

CASC3

Homo sapiens:

>NP_031385.2 protein CASC3 [Homo sapiens]
MADRRRQRASQDTEDEESGASGSDSGGSPLRGGGSCSGSAGGGGSGSLPSQRGGRTGALHLRRVESGGAK
SAEESCESEDGIEGDAVLSDYESAEDSEGEEGYSEENSKVELKSEANDAVNSSTKEEKGEKPDTKS
TVTGE**RQSGDQGL**STEPVENKVGGKPKHLDDDEDRKNPAYIPRKGLFFEHLRGQTQEEEVVRPKGRQRK
LWKDEGRWEHDKFREDEQAPKSRQELIALYGYDIRSAHNDDIKPRRIKPRYGSPPQRDPNWNGERLNK
SHRHQGLGGTLPPrTFINRNAAGTGRMSAPRNYSRSGGFKEGRAGFRPVEAGGQHGGRSGETVKHEISYR
SRRLEQTSVRDPSPEADAPVLGSPKEEAASEPPAAAPDAAPPPDRPIEKKSYSRARRTRTKVGDAVKL
AEVPPPPPEGLIPAPVPVETTPPTPTKTGTWEAPVDSSTSGLEQDVAQLNIAEQNWSPGQPSFLQPRELR
GMPNHIMGAGPPPPQFNRMEEEMVGQGRAKRYSSQRQRPVPEPPAPFVHISIMEGHYYDPLQFGQPIYTH
GDSAPLPPQGMIVQPEMHLPHFGLHPHQTAPLPLNPGLYPPPVSMSPGQPPPPQQLLAPTYFSAPGVMNFG
GNPSYYPAPGALPPPPPHLYPNTQAPSQVYGGVTTYNPAQQQVQPKPSPPRRTPQPVTIKPPPEVVSR
GSS

Pongo abelii:

>XP_024090145.1 protein CASC3 [Pongo abelii]
MADRRRQRASQDTEDEESGASGSDSGGSPLRGGGSCSGSAGGGGSGSLPSQRGGRIGALHLRRVESGGAK
SAEESCESEDGIEGDAVLSDYESAEDSEGEEGYSEENSKVELKSEANDAVNSSTKEEKGEKPDTKS
TVTGE**RQSGDQGL**STEPVENKVGGKPKHLDDDEDRKNPAYIPRKGLFFEHLRGQTQEEEVVRPKGRQRK
LWKDEGRWEHDKFREDEQAPKSRQELIALYGYDIRSAHNDDIKPRRIKPRYGSPPQRDPNWNGERLNK
SHRHQGLGGTLPPrTFINRNAAGTGRMSAPRNYSRSGGFKEGRAGFRPVEAGGQHGGRSGETVKHEISYR
SRHLEQT¹PVDRDPSPEADAPVLGSPKEEAAAPAAAPDAAPPPDRPIEKKSYSRARRTRTKVGDAVKLAE
EVPPPPPEGLIPAPVPVETTPPTPTKTGNWEAPVDSTTGGLEQDVAQLNIAEQSWSPGQPSFLQPRELRGM
PNHIMGAGPPPPQFNRMEEEMVGQGRAKRYSSQRQRPVPEPPAPFVHINIMEGHYYDPLQFGQPIYTHGD
SPAPLPPQGMIVQPEMHLPHFGLHPHQTAPLPLNPGLYPPPVSMSPGQPPPPQQLLAPTYFSAPGVMNFGN
PSYYPAPGALPPPPPHLYPNTQAPSQVYGGVTTYNPAQQQVQPKPSPPRRTPQPVTIKPPPEVVSRGS
S

Mus musculus:

>NP_619601.2 protein CASC3 [Mus musculus]
MADRRRQRASQDTEDEESGASGSDSGSPARGGGSCSGSVGGGGGSLPSQRGGRGGGLHLRRVESGGAKS
AEESCESEDGMGEDAVLSDYESAEDSEGEEDYSEENSKVELKSEANDAADS¹SAKEKGEEKPESKGTVT
GE**RQSGDQGL**STEPVENKVGGKPKHLDDDEDRKNPAYIPRKGLFFEHLRGQTQEEEVVRPKGRQRLWK
DEGRWEHDKFREDEQAPKSRQELIALYGYDIRSAHNDDIKPRRIKPRFGSSPQRDPNWIGDRSSKSHR
HQGGPGNLPPrTFINRNTAGTGRMSASRNYSRSGGFGDGRTSFRPVEVAGQHGGRSAETLKHEASYSRR
LEQT¹PVDRDPSPEPADPLLGSPKEEVA²SETPAAVPDITPPAPDRPIEKKSYSRARRTRTKVGDAVKAEE
VPPSEGLASTATVPETTPAAKTGNWEAPVDSSTTGGLEQDVAQLNIAEQSWSPGQPSFLQPRELRGVPNH
IMGAGPPPPQFNRMEEEMVGQGRAKRYSSQRQRPVPEPPAPFVHISIMEGHYYDPLQFGQPIYTHGDSPA
PLPPQGMIVQPEMHLPHFGLHPHQSFGPLPNPGLYPPPVSMSPGQPPPPQQLLAPTYFSAPGVMNFGNPNY
PYAPGALPPPPPHLYPNTQAPPQVYGGVTTYNPAQQQVQPKPSPPRRTPQPVSIKPPPEVVSRGSS

Gallus gallus:

>XP_046789397.1 protein CASC3 isoform X6 [Gallus gallus]
MADRRRQRASQDSEDDSDSAASDSGDSAASAARSRS¹SGSASPRPSHRPPRGAAGALSAGPRGRGADSAAGG
GAAKSAPQSECESEDGIEGDAVLSDYESAEDSEAEEDYSEESAKVELKQDSNGSCSAAKAEKGDEKP
DSKGAVTGE**RQSGDQGL**STEPVENKVGGKAPKHLDDDEDRKNPAYIPRKGLFFEHLRGQTQEEEVVRPKG
RQR²LWKDEGRWEHDKFREDEQAPKTRQELIALYGYDIRSAHNDDIRPRMRKPRFGSPQRDPNWSNER
PNKPRRHQGTGDTSAPRPTFTTSRSAGTGRMPPPRNYPRVGGYKESRPGYRASEVSAQPSRNGEQSKQES
GYRAKRAEQSPPRKKSFEVEAVHIHGSFVKEEGALENQDAAQPPPPDRPIEKKSYSRARRTRTKAGDAGK
LADDVPALEAPATPKPIQ³AETSPPPAKSSNWESPVESGLDGLQEMIQMNLTQ⁴QNWSPGQSQTQPRELR
GIPNHMHVGTGPPPPQFNRMEEEMAVQGGRVKRYSSQRQRPVPEPAPFVHISIMEGHYYDPLQFGQPIYTH
GENPAPLPPQGMIVQPEMHLPHFGLHPHQTAPMANPGLYPPPVSMPPGQPPPPQQLLAPTYFSPPGVMMNF
GNPGYPPPGALPPPPPHLYPNTQAQSQVYGGVTTYNTVQQQVQPKPSPPRRTSQPVTIKPPPEVVSR
APVNLSE

Xenopus laevis:

>AAH47246.1 MGC54001 protein [Xenopus laevis]
MADRRRRRRRASQDSEELGEEEEASDSAGSGGESVGP¹IRQERAEQSKTEPARAEQETRRAEPAREGKES
ECESEDGIEGDAVLSDYESADESEEEEAHNSEEDPLKTTLKQENNVEEAPATREQKPKSKGAVTGE**RQSG
DQGL**STEP²EENN³TSKKSKQLDDDEDRKNPAYIPRKGLFFEHLRGHVNDDEVVRPKGRHPRKLWKDEGRW
VH⁴DRFREDEQAPKSRRELVSIYGYDIRSCRNP⁵EEIHPRRPCKPRFSSPSRREENDEKPSRPSNRYQDSGV
TQPLRPY⁶TNRNAPPSSKVGPSRTYSRQGGYKENRASYQSEEEAAPHTYERRQDYGGHRSRSTDQGFPPPR
EYSPEADPIIKEEAFTEKQTAEPSPPPPDRPVEKKSYSRARRSRIKVGDAKSMEDTTAAELPPPPFVPP
AVAAETPAPLNVKQGNWEPPAEGGMSGIDEELSKMNLSEQSWNQGPAYISPRGIPNPMHMGAGPPQYS
RMESMAVQAGRVKRYSSQRQRPVDPDPAAMHISLMESHYYDSLQFGQPIYAHGDS⁷SSPSMP⁸PPQGMIVQPEMH
LSHPGMHPHQS⁹PATISTPNIYPAVSLTPGQPPPPQLLPPPYFTAPS¹⁰NVMNFGNPTYYPYPGALPPPPAH
LYPNAQAQSQVYGGVTTYNFVQQVQQQVLKPKSPPRRTSQPVTIKPPPEPEPQSLFVALTF

Salmo salar:

>XP_014047999.1 protein CASC3-like [Salmo salar]
MADRRRRRRRASQDSEEDDESCSGSESGKSLSTTKPRVRDPEPVEAPVRVVPKND¹AESECESEDGVGE
AVLSDYESADPEENGSHSEGGEEEEVVPPPAEPKPSPAADTPAAEGELQEGGGKEEGEKGVSK²EVKCE
DKGNLAGE**RQSGDQGL**STEDSENKGA³KPQKQLDDQDRNNPAYIPRKGMFFEHDVRGNQAQEEERPKGRNR
KLWKDEGRWEH⁴DRFREEQAPKSR⁵EELVAIYGYDIRNGGVSNERSYRQRKPRHSTSPVRDKRWRDGDGER
PIHTSWQGGGNSNRSAPLAVALQQSGPPPSAA⁶PNTQRNNNPPRPSSHP⁷PPRGFGQNRPPQAQYRNDNRQ
ESQRPFGKAHPAELQTRSLPMDGERGPRGRGNRGAHTERS⁸SSVVVEEIRSEEDDERNTT⁹TVT¹⁰SVYHN
RHYSGKDRERD¹¹SAPRRQ¹²QRRGGSAPADNPVTRDASPAERPV¹³EEKSSYLARRTRTRATELDKQASLE
EPASTASSALTSE¹⁴PWQPGQSQGDAGDSSQATVLTGLDQDLARLSLAGQNWQNPS¹⁵SFLRAEMRGIPNS
MHMGAGPPQYSNIEELGAGNRAKRYSSQRQRPSEPA¹⁶PMHIGVMESHYYE¹⁷PMYQ¹⁸GPIYAHGDSAPL¹⁹PF

PQGMVLVQPEMHLPHPGHPGHPGLHHPQSSGMPMPALYAAPPVSMSPGQPPFQQLLAPPFYPPPGVMTFG
NTNYPYPAGATLPPMYPNPPAQSQVYGQSQVYGGVTYYDFMQQQAQPKSPPRRSSQFVTVKPPPEVGYG
PE

Petromyzon marinus:

>XP_032831431.1 protein CASC3 isoform X2 [Petromyzon marinus]
MADRRRRRTGASQDSDEEEDEEEESDLSPGRCPEKAAATPARAAESECESECVPERDGVVLSGYESADDN
YSHYSEDEKEEEEGSCSVTDDDEVAEEGSSVPPAITGVVAGEKIASTPADKRPERPHRV**RKPSHGSQ**EAFE
DDAPPTGAGGKNSKRDEEEEDQKNPAFVPRKGLFFEHDIRGGNNKEDARAKVHNRKLWRDAGRWEHDFR
EDEQAPKSREELVALYGYDIRSGAHADDARPLRRPRYRSPTGRWSRESPPVNRGPYQAPKREPVERPARL
RDEDRDTERRPAPRRPGPTTAGPAALPGRPRAYVEQRAYVEPRARAHTQGDSSRDQPPGTPAARDGARSS
PQRHQQRHQHNGNGEEEGEKRAEILSAGTEAEVGARGAPAAAAAATVAPATGDAAFAVDLAQDKAPER
KSYSRVRRLRNKPSELPGQASTTDPVSPAPLAAPAPSTVPLVALPETQAATALPHQHNPQQLQQLQPQAP
PLKPLGERTRIAALLPQPLWDVPVLEPSFVGRLEHGMACIISLGQTNWPGAQPHYLPTQREHRGGATHLP
VNSVPPFFNRIEDLGGQAGRAKRYSSQSRSPVPEPHPTPPMHIPLIEGSIYDPNTAYQAPLYGHGGDSFA
AIPFQGIWQPDNLNPHGLHHPQSPHMYAPPVSMATGQPPPPGQMLGYFPSNIMYPGAALPNPGYTYT
PAPIPPPPPPAHFPPPPAQSQVYGGVTYYNTAQQAQPKSPPRRPSQPVSVKPPPEEGQAEKKE

Branchiostoma belcheri:

>XP_019629453.1 PREDICTED: protein CASC3-like [Branchiostoma belcheri]
MADRRRRRPSESEGEEGEETLSTSQASLGSTEDPSHSGEDDRDRQSPCESEGEHAEALSEYESAEEDRA
GEADESQAEQGDSDTEHEDTRADDDTETEDTQETSEETQETGDTROLDTSKSTVSTDGSDKGKKLE**KCS**
GTGSEAPDSEDQAEENLDDDDRNPAPFIPRKGDFFEHDIRGEEDDKQGRPPVKGRKLWQDEGKWQHD
FNEDEQRPKPVEELIAIYGYDPRRESSPDNIRPRRGRPPRGGGRGGRPPPTLRDFVERPPPPRRGFFP
RNRTDVQTRNRAQYTDQVQRWAANTNNYRDNGPLDNVSDENRNQPEVSRQKPSVEQAVPNVINNVPSNP
MPKNSENGVTVAPMPVKAPTSTESEHQHPAPQEKRSYTRYRRSTQAPRTSPFQQQNIKRKMENLSLQPG
ESVAQDRGHADGSPQHPEERHGPNRSDRPKRYSSLRQRPMEQVVPFNMVKGVTYYNQGYRGEQFARGST
PFVVDGFIQPHPTGPPAPPHQGMIVSDVNLPPGMAHPAMYNPAMTMAPVPPQLLPPFFSAGGMVNYAA
APNPVSSYAPIFQAGPTAPTNPVPPVYTSPPHPSAQVVRGVTYFNNQMPPQVLKRSPPARRNAAIPIEPP
PDVRGDTASEEGAQTPEA

Drosophila melanogaster:

No homolog found.

Hydra vulgaris:

No homolog found.

Nematostella vectensis:

No homolog found.

Amphimedon queenslandica:

No homolog found.

Alignment

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XP_019629453.1[B.belcheri] MADRRRRRPFSESEGEEGEE--ETLSTSQASLGST----- 32
XP_032831431.1[P.marinus] MADRRRRRT--GASQDSDEEEDEEEE--ESDLSGPRG----- 32
XP_014047999.1[S.salar] MADRRRRRRRASQDSDEEDDESGSGSESGKSLSPPTK-----PRVRD----- 41
AAH47246.1[X.laevis] MADRRRRRRRASQDSSEELG--EEEEASDSDAGSGGGE---SVGPTRQERAEQSKT--EP- 51
XP_046789397.1[G.gallus] MADRRRRQR--ASQDSEDDSDSAA--SDSGDSAASAARSRSGSASPRPSHRPPRGAAGALSA 57
NP_619601.2[M.musculus] MADRRRRQR--ASQDTEDEESGASGSDS--GSPARGGGSCSGSVG-----GGGSGSLPS 49
NP_031385.2[H.sapiens] MADRRRRQR--ASQDTEDEESGASGSDSGGSPLRGGGSCSGSAG-----GGGSGSLPS 50
XP_024090145.1[P.abelii] MADRRRRQR--ASQDTEDEESGASGSDSGGSPLRGGGSCSGSAG-----GGGSGSLPS 50
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XP_019629453.1[B.belcheri] -----EDPSHSGEDDRDRQSPCESEGEH---AEALSEYESAEEDRAGEADEDQA 79
XP_032831431.1[P.marinus] -----PE-----KAAAI PARAAESECSEGVPERDGVVLSGYESADDNYSHYSEDEKEE 81
XP_014047999.1[S.salar] -----PEPVEAPAVRVVFPKNDASECESEDGV-GE-AVLSDYESADPEENGSHSEGGEE 93
AAH47246.1[X.laevis] -----ARAEQETRAEPAREGKESECESEDGIEGD-AVLSDYESADEEEEEAHNSEED 104
XP_046789397.1[G.gallus] GPRGRG---ADSAAGGGAASAPQSECESEDGIEGD-AVLSDYESAEDSEAEEDYSEEE 113
NP_619601.2[M.musculus] QRGGRGGGLHLRRVESGGAKSAEESCESEDGMGEG-AVLSDYESAEDSEEGEE--DYSEEE 107
NP_031385.2[H.sapiens] QRGGRGTALHLRRVESGGAKSAEESCESEDGIEGD-AVLSDYESAEDSEEGEEGYSEEE 109
XP_024090145.1[P.abelii] QRGGRIGALHLRRVESGGAKSAEESCESEDGIEGD-AVLSDYESAEDSEEGEEGYSEEE 109
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XP_019629453.1[B.belcheri] EQGDSSTEHEDTR---ADDDTETEDTQET--SEETQETGDRDLDT-SKSTV----- 125
XP_032831431.1[P.marinus] EEGSCSVTD-----DEV-----AEEGS-----SVPPAITGVVAGEKIATST 116
XP_014047999.1[S.salar] EEVVVPPAAEPKPSPAADTPAAEGELQEGGGKEEGKGVSKVCEDKGNLAGERQ--- 150
AAH47246.1[X.laevis] PLKTTT-----K-----QENNVEEAP---ATREQPKPSKGAVTGERQ--- 138
XP_046789397.1[G.gallus] SAKVEL-----K-----QDSNGSCESAIAEKGDGKPSKGAVTGERQ--- 151
NP_619601.2[M.musculus] NSKVEL-----K-----SEANDAADSSA-KEKGEEKPESKGTVTGERQ--- 144
NP_031385.2[H.sapiens] NSKVEL-----K-----SEANDAVNSSTKEEKGEKPDTKSTVTGERQ--- 147
XP_024090145.1[P.abelii] NSKVEL-----K-----SEANDAVNSSTKEEKGEKPDTKSTVTGERQ--- 147
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XP_019629453.1[B.belcheri] -STDGS DKGKLE RQSGDGS EAPDSED-----QAENLDDDDRRNPAFIPRKGDFFE 176
XP_032831431.1[P.marinus] PADKRPERPHRV RKP SHGS QEAPEDDAPPTGAGGKNSKRDEEEEDQKNPAFVPRKGLFFE 176
XP_014047999.1[S.salar] -----SGDGGQSTEDSE--NKGAKP-GQKLDDQDRNNPAYIPRKGMFFE 192
AAH47246.1[X.laevis] -----SGDGGQSTEPVE--NNTSKKSQKQLDDDEDKKNPAYIPRKGLFFE 181
XP_046789397.1[G.gallus] -----SGDGGQSTEPVE--NKVGKKAPKHLDDDEDKKNPAYIPRKGLFFE 194
NP_619601.2[M.musculus] -----SGDGGQSTEPVE--NKVGKKGPKHLDDDEDKKNPAYIPRKGLFFE 187
NP_031385.2[H.sapiens] -----SGDGGQSTEPVE--NKVGKKGPKHLDDDEDKKNPAYIPRKGLFFE 190
XP_024090145.1[P.abelii] -----SGDGGQSTEPVE--NKVGKKGPKHLDDDEDKKNPAYIPRKGLFFE 190
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XP_019629453.1[B.belcheri] HDIRGEEDDKQGGRPVFKRRKLWQDEGKWQHDLFNEDEQRKPFVEELIAIYGYPDRRES 236
XP_032831431.1[P.marinus] HDIRGGNNKE-DARAKVHN--RKLWRDAGRWEHDFREDEQAPKSREELVALYGYDIRSGA 234
XP_014047999.1[S.salar] HDVVRGNAQEE--ERP KGRN--RKLWKDEGRWEHDFREDEQAPKSREELVAIYGDIRNGG 249
AAH47246.1[X.laevis] HDLRGHVNDE-EVRPKGRHPRKLWKDEGRWVHDFREDEQAPKSREELVSIYGDIRSCR 240
XP_046789397.1[G.gallus] HDLRGQTQEE-EVRPKGRQ--RKLWKDEGRWEHDKFREDEQAPKTRQELIALYGYDIRSAH 252
NP_619601.2[M.musculus] HDLRGQTQEE-EVRPKGRQ--RKLWKDEGRWEHDKFREDEQAPKSRLQELIALYGYDIRSAH 245
NP_031385.2[H.sapiens] HDLRGQTQEE-EVRPKGRQ--RKLWKDEGRWEHDKFREDEQAPKSRLQELIALYGYDIRSAH 248
XP_024090145.1[P.abelii] HDLRGQTQEE-EVRPKGRQ--RKLWKDEGRWEHDKFREDEQAPKSRLQELIALYGYDIRSAH 248
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XP_019629453.1[B.belcheri] SPDNIRPRRGRPPRGGRG---GGRPPPRRTL----- 264
XP_032831431.1[P.marinus] HADDARPLR--RPRYRST---GRWSRESFPVNRGPYQAPKREPVE--RPARLRDEDRT 287
XP_014047999.1[S.salar] VSNE-RSYRQKPRHSTSPVRDKWRDGDGERPIHTSWQGGGNSNSRSLAVALQQSGP 308
AAH47246.1[X.laevis] NP EEIHPRRPGKPRFSSPSRREEN--DEKPSRPSNRYQ-DSGVT---QPL----- 284
XP_046789397.1[G.gallus] NPDDIRPRMRKPRFGS--PQRPDPNWSNERPNKPPRHQGTGTS---APP----- 297
NP_619601.2[M.musculus] NPDDIKPRRIRKPRFGSSPQRPDPNWI GDRSSKSHRHQGTGTS---LPP----- 290
NP_031385.2[H.sapiens] NPDDIKPRRIRKPRYGSPPQRPDPNWNGERLNKSHRHQGTGTS---LPP----- 293
XP_024090145.1[P.abelii] NPDDIKPRRIRKPRYGSPPQRPDPNWNGERLNKSHRHQGTGTS---LPP----- 293
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XP_019629453.1[B.belcheri] -----RDFVERPPPP--RRGFPPRNRDVTQTRNRAQYTQDVQR-----WAANTNNY 308
XP_032831431.1[P.marinus] ERRPAPRRPGPTTAGPAALPGRPAYVE-----QRAYVEPRARAHTQ-GDS-----S 333
XP_014047999.1[S.salar] PPSAAPTQQRNNPPRPSSHPPRGFQGNR-PPQAQYRNDNRNQESQRP GPKAHPAEPLQT 367
AAH47246.1[X.laevis] -----RPYTNRNAPSSKVPSPRTYSR-----QGGYKEN-----RASYSQSEE----- 321
XP_046789397.1[G.gallus] -----RTFTSRSSACTGRMPPPRMYPR-----VCGYKES-----RPGYRASE----- 334
NP_619601.2[M.musculus] -----RTFINRNTAGTGRMSASRNYSR-----SGGFKDG-----RTSFRPVE----- 327
NP_031385.2[H.sapiens] -----RTFINRNAAGTGRMSAPRNYSR-----SGGFKEG-----RAGFRPVE----- 330
XP_024090145.1[P.abelii] -----RTFINRNAAGTGRMSAPRNYSR-----SGGFKEG-----RAGFRPVE----- 330
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XP_019629453.1[B.belcheri] RDNGPLDN-----VVS DENRNQPEVSRQKPSVEQ-----AVPNV---I--- 343
XP_032831431.1[P.marinus] RDQPPG-----T-PAARDGARSSPQRHQQRHQHNGNGEEEGEKRAEILS-AGTE--- 381
XP_014047999.1[S.salar] RSLPMDGGERGPRGRGNRGAHTERSSSVV-----VEEIRSEEDDERNTTTVTTSVYHNR 421
AAH47246.1[X.laevis] -----EAAPTYERR-----QDY-----GGHRSR 340
XP_046789397.1[G.gallus] -----VSAQP-SRNGEQS-----KQE-----SGYRSR 355
NP_619601.2[M.musculus] -----VAGQHGGRS AETL-----KHE-----ASYRSR 349
NP_031385.2[H.sapiens] -----AGGQHGGRSGETV-----KHE-----ISYRSR 352
XP_024090145.1[P.abelii] -----AGGQHGGRSGETV-----KHE-----ISYRSR 352
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XP_019629453.1[B.belcheri] -----NNVPSNPMPKNSE-----NGVTVAPMPVKAPTSTESEHQHPAPQEKRSY 387
XP_032831431.1[P.marinus] -----AEVGARGAPAAAAAATVAPA--TGDAAFVADLAQDKAPERKSY 423
XP_014047999.1[S.salar] HYSKGKDREDRSAPRRQ-----EQQ-RGGSAPPA--DNFVTRDASAPAPERVVEKSY 470
AAH47246.1[X.laevis] STDQGPPPPPREYSPEADPI-----IKE-EAFTE--K---QTAEPSPPPPDRPVEKSY 387
XP_046789397.1[G.gallus] RAE--QSPPRDKSPEVEAVHIHGSVPKE-EGAL--E---NQPDAAQPPPPDRPIEKSY 405
NP_619601.2[M.musculus] RLE--QTPVRDPSPEADAP-VLGSPEKE-EVASETPA---AVPDITPPAPDRPIEKSY 401
NP_031385.2[H.sapiens] RLE--QTSVRDPSPEADAP-VLGSPEKE-EAASEPFA---AAPDAAPPPPPDRPIEKSY 404
XP_024090145.1[P.abelii] HLE--QTPVRDPSPEADAP-VLGSPEKE-EAAS--PA---AAPDAAPPPPPDRPIEKSY 402
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XP_019629453.1[B.belcheri] TRYRRSTQAPRTSPFQ----- 403
XP_032831431.1[P.marinus] SRVRLRNKPSLPGQASTTDPVSPAPLAAPASTVPLVALPETQAATALPHQHNPPQQLQ 483
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XP_014047999.1[S.salar]	SLARRTRTRATELDKQASLEEP-----AS-----TAS-----	497
AAH47246.1[X.laervis]	SRARRSRIVGDAGKSMEDTTAAEL-PPPPVPP--AVAAEFTPA-----	429
XP_046789397.1[G.gallus]	SRARRTRVKAGDAGKLADDVPALEA-PAT----P---KP-IQAETS-----	442
NP_619601.2[M.musculus]	SRARRTRTKVGDAVKAAEEVPPFSE-GLA----S---TATVPETTP-----	439
NP_031385.2[H.sapiens]	SRARRTRTKVGDAVKAAEEVPPFPE-GLI----P---APPVPETTP-----	442
XP_024090145.1[P.abelii]	SRARRTRTKVGDAVKAAEEVPPFPE-GLI----P---APPVPETTP-----	440
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XP_019629453.1[B.belcheri]	-----QONIRKRMENLSL-	416
XP_032831431.1[P.marinus]	LQQPQAPPLKPLGERTRPIAALLPQPLWDVPVL-----EPSPVGRLEHGMQISL-	533
XP_014047999.1[S.salar]	-----SSALTSEPWQGFQSQSDAGDSSQATVLTGLDQDLARLSLA	538
AAH47246.1[X.laervis]	-----FLNVKQGNWEPP-----AEGGMSGIDEELSKMNLS	459
XP_046789397.1[G.gallus]	-----PPAKSSNWESP-----VESGLDGLQEQMIQMNLT	472
NP_619601.2[M.musculus]	-----AAKTGNWEAP-----VDSTTGGLEQDVAQLNIA	467
NP_031385.2[H.sapiens]	-----TPPTKTGTWEAP-----VDSTTGGLEQDVAQLNIA	472
XP_024090145.1[P.abelii]	-----TPPTKTGNWEAP-----VDSTTGGLEQDVAQLNIA	470
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XP_019629453.1[B.belcheri]	----QPGEESVAQD-RGHADGSPQHPEERH-----GPNRSDRPKRYSSLRQRM	460
XP_032831431.1[P.marinus]	GQTWNPGAQPHYLPTQREHRGGATHLPVNSVP-PFFNRIEDLGGQAGRAKRYSSQSRSPV	592
XP_014047999.1[S.salar]	GQNWAQNPSSFLR---AEMRGLPNSMHMGAP-PQYSNIEELGA-GNRAKRYSSQQRQPS	593
AAH47246.1[X.laervis]	EQSWNGQGPAYISP-----RGIPNFMHMGAGP-PQYSRMEGMAVQGRVKRYSSQQRQPV	513
XP_046789397.1[G.gallus]	EQNWSFGQSQFIQP--RELRGIPNHHMVGTPPPQFNRMEEMAVQGGRVKRYSSQQRQRP	530
NP_619601.2[M.musculus]	EQSWSPGQPSFLQP--RELRGVFNHIMHAGPPPPQFNRMEEMGVQSGRAKRYSSQQRQRPV	525
NP_031385.2[H.sapiens]	EQNWSFGQPSFLQP--RELRGMPNHHMAGPPPPQFNRMEEMGVQSGRAKRYSSQQRQRPV	530
XP_024090145.1[P.abelii]	EQSWSPGQPSFLQP--RELRGMPNHHMAGPPPPQFNRMEEMGVQSGRAKRYSSQQRQRPV	528
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XP_019629453.1[B.belcheri]	PEQVVPNNMVKGV---TYYNQ--GYRGEQFARGSTPPVVDGPIQPHFTGPPAPPHQGMIV	515
XP_032831431.1[P.marinus]	PEPHTPPMHIPLIEGSYYDPNTAYQAPLYGHGG-----DSPAAIPFQGMIV	639
XP_014047999.1[S.salar]	PE--PAPPMHIGVMESHYYEPM-SYQGPIYAHG-----DSPAPLPFQGMIV	636
AAH47246.1[X.laervis]	PDP-A--AMHISLMESHYYDSL-QFQGPITYAHG-----DSSPSMPPQGMIV	555
XP_046789397.1[G.gallus]	VPE-PAPPMHISIMEGHYYDPL-QFQGPITYTHG-----ENPAPLPFQGMIV	574
NP_619601.2[M.musculus]	PEP-PAPPVHISIMEGHYYDPL-QFQGPITYTHG-----DSPAPLPFQGMIV	569
NP_031385.2[H.sapiens]	PEP-PAPPVHISIMEGHYYDPL-QFQGPITYTHG-----DSPAPLPFQGMIV	574
XP_024090145.1[P.abelii]	PEP-PAPPVHINIMEGHYYDPL-QFQGPITYTHG-----DSPAPLPFQGMIV	572
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XP_019629453.1[B.belcheri]	S-DVNLP-----PGMAHPAMYN-PAMTMA--PPVPPQLLPPPPFSAGGM	555
XP_032831431.1[P.marinus]	QDNLNLPH-----PGLHPHQSPTHM---Y-APPVSMATGQPPPPQMLG-YFP--SN	684
XP_014047999.1[S.salar]	QPEMHLPHGHPGHPGLHPHQSSGMPNPAALYAAPVSMSPGQPPQQLLAPFFYPPP-G	695
AAH47246.1[X.laervis]	QPEMHLSH-----PGMHPHQSPATISTPNIYP-APVSLTPGQPPPPQQLLPPPYFTAPSN	608
XP_046789397.1[G.gallus]	QPEMHLPH-----PGLHPHQTPAPMANFGLYP-PPVSMPPGQPPPPQQLLAPTYFSPP-G	626
NP_619601.2[M.musculus]	QPEMHLPH-----PGLHPHQSPGFLPNFGLYP-PPVSMSPGQPPPPQQLLAPTYFSAP-G	621
NP_031385.2[H.sapiens]	QPGMNLPH-----PGLHPHQTPAPLPNFGLYP-PPVSMSPGQPPPPQQLLAPTYFSAP-G	626
XP_024090145.1[P.abelii]	QPEMHLPH-----PGLHPHQTPAPLPNFGLYP-PPVSMSPGQPPPPQQLLAPTYFSAP-G	624
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XP_019629453.1[B.belcheri]	VNYA--AAPNVSSYAPIPQAGPTAPTNNVPPVYTSHPHPSAQVVRGVTYFNNQMPP---	610
XP_032831431.1[P.marinus]	IMYPGAALPNPGYTYTPAPI-----PPPPPPPAHIFPPPAQSQVYGGVTYYNPAQQQ---	737
XP_014047999.1[S.salar]	VM---TFGNTNYPYPAGAT---LPP-MYNPPAQSQVYGGVTYYNPAQQQ---	743
AAH47246.1[X.laervis]	VM---NFGNPTYYPYPGAL---PP---PPAHLYPNAQAQSQVYGGVTYYNPAQQQ---	657
XP_046789397.1[G.gallus]	VM---NFGNPGYPYPGAL---PPP---PPPHLYSNTQAQSQVYGGVTYYNPAQQQ---	673
NP_619601.2[M.musculus]	VM---NFGNPNYPYPGAL---PPP---PPPHLYPNTQAQSQVYGGVTYYNPAQQQ---	668
NP_031385.2[H.sapiens]	VM---NFGNPSYPYPGAL---PPP---PPPHLYPNTQAQSQVYGGVTYYNPAQQQ---	673
XP_024090145.1[P.abelii]	VM---NFGNPSYPYPGAL---PPP---PPPHLYPNTQAQSQVYGGVTYYNPAQQQ---	671
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XP_019629453.1[B.belcheri]	-QVLKRSPPARRPNAAPIEPPDPVRGDPTASEEGAQPT	649
XP_032831431.1[P.marinus]	-AQPKPSPPRRPSQPVSVKPPPEEGQAEKE-----	767
XP_014047999.1[S.salar]	-AQPKPSPPRRSSQPVTVKPPPEVGYGPE-----	772
AAH47246.1[X.laervis]	-QVLKPSPPRRTSQPVTIKPPPEEQSL-FVALTF----	691
XP_046789397.1[G.gallus]	-VQPKPSPPRRTSQPVTIKPPPEVVSRAVNLSE----	707
NP_619601.2[M.musculus]	-VQPKPSPPRRTPQPVSIKPPPEVVSARGSS-----	698
NP_031385.2[H.sapiens]	-VQPKPSPPRRTPQPVTIKPPPEVVSARGSS-----	703
XP_024090145.1[P.abelii]	-VQPKPSPPRRTPQPVTIKPPPEVVSARGSS-----	701
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