTQLS	386
XP_014034661.1[S.salar]	-----QQHSLTTLGSQGGQGNQRTPTTHIKTEQLS	379
NP_989612.1[G.gallus]	-----A--QPPAQHTLPALSQE--QG--PAQQRPHIKTEQLS	381
NP_001087942.1[X.laervis]	-----QHSLSSTINSE--QS--QSQRTHIKTEQLS	369
NP_000337.1[H.sapiens]	-----PQAPPQQAAPPQQAAPP--QQPOAHTLTTLSS--P--GQSQRTHIKTEQLS	403
XP_009250264.1[P.abelii]	-----PQAPPQQAAPPQQAAPP--QQPOAHTLTTLSS--P--GQSQRTHIKTEQLS	403
NP_035578.3[M.musculus]	-----PQAPPQQAAPPQQAAPP--QQQAHTLTTLSS--P--GQSQRTHIKTEQLS	401
XP_002161752.2[H.vulgaris]	-----	404
NP_001266245.1[A.queenslandica]	-----SSAATSIFSPFNIDSC	367
CAB63903.1[D.melanogaster]	VAEYIEHLGYSPAASS-----ASQNPNGFPQQPYAN	485
XP_001630037.1[N.vectensis]	PSATMQQ-----RNQPSNSFFPFSESEV	359
XP_019645392.1[B.belcheri]	ASSYNYQPQYS-----SYQHSPPRPQYT-----	405
XP_032830402.1[P.marinus]	PSHYSDQQQQQQQPPQQQHSPPQQQQQQQQQPPQQAQQAQQVQQQQQLGYSFPFSIQHY	446
XP_014034661.1[S.salar]	PSHYNDQQNSS-----PPQHVITYGSFNLQHY	405
NP_989612.1[G.gallus]	PSHYSEQQHSFPQ-----QQ-----QQQQQLGYGSFNLQHY	413
NP_001087942.1[X.laervis]	PSHYSDQQQ-----QHSPPQLNYSFNLQHY	395
NP_000337.1[H.sapiens]	PSHYSEQ-Q-----QHSPPQIAYSFPNLPHY	428
XP_009250264.1[P.abelii]	PSHYSEQ-Q-----QHSPPQIAYSFPNLPHY	428
NP_035578.3[M.musculus]	PSHYSEQ-Q-----QHSPPQIAYSFPNLPHY	426
XP_002161752.2[H.vulgaris]	-----	404
NP_001266245.1[A.queenslandica]	STDFDPELPSDFADIFAQNAS-----EFD-----TSITTLTST-----	400
CAB63903.1[D.melanogaster]	GAASMTPTLGDPAPOQE-----LQSQQQEQQHONPSQHHLWGTYTYVNP-----	529
XP_001630037.1[N.vectensis]	NVCSSLAATRQ-----PAFLSS--PSTSGTLSSSSNSGRHT--	394
XP_019645392.1[B.belcheri]	---DYPPPAHS-----PQOFYSFH--PTSSSIPPPYNYMAPQRSL	441
XP_032830402.1[P.marinus]	GAAVVPAISRQYSYADHHHHHHHHQSSAAAAAYSGHSAGTAGLYSGFSYMGFSQRPS	506
XP_014034661.1[S.salar]	SSSSYPSITRAQYDFSDHGG-----TNSYSSHAAGQGQSGLYSFSSYMSFSQRPM	456
NP_989612.1[G.gallus]	GS-SYPPITRSQYDYTEHQNS-----GSYYSHA-AGQSGGLYSTFTYMNFTQRPM	461
NP_001087942.1[X.laervis]	SS-SYPTITRAQYDYTEHQGS-----NSYYTHA-SGQNSGLYNFTYMNFSQRPM	443
NP_000337.1[H.sapiens]	SP-SYPPITRSQYDYTDHQNS-----SSYYSHA-AGQGTGLYSTFTYMNPAQRPM	476
XP_009250264.1[P.abelii]	SP-SYPPITRSQYDYTDHQNS-----SSYYSHA-AGQGTGLYSTFTYMNPAQRPM	476
NP_035578.3[M.musculus]	SP-SYPPITRSQYDYADHQNS-----GSYYSHA-AGQSGGLYSTFTYMNPAQRPM	474
XP_002161752.2[H.vulgaris]	-----	404
NP_001266245.1[A.queenslandica]	-----	400
CAB63903.1[D.melanogaster]	-----	529
XP_001630037.1[N.vectensis]	-----LIWK-----	398
XP_019645392.1[B.belcheri]	YPTVAGAP-----STWE--PSYTQLARP	462
XP_032830402.1[P.marinus]	YTPIDATGVPSIPQPHSPP-SWE-QPVYTQLTRP	539
XP_014034661.1[S.salar]	YTPIDATTGVPSIPQTHSPQHQHWDQPVYVYQLSRP	491
NP_989612.1[G.gallus]	YTPIDATSGVPSIPQTHSPQ-HWE-QPVYTQLTRP	494
NP_001087942.1[X.laervis]	YTPIDATTGVPSIPQTHSPQ-HWE-QPVYTQLTRP	476
NP_000337.1[H.sapiens]	YTPIDATSGVPSIPQTHSPQ-HWE-QPVYTQLTRP	509
XP_009250264.1[P.abelii]	YTPIDATSGVPSIPQTHSPQ-HWE-QPVYTQLTRP	509
NP_035578.3[M.musculus]	YTPIDATSGVPSIPQTHSPQ-HWE-QPVYTQLTRP	507