

Supplementary Materials: Analysis of High Molecular Mass Compounds from the Spider *Pamphobeteus verdolaga* Venom Gland. A Transcriptomic and MS ID Approach

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Section S1. Full-length translated sequences for putative protein ORFs corresponding to phospholipases A₂, phospholipases D, phospholipases B, kunitz-type, hyaluronidases, lycotoxins toxins, CRISP proteins, Hephaestin-like protein and venom metalloproteinase.

Pairwise alignments and amino acid sequences of phospholipases A₂ translated from *Pamphobeteus verdolaga*. Residues highlighted in grey indicate the signal peptide, while magenta blue highlighted residues, indicates the propeptide according to Spider|ProHMM from the arachnoserver. Residues highlighted in yellow shows cysteines potentially forming disulfide bridges.

PhospholipaseA₂-1-Pverdolaga:

XLGTGKSPVVAVETIDVFRPDSLWDA^{CM}KMVALGVSAIGQLLIDQATQTDGRVIGRAQAM^{CS}MLNIPYYRLNPQLTENVGDLTDDNKTTLVKMLWETTAYMHSMRQELEQL^CNNYEDSGLD

CLUSTAL O(1.2.4) multiple sequence alignment

A0A087UHX4_Ca-ind_PLA2_(Fragment) PhospholipaseA2-1-Pverdolaga	MVLIQ ^{ML} DELERILGKPVVQHFDLIA ^{GT} STGGILALVLATGKSMKE ^{CL} YFRLKDKVFV	60 0
A0A087UHX4_Ca-ind_PLA2_(Fragment) PhospholipaseA2-1-Pverdolaga	GTRPYDADLLESFLKKELGESTVMGDI ^{EP} KIMITATRGDRKPADLHIFRNYKSPLEILN	120 0
A0A087UHX4_Ca-ind_PLA2_(Fragment) PhospholipaseA2-1-Pverdolaga	HIEKDILTNEPLNP ^{EQ} LIWQAARATGAAPTYFRASGPYIDGGLISNNPTLDALTEIHQ	180 0
A0A087UHX4_Ca-ind_PLA2_(Fragment) PhospholipaseA2-1-Pverdolaga	CNQSLTAVGKRDQVCKIKVIVSMGTGRPPLVAVDTIDVFRPDSLWGA ^{CRM} -ALGVTNLGQ -----X ^{LG} TGKSPVVAVETIDVFRPDSLWDACKMVALGVSAIGQ	239 39
A0A087UHX4_Ca-ind_PLA2_(Fragment) PhospholipaseA2-1-Pverdolaga	LLVDQATQTDGRV ^{TAR} ALAVCGMLNIPYFRLNPQLTENVALDETNTKTLVKMLWETTAYM LLIDQATQTDGRVIGRAQAMCSMLNIPYYRLNPQLTENVGDLTDDNKTTLVKMLWETTAYM	299 99
A0A087UHX4_Ca-ind_PLA2_(Fragment) PhospholipaseA2-1-Pverdolaga	RCMKDELEELKKLLTT---- HSMRQELEQLC ^{NN} YEDSGLD	315 119

PhospholipaseA₂-2-Pverdolaga:

MAAESVADDVLR^{CC}VNLSSEFRDFY^CPYDIPSV^{EG}PPTPLEFARNWVSPNKPVIFRNAVKHWP
ALKKWTVSYLR

CLUSTAL O(1.2.4) multiple sequence alignment

XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	MAEAAVEAVRRCLASFEEARELCFPEVPYLDSPPSPLQFFREWCPNKPCVIRNAF -MAAESVADDVLRCCVNLSEFRDFYCPYDIPSVEGPPTLEFARNWVSPNKPVIFRNAV **::: * ** ::: * *: * : * : :*: *: *: *: *: *: *	60 59
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	NHWPALKRWTLDYLRREIMGEKLVSAVTPNGYADAVYQDWFMPEERLTPFSAFLDILEK KHWPALKKWTVSYLK :*****: *: *	120 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	KVTSPGVFYVQKQCSNLTEEFPELMDLLEPEIPWMSEALGKKPDVNFNLGESAATSLH -----	180 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	KDHYENLYCVISGEKHFLHPSPDRPFIPHELYPPATYHISEDGNFIVMDKMSKVPWI -----	240 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	PLDPLNPDLERYPEYAKAKPLRQCTVKSGEMLYLPSLWFFHHVQQSHGCIANVWYDMEDYL -----	300 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	KYSYVQLDLSLTAMTPTYADTMILYLRQYPQWGIHSYGEVDSLPLSCKGTGVQYLEVY -----	360 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	GFHIIERTNYFNALKRFLPLPSIFHAMATQMPMVGTFFCYTLFVKIIQARHIPARDLWS -----	420 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	FSDCYVTLWLSTSKKAVTKTISNTSNPVWNEFQFVIQTQVKNVLEKLKYDEDDVTKD -----	480 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	DLIFIVTYDISKVKPGETIQENFTLNAGPESLEVEFKMEKICCGFEQIITNDILVAREV -----	540 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	SCLEIQMDKGNETCKEHNIELVWNEFEEAEKINQDSEAFQFHYVKNGEPIKAKLK -----	600 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	SNFFKEKFLGDTPAHSHVLLKTLPLEEETEVALSITENAEKLQLKVNDCLGDLDRLEEC -----	660 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	DLCAAEQDFLCKRKKHVARALENLLQKLNHEVPVIAVMATGGGARAMSAFYGHLSALQ -----	720 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	KLNLDCITYLCGASGSTWTMRSLYEDNDWSQKDLIGPIHKAQGHIVRNKSNVFSLEALQ -----	780 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	FYDQELRRRRQEGYSVSFTDMWLIIDRMFHDESNKSLDQQQAVNKGQNPLPLYVALNV -----	840 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	KEDAQTTFEFKENCEFSPYEVGFSGYGAIRSEDFGSEFYMGATDEDKPESRICFLEGIW -----	900 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	SNIFSLNLVDVWNLVQLWQWPFSGQEEDNSKGSTSTTQVSEYHATCDTPSIFHGLTRRP -----	960 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	IGEGKPNFLRGLQHLKDYQNKSFSGWQDSYLDQLPNHLTPLEKELCLVDAGYINTSFP -----	1020 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	PLLKERNVDVVISLDYHLMETKFKSIENMSKYCIDQKIPFPKIVLTEERSNPKCYLF -----	1080 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	EDKENPEAPIILHFLVNGSFKEYRKPQIKRKSAAKFEGEVLDSSMSPYKMTDLYTSD -----	1140 74
XP_003214621.2_cytosolic_PLA2_(predicted) PhospholipaseA2-2-Pverdolaga	EFNKLKSLCDYNIQNNELILQALWSAIEGGNISKL -----	1176 74

PhospholipaseA2-3-Pverdolaga:

MLSLSTHSRFVVSFTLLSLLISSTTSYRIPKRSVRPSPVIFVPGDGGSQLQAKLNKPETVHYYCN

KKTDYYFDLWLNLELLVPYVLD**C**WIDNMRLIYDNVTRKTTNAPGVDIRVPFGNTSTVEWLD
PSQIAPSAFYFVRIVQGLVDEGYTRGVLDKGAPYDYRKAPNEMANYYKNVKQMTEEMYFKLN
KTRITYV**C**HSMG**C**PVMLYFFNRQTQDWKDDTHVKALITLGGAWGGAVKAMKAFASGENLGV
YVINHLLLRKEQRTSPSLAYMTPSDFWKKDEILVVTEKQNYTIGNYYDFFQDIRFPVGVEMW
KDTYNLTRDLIPPGVEVH**C**MHG VNVSTIERLVYKHLEFPDSNPTLIQGDGDGTVNLRSLEG**C**L
RWKGNOKOKVVHKPLNNVDHMGVLYDDDVIQYIKOVSS

CLUSTAL O(1.2.4) multiple sequence alignment

Accession	Protein Name	Sequence	Length
A0A087U096_Group_XV_PLA2_ (Fragment)	PhospholipaseA2-3-Pverdolaga	MFISCNVSVLAAGVWFLAFLRLHVTANHLLNRADRHSPVLVPDGGGSLAKLDPKEI MLSLSTHSRFVWSVFTLLSLLSISSTYSRIPKRSVRPSPVIFVPGDGGSQLAKLNKPEI	60
A0A087U096_Group_XV_PLA2_ (Fragment)	PhospholipaseA2-3-Pverdolaga	VHYFCNRKKTENYFSLWLNLELLVPYVVDWVDNMRMRYVDNETRTSSNSPGVDIRVPGFGN VHYCYCNKKTIDYFDFLWLNLELLVPYVLDGWIDNMRLLYDNYTRKTTNAPGVDIRVPGFGN	120
A0A087U096_Group_XV_PLA2_ (Fragment)	PhospholipaseA2-3-Pverdolaga	TTSVDWLDPDSQISPAYFVNIIDMLVTQGYTRGVDRGAPYDFRKAPNEMTDYFKRLKNL TSTVEWLDPDSQIAPSAFYFRIVQGLVDEGYTRGVDLKGAPYDYRKAPNEMANYNKKVQKM	180
A0A087U096_Group_XV_PLA2_ (Fragment)	PhospholipaseA2-3-Pverdolaga	TEDTYEKNISQTKVTFICHSMGCPIMSYFFNQQTQAWKDEYIKALVSLGGAWGGAVKAMKT TEEMYFKLNKTRITTYVCHSMGCPVMLYFFNRQTQDWKDTHTVKALITLGGAWGGAVKAMKA	240
A0A087U096_Group_XV_PLA2_ (Fragment)	PhospholipaseA2-3-Pverdolaga	FTSGENLGVFVISQTNVRKEQRTCPSLAYMMPDLLWGKDEILMITANKNYTVSNYYEFF FASGENLGVYVIHLLRKEQRTSPSLAYMTPSDTFWKKDEILVVTETKQNYTIGNYYDDF	300
A0A087U096_Group_XV_PLA2_ (Fragment)	PhospholipaseA2-3-Pverdolaga	QDIDFPVGYEIKDYTRYARTGLSPPGVEVHCLHGLNVTDTVKLDFRNTSHFPDNPCLI QDIRFPVGWEMWKDNYNLTR-DLIPPGVEVHCHMGVNVST-IERLVYKHLFEPDSNPTLI	360
A0A087U096_Group_XV_PLA2_ (Fragment)	PhospholipaseA2-3-Pverdolaga	YGDGDGTVMNVRSLRACLQWGQKQKQVNVHAATYVNDHMGILADAHVLEYIKNVVHQQ QGSDGDGTVMNLRSLLEGCLRWKGNQKQKVNVHKLNNVDHMGVLYDDVDYIQKQVSS-	417

PhospholipaseA₂-4-Pverdolaga:

XFVNNIC¹TSSVLDTRKGAGLILNPLRGLSLIP²C³FNFS⁴PFSP⁵TSPSDDMLFKGLTEAVPTQSKTLY
LVDGGLTFENLPFPLLLRPORGIDVYLAFDFSSRDADH

CLUSTAL O(1.2.4) multiple sequence alignment

A0A087UL94_Cytosolic_PLA2_(Fragment)	MLNPGFWKDFINNIFTSSVLDRKGAGRVFNPLRGLSLIPCFPFSPFSPSPTSDNTLFK	60
PhospholipaseA2-4-Pverdolaga	-----X FVNINICTSSVLDRKGAGGLTLNPLRLGSLIPCFFNFSPFSPSPTSDDDMLFK	52
	::* *:	
A0A087UL94_Cytosolic_PLA2_(Fragment)	GLTEPAPTNSKTYLVLDGGLTFNLFPPLLRSQRAVDIYISDFSSREHDSPPFKELL	120
PhospholipaseA2-4-Pverdolaga	GLTEAVPTQS KTYLVLDGGLTFNLFPPLLRPQRIGDIVLYAFDSSRRADH-----	103
	::* *:	
A0A087UL94_Cytosolic_PLA2_(Fragment)	SEKWARLNNCLFPPIHDLAEEYIKHPKCEYVFKDPV	157
PhospholipaseA2-4-Pverdolaga	-----	103

PhospholipaseA₂-5-Pverdolaga:

XPSQSKKCTCSFDCSGGDSMEIVPQNCRVLCQLDGGGIRGLVLIQLLDQLEKVLGIPVNLQFDWI
AGTSTGGVLALLLAQGKSVKECRCLYFRLKDRVFVGMRPYDAEPLKILQKELGYETMMSDV
TGARVMVTATKSDRHPAELHVFERNYDSPMEILTQEDLDPFHNTPLPKPSEQLVWKVARATGS
APTYFRAFGAFLDGGGLISNNPTLDALTEIHOQNOAYRVTHOEKIKEIDX

CLUSTAL O(1.2.4) multiple sequence alignment

A0A087UHX4_Ca-ind_PLA2_(Fragment)	-----MVLIQMLDELEIRILGKPVVQH	21
PhospholipaseA2-5-Pverdolaga	XPSQSKKCTCSFDCSGGDSMEIVPQNCRLCLDGGGIRGLVLIQLLDQLEKVLGIPVNL	60

A0A087UHX4_Ca-ind_PLA2_(Fragment)	FDLIAGTSTGGILALVLATGKSMKECRCLYFRLKDKVFGTRPYDADLLESFLKKELGES	81
PhospholipaseA2-5-Pverdolaga	FDWIAGTSTGGVLALLAQGKSVKECRCLYFRLKDRVFGMRPYDAEPLKILQKELGYE	120

A0A087UHX4_Ca-ind_PLA2_(Fragment)	TVMGDIEKPKIMITATRGDRKPADLHIFRNYKSPLEILNHIEKDILTNEPLNPREQLIW	141
PhospholipaseA2-5-Pverdolaga	TMMSDVTGARVMVTATKSDRHPAELHVFNRNYDSPEILTQEDLPFHNTPLPKPSEQLW	180

A0A087UHX4_Ca-ind_PLA2_(Fragment)	QAAATGAAPTYYFRASGPYIDGGILSNPTLDALTEIHQCNSLTAVGKRQVCKIKVIV	201
PhospholipaseA2-5-Pverdolaga	KVARATGSAPTYYRAFGAFLDGGILSNPTLDALTEIHQCNSQAYRVTHQEKIKED--	238

A0A087UHX4_Ca-ind_PLA2_(Fragment)	SMGTGRPLVAVDTIDVFRPSLWAGACRMALGVTNLGLLDVQATQTDGRVTRALAVCG	261
PhospholipaseA2-5-Pverdolaga	-----	238
A0A087UHX4_Ca-ind_PLA2_(Fragment)	MLNIPYFRLNPQLTENVALDETNTKTLVKMLWETTAYMRCKDELEELKKLLTT	315
PhospholipaseA2-5-Pverdolaga	-----	238

PhospholipaseA2-6-Pverdolaga:

MTICTSNSKYLFLVLQILWILPFLA FNVKRWANNSDDCNYDLQVENDGPVTLDPITFYAVLE
 CAAEEHYVYIFQDNAVPPHRIQVDGSTGANVSFVYNANIYRPGVYILKVSFSGMWSPVLVG
 IASTSTFVISEYIPGSLNISDIKVRNQGGSLYISSGSVTNLTINLHYPSSVYPLLETSSYWNVEKDQ
 FITVDPFIYNFTQPGTYRISVSAVARVPVYNVLAVPTQIMKYKWGYFNTVATVKDSMTAVNLT
 GNTYLKHGQLNLNLDVSC TSGSPFEYCWKIFQPFENVTDLT CPSPIVTTKCSFPIIYFQESGNYQ
 VAILVDNYITSIQRNIEVHVYDVS LKQPLSTVILPLVCAVLAIFIITIGIVIHIRENQQFDIETADFD
 FLQSDVIVVETFWKMYHSILQVLC LRREVQSNNYLRLVSPDASSSHYGSVPXIGAVRRIIIIVTV
 WMIGRCHHVSKSLTAEFLYWFLRLRFQHTVKEKLFDSNPASTWNWPHFRNCNYLLVL

CLUSTAL O(1.2.4) multiple sequence alignment

A0A0J7L0J5_Ca-ind_PLA2	MYMVDVEVSY-RTWGIWTFDTSARIEFITEYLNQNVTAQTNTKIAGDYISSVNETKL	59
PhospholipaseA2-6-Pverdolaga	MTICTSNSKYLFLVLQILWIL-PFSLAFNVKRWANNSDDCNY-----DLQVENDGPV	51
	* : : * : * : : * : : : * : : : * : : : * : : : * : : : * : : : *	
A0A0J7L0J5_Ca-ind_PLA2	MIDIRKGDYDFIQKATAISTYFI-----DCKYYGQTNDFVFAYNFTSPGMTH	107
PhospholipaseA2-6-Pverdolaga	TLDPITFYAVLECAAAEYHYVYIFQDNAVPPHRIQVDGSTGANVSFVYNANIYRPGVYI	111
	: * : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *	
A0A0J7L0J5_Ca-ind_PLA2	-----EIGALVIASYNPQTTTTLVPPTTTTAPINVTTVSPNAIMTN	148
PhospholipaseA2-6-Pverdolaga	LKVSFSGMWSPVLVGIASTSTFVISEYIPGSL-----NISDIKVRNQGGSLYISS	163
	: : * : : * : : : * : : : * : : : * : : : * : : : * : : : * : : : *	
A0A0J7L0J5_Ca-ind_PLA2	PNGTRITVP--LTTTMLPT-----TVASADPSIKPATAAP--PIAVSTIDAA	191
PhospholipaseA2-6-Pverdolaga	GSVTNLTINLHYPSSVYPLLETSSYWNVEKDQFITVDPFIIYNFTQPGTYRISVSAVAR	223
	. * : * : : : : * : : : * : : : * : : : * : : : * : : : * : : : *	
A0A0J7L0J5_Ca-ind_PLA2	NIYLPYICSNTSLIPDPNKTYGYFYKKIHVRAPVTNISVEGTNWIQPDMLSLNVTCKG	251
PhospholipaseA2-6-Pverdolaga	PVYNV----LAVPTQIMKYKWGYFNTVATVKDSMTAVNLTGNTYLKHGQLNLNLDVSC	278
	: * : : : : : : : * : : : * : : : * : : : * : : : * : : : * : : : *	
A0A0J7L0J5_Ca-ind_PLA2	SGPFSKCLQFHGKYNVTGNETCNNAELRSCNFSILHYFLEPSVYTIILINNEVKNQV	311
PhospholipaseA2-6-Pverdolaga	SGPFEYCWKIFQPFEN-VTDLTCPSPIVTTKCSFPIIYFQESGNYQVAILVDNYITSIQ	337

A0A0J7L0J5_Ca-ind_PLA2	YPLTINIYKVTTPQLSVIWPVSCSLVAVVLVIFGVAYYIQSARFTVEVADFDFGQSN	371
PhospholipaseA2-6-Pverdolaga	RNIEVHVYDVS LKQPLSTVILPLVCAVLAIFIITIGIVIHIRENQQFDIETADFDLQSD	397
	: : : * : * : : * : : : * : : : * : : : * : : : * : : : * : : : *	

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CLUSTAL O(1.2.4) multiple sequence alignment

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A0A087SVA4_PLA2_(Fragment)      MLPDKFCVIFLWMSLAFAYVSSGKLRRLQDLDLADMFDTLTGLDPTDYPYGNWCGYG 60
PhospholipaseA2-7-Pverdolaga    -----MTLGAPNIRRKIKRDLADMFELTQLDPTTEYPYGNWCGYG 44
                                   ::  :  *  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
A0A087SVA4_PLA2_(Fragment)      GQGKPVVDHIDSCCQIHDECYGQS-EKKCSNVQVHVQYAWKINNATIIICSD-EANCEASI 118
PhospholipaseA2-7-Pverdolaga    GDGEILDRIIDRCCEIHRCYGVKSENVCNEQVHIINYQWNRENDTITCDGNTSKCEMEA 104
                                   *  *  :  :  *  *  *  *  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
A0A087SVA4_PLA2_(Fragment)      CKCDKEVEECIAQHSHSYSEHYRFIRKSR----- 147
PhospholipaseA2-7-Pverdolaga    CMCDRDVVLCHKHNGDYSHEVRYVDSKPKTSGVPQWSSMNDKTKRSDGSEIPLMGRM 164
                                   *  *  *  *  *  *  *  *  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
A0A087SVA4_PLA2_(Fragment)      ----- 147
PhospholipaseA2-7-Pverdolaga    GNMSLIFX 172

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PhospholipaseA2-8-Pverdolaga:

MGFLLTAALTFILLAGYSPFSAEKPLQIRRNKRSLFDLNDMIKQLTGRLGLDFIGYGNYC GFGGE
 GKPVDDIDRCCCKMHDICYDFAQNDDCAEDPNVVYKIKYGWQQKSFGVQCSFSQSKCMKV
 CICKDVRFAKCLKNYINEYNNSNKHEKDLQELLEEVQQMSK

CLUSTAL O(1.2.4) multiple sequence alignment

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A0A087TLC5_PLA2_(Fragment)      -----MVTLAWAVSSGVLFFVKGCSSVLDLGNMLRMVTGRNPLDFVNYGNIC 49
PhospholipaseA2-8-Pverdolaga    MGFLLTAALTFILLAGYSPFSAEKPLQIRRNKRSLFDLNDMIKQLTGRLGLDFIGYGNYC 60
                                   ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
A0A087TLC5_PLA2_(Fragment)      GLGSGPVVDKIDRCCKMHDICYDKASDTVCGEEKPHL--AAYTWKYAAGKIKCNKVDRLP 107
PhospholipaseA2-8-Pverdolaga    GFGGEGKPVDDIDRCCKMHDICYDFAQNDDCAEDPNVVYKIKYGWQQKSFGVQCSFSQSK 120
                                   *  *  *  *  *  *  *  *  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
A0A087TLC5_PLA2_(Fragment)      CGLASCKDAKFAICSIYKDSYDPRNKRTRPIFSIISNIAQLHPTRKSSSEGISIRIG 166
PhospholipaseA2-8-Pverdolaga    CMKVVCICKDVRFAKCLKNYINEYNNSNKHEKDLQELLEEVQQMSK----- 165
                                   *  *  *  *  *  *  *  *  :  :  :  :  :  :  :  :  :  :  :  :  :

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PhospholipaseA2-9-Pverdolaga:

MERKYLLEYCAVVLGSIITYPQSLFAGVKNVLDVSNVNAIVEEVSLGLRSLSAGLDFVDQFVQTAG
 SEECFLFHCPSPGKKLVNPQKYKPVPSGCGAYGVTLVKNVSPQKEFTECCNYHDIYGTCLSKKEI
 CDEKFDKCLNKA CAKQAKEIGEKKFGDC KMAAKVFYAGTVALGCKAFLDAQAEACICPEA
 WSVRLCVRSTRQICVVYGEDAIAPRTA

CLUSTAL O(1.2.4) multiple sequence alignment

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XP_011150082.1_Group_XIIA_Sec_PLA2_(Predicted) MDLSRYRKFIIVLTFLAYAWSGYSGLLSNLDAVLAAESVFHDFENAITVARIKIDI 60
PhospholipaseA2-9-Pverdolaga    ---MERKYLLEYCAVVLGSIITYPQSLFAGVKNVLDVSNVNAIVEEVSLGLRSLSAGLDFV 56
                                   *  *  *  *  *  *  *  *  :  :  :  :  :  :  :  :  :  :  :  :  :
XP_011150082.1_Group_XIIA_Sec_PLA2_(Predicted) HEVFDAAVEENCYFQCPDGSAPKPDWNHKKPRNCCSLGIEVSQEYLPLAEMTKCCDFHD 120
PhospholipaseA2-9-Pverdolaga    DQFVQTAGSEECFLFHCPSPGKKLVNPQKYKPVPSGCGAYGVTLVKNVSPQKEFTECCNYH 116
                                   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
XP_011150082.1_Group_XIIA_Sec_PLA2_(Predicted) ICYDICTDKENCLEFKPKYKPCDTY-QTTGLTIVNCGAAKVLFTGTTALGCCSFL 179
PhospholipaseA2-9-Pverdolaga    ICYGTICSKKEICDEKFDCLNKA CAKQAKEIGEKKFGDC KMAAKVFYAGTVALGCKAFL 176
                                   *  *  *  *  *  *  *  *  :  :  :  :  :  :  :  :  :  :  :  :  :
XP_011150082.1_Group_XIIA_Sec_PLA2_(Predicted) DAQKEACCPDKGSTRNKKPKKAA-QAGGEL----- 210
PhospholipaseA2-9-Pverdolaga    DAQKEACCPDEAVSVRLCVRSTRQICVVYGEDAIAPRTA 215
                                   *  *  *  *  *  *  *  *  :  :  :  :  :  :  :  :  :  :  :  :

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PhospholipaseA2-10-Pverdolaga:

FGYIMVLKNGSLSDNDSEEVATGENLTMIKILDGNGYLKDADIRCTWSIDMERFDLEGTSLN
 TYYPDGMYSYIAVAVFATLPSSKTVFGLFTKELVVKVPVSDITISGNPFIHHNEVLNLNVSWTGT
 PFEYCWDIINSNETVEGNFTCMVIVTYDTSFPVTRYFQKNGTYTMAIHVSNDVKLVKRNMEIIV

FSVLPKSQLSTVIIPIVCSLLTLVIIAIGIAYYRQRRQLIVEVASFDFHDNSDSYRERTFFEQLWDS
FRCRGCCPSLSVRSDCLPSENEPLLT

CLUSTAL O(1.2.4) multiple sequence alignment

E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	MQTAYFYCQFIWGWCFLQVTATDYVKLSYDGPVLGANITFRADLYEQSWFPQKQYKY	60 0
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	VWSDSLKNTYMIITLNTVFWNTSYPRNNTSGNYKMTLQVYNKIHKLFPIWIFVTSDSI	120 0
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	DFEITEYLNNGNMTIKQNNKIMRDYISSINEAKLIADIIHKEDYDFIIQKAMTISTFWFID	180 0
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	CQYYGQTNDFTFAYNFTNPGTTHEIEALVIASDNPTTTTILPPTTTTATNVTTPPNIT	240 29
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	TASLNGTHVTAVTTMLPTTIASANPAIIASPI TVS---MTDATNISFP-----YVC	289 74
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	SNISFIPDPKKIYGYFHKIYVRVPISNISVEGTNWIQPWDMLSLNVTCKGSGPFSKCL	349 134
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	QFHHGKYNVTGNETCSNVEHLHSCNFSILHYFLEPSVYIILILNNEIGAHYPLTINIY	409 193
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	KVTTKQLSVIVVPVTCSLVAWLIVFGVAYYIQRARFTVEANFDFGQKASGLIVPLP	469 252
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	QNI VTHHKISTMAWLGTIANNVLRN--IVFSDVPPNVVQEV RPEQYSNRRIHSREDGIVL	527 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	YGPGEIKNQDKYEIVLHRPCTETLHQAYS LFRSETLEEADARFLIYKDKVPVLVQIAREI	587 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	CNVGKIQKLCDTLVEHPAWTLAHLAAYFALHDAFMHAAVNSQLNSGDLTGISPLQVAIQ	647 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	TNNLRVTELLIAASKSLEHLHDNANTVYHYAATSTKEIILALGSGLPNSLNSNSNGHTP	707 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	IHVACQNDKPECVKALLIGADVNI PATEGQPSSPGYVGDFLHNKPNVLHAEDMKFGGTP	767 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	LHWSRSEVITALIDTNCIDALNFEGRTALHVMVMRKRLPCVALLSHMASVNIVDNDG	827 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	NTPLHLAVEAETLAIVQTLIGFGADIDARNWKSETPRHKANIDTTEGNKIIYLLHAVGAE	887 287

E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	KCPAEMTGCHLGCKYGENYGTIAPSEPPRYVPRITILDQMLHVSSMEKMAEQGRDKRIKGG	1007 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	RLLCLDGGGIRGLVLIQTLLLEIESVLKRPVWHCFDWIAGTSTGGILALGLAAGKSLRECQ	1007 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	ALYFRIKEDAFVGSRPYNSEGLEKVLKECLGTYTMADIDKPKIMITGVLADRPVDLHL	1067 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	FRNYESPALLKVPGNMFKTTLSSREQLLWKAARATGAAPSYFRAFGRFLDGGLIANNP	1127 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	TLDAMTEIHEYNLALKATGREKEAIPLSLVVSI GTGLMPTTVTLNEIDVFRPESLWDTAK	1187 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	LAFGISALGTL LVDQATASDGRVVD RARTWCSMIGIPYYRFNPQLTEDVAMDEKSD EILA	1247 287
E2B1P4_Ca-ind_PLA2 PhospholipaseA2-10-Pverdolaga	HMIWTAKAFMHANRDQVKELAAIIDRDTNLND	1280 287

PhospholipaseA2-11-Pverdolaga:

XGDLVDTDPYVVLKVPGPSNGKKRTKYFNNTINPTWKETFTFVLDPKKNYELEVLMDANYT
IDQRLGX

CLUSTAL O(1.2.4) multiple sequence alignment

A0A087UL97_Cytosolic_PLA2_(Fragment)	MECETLADQLLLSEQPISEVPPLSLQVFQVTPDSCNINLVTVVEAHKIKGWVGDLVDK	60
PhospholipaseA2-11-Pverdolaga	-----XGDLVDT	7

A0A087UL97_Cytosolic_PLA2_(Fragment)	PDPYVILRIPGSPNGMKRTKHFNNTSSPTWNEEFFVLDPQKEYELEITLMDANYTIDEK	120
PhospholipaseA2-11-Pverdolaga	PDPYVWLKVPGSPNGKKRTKYFNNNTINPTWKETFVLDPKEKNYELEVLMDANYTTDQR	67
	*****::***** ***** ***** *****::*****::*****::*****::	
A0A087UL97_Cytosolic_PLA2_(Fragment)	MG-	122
PhospholipaseA2-11-Pverdolaga	LGX	70
	.*	

PhospholipaseA₂-12-Pverdolaga:

MSIIRDILGGFRKVSQVDDPFRVLEVNVEDYLTVDVVCREDCLVLYKANDRGVMKLEIVVQL
HINHSSNKNNKVYSLHRSEDETNCQILFSQMCQKIPILIDYVPEVGLSKMALQNVSQVIRENLA
WNAAHIAAHFGYTDCKFKYKTMASEISEPCCEGLTQTPLVHAIKASQFPVVALVALDVVMDIV
DCNGDSIFHYAATTTKEIIQALS VKPCVPVINMLNHDGHTPLHLACMADKPECVKELLRAGA
DVNMA SIVDVDEVDRAQAAEMPSKLLSDVMHTHAQRLYMDDMKTGGTPLHWSKTSeltaI
LIEYGCHIDAKNFEGNTALHVMVLRNRISC AVTLLSHGANVDIQGADGNTPLHLAVKSGDIY
LVYAFVAFGANVNAINNKGETPRHILATEKRPGFEEMLYALHIVGAERCQRRTPWCKDGCCEP
GOHFNGIPSENPPVLNKTTLDDLLGAT

CLUSTAL O(1.2.4) multiple sequence alignment

XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	----- MSIIRDILGGFRKVSQVDDPFRVLEVNVEDYLYTDVVCREDCLVLYKANDRGVMKLEIV	0 60
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	---VSIPPADGAVSCSLLRTKDQVAAEVSVFQLRDKLPLLLCVPDLL-SKDLVQEVVL VQLIHNSNKNKVSLSHSEDETNCILFSQMCQKIPILIDYVPEVGLSKMALQNVSQ	55 120
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	LVRNNPSWTLAHLAHLGLVDCFKNQKVAAQICQPAQDTLATPLHIAVRAQKLSNVQVLM VIRENLAWNAAHIAAHFGYTDCFKYKTMASEISEPCEGTLQTPHVAIKASQFSPVVALV	115 180
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	GMDAPLNLTDHNGDTIYHAAVTTKELIKALSVPAPTAVINQVNNNGYTPQLACLTDK ALDVMDIVDCNGDSIFHYAATTTKEIIQALSVPKCV-PVINMLNHDGHTPLHLACMADK	175 239
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	PECVRELLKEGADVNSASSRGSNCT-----FFFFSLGRDHVEQNGHNFQIEDMKHGGTP PECVKELLRAGADVNMASIVDVDEVDRQAEMPSKLLSDVMHTHAQRLYMDDMKTGTP	230 299
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	LHWAKTTQCLEMIELGCDLDAKNFQGNLTHIMVARGRLACVISLLSHGASVNAVCGDG LHWKSTSELTAILIEYGCHIDAKNFEGNLTHVMVLRNISCALVLLSHGANVDIQGADG	290 359
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	DTPLHA AVR-GDVSLIHALIVFGADVNPQKGETARHLAATSKLSKRDSVLYTLHAVGA NTPLHLAVKSGDIYLVYAFVAFGANVNAINNKGTPPHILATEKRPGFEEMLYALHIVGA	349 419
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	RRCDRD-QGCSEGCSPGSGFVGVAPEKPNFFKASRREWAGLGGGASAIPLPLKLNRRSLA ERCQRRTPWCKDGCPEGQHFNGIPSENPPVLNKTLLDOLLGAT-----	408 463
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	VGSKWRLTDGRCAVGKTPRQCLQLYFSLKDKMGVGRRRSRELTPMGSKWRLNDGRCAVGK -----	468 463
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	TPRQCLQLYFSLKDKVFIGNRPHDADSLEKFLQREMGETTLMTDIKHPKLMITGVLAADRH -----	528 463
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	PAALHLFRNYDSPKKILGVTEDESDFPSCPTPPHEQLVWRAARASGAAPTYFRPFGRFLDG -----	588 463
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	GLISNNPTLDAMTEICEYNEALKATVRLWLPNIFENELFCIFDITYHINIHRDENVKVR -----	648 463
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	TQQATQANGRLVDRAQAWCRTIGVPYFRLNAPISEDVCLNETDNRLLRVVLWETLVYMRG -----	708 463
XP_002399324.1_Ca-ind_PLA2_(partial) PhospholipaseA2-12-Pverdolaga	RAELDELAQLVRP -----	722 463

PhospholipaseA2-13-Pverdolaga:

XRLHELDEPADA EPLIQNSGLPAKYPSFKMMLELINNCSQLELPVHKVASSIATNQSEPNTIS
KWSPWALWNGIVPGTKWCGVGDIASFEELGSQAVVDSCCRADHDHCPVKLKAFRVGYGMI
NLSFYTKSHCDCDRLFHSCCLKQTKNKLAVGNFYFNFIRVQCLKERKVYVCVENRTDVGDL
NECIRWSVDPDSRKX

Protein	Sequence	Score
XP_012259279.1_Secretory_PLA2_isoform_X2 PhospholipaseA2-13-Pverdolaga	MGLAVIFLLVITCSVQTLQOPTIFRNTYKGLRGVIPKVRPLDEEIRAAVFHDQTVAVIDL -----	60 0
XP_012259279.1_Secretory_PLA2_isoform_X2 PhospholipaseA2-13-Pverdolaga	SNSNQLKNCDDIEVYEPLAEAMVKNLSTVEQPVQVFIEMTTLMRQCEMLDMKEDAIS -----XRLHELDEPADAEPLIQNSG--LPAPKYPSEFKMMLELINNCSQLELPVHKVAS *: *	120 50
XP_012259279.1_Secretory_PLA2_isoform_X2 PhospholipaseA2-13-Pverdolaga	TLPTI-DTKNRGSKPGVNPPLSLFLFGILPGTKWCGTGDIAADNYHDLGQEARIDRCRSHDLC STATNQSEPNNTISKSPWALWNGIVPGTKWCGVGDIASFTFEELGSQAVVDSCCRAHDC *: *	179 110
XP_012259279.1_Secretory_PLA2_isoform_X2 PhospholipaseA2-13-Pverdolaga	PKVKVRAQKSRYNLTNNISYTKSHCVCEMLYHCLKKAYHPADVMGRIYFNFIRVQPCVED PVKLKAFRVGYGMINLSFYTKSHCCDRLFHSLCLKQTKNKLNAVGNFYFNFIRVQCLKE *: *	239 170
XP_012259279.1_Secretory_PLA2_isoform_X2 PhospholipaseA2-13-Pverdolaga	VTNGTQGSVKRFID--VKMNY----- RKVVYVCVENRTDVGDLNEICRWSVDPDSRK	258 200

X C R A H D L C D D T L A P G E T K H N L T N R S T F T K L N C Q C D Q E F Y E C L Q K V D S L V S N S I G N L Y F N V L R
R G C Y E Y D H P L T K C K S Y R T

A0A087UYP4_PLA2_(Fragment) PhospholipaseA2-14-Pverdolaga	MEHIVRCLLTFCLVWVISCXSAFREKMFFLQRPSEENKTLVVWTWSEGRQEATGCEIF -----	60 0
A0A087UYP4_PLA2_(Fragment) PhospholipaseA2-14-Pverdolaga	TNEELIQNILKLSPDQS VKKPSPEEMKS LLEDCTEISIRRKRS AEHETRRTGDDRRIYGN -----	120 0
A0A087UYP4_PLA2_(Fragment) PhospholipaseA2-14-Pverdolaga	EPHTRNDRSRSHSYESHTVNSRGKDFNNGNNRRVVI EESWSNGDRSSINENGANYDNTE DY -----	180 0
A0A087UYP4_PLA2_(Fragment) PhospholipaseA2-14-Pverdolaga	ESTTMIPP NEMEGPKKESSTTEGYDGLP VIFPGTKWCGAGDI AKSYDDLGLHQDTDRCCR -----XCR **	240 3
A0A087UYP4_PLA2_(Fragment) PhospholipaseA2-14-Pverdolaga	AHDLCNDT LAPGETRN NL TNNSPFTKLSC KCDQDFYDCLDRINSVTANTIGNMYFNLLKR AHDLCDDT LAPGETKHNL TRNSTFTKLNC QCDQFEYEC LQKVDSLVS NSIGNLYFNVLR *****.*****.*.*****.*.*****.*.*****.*.*****.*.*****.*.	300 63
A0A087UYP4_PLA2_(Fragment) PhospholipaseA2-14-Pverdolaga	ECYKKDYPRSSCKRYRSLLIKITCKEYEKDANAEVYQIWP AKRYKNLPVP GPF SVTL PF GCYEYDHPL-TKCKSYRT *. *. * .*** **.	360 80

MPRSQNAFSRNSSIYSSLYTRSVNISKEKR KLLLHKTYCTSKRSSDLNVSKPSSDKIPGNSIFSTIW
KSVVVASSMLRPGLSVTPPKSIPIREFISKVGNVVSTEKYSKLLQPYLKLRSVNSEENVNRQTTEKS
RTCSKPGVVSQAGNVISGEKESVFEQAAAEWITSANLQEKKQENLSNQKEKKSENLPKVLISKAS
LASRSRFLVRSLS CASSQSSQMLRLEEVC KHL LQHPQEKGT LVKEGLIRVALRLRRKSSNTDIQT
QACV AL TLLGYHEPPGGQGIRILSIDGGGTRGLMAIEILRQLQARTGKT VHEMFDYIC GVVSSGA
ILTFL L GGLRLSPDEC ES LYRELSLEVFKASGIWGAGRLMWYHAYYDTSMWVDVL RKTFTGDK
MLIDSVKEKSSPKLAAISAVMNL PALRA FVFRNYDYP IRVQSQYIGSANYRMWEAIRASGAAP
GYFEFH L NHLLHQDGGIMIN NPTALAIHEARLLWPSDYIQ CVFSLGSGRFTPATNTAFTSTTL
KTKVQKVIDSATDTEAVHISMNDLLSPGTYFRFN PYL TEF L HLDENRPDKLHQLKMDAQMYL
RRNEHKLEOSIKVLTRPRSTLKKINDWIOLOKTL LL

Protein Name	Sequence	Position
A0A087TW26_Ca-ind_PLA2-gamma_(Fragment)	-MKAHGVLSQAIWRSFPIFRAVSSSKKKRKFVFSHHYGTSSKPASSNLSSKNNFLNLI	59
PhospholipaseA2-15-Pverdolaga	MPRSQNAFNRSSNIYSSLYTRSVNISKEKRKLHLHKTYCTSKRSSD--LNVSKPSS--D	55
A0A087TW26_Ca-ind_PLA2-gamma_(Fragment)	RNTTDLNRPMIWKSVTVASSLFNNVTLRFSKNKIVEEPKSVSV-----	102
PhospholipaseA2-15-Pverdolaga	KIPGNSIFSTIWKSVVASSMLRPLGS-----VTPPKSIPIREFTSKVGNVSTEKYS	108
A0A087TW26_Ca-ind_PLA2-gamma_(Fragment)	-----STNIQKLEKSTSTSGG-KMTVIPGGQSDKREASLEQGAENLTGDE	147
PhospholipaseA2-15-Pverdolaga	LLQLQPYLKLRSVNSEENVRTTEKSRTECKPGVSGAGNVISGEKESVFEEQAAAEWITSAN	168
A0A087TW26_Ca-ind_PLA2-gamma_(Fragment)	LQTKKKEFFGG-KEEKYVEKSKKVVISKSSLQQRSLFVSSLLDATTSSGSQLRLLEEICKH	206
PhospholipaseA2-15-Pverdolaga	LQEKKQENLSNQKEKSENLPKVLISKASLASRSLFVRSLSLSCASSCSSQMLRLLEEVCCKH	228
A0A087TW26_Ca-ind_PLA2-gamma_(Fragment)	LLLYPDQKSTMCAGLVRTLHMKCNSSDNVRAQARCTLSLVGYNESPKGHGIRILSID	266
PhospholipaseA2-15-Pverdolaga	LLQHPQEKGLTVKEGLIRVALRLRRKSSNTDITQACVALTLGYHEPPGGQGIRILSID	288
A0A087TW26_Ca-ind_PLA2-gamma_(Fragment)	GGGTRGIIAEVLRLQLEARTNKRIEYLFDFMCGVSSGAVLSLLLGGRLSLDECEALYRR	326
PhospholipaseA2-15-Pverdolaga	GGGTRGLMAIEILRLQLARTGKTVHEMFYICGVSSGAILTFLGLGLSPDECEALYRE	348
A0A087TW26_Ca-ind_PLA2-gamma_(Fragment)	LSDEVFSQSSFSGWTSRLMWSHAYYDTTMVVKVKKTFGEKLLIDTCKEEFAPKLAASVAL	386
PhospholipaseA2-15-Pverdolaga	LSLEVFKASGIWAGRLMWHAYYDTSMVVDVLRKTFGDKMLIDSVKESSPKLAASVAL	408
A0A087TW26_Ca-ind_PLA2-gamma_(Fragment)	MNLPHLQAFVFRNYDFPPHVQSYHHGSCRYRMWEAIRASGAAPGYFEYCLDDYLHQDGG	446
PhospholipaseA2-15-Pverdolaga	MNLPALRAFFVFRNYDYPRVQSQYIGSANYRMWEAIRASGAAPGYFEFHLNHLHQDGG	468
A0A087TW26_Ca-ind_PLA2-gamma_(Fragment)	IMVNNPTALAIHEAQLLWPSDGIQCVMSLGSGRYPVPPQPNFTSTSLTKVKLVKVIDSATD	506
PhospholipaseA2-15-Pverdolaga	IMINNPALAIHEARLLWPSDYIQCVFSLGSGRFTPATNTAFTSTTLTKVKQKVIDSATD	528
A0A087TW26_Ca-ind_PLA2-gamma_(Fragment)	TEAVHISMNDLLSPGTYFRFNPLYTEFLHLDENRPDKLHQLKMDAQMYLRNHEHLEQSI	506
PhospholipaseA2-15-Pverdolaga	-----	588
A0A087TW26_Ca-ind_PLA2-gamma_(Fragment)	-----	506
PhospholipaseA2-15-Pverdolaga	KVLTRPRSTLKKINDWIKLQKLTLL	613

MAEEEEYHLMCSILAHGSDIRSVTTSYVPLGGIVTGSRDKTIKLWRPTGTTFTTEEHCMRGASHFIS
SLCALPPSDQYPDGLILAGSNDCAIYGFSLDSSEPILKLLGHSENVCALVAGNLGTIVSGSWDKT
ARVWHGQRCVATLSGHTQAVWAVALLPDHALVLTGSADKAVFLWNNGKCERKFIGHEDC
VRGLTVISDLEFLSCSNDTTVRRWQTSGECLGIYTGHTDYVYDICLSSCREYFISCSQDQTVKVV
KENVCVQTIKLPKSLWAVTYLYNGDIAVGGSDGSRVFTKDKSRRASPAEEARFNEEIVSMN
SKNMKQNIQDLELDDVPGPDALLQDGTSDGQTQLCKVGNEVSVFQWSVKEHKWLKLGKVL
DALDNRPAKGKTVYEGKEYDYVFTIDVAEGKLLKLPYNDTEDPWLV AHKFIEKHDLNPMFLD
QIANFIINNSKSAGVQAESMSEFSDPFTGASRYIPSNVGKPSLASNHGDNSSIQELPKSNPTGN
GDIEKASTGAHFPLITYVTFTDANTNGIRAKLCFTEKIEKSQQLSIEKIEHMLLLLDYPQAITD
DQMLSLEKALSWPAEFVFPALDVLRLAVRAEPVNSRVSKDGGVGLINHLLRYVSTGNPVSNQ
MLVLRTLSNFFVCPSGEQLLVSQAKKVLSLTRSCCASKNKHVQIALATLYANYSVAFQKSTSSE
DTYCKDMYLNDAVEALKQFNEPEALFRLIVCIGTAVQDKYCLQVAKALKIGEIVQSVLERCEV
SKIODFGATLIDIVSN

CLUSTAL O(1.2.4) multiple sequence alignment

EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	MASGASRYRLSCSLPGHELDVRGLVCCLYPPGAFVSVRDRTTTLWAPDSPNRGFTEMHC --MAEEHYHLMCSILAHGSDIRSVTTSYVPLGGIVTGSVDKTIKLWRPTG--TTFTEEH * * * * *	60 56
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	MSGHSNFVSCVCIIIPSSDIYPHGLIATGGNDHNICIFSLDSPMPLYILKGHKDVTCSLSS MRGASHFISLALPPSDQYDGLILAGSNDCAIYGFSLDSSEPIKLLGHSENVCAVLA * * * * *	120 116
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	GKFGTLLSGSWDTTAKVWLNCKMMLTQGHAAVWAVKILPEQLMLTGSADKTIKLWKA GNLGTIVSGSWDKTARVWHGQVCVATLSGHTQAVWAVALLPDHALVLTGSADKAVFLWNN * * * * *	180 176
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	GRCERTFLGHEDCVRLAILSETEFLSCANDASIRRWQITGECLEVFYGHNTIYISISVF GKCEKFIHGHEDCVRLTIVISDLFLSCSNDTTRVWQTSGECLGIYTGHTDYVDICLS * * * * *	240 236
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	PNSKDFVTTAEEDSLRIWKHGCAQTIPLPAQSIWCCCVLENGDIWVGASDGIIRVFTES SCREYFISCSDDQTVKRWKENVCQTIKPAKSLWAVTYLYNGDIAGGSDGVSFKDK * * * * *	300 296
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	EEERTASAEFIKAFERELSQATIDSKTGLDINAEQLPGREHLEPGTREGQTRLIRDGE KSRASPAEEARFNEEIVSMNSKNMKQNIQDLEDDVPDALLQDQSDGQTLCKVGN * * * * *	360 356
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	RVEAYQWSVSDGRWIKIGDVVGSSGANQQTSGKVLVEGKEFDYVFSIDVNEGGPSYKLPY EVSVFQWSVKHKLKGLKVDLAL-DNRPAKGKTVYEGKEYDYVFTIDVAEG-KLLKLPY * * * * *	420 414
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	NVSDPWLVAYNLFQKNDLNPMLDQVAKFIIDNTKGQTLG-LGNTSFDPFTGAGRYMP NDTEPWLVAKHFKIEKHDLPMLDQIANFIINNSKAGVQAESMSFSDPFTGASRYIP * * * * *	479 474
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	GSAGMDTTMTGVPFT-----GNSAYRSAASKTVNIYFPKKEALTFDQANPTQILG SNVGKPSLASNHGDNSSIQELPKSNPTGNGDIEKASTGAHFPLLTVTFTDANTNGIRA * * * * *	530 534
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	KLKELNGTAPEKKLTEDDLVLEKILSLICNNSSEKPTAQQQLIWLKAINWPEDIVFPA KLCEFTKEIKSQQLSIEKI---EHMLL--LLDYPQAITDDQMLSLKALSWPAEFVFP * * * * *	590 589
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	LDILRLSIKHPNVNENFCNEKGDQFSSHLINLLNPKGKPAQLLALRTFCNCFVSAQK LDVLRVAVRAEPVNSRVSKDGGVGLINHLVYVSTGNPVSQMLVRLTLNFFVCPSGEQ * * * * *	650 649
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	LMMSQRESLMSHAIELKSGSNKNIHIALTLTNYSVCFKHNDHIEGKAQ---CLSVIST LLVSQAKKVLSTLRSCCAKKNHVQIALATLYANYSVAFQKSTSSDITYCKMYLNDAVE * * * * *	707 709
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	ILEVVQDLEATFRLVALLGLISDDSNALQAKSLGVDSQIKKYVSVSEPAKVSECCRLV ALKQFNEPEALFRLVIGTAVQDK-YCLQVAKALKIGEIVQSVLERCEVSKIQDFGATL * * * * *	767 768
EDL30937.1_PLA2_isoform PhospholipaseA2-16-Pverdolaga	LHLL-- DIVSN * * *	771 774

Pairwise alignments and amino acid sequences of phospholipases D translated from *Pamphobeteus verdolaga*. Residues highlighted in grey indicate the signal peptide, while magenta blue highlighted residues, indicates the propeptide according to Spider|ProHMM from the arachnoserver. Residues highlighted in yellow shows cysteines potentially forming disulfide bridges. Residues highlighted in red shows amino acids implicated in the active site.

PhospholipaseD-1-Pverdolaga:

MKILKFLGCLIWYQVCVADEVDWRRPVWNIAMVNANYQIDYYLDMGANSIEFDVAFDNS
 GNARFTFHGVPCDCFRSCVRHEEIEENYLEYMRHLTTPGDPKFQEKLVLLFMDLKVKGSSRAR
 TNAGFSIARKLVRHYWQNGTSAARAHVLMSPVSDHMEVVRGFRDGLRVEGLSGYINKVGV
 DFSGNEDLNSIRRALMSEISDRIWQGDGITNCLPRGTGRLREAIQRRDQPLTHIEKVYWWTV
 DKMSTMATRLRLSVDAMITNYPRLVSVLDEDEFSGRFRMATIDDPWSKHELRTSALYALDE
 GPTARGGNITTYFDKEDDELLIIASTITQTMAGINFTRGLEESIPX

CLUSTAL O(1.2.4) multiple sequence alignment

Q1W694_LiSicTox-betaID1	MQLFIILCLAGSAVQLEGTLDGVERADNRRPIWNIAMVNDKGLIDEYLDDGANSVESD	60
PhospholipaseD-1-Pverdolaga	---MKILKFLGCLIWY---QVCVADEVDWRRPVWNIAMVNANYQIDYYLDMGANSIEFD	54
	* * * * *	
Q1W694_LiSicTox-betaID1	VSFDSNGKPEKMLHGSPCDCGRSCRQMSFADYLDYMRQLTTPGDPKFRENILVMDLK	120
PhospholipaseD-1-Pverdolaga	VAFDNSGNARFTFHGVPCDCFRSCVRHEEIEENYLEYMRHLTTPGDPKFQEKLVLLFMDLK	114
	* * * * *	
Q1W694_LiSicTox-betaID1	LKLLSSEQAYSAGQEVASQMLDKYWKRGESGARAYIVLSIPTITRVTFVNGFYDKLHSEG	180
PhospholipaseD-1-Pverdolaga	VKGLSSRARTNAGFSIARKLVRHYWQNGTSAARAHVLMSPVSDHMEVVRGFRDGLRVEG	174
	* * * * *	
Q1W694_LiSicTox-betaID1	FDQYREKVGVDVDFSGNEDLDTGKILKSRDILDHIWQSDGITNCLFRIMKRLKAAIRKRDS	240
PhospholipaseD-1-Pverdolaga	LSGYINKVGVDFSGNEDLNSIRRALMSEISDRIWQGDGITNCLPRGTGRLREAIQRRDQ	234
	* * * * *	
Q1W694_LiSicTox-betaID1	NGY--MVKVYTWSVDKYTTMRKALRAGADGMITNFPKRLVSVLNREFSGKFRLATYNDN	298
PhospholipaseD-1-Pverdolaga	PGLTHIEKVYWWTVDKMSTMATRLRLSVDAMITNYPRLVSVLDEDEFSGRFRMATIDDP	294
	* * * * *	
Q1W694_LiSicTox-betaID1	PWERYTG-----	305
PhospholipaseD-1-Pverdolaga	PWSKHELRTSALYALDEGPTARGGNITTYFDKEDDELLIIASTITQTMAGINFTRGLEES	354
	* * * * *	
Q1W694_LiSicTox-betaID1	---	305
PhospholipaseD-1-Pverdolaga	IPX	357

PhospholipaseD-2-Pverdolaga:

MANDISDAIYLLDQGANALEFDISFFNNGTVNRVYHGVPCDCFRVCTHEASLPDYLLSTIRKITD
 PQTGKYSQQMTFQFFDLKLQVTPWGKYVAGLEIANHVIDYLWGNDTKRQLVRVLFINDES
 DKDVVLGVRNAFLQRGMKKFLDQVGFDDGGTGTMKSIKDMWDSLGRGNLWQGDGIFNCLS
 EVYKDDRLREALHIRDSPNGFIDKVYHWTIDSRGRMRMSRLRGVDGMITNLPKDLIDVLNEDP
 YSNIFRLATAKDDPFSSRFHPSKSFK

CLUSTAL O(1.2.4) multiple sequence alignment

XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	MDLRRENSDGSDEVEEFEELEDEDEENLRNSPLDTCGIATHLSTHFGSIPFARIYD	60 0
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	SSQSVTDSSDGFVPGVPMCFKLLGFERDPRPSHMHVHPNLYVIEVTHGDFVWVLKKRYKH	120 0
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	FLELHTILKLFASLALPLPNESHQMRKSFDDRAKRKEVPQFPKRPESSAQVQAR	180 0
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	GEQLVSYLNKVVKVANYRNHPKMTFLEVSPYSFLNSTGPKGKEGAVSKRAGGHNPNSCF	240 0
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	IYMKSVWYKICKRWRRLIAKDTYILYHPKTGAVKSVILMDGRFRVHEDGPTGSRSG	300 0
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	VIISNLSRELLIDVWTKRQRMWVKHIEELVKTRAKDFVAENRHGSYAPVRSRTLARWYV	360 0
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	DGAMYMRAVANAIEANREEIFITDWLSPFLKRSNKNEDWRLDLLRRKASSGVRI	420 0
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	FIMLYKEVSSALAINSLYSKQKISTHPNIKVFRHPDHVNAAVYLWAHHEKLVIVDQKYAF -----XALPISKLDIK-----RHTSSIV----- * * . * * * * * * *	480 18
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	LGGIDLCYGRWDDAGHRLTDLVPDENKRQGVCDSDVDEVDGYMVKPSCCVSETRFLNVA -----PPPLFPVHKRSRS-----DSNV-----MTVPK-----KNQEFY-QS * * . * * * * * * *	540 48
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	GPPHNFERCLV---VPEYDQAEKIVN-SKSPSDRVSRRLMLQRVKAKLKALRAFKHLH RPHDDYHIKTLKNIPSKPQPVHKLQAKVKHDENRAKQRW--RVAVKKIQAISAFQNL * : : * : * : * : * : * : * : * : * : * : * : * : *	596 106
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	YLEGSTAEIMYEDPHSGYLSQFECL-----E-EKLEPFVTDGTYWIGKD -----SQVLLQVVDGAH--QDVCLSSLPADVHRTIQEIALVHLGLERTYRLWHGKD : : : * : : * * * * * : : : * : * : *	642 158
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	YSNFIYKDVNTLEKPFDDHIDRTKIPRMPWHDIGAVVLGRAARDLARHFIQRWNSIKIQK YSNFIKDLNKLNEPYTDSVNRYPETPRMPWHDVSCFLQGAARDVARHFIQRWNFTKLRT ***** : : : * : : * : * : * : * : * : * : * : * : * : *	702 218
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	AKKAKSYPWLIPKSYDSAEDIEV--KLFGLYRCVQILRSASSWSAGISETENSIHSA AKFDDVYPLLLPKCYEFPDPIPPILSSEVGSILMADCQVLRSTSMWSAGIITTEYSILNA * * * * * : * : * : * : * : * : * : * : * : * : * : * : *	759 278
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	YVDLILKAKHFIYIENQFFISLQSPDNIVYNEVADALFTRIVGAFKAKEKFRVYIVLPLL YKDAIMKAEHFIYIENQFFVSLQHGNKDVFNDSICLYQRIMKAHQENKRFQVYVIMPLL * * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	819 338
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	PAFEGEVGTSGVSIQAIHWNYSNLCRGEYSLLERLKRVEDDPKEYIGFYGLRKHDMLN PAFEGEVGTGTGLIQAVTHWNYSICRGPRLCQRLAKSIQDPLSYISFYGLRNFGLN ***** : * : * : * : * : * : * : * : * : * : * : * : *	879 398

XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	GIPVTELIYVHSKLMIVDDVQAIIGSANINDRSLGERSIAKWSQHFRLATFDGKP NKLVTETLIYVHSKLMIVDDKKAIGSANINDRSLGRRDSEIAVLVNDVSFVSVMDGKP *****	939 458
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	VKAGLYVSSLRRWIFREHLGIRDVEDPVADSFYSDVWKKIARRNTEIFEEVFKPLPTDCV YKAGHFCSLRKALFKHLGLLGGKHSKVEX----- *** : *** : * : *** : . : . :	999 489
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	KTFAELRAYSRVSPLAIEDPSAALEKLRDVQGHVLELPERFLEDENLTAPPTTKESLMPT -----	1059 489
XP_003744259.1_Phospholipase PhospholipaseD-4-Pverdolaga	RLWT 1063 ---- 489	

Pairwise alignments and amino acid sequences of phospholipases B translated from *Pamphobeteus verdolaga*. Residues highlighted in grey indicate the signal peptide, while magenta blue highlighted residues, indicates the propeptide according to Spider|ProHMM from the arachnoserver. Residues highlighted in yellow shows cysteines potentially forming disulfide bridges.

PhospholipaseB-1-Pverdolaga:

LEAIVLSLFRDNNVFLYGVFAPPRLVSAS^CSSVSL^CMKNLSPEASDWKF^CMMMLTLWVAIALLV
HV^CAASTEQKAYVTWDSSSYKFTVHSDPVENFVAYATFTNEINATGWSYLEVWNTNETFPDSV
QAYSAGLAEGVLTADLLKKHWNVTATY^CDGEESY^CCDRLKIFLETNLDPMNYNIARRRKYV
PYWHQVALALEQLSGLEDGYNNVSGKPHTKLNVTGVLMMVNIIFGDLEDLEGILNKTVSSRPL
GSGS^CCSGLIKVLPNNEDLYVSQDSWNTYSSMLRVLKKYNISVHSGMDRGSPVIPGQVMSFSSY
PGLI^CSGDDFYTISSGLATMETTIGNGNSSLWKYIRAKGTVLEWLSIVANRMARSGREWSRW
FSIMNSGTYNQWMMVVDYNKFLPGAPLQNDLLWVLEQLPGYIHSDDLTDVLRKQGYWPSY
NTPYFKDIFNLSGSQENADKYGDWFTYDKTPRALIFKRDHGTVDVKSMIKLMRYNDYTHD
PLSR^CN^CTPPYSAENASAR^CDLNPANGTYPFGALGHRSHGGIDMKLTTGSLFKNFEFVAFG
GPTYDSLPPFKWSESDFRTERHEGHPDLWKFEPIVRKWSQ

CLUSTAL O(1.2.4) multiple sequence alignment

XP_015925352.1_Phospholipase_B-like_Putative PhospholipaseB-1-Pverdolaga	-----MLVSSVLC 9 LEAIVLSLFRDNNVFLYGVFAPPRLVSAS ^C SSVSL ^C MKNLSPEASDWKF ^C MMMLTLWVAIA 60 *****	
XP_015925352.1_Phospholipase_B-like_Putative PhospholipaseB-1-Pverdolaga	LL---IALVKAKNASVTDQTTGKFQIHDIANDPVAYGTFTDEIFKVGWSYLEIKSYEK 66 LLVHVCAASTEQKAYVTWDSSSYKFTVHSDPVENFVAYATFTNEINATGWSYLEVWNTNET 120 ** * . : * * * . : * * * . : * * * . : * * * . : *	
XP_015925352.1_Phospholipase_B-like_Putative PhospholipaseB-1-Pverdolaga	YDPDIQAYAGVVEGYLTADLLRKHFNLVDGYCDGEEIYCDRLTSFLQENWDFIDSNVK 126 FPDSQAYAGVVEGYLTADLLRKHFNLVDGYCDGEEIYCDRLTSFLQENWDFIDSNVK 180 : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : *	
XP_015925352.1_Phospholipase_B-like_Putative PhospholipaseB-1-Pverdolaga	VRRKYDVYWHQIALTFEQLHGLEGGYKNTSQPSTKVDLMGLLLNMGDLEDLEVLKK 186 RRRKYVYWHQVALALEQLSGLEDGYNNVSGKPHTKLNVTGVLMMVNIIFGDLEDLEGILNK 240 * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : *	
XP_015925352.1_Phospholipase_B-like_Putative PhospholipaseB-1-Pverdolaga	NMRRVLGSGHCSGLIKVLPNNKILFSQVTSWSTYTSMLRIKKYSLKLHTSLADGSPVI 246 TVSSRPLGSGHCSGLIKVLPNNEDLYVSQDSWNTYSSMLRVLKKYNISVHSGMDRGSPVI 300 * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : *	
XP_015925352.1_Phospholipase_B-like_Putative PhospholipaseB-1-Pverdolaga	PGHTSTFSSQPGVLYSGDDFYVLSGLVAIETTFGNGDSSLWKYVVP-QTILEWQRIIA 305 PGQVMSFSSYPLGICSGDDFYTISSGLATMETTIGNGNSSLWKYIRAKGTVLEWLSIVA 360 * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : *	
XP_015925352.1_Phospholipase_B-like_Putative PhospholipaseB-1-Pverdolaga	NRLAKTGKQWTLFGILNSGTYNQWMMVVDYNKFKPGSLQDGLLYVLEQLPGYLHSEDR 365 NRMARSGREWSRWFSIMNSGTYNQWMMVVDYNKFLPGAPLQNDLLWVLEQLPGYIHSDDL 420 * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : *	

CLUSTAL O(1.2.4) multiple sequence alignment

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P0DJ76|VKT4_Kunitz-type-theraphotoxin-Hs1e  MGIARILSAVLFLSVLFVTFPALLADHHDGRIDTCRLPSDRGRCKASFERYWYNGRTC 60
Kunitz-3-Pverdolaga  MGIRNICSVISVFVTLFALTFFPVFLAGYH---LDICRQRPDRGMCLVNMERWFFNGRFC 57
                        ***  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
P0DJ76|VKT4_Kunitz-type-theraphotoxin-Hs1e  AKFIYGGCGGNGNKFPEKACMKRCAKA 88
Kunitz-3-Pverdolaga  STFVYGGCGGNGNFIKKAQCMARCARG 85
                        .  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

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Kunitz-4-Pverdolaga:

MLLMILVVASFQHSNADANGIDLCELDKEPGSCTSVINRYFFNRYSRRCERFIYTDCCGGNSNNF
HYEFECCERTCPGDLYIGDVCSLPKKVGPCRAAMPRIYFNKETGRCEFTFYGGCSGNYNFETK
EQCNSYCFQG

CLUSTAL O(1.2.4) multiple sequence alignment

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W4VSH9_Kunitz-type_U19-barytoxin-Tl1a  MNFELIYVSSLLLGICLANQADVVPSCNLPADAGMCYAYFPMFFYDASSRCKLNFIYGG 60
Kunitz-4-Pverdolaga  MLLMILVVA---SFQHSNADANGIDLCELDKEPGSCTSVINRYFFNRYSRRCERFIYTD 56
                        *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
W4VSH9_Kunitz-type_U19-barytoxin-Tl1a  CGGNANRFWSEAECKCGGGGGGGSSDGSQKTAKMLNLDLGIDCSLEKKVGPCKAHMP 120
Kunitz-4-Pverdolaga  CGGNSNNFHYEFECERTCPG-----DLYIGDVCSLPKKVGPCRAAMP 98
                        ***  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
W4VSH9_Kunitz-type_U19-barytoxin-Tl1a  RYFFNRETGLCEEFIYGGCSGNHNNFQTEQCESFCAPGNSPREEETRKRTKQSY 176
Kunitz-4-Pverdolaga  RYFFNKETGRCEFTFYGGCSGNYNFETKEQCNSYCFQG----- 137
                        ***  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

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Kunitz-5-Pverdolaga:

XYFLRNGCPSSTVCECTHSLGISRGNCCDSINSCHLIAKFPNXAEMHFTLACVFSLFCGICFANH
NVPDTCPSLPPDAGMCYAYFPMFFYDAPSGACINFIYGGCGGNANRFWTEEECMNRCAGVG
GTTKEPADEEKGPFLGPVDEGKGTISQKPIDEGKEVIIQKPVDEGKGAIYPQPTGGGKGVIFPQ
PVAGGKGVIFQPPVGGGKGVTVQHAPQADICNQEKPQGNCSQIIRYFFDKDSKKCDTFMYS
GCGKNDNNFNKYFECERTCSGEHDIGDTCNFKQDSGPCRAFFPRFYFSGESGQCEQFIYGGCQ
GNHNNFKTKEECLQFCTSGKGSPLP

CLUSTAL O(1.2.4) multiple sequence alignment

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KFM65460.1_kunitz-type_serine_protease_inhibitor  MRALILLCAVTVAFASQDVCPENEHFQCGTACPDNCENYDTPARPCVLMISGCFCDKG 60
Kunitz-5-Pverdolaga  ----- 0
KFM65460.1_kunitz-type_serine_protease_inhibitor  FVRGEDGRCKIPESCPSQAEIVCPANQHFERCGTACPDTCEN---YQ-DTLRCPVLM 113
Kunitz-5-Pverdolaga  -----XYFLRNGCPSST--VCETTHSLGISRGNCCDSINSCHLIAKFPNXAEMHFTLA 51
                        :  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
KFM65460.1_kunitz-type_serine_protease_inhibitor  CVPGCFCDKGLVKAIDGSCIKPESCPSQAKPLVQNCEDKPERGMCLAYIPSYYYDKETGT 173
Kunitz-5-Pverdolaga  CVFSLFCG-----ICFAN-----HNVPDTCPSLPPDAGMCYAYFPMFFYDAPSGA 96
                        *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
KFM65460.1_kunitz-type_serine_protease_inhibitor  CKKFIYGGCGGNGNRYATEEECKEKKGVTLAQTKSDDVCELPVATGPRCALFHRY--- 230
Kunitz-5-Pverdolaga  CINFIYGGCGGNANRFWTEEECMNRCAGVGGTKEPADEEKGPFLGPVDEGKGTISQKP 156
                        *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
KFM65460.1_kunitz-type_serine_protease_inhibitor  -----FDSASGQCKKFIYGGCGGNENN--FKT-----LKECERTCGAGGVLGLA 272
Kunitz-5-Pverdolaga  IDEGKEVIIQKPVDEGKGAIYPQPTGGGKGVIFQPPVAGGKGVIFQPPVGGGKGVTVQHA 216
                        :  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
KFM65460.1_kunitz-type_serine_protease_inhibitor  LDRPDCAPETGVCRAIRRFYDQKEGMCKTFIYGGCGGNRNRFVTEECYNKCGALA 332
Kunitz-5-Pverdolaga  PQADICNQEKPQGNCSQIIRYFFDKDSKKCDTFMYSGCGKNDNNFNKYFECERTCSGEH 276
                        :  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
KFM65460.1_kunitz-type_serine_protease_inhibitor  S-MSACQQKEKGTGPKAAFRFYFNKQTGECEPFIYGGCGGNSNFFLDKEDCEAVCKA-- 389
Kunitz-5-Pverdolaga  DIGDTCNFKQDSGCPRAFFPRFYFSGESGQCEQFIYGGCGGNHNNFKTEECLEQCTSGK 336
                        .  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
KFM65460.1_kunitz-type_serine_protease_inhibitor  ----- 389
Kunitz-5-Pverdolaga  GSPLP 341

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Kunitz-6-Pverdolaga:

VISVFTVLLALTFPPLFSADHHLDI CELPADSGT CFVRLHRWYFNGESC TKFLYRG CGGNENHF
MTEVE CMAK CGGA

CLUSTAL O(1.2.4) multiple sequence alignment

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B2ZBB6_Kunitz-type-theraphotoxin-Hs1b      MGIARILSAVLFLSVLFVWTFPALLSADHHDGRIDTCRLPSDRGRCKASFERWYFNGRTC 60
Kunitz-6-Pverdolaga                        -----VISVFTVLLALTFPPLFSADHH---LDICELPADSGTCFVRLHRWYFNGESC 49
                                         . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . *
                                         . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . *

B2ZBB6_Kunitz-type-theraphotoxin-Hs1b      AKFIYGGCGGNGNKFPTEACMKRCGKA 88
Kunitz-6-Pverdolaga                        TKFLYRGCGGNENHFMTVEECMAKCGGA 77
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *

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Kunitz-7-Pverdolaga:

XTSC KGIKES CTLDRAEAK EICMMPKEIG PCRGYFHRWYFDVNTLT C VTFVYGG C RGNNNNF
EFQRDC VRT CEPLFKASGNEDPSNVSTHDVAQGNSPID CMVTPWX

CLUSTAL O(1.2.4) multiple sequence alignment

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XP_002435922.1_secreted_protein_Kunitz_domain_(Partial)  -----FPEICLLPKDIGPCRGYFPRWYDSTKRMCLQFVYGGCRGNRN 43
Kunitz-7-Pverdolaga  XTSC KGIKESCTLDRAEAK EICMMPKEIGPCRGYFHRWYFDVNTLT C VTFVYGGCRGNNN 60
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *

XP_002435922.1_secreted_protein_Kunitz_domain_(Partial)  RFERYECNKMCEVTISR----- 61
Kunitz-7-Pverdolaga  NFEFQRDCVRTCEPLFKASGNEDPSNVSTHDVAQGNSPIDCMVTPWX 107
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *

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Kunitz-8-Pverdolaga:

DAGTC FASIPRWYFTGSK CRSFIYGG CGGNANNFDTELXMPKEMWKEMKRVTSHFTTETGT A
QNPSSGYLEVFEVRIV

CLUSTAL O(1.2.4) multiple sequence alignment

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B2ZBB6_Kunitz-type-theraphotoxin-Hs1b      MGIARILSAVLFLSVLFVWTFPALLSADHHDGRIDTCRLPSDRGRCKASFERWYFNGRTC 60
Kunitz-8-Pverdolaga                        -----DAGTCFASIPRWYFTGSKC 19
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *

B2ZBB6_Kunitz-type-theraphotoxin-Hs1b      AKFIYGGCGGNGNKFPTEACMKRCGKA----- 88
Kunitz-8-Pverdolaga                        RSFIYGGCGGNANNFDTELXMPKEMWKEMKRVTSHFTTETGT A QNPSSGYLEVFEVRIV 79
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *

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Kunitz-9-Pverdolaga:

QVATLHPPEAEKENLRNYVQRFP TGVMKSSLGV CELEKNSGP CAKSYKRWYYDAISKD CLP
FSYGG CLGNENRFRTKAACEET CKN

CLUSTAL O(1.2.4) multiple sequence alignment

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XP_011135446.1_kunitz-type_serine_protease_inhibitor  -----MGLKSCLLFTLIIVGILSHEIVAKPSSICQLPKVVGPCASLKRYRYD 48
Kunitz-9-Pverdolaga  QVATLHPPEAEKENLRN-----YVQRFPTGVVMKSSLGVCELEKNSGP C AKSYKRWYYD 54
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *

XP_011135446.1_kunitz-type_serine_protease_inhibitor  STTGQCEEFYGGCKGNENNFITREVCQENCINN 82
Kunitz-9-Pverdolaga  AISKDCLPF SYGGCLGNENRFRTKAACEETCKN- 87
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
                                         . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *

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Kunitz-10-Pverdolaga:

XLKLPPKMMKLLWVNLLLLVLAT CLC SEKTDKTNNGIC NQRMDSGNGNQ RITHFYDYDTGRQ
K CHFPYPYSGRGGNKNNFSTMQE CKKRM P

CLUSTAL O(1.2.4) multiple sequence alignment

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XP_012273912.1_kappaPI-actitoxin-Avd3d  -----MIANFVLPLVLLACLCAAPSKTAPTVCLEPMVKGNCRALMPRYRYDSRA  50
Kunitz-10-Pverdolaga                    XLKLPPKMKLLWVNLNLLVLATCLCEKTDKTNNGICNQRMDSGNGNQRIHFYDITGR  60
                                         ::  *  ***  :***:  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
XP_012273912.1_kappaPI-actitoxin-Avd3d  KDCLPFNYGGCGGNRNINFLSREQCMETCKGV  81
Kunitz-10-Pverdolaga                    QKCHFPYPSGRGGNKNFESTMQECKRMP--  89
                                         :. *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

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Kunitz-11-Pverdolaga: MRKSIMGTQVQGFRSSSPGALMSRVMASSTTLFFSGKVYLQA

CLUSTAL O(1.2.4) multiple sequence alignment

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B2ZBB6_Kunitz-type-theraphotoxin-Hs1b  -----MG-----IARILSAVLFSLVLFVTFPALLSADHHDGRIDTCRLPSDRGRCKASF  50
Kunitz-11-Pverdolaga                    MRKSIMGTQVQGFRSSSPGALM-----SRVMAST  29
                                         **  :  .  *  :
B2ZBB6_Kunitz-type-theraphotoxin-Hs1b  ERWYFNGRTCAKFIYGGCGGNNGKFPQTQECMKRCGKA  88
Kunitz-11-Pverdolaga                    TLCFFSGKVYLQA-----  42
                                         :*  *  *  :

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Kunitz-12-Pverdolaga:

MLLRNDVSRRRIMIKVSRQRFSLTFDLEDFCTAKDENNTDCQTLPA GDPTCY YDNC PMFY YD
TSSSTCMNVEYGGCGGKANRFWTEKECTDQCKNKEDDVANGAASEYSIGVSWLKV KYPFL

CLUSTAL O(1.2.4) multiple sequence alignment

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W4VSH9_Kunitz-type_U19-barytoxin-T11a  -----MNFELIYVSSLLLGICLANQADVPSDC-NLPAD-AGMCYAY  40
Kunitz-12-Pverdolaga                    MLLRNDVSRRRIMIKVSRQRFSLTFDLEDFCTAKDEN-NTDCQTLPA GDPTCY YD  56
                                         *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
W4VSH9_Kunitz-type_U19-barytoxin-T11a  FPMFFYDASSRKCLNFIYGGCGGNANRFWEAECEKCGGGGGGGSSDGSQKTAKMLNL  100
Kunitz-12-Pverdolaga                    CPMFY YDTSSSTCMNVEYGGCGGKANRFWTEKECTDQCKNKEDDVANGAASEYSIGV-  113
                                         ***  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
W4VSH9_Kunitz-type_U19-barytoxin-T11a  DLGDISCLSEKKVGPCKAHMPRYFNRGTGLCEEFIYGGCSGNHNNFQTKEQCSFCAPGN  160
Kunitz-12-Pverdolaga                    -----SWLKV KYPFL-----  124
                                         *  *  *  *
W4VSH9_Kunitz-type_U19-barytoxin-T11a  SPRPEETTRKRTKQSY  176
Kunitz-12-Pverdolaga                    -----  124

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Kunitz-13-Pverdolaga:

MGIARIFSVVSLFVFLALTFPPLFSADHHEGTDICYLPPERGVCKAYSEQWHFNGRRCAKFVF
GGCGGNANRFPTKDECI RRCRKA

CLUSTAL O(1.2.4) multiple sequence alignment

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P68425_Kunitz-type-theraphotoxin-Hs1a  MGIARILSAVLFSLVLFVTFPALLSADHHDGRIDTCRLPSDRGRCKASFERWYFNGRTC  60
Kunitz-13-Pverdolaga                    MGIARIFSVVSLFVFLALTFPPLFSADHHEG-TDICYLPPERGVCKAYSEQWHFNGRR  59
                                         *****  *  :  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
P68425_Kunitz-type-theraphotoxin-Hs1a  AKFIYGGCGGNNGKFPQTQECMKRCAKA  88
Kunitz-13-Pverdolaga                    AKFVFGGCGGNANRFPTKDECI RRCRKA  87
                                         ***  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

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Amino acid sequences of Hyaluronidases translated from *Pamphobeteus verdolaga*. Residues highlighted in grey indicate the signal peptide, while magenta blue highlighted residues, indicates the propeptide according to Spider|ProHMM from the arachnoserver. Yellow highlighted residues indicate

the cysteine position on hyaluronidase-like sequence (Cys17, Cys176, Cys183, Cys196, Cys218, Cys307, Cys332, Cys337, Cys343, Cys372, Cys374 and Cys383).

Hyaluronidase-1-Pverdolaga:

PRMYQSKLLQGLFPNSKDLPSVLLLDSEGA VKVIGH SRLSRVLEDNRG CWIASVIISKEKRG
QGLGKFLMMKTEEYAKVLGLTTAYLNTRDKQGFYEHLGYSY NPVSPHKGSFSMNGVGHL
NFHRQVLRRC EEGETNHSGSPVGD PKIAKSSSVSSAKTSTPPLPPPPPPSSSNVKTD CFTSATG
HNWMKKYL

Hyaluronidase-2-Pverdolaga:

MSVTLFLLLLLP CYTRQAEDPTVFTVRWNVPTIQ CRKTYGMDFVPLLKSYGILVNSGDEFKGEV
NTIFYESQLGLYPHLDQSGQRVNGGIPQLGDLPEHLKNAREDINKAIPDINFNGLGIIDWESWR
PVWNFNW GALKKYQDES FQEAL KQHPGWTND SLWQLAQQEWETSAKNFMLET LRLAQTM
RPN SLW CYLFPD CYN YNGQTPREFR CPSIVVTGNNQLSWLWHESKAV CPSLYVADGYLQKY
TFEQRTWYVDGRLKEALRVAPNSQLYPYIGYGYGVTPGAMVPEDDFWRILAQVASAGSSGTVI
WGASATLR SKDN CQLLQKYVKDILGPSVTIVKENAER CAKTM CNGKGR CTWLNDPNVIAWR
VYLDNRNHPFQRSEIT CH CVEGYSGRY CDVQRRVINQTKLRVSFKLSLDLYTLRRLLDN

Amino acid sequences of Lycotoxin translated from *Pamphobeteus verdolaga*.

Residues highlighted in grey indicate the signal peptide, while magenta blue highlighted residues, indicates the propeptide according to Spider|ProHMM from the arachnoserver. Yellow highlighted residues indicate the cysteine disposition commonly described in the ICK peptides.

Lycotoxin-1-Pverdolaga:

MEGR TKLLFLIAVFSIMHVITAELY CPQRLRIY CYVRTDR CCS DSDCGGGTIC CEENC GNTC RTP
RIIQSGGTRVDP SQI CKIG

Lycotoxin-2-Pverdolaga:

MDRLLMLFVTLAVLA QVLIVSPFMATSDADREILADYPDVTRYLYYNRKRS CIKRGGS CDHR
PND CCYNSS CRC NLWGTN CRC QRMGLFQKWGK

Lycotoxin-3-Pverdolaga:

MGKITEVLLIFLI CVLAIALVISAEVY CPAKSSII CKRSITK CCS DQDCPRGRI CCQEN CGNQ CNIP
SSVQTNGSKVLSDT CKIGQF

Lycotoxin-4-Pverdolaga:

XNARARSMDFLDADNREATLPPENKLGSGQGRVKSEHELRIERSLQNL TIPDWYKQSPW
SKKPKEGFILRRX

Amino acid sequences of CRISP proteins translated from *Pamphobeteus verdolaga*. Residues highlighted in grey indicate the signal peptide, while magenta blue highlighted residues, indicates the propeptide according to

Spider|ProHMM from the arachnoserver. Red highlighted residues indicate the cysteine disposition commonly described in the ICK peptides.

CRISP-1- Pverdolaga:

MNHVLLVLLAVTIC₁YAVPRLSRPKIYGNAIPYRDLDTN₂GATKKKIVLMHNFFRSRVQPSAS
DMLAMSWHEGAAEDAQRWAES₃Q₄LLLDHNTTGRWTQDFGT₅CGQ₆NIFVANVQVPWF₇FAAK
VWFLERDNFTY₈GKNVNDPDVVG₉HYTQMVWYSTHRVGC₁₀GFHYCGPDVTKVPYYSYV₁₁C₁₂NY₁₃CP
IGNHPERFDRPYTRGKPC₁₄SAC₁₅PGQ₁₆CKFKKLC₁₇TNT₁₈CPHADTWIN₁₉CRELNETWHDWL₂₀CGNEQN
EGHQA₂₁CKAT₂₂C₂₃CEGAIR

CRISP-2- Pverdolaga:

MRIRVILMLSWLWLGVS₁DGSCPALYRRYSKAHTYCLPPKSSSTILKSGISKSDIETIVRVHNELRS
KVATGEETYSMPKASNM₂RQMVWDSELA₃AVAQKHANQCLFKHDCNNCRKVKNFDV₄GQN
LFKRNPFVPPQPTWAQAVTDWYSEVNVFDQ₅QGIDGFIDGEGPPQTGHFTQDIWAESWRVGC
GYSVCEE₆GNVLELYTCNYGPAGNGENDPIYERGD₇PCTNCPLNSCCGSSCSGGTSYPGLCRISG
ENAPQYNRPEGLTFYCSFNNEHDCAKTVTGHNKWQVSKTL₈SGSYIGIVLNGGESSTLSFKNPA
KVPQKPLCFIINYRTGPQVDGEEVSGTANVIFKAGGSTF₉SELNSNGFQSF₁₀TKFSITLGWNMPT
MIDISISVPEGSSRYLEIKDMSATKESARTMALSSLLSGHYARTMELSSLLSGHYARTMELSSLL
SGHYARTMX

CRISP-3- Pverdolaga:

MLEMSWHKEAQESAQRWAE₁EC₂QILTYDGILGKYVEDYGS₃CGQ₄NIFVSNEKVPWTFVGEAWF
AERYDFSYSYNSVSEVGHYTQMVWNGSHRLG₅GFHYCAKDVKKPFYNYV₆C₇NY₈CPMGND
PKRLGMPYSSGKPC₉SECIKHCKYKKLC₁₀TNT₁₁CPYADLWVNCAQLNVTWNDWL₁₂CSNPEHQRH
RG₁₃CRATCLCPGKVI

Amino acid sequences of Hephaestin-like protein translated from *Pamphobeteus verdolaga*. Residues highlighted in grey indicate the signal peptide, while magenta blue highlighted residues, indicates the propeptide according to Spider|ProHMM from the arachnoserver. Red highlighted residues indicate the cysteine disposition commonly described in the ICK peptides.

Hephaestin-1- Pverdolaga:

MPTNLKIAIALTA₁AVMALVTAVILAVVLTS₂AKSVKTEAQQNVRTFYFAAE₃EVLWDYAPRETD
LLKERREDAGSSLEES₄EDPLRLGKRYKKA₅VFREYTDSTYSEAKSHPEWL₆GILGPLIETEVGDIVKI
NVYNNATHPVSLH₇THGARYLKHHEGAFYQDNT₈PKRDDKVFPGENYTYTWQISENRGP₉TES
DTPCMLWAYHSHVSGDEDIHTG₁₀LLGPLLI₁₁CRQGYLDTMYEHSEFSGRRHFVLLFLIFDENQSW
YLDENIAVKRTNTTQGNTEEIKENEQFQESNLMYSVNGLMYDNLKGLRM₁₂CHGSQVTWYLMG
MGNEADIIHAIT₁₃PGHPLL₁₄VREHRTDVVHL₁₅FPK₁₆FESALMTSNREGSWPIK₁₇CEVGDAHIVGME
ARFSVRQCGNRNTSEMSSQTGQVREFFIAAEETVWNYAPTGIN₁₈KMN₁₉GIPL₂₀NDSEAAPFFERG
ENRIGGTYKKVVYRGYMDQH₂₁FTEPLHHPAHLG₂₂LLGPTIRAEVGETVRVHFFNKATKAYAFQL
TAFV₂₃CSDCEMAGQNKSVAPSGNRTYSFVIREDLGSPKDPQCIPWRYFSAVEHLKDIYGG₂₄LNG
VLLI₂₅CRPGTLKADGTQKNVDKEFTLMFAVMDENKSPYIDENIAEYTTSGDNVDKEDEDFVESN
LMHSINGLMYGHLDGLE₂₆MC₂₇VNDNVSWNLFAIGAVVDMHVVYFSGNTILRDGLYRDTVDVM
PSGHQIVSMNPDLLGKWPMT₂₈CRTNDHLRGGMKARYEVKS₂₉C₃₀NHNGDVLSGGSQDLTADDKI
RKYFIAAVDEEWDYAPFDYHIVTGENLTENENSRI₃₁FVTRDATHIGSKYMK₃₂TLYREFTDSSFSQR
KTRTP₃₃EEHLG₃₄LLGPV₃₅IKAEVGETIQV₃₆FRNKAS₃₇RKFNI₃₈HTHGLPENSSQLYGV₃₉EPGGTQTYIW

KVPQRSGPTPGSFNCSSWMYYSAVDSIKDINTGLVGPLIICNPGILTNSGSRTDVDKEFSVLFTVF
DENESWYLEENVNNYCFEPEKVDVEDEDFKESNLKHSLNGLLYGALRGLGGTVGDTVAVWL
MGLGNEIDIHTAHFHGMSFVEKDDPLAGPKGHKADVTDLFPGFRTVEMTFDTPGTWLFHCH
VDDHLKGGMIALVTVNDRNATTLH

Hephaestin-2- Pverdolaga:

XGSKGTAFMRLSCPGRIPEASGQRPLHYSVNGRIYGTLEGLVAKNGTKTAWYLLGMGSEDDL
HTAHFHGQTFLQRTDTRRGDVVDLFPGYFDTVEMINDNPGTWILHCHVDDHMRYGMAAL
FTVTP

Amino acid sequences of venom metalloproteinase translated from *Pamphobeteus verdolaga*. Residues highlighted in grey indicate the signal peptide, while magenta blue highlighted residues, indicates the propeptide according to Spider|ProHMM from the arachnoserver. Red highlighted residues indicate the cysteine disposition commonly described in the ICK peptides.

Metalloproteinase-1- Pverdolaga:

XGKHVVYKRKFPIVKGLPTDYVTMDSEKMLNNTKHRSKRQAVPDTVWPEVLLVVDYETFIL
HGGNSRDVKRYFISFFNGVDLRYKLLHHPVRISLAGMIVAKDRDATPYLERNRLRPPNADAV
DAAGALTDMGKYLYREHRLPTYDLAVVITKLDMCRRRFPGGRCNRGTAGFAYVGGACVNV
KRLEKVNVAIIEDSGGFSGIIVAAHEIGHLLGVHDGSPPPSYLGGPGATHCPWEDGFIMSDL
RHTERGFKWSSCSVEQFKHFLHGETATCLYNFPHENDLLVRVLPGTMLTLDEQCKRDRGTTA
CFKDARVCAQLFCFDTASGYCVSYRPAAEGSPCGDGQVCKNGRCLAEIENIIPDFSHVTETYVE
AEERMDRSEEEITKSTDTTTFPSRRARIRRLYRGPNSRLRSTVPKENLPTISTGFPPKNDPSRNMK
TRL

Section S2. Full-length translated sequences for putative protein ORFs corresponding to proteins matching housekeeping and cellular process proteins.

Amino acid sequences of contig c6436_g1_i1 translated from *Pamphobeteus verdolaga*.

MCDDDDVAALVVDNGSGMCKAGFAGDDAPRAVFPISVGRPRHQGVMVGMGQKDSYVGDEA
QSKRGILTLKYPIEHGIVTNWDDMEKIW

Amino acid sequences of contig c62193_g1_i1 translated from *Pamphobeteus verdolaga*.

TQIMFETFNTPAMYVAIQAVLSLYASGRRTGIVLDSGDGVSHTVPIYEGYALPHAILRLDLAGR
DLTDYLMKILTERGYSFTTTAEREIVRDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVIT
IGNERFRCPEALFQPSFLGMESCGIHETTYNSIMKCDVDIRKDLANTVLSGGTTMYPGIADRM
QKEITALAPSTMKIKIIPPERKYSVW

Amino acid sequences of contig c13011_g1_i1 translated from *Pamphobeteus verdolaga*.

XEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYA
SGRTTGIVLDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIV
RDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNERFRCPEAMFQPSFLGMESCGI
HETTYNSIMKCDVDIRKDLYANTVLSGGTMYPGIADRMQKEITALAPSTMKIKIIPPERKYS
VWIGGSILASLSTFQX

Amino acid sequences of contig c15096_g1_i3 translated from *Pamphobeteus verdolaga*.

MEASHVTEDHINDESRSSESTNSMSHSRKYRATQHRVFNRSLSHLEKIKFFGFDMDYTLAQYN
SPEYEALQFRLMVGRMISIGYPAELKDFEYDPTFPIRGLWFDTTYGNLLKVDAYGNILVCCHGF
QFLKTSEIYNLYPNKFIQHDESRIYILNTLNLPEAYLLACLVDFFSNPQYTPSKTGKTNIFMS
YKSIFQDVRDAIDWVHMQGSLEKEETVNNIDKYVNKEDRLPMLFDRIHEVGKKTFLTNSTDYD
YTAKIMSYLEFDHPKSGGRDWKSYFDYILVDARKPLFFGGGTTLRQVDTGTGALRIGIHVGPLH
PGQVYSGGSCDVFTSLIGAKGKDVLYVGDIHYGDILKSKKTRGWRTFLIVPELQREVHVWTSK
WQLFNRLQELDIQLGDTYKDLDSCKDEPDISELMAIREVSHELDMSYGILGSTFRSGSRQTF
ANQICHYADLYACTFLNLMYYPFSYMFAPPMLMPHESTVEHDEGSIVNGEAYELEEEQVQE
PMRRRSRLEHSESSVPHLFAETPEAVTHHHDTDDEDEDTKSGEH

Amino acid sequences of contig c27174_g1_i1 translated from *Pamphobeteus verdolaga*.

MAKVPAIGIDLGTYSYCVGVFQHGKVEIANDQGNRTTPSYVAFTDTERLIGDAAKNQVAMN
PSNTVFDKRLIGRRFEDPSVQSDMKHWPFDVVS DSGPKIQVEYKGETKTFYPEEISSMVLTK
MKEIAEAYLGKTVTNVAVVTPAYFNDSQRQATKDAGTIAGLNVLRINEPTAAAIAYGLDKK
GQGERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNHVQEFKRKHKK
DLTTNKRALRRLRTACERAKRTLSSSTQASIEIDSLFEGVDFYSTITRARFEELNADLFRSTLEPVE
KALRDAKLDKAQVHDIVLVGGSTRIPKIQKLLQDFFNGKDLNKSINPDEAVAYGA AVQAAIL
NGDKSEQVQDLLLLDVTPSLGIETAGGVMTVLIKRNTPITRQTQTFTTYSNQPVGVLIVQVE
GERAMTKDNNLLGKFELTGIPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKENKITITNDKG
RLSKEEIERMVKDAEKYKDEDDKQKCRISKSNSLESYAFNVKSTVEDDKLKEKISEDDKKKVL
KVNETLRWLDSNQLADKEEYEHKQKELEGVCTPIITKLYQGAGGAPGMPGFPGAGAAPGG
GGTGSGGPTIEVD

Amino acid sequences of contig c15743_g1_i1 translated from *Pamphobeteus verdolaga*.

MPAIGIDLGTYSYCVGVFQHGQVEIANDQGNRTTPSYVAFTDTERLIGDPAKSQVVLNPENTV
FDKRLIGRKHDDPKIASDLKHWPQVCDAGGPKISVMYKGEKKLFNPEEISAMVLTCKMKE
TAEMYLGKVTAEVITVPAYFNDSQRQATKDAGIAGLNVLRINEPTAAALAYGLDKNLQGE
KNVLIFDLGGGTFDVSILTIDEGSLFEVRATAGDTHLGGEDFDNRMVNHFIIEFKRMHKKDL
QGNARALRRLRTACERAKRTLSSGTEASIEIDALYQGIDFYSKITRARFEELCMDLFRSTLEPVEK
ALTDKMDKNSIHVVVLVGGSTRIPKIQKLLRDFNGKELCMSINPDEAVAYGA AVQA AVL
GDKSEKIRDVLLVDVAPLSLGIETAGGVMKIVQRNSRIPCKTSQIFTTYSNQPVGVTIQVFEGE
RAMTKDNNHLLGKFDLSGIPPAQRGVPQIEVTFNLDANGILQVSACDKGTGKLQSIQITNDKGR
LTKEEIERMLAEAEKYQDEKQREKVSARNSLESYVYSVKQAASSVDNNRLSETDKKKVNDT
CDDVIRWLDNNTLAEKEEIEYKMKEVQSQLSPIMTKLHQAGGSPNNYSENSSATSSGPTVEEV
D

Amino acid sequences of contig c10792_g1_i2 translated from *Pamphobeteus verdolaga*.

MAKVPAIGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFTDTERLIGDAAKNQVAMN
PSNTVFDKRLIGRRX

Amino acid sequences of contig c2143_g1_i2 translated from *Pamphobeteus verdolaga*.

MARTKQTARKSTGGKAPRKQLATKAARKSAPSTGGVKKPHRYRPGTVALREIRRYQKSTELLI
RKLPFQRLVREIAQDFKTDLRFSAAIGALQEASE

Amino acid sequences of contig c16774_g1_i2 translated from *Pamphobeteus verdolaga*.

XGKQLEDGRMLSDYNIQKESTLHLVLRRLRGGMQIFVKTLTGKTITLEVEPSDTIENVKAKIQDK
EGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRRLRGGMQIFVKTLTGKTITLEVEPSDTI
ENVKAKI

Amino acid sequences of contig c17180_g4_i1 translated from *Pamphobeteus verdolaga*.

MCDDIAALVVDNGSGMCKAGFAGDDAPRAVFPISVGRPRHQGMVMVGMGQKDSYVGDEA
QSKRGILSLKYPIEHGIITNWDDMEKIWHHTFYNELRVAPEEHPILLTEAPLNPKANREKMTQI
MFETFNAPAMYVAIQAVLSLYASGRITGIVLDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLT
DYLKILTERGYSFVTTAEREIVRDIKEKLCYVALDFEQEMATAASSSTVEKSYELPDGQVITIG
NERFRCPETLFQPSFIGMESVGIHETTFNSIQKCDIDIRKDLANTVLSGGTMYPGIADRMQKE
ITALAPSTMKIKIIPPERKYSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHRKCF

Amino acid sequences of contig c16820_g1_i1 translated from *Pamphobeteus verdolaga*.

AAAIAYGLDKKGQGERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNH
FVQEFKRKHKKDLTTNKRSLRRLRTACERAKRTLSSSTQASIEIDSLFEGVDFYSTITRARFEELN
ADLFRGTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKIQKLLQDFNKGDLNKSINPDEAVA
YGA AVQAAILNGDKSEQVQDLLLLDVTPSLGIETA

Amino acid sequences of contig c9831_g1_i1 translated from *Pamphobeteus verdolaga*.

XLNGSPIPLPCADSRKFLPLLVEASHSRVTYVLSGVLYNLLYNPAVQLIKSNMPAIGIDLGTTY
SCVGVFQHGKVEIANDQGNRTTPSYVAFTDVERLIGDPAKSQAAMNPENTVFDKRLIGRRY
DDPKIAADIKNWPFEVCNVGGKPKVGVLYKGENKMFNPPEISAMVLTCKMKETAEMYLGKLV
TDAVVTVPAYFNDSQRQATKDAGAIAGLTVLRINEPTAAALAYGLDKNLKGEKVLIFDLGG
GTFDVSILTIDEGSLFEVKATAGDTHLGGEDFDNRMVNYFVEEFHRKHKKDLRSPRAIRRLRT
ACERAKRTLSSSTEAGIEVDAIFEGIDLYSKISRARFEELCIDLFRSTLEPVERALSDAKMNKASIH
DVVLVGGSTRIPKIQKLLRDFNKGELCMSINPDEAVAYGA AVQA AVLSGDTSKNIRDVLLVD
VIPLSLGIETAGGVMTKIVGRNSRIPCKTSQDFTTYSNQTSTVTVQVYEGERAMTKDNHLLGKF
NLGIPVPVPRGVPRIEVTFNLDNGLHVS AVEKSSGKSQSIRITNDKGRLSKQEIDRMLEDADK
YQREDEIQREKVAARNLTESYLYSVKQGADSANYSSLSPSDKAKVNNICEDAIRWLDNNSLAE
KEEILYKNKEVQAQLSPIMTKLHQRSSSGPIIEVD

Amino acid sequences of contig c16774_g1_i2 translated from *Pamphobeteus verdolaga*.

XGKQLEDGRMLSDYNIQKESTLHLVLRLRGGMQIFVKTLTGKTITLEVEPSDTIENVKAKIQDK
EGIPPDQQRLLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGMQIFVKTLTGKTITLEVEPSDTI
ENVKAKI

Amino acid sequences of contig c14336_g1_i1 translated from *Pamphobeteus verdolaga*.

XGIETAGGVMTVLIKRNTTIPTRQTQTFTTYSNQPGLVLIQVYEGERAMTKDNNLLGKFELTGI
PPAPRGVPQIEVTFDIDA

Amino acid sequences of contig c51913_g1_i1 translated from *Pamphobeteus verdolaga*.

DIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNERFRCPEALFQPSFLGMESCGIH
ETTYNSIMKCDVDIRKDLANTVLSGGTTMYPGIADRMQKEITALAPSTMKIKIAPPERKYSV
WIGGSILASLTFQQMWSKQYDESGPSIVHRKCF

Amino acid sequences of contig c2143_g1_i2 translated from *Pamphobeteus verdolaga*.

MARTKQTARKSTGGKAPRKQLATKAARKSAPSTGGVKKPHRYRPGTVLREIRRYQKSTELLI
RKLPFQRLVREIAQDFKTDLRFQSAAGALQEASE

Amino acid sequences of contig c4667_g1_i1 translated from *Pamphobeteus verdolaga*.

MARTKQTARKSTGGKAPRKQLATKAARKSAPSTGGVKKPHRYRPGTVLREIRRYQKSTELLI
RKLPFQRLVREIAQDFKTDLRFQSAAGALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQL
ARRIRGERA

Amino acid sequences of contig c15300_g1_i1 translated from *Pamphobeteus verdolaga*.

MFLKLPDVAQLCHAXTEENSAVKHRGHFRKWLTNPVRKLSHGRLDRSSSDNPKTSVKKPCPD
PTKVVNSKEEMGNKSSSPGPIKHAEGDIEPEVTVENTAPEVSPEAPDVNGESTDATSTCPVIP
SSSEAEGNSSAAVNLEPEGEPEEQVEQSSSEDNCPLTEQSNESKFLEHEEIEKALQKRKFVLQELVT
TEKQYVKDLGSLVEGYIELMKSGEITMPEDLKNKGDKIVFGNIEAIYEWHRDLFCAELEKCLEE
PERLGLLFRRYERRLNMYVVYCQNKPKSEYIVSEYLDTFEERQKLGHKLQLPDLLIKPVQRI
MKYQLLLKDILKYTEKAGIEEEAQNLRKAVHIMHVVPKAANDMMNVGRLQGFDGKITGQG
KLLQQGILFISDPSTGGKMKERQVFLFEQIIIFSDSVGPKTQFSNPVYIYKNHLQVNKMSLEERSE
ESDPTKFLKSKDPMQQGLTFVIQASQEERDEWVANIRAILDTQLDFLRALQSPIAYQKELTK
DISAPELGSLWNPSLRKTLSHPAAHKTVKSGSATTGPSLTSKSLRHPGRDKKVRADVTKPKS
VSAGTSGENLKEQTDGLVKECRAHSLAVPPLTLGDQSSDSESCNKNNGNSTPDVTS DGQRK
HSLPIEKRSNLAQQSPKSKRNFFEGFRNTLRPKSKTDSVLSGSGESTAVLSSSHLSDSASAAQG
KQDLSLNNKSDSMIRRWSETNPSRSVKGRRDMRWPHLTPRLSPALCSATEDYSASQSDEIPLS
KGD TVHLISKH SR CFVKKYSEDDDDNGTTEGWVPSYVIGQDVRKNRSFRLRLGLSMERLGH
KWTSGGD KKTETPKLND SKNLQTPNDLPDSVVSND EKKSLIFIESVSNMEVPEGEDATLAGRV
APADCLVVKWTL PDN SEIESK SIESDELSDSQFSPSTSPDSPMFDIKVQAFVFS DGGFSLTIRNCA
NSYSGQYVCTVNSPFGKIQTTC HLTVLGKPTPPGRPYVVERCGDSVCLQWSPPLCTGNLQLI

Amino acid sequences of contig c34105_g1_i1 translated from *Pamphobeteus verdolaga*.

CSQLSCSFPGISSLPNFYHEVGEQHQHVGNPIVFRGKDSVSFSALSQVPPATSFSSSTTTVGHMNS
HTQEWSSSHQGKAGGVLRRSSKSVSDLHSLPQLEDSSSFPTSVRSHTPPPNIANQVLDNEKGLKK
DSSRENDASASLPDPYFELEESERQFVDSVTDMGFPRGQVARTVKHLGTDDKKVVEHLCQIQTL
EESGYDSLEAEAAHLHDYNSDEARKYLDLLIKIQLGFDKTARS

Amino acid sequences of contig c5964_g1_i2 translated from *Pamphobeteus verdolaga*.

XHLVPFSPLSDRDRGLRHPFGKAQYCRGVSLQPRAGKSKIAQRAPAAGESVTAIVHSQYNSPA
AMYSMNAIADTLSAHAEMIAPGVMGINFMKPEKPINTMSEVYKLVQEEEQMKGDRTSPAA
PSQKKPYFGSLKVAQATSPTPPSSTPPVRQVRVSAPPVKTPPPVAPKPVLPVLPVAPPAPAA
PTSPGVTPPQANCSDCGRFIAGIFVRLNDRTLHEECFRCSTCGTSLKNMGYVNISNKLYCDIHA
KLAAKIIPPEDVSPTPPVNNAPAAPAPAFTPAPAFTPAPPPAPAPAQVPPPLPMPAAVAPK
VTQTAPSPFSPQLQQLTGGDLGNLPHTPSSSGGLPFRSISPQPFRAAGDYHKVIAPMSPTTGS
TAAPYFPQSGPLPFEMTPYMPPEVPVSSVFSSSSQQTQVSQTSQQTQITQQTQTSQTSQFSVDYRK
VIAQQSGRTGTFKIWPFPKPGAPVLESNTMPPTYPNTQHYSPLAMQSTPSSLSQTLFSR
SVQPPVPAPPAPSAAPPAPAPPAPAPLPFVPPPLSSFTKPAEPEPPKQEPKSEPQATEAAPEQ
KETSKEPPPPQPLPLPTSAPSGPSAPGFAPVLAPVVDPSSEPKPSAPQSGVPTGAGSRPAPKRG
RGQLKEQTPGSRIPICAVCGSPIRGPFVLTALGKTWCPDHFHCNNVHCKAPLQDIGFVEEHGQL
YCENCYEAFLAPICNKCTVRIKGDCLNALDKQWHPECFICAYCSKPFGNTSFYLEDGLPYCEK
DWNELFTTKCVGCGYPIEAGDRWVEALNNNYHSQCFCSCICNKNLEGQSFYAKGGRPFCKA
HAR

Amino acid sequences of contig c14908_g1_i2 translated from *Pamphobeteus verdolaga*.

MSYGSSYGSGRYGSGYGSSSYGSGSRRTGGSSYTPSTISSSYVPYRRSNGGSSYGLMQSKSASYIS
PTSSPRSSISSASGTTYLSSRIPSSNSYRNSTSYDPSYGSSKGVYKTLDSKKSDYVPDTEERCKLT
ASRSTGSVDQDDVSDSSKEEEDDEEEEDDDISERAKQKYGSSTSLPDTSSSEVSSRGETPSRYSS
VSSSRSSLIEDSNKDYKKLYEETKKENERLREKLKXSEDELERVKQQLQKSTQNNNTRNSISET
KKERRALERRISEMEMEEVKTLTKLKAENEKLAENRALSRRVCKLSK

Amino acid sequences of contig c4688_g1_i1 translated from *Pamphobeteus verdolaga*.

XLRELNECVGEEQSFKPVSSSEVDAIRSQQDEFKHYHQDRLEPLGKQIDGMNKMGGGLIQSAAP
GVSTSVLECDLDVLNDRWNSLKQRMNERERRLDVAFLQSGKFQEAMAGVQKWLEDTEEMV
ANQKPPSADYKVVKAQLQEQLKFLNKLDRQSSMSSMTMGTEIMNNMEPMERIQLEAQLS
DLMQRFDELMNGAQERTDALERTIPVAKDFQDRMSPLVEWLEQTEKKLAGMATIPTDQEKIR
QRMVEHEALHEDIMDHKEAFEELTEIAQMLMGLVGDDEAQVVVEKLQEVTDFHAKVVEDSE
HIGQLLAAYQGMGSFTVNYEDLMAWIDEMASRLSRFHVLSVYVEKLQEQLDELVELSEEIAD
HQQQVDDVASAGQDIMKHASGDDVIRMKEKLDLSVKFTDLTSRAADRLRQAQDSLPLVQN
FHSSHEKVTAWMDSAERQLKSLNVGLTSQETSIQKLEAEIQEYRPMVDTLNHLGPQLCQMSF
GEGAAVIETQVSRVNRFDACEQVQRKAERIDLSKQRNVEVIGDIEDLLDWFHEVEKQMMQ
AEPLSADPDSL TALLKEQKILNEEVSSQKGRVRDILVAAKKLMRESSGDDLAEVRDKADELKD
VTNAVASLCAADRLAALPLAEHFFETHADLCQWLDEIESEAELEAPALNANQIKKQQE
RNKALMQSVNDHKALVDKLNKTGEALKKLTPEEASRVQDVMDSDNSRYSSLKDILDRQN
ALEEALQATSQFSKLDGMLNALSNTADQLNNAEPVSAHPEKIEEQIDENKAVLKDLDKRSN
ALEAVKRAADDVIVKAGGARDPAVKDIKQLDKLNDLWDNIQKLARNRGRSLEDALAAAE
RFWDELTTVMKALKDLQDSLAAQEPPAIEPNAIQQQQEVLEI

Amino acid sequences of contig c14491_g1_i2 translated from *Pamphobeteus verdolaga*.

MEFPALGKHCFEKSNCMLDFLPMKCDACGNVFCKDHIHYIKHSCERAYQKDIQVPVCPLCN
KPVPSKRSEPPDIAVGEHIDRDCQSDPAVAKRKIYTNRCVKSCKRKEVIPLSCDNCRKNFCLK
HRHSADHECRDIKTSHELSPSGAAALVRMQASNKCTSKTSSKQSFSNAVMTANLPGSVIETE
KSVRSASACMSEDEALALALQKSLSDCNKAPPLPKDVQEEEDRLLAQAALAAEIDQRTAVSGV
QRHNXGQELYSVLA AVL SMLLN

Amino acid sequences of contig c9864_g1_i1 translated from *Pamphobeteus verdolaga*.

MSYRNQYSGSPWQQGGPPFGVGGYGQSYGGYGLNDQYAMMNSGYRSRQGGYGSMYSSG
MSQMRSMGYGGPSPSRHYLNDRMGGRQSGRGQMQRKRLPQRSPAGGPRSKRPNLDESRRN
RSKPRRRRDSRGSGSKGRRDHSDDEKGDPEYNPAEPTDDASDINYDDYESWKSSSDDENETKEV
TQNGEEQPAIDGEETKTTEKTDES DAKAKVD AKKPLICHVCKITCSNPERFRKHTISRTHRSKM
DTLLALQREKKQVLEASMKASQQVESRDSSKKS RKP GNWCTVCECSFSGNFLAHRRTKEHR
KKRDKKYPKCRPCR VGFSSSEYKEHCKKEDHKLKSAEFHYLKNLASGSDDDEAAIEPIAEYIE
AEDETKKDAEMKEEKEGSEEKKEEQEKMD EAKDGEETTDEKKDKKDDGKDSKSSKQKDS
KESKEPKAIGQSFVVS VQGYCKLCHKFFKDVTVAKVKHCRSIMHNGAFKKAMEEAMEQEEE
RQKLADQQEKIEREIAEAARLAADIAAVEKAAKEAAKREAAEKKAAQAKDSETKESVDQN
ENAAVEKMETDVANGEKEEMEVTETKESGEETKGKTEPQPPAPVAAAEEEEKPAETAQSDS
QGDEEVEEEPEKAKEEPTSSPATRRGRGRGRGQSRGKGKRR

Amino acid sequences of contig c62910_g1_i1 translated from *Pamphobeteus verdolaga*.

MFRMQNNTTVVDLLHPDLLSTTVLQEILVERKIGEEHINGASREQLLSLYSKVILPLPQREFRKNR
RGAYLSKKCGRNALQEKSTESQVEVKAKSTSPVPCPETQSRLPATKNKIVGLHATEPQSRLKPP
PISTESGKIIKLSRATNGDSIISPKRSMSPPGDSKRPKLIRLNRTLPPQNNKSKDDHCEETDTPSP
PKKKHKPILWP

Amino acid sequences of contig c29740_g1_i1 translated from *Pamphobeteus verdolaga*.

MIQTAMPGVDVWRISPEVKAKYDEQFFQLKPINGYVTGDQAKNLFQSGLPQILAQIWALA
DRNADGKMDSFEFAIAMHLIQMKLKGAE LPKILPSSMQVAAPQSVAIAPGFRPPVAVGPPVP
AVPTSTMAPL TAGFIRPASP VDAKLQRSGSVSSQDSPTGVPPPLIEWAVPQQSKLKYTQLFNSY
DRTRTGFLTGAQARNILVQTGLSHVILAQIWSLADIDADGRLSCEEFLAMHLTDCVKAGDTL
PPALPPDLIPPSHRRKRSTSIQSNVSISSHSNIGDMLLLGDLKEEDKLKGLPATFEDKRRENFEG
QAE LERRRLALLESQRKEQEERERKEREEQERRERIRQEERRRQLELEKQLAKQRELEQEE
QRRKALEQREAA REMERQRQLEWEKQRQ QE LLSQRQKEQETVCHLKNVNKNLTFELEELA
GKIKDLNEKISETRKGVTAMKSSIDDMRNERDSKLKEIADVKSKEFNDRLLV

Amino acid sequences of contig c11572_g1_i1 translated from *Pamphobeteus verdolaga*.

MVLVSAEGSERRPPMDAPENPVLLPKQSTWTKGDEH MVYLDNARAKREQSKQPTSMY GQLV
TQDQLVAISTR TQGSQNDLVALQSPTPYKCRDPSSAPLRKLSVDLIKTYKHINEVYYAKKKRA
QQTQGGDTSHKKERKIFNDGYDDDNHDYIIRNGEKFLDRYEIDSLIGKGSFGQVVKAYDHED
QCHVAIKIIKNKKPFLNQAQIEVKLLEMMNNHDSGSCYPVGQDKIVKLKGFHFMWRNHLCL
VFELLSYNLYDLLRNTNFRGVSLNLTRKFAQQMCTALMFLSSDLNIIHCDLKPENILL CNPKR

SAIKIVDFGSSCQLGQRIYQYIQSRFYRSPEVLLGIPYDMAIDMWSLGCILVEMHTGEPLFSGAN
 EVDQMNKIVEVLGMPPKHILDQAHKSRKYFDRLPDGTFVLKKTGDGKKYKSPGTRKLHDILG
 VETGGPGGRRLGEPGHTVSDYLFKDLILRMLDYDPKTRISPYHALQHSFFKRTSDESTNTSHS
 ASTSPAMEQGSVGNTNTGAGGAGSGSSSGSSSCAPPQVAGRARSDPTHQHHPFGQLQHSYTQ
 TGSYSMQFGTQVSITTAATAAALSAMECESPITSAGAGIFRSSQKIHAWSALGAAGTPTTLTPA
 IGAFTGTVTVGQHSHTSAPTSTRVGSHSHHSHNHSYRRHLHHQTQSSASGQTSASTSHAMNAV
 SFDPLQSFQPPATFSVVSSSRNQACSSSSVASSQLMPMDINSSNNLFASLDCTQTGSLNIQLGSSY
 QPLLYTGTVYSGQTTVPSYLGNTNFSQLGIHPSTPTTQPSSVVSPDVVSQKQSTDRDESPMVGVC
 VEQSPVASH

Amino acid sequences of contig c5016_g1_i1 translated from *Pamphobeteus verdolaga*.

KEYYEDDESIPKNTSVIVARVPVWSCNKKSWERSDLPLPVDDDELSGQINFDKVVKSADLVN
 ANVSEEDKVKAMISQSSQEYDPSKYLKCRSMTGPLPPSYTCFRCGKQGHWIKNCPTNNVDIKR
 STGIPRSFMVPVDGPEHKGALLTSSGEYAVPLIDHVAAYKEVKREKPPFVNVPEPEVEPEAQIPEE
 LLCMVCRDLLQDAVLIPCCGNSFCDECVRQVLLDSDNHECPLCHETGISPDVIPNRFLRTAVL
 NFRNETGYTRVKRMPSIPFPQPSHMDSPQSPDSTVENQAAPPEPVPEEAATVEDGTAVPITTV
 PEPENVEPECNETTESTPQPPDPPVQEETEETVEPGNEDLQPGTPLADEPPVHNVPEPELAENE
 QYPSHNQYDEENKFSYSHYYNENMDSDSRDEGHVSSSEINQISTIETITTRLNYKSRSDRPSHS
 FSQQRPVHHGHTRDPDSSSLPSRRGGSSHTYRSKPQEWPKGSLTVLVERDYNHDRLDYRDRYD
 RRNRDRPTNTSRFPQRSHNRYERPRETRYNQSDYHSENRCEYRDYSNNSELREDVNYEIRTNS
 GESTHSHAQRYNSPPASEHTQNKINVAAPPPPPPX

Amino acid sequences of contig c17992_g1_i1 translated from *Pamphobeteus verdolaga*.

MAYLXIVISDNGPQYASAEFHNFFVQQYDFQHITSSPGYPQANREVERMVRAVKDLLKRYPLP
 LILPQYAWSDWCLTSTVLYGSQASNEXCLLIIVNSSLGQIFDSTRRKITTLKSSNKSIGITAVTQP
 DLFQFSTPEITLPRFGYIRDCPQFLYYSPIQSHYRQGHSEKELPPPGETTPAICWDITPCSLLE
 PKPMPATASQVLPTHASEADNTMSDKPLEPASPAARTEIXVTDENQQRDHEASKVPQSESEG
 DVVVLTQ

Section S3. Raw material of proteomic reports.

Header -----

Search title Sebastian-AS-pep-5600 (\\nucleus.ecn.purdue.edu\vhedrick\My Documents\Mascot Daemon\Sebastian_AS-peptides_5600.par), submitted from Daemon on 1212-B119PC12

Timestamp 2015-08-20T14:01:03Z

User

Email

Report URI

http://mascot.bbc.purdue.edu/mascot/cgi/master_results.pl?file=../data/20150820/F020650.dat

Peak list data path C:\ProgramData\Matrix Science\Mascot Daemon\MGF\833 Sebastian-AS-pep-5600\mascot_daemon_merge.mgf

Peak list format Mascot generic

Search type MIS

Mascot version 2.5.1

Database AS_peptides_081915

Fasta file AS_peptides_081915_20150819.fasta

Total sequences 1834

Total residues 175871

Sequences after taxonomy filter 1834

Number of queries 271399

Decoy -----

Number of matches above identity threshold in search of real database 78

Number of matches above identity threshold in search of decoy database 25

Number of matches above homology threshold in search of real database 78

Number of matches above homology threshold in search of decoy database 25

Fixed modifications-----

Identifier Name Delta Neutral loss

1 Ethanolyl (C) 44,026215

Variable modifications -----

Identifier Name Delta Neutral loss(es)

1 Acetyl (K) 42,010565

2 Oxidation (M) 15,994915 0 63,998285

Search Parameters -----

Taxonomy filter All entries

Enzyme Trypsin

Maximum Missed Cleavages 1

Fixed modifications Ethanolyl (C)

Variable modifications Acetyl (K),Oxidation (M)

Peptide Mass Tolerance 0,05

Peptide Mass Tolerance Units Da

Fragment Mass Tolerance 0,2

Fragment Mass Tolerance Units Da

Mass values Monoisotopic

Instrument type ESI-QUAD-TOF

Decoy database also searched 1

Format parameters -----

Significance threshold 0,05

Max. number of hits 0

Use MudPIT protein scoring 1

Ions score cut-off 0

Include same-set proteins 0

Include sub-set proteins 1

Include unassigned 0

Require bold red 0

Use homology threshold 1

Group protein families 1

Re-score using Percolator 0

Show duplicate peptides 1

Protein hits -----

prot_hit_num	prot_family_member	prot_acc	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	pep_query	pep_rank	pep_isbold	pep_isunique	pep_exp_mz	pep_exp_mr	pep_exp_z	pep_calc_mr	pep_delta	pep_miss	pep_score	pep_expect	pep_res_before	pep_seq	pep_res_after	pep_var_mod	pep_var_mod_pos	pep_summed_mod_pos	pep_local_mod_pos
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4 1 >Hyaluronidase-1-Loxosceles intermedia|sp:R4J7Z9|1899
 Hyaluronidase from the venom of the spider Loxosceles intermedia 22
 46697 18 4 4 1 12,8 87360 1 1 1
 536,2918 2141,138 4 2141,1595 -0,0214 1 2,09
 0,62 K YGMK FVPLLEQYSILV NK E

6 1 >U16-lycotoxin-Ls1a|sp:B6DD52|1075 Toxin from venom of the
 spider Lycosa singoriensis with unknown molecular target and function 15
 2174 1 2 1 18005 1 1 1 421,7672
 841,5198 2 841,5385 -0,0187 1 1,37 0,73 K
 GIIRTIK D Acetyl (K) 0.0000001.0

6 1 >U16-lycotoxin-Ls1a|sp:B6DD52|1075 Toxin from venom of the
 spider Lycosa singoriensis with unknown molecular target and function 15
 2174 1 2 1 63948 1 1 1 498,2414
 994,4682 2 994,5124 -0,0441 1 2,99 0,5 R
 TIKDWYK G Acetyl (K) 0.0010000.0

7 1 >SphingomyelinaseD(LISicTox-alphaIII1i)|sp:Q8I914|132
 Sphingomyelinase D (EC 3.1.4.41; LISicTox-alphaIII1i) from the spider
 Loxosceles laeta 14 34985 45 3 2 1 5,1 3983 1
 1 1 406,695 811,3755 2 811,3348 0,0407 0
 5,38 0,29 K ESGYNDK Y

7 1 >SphingomyelinaseD(LISicTox-alphaIII1i)|sp:Q8I914|132
 Sphingomyelinase D (EC 3.1.4.41; LISicTox-alphaIII1i) from the spider
 Loxosceles laeta 14 34985 45 3 2 1 5,1 67559 1
 1 1 504,2342 1006,4539 2 1006,472 -0,018 0
 0,06 1,7 R DSANGFINK I Acetyl (K)
 0.000000001.0

8 1 >CRISP-2-Grammostola rosea|sp:M5WW7 |1844 Translation of a
cysteine rich secretory protein (CRISP) from the spider Grammostola rosea

13 46078 40 1 5 1 11,5 61364 1 1 1
493,2478 984,481 2 984,524 -0,043 1 0,01 3,3
R TGPQVKGEK S Acetyl (K) 0.000001000.0

8 1 >CRISP-2-Grammostola rosea|sp:M5WW7 |1844 Translation of a
cysteine rich secretory protein (CRISP) from the spider Grammostola rosea

13 46078 40 1 5 1 11,5 85926 2 0 1
533,2644 1064,5143 2 1064,5178 -0,0035 1 1,14
0,77 K DWYKEIK D 2 Acetyl (K) 0.0001001.0

8 1 >CRISP-2-Grammostola rosea|sp:M5WW7 |1844 Translation of a
cysteine rich secretory protein (CRISP) from the spider Grammostola rosea

13 46078 40 1 5 1 11,5 152184 1 1
1 728,3399 1454,6653 2 1454,7075 -0,0423 1
9,26 0,12 K VATGKETQYSMPK A Oxidation (M)
0.0000000000200.0

8 1 >CRISP-2-Grammostola rosea|sp:M5WW7 |1844 Translation of a
cysteine rich secretory protein (CRISP) from the spider Grammostola rosea

13 46078 40 1 5 1 11,5 67400 1 1 1
503,7584 2011,0045 4 2010,9973 0,0072 1 0,4 2,8
K SFPTVLTSSSMSFTKFTK K Oxidation (M)
0.000000000020000000.0

Section S4. Gen Ontology terms using the Panther database of the different proteins with catalytic activity.

Oxidoreductase Activity

HUMAN HGNC=3482 UniProtKB=P38117	ETFB	Electron transfer flavoprotein subunit beta;ETFB;ortholog	ELECTRON TRANSFER FLAVOPROTEIN SUBUNIT BETA (PTHR21294:SF8)	hydroxylase(PC00122)	<i>Homo sapiens</i>
HUMAN HGNC=7695 UniProtKB=O75438	NDUB1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1;NDUB1;ortholog	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 1 (PTHR15222:SF4)	dehydrogenase(PC00092);mitochondrial carrier protein(PC00158);transfer/carrier protein(PC00219)	<i>Homo sapiens</i>
HUMAN HGNC=15987 UniProtKB=O76003	GLRX3	Glutaredoxin-3;GLRX3;ortholog	GLUTAREDOXIN-3 (PTHR10293:SF40)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=11180 UniProtKB=P04179	SODM	Superoxide dismutase [Mn], mitochondrial;SOD2;ortholog	SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL (PTHR11404:SF35)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=6052 UniProtKB=P20839	IMDH1	Inosine-5'-monophosphate dehydrogenase 1;IMPDH1;ortholog	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1 (PTHR11911:SF74)	dehydrogenase(PC00092);metalloprotease(PC00153);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=10683 UniProtKB=O14521	DHSD	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial;SDHD;ortholog	SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT-RELATED (PTHR13337:SF6)	transfer/carrier protein(PC00219)	<i>Homo sapiens</i>
HUMAN HGNC=30231 UniProtKB=O75663	TIPRL	TIP41-like protein;TIPRL;ortholog	TIP41-LIKE PROTEIN (PTHR21021:SF16)		<i>Homo sapiens</i>
HUMAN HGNC=1334 UniProtKB=Q96IV6	FXDC2	Fatty acid hydroxylase domain-containing protein 2;FAXDC2;ortholog	FATTY ACID HYDROXYLASE DOMAIN-CONTAINING PROTEIN 2 (PTHR11863:SF26)	hydroxylase(PC00122);oxidase(PC00175)	<i>Homo sapiens</i>

HUMAN HGNC=29836 UniProtKB=Q9NRX3	NUA4L	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4-like 2;NDUFA4L2;ortholog	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 4-LIKE 2 (PTHR14256:SF5)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=23287 UniProtKB=O95571	ETHE1	Persulfide dioxygenase ETHE1, mitochondrial;ETHE1;ortholog	PERSULFIDE DIOXYGENASE ETHE1, MITOCHONDRIAL (PTHR43084:SF4)	hydrolase(PC00121)	<i>Homo sapiens</i>
HUMAN HGNC=2638 UniProtKB=P20815	CP3A5	Cytochrome P450 3A5;CYP3A5;ortholog	CYTOCHROME P450 3A5 (PTHR24302:SF20)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=12009 UniProtKB=P60174	TPIS	Triosephosphate isomerase;TPI1;ortholog	TRIOSEPHOSPHATE ISOMERASE (PTHR21139:SF22)	isomerase(PC00135)	<i>Homo sapiens</i>
HUMAN HGNC=2861 UniProtKB=P00374	DYR	Dihydrofolate reductase;DHFR;ortholog	DIHYDROFOLATE REDUCTASE (PTHR22778:SF46)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=7699 UniProtKB=O95168	NDUB4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4;NDUFB4;ortholog	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 4 (PTHR15469:SF1)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=2570 UniProtKB=P00167	CYB5	Cytochrome b5;CYB5A;ortholog	CYTOCHROME B5 (PTHR19359:SF78)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=12587 UniProtKB=P47985	UCRI	Cytochrome b-c1 complex subunit Rieske, mitochondrial;UQCRFS1;ortholog	CYTOCHROME B-C1 COMPLEX SUBUNIT RIESKE, MITOCHONDRIAL-RELATED (PTHR10134:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=382 UniProtKB=O60218	AK1BA	Aldo-keto reductase family 1 member B10;AKR1B10;ortholog	ALDO-KETO REDUCTASE FAMILY 1 MEMBER B10 (PTHR11732:SF278)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=4866 UniProtKB=Q9BQS7	HEPH	Hephaestin;HEPH;ortholog	HEPHAESTIN (PTHR11709:SF221)	oxidase(PC00175)	<i>Homo sapiens</i>

HUMAN HGNC=2898 UniProtKB=P09622	DLDH	Dihydrolipoyl dehydrogenase, mitochondrial;DLD;ortholog	DIHYDROLIPOYL DEHYDROGENASE, MITOCHONDRIAL (PTHR22912:SF151)	dehydrogenase(PC00092);oxidase(PC00175);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=30862 UniProtKB=O14957	QCR10	Cytochrome b-c1 complex subunit 10;UQCR11;ortholog	CYTOCHROME B-C1 COMPLEX SUBUNIT 10 (PTHR15420:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=17194 UniProtKB=Q9P0J0	NDUAD	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13;NDUFA13;ortholog	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 13 (PTHR12966:SF0)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=17366 UniProtKB=Q9UDR5	SDHAAS	Alpha-aminoadipic semialdehyde synthase, mitochondrial;AAS;ortholog	ALPHA-AMINOADIPIC SEMIALDEHYDE SYNTHASE, MITOCHONDRIAL (PTHR11133:SF18)		<i>Homo sapiens</i>
HUMAN HGNC=7422 UniProtKB=P00414	COX3	Cytochrome c oxidase subunit 3;MT-CO3;ortholog	CYTOCHROME C OXIDASE SUBUNIT 3 (PTHR11403:SF7)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=11476 UniProtKB=O15260	SURF4	Surfeit locus protein 4;SURF4;ortholog	SURFEIT LOCUS PROTEIN 4 (PTHR23427:SF1)	oxidase(PC00175);transmembrane receptor regulatory/adaptor protein(PC00226)	<i>Homo sapiens</i>
HUMAN HGNC=4313 UniProtKB=P23378	GCDP	Glycine dehydrogenase (decarboxylating), mitochondrial;GLDC;ortholog	GLYCINE DEHYDROGENASE (DECARBOXYLATING), MITOCHONDRIAL (PTHR11773:SF1)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=29079 UniProtKB=O60341	KDM1A	Lysine-specific histone demethylase 1A;KDM1A;ortholog	LYSINE-SPECIFIC HISTONE DEMETHYLASE 1A (PTHR10742:SF350)	DNA methyltransferase(PC00013);oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=5385 UniProtKB=O43837	IDH3B	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial;IDH3B;ortholog	ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT BETA, MITOCHONDRIAL (PTHR11835:SF42)	dehydrogenase(PC00092)	<i>Homo sapiens</i>

HUMAN HGNC=4455 UniProtKB=P21695	GPD A	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic;GPD1;ortholog	GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD(+)], CYTOPLASMIC (PTHR11728:SF32)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=4801 UniProtKB=P40939	ECH A	Trifunctional enzyme subunit alpha, mitochondrial;HADHA;ortholog	TRIFUNCTIONAL ENZYME SUBUNIT ALPHA, MITOCHONDRIAL (PTHR43612:SF5)	dehydrogenase(PC00092);epimerase/racemase(PC00096);hydratase(PC00120)	<i>Homo sapiens</i>
HUMAN HGNC=2640 UniProtKB=P24462	CP3 A7	Cytochrome P450 3A7;CYP3A7;ortholog	CYP3A7-CYP3A51P READTHROUGH-RELATED (PTHR24302:SF31)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=17450 UniProtKB=Q9HB55	CP34 3	Cytochrome P450 3A43;CYP3A43;ortholog	CYTOCHROME P450 3A43 (PTHR24302:SF6)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=2269 UniProtKB=P10606	COX 5B	Cytochrome c oxidase subunit 5B, mitochondrial;COX5B;ortholog	CYTOCHROME C OXIDASE SUBUNIT 5B, MITOCHONDRIAL (PTHR10122:SF0)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=19691 UniProtKB=Q9BV79	MEC R	Enoyl-[acyl-carrier-protein] reductase, mitochondrial;MECR;ortholog	ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE, MITOCHONDRIAL (PTHR43981:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=29958 UniProtKB=Q8NEX9	DR9 C7	Short-chain dehydrogenase/reductase family 9C member 7;SDR9C7;ortholog	SHORT-CHAIN DEHYDROGENASE/REDUCTASE FAMILY 9C MEMBER 7 (PTHR43313:SF5)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=410 UniProtKB=P43353	AL3 B1	Aldehyde dehydrogenase family 3 member B1;ALDH3B1;ortholog	ALDEHYDE DEHYDROGENASE FAMILY 3 MEMBER B1 (PTHR43570:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=976 UniProtKB=P54687	BCA T1	Branched-chain-amino-acid aminotransferase, cytosolic;BCAT1;ortholog	BRANCHED-CHAIN-AMINO-ACID AMINOTRANSFERASE, CYTOSOLIC (PTHR11825:SF70)	transaminase(PC00216)	<i>Homo sapiens</i>
HUMAN HGNC=21492 UniProtKB=Q8N0U8	VKO RL	Vitamin K epoxide reductase complex subunit 1-like protein 1;VKORC1L1;ortholog	VITAMIN K EPOXIDE REDUCTASE COMPLEX SUBUNIT 1-LIKE PROTEIN 1 (PTHR14519:SF5)	oxidoreductase(PC00176)	<i>Homo sapiens</i>

HUMAN HGNC=7690 UniProtKB=P56556	NDU A6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6;NDUFA6;ortholog	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 6 (PTHR12964:SF2)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=18503 UniProtKB=Q9BYV7	BCD O2	Beta,beta-carotene 9',10'-oxygenase;BCO2;ortholog	BETA,BETA-CAROTENE 9',10'-OXYGENASE (PTHR10543:SF61)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=9353 UniProtKB=P32119	PRD X2	Peroxioredoxin-2;PRDX2;ortholog	PEROXIREDOXIN-2 (PTHR10681:SF151)	peroxidase(PC00180)	<i>Homo sapiens</i>
HUMAN HGNC=5384 UniProtKB=P50213	IDH3 A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial;IDH3A;ortholog	ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT ALPHA, MITOCHONDRIAL (PTHR11835:SF34)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=9752 UniProtKB=P09417	DHP R	Dihydropteridine reductase;QDPR;ortholog	DIHYDROPTERIDINE REDUCTASE (PTHR15104:SF0)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=2277 UniProtKB=P12074	CX6 A1	Cytochrome c oxidase subunit 6A1, mitochondrial;COX6A1;ortholog	CYTOCHROME C OXIDASE SUBUNIT 6A1, MITOCHONDRIAL (PTHR11504:SF4)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=380 UniProtKB=P14550	ALR	Alcohol dehydrogenase [NADP(+)];AKR1A1;ortholog	ALCOHOL DEHYDROGENASE [NADP(+)] (PTHR11732:SF401)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=30086 UniProtKB=Q6P1R4	DUS 1L	tRNA-dihydrouridine(16/17) synthase [NAD(P)(+)]-like;DUS1L;ortholog	TRNA-DIHYDROURIDINE(16/17) SYNTHASE [NAD(P)(+)]-LIKE (PTHR11082:SF5)		<i>Homo sapiens</i>
HUMAN HGNC=4795 UniProtKB=O95479	6PG L	GDH/6PGL endoplasmic bifunctional protein;H6PD;ortholog	GDH/6PGL ENDOPLASMIC BIFUNCTIONAL PROTEIN (PTHR23429:SF7)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=10451 UniProtKB=P23921	RIR1	Ribonucleoside-diphosphate reductase large subunit;RRM1;ortholog	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE SUBUNIT (PTHR11573:SF6)	reductase(PC00198)	<i>Homo sapiens</i>

HUMAN HGNC=25996 UniProtKB=Q6P6C2	ALK B5	RNA demethylase ALKBH5;ALKBH5;ortholog	RNA DEMETHYLASE ALKBH5 (PTHR32074:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=15472 UniProtKB=O94788	AL1 A2	Retinal dehydrogenase 2;ALDH1A2;ortholog	RETINAL DEHYDROGENASE 2 (PTHR11699:SF102)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=4555 UniProtKB=P22352	GPX 3	Glutathione peroxidase 3;GPX3;ortholog	GLUTATHIONE PEROXIDASE 3 (PTHR11592:SF32)	peroxidase(PC00180)	<i>Homo sapiens</i>
HUMAN HGNC=4923 UniProtKB=P52789	HXK 2	Hexokinase-2;HK2;ortholog	HEXOKINASE-2 (PTHR19443:SF4)		<i>Homo sapiens</i>
HUMAN HGNC=15814 UniProtKB=Q9NR19	ACS A	Acetyl-coenzyme A synthetase, cytoplasmic;ACSS2;ortholog	ACETYL-COENZYME A SYNTHETASE, CYTOPLASMIC (PTHR24095:SF126)	dehydrogenase(PC00092);ligase(PC00142)	<i>Homo sapiens</i>
HUMAN HGNC=964 UniProtKB=O75936	BOD G	Gamma-butyrobetaine dioxygenase;BBOX1;ortholog	GAMMA-BUTYROBETAINE DIOXYGENASE (PTHR10696:SF33)	hydroxylase(PC00122);oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=7693 UniProtKB=Q16795	NDU A9	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial;NDUFA9;ortholog	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 9, MITOCHONDRIAL (PTHR12126:SF10)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=16631 UniProtKB=RT36P82909		28S ribosomal protein S36, mitochondrial;MRPS36;ortholog	28S RIBOSOMAL PROTEIN S36, MITOCHONDRIAL (PTHR31601:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=6666 UniProtKB=Q9Y4K0	LOX L2	Lysyl oxidase homolog 2;LOXL2;ortholog	LYSYL OXIDASE HOMOLOG 2 (PTHR45817:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=1063 UniProtKB=P30043	BLV RB	Flavin reductase (NADPH);BLVRB;ortholog	FLAVIN REDUCTASE (NADPH) (PTHR43355:SF2)	reductase(PC00198)	<i>Homo sapiens</i>

HUMAN HGNC=25598 UniProtKB=Q9NV66	TYW1	S-adenosyl-L-methionine-dependent tRNA 4-demethylwyosine synthase;TYW1;ortholog	S-ADENOSYL-L-METHIONINE-DEPENDENT TRNA 4-DEMETHYLWYOSINE SYNTHASE (PTHR13930:SF0)	oxidoreductase(PC00176);trans porter(PC00227)	<i>Homo sapiens</i>
HUMAN HGNC=24288 UniProtKB=Q8NE62	CHDH	Choline dehydrogenase, mitochondrial;CHDH;ortholog	CHOLINE DEHYDROGENASE, MITOCHONDRIAL (PTHR11552:SF147)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=7459 UniProtKB=P03905	NU4M	NADH-ubiquinone oxidoreductase chain 4;MT-ND4;ortholog	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (PTHR43507:SF1)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=19331 UniProtKB=Q96EY8	MMAB	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial;MMAB;ortholog	COB(I)YRINIC ACID A,C-DIAMIDE ADENOSYLTRANSFERASE, MITOCHONDRIAL (PTHR12213:SF0)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=12582 UniProtKB=P14927	QCR7	Cytochrome b-c1 complex subunit 7;UQCRB;ortholog	CYTOCHROME B-C1 COMPLEX SUBUNIT 7 (PTHR12022:SF2)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=6971 UniProtKB=P40926	MDHM	Malate dehydrogenase, mitochondrial;MDH2;ortholog	MALATE DEHYDROGENASE, MITOCHONDRIAL (PTHR11540:SF16)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=4335 UniProtKB=P00367	DHE3	Glutamate dehydrogenase 1, mitochondrial;GLUD1;ortholog	GLUTAMATE DEHYDROGENASE 1, MITOCHONDRIAL (PTHR11606:SF25)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=19086 UniProtKB=Q96DB2	HDA11	Histone deacetylase 11;HDAC11;ortholog	HISTONE DEACETYLASE 11 (PTHR43497:SF2)	deacetylase(PC00087);nucleic acid binding(PC00171);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=10603 UniProtKB=O75880	SCO1	Protein SCO1 homolog, mitochondrial;SCO1;ortholog	PROTEIN SCO1 HOMOLOG, MITOCHONDRIAL (PTHR12151:SF4)	oxidase(PC00175)	<i>Homo sapiens</i>

HUMAN HGNC=21298 UniProtKB=Q86V21	AACS	Acetoacetyl-CoA synthetase;AACS;ortholog	ACETOACETYL-COA SYNTHETASE (PTHR42921:SF1)	dehydrogenase(PC00092);ligase(PC00142)	<i>Homo sapiens</i>
HUMAN HGNC=20837 UniProtKB=Q6QHF9	PAOX	Peroxisomal N(1)-acetyl-spermine/spermidine oxidase;PAOX;ortholog	PEROXISOMAL N(1)-ACETYL-SPERMINE/SPERMIDINE OXIDASE (PTHR10742:SF43)	DNA methyltransferase(PC00013);oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=2571 UniProtKB=P49447	CY561	Cytochrome b561;CYB561;ortholog	CYTOCHROME B561 (PTHR10106:SF14)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=18685 UniProtKB=Q7Z5P4	DHB13	17-beta-hydroxysteroid dehydrogenase 13;HSD17B13;ortholog	17-BETA-HYDROXYSTEROID DEHYDROGENASE 13 (PTHR24322:SF499)		<i>Homo sapiens</i>
HUMAN HGNC=14966 UniProtKB=Q92626	PXD N	Peroxidasin homolog;PXD N;ortholog	PEROXIDASIN HOMOLOG (PTHR11475:SF75)	peroxidase(PC00180)	<i>Homo sapiens</i>
HUMAN HGNC=6053 UniProtKB=P12268	IMDH2	Inosine-5'-monophosphate dehydrogenase 2;IMPDH2;ortholog	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2 (PTHR11911:SF121)	dehydrogenase(PC00092);metallopeptidase(PC00153);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=17169 UniProtKB=Q13162	PRDX4	Peroxiredoxin-4;PRDX4;ortholog	PEROXIREDOXIN-4 (PTHR10681:SF128)	peroxidase(PC00180)	<i>Homo sapiens</i>
HUMAN HGNC=13280 UniProtKB=Q96HE7	ERO1L	ERO1-like protein alpha;ERO1A;ortholog	ERO1-LIKE PROTEIN ALPHA (PTHR12613:SF1)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=15862 UniProtKB=Q9NWM0	SMOX	Spermine oxidase;SMOX;ortholog	SPERMINE OXIDASE (PTHR10742:SF347)	DNA methyltransferase(PC00013);oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=30141 UniProtKB=Q96Q83	ALKB3	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 3;ALKBH3;ortholog	ALPHA-KETOGLUTARATE-DEPENDENT DIOXYGENASE ALKB HOMOLOG 3 (PTHR31212:SF4)		<i>Homo sapiens</i>

HUMAN HGNC=11474 UniProtKB=Q15526	SURF1	Surfeit locus protein 1;SURF1;ortholog	SURFEIT LOCUS PROTEIN 1 (PTHR23427:SF2)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=4458 UniProtKB=P06744	G6PI	Glucose-6-phosphate isomerase;GPI;ortholog	GLUCOSE-6-PHOSPHATE ISOMERASE (PTHR11469:SF4)	isomerase(PC00135)	<i>Homo sapiens</i>
HUMAN HGNC=8891 UniProtKB=P52209	6PGD,PGDH	6-phosphogluconate dehydrogenase, decarboxylating;PGD;ortholog	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (PTHR11811:SF53)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=6041 UniProtKB=A1L0T0	ILVBL	Acetolactate synthase-like protein;ILVBL;ortholog	ACETOLACTATE SYNTHASE-LIKE PROTEIN (PTHR18968:SF155)	decarboxylase(PC00089);dehydrogenase(PC00092);transferase(PC00220)	<i>Homo sapiens</i>
HUMAN HGNC=3481 UniProtKB=P13804	ETFA	Electron transfer flavoprotein subunit alpha, mitochondrial;ETFA;ortholog	ELECTRON TRANSFER FLAVOPROTEIN SUBUNIT ALPHA, MITOCHONDRIAL (PTHR43153:SF1)	dehydrogenase(PC00092);oxidase(PC00175);transferase(PC00220)	<i>Homo sapiens</i>
HUMAN HGNC=4623 UniProtKB=P00390	GSHR	Glutathione reductase, mitochondrial;GSR;ortholog	GLUTATHIONE REDUCTASE, MITOCHONDRIAL (PTHR42737:SF2)	dehydrogenase(PC00092);oxidase(PC00175);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=2494 UniProtKB=Q13363	CTBP	C-terminal-binding protein 1;CTBP1;ortholog	C-TERMINAL-BINDING PROTEIN 1 (PTHR46029:SF2)	transcription cofactor(PC00217)	<i>Homo sapiens</i>
HUMAN HGNC=2596 UniProtKB=P05177	CP1A2	Cytochrome P450 1A2;CYP1A2;ortholog	CYTOCHROME P450 1A2 (PTHR24299:SF7)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=3773 UniProtKB=P49326	FMO5	Dimethylaniline monooxygenase [N-oxide-forming] 5;FMO5;ortholog	DIMETHYLANILINE MONOOXYGENASE [N-OXIDE-FORMING] 5 (PTHR23023:SF78)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=7432 UniProtKB=P11586	C1TC	C-1-tetrahydrofolate synthase, cytoplasmic;MTHFD1;ortholog	C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (PTHR43274:SF2)	ligase(PC00142)	<i>Homo sapiens</i>

HUMAN HGNC=23198 UniProtKB=CP4 V2 Q6ZWL3	Cytochrome P450 4V2;CYP4V2;ortholog	CYTOCHROME P450 4V2 (PTHR24291:SF56)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=5386 UniProtKB=IDH3 G P51553	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial;IDH3G;ortholog	ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT GAMMA, MITOCHONDRIAL (PTHR11835:SF60)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=32487 UniProtKB=ALK B2 Q6NS38	DNA oxidative demethylase ALKBH2;ALKBH2;ortholog	DNA OXIDATIVE DEMETHYLASE ALKBH2 (PTHR31573:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=7473 UniProtKB=MTR R Q9UBK8	Methionine synthase reductase;MTRR;ortholog	METHIONINE SYNTHASE REDUCTASE (PTHR19384:SF84)		<i>Homo sapiens</i>
HUMAN HGNC=18985 UniProtKB=DCX R Q7Z4W1	L-xylulose reductase;DCXR;ortholog	L-XYLULOSE REDUCTASE (PTHR44252:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=4892 UniProtKB=HGD Q93099	Homogentisate 1,2-dioxygenase;HGD;ortholog	HOMOGENTISATE 1,2-DIOXYGENASE (PTHR11056:SF0)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=11179 UniProtKB=SOD C P00441	Superoxide dismutase [Cu-Zn];SOD1;ortholog	SUPEROXIDE DISMUTASE [CU-ZN] (PTHR10003:SF58)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=6983 UniProtKB=MA OX P48163	NADP-dependent malic enzyme;ME1;ortholog	NADP-DEPENDENT MALIC ENZYME (PTHR23406:SF17)	acyltransferase(PC00042);decarboxylase(PC00089);dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=10293 UniProtKB=RPE Q96AT9	Ribulose-phosphate 3-epimerase;RPE;ortholog	RIBULOSE-PHOSPHATE 3-EPIMERASE-RELATED (PTHR11749:SF9)		<i>Homo sapiens</i>
HUMAN HGNC=28242 UniProtKB=HPD L Q96IR7	4-hydroxyphenylpyruvate dioxygenase-like protein;HPDL;ortholog	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE-LIKE PROTEIN (PTHR11959:SF10)	oxygenase(PC00177)	<i>Homo sapiens</i>

HUMAN HGNC=26222 UniProtKB=Q8WVX9	FAC R1	Fatty acyl-CoA reductase 1;FAR1;ortholog	FATTY ACYL-COA REDUCTASE 1 (PTHR11011:SF45)		<i>Homo sapiens</i>
HUMAN HGNC=7891 UniProtKB=Q9NPH5	NOX 4	NADPH oxidase 4;NOX4;ortholog	NADPH OXIDASE 4 (PTHR11972:SF78)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=28697 UniProtKB=Q8N4Q0	PTG R3	Prostaglandin reductase 3;ZADH2;ortholog	PROSTAGLANDIN REDUCTASE 3 (PTHR43677:SF3)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=987 UniProtKB=P21953	ODB B	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial;BCKDHB;ortholog	2-OXOISOVALERATE DEHYDROGENASE SUBUNIT BETA, MITOCHONDRIAL (PTHR42980:SF1)	dehydrogenase(PC00092);lyase(PC00144);transketolase(PC00221)	<i>Homo sapiens</i>
HUMAN HGNC=4829 UniProtKB=P02042	HBD	Hemoglobin subunit delta;HBD;ortholog	HEMOGLOBIN SUBUNIT DELTA (PTHR11442:SF50)		<i>Homo sapiens</i>
HUMAN HGNC=4803 UniProtKB=P55084	ECH B	Trifunctional enzyme subunit beta, mitochondrial;HADHB;ortholog	TRIFUNCTIONAL ENZYME SUBUNIT BETA, MITOCHONDRIAL (PTHR18919:SF141)	acetyltransferase(PC00038)	<i>Homo sapiens</i>
HUMAN HGNC=2577 UniProtKB=P13498	CY24 A	Cytochrome b-245 light chain;CYBA;ortholog	CYTOCHROME B-245 LIGHT CHAIN (PTHR15168:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=3951 UniProtKB=Q16595	FRD A	Frataxin, mitochondrial;FXN;ortholog	FRATAXIN, MITOCHONDRIAL (PTHR16821:SF4)	cation transporter(PC00068);kinase(PC00137)	<i>Homo sapiens</i>
HUMAN HGNC=7702 UniProtKB=P17568	NDU B7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7;NDUFB7;ortholog	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 7 (PTHR20900:SF0)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=404 UniProtKB=P05091	ALD H2	Aldehyde dehydrogenase, mitochondrial;ALDH2;ortholog	ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL (PTHR11699:SF233)	dehydrogenase(PC00092)	<i>Homo sapiens</i>

HUMAN HGNC=4057 UniProtKB=P11413	G6PD	Glucose-6-phosphate 1-dehydrogenase;G6PD;ortholog	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (PTHR23429:SF0)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=7715 UniProtKB=O00217	NDUS8	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial;NDUFS8;ortholog	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 8, MITOCHONDRIAL (PTHR10849:SF24)	Homo sapiens	
HUMAN HGNC=9083 UniProtKB=O60568	PLOD3	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3;PLOD3;ortholog	PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 3 (PTHR10730:SF7)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=29838 UniProtKB=Q9UHB4	NDOR1	NADPH-dependent diflavin oxidoreductase 1;NDOR1;ortholog	NADPH-DEPENDENT DIFLAVIN OXIDOREDUCTASE 1 (PTHR19384:SF10)		<i>Homo sapiens</i>
HUMAN HGNC=26927 UniProtKB=Q96CU9	FXRD1	FAD-dependent oxidoreductase domain-containing protein 1;FOXRED1;ortholog	FAD-DEPENDENT OXIDOREDUCTASE DOMAIN-CONTAINING PROTEIN 1 (PTHR13847:SF44)	dehydrogenase(PC00092);oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=18308 UniProtKB=Q9NVH6	TMLH	Trimethyllysine dioxygenase, mitochondrial;TMLHE;ortholog	TRIMETHYLLYSINE DIOXYGENASE, MITOCHONDRIAL (PTHR10696:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=4570 UniProtKB=Q9UBQ7	GRHPR	Glyoxylate reductase/hydroxypyruvate reductase;GRHPR;ortholog	GLYOXYLATE REDUCTASE/HYDROXYPYRUVATE REDUCTASE (PTHR10996:SF137)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=24475 UniProtKB=Q9UI17	DMGDH	Dimethylglycine dehydrogenase, mitochondrial;DMGDH;ortholog	DIMETHYLGLYCINE DEHYDROGENASE, MITOCHONDRIAL (PTHR13847:SF187)	dehydrogenase(PC00092);oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=4907 UniProtKB=P31937	3HIDH	3-hydroxyisobutyrate dehydrogenase, mitochondrial;HIBADH;ortholog	3-HYDROXYISOBUTYRATE DEHYDROGENASE, MITOCHONDRIAL (PTHR22981:SF7)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=7863 UniProtKB=Q13423	NNTM	NAD(P) transhydrogenase, mitochondrial;NNT;ortholog	NAD(P) TRANSHYDROGENASE, MITOCHONDRIAL (PTHR10160:SF22)	dehydrogenase(PC00092)	<i>Homo sapiens</i>

HUMAN HGNC=408 UniProtKB=P51649	SSD H	Succinate-semialdehyde dehydrogenase, mitochondrial;ALDH5A1;ortholog	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE, MITOCHONDRIAL (PTHR43353:SF5)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=253 UniProtKB=P11766	ADH X	Alcohol dehydrogenase class-3;ADH5;ortholog	ALCOHOL DEHYDROGENASE CLASS-3 (PTHR43880:SF4)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=7706 UniProtKB=O95298	NDU C2	NADH dehydrogenase [ubiquinone] 1 subunit C2;NDUFC2;ortholog	NADH DEHYDROGENASE [UBIQUINONE] 1 SUBUNIT C2-RELATED (PTHR13099:SF0)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=1516 UniProtKB=P04040	CAT A	Catalase;CAT;ortholog	CATALASE (PTHR11465:SF9)	peroxidase(PC00180)	<i>Homo sapiens</i>
HUMAN HGNC=16232 UniProtKB=Q96KJ9	COX 42	Cytochrome c oxidase subunit 4 isoform 2, mitochondrial;COX4I2;ortholog	CYTOCHROME C OXIDASE SUBUNIT 4 ISOFORM 2, MITOCHONDRIAL (PTHR10707:SF11)		<i>Homo sapiens</i>
HUMAN HGNC=7179 UniProtKB=Q02252	MMS A	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial;ALDH6A1;ortholog	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE [ACYLATING], MITOCHONDRIAL (PTHR43866:SF3)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=10452 UniProtKB=P31350	RIR2	Ribonucleoside-diphosphate reductase subunit M2;RRM2;ortholog	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SUBUNIT M2 (PTHR23409:SF20)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=7873 UniProtKB=P35228	NOS 2	Nitric oxide synthase, inducible;NOS2;ortholog	NITRIC OXIDE SYNTHASE, INDUCIBLE (PTHR19384:SF56)		<i>Homo sapiens</i>
HUMAN HGNC=8923 UniProtKB=O43175	SER A	D-3-phosphoglycerate dehydrogenase;PHGDH;ortholog	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PTHR42938:SF9)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=7455 UniProtKB=P03886	NU1 M	NADH-ubiquinone oxidoreductase chain 1;MT-ND1;ortholog	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (PTHR11432:SF3)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>

HUMAN HGNC=10297 UniProtKB=RPIA P49247	Ribose-5-phosphate isomerase;RPIA;ortholog	RIBOSE-5-PHOSPHATE ISOMERASE (PTHR11934:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=2689 UniProtKB=DOP O P09172	Dopamine beta-hydroxylase;DBH;ortholog	DOPAMINE BETA-HYDROXYLASE (PTHR10157:SF29)		<i>Homo sapiens</i>
HUMAN HGNC=5398 UniProtKB=GILT P13284	Gamma-interferon-inducible lysosomal thiol reductase;IFI30;ortholog	GAMMA-INTERFERON-INDUCIBLE LYOSOMAL THIOL REDUCTASE (PTHR13234:SF8)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=17822 UniProtKB=PGE S2 Q9H7Z7	Prostaglandin E synthase 2;PTGES2;ortholog	PROSTAGLANDIN E SYNTHASE 2 (PTHR12782:SF5)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=4195 UniProtKB=GCK P35557	Glucokinase;GCK;ortholog	GLUCOKINASE (PTHR19443:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=9081 UniProtKB=PLO D Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1;PLOD1;ortholog	PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 (PTHR10730:SF5)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=11834 UniProtKB=TKT P29401	Transketolase;TKT;ortholog	TRANSKETOLASE (PTHR43195:SF3)	dehydrogenase(PC00092);lyase (PC00144);transketolase(PC00221)	<i>Homo sapiens</i>
HUMAN HGNC=412 UniProtKB=AL9 A1 P49189	4-trimethylaminobutyraldehyde dehydrogenase;ALDH9A1;ortholog	4-TRIMETHYLAMINO BUTYRALDEHYDE DEHYDROGENASE (PTHR11699:SF228)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=7688 UniProtKB=NDU A5 Q16718	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5;NDUFA5;ortholog	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 5 (PTHR12653:SF0)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=23316 UniProtKB=H17B 6 O14756	17-beta-hydroxysteroid dehydrogenase type 6;HSD17B6;ortholog	17-BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 6 (PTHR43313:SF4)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>

HUMAN HGNC=8768 UniProtKB=O95831	AIF M1	Apoptosis-inducing factor 1, mitochondrial;AIFM1;ortholog	APOPTOSIS-INDUCING FACTOR 1, MITOCHONDRIAL (PTHR43557:SF4)	dehydrogenase(PC00092);oxidase(PC00175);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=26101 UniProtKB=Q96CM8	ACS F2	Acyl-CoA synthetase family member 2, mitochondrial;ACSF2;ortholog	ACYL-COA SYNTHETASE FAMILY MEMBER 2, MITOCHONDRIAL (PTHR43201:SF9)	dehydrogenase(PC00092);ligase(PC00142)	<i>Homo sapiens</i>
HUMAN HGNC=28218 UniProtKB=Q9BRA2	TXD 17	Thioredoxin domain-containing protein 17;TXNDC17;ortholog	THIOREDOXIN DOMAIN-CONTAINING PROTEIN 17 (PTHR12452:SF0)	transporter(PC00227)	<i>Homo sapiens</i>
HUMAN HGNC=26920 UniProtKB=Q96G46	DUS 3L	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like;DUS3L;ortholog	TRNA-DIHYDROURIDINE(47) SYNTHASE [NAD(P)(+)]-LIKE (PTHR45846:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=20499 UniProtKB=Q9H9P8	L2H DH	L-2-hydroxyglutarate dehydrogenase, mitochondrial;L2HGDH;ortholog	L-2-HYDROXYGLUTARATE DEHYDROGENASE, MITOCHONDRIAL (PTHR43104:SF2)	dehydrogenase(PC00092);oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=12590 UniProtKB=P07919	QCR 6	Cytochrome b-c1 complex subunit 6, mitochondrial;UQCRH;ortholog	CYTOCHROME B-C1 COMPLEX SUBUNIT 6, MITOCHONDRIAL (PTHR15336:SF3)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=20667 UniProtKB=Q86VQ6	TRX R3	Thioredoxin reductase 3;TXNRD3;ortholog	THIOREDOXIN REDUCTASE 3 (PTHR43256:SF7)	dehydrogenase(PC00092);oxidase(PC00175);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=11184 UniProtKB=Q00796	DHS O	Sorbitol dehydrogenase;SORD;ortholog	SORBITOL DEHYDROGENASE (PTHR43161:SF9)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=9722 UniProtKB=P54886	P5CS	Delta-1-pyrroline-5-carboxylate synthase;ALDH18A1;ortholog	DELTA-1-PYRROLINE-5-CARBOXYLATE SYNTHASE (PTHR11063:SF8)	amino acid kinase(PC00045);dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=3012 UniProtKB=Q12882	DPY D	Dihydropyrimidine dehydrogenase [NADP(+)];DPYD;ortholog	DIHYDROPYRIMIDINE DEHYDROGENASE [NADP(+)] (PTHR43073:SF2)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>

HUMAN HGNC=23396 UniProtKB=Q5SRE7	PHY D1	Phytanoyl-CoA dioxygenase domain-containing protein 1;PHYHD1;ortholog	PHYTANOYL-COA DIOXYGENASE DOMAIN-CONTAINING PROTEIN 1 (PTHR20883:SF15)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=26506 UniProtKB=Q96MI6	PPM1E	Protein phosphatase 1M;PPM1M;ortholog	PROTEIN PHOSPHATASE 1M (PTHR13832:SF236)	kinase inhibitor(PC00139);protein phosphatase(PC00195)	<i>Homo sapiens</i>
HUMAN HGNC=20797 UniProtKB=Q53TN4	CYBR1	Cytochrome b reductase 1;CYBRD1;ortholog	CYTOCHROME B REDUCTASE 1 (PTHR10106:SF12)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=30264 UniProtKB=Q8NCN5	PDP R	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial;PDPR;ortholog	PYRUVATE DEHYDROGENASE PHOSPHATASE REGULATORY SUBUNIT, MITOCHONDRIAL (PTHR13847:SF193)	dehydrogenase(PC00092);oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=1613 UniProtKB=O14618	CCS	Copper chaperone for superoxide dismutase;CCS;ortholog	COPPER CHAPERONE FOR SUPEROXIDE DISMUTASE (PTHR10003:SF27)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=26398 UniProtKB=Q96NN9	AIF M3	Apoptosis-inducing factor 3;AIFM3;ortholog	APOPTOSIS-INDUCING FACTOR 3 (PTHR43557:SF8)	dehydrogenase(PC00092);oxidase(PC00175);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=4236 UniProtKB=P55789	ALR	FAD-linked sulfhydryl oxidase ALR;GFER;ortholog	FAD-LINKED SULFHYDRYL OXIDASE ALR (PTHR12645:SF0)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=12390 UniProtKB=Q13630	FCL	GDP-L-fucose synthase;TSTA3;ortholog	GDP-L-FUCOSE SYNTHASE (PTHR43238:SF1)	dehydratase(PC00091);epimerase/racemase(PC00096);oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=7419 UniProtKB=P00395	COX 1	Cytochrome c oxidase subunit 1;MT-CO1;ortholog	CYTOCHROME C OXIDASE SUBUNIT 1 (PTHR10422:SF18)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=1548 UniProtKB=P16152	CBR 1	Carbonyl reductase [NADPH] 1;CBR1;ortholog	CARBONYL REDUCTASE [NADPH] 1 (PTHR43963:SF2)		<i>Homo sapiens</i>

HUMAN HGNC=20390 UniProtKB=Q9Y6N5	SQOR	Sulfide:quinone oxidoreductase, mitochondrial;SQOR;ortholog	SULFIDE:QUINONE OXIDOREDUCTASE, MITOCHONDRIAL (PTHR10632:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=2593 UniProtKB=P05093	CP17A	Steroid 17-alpha-hydroxylase/17,20 lyase;CYP17A1;ortholog	STEROID 17-ALPHA-HYDROXYLASE/17,20 LYASE (PTHR24289:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=25812 UniProtKB=Q9H8P0	POR ED	Polyprenol reductase;SRD5A3;ortholog	POLYPRENOL REDUCTASE (PTHR14624:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=7377 UniProtKB=Q9UJ68	MSRA	Mitochondrial peptide methionine sulfoxide reductase;MSRA;ortholog	MITOCHONDRIAL PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PTHR42799:SF2)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=7714 UniProtKB=O75251	NDU S7	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial;NDUFS7;ortholog	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 7, MITOCHONDRIAL (PTHR11995:SF22)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=2321 UniProtKB=P36551	HEM 6	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial;CPOX;ortholog	OXYGEN-DEPENDENT COPROPORPHYRINOGEN-III OXIDASE, MITOCHONDRIAL (PTHR10755:SF0)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=2267 UniProtKB=P20674	COX 5A	Cytochrome c oxidase subunit 5A, mitochondrial;COX5A;ortholog	CYTOCHROME C OXIDASE SUBUNIT 5A, MITOCHONDRIAL (PTHR14200:SF13)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=7872 UniProtKB=P29475	NOS 1	Nitric oxide synthase, brain;NOS1;ortholog	NITRIC OXIDE SYNTHASE, BRAIN (PTHR19384:SF63)		<i>Homo sapiens</i>
HUMAN HGNC=18583 UniProtKB=Q9ULR3	PPM 1H	Protein phosphatase 1H;PPM1H;ortholog	PROTEIN PHOSPHATASE 1H (PTHR13832:SF287)	kinase inhibitor(PC00139);protein phosphatase(PC00195)	<i>Homo sapiens</i>
HUMAN HGNC=17772 UniProtKB=Q99757	THI OM	Thioredoxin, mitochondrial;TXN2;ortholog	THIOREDOXIN, MITOCHONDRIAL (PTHR43601:SF3)	oxidoreductase(PC00176)	<i>Homo sapiens</i>

HUMAN HGNC=7421 UniProtKB=P00403	COX 2	Cytochrome c oxidase subunit 2;MT-CO2;ortholog	CYTOCHROME C OXIDASE SUBUNIT 2 (PTHR22888:SF9)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=20372 UniProtKB=Q9NX14	NDU BB	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial;NDUFB11;ortholog	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 11, MITOCHONDRIAL (PTHR13327:SF0)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=30576 UniProtKB=Q9BV57	MTN D	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase;ADI1;ortholog	1,2-DIHYDROXY-3-KETO-5-METHYLTHIOPENTENE DIOXYGENASE (PTHR23418:SF0)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=7700 UniProtKB=O43674	NDU B5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial;NDUFB5;ortholog	NADH DEHYDROGENASE [UBIQUINONE] 1 BETA SUBCOMPLEX SUBUNIT 5, MITOCHONDRIAL (PTHR13178:SF0)	oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=9021 UniProtKB=P14618	KPY M	Pyruvate kinase PKM;PKM;ortholog	PYRUVATE KINASE PKM (PTHR11817:SF15)		<i>Homo sapiens</i>
HUMAN HGNC=406 UniProtKB=P30038	AL4 A1	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial;ALDH4A1;ortholog	DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE, MITOCHONDRIAL (PTHR14516:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=10536 UniProtKB=Q9UL12	SAR DH	Sarcosine dehydrogenase, mitochondrial;SARDH;ortholog	SARCOSINE DEHYDROGENASE, MITOCHONDRIAL (PTHR13847:SF200)	dehydrogenase(PC00092);oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=30863 UniProtKB=Q9UDW1	QCR 9	Cytochrome b-c1 complex subunit 9;UQCR10;ortholog	CYTOCHROME B-C1 COMPLEX SUBUNIT 9 (PTHR12980:SF0)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=13709 UniProtKB=O15121	DEG S1	Sphingolipid delta(4)-desaturase DES1;DEGS1;ortholog	SPHINGOLIPID DELTA(4)-DESATURASE DES1 (PTHR12879:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=28639 UniProtKB=Q6UWP2	DHR 11	Dehydrogenase/reductase SDR family member 11;DHRS11;ortholog	DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 11 (PTHR43115:SF4)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>

HUMAN HGNC=6229 UniProtKB=Q13303	KCA B2	Voltage-gated potassium channel subunit beta-2;KCNA2;ortholog	VOLTAGE-GATED POTASSIUM CHANNEL SUBUNIT BETA-2 (PTHR43150:SF1)	reductase(PC00198);voltage-gated potassium channel(PC00242)	<i>Homo sapiens</i>
HUMAN HGNC=877 UniProtKB=P49419	AL7 A1	Alpha-amino adipic semialdehyde dehydrogenase;ALDH7A1;ortholog	ALPHA-AMINOADIPIC SEMIALDEHYDE DEHYDROGENASE (PTHR43521:SF5)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=20134 UniProtKB=Q86SX6	GLR X5	Glutaredoxin-related protein 5, mitochondrial;GLRX5;ortholog	GLUTAREDOXIN-RELATED PROTEIN 5, MITOCHONDRIAL (PTHR10293:SF16)	reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=20233 UniProtKB=Q9Y2Z9	COQ 6	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial;COQ6;ortholog	UBIQUINONE BIOSYNTHESIS MONOOXYGENASE COQ6, MITOCHONDRIAL (PTHR43876:SF7)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=29594 UniProtKB=O14949	QCR 8	Cytochrome b-c1 complex subunit 8;UQCRCQ;ortholog	CYTOCHROME B-C1 COMPLEX SUBUNIT 8 (PTHR12119:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=21577 UniProtKB=Q8NB78	KDM1B, L SD2	Lysine-specific histone demethylase 1B;KDM1B;ortholog	LYSINE-SPECIFIC HISTONE DEMETHYLASE 1B (PTHR10742:SF359)	DNA methyltransferase(PC00013);oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=21063 UniProtKB=Q6UVY6	MOXD1	DBH-like monooxygenase protein 1;MOXD1;ortholog	DBH-LIKE MONOOXYGENASE PROTEIN 1 (PTHR10157:SF28)		<i>Homo sapiens</i>
HUMAN HGNC=8903 UniProtKB=O95336	6PG L	6-phosphogluconolactonase;PGLS;ortholog	6-PHOSPHOGLUCONOLACTONASE (PTHR11054:SF0)	hydrolase(PC00121)	<i>Homo sapiens</i>
HUMAN HGNC=18246 UniProtKB=Q9Y2S2	CRYL1	Lambda-crystallin homolog;CRYL1;ortholog	LAMBDA-CRYSTALLIN HOMOLOG (PTHR43492:SF2)	dehydrogenase(PC00092);epimerase/racemase(PC00096);hydratase(PC00120)	<i>Homo sapiens</i>
HUMAN HGNC=17804 UniProtKB=Q9P0Z9	SOX	Peroxisomal sarcosine oxidase;PIPOX;ortholog	PEROXISOMAL SARCOSINE OXIDASE (PTHR10961:SF7)	oxidase(PC00175)	<i>Homo sapiens</i>

HUMAN HGNC=7064 UniProtKB=O14880	MGS T3	Microsomal glutathione S-transferase 3;MGST3;ortholog	MICROSOMAL GLUTATHIONE S-TRANSFERASE 3 (PTHR10250:SF17)	transferase(PC00220)	<i>Homo sapiens</i>
HUMAN HGNC=16753 UniProtKB=P30041	PRD X6	Peroxiredoxin-6;PRDX6;ortholog	PEROXIREDOXIN-6 (PTHR43503:SF11)	peroxidase(PC00180)	<i>Homo sapiens</i>
HUMAN HGNC=2595 UniProtKB=P04798	CP1 A1	Cytochrome P450 1A1;CYP1A1;ortholog	CYTOCHROME P450 1A1 (PTHR24299:SF8)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=19708 UniProtKB=Q86WU2	LDH D	Probable D-lactate dehydrogenase, mitochondrial;LDHD;ortholog	D-LACTATE DEHYDROGENASE, MITOCHONDRIAL-RELATED (PTHR11748:SF35)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=9605 UniProtKB=P35354	COX 2	Prostaglandin G/H synthase 2;PTGS2;ortholog	PROSTAGLANDIN G/H SYNTHASE 2 (PTHR11903:SF8)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=6381 UniProtKB=O15229	KMO O	Kynurenine 3-monooxygenase;KMO;ortholog	KYNURENINE 3-MONOOXYGENASE (PTHR46028:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=121 UniProtKB=O15254	ACO X3	Peroxisomal acyl-coenzyme A oxidase 3;ACOX3;ortholog	PEROXISOMAL ACYL-COENZYME A OXIDASE 3 (PTHR10909:SF315)	dehydrogenase(PC00092);oxidase(PC00175);transferase(PC00220)	<i>Homo sapiens</i>
HUMAN HGNC=13815 UniProtKB=Q9HAY6	BCD O1	Beta,beta-carotene 15,15'-dioxygenase;BCO1;ortholog	BETA,BETA-CAROTENE 15,15'-DIOXYGENASE (PTHR10543:SF34)	oxygenase(PC00177)	<i>Homo sapiens</i>
HUMAN HGNC=8896 UniProtKB=P00558	PGK 1	Phosphoglycerate kinase 1;PGK1;ortholog	PHOSPHOGLYCERATE KINASE 1 (PTHR11406:SF14)	carbohydrate kinase(PC00065)	<i>Homo sapiens</i>
HUMAN HGNC=14355 UniProtKB=Q86YB8	ERO 1B	ERO1-like protein beta;ERO1B;ortholog	ERO1-LIKE PROTEIN BETA (PTHR12613:SF2)	oxidoreductase(PC00176)	<i>Homo sapiens</i>

HUMAN HGNC=4551 UniProtKB=Q9NZ01	TEC R	Very-long-chain enoyl-CoA reductase;TECR;ortholog	VERY-LONG-CHAIN ENOYL-COA REDUCTASE (PTHR10556:SF31)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=3976 UniProtKB=P02794	FRIH	Ferritin heavy chain;FTH1;ortholog	FERRITIN HEAVY CHAIN (PTHR11431:SF37)	storage protein(PC00210)	<i>Homo sapiens</i>
HUMAN HGNC=20968 UniProtKB=Q9H6W3	RIO X1	Ribosomal oxygenase 1;RIOX1;ortholog	RIBOSOMAL OXYGENASE 1 (PTHR13096:SF4)		<i>Homo sapiens</i>
HUMAN HGNC=1027 UniProtKB=Q02338	BDH	D-beta-hydroxybutyrate dehydrogenase, mitochondrial;BDH1;ortholog	D-BETA-HYDROXYBUTYRATE DEHYDROGENASE, MITOCHONDRIAL (PTHR43313:SF25)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=5211 UniProtKB=P37059	DHB 2	Estradiol 17-beta-dehydrogenase 2;HSD17B2;ortholog	ESTRADIOL 17-BETA-DEHYDROGENASE 2 (PTHR43313:SF3)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=16354 UniProtKB=Q8IWW8	HOT	Hydroxyacid-oxoacid transhydrogenase, mitochondrial;ADHFE1;ortholog	HYDROXYACID-OXOACID TRANSHYDROGENASE, MITOCHONDRIAL (PTHR11496:SF83)		<i>Homo sapiens</i>
HUMAN HGNC=21497 UniProtKB=Q9H845	ACA D9	Acyl-CoA dehydrogenase family member 9, mitochondrial;ACAD9;ortholog	ACYL-COA DEHYDROGENASE FAMILY MEMBER 9, MITOCHONDRIAL (PTHR43884:SF9)	dehydrogenase(PC00092);oxidase(PC00175);transferase(PC00220)	<i>Homo sapiens</i>
HUMAN HGNC=3062 UniProtKB=Q9NRD9	DUOX X	Dual oxidase 1;DUOX1;ortholog	DUAL OXIDASE 1 (PTHR11972:SF75)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=2418 UniProtKB=Q14894	CRY M	Ketimine reductase mu-crystallin;CRYM;ortholog	KETIMINE REDUCTASE MU-CRYSTALLIN (PTHR13812:SF19)	lyase(PC00144)	<i>Homo sapiens</i>
HUMAN HGNC=14874 UniProtKB=Q96PH1	NOX 5	NADPH oxidase 5;NOX5;ortholog	NADPH OXIDASE 5 (PTHR11972:SF58)	oxidase(PC00175)	<i>Homo sapiens</i>

HUMAN HGNC=6970 UniProtKB=P40925	MD HC	Malate dehydrogenase, cytoplasmic;MDH1;ortholog	MALATE DEHYDROGENASE, CYTOPLASMIC (PTHR23382:SF3)	dehydrogenase(PC00092)	<i>Homo sapiens</i>
HUMAN HGNC=9280 UniProtKB=P50336	PPO X	Protoporphyrinogen oxidase;PPOX;ortholog	PROTOPORPHYRINOGEN OXIDASE (PTHR42923:SF3)	DNA methyltransferase(PC00013);oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=2867 UniProtKB=Q02127	PYR D	Dihydroorotate dehydrogenase (quinone), mitochondrial;DHODH;ortholog	DIHYDROOROTATE DEHYDROGENASE (QUINONE), MITOCHONDRIAL (PTHR43517:SF1)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>
HUMAN HGNC=13273 UniProtKB=Q9NRD8	DUO X2	Dual oxidase 2;DUOX2;ortholog	DUAL OXIDASE 2 (PTHR11972:SF67)	oxidase(PC00175)	<i>Homo sapiens</i>
HUMAN HGNC=2265 UniProtKB=P13073	COX 41	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;COX4I1;ortholog	CYTOCHROME C OXIDASE SUBUNIT 4 ISOFORM 1, MITOCHONDRIAL (PTHR10707:SF12)		<i>Homo sapiens</i>
HUMAN HGNC=20588 UniProtKB=Q9UHG3	PCY OX	Prenylcysteine oxidase 1;PCYOX1;ortholog	PRENYLCYSTEINE OXIDASE 1 (PTHR15944:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=17693 UniProtKB=O75911	DHR S3	Short-chain dehydrogenase/reductase 3;DHRS3;ortholog	SHORT-CHAIN DEHYDROGENASE/REDUCTASE 3 (PTHR24322:SF483)		<i>Homo sapiens</i>
HUMAN HGNC=7708 UniProtKB=O75306	NDU S2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial;NDUFS2;ortholog	NADH DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN 2, MITOCHONDRIAL (PTHR11993:SF10)	dehydrogenase(PC00092);reductase(PC00198)	<i>Homo sapiens</i>

Lipases

HUMAN HGNC=24768 UniProtKB=Q6ZV29	PL 7	Patatin-like phospholipase domain-containing protein 7;PNPLA7;ortholog	PATATIN-LIKE PHOSPHOLIPASE DOMAIN-CONTAINING PROTEIN 7 (PTHR14226:SF23)	esterase(PC00097)	<i>Homo sapiens</i>
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HUMAN HGNC=PL 16268 UniProtKB=PL Q8IY17 6	Neuropathy target esterase;PNPLA6;ortholog	NEUROPATHY TARGET ESTERASE (PTHR14226:SF26)	esterase(PC00097)	<i>Homo sapiens</i>
HUMAN HGNC=PL 9059 UniProtKB=CB Q15147 4	1-phosphatidylinositol 4,5- bisphosphate phosphodiesterase beta-4;PLCB4;ortholog	1-PHOSPHATIDYLINOSITOL 4,5- BISPHOSPHATE PHOSPHODIESTERASE BETA-4 (PTHR10336:SF106)	calcium-binding protein(PC00060);guanyl- nucleotide exchange factor(PC00113);phospholipase(PC00186);signali ng molecule(PC00207)	<i>Homo sapiens</i>
HUMAN HGNC=PL 9062 UniProtKB=C Q9BRC7 D4	1-phosphatidylinositol 4,5- bisphosphate phosphodiesterase delta-4;PLCD4;ortholog	1-PHOSPHATIDYLINOSITOL 4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA-4 (PTHR10336:SF31)	guanyl-nucleotide exchange factor(PC00113);signaling molecule(PC00207)	<i>Homo sapiens</i>
HUMAN HGNC=G 4390 UniProtKB=NA P50148 Q	Guanine nucleotide-binding protein G(q) subunit alpha;GNAQ;ortholog	GUANINE NUCLEOTIDE-BINDING PROTEIN G(Q) SUBUNIT ALPHA (PTHR10218:SF318)	heterotrimeric G-protein(PC00117)	<i>Homo sapiens</i>
HUMAN HGNC=LI 18483 UniProtKB=PH Q8WWY8	Lipase member H;LIPH;ortholog	LIPASE MEMBER H (PTHR11610:SF12)	esterase(PC00097);lipase(PC00143);storage protein(PC00210)	<i>Homo sapiens</i>
HUMAN HGNC=5H 5293 UniProtKB=T2 P28223 A	5-hydroxytryptamine receptor 2A;HTR2A;ortholog	5-HYDROXYTRYPTAMINE RECEPTOR 2A (PTHR24247:SF30)	G-protein coupled receptor(PC00021)	<i>Homo sapiens</i>
HUMAN HGNC=PL 17175 UniProtKB=CE Q9P212 1	1-phosphatidylinositol 4,5- bisphosphate phosphodiesterase epsilon-1;PLCE1;ortholog	1-PHOSPHATIDYLINOSITOL 4,5- BISPHOSPHATE PHOSPHODIESTERASE EPSILON-1 (PTHR10336:SF6)	calcium-binding protein(PC00060);guanyl- nucleotide exchange factor(PC00113);phospholipase(PC00186);signali ng molecule(PC00207)	<i>Homo sapiens</i>
HUMAN HGNC=A 277 UniProtKB=PA1 35348 A	Alpha-1A adrenergic receptor;ADRA1A;ortholog	ALPHA-1A ADRENERGIC RECEPTOR (PTHR24248:SF16)	G-protein coupled receptor(PC00021)	<i>Homo sapiens</i>
HUMAN HGNC=LI 9156 UniProtKB=PR P54315 1	Inactive pancreatic lipase-related protein 1;PNLIPRP1;ortholog	INACTIVE PANCREATIC LIPASE- RELATED PROTEIN 1 (PTHR11610:SF147)	esterase(PC00097);lipase(PC00143);storage protein(PC00210)	<i>Homo sapiens</i>

HUMAN HGNC=LI 6619 UniProtKB=PC P11150	Hepatic triacylglycerol lipase;LIPC;ortholog	HEPATIC TRIACYLGLYCEROL LIPASE (PTHR11610:SF2)	esterase(PC00097);lipase(PC00143);storage protein(PC00210)	<i>Homo sapiens</i>
HUMAN HGNC=PA 17163 UniProtKB=G1 Q8NCC3	Group XV phospholipase A2;PLA2G15;ortholog	GROUP XV PHOSPHOLIPASE A2 (PTHR11440:SF47)	acyltransferase(PC00042);phospholipase(PC0018 6)	<i>Homo sapiens</i>
HUMAN HGNC=S2 17018 UniProtKB=3I Q9Y6Y8	SEC23-interacting protein;SEC23IP;ortholog	SEC23-INTERACTING PROTEIN (PTHR23509:SF4)	membrane traffic protein(PC00150);phospholipase(PC00186)	<i>Homo sapiens</i>
HUMAN HGNC=LI 9155 UniProtKB=PP P16233	Pancreatic triacylglycerol lipase;PNLIP;ortholog	PANCREATIC TRIACYLGLYCEROL LIPASE (PTHR11610:SF115)	esterase(PC00097);lipase(PC00143);storage protein(PC00210)	<i>Homo sapiens</i>
HUMAN HGNC=LI 9157 UniProtKB=PR P54317	Pancreatic lipase-related protein 2;PNLIPRP2;ortholog	PANCREATIC LIPASE-RELATED PROTEIN 2 (PTHR11610:SF85)	esterase(PC00097);lipase(PC00143);storage protein(PC00210)	<i>Homo sapiens</i>
HUMAN HGNC=LP 15520 UniProtKB=A P43657	Lysophosphatidic acid receptor 6;LPAR6;ortholog	LYSOPHOSPHATIDIC ACID RECEPTOR 6 (PTHR24232:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=AB 18718 UniProtKB=H Q8WU67	Phospholipase ABHD3;ABHD3;ortholog	PHOSPHOLIPASE ABHD3 (PTHR10794:SF50)	serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=A 278 UniProtKB=P 35368	Alpha-1B adrenergic receptor;ADRA1B;ortholog	ALPHA-1B ADRENERGIC RECEPTOR (PTHR24248:SF17)	G-protein coupled receptor(PC00021)	<i>Homo sapiens</i>

Peptidase Activity

HUMAN HGNC=500 UniProtKB=P15144	AMP N	Aminopeptidase N;ANPEP;ortholog	AMINOPEPTIDASE N (PTHR11533:SF172)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=2524 UniProtKB=P40313	CTRL	Chymotrypsin-like protease CTRL-1;CTRL;ortholog	CHYMOTRYPSIN-LIKE PROTEASE CTRL-1 (PTHR24250:SF28)	serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=9509 UniProtKB=P49810	PSN2	Presenilin-2;PSEN2;ortholog	PRESENILIN-2 (PTHR10202:SF26)	aspartic protease(PC00053);calcium-binding protein(PC00060);membrane-bound signaling molecule(PC00152)	<i>Homo sapiens</i>
HUMAN HGNC=9344 UniProtKB=P42785	PCP	Lysosomal Pro-X carboxypeptidase;PRCP;ortholog	LYSOSOMAL PRO-X CARBOXYPEPTIDASE (PTHR11010:SF38)	serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=25679 UniProtKB=Q9BSB4	ATG A1	Autophagy-related protein 101;ATG101;ortholog	AUTOPHAGY-RELATED PROTEIN 101 (PTHR13292:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=12623 UniProtKB=Q9UPU5	UBP2 4	Ubiquitin carboxyl-terminal hydrolase 24;USP24;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 24 (PTHR24006:SF729)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=25072 UniProtKB=Q5MNZ6	WIPI3	WD repeat domain phosphoinositide-interacting protein 3;WDR45B;ortholog	WD REPEAT DOMAIN PHOSPHOINOSITIDE-INTERACTING PROTEIN 3 (PTHR11227:SF18)		<i>Homo sapiens</i>
HUMAN HGNC=18173 UniProtKB=Q9NZ08	ERAP 1	Endoplasmic reticulum aminopeptidase 1;ERAP1;ortholog	ENDOPLASMIC RETICULUM AMINOPEPTIDASE 1 (PTHR11533:SF156)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=589 UniProtKB=Q9H1Y0	ATG5	Autophagy protein 5;ATG5;ortholog	AUTOPHAGY PROTEIN 5 (PTHR13040:SF2)	membrane trafficking regulatory protein(PC00151)	<i>Homo sapiens</i>
HUMAN HGNC=20635 UniProtKB=Q14997	PSME 4	Proteasome activator complex subunit 4;PSME4;ortholog	PROTEASOME ACTIVATOR COMPLEX SUBUNIT 4 (PTHR32170:SF3)		<i>Homo sapiens</i>

HUMAN HGNC=11280 UniProtKB=SQSTM1	Sequestosome-1;SQSTM1;ortholog	SEQUESTOSOME-1 (PTHR15090:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=2301 UniProtKB=CBPD	Carboxypeptidase D;CPD;ortholog	CARBOXYPEPTIDASE D (PTHR11532:SF57)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=20068 UniProtKB=UBP4	Ubiquitin carboxyl-terminal hydrolase 42;USP42;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 42 (PTHR24006:SF727)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=12666 UniProtKB=TERA	Transitional endoplasmic reticulum ATPase;VCP;ortholog	TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (PTHR23077:SF69)		<i>Homo sapiens</i>
HUMAN HGNC=9532 UniProtKB=PSA3	Proteasome subunit alpha type-3;PSMA3;ortholog	PROTEASOME SUBUNIT ALPHA TYPE-3 (PTHR11599:SF10)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=12632 UniProtKB=USP9X	Probable ubiquitin carboxyl-terminal hydrolase FAF-X;USP9X;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-X-RELATED (PTHR24006:SF732)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=588 UniProtKB=ATG1	Ubiquitin-like protein ATG12;ATG12;ortholog	UBIQUITIN-LIKE PROTEIN ATG12 (PTHR13385:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=12624 UniProtKB=UBP2	Ubiquitin carboxyl-terminal hydrolase 25;USP25;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 25 (PTHR24006:SF666)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=29169 UniProtKB=TPPC	Trafficking protein particle complex subunit 8;TRAPPC8;ortholog	TRAFFICKING PROTEIN PARTICLE COMPLEX SUBUNIT 8 (PTHR12975:SF6)		<i>Homo sapiens</i>
HUMAN HGNC=1361 UniProtKB=AMP	Aminopeptidase O;AOPEP;ortholog	AMINOPEPTIDASE O (PTHR46627:SF1)		<i>Homo sapiens</i>

HUMAN HGNC=9531 UniProtKB=PSA2 P25787	Proteasome subunit alpha type-2;PSMA2;ortholog	PROTEASOME SUBUNIT ALPHA TYPE-2 (PTHR11599:SF16)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=21498 UniProtKB=A16L1 Q676U5	Autophagy-related protein 16-1;ATG16L1;ortholog	AUTOPHAGY-RELATED PROTEIN 16-1 (PTHR19878:SF6)		<i>Homo sapiens</i>
HUMAN HGNC=20944 UniProtKB=SEN6 Q9GZR1	Sentrin-specific protease 6;SEN6;ortholog	SENTRIN-SPECIFIC PROTEASE 6 (PTHR46896:SF1)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=30227 UniProtKB=SPP2A Q8TCT8	Signal peptide peptidase-like 2A;SPPL2A;ortholog	SIGNAL PEPTIDE PEPTIDASE-LIKE 2A (PTHR12174:SF34)		<i>Homo sapiens</i>
HUMAN HGNC=15859 UniProtKB=TASP1 Q9H6P5	Threonine aspartase 1;TASP1;ortholog	THREONINE ASPARTASE 1 (PTHR10188:SF8)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=15991 UniProtKB=LMLN Q96KR4	Leishmanolysin-like peptidase;LMLN;ortholog	LEISHMANOLYSIN-LIKE PEPTIDASE (PTHR10942:SF0)	cell adhesion molecule(PC00069);metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=28430 UniProtKB=EMC6 Q9BV81	ER membrane protein complex subunit 6;EMC6;ortholog	ER MEMBRANE PROTEIN COMPLEX SUBUNIT 6 (PTHR20994:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=4248 UniProtKB=GGH Q92820	Gamma-glutamyl hydrolase;GGH;ortholog	GAMMA-GLUTAMYL HYDROLASE (PTHR11315:SF0)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=16702 UniProtKB=CSN4 Q9BT78	COP9 signalosome complex subunit 4;COPS4;ortholog	COP9 SIGNALOSOME COMPLEX SUBUNIT 4 (PTHR10855:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=586 UniProtKB=ACP H 13798	Acylamino-acid-releasing enzyme;APEH;ortholog	ACYLAMINO-ACID-RELEASING ENZYME (PTHR42776:SF4)	serine protease(PC00203)	<i>Homo sapiens</i>

HUMAN HGNC=11820 UniProtKB=P01033	TIMP1	Metalloproteinase inhibitor 1;TIMP1;ortholog	METALLOPROTEINASE INHIBITOR 1 (PTHR11844:SF20)	protease inhibitor(PC00191)	<i>Homo sapiens</i>
HUMAN HGNC=2240 UniProtKB=Q92905	COP9 CSN5	signalosome complex subunit 5;COP5;ortholog	COP9 SIGNALOSOME COMPLEX SUBUNIT 5 (PTHR10410:SF6)	metalloprotease(PC00153);transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=27912 UniProtKB=Q6ZMM2	ADAMTS-like protein 5;ADAMTSL5;ortholog	ADAMTS-LIKE PROTEIN 5 (PTHR13723:SF173)	extracellular matrix glycoprotein(PC00100);metalloprotease(PC00153);serine protease inhibitor(PC00204)		<i>Homo sapiens</i>
HUMAN HGNC=14348 UniProtKB=O43464	HTRA2	Serine protease HTRA2, mitochondrial;HTRA2;ortholog	SERINE PROTEASE HTRA2, MITOCHONDRIAL (PTHR22939:SF109)	chaperone(PC00072);serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=1499 UniProtKB=P29466	CASP1	Caspase-1;CASP1;ortholog	CASPASE-1 (PTHR10454:SF216)	cysteine protease(PC00081);protease inhibitor(PC00191)	<i>Homo sapiens</i>
HUMAN HGNC=15722 UniProtKB=Q8WXQ8	CBPA5	Carboxypeptidase A5;CPA5;ortholog	CARBOXYPEPTIDASE A5 (PTHR11705:SF16)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=14605 UniProtKB=P58397	A disintegrin and metalloproteinase with thrombospondin motifs 12;ADAMTS12;ortholog	A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 12 (PTHR13723:SF189)	extracellular matrix glycoprotein(PC00100);metalloprotease(PC00153);serine protease inhibitor(PC00204)		<i>Homo sapiens</i>
HUMAN HGNC=6746 UniProtKB=Q14596	NBR1	Next to BRCA1 gene 1 protein;NBR1;ortholog	NEXT TO BRCA1 GENE 1 PROTEIN (PTHR20930:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=24969 UniProtKB=Q8WTW4	NPRL2	GATOR complex protein NPRL2;NPRL2;ortholog	GATOR COMPLEX PROTEIN NPRL2 (PTHR12991:SF10)	nuclease(PC00170);transcription factor(PC00218)	<i>Homo sapiens</i>

HUMAN HGNC=20492 UniProtKB=Q96IL0	APOP1	Apoptogenic protein 1, mitochondrial;APOPT1;ortholog	APOPTOGENIC PROTEIN 1, MITOCHONDRIAL (PTHR31107:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=14124 UniProtKB=Q12980	NPRL3	GATOR complex protein NPRL3;NPRL3;ortholog	GATOR COMPLEX PROTEIN NPRL3 (PTHR13153:SF5)		<i>Homo sapiens</i>
HUMAN HGNC=9530 UniProtKB=P25786	PSA1	Proteasome subunit alpha type-1;PSMA1;ortholog	PROTEASOME SUBUNIT ALPHA TYPE-RELATED (PTHR11599:SF12)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=3942 UniProtKB=P42345	MTOR	Serine/threonine-protein kinase mTOR;MTOR;ortholog	SERINE/THREONINE-PROTEIN KINASE MTOR (PTHR11139:SF9)	non-receptor serine/threonine protein kinase(PC00167);nucleic acid binding(PC00171);nucleotide kinase(PC00172)	<i>Homo sapiens</i>
HUMAN HGNC=3355 UniProtKB=Q07075	AME	Glutamyl aminopeptidase;ENPEP;ortholog	GLUTAMYL AMINOPEPTIDASE (PTHR11533:SF269)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=9533 UniProtKB=P25789	PSA4	Proteasome subunit alpha type-4;PSMA4;ortholog	PROTEASOME SUBUNIT ALPHA TYPE-4 (PTHR11599:SF13)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=9559 UniProtKB=Q13200	PSMD2	26S proteasome non-ATPase regulatory subunit 2;PSMD2;ortholog	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 2 (PTHR10943:SF15)	enzyme modulator(PC00095)	<i>Homo sapiens</i>
HUMAN HGNC=590 UniProtKB=Q13490	BIRC2	Baculoviral IAP repeat-containing protein 2;BIRC2;ortholog	BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 2 (PTHR10044:SF79)	protease inhibitor(PC00191)	<i>Homo sapiens</i>
HUMAN HGNC=9358 UniProtKB=P48147	PREP, PEP	Prolyl endopeptidase;PREP;ortholog	PROLYL ENDOPEPTIDASE (PTHR42881:SF2)	serine protease(PC00203)	<i>Homo sapiens</i>

HUMAN HGNC=7160 UniProtKB=P50281	MMP14	Matrix metalloproteinase-14;MMP14;ortholog	MATRIX METALLOPROTEINASE-14 (PTHR10201:SF24)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=21408 UniProtKB=P20D2Q8IYS1		Peptidase M20 domain-containing protein 2;PM20D2;ortholog	PEPTIDASE M20 DOMAIN-CONTAINING PROTEIN 2 (PTHR30575:SF0)	metalloprotease(PC00153);oxidoreductase(PC00176)	<i>Homo sapiens</i>
HUMAN HGNC=3008 UniProtKB=Q9NY33	DPP3	Dipeptidyl peptidase 3;DPP3;ortholog	DIPEPTIDYL PEPTIDASE 3 (PTHR23422:SF11)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=9119 UniProtKB=O75439	MPPB	Mitochondrial-processing peptidase subunit beta;PMPCB;ortholog	MITOCHONDRIAL-PROCESSING PEPTIDASE SUBUNIT BETA (PTHR11851:SF103)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=10701 UniProtKB=Q15436	SC23A	Protein transport protein Sec23A;SEC23A;ortholog	PROTEIN TRANSPORT PROTEIN SEC23A (PTHR11141:SF7)	G-protein modulator(PC00022)	<i>Homo sapiens</i>
HUMAN HGNC=25402 UniProtKB=Q96G74	OTU D5	OTU domain-containing protein 5;OTUD5;ortholog	OTU DOMAIN-CONTAINING PROTEIN 5 (PTHR12419:SF4)	cysteine protease(PC00081);nucleic acid binding(PC00171)	<i>Homo sapiens</i>
HUMAN HGNC=29331 UniProtKB=Q9HCE0	EPG5	Ectopic P granules protein 5 homolog;EPG5;ortholog	ECTOPIC P GRANULES PROTEIN 5 HOMOLOG (PTHR31139:SF4)		<i>Homo sapiens</i>
HUMAN HGNC=30627 UniProtKB=Q8TCT7	SPP2B	Signal peptide peptidase-like 2B;SPPL2B;ortholog	SIGNAL PEPTIDE PEPTIDASE-LIKE 2B (PTHR12174:SF39)		<i>Homo sapiens</i>
HUMAN HGNC=28912 UniProtKB=Q9Y484	WIPI4	WD repeat domain phosphoinositide-interacting protein 4;WDR45;ortholog	WD REPEAT DOMAIN PHOSPHOINOSITIDE-INTERACTING PROTEIN 4 (PTHR11227:SF44)		<i>Homo sapiens</i>
HUMAN HGNC=13557 UniProtKB=Q9BYF1	ACE2	Angiotensin-converting enzyme 2;ACE2;ortholog	ANGIOTENSIN-CONVERTING ENZYME 2 (PTHR10514:SF24)	metalloprotease(PC00153)	<i>Homo sapiens</i>

HUMAN HGNC=20962 UniProtKB= ATG3 Q9NT62	Ubiquitin-like-conjugating enzyme ATG3;ATG3;ortholog	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG3 (PTHR12866:SF2)	ligase(PC00142)	<i>Homo sapiens</i>
HUMAN HGNC=9540 UniProtKB= PSB3 P49720	Proteasome subunit beta type-3;PSMB3;ortholog	PROTEASOME SUBUNIT BETA TYPE-3 (PTHR11599:SF62)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=SPCS2 28962 UniProtKB= ,SPC2 Q15005 5	Signal peptidase complex subunit 2;SPCS2;ortholog	SIGNAL PEPTIDASE COMPLEX SUBUNIT 2 (PTHR13085:SF2)	enzyme modulator(PC00095)	<i>Homo sapiens</i>
HUMAN HGNC=2482 UniProtKB= CYTB P04080	Cystatin-B;CSTB;ortholog	CYSTATIN-B (PTHR11414:SF22)	cysteine protease inhibitor(PC00082)	<i>Homo sapiens</i>
HUMAN HGNC=2311 UniProtKB= CBPM P14384	Carboxypeptidase M;CPM;ortholog	CARBOXYPEPTIDASE M (PTHR11532:SF84)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=12628 UniProtKB= UBP5 P45974	Ubiquitin carboxyl-terminal hydrolase 5;USP5;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 5 (PTHR24006:SF655)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=19962 UniProtKB= BAKO R Q6ZNE5	Beclin 1-associated autophagy-related key regulator;ATG14;ortholog	BECLIN 1-ASSOCIATED AUTOPHAGY-RELATED KEY REGULATOR (PTHR13664:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=24281 UniProtKB= OTU6 B Q8N6M0	OTU domain-containing protein 6B;OTUD6B;ortholog	OTU DOMAIN-CONTAINING PROTEIN 6B (PTHR12419:SF21)	cysteine protease(PC00081);nucleic acid binding(PC00171)	<i>Homo sapiens</i>
HUMAN HGNC=9472 UniProtKB= LGM N Q99538	Legumain;LGMN;ortholog	LEGUMAIN (PTHR12000:SF38)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=2088 UniProtKB= CLPX O76031	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial;CLPX;ortholog	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX-LIKE, MITOCHONDRIAL (PTHR11262:SF4)	chaperone(PC00072)	<i>Homo sapiens</i>

HUMAN HGNC=1509 UniProtKB=Q14790	CASP8	Caspase-8;CASP8;ortholog	CASPASE-8 (PTHR10454:SF162)	cysteine protease(PC00081);protease inhibitor(PC00191)	<i>Homo sapiens</i>
HUMAN HGNC=9541 UniProtKB=P28070	PSB4	Proteasome subunit beta type-4;PSMB4;ortholog	PROTEASOME SUBUNIT BETA TYPE-4 (PTHR11599:SF5)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=26212 UniProtKB=SPCS3P61009	SPCS3	Signal peptidase complex subunit 3;SPCS3;ortholog	SIGNAL PEPTIDASE COMPLEX SUBUNIT 3 (PTHR12804:SF0)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=9251 UniProtKB=P10619	PPGB	Lysosomal protective protein;CTSA;ortholog	LYSOSOMAL PROTECTIVE PROTEIN (PTHR11802:SF293)	serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=29507 UniProtKB=Q9HB40	RISC, SCP1	Retinoid-inducible serine carboxypeptidase;SCPEP1;ortholog	RETINOID-INDUCIBLE SERINE CARBOXYPEPTIDASE (PTHR11802:SF3)	serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=15912 UniProtKB=Q9UNZ2	NSFL1 C	NSFL1 cofactor p47;NSFL1C;ortholog	NSFL1 COFACTOR P47 (PTHR23333:SF24)	membrane trafficking regulatory protein(PC00151)	<i>Homo sapiens</i>
HUMAN HGNC=2707 UniProtKB=P12821	ACE	Angiotensin-converting enzyme;ACE;ortholog	ANGIOTENSIN-CONVERTING ENZYME (PTHR10514:SF25)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=18533 UniProtKB=Q86UV5	UBP48	Ubiquitin carboxyl-terminal hydrolase 48;USP48;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 48 (PTHR24006:SF722)		<i>Homo sapiens</i>
HUMAN HGNC=1508 UniProtKB=P55210	CASP7	Caspase-7;CASP7;ortholog	CASPASE-7 (PTHR10454:SF31)	cysteine protease(PC00081);protease inhibitor(PC00191)	<i>Homo sapiens</i>
HUMAN HGNC=9534 UniProtKB=P28066	PSA5	Proteasome subunit alpha type-5;PSMA5;ortholog	PROTEASOME SUBUNIT ALPHA TYPE-5 (PTHR11599:SF14)	protease(PC00190)	<i>Homo sapiens</i>

HUMAN HGNC=8974 UniProtKB=Q8NEB9	PK3C 3	Phosphatidylinositol 3-kinase catalytic subunit type 3;PIK3C3;ortholog	PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT TYPE 3 (PTHR10048:SF7)	kinase(PC00137)	<i>Homo sapiens</i>
HUMAN HGNC=11345 UniProtKB=RECKO95980		Reversion-inducing cysteine-rich protein with Kazal motifs;RECK;ortholog	REVERSION-INDUCING CYSTEINE-RICH PROTEIN WITH KAZAL MOTIFS (PTHR13487:SF3)	protease inhibitor(PC00191)	<i>Homo sapiens</i>
HUMAN HGNC=20066 UniProtKB=Q70CQ2	UBP3 4	Ubiquitin carboxyl-terminal hydrolase 34;USP34;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 34 (PTHR24006:SF671)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=29028 UniProtKB=Q2TAZ0	ATG2 A	Autophagy-related protein 2 homolog A;ATG2A;ortholog	AUTOPHAGY-RELATED PROTEIN 2 HOMOLOG A (PTHR13190:SF21)		<i>Homo sapiens</i>
HUMAN HGNC=9537 UniProtKB=P20618	PSB1	Proteasome subunit beta type-1;PSMB1;ortholog	PROTEASOME SUBUNIT BETA TYPE-1 (PTHR11599:SF59)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=30748 UniProtKB=Q9UKU6	TRHD E	Thyrotropin-releasing hormone-degrading ectoenzyme;TRHDE;ortholog	THYROTROPIN-RELEASING HORMONE-DEGRADING ECTOENZYME (PTHR11533:SF40)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=318 UniProtKB=P20933	ASPG	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase;AGA;ortholog	N(4)-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE (PTHR10188:SF6)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=12822 UniProtKB=Q9NQW7	XPP1	Xaa-Pro aminopeptidase 1;XPNPEP1;ortholog	XAA-PRO AMINOPEPTIDASE 1 (PTHR43763:SF6)	metalloprotease(PC00153);nucleic acid binding(PC00171);transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=12608 UniProtKB=Q14694	UBP1 0	Ubiquitin carboxyl-terminal hydrolase 10;USP10;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 10 (PTHR24006:SF687)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=3535 UniProtKB=P00734	THRB	Prothrombin;F2;ortholog	PROTHROMBIN (PTHR24254:SF10)	serine protease(PC00203)	<i>Homo sapiens</i>

HUMAN HGNC=18667 UniProtKB=Q10713	MPP A	Mitochondrial-processing peptidase subunit alpha;PMPCA;ortholog	MITOCHONDRIAL-PROCESSING PEPTIDASE SUBUNIT ALPHA (PTHR11851:SF190)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=15759 UniProtKB=Q16186	ADR M1	Proteasomal ubiquitin receptor ADRM1;ADRM1;ortholog	PROTEASOMAL UBIQUITIN RECEPTOR ADRM1 (PTHR12225:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=9544 UniProtKB=Q99436	PSB7	Proteasome subunit beta type-7;PSMB7;ortholog	PROTEASOME SUBUNIT BETA TYPE-7 (PTHR11599:SF42)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=9758 UniProtKB=P62820	RAB1 A	Ras-related protein Rab-1A;RAB1A;ortholog	RAS-RELATED PROTEIN RAB-1A (PTHR24073:SF999)		<i>Homo sapiens</i>
HUMAN HGNC=20187 UniProtKB=Q96BY7	ATG2 B	Autophagy-related protein 2 homolog B;ATG2B;ortholog	AUTOPHAGY-RELATED PROTEIN 2 HOMOLOG B (PTHR13190:SF20)		<i>Homo sapiens</i>
HUMAN HGNC=7900 UniProtKB=P55786	PSA	Puromycin-sensitive aminopeptidase;NPEPPS;ortholog	PUROMYCIN-SENSITIVE AMINOPEPTIDASE-RELATED (PTHR11533:SF261)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=20076 UniProtKB=Q96K76	UBP4 7	Ubiquitin carboxyl-terminal hydrolase 47;USP47;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 47 (PTHR24006:SF702)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=9479 UniProtKB=P36776	LON M	Lon protease homolog, mitochondrial;LONP1;ortholog	LON PROTEASE HOMOLOG, MITOCHONDRIAL (PTHR43718:SF2)	serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=9543 UniProtKB=P28072	PSB6	Proteasome subunit beta type-6;PSMB6;ortholog	PROTEASOME SUBUNIT BETA TYPE-6 (PTHR11599:SF46)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=23080 UniProtKB=Q7RTY7	OVC H1	Ovochymase-1;OVCH1;ortholog	OVOCHYMASE-1 (PTHR24251:SF21)	serine protease(PC00203)	<i>Homo sapiens</i>

HUMAN HGNC=16889 UniProtKB=PSDEO00487	26S proteasome non-ATPase regulatory subunit 14;PSMD14;ortholog	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 14 (PTHR10410:SF5)	metalloprotease(PC00153);transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=22408 UniProtKB=ATG9A Q7Z3C6	Autophagy-related protein 9A;ATG9A;ortholog	AUTOPHAGY-RELATED PROTEIN 9A (PTHR13038:SF13)		<i>Homo sapiens</i>
HUMAN HGNC=24554 UniProtKB=PAMR1 Q6UXH9	Inactive serine protease PAMR1;PAMR1;ortholog	INACTIVE SERINE PROTEASE PAMR1 (PTHR24254:SF9)	serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=20069 UniProtKB=UBP4 Q9NVE5	Ubiquitin carboxyl-terminal hydrolase 40;USP40;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 40 (PTHR24006:SF704)		<i>Homo sapiens</i>
HUMAN HGNC=7162 UniProtKB=MMP16 P51512	Matrix metalloproteinase-16;MMP16;ortholog	MATRIX METALLOPROTEINASE-16 (PTHR10201:SF26)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=32583 UniProtKB=MAP1 Q6UB28	Methionine aminopeptidase 1D, mitochondrial;METAP1D;ortholog	METHIONINE AMINOPEPTIDASE 1D, MITOCHONDRIAL (PTHR43330:SF8)	metalloprotease(PC00153);nucleic acid binding(PC00171);transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=16435 UniProtKB=HM13 Q8TCT9	Minor histocompatibility antigen H13;HM13;ortholog	MINOR HISTOCOMPATIBILITY ANTIGEN H13 (PTHR12174:SF23)	membrane-bound signaling molecule(PC00152)	<i>Homo sapiens</i>
HUMAN HGNC=3273 UniProtKB=EIF3H O15372	Eukaryotic translation initiation factor 3 subunit H;EIF3H;ortholog	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT H (PTHR10410:SF3)	metalloprotease(PC00153);transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=19168 UniProtKB=TINA Q9GZM7	Tubulointerstitial nephritis antigen-like;TINAGL1;ortholog	TUBULOINTERSTITIAL NEPHRITIS ANTIGEN-LIKE (PTHR12411:SF270)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=9570 UniProtKB=PSME3 P61289	Proteasome activator complex subunit 3;PSME3;ortholog	PROTEASOME ACTIVATOR COMPLEX SUBUNIT 3 (PTHR10660:SF4)		<i>Homo sapiens</i>

HUMAN HGNC=1480 UniProtKB=NCL1 P20807	Calpain-3;CAPN3;ortholog	CALPAIN-3 (PTHR10183:SF329)	annexin(PC00050);calmodulin(PC00061);cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=7157 UniProtKB=MMP11 P24347	Stromelysin-3;MMP11;ortholog	STROMELYSIN-3 (PTHR10201:SF20)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=16856 UniProtKB=ESPL1 Q14674	Separin;ESPL1;ortholog	SEPARIN (PTHR12792:SF0)	cysteine protease(PC00081);nucleic acid binding(PC00171)	<i>Homo sapiens</i>
HUMAN HGNC=19262 UniProtKB=PPN O95428	Papilin;PAPLN;ortholog	PAPILIN (PTHR13723:SF179)	extracellular matrix glycoprotein(PC00100);metalloprotease(PC00153);serine protease inhibitor(PC00204)	<i>Homo sapiens</i>
HUMAN HGNC=9542 UniProtKB=PSB5 P28074	Proteasome subunit beta type-5;PSMB5;ortholog	PROTEASOME SUBUNIT BETA TYPE-5 (PTHR11599:SF51)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=9536 UniProtKB=PSA7 O14818	Proteasome subunit alpha type-7;PSMA7;ortholog	PROTEASOME SUBUNIT ALPHA TYPE-7 (PTHR11599:SF40)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=29091 UniProtKB=ATG13 O75143	Autophagy-related protein 13;ATG13;ortholog	AUTOPHAGY-RELATED PROTEIN 13 (PTHR13430:SF4)		<i>Homo sapiens</i>
HUMAN HGNC=19703 UniProtKB=ULK3 Q6PHR2	Serine/threonine-protein kinase ULK3;ULK3;ortholog	SERINE/THREONINE-PROTEIN KINASE ULK3 (PTHR24348:SF43)	non-receptor serine/threonine protein kinase(PC00167)	<i>Homo sapiens</i>
HUMAN HGNC=9554 UniProtKB=PSMD1 Q99460	26S proteasome non-ATPase regulatory subunit 1;PSMD1;ortholog	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 1 (PTHR10943:SF2)	enzyme modulator(PC00095)	<i>Homo sapiens</i>

HUMAN HGNC=32225 UniProtKB=WIPI2 Q9Y4P8	WD repeat domain phosphoinositide-interacting protein 2;WIPI2;ortholog	WD REPEAT DOMAIN PHOSPHOINOSITIDE-INTERACTING PROTEIN 2 (PTHR11227:SF27)		<i>Homo sapiens</i>
HUMAN HGNC=23400 UniProtKB=SC11 C Q9BY50	Signal peptidase complex catalytic subunit SEC11C;SEC11C;ortholog	SIGNAL PEPTIDASE COMPLEX CATALYTIC SUBUNIT SEC11C (PTHR10806:SF12)	serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=2303 UniProtKB=CBPE P16870	Carboxypeptidase E;CPE;ortholog	CARBOXYPEPTIDASE E (PTHR11532:SF62)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=4067 UniProtKB=GBRAP O95166	Gamma-aminobutyric acid receptor-associated protein;GABARAP;ortholog	GABARAP-A-RELATED (PTHR10969:SF20)	non-motor microtubule binding protein(PC00166)	<i>Homo sapiens</i>
HUMAN HGNC=15574 UniProtKB=RBCC1 Q8TDY2	RB1-inducible coiled-coil protein 1;RB1CC1;ortholog	RB1-INDUCIBLE COILED-COIL PROTEIN 1 (PTHR13222:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=16935 UniProtKB=ATG7 O95352	Ubiquitin-like modifier-activating enzyme ATG7;ATG7;ortholog	UBIQUITIN-LIKE MODIFIER-ACTIVATING ENZYME ATG7 (PTHR10953:SF3)	ligase(PC00142);transfer/carrier protein(PC00219)	<i>Homo sapiens</i>
HUMAN HGNC=15789 UniProtKB=MAP11 P53582	Methionine aminopeptidase 1;METAP1;ortholog	METHIONINE AMINOPEPTIDASE 1 (PTHR43330:SF7)	metalloprotease(PC00153);nucleic acid binding(PC00171);transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=1478 UniProtKB=CAN11 Q9UMQ6	Calpain-11;CAPN11;ortholog	CALPAIN-11 (PTHR10183:SF322)	annexin(PC00050);calmodulin(PC00061);cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=8982 UniProtKB=PI3R4 Q99570	Phosphoinositide 3-kinase regulatory subunit 4;PIK3R4;ortholog	PHOSPHOINOSITIDE 3-KINASE REGULATORY SUBUNIT 4 (PTHR17583:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=2312 UniProtKB=ACBP P15169	Carboxypeptidase N catalytic chain;CPN1;ortholog	CARBOXYPEPTIDASE N CATALYTIC CHAIN (PTHR11532:SF80)	metalloprotease(PC00153)	<i>Homo sapiens</i>

HUMAN HGNC=7104 UniProtKB=Q99797	MIPEP	Mitochondrial intermediate peptidase;MIPEP;ortholog	MITOCHONDRIAL INTERMEDIATE PEPTIDASE (PTHR11804:SF5)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=12877 UniProtKB=O75844	FACE1	CAAX prenyl protease 1 homolog;ZMPSTE24;ortholog	CAAX PRENYL PROTEASE 1 HOMOLOG (PTHR10120:SF24)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=1034 UniProtKB=Q14457	BECN1	Beclin-1;BECN1;ortholog	BECLIN-1 (PTHR12768:SF6)	protease inhibitor(PC00191)	<i>Homo sapiens</i>
HUMAN HGNC=9535 UniProtKB=P60900	PSA6	Proteasome subunit alpha type-6;PSMA6;ortholog	PROTEASOME SUBUNIT ALPHA TYPE-6 (PTHR11599:SF11)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=24185 UniProtKB=P46736	BRCC3	Lys-63-specific deubiquitinase BRCC36;BRCC3;ortholog	LYS-63-SPECIFIC DEUBIQUITINASE BRCC36 (PTHR10410:SF19)	metalloprotease(PC00153);transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=20315 UniProtKB=Q9H0Y0	ATG10	Ubiquitin-like-conjugating enzyme ATG10;ATG10;ortholog	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG10 (PTHR14957:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=14263 UniProtKB=Q9ULC3	RAB23	Ras-related protein Rab-23;RAB23;ortholog	RAS-RELATED PROTEIN RAB-23 (PTHR24073:SF209)		<i>Homo sapiens</i>
HUMAN HGNC=9539 UniProtKB=P49721	PSB2	Proteasome subunit beta type-2;PSMB2;ortholog	PROTEASOME SUBUNIT BETA TYPE-2 (PTHR11599:SF6)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=223 UniProtKB=Q9UKP4	ATS7	A disintegrin and metalloproteinase with thrombospondin motifs 7;ADAMTS7;ortholog	A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7 (PTHR13723:SF142)	extracellular matrix glycoprotein(PC00100);metalloprotease(PC00153);serine protease inhibitor(PC00204)	<i>Homo sapiens</i>

HUMAN HGNC=12630 UniProtKB=UBP7Q93009	Ubiquitin carboxyl-terminal hydrolase 7;USP7;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (PTHR24006:SF753)	cysteine protease(PC00081)	<i>Homo sapiens</i>
HUMAN HGNC=11793 UniProtKB=THOP1P52888	Thimet oligopeptidase;THOP1;ortholog	THIMET OLIGOPEPTIDASE (PTHR11804:SF50)	metalloprotease(PC00153)	<i>Homo sapiens</i>
HUMAN HGNC=8840 UniProtKB=PEPD P12955	Xaa-Pro dipeptidase;PEPD;ortholog	XAA-PRO DIPEPTIDASE (PTHR43226:SF1)	metalloprotease(PC00153);nucleic acid binding(PC00171);transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=16448 UniProtKB=ASGL1Q7L266	Isoaspartyl peptidase/L-asparaginase;ASRGL1;ortholog	ISOASPARTYL PEPTIDASE/L-ASPARAGINASE (PTHR10188:SF30)	protease(PC00190)	<i>Homo sapiens</i>
HUMAN HGNC=20062 UniProtKB=UBP3Q9P275	Ubiquitin carboxyl-terminal hydrolase 36;USP36;ortholog	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 36 (PTHR24006:SF653)	cysteine protease(PC00081)	<i>Homo sapiens</i>

Hydrolase Activity, ester bonds

HUMAN HGNC=33911 UniProtKB=Q6P RNK5S7	Ribonuclease kappa;RNASEK;ortholog	RIBONUCLEASE KAPPA (PTHR31733:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=12379 UniProtKB=Q156 TSN31	Translin;TSN;ortholog	TRANSLIN (PTHR10741:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=23287 UniProtKB=O95571	ETH Persulfide dioxygenase ETHE1, mitochondrial;ETHE1;ortholog	PERSULFIDE DIOXYGENASE ETHE1, MITOCHONDRIAL (PTHR43084:SF4)	hydrolase(PC00121)	<i>Homo sapiens</i>
HUMAN HGNC=24616 UniProtKB=Q8N1G1	RNA exonuclease 1 homolog;REXO1;ortholog	RNA EXONUCLEASE 1 HOMOLOG (PTHR12801:SF62)	exoribonuclease(PC00099)	<i>Homo sapiens</i>

HUMAN HGNC=24768 UniProtKB=Q6ZV29	PLP L7	Patatin-like phospholipase domain-containing protein 7;PNPLA7;ortholog	PATATIN-LIKE PHOSPHOLIPASE DOMAIN-CONTAINING PROTEIN 7 (PTHR14226:SF23)	esterase(PC00097)	<i>Homo sapiens</i>
HUMAN HGNC=4056 UniProtKB=P35575	G6P C	Glucose-6-phosphatase;G6PC;ortholog	GLUCOSE-6-PHOSPHATASE (PTHR12591:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=8773 UniProtKB=Q9HCR9	PDE 11	Dual 3',5'-cyclic-AMP and -GMP phosphodiesterase 11A;PDE11A;ortholog	DUAL 3',5'-CYCLIC-AMP AND -GMP PHOSPHODIESTERASE 11A (PTHR11347:SF130)		<i>Homo sapiens</i>
HUMAN HGNC=3606 UniProtKB=P09467	FBP1 F16 P1	Fructose-1,6-bisphosphatase 1;FBP1;ortholog	FRUCTOSE-1,6-BISPHOSPHATASE 1 (PTHR11556:SF11)	carbohydrate phosphatase(PC00066)	<i>Homo sapiens</i>
HUMAN HGNC=26911 UniProtKB=Q8N2G6	ZCH 24	Zinc finger CCHC domain-containing protein 24;ZCCHC24;ortholog	ZINC FINGER CCHC DOMAIN-CONTAINING PROTEIN 24 (PTHR15439:SF4)	nuclease(PC00170)	<i>Homo sapiens</i>
HUMAN HGNC=16268 UniProtKB=Q8IY17	PLP L6	Neuropathy target esterase;PNPLA6;ortholog	NEUROPATHY TARGET ESTERASE (PTHR14226:SF26)	esterase(PC00097)	<i>Homo sapiens</i>
HUMAN HGNC=3465 UniProtKB=P10768	EST D	S-formylglutathione hydrolase;ESD;ortholog	S-FORMYLGLUTATHIONE HYDROLASE (PTHR10061:SF0)	esterase(PC00097);serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=7618 UniProtKB=O14974	MYP T1	Protein phosphatase 1 regulatory subunit 12A;PPP1R12A;ortholog	PROTEIN PHOSPHATASE 1 REGULATORY SUBUNIT 12A (PTHR24179:SF20)		<i>Homo sapiens</i>
HUMAN HGNC=7619 UniProtKB=O60237	MYP T2	Protein phosphatase 1 regulatory subunit 12B;PPP1R12B;ortholog	PROTEIN PHOSPHATASE 1 REGULATORY SUBUNIT 12B (PTHR24179:SF18)		<i>Homo sapiens</i>
HUMAN HGNC=20604 UniProtKB=Q9Y2L1	RRP 44	Exosome complex exonuclease RRP44;DIS3;ortholog	EXOSOME COMPLEX EXONUCLEASE RRP44 (PTHR23355:SF35)	endoribonuclease(PC00094);exoribonuclease(PC00099);hydrolase(PC00121)	<i>Homo sapiens</i>

HUMAN HGNC=87 79 UniProtKB=Q1337 0	PDE 3B	cGMP-inhibited 3',5'-cyclic phosphodiesterase B;PDE3B;ortholog	PHOSPHODIESTERASE (PTHR11347:SF29)		<i>Homo sapiens</i>
HUMAN HGNC=99 89 UniProtKB=Q1549 3	RGN	Regucalcin;RGN;ortholog	REGUCALCIN (PTHR10907:SF54)	calcium-binding protein(PC00060);esterase(PC00097)	<i>Homo sapiens</i>
HUMAN HGNC=17 851 UniProtKB=Q9Y 3B8	ORN	Oligoribonuclease, mitochondrial;REXO2;ortholog	OLIGORIBONUCLEASE, MITOCHONDRIAL (PTHR11046:SF0)	exoribonuclease(PC00099);hydrolase(PC00121)	<i>Homo sapiens</i>
HUMAN HGNC=16 219 UniProtKB=Q8T EA8	DTD 1	D-aminoacyl-tRNA deacylase 1;DTD1;ortholog	D-AMINOACYL-TRNA DEACYLASE 1 (PTHR10472:SF5)	esterase(PC00097)	<i>Homo sapiens</i>
HUMAN HGNC=17 689 UniProtKB=Q969 H6	POP 5	Ribonuclease P/MRP protein subunit POP5;POP5;ortholog	RIBONUCLEASE P/MRP PROTEIN SUBUNIT POP5 (PTHR10993:SF12)		<i>Homo sapiens</i>
HUMAN HGNC=22 197 UniProtKB=O432 99	AP5 Z1	AP-5 complex subunit zeta- 1;AP5Z1;ortholog	AP-5 COMPLEX SUBUNIT ZETA-1 (PTHR46488:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=21 58 UniProtKB=P0954 3	CN3 7	2',3'-cyclic-nucleotide 3'- phosphodiesterase;CNP;orthol og	2',3'-CYCLIC-NUCLEOTIDE 3'- PHOSPHODIESTERASE (PTHR10156:SF0)	phosphodiesterase(PC00185)	<i>Homo sapiens</i>
HUMAN HGNC=29 170 UniProtKB=Q9Y 2M0	FAN 1	Fanconi-associated nuclease 1;FAN1;ortholog	FANCONI-ASSOCIATED NUCLEASE 1 (PTHR15749:SF4)		<i>Homo sapiens</i>
HUMAN HGNC=23 292 UniProtKB=P603 21	NOS 2	Nanos homolog 2;NANOS2;ortholog	NANOS HOMOLOG 2 (PTHR12887:SF14)	nuclease(PC00170)	<i>Homo sapiens</i>
HUMAN HGNC=17 687 UniProtKB=Q9Y 2P8	RCL 1,RP C2	RNA 3'-terminal phosphate cyclase-like protein;RCL1;ortholog	RNA 3'-TERMINAL PHOSPHATE CYCLASE-LIKE PROTEIN (PTHR11096:SF1)	RNA binding protein(PC00031);cyclase(PC00079)	<i>Homo sapiens</i>

HUMAN HGNC=3367 UniProtKB=O75356	ENTP5	Ectonucleoside triphosphate diphosphohydrolase 5;ENTPD5;ortholog	ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 5 (PTHR11782:SF35)	lyase(PC00144);nucleotide phosphatase(PC00173)	<i>Homo sapiens</i>
HUMAN HGNC=18884 UniProtKB=Q9NUW8	TYDP1	Tyrosyl-DNA phosphodiesterase 1;TDP1;ortholog	TYROSYL-DNA PHOSPHODIESTERASE 1 (PTHR12415:SF0)	phosphodiesterase(PC00185)	<i>Homo sapiens</i>
HUMAN Ensembl=ENSG00000005189 UniProtKB=Q96IC2	REXO5	RNA exonuclease 5;REXO5;ortholog	RNA EXONUCLEASE 5 (PTHR12801:SF82)	exoribonuclease(PC00099)	<i>Homo sapiens</i>
HUMAN HGNC=20154 UniProtKB=Q8TB40	ABHD4	Protein ABHD4;ABHD4;ortholog	PROTEIN ABHD4 (PTHR42886:SF21)		<i>Homo sapiens</i>
HUMAN HGNC=17059 UniProtKB=Q9NTJ5	SAC1	Phosphatidylinositol phosphatase SAC1;SACM1L;ortholog	PHOSPHATIDYLINOSITIDE PHOSPHATASE SAC1 (PTHR45662:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=8782 UniProtKB=Q08493	PDE4C	cAMP-specific 3',5'-cyclic phosphodiesterase 4C;PDE4C;ortholog	CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE 4C (PTHR11347:SF135)		<i>Homo sapiens</i>
HUMAN HGNC=20614 UniProtKB=Q8NAT2	TDRD5	Tudor domain-containing protein 5;TDRD5;ortholog	TUDOR DOMAIN-CONTAINING PROTEIN 5 (PTHR22948:SF19)	nuclease(PC00170)	<i>Homo sapiens</i>
HUMAN HGNC=15594 UniProtKB=Q9UK59	DBR1	Lariat debranching enzyme;DBR1;ortholog	LARIAT DEBRANCHING ENZYME (PTHR12849:SF0)	endoribonuclease(PC00094);hydrolase(PC00121)	<i>Homo sapiens</i>
HUMAN HGNC=15506 UniProtKB=Q9BSV6	SEN34	tRNA-splicing endonuclease subunit Sen34;TSEN34;ortholog	TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN34 (PTHR13070:SF0)	endoribonuclease(PC00094)	<i>Homo sapiens</i>
HUMAN HGNC=25671 UniProtKB=Q5TBB1	RNH2B	Ribonuclease H2 subunit B;RNASEH2B;ortholog	RIBONUCLEASE H2 SUBUNIT B (PTHR13383:SF11)		<i>Homo sapiens</i>

HUMAN HGNC=24599 UniProtKB=Q9UHY7	ENO PH	Enolase-phosphatase E1;ENOPH1;ortholog	ENOLASE-PHOSPHATASE E1 (PTHR20371:SF2)	phosphatase(PC00181)	<i>Homo sapiens</i>
HUMAN HGNC=12269 UniProtKB=Q9NSU2	TRE X1	Three-prime repair exonuclease 1;TREX1;ortholog	THREE-PRIME REPAIR EXONUCLEASE 1 (PTHR13058:SF19)		<i>Homo sapiens</i>
HUMAN HGNC=9059 UniProtKB=Q15147	PLC B4	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-4;PLCB4;ortholog	1-PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA-4 (PTHR10336:SF106)	calcium-binding protein(PC00060);guanylnucleotide exchange factor(PC00113);phospholipase(PC00186);signaling molecule(PC00207)	<i>Homo sapiens</i>
HUMAN HGNC=8792 UniProtKB=Q9NP56	PDE 7B	cAMP-specific 3',5'-cyclic phosphodiesterase 7B;PDE7B;ortholog	CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE 7B (PTHR11347:SF72)		<i>Homo sapiens</i>
HUMAN HGNC=20097 UniProtKB=Q96LQ0	PPR3 6	Protein phosphatase 1 regulatory subunit 36;PPP1R36;ortholog	PROTEIN PHOSPHATASE 1 REGULATORY SUBUNIT 36 (PTHR21055:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=9062 UniProtKB=Q9BRC7	PLC D4	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-4;PLCD4;ortholog	1-PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA-4 (PTHR10336:SF31)	guanylnucleotide exchange factor(PC00113);signaling molecule(PC00207)	<i>Homo sapiens</i>
HUMAN HGNC=18344 UniProtKB=Q9BX68	HINT T2	Histidine triad nucleotide-binding protein 2, mitochondrial;HINT2;ortholog	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN 2, MITOCHONDRIAL (PTHR23089:SF18)	nucleotide phosphatase(PC00173)	<i>Homo sapiens</i>
HUMAN HGNC=27696 UniProtKB=Q2TAA2	IAH 1	Isoamyl acetate-hydrolyzing esterase 1 homolog;IAH1;ortholog	ISOAMYL ACETATE-HYDROLYZING ESTERASE 1 HOMOLOG (PTHR14209:SF9)		<i>Homo sapiens</i>
HUMAN HGNC=12380 UniProtKB=Q99598	TSN AX	Translin-associated protein X;TSNAX;ortholog	TRANSLIN-ASSOCIATED PROTEIN X (PTHR10741:SF7)		<i>Homo sapiens</i>

HUMAN HGNC=14099 UniProtKB=Q9ULM6	CCR4A	CCR4-NOT transcription complex subunit 6;CNOT6;ortholog	CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 6 (PTHR12121:SF33)	exoribonuclease(PC00099)	<i>Homo sapiens</i>
HUMAN HGNC=14101 UniProtKB=Q9UIV1	CNOT7,CAF1	CCR4-NOT transcription complex subunit 7;CNOT7;ortholog	CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 7 (PTHR10797:SF2)	transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=18466 UniProtKB=O60930	RNH1	Ribonuclease H1;RNASEH1;ortholog	RIBONUCLEASE H1 (PTHR10642:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=9040 UniProtKB=Q13093	PAFA	Platelet-activating factor acetylhydrolase;PLA2G7;ortholog	PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE (PTHR10272:SF12)	esterase(PC00097)	<i>Homo sapiens</i>
HUMAN HGNC=28417 UniProtKB=Q9BTE6	AASD1	Alanyl-tRNA editing protein Aarsd1;AARSD1;ortholog	ALANYL-TRNA EDITING PROTEIN AARSD1 (PTHR43462:SF1)	RNA binding protein(PC00031)	<i>Homo sapiens</i>
HUMAN HGNC=21396 UniProtKB=Q8WTS1	ABHD5	1-acylglycerol-3-phosphate O-acyltransferase ABHD5;ABHD5;ortholog	1-ACYLGLYCEROL-3-PHOSPHATE O-ACYLTRANSFERASE ABHD5 (PTHR42886:SF34)		<i>Homo sapiens</i>
HUMAN HGNC=4390 UniProtKB=P50148	GNAQ	Guanine nucleotide-binding protein G(q) subunit alpha;GNAQ;ortholog	GUANINE NUCLEOTIDE-BINDING PROTEIN G(Q) SUBUNIT ALPHA (PTHR10218:SF318)	heterotrimeric G-protein(PC00117)	<i>Homo sapiens</i>
HUMAN HGNC=30831 UniProtKB=Q8NHU6	TDRD7	Tudor domain-containing protein 7;TDRD7;ortholog	TUDOR DOMAIN-CONTAINING PROTEIN 7 (PTHR22948:SF14)	nuclease(PC00170)	<i>Homo sapiens</i>
HUMAN HGNC=4422 UniProtKB=P15586	GNS	N-acetylglucosamine-6-sulfatase;GNS;ortholog	N-ACETYLGLUCOSAMINE-6-SULFATASE (PTHR43108:SF5)	hydrolase(PC00121)	<i>Homo sapiens</i>
HUMAN HGNC=28698 UniProtKB=Q8TF46	DIS3L1	DIS3-like exonuclease 1;DIS3L1;ortholog	DIS3-LIKE EXONUCLEASE 1 (PTHR23355:SF30)	endoribonuclease(PC00094);exoribonuclease(PC00099);hydrolase(PC00121)	<i>Homo sapiens</i>

HUMAN HGNC=12791 UniProtKB=Q14191	WRN	Werner syndrome ATP-dependent helicase;WRN;ortholog	WERNER SYNDROME ATP-DEPENDENT HELICASE (PTHR13710:SF120)	DNA helicase(PC00011)	<i>Homo sapiens</i>
HUMAN HGNC=18483 UniProtKB=Q8WY8	LIPH	Lipase member H;LIPH;ortholog	LIPASE MEMBER H (PTHR11610:SF12)	esterase(PC00097);lipase(PC00143);storage protein(PC00210)	<i>Homo sapiens</i>
HUMAN HGNC=2326 UniProtKB=Q9UKF6	CPSF3	Cleavage and polyadenylation specificity factor subunit 3;CPSF3;ortholog	CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 3 (PTHR11203:SF11)	endoribonuclease(PC00094);mRNA polyadenylation factor(PC00146)	<i>Homo sapiens</i>
HUMAN HGNC=24860 UniProtKB=Q5MY95	ENTP8	Ectonucleoside triphosphate diphosphohydrolase 8;ENTPD8;ortholog	ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 8 (PTHR11782:SF31)	lyase(PC00144);nucleotide phosphatase(PC00173)	<i>Homo sapiens</i>
HUMAN HGNC=9889 UniProtKB=Q7Z6E9	RBBP6	E3 ubiquitin-protein ligase RBBP6;RBBP6;ortholog	E3 UBIQUITIN-PROTEIN LIGASE RBBP6 (PTHR15439:SF0)	nuclease(PC00170)	<i>Homo sapiens</i>
HUMAN HGNC=19909 UniProtKB=Q8N5L8	RP25L	Ribonuclease P protein subunit p25-like protein;RPP25L;ortholog	RIBONUCLEASE P PROTEIN SUBUNIT P25-LIKE PROTEIN (PTHR13516:SF8)	nuclease(PC00170)	<i>Homo sapiens</i>
HUMAN HGNC=11407 UniProtKB=Q9BXU1	STK31	Serine/threonine-protein kinase 31;STK31;ortholog	SERINE/THREONINE-PROTEIN KINASE 31 (PTHR12302:SF3)	nucleic acid binding(PC00171);transcription cofactor(PC00217)	<i>Homo sapiens</i>
HUMAN HGNC=18042 UniProtKB=Q96LI5	CNO6L	CCR4-NOT transcription complex subunit 6-like;CNOT6L;ortholog	CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 6-LIKE (PTHR12121:SF35)	exoribonuclease(PC00099)	<i>Homo sapiens</i>
HUMAN HGNC=19949 UniProtKB=O75817	POP7	Ribonuclease P protein subunit p20;POP7;ortholog	RIBONUCLEASE P PROTEIN SUBUNIT P20 (PTHR15314:SF1)	endoribonuclease(PC00094);hydrolase(PC00121)	<i>Homo sapiens</i>
HUMAN HGNC=8021 UniProtKB=P21589	5NTD	5'-nucleotidase;NT5E;ortholog	5'-NUCLEOTIDASE (PTHR11575:SF25)	phosphodiesterase(PC00185)	<i>Homo sapiens</i>

HUMAN HGNC=13 236 UniProtKB=O947RMP 63		Unconventional prefoldin RBP5 interactor 1;URI1;ortholog	UNCONVENTIONAL PREFOLDIN RBP5 INTERACTOR 1 (PTHR15111:SF0)	transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=30 802 UniProtKB=Q96 AD5	PLP L2	Patatin-like phospholipase domain-containing protein 2;PNPLA2;ortholog	PATATIN-LIKE PHOSPHOLIPASE DOMAIN-CONTAINING PROTEIN 2 (PTHR12406:SF29)	acyltransferase(PC00042);phospholipase(PC0018 6)	<i>Homo sapiens</i>
HUMAN HGNC=52 93 UniProtKB=P2822 3	5HT 2A	5-hydroxytryptamine receptor 2A;HTR2A;ortholog	5-HYDROXYTRYPTAMINE RECEPTOR 2A (PTHR24247:SF30)	G-protein coupled receptor(PC00021)	<i>Homo sapiens</i>
HUMAN HGNC=16 650 UniProtKB=Q9H 9J2	RM4 4	39S ribosomal protein L44, mitochondrial;MRPL44;ortholo g	39S RIBOSOMAL PROTEIN L44, MITOCHONDRIAL (PTHR11207:SF5)	endoribonuclease(PC00094)	<i>Homo sapiens</i>
HUMAN HGNC=23 845 UniProtKB=Q8IYSLX4 92		Structure-specific endonuclease subunit SLX4;SLX4;ortholog	STRUCTURE-SPECIFIC ENDONUCLEASE SUBUNIT SLX4 (PTHR21541:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=24 84 UniProtKB=P3324 0	CST F2	Cleavage stimulation factor subunit 2;CSTF2;ortholog	CLEAVAGE STIMULATION FACTOR SUBUNIT 2 (PTHR45735:SF6)	mRNA splicing factor(PC00148)	<i>Homo sapiens</i>
HUMAN HGNC=10 293 UniProtKB=Q96 AT9	RPE	Ribulose-phosphate 3- epimerase;RPE;ortholog	RIBULOSE-PHOSPHATE 3- EPIMERASE-RELATED (PTHR11749:SF9)		<i>Homo sapiens</i>
HUMAN HGNC=17 175 UniProtKB=Q9P 212	PLC E1	1-phosphatidylinositol 4,5- bisphosphate phosphodiesterase epsilon- 1;PLCE1;ortholog	1-PHOSPHATIDYLINOSITOL 4,5- BISPHOSPHATE PHOSPHODIESTERASE EPSILON-1 (PTHR10336:SF6)	calcium-binding protein(PC00060);guanyl- nucleotide exchange factor(PC00113);phospholipase(PC00186);signali ng molecule(PC00207)	<i>Homo sapiens</i>
HUMAN HGNC=21 300 UniProtKB=Q9H 633	RPP2 1	Ribonuclease P protein subunit p21;RPP21;ortholog	RIBONUCLEASE P PROTEIN SUBUNIT P21 (PTHR14742:SF0)	hydrolase(PC00121);nuclease(PC00170)	<i>Homo sapiens</i>

HUMAN HGNC=17 641 UniProtKB=Q9H 816	DCR 1B	5' exonuclease Apollo;DCLRE1B;ortholog	5' EXONUCLEASE APOLLO (PTHR23240:SF27)		<i>Homo sapiens</i>
HUMAN HGNC=36 50 UniProtKB=P3974 8	FEN 1	Flap endonuclease 1;FEN1;ortholog	FLAP ENDONUCLEASE 1 (PTHR11081:SF54)	damaged DNA-binding protein(PC00086);endodeoxyribonuclease(PC000 93);exodeoxyribonuclease(PC00098);hydrolase(P C00121)	<i>Homo sapiens</i>
HUMAN HGNC=27 7 UniProtKB=P35348	ADA 1A	Alpha-1A adrenergic receptor;ADRA1A;ortholog	ALPHA-1A ADRENERGIC RECEPTOR (PTHR24248:SF16)	G-protein coupled receptor(PC00021)	<i>Homo sapiens</i>
HUMAN HGNC=21 339 UniProtKB=O605 22	TDR D6	Tudor domain-containing protein 6;TDRD6;ortholog	TUDOR DOMAIN-CONTAINING PROTEIN 6 (PTHR22948:SF15)	nuclease(PC00170)	<i>Homo sapiens</i>
HUMAN HGNC=26 019 UniProtKB=Q9N X62	IMP A3	Inositol monophosphatase 3;IMPAD1;ortholog	INOSITOL MONOPHOSPHATASE 3 (PTHR43028:SF6)	phosphatase(PC00181)	<i>Homo sapiens</i>
HUMAN HGNC=21 416 UniProtKB=Q924 85	ASM 3B	Acid sphingomyelinase-like phosphodiesterase 3b;SMPDL3B;ortholog	ACID SPHINGOMYELINASE-LIKE PHOSPHODIESTERASE 3B (PTHR10340:SF25)	phosphodiesterase(PC00185)	<i>Homo sapiens</i>
HUMAN HGNC=17 660 UniProtKB=Q6PJ P8	SNM 1,DC R1A	DNA cross-link repair 1A protein;DCLRE1A;ortholog	DNA CROSS-LINK REPAIR 1A PROTEIN (PTHR23240:SF6)		<i>Homo sapiens</i>
HUMAN HGNC=17 889 UniProtKB=Q9U BZ4	APE X2	DNA-(apurinic or apyrimidinic site) lyase 2;APEX2;ortholog	DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE 2 (PTHR22748:SF4)		<i>Homo sapiens</i>
HUMAN HGNC=21 185 UniProtKB=Q8N A58	PND C1	Poly(A)-specific ribonuclease PNLDC1;PNLDC1;ortholog	POLY(A)-SPECIFIC RIBONUCLEASE PNLDC1 (PTHR15092:SF22)	mRNA polyadenylation factor(PC00146)	<i>Homo sapiens</i>
HUMAN HGNC=25 044 UniProtKB=Q587 J7	TDR 12	Putative ATP-dependent RNA helicase TDRD12;TDRD12;ortholog	ATP-DEPENDENT RNA HELICASE TDRD12-RELATED (PTHR22948:SF31)	nuclease(PC00170);signaling molecule(PC00207)	<i>Homo sapiens</i>

HUMAN HGNC=24763 UniProtKB=Q6ZVT6	CC067	Uncharacterized protein C3orf67;C3orf67;ortholog	ZGC:162324 (PTHR12458:SF7)	nuclease(PC00170);transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=17098 UniProtKB=Q9UPY3	DICER	Endoribonuclease Dicer;DICER1;ortholog	ENDORIBONUCLEASE DICER (PTHR14950:SF37)	endodeoxyribonuclease(PC00093)	<i>Homo sapiens</i>
HUMAN HGNC=12836 UniProtKB=Q9H0D6	XRN2	5'-3' exoribonuclease 2;XRN2;ortholog	5'-3' EXORIBONUCLEASE 2 (PTHR12341:SF59)	exoribonuclease(PC00099)	<i>Homo sapiens</i>
HUMAN HGNC=20074 UniProtKB=Q504Q3	PAN2	PAN2-PAN3 deadenylation complex catalytic subunit PAN2;PAN2;ortholog	PAN2-PAN3 DEADENYLATION COMPLEX CATALYTIC SUBUNIT PAN2 (PTHR15728:SF0)	cysteine protease(PC00081);esterase(PC00097);exoribonuclease(PC00099)	<i>Homo sapiens</i>
HUMAN HGNC=24660 UniProtKB=Q8IXG06	GOR	Putative exonuclease GOR;REXO1L1P;ortholog	EXONUCLEASE GOR-RELATED (PTHR12801:SF22)	exoribonuclease(PC00099)	<i>Homo sapiens</i>
HUMAN HGNC=25026 UniProtKB=Q8NEB5	PLP5	Phospholipid phosphatase 5;PLPP5;ortholog	PHOSPHOLIPID PHOSPHATASE 5 (PTHR10165:SF87)	phosphatase(PC00181);pyrophosphatase(PC00196)	<i>Homo sapiens</i>
HUMAN HGNC=10297 UniProtKB=P49247	RPIA	Ribose-5-phosphate isomerase;RPIA;ortholog	RIBOSE-5-PHOSPHATE ISOMERASE (PTHR11934:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=9156 UniProtKB=P54315	LIPR1	Inactive pancreatic lipase-related protein 1;PNLIPRP1;ortholog	INACTIVE PANCREATIC LIPASE-RELATED PROTEIN 1 (PTHR11610:SF147)	esterase(PC00097);lipase(PC00143);storage protein(PC00210)	<i>Homo sapiens</i>
HUMAN HGNC=6619 UniProtKB=P11150	LIPC	Hepatic triacylglycerol lipase;LIPC;ortholog	HEPATIC TRIACYLGLYCEROL LIPASE (PTHR11610:SF2)	esterase(PC00097);lipase(PC00143);storage protein(PC00210)	<i>Homo sapiens</i>
HUMAN HGNC=6737 UniProtKB=O75608	LYPA1	Acyl-protein thioesterase 1;LYPLA1;ortholog	ACYL-PROTEIN THIOESTERASE 1 (PTHR10655:SF22)		<i>Homo sapiens</i>

HUMAN HGNC=23044 UniProtKB=Q8WY41	NOS1	Nanos homolog 1;NANOS1;ortholog	NANOS HOMOLOG 1 (PTHR12887:SF6)	nuclease(PC00170)	<i>Homo sapiens</i>
HUMAN HGNC=17163 UniProtKB=Q8NCC3	PAG15	Group XV phospholipase A2;PLA2G15;ortholog	GROUP XV PHOSPHOLIPASE A2 (PTHR11440:SF47)	acyltransferase(PC00042);phospholipase(PC00186)	<i>Homo sapiens</i>
HUMAN HGNC=3066 UniProtKB=O75319	DUS11	RNA/RNP complex-1-interacting phosphatase;DUSP11;ortholog	RNA/RNP COMPLEX-1-INTERACTING PHOSPHATASE (PTHR10367:SF9)	nucleotidyltransferase(PC00174);phosphatase(PC00181)	<i>Homo sapiens</i>
HUMAN HGNC=25364 UniProtKB=Q9H0R4	HDHD2	Haloacid dehalogenase-like hydrolase domain-containing protein 2;HDHD2;ortholog	HALOACID DEHALOGENASE-LIKE HYDROLASE DOMAIN-CONTAINING PROTEIN 2 (PTHR19288:SF43)	Homo sapiens	
HUMAN HGNC=24220 UniProtKB=Q6P1N9	TATD1	Putative deoxyribonuclease TATDN1;TATDN1;ortholog	DEOXYRIBONUCLEASE TATDN1-RELATED (PTHR10060:SF15)		<i>Homo sapiens</i>
HUMAN HGNC=17086 UniProtKB=Q9H0L4	CSTFT	Cleavage stimulation factor subunit 2 tau variant;CSTF2T;ortholog	CLEAVAGE STIMULATION FACTOR SUBUNIT 2 TAU VARIANT (PTHR45735:SF3)	mRNA splicing factor(PC00148)	<i>Homo sapiens</i>
HUMAN HGNC=9827 UniProtKB=Q99638	RAD9A	Cell cycle checkpoint control protein RAD9A;RAD9A;ortholog	CELL CYCLE CHECKPOINT CONTROL PROTEIN RAD9A (PTHR15237:SF1)	kinase activator(PC00138)	<i>Homo sapiens</i>
HUMAN HGNC=11120 UniProtKB=P17405	ASMP	Sphingomyelin phosphodiesterase;SMPD1;ortholog	SPHINGOMYELIN PHOSPHODIESTERASE (PTHR10340:SF34)	phosphodiesterase(PC00185)	<i>Homo sapiens</i>
HUMAN HGNC=17018 UniProtKB=Q9Y6Y8	S23IP	SEC23-interacting protein;SEC23IP;ortholog	SEC23-INTERACTING PROTEIN (PTHR23509:SF4)	membrane traffic protein(PC00150);phospholipase(PC00186)	<i>Homo sapiens</i>

HUMAN HGNC=24 644 UniProtKB=Q9U PR3	SMG 5	Protein SMG5;SMG5;ortholog	PROTEIN SMG5 (PTHR15696:SF7)		<i>Homo sapiens</i>
HUMAN HGNC=33 882 UniProtKB=Q9B T40	PPS,I NP5 K	Inositol polyphosphate 5-phosphatase K;INPP5K;ortholog	INOSITOL POLYPHOSPHATE 5-PHOSPHATASE K (PTHR11200:SF117)	phosphatase(PC00181)	<i>Homo sapiens</i>
HUMAN HGNC=14 254 UniProtKB=Q9U K39	NOC	Nocturnin;NOCT;ortholog	NOCTURNIN (PTHR12121:SF45)	exoribonuclease(PC00099)	<i>Homo sapiens</i>
HUMAN HGNC=28 142 UniProtKB=Q9B T23	LIM D2	LIM domain-containing protein 2;LIMD2;ortholog	LIM DOMAIN-CONTAINING PROTEIN 2 (PTHR24206:SF58)	actin family cytoskeletal protein(PC00041);nuclease(PC00170);transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=58 7 UniProtKB=P27695	APE X1	DNA-(apurinic or apyrimidinic site) lyase;APEX1;ortholog	DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE (PTHR22748:SF6)		<i>Homo sapiens</i>
HUMAN HGNC=92 07 UniProtKB=Q9UF F9	CAF 1B	CCR4-NOT transcription complex subunit 8;CNOT8;ortholog	CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 8 (PTHR10797:SF1)	transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=91 55 UniProtKB=P1623 3	LIPP	Pancreatic triacylglycerol lipase;PNLIP;ortholog	PANCREATIC TRIACYLGLYCEROL LIPASE (PTHR11610:SF115)	esterase(PC00097);lipase(PC00143);storage protein(PC00210)	<i>Homo sapiens</i>
HUMAN HGNC=28 424 UniProtKB=Q9B Q61	TRIR	Telomerase RNA component interacting RNase;TRIR;ortholog	TELOMERASE RNA COMPONENT INTERACTING RNASE (PTHR34753:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=87 78 UniProtKB=Q1443 2	PDE 3A	cGMP-inhibited 3',5'-cyclic phosphodiesterase A;PDE3A;ortholog	PHOSPHODIESTERASE (PTHR11347:SF104)		<i>Homo sapiens</i>
HUMAN HGNC=15 984 UniProtKB=Q7Z 2E3	APT X	Aprataxin;APTX;ortholog	APRATAXIN (PTHR12486:SF4)	damaged DNA-binding protein(PC00086)	<i>Homo sapiens</i>

HUMAN HGNC=9177 UniProtKB=Q07864	DPO E1	DNA polymerase epsilon catalytic subunit A;POLE;ortholog	DNA POLYMERASE EPSILON CATALYTIC SUBUNIT A (PTHR10670:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=20999 UniProtKB=Q9NPJ3	ACO 13	Acyl-coenzyme A thioesterase 13;ACOT13;ortholog	ACYL-COENZYME A THIOESTERASE 13 (PTHR21660:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=11712 UniProtKB=Q9BXT4	TDR D1	Tudor domain-containing protein 1;TDRD1;ortholog	TUDOR DOMAIN-CONTAINING PROTEIN 1 (PTHR22948:SF4)	nuclease(PC00170)	<i>Homo sapiens</i>
HUMAN HGNC=9891 UniProtKB=Q99708	CTIP SAE 2	DNA endonuclease RBBP8;RBBP8;ortholog	DNA ENDONUCLEASE RBBP8 (PTHR15107:SF4)	transcription cofactor(PC00217)	<i>Homo sapiens</i>
HUMAN HGNC=12270 UniProtKB=Q9BQ50	TRE X2	Three prime repair exonuclease 2;TREX2;ortholog	THREE PRIME REPAIR EXONUCLEASE 2 (PTHR13058:SF24)		<i>Homo sapiens</i>
HUMAN HGNC=28422 UniProtKB=Q8NCE0	SEN 2	tRNA-splicing endonuclease subunit Sen2;TSEN2;ortholog	TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN2 (PTHR21227:SF0)	endodeoxyribonuclease(PC00093);hydrolase(PC00121)	<i>Homo sapiens</i>
HUMAN HGNC=23994 UniProtKB=Q8IV48	ERI1	3'-5' exoribonuclease 1;ERI1;ortholog	3'-5' EXORIBONUCLEASE 1 (PTHR23044:SF27)	esterase(PC00097);exoribonuclease(PC00099)	<i>Homo sapiens</i>
HUMAN HGNC=16205 UniProtKB=Q9BQP7	MG ME1	Mitochondrial genome maintenance exonuclease 1;MGME1;ortholog	MITOCHONDRIAL GENOME MAINTENANCE EXONUCLEASE 1 (PTHR31340:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=8909 UniProtKB=A6NDG6	PGP	Glycerol-3-phosphate phosphatase;PGP;ortholog	GLYCEROL-3-PHOSPHATE PHOSPHATASE (PTHR19288:SF69)		<i>Homo sapiens</i>
HUMAN HGNC=9229 UniProtKB=O14495	PLP P3	Phospholipid phosphatase 3;PLPP3;ortholog	PHOSPHOLIPID PHOSPHATASE 3 (PTHR10165:SF79)	phosphatase(PC00181);pyrophosphatase(PC00196)	<i>Homo sapiens</i>

HUMAN HGNC=91 57 UniProtKB=P5431 7	LIPR 2	Pancreatic lipase-related protein 2;PNLIPRP2;ortholog	PANCREATIC LIPASE-RELATED PROTEIN 2 (PTHR11610:SF85)	esterase(PC00097);lipase(PC00143);storage protein(PC00210)	<i>Homo sapiens</i>
HUMAN HGNC=20 217 UniProtKB=Q9N VH0	EXD 2	Exonuclease 3'-5' domain- containing protein 2;EXD2;ortholog	EXONUCLEASE 3'-5' DOMAIN- CONTAINING PROTEIN 2 (PTHR13620:SF0)	nuclease(PC00170)	<i>Homo sapiens</i>
HUMAN HGNC=23 719 UniProtKB=Q96 FM1	PGA P3	Post-GPI attachment to proteins factor 3;PGAP3;ortholog	POST-GPI ATTACHMENT TO PROTEINS FACTOR 3 (PTHR13148:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=49 12 UniProtKB=P4977 3	HIN T1,H INT	Histidine triad nucleotide- binding protein 1;HINT1;ortholog	HISTIDINE TRIAD NUCLEOTIDE- BINDING PROTEIN 1 (PTHR23089:SF44)	nucleotide phosphatase(PC00173)	<i>Homo sapiens</i>
HUMAN HGNC=25 499 UniProtKB=Q9N W75	GPT C2	G patch domain-containing protein 2;GPATCH2;ortholog	G PATCH DOMAIN-CONTAINING PROTEIN 2 (PTHR14195:SF4)	nucleic acid binding(PC00171)	<i>Homo sapiens</i>
HUMAN HGNC=91 79 UniProtKB=P5409 8	DPO G1	DNA polymerase subunit gamma-1;POLG;ortholog	DNA POLYMERASE SUBUNIT GAMMA-1 (PTHR10267:SF0)	DNA-directed DNA polymerase(PC00018);exodeoxyribonuclease(PC 00098);nucleotidyltransferase(PC00174)	<i>Homo sapiens</i>
HUMAN HGNC=30 081 UniProtKB=O957 07	RPP2 9	Ribonuclease P protein subunit p29;POP4;ortholog	RIBONUCLEASE P PROTEIN SUBUNIT P29 (PTHR13348:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=26 023 UniProtKB=Q8N 9H8	MUT 7	Exonuclease mut-7 homolog;EXD3;ortholog	EXONUCLEASE MUT-7 HOMOLOG (PTHR13620:SF42)	nuclease(PC00170)	<i>Homo sapiens</i>
HUMAN HGNC=90 35 UniProtKB=P4771 2	PA2 4A	Cytosolic phospholipase A2;PLA2G4A;ortholog	CYTOSOLIC PHOSPHOLIPASE A2 (PTHR10728:SF13)	phospholipase(PC00186)	<i>Homo sapiens</i>
HUMAN HGNC=19 124 UniProtKB=Q6U N15	FIP1	Pre-mRNA 3'-end-processing factor FIP1;FIP1L1;ortholog	PRE-MRNA 3'-END-PROCESSING FACTOR FIP1 (PTHR13484:SF5)		<i>Homo sapiens</i>

HUMAN HGNC=29 523 UniProtKB=Q9Y 6A4	CFA 20	Cilia- and flagella-associated protein 20;CFAP20;ortholog	CILIA- AND FLAGELLA- ASSOCIATED PROTEIN 20 (PTHR12458:SF8)	nuclease(PC00170);transcription factor(PC00218)	<i>Homo sapiens</i>
HUMAN HGNC=15 520 UniProtKB=P436 57	LPA R6	Lysophosphatidic acid receptor 6;LPA6;ortholog	LYSOPHOSPHATIDIC ACID RECEPTOR 6 (PTHR24232:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=19 958 UniProtKB=O150 91	MRP P3	Mitochondrial ribonuclease P catalytic subunit;KIAA0391;ortholog	MITOCHONDRIAL RIBONUCLEASE P CATALYTIC SUBUNIT (PTHR13547:SF1)		<i>Homo sapiens</i>
HUMAN HGNC=36 7 UniProtKB=Q92667	AKA P1	A-kinase anchor protein 1, mitochondrial;AKAP1;ortholog	A-KINASE ANCHOR PROTEIN 1, MITOCHONDRIAL (PTHR22948:SF48)	nuclease(PC00170);signaling molecule(PC00207)	<i>Homo sapiens</i>
HUMAN HGNC=89 03 UniProtKB=O9533 6	6PG L	6- phosphogluconolactonase;PGL S;ortholog	6-PHOSPHOGLUCONOLACTONASE (PTHR11054:SF0)	hydrolase(PC00121)	<i>Homo sapiens</i>
HUMAN HGNC=95 77 UniProtKB=P7833 0	SER B	Phosphoserine phosphatase;PSPH;ortholog	PHOSPHOSERINE PHOSPHATASE (PTHR43344:SF2)	phosphatase(PC00181)	<i>Homo sapiens</i>
HUMAN HGNC=92 28 UniProtKB=O1449 4	LPP1	Phospholipid phosphatase 1;PLPP1;ortholog	PHOSPHOLIPID PHOSPHATASE 1 (PTHR10165:SF26)	phosphatase(PC00181);pyrophosphatase(PC0019 6)	<i>Homo sapiens</i>
HUMAN HGNC=14 451 UniProtKB=Q9B QK8	LPI N3	Phosphatidate phosphatase LPIN3;LPIN3;ortholog	PHOSPHATIDATE PHOSPHATASE LPIN3 (PTHR12181:SF60)		<i>Homo sapiens</i>
HUMAN HGNC=10 8 UniProtKB=P22303	ACE S	Acetylcholinesterase;ACHE;ort holog	ACETYLCHOLINESTERASE (PTHR11559:SF393)	lipase(PC00143);serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=23 409 UniProtKB=Q6U WR7	ENP P6	Ectonucleotide pyrophosphatase/phosphodiesterase family member 6;ENPP6;ortholog	ECTONUCLEOTIDE PYROPHOSPHATASE/PHOSPHODIESTERASE FAMILY MEMBER 6 (PTHR10151:SF66)	nucleotide phosphatase(PC00173);pyrophosphatase(PC0019 6)	<i>Homo sapiens</i>

HUMAN HGNC=4908 UniProtKB=Q6N VY1	HIBCH	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial;HIBCH;ortholog	3-HYDROXYISOBUTYRYL-COA HYDROLASE, MITOCHONDRIAL (PTHR43176:SF13)	acetyltransferase(PC00038);acyltransferase(PC00042);dehydrogenase(PC00092);epimerase/racemase(PC00096);hydratase(PC00120);ligase(PC00142)	<i>Homo sapiens</i>
HUMAN HGNC=6071 UniProtKB=P4944 1	IPP	Inositol polyphosphate 1-phosphatase;INPP1;ortholog	INOSITOL POLYPHOSPHATE 1-PHOSPHATASE (PTHR43028:SF3)	phosphatase(PC00181)	<i>Homo sapiens</i>
HUMAN HGNC=3363 UniProtKB=P4996 1	ENTP1	Ectonucleoside triphosphate diphosphohydrolase 1;ENTPD1;ortholog	ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 1 (PTHR11782:SF32)	lyase(PC00144);nucleotide phosphatase(PC00173)	<i>Homo sapiens</i>
HUMAN HGNC=17904 UniProtKB=Q9N RR4	RNC	Ribonuclease 3;DROSHA;ortholog	RIBONUCLEASE 3 (PTHR11207:SF0)	endoribonuclease(PC00094)	<i>Homo sapiens</i>
HUMAN HGNC=25792 UniProtKB=Q9B Q65	USB1	U6 snRNA phosphodiesterase;USB1;ortholog	U6 SNRNA PHOSPHODIESTERASE (PTHR13522:SF3)		<i>Homo sapiens</i>
HUMAN HGNC=8781 UniProtKB=Q0734 3	PDE4B	cAMP-specific 3',5'-cyclic phosphodiesterase 4B;PDE4B;ortholog	CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE 4B (PTHR11347:SF108)		<i>Homo sapiens</i>
HUMAN HGNC=15925 UniProtKB=Q9Y 3Z3	SAMH1	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1;SAMHD1;ortholog	DEOXYNUCLEOSIDE TRIPHOSPHATE TRIPHOSPHOHYDROLASE SAMHD1 (PTHR11373:SF4)		<i>Homo sapiens</i>
HUMAN HGNC=18718 UniProtKB=Q8W U67	ABHD3	Phospholipase ABHD3;ABHD3;ortholog	PHOSPHOLIPASE ABHD3 (PTHR10794:SF50)	serine protease(PC00203)	<i>Homo sapiens</i>
HUMAN HGNC=1864 UniProtKB=O0074 8	CES2	Cocaine esterase;CES2;ortholog	COCAINE ESTERASE (PTHR11559:SF394)	lipase(PC00143);serine protease(PC00203)	<i>Homo sapiens</i>

HUMAN HGNC=60 50 UniProtKB=P2921 8	IMP A1	Inositol monophosphatase 1;IMP A1;ortholog	INOSITOL MONOPHOSPHATASE 1 (PTHR20854:SF26)	phosphatase(PC00181)	<i>Homo sapiens</i>
HUMAN HGNC=25 386 UniProtKB=Q6L 8Q7	PDE 12	2',5'-phosphodiesterase 12;PDE12;ortholog	2',5'-PHOSPHODIESTERASE 12 (PTHR12121:SF37)	exoribonuclease(PC00099)	<i>Homo sapiens</i>
HUMAN HGNC=80 22 UniProtKB=P4990 2	5NT C	Cytosolic purine 5'- nucleotidase;NT5C2;ortholog	CYTOSOLIC PURINE 5'- NUCLEOTIDASE (PTHR12103:SF17)	nucleotide phosphatase(PC00173)	<i>Homo sapiens</i>
HUMAN HGNC=29 991 UniProtKB=Q58 A45	PAN 3	PAN2-PAN3 deadenylation complex subunit PAN3;PAN3;ortholog	PAN2-PAN3 DEADENYLATION COMPLEX SUBUNIT PAN3 (PTHR12272:SF11)		<i>Homo sapiens</i>
HUMAN HGNC=29 540 UniProtKB=Q9U LX3	NOB 1	RNA-binding protein NOB1;NOB1;ortholog	RNA-BINDING PROTEIN NOB1 (PTHR12814:SF2)		<i>Homo sapiens</i>
HUMAN HGNC=30 646 UniProtKB=Q7K ZF4	SND 1	Staphylococcal nuclease domain-containing protein 1;SND1;ortholog	STAPHYLOCOCCAL NUCLEASE DOMAIN-CONTAINING PROTEIN 1 (PTHR12302:SF2)	nucleic acid binding(PC00171);transcription cofactor(PC00217)	<i>Homo sapiens</i>
HUMAN HGNC=86 09 UniProtKB=O9545 3	PAR N	Poly(A)-specific ribonuclease PARN;PARN;ortholog	POLY(A)-SPECIFIC RIBONUCLEASE PARN (PTHR15092:SF26)	mRNA polyadenylation factor(PC00146)	<i>Homo sapiens</i>
HUMAN HGNC=25 495 UniProtKB=Q9N W82	WD R70	WD repeat-containing protein 70;WDR70;ortholog	WD REPEAT-CONTAINING PROTEIN 70 (PTHR16017:SF0)		<i>Homo sapiens</i>
HUMAN HGNC=27 8 UniProtKB=P35368	ADA 1B	Alpha-1B adrenergic receptor;ADRA1B;ortholog	ALPHA-1B ADRENERGIC RECEPTOR (PTHR24248:SF17)	G-protein coupled receptor(PC00021)	<i>Homo sapiens</i>
HUMAN HGNC=18 518 UniProtKB=O757 92	RNH 2A	Ribonuclease H2 subunit A;RNASEH2A;ortholog	RIBONUCLEASE H2 SUBUNIT A (PTHR10954:SF7)	endoribonuclease(PC00094);hydrolase(PC00121)	<i>Homo sapiens</i>

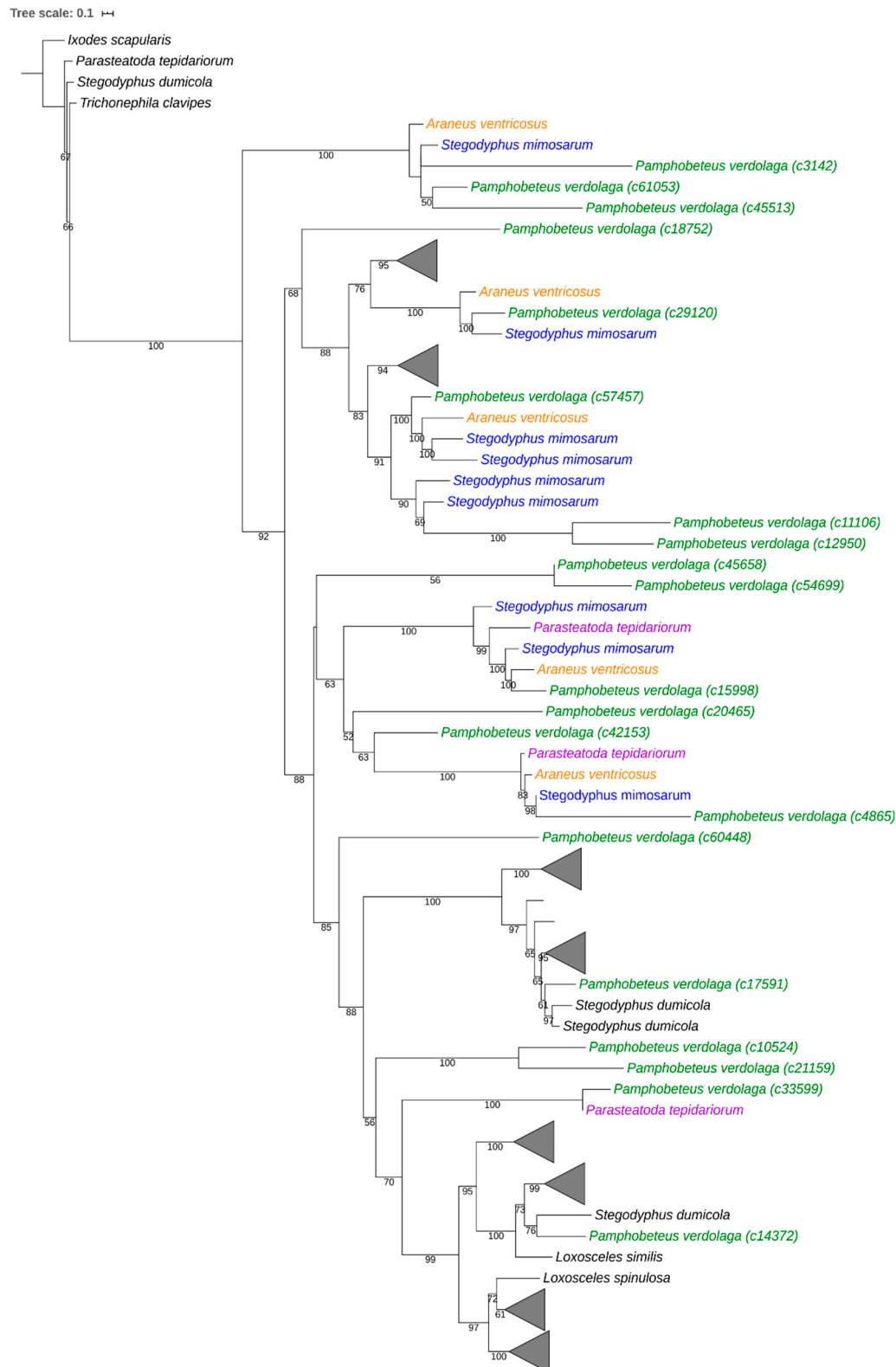


Figure S1. Phylogenetic tree of phospholipase A2. The tree includes sequences of phospholipase A2 reported for different spider families. *P. verdolaga* sequences (green) are orthologous with different species, grouped with good branch supports (> 50%), multiples duplication event underwent during the evolution of phospholipase A2 in *P. verdolaga*. The triangle represents collapsed sequences from other species used to build the tree. Phospholipase A2 from *Ixodes scapularis* was used as outgroup.

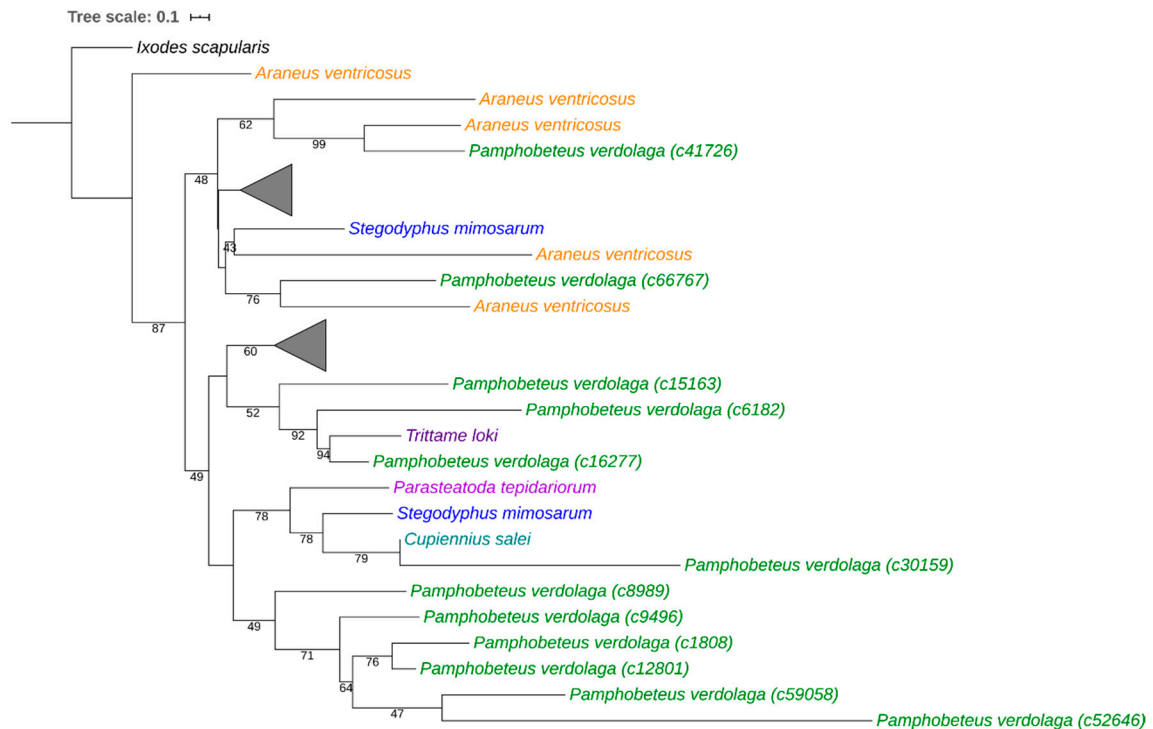


Figure S2. Phylogenetic tree of Kunitz-like protein family. The tree includes the Kunitz reported in data bases for different spider families. The Phylogenetic tree show that *P. verdolaga* sequences (green) are orthologous with different species, grouped with good branch supports (> 50%). The triangle represents collapsed sequences from other species used to build the tree. Kunitz from *Ixodes scapularis* was used as outgroup.

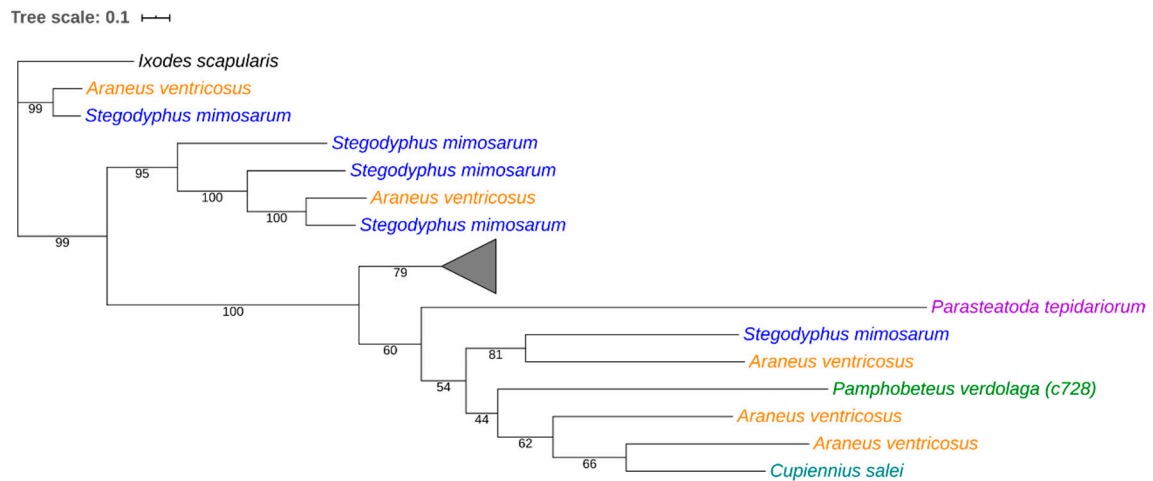


Figure S3. Phylogenetic tree of the metalloproteinase. The tree includes the metalloproteinase reported in data bases for different spider families. The Phylogenetic tree show that *P. verdolaga* sequence (green) is orthologous with the sequences reported for *Araneus ventricosus* with a branch support of 44%. The triangle represents collapsed sequences from other species used to build the tree. Metalloproteinase sequence from *Ixodes scapularis* was used as outgroup.

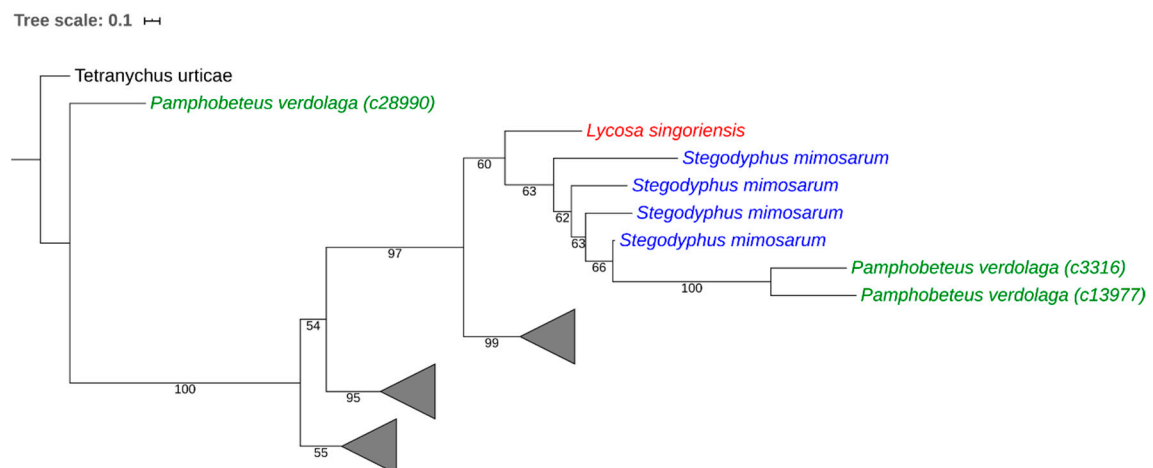


Figure S4. Phylogenetic tree of Lycotoxin-like protein. The tree includes the Lycotoxin-like proteins reported in data bases for different spider families. The Phylogenetic tree supports (branch support 100%) that *P. verdolaga* sequence c28990 is a basal protein that belong to the Lycotoxin-like family in spiders and multiples duplication events allow the diversification of the protein in different spider species. The triangle represents collapsed sequences from other species used to build the tree. Lycotoxin from *Tetranychus urticae* was used as outgroup.