

Notch2

Homo sapiens:

>Q04721.3 NOTCH2_HUMAN Neurogenic locus notch homolog protein 2 OS=Homo sapiens OX=9606 GN=NOTCH2 PE=1 SV=3
MPALRPALLWALLALWLC AAPAHALQCRDGYEPCVNEGMCVITYHNGTGYCKCEPGEFLGEYQCQRHDPCEKNRCQNGGT CVAQAMLGKATCRCA SGFTGEDCQYSTSHPCFVSRPCLNGGTC HMLS RDTY
ECTCQVGFTTGKECQWTDACL SHPCANGSTCTT VANQFSCCKLTGFTGQKCETDVNECDIPGHCGHG GTCLNLPGSYQCQCQPGFTGQYCD SLYVPCAPSPCVNGGTCRQTGDFTFE CNCLPGFEGSTCE
RNIDDCPNHR CQNGGVCVDGVNTYNCRCPPQWTGQFCTEDVDECLLQPNACQNGGTCANRNGG YGCVCVNWSGDDCSENIDDCAFASCTPGSTCIDRVASFSCMCPEGAGLLCHLDDACISN PCHKG
ALCDTNPLNGQYICTCPQGYKGADCTEDVDECAMANSNPCEHAGKCVNTDGA FHCECLKGYAGPRCEMDINECHSDP CQN DATCLDKIGGFTCLCMPGFKGVHCELEINECQSNPCVNNGQCVDKVNRF
QCLCPGFTGPVQCIDIDDCSS TPC LINGAKC I DHPNGYECQCATGFTGVLCEENIDMCDPDPCHHGQ CQDGDISTYTCINPGYMGAI CSDQIDECYSSPC LNDGRC I DLVNGYQCNCQPGTSGVNC E IN
FDDCASNP C I H G I C M D G I N R Y S C V C S P G F T G Q R C N I D I D E C A S N P C R K G A T C I N G V N G F R C I C P E G P H P F S C Y S Q V N E C L S N P C I H G N C T G G L S G Y K K C L D A G W V G I N C E V D K N E C L S N P C Q N G G T C D N
LVNGYRCTCKKGFKGYNCQVNI DECA SNPCLNQGTCFDDISGYTCHCVLPYTGKNQCQTVLAPCS PNP CENAAVCKESPNFESY TCLCAPGWQ GQRCITIDI DECISKPCMNHGLCHNTQGSYMCCEPPGF
SGMDCEEDIDDCLANPCQNGGSCMDGVNTFSCLCLPGFTGDKCQ TDMNECLSEPCKNNGTCS DVS YNSYTCCKQAGDFGVHCENNINECTESSCFNGGTCVDGINSFSC LCPVGTGSCFLHEINECSSH
PCLNEGTCVDGLGTYRCS C P L G Y T G K N C Q T L V N L C S R S P C K N K G T C V Q K K A E S Q C L P S G W A G A Y C D V P N V S C D I A A S R R G V L V E H L C Q H S G V C I N A G N T H Y C C Q L P G Y T G S Y C E E Q L D E C A S N P C Q H G
ATCSDFTIGGYRCECVPGYQGVNCEYEVDE CQNQPCQNGGTC I D L V N H F K C S C P P G T R G L L C E E N I D D C A R G P H C L N G G Q C M D R I G G Y S C R C L P G F A G E R C E G D I N E C L S N P C S S E G S L D C I Q L T N D Y L C
VCRSAFTGRHCETFLVDVCQMPCLNGGTCAVASNM PDGFI CRCP P G F S G A R C Q S S C G Q V K C R K G E Q C V H T A S G P R C F C P S P R D C E S G A S S P C Q H G S C H P Q R P P P Y S C Q C A P P F S G S R C E L Y T A P P S
TPPATCLSQYCADKARDGYCDEACNSHACQWDG GDCSLTMENPWANCSSPLPCWDYINNQCDEL CNTVECLDFNFECQGN SKTCKYDKYCADHFKDNHCDQGCNSEECGWDGLDCAADQPENLAEGTLV
IVVLMPEQLLQDARSFLRALGTLTLHNLRIK RDSQ GELMVYPYGEKSAAMKQRMTRRSLPGEQE QEVAGSKVFLEIDNRQCVQDS DHCFKNTDAAAALLASHAIQGTLSYPLVS VVS E S L T P E R T Q
L L Y L L A V A V V I I L F I L L G V I M A K R K R K H G S L W L P E G F T L R R D A S N H K **REFVEQCL**AVGLKNLSVQVSEANLIGTGTSEHWVDDEGPQPKKVAE D A L L S E E D D P I D R R P W T Q Q H L E A A D I R H T P S L A
LTPPQAEQEV D V L D V N V R G P D G C T P L M L A S L R G G S S D L S D E D E D A E D S S A N I I T D L V Y Q G A S L Q A Q T D R T G E M A L H L A A R Y S R A D A A K R L L D A G A D A N A Q D N M G R C P L H A A V A A D A Q G V F Q I L I R N R V T
D L D A R M N D G T T P L I L A A R L A V E G M V A E L I N C Q A D V N A V D D H G K S A L H W A A V N N V E A T L L L K N G A N R M D Q N K E E T P L F L A A R E G S Y E A A K I L L D H F A N R D I T D H M D R L P R D V A R D R M H D I V R L L D E
Y N V T P S P P G T V L T S A L S P V I C G P N R S F L S L K H T P M G K S R R P S A K S T M P T S L P N L A K E A K D A K S R R K K S L S E K V Q L S E S S V T L S P V D S L E S P H T Y V S D T T S S M I T S P G L I Q A S P N P M L A T A A P P A P V
H A Q H A L S F S N L H E M Q P L A H G A S T V L P S V Q L L S H H I V S P G S G A G S L S R L H P V P V P A D W M N R M E V N E T Q Y N E M F G M V L A P A E G T H P G I A P Q S R P P E G K H I T T P R E L P P I V T F Q L I P K G S I A Q P A G A P
Q Q S T C P P A V A G P L P T M Y Q I P E M A R L P S V A F T T A M P P Q D G Q V A Q T I L P A Y H P P F A S V G K Y T P P S Q H S Y A S S N A A E R T P S H S G H L Q G E H P Y L T P S P E S P D Q W S S S P H S A S D W S D V T T S P T P G G A G G G
Q R G P G T H M S E P P H N M Q V Y A

Pongo abelii:

>XP_009243797.2 neurogenic locus notch homolog protein 2 isoform X1 [Pongo abelii]
MPAIRPALFWALLALWLC AAPARALQCRDGYEPCVNEGMCVITYHNGTGYCKCEPGEFLGEYQCQRHDPCEKNRCQNGGT CVAQAMLGKATCRCA SGFTGEDCQYSTSHPCFVSRPCLNGGTC HMLS RDTY
ECTCQVGFTTGKECQWTDACL SHPCANGSTCTT VANQFSCCKCLPGFTGQKCETDVNECDIPGHCGHG GTCLNLPGSYQCQCQPGFTGQYCD SLYVPCAPSPCVNGGTCRQTGDFTFE CSCLPGFEGSTCE
RNIDDCPNHR CQNGGVCVDGVNTYNCRCPPQWTGQFCTEDVDECLLQPNACQNGGTCANRNGG YGCVCVNWSGDDCSENIDDCAFASCTPGSTCIDRVASFSCMCPEGAGLLCHLDDACISN PCHKG
ALCDTNPLNGQYICTCPQGYKGADCTEDVDECAMANSNPCEHAGKCVNTDGA FHCECLKGYAGPRCEMDINECHSDP CQN DATCLDKIGGFTCLCMPGFKGVHCELEINECQSNPCVNNGQCVDKVNRF
QCLCPGFTGPVQCIDIDDCSS TPC LINGAKC I DHPNGYECQCATGFTGVLCEENIDMCDPDPCHHGQ CQDGDISTYTCINPGYMGAI CSDQIDECYSSPC LNDGRC I DLVNGYQCNCQPGTSGVNC E IN
FDDCASNP C I H G I C M D G I N R Y S C V C S P G F T G Q R C N I D I D E C A S N P C R K G A T C I N G V N G F R C I C P E G P H P F S C Y S Q V N E C L S N P C I H G N C T G G L S G Y K K C L D A G I N G C E V D K N E C L S N P C Q N G G T C D N
LVNGYRCTCKKGFKGYNCQVNI DECA SNPCLNQGTCFDDISGYTCHCVLPYTGKNQCQTVLAPCS PNP CENAAVCKESPNFESY TCLCAPGWQ GQRCITIDI DECISKPCMNHGLCHNTQGSYMCCEPPGF
SGMDCEEDIDDCLANPCQNGGSCVDGVNAFSC LLLGFTGDKCQ TDMNECLSEPCKNNGTCS DVS YNSYTCCKQAGDFGVHCENNINECTESSCFNGGTCVDGINSFSC LCPVGTGSCFLHEINECSSH
PCLNEGTCVDGLGTYRCS C P L G Y T G K N C Q T L V N L C S R S P C K N K G T C V Q K K A E S Q C L P S G W A G A Y C D V P N V S C D I A A S R R G V L V E H L C Q H S G V C I N A G N T H Y C C Q L P G Y T G S Y C E E Q L D E C V S N P C Q H G
ATCSDFTIGGYRCECVPGYQGVNCEYEVDE CQNQPCQNGGTC I D L V N H F K C S C P P G T R G L L C E E N I D D C A R G P H C L N G G Q C M D R I G G Y S C R C L P G F A G E R C E G D I N E C L S N P C S S E G S L D C I Q L T N D Y L C
VCRSAFTGRHCETFLVDVCQMPCLNGGTCAVASNM PDGFI CRCP P G F S G A R C Q S S C G Q V K C R K G E Q C V H T A S G P R C F C P S P R D C E S G A S S P C Q H G S C H P Q R P P P Y S C Q C A P P F S G S R C E L Y T A P P S
TPPATCLSQYCADKARDGYCDEACNSHACQWDG GDCSLTMENPWANCSSPLPCWDYINNQCDEL CNTVECLDFNFECQGN SKTCKYDKYCADHFKDNHCDQGCNSEECGWDGLDCAADQPENLAEGTLV
IVVLMPEQLLQDARSFLRALGTLTLHNLRIK RDSQ GELMVYPYGEKSAAMKQRMTRRSLPGEQE QEVAGSKVFLEIDNRQCVQDS DHCFKNTDAAAALLASHAIQGTLSYPLVS VVS E S L T P E R T Q
L L Y L L A V A V V I I L F I L L G V I M A K R K R K H G S L W L P E G F T L R R D A S N H K **REFVEQCL**AVGLKNLSVQVSEANLIGTGTSEHWVDDEGPQPKKVAE D A L L S E E D D P I D R R P W T Q Q H L E A A D I R H T P S L A
LTPPQAEQEV D V L D V N V R G P D G C T P L M L A S L R G G S S D L S D E D E D A E D S S A N I I T D L V Y Q G A S L Q A Q T D R T G E M A L H L A A R Y S R A D A A K R L L D A G A D A N A Q D N M G R C P L H A A V A A D A Q G V F Q I L I R N R V T
D L D A R M N D G T T P L I L A A R L A V E G M V A E L I N C Q A D V N A V D D H G K S A L H W A A V N N V E A T L L L K N G A N R M D Q N K E E T P L F L A A R E G S Y E A A K I L L D H F A N R D I T D H M D R L P R D V A R D R M H D I V R L L D E
Y N V T P S P P G T V L T S A L S P V I C G P N R S F L S L K H T P M G K S R R P S A K S T M P T S L P N L A K E A K D A K S R R K K S L S E K V Q L S E S S V T L S P V D S L E S P H T Y V S D T T S S M I T S P G L I Q A S P N P M L A T A A P P A P V
H A Q H A L S F S N L H E M Q P L A H G A S T V L P S V Q L L S H H I V S P G S G A G S L S R L H P V P V P A D W M N R M E V N E T Q Y N E M F G M V L A P A E G T H P G I A P Q S R P P E G K H I T T P R E L P P I V T F Q L I P K G S I A Q P A G A P
Q Q S T C P P A V A G P L P T M Y Q I P E M A R L P S V A F T T A M P P Q D G Q V A Q T I L P A Y H P P F A S M G K Y T P P S Q H S Y A S S N A A E R T P S H S G H L Q G E H P Y L T P S P E S P D Q W S S S P H S A S D W S D V T T S P T P G G A G G G
Q R G P G T H M S E P P H N M Q V Y A

Mus musculus:

>NP_035058.2 neurogenic locus notch homolog protein 2 precursor [Mus musculus]
MPALRPAARALLWLLWLCAGAPAHALQCRGGQEPVCNEGTCVITYHNGTGFCRCPEGLGEYQCQRHDPCEKNRCQNGGT CVPQGMGLKATCRCA PGTGEDCQYSTSHPCFVSRPCQNGGTC HMLS RDTY
ECTCQVGFTGQKCQWTDACL SHPCENGSTCTSVASQFSCCKCPAGLTGQKCEADINNECDIPGRCQHGGTCLNLPGSYRCQCQPGFTGQHCDS PYPVPCAPSPCVNGGTCRQTGDFTFE CNCLPGFEGSTCE
RNIDDCPNH K C Q N G G V C V D G V N T Y N C R C P P Q W T G Q F C T E D V D E C L L Q P N A C Q N G G T C T N R N G G Y G C V C V N W S G D D C S E N I D D C A Y A S C T P G S T C I D R V A S F S C L P E G K A G L L C H L D D A C I S N P C H K G
ALCDTNPLNGQYICTCPQGYKGADCTEDVDECAMANSNPCEHAGKCVNTDGA FHCECLKGYAGPRCEMDINECHSDP CQN DATCLDKIGGFTCLCMPGFKGVHCELEINECQSNPCVNNGQCVDKVNRF
QCLCPGFTGPVQCIDIDDCSS TPC LINGAKC I DHPNGYECQCATGFTGILCDENIDMCDPDPCHHGQ CQDGDISTYTCINPGYMGAI CSDQIDECYSSPC LNDGRC I DLVNGYQCNCQPGTSGNLCE IN
FDDCASNP CMHG C V D G I N R Y S C V C S P G F T G Q R C N I D I D E C A S N P C R K G A T C I N G V N G F R C I C P E G P H P F S C Y S Q V N E C L S N P C I H G N C T G G L S G Y K K C L D A G I N G C E V D K N E C L S N P C Q N G G T C N N
LVNGYRCTCKKGFKGYNCQVNI DECA SNPCLNQGTCFDDVSGYTGCHMPLYTGNKQCQTVLAPCS PNP CENAAVCKEAPNFESFSC LCAPGWQ GQRCITVDVDECISKPCMNNGVCHNTQGSYVCECP P G F
SGMDCEEDIDDCLANPCQNGGSCVDHVN T F S C Q C H P G F I G D K C Q T D M N E C L S E P C K N G G T C S D V N S Y T C T C P A G F H G V H C E N N I D E C T E S S C F N G G T C V D G I N S F S C L C P V G T G P F C L H D I N E C S N
PCLNAGTCVDGLGTYR C I C P L G Y T G K N C Q T L V N L C S R S P C K N K G T C V Q E K A R P H C L P P G W D G A Y C D V L N V S C K A A L Q K G V P V E H L C Q H S G I C I N A G N T H Y C C Q L P G Y T G S Y C E E Q L D E C A S N P C Q H G
ATCNDFTIGGYRCECVPGYQGVNCEYEVDE CQNQPCQNGGTC I D L V N H F K C S C P P G T R G L L C E E N I D E C A G P H C L N G Q C V D R I G G Y T C R C L P G F A C E R C E G D I N E C L S N P C S S E G S L D C I Q L K N N Y N C
ICRSAFTGRHCETFLVDVCQPKCLNGGTCAVASNM PDGFI CRCP P G F S G A R C Q S S C G Q V K C R R G E Q C I H T D S G P R C F C L N P K D C E S G C A S N P C Q H G G T C Y P Q R P P H Y S C R C P S P F G G S H C E L Y T A P T S
TPPATCQSQYCADKARDGICDEACNSHACQWDG GDCSLTMDPWANCTSTLRWEYINNQCDEQCNTAECLDFNFECQRNSKTCKYDKYCADHFKDNHCDQGCNSEECGWDGLDCAADQPENLAEGTLI
IVVLLPPEQLLQDSR S F L R A L G T L L H N L R I K R D S Q G A L M V Y P Y F G E K S A A M K Q K M T R R S L P E E Q E Q E V I G S K I F L E I D N R Q C V Q D S D Q C F K N T D A A A L L A S H A I Q G T L S Y P L V S V F S E L S P R N
A Q L L Y L L A V A V V I I L F I L L G V I M A K R K R K H G F L W L P E G F T L R R D S S N H K **REFVEQCL**AVGLKNLSVQVSEANLIGSGTSEHWVDDEGPQPKKA E D A L L S E E D D P I D R R P W T Q Q H L E A A D I R H T P S L
ALTTPPQAEQEV D V L D V N V R G P D G C T P L M L A S L R G G S S D L S D E D E D A E D S S A N I I T D L V Y Q G A S L Q A Q T D R T G E M A L H L A A R Y S R A D A A K R L L D A G A D A N A Q D N M G R C P L H A A V A A D A Q G V F Q I L I R N R V T
D L D A R M N D G T T P L I L A A R L A V E G M V A E L I N C Q A D V N A V D D H G K S A L H W A A V N N V E A T L L L K N G A N R M D Q N K E E T P L F L A A R E G S Y E A A K I L L D H F A N R D I T D H M D R L P R D V A R D R M H D I V R L L D E
Y N V T P S P P G T V L T S A L S P V I C G P N R S F L S L K H T P M G K K A R R P N T K S T M P T S L P N L A K E A K D A K S R R K K L S E K V Q L S E S S V T L S P V D S L E S P H T Y V S D T T S P G L I Q A S P T P L A A A P A A P
V H T Q H A L S F S N L H D M Q P L A P A G A S T V L P S V Q L L S H H I A P P G S S A G S L G R L H P V P V P A D W M N R M E V N E T Q Y S E M F G M V L A P A E G A H P G I A A P Q S R P P E G K H M S T Q R E P L P P I V T F Q L I P K G S I A Q A A G
A P Q T Q S S C P P A V A G P L P S M Y Q I P E M P R L P S V A F P P T M M Q Q E G G V A Q T I V T Y T H P P F A S V G K Y T P P S Q H S Y A S S N A A E R T P S H G H L Q G E H P Y L T P S P E S P D Q W S S S P H S A S D W S D V T T S P T P G G G G
G Q R G P G T H M S E P P H S N M Q V Y A

Gallus gallus:

>NP_001238962.2 neurogenic locus notch homolog protein 2 precursor [Gallus gallus]
MARGAGAFALFGLVLAVLSRAEPAAALQCMDDSKPCVNEGKCIYPQNGTGYCKREGLDYGCYQRPNESNTCKNGGTCETTSLIGKATCKCAPGFTGEDCQYSESHICYVSQ PCLNGGTC HPHSQ
ETNEVCVCPGYTGKDCQWTDAC T G Q P C A N G S T C T V S G H K F S C I C Q S G Y T G Q K C I D V N E C A T S G L C H H G G T C I N L P G S F R C Q C K P G Y T G H R C E S N Y V P C S P S P C M N G G T C H Q T S D F T F E C N C L P G F E G S T C E
ICEKNYDCPNHNCQNGGTCVDGVNTYNCRCPPQWTGQFCTEDVDE CQLQPNACQNGGTC T N H N G Y A C V C V N W S G D D C S K N I D D C T A S C A N G S T C I D R V A S F S C I C P E G K A G L L C H L D D A C V S N P C
QKGA L C D T P N V N G H Y I C T C P Q C H K G A D C T E D V D E C A M A N S N P C E H A G K C V N T E D S F G H C E C L K G Y T P R C E M D I N E C H S N P C Q N D A T C L D K I G G F T C L C M P G F K G V H C E B D I D E C L S N P C V N N G C E L D K V
N R F L C S C P P F S G A V Q C I D I D D C S T P C L N G A K C I D H P N G Y E C Q C A T G F T G V L C E E N I D M C D P D P C H H G Q C Q D G I D S Y T C I N P G Y M G A I C S E Q I N E C H S N P C S S E G S L D C I Q L K N N Y N C
ENNFDCCASNPCVHGDCIDGINRYNCA CKPGFTGPRCNVDIDE CASSPCNNGGTCINEVNGFRVCPEGYHHPCQSGADGCLSNPCVHGNC THIVSGYKVCVDPGWIGDYCSTEGNECKSNPCQNGGT
CEDILLNGYRCTCRKGFKGYNCQVVAPCS P D P C E N S G I Q E S P D S E G Y T C C A P G W E G E R C T V D I D E C L S K P C N A L H C N I Q G S Y L C E C R P G T T G G C D S N I D D C L S N P C Q N G A S C V D G I N S F C I C L
P G F H G D K Q C T D N E C L S E P C R N G G T C T H V N S Y T C K Q C P G F E G T N C E N N I D E C T E S S C F N G G T C V D G I N S T C Q C P V G T G P F C L M E I N E C D S H P C L N K G S C V S L D K Y N C I P L G Y T G S R C E Q T P M D L C
S C S P C K N K G T C F Q S G A Q T R C D C P S G W T G A Y C D V P N V S C Q V A A S Q R G I T V D Q L C Q H S H C L N V N T H R C Q R V G Y T G S Y C E E Q L D E C D S S P C Q N G A T C R H L L G G Y Q C E C V P G Y Q G V N C E Y E V D E C Q F C P C
Q N G T C I D L V N H F R C S C P P G T R G L E N A V D D C I S E S G G R P C F N G G Q C I D Q I G G Y S C L C L P G F A G E R C E G D I N E C L S N P C N P R G S L D C I Q L I N D Y T C I C R S A F T G R H C E S V I D V C P R K P C Q N G G T C A V A
S N M P D G F I C Q C P P G Y S A K C E F S S H S T C G Q V K K K G E Q C I H T S S G P R C Y C P R L A V G E E Q C T N T G C A S A P C Q N G S S C H P R S Q P P Y Y C Q C P A H A G S C Q E Q L V H P S Q E P L G C L D S Q C A E K A R D Y G C D E D C

NTHACQWDGDCSLTMEDPWANCSSSLRCWMLFNGQCDEFNTPCECLFDNFECQQNSRMCKYDKYCADHYGDGRCDQGCNSEECGWDGLDCAGDKAERLAEGTLIIIVLMRPPDELLDRDVSFLRTLGTLLHTNLRILKLDSSQGNPMVFPYYEGKSAARSSRVVVVRKHRELEQEVILGTRVFLIEDNRQCAEDSEQFHNTAAALAAQAIKGMLPYFPFVSQSEPLLPKTKQLLYLLAVALIILLILLGVMMAKRRKHGSLWLPPEGFIILRRPDSNH**REFPVQGL**AVGLKNLSVQIPEGNMADSGPTEHWAGDGGGPKRKRVTEDQALLPEADEQIDQRQWTOQHLEAADVCGSTSLATLPQADQEVVDLVNNVGRPDGCTPLMLASLRVSGSDISEDDGEDSSANITIDLIIYQGANLQAQTDRTGEMALHLAARYSRADAARLLDAGADANARDNMGRTPLHAAVAADAQGVFQJILIRNRVITDLDRMADGTEFPLILAAARLAVEGMVAELINCQADVNAVDDHGKSALHWAAAVNNVEATLVLLKNGANRDMQDNKEETPLFLAAREGSFEAAKILLDHFANRDTIDHMDRLPRDVAQDRMHHDIVQLLNEYNVAHSPTGHGPAMLNSALSPVICGPNRSFLNLKHASLSKKSRRKPNAGIMPTNLTKDAKRRRKKSLSESKGQFSESSVTLSPVDSLESPLHAFASEPTSSPMPSPGVLHSSPSSLTAPSVQAAHSMSPSNLHMQLPGRGSSVTLPSPVSQQLSQHRTTTPSSGLGRLPANVSTEWNNRMEMNESQYNEMFGMVPVVMHSHSPVSQSQGLVQADTKHLGVSRSEPTSPMITPQLVPKGINQQALPQQAQSNCAQNMAGPLSSSMYQISDLAQLPSASFMAAIPQQDGQVPQTILPAYHQFQSSGMKYPTPPSQHSYSSATERTPSHNRHLQGEHPYLTSPSPESPDQWSSSSPHSASDWSDVATSPGNINQRGPAAAHVPEQQRNNMQVYA

Xenopus laevis:

>XP_018114267.1 neurogenic locus notch homolog protein 2 isoform X1 [Xenopus laevis]
MGVQAVFGLCVLLGMPCCDGLQCRGASEPCLNEGRCITSDDGSAYCKCPDAFVGVEYQCLQNPQJETVCLNNGGSKCVSPDLSKGVCTCAPFGSGENCKQPVASVCSLTQPCMNNGGTCRLLTLEHYECICPFGWRGKDCEFIDACASQPCANGSTCLPNEQNQYSCTCQAGYTLGKCEMDVNECTSPGLCKNGGTCENLPGSRYCQCHPGYIGORCESPFIPCSFSPCMNGGTCRQTSEFAYECNCLPFGDGKNCESNIDDCPSHHKQNGGTCVDGVNTYRCNCPFPQWTGQFCETEDVDECLLQPNACQNGGTCITNSNGYCNVCVNGWSGDDCQNIIDDCATAACANGSTCIDRVASFICVCPPEGKIGILLCHKNDACFSNPCIHGISLCDTNPLTGAICTCPCPGYKGTACTEIDECSLVNSPCEHAGKCVNTEGSFYCECSKSGTGPCEMDINECLSEPCNDCTCLDKIGGFTCLCMPGYKGIHCEIHEVEDECLSNPCVNNVGVCDVKNRNVFCICPPGTFPGVQCIDIDDDCSSTPQNQAGKCVDPHAGFYDCLCATGFTGLVCEENINCEPFPCHYQCDQIGDSYTCICEFPGMGAICSDQIDECHSNPCLNEGRCVLDVNGQCNCLPSTGSPRCKENVDDCASNPCTGKNCVDGNIIRDVCVSPGFTGPQCKDDIDECASSPCHNGGTCVNEQNRFRCICEPFGRPQSPCFSQVDECVNPNCIHGNCITDDEVNGYKCLCQPGWNGKCEVDRNECLSDPCQNGGTCDDLVNGYRCSCKTKYGNKQCIDTNECASPNCLNHGTCRDGINGYTHCHALPYTGTRNCQNIILTPCSPEPCHNGGICQSESDFKFSFSLCATGWQQRCTIDVDECVNTPNCRNYGRCTNRTGGYKXCHCPCDFGSGFNCENNIDDCLSNFCQNGASCLDGINTFSCNCLAGFHGDKQQRDVBECASNPKCNGGSCITYDINSYTCCKQCPGFDGICHDNNIDECTDTSCFNATGCTVDGVNSFSCQCPQGTGPFCLFEINECGSHPCINGGTCVDGMGTGTHCTCPIGYRGKNCEVLDLNCQADVNAVDDHGKSALHWAAAVNNVEATVLLKNGANRDMQDNKEETPLFLAAREGSFEAAKMLLDYFANREITDHDMDRLPRDIAKDRMHHDIVRLLEDEYNLHNSLTGQGPGLSMNLSLPSQSGNSRSLNLKHAAQAKKTRRPSAKNVGRCPNLPLNAKEPKDTKNRRRKKSDTDNKGQLESSESVTLSPVDSLESPLHAFASEPTSSPMTPLTSPGTLTSPGQMHAATSTLQPPHTTMSMTNLSTIGCAANNMLPSVQGLLSQAQNNVLDAQORQLNLLSSDWLSRMERNNITQYNEMFGLVHHDTNNHSCIQNGIMQADIKPTLHMGVARDALPITMTFQLIPKSGMMQQTLLVQQTSHAQNVAGMYQMPDRARITGSSVPIAMMHQHDGQLSQTMLTSYHPLQNPMGKYPTPPSQHSYASTDKTPNNHNGHLPEGHPYLTSPSPESPDQWSSSSPNSASDWSDVTTSTPTNGSQRMFATHMFEQSHNGMQVYA

Salmo salar:

>XP_014025097.1 neurogenic locus notch homolog protein 2-like isoform X3 [Salmo salar]
MGQLPVFSSGKVLVIVVCCVRLSLALQCLDIAVKPCVNNATCATFTNGTGYCRCAAGFLGDYCHKHDKPCHPGYCLNNGNCVAVSGIPGSPSTCSCPLGYTGHCQCTPQNSTCYPNPNCANQGVCTLLSLDKYKQCAHNGTGMRCNREDSCLSGPCANGGTCSSPPGGKFGCTCPPGYLGPRLCNDTDECAASAPVCQNGRCVNTPGSYRCNCAPEGFTGRQCBETPYIPCSFSPCLNNGGTCRPTSETSYWCHCLPGFNGTNCENIIDDCPDHGCNRNGTCMDGVNTYNCQCPPEWTGQFCTEDVDECLRLQNPCTQNGGTCINSQGSYTCVVCVNGWSGLDCSENIIDDCATAACTKGSTCIDRVASFICVCPYKGTGLLCHVNDACISSPCRDGAQCDTNPIINGMFCNCAFPYIGSTCNDVDNECIIIPNPCEHHGSCVNTDGSFTCNCAQGDYGRCEITINEACSSPCQNDGTCDLRIDYDYSICIMEGFEHTHCEIDINECASSPCNLNGQCTCLDQVKRYVCWCPGLFGSGEMQCIDIDECSSSTPCNLNGAKCIDRPNGYECECAEGFSGLCENIIDDCDPEPCHHGVCRDGIATFSCDDCPGYTGSCINVQVMECHSNPCQNGRCIDLVNMYQCNCLPGTSGVNCERNVDDCASNPCEYEQCDQGINEXYKVCAPGYTGAKCDVDIHCNSSPCMSGSGCTVDKXNGEIQCCPPTHGFLCHSGTIDHCAQPQCVPHGDCVQSQSGRYNCECCSGWVGQHCDCQSSQSSPQHSKCSVDRLNGYCGSCQRPGFTGVCNEECASSPCENHGTCTVDGVNTYSLCLDPFYSKGHCHEELYPGASHPHCEYGGVCQTPDYTYFTRCPRGQGRCTEDVDECKNRQCNKRCINQSGVYKCRPGYSGLNCQITIIDDCSPNPLCNGGSCVDVEVGGSFSCDRQGFDFGERCEAEVDECASQPCQNGAVCRDYNVSFVCVCRPGFDGILCEHNIPECTESSCLNNGTCVDDINTFSRCRCPFGYGTFCFCEYQNECDSQPCKNNGTCITDGLGSYRCTCPVYNGNQCNQNFVNLCSQPLCQNGGSCSQSETTWLCKHPVGTGMYDDVPNMSQDYAARNQIQVELVCKHSGRCVNVNQAHHQCLPGYTGSGYCNEMVEDCLSNPCRNAGATMDQYGTCECMCKAGYQVNCHEYDVDECHSNPCHHGCTCINLIRNFASCAPPGTNGVNDCAAPKPGSWELRCLNNGGQVDGVGRYTCNCPGFAHGGGCVNCLSGHSCPSGLDCVQLANDYQCRCLRGYTGHRHCSMVDLQSKPCHNSGTCSMNMSVHYGTICIQPGFTGFNCEVEBVGYNCAKLRQCNQNGHCQETQVGRPHRCRQCPGFSGPRCETVHSQCNRPCLNNGGTCMKDPHYQYSCHCAHFSGRHNEGVIDFDPSPSTAPCEPYVECEQHSQGDVCPQCNSHCEQWDGDCSLHWRQPVWNCTAPVPWEFLFNRGRCDPDCDNSGCLFDSFCEQESAQSYCKYDKYCAAHYANKIKDKGCNTEACGWDLGDCSGDTPAEVAADGTILVIVLLQPEELMGDMRGFLRSLGTLHTNLNRVKMDDQKQPMPLYPPYLEHDDNGEGQPTMTLRKRELDKKEIVISGVLYLEIDNRKCSERSMDCSFSTELAASFIAEAYLEKSELPYPVSVSNPDTEPYKFNFLLYLAVGAAMIIILLIIVLGVLAARKRRKHGVLWLPDGLFLAKDD**REFPVQGL**DFGMKNKFTQDGGMIDGGQRMEEEAAPKKVTRTEDKPLPMGVDCGVDRREITLQHHKAADISLTTPQTDLEADCLDVNVKPGDGTPLMLASLRNGGASDCGLQAEEEEEESGGDEPCPNAISDLITQGATLMAQTDRTGETALHLAARYARADAARLLDAGADANAHNDMGRTPLHAAVAADAGQGVFQJILIRNRATELDARMNDGTPPLILAAARLAVEGMVEELVHCHADINAVDDHGKSALHWAAAVNNVEATLVLLKNGANRDMQDNKEETPLFLAAREGSFEAAQLLDHYSNRDTIDHLDRLPRDTAQERMHHDIVRLLDQYNLVHSPHNGFNMGHGHSLVCGNGAGYMGMRPGQKKRSRGAAGVGGVAGTAQQLKMDKAKRRKKTPGTGEGPAGVGASGNGTKAAGGLLESPLMSPVDSLESPLIYFGDAAGASAKTTNSPLLGSPPSRPLLPVPSHMLGQQQSWGLKHGYGGHMFSLLPQQMGSGHPSMSQHHQGGLLTPMNVMTSREQLPPIVTFQMMAPEGGQALLKQPGQGVQSQQQGQPGQSQQQGPTHLCGPCQMLYQMPNVSLQHSLSLGHPLHAGVMVDGQSRQQLPPYQAMQSFVVKYPTPPSQHSYATAGSETTTPGPAHPSHHPYLTSPSPESPDQWSSSSPHSNSDWSDVTTSTPTPLGNHALPPLHHTHIEQLQPGSQQTQQNFPQQRGNMQVFA

Petromyzon marinus:

>XP_032815028.1 neurogenic locus notch homolog protein 1-like isoform X1 [Petromyzon marinus]
MEPFLALPILLRLLLLLALGARISRGLCQQDSNQPCINGGTCTCFANGTGIKCKQHNFVGIYQCLDNHCASSPCQNGGTCSTVVRGGVPDYACEPLGFMDPVCLITPADNACLGVPCHNNGGTCRLLSLHRFECHELLGWSGCTEKADPCASNPCAQHGSCRAVGSRYACACRPGFSGMCRNADTDECAASPCNRNGGSCAVNPVGSYACACPAAYTGRHCETAYVFCAPSPLNNGGTCRGTGDTAYDCSLCPGFGEGRDCNVNDDCPGNRCNDGATCVDGVNTYNCQSPQWTGYCTEDVDECLQLPACNLNGGTCNHTHGGYCNVCVNGWGTDCENIIDCAIACFNAGTACHDRVSLFGCTPGKLTGLLCHLDDACSDPCHEGAICTDNPINGKAICTCRAGFTGGACNQDVDECSIGANPCEHGGRCINTQGSFRNQCQTAGTTPGRCETDINECNSMPLCNDATCLDKIGEFTCICMPGFEGRHCEIDINECGSGPCLNDGNCTDHVNGFLRCRPPFGTGMQCIDMDECASTPCNLGAKCVDRPNAYSCETEGFAGLVCELVNNECQDPDCHHGKGVGDIASFYCVCSFGPYTGFLCDSQLNECQSSPGWKGKCVLDVNRHYHCTEGVNCETNFDGAGELCQRGKCVDGVNEYRCLDAGYTGLOCDVELNECESSPCHNGGSCCKLDVADAFCEVCLPGFHGFLCYSETDACYASPCLHGTCLDHGESYRACAEAGWTGPLCEVIDIECESSPGQNGGACQEHDDGYTCRCRDGKFGKTCQKNRYECVSNPCNLNRGTCVDGVAGYTCLTDLPTFGRNCEAVMAPACQSPCHNAATCYCSESVNLSFSFCACPPGWRGATGCLDIDECAGAPCGQGGACMNTGGFRCSRCPGYTGPTCQTDIDDCSPNCPQNGSGCTDGVGAFSCKCRGFERGSRCETEVNECASNPCKNRNGGSCADYNSYTCRCRPFNGIHCEHDIETCTDSSCLNGGSCVDGINATYCLCRGGFTGSVCYQFDIECESQPQCQHGCTCLDGLGTKYCTCRPGTYKNGQALVDWCSSSPCKNSGSCVQSRSTSYRDCSHGWTGLYCDIPNMSDCDIAARNKGLSVSHLCRHGGRCIDAGNTHQCTCRGFGESYCEKEVDECTSNPNCGATCRNFLSGYKCECPVGYHGLNCDYEINECLSQPCQNGGKCIDLVRNFCVCPPGTQGILCEINTDDCNPGDPAMPGPRCFNGGSCVDGVGSFTCSCPPGFGVGERCEGDVNECLSNPCDPRGSLDCIQLVNDYKQCRPGFTGHNCEVVINTCRLEPCRNNGTCMITVNTLLGTCLCAPGYAGHACEDNAYACGNLSCRNGGTCLPDRAAGPLCVCPRAWRGPEQYHSGGGGSSACASSPCENGAACYEEVVRPFYRCVCPPLFTGPRCVRVLGPKVPGDASSGRALPVPPVPLEESCPVAECESHAGDGLCDRDCNNHACAWDGGDCSLHFPSPWRNCSVRLQCWLRFRNGECEQCNLSLGLCDFDQGLGMKNCNPLYNAYCTAHYADQHCDDQGCNSDECWDDGGDCAGEVERLADGVLLIMLPLPARVHNSANFLRQLGSLLHATVRFKIDTNGQDMIFFYYGDEARGGGPRLERAAARSLSRFVREMERPLIGSKVYVEIDNRHCYQTSDRCFSSAAADAAFLAAQATHGSLPLPLLGVSSSEVPDVVTAAPRVQVYVLLGLVLLVLMVVVLLGLVLRKRRREOGTLWFFPEGFILGPPSDKK**REFPVQGL**DVGMTLLSQSSVEDSLIDGNQNEAWLDGSPVTKRRKLEEQMLPEAEFEPVDRHWTQQLHEAADIRTAPALVIALTPPQGEADDGMVNRHOGTPTPLMVASFHGGGLDSSLDBEESSDGLFEDGTDDGASANVITDLICQGAALHAQTDRTGETALHLAARYARSDAARLLDAGADANLCPDNMGRSPLHAASVADAGQGVFQJILIRNRATDVDMVNRHGTTPPLILAAARLAVEGMAEELINCHADVNVKVDLGRKSLHWAAAVNNVEATLVLLKNGANKDMQDNKEETPLFLAAREGSYETAKLLLDHFASRDITDHDVRLPRDIAQERLHHDIVRLLEYNVVRNPSGPNGLASPPQANGAYAHGAKAGKGVRRPGNKSGVAHDAACKKCAQKKNVNGVASGGGSDGAPLLGLDGSASLSPVNSESSQSGDGTSPSLTSPHVAHSLYASMEAVGCGPPRVGHPMAFRNGAIAVASGWINPMQNVPLSQGTTHQGHSGLTSSHPQSNHRAMSSPLHPAMINQHQMILAFOQNNLYSRNPKLMEAPQHHPPEARAGGAFFQSGKMPMIQFSNQLAASQSQLLASVSGNFPPLSQQQHQIAPVQMOSFVGSEGFESFASNDYKPNKESHQSCTVLQTPVPPPEQANVSQSSQLAKREGAAPAEQFPTTPSQHSRSGSGPHAPPFTGEPHYLTSPPETPERWSTCSPRSASDWSDDGVSSPGLAARAQRRPADQQLHNLQALM

Branchiostoma belcheri:

>XP_019643529.1 PREDICTED: neurogenic locus notch homolog protein 1-like [Branchiostoma belcheri]
MRSFLGAVTLLAAAGPALVQGLVQANNPCLNGGICETDSSSGQSCVCTDGVWGVEYQCEVDPASNPCRHHGTCVVHNDATWSCDPCPLGYRDMICLTVVNDPCVTNPNNGGTCCELITIDEYRCNCQPGYTGDGTCVVHEYCSQPKNGGTCSTSESGYTCACLGGFEGSTCQTDIDECAGTQNGGQCNQTMGFTCTCPKERTGRCLBEEYIPCSFSPCQHGGTCESEYDTEYTHCMSGFTGDDCEVNVDDCVHLCENGAACVQDGVNEYTCTPSEWQGRYCNEDVDECMQSPNICNSGTCHNTVGGYSCVCVNGIWDGDCSENFDDCATAACHFACGTACHDRVGFMMCECAPGKTGLLLCHLDDACESSPCEAGIACDTNPFVNGPCTCTCPDGYAGQLCAGDLCSLGENPCEHDCGNPNVPGSFCTCTGDTGDRCEVNEINCASNPQNGQCTIDICEFRACMPGFAGLDCLCTDIDAGVSCPLCINGICRDNINKYCECEDPGYEGTTCEVNNINECASGFCRNGAHCTDLVTATYCTCLEGFTGTDCENIIDCQSNQCGHGTCDVEVASFTCSCEPGYNGPLCESPVDECDSDPCQNGGTCEDLVNGYRCNCLPGTSGDNCENVQDDCTGNLCVHVGQDGLNTYTCMCDGGYEGENCBESIDECASSPCHNGGICHLVNAFSCBCEPFGYHLLCYHLLCYNECESSPCEHGTQDQGINDYTCTCTGYEGNCKNDVNIDECASNPCQHGEGQDDGIGRYECPCLPGYEGVNCQITDCEGQNPQNGGQGLDGVNNYQCHCELPFVGINQCIELACPENPCNANGSNCISPNADYQTTFTCDCAEGFEGTCADDINECQSNPKNCQNIINLEGDFRCDCLDGLSCVNIIDDCDPPCHNGGTCNDGINSYTCSCMPGFGGTNCEIDIECYSNPCQNGGQCTDAVNGYACDVLGFTGTNGCTNKKDDCTSSSCFSGGTICDGINFTTCQCPGFTGSGNQHIEINESCHFPQNGATCVDQTYGFSCICTGYEGVNTCQKDLCDASDRCRNGGTCQSGDRYECLEDEWTGLICDMTKTYSACAAASERGVLGELCQNGGSCVDTGNSHNCNCPAGRYGSCSEIDECASSPCQNGAQCRDGLGTYSVCVRAGYQVNCQEINEICISNPQNGGTCIDMVNRYRCSPPGTQGLLCEINNDNCFAGACYHDTGTVDGIETTCRCRPGYVGRCEGDVNECLSNPCDAEGTQDCVQLENDRYRCDCKPGYTTG

RRDPVGQEVGMKSFT

[illegible][illegible]

XP_032230096.1 neurogenic locus notch homolog protein 1 [Nematostella vectensis]
MSSVLLNFWFLTLFVNAAAGFYQRLKTSSEGKTRPRLAEKLPKYCGSHSTPCENIKDCTKPNQDQICDEBDCNICTDPTTNCCTGCTNGGVCSEAGGVVTCSPKPNFTGAARCELDVDECTTSLSPQC
GSGVTCDSNVYGVGMCRCITGWDGADCSVNIEDCKQNDFFKCEAGKCTVDKJIGSYICICPPGKTGLNVCDFEACASNPSCANATCTVYGFSGKASICNSGWTGKNCDDVIECEBQDSSTCYPHGCTCRDI
PGSFVGCDCVPFGAGACREINCEBSPNVHGLLCKDQNPFRKFCACSKGQYTGRLCDVEINCEBSPNLGNCCQDGLNGYSCICTQVGVVGEICQTYNDDCASNPQDCQDQJGDIACPLGLFTGKCK
CETNTNCECAGNPMCMNGTCIDGINSFRCQCPGLGFTGNRCETEIDECSSPCQNGGCTCKDKINGVYVICPPGASGTHCENDPNDCPANACQNGGVICIDGMNTYSCKCHKPGFTGFGSCGVVNECASSPCRN
GCTEDGGVAYQYCCRDGVTGKNCVRLISDCHITQNGACSVSTPYASQCKPGYTGQYCTEDVDECAARPVCNAGVCADGVNGFICRCDPFGTGDRGCINVDQCSSPCVHGSSGIDSLINTYTCQY
CKPGFTGPRCEIHINCEBSSDPGKCEGDCSRIAGSYSCYRPGYTGSNQYGLPDRACNDPCRNAGTCRTGDELDSPFCECKPLGKYGITCDPVCBSAVAGAITCANGGTGCTPSNQGVSCTCKPGFTGYSYCR
TNIECAKCEPKCYKQACHDAVANYTCTTAGTGTGNKDININECASNPQCRGSLDLNLVNGLYLSCCKPGYIGKHCENIADDFVACNFGNGSCVDGIAEFKCTCPLFGSGSREVDVDECASSPCSAJLT
QCEINNI GAYHCKQKQFGLGRHCLDINELCSYPCRNCGEKGDKAGYEYTCGLCPHGSGFDCERRVYCTDQPCLNSTGTCRTVHNTYSCSPRGVYGKCEWNNKDCAPACRNGGTIDGYSYSCYKCP
LPGFAGANCEGIDNCSYCPCKNGGSCRDIVNGYCKDCPSMKITGKNCETVVLQDCVPVNCAGKFDGGKCNPKNCTHENCWDTGTSCLGIEPWSNCTYTGTSKACYQVANGVCDRENTGCGCLDFDGGC
KPSVPGKCAADYCAARFANAEACTCNVACQNDGLDCSKFKFEIVETGLIVLVVLEAPFMNRSVFMRLSRTLNTAIFKSDSGEKLKVYVLPSPAPVPAERKRKRSAEIKFVIDSJLTSHRFR
RAAQVQSGVQVQINILNDRGCECTFQSTQEAQYILGAQSTGKLNLYPEKYSVTEKEPTVETPGTGPELWIALILCVGVLPIFVGLAGGKRVYITKLWLEPGVRRVPHQSS[Redacted]SHMS
MNRKSDLEEEBAGVGDLTLPQEARADAKRVLEEVDSQVRKVESEKDTQWRLHREAADTVNRNLTALTPQGESEKPGITGVDAARGPGETLPHLASCRTGLDRCSSIDDDKESDGGAMV
SDLLALGASYGARTDIEKETPLHLAARHSADAAKRLLHAGADPNARDKLGRTPLHLAVGADAQGVQILLNRNTDLEAAMEDGTTPLILAARLDLLDIVDKLIKASCKVMNVDAQGSALHWAAMVN
SHEVTSLECNKNAQNKQDQKQGTPLFLGAREDSLEAVRILLYSANRMIADMDKTFEEVARQANDIVELSDSSGSCSAPAAPTSPDQRSPLNGTASPDSPMDISQGNKVYTHFFVSAGTTR
PTKNTSTTRGARSQVQENMGAKKKRKKRRLDLPNGNKASQGGASSTYSPYGLKCSGSGANSPAPFVNVNGLSPQGSAGTSPSNSTLSLPQSHSDSPMSQFPLSDSPFDGGLDLDIFDL
TDQDLDHGFASPCACGLRGSTDLHDLSIMLPEPTIGPVQNDSSVPTTSCMYPPLRSHVAFGHTAPRLYSAHSSPNLCADNESRQLIVASHNGYPSNQSSIQACKLSNRLEEHVMMETTLHHNNQSMC
VPVESGPRFREKHTTTPSAHSGTSSYSDSPQKPLISYLTSPSPSPKDWSSACVSSDWSNIC

XP_018853114.1 PREDICTED: neurogenic locus notch homolog protein 1-like [Amphimedon queenslandica]
MDTRTKAAIIYLGVGSLVFSVAQNLCFVNCTSNNGTCTIENGSDVCMCPSPYSTGMTCEIENVVSGCSTTKCKNGCTCNDEDGVRKCDLPIFTGQFCDSLNMGDCSNPFCNEATCSNFFGAFCVSCPPG
FTGRCQCTETDNDCAASNPCADGGTCTIDEVNGTCECPGPTGNSCNVDDCRGSDVECHNMGDGLDLVDVYDCTEEFGGRNCIEBSCDPLDNLTKCENNGFCFHRNTSSCSCTGYGTTCYETELNEC
DSNPNCNGCTCVDKIGTGSFCSCNPFPGYTQCEEVIDMCPQCYNMGACINSSDPCFCRQGYTGQCLVDEIDCLSSCPGNGCNTCEIEMDFGSCGLPGYSGTGQCIDESCSQCNQDGTCTIAGNLT

SCVCSLDYTDENCTTFFITPCYFEPCLNGATCINEDLDNYTCSCLPGFTEEDCSVNIDDCGSNPCQNEGTCLDLVNDYQCDCSAGYTGSDCQTDIDECLMTPCFNNGTCTDLVNSVSCECPPGFNGSLCQ
NNINECSSSPCSSGSTCIDEIDDFTCCLPMGLTGTCQDISIIDCSMDPCGNNGTCTDTPGGYECSSSGYTGVMCMVNINDCLPHPCNNGTCIDGINEYVCICPEDYTDNCETPIDHCDNPPCSSLAT
CITNPGGYQCICPIDFTGTDCDFDINDCQPNPCNNGTCSDLIGTFNCSCPLGFEGSICEYDINECASPLCLNGGNCITDLVNGYSCSPHGFNGTNCENSTITTTCESVVCENGGMCDPTTGFECCLCPN
GYTGPHYCQNNIDDCLSNPCLNNATCIDEIANYTCECTEGFDCRNCAIDTDLCSPPCFNNGGTCSSETSDFSFTCTCLGYFGSHCQNTLDPCSSSPCLNSGICTNVNGTNFSCACSQAYGGERCEIKLFPPD
CLDMPCLNNGTCAELVSGSGNIGGSGAGEPGPRIYCCQPLGYAGEFCENITDLCVSSPCKNNATCIGDSANFTCTCLPGFTGTLCETELTGCHTELYPCLNGGECMEMDGGQFMCNCAPGFTGPLCGYGIN
ECRNQPCLNNGGTCRDFFRYYVICPPNFTGTDCESMIDPCTNIDCNGGSCIGDMGTYTCQCDPGWTGLQCESEINECDGVDCITNGTCVDLINNYTCQCSDGFTGQFCEINIDDCAGINCNNGTCTVDGIG
SYQCDCLLGYTGPSCDTIIIDCAGMPCMNNASCIDLFNNYTCVCSDGFTGRFCEVNIDCLNINCNNGSCEDLINDHMCNCFPGFTDQRCETDINECDGNPCNDGTCTDGINSFSCCPPDYTGDTCDT
EINLCLEMQPCLNNGTCTSDKIEGPIYNCSCSVPLYSGDNCEQINCSLSPCQNNATCTGNLTGDYTCCHCSENYGTHCERFDYCHSNPCQNDGTCTINGSPGNLISDTFLCICMPQFNGSDCSMELS
PCSIDPCMNGGTCTVEDGSTYCCQCPVGYTGNNCEVFSSDTPYFNGDSYTLVPYSPNNNNSQSLINLHFRSSQSGLLLYISEEDHSSYLSLGEAGLLSLMRQEGSFQSVARYHPVSDDRWHYVEV
TQNGLEIKTEIDGYPNSTSLIDMFLIFEPAVTYIGGFNDYTSLPFAVLQSSGFIGYINATIQLGGEALHIIDDSIAGRDIAGGEAAGSCGPETCSNGGICVEESQSSFLCLCPIGFRGDTCEQDTEIIV
PYFNTRSyaIVSNDAFSLYGGIDIDITLHTSSPNGLIYYLYDSTNVTNDYFTLYLEEGGIGIEYSMEGSAHIVSYQGNVSDNEWHLMTVQLNTSGLYLILDGSVLVLYSNNATLSSIIYLTSPFLGGLPN
GLIADSVSGSGLNGCIRDVQISNTSLGLIENNVLVYGLGLECPQSLCPLVQCLNGGTCVSDSVSFGFECSCSPSGYNGTYCEVLLSTCIPNPFCLFDGVCTDFNNMTYSQCQCTLGRQGRICDEELNITVP
AFYGNsYLAYSSLSITNVQSNLILSLTFKTPSPSGLLLFNHGSNTDFSQYVSI SLVNSSVYKFDLGSGLATISSPITLGLNQWHTITAYRTGRVGFRLVNDEELNTSLGLTNGLNLIAGDMWLGGT
DRFNIISQHAGVGTGLTGCISSSVNGIISINLVSSAERGLNIGECNMTSCSSFPFCFNGGTCTETGSSFFICQCPAGYEGGLCGLQTFSCLSPPCGNGGTCTIEGVAEGGYNCLPLGFGGNNCNEMLQVST
PSFNRTSYQEYSSPAPISLSTIISLSFHPTSSNGLILYIGDVSTTRDFLSLSLVSGRIQLRYDLGSGPAI IASPSV I PLNQWTSVTNVRVRKDVVLVVDVSVSTNGSSPGFAGLLNPAGNLYIGGGAGGV
GGYQVSPNAGSHVGLTGCVDTATLRVNSFGLGAVISSRGVIQCQVDPCSHSPCQNGGSCVSSDLTYSCVCPLGYSGDQCQEISNATEGAAISQCPTSVA CNVNPNCLNGGKCI AVLNGIIEERCQCSLP
FAAGAKCEQRVSFSSAFFAGDGYLLFFAVNIPLSSITIHTEIRLSIIPSNGSGLLLYIGHANPSTGNVLLVGMNEGVLEFRFQLGSGVGLVETSQPLAIGQQHNITLLRTDYRGRILMSQGNNTTVFTDG
MSQSSSRHLNLSPYDFVFLFGLGAPNVPLISQQVYQTGFSGCLVSVVQLGYSMNPEVPVPTDSSYGENVITCS

Alignment:

XP_012554603.1[H.vulgaris]	MVFYMLLLFHVLMVACNTNVKGYVDSKQNNFEYAANYKCPNGWQQRCEKCYLYVNESKQ	60
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	WTDAQYYCKQNGGNLVTIKEDAVNLFRLARYVQYSSRLAITIWTGLHARKVHKEFQWVDNS	120
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
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XP_019853114.1[A.queenslandica]	-----	0
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NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	DNGKCVSKHLFCDSKNDCGDFSDEKNCTKCNEHYTAQEGSISSPNFPQHYGNRDCRWLI	240
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	EVESYIIIEIKFLEFFIENSFDWVEVFDGPTLASKSFGKFSGNFKPEVILSSSSKILVHL	300
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	KSDKSTSDDKFFARYKAVKGCNVDLIINSNKPEYISSPNFPLNYPDNTKCEWTIRNEDP	360
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	SKILTFQLELETEENDFIEVRDGLTEDNALLGKFFGNFSNIQKRHIFTSNFKMHVKFQS	420
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0

NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	NFQLNQKGFRVIFSGCTATINATHGTISSPNFGVGNYPNNILCSWTVHAQTDEKVSIVIF	480
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laervis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	HSFDTEYKQDVTVLRTCDDVMIKECYGSNKTTLGKEMPLLEPIVFNSSCFKVIKSDETY	540
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laervis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	SLEGFNATFSIGCPMLPAINGGSFRQDQKFYGASVEYKCDRSFRIKSENGNVRKCMYGGN	600
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laervis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	WSEPAFPCEEINCGHPGTIENGGFIEIYPLNSTFVFMSTVKYSCNVGYILVGEPNRVCQVN	660
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laervis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	STWSGGVERKCEVLKCPDPGTPVNGTRSGNEFNVGSSITFSCEKGFRRHGARTITCGITG	720
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laervis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	KWSSETPLCKVVVCQLPSFSLNTIISSSSIGFNTPYKTVLHISCKKGFELIGSVNITCTE	780
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laervis]	-----	0
NF_001238962.2[G.gallus]	-----	0
NF_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	SGAWKPDVPQCIDINECLNNPCRGLGSQCTNLMGSYKCTCKSGFRQIDETTCEDIDECKS	840
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0

XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NP_001238962.2[G.gallus]	-----	0
NP_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	SGKTVKCNQKCTNIDGGYFCSCEDGYFLYDGDNKTVNRVEAEESFVNHTCLGNPCKLPKI	900
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NP_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NP_001238962.2[G.gallus]	-----	0
NP_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	PENGYILNYGNRYPTTEITFCQDKGWIVDGDLSIKCLKNGSWGSGISDCIAARCNPDPVP	960
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NP_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NP_001238962.2[G.gallus]	-----	0
NP_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	NSSSVVDGGLVKGQYSQGTIYTYTCINGYEIISGNSKRMCSQNATASFWSGSSPVCERVS	1020
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NP_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NP_001238962.2[G.gallus]	-----	0
NP_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	CGPLENPKNGHVNITGDKYGDSSKFFCDGGYIITGNDSSTCQANGRWSASSPFCLASPCP	1080
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NP_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NP_001238962.2[G.gallus]	-----	0
NP_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	DPGIPINGEIIIGLISLDQTTIFRCLVNGSILIGDNKRTCIFNKSTGLNQWNGSQPFCKDT	1140
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NP_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NP_001238962.2[G.gallus]	-----	0
NP_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	STPTFKFCPMSTIEFTLPQSEKSMVNWTLPTLTDNVHLLNITVSPDYVSPMVMPAGLN	1200
XP_019853114.1[A.queenslandica]	-----	0
XP_032230096.1[N.vectensis]	-----	0
NP_001245510.1[D.melanogaster]	-----	0
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----	0
XP_014025097.1[S.salar]	-----	0
XP_018114267.1[X.laevis]	-----	0
NP_001238962.2[G.gallus]	-----	0
NP_035058.2[M.musculus]	-----	0
Q04721.3[H.sapiens]	-----	0
XP_009243797.2[P.abelii]	-----	0
XP_012554603.1[H.vulgaris]	IITYTATYKDGSTAVCEVKINVQDKEIPKIFCPKNIVIKSDLSSKVFWSGDIYTDNVGIK	1260
XP_019853114.1[A.queenslandica]	-----MDTR-----	4

XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	-----MQSQSRRRRSRAPN-----TWICFWINKMHAV----	27
XP_019643529.1[B.belcheri]	-----	0
XP_032815028.1[P.marinus]	-----MEPRAL-----	6
XP_014025097.1[S.salar]	-----MGQL-----	4
XP_018114267.1[X.laavis]	-----	0
NF_001238962.2[G.gallus]	-----MARGAG-----	6
NF_035058.2[M.musculus]	-----MP--A-----	3
Q04721.3[H.sapiens]	-----MP--A-----	3
XP_009243797.2[P.abelii]	-----MP--A-----	3
XP_012554603.1[H.vulgaris]	NVIFNPNG--TILESNKYHKVTMTVEDISGNSDSCVMEIYVEGCGCTQRTCDYKQRNGQ	1318
XP_019853114.1[A.queenslandica]	-----TKAAILYLLVGCWLSFS-----VAQNLCFVNTCSNNGTCYI-ENG	44
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	--ASLPASLPL-LLTLAFANLPNTV---R-GTDTALVAASCTSVGCQNGGTCVTQLNGK	80
XP_019643529.1[B.belcheri]	---MRSLFAVVLALLAAGPALV-----Q-----GLVCQANNSPCLNGGTCETDSSGQ	44
XP_032815028.1[P.marinus]	--LPL-LRL-LLLLALLGARLS-----R-----GLQCQDSNQPCINGGTCETFANGT	50
XP_014025097.1[S.salar]	--PVF-SSG-KVLIVTVCCVRLS-----L-----ALQCLDAVKPCVNNATCATFTNGT	48
XP_018114267.1[X.laavis]	--MGVQAVF-GLCVL-LLGMPC-----D-----GLQCRGASEPCVNEGRCITSDDGS	44
NF_001238962.2[G.gallus]	--PAPAALF-GLVLAVLSRAEPA-----A-----ALQCMDDSKPCVNEGKCIPYQNGT	51
NF_035058.2[M.musculus]	--LRPALR-ALLWLWLCGAGPA-----H-----ALQCRGQEPVCVNEGTCVTYHNGT	48
Q04721.3[H.sapiens]	--LRPALLW-ALLALWLCCAAPA-----H-----ALQCRDGYEPCVNEGMCVTYHNGT	48
XP_009243797.2[P.abelii]	--LRPALPW-ALLALWLCCAAPA-----R-----ALQCRDGYEPCVNEGMCVTYHNGT	48
XP_012554603.1[H.vulgaris]	SVCTIAPGVVPTDVII-----S	1335
XP_019853114.1[A.queenslandica]	DVCMCPSPSYTGMTCEIEVVSGQSTTKNGGTCND---EDGVVRCDCLPIFTGQFCDL	100
XP_032230096.1[N.vectensis]	-----	0
NF_001245510.1[D.melanogaster]	TYCACDSHYVGDYCEH--RNPCNSMRCQNGGTCQVTFRNGRPGISCKPLGFDESLSCEIA	138
XP_019643529.1[B.belcheri]	GSCVCTDGMVGEYQCE--VDPASNPCRHGCTCVVH---DNATWSCDCPLGYRDMICLTV	99
XP_032815028.1[P.marinus]	GICKQHNFFVGIYQQL--DNRCASSPCQNGGTCSTVVRGGVDPDYACEPLGFMDPVCLTP	108
XP_014025097.1[S.salar]	GYCRCAAGFLGDYCHH--KDPCHPGYCLNGGNCVAVSGIPGSPTCSCPLGYTGQHCQTP	106
XP_018114267.1[X.laavis]	AYCKCPDAFVGEYQCL--QNPCEVTVCLNGGSKV--SPDLSKGVCTCAPGFSGENCKQP	100
NF_001238962.2[G.gallus]	GYCKCREGLDGYCQY--RNPCESNTCKNGGTCET--TSLIGKATCKCAPGFTGEDCQYS	107
NF_035058.2[M.musculus]	GFCRCPEGLGEYQCH--RDPCEKNRCQNGGTCVP--QGMLGKATCRCAPGFTGEDCQYS	104
Q04721.3[H.sapiens]	GYCKCPEGLGEYQCH--RDPCEKNRCQNGGTCVA--QAMLGKATCRCASGFTGEDCQYS	104
XP_009243797.2[P.abelii]	GYCKCPEGLGEYQCH--RDPCEKNRCQNGGTCVA--QAMLGKATCRCASGFTGEDCQYS	104
XP_012554603.1[H.vulgaris]	CNLN-----CFQNKTTFRVSNTEFEKTSNVMCIPNKGWENKSPSGCVERKPLISCLKGS	1389
XP_019853114.1[A.queenslandica]	LN-GC-DSNPCFNEATCSNF-FGA-----FVSCSPPGTGRQCTDNNDCASNPADGG	151
XP_032230096.1[N.vectensis]	-----MWSVLNIFWF-LTIFVNAKA---	19
NF_001245510.1[D.melanogaster]	VPNAC-DHVTCLNGGTCQLKLEE-----YTACANGYTGERCETK-NLCASSPCRNGA	190
XP_019643529.1[B.belcheri]	VDPNC-VTPNCPNNGGTCELITIDE-----YRCNCQPGYTGDTCDDV-EHCYSQPCKNNG	151
XP_032815028.1[P.marinus]	ADNAC-LGVPCPNNGGTCRLLSLHR-----FECHLLGWSGKTCEKA-DPCASNPCAHHG	160
XP_014025097.1[S.salar]	QNSTCYPNNPCANQGVCTLLSLDK-----YKCCQAHGWTGMRNRE-DSCLSGPCANGG	159
XP_018114267.1[X.laavis]	VASVCSLTQPCMNNGGTCRLLTLEH-----YECICPFGRGKDCEFI-DACASQPCANGS	153
NF_001238962.2[G.gallus]	ESHICYVSQPCNLNGGTCPHSQET-----YECVCPPGYTGKDCQWI-DACTSQPCANGS	160
NF_035058.2[M.musculus]	TSHPCFVSRRPCQNGGTCCHLSRDT-----YECTCQVGTGKQCQWT-DACLSPCANGS	157
Q04721.3[H.sapiens]	TSHPCFVSRRPCNLNGGTCCHLSRDT-----YECTCQVGTGKQCQWT-DACLSPCANGS	157
XP_009243797.2[P.abelii]	TSHPCFVSRRPCNLNGGTCCHLSRDT-----YECTCQVGTGKQCQWT-DACLSPCANGS	157
XP_012554603.1[H.vulgaris]	LSIDFTTGDNTNEKPLDIFTFLNNLNKSTCSFIYQTGNLISNGTSVAGDFKILSHDDG	1449
XP_019853114.1[A.queenslandica]	TCIDE--VNGYT-----CECPPGFTGSNCS-----	174
XP_032230096.1[N.vectensis]	-----AGFY-----YQRLKTSEKTCR-----	36
NF_001245510.1[D.melanogaster]	TCTALAGSSSFT-----CSCPFGTGDTC-----	215
XP_019643529.1[B.belcheri]	TCTS-TE-SGYT-----CACLGFEFGSTCQ-----	174
XP_032815028.1[P.marinus]	SCRA-VG-SRYA-----CACRPFSGPMCR-----	183
XP_014025097.1[S.salar]	TCSSPPG-GKFG-----CTCPCGYLGRCL-----	183
XP_018114267.1[X.laavis]	TCPL-NE-NQYS-----CTCQAGYTLKCE-----	176
NF_001238962.2[G.gallus]	TCTV-SG-HKFS-----CICQSGYTGQKCE-----	183
NF_035058.2[M.musculus]	TCTS-VA-SQFS-----CKCPAGLTGQKCE-----	180
Q04721.3[H.sapiens]	TCTT-VA-NQFS-----CKCLTGFTGQKCE-----	180
XP_009243797.2[P.abelii]	TCTT-VA-NQFS-----CKCLPGFTGQKCE-----	180
XP_012554603.1[H.vulgaris]	VIPLLNGLHECKTILLKDLDFKTLNLLQTLSSVDIKLLNISSCCPLNKSYYCCPTGHLIK	1509
XP_019853114.1[A.queenslandica]	-----INIDDCRG-----DVECHNDGECLDLVDDYDCDTEE--	207
XP_032230096.1[N.vectensis]	-----PRLEAKL-----YKPF-----	46
NF_001245510.1[D.melanogaster]	-----YDIEECQSN-----PCKYGGTCVNTHGSYQCMCTG--	246
XP_019643529.1[B.belcheri]	-----TDIDECAGT-----NPCQSGGQCNQTMGSFTCTCPKE--	206
XP_032815028.1[P.marinus]	-----ADVDECAAS-----PCRNNGGSCANVPGSYACAPAA--	214
XP_014025097.1[S.salar]	-----NDTDECAAS-----APVCQNGRCVNTPGSYRCNCAPG--	216
XP_018114267.1[X.laavis]	-----MDVNECTSP-----GLCKNGGTCENLPGSYRCQCHPG--	208
NF_001238962.2[G.gallus]	-----IDVNECATS-----GLCHHGGTCINLPGSYRCQCPQG--	215
NF_035058.2[M.musculus]	-----ADINECDIP-----GRCQHGCTCLNLPGSYRCQCPQG--	212
Q04721.3[H.sapiens]	-----TDVNECDIP-----GHCQHGCTCLNLPGSYRCQCPQG--	212
XP_009243797.2[P.abelii]	-----TDVNECDIP-----GHCQHGCTCLNLPGSYRCQCPQG--	212
XP_012554603.1[H.vulgaris]	TTGLTVKASY-CIPG----LGMYNHSTNN--KCLNCPVGFYNDLEFADQCKRCPNETN	1561
XP_019853114.1[A.queenslandica]	FGGRNCEIESDCPLDNLTCENNGFCHRNST---SCSCITGYTGTYC-ETELNECDS--	260
XP_032230096.1[N.vectensis]	YC-----GSHTPCENIKDCTKPN--QCICD-EDCGNIC-TDPTNCTT--	86
NF_001245510.1[D.melanogaster]	YTGKDDCTKYK--PCSPSPCQNGGTCISNG-LSYECKCPKGFEGKNC-EQNYDDCLG--	299
XP_019643529.1[B.belcheri]	RTGLCEEEYI--PCSPSPCQHGCTCESVDTYEYTHCMSGFTGDDC-EVNVDCCVD--	260
XP_032815028.1[P.marinus]	YTRGHCETAYV--PCAPSPCLNGGTCRQTGDTAYDCSCCLPGFEGRDC-DVNVDDCPG--	268
XP_014025097.1[S.salar]	FTGRQCETPYI--PCSPSPCLNGGTCRPTSETSYWCHCLPGFNNGTNC-ENNIDDCPD--	270
XP_018114267.1[X.laavis]	YIGQRCESPFI--PCSPSPCMNGGTCRQTSEFAYECNCLPGFDGKNC-ESNIDDCPS--	262
NF_001238962.2[G.gallus]	YTHRCESNYV--PCSPSPCMNGGTCRQTSDTFECNCLPGFEGKNC-EKNVDDCPN--	269
NF_035058.2[M.musculus]	FTGQHCDSYV--PCAPSPCVNGGTCRQTGDTFECNCLPGFEGSTC-ERNIDDCPN--	266
Q04721.3[H.sapiens]	FTGQYCDLSYV--PCAPSPCVNGGTCRQTGDTFECNCLPGFEGSTC-ERNIDDCPN--	266
XP_009243797.2[P.abelii]	FTGQYCDLSYV--PCAPSPCVNGGTCRQTGDTFECNCLPGFEGSTC-ERNIDDCPN--	266

XP_012554603.1[H.vulgaris]	NLKVQSDSCTKMAAGSYSTGLEP-----TCRK-----C-DYGEY	1596
XP_019853114.1[A.queenslandica]	-----NPCNN-GTCVDKIGSFSCNCFPGYTQQCEEVIDMCQ---PQPCYNGAMC	306
XP_032230096.1[N.vectensis]	-----GWCNTGGVCSSEAGGVVTCSPKNTFGARCEIDVDECTTL-SQPCQNGGTC	135
NP_001245510.1[D.melanogaster]	-----HLCQNGGTCIDGISDYTCRCPPNFTGRFCQDDVDECAQRDHPVCQNGATC	349
XP_019643529.1[B.belcheri]	-----HLCENGAAACVDGVNEYTCTCPSEWQGRYCNEDVDECMQS-PNICLNSGTC	309
XP_032815028.1[P.marinus]	-----NRCDNAGTCVDGVNTYNCQCSPPQWTGGYCTEDVDECLQ-PNACLNGGTC	317
XP_014025097.1[S.salar]	-----HQCNRGGTCMDGVNTYNCQCPPEWTGQFCTEDVDECLQ-PNTCQNGGTC	319
XP_018114267.1[X.laavis]	-----HLCQNGGTCVDGVNTYNCRCPPQWTGQFCTEDVDECLQ-PNACQNGGTC	311
NP_001238962.2[G.gallus]	-----HNCQNGGICVDGVNTYNCRCPPQWTGQFCTEDVDECLQ-PNACQNGGTC	318
NP_035058.2[M.musculus]	-----HRCQNGGVCVDGVNTYNCRCPPQWTGQFCTEDVDECLQ-PNACQNGGTC	315
Q04721.3[H.sapiens]	-----HRCQNGGVCVDGVNTYNCRCPPQWTGQFCTEDVDECLQ-PNACQNGGTC	315
XP_009243797.2[P.abelii]	-----HRCQNGGVCVDGVNTYNCRCPPQWTGQFCTEDVDECLQ-PNACQNGGTC	315
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XP_012554603.1[H.vulgaris]	QSQVGAYNCIKCPYNLTSRSGSENISEKACQSPGTYSSSTGLEPCTKCAKGLFQNEIGR	1656
XP_019853114.1[A.queenslandica]	VSSINGFDCFCRQ--GYTGQFCQVDIDECLSS-----PCQNGGNCCTEMVN	349
XP_032230096.1[N.vectensis]	SNVYGGVMCRCT--GWDGADCSVNIDECKQN-----DPFPRCQHGCTCVKIG	182
NP_001245510.1[D.melanogaster]	TNTHCSYSICIVN--GWAGLDCSNNTDDCKQA-----ACFYGATCIDGVC	392
XP_019643529.1[B.belcheri]	HNTVGGYSCVVCV--GWIGDDCSSENFDDCATA-----ACFHGATCHDRVG	352
XP_032815028.1[P.marinus]	HNTGGYNCVVCV--GWTGEDCSSENIDDCAIA-----ACFNAGATCHDRVA	360
XP_014025097.1[S.salar]	SNIQGSYTCVVCV--GWSGLDCSENIDDCATA-----ACTKGSTCIDRVA	362
XP_018114267.1[X.laavis]	TNSNGGYNCVVCV--GWSGDDCSQNIDDCATA-----ACANGSTCIDRVA	354
NP_001238962.2[G.gallus]	TNHNNGYACVVCV--GWSGDDCSKNIDDCFTA-----SCANGSTCIDRVA	361
NP_035058.2[M.musculus]	TNRNGGYGCVCV--GWSGDDCSSENIDDCAYA-----SCTPGSTCIDRVA	358
Q04721.3[H.sapiens]	ANRNGGYGCVCV--GWSGDDCSSENIDDCAFA-----SCTPGSTCIDRVA	358
XP_009243797.2[P.abelii]	ANRNGGYGCVCV--GWSGDDCSSENIDDCAFA-----SCTPGSTCIDRVA	358
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XP_012554603.1[H.vulgaris]	SYCKLCPSSGIYLMGEA-----TSEANCPKSNACDE	1688
XP_019853114.1[A.queenslandica]	GFSCGCLPGYSGTQCEIDSCSSQPCQNDGTCIANGLTYSVCVSLDYTDENCTFTITPCYF	409
XP_032230096.1[N.vectensis]	SYTCICPPGKTLGLVCFND-----DECAS	205
NP_001245510.1[D.melanogaster]	SFYCQCTKGKTLGLCHLD-----DACTS	415
XP_019643529.1[B.belcheri]	FFMCECAPKGTGLLCHLD-----DACES	375
XP_032815028.1[P.marinus]	SFFCQCPGLKGTGLLCHLD-----DACVS	383
XP_014025097.1[S.salar]	SFLCVCPYKGTGLLCHVN-----DACIS	385
XP_018114267.1[X.laavis]	SFICVCPGKIGLGLCHKN-----DACFS	377
NP_001238962.2[G.gallus]	SFSCICPEGKAGLLCHLD-----DACVS	384
NP_035058.2[M.musculus]	SFSCLCPEGKAGLLCHLD-----DACIS	381
Q04721.3[H.sapiens]	SFSCMCPEGKAGLLCHLD-----DACIS	381
XP_009243797.2[P.abelii]	SFSCMCPEGKAGLLCHLD-----DACIS	381
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XP_012554603.1[H.vulgaris]	KPCRNGATCNAGN--YSYTCCKPGWTGVNCEVDIDEC---ASSPCGRHGTCTNLINDFN	1743
XP_019853114.1[A.queenslandica]	EPCLNGATCINEDL-DNYTCSCLPGFTEEDCSVNIDDC---GSNFCQNEGTCTDLVNDYQ	465
XP_032230096.1[N.vectensis]	NPCSANATCVTS-FSGKASCICNSGWTGKNCDDVDIKECEG-DSSPCYHGGTCRDI PGSFV	263
NP_001245510.1[D.melanogaster]	NPCHADAICTSPINGSYACSCATGYKGVDCSEDI DECDQ---GSPCEHNGICVNTPGSYR	473
XP_019643529.1[B.belcheri]	SPCNEGAICDTPNPVNGQPICTPCDGYAGQLCMQDIDECSL-GENPCEHDEGCNNVPGSFT	434
XP_032815028.1[P.marinus]	DPCHEGAICDTPNPINGKAICTCRAGFTGGACNQDVDECSI-GANPCEHGGRCINTQGSFR	442
XP_014025097.1[S.salar]	SPCRDGAQCDTPNPINGMFCNCAPGYIGSTCNDVNECII-GPNPCEHGGSCVNTDGSFT	437
XP_018114267.1[X.laavis]	NPCHIGSLCDTNPILTGQAICTCPPGYKGTACTEDIDECSLVNSNPCEHAGKCVNTEGSFY	444
NP_001238962.2[G.gallus]	NPCQKALCDTNPVNGHYICTCPQGHKGADCTEDVDECAMANSNPCEHAGKCVNTEGSFH	444
NP_035058.2[M.musculus]	NPCHKALCDTNPVNGQYICTCPQGYKGADCTEDVDECAMANSNPCEHAGKCVNTDGAFH	441
Q04721.3[H.sapiens]	NPCHKALCDTNPVNGQYICTCPQGYKGADCTEDVDECAMANSNPCEHAGKCVNTDGAFH	441
XP_009243797.2[P.abelii]	NPCHKALCDTNPVNGQYICTCPQGYKGADCTEDVDECAMANSNPCEHAGKCVNTDGAFH	441
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XP_012554603.1[H.vulgaris]	CTCIKIGIIGKQCEINIDDKNDTCRNGGICNDLVDDFKCLCAAGFEGKRCEINKNECEPN	1803
XP_019853114.1[A.queenslandica]	CDCSAGYTGSDQCTDIDECMLTPCFNNGTCTDLVNSVSCCEPPGFNGSLCQNNINECSSS	525
XP_032230096.1[N.vectensis]	CDVCPGFAGARCEBINECESNPVH-GLCLDYQNKFEACACSKGYTGRLCDVEINECDN	322
NP_001245510.1[D.melanogaster]	CNCSQGTGPRCETINECESHPCQNEGSLDDPGTFRVCVMPGFTGTQCEIDIDECQSN	533
XP_019643529.1[B.belcheri]	CTCTDGTGDRCEVINECASNPQNGTCTIDDIGEFRCACMPGFAGDLCECTDVDECASS	494
XP_032815028.1[P.marinus]	CQCTAGTGTGPRCETINECSMPCNDATCLDKIGFTCTCMPGFEGRHCEIDINECQSG	502
XP_014025097.1[S.salar]	CNCARGYDGRPCETIDINECASSPCQNDGTCLDRIGDYSCIMEGFEHGTCEIDINECASS	504
XP_018114267.1[X.laavis]	CECSKGTGTGPRCEMDINECLSEPCQNDATCLDKIGGFTCLCMPGYKGIHCEIEVDECLSN	497
NP_001238962.2[G.gallus]	CECLKGYTGPRCEMDINECHSNPCQNDATCLDKIGGFTCLCMPGFKGVHCEEDIDECCLN	504
NP_035058.2[M.musculus]	CECLKGAGPRCEMDINECHSDPCQNDATCLDKIGGFTCLCMPGFKGVHCELEVNQCQN	501
Q04721.3[H.sapiens]	CECLKGAGPRCEMDINECHSDPCQNDATCLDKIGGFTCLCMPGFKGVHCELEINECQSN	501
XP_009243797.2[P.abelii]	CECLKGAGPRCEMDINECHSDPCQNDATCLDKIGGFTCLCMPGFKGVHCELEINECQSN	501
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XP_012554603.1[H.vulgaris]	PCLKNSTCEDLINDFKNCIPGYVGLCDVDIDECAMSPCFNNATCVDKVNAFECKCQPG	1863
XP_019853114.1[A.queenslandica]	PCSSGSTCIDEIDFPTCLCPMGLTGTQCDISIIDCSDMPCGNGNTCTDTPGGYECSSSG	585
XP_032230096.1[N.vectensis]	PCLNGGQCHDGLNYSTCQGVYVGEICQTNYYDCASNPCQNDGTQDGLAQYTCCLPLG	382
NP_001245510.1[D.melanogaster]	PCLNDGTCHDKINGFKSCALGFTGARCQINIDDCSQSPCRNRGICHDSIAGYSECPPG	593
XP_019643529.1[B.belcheri]	PCLN-GICRDGINKYCECDPGYEGTTCEVNIINECASGPCRNAGHCTDLVTAYTCTCLEG	553
XP_032815028.1[P.marinus]	PCLNDGNTDHNVGLCRCPGFTGPMQIDMDECASTPCLNGAKCVDRPNAYSECTEG	562
XP_014025097.1[S.salar]	PCLNQGTCLDQVVRVVCQPLGFSGEMCQIDIDECSSTPCLNGAKCIDRPNGYECECAEG	564
XP_018114267.1[X.laavis]	PCVNNGVCCVDKVNRFVCI CPGFTGPVCQIDIDDCSSTPCQNGAKCVDPHAGYDCLCATG	557
NP_001238962.2[G.gallus]	PCVNNGECLDKVNRFVLCVPPGFSGAVCQIDIDDCSSTPCLNGAKCIDHPNGYECQCATG	564
NP_035058.2[M.musculus]	PCVNNGQCVDKVNRFQCLCPGFTGPVCQIDIDDCSSTPCLNGAKCIDHPNGYECQCATG	561
Q04721.3[H.sapiens]	PCVNNGQCVDKVNRFQCLCPGFTGPVCQIDIDDCSSTPCLNGAKCIDHPNGYECQCATG	561
XP_009243797.2[P.abelii]	PCVNNGQCVDKVNRFQCLCPGFTGPVCQIDIDDCSSTPCLNGAKCIDHPNGYECQCATG	561
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XP_012554603.1[H.vulgaris]	FNGTLC-----ETDIDECSTQPCANNGS	1886
XP_019853114.1[A.queenslandica]	YTVHCMVNNIDCLPHPCNNGTCIDGINEYVICPEDYTGDNCTETPDHDCSNPCSSLAT	645
XP_032230096.1[N.vectensis]	FTGKSC-----	388
NP_001245510.1[D.melanogaster]	YTGTSCEININDCDSNPCHRGKCIDVNSFKCLCDPGYTGTYICQKQINECESNPQFDDH	653
XP_019643529.1[B.belcheri]	FTGTDEINIDDCQSNQCQHGTCVDEVASFTCEPFGYNGPLCESPVDECDSDPCQNGGT	613
XP_032815028.1[P.marinus]	FAGLVCELNVNECQDPDCHHGKVDGIAFYCVCSPGYTGFLCDSQLNECQSSPCQNGGK	622
XP_014025097.1[S.salar]	FSGPLCKENIDDCDEPCHHGVCRDGIATFSCDCDPGYTGSI CNVQVMECHSNPCQNRGR	624
XP_018114267.1[X.laavis]	FTGVLCENINNCEPPCHYGTQDQIDSYTCICEPFGYMAICSDQIDECCHSNPCLNEGR	617
NP_001238962.2[G.gallus]	FTGVLCENINNCDPCHHGECQDQIDSYTCICNPGYMAICSEQINECHSNPCLHQGR	624
NP_035058.2[M.musculus]	FTGILCENIDNCDPCHHGQCDQIDSYTCICNPGYMAICSDQIDECYSSPCLNDGR	621

Q04721.3[H.sapiens]	FTGVLCEENIDNCDPDPCHHGQCQDGDIDSYTCICNPGYMGAIACSDQIDECYSSPCLNDGR	621
XP_009243797.2[P.abelii]	FTGVLCEENIDNCDPDPCHHGQCQDGDIDSYTCICNPGYMGAIACSDQIDECYSSPCLNDGR	621
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XP_012554603.1[H.vulgaris]	CIDIVNGFLCKCIDGFRGSNCISINIDCDPSPCLHNSCTVDQINGFGQCECSPGYFGLRCE	1946
XP_019853114.1[A.queenslandica]	CITNPGGYQCICPIDFTGTDFDQINDCQPNPCNNGGTCSDLIGTFNCSCPLGFEGSICE	705
XP_032230096.1[N.vectensis]	-----ETNTNECAGNPCMNMGTICIDGINSFRCQCPGLFTGNRCE	427
NP_001245510.1[D.melanogaster]	CQDRVGSYYCQAGTSGKNCENVNNECHSNPCNNGATCIDGINSYKCCQCPGFTGQHCE	713
XP_019643529.1[B.belcheri]	CEDLVNGYRCNCLPGTSGDNCEVNQDDCTGNLCVHG-VQDGLNTYTCMCDGGYEGENCE	672
XP_032815028.1[P.marinus]	CVDLVNRYHCQCLEGTGVCNEFTNFDDCAGELCQQRG-KCVDGNEYRCLCDAGYTGLOCD	681
XP_014025097.1[S.salar]	CIDLNVKYQCNCPLPGTSGVNCENFNVDDCASNPCEYG-ECQDGINEYKVCVAPGYTGAKCD	683
XP_018114267.1[X.laevis]	CVDLVNGYQCNCPLPGTSGPRCEKNVDDCASNPCTYG-NCVDGINRYDCVCSPGFTGPQCK	676
NP_001238962.2[G.gallus]	CIDLNVGYQCNCPLPGTSGVNCENFDDCASNPVHG-DCIDGINRYNCACKPGFTGPRCN	683
NP_035058.2[M.musculus]	CIDLNVGYQCNCQPGTSGLNCEINFDDCASNPCHMG-VCDGINRYSCVCSPGFTGQRGN	680
Q04721.3[H.sapiens]	CIDLNVGYQCNCQPGTSGVNCINFDDCASNPCHMG-ICMDGINRYSCVCSPGFTGQRGN	680
XP_009243797.2[P.abelii]	CIDLNVGYQCNCQPGTSGVNCINFDDCASNPCHMG-ICMDGINRYSCVCSPGFTGQRGN	680
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XP_012554603.1[H.vulgaris]	TEINECESQPSCNNATCVDKINDYQCLCNIGFEKQCEIDINECQNPNCVN-GSCKDLVG	2005
XP_019853114.1[A.queenslandica]	YDINECASLPCLNGNCTDLNVNGYSCSCPFGFNGT-----	740
XP_032230096.1[N.vectensis]	TEIDECESSPCQNGGTCKDKINGVYVICPPGASG-----	461
NP_001245510.1[D.melanogaster]	KNVDECISPPCANNGVCIQVNGYKCECPRGFYDAHLSDVDECASNPVNEGRCEDEGIN	773
XP_019643529.1[B.belcheri]	SEIDECASSPCHNGGICHDLVNAFSCPCPGYHDLCLCYSNVNECESSPCEH-GTCQDGIN	731
XP_032815028.1[P.marinus]	VELNECESSPCHNGGSKDLVDAFEVCVCLPGFHPGLCYSETDACYASPCILH-GTCLDHGE	740
XP_014025097.1[S.salar]	VDIHECNSSPCMSGGTCTVDKVNFGICQCPFGTHGPLCHSGTDHCAPOPCVH-GDCVEQQS	742
XP_018114267.1[X.laevis]	DDIDECASSPCHNGGTCTVNEQNRFRCICPEGFRQPSCFSQSDECVNPNCH-GNCTDDVN	735
NP_001238962.2[G.gallus]	VDIDECASSPCNNNGGTCTINEVNGFRVCPEGYHHPHCQSQADGCLSNPCVH-GNCTHIVS	742
NP_035058.2[M.musculus]	IDIDECASNPCKRGATCINDVNGFRVCICPEGPHHPCSYQVNECLSNPCH-GNCTGGLS	739
Q04721.3[H.sapiens]	IDIDECASNPCKRGATCINGVNGFRVCICPEGPHHPCSYQVNECLSNPCH-GNCTGGLS	739
XP_009243797.2[P.abelii]	IDIDECASNPCKRGATCINGVNGFRVCICPEGPHHPCSYQVNECLSNPCH-GNCTGGLS	739
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XP_012554603.1[H.vulgaris]	DYLCECQPGFDRNCNSNL-IDNCFSLPCKNNGNCTNKVNNYTCTCQAGFSGSDCETNINE	2064
XP_019853114.1[A.queenslandica]	-----CENSTITTTCESVVCENGMCDDTPTGFECLCPNGYTGYPYQNNIDD	787
XP_032230096.1[N.vectensis]	-----THCEND-PNDCEPANACQNGGVCIDGMNTYSCKCHPGTGFSGVFPVNE	508
NP_001245510.1[D.melanogaster]	EFICHCPPGYTGKRCELD-IDCESSNPCQHGHTCYDKLNAFSCQMPGYTGQKCEINIDD	832
XP_019643529.1[B.belcheri]	DYTCCTCTGYEGKNCNVN-IDECASNPCQHEGQCDGIGRYECQCLPGYEGVNCQINTDE	790
XP_032815028.1[P.marinus]	SYRCACEAGWTGPLCEVD-IDCESSPCQNGGACQHELDGTYCRCRDGFKGPTCQKNVNE	799
XP_014025097.1[S.salar]	GYNCECDSPGWGQHCQDE-KDECSPPCQSHSGSCVDRLNGYSCQCRPGFTGVNCEFNME	801
XP_018114267.1[X.laevis]	GYKCLCQPGWNGKKEVD-KNECLSDPCQNGGTCDLVNGYRCSCKKGFKGYNCQIDTNE	794
NP_001238962.2[G.gallus]	GYKVCVDPGWIGDYCSTE-GNECKSNPCQNGGTCEDDLNGYRCTCRKGFKGYNVCQ----	796
NP_035058.2[M.musculus]	GYKCLCDAGWVGVNCEVD-KNECLSNPCQNGGTCTNNLVNGYRCTCKKGFKGYNQVNI	798
Q04721.3[H.sapiens]	GYKCLCDAGWVGINCEVD-KNECLSNPCQNGGTCDNLVNGYRCTCKKGFKGYNQVNI	798
XP_009243797.2[P.abelii]	GYKCLCDAGWIGINCEVD-KNECLSNPCQNGGTCDNLVNGYRCTCKKGFKGYNQVNI	798
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XP_012554603.1[H.vulgaris]	CDPDPSCSNALNCTDLINGYICYCKLGRGENCSEIIDNCPQPCRNHSTCTNRFTVND-	2123
XP_019853114.1[A.queenslandica]	CLSNPCLNN-ATCIDIANYTECECTEGFDGRNCAIDTDLCSQPQCFNGGTSETSD--SF	844
XP_032230096.1[N.vectensis]	CASSPCRNNG-GTCEDGVAQYRCRCDGYTGKNCVEVRIDSCIDHTCQNGASCVSSTP----	563
NP_001245510.1[D.melanogaster]	CVTNPCQNGG-GTCDKVNKYKCVCKVPFTGRDCESKMDPCASNRCNKAECTPSSNFLDF	891
XP_019643529.1[B.belcheri]	CGSNPCQNGG-GQCLDGVNNGYQCHCELPFVGINQCIELAPCNPNPCANSNGSCIPADYQTF	849
XP_032815028.1[P.marinus]	CVSNPCLNLR-GTCVDGVAGYTCCLTLPFTGRNCEAVMAPCASQPCNNAATCKESVNLSSF	858
XP_014025097.1[S.salar]	CASSPCRNH-GTCDVGNTYISCLDPPYSKGHCEELVPCASHPCERGVCQPTPDYTFY	860
XP_018114267.1[X.laevis]	CASNPCLNH-GTCRDGINGYTCCHALPYTGTCNQILTPCSPEPCHNGGICQESDFKSF	853
NP_001238962.2[G.gallus]	-----VVVAPCSPPDCENSIGICQESPDSEGY	822
NP_035058.2[M.musculus]	CASNPCLNQ-GTCFDDVSGYTCCHMLPYTGKNCQTVLAPCSNPNCENAAVCKEAPNFESF	857
Q04721.3[H.sapiens]	CASNPCLNQ-GTCFDDISGYTCHVLPYTGKNCQTVLAPCSNPNCENAAVCKEAPNFESY	857
XP_009243797.2[P.abelii]	CASNPCLNQ-GTCFDDISGYTCHVLPYTGKNCQTVLAPCSNPNCENAAVCKEAPNFESY	857
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XP_012554603.1[H.vulgaris]	-----	2123
XP_019853114.1[A.queenslandica]	FCTCPLGYFGSHCQNTLDPCS-SSPCLNSGICTNVNGTNFSCACSQAYGGERCEIKLFPD	903
XP_032230096.1[N.vectensis]	-----Y-----	563
NP_001245510.1[D.melanogaster]	SCTCKLGYTGRYCEDIDECSSSPCRNGASCLNVPG-SYRCLCTKGYEGRDCAIN-TDD	949
XP_019643529.1[B.belcheri]	TCDCAEFGFEGETCADDINECQ-SNPCKNGAPCINLEG-DFRCDCLTGFSGELCSVN-IDD	906
XP_032815028.1[P.marinus]	SCACPPGWRGATCSLIDIECA-GAPCQHGGAAMNTQG-GFRCSRPGYTGPTCQTD-IDD	915
XP_014025097.1[S.salar]	TCRCPRGQWGPRCTDVIDECL-KNPCNRRARCINSQG-SYVCKCRPGYSGLNCQTN-IDD	917
XP_018114267.1[X.laevis]	SLCLCATGWQQRCTIDVDECV-TNPCRNYGRQCNTKG-GYKCHCPDGFSGFNCENN-IDD	910
NP_001238962.2[G.gallus]	TCQCAPGWEGERCTVIDIECL-SKPCRNHALCHNIQG-SYLCECRPGFTGGDCDSN-IDD	879
NP_035058.2[M.musculus]	SLCLAPGWQQRCTVDVDECI-SKPCMNHGVCHNTQG-SYVCECPGFSGMDCEED-IDD	914
Q04721.3[H.sapiens]	TCLCAPGWQQRCTIDIECI-SKPCMNHGLCHNTQG-SYMCECPGFSGMDCEED-IDD	914
XP_009243797.2[P.abelii]	TCLCAPGWQQRCTIDIECI-SKPCMNHGLCHNTQG-SYMCECPGFSGMDCEED-IDD	914
XP_012554603.1[H.vulgaris]	-----FHNCNSLGYEGDRCEIEIDECKALPCKN	2151
XP_019853114.1[A.queenslandica]	CLDMPCLNNGTCAELVGSNGIGSGAGEPGPRIYQCPLGYAGEFCENITDLCVSSPCKN	963
XP_032230096.1[N.vectensis]	-----Y-----AYSQCCKPGYTGQYCEITDVIDECAARPCVN	593
NP_001245510.1[D.melanogaster]	CASFPCQNGTCLDGI-----DYSCLCVDGFDGKHCEITDINECLSQPCQN	995
XP_019643529.1[B.belcheri]	CDPDPCHNGGTCTNDGIN-----SYTSCMPGFGGTNCEEDIDECYSNPQCN	952
XP_032815028.1[P.marinus]	CSPNPCCQNGSGCTDGVG-----AFSCKCRPGFRGSRCETEVNECASNPCKN	961
XP_014025097.1[S.salar]	CSPNPCLNGSGCVDEVG-----GFSCDRCQFGDGERCEAEVDECAASQPCQN	963
XP_018114267.1[X.laevis]	CLSNPCQNGASCLDGIN-----TFSCNCLAGFHGDKCQTDVDECAASNPCKN	956
NP_001238962.2[G.gallus]	CLSNPCQNGASCVDGIN-----SFSCICLPGFHGDQCTDTNECLSEPCRN	925
NP_035058.2[M.musculus]	CLANPCQNGGSCVDHVN-----TFSCQCHPGFTGDKCQTDMECLSEPCRN	960
Q04721.3[H.sapiens]	CLANPCQNGGSCMDGVN-----TFSCCLCPGFTGDKCQTDMECLSEPCRN	960
XP_009243797.2[P.abelii]	CLANPCQNGGSCVDGVN-----AFSCLCLLGTGDKCQTDMECLSEPCRN	960
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XP_012554603.1[H.vulgaris]	GGNCTDLPGKYLCTCPPGFTGVDCEINIDCKN--VSCLNGGKCIDLINSYVCECPVTHK	2209
XP_019853114.1[A.queenslandica]	NATCIGDSANFTCTCLPGFTGTLCETELTGCHTELYPCLNGGECMEMDQGFMCNAPGFT	1023
XP_032230096.1[N.vectensis]	G-ACVDGVNGFICRCDPGFTGDRQCINVDQCS--SPCVHGGSCIDSINTYTCQCPKGFT	650
NP_001245510.1[D.melanogaster]	GATCSQVNSYTYCTCLPGFSGINCQTNDECTE--SSCLNGGSCIDGINGYNCSCLAGYS	1053
XP_019643529.1[B.belcheri]	GGQCIDAVNGYACDVLGFTGNTCQTNKDDCTS--SSCFSGGTCTIDINTTCQCPKGFT	1010
XP_032815028.1[P.marinus]	GGSCADVNSYTCRCRPGFNHCEHDIETCTD--SSCLNGGSCVDGINAYTCLCRGGFT	1019
XP_014025097.1[S.salar]	GAUCRDYVNSFVVCVRPGFDGILCEHNIPECTE--SSCLMNGTCVDDINTFSCRCRPGFY	1021

XP_018114267.1[X.laewis]	GGSCDTYVNSYTKCKQPGFDGIHCNNIDECD--TSCFNGATCVDGVNSFSCQCPQGFT	1014
NP_001238962.2[G.gallus]	GGTCTHYVNSYTKCKQPGFEGTNCENNIDECE--SSCFNGGTCVDGINSFTCCQCPVGFT	983
NP_035058.2[M.musculus]	GGTCSDYVNSYTKCTCPAGFHGVHCENNIDECE--SSCFNGGTCVDGINSFSCCLCPVGFT	1018
Q04721.3[H.sapiens]	GGTCSDYVNSYTKCKQAGFDGVHCENNINECTE--SSCFNGGTCVDGINSFSCCLCPVGFT	1018
XP_009243797.2[P.abelii]	GGTCSDYVNSYTKCKQAGFDGVHCENNINECTE--SSCFNGGTCVDGINSFSCCLCPVGFT	1018
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XP_012554603.1[H.vulgaris]	GKHCEKKIPDDVDI-----TFPGGDSYIKHCVKGNASKEFSISLWFRFLGRSRGVFLN	2263
XP_019853114.1[A.queenslandica]	GPLCGYGINECRNQPCNLNGGTCRDFFRYYVICPPNFTGTDCES-----MID	1070
XP_032230096.1[N.vectensis]	GPRCIHIHNECSSDPCQHGGTCSDRIGSYSCYCRPGYTGSNCQH-----PLD	697
NP_001245510.1[D.melanogaster]	GANCCYKLNKCDSPNCLNGATCHEQNNIYTHCPSGFTGKQCSE-----YVD	1100
XP_019643529.1[B.belcheri]	GSNCQHEINECESHPCONGATCVDQTYGFCICTYGYEGVTCQN-----QKD	1057
XP_032815028.1[P.marinus]	GSYCQFDIDECESSQPCQHGGTCLDGLGYKCTCPRGYTGGNCQA-----LVD	1066
XP_014025097.1[S.salar]	GTFCHEYQNECDSQPCKNNGTCTDGLGSYRCTCPVYNGNQNCQN-----FVN	1068
XP_018114267.1[X.laewis]	GPFCLEINEECGSHPCINGGTCVDGMGTYHCTCPIGYRGNKEE-----LVD	1061
NP_001238962.2[G.gallus]	GPFCLEINEECDSHPCLNKGSCVSLGKYRCICPLGYTGKNCQT-----PMD	1030
NP_035058.2[M.musculus]	GPFCLEINEECSSNPCLNAGTCVDGLGYRCICPLGYTGKNCQT-----LVN	1065
Q04721.3[H.sapiens]	GSFCLHEINECSSHPCLNEGTCTVDGLGYRCSPLGYTGKNCQT-----LVN	1065
XP_009243797.2[P.abelii]	GSFCLHEINECSSHPCLNEGTCTVDGLGYRCSPLGYTGKNCQT-----LVN	1065
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XP_012554603.1[H.vulgaris]	L--GFGCETVRPFLIMSHSSIRFQFRNQFSFVMDNLKINNEKLVINNGVWHHIYIALSS	2321
XP_019853114.1[A.queenslandica]	PCTNIDCNGGSCI-----GDM-----GTYTCQCDPFGWTGLQCESEI	1106
XP_032230096.1[N.vectensis]	RCANDPCRNAGATC-----RRGTGDL-----SDFHCECPLGYKGTICDVKE	737
NP_001245510.1[D.melanogaster]	WCGQSPCENGATC-----SQMK-----HQFSCCKSAGWTGKLCVDVQT	1137
XP_019643529.1[B.belcheri]	LCASDFCRNGGTC-----TQSG-----DRYECLCEDEWTGLICDMTK	1094
XP_032815028.1[P.marinus]	WCSSSPCKNSGSC-----VQSR-----TSYRCDCHSGWTGLYCDIPN	1103
XP_014025097.1[S.salar]	LCSQPLCQNGGSC-----SQSE-----TTWLCHCPVGWTGMXCDVFN	1105
XP_018114267.1[X.laewis]	LCNGFPCKNKGIC-----KQVK-----TEPKCICPTGWTGYCDIPD	1098
NP_001238962.2[G.gallus]	LCSSPCKNKGTC-----FQSG-----AQTRCDPCSGWTGAYCDVFN	1067
NP_035058.2[M.musculus]	LCSSPCKNKGTC-----VQEK-----ARPHCLCPPGWDGAYCDVFN	1102
Q04721.3[H.sapiens]	LCSSPCKNKGTC-----VQKK-----AESQCLCPSGWAGAYCDVFN	1102
XP_009243797.2[P.abelii]	LCSSPCKNKGTC-----VQKK-----AESQCLCPSGWAGAYCDVFN	1102
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XP_012554603.1[H.vulgaris]	VTLNFKVVLGGIIVQEEQKAELSGMTFFNESGTILIGKSLLDGKLIESGFIGDVSQVALF	2381
XP_019853114.1[A.queenslandica]	NECDGVD-----C-----TNGTCV-DLINNYTCQCSGFTGQFCEINID	1144
XP_032230096.1[N.vectensis]	VSCAVA-----GTIC-----ANGGTCF-DSNGVQSCCTCKPGFTGSYCRNTID	778
NP_001245510.1[D.melanogaster]	ISCDQAADRKGLSLRQLC-----NN-GTCK-DYGNSHVCYCSQGYAGSYCKEID	1185
XP_019643529.1[B.belcheri]	VSCAAAASERGVLLGELC-----QNGGSCV-DTGNSHNCCNCPAGYRGSYCSBEID	1143
XP_032815028.1[P.marinus]	MSCDTAARNKGLSVSHLC-----RHGGRCI-DAGNTHHCQCSRGFEGSYCEKEVD	1152
XP_014025097.1[S.salar]	MSCQDYAARNGIQVELVC-----KHSGRGV-NVGNHAGQCQCLPGYTGSCYCNEMVD	1154
XP_018114267.1[X.laewis]	VSCVEAASQRGVAVQDLC-----QHAGVCI-NTGFSHRCQCRQGYIGSYCEGELD	1147
NP_001238962.2[G.gallus]	VSCQVAASQRGITVDQLC-----QSSHCL-NVGNTHRCQCRVGYTGSYCEEQLD	1116
NP_035058.2[M.musculus]	VSCKAAALQKGVVPEHLC-----QHSIGCI-NAGNTHHCQCLPGYTGSYCEEQLD	1151
Q04721.3[H.sapiens]	VSCDIAASRRGVLEHLC-----QHSGVCI-NAGNTHYCCQCLPGYTGSYCEEQLD	1151
XP_009243797.2[P.abelii]	VSCDIAASRRGVLEHLC-----QHSGVCI-NAGNTHYCCQCLPGYTGSYCEEQLD	1151
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XP_012554603.1[H.vulgaris]	KRV-----LDS---TETAGL-VRNCSRNISDSIIPWVGLMADAGPNVSLLET	2424
XP_019853114.1[A.queenslandica]	DCAGINCNGN-TCVDIGISYQCDCLLGYTGPSCDTIIDDCAG---MPCMNASCIDLFNN	1200
XP_032230096.1[N.vectensis]	ECAGKPCYKYGATCHADVANTCTCTAGFTGKNCININECAS---NPCQR-GSCLDLVNG	834
NP_001245510.1[D.melanogaster]	ECQSQPCQNGGTCRDILGAYECQCRQFQGCQNCENLIDDCAP---NPCQNGGTCRDVRN	1242
XP_019643529.1[B.belcheri]	ECASSPCQNGAQCRDGLGTYSVCRCRAGYQGVNCEQEINECIS---NPCQNGGTCIDMVNE	1200
XP_032815028.1[P.marinus]	ECSNPNCHNGATCRNFGSYKCECPVGYHGLNCDYENECLS---QPCQNGGTCIDLVNR	1209
XP_014025097.1[S.salar]	ECLSNPCRNAGATCMDYQGTCECMCKAGYQGVNCEYDVECHS---NPCHHGGTCINLINR	1211
XP_018114267.1[X.laewis]	ECASNPCQNSAACVDRHGGYECKCLPGYQGVNCEYEIDEQCL---QPCNNGGTCVDLVNQ	1204
NP_001238962.2[G.gallus]	ECDSPPCQNGATCRDLGGYQCECPVGYQGVNCEYEVDEQCF---QPCQNGGTCIDLVNH	1173
NP_035058.2[M.musculus]	ECASNPCQHGATCNDFIGGYRCECPVGYQGVNCEYEVDEQCN---QPCQNGGTCIDLVNH	1208
Q04721.3[H.sapiens]	ECASNPCQHGATCSDFIGGYRCECPVGYQGVNCEYEVDEQCN---QPCQNGGTCIDLVNH	1208
XP_009243797.2[P.abelii]	ECVSNPCQHGATCSDFIGGYRCECPVGYQGVNCEYEVDEQCN---QPCQNGGTCIDLVNH	1208
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XP_012554603.1[H.vulgaris]	WTCGTNVCPPEFTGKFCQTKIDKIPTTVVF-----CPSPIKVYTEESSVFVWTW	2472
XP_019853114.1[A.queenslandica]	YTC---VCSGDTGRFCEVNIDDCINI-----NCNNGSCEDLINDHM--CNCFPGF	1246
XP_032230096.1[N.vectensis]	YLC---SCPKGYIGKHCEVNADDCFVN-----ACFNNGSCVDGIAEFK--CTCPPLGF	881
NP_001245510.1[D.melanogaster]	FSC---SCPPGTGMIIICEINKDDCKPG-----ACHNNGSCIDRVGGFE--CVCPQPGF	1289
XP_019643529.1[B.belcheri]	YRC---SCPPGTQGLLCEINNDCNCFAG-----ACYHDGTCVDGIGFT--CRCRPGY	1247
XP_032815028.1[P.marinus]	FNC---VCPPGTGQRLCEINTDDCNPGDPAMPGPGRFCFNGGSCVDGVGSFT--CSCPPGF	1264
XP_014025097.1[S.salar]	FSC---ACPPGTNGVQCEVNDDCAPKPG--SWELRCLNGGQCVGVGGRYT--CSCPPGF	1264
XP_018114267.1[X.laewis]	FRC---SCPPGTGRGLCEENIDDCAPSAE-----GPHCFNGGRCIDRIGGYR--CECLPGF	1255
NP_001238962.2[G.gallus]	FRC---SCPPGTGRGLCEENVDCCISESG---GPRCFNGGQCIDQIGGYS--CLCLPGF	1224
NP_035058.2[M.musculus]	FKC---SCPPGTGRGLCEENIDEC---AG---GPHCLNGGQCVDRIGGYT--CRCLPGF	1256
Q04721.3[H.sapiens]	FKC---SCPPGTGRGLCEENIDDC---AR---GPHCLNGGQCMRIGGYS--CRCLPGF	1256
XP_009243797.2[P.abelii]	FKC---SCPPGTGRGLCEENIDDC---AR---GPHCLNGGQCMRIGGYS--CRCLPGF	1256
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XP_012554603.1[H.vulgaris]	KEPQFDDDVAVVEVIRSHSPNGLFSWGDYVITYI-----AK-DAFE	2512
XP_019853114.1[A.queenslandica]	TDQRCETDINECDGN-PCNDG---TCTDGINSFSCSCPPDYTGDTCDTEINLCLMEQFCL	1302
XP_032230096.1[N.vectensis]	SGSRCEVDVDECASS-PCSALGTEKCNINNGAYHCQKQGLGRHCDLNECLSL-YPGR	939
NP_001245510.1[D.melanogaster]	VGARCEGDINECLSN-PCSNAGTLDCVQLVNNYHCNCRPHGMGRHCEHKVDFCAQ-SPCQ	1347
XP_019643529.1[B.belcheri]	VGPRCEGDVNECLSN-PCDAEGTQDCVQLENDYRCDCKPGYTGRCERTVDSCE-SDPCL	1305
XP_032815028.1[P.marinus]	VGERCEGDVNECLSN-PCDPRGSLDCIQLVNDYKQCRCRPGFTGHNCVINTCRL-EPGR	1322
XP_014025097.1[S.salar]	AGEHCEGDVNECLSG-PCSPGSLDCVQLANDYQCRCLRYGTGRHCESMVLDCCS-KPCH	1322
XP_018114267.1[X.laewis]	AGERCEGDVNECLSS-PCSSGSLDCIQLANNYLCKCKPVFTGRHCETIQDLCP-SRPL	1313
NP_001238962.2[G.gallus]	AGERCEGDINECLSN-PCNPRGSLDCIQLINDYTCICRSATGRHCESVIDVCP-KPCQ	1282
NP_035058.2[M.musculus]	AGERCEGDINECLSN-PCSSGSLDCVQLKNNYCNICRSATGRHCETFLDVCP-KPCL	1314
Q04721.3[H.sapiens]	AGERCEGDINECLSN-PCSSGSLDCIQLTNDYLCVCRSAFTGRHCETFDVCPQ-MPCL	1314
XP_009243797.2[P.abelii]	AGERCEGDINECLSN-PCSSGSLDCIQLTNDYLCVCRSAFTGRHCETFDVCPQ-MPCL	1314
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XP_012554603.1[H.vulgaris]	NSVSTCFEI-N-VTFPN-----CSE-----FQTANNSIH	2539
XP_019853114.1[A.queenslandica]	NNGTCTSDKIEGPIYNCSSVPLYSGDNCEQIN--SCSLSPCQNNATCTGNLTGDTYC	1360
XP_032230096.1[N.vectensis]	NGGCEKDA---GEYTCCLP-HGFSGDDCERRV-YTCSQPCLNSGTCT--VHNTYNC	991
NP_001245510.1[D.melanogaster]	NGGNCNIRQ---SGHHICCN-NGFYGNKCELSG-QDCDS-----	1381

XP_019643529.1[B.belcheri]	NGGACSQSG----NNYVDCDQ-PGFGGDNCELVC-----D-----	1335
XP_032815028.1[P.marinus]	NGGTCTMTV-NTLLGFTCLCA-PGYAGHACEDNA-YACGN-----	1359
XP_014025097.1[S.salar]	NSGTCSMMN-SSVHGTYCICQ-PGFTGFNCGEVGYNCAK-----	1360
XP_018114267.1[X.laavis]	NGGTCAVAV-NMPEGFTCCQP-SGFLGSKQYSN-NTCEH-----	1350
NP_001238962.2[G.gallus]	NGGTCAVAS-NMPDGFICQCP-PGYSGAKCEFSSHSTCGQ-----	1320
NP_035058.2[M.musculus]	NGGTCAVAS-NMPDGFICRCP-PGFSGARCG-----SSCGQ-----	1348
Q04721.3[H.sapiens]	NGGTCAVAS-NMPDGFICRCP-PGFSGARCG-----SSCGQ-----	1348
XP_009243797.2[P.abelii]	NGGTCAVAS-NMPDGFICRCP-PGFSGARCG-----SSCGQ-----	1348
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XP_012554603.1[H.vulgaris]	ACGTWKYGRFCDYKCH-----EKY-	2558
XP_019853114.1[A.queenslandica]	HCSENNYGTHCER-FDYCHSNPCQNDGTICNGSPGNLISDTFLCICMPQFNNGSDCSMEL-	1418
XP_032230096.1[N.vectensis]	SCRPGVYGRKQCEWNKDECLSAPCRNNGGTCIDYGS-----YSCKPLGFAGANCEESI-	1044
NP_001245510.1[D.melanogaster]	-----NPCRVGNVVADEGF-----GYRCECPRGTLGEHCEIDT-	1415
XP_019643529.1[B.belcheri]	-----RECKNRGQCLYTDGE-----FRCSCPSNYAGDSQCFHE-	1368
XP_032815028.1[P.marinus]	-----LSCRNGGTCLPDRAA-----GPLCVCPRAWRGPECQYHSG	1394
XP_014025097.1[S.salar]	-----LRCQNGHGCOETQVG-----RPHCRCPQFSGPRCETVH-	1394
XP_018114267.1[X.laavis]	-----YKCKVGENCIQTHMG-----PRCYCPMGPAGYACQSNL-	1383
NP_001238962.2[G.gallus]	-----VKCKKGEQCIHTSSG-----PRCYCPRLAVGEECQNT-	1353
NP_035058.2[M.musculus]	-----VKCRRGECQIHTDSG-----PRCFCLNPK-----DCES-	1376
Q04721.3[H.sapiens]	-----VKCRKGEQCVHTASG-----PRCFCPSPR-----DCES-	1376
XP_009243797.2[P.abelii]	-----VKCRKGEQCVHTASG-----PRCFCPSPR-----DCES-	1376
XP_012554603.1[H.vulgaris]	-----ELAVPKPPFYVCGRPGTWSHGPT--YPENPDLLVSECT--	2595
XP_019853114.1[A.queenslandica]	-----SPCSDPCMMNGGTCVDEG--STRYQCQPVGYTGNNCEVFSSDTPYFNGDSY--	1468
XP_032230096.1[N.vectensis]	-----NECLSQPCKNNGGSCARDI--VNGYKCDPCSMKMGKNCETVV-----	1082
NP_001245510.1[D.melanogaster]	----LDECSFNPCAQGAACEDL--LGDIYELCPKSKWKGRCDIYDANYPGWNGSGSGND	1469
XP_019643529.1[B.belcheri]	-----SNPCFSLPCYNNNGECQQTG-IDSYRCMCPEDYNGVLCEIYIPDVTP-----GP---	1415
XP_032815028.1[P.marinus]	GGGGSSACASSPCENGAAACEYEVPRFPYRCVCPPLFTGPRCVRVLGPKVPGDASS-GR---	1450
XP_014025097.1[S.salar]	-----SCQNRPCNLNGTCKMKDP-HYQYSCHCPAHFSGRHCENVIF-----	1433
XP_018114267.1[X.laavis]	-----GCASQPCKNNGVCQKRAQPPFYTCCHCPKGVVGPQCEIPI-----	1422
NP_001238962.2[G.gallus]	-----GCASAPCQNGGCHPRSPQPPYYQCFAHAGQSQCEQLV-----	1392
NP_035058.2[M.musculus]	-----GCASNPCQHGTCTYFQRPQPHYSCRCPPSFGGSHCELYT-----	1415
Q04721.3[H.sapiens]	-----GCASSPCQHGGSCHPQRPQPPYYSCQCAPFFSGSRCELYT-----	1415
XP_009243797.2[P.abelii]	-----GCASSPCQHGGSCHPQRPQPPYYSCQCAPFFSGSRCELYT-----	1415
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XP_012554603.1[H.vulgaris]	--ATTPFNITITNKISFPTSSCDDSFKNDFV----E----S-----FKQLITELQDVW	2638
XP_019853114.1[A.queenslandica]	--TLVPYSPNNNNSSQLINLHFTSSQSGLLLYISEEDHSSVLSLGIEAGLLSLMRQEG	1526
XP_032230096.1[N.vectensis]	-----KDQCPV-----PNCAKKFDGGKC-----NPKCNT-HECNWDGTCTSLG-IEPW	1123
NP_001245510.1[D.melanogaster]	RYAADLEQQRAMCDK---RGCTEKQNGNIC-----DSDCNT-YACNFDGNDCSLG-INPW	1519
XP_019643529.1[B.belcheri]	GVTMIPPHIEPSCPF---EHCASKARDGRC-----DEECNI-HECDWDGTDGALG-NNPW	1465
XP_032815028.1[P.marinus]	ALPVPFPVLEESCPV---AECESHAGDGLC-----DRDCNN-HACAWDGGDCSLHFPSPW	1501
XP_014025097.1[S.salar]	----DPSPSTPASCYP---VECEQHSQDKVC-----DPQCNS-HECQWDGGDCSLHWRQPW	1481
XP_018114267.1[X.laavis]	---E-----TDRCHK---YQCEPKARDGYC-----DQECNI-HECLWDGGDCSLTMGDWP	1465
NP_001238962.2[G.gallus]	---HPSQE-PLGCLD---SQCAEKARDGYC-----DEDNT-HACQWDGGDCSLTMEDPW	1439
NP_035058.2[M.musculus]	---APTSTPPATCQS---QYCADKARDGIC-----DEACNS-HACQWDGGDCSLTMEDPW	1463
Q04721.3[H.sapiens]	---APPSTPPATCLS---QYCADKARDGVC-----DEACNS-HACQWDGGDCSLTMENPW	1463
XP_009243797.2[P.abelii]	---APPSTPPATCLS---QYCADKARDGVC-----DEACNS-HACQWDGGDCSLTMENPW	1463
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XP_012554603.1[H.vulgaris]	SICGTTCDKFKNIKVSCPKDAKRFRDMDPK-----WTGPKFILD-----SFD	2681
XP_019853114.1[A.queenslandica]	SFIQSVARYHPVSDRWHYVEVTQNGLEIKTEIDGYPNSTSLIDMFLIFEPATYIGGFD	1586
XP_032230096.1[N.vectensis]	SNCTTV---TKSGKACYQVFANGVCDRECN-----GGCL-----FDGFD	1160
NP_001245510.1[D.melanogaster]	ANCTA-----NECWNKFKNGKNEECNN-----AACH-----YDGH	1551
XP_019643529.1[B.belcheri]	ANCTSS-----LQCNWYFSNGHCDQCCNN-----EECL-----YDGR	1498
XP_032815028.1[P.marinus]	RNCVSR-----LQCNLRFNRGECDEQCNS-----LGCL-----FDGFD	1534
XP_014025097.1[S.salar]	VNCTAP-----VPCWELFRNGRCDPDCN-----SGCL-----FDSFE	1514
XP_018114267.1[X.laavis]	ANCSSS-----LRCWEYF-NGQCDELNT-----PECL-----FDNFE	1497
NP_001238962.2[G.gallus]	ANCSSS-----LRCWMLF-NGQCDEFNT-----PECL-----FDNFE	1471
NP_035058.2[M.musculus]	ANCTST-----LRCWEYI-NNQCDEQCN-----AECL-----FDNFE	1495
Q04721.3[H.sapiens]	ANCSSP-----LPCWDYI-NNQCDELNT-----VECL-----FDNFE	1495
XP_009243797.2[P.abelii]	ANCSSP-----LPCWDYI-NNQCDELNT-----AECL-----FDNFE	1495
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XP_012554603.1[H.vulgaris]	ATNETNLAKIQNGIKTFKNMTVIVNNVSISSDLLNVEKTVCNNGSILKNDICVKCPAG	2741
XP_019853114.1[A.queenslandica]	NYTSLPSAVLQSS---GF-IGYINATIQLGGEAL-----HIIDDSIAGRDI-	1629
XP_032230096.1[N.vectensis]	CKPSVP---KC---GA-----DKYCAARFA-	1179
NP_001245510.1[D.melanogaster]	CERKLG-S-CDS---LF-----DAYCQKHYG-	1572
XP_019643529.1[B.belcheri]	CEENFHPT--CNP---VY-----DTYCGNFR-	1520
XP_032815028.1[P.marinus]	CQLGMK-N-CNP---LY-----NAYCTAHYA-	1555
XP_014025097.1[S.salar]	CQESAQ-S---YC---KY-----DKYCAAHYA-	1534
XP_018114267.1[X.laavis]	CQQKE--P---IC---KY-----DKYCEDHYA-	1516
NP_001238962.2[G.gallus]	CQQNS--R---MC---KY-----DKYCADHYG-	1490
NP_035058.2[M.musculus]	CQRNS--K---TC---KY-----DKYCADHFK-	1514
Q04721.3[H.sapiens]	CQGNS--K---TC---KY-----DKYCADHFK-	1514
XP_009243797.2[P.abelii]	CQGNS--K---TC---KY-----DKYCADHFK-	1514
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XP_012554603.1[H.vulgaris]	TFKNVTNELCEKCPFGSYSKEAGSEMC---INCPANT--TTTSEGSTEESCKVKCLFG	2795
XP_019853114.1[A.queenslandica]	-----HGEA---AG---SCGPETCSNGGICVEES-----	1652
XP_032230096.1[N.vectensis]	-----NAEC---DA---ICNNVACQNDGLDCSFKK--PEIVEGTL-----VLV----	1214
NP_001245510.1[D.melanogaster]	-----DGFC---DY---GCNNAECSDWGLDCENKTQSPVLAEGAM-----SVV----	1609
XP_019643529.1[B.belcheri]	-----DGNL---DS---GCNNLECGYDGGDCDEY-PPVTAKGYL-----VMI----	1556
XP_032815028.1[P.marinus]	-----DQHC---DQ---GCNSEDGWDGDCAGEV-PERLADGVL-----VLI----	1591
XP_014025097.1[S.salar]	-----NKIC---DK---GCNTEACGWDGLDCSGDT-PAEVADGTL-----VIV----	1570
XP_018114267.1[X.laavis]	-----NGHC---DK---SCNTKECGWDGLDCSTDR-PENLAEGTL-----VVV----	1552
NP_001238962.2[G.gallus]	-----DGRG---DQ---GCNSEECGWDGLDCAGDK-AERLAEGTL-----IIV----	1526
NP_035058.2[M.musculus]	-----DNHC---DQ---GCNSEECGWDGLDCASQ-PENLAEGTL-----IIV----	1550
Q04721.3[H.sapiens]	-----DNHC---DQ---GCNSEECGWDGLDCAADQ-PENLAEGTL-----VIV----	1550
XP_009243797.2[P.abelii]	-----DNHC---DQ---GCNSEECGWDGLDCAADQ-PENLAEGTL-----VIV----	1550
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XP_012554603.1[H.vulgaris]	AYLENNECKDCPIGFYKETAGFEKQCPALGLTTKTKTGAUTKQCKNDCTLGQELVNNTC	2855

XP_019853114.1[A.queenslandica]	-----QSSFL-----CLC-----	1660
XP_032230096.1[N.vectensis]	LLV-----VPEAFMNGSRVFM-----RELSRTL-----	1237
NP_001245510.1[D.melanogaster]	MLM-----NVEAFREIQAQFL-----RNMSHML-----	1632
XP_019643529.1[B.belcheri]	VAA-----PPEVLLNNSISFL-----RMLSIIIL-----	1579
XP_032815028.1[P.marinus]	MLL-----PPARVHNSANFL-----RQLGSL-----	1614
XP_014025097.1[S.salar]	VLL-----QPEELMGDMGRFL-----RSLGTLL-----	1593
XP_018114267.1[X.laavis]	VLM-----PPSELLKNSRNFL-----RVLGSL-----	1575
NP_001238962.2[G.gallus]	VLM-----RPDELLRDRVSFL-----RTLGTLL-----	1549
NP_035058.2[M.musculus]	VLL-----PPEQLQDSRSFL-----RALGTLL-----	1573
Q04721.3[H.sapiens]	VLM-----PPEQLQDARSFL-----RALGTLL-----	1573
XP_009243797.2[P.abelii]	VLM-----PPEQLQDARSFL-----RALGTLL-----	1573
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XP_012554603.1[H.vulgaris]	QPCRMGYRRNNSDQFVCLPCPNYQST-YQLGATSP-VCY-AVCEVGKEIS-SDGLK---C	2908
XP_019853114.1[A.queenslandica]	---PIGFRGDTCEQDTEIIVPYFNTRSYAIVSNDAFSLYGG---IDIDI-----TLHTS	1708
XP_032230096.1[N.vectensis]	---NTIAFIKKDSEKELVKVYPLPPSAPVPAERRKRSAEKIWFIDSDLTESHRRFRAAV	1294
NP_001245510.1[D.melanogaster]	---RTTVRLKDALGHDIIINWKNVVRPEIEDTD--FA-----RKNKILYTTQV	1677
XP_019643529.1[B.belcheri]	---RSSMSFKVDEGNPMVYPWYGEVDETISKRAIRSVFR-----ALSGRYRRATES	1629
XP_032815028.1[P.marinus]	---HATVRVKFIDTNGQDMIFPYQDEARGCGGFRLEAAR-----SLSRFVREMER	1662
XP_014025097.1[S.salar]	---HTNLRVKMDDQKPMLYPYGLEHDDGNEG--QPST-----MTLRGKRELDK	1638
XP_018114267.1[X.laavis]	---HTNLRKKNPDGSYMVFYFRENASSQSRRR--SLK-----LRVIREL-E	1618
NP_001238962.2[G.gallus]	---HTNLRKLDGSGNPMVYPYGEKSAARSRR--SVV-----VVRKHRELEQ	1592
NP_035058.2[M.musculus]	---HTNLRKQDSQGALMVYPYGEKSAAMKKQ--KMTR-----RSLPEEQEQEQ	1618
Q04721.3[H.sapiens]	---HTNLRKRDGSGELMVYPYGEKSAAMKKQ--RMTR-----RSLPGEQ--EQ	1616
XP_009243797.2[P.abelii]	---HTNLRKRDGSGELMVYPYGEKSAAMKKQ--RMTR-----RSLPGEQ--EQ	1616
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XP_012554603.1[H.vulgaris]	MECAIGYKNNNNNAKTSCKCPAGLTTKQLASTSIDQCIEKSSDS-KYYDVQVAITSLTWS	2967
XP_019853114.1[A.queenslandica]	SPNGLIYYL-YDS-----TNVNDYFTLYLEEGGIG--	1738
XP_032230096.1[N.vectensis]	QKNGVQVQINLNRG-CE-----TDCFQSTEQAAKYLGAQOSTGKLN--	1335
NP_001245510.1[D.melanogaster]	HQTGIQIYLEIDNRK-CT-----ECFTHAVEAAEFLAATAAKHQLR--	1717
XP_019643529.1[B.belcheri]	EVQGSIVYLEMDNSK-CY-----RVHDDCFETAKEAADFLAALFLHNGLS-	1673
XP_032815028.1[P.marinus]	PLIGSKVYVEIDNRH-CY-----QTSDRCFSSAADAALFLAAQATHG----	1703
XP_014025097.1[S.salar]	EVIGSKVYLEIDNRK-CE-----ERSMDCFSSTELAAAFIAEYKLS-----	1679
XP_018114267.1[X.laavis]	QPIGSKVSLEINNQE-CV-----MDSQDCFKTSESAALLAAHAVRG----	1659
NP_001238962.2[G.gallus]	EVIGTRVFLEIDNRQ-CA-----EDSEQCFHNTAAAAALLAAQAIKG--	1633
NP_035058.2[M.musculus]	EVIGSKIFLEIDNRQ-CV-----QDSQCFKNTDAAAALLASHAIQG-----	1659
Q04721.3[H.sapiens]	EVAGSKVFLEIDNRQ-CV-----QSDHCFKNTDAAAALLASHAIQG-----	1657
XP_009243797.2[P.abelii]	EVAGSKVFLEIDNRQ-CV-----QSDHCFKNTDAAAALLASHAIQG-----	1657
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XP_012554603.1[H.vulgaris]	DNLNQNQSVVEYRDVAYKIIIE-----SVYGVYLNMSYLLFVNITKLSSGSVVANLT	3017
XP_019853114.1[A.queenslandica]	-----IEYSMEGSAHIVSYQ-GNVS-DNEW--HMTVQLNTSGLYLILDGSLVLYS-	1785
XP_032230096.1[N.vectensis]	-----LPYPVYSVKTEEK---PTVEPETGFQPEPLWIALCVGVPFLFVIGVL--AG-	1381
NP_001245510.1[D.melanogaster]	-----NDQFIHSVRGINKPGDEDNGEPANVKYVITG-IILVIALAFFGMVLSTQ-	1767
XP_019643529.1[B.belcheri]	-----QLNYPVKLSYS---GDDPEPSTPTFNPLVYVVAAVGLLVMVGLVGLMTTK-	1722
XP_032815028.1[P.marinus]	-----SLPLPLLVGSS---EV-PDVVTAAPRVQVYVLLGLVLLVMVVLGVLVGRK-	1751
XP_014025097.1[S.salar]	-----ELPYPVVSVNS---DP-TEPY-KPNFLLYLAVGAA-VIILLILVLGVL-AAK-	1724
XP_018114267.1[X.laavis]	-----TLNYPVLSVEV---EN-APMS-HQTLM-YILPVTI-AIIVILLMVVV-LAK-	1703
NP_001238962.2[G.gallus]	-----MLPYPFVSVQS---EP-LLPP-KTQLL-YLLAVAA-LIILLILLGVM-MAK-	1677
NP_035058.2[M.musculus]	-----TLYSPLVSVS---EL-ESPR-NAQLL-YLLAVAV-VIILFFILLGVI-MAK-	1703
Q04721.3[H.sapiens]	-----TLYSPLVSVS---ES-LTPE-RTQLL-YLLAVAV-VIILFILLGVI-MAK-	1701
XP_009243797.2[P.abelii]	-----TLYSPLVSVS---ES-LTPE-RTQLL-YLLAVAV-VIILFILLGVI-MAK-	1701
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XP_012554603.1[H.vulgaris]	LGFNSSVKDPLFAFDSAVKSQQFYKLTVPDPSLIADRCCKHIV-----CPMEQV----	3065
XP_019853114.1[A.queenslandica]	---NNATLSSIYL-TSP-----LFLGGLPNGLIADSVSGSL-NGCIRDVOISNTSLGL	1834
XP_032230096.1[N.vectensis]	---GKRVYTKLWL-----PEGFVRPVPVH---RRLSLR RPVVGQ -HSM	1417
NP_001245510.1[D.melanogaster]	---RRRAHGVTWF-----PEGFRAPAAVMSRR--- RRDPHGQ ---M	1800
XP_019643529.1[B.belcheri]	---RRRESGQLWY-----PEGFKLTKEKRKDARRSTR RRDPVQ -HVM	1762
XP_032815028.1[P.marinus]	---RRREQGTLWF-----PEGFILGPPSDKKK--- RRFPVQ QDVGM	1787
XP_014025097.1[S.salar]	---RRKRKHGVLWL-----PDGFLAKD--DK--- RRFPVQ QDFGM	1757
XP_018114267.1[X.laavis]	---RRKRKHGALWF-----PEGFFLHRENSNQ--- RRFPVQ QAVGM	1739
NP_001238962.2[G.gallus]	---RRKRKHGSLWL-----PEGFILRRDPSNHK--- RRFPVQ QAVGL	1713
NP_035058.2[M.musculus]	---RRKRKHGFLWL-----PEGFTLRDSSNHK--- RRFPVQ QAVGL	1739
Q04721.3[H.sapiens]	---RRKRKHGSLWL-----PEGFTLRDASNHK--- RRFPVQ QAVGL	1737
XP_009243797.2[P.abelii]	---RRKRKHGSLWL-----PEGFTLRDASNHK--- RRFPVQ QAVGL	1737
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XP_012554603.1[H.vulgaris]	CSYDTRV-ECKCTVGK-----QKSPDGE-K-CYDTCCLKGCPGQECFSNSTF---N	3111
XP_019853114.1[A.queenslandica]	I-----ENNVLVYGL-----GLLECPQSLCLPLVQCLNGGTCVDSVSVFGF	1874
XP_032230096.1[N.vectensis]	RSMNKSSDLEEGAVGG-----DLTPPQEARDAKRVKLE-----EVD----	1454
NP_001245510.1[D.melanogaster]	RNLNKQVAMQSQGVGQ-----PGAHSDDSDMPLPKRQR-----SDPVSQV	1842
XP_019643529.1[B.belcheri]	KSFTFPQGATAANVDNDNETVRDSSAWEDDMVPPEAKRMKT-----QQPTPGS	1810
XP_032815028.1[P.marinus]	KTLSQSSVEDSLIDGNQ-----NEAWLDGSPVSTKRRKLE-----EQGM---	1826
XP_014025097.1[S.salar]	KNFKTQ--DGGMIDGG-----QRWMEEEP-PKKV RTE-----DKPL---	1791
XP_018114267.1[X.laavis]	KNLSVPIVDVNLDSNQ-----NDHWSDDRGPPKKSKSE-----GQAL---	1778
NP_001238962.2[G.gallus]	KNLSVQIPEGNMADSGP-----TEHWAGDGGPPKKRVKTE-----DQAL---	1752
NP_035058.2[M.musculus]	KNLSVQVSEANLIGSGT-----SEHWVDDEGPPKKAKAE-----DEAL---	1778
Q04721.3[H.sapiens]	KNLSVQVSEANLIGTGT-----SEHWVDDEGPPKKVKAE-----DEAL---	1776
XP_009243797.2[P.abelii]	KNLSVQVSEANLIGSGT-----SEHWVDDEGPPKKVKAE-----DEAL---	1776
XP_012554603.1[H.vulgaris]	ECRCKDGG---VLS-----SDKKECIYTCEL-----KG-----	3136
XP_019853114.1[A.queenslandica]	ECSCPSGYNGTYCEVLLSTCIPNCLFDGVCDFNNMTYSCQCTL--GRQGRICDEELNI	1932
XP_032230096.1[N.vectensis]	-----ESQ-R-----VKVSEKEKDRQWTRLHREAADVTVRNCT-ALAL	1491
NP_001245510.1[D.melanogaster]	GL----GNNGGYASDHT-----MVSEYEEADQRVWSQAHLVDVVDVRA-----IM	1882
XP_019643529.1[B.belcheri]	-----DATADQ-----TLDYDDTDHRQWTQQHLEAADIRNPACLAQVAL	1850
XP_032815028.1[P.marinus]	-----L-----PEAEPEVDHRPWTQQHLEAADIRTPAL-VLAL	1859
XP_014025097.1[S.salar]	-----L-----PMGVDGGVDRREWTLQHHKAADI-----SL	1817
XP_018114267.1[X.laavis]	-----L-----LGGDDQVDSRQWTQQHLEAADIRMTPSL---AL	1809
NP_001238962.2[G.gallus]	-----L-----PEADEIDQRQWTQQHLEAADVCGSTSL---AL	1783
NP_035058.2[M.musculus]	-----L-----S-EDDPIDRRPWTQQHLEAADIRHTPSL---AL	1808
Q04721.3[H.sapiens]	-----L-----SEEDDPIDRRPWTQQHLEAADIRHTPSL---AL	1807
XP_009243797.2[P.abelii]	-----L-----SEEDDPIDRRPWTQQHLEAADIRHTPSL---AL	1807

XP_012554603.1[H.vulgaris]	C-----		3137
XP_019853114.1[A.queenslandica]	TVPAFYGNISLAYSSLSITNVQSNLILSLTFKPTSPSGLLLFNHGSNTDFSQYVSISLV		1992
XP_032230096.1[N.vectensis]	TPPQEGES-----EKPGLDITGDVARGPGGFT-----	PLHLASCR	1525
NP_001245510.1[D.melanogaster]	TPPA-HQ-----DGG--KHDVDARGPCGLT-----	PLMIAAVR	1912
XP_019643529.1[B.belcheri]	TPPQTEG-----EADPCSVDVNVVRGPDGLT-----	PLMLASFR	1883
XP_032815028.1[P.marinus]	TPPQGEA-----DD--GMDVNVVRGPNGFT-----	PLMVASFH	1889
XP_014025097.1[S.salar]	TPPQTDL-----EAD--CLDVNVVRGPDGFT-----	PLMLASLR	1848
XP_018114267.1[X.laevis]	TPPQAEQ-----DID--VIDVNVVRGPDGCT-----	PLMLASLR	1840
NP_001238962.2[G.gallus]	TPPQADQ-----EVD--VLDVNVVRGPDGCT-----	PLMLASLR	1814
NP_035058.2[M.musculus]	TPPQAEQ-----EVD--VLDVNVVRGPDGCT-----	PLMLASLR	1839
Q04721.3[H.sapiens]	TPPQAEQ-----EVD--VLDVNVVRGPDGCT-----	PLMLASLR	1838
XP_009243797.2[P.abelii]	TPPQAEQ-----EVD--VLDVNVVRGPDGCT-----	PLMLASLR	1838
XP_012554603.1[H.vulgaris]	-----		3137
XP_019853114.1[A.queenslandica]	NSSVVY-----KFDLGSGLATISSPITLGLNQWHITITAYRTGRVG----		2032
XP_032230096.1[N.vectensis]	CTLVDCCSIDD-----DKESDDSGAMVSDLLALGASYGA--RTDIEKETPLHLAAR		1575
NP_001245510.1[D.melanogaster]	GGGLDTG-----E-----DIENNEDSTAQVISDLLAQGAELNA--TMDKTGETSLHLAAR		1960
XP_019643529.1[B.belcheri]	GGGLEYY-----ED-----HQEDGEDESANVITDMLMQGANINA--QDRTGETSLHLAAR		1932
XP_032815028.1[P.marinus]	GGGLDSSLCDDEESSDGLFEDGTDDGSANVITDLICQGAALHA--QDRTGETALHLAAR		1947
XP_014025097.1[S.salar]	NGGASDCGLQAEED-----ESGGDEPCPNAISDLITQGATLMA--QDRTGETALHLAAR		1902
XP_018114267.1[X.laevis]	MGSPhL-----EE-----DDEADDPANVITDLIYQGACQLA--QDRTGETALHLAAR		1888
NP_001238962.2[G.gallus]	VGGSID-----SE-----DDEGEDSSANITDLIYQGANLQA--QDRTGEMALHLAAR		1862
NP_035058.2[M.musculus]	GGSSDL-----SD-----EDEADDPANVITDLVYQGASLQA--QDRTGEMALHLAAR		1887
Q04721.3[H.sapiens]	GGSSDL-----SD-----EDEADDPANVITDLVYQGASLQA--QDRTGEMALHLAAR		1886
XP_009243797.2[P.abelii]	GGSSDL-----SD-----EDEADDPANVITDLVYQGASLQA--QDRTGEMALHLAAR		1886
XP_012554603.1[H.vulgaris]	-----	PEGQECFSNSTFN--	3150
XP_019853114.1[A.queenslandica]	FLRVNDEELLTNTSLGTNLGLNIAGDMWLGGTDRFNIISQHAGVGTGLTGCISSVSVNGI		2092
XP_032230096.1[N.vectensis]	HSRADAARLLDHAGA-----D--PNARDKLGRTPLHLAVGADAQGVFQILLRNR-		1622
NP_001245510.1[D.melanogaster]	NP_001245510.1[D.melanogaster]	NP_001245510.1[D.melanogaster]	2007
XP_019643529.1[B.belcheri]	YARADRAKRLLDAGA-----D--ANARDNTGRTPLHAAIASDAQGVFQILLRNR-		1979
XP_032815028.1[P.marinus]	YARSDAAKRLLDAGA-----D--ANLPDNGMGRPLHAAVSADAQGVFQILLRNR-		1994
XP_014025097.1[S.salar]	YARADAARLLLDAGA-----D--ANAHDNMGRTPHAAVAADAQGVFQILLRNR-		1949
XP_018114267.1[X.laevis]	YSRADAARLLLDAGA-----D--ANSQDSMGRTPHAAVSADAQGVFQILLRNR-		1935
NP_001238962.2[G.gallus]	NP_001238962.2[G.gallus]	NP_001238962.2[G.gallus]	1909
NP_035058.2[M.musculus]	YSRADAARLLLDAGA-----D--ANAQDNMGRCPHAAVAADAQGVFQILLRNR-		1934
Q04721.3[H.sapiens]	YSRADAARLLLDAGA-----D--ANAQDNMGRCPHAAVAADAQGVFQILLRNR-		1933
XP_009243797.2[P.abelii]	YSRADAARLLLDAGA-----D--ANAQDNMGRCPHAAVAADAQGVFQILLRNR-		1933
XP_012554603.1[H.vulgaris]	-----	ECRCKDKVLSFDPKKRCINQCSLHYCKNGGSCQLKETGPVCRCSKNYSGDQC	3202
XP_019853114.1[A.queenslandica]	SINLVSSAERGLNIGE-----CNMTSCSSFPFCFNGGTCTETGSSFCQCPAGYEGGLC		2145
XP_032230096.1[N.vectensis]	---TTDLAEMEDGT-----	TPILAAARLLDLIDIV	1650
NP_001245510.1[D.melanogaster]	---ATNLNARMHDGT-----	TPILAAARLAIEGMVE	2035
XP_019643529.1[B.belcheri]	---ATDLADARTNDGT-----	TPILAAARLAVEGVVE	2007
XP_032815028.1[P.marinus]	---ATDVDARMHDGT-----	TPILAAARLAVEGMAE	2022
XP_014025097.1[S.salar]	---ATELDARMNDGT-----	TPILAAARLAVEGMVE	1977
XP_018114267.1[X.laevis]	---VTDLARMNDGT-----	TPILAAARLAVEGMVA	1963
NP_001238962.2[G.gallus]	---VTDLARMNDGT-----	TPILAAARLAVEGMVA	1937
NP_035058.2[M.musculus]	---VTDLARMNDGT-----	TPILAAARLAVEGMVA	1962
Q04721.3[H.sapiens]	---VTDLARMNDGT-----	TPILAAARLAVEGMVA	1961
XP_009243797.2[P.abelii]	---VTDLARMNDGT-----	TPILAAARLAVEGMVA	1961
XP_012554603.1[H.vulgaris]	QTLQTKSN--AL-----MIVLVSLSTVAVVLIVIVLKNRKKRIYN--ECRNDLM--		3248
XP_019853114.1[A.queenslandica]	GLQTFSCLSPPCGNGGTCIEGVAEGGYN---C---LCPLGFGGNNCNEMLQVSTPSPNRT		2199
XP_032230096.1[N.vectensis]	DLIKASCKVNVNDAQGKSALHWAAVNNEHEVT--SELCKNGAKKMDQDKGTPLFLGA		1707
NP_001245510.1[D.melanogaster]	DLITADADINAADNSGTALHWAAVNNEATEV--NILLMHANRDAQDDKDETPFLFAA		2092
XP_019643529.1[B.belcheri]	ELLNSHADANACDDNGKSALHWAATNNEEAV--ISLLSHGVNVDQDNKEETPLFLAA		2064
XP_032815028.1[P.marinus]	ELINCHADVKNVDDHGKSALHWAAVNNEATEV--LVLLKNGANKDMQDNKEETPLFLAA		2079
XP_014025097.1[S.salar]	ELVHCHADINAVDDHGKSALHWAAVNNEATEV--LVLLKNGANRDMQDNKEETPLFLAA		2034
XP_018114267.1[X.laevis]	DLINCQADVNAVDDHGKSALHWAAVNNEATEV--MVLLKNGANRDMQDNKEETPLFLAA		2020
NP_001238962.2[G.gallus]	ELINCQADVNAVDDHGKSALHWAAVNNEATEV--LVLLKNGANRDMQDNKEETPLFLAA		1994
NP_035058.2[M.musculus]	ELINCQADVNAVDDHGKSALHWAAVNNEATEV--LLLLKNGANRDMQDNKEETPLFLAA		2019
Q04721.3[H.sapiens]	ELINCQADVNAVDDHGKSALHWAAVNNEATEV--LLLLKNGANRDMQDNKEETPLFLAA		2018
XP_009243797.2[P.abelii]	ELINCQADVNAVDDHGKSALHWAAVNNEATEV--LLLLKNGANRDMQDNKEETPLFLAA		2018
XP_012554603.1[H.vulgaris]	-----	YDDEKSLELSVKNSNLDKKS-VTL	3271
XP_019853114.1[A.queenslandica]	SYQYSSPAPISLSTIISLSFHTSSNGLILYIGDVSTTRDFLSLSLVSGR-----IQ		2252
XP_032230096.1[N.vectensis]	REGSLEAV-----RILLLSYAN-----RMIADNMDKTPPEVARQRAHNDIVELL		1751
NP_001245510.1[D.melanogaster]	REGSYEAC-----KALLDNFAN-----REITDHMDRLPRDVASERLHHDIVRLL		2136
XP_019643529.1[B.belcheri]	REGSFQAA-----KILLDHYAN-----RDITDHMDRLPRDIAQERMHSDIVKLL		2108
XP_032815028.1[P.marinus]	REGSYETA-----KLLLDHFAS-----RDITDHMDRLPRDIAQERLHHDIVRLL		2123
XP_014025097.1[S.salar]	REGSFEAA-----QVLLDHYSN-----RDITDHMDRLPRDIAQERMHHDIVRLL		2078
XP_018114267.1[X.laevis]	REGSFEAA-----KMLLDYFAN-----REITDHMDRLPRDIAKDRMHHDIVRLL		2064
NP_001238962.2[G.gallus]	REGSFEAA-----KILLDHAN-----RDITDHMDRLPRDVAQDRMHHDIVQLL		2038
NP_035058.2[M.musculus]	REGSYEAA-----KILLDHAN-----RDITDHMDRLPRDVARDRMHHDIVRLL		2063
Q04721.3[H.sapiens]	REGSYEAA-----KILLDHAN-----RDITDHMDRLPRDVARDRMHHDIVRLL		2062
XP_009243797.2[P.abelii]	REGSYEAA-----KILLDHAN-----RDITDHMDRLPRDVARDRMHHDIVRLL		2062
XP_012554603.1[H.vulgaris]	TRYDHLRSSEKLG-----		3284
XP_019853114.1[A.queenslandica]	LRDYLGSPPAITASPSVPLNQWTSVTNVNRVRKDGVLVVDVSSTNGSSPGFAGLLNPAGN		2312
XP_032230096.1[N.vectensis]	SDWSIGCNSPKAAPSPSPDQSRPL--NGTASPPSMDQIS--GN-----		1792
NP_001245510.1[D.melanogaster]	DEHVP-RSPQMLSMTPQA--MIGSPP--PGQQPQLITQPTVISAGNG-----G		2180
XP_019643529.1[B.belcheri]	DEYNLVRSPPSQA-----AANCQNSF-----G--G-----H		2131
XP_032815028.1[P.marinus]	DEYNVVRNPSGP-----NGLASFPQ-----ANG-----		2146
XP_014025097.1[S.salar]	DQYNLVHSPHNG-----PNHMGGGH-----SSLVCGGNG-----A		2108
XP_018114267.1[X.laevis]	DEYNLVHSTQCG-----PGSMLSNS-----LSPAVCGSN-----R		2094
NP_001238962.2[G.gallus]	NEYNVHSPSTGH-----PGAMLNSA-----LSPVICGPN-----R		2068

NF_035058.2[M.musculus]	DEYNVTSP-----PGTVLTSA---LSPVLCGPN-----R	2090
Q04721.3[H.sapiens]	DEYNVTSP-----PGTVLTSA---LSPVICGPN-----R	2089
XP_009243797.2[P.abelii]	DEYNVTSP-----PGTVLTSA---LSPVICGPN-----R	2089
.		
XP_012554603.1[H.vulgaris]	-RINGGATFD-----DNSPAPLIRNS-----DQK--R----	3308
XP_019853114.1[A.queenslandica]	LYIGGGAGGV---GGYQVSPNAGSH--VGL-----TGCV-----DTATLR----	2347
XP_032230096.1[N.vectensis]	KVV---THFP---VSAGTTRPKTNSTSTRGARS-----KVQENNGAKRRKRRRK	1835
NF_001245510.1[D.melanogaster]	NNNGNGASGKQSNQTAQKQ-AAKKAKLIEGSPDNGLDATGSLRRKASSKKTSAASKKAAN	2239
XP_019643529.1[B.belcheri]	HFMNGPTTKQ---QRAKPKRPNGK--MQHHT-----IARADASKMRKKK	2171
XP_032815028.1[P.marinus]	AYA-HG-AKA---GKKGVRRPKNKSGVAHDAK-----CKKAQ-KKV	2182
XP_014025097.1[S.salar]	GYMGMR-PGP---QKKSRRGGAKEVGVGG--A-----TAKELKDMKAKRRKKP	2151
XP_018114267.1[X.laavis]	SFLNLK-HAA---QAKKTRRPSAKNVGPRSLPN-----LAKEPKDTKNRRRKK	2139
NF_001238962.2[G.gallus]	SFLNLK-HAS---LSKKSRKPNAGKIMPTNLTK-----D-----AKRRRK-KS	2106
NF_035058.2[M.musculus]	SFLSLK-HTP---MGKKARRPNTKSTMTPSLNP-----LAKEAKDAKGSRR-KK	2134
Q04721.3[H.sapiens]	SFLSLK-HTP---MGKKSRRPSAKSTMTPSLNP-----LAKEAKDAKGSRR-KK	2133
XP_009243797.2[P.abelii]	SFLSLK-HTP---MGKKSRRPSAKSTMTPSLNP-----LAKEAKDAKGSRR-KK	2133
:		
XP_012554603.1[H.vulgaris]	-----VNSFGLGAVISSRGVQCQVDPCHSHSPCQNG--GSCV	3308
XP_019853114.1[A.queenslandica]	DDDLPHGNRKAS-----QGG---ASSTY-----SPYGKE-LSPC--SSGANFS	2382
XP_032230096.1[N.vectensis]	LNGLN--PGQLTGGVSGVPGVPPNTNSAAQAAAAA-AAVAAMSHLEGSFVGVGMGGNLP	1872
NF_001245510.1[D.melanogaster]	LEGTGTMF-----RHMDSTAL-----SPDGLGGSFPHGNTG-TP	2296
XP_019643529.1[B.belcheri]	NGGVASGGGGDG-----APLLGLDGSASL-----SPVNSE-SSQ---SDG-TS	2206
XP_032815028.1[P.marinus]	TGGEPAVGASGNGTKAAGLLESSVTM-----SPVDSL-ESPHLYIGDA-AG	2220
XP_014025097.1[S.salar]	-----DTDNKGQLESSESVTL-----SPVDSL-ESPHA-----TS	2198
XP_018114267.1[X.laavis]	-----LSEKGVQLESSESVTL-----SPVDSL-ESPHAFASEP-TS	2167
NF_001238962.2[G.gallus]	-----CLNEKVQLESSESVTL-----SPVDSL-ESPHYTVSDA-TS	2139
NF_035058.2[M.musculus]	-----SLSEKVQLESSESVTL-----SPVDSL-ESPHYTVSDT-TS	2167
Q04721.3[H.sapiens]	-----SLSEKVQLESSESVTL-----SPVDSL-ESPHYTVSDT-TS	2166
XP_009243797.2[P.abelii]	-----SLSEKVQLESSESVTL-----SPVDSL-ESPHYTVSDT-TS	2166
:		
XP_012554603.1[H.vulgaris]	-----SSDLTYSVCVPLGYSGDQCCEISNATEGAAISQCPTSVA-----CNVNPCL	3308
XP_019853114.1[A.queenslandica]	PPAFSVVNGL-----SPQSSATG-----ISPSNSTTLSPQQ	2428
XP_032230096.1[N.vectensis]	SPYDT-----SSMYSNAMAAPLANGNPNTGAKQPPSYEDCIKNAQSMQSLQ	1904
NF_001245510.1[D.melanogaster]	PPNSMYGVGSQHLALS-----HPNLHGVDTVHTTSTPQIV-----NSFSFTNGQPMRRLS	2342
XP_019643529.1[B.belcheri]	PSLLT---SPHVAHS---LYASMEAVGC--GPPRVG-----HPMAFRN-----	2257
XP_032815028.1[P.marinus]	ASKTT---NSPL-----LGSP-----	2255
XP_014025097.1[S.salar]	SPTIT---SPGTLHT---SPGQMHAATSTLQPH-----TTM---SMTNLQSIG	2211
XP_018114267.1[X.laavis]	SPVMP---SPGVLSH---SPSLLTAP---SVQAA---HSMFSNLHEMQPLG	2206
NF_001238962.2[G.gallus]	SPMIT---SPGILQA---SPTPLAAAPAPVHTQ---HALSFSNLHDMQPLA	2180
NF_035058.2[M.musculus]	SPMIT---SPGILQA---SPNFMATAAPAPVHAQ---HALSFSNLHEMQPLA	2212
Q04721.3[H.sapiens]	SPMIT---SPGILQA---SPNFMATAAPAPVHAQ---HALSFSNLHEMQPLA	2211
XP_009243797.2[P.abelii]	SPMIT---SPGILQA---SPNFMATAAPAPVHAQ---HALSFSNLHEMQPLA	2211
:		
XP_012554603.1[H.vulgaris]	-----NGGKCI AVL-----V-NGIIEERCQCSLPFA---AGAKCEQRVSFSSAFFA----	3308
XP_019853114.1[A.queenslandica]	HSSLD-----GDGYLLFPA-----VNIPLSSITIHTIIRLSIIPNSGSL-----L	2470
XP_032230096.1[N.vectensis]	GNGLDMIKLDNYAYSMGSPFQQLLNG--QGLMGNGNGRNG---VGPGVLPGLGCMGG	1932
NF_001245510.1[D.melanogaster]	HH---T-----ADSN-S---HQ-DQSTLGRGETGLGLHLDPPVSPVSDWLASLDS	2398
XP_019643529.1[B.belcheri]	-----SQRTHQGHSLGLTSSHPQSNHR-----GAIVASGWINPMQN	2299
XP_032815028.1[P.marinus]	-----SSRPL-----LPPV-SHMLGO-Q-----QSWVG---L	2270
XP_014025097.1[S.salar]	CAANNM-----LPSV-QQLLSQ-AAQN-----NVLAGQRQLNLSDDLSRMR	2233
XP_018114267.1[X.laavis]	RGSSTV-----LPSV-SQLLSQ-HRTTPPSS---GLGRLRPANVSTWEMNRMEM	2247
NF_001238962.2[G.gallus]	PGASTV-----LPSV-SQLLSH-HHIAPPGSSSAGSLRLHPVPVPADWMNRVEM	2224
NF_035058.2[M.musculus]	HGASTV-----LPSV-SQLLSH-HHIVSPGSGSAGSLRLHPVPVPADWMNRMEV	2260
Q04721.3[H.sapiens]	HGASTV-----LPSV-SQLLSH-HHIVSPGSGSAGSLRLHPVPVPADWMNRMEV	2259
XP_009243797.2[P.abelii]	HGASTV-----LPSV-SQLLSH-HHIVSPGSGSAGSLRLHPVPVPADWMNRMEV	2259
:		
XP_012554603.1[H.vulgaris]	-----EDLTDQDLHGDFASPCGLRGS-----TSDLHDSISMPLPETTIGVPQDSSVPTTSACM	3308
XP_019853114.1[A.queenslandica]	SGA-----GNGNSHEQGLSPPYSNQSPPHSVQSSSLALSPHAYLGSPSPAKSRP---SLP	2506
XP_032230096.1[N.vectensis]	RNH---HYTQFSFRMHMTA---GLNHMPQ-----SQSPP---SGL	1986
NF_001245510.1[D.melanogaster]	VPL-----SQFTHQGHSLGLTSSHPQSNHR-----AM	2449
XP_019643529.1[B.belcheri]	KH-----GYGGMFSLLPQOMSGHPSMSQH-----HGQG-----L	2332
XP_032815028.1[P.marinus]	NN-----TQYNEMFGLVHHDNTN--HS-CIQ-----NGIMQ---ADI	2297
XP_014025097.1[S.salar]	NE-----SQYNEMFGMVPVPMH-SHPVSQ-----SGLVQ-----	2264
XP_018114267.1[X.laavis]	NE-----TQYSEMFGMVLAPAEGAHPGIA-----PQSRP-----	2279
NF_001238962.2[G.gallus]	NE-----TQYNEMFGMVLAPAEGTHPGIA-----PQSRP-----	2254
NF_035058.2[M.musculus]	NE-----TQYSEMFGMVLAPAEGTHPGIA-----PQSRP-----	2290
Q04721.3[H.sapiens]	NE-----TQYSEMFGMVLAPAEGTHPGIA-----PQSRP-----	2288
XP_009243797.2[P.abelii]	NE-----TQYSEMFGMVLAPAEGTHPGIA-----PQSRP-----	2288
:		
XP_012554603.1[H.vulgaris]	-----LYIGHAN-----PSTGNYLLVGMNE-----GVLEFRFQ	3308
XP_019853114.1[A.queenslandica]	YLPKHS-----VAPFGHT-----	2534
XP_032230096.1[N.vectensis]	TSPTHQAMRHATQKQFGGSNLNSLLGGANGGVVGGGGGGGGVGGQGPQNSPVSLGII	1999
NF_001245510.1[D.melanogaster]	LSPPHSH-----GSITGGSPAQMAAFQAL	2509
XP_019643529.1[B.belcheri]	MSPLHP-----AMINNHQHMLAFQQN	2356
XP_032815028.1[P.marinus]	LTPMNV-----TMSREQLPPIVTFQMM	2319
XP_014025097.1[S.salar]	KPTLHM-----GVARDALPPIVTFQLI	2286
XP_018114267.1[X.laavis]	ADTKHL-----GVSRSLPPIVTFQLI	2301
NF_001238962.2[G.gallus]	PEGKHM-----STQREPLPPIVTFQLI	2276
NF_035058.2[M.musculus]	PEGKHI-----TTPREPLPPIVTFQLI	2312
Q04721.3[H.sapiens]	PEGKHI-----TTPREPLPPIVTFQLI	2310
XP_009243797.2[P.abelii]	PEGKHI-----TTPREPLPPIVTFQLI	2310
:		
XP_012554603.1[H.vulgaris]	-----LGSGV---GLVETSQ---PL-----AIGQQHNITLLRTDYRGRILMSQNTTVF	3308
XP_019853114.1[A.queenslandica]	A-----PRLYSAH-----SSPN-----LCADNESRQLIVAHISINGY	2577
XP_032230096.1[N.vectensis]	SPTGSDMGIMLAPPQ-----SSKNSAIMQTIISPQQQ---QQQQQQQQQQQQQQQQQQQ	2030
NF_001245510.1[D.melanogaster]	SSSNAKQ-----QLAHS---NHNHNRMY	2560
XP_019643529.1[B.belcheri]	LYSPRNKPLMEAPQHHPQARGGAFFQSKMPMIQPSN---LQAASQSQLLASVSQSNMF	2379
XP_032815028.1[P.marinus]		2377

XP_014025097.1[S.salar]	-----APGGGQA-----LLKQPQPGQVQSQGQNGQ	2312
XP_018114267.1[X.laervis]	-----PKSGMNQ-----QTLVQQT-----	2315
NP_001238962.2[G.gallus]	-----PKGGINQ-----QALPQQA-----	2290
NP_035058.2[M.musculus]	-----PKGSIAQ-----AAGAPQT-----	2326
Q04721.3[H.sapiens]	-----PKGSIAQ-----PAGAPQP-----	2324
XP_009243797.2[P.abelii]	-----PKGSIAQ-----PAGAPQP-----	2324

XP_012554603.1[H.vulgaris]	-----	3308
XP_019853114.1[A.queenslandica]	TDGMSQGSSRHLNLSFYDFV---LFLGG---APNVPLISQ---QVYQTGFSGL---	2622
XP_032230096.1[N.vectensis]	PSN--QSSIQAC--K-----LS--NRLEEHVMMET-----T	2055
NP_001245510.1[D.melanogaster]	Q-Q--QQQQQL--GGLEFGSAGLDLNGFCGSPD--SFHSGQMNPSSIQS-----	2603
XP_019643529.1[B.belcheri]	H-D--QHGNAGH--GS-----PLGGG-----GRMHDPIPLNVI PPGE-----	2412
XP_032815028.1[P.marinus]	PSL--QQHQGI--AV-----FMQSFVGSFEGESFASNDYKFKNEKSHSQTSCVLTQT	2425
XP_014025097.1[S.salar]	PQS--QQGPETHL--HC-----PQGMLYQMPNVSLQHSLSHSLP-HPHG-----L	2351
XP_018114267.1[X.laervis]	--S-H-----AQ-----NVAGMYQMPDRARITGSSVPIA-M-----	2342
NP_001238962.2[G.gallus]	--Q--SNCAQNM--AG-----PLSSMYQISDLAQLPSASFMA-A-----	2323
NP_035058.2[M.musculus]	--Q--SSCPCPAV--AG-----PLPSMYQIPEMPRLPSVAFPTA-M-----	2359
Q04721.3[H.sapiens]	--Q--STCCPAV--AG-----PLPTMYQIPEMARLPSVAFPTA-M-----	2357
XP_009243797.2[P.abelii]	--Q--STCCPAV--AG-----PLPTMYQIPEMARLPSVAFPTA-M-----	2357

XP_012554603.1[H.vulgaris]	-----	3308
XP_019853114.1[A.queenslandica]	-----VSVVQLGYSMNPEVPVFDTSVGENVTTC-S-----	2652
XP_032230096.1[N.vectensis]	LH---HN---NQSMCV-PVESGMFKEKHHTPPSAHSYGTSSYDS-SPQ-----KLPI	2099
NP_001245510.1[D.melanogaster]	--SMSSGSSPSTNMLSPSSQHNAQAFYQYLTSPSSQHSQSGH-----TPQH-----LVQTLD	2650
XP_019643529.1[B.belcheri]	LPPHSHQTVLPFGSCAQFSSNNPAEQLTPTPSQHSNGNPQSHECTPTHYLSHAETIVPE	2472
XP_032815028.1[P.marinus]	VPPPQEANPSVQSSQLAKREGAAPAEQFTPTPSQHSRGEQSPGH---APPP---GTPGEH	2479
XP_014025097.1[S.salar]	AHGMVQDGG--SRQQLPYQAMQSPVDKYPTPPSQHSYATAGSEGTTPGYPA---HPPSEH	2407
XP_018114267.1[X.laervis]	--MHQHDGQLSQTMLTSYHPLQNPMGKYPTPPSQHSYAS---TDKTPNHNG---HLPGEH	2394
NP_001238962.2[G.gallus]	--IPQDGGQVPQTILPAYHQFQSSMGKYPTPPSQHSYAS-SATERTPSHNR---HLQGEH	2377
NP_035058.2[M.musculus]	--MPQDGGQVAQTIIVPTYHFFPASVGKYPTPPSQHSYASSNAERTPSHGG---HLQGEH	2414
Q04721.3[H.sapiens]	--MPQDGGQVAQTIILPAYHFFPASVGKYPTPPSQHSYASSNAERTPSHSG---HLQGEH	2412
XP_009243797.2[P.abelii]	--MPQDGGQVAQTIILPAYHFFPASMGKYPTPPSQHSYASSNAERTPSHSG---HLQGEH	2412

XP_012554603.1[H.vulgaris]	-----	3308
XP_019853114.1[A.queenslandica]	-----	2652
XP_032230096.1[N.vectensis]	SYLTSPSPESPKDWSSS-PSS-HSDWSNC-----	2125
NP_001245510.1[D.melanogaster]	SYPTSPSPESPGHWSSSSPRS-NSDWSEGVQSPAANNLYIS-----GGHQ-----	2693
XP_019643529.1[B.belcheri]	NYLTSPSPSPDQWSSSSPHSATSDWSGDISPPAAQSQRQPYI-PETHN-----	2520
XP_032815028.1[P.marinus]	PYLTSPSPETPERWSTCSPRSGASDWSGVSPPGLAARARRPA-----	2523
XP_014025097.1[S.salar]	PYLTSPSPSPDPWSSSSSPHS-NSDWSDVTTSTPTPLGNPHALPPLHHTHIPEQLQPQSQQT	2466
XP_018114267.1[X.laervis]	PYLTSPSPSPDQWSSSSSPNS-ASDWSDVTTSTPTPNGS---QRM-PATHMPE-----	2440
NP_001238962.2[G.gallus]	PYLTSPSPSPDQWSSSSSPHS-ASDWSDVATSPGNN-----QRGPAAAHVPE-----	2422
NP_035058.2[M.musculus]	PYLTSPSPSPDQWSSSSSPHS-ASDWSDVTTSTPTGGGGGQGRGP-GTHMSE-----	2463
Q04721.3[H.sapiens]	PYLTSPSPSPDQWSSSSSPHS-ASDWSDVTTSTPTGGAGGGQGRGP-GTHMSE-----	2461
XP_009243797.2[P.abelii]	PYLTSPSPSPDQWSSSSSPHS-ASDWSDVTTSTPTGGAGGGQGRGP-GTHMSE-----	2461

XP_012554603.1[H.vulgaris]	-----	3308
XP_019853114.1[A.queenslandica]	-----	2652
XP_032230096.1[N.vectensis]	-----	2125
NP_001245510.1[D.melanogaster]	-----ANKGSEAIYI	2703
XP_019643529.1[B.belcheri]	---TRQGGHSALPVFI	2533
XP_032815028.1[P.marinus]	--DPQQQ-LHNLQALM	2536
XP_014025097.1[S.salar]	QQNPQQPQRGNMQVFA	2482
XP_018114267.1[X.laervis]	-----QSHNGMQVYA	2450
NP_001238962.2[G.gallus]	-----QQRNNMQVYA	2432
NP_035058.2[M.musculus]	-----PPHSNMQVYA	2473
Q04721.3[H.sapiens]	-----PPHNNMQVYA	2471
XP_009243797.2[P.abelii]	-----PPHNNMQVYA	2471