Table S1. Distribution of transcripts that putatively code for venom components.

						Sodium toxins	
ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatNaTAlp01	P63019.1	2 e-28	PF00537	--	alpha toxin	ILLLGIERSES**RDGYPIASNGCKFGCSGLGENNPTCNH VCEKKAGSDYGYCYAW**	ATTCTACTCTTAGGAATAGAAAGAAGCGAGTCGAGAGATGGTTATCC TATAGCTTCAAATGGTTGCAAATTTGGATGCAGTGGATTAGGTGAGA ACAATCCAACTTGTAATCACGTTTGTGAAAAGAAAGCCGGAAGTGAC TACGGCTATTGCTATGCCTGG
TatNaTAlp02	Q5MJP5.1	6 e-24	N/D	8500.77	alpha toxin	MNTLSTFTLTSLLLLIIGFYQYQAQA**RFVRRKNMTFYE CSELSGHDPYCVRTCEEHESKEEGYCKEFDRYGISAC YCPNIVGTKVVMCYAALQRKCKF***	ATGAATACACTAAGCACCTTTACCCTCACTTCATTACTTCTTCTTATT ATTGGCTTTTATCAATATCAAGCACAGGCAAGATTTGTGAGAAGGAA AAACATGACATTTTACGAATGCAGCGAATTATCTGGCCATGATCCCT ATTGTGTTCGTACTTGCGAAGAGCACGAATCAAAAGAGGAGGGATA TTGTAAAGAATTTGACCGTTATGGAATTTCTGCTTGTTACTGCCCAAA CATTGTAGGAACCAAAGTTGTTATGTGCTACGCAGCTCTTCAAAGAA AATGCAAATTC
TatNaTAlp03	Q5MJP5.1	5 e-34	PF00537	7986.39	alpha toxin	MKTIANMTYYFYCLLLFVGIFNIQVGGK**FVRKPNGSFY ECGMLIGYQPYCVQTCKEHKAPEKGYCKEMYPFGL PGGCYCPNIPQNKIRMCRGALKNEC***	ATGACTTATTATTTCTACTGTCTCTTGCTTTTCGTAGGCATTTTTAATA TTCAAGTAGGAGGAAAATTTGTGAGAAAACCCAATGGCTCATTTTAT GAATGCGGTATGTTAATAGGGTACCAGCCATATTGCGTTCAGACTTG TAAAGAACACAAAGCTCCTGAAAAAGGCTACTGCAAAGAAATGTAT CCTTTTGGACTCCCTGGTGGCTGCTACTGTCCAAATATTCCTCAAAAT AAAATAAGAATGTGTCGCGGTGCCCTTAAAAATGAGTGT
TatNaTBet01	P0CI45.1	9 e-17	PF00537	6672	beta toxin	MNCSTVLIFCLIAIVFEFAGVEC**KKDGYPLTTEGLKFSC AAGMLGDNRFCLSICRSRGSNYGYCYFFGCYCEGLN DDVKIWSG***	ATGAATTGCTCTACTGTTCTCATTTTCTGCCTAATTGCCATTGTTTTTG AATTTGCTGGTGTGGAGTGCAAAAAGGATGGATATCCTTTGACTACA GAAGGATTGAAGTTCAGTTGTGCTGCAGGAATGTTAGGTGATAACAG ATTCTGTCTATCTATCTGTAGAAGTCGTGGTTCAAATTATGGTTATTG TTACTTCTTTGGTTGTTATTGTGAAGGCTTAAATGATGATGTTAAAAT TTGGAGTGGCTAA
TatNaTBet02	P01491.3	3 e-16	PF00537	6544.9	beta toxin	MNCSTVLIFCLIAIVFEFAGVEC**KKDGYPVTKEGLKVS CAAGMILGDNRFCQAICKGDGADYGYCYGFGCYCE GLNDDVKIWSG***	ATGAATTGCTCTACTGTTCTCATTTTCTGCCTAATTGCCATTGTTTTTG AATTTGCTGGTGTGGAGTGCAAAAAGGATGGATATCCTGTGACTAAG GAAGGATTGAAGGTCAGTTGTGCTGCAGGAATGATATTAGGCGATA ACAGATTCTGTCAAGCCATCTGTAAAGGCGATGGTGCCGATTATGGT TATTGTTACGGGTTTGGTTGTTACTGTGAAGGCTTAAATGATGATGTT AAAATTTGGAGTGGCTAA
TatNaTBet03	D9U299.1	4 e-12	PF00537	5193.2	beta toxin	MHISMAAILPLLCLIVTLVFVAETAYS**GFFPLDENGKVY RCEDLGPNQLCNATCVFHGGTYGYCAVSSCYCENR***	ATGCATATCAGCATGGCAGCCATTTTGCCTCTTCTCTGTCTGATCGTT ACTTTAGTCTTTGTTGCTGAAACTGCATACAGCGGATTTTTTCCGCTG GACGAGAATGGGAAAGTGTACCGCTGCGAAGATTTGGGGCCTAATC AGCTGTGCAATGCTACCTGTGTCTTCCATGGTGGAACTTATGGCTACT GTGCCGTCTCCAGCTGTTACTGCGAAAATCGATAA
TatNaTBet04	Q7YT61.1	2 e-27	N/D	--	beta toxin	MNSLLIITACLVLFGTVWA**KEGYLVNKSTGCKYGCFW LGKNENC**	ATGAACTCTTTGTTGATAATCACTGCTTGTTTGGTCCTATTCGGAACA GTGTGGGCAAAAGAAGGTTATCTGGTAAACAAGAGCACGGGCTGCA AATACGGTTGCTTCTGGTTGGGAAAAAACGAAAACTGC
TatNaTBet05	ACJ23108.1	2 e-10	N/D	--	beta toxin	IMRVIVFTATVFALSLLGGYSA**KNAYPRNYEGNCYRCR YPDKDDFCNDICKSLHKANAGECSVSNLFCFCVGIKE ENISIKDVGKA**	ATCATGAGGGTTATTGTCTTTACTGCCACGGTATTTGCTCTTTCTCTG TTGGGCGGATACAGTGCCAAAAATGCGTATCCACGCAACTACGAAG GGAACTGCTATCGATGTCGTTATCCCGATAAAGATGATTTTTGCAAT GACATCTGTAAAAGTTTGCACAAAGCAAACGCTGGTGAATGCAGCGT ATCTAATTTATTCTGTTTCTGCGTTGGCATCAAAGAGGAAATATTAG CATAAAAGACGTTGGAAAAGCA
TatNaTBet06	P0C1B8.1	4 e-11	PF00537	--	beta toxin	MAVILSIFCFVVALTVIDS**ENTYNGFFPLDENGEVYRC EFLGYDQLCNATCAFHGGIYGYCAISSCYCERGRNST AAT**	ATGGCAGTCATCTTGTCTATTTTCTGCTTTGTCGTTGCTTTAACCGTTA TTGATAGTGAAAATACGTATAATGGATTTTTTCCCTTGGATGAGAAC TGCTACTTGTGCCTTCCATGTGGGATTTATGGATATTGTGCCATCTC CAGTTGTTATTGCGAAAGAGGTAGAAATTCAACGGCAGCTACA

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatNaTBet07	P59865.1	3 e-9	N/D	--	beta toxin	<u>MIFAAYWITLFLFYVLFVPVAT</u>**TPSPTSDDVKRVYIPGYADKTCWKLGSNSFCRDICQETAGHGYCHLFVCYCESIS**	ATGATATTTGCTGCTTATTGGATAACGCTGTTCCTATTTTACGTTCTTTTTGTTCCAGTAGCTACCACTCCATCACCAACGTCTGATGATGTTAAAAGAGTTTACATTCCTGGCTATGCTGACAAAACTTGCTGGAAATTAGGATCGAATTCCTTCTGCAGAGATATTTGCCAGGAAACAGCAGGACATGGATATTGTCATCTTTTCGTTTGCTATTGTGAAAGCATTTCA
TatNaTBet08	P15223.3	6 e-9	PF00537	6191.6	beta toxin	<u>MKCFAFLTVCLAVVLFEFTEVEG</u>**KDGYPVDANGNVFNCVPGKLEVCKSACGERGSDQISCLAFTCWCDGMNDDAETWKHD***	ATGAAGTGTTTTGCCTTTCTCACAGTTTGCCTGGCTGTCGTCCTTTTTGAATTTACTGAGGTGGAAGGAAAGGATGGATATCCAGTGGATGCGAATGGAAATGTTTTCAACTGCGTTCCAGGGAAGTTAGAAGTTTGTAAATCTGCGTGTGGTGAGCGTGGATCTGATCAAATTTCCTGCCTCGCATTCACTTGCTGGTGTGATGGGATGAACGATGATGCCGAAACATGGAAACACGAC
TatNaTBet09	Q4LCT0.1	6 e-9	N/D	5178.1	beta toxin	<u>MQDADNNKILQQKQGIFITGMEG</u>**CDFVGGKGVYLDVGCTELGKNSLCEEKCRQVCNSYGYCYSFECWCE***	ATGCAAGATGCCGACAATAATAAAATATTGCAGCAAAAACAAGGAATTTTCATAACTGGAATGGAAGGCTGTGATTTTGTTGGTGGAAAGGAGTGTATCTCGATGTTGGCTGTACAGAACTGGGCAAAAATTCGTTGTGTGAAGAGAAGTGCCGACAAGTTTGCAATTCCTATGGTTATTGCTACAGTTTCGAATGTTGGTGTGAA
TatNaTBet10	Q4LCT0.1	7 e-11	N/D	5392.13	beta toxin	<u>MQLRLFSILIVFGMFKTSMEG</u>**CAVSGGIGTTYINDLCSNLGKNDFCKEKCREICYSYGYCYFFQCWCE***	ATGCAGCTGCGATTGTTTTCGATCTTGATTGTATTTGGAATGTTCAAAACCAGTATGGAAGGCTGTGCTGTTTCTGGTGGAATAGGAACCACCTACATCAATGACCTCTGTTCGAATCTCGGCAAAAATGATTTTTGTAAAGAGAAGTGCAGAGAAATTTGTTATTCTTACGGTTATTGCTACTTCTTCCAATGCTGGTGCGAA

Potassium toxins

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatKTxAlp01	API81322.1	1 e-22	PF14866	4563.34	alpha toxin	<u>MNKALFATVLIVLMVFAVSG</u>**IPAKNYAPTGGCPLSDALCANYCKKNKFGNGGKCDGTKCKCSIK***	ATGAATAAGGCTTTATTTGCAACTGTTCTAATTGTTTTTGATGGTGTTCGCCGTTAGTGGTATTCCAGCAAAAAACTATGCACCAACTGGAGGCTGCCCATTGTCAGACGCCCTTTGTGCTAATTACTGCAAGAAAAACAAATTTGGAAATGGTGGGAAATGCGATGGAACTAAATGCAAATGTTCTATTAAG
TatKTxAlp02	P45696.1	1 e-9	PF00451	--	alpha toxin	<u>MRLAIILLLMTTLVLTIG</u>**APPNGAKCSSSVQCTRPCRHGGGTHGKCMNGR**	ATGAGGCTAGCAATTATTTTGCTGTTGATGACAACATTGGTGTTGACAATTGGTGCACCTCCCAATGGTGCAAAATGTTCATCATCTGTCCAGTGCACACGTCCTTGCCGACATGGAGGAGGAACACATGGAAAATGCATGAACGGAAGA
TatKTxAlp03	API81318.1	3 e-13	PF00451	3933.78	alpha toxin	<u>MIGSFILTFDVVTTEG</u>**GKACTRTKECWSYCKKKDGCPKGKCINKICHCYGC***	ATGATCGGCTCTTTTATATTAACGTTTGATGTAGTGACAACTGAAGGAGGAAAGGCCTGCACTAGAACTAAAGAATGTTGGTCCTATTGTAAAAGAAGGACGGATGTCCTAAAGGAAAATGTATAAACAAAATATGCCATTGCTATGGATGT
TatKTxAlp04	API81318.1	4 e-13	PF00451	4491.24	alpha toxin	<u>MRTVCKKMNTKFAIFLIFTIVILLEGATT</u>**LEKGAKCETSKYCSDYCDRINKCPRGKCISRECKCYVCGG***	ATGAGAACCGTGTGCAAAAAGATGAATACAAAATTTGCTATCTTCCTTATTTTTACCATTGTGTACTGCTTGAAGGTGCAACGACACTCGAAAAAGGAGCCAAATGCGAAACGAGCAAATACTGTTCGGATTACTGTGATAGGATCAACAAATGTCCACGTGGAAAATGCATAAGCAGGGAATGCAAGTGCTATGTTTGTGGAGGC
TatKTxAlp05	API81318.1	3 e-12	PF00451	4606.35	alpha toxin	<u>MVLKFAFILLMFTATILTIGAMA</u>**LEKGAECQTTRYCWDYCGMINNCPRGKCINWECKCYICGG***	ATGGTTCTAAAATTTGCTTTCATTCTCCTTATGTTTACCGCTACGATATTGACAATTGGTGCAATGGCACTCGAAAAAGGAGCCGAATGCCAAACGACAAGATACTGTTGGGATTATTGTGGTATGATCAACAACTGTCCACGTGGAAAATGTATAAACTGGGAATGCAAATGCTACATTTGTGGGGGA
TatKTxAlp06	API81318.1	2 e-21	PF00451	4004.59	alpha toxin	<u>MGTKFVFITLLATTVILAFGALTVEG</u>**GKNCSGSKECYDYCYKTTGCSRAKCINRACKCYGCSG***	ATGGGTACAAAATTCGTCTTCATTACACTCTTGGCCACCACTGTGATATTAGCGTTTGGTGCACTGACAGTTGAAGGAGGGAAGAATTGCAGCGGATCTAAAGAATGTTATGATTATTGTTATAAGACAACCGGATGTTCTCGTGCAAAATGCATCAATAGGGCATGTAAATGTTACGGTTGTAGTGG
TatKTxAlp07	AHJ59318.1	2 e-16	PF00451	4656	alpha toxin	<u>MSTKFFVLMLMVSTVILT</u>**FDVMTTEGGKTCTGSNQCYPYCRKQTGYNAGKCINGRCKCYGG***	ATGAGCACGAAATTTTTCGTCCTTATGCTTATGGTTCAGCACTGTTATACTGACATTTGATGTAATGACAACTGAAGGAGGAAAGACCTGCACTGGAAGTAACCAATGTTATCCTTATTGTAGGAAGCAGACTGGATATAATGCTGGAAAATGTATAAACGGAAGATGCAAATGCTATGGAGGT

						Sequence	Nucleotide
TatKTxAlp08	AFB73769.1	7 e-13	PF00451	3533.5	alpha toxin	MSTKFFILMLMVGSVILTFDVMTTEG**GKTCTGSHQCRP YCIEQTGYNNGKCMNGRCKC***	ATGAGCACAAAATTTTTCATCCTTATGCTTATGGTCGGCTCTGTTATA CTGACATTTGATGTAATGACAACTGAAGGAGGAAAGACCTGCACTG GAAGTCACCAATGTCGGCCCTATTGTATAGAGCAGACTGGATATAAT AATGGAAAATGTATGAACGGAAGATGCAAATGCTAG
TatKTxAlp09	AHJ59318.1	5 e-19	PF00451	4560.25	alpha toxin	KFFILMLVVSSVILTFGVMTTEG**GLPCNGSHQCWDYC RAKTGCFSAKCMNGRCKCYGCSSVNSLQ***	AAATTTTTCATCCTTATGCTTGTGGTCAGCTCTGTTATATTGACCTTTG GTGTAATGACAACTGAAGGAGGACTGCCCTGCAATGGAAGTCACCA ATGTTGGGACTATTGTCGAGCTAAGACAGGATGTTTTAGTGCAAAAT GTATGAACGGAAGATGCAAATGCTACGGTTGTTCTTCTGTTAATTCTT TACAA
TatKTxAlp10	P0DJ32.1	2 e-16	PF00451	3607.4	alpha toxin	MKTNIVLAFLLLSFLIAVAA*GEGERSTR***AISCVGSKECV PKCRNQGCKNGKCMNKKCKCYC***	ATGAAAACGAATATTGTCCTGGCATTTCTTTTGCTAAGCTTCTTAATA GCCGTTGCAGCTGGTGAAGGTGAGAGAAGCACTCGGGCTATCAGCT GTGTCGGTAGCAAGGAATGTGTTCCAAAGTGTAGAAATCAAGGATGT AAAAATGGAAAATGCATGAATAAGAAGTGCAAATGTTACTGCTAA
TatKTxAlp11	P55928.1	7 e-10	PF00451	--	alpha toxin	ILTFDVMKTEGR**MSCTANRQCWPFCRDHTGYISGKCI NRSCKCYRG**	ATACTGACATTTGATGTAATGAAGACTGAAGGAAGAATGTCCTGCAC TGCAAATCGCCAATGTTGGCCCTTTTGTAGAGACCATACTGGATATA TTAGTGGAAAATGTATAAACAGAAGTTGCAAATGCTACCGAGGTTAA
TatKTxAlp12	API81324.1	5 e-23	N/D	4114.86	alpha toxin	MNKLPCFILISLLFIVITNVAVVDG**ISAGCPLSEKLCTSY CKRGRFGSKGKCVGSIGTDCKCYI***	ATGAACAAATTACCTTGCTTTATTCTGATTTCATTGCTGTTCATCGTT ATAACTAACGTTGCAGTCGTGGATGGGATATCAGCTGGCTGCCCGTT GTCTGAAAAACTCTGCACCAGTTATTGCAAAAGAGGACGATTCGGAT CAAAGGGGAAGTGTGTTGGAAGCATAGGAACTGACTGCAAATGTTA CATT
TatKTxAlp13	ACJ23158.1	7 e-10	N/D	4436.1	alpha toxin	MKLKHLLIFLILCTIASCEDHRYR**RSRGCSRTGACMDY CSIRVHEPQNHRRCPPGEYCCTLVV***	ATGAAGCTTAAACATTTACTGATTTTCTTAATATTATGTACAATTGCT AGCTGTGAAGATCATCGTTACAGACGTTCTAGAGGATGCAGTCGTAC TGGAGCCTGTATGGATTACTGTAGTATACGTGTTCATGAGCCACAAA ACCACAGAAGATGCCCTCCAGGAGAATACTGTTGTACTCTGGGTAGTT
TatKTxAlp14	AOF40181.1	7 e-11	N/D	3644.13	alpha toxin	MKLIILLLLLTLEIATILPTIEG**RKCYDSGWCGGPCRDK GASYGKCIDNQCRCYR***	ATGAAGCTGATTATATTACTGCTTTTGCTTACTCTAGAAATAGCAACG ATTCTTCCAACTATCGAAGGCAGAAAGTGCTATGATTCCGGATGGTG CGGAGGACCGTGTCGAGATAAGGGAGCATCTTACGGTAAATGCATA GACAACCAATGTCGGTGCTACAGA
TatKTxAlp15	API81322.1	7 e-31	N/D	3701.21	alpha toxin	MNKAYCAIFLVVLVMFAVSVLPTES**VPTGGCPSDSLCA KYCKSNKYGSTGKCDGTSCKCSLG***	ATGAATAAGGCTTATTGCGCTATATTCCTTGTGGTGCTAGTAATGTTT GCTGTCAGTGTGCTGCCAACTGAGAGCGTACCAACTGGTGGATGCCC AAGTGATTCCCTCTGTGCAAAATACTGCAAAAGTAACAAAATATGGTT CTACTGGAAAATGCGATGGCACCAGTTGTAAGTGTTCCCTTGGATGA
TatKTxScr01	P0C8W5.1	4 e-39	PF14866	9051.78	scorpine like	MQKLFAVLCILSLATFCTC**GLIKEKHVQKGVDALTNLI PAPVVGGIINKVAKQMVHKMGKVQELCAFNKDVMG WCDKACLEKEQTNGFCHGTKCKCGKPLSY***	ATGCAGAAACTTTTCGCTGTTTTGTGTATTCTCAGTTTGGCAACTTTC TGCACATGTGGTTTAATCAAAGAGAAACACGTTCAGAAAGGAGTTG ATGCTTTGACCAATTTAATACCTGCGCCAGTTGTAGGAGGAATCATA AATAAGGTTGCGAAACAGATGGTGCACAAGATGGGTAAAGTTCAAG AATTATGTGCTTTCAACAAAGATGTGATGGGTTGGTGTGATAAAGCC TGCCTGGAGAAGAACAGACAAATGGATTTTGTCACGGCACTAAAT GCAAGTGCGGGAAACCTTTGAGCTATTAA
ViScplp2	API81325.1	8 e-42	PF14866	8497.85	scorpine like	MNAKITVLFFLVAITIASC**AWISEKKIQDAIDKRLPNGA VKSAIKAVVHKAAKNKHGCLADFDVGGGCEQHCRK TEDKEGVCHGTKCKCGIPRAYRK***	ATGAACGCTAAAATAACTGTCCTATTTTTTCTGGTAGCCATTACAATT GCTTCTTGTGCCTGGATAAGCGAGAAAAAAATCCAAGATGCTATCGA TAAGAGGTTGCCAAACGGAGCTGTGAAAAGCGCAATCAAAGCCGTA GTACACAAAGCTGCCAAAAATAAGCATGGCTGTCTAGCTGATTTTGA TGTAGGAGGTGGATGCGAACAGCACTGCAGAAAAACTGAAGATAAA GAAGGAGTCTGCCACGGAACCAAGTGCAAATGCGGTATTCCCCGTGC ATATAGAAAA
TatKTxScr02	P0C8W5.1	2 e-49	PF14867	9228.06	scorpine like	MQIKFTILILLVISTFCSC**GLIREKYFHQGVDALTPLIPV PVVGGVVNKVAKQMIHKIGKIQSLCAFNKDMAGLC EKKCQETEKVKGYCHGTKCKCGKPLSYK***	ATGCAGATAAAATTTACCATTCTGATTTTTACTTGTGATTTCAACATTT TGTTCGTGTGGCTTAATCCGTGAGAAATATTTTCACCAAGGAGTGGA CGCTTTAACTCCATTAATACCAGTTCCTGTGGTTGGAGGAGTCGTAA ATAAAGTTGCAAAACAGATGATTCACAAAATCGGCAAAATTCAAAG CCTATGTGCTTTCAACAAAGACATGGCTGGTTTATGTGAGAAAAAT GTCAGGAAACAGAAAAGGTGAAAGGATACTGCCACGGTACTAAATG CAAGTGCGGGAAAGCCTTTGAGCTACAAA

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatKTxKap01	P0DJ41.1	5 e-24	N/D	3092.71	kappa toxin	MKLLSIVFVLVLVFALLPMEVSC*EPNAIENSRKNYEDISRNIVKR***SCKRVCSGSRRSKQCMQKCKPTPGR***	ATGAAACTGCTATCAATCGTGTTTGTGTTGGTGCTGGTTTTTGCTTTGCTTCCAATGGAAGTTTCCTGTGAACCCAATGCCATAGAGAATAGCAGAAAAAATTATGAAGACATTTCAAGAAATATTGTCAAAAGATCTTGCAAACGAGTATGTTCTGGAAGCAGGCGTTCCAAGCAGTGTATGCAGAAATGTAAACCGACTCCTGGTCGTTGAGAAACAAATTCGGTTCTAAGTTTGTATTCCAAT
TatKTxDel01	P0C8W3.1	1 e-39	PF00014	7457.59	delta toxin kunitz type	MIFAGCLLLILASNALLVTVAG**HHKKQVNCLLPPKAGPCKGSFARYYFDIESGSCKAFIYGGCDANSNNFAKRHHCEKRCRRFSVLGI***	CGCACAAAGAAAAAATTAATTATTACGGAAAAAATGATTTTCGCCGGCTGCCTTTTGTTGATTTTGGCTTCCAATGCCTTGTTAGTGACAGTGGCTGGGCACCACAAGAAACAAGTTAACTGCTTACTTCCACCTAAGGCAGGACCCTGCAAAGGTTCTTTTGCAAGATATTACTTTGATATAGAATCTGGAAGTTGTAAAGCGTTTATCTATGGAGGATGTGATGCAAATTCTAACAACTTCGCCAAAAGACACCACTGTGAAAAGCGTTGCCGAAGATTTTCCGTTCTTGGAATTAGAAAAAGCCAC
TatKTxDel02	ACV66786.1	3 e-16	PF00014	6537.68	delta toxin kunitz type	MASFLLFFLLIALVNS**EDDVCELPPETGPCKARMLMFYYNSTCKCCDDFTYGGCNGNGNRFLTVDECLYKCAED***	AGAATTTCTATATATTTAGAGAATAAGGCTATTAGTTATAAATTCCTCGTCGAAGAGATGGCCTCATTTTTGTTATTCTTTCTGCTTATAGCTTTAGTTAATTCGGAAGACGATGTCTGTGAACTTCCTCCAGAAACAGGACCTTGCAAGGCACGTATGCTAATGTTTTATTACAACTCTACATGCAAATGTTGCGATGACTTCACTTATGGAGGATGCAATGGAAATGGCAATAGATTCTTAACAGTAGATGAGTGCTTATATAAATGTGCAGAAGATTAG

Calcium toxins

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatCaTOme01	JAV47697.1	3 e-26	PF02819	6006.83	Agatoxin-like	MKLFVTTLFLCLLFLEISSFG**DEYTRTDLSPRKGCIRKYRSCDHNKSGCCDNASCKCNLFGSNCKCQRKGMFQG***	ATGAAACTCTTCGTTACAACATTGTTTCTGTGTTTATTGTTTCTCGAAATCAGCTCATTTGGGGATGAATACACGCGAACGGACTTATCACCACGAAAAGGTTGTATTCGAAAATACAGAAGCTGTGATCATAACAAGAGTGGATGCTGCGATAATGCCTCTTGTAAATGCAATCTATTTGGGAGCAACTGCAAGTGCCAGAGAAAGGGAATGTTCCAAGGT
TatCaTClc01	A0A1L4BJ42	2 e-26	PF08099	3788.48	Calcin-like	MKQNTMTIIFIVFIVTFASLTIYGAEA*SEANFLERR***ADCLAHLKLCKKNKDCCSKKCSRRGTNPEQRCR***	ATGAAGCAAAATACAATGACCATTATTTTTATTGTTTTCATTGTCACATTTGCTTCATTGACCATCTATGGTGCAGAAGCAAGTGAAGCCAACTTTTTGGAGAGAAGGGCAGATTGCTTAGCACATCTCAAACTCTGTAAAAAGAACAAGGATTGTTGCAGCAAGAAATGTTCCAGAAGAGGAACAAATCCTGAGCAGAGATGCAGA
TatCaTClc02	P60252.1	9 e-12	PF08099	4866.3	Calcin-like	MKAIIFLITFIMATTFVSCIKFYVNPYSSSSSDVDY*ADDDDQSND***DKESCAGYMEDCSKNSDCCSDRCRRKGTRSRKRCRSNPHDDD***	ATGAAGGCAATTATTTTTTCTGATCACCTTTATCATGGCTACAACATTTGTTTCCTGTATCAAGTTTTACGTAAATCCCTATAGTTCTTCGTCGACGTGGATTACGCAGATGATGACGATCAATCTAATGATGACAAAGAAAGCTGTGCAGGTTATATGGAGGATTGTAGCAAAAATAGCGACTGTTGCAGTGACAGATGTAGGAGAAAAGGGACGAGGTCAAGAAAACGATGTCGTTCAAATCCTCACGACGACGATTGA
TatCaTLio01	P0DJ08.1	7 e-32	N/D	4149.85	Liotoxin-like	MSFVAKISFLLLLVAVISTVT*GRDVTNLFESEKSDVER***DLPLSDEYQPCVRPRKCKPHLKCSKAQICVDPNKGW***	ATGAGCTTTGTAGCGAAAATATCCTTCCTTCTTTTGCTGGTAGCTGTGATCTCTACAGTCACAGGTAGAGATGTCACCAATTTATTTGAATCTGAGAAAAGTGACGTAGAAGAGACCTTCCTCTGAGTGACGAATATCAGCCATGCGTTCGCCCCAGAAAATGTAAACCTCACCTGAAATGCAGCAAGGCACAAATCTGCGTTGATCCTAACAAAGGATGG
TatCaTLio02	P0DJ08.1	4 e-32	N/D	4178.85	Liotoxin-like	MSPAAKISLLLLLIAVMSTVT*GGDVVNLFESEKSDVER***DLPLSDEYEPCVRPRKCKPHLKCSKAQICVDPNRGW***	ATGAGCCCTGCAGCGAAAATATCCCTCCTTCTGTTGCTGATAGCTGTGATGTCTACAGTTACAGGTGGAGATGTCGTCAATTTGTTTGAATCTGAGAAAAGTGACGTAGAAGAGACCTTCCTCTGAGTGACGAATATGAGCCGTGCGTTCGCCCCAGAAAATGTAAACCTCACCTGAAATGCAGCAAGGCACAAATCTGCGTTGATCCTAATAGAGGATGG
TatCaTLio03	P0DJ08.1	1 e-33	N/D	4149.85	Liotoxin-like	MSFVAKISFLLLLITVISTVT*GGDVLNLFESEESDTER***DLPLSDEYQPCVRPRKCKPHLKCSKAQICVDPNKGW***	ATGAGCTTCGTAGCAAAAATATCCTTCCTTCTGTTGCTGATAACTGTAATCTCTACAGTCACAGGTGGGGATGTCCTCAATTTGTTTGAATCTGAGGAAAGTGACACAGAAAGAGACCTTCCTCTGAGTGACGAATATCAGCCATGCGTTCGCCCCAGAAAATGTAAACCTCACCTGAAATGCAGCAAGGCACAAATCTGCGTTGATCCTAACAAAGGATGG

TatCaTLio04	P0DJ08.1	7 e-30	N/D	4143.81	Liotoxin-like	MSFVAKISFFLLLIAVISTVTG*RDVTNLFESEKSDVER*GFSLSDEYQPCVRPRKCKPHLKCSKAQICVDPNRGW*	ATGAGCTTTGTAGCGAAAATATCCTTCTTTCTTTTGCTGATAGCTGTGATCTCTACAGTCACAGGTAGAGATGTCACCAATTTATTTGAATCTGAGAAAAGTGACGTAGAAAGAGGCTTTTCTCTGAGTGACGAATACCAGCCTTGCGTTCGCCCCAGAAAATGTAAACCTCACCTGAAATGCAGCAAGGCACAAATCTGCGTTGATCCTAATAGAGGATGG

Host Defense Peptides (HDPs)

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatHDPDef01	KFM64187.1	2 e-12	PF01097	--	Defensin-like	ILCTFETAKAQFGFGCPLFPNDCNKHCQTLKYRGGYCTNFLERTCKCYG	ATCTTGTGCACCTTTGAAACTGCAAAAGCCCAATTTGGATTTGGATGTCCTTTGTTTCCAAACGATTGCAATAAACATTGTCAGACCTTGAAGTATAGAGGGGGATACTGTACAAACTTCTTGGAACGTACCTGCAAATGCTATGGA
TatHDPDef02	AIX87626.1	1 e-21	PF01097	4544.3	Defensin-like	MKFVAIMLIILVAFCILEDGLVEA**DYGCPFNPGKCHRSCIYLGYKEGRCKGTFKKNCACYRPKG***	ATGAAATTCGTAGCCATTATGTTAATCATCCTGGTTGCCTTCTGTATTTTGGAGGATGGACTTGTGGAAGCTGATTATGGATGTCCCTTTAATCCTGGAAAATGCCATAGAAGTTGTATATACCTTGGATACAAAGAAGGACGTTGTAAAGGAACGTTCAAGAAAAACTGTGCTTGCTATAGGCCTAAGGGTTGA
TatHDPDef03	AIX87626.1	3 e-23	PF01097	4099.64	Defensin-like	AFCILEDELVEA**GFGCPFNAGTCHNHCRSIGRRGGYCSGTFRTTCVCYKS***	GCCTTCTGTATTTTGGAGGATGAGCTTGTGGAAGCTGGTTTTGGATGTCCCTTTAATGCTGGAACATGCCATAATCATTGTAGGAGCATTGGACGCAGGAGGGGGTATTGCAGCGGAACCTTCAGGACAACCTGCGTTTGCTATAAGAGT
TatHDPDef04	AIX87626.1	1 e-17	PF01097	--	Defensin-like	AFCILEDGIVEA**EFGCPVDRKKCDRYCKSIGRSGGYCGGISGTTCICYES**	GCCTTCTGTATTTTGGAGGATGGGATTGTGGAAGCTGAATTTGGATGTCCGTGGATCGTAAAAAATGCGATAGATATTGTAAGAGCATTGGACGCAGTGGAGGGTATTGCGGCGGAATCTCCGGGACAACCTGTATTTGCTATGAGAGT
ViVlp1	AGK88593.1	5 e-33	PF08102	6158.03	NDBP-2	MNGKALLVVFLVTMLVMEPTEA**GIFSWVKKAWNSGVGKSLRKQAVKAAKNYVANKLGGTPEEAGAMPFDEFMDVLHYN***	ATGAACGGAAAAGCACTCCTCGTTGTTTTCTTGGTTACCATGCTTGTAATGGAGCCTACTGAAGCAGGAATTTTCTCATGGGTCAAGAAAGCATGGAACTCAGGTGTAGGCAAATCACTAAGAAAACAGGCTGTCAAAGCAGCGAAAAATTACGTAGCAAATAAACTTGGAGGAACGCCCGAGGAAGCTGGAGCAATGCCGTTCGATGAATTTATGGATGTGCTGCATTATAACTAA
TatHDPND201	F1AWB0.1	7 e-52	PF08102	6510.42	NDBP-2	MNAKTIFAIFLIGMLVTEQAEA**GIWSTIKKYASKAWNSDIGKSLRNKAAGAINKFVADKIGVTPSQAASMTLDQIVDAMYYD***	ATGAATGCAAAAACCATCTTCGCTATTTTCTTGATTGGGATGCTCGTGACTGAACAAGCAGAAGCAGGAATCTGGAGTACAATTAAGAAATATGCTTCAAAAGCATGGAATTCCGACATAGGCAAATCTCTAAGAAACAAGGCAGCTGGCGCTATCAACAAATTTGTGGCAGATAAAATAGGTGTAACACCCTCACAAGCAGCCTCTATGACCCTTGATCAAATAGTAGATGCTATGTATTACGATTAA
TatHDPND301	ALG64974.1	1 e-44	N/D	2070.59	NDBP-3	MKLVNLVPVFFVLIIVVDYCHS**LPFFLLSLVPTAISAIKKL***GKRNVESQRYVDLKRRDLDEDLQALQDLLDQLSED***	ATGAAGCTGGTTAATTTGGTTCCAGTTTTCTTTGTTCTGATAATAGTTGTTGATTACTGCCATTCTCTTCCTTTTTTCCTTCTGAGTCTCGTACCTACAGCAATCTCAGCAATCAAGAAACTTGGCAAACGAAACGTAGAATCCCAACGTTATGTGGATCTTAAGAGACGTGATCTAGATGAAGATCTGCAAGCTCTGCAGGATTTACTCGACCAGCTGTCTGAGGATTAG
ViAMP1	ALG64975.1	1 e-52	N/D	2509.97	NDBP-3	MQLRKALLVIFVAYLLVTDEAEA**FWGFLGKLAMKAIPSLIGGNKSSS***KRKREIEDLFDPYQKDLDLQRLDRFFSQFQ***	ATGCAGCTCAGAAAAGCACTGTTGGTAATCTTTGTGGCTTATCTCTTAGTGACCGATGAAGCAGAAGCTTTCTGGGGATTCCTGGGTAAACTTGCAATGAAGGCCATCCCATCGTTAATTGGAGGAAACAAAAGTTCATCAAAGAGAAAGCGTGAAATTGAAGATTTATTCGACCCATACCAAAAAGACTTAGATCTGCAACGGTTAGATCGTTTCTTCTCCCAGTTCCAGTAG
ViCT2	I0DEB3.1	1 e-32	N/D	1461.71	NDBP-4	MKTQLVVLIVALVFMQLFAQSHA**FWGAVWNAAKSIL***GKRGLRNLDDLDQFDDSFEPELSEADLKYLEDLLR***	ATGAAAACTCAGCTTGTAGTCCTGATCGTAGCTCTTGTATTCATGCAACTGTTTGCTCAGTCACATGCTTTCTGGGGTGCAGTTTGGAATGCAGCAAAGTCAATATTAGGGAAGAGAGGTCTCCGAAATTTGGATGATTTGGATCAATTTGATGATAGCTTTGAGCCTGAACTGTCAGAAGCTGATCTTAAATATTTGGAAGATCTGCTCCGATAG
ViCT7	I0DEB5.1	7 e-27	N/D	1503.77	NDBP-4	A**FLKGIIDTVSNWL***GKRSLKNLDQYNDLFDGEISDADINFLRNLMR*	GCATTTCTTAAGGGAATCATTGATACTGTGAGCAACTGGCTTGGGAAACGAAGTTTGAAGAATCTAGACCAATACAATGATTTATTCGATGGTGAAATATCCGATGCTGATATCAACTTTCTAAGGAATTTGATGCGATGA

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatHDPND401	I0DEB5.1	8 e-42	N/D	1487.87	NDBP-4	<u>MKTQIVILIVAVLFLQLVSQSDA</u>**FLKGIIDTVGKWL***G KRGLKNLDQYNDLFDGEISDADIKYLQDLMR**	ATGAAGACCCAAATTGTAATTTTGATAGTTGCAGTACTATTCCTTCAAT TGGTCTCCCAATCAGATGCATTTCTTAAGGGAATCATTGACACTGTGGG CAAGTGGCTTGGAAAACGAGGCCTTAAGAACCTAGATCAATACAATGA TCTTTTTGATGGAGAAATATCTGATGCTGATATCAAGTATTTGCAAGAT TTGATGCGCTGA
TatHDPND402	I0DEB5.1	2 e-41	N/D	1487.87	NDBP-4	<u>MKTQIVILIVAMLFLQLVSQSDA</u>**FLKGIIDTVGKWL***G KRGLKNLDQYNDLFDGEISDADIKYLQDLMR**	ATGAAGACCCAAATCGTGATTTTGATAGTGGCAATGTTATTCCTTCAAT TGGTTTCCCAATCAGATGCATTTCTTAAGGGAATCATTGACACTGTGGG CAAGTGGCTTGGAAAACGAGGCCTTAAGAACCTAGATCAATACAATGA TCTTTTTGATGGAGAAATATCTGATGCTGATATCAAGTATTTGCAAGAT TTGATGCGCTGA
TatHDPND403	I0DEB3.1	2 e-24	N/D	1475.83	NDBP-4	<u>MKNQFAVLLVALVLLQLFSQSEGS</u>**FWNTLLSVGKSL L***GKRGLRNFDFDQLDDTYEPELSEADLRYL**	ATGAAGAACCAATTTGCAGTTCTCCTCGTAGCTCTTGTTCTCTTACAACT GTTTTCTCAATCAGAAGGATCCTTCTGGAACACACTTCTAAGTGTTGGG AAGTCCTTACTGGGGAAGAGAGGTCTCAGAAATTTTGATTTTGATCAGC TGGATGACACCTATGAGCCCGAATTGTCAGAAGCTGATCTTAGGTACCT TCAAGACTTGCTACGT
TatHDPND404	I0DEB3.1	2 e-27	N/D	1313.81	NDBP-4	<u>MKNQFVILIIAVVLLQLISQSEALWG</u>**TLLGLGSTLLSK L***GKRGTQNLDQFDDIFEPELSEADLRYLQDLLR**	ATGAAGAACCAATTTGTCATCCTGATCATTGCCGTTGTACTCCTACAAT TGATTTCTCAGTCAGAAGCCCTCTGGGGTACACTTTTAGGTTTGGGGAG TACCTTACTGAGCAAATTAGGAAAGAGAGGTACCCAAAACTTGGATCA ATTCGATGATATCTTTGAGCCCGAATTGTCAGAAGCTGATCTTAGGTAT TTACAAGACCTTCTGCGA
TatHDPND405	I0DEB3.1	6 e-29	N/D	1283.8	NDBP-4	<u>MKTQFVILIIAVVLLQLISQSEALWG</u>**ALLGLGSTLLSK L***GKRGTQNLDQFDDIFEPELSEADLRYLQDLLR**	ATGAAGACCCAATTTGTCATCCTGATCATTGCCGTTGTACTCCTACAAT TGATTTCTCAATCAGAAGCCCTCTGGGGTGCACTTTTAGGTTTGGGAAG TACCTTACTGAGCAAATTAGGAAAGAGAGGTACCCAAAACTTGGATCA ATTCGATGATATCTTTGAGCCCGAATTGTCAGAAGCTGATCTTAGGTAT TTACAAGACCTTCTGCGATAA
TatHDPAni01	AOF40247.1	8 e-10	N/D	5893.99	Anionic peptide	<u>MVSRTLIFLMIVALLATTFTSSYG</u>**FPAQNMDDDDDSF DDLFDDYDDADDDSFDLDLDPADLAMLDMFANLF DSDSS**	ATGGTATCAAGGACTCTCATTTTTCTGATGATAGTGGCTCTGTTAGCAA CCACCTTTACTTCATCTTATGGCTTCCCAGCTCAAAATATGGATGATGA TGATGACTCGTTTGATGACTTGTTTGATGACTATGACGACGCCGATGAT GACTCCTTTGATCTAGACCTGGATCCTGCTGACCTAGCGATGCTGGACA TGTTTGCAAATCTATTTGACAGCGACAGTTCTTAA
TatHDPWap01	XP_015928629.1	7 e-47	PF00095	12082.96	Putative waprin-like	<u>MYAPQLFLLVAITVWGSAE</u>**GGSRPFPFGPRRRILPG QRASGCVDCATELKQCVQKCLQQHDCSEMDVKE GFCPAGSPRPEKCPVSAVLSVCENDTDCPGTKKCC ENGCSRICANALPVPSAIRQSKRTPKLG**	ATGTACGCTCCACAACTTTTTCTACTCGTAGCTATTACAGTATGGGGGT CGGCTGAGGGTGGCAGTCGCCCTTTTCCTTTCGGTCCAAGACGTAGGAT CCTACCTGGACAAAGAGCATCAGGATGCGTGGATTGCGCAACGGAATT AAAGCAGTGTGTCCAGAAATGTCTCCAGCAACATGACTGCTCAGAAAT GGACGTTAAAGAAGGCTTCTGCCCAGCTGGATCACCTAGACCAGAGAA ATGCCCAGTGAGTGCTGTTCTTTCAGTATGCGAAAACGACACCGACTGC CCAGGTACTAAGAAATGCTGCGAAAATGGATGCTCAAGGATCTGCGCA AATGCACTTCCGGTTCCATCAGCTATCCGACAGTCGAAGAGAACTCCA AAATTAGGT

<div align="center">**La1-like peptides**</div>

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
ViLa1lp1	AOF40216.1	3 e-43	PF15430	8728.18	Other	<u>MRHLCVVALFGCLSLCTLFSFSKG</u>**VGEICQVGSMSINV GKKMQDPKSCVIYECVEQNYRILLSKMSCSPQVPKR GCRNVPGPVDAPFPDCCPTSLCRGKQWDE**	ATGAGGCATTTGTGCGTAGTTGCTCTTTTTTGGTTGTTTATCATTATGC ACTCTTTTCTCTTTTTCAAAAGGAGTTGGAGAAATTTGCCAAGTGGG GAGCATGTCAATAAATGTTGGAAAAAAGATGCAAGATCCTAAAAGC TGCGTCATTTATGAATGTGTTGAGCAAAACTATAGAATACTTCTCAG TAAAATGAGTTGTTCTCCGCAAGTACCAAAACGTGGATGCAGAAATG TGCCTGGTCCAGTTGATGCTCCATTCCCTGACTGCTGTGTCCCACGTCTC TTTGCCGAGGAAAACAATGGGATGAATAA
TatOthLa101	AOF40202.1	3 e-43	PF15430	8260.58	Other	<u>MENKFTCLLLGSLLMFSFCSLSAG</u>**FGETCQAGGKYNV RVGQPIQDPNSCVLYKCLNYNRRYVLQTLSCATQTL KSGCRFAAAAPGTPFPNCCPMVICKGSG**	ATGGAGAACAAATTCACGTGTCTGTTATTGGGCAGTTTGCTAATGTTT TCTTTTTGTTCGTTATCTGCTGGATTTGGAGAAACCTGTCAAGCAGGG GGAAAGTATAATGTTCGGGTTGGTCAGCCGATACAAGATCCAAATTC ATGTGTTCTGTATAAAATGTCTTAATTATAACCGGAGATATGTGCTTCA AACATTAAGTTGCGCTACTCAGACATTGAAAAGTGGATGTCGTTTTG CTGCTGCAGCCCCAGGAACACCATTTCCTAACTGTTGTCCCATGGTG ATTTGCAAAGGAAGTGGTTAA
TatOthLa102	API81329.1	3 e-14	PF15430	--	Other	GEEKQHPNSCALYRCERYLSRIVLYKLICANQTMKSGC RLAAAAGRTPFPNC	GGGGAAGAAAAACAACATCCTAACTCATGTGCATTGTATAGATGCG AAAGATATCTTTCAAGGATTGTTCTTTATAAACTGATTTGCGCAAATC AGACAATGAAAAGTGGATGTCGACTTGCTGCTGCAGCTGGAAGAAC ACCATTTCCTAACTGT

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid Sequence	Nucleotide sequence
TatOthLa103	ADY39631.1	3 e-6	PF15430	8693.97	Other	<u>MNTTWIVVFVFLGLVLAATA</u>SHKDPYIRTCPIGDKDIS NGEEWADQKRCVKYKCQVRGPDAALLITRCPSVGV YPTDKCREVPGKGDFPTCCPKLQCD*	TGAGATATGAACACCACTTGGATCGTTGTCTTCGTTTTCCTTGGCTTG GTACTAGCTGCTACAGCCAGCCACAAAGATCCCTACATCAGAACTTG CCCGATTGGTGACAAGGATATTAGCAATGGAGAAGAATGGGCTGAT CAAAAACGCTGCGTGAAATATAAATGTCAAGTGCGTGGACCAGATG CTGCTCTGCTTATAACAAGATGCCCATCAGTTGGAGTATATCCAACA GACAAATGCAGAGAGGTTCCCGGAAAAGGTGACTTTCCCACTTGCTG TCCAAAACTGCAGTGCGACTGA
TatOthLa104	ADY39631.1	4 e-5	PF15430	8762.05	Other	<u>MNTTWIVVFVFLGLVLAATA</u>QHRDPYIRTCPIGDKDIS NGNEWADQKRCVKYKCQVRGPDASLLIIRCPSVGVY PTDKCREVPGKGDFPSCCPKLQCD*	ATGAACACCACTTGGATCGTTGTCTTCGTTTTCCTTGGCTTGGTACTA GCTGCTACAGCCCAGCACAGAGATCCTTACATCAGAACTTGCCCGAT TGGTGACAAGGATATTAGTAATGGGAATGAATGGGCTGATCAAAAA CGCTGCGTGAAATATAAATGTCAAGTGCGTGGACCAGATGCCTCTCT ACTTATAATAAGATGCCCATCAGTAGGAGTATATCCAACAGACAAAT GTAGAGAGGTTCCCGGTAAAGGTGATTTTCCCTCTTGCTGCCCAAAA CTGCAGTGCGACTAA
TatOthLa105	L0GCW8.1	2 e-24	PF15430	9112.04	Other	<u>MKVWNTILCIWLLVVLNVSFVVVEG</u>YTYVVVNQKEGA VVCTDELGVEHQPGDQWFNDENCEMLLCDNATENL VIGALGCGSVYAPDCELKRGSGSYPNCCPRPVCDGN DQ*	ATGAAAGTCTGGAATACAATATTATGTATTTGGTTGTTAGTTGTACTT AATGTTTCATTCGTAGTTGTTGAAGGTTATACGTATGTAGTGAATCAG AAGGAAGGAGCAGTGGTTTGTACCGACGAATTAGGTGTTGAACACC AACCAGGTGATCAGTGGTTCAATGATGAAAATTGCGAGATGTTGCTT TGTGATAATGCTACAGAAAATTTGGTTATTGGAGCATTAGGGTGCGG CAGTGTCTATGCCCCTGATTGTGAATTAAAGCGTGGTTCTGGTTCATA TCCTAACTGCTGTCCAAGACCTGTTTGTGATGGGAATGATCAGTAA
TatOthLa106	L0GCW8.1	4 e-22	PF15430	9101.01	Other	<u>MKVWNTILCIWLLVVLNVSFVVVEG</u>YTYVVVNQKEGA VVCTDELGVEHQPGDQWFNDENCEMLLCDNATENL VIGALGCGSVYAPDCELKRGSGSYPNCCLEPVCDGN DQ*	ATGAAAGTCTGGAATACAATATTATGTATTTGGTTGTTAGTTGTACTT AATGTTTCATTCGTAGTTGTTGAAGGTTATACGTATGTAGTGAATCAG AAGGAAGGAGCAGTGGTTTGTACCGACGAATTAGGTGTTGAACACC AACCAGGTGATCAGTGGTTCAATGATGAAAATTGCGAGATGTTGCTT TGTGATAATGCTACAGAAAATTTGGTTATTGGAGCATTAGGGTGCGG CAGTGTCTATGCCCCTGATTGTGAATTAAAGCGTGGTTCTGGTTCATA TCCTAACTGCTGTCTAGAACCTGTTTGTGATGGAAATGATCAGTAA

| | | | | Phospholipases | | | |

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid Sequence	Nucleotide sequence
TatEnzPA201	API81339.1	7 e-96	PF05826	21335.9	A2	<u>MEVAIILALISAALA</u>*ESIEKELYVNFEPLPGQRDGWPMTK AVRMQFMKRSENGR*TLRTFHGCQILQSLTDIAREVSILP KYAIRRISKQELESFQSRCEHVGEEERTIWGTKWCG AGNESSGYEDLGYFYNVDSCCRDHDHCDSIPSGGTK YSLKNEGKFTMMNCECEDAFAKCLDKVVEGTSWYD YLATLGLIKSFKGVYFNLYGNGCFHVKCNSGRSERR ALCANPTAEYTGESGFAKLLNG*	ATGGAAGTAGCTATTATTCTAGCACTGATCTCTGCGGCCTTAGCAGA GTCTATCGAGAAAGAGCTATATGTGAACTTCGAGCCATTGCCTGGCC AGCGCGATGGTTGGCCAATGACGAAAGCAGTCCGTATGCAGTTTATG AAAAGATCTGAAAATGGAAGAACACTCAGAACATTCCACGGATGCC AAATACTTCAATCACTAACTGACATCGCAAGAGAAGTTAGCATCTTG CCAAAGTATGCTATTAGAAGGATATCAAAACAAGAATTGGAATCATT CCAAAGTAGGTGCGAACACGTAGGAGAGGAAGAAAGGACTATATGG GGAACTAAGTGGTGCGGAGCAGGGAATGAATCAAGTGGCTATGAAG ATTTAGGATATTTTTATAATGTGGATAGCTGTTGCCGCGATCATGATC ACTGCGATAGTATTCCTTCAGGTGGAACAAAGTACAGTCTGAAGAAC GAAGGGAAATTTACAATGATGAATTGCGAATGCGAAGAGCGCGTTCG CTAAATGTCTGGATAAAGTTGTAGAAGGGACAAGTTGGTACGATTAT CTTGCTACCCTGGGATTGATTAAAAGTTTCAAAGGGGTTTATTTCAAT TTATATGGAAACGGATGTTTTCACGTAAAGTGCAACAGTGGACGATC AGAAAGAAGGGCATTATGTGCCAACCCAACTGCCGGAGTACACTGGC GAATCCGGATTTGCAAAATTACTTAACGGTTAG

TatEnzPA202	API81335.1	7 e-73	PF05826	22373	A2	<u>MTALFLTAFIALLATGRT</u>*RTVQRELYLNLESSPHQEDSWP SVRAIIVNSNERHEEGR***TFSKCRMLNSTKEAAREVSKFP QHLIKRVSKEEMDNLERRCSGPLETRGFTDNFAFKG TKWCGPGTMAENEDDLGPLEADKCCRAHDHCDSIE SGGFKYNLKNNAYRTLLNCECEEAFDRCLQATADRV EGTEKEETKMLRNYYFNILHVQCYRLYCRNGGPASE NNCTDKFGVWMENYYEENFERKDITFY***	AGTTTATATATGGACCATAACTGCTATACATGTATGACTGCGTTATTT CTTACCGCATTCATAGCGTTGTTAGCTACAGGCCGCACTCGCACTGTC CAAAGAGAACTCTATTTAAATCTGGAATCGTCACCTCATCAAGAAGA TTCGTGGCCATCTGTAAGAGCAATCATAGTTAATTCCAATGAGAGGC ACGAAGAAGGACGAACATTTTCTAAATGTAGGATGCTGAATTCCACG AAAGAAGCAGCTAGAGAAGTATCTAAATTTCCACAACATTTGATAAA AAGAGTTTCCAAAGAAGAAATGGACAACTTGGAGAGAAGATGCTCA GGGCCATTAGAAACAAGAGGATTTACTGACAATTTCGCATTCAAAGG AACAAAATGGTGTGGCCCTGGTACGATGGCAGAAAATGAAGACGAT CTTGGACCTTTAGAAGCAGATAAGTGCTGTCGCGCTCATGATCACTG TGACAGTATTGAATCAGGAGGATTTAAGTATAACCTGAAGAACAATG CGTACCGTACTTTGTTGAATTGTGAATGTGAAGAAGCTTTCGATCGTT GCTTGCAGGCGACTGCAGATAGGGTAGAAGGTACTGAGAAGAAGA AACTAAAATGCTTAGGAATTATTACTTTAATATTCTTCATGTTCAGTG TTACCGTTTGTATTGTCGAAATGGGGGACCTGCCAGCGAAAACAACT GTACAGACAAATTTGGTGTGTGGATGGAAAATTATTACGAGGAGAA CTTTGAAAGAAAAGATATTACATTCTAT
TatEnzPA203	Q3YAU5.1	2 e-20	PF05826	--	A2	WTFYSPYFVYMLSRSGTKWCGAGNEATDENDLGLLYN VDSCCRDHDHCDNIASGETKYGLRNNGKYTM	TGGACCTTTTATAGTCCATATTTTGTTTATATGCTTTCTCGCTCAGGA ACAAAGTGGTGCGGAGCTGGAAACGAAGCCACTGATGAGAATGATC TAGGGTTATTGTACAACGTTGACAGCTGTTGCCGTGACCACGATCAC TGTGATAATATTGCGTCGGGTGAAACAAAGTATGGTTTGAGAAACAA TGGGAAATATACAATG
TatEnzPA204	KFM56793.1	4 e-30	PF05826	--	A2	KKCRSLERKRRSLADLAKMVSLTTKRKATDFVPYGNW CGIGGSGKVMDPIDKCCQVHDNCYLKARDKGICKAIVS LYLGKYNWKMENGEIVCSIPEDANACDEASCLCDKEVA ICLAKNIDSYQKDHRYVRSLFKS	AAGAAATGCCGATCGTTAGAGAGGAAACGACGGAGTTTAGCAGATT TAGCAAAAATGGTTAGCTTAACTACCAAAAGGAAAGCAACAGATTTT GTGCCATATGGAAACTGGTGTGGTATTGGCGGTAGTGGTAAAGTCAT GGACCCTATTGATAAATGCTGCCAAGTGCATGATAATTGCTATTTGA AAGCACGCGATAAAGGGATATGCAAAGCTATTGTCAGTCTTTATCTC GGAAAATACAATTGGAAGATGGAAAATGGAGAAATTGTCTGCTCCA TACCAGAAGATGCGAATGCATGTGACGAAGCAAGTTGCCTCTGCGAT AAGGAAGTAGCAATATGTTTAGCAAAAAATATTGATAGCTATCAAA AAGACCATAGATACGTTAGATCATTGTTTAAGAGT
TatEnzPA205	KFM56793.1	5 e-31	PF05826	--	A2	SQFSGSSDMYFKVFFIIVILASVCYQVNECRSLERKRRSL ADLAKMVSLTTKRKATDFVPYGNWCGIGGSGKVMDPI DKCCQVHDNCYLKARDKGICKAIVSLYLGKYNWKMEN GEIVCSIPEDANACDEASCLCDKEVAICLAKNIDSYQKD HRYVRSLFKS	ATCACAATTCAGTGGGTCCAGCGATATGTATTTTAAAGTCTTTTTCAT TATTGTAATATTGGCCTCAGTATGCTACCAAGTTAACGAATGCCGAT CGTTAGAGAGGAAACGACGGAGTTTAGCAGATTTAGCAAAAATGGT TAGCTTAACTACCAAAAGGAAAGCAACAGATTTTGTGCCATATGGAA ACTGGTGTGGTATTGGCGGTAGTGGTAAAGTCATGGACCCTATTGAT AAATGCTGCCAAGTGCATGATAATTGCTATTTGAAAGCACGCGATAA AGGGATATGCAAAGCTATTGTCAGTCTTTATCTCGGAAAATACAATT GGAAGATGGAAAATGGAGAAATTGTCTGCTCCATACCAGAAGATGC GAATGCATGTGACGAAGCAAGTTGCCTCTGCGATAAGGAAGTAGCA ATATGTTTAGCAAAAAATATTGATAGCTATCAAAAAGACCATAGATA CGTTAGATCATTGTTTAAGAGT
TatEnzPA206	JAT91104.1	7 e-85	PF05826	--	A2	MSKQTAMKTLLATILATLSLVDGGIFDAVDDVLPITTTF YREKDGHRMVETIEVNTYVSGKKTVDCYMYGDNYIIN KMVELIPTSITKEVDKEEMSDLVNQCSDLLLNELNSGVF HFVKSPFDSIRKAFKSLLIFPGTKWCGAGNVADDYEDLG RAEDTDKCCRTHDHCDDTIPGFETKYGLKNKDFYTKST CDCDLTFHSCLYEGENLPSDLVGKVFFNILQTQCFKEDY PQVECLEKSGIPLIRESCQEYELDYNGTKKYQFFDAKSY ESKDNASILERILS	ATGTCAAAGCAAACGGCAATGAAGACTTTACTGGCAACAATTCTGGC AACACTTTCGTTAGTAGATGGTGGTATTTTCGATGCAGTAGACGATG TTCTTCCCATAACCACAACCTTTTATCGAGAGAAAGATGGCCATAGA ATGGTTGAAACAATCGAAGTTAATACCTACGTAAGCGGAAAGAAAA CTGTGGATTGTTACATGTATGGAGATAATTACATTATCAACAAGATG GTAGAATTGATTCCAACAAGCATTACCAAAGAAGTGGATAAGGAAG AAATGAGTGATTTGGTAAATCAATGCAGCGACCTGTTATTGAATGAA CTGAACAGTGGCGTATTCCATTTTGTTAAAAGTCCTTTTGACTCCATT AGGAAAGCCTTCAAATCACTGCTGATATTCCCTGGAACTAAGTGGTG TGGAGCAGGTAATGTTGCTGATGATTATGAAGATTTGGGACGTGCTG AAGACACCGACAAGTGTTGTAGAACACATGACCATTGCGATGACACT ATACCTGGATTTGAAACGAAATATGGTCTTAAAAAACAAGGATTTTTA TACAAAGAGCACCTGTGATTGTGATCTGACATTTCATTCGTGTTTATA TGAAGGAGAGAACCTGCCATCTGATTTAGTTGGTAAAGTATTTTTCA ACATCCTTCAAACACAATGCTTCAAAGAGGATTATCCACAGGTGGAA TGCTTAGAAAAAAGCGGGATACCATTAATCAGAGAAAGTTGTCAAG AATATGAACTGGATTACAATGGAACAAAGAAGTACCAATTCTTTGAT GCAAAAAGCTACGAATCTAAAGACAACGCCTCAATTCTTGAAAGAA TACTGTCT

TatEnzPA207	API81338.1	2 e-74	PF05826	--	A2	MQFIKRSEEGREFRRFHGCQILQSLNDIAREAYRTPRHSMKRISKEEMRSFESRCERIGVDERTVLGTKWCGAGNEATDENDLGLLYNVDSCCRDHDHCDNIASGETKYGLRNNGKYTMMNCKCEDKFSACLESVIEKTNFLDYLPTLAAIKGFKAIYFDLYGNGCFNLTCSSGRSER	ATGCAGTTTATAAAGAGATCAGAAGAAGGAAGAGAGTTCAGAAGATTCCATGGATGTCAGATACTTCAATCCTTAAATGACATTGCGAGAGAAGCATACAGAACCCCAAGCATTCTATGAAAAGAATATCAAAAGAGGAAATGAGGTCGTTTGAATCAAGATGTGAACGTATTGGAGTTGATGAAAGAACTGTACTTGGAACAAAGTGGTGCGGAGCTGGAAACGAAGCCACTGATGAGAATGATCTAGGGTTATTGTACAACGTTGACAGCTGTTGCCGTGACCACGATCACTGTGATAATATTGCGTCGGGTGAAACAAAGTATGGTTTGAGAAACAATGGGAAATATACAATGATGAATTGCAAATGTGAGGACAAGTTCTCTGCATGCTTGGAGTCAGTAATAGAAAAAACTAATTTTCTTGATTATCTTCCAACTTTGGCTGCAATTAAAGGTTTCAAAGCTATTTATTTCGATCTCTATGGTAACGGATGTTTTAATTTAACATGCAGCAGTGGGCGATCAGAGAGGTGA
TatEnzPA208	API81341.1	2 e-38	PF05826	--	A2	MLSRSGTKWCGAGNEATDENDLGLLYNVDSCCRDHDHCDNIASGETKYGLRNNGKYTMMNCKCEDKFSACLESVIEKTNFLDYLPTLAAIKGFKAIYFDLYGNGCFNLTCSSGRSER	ATGCTTTCTCGCTCAGGAACAAAGTGGTGCGGAGCTGGAAACGAAGCCACTGATGAGAATGATCTAGGGTTATTGTACAACGTTGACAGCTGTTGCCGTGACCACGATCACTGTGATAATATTGCGTCGGGTGAAACAAAGTATGGTTTGAGAAACAATGGGAAATATACAATGATGAATTGCAAATGTGAGGACAAGTTCTCTGCATGCTTGGAGTCAGTAATAGAAAAAACTAATTTTCTTGATTATCTTCCAACTTTGGCTGCAATTAAAGGTTTCAAAGCTATTTATTTCGATCTCTATGGTAACGGATGTTTTAATTTAACATGCAGCAGTGGGCGATCAGAGAGGTGA
TatEnzPA209	P0C8L9.1	1 e-82	PF05826	--	A2	MQFIKRSEEGREFRRFHGCQILQSLNDIAREAYRTPRHSMKRISKEEMRSFESRCERIGVDERTVLGTKWCGAGNEATDENDLGLLYNVDSCCRDHDHCDNIASGETKYGLRNNGKYTMMNCKCEDKFSACLESVIEKTNFLDYLPTLAAIKGFKAIYFDLYGNGCFNLTCSSGRSESNAKCPNPTAAYTGESGAAKLINYLSG	ATGCAGTTTATAAAGAGATCAGAAGAAGGAAGAGAGTTCAGAAGATTCCATGGATGTCAGATACTTCAATCCTTAAATGACATTGCGAGAGAAGCATACAGAACCCCAAGCATTCTATGAAAAGAATATCAAAAGAGGAAATGAGGTCGTTTGAATCAAGATGTGAACGTATTGGAGTTGATGAAAGAACTGTACTTGGAACAAAGTGGTGCGGAGCTGGAAACGAAGCCACTGATGAGAATGATCTAGGGTTATTGTACAACGTTGACAGCTGTTGCCGTGACCACGATCACTGTGATAATATTGCGTCGGGTGAAACAAAGTATGGTTTGAGAAACAATGGGAAATATACAATGATGAATTGCAAATGTGAGGACAAGTTCTCTGCATGCTTGGAGTCAGTAATAGAAAAAACTAATTTTCTTGATTATCTTCCAACTTTGGCTGCAATTAAAGGTTTCAAAGCTATTTATTTCGATCTCTATGGTAACGGATGTTTTAATTTAACATGCAGCAGTGGGCGATCAGAGAGCAACGCCAAATGCCCCAATCCAACAGCAGCATACACTGGTGAATCTGGAGCTGCAAAATTAATTAATTATCTTAGTGGTTAA
TatEnzPA210	JAT91104.1	7 e-94	PF05826	--	A2	MKVAAAVIFALTFVFAKCGIFDIADKLLPITTTFYREKDGHRMVETIEINTYIGGKKLVDCYLYGHVYIIDKMMEVVPPDIVKEVGKKKMSKLVNTCSDLHVTKLRKGIFDIIKSPFDFARKLFKSLLIFPGTKWCGAGDVADDYDDLGVYEDTDKCCRTHDHCNDSIVGFETKYDLKNKDFYTKSSCDCDLPFHECLYQKEAIHSDAVGHLFFNILQTQCFKEEYPIVKCLKKWGIPLIRESCQKYELDYNGTKKHQFFDAKMYKGKNESPFLKQLLSH	CATATCATCACTAGCATATATAGGGTGATTATATTGTTATTTTTATTGCAGCAGAAAATGAAGGTAGCAGCGGCTGTTATTTTCGCGTTAACTTTCGTTTTCGCGAAGTGTGGGATATTTGACATTGCGGACAAACTTCTCCCCATTACCACAACCTTCTATCGAGAGAAAGATGGACACAGAATGGTTGAAACTATCGAAATTAATACTTACATCGGTGGGAAGAAACTGGTTGATTGTTACTTGTATGGACATGTGTACATTATTGACAAAATGATGGAAGTGGTTCCTCCCGATATTGTAAAAGAAGTAGGTAAAAAGAAAATGAGTAAATTGGTCAATACGTGCAGCGATTTACACGTAACTAAACTCCGAAAGGGGATTTTTGACATTATTAAGAGCCCATTCGACTTTGCCAGGAAGCTTTTCAAATCGCTTCTTTATATTTCCTGGTACTAAGTGGTGTGGAGCAGGTGACGTAGCTGATGACTACGATGACCTTGGAGTATATGAAGACACTGATAAATGTTGTAGAACCCACGATCATTGCAACGATAGTATTGTTGGATTCGAAACCAAATATGATCTTAAGAATAAGGATTTTTATACAAAGAGCAGTTGTGACTGTGACTTGCCATTCCACGAATGCTTATATCAGAAAGAAGCGATACATTCAGACGCGGTTGGGCATCTATTTTTTAACATTCTGCAAACACAGTGTTTTAAAGAGGAGTATCCGATAGTAAAGTGTTTAAAGAAATGGGGGATACCACTAATAAGGGAATCTTGCCAGAAGTATGAGTTGGATTACAACGGGACGAAGAAACACCAGTTCTTCGATGCGAAGATGTATAAAGGGAAGAATGAATCTCCGTTTCTTAAGCAGTTATTGTCACAT

						Sequence (protein)	Sequence (DNA)
TatEnzPA211	JAT95961.1	8 e-39	PF05826	--	A2	IRYRLTLYTLWTPLNTTEMTYKGHQMLLLILTAFLSFVQ PLPSAVIELPHENKLTGYYQSEKNPYMLIIGQTGKVIHCH QYEDRNEAKRVLAALHLEDVERVTPQKMDDLLKFCTE EERIEHPKKDVKKVFIYPGTKWCGMGDDAANENELGK EKEADSCCRDHDHCKDSIPAFSIKHNLTNYSPFTKSHCS CDREFHLCLAKAGTEAAKIISGLYFNMLKMECFQTTNCS SSNETCVKTWQWTLSSSYI	TGCCACCATTTCCAACAGTCGTTCTTTAGTAGACTGCATTACATCCTT AAGGGCCCATCAGATGTTGCTTCTCATACTAACAGCTTTCTTATCATTT GTACAACCTTTGCCATCCGCTGTTATAGAATTACCGCACGAAAACAA GTTAACTGGATACTACCAAAGTGAAAAAAATCCTTATATGTTGATTA TTGGACAAACAGGAAAAGTAATACACTGCCATCAGTATGAAGACAG GAATGAGGCTAAAAGAGTGCTGGCAGCTTTGCATTTGGAAGATGTGG AAAGAGTAACACCTCAAAAAATGGACGATCTATTAAAGTTTTGTACT GAGGAAGAAACGTATAGAGCATCCTAAAAAAGATGTAAAGAAGGTAT TTATTTATCCAGGCACTAAATGGTGTGGAATGGGAGACGATGCAGCT AATGAAAATGAATTGGGTAAAGAGAAAGAAGCTGATTCTTGTTGTCG TGATCACGATCATTGTAAAGATTCAATCCCTGCATTCAGCATTAAAC ATAATCTAACGAACTATTCACCATTCACTAAGAGCCACTGCAGTTGT GACAGAGAATTTCATCTTTGTTTAGCCAAGGCAGGAACTGAGGCAGC TAAAATAATTTCAGGTTTATATTTCAATATGTTAAAAATGGAGTGTTT CCAAACGACAAACTGCAGCAGTTCCAACGAAACCTGTGTCAAAACTT GGCAATGGACTTTATCCAGCTCTTATATC
TatEnzPA212	JAT95961.1	8 e-39	PF05826	--	A2	IRYRLTLYTLWTPLNTTEMTYKGHQMLLLILTAFLSFVQ PLPSAVIELPHENKLTGYYQSEKNPYMLIIGQTGKVIHCH QYEDRNEAKRVLAALHLEDVERVTPQKMDDLLKFCTE EERIEHPKKDVKKVFIYPGTKWCGMGDDAANENELGK EKEADSCCRDHDHCKDSIPAFSIKHNLTNYSPFTKSHCS CDREFHLCLAKAGTEAAKIISGLYFNMLKMECFQTTNCS SSNETCVKTWQWTLSSSYI	ATACGCTACAGACTAACATTATACACATTATGGACTCCCCTGAATAC AACAGAGATGACCTACAAGGGCCATCAGATGTTGCTTCTCATACTAA CAGCTTTCTTATCATTTGTACAACCTTTGCCATCCGCTGTTATAGAAT TACCGCACGAAAACAAGTTAACTGGATACTACCAAAGTGAAAAAAA TCCTTATATGTTGATTATTGGACAAACAGGAAAAGTAATACACTGCC ATCAGTATGAAGACAGGAATGAGGCTAAAAGAGTGCTGGCAGCTTT GCATTTGGAAGATGTGGAAAGAGTAACACCTCAAAAAATGGACGAT CTATTAAAGTTTTGTACTGAGGAAGAACGTATAGAGCATCCTAAAAA AGATGTAAAGAAGGTATTTATTTATCCAGGCACTAAATGGTGTGGAA TGGGAGACGATGCAGCTAATGAAAATGAATTGGGTAAAGAGAAAGA AGCTGATTCTTGTTGTCGTGATCACGATCATTGTAAAGATTCAATCCC TGCATTCAGCATTAAACATAATCTAACGAACTATTCACCATTCACTA AGAGCCACTGCAGTTGTGACAGAGAATTTCATCTTTGTTTAGCCAAG GCAGGAACTGAGGCAGCTAAAATAATTTCAGGTTTATATTTCAATAT GTTAAAAATGGAGTGTTTCCAAACGACAAACTGCAGCAGTTCCAACG AAACCTGTGTCAAAACTTGGCAATGGACTTTATCCAGCTCTTATATC
TatEnzPA213	API81335.1	4 e-76	PF05826	23742.5	A2	<u>MYLAAFITILSLSCSYA</u>**AERELHVNFDPWPVARAAIVN FDYNSETRREFSDCRMITSLDEITREGLDLPEHLIKRV SKEEMDALEKRCSGSAEMERFGMIYPGTKWCGPGNI SSSYSDLGELEADKCCRDHDHCDSIPAGQTKYGLSNT GEYTLMNCDCEKAFDSCLGDAADKEYLWNSMRTKT LRWTYFSAYSPKCYSVSCSAKRLDMEARCANGIGEW KSSYNV**	ATGTATCTCGCTGCATTTATAACAATTCTATCATTGTCCTGCTCTTAT GCTGCCGAAAGAGAACTCCATGTAAATTTTGACCCTTGGCCCGTAGC AAGAGCCGCTATTGTGAATTTTGATTACAACTCTGAAACGAGAAGAG AATTTTCTGACTGCCGCATGATTACTTCGCTGGATGAGATCACTAGA GAAGGTCTGGATTTACCAGAACATTTGATAAAAAGGGTTTCAAAAGA AGAAATGGATGCCTTAGAGAAAAGATGCTCAGGTTCTGCAGAAATG GAACGATTTGGAATGATATATCCTGGAACAAAATGGTGCGGACCTGG AAACATTTCAAGCAGTTATTCTGATCTAGGAGAACTAGAAGCAGACA AATGTTGCCGTGATCACGACCACTGTGACAGCATTCCAGCTGGTCAA ACTAAATATGGTCTTTCAAATACTGGCGAATATACATTAATGAACTG CGACTGTGAAAAAGCCTTTGACTCCTGTTTGGGAGATGCTGCTGATA AAGAATATTTATGGAATAGTATGAGGACTAAAACCTTAAGGTGGAC GTACTTCAGCGCTTATTCACCGAAATGTTACTCTGTTAGTTGCTCCGC AAAGAGATTAGATATGGAGGCAAGATGTGCGAATGGGATTGGTGAA TGGAAGAGTAGTTACAACGTATAG

TatEnzPA214	XP_015925461.1	7 e-51	PF05826	--	A2	MMMTPLNLVLAMLSVVARSVSNEANGRFELTTTFYIEK DGHRMVEMVEGARYKGRSENVACYVYGDRYTIDRMM KFVEKNSMKDVTRAEMRELLNQCSSLNQPEKEEFRRM KNPINYIKNITDKFGIFPGTKWCGSGNIAENDDDLGSSVE TDKCCRAHDKCNDSIPANGTKHGLKNDGSYTKSNCNC DEEFYSCLKRVDDKTSTAVGTTYFDILRTQCFKYEYPIIK CEKTCSILRRNCENYELNYNATKKYQFFDARCFL	ATGATGATGACACCACTGAATCTGGTCTTGGCAATGTTGTCTGTAGT AGCGAGAAGTGTTTCTAACGAAGCTAATGGTAGGTTTGAATTAACCA CAACCTTCTATATAGAAAAGGATGGCCACAGAATGGTAGAAATGGT CGAAGGTGCTAGATACAAGGGCAGAAGTGAAAACGTTGCTTGCTAC GTTTATGGAGACAGATACACTATTGACAGAATGATGAAGTTTGTTGA AAAAAATTCCATGAAGGATGTAACCAGAGCAGAAATGAGAGAATTG CTGAATCAATGTAGTTCATTGAACCAACCGGAAAAAGAAGAATTTCG CAGAATGAAAAATCCCATTAATTATATTAAGAATATTACTGATAAAT TTGGAATCTTTCCTGGTACTAAATGGTGCGGATCTGGGAATATAGCT GAGAATGACGACGATTTGGGCAGTTCAGTAGAAACAGACAAATGCT GTAGGGCTCATGACAAATGTAATGATTCTATACCTGCCAATGGAACA AAACATGGCCTTAAAAATGATGGATCTTATACTAAGAGTAATTGTAA TTGCGATGAAGAGTTTTACTCCTGCTTGAAAAGGGTGGACGATAAAA CGTCTACAGCTGTCGGTACAACATATTTCGATATCTTGAGGACACAG TGCTTCAAATACGAATACCCCATAATTAAATGCGAGAAGACGTGTAG CATACTTAGAAGAAACTGCGAGAACTATGAGCTGAATTACAATGCA ACGAAGAAATACCAATTTTTTGACGCTAGATGCTTTTTATAA
TatEnzPA215	API81335.1	2 e-88	PF05826	--	A2	MYLAVFTALLSLCCSRAAQRELYINFEPLPGQRDSWPIA RAAIVNFEEKSEMGREFSGCRMISSVDELAREGTDLPEH LIKRASKEEMDALQERCSGSAEMERFTMIYPGTKWCGP GNKAKNESDLGSLEADKCCRAHDHCDNIGAGKSKYGL TNTGSFTLLNCDCENTFDRCLSDAAEKEGWFKKQGTKA LRWTYFTAYSPKCYSLSCNKKRSILEARCANPVGKWKE NYKL	TGGATTTTGCAAGCACATCTTGGAACGCATCCATCTTTGAAGGGAAC AGACTTTCCAGTCAATATGTATCTCGCAGTATTTACAGCACTTTTGTC TTTGTGCTGCTCTCGTGCTGCTCAAAGAGAACTCTACATAAATTTTGA ACCACTACCTGGTCAAAGAGATTCTTGGCCCATAGCAAGAGCCGCCA TTGTGAACTTTGAGGAAAAATCCGAAATGGGAAGAGAATTTTCTGGA TGTCGCATGATCAGTTCTGTAGATGAACTGGCTAGAGAAGGAACGGA TTTGCCGGAGCATCTGATTAAAAGAGCTTCCAAAGAAGAAATGGATG CTTTACAGGAAAGATGCTCGGGTTCTGCAGAAATGGAACGCTTCACA ATGATATATCCCGGAACAAAAATGGTGTGGACCTGGTAACAAGGCGA AAAACGAATCTGACCTCGGTAGCTTGGAAGCAGATAAATGTTGCCGC GCTCACGACCACTGTGATAATATTGGAGCTGGTAAATCTAAATATGG CCTAACAAACACAGGAAGTTTTACATTATTGAACTGTGATTGCGAAA ATACATTTGACAGATGTTTGAGTGATGCTGCTGAAAAGGAAGGTTGG TTTAAAAAACAGGGCACAAAAGCATTGAGGTGGACGTATTTCACCGC TTATTCACCAAAATGCTATTCACTCAGTTGCAATAAAAAGAGATCTA TTCTGGAGGCTAGATGTGCTAATCCTGTCGGAAAGTGGAAGGAAAAC TATAAACTA
TatEnzPA216	XP_012232705.1	3 e-40	PF05826	--	A2	MVVMIESGRTETPFCFRYGDRRTFQEIVKLIPKDIVKEVS KEEMTELLNKCSEFSFNELENEAFRIQKRQIATYEEFLDL IKRILRFYSISESSIGTFLKSLADYISKNGVISPENPLLFPGT KWCGPGNRGENYNDLGIFSDTDACCRDHDNCNNSIKV GETKCNLTNNGLLTRMSCDCDDALYSCLKNSCNVISEL VGIMFFNVLRNKCFEEEYPQVRCKKPCSTLLFLENCNEY ELDTTKEKKCQFFDPRCYYASQNCLLSTPNGTSPTLLKIL LQLLGIN	ATGGTTGTAATGATTGAAAGTGGCAGAACCGAAACACCTTTTTGCTT TCGTTATGGCGATAGGCGTACATTTCAAGAAATTGTGAAGTTGATTC CAAAGGATATTGTAAAGGAAGTGAGCAAAGAAGAGATGACCGAATT ATTGAATAAATGTAGCGAATTTTCGTTCAACGAATTGGAAAATGAGG CTTTTCGCATCCAGAAAAGACAAATTGCTACCTACGAAGAGTTTTTG GATCTGATTAAACGTATTCTTCGTTTTTATTCGATTTCTGAGAGTTCA ATTGGAACGTTCCTGAAGAGTCTTGCCGACTACATTAGTAAAAATGG TGTTATTAGTCCTGAAAATCCTTTGCTGTTTCCTGGAACTAAATGGTG CGGACCTGGAAACAGAGGTGAAAATTACAACGATTTGGGGATTTTTA GTGACACAGATGCATGCTGTAGGGACCATGATAATTGCAATAACTCC ATAAAAGTAGGAGAAACGAAGTGCAATCTTACAAATAATGGACTTTT AACAAGGATGAGTTGTGATTGCGATGATGCGCTATACTCTTGTTTGA AAAACTCATGTAATGTGATATCTGAGCTTGTTGGAATAATGTTCTTCA ACGTTTTGAGAAACAAGTGCTTCGAAGAAGAATATCCACAAGTTAGG TGTAAGAAACCGTGTAGCACACTTCTGTTCCTGGAAAATTGCAATGA ATATGAATTGGATACTACTAAAGAAAAGAAATGCCAATTCTTTGATC CGAGATGCTACTATGCCTCTCAAAATTGTTTGCTTTCCACTCCCAATG GTACCTCACCAACCTTGTTGAAAAATATTGTTGCAACTATTAGGCATA AACTGA

TatEnzPhB01	XP_013790770.1	0	PF04916	61028.7	B-like 2	<u>MECYVIIFCLLPCLVMA</u>**LPPRNVSVSWDSIKGDFSIHDT VVKDWVAWASFSNEINSTGWSYLEVHTSEYYKDSYQ AYAAGLVEGYVTSDLIKKHWNNLYADYCDGEKAYC DRLQQFLKINLDFLNDQISNNRTNAYWHQVALVLEQ VKGLEDGYNNKPSFPTTRPSIFGPMFFNLFGDLEDLE AVLNKTVKKRVLGSGHCSGLIKLLPGYKDLYVAQDS WNTYNSMLRILKKYVMPLKSSTSTGSKRIAGSTMSFS SYPATIFSGDDFYIISSRLIALETTIGNSNSSLWKYVVP NKIVLEWIRNIVANRLARTGEAWTYLFSLYNSGTYNN QWMVVDYNRFFPGQSPRRGLLWVLEQLPGHIERKD QTHHLLKETYWPSYNSPFYPDIFNLSGTLDMVKKYG DWFTYDKTPRALIFKRDHKKVHDLASMMHLMRYND YKNDALSRCNCTPPYSAENAIAARSDLNPPNGTYPFPS LGHRSHGAIDMKLTNYSMHMKYQFVAYGGPTYDQQ PPFQWSKSDFGSEHHDGHPDLWKFKPVVHKWLSDN *****	ATGGAGTGCTATGTGATAATTTTCTGTCTTCTGCCATGTCTTGTAATG GCATTACCTCCAAGAAATGTATCAGTTTCATGGGATTCTATTAAAGG AGATTTCTCCATTCATGACACAGTTGTTAAGGACTGGGTAGCTTGGG CTAGTTTTTCTAATGAAATAAATAGTACTGGTTGGTCGTACTTAGAG GTTCACACAAGTGAATACTATAAGGATTCTTATCAAGCTTATGCTGC AGGGCTTGTTGAGGGATATGTAACATCTGATCTGATTAAAAAGCATT GGAACAATTTATATGCTGACTATTGTGATGGAGAAAAGCATATTGT GATAGGTTGCAACAGTTTTTGAAGATAAACCTGGATTTTCTGAATGA TAGTGTTGGAACAAGTAAAAGGGTTGGAAGATGGTTACAATAATAA ACCTTCCTTTCCTACCACAAGACCAAGCATCTTTGGACCAATGTTTTT TAATTTGTTTGGTGATTTGGAAGATTTAGAAGCTGTTCTTAACAAAAC AGTTAAAAAACGAGTATTAGGAAGTGGTCATTGCTCTGGATTAATCA AACTTTTACCTGGATACAAAGATTTTATATGTTGCTCAAGATTCATGG AATACATACAATTCTATGCTTCGTATTCTTAAAAAATATGTTATGCCA CTTAAGTCTTCTACATCTACAGGTAGCAAGAGAATAGCTGGCAGCAC AATGAGCTTTTCCTCTTATCCTGCCACAATATTTTCTGGTGATGATTT TTATATAATATCAAGTAGACTGATTGCTCTTGAGACAACAATTGGTA ATAGTAATTCAAGTCTTTGGAAGTATGTTGTGCCAAACAAAATTGTG TTAGAGTGGATTAGAAATATTGTTGCCAACAGACTAGCAAGGACAG GTGAAGCTTGGACATACTTGTTCAGTCTTTACAATAGTGGAACTTAC AACAACCAATGGATGGTTGTTGATTACAATAGGTTTTTTCCTGGTCA ATCTCCAAGGAGAGGTTTGCTTTGGGTTTTAGAACAATTACCGGGAC ATATTGAACGTAAGGATCAGACACATCACCTTCTAAAAGAAACATAT TGGCCATCATACAACAGTCCCTTTTATCCTGATATTTTCAATCTCAGT GGAACTTTGGACATGGTGAAAAAATATGGAGATTGGTTTACATATGA CAAAACTCCTCGTGCCCTCATTTTTAAAAGGGATCATAAAAAAGTGC ATGATTTGGCATCCATGATGCATCTGATGAGGTATAATGACTACAAA AATGATGCCCTCTCAAGATGCAACTGCACTCCACCATACAGTGCTGA AAATGCAATTGCTGCAAGGAGTGACCTCAATCCACCAAATGGAACTT ATCCATTTCCATCCTTGGGGCATCGTTCTCATGGAGCTATTGACATGA AGCTTACAAATTATTCCATGCATATGAAATACCAGTTTGTGGCATAT GGTGGACCTACTTATGACCAGCAACCACCCTTTCAGTGGAGCAAGTC TGATTTTGGTAGTGAACACCATGATGGTCATCCTGATCTATGGAAAT TCAAGCCTGTAGTTCATAAGTGGCTAAGTGACAAT
TatEnzPhD01	API81381.1	7 e-77	N/D	--	D	QLFHHVNDNAFLFSTGVISEGAKSQLWILLSLPYSTDSDF IIGFKQTLKVYGYQHMQHRVGWDMYGNERLDVIKKTY QKLGISTAVWQGDGINNCLPRSGRRLRKAIHKRDCDAE WTFLKKVYYWTVDKSSTMKEALRMGVDAILTNRPDKF YSALGDDEFSTTHRLATIRDNPWQKVRGSKRSVYC	CAGCTTTTTCACCATGTCAACGACAATGCTTTTCTATTTAGTACCGGC GTTATTTCAGAGGGAGCCAAGTCACAGTTATGGATACTGCTGTCTTT GCCATATAGCACCGACTCCGATTTTATAATAGGGTTTAAGCAGACAC TGAAAGTATATGGTTACCAACATATGCAGCACAGGGTTGGATGGGAT ATGTATGGAAATGAAAGATTAGATGTAATCAAGAAGACGTACCAAA AACTAGGAATTTCCACAGCAGTATGGCAGGGCGATGGGATCAACAA CTGCTTGCCTCGTTCCGGTAGGCGTTTGCGGAAAGCAATACACAAAA GAGATTGCGATGCAGAATGGACATTTCTCAAAAAGGTTTATTACTGG ACGGTAGACAAATCAAGTACCATGAAGGAAGCCCTAAGGATGGGAG TAGATGCAATCCTCACCAATCGCCCCGACAAGTTTTACTCGGCTCTA GGAGATGATGAATTTTCTACAACCCATCGATTGGCAACAATAAGAGA TAATCCATGGCAGAAAGTGCGAGGATCTAAAAGATCAGTATATTGC

TatEnzPhD02	API81381.1	0	N/D	--	D	MSTTMLFYLVPALFQILFSSAEVRPIWNIGHMVNSLSQID QFLNLGANALETDFTFNSDGVAEWTYHGYPCDCFRSCR RYATVEDYLRYVRELTSPDSPKFRSDFVLLQIDLKVSGL SDDATHNAGVDVAVKLIRYLWSGKGAKSQLWILLSFPY STDSDFVIGFMQTLRANGYQNMHQRVGWDMSGNESLD VIKKTYQRLGVSRAVWQSDGITNCLPRSIKRLLEAIHRR DWDAEWEFLDKVYYWTLDKSSSMKQALRIGVDAIITN HPDRFYSVLGDDEFSTTHRLATIRDNPWQKVRGAKRYL SQYTADVNYVFYECNLEEETEKEDIDE	ATGGTAAATTCACTCTCTCAAATTGATCAGTTCCTCAACCTAGGCGC AAATGCTTTGGAGACAGATTTCACATTTAACAGTGACGGAGTCGCTG AATGGACGTACCATGGGTATCCCTGTGACTGTTTTAGAAGCTGCAGG CGATACGCGCGACAGTTGAAGATTATCTTCGTTATGTTAGAGAACTGAC TTCTCCAGACAGTCCCAAATTCCGTAGTGACTTTGTTCTGTTACAAAT TGACCTGAAAGTCTCAGGATTGTCAGATGATGCGACACACAACGCTG GTGTAGATGTTGCTGTGAAACTTATTAGGTATTTGTGGAGCGGAAAG GGAGCCAAGTCACAATTGTGGATACTGCTGTCTTTTCCATATAGCAC AGATTCCGATTTCGTAATAGGGTTTATGCAGACACTGAGAGCAAATG GTTACCAAAATATGCACCAAAGGGTTGGATGGGATATGTCTGGCAAC GAAAGTTTAGATGTAATCAAGAAGACATATCAAAGATTAGGAGTTTC CAGAGCAGTATGGCAGAGCGATGGGATCACCAACTGTTTGCCACGTT CCATTAAACGTTTGCTAGAAGCAATACACAGAAGAGACTGGGATGC AGAATGGGAATTTCTGGACAAGGTTTATTACTGGACGTTAGATAAAT CGAGTTCCATGAAGCAAGCCCTAAGGATAGGAGTAGATGCAATCAT CACCAACCACCCTGACAGGTTTTACTCGGTTCTGGGAGATGACGAAT TTTCTACAACCCATCGGTTAGCAACTATAAGAGACAATCCATGGCAG AAGGTACGAGGAGCTAAAAGATATCTCAGCCAGTACACTGCTGATGT TAACTATGTATTTTATGAATGTAACCTTGAAGAAGAAACCGAGAAGG AAGATATAGATGAA
TatEnzPhD03	XP_002399661.1	7 e-78	N/D	--	D	KYLSQDLTYFIRYLKIIGVDKGISTFIMIENISLIIILLSSVV QVQGTEEDRRHPVYIIAHMANSIHEVDDYLRRGANAIE ADVTFTSKGEVDSIYHGYPCDCFRVCSRKEKFSKYISYIR NITTPGTKNYKENFTLLFLDLKVKNLIPQLKYAAGIKLT KALVKYLWNGGDNVTVINVLLSVGTTEDSQVIRAAKRT LQRDNLTYLLPRIGFDVGMNDHPLKISNMWKSLGMELN KWQGDGISNCVFPMRSTRRLDWLLRKQRDGESYMSKI YQWTVDFSVHFRRYLGSGVEAFITNYPERLSSLLQESKI RQFYRLATINDNIWERVPIYPSVVRAEVTDTPISSNVYTI GQEVMDSLATFFTDAFSNTINRGVINSEYLSLMNYFADT NNDRSEPEQPDPQDFCRYSLCLFYQLYSNQTASRRLQFV TDCMQRSDSPFMEISTICRSLDKLVHNLFVSNVTSVA	AAGTATCTGTCCCAAGATTTAACATACTTCATCAGATACCTGAAAAT AATTGGAGTGGACAAAGGTATAAGCACTTTCATTATGATTGAAAACA TTTCGTTAATCATCATTCTTCTGTCATCAGTTGTGCAGGTGCAGGGGA CAGAAGAAGATAGAAGGCATCCTGTTTACATCATTGCTCACATGGCG AACAGCATTCATGAAGTTGATGACTACCTACGTAGAGGAGCTAATGC TATCGAAGCAGATGTAACGTTTACTAGTAAAGGAGAGGTAGACTCA ATTTACCACGGATATCCTTGCGACTGCTTTCGTGTATGCTCGAGAAA AGAAAAATTCTCCAAATATATTTCTTACATTCGTAATATTACAACACC AGGTACTAAAAACTACAAGGAAAATTTTACACTATTATTTCTGGACC TAAAAGTAAAAAATTTGATTCCACAATTGAAATACGCTGCTGGAATA AAGCTCACTAAAGCGTTAGTAAAATATCTATGGAATGGTGGCGATAA CGTCACTGTGATAAATGTTCTGTTATCCGTTGGTACCACGGAAGATA GTCAAGTAATAAGAGCTGCAAAACGCACTCTTCAACGAGATAACTTA ACATATCTGCTTCCAAGAATAGGTTTCGATGTTGGGATGAACGATCA CCCACTTAAGATTTCCAACATGTGGAAGAGTTTAGGAATGGAGCTGA ACAAATGGCAAGGTGATGGAATAAGCAATTGTGTCTTTCCAATGAGA TCTACTAGGAGACTCGACTGGCTTCTAAGGAAACAAAGAGATGGAG AAAGTTACATGAGTAAAATATATCAATGGACAGTGGATTTCTCTGTA CATTTCAGAAGATACCTTGGGTCAGGTGTAGAAGCGTTCATCACCAA TTATCCTGAGAGATTAAGCAGTTTACTTCAAGAGTCGAAAATTCGTC AATTCTACAGACTAGCAACAATAAATGATAATATCTGGGAACGCGTG CCAATTTACCCCTCTGTTGTCAGAGCTGAAGTAACCGATACACCAAT CTCTTCTAACGTTTATACAATTGGACAAGAAGTTATGGACTCCTTAGC AACCTTCTTTACCGATGCCTTTAGTAACACCATTAATCGAGGGGTTAT CAACTCAGAATATCTTTCATTGATGAATTACTTCGCGGACACTAACA ATGACAGATCAGAACCTGAGCAACCAGATCCTCAAGACTTTTGTCGG TATTCATTGTGCCTCTTTTACCAACTATATAGTAATCAAACTGCATCA CGCCGCTTGCAGTTTGTCACTGACTGTATGCAAAGAAGCGATTCACC ATTTATGGAAATTTCGACCATATGTAGGTCTCTAGACAAACTAGTAC ATAATTTATTTGTATCTAATGTGACTTCAGTTGCA

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatEnzPhD04	XP_015792031.1	1 e-77	N/D	--	D	KYLSQDLTYFIRYLKIIGVDKGISTFIMIENISLIIILLSSVV QVQGTEEDRRHPVYIIAHMANSIHEVDDYLRRGANAIE ADVTFTSKGEVDSIYHGYPCDCFRVCSRKEKFSKYISYIR NITTPGTKNYKENFTLLFLDLKVKNLIPQLKYAAGIKLT KALVKYLWNGGDNVTINVLLSVGTTEDSQVIRAAKRT LQRDNLTYLLPRIGFDVGMNDHPLKISNMWKSLGMELN KWQGDGISNCVFPMRSTRRLDWLLRKQRDGESYMSKI YQWTVDFSVHFRRYLGSGVEAFITNYPERLISVLQEKNI RQHYRLATANDNPWETVPNYPTVISDQTANQPISSNVYS IAQEAVESLMMFVGNVFNININRRISNSDIFTTIDYLVNG YRSESELTEPEIFCQYALCTLYEIYSNQTIAYRFKLESKC MQKSGTPGVEISTICKSLHKMVSPWPII	AAGTATCTGTCCCAAGATTTAACATACTTCATCAGATACCTGAAAAT AATTGGAGTGGACAAAGGTATAAGCACTTTCATTATGATTGAAAACA TTTCGTTAATCATCATTCTTCTGTCATCAGTTGTGCAGGTGCAGGGGA CAGAAGAAGATAGAAGGCATCCTGTTTACATCATTGCTCACATGGCG AACAGCATTCATGAAGTTGATGACTACCTACGTAGAGGAGCTAATGC TATCGAAGCAGATGTAACGTTTACTAGTAAAGGAGAGGTAGACTCA ATTTACCACGGATATCCTTGCGACTGCTTTCGTGTATGCTCGAGAAA AGAAAAATTCTCCAAATATATTTCTTACATTCGTAATATTACAACACC AGGTACTAAAAACTACAAGGAAAATTTTACACTATTATTTCTGGACC TAAAAGTAAAAAATTTGATTCCACAATTGAAATACGCTGCTGGAATA AAGCTCACTAAAGCGTTAGTAAAATATCTATGGAATGGTGGCGATAA CGTCACTGTGATAAATGTTCTGTTATCCGTTGGTACCACGGAAGATA GTCAAGTAATAAGAGCTGCAAAACGCACTCTTCAACGAGATAACTTA ACATATCTGCTTCCAAGAATAGGTTTCGATGTTGGGATGAACGATCA CCCACTTAAGATTTCCAACATGTGGAAGAGTTTAGGAATGGAGCTGA ACAAATGGCAAGGTGATGGAATAAGCAATTGTGTCTTTCCAATGAGA TCTACTAGGAGACTCGACTGGCTTCTAAGGAAACAAAGAGATGGAG AAAGTTACATGAGTAAAATATATCAATGGACAGTGGATTTCTCTGTA CATTTCAGAAGATACCTTGGGTCTGGCGTGGAAGCCTTCATTACAAA TTACCCTGAGAGGTTAATCAGCGTACTCCAAGAAAAGAATATTCGTC AGCACTACCGGCTAGCGACAGCAAATGATAATCCCTGGGAAACAGT TCCGAATTATCCAACTGTTATTAGCGACCAAACAGCTAATCAGCCAA TCTCTAGCAATGTTTATAGTATTGCTCAAGAAGCCGTGGAATCTCTG ATGATGTTTGTTGGAAATGTTTTTAATATAAATATCAACAGAAGGAT CAGTAACTCGGATATTTTTACCACAATTGACTACTTAGTTAATGGATA TAGATCAGAGTCTGAATTAACGGAGCCTGAAATCTTCTGTCAGTATG CTCTATGCACTCTATACGAAATATATAGCAATCAGCTATAGCGTAT CGCTTCAAGCTTGAAAGTAAATGCATGCAGAAGAGTGGCACACCAG GTGTGGAAATATCGACGATATGTAAGTCTCTGCATAAAATGGTTTCT CCATGGCCCATTATC

<div align="center">

Hyaluronidases

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ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatEnzHya01	API81375.1	2 e-160	PF01630	--	Other	MSIFSTFIISIFAFSIVKANFEVFWNVPSLLCSIKFGVNLTQ TLLKYKILVNNGESFIGDKIALIYENGIGKYPHIDPKKGDI NGGIPQLDKLNEHLKLAENDIQKLIPNPDFNGLGIIDWEA WRPIWEYHWGSLGIYKNRTLEMVKKDHPTWSEQLVQS TAKNIWENSAKQWMLKTLELAKKLRPHGRWCYYLFPD CYNYFGKDQPSQFFCSAMIQNNNDRLSWMWDASTALC PSIYFIENQMKYNGSQRTWFLYGKLAEAVRVARPHTRIY PYINYMVHVSRIPVPEDHFWKMLSLIASLGLDGAIIWGS SSYLSDITSCQDLETYVNNVIGPAVTTVSSNVERCSQMV CNGRGKCTWPNDPFTSWKYLTDINSDFDSKEITCRCQT HKGRYCD	ATGTCCATATTTTCTACATTTATAATTTCTATTTTTGCATTTAGTATTG TCAAGGCCAATTTTGAAGTCTTCTGGAACGTACCTTCTTTGTTATGTT CGATTAAGTTCGGTGTAAATCTGACTCAAACTCTTTTGAAGTATAAA ATATTGGTGAACAACGGGGAAAGTTTTATTGGGGATAAAATAGCCTT AATTTATGAAAATGGAATTGGAAAGTATCCACACATAGATCCTAAGA AAGGTGACATCAATGGAGGAATTCCACAATTGGATAAATTGAATGA GCATTTAAAATTGGCAGAGAATGATATTCAGAAACTAATACCAAATC CCGACTTTAATGGTCTTGGAATTATCGACTGGGAAGCATGGCGTCCA ATCTGGGAGTATCATTGGGGATCGTTGGGCATTTACAAGAATAGGAC TTTGGAAATGGTGAAGAAAGATCATCCAACATGGTCTGAACAGCTCG TCCAAAGTACAGCCAAGAATATATGGGAGAACAGCGCTAAGCAATG GATGCTGAAAACGTTGGAACTTGCAAAGAAGTTACGTCCACATGGA AGATGGTGTTACTATCTTTTTCCCGACTGTTATAATTATTTTGGAAAG GATCAGCCATCTCAATTCTTTTGTAGTGCTATGATACAAAATAATAA CGATAGATTGTCTTGGATGTGGGACGCCAGTACTGCCCTCTGTCCAT CGATATATTTTATTGAAAATCAAATGAAAATATAATGGGAGTCAACGT ACGTGGTTTCTTTATGGAAAATTAGCTGAAGCTGTAAGAGTTGCTCG ACCGCACACAAGAATATACCCATATATTAACTATATGGTCCACGTTT CCCGGATTCCAGTTCCAGAGGACCATTTCTGGAAAATGCTGTCTCTT ATAGCATCCCTGGGATTAGATGGAGCAATTATATGGGGATCATCCAG CTATCTCTCAGACATAACCTCTTGCCAAGATCTTGAAACTTACGTTAA TAATGTGATTGGTCCTGCCGTAACTACAGTTTCATCGAATGTCGAAC GGTGTAGCCAAATGGTCTGCAATGGAAGAGGAAAATGTACATGGCC AAATGATCCGTTTACTTCGTGGAAATATTTAACTGACATAAATAGCG ATTTTGATTCCAAAGAAATTACATGCAGATGTCAAACCCATAAAGGA AGATATTGTGATTAA

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatEnzHya02	API81375.1	0	PF01630	--	Other	MNSRILIGIILNYIICVIEASFKIYWNVPSYMCSVRFGINV TETLINSNVMVNNKEEFLGEKLVIFYENRLGKYPYIDPK EGDINGGLPQLGNLEEHLEVAEKDIQEIIPNPNFDGLGIID WEKWRPIWDFNWGKMRIYKTRSMELMKKKHPSWPWK LIENASRKEWEETAMQWMLKTIQLTKKMRPKGRWCFY HLPDCYNYAGKDNPEQFLCSSLVRKHNDRLIWLWNSTT ALCPSIYYDERQMKYNETQDVWFLYGRLCEVMRVSQP NTPIYPYINYKVHTSLENVPKEHFWLMLSHLASLGLDGA VIWGSSNYVKTEEDCKSLELYVKEVIGPAAYTISTNVNY CSETVCNNNGLCTWPHQPYTSWKYLTDPNITVFNPENIT CRCQLYKGRYCDMFESNSTDLL	ATGAATTCGCGCATTTTGATAGGGATAATTTTAAACTATATTATCTGT GTGATCGAGGCATCTTTTAAAATCTACTGGAATGTTCCTTCTTATATG TGCTCAGTGAGATTTGGCATCAATGTTACAGAAACGCTGATAAATAG CAATGTGATGGTGAACAACAAAGAAGAATTTCTTGGTGAGAAGTTG GTGATTTTTTATGAAAATAGATTAGGAAAATATCCATATATTGATCC CAAAGAAGGTGATATTAATGGAGGGTTACCGCAGTTAGGAAATCTA GAAGAACATTTAGAAGTGGCAGAAAAGGATATTCAAGAAATAATTC CCAATCCAAATTTTGATGGACTTGGAATAATTGATTGGGAAAAATGG CGTCCGATTTGGGATTTCAATTGGGGAAAAATGAGAATTTACAAGAC AAGGTCGATGGAGCTAATGAAGAAGAAACATCCTTCTTGGCCATGG AAACTTATTGAGAATGCTTCTAGGAAAGAGTGGGAAGAAACAGCAA TGCAATGGATGTTGAAAACGATTCAACTTACAAAGAAAATGCGTCCT AAAGGAAGATGGTGCTTTTATCATTTGCCTGATTGTTACAATTATGCA GGAAAAGATAATCCAGAACAGTTCCTCTGCAGTTCATTGGTTAGAAA ACACAATGACAGATTGATTTGGCTGTGGAATTCAACAACGGCTCTTT GCCCATCAATATACTATGACGAACGTCAAATGAAATACAACGAAACT CAAGACGTTTGGTTCCTTTATGGCAGACTGTGTGAAGTTATGCGAGT TTCGCAACCAAACACACCTATATACCCTTACATCAATTACAAAGTAC ACACTTCTTTGGAAAATGTACCAAAGGAACATTTCTGGCTAATGTTG TCTCATTTAGCGTCACTTGGCTTAGATGGAGCTGTTATTTGGGGATCT TCCAATTACGTTAAAACAGAAGAGGATTGCAAAAGTCTTGAACTCTA TGTGAAAGAAGTGATTGGGCCTGCTGCATATACCATTTCTACCAATG TCAACTACTGCAGTGAAACAGTGTGCAACAATAATGGACTGTGCACA TGGCCTCATCAGCCTTATACTTCCTGGAAATACCTGACTGACCCAAA CATAACAGTATTCAATCCAGAAAATATCACGTGCAGGTGTCAATTGT ATAAAGGACGCTATTGTGATATGTTTGAATCAAATTCAACTGATTTA CTGTAA

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatEnzSeP01	AFS65328.1	6 e-156	PF00089	--	Trypsin-like	SENLKMCFKMNFSFVTIPLLLFILSRASAMSRHRRQNFIF PSEGENCRTPNEQPGFCIPLSRCEALRRSNDFNLLRNSIC GYDRDVPRVCCPSTNRVVTENPVVVDVSTSNPVPIEVTT RRTVPDGPVIVEVTPRPRTQSTNNNTTRQKPAILPDDCG RSTVSLPKIVNGIPAELAAWPWMAAVYVTRSGLTRGTD CGGALISPRHVMTAAHCVTDRRGNQMSASTFTVRLGEH ILNDDNDGASPVDIPVVRIVRHENFQRRVFRNDIAILTLQ RDVEFNRFIRPICLPYDRFSNDDLAPRGAFVAGWGTTVF DGEYSPILSQIQVPIWRNEDCHRVYQAERVPITREYLCA GVSDGSKDSCQGDSGGPLMLPSEENKFYLVGIVSFGKR CATVGYPGVYTRVNMFLDWIAANLT	TCAGAAAATTTAAAAATGTGTTTCAAAATGAACTTCAGTTTCGTTAC CATTCCACTACTACTGTTTATTTTAAGTCGAGCTTCAGCCATGTCAAG ACATCGAAGGCAAAATTTCATTTTTCCTAGTGAGGGTGAAAATTGTA GAACTCCAAATGAGCAACCAGGATTTTGTATTCCACTTAGCAGGTGT GAAGCATTAAGAAGAAGTAACGATTTTAATCTACTCAGGAACTCAAT TTGTGGATACGACAGAGACGTGCCAAGGGTATGTTGTCCTTCTACAA ATCGCGTTGTTACTGAAAATCCTGTTGTAGTTGATGTGTCAACTTCCA ATCCAGTACCTATTGAGGTAACAACTAGACGAACTGTTCCTGATGGT CCAGTAATTGTTGAAGTAACTCCTAGACCTAGAACTCAATCTACAAA TAATAATACTACAAGACAAAAACCAGCTATTCTTCCGGATGACTGTG GACGTTCAACCGTATCACTTCCAAAAATTGTCAATGGTATACCAGCA GAACTTGCAGCCTGGCCTTGGATGGCAGCTGTATATGTTACAAGAAG TGGACTCACTAGAGGTACTGACTGTGGAGGTGCATTAATCAGCCCTC GTCATGTAATGACAGCTGCGCACTGTGTTACAGATCGCCGTGGAAAT CAGATGAGTGCATCTACATTTACAGTCCGTCTAGGAGAACATATTTT GAATGATGATAATGATGGAGCTTCACCTGTAGACATCCCTGTTGTCA GAATAGTTCGCCATGAGAACTTTCAAAGACGGGTTTTCAGAAACGAT ATTGCAATATTAACGCTACAGAGAGATGTAGAGTTTAACAGGTTCAT ACGTCCAATCTGCCTACCATATGATAGATTCAGTAATGATGACTTAG CTCCAAGAGGTGCATTCGTTGCTGGATGGGGAACCACAGTTTTTGAT GGAGAATACAGTCCAATACTGTCACAGATACAGGTTCCAATATGGAG AAATGAAGATTGTCATCGTGTCTACCAAGCAGAAAGGGTACCAATCA CTCGAGAGTATCTATGTGCAGGTGTAAGTGATGGGAGTAAAGACTCA TGTCAGGGTGACTCTGGAGGTCCTTTGATGTTACCCTCTGAAGAGAA TAAATTTTACTTGGTGGGTATAGTTTCTTTTGGAAAACGTTGTGCAAC AGTTGGATACCCAGGAGTATATACCAGAGTTAATATGTTCTTAGATT GGATAGCAGCAAATCTGACA

TatEnzSeP02	JAT91153.1	3 e-94	PF00089	--	Serin protease	SRIVGGEESSPGSWPWLAALHGGPEEVFFCGGILISPWW VLSAAHCVGNQTNPSGWTMKLGMTRRTSAPFFVHKRG VSLIIKHPDFLSNPFFDDDLVLLMLDKPVNFDEFLRPICLP TLNLSLEGYDSCVVTGWGKAMYDDEADYQVVIHQVK VPIVEFEDCAKWYSLHQVNISEKMICAGYLEGEKDACQ GDSGG	TCGAGGATAGTGGGTGGGGAGGAATCATCTCCTGGTAGCTGGCCTTG GTTAGCTGCACTTCATGGTGGTCCAGAGGAAGTCTTCTTTTGTGGAG GAATATTAATTTCACCTTGGTGGGTGCTATCTGCTGCACATTGTGTGG GAAATCAAACAAATCCAAGCGGATGGACCATGAAACTTGGAATGAC CAGAAGAACTTCTGCACCCTTCTTCGTTCACAAGAGAGGAGTTTCTC TAATTATCAAACATCCTGATTTTCTCTCAAACCCATTCTTTGATGACG ATTTGGTTTTGTTAATGTTGGATAAGCCAGTTAACTTTGACGAGTTCT TGAGGCCCATATGTCTACCAACTTTGAACTTATCTCTCGAAGGCTAC GATTCCTGTGTTGTGACTGGTTGGGGAAAAGCTATGTATGATGATGA AGCAGATTATCAAGTTGTCATTCATCAAGTAAAAGTGCCAATTGTTG AATTCGAAGATTGTGCTAAGTGGTATTCCTTACATCAAGTGAATATA TCAGAGAAGATGATTTGTGCTGGATATCTTGAAGGTGAAAAAGATGC CTGCCAGGGTGATAGCGGAGGG
TatEnzSeP03	XP_015906323.1	1 e-55	PF00089	--	Trypsin-like	AAHCVYRTATSGLRVRVGEHNIKQTSEPYPHEEYPVRR KIVNPGYHPATYKDDIALLELSHPVIYRKHVIPACLPEKG EDFAGNVASVTGWGRLQYGNRNAPSILQRVEVKVFNL DECREMYKKIGRRETIYSTM	GCAGCTCATTGTGTATATAGAACCGCCACTTCTGGTCTTCGAGTAAG AGTGGGAGAACATAACATAAAGCAAACTAGCGAACCATATCCTCAT GAAGAGTATCCGGTGAGGCGAAAGATTGTTAATCCAGGTTATCATCC AGCAACATACAAGGACGATATCGCGTTACTTGAACTCAGCCATCCGG TGATTTACAGGAAGCACGTTATACCTGCTTGTTTGCCAGAAAAAGGA GAGGACTTTGCTGGTAATGTAGCGTCTGTTACTGGATGGGGTCGTTT ACAGTATGGTAACAGAAATGCACCTAGCATCTTACAAAGAGTTGAA GTGAAGGTCTTCAACCTCGATGAGTGCAGGGAGATGTACAAGAAGA TTGGAAGGCGTGAAACTATATATTCTACAATG
TatEnzSeP04	JAT91142.1	9 e-68	PF00089	--	Serin protease	LTAAHCFGENVGRFPSNYQVRAGGHTRTDGEYYAVEEI RKHPSYTSGRHYYDIAILKVNETFIFGDTVSPACLPSVDE SYSNSQVAAFGWGDTSFGGIPSDALQVIIINVLSNFRCDQ SYRTLSLSSFPSGITDDLLCAGLSQGGKDTCQGDSGGPL MIKDNSTSKWTVIGVVSFGYQCAVAGYPGVYTRVSSYL PWISENMIN	CTTACAGCGGCTCATTGTTTTGGCGAAAATGTAGGAAGATTCCCTTC CAATTACCAGGTAAGGGCAGGAGGTCATACGAGAACAGATGGAGAG TACTATGCTGTTGAAGAAATCAGGAAACATCCTTCATACACATCAGG ACGACATTATTACGATATTGCCATATTGAAAGTGAATGAAACTTTTA TTTTTGGTGATACAGTTTCCCCTGCTTGCTTACCTTCAGTGGACGAAA GTTACAGCAATAGTCAAGTAGCTGCGTTTGGATGGGGAGATACCTCC TTCGGTGGAATCCCAAGCGACGCCCTCCAAGTAATAATTATCAATGT TTTGAGTAATTTTCGTTGCGACCAATCTTACAGAACACTGAGCCTGTC TTCTTTTCCAAGCGGGATTACAGATGATTTGCTTTGTGCTGGGTTAAG TCAAGGTGGTAAAGATACTTGTCAGGGAGATTCCGGAGGACCTCTTA TGATTAAGGATAATTCAACTTCGAAATGGACAGTAATCGGTGTTGTA TCATTTGGATATCAGTGTGCTGTTGCTGGATACCCAGGAGTATATAC CAGGGTCTCCAGCTACCTTCCTTGGATTTCTGAAAAATATGATAAAC

| TatEnzSeP05 | XP_015907406.1 | 0 | PF00089 | -- | Trypsin-like | ASAKTLPAIFAFTIVIAYVILVVKASSLQRISENQDKLKLL KTLDSYNKNILQRQKRETECSANYTVGSKGGNLISPGYP KQYPESLHCQWRLKSSTSSNLILKFTDVSIEEAEDCGYD YLALYDETNNMVEKICGTHSNKVVVLNSTTANIVFHSD ETYTEKGFALEYFLEVTLDCKAILNDSEGTVTSPLYPDN YPGNTDCHTTIMVEPGAKISLKFDVLNLEFDENCDYDY VDIYDGETTDSPLLGHFCSNPEDAVVMSTNNTLMVHFH SDPLINYNGFSASYTSVFPGIQEIGNCVWEKGKNDGTITS PNYPERYPSNSNCRIKIQAAEGYVISIDIDSIKLEVDANCT YDRLEIRDGLNEDSPLLGYFCGQTNEMKHITSAQNGAYI IFVSDSFTEFDGFRIEYRIHRKESEIVSSEDGTVSPSTEIILP SQLFREQPQDFTAIEGEPHVMSCKPEDPNIEVQWTKDGL EIDLFLNIDLHDHGKILWIHSMSEELKGTYTCTAINPHGD SYSVHAILDMKEREWNCDIIFRHTPKNTSILEGDTKLIEC SLSSSKSAQITWTKNGLPLAKSNNYQQIPNGFLLITDATL EMSGIYSCVAEEKSGCVRQHSASIQVSPRISIMNICGRPV MGKPSKRKPQMSHGRILGGKNAKKGAYPWQVIIRNFK HQTACGGTLVNEHWVVTAAHCLYIPKTNHRVEASAFT VKLGEYDVEKKEPEEVLTGMEEYFVHPEFHRATFDNDI AMVKLLDSIQFTDYISPVCLGDHRFIRGVLFEKDLPMGT VTGWGRITESGPTPQFLQELRMPVVDFETCQQSTNYKV TENMFCAGYAQETARDACQGDSGGPFVMEHDDVWYL VGIVSWGEGCGKKGQYGFYTKVDNYHSWIKSIIN | GCAAGTGCCAAAACACTGCCAGCAATTTTCGCTTTTACTATCGTAATT GCCTACGTTATACTGGTAGTTAAAGCTTCGTCGTTGCAAAGGATTTC AGAAAATCAAGATAAGTTAAAATTATTGAAGACCTTGGATAGTTACA ACAAAAATATACTACAACGACAAAAAAGAGAAACAGAATGCTCCGC CAACTATACTGTAGGTTCTAAAGGAGGGAAATTTGATCAGTCCTGGGT ATCCAAAACAATATCCTGAAAGTCTGCATTGTCAATGGCGACTGAAA TCCTCAACATCGTCAAATTTAATACTGAAGTTCACTGATGTGAGTAT AGAAGAAGCAGAAGATTGCGGATATGACTATCTGGCTCTCTACGATG AAACAAATAATATGGTTGAGAAAATATGCGGAACCCACAGTAACAA AGTTGTTGTTTTAAACTCAACAACTGCAAATATTGTCTTTCATTCTGA TGAAACTTACACAGAAAAAGGATTTGCTTTGGAATACTTTCTAGAAG TGACATTGGATTGTAAAGCAATTCTGAATGATAGTGAAGGAACTGTA ACAAGCCCACTTTACCCAGATAACTATCCTGGAAACACAGATTGCCA TACAACTATCATGGTTGAACCTGGTGCTAAGATAAGTCTGAAGTTTG ATGTCCTCAACCTAGAGTTTGATGAAAACTGCGATTATGATTATGTA GATATATATGATGGTGAAACAACAGATTCTCCCCTGTTAGGCCATTT CTGTTCAAATCCAGAAGATGCTGTGGTGATGTCAACCAATAATACTC TGATGGTTCATTTTCATTCTGACCCTTTGATAAACTATAATGGTTTCA GTGCATCATATACATCCGTTTTCCCTGGGATACAAGAAATAGGAAAT TGCGTATGGGAAAAAGGAAAGAATGATGGCACAATCACTAGCCCTA ACTATCCAGAAAGATATCCAAGCAACTCTAATTGCAGAATAAAAATC CAAGCAGCTGAAGGTTATGTTATAAGCATTGATATTGATAGTATAAA GCTCGAGGTTGATGCAAACTGCACCTATGACAGACTGGAAATAAGA GATGGGCTAAATGAAGATTCACCATTACTAGGATACTTCTGTGGACA AACAAACGAAATGAAACACATCACATCAGCACAAAATGGTGCCTAC ATTATTTTCGTCAGTGATAGTTTTACAGAATTCGATGGATTTCGTATT GAGTATCGTATACATCGAAAAGAAAGTGAAATTGTATCTTCAGAAGA TGGCACTGTATCTCCCTCTACTGAGATTATTTTGCCATCGCAGTTATT CAGGGAACAACCACAAGATTTTACTGCTATAGAAGGAGAACCTCAC GTTATGTCATGCAAACCAGAAGATCCTAACATCGAAGTGCAATGGAC AAAAGACGGGTTAGAAATAGATTTGTTTCTAAATATCGATTTGCATG ACCATGGAAAAATATTGTGGATACATTCTATGTCAGAAGAATTAAAA GGCACTTACACATGTACAGCAATCAACCCACATGGTGATTCATATTC AGTCCATGCAATACTTGACATGAAAGAACGAGAATGGAACTGTGAT ATAATTTTCAGGCATACTCCAAAGAATACCTCAATCTTAGAAGGAGA TACCAAGCTCATTGAATGCTCATTGTCAAGCTCAAAATCAGCACAGA TAACATGGACGAAAAACGGTCTTCCACTTGCAAAGAGCAACAATTAT CAGCAGATACCAAATGGATTTCTTCTGATAACAGATGCAACTTTGGA AATGAGTGGGATTTATTCTTGCGTGGCTGAAGAAAAAAGTGGATGTG TGAGACAGCACTCTGCATCGATACAAGTTTCCCCTAGGATCAGTATA ATGAATATTTGTGGCCGCCCTGTAATGGGAAAACCAAGCAAAAGAA AACCACAAATGTCTCATGGAAGGATTTTAGGTGGTAAAAATGCCAAG AAAGGAGCATATCCATGGCAGGTGATCATAAGAAACTTCAAACATC AAACGGCTTGTGGAGGCACACTAGTAAATGAGCATTGGGTGGTCAC AGCTGCACATTGTCTTTATATTCCCAAAACTAATCATCGAGTAGAGG CAAGTGCATTCACTGTCAAACTGGGAGAGTATGATGTGGAAAAGAA GGAACCTGAAGAAGTTTTAACTGGGATGGAGGAATATTTTGTTCATC CAGAATTTCATAGAGCTACATTTGACAATGATATTGCTATGGTCAAA CTGCTGGACAGCATTCAGTTTACTGACTATATTTCTCCAGTATGCCTA GGGGACCACAGATTCATACGAGGTGTACTTTTTGAGAAGGATTTACC CATGGGGACTGTAACAGGTTGGGGAAGGATAACAGAGTCTGGACCT ACTCCACAGTTTCTACAGGAATTACGAATGCCTGTGGTGGACTTTGA GACCTGCCAGCAGTCTACAAATTATAAGGTAACTGAAAATATGTTCT GTGCTGGATATGCTCAAGAAACTGCTCGTGATGCTTGCCAAGGTGAC AGTGGTGGACCATTTGTTATGGAGCATGATGATGTTTGGTATCTAGTT GGTATTGTAAGTTGGGGTGAAGGATGTGGAAAAAAGGGACAGTATG GTTTCTATACAAAAGTAGACAATTATCACTCATGGATTAAATCAATT ATTAAC |

TatEnzSeP06	JAT91140.1	4 e-120	PF00089	--	Trypsin-like	TVRFERVNYRMIVSLMLLFCGNVALSSWVDDYNNDPRP ICITDFDTNPLNSRIVGGSDAGAGTFPYAVAILMGSPGDS KFRTDNSFCGGTMITESHVLTAAHCLYKNQYLADYLWL NVNDYDTRDSTETRNHVSRVKSITIHPRYVDETFDNDIAI IELSNPVSRNEKDIRMAILPPMGRTLDIGIVCTVWGWGR TSYKGRRPTVMQKVDLPITSREACQEHLSHIITENMICA GGKEGEDACLGDSGGSLLSRDGNVYCLAGIVSFGKGCA MKDVSGVYTNVARYIDWIYENTRTAECKPRILQ	ACTGTTAGGTTTGAAAGAGTGAATTATAGAATGATAGTGTCATTAAT GTTATTGTTTTGCGGCAATGTTGCATTAAGCTCGTGGGTTGACGATTA TAATAACGATCCAAGACCTATCTGTATAACAGATTTCGATACAAATC CCTTGAATAGCCGAATTGTTGGAGGAAGCGACGCTGGTGCTGGAACC TTTCCTTATGCGGTTGCAATACTAATGGGTAGCCCGGGAGATAGTAA ATTTAGAACAGACAATTCGTTCTGTGGAGGAACGATGATCACTGAAT CTCACGTGCTGACAGCTGCTCATTGCTTGTACAAAAATCAATATTTA GCTGATTATTTATGGCTGAATGTGAACGATTATGATACCCGTGATTCT ACCGAAACTAGAAATCATGTGAGCCGAGTTAAAAGTATTACTATACA TCCTAGATATGTGGATGAGACCTTCGATAATGACATCGCAATAATTG AACTAAGTAATCCGGTATCACGCAACGAAAAGGATATAAGGATGGC AATTTTACCTCCTATGGGCAGGACTTTGGATATAGGAATTGTATGTA CAGTATGGGGATGGGGAAGAACTTCTTATAAGGGAAGAAGACCTAC AGTAATGCAAAAGTAGATCTTCCAATTACGAGTAGGGAGGCGTGC CAAGAACATCTCTCACATATTATTACCGAAAATATGATATGTGCTGG AGGAAAAGAAGGGGAGGACGCTTGCTTGGGTGATTCTGGTGGATCT CTTCTTTCTAGAGATGGAAATGTTTATTGCTTGGCTGGAATTGTGTCC TTTGGCAAAGGATGTGCAATGAAAGATGTATCAGGTGTATATACAAA TGTTGCTAGATATATTGACTGGATTTATGAAAACACAAGGACAGCAG AGTGTAAACCTCGAATACTCCAAT
TatEnzSeP07	JAT91142.1	1 e-83	PF00089	--	Serin protease	RNSWPWMVEIEKKVGPFVQHLCGGCIIGDRYILTAAHC FSQNAERSPSNYTVRTGGHTRTDGVRYTVEEIRRHPSYK AGIHYHDIAILKLKEVIQFYDKVSPACLPSNGDDYVNKR VAVIGWGDTSFGGIPSNVLQEVYINVVNNSLCDQSYRM LSLSSFPRGITQDLLCAGVSKGGKDACQGDSGGPLMIPD FSSLRWEVIGVVSFGYQCAVEGYPGIYTRISSYLPWIAEN MKQ	CGTAATTCCTGGCCATGGATGGTGGAAATTGAGAAGAAGGTTGGCCC ATTTGTTCAGCATCTATGTGGAGGTTGCATTATCGGTGATCGTTATAT TCTTACAGCGGCACACTGTTTTAGCCAAAACGCAGAGAGGTCCCCTT CTAATTATACCGTAAGGACGGGAGGACACACAAGAACAGATGGAGT GAGATATACAGTTGAGGAAATCAGGAGGCATCCTTCGTATAAAGCA GGAATACATTATCATGACATTGCGATATTGAAATTGAAGGAAGTCAT TCAGTTCTACGATAAAGTCTCTCCCGCTTGTTTGCCATCCAATGGTGA TGATTACGTCAATAAAAGAGTGGCTGTCATTGGATGGGGAGATACCT CTTTCGGTGGCATTCCAAGTAATGTTCTTCAAGAAGTTTATATCAACG TGGTCAATAATTCTCTTTGCGATCAATCCTATAGGATGCTAAGTCTGT CGTCATTTCCAAGAGGAATTACTCAGGATTTGCTTTGTGCTGGAGTA AGTAAAGGCGGTAAAGATGCTTGTCAGGGAGATTCTGGAGGTCCCCT GATGATTCCAGATTTCTCTTCATTAAGATGGGAGGTGATTGGGGTGG TGTCATTTGGATATCAATGCGCTGTTGAGGGATACCCAGGAATTTAT ACAAGGATCTCCAGCTACCTTCCTTGGATCGCTGAAAATATGAAGCA

TatEnzSeP08	JAT91148.1	0	PF00089	--	Serin protease	CFQEINFRSLRNRTLPISMKVIFSSMSVSLFPPSTLFTGIPG TDVVSLARLEDWTNSFIKCDRPHHKLDSWWCVWDTDT MRVIFALLVTVCFVSCQSPKEADYERPPKPVKPIGDYDG GDVGGPPPKINDYDEDGKVPLPNPGLKPDVPSDFNDPAP GGGGFDNKPSGDENCVCVPYYQCKEGEIVTDGTGIIDA RKKPPPEEELPLDSQFEPPFCGSFHVCCKTPQQDVVKPY EHKCGIRNPGGIFGKILAPDKKGEANFGEWPWQAAVLK VEGKVNIFQCGGVLVDKKHIATVAHCVCHYKGYNQYP LKVRLGEYDTQKTDEFLAHDDYNVERIFCHPQFRNNSL WNDMALLKLDRDVIFAPHIDSICLPTYEEVFEGQSCVVT GWGKDAYKGGSYSNIMKEVNIPVIDNAKCQEQLRKTRL GRYYRLHDSFICAGGEEGLDSCKGDGGGPLVCYRKDGS YALAGLVSWGIDCGQPGVPGVYVRVQKFLEWVTQQTG LQLNEYWPKVY
TatEnzSeP09	XP_002411811.1	7 e-43	PF00089	--	Trypsin-like	EGKTMSKCFFENQQCGRTVPAREIDEVLYRNDSTDLDR GSERLEINTDGTFVIQPRILIRERFRVLSGEWPWMIAIYLK SNGSFVCNGFIIDNSHLLTAAHCFHEKRRQLQDYYIGTIH NEEILNVEVTELHIHHHYKDNYYKDIALLKMSPRLTDV ASICMPSSVNESNYLLGKEITVLDWVGTEYVMQRNRIA ETQLCNQLYTNLTNSPFPNGIVDELICAIPVEKTDNVCLV HSGGPVMIEENGKWIAIGIATFGIPCTLPTYPAVYTRISPY LQWIRDNE

TatEnzSeP10	AFS65328.1	5 e-173	PF00089	--	Trypsin-like	KRGVVINMKYILAIIVVLFLVLIQAARETRKRRQIYFPDD EEEEGCRTPNERRGSCVPLNRCPALRRASIPYLRESICRY NRNTPLVCCPSSRPQEVTPRPVRPTRPTRPTRPTRPTRPP APPPTPRPRNPIVGPNSRKPSILPTECGKSTVPVSRIIGGR KSEVGAWPWMAAVYLTRTGLSRGTDCGGALVSNRHIIT AAHCVVDTRRGTVMSPSSFTVRLGEHTLNDDNDGASPI DFAVSNIVAHEDFERRTFKNDIAILTLRDRVQFNSFIRPIC LPYDSVSQQNLVSRSAFVVGWGTTAFDGNFNPVMSEIQI PIWENDECRRIYQREVPITREYLCAGVSDGSKDSCQGDS GGPLMLPTSDTRFFLVGVVSFGKRCATPGYPGVYTRVT MYLDWLAENLN	AAGCGCGGTGTTGTGATCAATATGAAGTATATTCTTGCCATTATTGTC GTATTATTTCTAGTCCTAATCCAAGCTGCCAGAGAAACAAGAAAACG CAGACAGATATATTTTCCTGATGACGAGGAAGAAGAAGGATGTAGA ACTCCAAACGAAAGGAGAGGATCTTGTGTCCCATTAAATAGATGTCC TGCCTTAAGAAGAGCCAGTATTCCGTATCTAAGAGAATCGATATGTC GGTATAATAGAAATACACCGTTAGTGTGCTGTCCATCATCTAGACCC CAAGAAGTCACCCCACGTCCTGTTAGACCGACAAGGCCTACCAGACC AACTAGGCCAACGAGGCCTACTCGACCCCCAGCACCCACCTCCCACAC CACGACCAAGGAATCCCATAGTAGGACCTAATAGTCGAAAGCCCTC AATTTTGCCAACAGAATGTGGAAAAAGCACGGTACCTGTTAGTAGAA TCATCGGAGGAAGGAAGTCAGAAGTAGGTGCTTGGCCTTGGATGGC GGCAGTTTATTTGACACGAACTGGTCTGAGCAGAGGAACCGATTGTG GAGGGGCGCTGGTTTCTAACAGACACATAATTACAGCCGCGCACTGT GTTGTTGACACCAGAAGAGGAACAGTAATGAGCCCTTCCAGCTTTAC AGTTAGATTGGGTGAACACACTTTGAATGATGACAATGATGGCGCCT CACCTATCGACTTTGCCGTAAGCAATATTGTAGCTCATGAAGATTTTG AAAGGAGGACATTCAAAAATGATATCGCTATACTGACTCTGAGGGAT AGGGTTCAGTTCAATTCTTTCATTCGTCCAATTTGTTTGCCTTATGAC AGTGTAAGCCAACAAAATTTAGTTTCAAGATCAGCATTCGTTGTTGG TTGGGCACTACAGCTTTTGATGGTAATTTTAACCCAGTTATGTCAGA AATCCAAATACCAATATGGGAGAATGATGAGTGTAGACGAATATAC CAACGAGAAGTTCCAATTACCAGAGAATACTTATGCGCGGGAGTCA GTGATGGTTCCAAGGATTCCTGTCAGGGTGATTCAGGAGGACCGTTG ATGTTACCTACAAGTGACACTAGGTTTTTCCTTGTAGGCGTTGTGTCA TTTGGAAAGCGCTGCGCAACTCCAGGATACCCAGGTGTTTATACTCG CGTTACTATGTACTTGGACTGGTTAGCAGAAAAATTTGAAT
TatEnzSeP11	XP_011185363.1	3 e-27	PF00089	--	Serin protease	LTMLRLLLLVLYFLSAIASPINDDEDSSRIWNGNIATQGQ FPFVASLQLVYPDGYHSHTCTVSLISTKSCLGAAHCVFR KDETVKGPDEFCVIVGSYVQNDKLPCQELKSLVYHEKF DHKDPIYDIALFELSNEIMLNDDIRTVKLAGPSIEVFGSIV TAIGWGRIVADRRSPHRLRYAFFDVVANSVCKDILNPE MKDDICIYSNEYSICPGDSGGPIVLEGSDIEIGLSSYGGKI CGKIPVAVYTDVRKYLDWIKEHAVGEIEIVEISDDNALY HQQS	TTGACCATGCTAAGGCTTCTGTTGCTAGTTCTATATTTCCTCTCCGCC ATAGCATCACCCATTAACGATGATGAAGATAGTTCAAGAATTTGGAA CGGAAATATTGCTACGCAAGGACAATTCCCTTTTGTGGCGTCTCTGC AGTTAGTTTACCCTGATGGGTACCACAGTCATACCTGTACAGTTTCGC TGATTTCAACAAAATCCTGTCTAGGAGCTGCTCACTGTGTCTTCCGGA AAGACGAAACTGTGAAAGGACCTGATGAATTTTGCGTAATCGTTGGT TCTTACGTGCAAAATGATAAACTTCCTTGTCAAGAACTTAAAAGCCT TGTTTACCATGAAAAGTTTGATCATAAGGATCCAATATATGACATTG CTTTGTTTGAGTTGTCAAATGAAATCATGCTTAATGATGACATAAGA ACAGTAAAGTTAGCTGGACCAAGCATAGAAGTTTTTGGAAGCATAGT AACAGCAATTGGTTGGGGAAGAATAGTAGCAGATAGACGTAGCCCA CATCGATTGAGATATGCTTTTTTCGATGTGGTAGCTAATTCCGTGTGC AAAGACATCCTTAATCCCGAAATGAAAGATGACATTTGTATTTACAG CAATGAGTACAGCATTTGCCCGGGTGATTCTGGAGGACCCATCGTTC TTGAGGGCAGCGACATAGAAATTGGTCTTTCATCTTATGGAGGAAAA ATTTGTGGTAAAATACCAGTAGCTGTATATACAGACGTCCGAAAATA TCTCGATTGGATTAAAGAACATGCTGTTGGAGAGATAGAAATCGTTG AGATATCGGATGATAATGCCTTGTATCACCAACAGTCC

| TatEnzSeP12 | XP_018529593.1 | 2 e-30 | PF00089 | -- | Serin protease | MTSSNSAFLLLLLVDYHLTSFSKDITDKFEVAETSRIIGG NQAKPKQFPYAVSIQEYNEDFQTYEHICTFSLITTQSVLG VAHCVVGQNNEILDVDDYIGVLGTVDQWNRTNSVTFD EFIVHRGYNIEYFSNDIAIFVLSESVKLGDSIQTIPLIGQGV SFIGKRGTTFGWGFIYPSATSSTRILRYVDVDIVENEECE QYYGFLDKGQFCFGTEGRSGCDGDSGAPIIVRYRKKEV QMGILSFNTDPCARDPSTGTNISSYNSWIRKNVVGKPVFI N | ATGACTTCTTCAAATTCAGCATTTCTCCTTTTGCTATTGGTTGATTATC ATTTGACTTCATTTTCCAAGGATATTACTGACAAATTTGAAGTTGCGG AAACGTCGAGGATCATTGGTGGAAATCAAGCAAAACCTAAGCAGTT CCCATATGCAGTGTCAATTCAAGAATACAATGAAGATTTCCAAACTT ACGAACACATCTGCACTTTTTCCTTGATTACAACTCAATCAGTTCTAG GGGTAGCGCATTGTGTAGTAGGACAGAATAATGAAATTTTAGATGTA GACGATTACATTGGAGTTTTAGGAACTGTGGATCAGTGGAACAGAAC CAACAGTGTAACTTTCGATGAATTCATTGTTCATCGTGGTTATAACAT CGAATACTTTTCGAATGACATTGCAATATTTGTACTTTCCGAATCGGT AAAACTGGGTGATTCTATTCAAACTATACCTTTGATTGGACAAGGTG TCTCGTTTATTGGAAAGCGAGGTACAACTTTCGGATGGGGTTTCATCT ACCCTTCAGCCACGAGTTCAACTCGTATATTGAGATACGTTGATGTT GATATTGTGGAAAATGAGGAATGTGAACAATATTATGGTTTCCTAGA TAAAGGTCAGTTTTGTTTCGGAACAGAAGGAAGAAGTGGTTGCGATG GAGATAGTGGCGCTCCAATCATAGTAAGATATCGGAAGAAGGAAGT ACAAATGGGTATTTTATCATTTAACACAGATCCTTGTGCAAGAGATC CAAGCACGGGTACAAATATCAGTTCTTATAATTCGTGGATTCGAAAG AATGTTGTGGGAAAGCCAGTTTTCATTAAT |

| TatEnzSeP13 | XP_019869370.1 | 0 | PF00089 | -- | Nudel-like | TLMREHQKTETPRLDNLAFVTTFPKDYLPYARQKRKSDPMESNPHWKYKRKRWWPFRRCCNLSSATTIISITVTILAFMAALGVSIYFGVLTSMYTSPVFHIYGKIRVTEGDEFDSSLLDANSANFASKAAIYENKLRSTYLRSLFQYVLHEVRIYGFREPGLNIFFRLHLDRRKGTRIQGINNLARTVLLNEIHNGEIFEGLKIDPESVSFSGISCLDDCPTQAPTNTTTPLLVSDWFNTIDVTTKKNEQDEAHFKRLNGTNNNETVVQWVTPSNTKITNVTILQIDANSTLLPWKNASEWDNTTVSAKYNDTGVTVSSPKFVSQFTNREENTLFHQENDKQNRNLSVIEDDLIVPVNETTLSSTTDLWNEFDVVNIKDGKNKIPECGKEGFRCADNKCIPGYRKCDRFSDCSDSSDEANCTCSDYLISLEQPRKICDGFMDCWDYSDETHCPWCSDDMFHCPGAKVCINKTKVCDGIRDCPSGSDEATCMKIAKDVSGANGFTFAKEGYLMIQREGQWKKLCLDNNNLIDKPRWNVEKLGYTVCSSLTYKALESIVLSPRKYQEDSYYELIPATERSGTKFLISDCADGKIARIRCRDLACGLGTPVQLPTKRIVGGDSVPMGARPWLAALYREGQFQCGAIVIADRWLLSAGHCFFHTKHSYWVARMGLLRRGTDMPTPYEIVKRIIQIKVNPQYINKNFINDIAVLKLESAVPFSNYIRPICLPQPEDDVVKWNGKKCSVVGWGKLGENGDEFPDTLQEVQLPVISTEECRKRTLFLSIYQITDNMFCAGYERGGRDACLGDSGGPMMCQKEDGRWVLIGIISNGDGCARPSRPGVYTKVGNFMNWIDSIMNENATDEVKPDSCLGTRCKLGMCLFPESNCDGNADCPDGSDEKGC | ACACTGATGAGGGAACACCAGAAGACAGAAACGCCACGCCTGGATAATTTAGCGTTTGTAACTACATTTCCGAAGGATTACCTACCGTACGCTCGACAGAAAAGAAAATCGGATCCGATGGAATCTAATCCTCATTGGAAATATAAGAGGAAACGATGGTGGCCTTTCAGAAGATGTTGCAATCTCTCCTCAGCGACTACAATTATTTCAATAACTGTTACCATTTTAGCATTTATGGCAGCTTTAGGTGTATCGATATATTTTGGCGTTTTAACCAGTATGTACACCTCTCCAGTCTTTCACATATACGGAAAAATACGGGTAACGGAGGGTGACGAATTTGACTCTTCCTTGTTAGATGCCAACTCTGCTAATTTTGCTAGCAAAGCAGCTATTTACGAAAACAAGCTTAGAAGCACGTATCTTAGAAGTTTATTTCAGTACGTATTACACGAAGTCAGGATTTACGGTTTTAGGGAACCTGGCTTGAATATTTTCTTCAGACTTCATTTAGACAGAAGAAAAGGTACCCGGATACAAGGTATTAATAATTTGGCAAGGACTGTTCTTTTAAACGAGATACATAATGGAGAAATATTTGAGGGCTTGAAAATCGATCCTGAATCGGTGTCCTTCTCCGGTATTAGTTGCCTTGACGACTGTCCAACTCAGGCTCCCACTAACACGACCACACCTTTATTGTATCTGACTGGTTTAATACTATTGATGTCACTACAAAAAAGAATGAGCAAGATGAAGCGCATTTCAAAAGGCTTAACGGTACTAACAACAATGAAACCGTTGTTCAATGGGTCACTCCATCCAATACCAAGATCACTAACGTTACAATTCTCCAAATTGATGCAAACAGTACGTTATTACCCTGGAAAAATGCTTCAGAATGGGATAATACCACAGTAAGTGCCAAATACAATGATACTGGAGTCACTGTCAGTTCACCGAAATTCGTATCGCAATTCACGAACAGAGAAGAGAACACACTCTTTCATCAGGAGAATGATAAGCAGAACCGGAATTTAAGTGTAATTGAAGATGATTTGATTGTACCTGTTAACGAAACTACACTAAGTTCGACCACCGATTTGTGGAATGAGTTTGATGTCGTCAATATTAAAGATGGCAAAAATAAAATTCCAGAATGCGGCAAAGAAGGATTTCGCTGTGCTGACAACAAATGTATTCCTGGTTATCGTAAATGCGATCGCTTCTCGGATTGTTCAGATAGTTCTGATGAAGCGAACTGCACCTGTTCTGACTATTTGATATCGCTCGAACAGCCGAGGAAAATATGCGATGGTTTTATGGACTGCTGGGATTATAGTGATGAAACCCATTGCCCGTGGTGTTCTGATGATATGTTCCATTGTCCTGGTGCAAAAGTGTGTATCAATAAAACTAAAGTATGCGATGGTATTCGAGACTGCCCTTCCGGTTCTGATGAGGCCACATGCATGAAAATAGCCAAGGACGTAAGCGGAGCTAATGGTTTTACTTTTGCCAAGGAAGGTTACTTAATGATTCAGAGAGAGGGTCAATGGAAAAAGTTATGTCTTGACAACAATAATCTAATCGACAAACCTAGATGGAATGTCGAAAAGCTTGGATACACCGTTTGTTCTTCTCTGACTTATAAGGCTTTAGAATCGATTGTTTTATCACCACGGAAGTATCAAGAAGATTCATATTATGAACTGATACCAGCTACAGAAAGGTCTGGCATTTAAGTTTCTTATATCCGATTGTGCAGATGGAAAAATCGCCCCGAATAAGATGTCGAGACTTGGCGTGTGGATTGGGAACGCCTGTTCAGTTACCTACCAAAAGAATCGTCGGAGGTGACAGCGTACCGATGGGAGCGAGACCATGGCTTGCTGCTCTTTATAGAGAAGGACAGTTCCAATGCGGAGCTATCGTTATTGCGGACAGATGGCTTTTGTCGGCGGGACATTGTTTTTTTCACACCAAGCATTCTTATTGGGTGGCAAGAATGGGCTTGCTTAGAAGAGGGACAGATATGCCAACGCCTTACGAGATAGTGAAGAGGATTATTCAGATTAAAGTCAATCCTCAATACATAAATAAGAACTTCATCAATGATATAGCCGTTCTTAAATTAGAGAGTGCCGTCCCCTTCAGTAATTACATTCGTCCAATCTGCTTACCACAACCAGAAGATGATGTTGTTAAATGGAATGGTAAAAAATGTTCAGTTGTAGGATGGGGAAAATTAGGAGAAAATGGTGATGAATTTCCCGACACTCTTCAAGAAGTGCAGTTACCCGTCATCTCAACCGAAGAATGCAGGAAAAGAACTTTATTTTTATCTATCTATCAAATAACCGATAACATGTTTTGTGCCGGATACGAAAGAGGGGGTCGGGATGCGTGTTTGGGTGACTCGGGTGGTCCCATGATGTGCCAGAAGGAAGATGGTCGTTGGGTGTTAATTGGCATTATAAGCAACGGTGACGGATGTGCGAGACCTTCTCGTCCGGGGGTATATACTAAAGTTGGAAATTTTATGAACTGGATAGATTCTATAATGAATGAAAACGCTACAGACGAAGTAAAACCTGACAGCTGCCTTGGAACTAGGTGTAAGCTAGGCATGTGTCTTTTTCCCAGAATCAAACTGTGATGGAAATGCAGATTGCCCGGATGGTTCCGACGAAAAAGGGTGC |

| TatEnzSeP14 | JAT91142.1 | 7 e-94 | PF00089 | -- | Chymotrypsin-like | VLTPLTKMNYALLMVSFLHFSKYCVLSQNEQSPSKKLS YDDDVMVEGDGCFTQFRATGVCRAITACKTLSKTERQN PKLCSWDRDVPVICCPVPLADVLKPAAITNQECGIRTAV TIITDGRLKRMALEFANRQNKPTVVGGKDVIRNSWPWM VSIRKNTQIHCGGCIIGDRYILTAAHCFDGNNRSPSDFTV RVGGHTRADGVDYSVEEIKKHLLYKAGIRYHDIAILKTK ESIRFHRTVSPACLPSSEDTYVNRTATVIGWGDTFFGGIP SSVLQEASISVVSNSICDQSYRTLSLSSFPEGITDNLLCAG LSEGGKDACQGDSGGPLMIFDLPSLKWMVTGVVSFGY QCAVKGFPGIYTRVSSYLPWISEIMGS | GTGCTAACACCCTTAACGAAAATGAACTACGCTTTGTTAATGGTATC GTTTCTGCATTTTTCTAAATACTGTGTTCTTTCTCAGAATGAACAATC ACCTTCCAAGAAACTTAGCTATGACGATGATGTTATGGTTGAAGGAG ACGGTTGCTTCACTCAGTTCCGTGCAACGGGAGTATGTCGAGCAATA ACAGCCTGCAAAACTCTATCAAAAACGGAGAGACAAAATCCTAAAT TATGTAGCTGGGATAGAGATGTGCCAGTTATATGTTGCCCCGTACCA TTAGCTGACGTACTAAAGCCAGCTGCTATCACAAACCAAGAATGTGG AATAAGAACAGCTGTAACAATAATAACGGATGGCAGACTAAAGAGA ATGGCCCTCGAATTCGCGAACCGTCAGAACAAACCTACCGTAGTTGG CGGTAAGGACGTAATTCGTAATTCCTGGCCATGGATGGTATCCATCC GCAAAAATACCCAAATCCATTGCGGAGGATGCATCATAGGCGACCG TTATATTCTTACAGCTGCTCACTGTTTTGATGGAAATAACAGATCGCC TTCTGATTTTACCGTAAGGGGTTGGTGGCCATACTCGGGCTGATGGAG TAGACTATAGTGTGGAAGAAATTAAGAAGCACCTATTATACAAGGC AGGCATACGTTATCACGATATTGCCATACTGAAAACAAAAGAAAGT ATTCGTTTCCATAGGACAGTTTCTCCAGCTTGCTTGCCTTCGTCAGAG GATACTTACGTAAATAGGACAGCCACTGTTATTGGATGGGGAGATAC GTTTTTCGGGGGTATTCCCAGCAGCGTGCTTCAGGAAGCAAGTATTA GTGTGGTCAGCAATTCTATCTGTGACCAGTCTTACAGAACATTAAGC CTATCTTCTTTTCCTGAAGGAATTACAGATAATCTCCTTTGTGCTGGT TTAAGCGAAGGTGGTAAAGACGCCTGTCAGGGTGATTCTGGGGGTCC TCTTATGATTTTCGACTTACCCTCATTGAAATGGATGGTGACTGGTGT AGTATCATTTGGGTATCAATGTGCTGTTAAAGGATTCCCAGGAATTT ACACCAGGGTCTCCAGCTACTTACCTTGGATTTCTGAAATTATGGGT AGC |
| TatEnzSeP15 | XP_013781651.1 | 1 e-141 | PF00089 | -- | Trypsin-like | GTHADDGVESVACTRAGQRLSGPSGIITTPGFKDSKPYP PRAVCTWLFQLPPMKYISFEFEEFDVELSNDCKTDGVDI FAMNPPKLLRKFCGSEVPKIVILPTNDGIRLKFRSDDLYE RKGAKIKYEILNTYPDCGKDHIRCKNGKCVSKDKKCNK IDDCGDGTDEECSNILEHPKTCGKPKYSPVIGNGDRIIGG QETAPHSWPWQVSIQNAISFPSGHYCGGALINNLWVVT AGHCLYGRDIGSIRIHLGMHNRFYKDDGEIVRYASKSCV HPDFRRQLLKDDIALIKLNAPVAYNDNIQPVCMPPLTES LREGTYCHVTGWGTTFGTGNFHVLKQTMVPIIDHDKCK KMVKLLPLSPNAICSGFEDGYHSPCFGDSGGPFVCDYNK TWHLTGVVSWGPMMCGIREEPSVYTKVADYKPWLERII ENDEKGIQNRCL | GGAACACATGCTGATGATGGCGTGGAGTCTGTGGCTTGTACTCGTGC TGGGCAGAGACTGAGTGGTCCATCAGGTATAATTACAACTCCTGGTT TCAAAGACTCTAAACCATACCCTCCACGAGCAGTATGCACATGGTTG TTCCAGCTACCACCTATGAAATATATTTCTTTTGAATTCGAGGAGTTC GATGTAGAATTGTCAAATGACTGCAAGACTGATGGTGTTGACATATT TGCAATGAATCCACCTAAATTGCTTCGAAAGTTTTGTGGTTCTGAAGT GCCAAAAATCGTTATTTTGCCTACGAATGATGGAATTCGACTGAAGT TTCGCAGCGATGACTTGTATGAGAGGAAGGGGTGCAAAAATCAAATA TGAGATCCTAAATACTTATCCTGATTGTGGGAAAGATCACATTAGAT GCAAGAATGGCAAATGTGTCTCCAAAGATAAAAAATGCAATAAAAT TGACGACTGTGGAGACGGTACTGACGAAGAGTGCTCTAACATCTTGG AGCATCCAAAGACCTGTGGCAAGCCAAAATACAGCCCAGTAATAGG AAATGGCGATAGAATAATCGGAGGACAAGAAACTGCACCTCACAGC TGGCCATGGCAAGTCAGTATTCAAAATGCGATATCTTTTCCATCTGG ACATTACTGCGGAGGTGCTCTTATTAACAATCTGTGGGTAGTTACCG CCGGGCATTGCCTTTACGGAAGGGATATTGGAAGTATCAGAATTCAC CTGGGAATGCACAATCGTTTTTATAAAGACGATGGTGAAATTGTTAG GTATGCATCTAAATCGTGTGTCCATCCAGACTTTAGAAGGCAACTAC TGAAGGATGACATTGCCTTGATAAAGCTGAACGCTCCTGTCGCATAT AATGATAATATTCAACCTGTTTGTATGCCTCCACTGACCGAAAGTTTA AGAGAAGGAACGTACTGTCATGTGACAGGATGGGGAACTACGTTTG GGACTGGAAATTTCCATGTTTTGAAGCAAACTATGGTTCCAATTATT GATCATGATAAATGTAAGAAAATGGTAAAACTTCTTCCACTTTCGCC TAATGCCATTTGCTCCGGATTTGAAGATGGTTATCATTCACCCTGCTT TGGTGATAGCGGTGGTCCATTCGTTTGTGATTATAACAAAACATGGC ATTTAACTGGAGTAGTTTCTTGGGGTCCAATGATGTGTGGAATTAGA GAAGAACCTTCTGTTTATACAAAGGTTGCTGATTATAAGCCATGGTT AGAGAGAATTATTGAAAACGATGAGAAGGGTATCCAAAATCGTTGT TTG |

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatEnzSeP16	EZA52937.1	5 e-25	PF00089	--	Serin protease	IGAANVRKLFFALLTTLCLLPSIYVDGVEVLSPRIVGGET AMAGEMPCVLAVEDVRLHGNQSYCTFCLINEQTSIGGA LCVYQAKENIKTVGLFIYLIGGDVDRRNGTILPVKDIKIH EEFNYTSMRNDISLITVVKPITITPNLKPVLLPSPDQEFEGI TAKISGWGSTTFDTWYTTRYLRISEVKVLPDSDCNSFEE FYQPEEHLCAGASESGLAAYDSGVPLIISMNDEQIIIGVG SLADTNTTDTGNNAAYTNIKHYIPWIKENALGEVKLFN ASSTF	ATTGGTGCTGCTAACGTCAGAAAATTATTCTTCGCATTGCTGACGAC CTTATGTCTACTTCCTTCGATATATGTGGATGGGAGTGGAGGTACTCTC ACCGAGGATTGTGGGAGGAGAAACAGCAATGGCGGGTGAAATGCCT TGTGTGTTGGCCGTGGAAGATGTCAGACTCCATGGTAACCAATCCTA TTGCACATTCTGTCTGATTAACGAACAAACATCCATTGGAGGTGCAC TCTGCGTATATCAAGCTAAAGAAAATATAAAAACAGTAGGTCTGTTC ATCTACCTTATTGGCGGTGATGTGGATAGGCGTAATGGAACCATTTT GCCGGTAAAAGACATAAAAATACACGAAGAATTTAATTATACAAGT ATGAGGAATGACATTTCTCTAATAACAGTTGTGAAGCCTATTACAAT AACACCAAATTTGAAGCCAGTCCTCCTTCCATCGCCAGACCAAGAGT TTGAAGGAATAACTGCCAAAATATCTGGATGGGGAAGCACTACATTT GACACTTGGTATACAACTAGATATCTTCGAATATCAGAAGTTAAAGT CCTTCCTGATTCAGACTGTAATTCTTTTGAAGAATTTTATCAACCAGA GGAGCATCTTTGCGCTGGTGCAAGCGAATCAGGTCTTGCAGCGTATG ATTCTGGTGTACCTCTGATAATATCTATGAATGACGAGCAAATAATT ATTGGGGTTGGATCTCTAGCTGATACCAATACAACGGATACTGGAAA TAATGCAGCATACACAAATATAAAACATTACATCCCTTGGATTAAGG AAAATGCACTGGGTGAAGTCAAGCTTTTTAACGCTTCCAGCACATTC
TatEnzSeP17	XP_015911504.1	1 e-158	PF00089	--	Serin protease	DPYCGRNAVKTSRIVGGNDASFGQFPWQALIQVGGSRC GGALVGRCHVVTAGHCVARSQHNPSNIRVTLGDFVLHS NIESLPTETIGVSQVKLHPNFRFTPQADRFDVAVLILKRA APYRANIKPICLPRKNARFLGRTAYAAGWGAVQPGSKL RPKILQYVGVPIIENKICETWHKKRGINIRIHDEMMCAG YERGGRDACQGDSGGPLMMKEYNVWYLIGIVSAGYSC AKQHQPGIYHRVSSSSDWISSNLF	GATCCTTATTGTGGCAGAAATGCGGTGAAAACTAGTAGAATAGTTGG TGGAAATGATGCGTCCTTTGGACAATTTCCATGGCAGGCTTTAATTC AAGTAGGAGGAAGCAGGTGTGGTGGCGCTCTTGTCGGACGCTGCCAT GTTGTGACTGCTGGTCACTGTGTGGCACGATCGCAGCACAATCCTTC CAATATCCGCGTTACTTTAGGTGACTTCGTTCTCCACTCAAATATCGA AAGTTTGCCAACGGAAACAATTGGAGTCAGCCAGGTGAAGTTGCATC CGAATTTTCGTTTCACCCCACAAGCTGATCGTTTCGACGTGGCCGTGT TGATTTTGAAGAGAGCAGCACCTTATCGTGCTAATATCAAACCCATT TGTCTACCAAGGAAGAATGCTAGATTTTTGGGAAGGACGGCTTACGC TGCTGGATGGGGAGCTGTTCAGCCAGGTTCAAAGTTACGGCCGAAGA TTCTGCAGTACGTAGGCGTCCCTATTATAGAAAATAAAATATGTGAA ACGTGGCACAAAAAGCGTGGGATCAATATTCGAATACATGATGAAA TGATGTGTGCTGGTTATGAAAGGGGGAGGAAGGGATGCCTGTCAGGG TGATTCCGGAGGACCACTGATGATGAAAGAATACAATGTGTGGTATT TGATAGGAATAGTTTCTGCTGGTTATTCTTGCGCCAAACAGCACCAA CCTGGAATTTACCACCGAGTTAGCAGTTCCTCAGACTGGATATCGTC TAATCTCTTT
TatEnzSeP18	AAD00320.1	6 e-60	PF00089	--	Serin protease	LVMKTVHIWFLLSISSAAVSVIHSVKCGVSSKRDDGKFR LIVGGKPVPSGEWPWQVSLQVREGQNSFKHFCGGTLLN ENWILTAAHCFGSYGIPERVVLGEHNLKVKEKTEVHRNI AKTVLHPLYDRETISHDVALVKFLEPLDLEYEHNHLVPI CIPDKDTDVDNLSCVATGWGHLTPRGRRPDILQAVVLPI IDQEECKDRYTNVISYPITSDMICAGASEDGKGTCQGDS GGPLQCRMGQQWYQVGITSWGIDCASGLFPDVYARVS SVHEWIRSTINGQ	TTAGTCATGAAGACAGTACATATTTGGTTCCTGCTTTCCATTTCTTCA GCTGCAGTTTCGGTCATCCATAGTGTAAAATGTGGCGTTTCGTCGAA AAGAGATGATGGCAAGTTTAGGTTGATTGTAGGAGGAAAGCCAGTG CCCTCTGGTGAGTGGCCTTGGCAAGTATCTTTGCAAGTCAGAGAAGG GCAAAATAGTTTCAAACATTTCTGTGGAGGGACTCTTTTGAATGAAA ATTGGATTTTAACAGCAGCCCATTGCTTTGGAAGTTATGGTATTCCCG AAAGAGTTGTTCTTGGAGAACATAATTTAAAGGTGAAGGAGAAAAC GGAAGTTCACAGGAACATTGCAAAGACTGTGCTTCATCCTCTATATG ATCGAGAAACTATATCCCATGATGTAGCTTTAGTAAAGTTTTTGGAA CCTTTAGATTTGGAATATGAGCATAATCACTTGGTCCCAATATGTATT CCTGACAAAGACACAGATGTAGACAACTTGTCCTGCGTAGCCACTGG TTGGGGACACCTTACTCCTAGAGGAAGACGTCCAGATATACTGCAGG CAGTAGTCCTGCCAATTATAGATCAGGAAGAGTGCAAAGATCGATAC ACAAATGTAATTTCTTATCCAATCACATCTGATATGATCTGCGCTGGA GCATCTGAAGATGGAAAAGGCACTTGTCAAGGCGATTCTGGTGGACC ATTACAATGTAGAATGGGGCAGCAGTGGTACCAGGTTGGAATTACAT CTTGGGGCATAGATTGTGCATCGGGATTGTTTCCAGATGTGTACGCT CGTGTCTCTAGTGTTCATGAGTGGATTCGTTCAACTATCAATGGTCAA

Metalloproteinases

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence

TatEnzMtp01	AMO02512.1	3 e-118	PF00200	--	ADAM-like	SPNARHGGSYLMYTYSVSGYDPNNKKFSPCSIRSVRAV LLAKASKCFSTPEESFCGNSLVEVGEQCDAGLIGSEDND PCCDTNCTFRKDVICSDKNSPCCRDCRYVAAGEKCRDA QTTACKKEAYCSGDSSDCPPSAPQPNKTLCLDRGQCLM GECIPFCETRDRLSCMCDREEDACKRCCRRSQNDTCDP MEPVEILRDG	TCACCTAATGCACGGCATGGTGGTTCCTATCTGATGTATACATACTCT GTTAGTGGTTATGATCCAAATAATAAGAAATTCTCGCCTTGCAGTAT ACGTTCTGTTCGAGCAGTATTGCTAGCTAAAGCGAGCAAATGTTTTT CCACACCAGAAGAGTCATTCTGCGGCAATTCACTAGTTGAAGTTGGA GAACAGTGTGATGCTGGTTTGATTGGAAGTGAAGATAATGATCCTTG TTGTGATACAAATTGTACCTTTAGAAAGGATGTGTATATGCAGTGACA AAAATTCACCTTGTTGTCGTGATTGTCGGTATGTAGCAGCAGGGGAG AAATGTAGAGATGCGCAGACAACAGCATGTAAAAAAGAAGCATACT GCAGTGGGGACTCATCTGATTGCCCGCCATCTGCACCTCAGCCTAAC AAAACACTTTGTTTAGATAGAGGGCAATGCTTGATGGGAGAATGCAT TCCTTTCTGTGTGAGACAAGAGACCGGCTATCATGCATGTGTGACAGAG AGGAAGATGCATGTAAGCGATGTTGTCGCCGTTCACAAAATGACACC TGTGATCCTATGGAGCCTGTAGAAATTCTAAGAGATGGC
TatEnzMtp02	XP_013793082.1	0	PF13574, PF00200	--	Disintegrin-like	MIQNKFFLSLLVCFVTGGETGRLNQYISYFEPLRYNHET VHQGHLRAKRSPSDSLVYVNFHAHGRHFNIRLKRDTSA FAPDVVIETTNGVAEVDTSHLYDGHLLGESGSTVYGSIR NGVFEGKIHTPNKVYYVERSHKYFSSNPQPFHSVIYSSD DVEDPYADKRESHAGGCGITEDVLQWMQEVSNSADPK EMSPTNKTTNPEQSHLERSERSTAAENAPHNIYTREAQR DINQIDQLQAKRACTLYVQTDVFLWKHILTYEKTASSA REEISSLISQHVRAVNYIYENTDFDGYRGIKFVVQRIKIN DTSSCSNQGLDYKRTNPFCSPNIDVSNFLNLNSQFNHDD FCLAYIFTYRDFSGGTLGLAWVASASGASGGICEKYKPY NENINGRQVQTKRSLNTGVITFVNYNSRVPPKVSELTLA HEIGHNFGSPHDYPIDCRPGGSDGNFIMYASATSGDRKN NNKFSQCSIRNITTVLRAVFNGEGKENCFQRSDGAFCGN KIVENTEECDCGYDAKECNDECCYPRDVTLFQMKDPNA QRCKLRPRKVCSPSQGPCCSPSCNYVANGTICRGESECT LISLCNGSSAVCPASKPRPNRTECNKGTQVCWNGECTGS ICQKYNMEECFLTSLNGAKPEEMCEVACQKLGQPATCE STYGIAKMKNISGLKLQPGSPCNEFQGYCDVFQKCRAV DAEGPLARLKNLLLNQQTLRTIKQWITTYWWAVMLML VGLAIFMGLFIKCCAVHTPSSNPRKAPALRISDTLRHPAD TLRRKRHRPPPQPGIPSGPPPPYPGPQPSAPPSRSRSSAGP SRGYGEGRGHYNRRDRGQMHHGERGKLYIEDPSYAPA HPGRGSAMEMRVKSQA	ATGATACAAAACAAGTTCTTTTTGTCACTGCTTGTTTGTTTTGTGACA GGAGGTGAAACCGGTCGACTTAATCAGTATATAAGTTATTTTGAGCC ACTGAGGTACAACCACGAAACTGTACATCAAGGTCATTTACGTGCCA AACGTTCACCTTCAGATTCCTTAGTTTATGTGAATTTCCATGCACATG GAAGGCATTTTAATATTCGACTTAAAAGGGACACATCAGCTTTTGCT CCAGATGTTGTTATAGAAACTACTAATGGTGTAGCAGAAGTTGACAC ATCCCACTTATATGATGGGCATTTGTTAGGGGGAATCAGGATCCACTG TATATGGCTCAATAAGGAATGGTGTATTTGAGGGAAAGATTCATACA CCGAACAAAGTTTATTATGTAGAACGCTCTCACAAATATTTTTCATCA AACCCTCAACCATTTCACTCTGTGATATACTCATCAGATGATGTGGA AGATCCATATGCTGACAAACGGGAGTCACATGCAGGTGGATGTGGC ATCACAGAGGATGTTTTACAGTGGATGCAAGAAGTTAGCAATTCAGC AGATCCTAAAGAAATGTCCCCTACAAACAAGACAACAAACCCGGAG CAGTCTCATTTGGAAAGAAGTGAACGTTCAACAGCTGCGGAAAATGC ACCTCATAATATCTATACAAGAGAAGCGCAACGTGATATTAATCAGA TAGACCAATTACAAGCAAAAAGAGCATGTACATTATATGTGCAAAC AGATGTATTTCTATGGAAGCATATTTTGACGTATGAAAAAACTGCTA GTAGTGCACGAGAAGAAATATCTTCATTAATATCTCAACATGTGAGA GCCGTTAACTATATTTATGAAAATACTGACTTTGATGGCTATCGGGG CATAAAGTTTGTGGTGCAAAGAATTAAGATAAATGACACATCATCGT GTTCCAATCAAGGGGTTGGATTACAAACGAACAAATCCATTCTGCTCG CCAAATATTGATGTATCAAACTTTTTAAATTTGAATTCTCAATTCAAC CATGATGATTTCTGTTTAGCATACATTTTTACGTACAGAGATTTCTCT GGTGGTACATTAGGACTTGCATGGGTTGCATCAGCATCAGGTGCTTC TGGAGGAATCTGTGAGAAATACAAGCCATACAATGAAAATATTAAT GGCAGACAAGTACAAACCAAAAGAAGCCTGAACACTGGTGTGATTA CCTTTGTCAATTACAACAGCCGAGTACCTCCAAAAGTGTCAGAATTG ACATTGGCTCATGAAATTGGACACAACTTTGGTTCACCTCATGATTAT CCTATTGACTGCAGACCTGGTGGTAGTGACGGAAACTTTATTATGTA TGCAAGTGCTACATCTGGGGATAGGAAGAACAATAACAAATTTTCTC AGTGCAGTATCAGAAACATTACTACTGTCCTCCGTGCTGTGTTCAAT GGCGAAGGAAAGGAAAATTGCTTTCAGCGAAGTGATGGTGCTTTCTG TGGTAATAAAATTGTGGAAAATACTGAAGAATGCGACTGTGGGTATG ATGCAAAGGAATGCAATGATGAATGCTGCTATCCACGAGACGTCACT CTTTTCCAAATGAAAGATCCAAATGCACAACGATGCAAACTACGTCC AAGAAAAGTTTGCAGTCCAAGCCAAGGACCATGTTGCTCACCATCTT GCAATTATGTTGCGAATGGCACCATTTGCAGAGGAGAATCTGAATGC ACTCTCATTTCCTTGTGCAATGGAAGCAGTGCAGTGTGCCCTGCATC AAAACCAAGGCCTAATAGAACAGAATGTAATAAAGGAACACAAGTC TGTTGGAATGGTGAATGTACTGGTTCTATTTGCCAGAAATATAATAT GGAAGAGTGTTTCCTGACTAGTCTGAATGGTGCAAAACCAGAAGAG ATGTGTGAAGTAGCTTGCCAGAAATTAGGTCAACCAGCAACATGCGA AAGTACATATGGAATTGCAAAAATGAAAAATATTAGTGGGTTAAAG CTACAACCAGGATCACCATGCAATGAATTTCAAGGCTACTGTGATGT ATTTCAAAAGTGCAGAGCTGTTGATGCAGAAGGACCATTAGCACGCC TCAAGAACTTACTATTAAACCAGCAAACTTTGAGAACTATTAAGCAA TGGATAACAACATATTGGTGGGCTGTCATGCTGATGCTAGTAGGATT GGCCATCTTCATGGGTTTGTTTATAAAGTGTTGTGCTGTACATACACC TAGCAGTAATCCTAGGAAAGCTCCAGCACTTCGTATCAGCGACACGT TGCGTCATCCTGCTGACACTCTTCGCAGAAAGCGGCACCGTCCACCA CCACAACCAGGCATTCCTAGCGGACCACCTCCACCTTATCCAGGACC TCAGCCTTCAGCACCTCCCTCTAGGAGTAGATCTTCAGCTGGACCAT CACGTGGTTACGGAGAAGGTCGGGGACATTACAACAGAAGGGACAG

AGGCCAAATGCATCATGGTGAAAGGGGGAAGTTGTATATTGAAGAC
CCGTCCTATGCTCCTGCTCATCCTGGTCGGGGCAGTGCAATGGAAAT
GAGGGTTAAATCACAGGCCTGA

Name	Accession	E-value	Pfam		Description	Protein sequence	DNA sequence
TatEnzMtp03	XP_021004202.1	0	PF01421, PF00200	--	Disintegrin-like	MHWIYIVIIFFCYGTTLRICALLKRKREADSFPFDDVGDE NWPVAEADRLRRIYPENERLIANIPSRFFEVIYPVQVRQH QKLGISTRDATANKVSLPSTGKHFHQTSLLVKAFNYKFR LELELNMYLLAPNLIQKHFLPEGAQQISTQEIEHCYYHA VIKDYPGALAALRTCNGVSGIIHVSNETFVIHPFYGGDLS RKHPHVIYRYFGEAKEKHMCGNTGMHEWGFKQFRIQP GRIKRDVREVFKFIELALVLDQAMFDNRNATRSEVVND AIQVVNCVDMYFRTVNTRVSVLYVETWAHGDQMEINN DVRQTLLNFMEYASRKLYKVAKDATHLLTGHHFKGAE VGMSVPDSICTAKAVGVSQDTNIHEPHLVASTMTHMLG HNIGMSHDQYDNNDECECQDWWGCIMAQTILGQNRIQ PYHFSKCSFQDYINALRIGHGICLFNKPNQLEDFRSCGNK LVEEGEQCDCGSIDECLEHDQCCDPITCKLRVEAECSKG PCCADCKLKASGQPCREAIDECDIPEYCNGRDGQCPTDL FKRNGALCKNGIGFCFNGRCPSADERCEYIWDFGAVSS DIQCYEQFNTQGSLNGHCGTDGKGGYIKCTEENILCGTV QCQQGRRVPIVQGMNKQYARTIVSIGGAEYECKVASGN LDLDIVDLGMMPDGSKCAENKICVNQTCLRLDLFVEPG SCLSNNVALPCSGHGVCSNINTCFCDEGWTAADCSQRL NGDDPAADHTDEPFGGGNHAYIPVSTTQGSASENGQNL KKTPKSTTYGKKDALSAPSLVVVLVSVVGGVFIFFALLA TCYRRSTLPKQEPPHMKKHIVRKHTLPLTVATKRDEDSS QENVNRIITFGSMPSYREDKQRQQLQLKDTSLSEEGESH	ATGCATTGGATATATATAGTTATCATATTTTTCTGTTATGGAACAACG TTACGGATCTGCGCTTTGTTGAAGAGGAAAAGAGAAGCTGATTCATT CCCTTTTGATGATGTTGGAGATGAGAATTGGCCTGTTGCTGAGGCTG ATCGCTTAAGGCGAATATATCCAGAGAATGAACGTCTCATAGCCAAC ATTCCGAGTCGTTTCTTTGAAGTTATCTATCCTGTGCAGGTACGACAG CATCAAAAGCTGGGTATTTCCACAAGGGATGCCACAGCCAACAAAG TAAGCCTCCCTAGTACTGGCAAGCACTTCCATCAGACATCCCTCCTTG TCAAAGCTTTCAATTACAAATTCCGTCTTGAATTGGAATTGAATATGT ACCTTTTGGCACCAAACCTTATCCAAAAGCATTTTTTGCCTGAAGGA GCACAACAAATATCTACTCAGGAAATAGAACATTGTTACTATCATGC TGTTATCAAAGATTATCCAGGTGCTCTTGCTGCACTTAGGACCTGTAA TGGAGTTAGTGGCATTATTCATGTCAGTAATGAAACTTTTGTAATTCA TCCTTTCTATGGAGGTGATCTTTCTAGGAAGCATCCACATGTAATTTA TCGATATTTTGGTGAAGCAAAAGAAAAACATATGTGTGGAAATACA GGAATGCATGAATGGGGCTTCAAACAATTTAGAATACAACCAGGAA GAATTAAGCGGGATGTACGAGAAGTTTTCAAATTCATAGAACTTGCT TTAGTGTTAGATCAGGCAATGTTTGACAATCGGAATGCAACTAGATC TGAAGTAGTAAATGATGCTATCCAGGTTGTTAATTGTGTGGATATGT ACTTTCGAACTGTTAACACTAGAGTATCTGTTTTGTATGTGGAGACAT GGGCTCATGGTGATCAAATGGAAATTAACAACGATGTACGACAGAC ATTGCTAAACTTTATGGAATATGCTTCCCGAAAATTATATATAAAGTTG CAAAGGATGCCACCCATTTATTAACAGGCCATCATTTTAAAGGTGCT GAAGTGGGCATGTCTGTGCCAGATAGTATTTGTACAGCTAAAGCAGT TGGAGTTAGTCAAGATACCAATATCCATGAACCCCATCTAGTAGCAA GTACGATGACTCATATGTTAGGACACAACATTGGAATGAGCCATGAC CAGTATGATAATAATGATGAATGTGAATGTCAAGATTGGTGGGGGTG CATTATGGCACAAACAATTCTGGGTCAAAATAGGATACAACCATATC ACTTTTTCCAAGTGTAGCTTTCAGGATTATATTAATGCTCTTCGCATTG GTCATGGTATCTGTCTATTCAACAAGCCAAATCAGCTAGAAGACTTC AGGAGTTGTGGAAATAAGCTAGTTGAAGAAGGTGAACAGTGTGATT GTGGTAGTATTGATGAATGCTTAGAACATGATCAGTGTTGTGATCCT ATCACTTGCAAGCTGCGAGTTGAAGCTGAATGCTCCAAAGGTCCATG CTGTGCTGACTGCAAGCTAAAGGCTAGTGGACAACCCTGTCGAGAGG CAATTGATGAGTGTGATATTCCAGAATATTGTAATGGACGTGATGGG CAGTGTCCAACTGACTTGTTCAAGAGAAATGGTGCCTTGTGTAAAAA TGGAATTGGTTTTTTGCTTCAATGGTAGATGTCCAAGTGCTGATGAAC GTTGTGAATACATTTGGGATTTTGGTGCAGTATCCTCAGATATCCAAT GTTATGAACAGTTTAACACACAAGGAAGTCTAAATGGTCATTGTGGC ACTGATGGAAAAGGTGGATACATCAAGTGTACAGAAGAAAATATTC TCTGTGGTACTGTTCAGTGTCAGCAAGGTAGACGTGTGCCTATTGTG CAAGGAATGAATAAACAGTATGCACGTACAATTGTATCTATTGGTGG GGCAGAGTATGAATGCAAAGTTGCTAGTGGAAATCTGGACTTAGATA TAGTTGACCTTGGAATGATGCCTGATGGCTCAAAGTGTGCTGAAAAT AAGATATGTGTGAATCAGACTTGCCTCAGGTTAGATCTGTTTGTGGA GCCAGGTAGCTGTCTGTCCAATAATGTTGCACTTCCTTGCTCTGGCCA TGGTGTATGTTCAAATATTAATACTTGCTTTTGTGATGAGGGCTGGAC AGCAGCAGATTGTAGCCAACGTTTAAATGGTGATGATCCTGCAGCTG ATCATACTGATGAACCTTTTGGAGGAGGAAACCATGCTTATATCCCT GTCTCAACTACGCAAGGATCTGCATCAGAAAATGGACAAAATCTAA AAAAGACACCAAAGTCAACAACTTACGGGAAGAAGGATGCTTTAAG TGCACCATCACTTGTGGTTGTGCTCGTTTCAGTTGTTGGAGGGGTTTT TATATTCTTCGCTCTACTAGCAACATGCTACAGAAGAAGCACACTTC CAAAGCAAGAACCACCTCATATGAAAAAGCACATAGTTAGAAAGCA CACACTGCCATTAACTGTTGCTACTAAACGTGATGAAGATTCATCTC AAGAAAATGTGAATAGAATAATTACCTTTGGTAGCATGCCATCTTAT CGGGAAGACAAACAAAGGCAGCAACTGCAGTTAAAAGACACTTCAC TTTCTGAAGAAGGGGAAAGTCAT
TatEnzMtp04	XP_021001151.1	3 e-86	PF00200	--	Disintegrin-like	LKGCFTEPQDAICGNEVVEKGEECDCGWEEDCEEPCCF PMRSNPPRDEPPCHLRPNVVCSPSQGPCCTHDCRIKVGE ECRGDNGCRSASYRDGQGPHCPSSTNKPNKTVCNDEFV CYMGECTGSICMAYGLESCQCKRGLHDPLTKACELCCK LPRD	TTAAAAGGTTGTTTCACTGAGCCACAAGATGCCATCTGTGGAAATGA AGTAGTGGAGAAAGGTGAAGAATGTGACTGTGGCTGGGAAGAGGAC TGTGAAGAACCATGTTGTTTTCCCATGCGTAGCAATCCCCCTAGAGA TGAACCACCTTGTCACCTTAGACCCAATGTAGTTTGCAGCCCAAGCC AAGGTCCTTGTTGTACACATGACTGTAGGATAAAAGGTTGGAGAAGAG

						TGTCGTGGAGATAATGGTTGTAGAAGTGCAAGCTACCGTGATGGTCA AGGACCACATTGCCCATCATCCACCAACAAACCAAATAAAACTGTCT GCAACGATGAATTTGTTTGTTATATGGGAGAATGTACAGGCTCGATA TGTATGGCATATGGACTAGAGTCTTGCCAGTGCAAACGTGGCCTACA TGATCCTTTAACAAAAGCATGTGAACTTTGTTGTAAGCTGCCAAGGG AT
TatEnzMtp05	XP_015912698.1	0	PF00557	--	Other	MADKEENEPTIAQDLVVTKYKMAGEMVNRVLGQLIKK CQTGESVINICELGDKLLLDETGKVFKREKEMKKGIAFP TCLSVNNCICHFSPLKSEPDYILKDGDMVKVDLGAHIDG FIAVVAHTLIVGSEKDCKIAGKKADVIKAAYYAAEAAL RLVKPGGENSEVTEAVQKVAESFKCRPVEGMLSYQLKQ YRIDGEKSIIQNPTEAQRKEHEKCEFELHEVYAVDVLIST GEGKGREMDTRTTVYKKTDEIYQLKMKASRAFFSEVD KRFGNMPFTLRAFDDEKKARMGVVECVNHKLVEPFTV LYEKEGEYVAQFKFTVLLMPTGSHKITTGPIDMDIYESE FKLEDESLKSLLNRSVAPKSAKKKKKKAEKAVASSVET GDKIEDEKLNENNTLVED	ATGGCGGACAAAGAAGAAAATGAACCGACAATTGCTCAAGATCTTG TTGTGACTAAATATAAAATGGCTGGAGAAATGGTTAATAGAGTTCTA GGTCAACTGATAAAAAAATGCCAGACTGGAGAGAGTGTAATCAACA TATGCGAATTGGGTGATAAATTGTTACTGGATGAAACAGGGAAGGTT TTTAAAAGGGAAAAAGAAATGAAAAAAGGTATTGCATTTCCAACAT GTTTATCAGTGAACAACTGTATTTGTCATTTTTCACCATTGAAAAGTG AACCTGATTATATTTTAAAAGATGGGGATATGGTTAAAGTGGATTTG GGAGCACACATTGATGGATTTATTGCAGTGGTTGCTCACACATTGAT TGTTGGCTCAGAAAAGGACTGCAAAATTGCTGGTAAGAAGGCAGAT GTCATTAAAGCTGCTTACTATGCTGCAGAAGCTGCTCTAAGACTAGT AAAGCCAGGTGGAGAGAATTCTGAAGTCACTGAAGCTGTTCAGAAA GTAGCAGAATCATTTAAATGTAGGCCTGTTGAAGGTATGCTATCATA TCAGTTAAAACAATACAGGATAGATGGTGAAAAATCGATAATTCAA AATCCTACAGAAGCTCAAAGGAAGGAACATGAAAAATGTGAATTTG AGCTACATGAAGTTTATGCGGTAGATGTTTTAATTAGTACAGGTGAA GGAAAGGGTCGTGAAATGGATACACGTACCACTGTATACAAGAAAA CAGATGAAATATATCAATTAAAGATGAAAGCATCTAGGGCATTTTTT AGTGAAGTAGACAAGAGATTTGGTAATATGCCTTTCACATTAAGAGC ATTTGATGATGAGAAGAAAGCCAGGATGGGTGTAGTTGAATGTGTCA ATCACAAACTTGTTGAACCTTTTACAGTTTTATATGAAAAAGAAGGA GAATATGTAGCACAGTTCAAATTTACTGTTTTGTTAATGCCTACTGGG TCCCATAAAATTACAACTGGTCCTATTGATATGGATATTTATGAATCA GAATTCAAATTAGAAGATGAATCGTTAAAGTCATTGTTAAATCGTTC TGTGGCACCAAAGTCAGCTAAGAAGAAAAAGAAAAAGGCAGAAAA AGCTGTAGCATCATCGGTAGAAACAGGTGACAAAATTGAAGATGAA AAACTAAATGAAAATAATACCTTGGTTGAAGATTGA

| TatEnzMtp06 | AMO02513.1 | 0 | PF01421, PF00200 | -- | Disintegrin-like | MEWLVRSDALLGRLVCFIIVLRTCSTLRSKDVRSEFHNH YVIQPKLHTLDGRERRDVNGAKEVPKDNLVMTFEVLGE EFVLDLKMNTDLLPENYFEKYQLNSRTILNKPMKKFRR HCHYLGQIRGIPTSWAAISMCRGINGMVFDGKENYYVH AVNESNHILLKASDWKANNLTCGYKEHYDSNLRSQML NNIKRNRRSAVIQPPSGSSSDSRYVELILVNDYKEFKELN EDVESVFERSKQIANILNGLYIPLNIYIALVGVITWTEKDP IVMSPDGDATLTNFLHYRRQRLAREHPNDNAQLITAMT FDGGVVGKALKGPICTYEYSGGVNMDHSHIVGLVATTV AHELGHNFGMEHDTDECECPEDKCIMAPASSATSPHHW SSCSREYVHMAFQHGMDYCLRNVPSNIVGPICGNGFLE DGEECDCGLKEFCNNLCCNATTCRLNPNATCATGLCCD VHTCKMKHVATLCRGSVSECDLPEYCDGVTEYCPSDV HVQDGTDCGDGKGYCYDGACQSHSNQCKLLWGSTGK TSHHHCYDQNSNGNVNGNCGYNRINKTYKACAKKDVR CGMLQCTHLNERLEFGMPSAAILSRSFINVQGKILPCRT AVIDLGLTSVDPGLTPNGAKCGDGMACLNQKCVPVSHL RKKTCSQNCNDNGICNNRINCHCNYGYGPPHCDGPGHG GSIDSGPPSDPNAGQSFFIAMLIIFLGIIPFIAITAYVVYHY NHHLKNWWLLKIRKEPKKPPEPKSAPPPKKFNYPHGTV KKLEISAPFLQHGPSDPIVTVPLETAQRHIHNGNLPIKAT TSQETPRPVPLRAAPPVPPGPVQRSHSSVGATSSNRRASR PLSEASFSKRNLPPPPRPPPPKHLKPSVRPQSFSAGSNRVT ANDNATNVNNVELSRKGSNASNQNQVKKTATNNASVS AAASVGKPNRQTKPNSAFKPARNSDPNVGRTNSGQISR VASLTQRFEQQGGVNAKV | ATGGAGTGGTTAGTGCGAAGTGATGCTTTGTTGGGGGAGATTAGTTTG CTTTATCATCGTTCTGCGCACTTGTTCAACATTAAGAAGTAAAGATGT CCGCTCCGAGTTCCACAACCATTACGTCATCCAACCGAAACTCCACA CCCTGGACGGAAGGGAGAGGCGAGACGTTAACGGCGCAAAGGAAGT CCCCAAAGATAATTTAGTTATGACATTTGAAGTACTTGGTGAAGAAT TTGTGCTAGATCTAAAAATGAATACAGATCTACTGCCAGAAAACTAC TTTGAAAAATATCAACTTAATTCACGCACAATTTTAAATAAACCAAT GAAAAGTTCAGGAGACACTGTCATTACTTAGGGCAGATCCGAGGC ATTCCTACTTCTTGGGCGGCTATAAGCATGTGTCGTGGAATCAATGG AATGGTATTTGATGGAAAGGAAAATTATTATGTTCATGCAGTTAATG AAAGCAATCATATTCTACTTAAAGCTTCTGACTGGAAAGCAAACAAT CTCACTTGCGGGTACAAAGAACACTATGATAGCAATCTAAGATCTCA AATGTTAAACAATATAAAGAGGAATCGTCGATCAGCTGTGATACAGC CACCATCAGGATCTTCCAGTGACTCCCGCTATGTAGAGCTAATACTT GTCAATGATTATAAGGAGTTCAAAGAACTTAATGAAGATGTTGAAAG TGTTTTTGAAAGAAGTAAACAAATTGCTAATATTCTCAATGGGCTAT ATATTCCACTCAATATTTATATTGCATTGGTTGGTGTCATTACCTGGA CAGAAAAAGATCCAATTGTAATGTCTCCAGATGGTGATGCAACTCTC ACTAATTTCCTTCACTATCGTCGGCAACGTTTAGCACGTGAGCATCCA AATGATAATGCCCAGCTAATTACAGCTATGACATTTGATGGTGGAGT AGTAGGCAAAGCACTAAAGGGACCAATATGTACATATGAATACTCT GGGGGAGTTAATATGGATCATAGCCACATTGTGGGTCTTGTAGCTAC TACTGTTGCACATGAACTTGGGCATAATTTTGGAATGGAGCATGACA CAGATGAGTGTGAGTGTCCAGAAGATAAATGCATAATGGCCCCAGCT TCCAGTGCTACAAGTCCACATCATTGGTCATCATGCTCAAGAGAATA TGTCCATATGGCATTTCAGCATGGGATGGACTATTGCCTAAGAAATG TTCCTTCAAATATTGTTGGACCAATTTGTGGAAATGGATTTTTAGAAG ATGGGGAAGAGTGTGACTGTGGATTAAAGGAGTTTTGTAATAATCTT TGTTGTAATGCAACAACTTGTCGACTAAATCCTAATGCCACTTGTGCT ACAGGACTGTGTTGTGATGTTCATACATGCAAGATGAAGCATGTTGC TACTCTGTGCCGTGGCTCAGTTTCTGAATGTGACCTTCCTGAATACTG TGATGGAGTAACAGAGTATTGCCCATCTGATGTTCATGTCCAAGATG GAACTGATTGTGGAGATGGAAAGGGTTATTGCTATGATGGAGCATGT CAGTCACATAGTAACCAGTGCAAGCTATTATGGGGATCAACTGGTAA AACCTCTCATCATCACTGCTATGATCAAAATAGTAATGGAAATGTTA ATGGAAATTGTGGTTACAACAGAATTAATAAGACCTATAAAGCCTGT GCTAAAAAGGATGTCCGTTGTGGAATGCTTCAGTGCACACACTTGAA TGAACGACTTGAATTTGGTATGCCTTCAGCTGCTATTTTATCAAGATC ATTCATAAATGTGCAAGGGAAAATTCTTCCATGTCGAACAGCTGTCA TTGATTTAGGACTCACGTCAGTTGATCCAGGCCTAACCCCCAATGGA GCAAAGTGTGGTGATGGCATGGCATGTCTGAACCAAAAGTGTGTGCC AGTTTCTCACTTGAGGAAGAAAACCTGCTCGCAAAACTGCAATGACA ATGGGATATGCAATAACCGTATTAACTGTCATTGTAATTACGGCTAT GGCCCACCGCATTGTGATGGCCCAGGTCATGGTGGCAGTATAGATAG TGGACCACCATCTGATCCAAACGCTGGACAGAGCTTTTTTCATTGCAA TGCTTATCATCTTTCTTGGTATCATACCATTCATTGCCATCACTGCAT ATGTTGTGTATCACTACAACCATCATCTCAAGAATTGGTGGCTTCTTA AGATAAGGAAGGAACCAAAGAAGCCACCTGAACCTAAAAGTGCACC TCCACCAAAGAAATTCAATTATCCTCATGGTACAGTAAAAAAGTTGG AAATATCAGCTCCATTCCTACAACATGGCCCTTCTGATCCTATAGTAA CAGTCCCATTGGAAACAGCACAGAGGCATATTCACAATGGCAATTTG CCAATTAAGGCAACAACGTCACAAGAAACTCCTCGTCCTGTGCCTCT CAGAGCTGCTCCACCAGTCCCACCTGGACCAGTGCAGAGATCTCATT CATCAGTTGGTGCAACGTCATCAAATCGAAGAGCCTCTCGACCCCTG AGCGAGGCATCCTTTAGTAAGCGTAATTTACCGCCTCCACCTCGTCC ACCACCACCTAAACATTTAAAACCAAGTGTTCGACCACAGTCTTTCA GTGCAGGTAGTAATAGGGTGACAGCAAATGACAATGCAACAAATGT TAATAATGTAGAACTGAGTCGGAAAGGTAGTAATGCTTCTAATCAGA ATCAAGTTAAAAAGACTGCAACGAATAATGCTTCTGTGAGTGCAGCA GCTTCTGTAGGAAAGCCTAATAGACAGACAAAACCCAACAGTGCCTT CAAACCAGCAAGGAATTCAGATCCTAATGTTGGAAGGACCAATAGT GGACAAATATCGAGGGTAGCATCATTAACACAACGGTTTGAGCAAC AGGGTGGTGTAAATGCTAAAGTATAA |

TatEnzMtp07	XP_021004202.1	0	PF01421, PF00200	--	Disintegrin-like	MHWIYIVIIFFCYGTTLRICALLKRKREADSFPFDDVGDE NWPVAEADRLRRIYPENERLIANIPSRFFEVIYPVQVRQH QKLGISTRDATANKVSLPSTGKHFHQTSLLVKAFNYKFR LELELNMYLLAPNLIQKHFLPEGAQQISTQEIEHCYYHA VIKDYPGALAALRTCNGVSGIIHVSNETFVIHPFYGGDLS RKHPHVIYRYFGEAKEKHMCGNTGMHEWGFKQFRIQP GRIKRDVREVFKFIELALVLDQAMFDNRNATRSEVVND AIQVVNCVDMYFRTVNTRVSVLYVETWAHGDQMEINN DVRQTLLNFMEYASRKLYKVAKDATHLLTGHHFKGAE VGMSVPDSICTAKAVGVSQDTNIHEPHLVASTMTHMLG HNIGMSHDQYDNNDECECQDWWGCIMAQTILGQNRIQ PYHFSKCSFQDYINALRIGHGICLFNKPNQLEDFRSCGNK LVEEGEQCDCGSIDECLEHDQCCDPITCKLRVEAECSKG PCCADCKLKASGQPCREAIDECDIPEYCNGRDGQCPTDL FKRNGALCKNGIGFCFNGRCPSADERCEYIWDFGAVSS DIQCYEQFNTQGSLNGHCGTDGKGGYIKCTEENILCGTV QCQQGRRVPIVQGMNKQYARTIVSIGGAEYECKVASGN LDLDIVDLGMMPDGSKCAENKICVNQTCLRLDLFVEPG SCLSNNVALPCSGHGVCSNINTCFCDEGWTAADCSQRL NGDDPAADHTDEPFGGGNHAYIPVSTTQGSASENGQNL KKTPKSTTYGKKDALSAPSLVVVLVSVVGGVFIFFALLA TCYREDKQRQQLQLKDTSLSEEGESH	ATGCATTGGATATATATAGTTATCATATTTTTCTGTTATGGAACAACG TTACGGATCTGCGCTTTGTTGAAGAGGAAAAGAGAAGCTGATTCATT CCCTTTTGATGATGTTGGAGATGAGAATTGGCCTGTTGCTGAGGCTG ATCGCTTAAGGCGAATATATCCAGAGAATGAACGTCTCATAGCCAAC ATTCCGAGTCGTTTCTTTGAAGTTATCTATCCTGTGCAGGTACGACAG CATCAAAAGCTGGGTATTTCCACAAGGGATGCCACAGCCAACAAAG TAAGCCTCCCTAGTACTGGCAAGCACTTCCATCAGACATCCCTCCTTG TCAAAGCTTTCAATTACAAATTCCGTCTTGAATTGGAATTGAATATGT ACCTTTTGGCACCAAACCTTATCCAAAAGCATTTTTTGCCTGAAGGA GCACAACAAATATCTACTCAGGAAATAGAACATTGTTACTATCATGC TGTTATCAAAGATTATCCAGGTGCTCTTGCTGCACTTAGGACCTGTAA TGGAGTTAGTGGCATTATTCATGTCAGTAATGAAACTTTTGTAATTCA TCCTTTCTATGGAGGTGATCTTTCTAGGAAGCATCCACATGTAATTTA TCGATATTTTGGTGAAGCAAAAGAAAAACATATGTGTGGAAATACA GGAATGCATGAATGGGGCTTCAAACAATTTAGAATACAACCAGGAA GAATTAAGCGGGATGTACGAGAAGTTTTCAAATTCATAGAACTTGCT TTAGTGTTAGATCAGGCAATGTTTGACAATCGGAATGCAACTAGATC TGAAGTAGTAAATGATGCTATCCAGGTTGTTAATTGTGTGGATATGT ACTTTCGAACTGTTAACACTAGAGTATCTGTTTTGTATGTGGAGACAT GGGCTCATGGTGATCAAATGGAAATTAACAACGATGTACGACAGAC ATTGCTAAACTTTATGGAATATGCTTCCCGAAAATTATATAAAGTTG CAAAGGATGCCACCCATTTATTAACAGGCCATCATTTTAAAGGTGCT GAAGTGGGCATGTCTGTGCCAGATAGTATTTGTACAGCTAAAGCAGT TGGAGTTAGTCAAGATACCAATATCCATGAACCCCATCTAGTAGCAA GTACGATGACTCATATGTTAGGACACAACATTGGAATGAGCCATGAC CAGTATGATAATAATGATGAATGTGAATGTCAAGATTGGTGGGGGTG CATTATGGCACAAACAATTCTGGGTCAAAATAGGATACAACCATATC ACTTTTCCAAGTGTAGCTTTCAGGATTATATTAATGCTCTTCGCATTG GTCATGGTATCTGTCTATTCAACAAGCCAAATCAGCTAGAAGACTTC AGGAGTTGTGGAAATAAGCTAGTTGAAGAAGGTGAACAGTGTGATT GTGGTAGTATTGATGAATGCTTAGAACATGATCAGTGTTGTGATCCT ATCACTTGCAAGCTGCGAGTTGAAGCTGAATGCTCCAAAGGTCCATG CTGTGCTGACTGCAAGCTAAAGGCTAGTGGACAACCCTGTCGAGAGG CAATTGATGAGTGTGATATTCCAGAATATTGTAATGGACGTGATGGG CAGTGTCCAACTGACTTGTTCAAGAGAAATGGTGCCTTGTGTAAAAA TGGAATTGGTTTTTGCTTCAATGGTAGATGTCCAAGTGCTGATGAAC GTTGTGAATACATTTGGGATTTTGGTGCAGTATCCTCAGATATCCAAT GTTATGAACAGTTTAACACACAAGGAAGTCTAAATGGTCATTGTGGC ACTGATGGAAAAGGTGGATACATCAAGTGTACAGAAGAAAATATTC TCTGTGGTACTGTTCAGTGTCAGCAAGGTAGACGTGTGCCTATTGTG CAAGGAATGAATAAACAGTATGCACGTACAATTGTATCTATTGGTGG GGCAGAGTATGAATGCAAAGTTGCTAGTGGAAATCTGGACTTAGATA TAGTTGACCTTGGAATGATGCCTGATGGCTCAAAGTGTGCTGAAAAT AAGATATGTGTGAATCAGACTTGCCTCAGGTTAGATCTGTTTGTGGA GCCAGGTAGCTGTCTGTCCAATAATGTTGCACTTCCTTGCTCTGGCCA TGGTGTATGTTCAAATATTAATACTTGCTTTTGTGATGAGGGCTGGAC AGCAGCAGATTGTAGCCAACGTTTAAATGGTGATGATCCTGCAGCTG ATCATACTGATGAACCTTTTGGAGGAGGAAACCATGCTTATATCCCT GTCTCAACTACGCAAGGATCTGCATCAGAAAATGGACAAAATCTAA AAAAGACACCAAAGTCAACAACTTACGGGAAGAAGGATGCTTTAAG TGCACCATCACTTGTGGTTGTGCTCGTTTCAGTTGTTGGAGGGGTTTT TATATTCTTCGCTCTACTAGCAACATGCTACAGGGAAGACAAACAAA GGCAGCAACTGCAGTTAAAAGACACTTCACTTTCTGAAGAAGGGGA AAGTCAT

| TatEnzMtp08 | XP_021000996.1 | 0 | PF13574 | -- | Disintegrin-like | MIQNKFFLSLLVCFVTGGETGRLNQYISYFEPLRYNHET VHQGHLRAKRSPSDSLVYVNFHAHGRHFNIRLKRDTSA FAPDVVIETTNGVAEVDTSHLYDGHLLGESGSTVYGSIR NGVFEGKIHTPNKVYYVERSHKYFSSNPQPFHSVIYSSD DVEDPYADKRESHAGGCGITEDVLQWMQEVSNSADPK EMSPTNKTNPEQSHLERSERSTAAENAPHNIYTREAQRD INQIDQLQAKRACTLYVQTDVFLWKHILTYEKTASSARE EISSLISQHVRAVNYIYENTDFDGYRGIKFVVQRIKINDT SSCSNQGLDYKRTNPFCSPNIDVSNFLNLNSQFNHDDFC LAYIFTYRDFSGGTLGLAWVASASGASGGICEKYKPYN ENINGRQVQTKRSLNTGVITFVNYNSRVPPKVSELTLAH EIGHNFGSPEVMVLSVVIKLWKILKNATVGMMQRNAM MNAAIHETSLFSK | ATGATACAAAACAAGTTCTTTTTGTCACTGCTTGTTTGTTTTGTGACA GGAGGTGAAACCGGTCGACTTAATCAGTATATAAGTTATTTTGAGCC ACTGAGGTACAACCACGAAACTGTACATCAAGGTCATTTACGTGCCA AACGTTCACCTTCAGATTCCTTAGTTTATGTGAATTTCCATGCACATG GAAGGCATTTTAATATTCGACTTAAAAGGGACACATCAGCTTTTGCT CCAGATGTTGTTATAGAAACTACTAATGGTGTAGCAGAAGTTGACAC ATCCCACTTATATGATGGGCATTTGTTAGGGGAATCAGGATCCACTG TATATGGCTCAATAAGGAATGGTGTATTTGAGGGAAAGATTCATACA CCGAACAAAGTTTATTATGTAGAACGCTCTCACAAATATTTTTCATCA AACCCTCAACCATTTCACTCTGTGATATACTCATCAGATGATGTGGA AGATCCATATGCTGACAAACGGGAGTCACATGCAGGTGGATGTGGC ATCACAGAGGATGTTTTACAGTGGATGCAAGAAGTTAGCAATTCAGC AGATCCTAAAGAAATGTCCCCTACAAACAAGACAAACCCGGAGCAG TCTCATTTGGAAAGAAGTGAACGTTCAACAGCTGCGGAAAATGCACC TCATAATATCTATACAAGAGAAGCGCAACGTGATATTAATCAGATAG ACCAATTACAAGCAAAAAGAGCATGTACATTATATGTGCAAACAGA TGTATTTCTATGGAAGCATATTTTGACGTATGAAAAAACTGCTAGTA GTGCACGAGAAGAAATATCTTCATTAATATCTCAACATGTGAGAGCC GTTAACTATATTTATGAAAATACTGACTTTGATGGCTATCGGGGCAT AAAGTTTGTGGTGCAAAGAATTAAGATAAATGACACATCATCGTGTT CCAATCAAGGGTTGGATTACAAACGAACAAATCCATTCTGCTCGCCA AATATTGATGTATCAAACTTTTTAAATTTGAATTCTCAATTCAACCAT GATGATTTCTGTTTAGCATACATTTTTACGTACAGAGATTTCTCTGGT GGTACATTAGGACTTGCATGGGTTGCATCAGCATCAGGTGCTTCTGG AGGAATCTGTGAGAAATACAAGCCATACAATGAAAATATTAATGGC AGACAAGTACAAACCAAAAGAAGCCTGAACACTGGTGTGATTACCT TTGTCAATTACAACAGCCGAGTACCTCCAAAAGTGTCAGAATTGACA TTGGCTCATGAAATTGGACACAACTTTGGTTCACCTGAAGTGATGGT GCTTTCTGTGGTAATAAAATTGTGGAAAATACTGAAGAATGCGACTG TGGGTATGATGCAAAGGAATGCAATGATGAATGCTGCTATCCACGAG ACGTCACTCTTTTCCAAATGA |

| TatEnzMtp09 | XP_021000340.1 | 0 | PF13582 | -- | Disintegrin-like | SDSSHIEPYSTRHLFRHGKSPSVFPVAKRPMYLCSILLAT LWICGVYTYQNIKVHERMTPEELRQIFHVDLHNEVPEY DVVNVRSLSKRSTPSGNRKQLHLSAFGKKLHLNLKKNE EFENKLASMKVFEAETNQNGLKYREMEPQEHASDMGV SFQDEQQMAAVLVRHSDSGTVQVEGTIGNNLVIKPVPPS LVAFDDAYVDDEMFLDEDGINSTKPSQRHLPILNATSHII YMRKGYGSEQLSDYMDLESGHTDKQNWTMRSPRVKR KAPSTVFPEVLVVVDYNTLLMHGSDSRALKRYFVSFWN GVDLRYKTLSNPRVKVSLAGMVVAKDKDATPYLEKNR LRPPNYDAVDAAGALSDMGKYLYREDRLPTFDVAVVIT KLDMCRRQFNGGRCSRGTAGFAYVGGACVVNKRLEKV NSVAIIEDSGGFSGIIVAAHEVGHLLGCVHDGSQPPSYLG GPGATSCPWEDGYIMSDLRHTDRGFKWSPCSVQQFKHF LHGETAVCLYNYPHDNQALARILPGTTMSLDDQCRKDR GTTACFKDARVCAQLFCYDTSSGFCVSFRPAAEGSTCG HGQVCR | TCGGATTCAAGTCACATCGAACCATATTCCACCCGCCATCTTTTCCGG CACGGAAAAAGTCCGTCCGTATTTCCGGTGGCAAAACGACCCATGTA CCTGTGTTCCATTCTCTTAGCCACTCTGTGGATATGTGGCGTATATAC GTATCAAAATATAAAGGTTCACGAAAGGATGACGCCCGAAGAATTA AGACAAATATTTCATGTGGATTTACATAACGAAGTGCCGGAATATGA CGTCGTTAACGTTCGATCCTTGTCAAAACGTTCAACGCCCTCTGGCA ACAGGAAACAGCTGCATCTATCAGCGTTCGGGAAAAAATTGCATTTA AATTTAAAAAAGAATGAAGAATTTGAAAACAAGTTGGCATCGATGA AAGTATTTGAAGCAGAAACCAATCAAAATGGACTTAAATATCGAGA AATGGAACCACAAGAGCACGCGTCTGACATGGGTGTTAGTTTCCAAG ATGAGCAACAGATGGCAGCAGTATTAGTAAGACACTCAGACAGCGG AACAGTACAAGTGGAAGGCACAATCGGTAACAACCTTGTAATTAAA CCAGTACCTCCATCGTTGGTTGCATTTGATGATGCTTACGTCGATGAC GAGATGTTCCTTGATGAAGATGGAATTAATAGTACAAAGCCAAGTGA GCGCCATCTACCGATACTAAATGCAACTAGTCATATCATTTATATGA GAAAAGGATATGGTTCGGAACAACTTAGTGATTACATGGATTTGGAA AGTGGTCATACAGACAAGCAAAACTGGACAATGAGGAGTCCAAGAG TCAAAAGAAAAGCTCCTTCAACCGTTTTTTCCTGAGGTTTTAGTAGTTG TGGATTATAATACTCTGTTGATGCACGGAAGTGATAGTCGGGCATTA AAAAGATACTTTGTCAGTTTTTGGAACGGGGTAGATTTGCGTTACAA GACACTCTCGAATCCTAGGGTTAAAGTTAGTTTAGCTGGGATGGTAG TGGCAAAGGATAAAGATGCTACGCCTTATCTAGAAAAGAATCGCCTT AGGCCACCAAATTACGATGCTGTGGATGCTGCGGGAGCCTTGTCTGA CATGGGAAAGTACTTATATAGAGAAGACAGGCTACCGACCTTCGATG TTGCTGTTGTCATCACTAAATTAGATATGTGTAGAAGACAGTTCAAT GGGGGACGATGTAGCCGTGGAACTGCGGGTTTCGCTTATGTGGGTGG TGCTTGTGTAGTTAATAAAAGACTAGAAAAAGTAAACAGTGTTGCCA TTATCGAGGACAGTGGTGGATTTAGTGGTATCATTGTAGCAGCTCAT GAGGTTGGCCACCTGTTAGGCTGCGTTCACGATGGCTCCCAACCACC CAGTTACTTAGGAGGACCAGGTGCTACCAGTTGTCCATGGGAAGATG GTTATATCATGAGTGACCTTCGACACACTGATAGGGGGTTCAAATGG TCACCTTGCAGCGTACAGCAGTTTAAACATTTTTTACATGGAGAAAC TGCTGTGTGTCTTTACAACTATCCTCATGACAACCAAGCTCTAGCAA GAATATTACCTGGAACTACGATGTCTTTGGATGATCAATGTAGAAAG GATAGAGGCACCACTGCTTGTTTTAAAGATGCCAGAGTATGTGCGCA GTTATTTTGTTATGATACATCATCAGGCTTCTGTGTGTCGTTCAGGCC AGCAGCAGAAGGTTCTACTTGCGGCCATGGTCAAGTATGCCGA |

TatEnzMtp10	KFM63257.1	5 e-25	PF13582	--	Disintegrin-like	RKPSMLSLFLLASFTFVIGKAQDHEIVYPRMIISRSGEKR VLFRAFDRDFRLRLEPVDALTDDLVVHTTDDNGEEVFY KPNVDNLRETILQDPNVGATISIDDNGPLKIKGVINEKLR IEPDVSSHHKGGHHGGHYGKKGKKGKYYGKYMRQYD EFSEGIEQEREDPMEQIPHRVYEVTQRINDPEFFYDEIMP PDLKYNLSNEKTIENRADIIIVEVAVVSDVEHSKMLGSN DDCAVYHVILMNSVNLRFRTMEKTNIRFLLTDIVRNQPG QQPYIDGCMVDGHALSSETLYALCKYVYDNPTKFQADI VHLVTKTPLGDLDKSTNTINPGVIGIAFVGAACNRKYKC GISEDDGSCFSGSSTIAHENGHLLGCSHDGDPCAYDGCP GSTQCSWNDGFIMSYVRNNEDQYAFSSCCDDCVSYFAS LRSSYCLSVNNTKRIVNVYDNRLSGTFLKEKWGTTTSES YYDIKCKKARVDWSIYRYFPGCCIDAYYCRTVADSRGS FYYWKCNADDGDPCNENKHCENGYCVDN	CGAAAGCCGAGTATGCTGTCCTTGTTCCTATTAGCAAGCTTTACTTTT GTTATTGGTAAAGCCCAAGATCATGAAATCGTTTATCCACGTATGAT CATAAGCCGATCCGGTGAAAAACGAGTGCTTTTTCGAGCATTTGACC GAGATTTTCGTTTAAGATTAGAACCAGTCGATGCGTTAACAGACGAT TTGGTAGTTCACACGACAGACGATAATGGAGAAGAAGTCTTTTATAA GCCCAATGTTGACAATTTGAGAGAAACCATTCTACAGGATCCCAAATG TTGGAGCCACCATCTCCATTGACGATAATGGACCTCTGAAGATTAAA GGAGTCATCAATGAGAAATTGCGTATTGAACCAGATGTGAGCAGCC ATCATAAAGGCGGACATCATGGAGGACATTATGGAAAAAAAGGGAA AAAAGGCAAATACTATGGGAAATATATGCGCCAATATGATGAATTTA GTGAAGGAATAGAACAAGAAAGAGAAGATCCTATGGAACAGATTCC GCATAGAGTATATGAGGTCACTCAGAGGATTAACGATCCTGAATTTT TTTATGATGAAATCATGCCTCCTGATCTCAAGTATAACTTATCCAATG AGAAAACTATTGAAAACCGTGCAGACATAATAATCGTGGAAGTTGCT GTGGTTTCAGACGTTGAACATTCAAAAATGCTTGGTTCAAACGACGA TTGCGCTGTATATCATGTCATCTTAATGAATTCCGTTAACTTAAGGTT TCGAACCATGGAAAAAACCAACATAAGATTTTTGTTAACTGATATTG TGAGAAACCAACCAGGGCAACAGCCATACATTGATGGTTGTATGGTC GATGGTCATGCTCTATCGAGCGAAACTTTATACGCTTTGTGCAAATA TGTGTATGATAACCCAACGAAATTTCAAGCAGATATTGTTCACTTAG TAACTAAGCACCATTGGGAGACCTGGACAAATCAACCAATACAAT AAATCCTGGTGTTATAGGAATTGCCTTCGTAGGAGCAGCTTGTAACA GAAAGTATAAGTGTGGTATTTCTGAAGATGATGGTAGCTGCTTTAGT GGAAGTTCAACCATTGCCCATGAGAATGGTCATTTACTTGGTTGTTCC CATGATGGAGATCCATGTGCCTATGATGGATGTCCCGGATCAACACA ATGCTCTTGGAATGATGGTTTTATAATGAGTTATGTGAGAAATAACG AAGATCAAATATGCGTTCTCATCGTGTTGCGACGATTGCGTATCGTATT TTGCATCGTTACGCTCCTCTTACTGCCTGTCAGTAAACAATACTAAAA GGATAGTTAACGTTTATGATAATCGTCTGTCTGGAACTTTTTTAAAAG AAAAATGGGGAACCACAACATCAGAAAGTTATTACGATATCAAATG CAAGAAAGCAAGAGTTGATTGGTCTATTTATCGATATTTTCCTGGTTG CTGTATAGATGCATATTACTGTAGAACAGTAGCAGATAGTCGTGGTT CTTTCTATTATTGGAAGTGCAATGCCGACGATGGAGACCCTTGCAAT GAGAACAAACACTGCGAGAACGGATATTGTGTTGACAAT
TatEnzMtp11	AMO02515.1	1 e-93	PF01421	--	Disintegrin-like	GNTGMHEWGFKQFRIRPAKLKRDVSQVFKYIELALVID QAMFDNRNATRSEVVNDAVQIVNCVDMYFRTVNTRVS VVYVETWAHGDQIEAGSDVRQTLLNFMEYTSRKLYKV AKDATHLITGRHFRGNEVGMAVPDSICTAKA	GGAAACACAGGAATGCACGAATGGGGTTTTAAGCAATTTCGGATAC GTCCAGCTAAGCTCAAGCGTGACGTGAGCCAGGTATTTAAATATATT GAATTGGCACTTGTGATCGATCAAGCTATGTTTGACAACAGAAATGC TACCAGATCTGAAGTTGTAAATGATGCTGTTCAGATAGTCAACTGTG TGGATATGTATTTTCGCACAGTGAACACACGGGTTTCTGTTGTGTATG TTGAAACATGGGCACATGGGGACCAAATTGAAGCAGGCAGTGATGT GCGACAAACCTTGCTCAATTTCATGGAATACACATCACGCAAACTTT ATAAAGTCGCCAAAGATGCAACACATTTAATAACTGGTAGGCATTTT CGAGGCAATGAAGTTGGGATGGCTGTTCCTGATAGCATTTGCACTGC CAAAGCT
TatEnzMtp12	XP_019771969.1	7 e-8	PF01421	--	Disintegrin-like	SPYVNMASLSILILVLSTFSLYGALNGDNTKVEILAVVEK ELSDEFKLDNWRKSYFCRIFNEVQRYYDTIEGVKIKIILS GLKIITESKDQPFIERWTWKRGNRTYLRTICLQKFSRFAR GQLWSKDYDVIFLLTRKAIADIYSEIDGIAYKYGTCNFEE KFGVMVPDPKIIAHELGHLLGASNDGSRNPCSSDDGFV MAEYSHLVTENYGRFSSCTTDAIKMHLKSPKSYCLRRN DVQNTVMCENKTSFHDICYPISSVVSRMKGGGKIDKL	TCGCCTTATGTTAATATGGCATCGCTTTCAATCCTAATTTTAGTTTTG AGCACCTTCTCACTTTATGGAGCTTTGAATGGTGATAACACGAAAGT CGAAATTCTTGCCGTTGTGGAGAAGGAACTTTCTGATGAGTTTAAAT TAGACAACTGGAGAAAATCATACTTTTGTCGTATATTCAATGAGGTG CAACGATATTACGATACCATAGAGGGAGTCAAAATAAAAATTATTCT CAGCGGATTAAAGATTATTACGGAATCTAAGGATCAACCTTTTATTG AACGCTGGACTTGGAAAAGGGGGAAACAGAACTTATCTAAGAACCAT ATGTCTACAGAAGTTTTCGAGATTCGCGCGAGGGCAATTATGGAGTA AAGATTATGACGTCATATTCCTGTTAACCAGGAAAGCTATAGCAGAC ATCTATTCTGAAATCGATGGTATAGCTTACAAGTATGGCACCTGCAA TTTTGAGGAAAAATTTGGAGTAATGGTTCCTGATCCGAAAATAATTG CGCACGAGCTTGGTCATCTGTTAGGTGCTTCCAACGATGGTTCAAGG AATCCATGTTCTAGCGATGATGGCTTTGTAATGGCTGAGTATTCACAT CTCGTGACAGAAAACTATGGAAGGTTTTCTAGTTGTACAACTGACGC AATTAAAATGCATCTGAAATCTCCTAAGAGCTACTGTCTTCGAAGAA ACGATGTTCAGAATACAGTAATGTGTGAAAACAAAACGTCTTTCCAC GATATCTGCTATCCAATAAGCTCAGTGGTTTCCAGAATGAAGGGAGG AGGCAAAATTGATAAGCTA

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatEnzMtp13	XP_013781814.1	1 e-13	PF01421	--	Disintegrin-like	RLYREERGLNMPAFSIQIFVLSMSIFALTEVLYSEEITVEVLAVLEKEIADEYKFESERKANLCSIFKEVQGYYDNFEGVKINIVLNGIKTLTGPYFRPSTDFPHYKYATTMKDERVVQFSRFMQTQTWSNRYDVILLLMKEVFLGKASLFGGLSYLNGSCEHKRKVGIVIPDPRIIAHEIGHLLGAQNDGTNNSCSSEDGYIMQSTATVSVENYHRFSNCSIEEIKRRIRSPEAHCLYTNDIMDSVKCGQMTSCHEHCLPITSVVSSTIDDWKN	CGGTTATACAGAGAAGAAAGAGGATTAAACATGCCTGCATTTTCTATCCAAATTTTTGTTTTGAGTATGAGCATATTTGCATTAACTGAAGTTCTGTATAGTGAAGAAATAACAGTAGAAGTTCTTGCAGTTCTGGAGAAGGAAATAGCCGATGAGTATAAATTTGAGTCCGAGAGAAAAGCAAATCTTTGCAGTATTTTCAAAGAGGTGCAGGGATATTATGATAATTTTGAAGGAGTTAAAATAAACATTGTTCTCAATGGAATCAAGACCCTTACGGGCCCGTATTTCCGTCCATCTACTGATTTTCCGCATTATAAATATGCAACTACAATGAAAGATGAAAGAGTGGTGCAATTTTCTCGCTTCATGCAAACACAAACGTGGAGTAACAGATATGATGTCATATTACTTTTAATGAAAGAAGTTTTTTTAGGCAAGGCCTCGTTATTCGGTGGTCTCTCTTATCTCAATGGTTCCTGCGAACATAAGCGGAAAGTAGGAATAGTGATCCCTGATCCGAGAATAATAGCGCACGAAATTGGCCATTTATTAGGTGCTCAGAACGATGGTACCAATAATTCATGTTCAAGCGAAGACGGATATATAATGCAATCAACAGCTACTGTATCTGTAGAAAATTACCATAGATTTTCCAATTGTTCAATTGAAGAAATTAAGAGACGTATAAGATCGCCTGAAGCTCATTGTCTCTATACCAATGATATAATGGATAGTGTAAAATGTGGACAGATGACATCTTGCCATGAACACTGCCTCCCAATAACCTCTGTGGTTTCCAGCACAATTGATGACTGGAAAAATTGATTAAGAAAACATAACATTGAA
TatEnzMtp14	XP_013781814.1	6 e-14	PF01421	--	Disintegrin-like	EKQVNLMSNCCLIAMLALSIEIFVFSIFPLIEAQNSKKEEAEVEVLAILEKEYSDEFESDSKRKLDICDIFNEKTEDQPFIEHSSWRNNNVTYLNKTVLAKFSSFLQKEVWNNQYDVILLLTKKLMAGKNWSLKGAAYRYGSCRHSLKFGIVFPDPRMIAHEIGHLLGADNDGANNTCSSDDGYLMRAYSDIVSYENHRKFSHCSIEAIKQHLESHWSDCLRDTGVKDTVRCGERTSCNNHCRII	GAAAAGCAAGTTAATTTAATGAGTAACTGCTGCCTTATTGCCATGCTCGCGCTTTCAATTGAGATTTTCGTTTTTAGTATCTTCCCACTTATTGAAGCTCAGAATAGCAAAAAAGAAGAAGCAGAAGTCGAAGTTCTTGCCATTCTAGAGAAGGAATATTCTGATGAGTTTGAATCTGACTCCAAAAGAAAATTAGATATTTGTGATATTTTTAATGAGAAACGGAGGACCAGCCTTTCATTGAACACTCGTCTTGGCGAAATAACAACGTAACTTACCTAAACAAAACCGTTCTGGCCAAATTTTCAAGTTTCTTGCAAAAAGAAGTATGGAATAATCAGTATGATGTCATACTGCTTTTAACAAAGAAATTGATGGCAGGCAAAAATTGGAGTCTAAAAGGTGCAGCTTACCGATATGGATCCTGCAGGCATTCGCTAAAATTCGGAATAGTTTTTCCTGATCCAAGGATGATAGCACACGAAATTGGCCATCTGTTAGGTGCTGACAATGATGGCGCAAATAATACATGTTCCAGCGACGATGGCTATTTAATGAGAGCATATTCGGATATTGTATCTTATGAAAACCATAGGAAATTTTCTCATTGTTCAATTGAAGCTATTAAACAGCATCTGGAGTCACATTGGAGCGACTGTCTTCGAGATACCGGCGTTAAAGACACAGTAAGATGTGGAGAGAGAACGTCTTGCAACAACCACTGCCGAATAATA

CAP-Superfamily

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence

TatOthCRI01	JAV48224.1	0	PF00188	--	CRISP	MIKKITRFTVSFVPQIWIIVLLILSSSSSHGETICEAKYRNI HPEHSMCKARNNTCKFRQGLEENAKELVDFHNRIRKSI RQIIGNNFSEGKSMKNMQWDHELYLIAQKHVLQCTGLP DCYQCHQTDRFYVEQNFAVKTFNSVKESFNGTIERFKA VIKEWAEELSEYGPEVVNKFHFTGLPTNWTNIFRATTNK VGCASIAYDTQKEGTFTEVYVCNYGPAILTENEVIYEPV YTNCNNGLCKNQFLEKYGNSNFYRSNRPPERGKRSGAQ LQHNNGRLSRNSEEEECPAKYRNITVDHSYCKPDVEGC VFSRKYVRYRKKLLDTHNEIRNSVEAYAGWAYGTATN MRVMEWDDELYDIAKRYVIQCLVEPDCHLCHQAADFP VEQNFAVKVISYNGPQSQERFGAVIKGWAMELKNFAQS DVEHLSKEIIQRDDKNWINVFRASAWKVGCASISFETSP KPDLIVKEVYICNYGPAELSEGEEVYQIGESCSNCDPGFD CDEKYPNLCSKKEKPESNDDWLTQTMAAKTTAETTAS KNSIRTESDIFADEVDGSTVGSVKTSVNITTPTMTTAITTP SAPTTTITVSPVPTVSLSTENPHATEMPVETSTVSAVTS KQIVLYNNKTKTSKGNIVWNCTLRFFDDEECRREQQCF QAWTMSNDGKQPFMEIDIPENRRTALLFLHQIYIEKPSCF TFTYMKDGLSRLSSLDSTLYGIVVRTESNEHVMVDVNG NVPVWNSLAVDIPWEKVFVQVGVAVKTYDGRGEQHIQ IKDLLIHVGPCTAL	ACACAATGTAGAATAGGATCAGTAAATCCAAAGTTAACAGGAGATA ATCTTATAATGATTAAGAAAATAACTCGATTCACTGTCAGTTTTGTTC CACAAATTTGGATTATCGTTTTGCTCATTCTGAGTTCCAGCTCAAGTC ATGGGGAAACTATTTGTGAAGCCAAATATCGAAATATACATCCGGAA CATTCGATGTGCAAGGCTAGGAATAATACCTGCAAATTTAGGCAAGG ATTGGAGGAAAACGCTAAGGAACTTGTGGACTTTCATAACCGAATCC GAAAGTCGATACGACAGATTATTGGAAACAACTTTTCCGAAGGGAA AAGTATGAAAAATATGCAATGGGATCACGAGCTCTATCTCATAGCTC AAAAACACGTGCTTCAATGCACAGGATTACCCGATTGCTACCAGTGT CATCAAACAGATAGATTTTACGTGGAACAAAATTTTGCGGTCAAAAC CTTCAATTCTGTTAAAGAAAGCTTCAACGGAACCATTGAACGGTTTA AAGCAGTTATAAAAGAATGGGCTGAAGAACTAAGCGAGTATGGTCC AGAGGTAGTTAACAAGTTCCATTTCACTGGGCTTCCTACTAATTGGA CAAATATATTTCGCGCGACAACTAATAAAGTGGGGGTGTGCGTCGATA GCTTATGACACGCAGAAAGAGGGCACTTTTACAGAGGGTTTACGTATG TAATTACGGTCCTGCAATTCTTACAGAGAACGAAGTTATTTACGAAC CAGTATATACAAATTGCAACAATGGTTTATGTAAAAATCAGTTCTTG GAGAAATATGGAAACAGCAACTTCTATCGTTCCAATAGACCGCCCGA GAGAGGAAAACGTAGCGGTGCACAGTTGCAACATAATAATGGACGT CTATCTCGAAATTCAGAAGAGGAAGAGTGCCCAGCTAAGTATCGAA ATATTACAGTAGATCATTCCTATTGCAAACCAGATGTTGAAGGATGC GTATTTAGCAGAAAAATATGTCAGATACAGAAAGAAACTCTTAGATAC TCATAACGAAATTCGTAATTCAGTTGAAGCTTATGCAGGTTGGGCTT ATGGTACTGCAACGAACATGCGAGTAATGGAATGGGATGATGAACT GTATGATATTGCTAAACGCTATGTCATTCAATGTCTTGTGGAACCAG ACTGTCATTTATGCCACCAAGCAGCTGACTTCCCTGTGGAGCAGAAC TTTGCTGTTAAAGTTATAAGCTATAATGGACCCCAATCACAAGAAAG ATTTGGAGCAGTAATTAAGGGATGGGCTATGGAATTAAAGAATTTTG CACAGAGTGATGTGGAGCATCTCTCCAAGGAAATTATACAAAGAGA TGATAAAAACTGGATAAATGTATTTCGAGCGAGTGCATGGAAGGTA GGATGTGCATCAATATCATTTGAAACGTCACCAAAACCAGATCTTAT TGTGAAGGAAGTGTATATATGCAATTATGGCCCAGCTGAATTATCTG AAGGTGAAGAAGTATATCAAATTGGAGAGTCTTGTAGCAACTGCGA CCCAGGGTTTGATTGTGATGAAAAATACCCTAATTTATGTAGCAAAA AAGAGAAACCTGAATCCAACGATGATTGGCTAACTCAAACGATGGC AGCAAAGACAACTGCAGAAACTACAGCTAGCAAAAATTCTATTAGG ACTGAAAGTGATATCTTTGCAGACGAGGTTGATGGATCTACTGTTGG TTCAGTGAAGACAAGTGTAAATATAACCACTCCCACCATGACAACTG CAATTACAACCCCTTCAGCTCCAACCACCACAACAATTACAGTTTCA CCAGTGCCAACTGTATCCCTTAGCACAGAGAACCCACACGCAACTGA AATGCCTGTTGAGACTAGCACAGTATCTGCTGTCACAAGTAAGCAAA TTGTGTTATATAATAATAAAACAAAAACTTCTAAAGGCAACATAGTG TGGAACTGCACCTTGCGGTTTTTCGATGATGAGGAATGTAGACGTGA GCAACAGTGTTTTCAAGCATGGACTATGTCAAATGATGGAAAACAGC CGTTTATGGAAATTGATATTCCAGAAAACCGGAGAACAGCCTTATTG TTTCTTCATCAAATTTATATTGAAAAACCTTCTTGTTTTACTTTTACCT ATATGAAAGATGGGCTCAGCAGATTGTCTTCTCTTGACAGCACTCTTT ACGGTATTGTTGTTAGGACAGAAAGCAACGAACATGTAATGGTGGAT GTGAACGGTAATGTTCCTGTCTGGAATTCTCTAGCTGTGGATATTCCT TGGGAGAAAGTTTTTGTCCAGGTGGGAGTTGCTGTTAAAACATATGA TGGAAGGGGGTGAGCAGCACATTCAAATAAAGGATTTACTAATCCATG TTGGACCATGTACTGCATTG

TatOthCRI02	XP_013781883.1	1 e-119	PF00188, PF08562	--	CRISP	MAILGKNLFIKPQLFNSAIVEICLILLVSAYPRLQRPKLYG DAIPLRDLDPTHFKTRRKIVLLHNSYRARVDPPASNMLA MSWHEEAAKDAQRWAEACELLVHDSPTGRWVNNYGS CGQNIFVANMKVSWSFALKAWNVERYDFEYGSNKNIPS VVGHYTQMVWYKSHKVGCGFHYCGENRVKKPFYNYV CNYCPIGNDPATFNEPYGIGKPCSKCPGKCKYKKLCTNG CRYGDSWSNCAELNATWSNWLCSDPKQQRYHSCMGT CRCGSEFIK	ATGGCCATCTTAGGAAAGAATTTATTTATCAAACCACAACTTTTTAAT TCTGCGATTGTAGAAATATGTTTGATTCTACTGGTCTCTGCCTACCCT CGGCTCCAACGTCCTAAACTATACGGCGATGCCATACCGCTTCGTGA TTTAGATCCTACTCATTTCAAAACTCGAAGAAAGATTGTTCTTCTGCA CAATTCTTATCGCGCAAGAGTGGATCCTCCAGCAAGTAATATGTTAG CAATGTCATGGCATGAGGAAGCAGCAAAAGACGCTCAGCGGTGGGC GGAAGCTTGTGAATTACTTGTTCATGACAGCCCAACTGGTCGTTGGG TGAATAATTATGGATCCTGTGGGCAAAATATTTTCGTAGCAAATATG AAAGTGAGTTGGTCTTTCGCTCTAAAAGCTTGGAATGTGGAAAGATA TGATTTCGAATACGGCAGCAATAAAAACATCCCATCTGTGGTGGGAC ACTACACTCAGATGGTATGGTATAAAATCTCACAAGGTAGGATGTGGA TTCCATTACTGTGGAGAAAATAGGGTGAAAAAGCCTTTTTACAATTA CGTATGCAATTACTGTCCAATAGGTAATGATCCTGCTACATTTAATG AACCATACGGAATTGGAAAACCTTGTTCAAAATGTCCAGGAAAATGC AAATATAAAAAACTATGCACTAATGGGTGTAGATATGGCGATTCTTG GAGTAACTGTGCAGAACTAAATGCAACTTGGAGCAACTGGTTATGCA GTGACCCTAAACAACAACGCTATCATTCCTGCATGGGTACTTGTCGT TGTGGATCTGAATTCATCAAATGAATTATAAAGCACTTCAAACAACG AGAACGCGAC
TatOthCRI03	XP_015929114.1	3 e-66	PF00188	--	CRISP	MLFLLAFLVPLFLKDWCYGKESPVGITAWKSEFDNMES NYVTLDYAVSNKSRRGATNMGVPIPLSDEEKVEIVSTH NKYRSQVFPPAANMRYMKWNDEVADSAQTWANKCVF KHGRPSVSKFKGAMGQNIYKGSNAPLSFYMSLWYDEV HDFDMRLKQCNGSKCGHYIQIAWAESFLIGCGHTKCEG KRGPFNIFVCHYHKPFEKEDPYIIGRPCSMCNVETGGFC YNNMCVSKEDCERESWPCECNLKCHNCGVLNKSTCSC ECPPGWDFQDCSQQCIDEDSWCGKEGGYQGWVGCAM LEDNGFCRKMCGICEDITKDNEHMTCCEGKRCETGYVL NLVNNNCSCQLLCPGPECFTIPDSGHALQGRYYVLLTV MISMCIVLYSCM	ATGCTGTTTCTTTTAGCATTTCTGGTGCCATTGTTTTTAAAAGACTGG TGTTATGGGAAAGAAAGTCCAGTTGGTATTACTGCGTGGAAAAGTGA ATTTGATAATATGGAATCTAATTATGTGACATTAGATTACGCAGTAT CTAATAAGTCGAGAAGAGGGGGCCACTAATATGGGAGTACCTATACC ACTTAGTGATGAAGAGAAGGTAGAAATAGTCAGCACCCACAACAAG TACAGAAGTCAAGTGTTTCCACCAGCTGCCAATATGAGATACATGAA ATGGAATGACGAAGTAGCCGACTCAGCTCAAACCTGGGCGAACAAA TGCGTTTTCAAACATGGCCGTCCCTCAGTGTCGAAGTTTAAAGGAGC GATGGGTCAAAACATATACAAAGGAAGTAATGCGCCTTTGTCATTCT ACATGTCACTCTGGTATGATGAAGTACACGATTTTGATATGAGGCTA AAACAATGTAATGGTAGCAAATGCGGGCATTATATTCAGATTGCATG GGCTGAATCTTTTTTAATAGGCTGTGGTCACACTAAATGCGAAGGAA AACGGGGTCCTTTTAACATTTTTGTATGCCATTACCATAAACCTTTTG AAAAGGAGGATCCATATATCATTGGTAGGCCATGTTCTATGTGCAAT GTAGAAACAGGAGGATTTTGTTACAATAATATGTGTGTCTCTAAAGA GGATTGCGAAAGAGAGAGTTGGCCTTGTGAGTGCAATTTGAAGTGTC ACAACTGTGGTGTGCTTAACAAATCAACGTGTTCCTGCGAATGTCCA CCAGGGTGGGATTTTCAAGATTGTTCGCAACAATGTATAGACGAAGA TAGTTGGTGCGGAAAGGAAGGTGGTTACCAAGGTTGGGTTGGTTGTG CAATGTTGGAAGATAACGGGTTTTGTAGAAAGATGTGTGGAATTTGC GAAGACATCACAAAAGACAATGAACATATGACATGCTGCGAAGGTA AAAGATGCGAAACTGGATATGTCCTAAATCTCGTTAATAATAACTGC AGTTGTCAGCTGTTATGTCCGGGACCAGAATGCTTTACAATACCGGA CAGCGGGCATGCACTGCAAGGAAGATATTATGTGTTACTTACTGTAA TGATATCAATGTGTATAGTTTTGTATAGCTGTATG

TatOthCRI04	JAV45657.1	3 e-16	PF00188	--		CRISP	MQATMKLMLGITSLLFAVPSILCLTCSQSSYGNYDETSLESTRDETIPIDWWKILKINPGFAERKSIIVQKECPEIYQRFSVNHTFCKEAAEGIITEGVTDEDKNVILDIHNTLRSKLASGEEARYRQLPSAANMMQMEWDDELAAVAQAHSNLCKFEHDESDQRAVENFRVGQNLLLSTSPNKNWNSSQRWYKEEVCFFFPEYINPFQFQSDFGHFSQVTWATTWKVGCGFTAYQEGSGTRTLYTCNYGPGGNVDGGVQYIVGEPCSQCPDNTECSTQYPGLCKSLTENGPQIPRPAADEYILFCDFSEEDPEECININVEGSKNFSTGHIYSGNYKTVILEEGEHITIDFGEAQNDGGFCPFLYSRFGPNNAKESNGAVMEFLFRSPNTVPQPPTKMPPRGPNFSTFGIYMMYNGKLKTTVTLRAEEGAAPQYFDIKYWGIRRGNCKTNF

ATGCAAGCCACCATGAAGTTGATGTTGGGAATAACTTCACTGCTTTTCGCAGTTCCCTCCATTTTGTGCCTTACATGCTCTCAGAGTTCATATGGAAATTACGATGAAACCTCCCTAGAATCCACAAGAGATGAGACGATTCCCATTGATTGGTGGAAAATACTAAAAATCAACCCTGGGTTTGCTGAAAGAAAATCAATTATAGTTCAGAAAGAATGTCCAGAAATCTACCAACGTTTCAGTGTTAATCACACTTTCTGTAAGGAAGCAGCAGAAGGTATTATAACAGAAGGAGTGACTGACGAAGACAAGAATGTTATTTTGGACATACATAATACATTAAGAAGCAAGCTGGCTAGTGGAGAAGAAGCACGTTATCGTCAATTGCCTTCTGCAGCAAACATGATGCAAATGGAATGGGATGATGAATTAGCAGCTGTAGCTCAAGCCCATTCGAACCTTTGCAAGTTTGAACATGACGAGAGTGATCAGAGAGCTGTAGAAAACTTCCGGGTTGGACAAAATTTGTTGCTATCAACTTCTCCAAACAAGAACTGGAATTCTTCTCAGAGGTGGTATAAAGAAGAAGTGTGCTTTTTCTTTCCTGAATATATTAACCCATTTCAATTCCAAAGCGATTTTGGACATTTCTCTCAGGTAACATGGGCAACAACATGGAAGGTAGGATGTGGATTTACAGCTTACCAAGAGGGTAGTGGAACGAGGACACTCTATACATGCAATTATGGACCTGGGGGTAATGTTGATGGAGGTGTACAATACATTGTAGGAGAGCCTTGTTCTCAATGTCCTGACAACACAGAGTGTTCGACTCAGTATCCAGGACTTTGTAAATCTCTAACCGAAAATGGACCACAGATACCAAGACCAGCAGCAGATGAATACATACTGTTCTGCGATTTTAGTGAGGAAGACCCAGAAGAATGTATTAACATTAATGTTGAAGGTTCAAAGAACTTCTCAACAGGACACATATATTCTGGTAATTACAAAACAGTCATTCTTGAAGAAGGCGAGCATATAACCATTGATTCGGGGAAGCACAGAATGATGGGGGTTTCTGCCCATTCTCTACAGTCGTTTTGGTCCTAACAATGCTAAAGAAAGCAATGGAGCTGTAATGGAATTCCTTTTCAGAAGTCCAAACACTGTACCACAGCCTCCAACAAAAATGCCTCCACGTGGTCCTAACTTTTCCACATTTGGTATATATATGATGTACAATGGCAAGCTTAAGACGACTGTAACACTTAGAGCAGAAGAGGGCGCTGCACCGCAATATTTTGACATTAAGTACTGGGGTATTCGCAGGGGAAATTGCAAAACTAATTTCT

| TatOthCRI05 | JAV45657.1 | 4 e-83 | PF00188 | -- | | CRISP | MVKLMNLHHYYSIMVFLIFISFLLCGVSCSNKLPEDEDEQRYIFINKKKSCIIGQENDCNSNMFRDIFLHHQNTERKTIGAKLNMNLAASNMLQMEWDQTLADGAWKYVETCFLDYPTYVGIEVCREASIVTTFDGGVNYYRKTYKEDYPHVVDRILNAIANWTNYINDYDKSKLKVLHLYQESGAAEDSWSQVVRATTWKFGCALADGRTENTRLDEFVEVIACFYGNTKLQKGDEIFKPGKPCSSCPLGTHCNEYLCEVEPGQCPVPGNDFALEGQHCHKIDIVEIQEDSEESGEILWECNLQKYGEQCEILPSCSPFWNIDLIGNFKTITVKGNCVSANVFLEEISVVVPSCFRFQYIKERNPTRRFHTMVMGFAFNLNSGESINIMKNEDANSWADVNLDIPWTNTVIQVGILVRSYSDNIFQQHVTVGNFSVFEGNCS |

ATGGTTAAGTTGATGAATCTTCATCATTATTATTCAATTATGGTGTTCCTTATCTTTATAAGTTTCTTATTGTGCGGAGTTTCATGTTCCAATAAACTGCCAGAGGATGAGGATGAACAAAGATACATATTTATCAACAAAAAAGTCATGCATCATTGGTCAAGAAAATGATTGTAATTCAAACATGTTTCGAGACATATTTTTACATCATCAGAACACTGAGCGTAAAACAATTGGTGCTAAACTAAATATGAATTTAGCTGCATCAAATATGTTACAGATGGAATGGGATCAGACACTTGCAGACGGTGCATGGAAATATGTTGAAACATGCTTTTTAGACTACCCAACTTACGTCGGGATTGAAGTTTGTAGAGAAGCAAGCATAGTAACTACTTTTGATGGTGGTGTTAATTACTACCGGAAAACTTACAAAGAAGATTATCCACATGTTGTAGATCGTATCCTTAATGCAATTGCTAATTGGACTAACTACATCAATGATTATGATAAAAGCAAACTGAAAGTACTTCATCTCTATCGGAAAGTGGCGCTGCTGAGGATTCGTGGTCCCAGGTAGTTCGAGCAACCACATGGAAATTCGGATGTGCACTTGCTGATGGTCGTACTGAAAACACTAGATTAGACGAATTCGTAGAAGTTATAGCTTGCTTTTTATGGAAACACAAAGTTGCAAAAAGGTGATGAGATATTTAAACCAGGAAAACCCTGTTCGTCTTGTCCTCTTGGAACACATTGCAACGAATATTTATGCGAAGTAGAGCCAGGCCAGTGTCCTGTACCAGGCAATGATTTTGCACTTGAAGGACAACATTGTCACAAAATAGACATAGTTGAGATTCAAGAAGATTCAGAAGAGAGTGGAGAAATTCTTTGGGAATGCAACTTGCAGAAAATATGGAGAACAATGTGAAATCTTACCTTCATGCTCACCATTCTGGAACATTGATCTAATTGGGAATTTCAAAACTATTACAGTTAAAGGTAACTGTGTATCAGCCAATGTATTTTAGAAGAGATCAGCGTCGTAGTTCCATCTTGCTTTAGATTTCAATACATTAAAGAAAGGAATCCAACGCGACGATTTCATACTATGGTAATGGGATTCGCCTTTAATTTAAACTCTGGAGAAAGCATTAATATAATGAAGAATGAAGATGCAAATAGTTGGGCTGATGTCAATTTGGATATCCCATGGACGAATACTGTAATACAGGTTGGAATACTTGTCCGTTCGTACTCCGATAACATTTTCCAGCAGCATGTAACTGTAGGGAATTTCAGCGTTTTCGAAGGAAATTGTTCC

TatOthCRI06	JAV48225.1	5 e-145	PF00188	--	CRISP	MASVIITILVLWVTTIQSFEANDECDERYSSITQEHTMCK SINENCHFLRHGGKTYEQQLLRTHNLIRNSIWKYVGKN YPLATNMEIMQWDDELYEIARMHSLQCVEQPDCDLCH QIGYFPVEQNFAVKTYKKSEVANNGPVKRFQTVIKEWA AELKQYDPSIVNDFTVTEELPTNWTNILRANTSFVGCAS MNFYTDETDVFTEVYVCNYGPAKLTTGEEIYKTGGKPC SDCEDDGICDEEFKNLCVPADLELNITIVIPEEEDTEIWLG EGNYNGTSLSEEIEGTTSPNEFTTAESAKTFLYRQTGTPE ETHTAIGEENSSVVFTETAPEETSIVEFTTELSNEPVTTEV EESGERRKRKVHPLISRLLRYSNKRRKRHQEHSLFPMN	ATGGCGTCAGTGATTATTACCATTTTAGTTCTATGGGTGACAACGATT CAAAGCTTTGAAGCCAATGATGAATGTGACGAAAGGTACAGCAGCA TTACTCAGGAACACACCATGTGCAAAAGTATAAATGAAAACTGCCAT TTTCTTAGGCACGGTGGTAAAACATATGAGCAGCAACTACTTCGCAC TCATAACTTGATACGAAATTCAATTTGGAAGTATGTTGGAAAAAACT ACCCTTTGGCAACTAATATGGAAATAATGCAATGGGATGATGAACTG TATGAAATAGCCAGGATGCATAGTCTTCAATGTGTTGAGCAACCTGA CTGTGATCTATGCCACCAGATCGGTTACTTTCCTGTGGAGCAAAATTT CGCCGTTAAAACGTATAAAAAGTCAGAGGTTGCTAACAATGGTCCCG TCAAACGATTCCAAACTGTCATTAAAGAGTGGGCAGCCGAACTGAA ACAGTATGACCCTAGTATCGTTAATGATTTTACAGTTACCGAAGAAC TTCCCACTAATTGGACTAATATCCTGCGTGCTAATACATCGTTCGTTG GATGCGCGTCCATGAATTTCTATACTGATGAAACAGACGTCTTCACA GAGGTATATGTGTGCAATTACGGACCTGCGAAACTTACTACAGGAGA AGAGATATATAAAACAGGTGGTAAACCTTGCAGCGATTGCGAAGAC GATGGAATATGCGATGAGGAGTTTAAAAACCTATGTGTTCCAGCTGA TTTAGAGCTAAATATCACAATAGTTATTCCTGAAGAAGAAGACACGG AAATTTGGCTAGGTGAGGGAAATTACAATGGAACCAGTCTAAGTGA AGAAATCGAGGGAACCACGTCACCTAACGAATTCACTACGGCAGAA TCAGCAAAAACGTTCCTTTATAGACAAACTGGAACTCCTGAAGAAAC ACATACTGCAATAGGCGAGGAAAATTCTTCTGTGTGGTATTCACAGAAA CAGCTCCAGAGGAAACTTCAATTGTTGAGTTTACAACAGAACTTTCT AACGAACCTGTCACTACAGAAGTCGAAGAAAGTGGAGAGAGGCGTA AAAGGAAAGTTCATCCCTTGATATCAAGATTGCTTAGATATAGTAAC AAACGCAGAAAGAGACATCAAGAACATAGCCTATTTCCTATGAAT
TatOthCRI07	API81352.1	0	PF00188	--	CRISP	MNFLLLSCLVLFSCQAVFAQTCPALYLRFSKDHTYCRHS TCQTEKSGVSEKDKEIIVNMHNEFRSKIAMGKETTPMQ QPPAANMMQISWDEELAAVAQAHANGCKFDHDTAPQR QVENFNVGQNLYITMMSKRIDWRKAALWYTSEVKDFY PQYREPFVFGTYGHFSQVVWAETWKVGCGMAMYYDQ SDNMDKVLYTCNYGPAGNMQGAAMYIKGQPCSQCPK NTKCSDEYEGLCKPITKDGPQNDIAKSSNDFIFYCEFSKN DPSECSKVKVEGTKGFETRKIYSGIYKSVILNGGESITIKL GKAQDAGGICPFIYGSFGPNKDGDAKMSAVSFGFSAPGI IFGDPIKIEQGGSAFWTIGMHMQFDQEMESTIKLEAYPG ATPQYFNVKAFGIGKGKCPKL	ATGAATTTCCTACTGCTGTCCTGTCTTGTCTTGTTTTCTTGCCAAGCTG TTTTTGCTCAAACCTGCCCTGCGTTGTACCTAAGATTCAGTAAGGATC ACACATACTGTCGACATTCAACATGCCAAACTGAGAAAAGTGGTGTT TCTGAAAAGGACAAGGAAATAATTGTAAACATGCATAACGAATTCA GAAGTAAAATCGCTATGGGAAAGGAAACCACACCCATGCAGCAACC CCCTGCAGCTAATATGATGCAAATATCATGGGATGAAGAGCTGGCTG CAGTTGCGCAAGCCCACGCTAATGGATGTAAATTTGACCACGACACT GCACCTCAACGACAAGTAGAAAACTTCAATGTTGGGCAAAATCTGTA TATAACCATGATGTCAAAGAGGATAGATTGGAGGAAAGCTGCTTTGT GGTACACTTCTGAAGTGAAAGATTTCTATCCACAATATAGAGAACCA TTTGTATTTGGCACATATGGGCATTTCAGTCAGGTAGTCTGGGCTGA AACATGGAAAGTGGGTTGTGGAATGGCTATGTATTATGACCAAAGCG ATAATATGGATAAAGTGCTATACACCTGTAATTATGGACCTGCAGGA AATATGCAAGGGGCTGCAATGTATATTAAAGGGCAACCATGCTCTCA GTGTCCAAAGAATACAAAATGCTCAGATGAATATGAAGGACTTTGCA AACCAATAACCAAAGATGGCCCCCAAAATGATATTGCCAAATCTTCA AATGATTTCATCTTTTACTGTGAGTTTAGTAAGAATGACCCAAGTGA GTGCAGTAAAGTCAAAGTTGAAGGAACAAAAGGATTTGAAACAAGG AAAATATACAGTGGCATATACAAGAGTGTTATTCTTAATGGAGGAGA ATCCATTACCATAAAATTAGGAAAAGCTCAAGACGCTGGAGGAATA TGCCCTTTTATTTATGGATCTTTTGGCCCCAACAAAGATGGTGATGCT AAAATGTCTGCGGTATCTTTTGGCTTTTCTGCACCTGGAATCATATTT GGAGATCCTATTAAAATAGAGCAAGGTGGTAGTGCTTTCTGGACAAT AGGAATGCATATGCAGTTTGATCAGGAAATGGAGAGCACTATTAAG CTAGAAGCATATCCTGGAGCAACTCCTCAATATTTCAATGTAAAAGC ATTTGGAATTGGGAAAGGAAAATGCCCAAAACTT

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatOthCRI08	XP_015929114.1	4 e-83	PF00188	--	CRISP	GLVSKVAVERPMNIMVKETVIKLSEEERFYIAQIHNLFRS NATPPAANMRYVQWDETLEKTAQAWASLCVMRHGTP ASPRYHDSYGQNLYYGPSSSTHRAMWLWYNELHDYDH RNAKCALGRECGHYIQMMWWKTKLIGCSLAQCGKSEF FFVCHYYPQFFNNTAPYTVGEPCSLCNIGHGGLCNNSLC VTKTACEKYGLECECHLKCHNCGRFNNSTCSCDCVDG WDFLDCSTQCKDESEHCGKDDGYPSMLNCPMYKGQVK NEHCRKMCQACESVNSSYLRRTCCDGIVCSPGYVIDLE NRPCSCRLLCPGPECYSSFGKIWQVDLFLFEIGICAVLCM IWSR	GGTTTAGTTTCGAAGGTTGCGGTAGAAAGACCAATGAATATAATGGT TAAGGAGACCGTTATTAAACTTAGTGAAGAAGAGAGATTTTATATTG CCCAAATCCATAACTTGTTTCGAAGCAACGCCACACCACCAGCAGCT AATATGAGATACGTGCAGTGGGATGAAACATTAGAGAAAACGGCAC AAGCTTGGGCAAGCTTGTGTGTGATGCGCCATGGCACTCCAGCATCT CCTAGGTACCACGATTCCTATGGGCAGAATTTATATTATGGACCCAG TAGCTCCACTCACAGGGCAATGTGGTTGTGGTATAACGAATTACATG ATTATGATCATCGCAATGCTAAATGTGCTCTAGGAAGAGAATGCGGG CACTATATTCAGATGATGTGGTGGAAGACAAAATTGATTGGTTGTTC ATTGGGCCCAATGCGGAAAATCTGAATTCTTTTTCGTATGTCATTACTA TCCTCAGTTCTTTAATAACACAGCACCTTACACAGTTGGGGAACCTT GCTCCCTTTGCAATATTGGTCACGGAGGATTATGTAATAACAGTTTGT GTGTAACGAAGACAGCGTGTGAGAAATATGGTTTAGAATGTGAATG CCATTTGAAATGTCATAATTGTGGTCGATTTAATAATTCAACGTGCA GCTGTGACTGTGTGGATGGATGGGACTTTCTAGACTGTTCAACACAA TGCAAGGATGAGAGTGAACACTGTGGAAAAGATGATGGCTATCCAA GTATGTTAAATTGTCCAATGTACAAAGGTCAAGTCAAGAATGAACAT TGCAGAAAGATGTGCCAAGCATGTGAAAGTGTTAATTCAAGTTATCT AAGACGAACATGCTGTGATGGCATAGTTTGCTCTCCTGGGTATGTTA TTGATTTAGAAAATCGTCCCTGTTCTTGCAGGCTTCTATGTCCCGGAC CAGAATGTTATTCTTCATTTGGGAAGATTTGGCAAGTGGATTTATTTC TATTTGAAATTGGAATATGTGCAGTACTATGTATGATATGGAGCAGA

<div align="center">Protease inhibitor</div>

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatPInSrp01	JAT91131.1	4 e-58	PF00079	--	Serpin-like	FQGGEEVVSVQMMETRNTVFYGNFSEYGFEAVKMPYK GEDISMLVLLPFERNGLSGVEQELNSSKLDDVISKMKKG KFNVKIPKFRLKDRKHLRKNLNFLGVKSAFTNKANFTGI SGEGNLEVSKIIYRAVVEVNEKGSEAAGATAEFARFGKS RGRPKPGNFYVNHPFVFFIREDRTGMILFYGRVNKL	TTTCAGGGCGGCGAAGAGGTAGTTTCAGTTCAAATGATGGAAACAA GGAATACAGTTTTTTATGGAAATTTCAGCGAATATGGTTTTGAAGCT GTGAAAATGCCATACAAAGGTGAGGATATCAGTATGTTAGTGCTTCT ACCATTTGAAAGAAACGGCCTAAGTGGGGTAGAACAGGAGTTGAAT TCCAGTAAATTAGACGATGTTATCTCCAAGATGAAAAAGGGAAAGTT TAATGTAAAGATCCCAAAAATTTAGACTGAAAGACAGGAAACACCTA AGAAAAAATCTAAACTTCTTAGGGGTGAAAAGTGCATTCACAAATA AGGCAAATTTTACTGGAATTTCTGGAGAAGGAAATTTGGAAGTGTCA AAGATTATTTACAGAGCTGTGGTTGAAGTCAATGAAAAGGGTAGCG AAGCAGCAGGGGCCACTGCCGAATTTGCCAGGTTTGGGAAATCCAG AGGTAGACCAAAGCCGGGAAATTTTTATGTAAACCATCCTTTTGTCT TCTTCATTAGAGAAGACAGGACTGGAATGATTCTTTTCTATGGAAGG GTCAATAAATTGTAA

TatPInSrp02	CAX51426.1	9 e-89	PF00079	--	Serpin-like	MLRTMPSKDQSLLKDTEWDVSVKKKPTMWKTWVRCSI IFFLMLVVLAVVLLVMCGYVYRHDFLGFIQLKPFTEPTS HAFRDERIHAGTVRMVARWLNHANQNENAVWSPLTVI LGLSLLLEGTTGQTAYEIKSTMGWIGIDKSYVRSYLSRVI TRLNNLQHLDVIVANRMFLHDSYDVTSAYKNILNQHYQ VSIDHLDFTNANALQSINKWGLEESRGQIKELIPLDVIDP TTKMVLSTLLTFKGEWKLPFSPNRTKKAEFTSISGKKRQ VDMMYQTGKFMYGEFPAHGFSALELPYSEPNMTMVVL LPRSLSLLKAMLKEQDGTMLMNLSSKMTRTDVEVCIPK FTIEKGTTIENQLSSLGIRRLFDPSFANLELISPNSELYVQ KITHRVKIEVFESGTSGQASSSSILEGRSLTSSFCADHPFIF YVEDKETNSVVFWGEFNGPED	ATGCTAAGAACGATGCCGTCTAAAGATCAGTCGCTGTTAAAAGACAC AGAATGGGATGTAAGTGTCAAGAAAAAGCCAACTATGTGGAAAACG TGGGTGAGATGCAGTATAATATTTTTTCTGATGTTAGTCGTGCTGGCC GTTGTATTGTTAGTTATGTGCGGTTACGTATATCGACACGATTTCCTT GGATTCATTCAATTGAAGCCTTTCACAGAACCGACTTCTCACGCCTTT AGAGATGAACGTATTCACGCTGGAACAGTGCGTATGGTGGCTAGATG GCTTAATCACGCGAACCAGAATGAAAACGCAGTGTGGTCACCCCTTA CTGTCATATTAGGCTTAAGTCTATTGCTAGAAGGCACAACTGGACAG ACTGCGTACGAAATCAAGTCAACTATGGGATGGATTGGTATAGACAA AAGCTACGTACGTTCTTACCTTTCACGGGTGATAACACGCTTGAACA ATTTGCAGCACTGGATGTAATAGTCGCTAACCGGATGTTCCTTCATG ATTCCTACGACGTCACTTCCGCGTATAAAAATATTTTGAATCAACACT ACCAAGTTTCCATCGATCACCTAGATTTTACTAACGCTAATGCACTGC AAAGTATTAATAAATGGGGATTAGAAGAAAGCCGCGGACAGATCAA AGAATTAATTCCATTAGATGTTATTGACCCAACCACTAAAATGGTAC TATCGACGCTTCTTACTTTTAAAGGTGAGTGGAAGCTACCTTTTTCTC CAAATCGTACCAAGAAGGCAGAGTTTACATCAATAAGCGGAAAGAA ACGTCAAGTCGACATGATGTACCAGACGGGAAAATTTATGTACGGTG AATTTCCGGCTCACGGATTTTCTGCGCTGGAATTACCATATTCTGAAC CTAATATGACCATGGTGGTTTTGTTACCTCGGAGTTTGTCTCTTCTGA AAGCGATGCTAAAGGAACAAGATGGGACAATGCTAATGAACCTGAG CTCTAAAATGACGAGAACTGACGTGGAAGTGTGCATACCCAAATTTA CGATAGAAAAGGGACAACGATAGAAACCAGCTGTCATCTTTGGG AATCAGGAGATTATTTGATCCATCATTTGCAAATCTAGAATTGATAT CACCTAATTCTGAACTGTATGTGCAGAAAATAACCCACAGAGTAAAA ATAGAAGTATTTGAAAGCGGAACTTCAGGTCAAGCTTCTTCATCGTC CATTTTGGAAGGACGTTCACTGACGTCATCATTCTGCGCGGATCACC CGTTTATATTCTACGTCGAAGACAAGGAAACTAATTCTGTTGTGTTTT GGGGGCGAATTCAACGGGCCTGAGGATTAA
TatPInSrp03	JAT91147.1	0	PF00079	--	Serpin-like	MLQAFFALFLLPLAHGLGFTRAIPSSGITALIEGSNNFGFE LYKAIQSDDNLVFSPWSISVGMAMLYLGARNYTAREIES VLYQNDQGVSAREMMVAYGQLDRLMKRKAQLELTKF NAAVIQQGSPVSETYRHRLFHYFNSVLYDLDMKQNGKL VKDWINILAEIKTGGLIKDILTRVPTEDSKLILLSGIHYKG QWVEKFDPEKTTNGKFFNHGNMATTAALMLSTSNYTY YYSYANNLHVLQIPLEGRFAMTFVMPEENATLEEVAQK LNPKLLQKVLEQDASSKMIKLVLPKFKLEVRKDLSEPLK EMGMHTLFSPVNSDLTGIDATGDLFLKDVVHQATVEVN EEGVEAAATTVLGVESRLGAPYISFNRPFMFFVRDLDTR LILFMGHLKDCSEVCGVSNYVQQESQSLFR	ATGCTACAAGCGTTCTTCGCGTTGTTCCTCCTGCCTTTAGCTCATGGC TTAGGCTTTACCAGAGCGATACCATCCTCAGGAATCACAGCTCTAAT AGAAGGCAGCAATAACTTTGGTTTCGAATTGTATAAAGCCATCCAAA GCGATGATAACCTCGTATTCTCACCATGGAGCATCTCAGTAGGTATG GCCATGTTATATCTGGGTGCTAGGAACTATACAGCTCGTGAAATAGA GTCAGTTCTCTATCAAAATGATCAGGGTGTTTCTGCTAGAGAAATGA TGGTGGCATATGGACAGTTAGATCGTCTAATGAAAAGAAAAGCTCA GCTGGAACTCACAAAATTTAATGCTGCAGTTATTCAGCAAGGTTCCC CTGTTTCAGAGACCTACAGACATAGACTCTTCCATTATTTCAATTCCG TTCTTTATGATTTGGATATGAAGCAAAATGGAAAACTGGTGAAAGAT TGGATAAACATCTTAGCAGAAATCAAAACTGGAGGATTGATAAAAG ACATCCTTACGAGAGTCCCTACTGAAGATAGCAAACTAATATTGCTC AGTGGGATCCATTATAAAGGACAATGGGTAGAAAGTTCGATCCTG AGAAAACCACTAATGGGAAGTTTTTTAACCACGGAAATATGGCCACT ACTGCAGCTTTGATGTTGTCTACTTCTAATTATACGTATTACTACAGC TACGCAAATAATTTGCACGTGCTCCAAATTCCACTTGAGGGTAGATT TGCAATGACCTTCGTTATGCCAGAAGAGAATGCCACTCTCGAAGAAG TAGCACAGAAACTTAATCCCAAATTGCTACAGAAGGTTCTTGAACAA GATGCTTCATCTAAAATGATTAAGCTTGTATTGCCTAAGTTTAAATTG GAAGTAAGAAAAGATCTCTCTGAACCCTTAAAAGAAATGGGGATGC ACACGTTGTTTTCACCTGTAAATTCTGATCTAACTGGGATAGATGCA ACTGGAGACTTGTTTCTCAAAGACGTCGTTCATCAAGCCACAGTTGA AGTAAATGAAGAAGGTGTCGAGGCAGCAGCCACTACAGTACTTGGG GTAGAAAGTAGATTAGGAGCCCCGTATATTTCATTCAACCGTCCATT CATGTTCTTTGTTCGAGACCTTGACACTAGACTCATTTTGTTTATGGG ACATCTTAAGGACTGCAGTGAAGTATGCGGAGTTTCCAACTATGTGC AGCAAGAAAGTCAATCGCTTTTCCGTTAA

TatPInSrp04	KFM76460.1	4 e-120	PF00079	--	Serpin-like	MIWLSLVLAVLVLENAQRYEAKSDILFPTEPQFFLPRFT GDENLKVIEAINDFAFSLYWKLPREGNLLTSPMSLSTAM AMLYYGAQNETKREMSKALGYDGAKLDYDEVHRGFH QVLKSLKNKNAEYDLETANAVLIQKDYPVLASYKSQVE QIYNATIQELDFAQGDIALKMINAWTAWRTRDKIKELL KKPLDSLTRLFLLNAVYFKGTWKTKFDQRITTPDTFYNN GRIPKTVPMMRLKAKLAFGIDRRLKCSILEMPYTGEEVS MVILLPLERDGLPELEKSMSAEVLSNLTSSLRKETVQVTI PRFKLDDEHELKDVLKSMGMPSLFDPYTANLSGISKIEQ LYVTLVVHKTVLDVNEEGTEAAGVTGIAAGVRIGGPYF SAQHPFLIFIRDIRSNMIYFMARVNEL	ATGATTTGGCTGTCATTGGTGTTAGCTGTGTTGGTTTTGGAAAATGCT CAGAGGTATGAAGCAAAATCAGATATCCTGTTCCCAACAGAACCAC AATTTTTCCTACCTCGATTTACTGGTGATGAAAACCTTAAAGTAATTG AGGCTATCAACGATTTTGCGTTCTCTCTATACTGGAAGTTACCAAGA GAAGGAAATCTATTAACATCTCCAATGAGTTTGTCCACTGCAATGGC TATGTTGTATTACGGTGCACAAAACGAAACGAAAAGAGAAATGTCA AAAGCGTTAGGGTATGATGGTGCAAAGTTAGATTATGATGAAGTTCA CCGAGGGTTCCATCAGGTATTGAAAAGCTTAAAGAACAAGAATGCA GAATACGATCTGGAGACTGCAAATGCTGTTCTAATTCAGAAAGATTA TCCAGTGTTAGCCTCTTACAAATCTCAAGTGGAGCAAATATACAACG CTACCATTCAAGAATTAGACTTCGCCCAAGGAGACATAGCTCTTAAA ATGATCAATGCATGGACCGCCATGGAGGACTCGCGATAAAATCAAAG AATTGTTAAAGAAGCCACTGGATTCGCTAACAAGGCTATTTCTATTA AATGCTGTTTATTTTAAAGGAACATGGAAAACTAAGTTTGACCAGCG TATCACAACACCAGATACTTTCTACAACAATGGGCGCATACCAAAAA CTGTACCCATGATGAGATTAAAAGCTAAACTGGCTTTTGGAATAGAT CGTCGGTTGAAGTGTTCCATCTTAGAAATGCCATACACGGGTGAAGA GGTCAGTATGGTAATCTTGTTGCCATTGGAAAGAGACGGTCTCCCTG AACTGGAAAAGTCAATGTCTGCAGAAGTGCTATCCAACCTTACATCG TCTCTTAGAAAAGAAACAGTTCAAGTAACGATACCACGTTTTAAACT AGACGATGAACACGAATTGAAAGATGTGCTAAAGAGTATGGGAATG CCATCTTTGTTTGATCCATATACCGCAAACCTATCAGGTATTAGCAAA ATAGAACAGCTGTACGTTACTTTAGTGGTGCACAAAACCGTTTTAGA CGTCAACGAAGAAGGTACAGAAGCGGCAGGTGTTACAGGCATAGCT GCGGGTGTGAGGATAGGAGGCCCATATTTTTCGGCTCAGCATCCATT TTTAATTTTTATTCGCGACATTAGATCAAATATGATTTACTTCATGGC TCGCGTTAATGAGTTGTAG
TatPInSrp05	JAT91131.1	7 e-81	PF00079	--	Serpin-like	MTVDQSCIVYIITILATLIVFSTATSPDNDLTNVTAANND FAFKFLKTIEWKENAFFSPASLFIGLGMLYRGARSNTAK EMRHALSYDLADVDPTNLHRRIRVLLNSLNDNKGQYVL EIANALITQMGYRVRNEYRKALRRYYDTYFKEVDFKSN KEKAIKDINEWVIEKSKGKVPKIVDDLEDDTRLILLNAA YFKGTWKVEFNPTFTSTETFYNYGKDAVTVTMMNTKN RFPYGVFINRGIQALQLPYKGEDIRMVILLPLKLDGLKEL EEILNAEEFNSIIAGMEESLVAVSLPKFKLKDARSLKDNL KDLGMVSAFGNRADFSAISWNNNLLLSDIIHKSVIEVNE EGSEAVSFVAMLMRSKSAADEVDTFIVDGPFLFFIRDNR NNGMILFMGRVDKL	ATGACAGTTGACCAAAGTTGCATCGTATATATTATAACAATACTGGC AACACTGATTGTTTTCAGTACCGCAACAAGCCCAGATAATGATCTTA CTAATGTAACAGCTGCCAATAACGACTTTGCCTTCAAATTTCTGAAA ACAATAGAATGGAAAGAAAATGCTTTTTTCTCCCCAGCCAGTCTGTT TATTGGTTTGGGTATGCTCTACCGAGGTGCTCGGTCTAATACAGCTA AAGAAATGCGCCATGCCCTTTCGTATGATCTAGCAGATGTAGATCCA ACAAATCTTCATAGGCGTATAAGAGTGCTACTAAATTCTCTGAATGA TAACAAAGGACAGTATGTACTAGAAATTGCCAATGCCCTCATAACAC AGATGGGCTATCGAGTAAGAAATGAATATAGAAAAGCTCTAAGGAAG ATACTACGACACTTACTTCAAAGAAGTGGACTTTAAGTCAAACAAAG AAAAAGCAATCAAAGATATCAATGAGTGGGTTATTGAAAAAGAGTAA AGGAAAGGTACCGAAGATCGTTGATGACCTAGAAGATGATACCAGG TTGATTCTTTTGAATGCTGCTTACTTCAAAGGAACTTGGAAGGTTGAA TTCAACCCTACATTCACTTCAACAGAAACGTTTTACAATTATGGTAA GGATGCTGTGACTGTTACTATGATGAATACTAAAAATAGATTTCCTT ATGGTGTTTTCATAAATAGAGGGATTCAAGCTCTTCAGCTACCCTAC AAAGGTGAGGATATAAGGATGGTTATATTGCTTCCTCTAAAACTAGA TGGTTTGAAAGAACTGGAGGAAATTCTGAATGCTGAAGAGTTTAATT CTATAATTGCTGGTATGGAAGAATCACTAGTGGCAGTCTCTCTGCCG AAGTTTAAGCTCAAAGATGCTAGGAGTTTGAAGGATAATTTGAAAGA TTTAGGGATGGTGTCAGCATTTGGAAACAGAGCAGACTTTTCCGCTA TTAGTTGGAATAATAATTTACTGTTATCTGACATCATACATAAATCTG TTATTGAGGTGAATGAGGAAGGAAGTGAAGCTGTCTCATTTGTTGCC ATGTTGATGAGGTCAAAATCAGCTGCTGATGAAGTAGACACTTTTAT TGTTGATGGGCCTTTTTTATTCTTTATTAGGGATAATCGAAATGGAAT GATTTTATTTATGGGCCGTGTTGACAAGTTGTAA

TatPInSrp06	JAT91131.1	3 e-66	PF00079	--	Serpin-like	FKGTWKTRFSRRHTREHLFYNGGEEVVSVQMMETRNT VFYGNFSEYGFEAVKMPYKGEDISMLVLLPFERNGLSG VEQELNSSKLDDVISKMKKGKFNVKIPKFRLKDRKHLR KNLNFLGVKSAFTNKANFTGISGEGNLEVSKIIYRAVVE VNEKGSEAAGATAEFARFGKSRGRPKPGNFYVNHPFVF FIREDRTGMILFYGRVNKL	TTCAAAGGTACATGGAAAACTCGGTTTTCTCGAAGACATACAAGGGA ACATCTCTTTATAATGGCGGCGAAGAGGTAGTTTCAGTTCAAATGA TGGAAACAAGGAATACAGTTTTTTATGGAAATTTCAGCGAATATGGT TTTGAAGCTGTGAAAATGCCATACAAAGGTGAGGATATCAGTATGTT AGTGCTTCTACCATTTGAAAGAAACGGCCTAAGTGGGGTAGAACAG GAGTTGAATTCCAGTAAATTAGACGATGTTATCTCCAAGATGAAAAA GGGAAAGTTTAATGTAAAGATCCCAAAATTTAGACTGAAAGACAGG AAACACCTAAGAAAAAATCTAAACTTCTTAGGGGTGAAAAGTGCATT CACAAATAAGGCAAATTTTACTGGAATTTCTGGAGAAGGAAATTTGG AAGTGTCAAAGATTATTTACAGAGCTGTGGTTGAAGTCAATGAAAAG GGTAGCGAAGCAGCCAGGGGCCACTGCCGAATTTGCCAGGTTTGGGA AATCCAGAGGTAGACCAAAGCCGGGAAATTTTTATGTAAACCATCCT TTTGTCTTCTTCATTAGAGAAGACAGGACTGGAATGATTCTTTTCTAT GGAAGGGTCAATAAATTGTAA
TatPInSrp07	XP_011215073.1	2 e-85	PF00079	--	Serpin-like	MDSAVASSNELSLKLLRICRNSTPEANLFYSPASITICLS MLKTGAKEETLKQIEEILSIGEDQCKDDGFGVLSRYLQE SKGPITLKISNILAVDQQFAIEPEFVNNLKLNYNSEMKEL PFQSDPEKSRKEINRLVEEGTNGKIKDMLVPGSISSDSRL VLANAIYFMGKWQTRFKRYETRKVPFYTINEENSMVD MMFKMESYKYIHSKDLNADIIEVPYLGETVSLIILLPFER FGLPLLEKNISVQKLNHAVGQMQMENYVELGLPKFKLE EKISLEEHLQNMGMTEAFIKGAANFSGISGEGNLCLSSAI HKTFLDINEEGTEAAAATGLEIMLCCLPPPPRFHFTVDHP FMLLIRESTTGLILFLGSVNNL	ATGGATTCTGCAGTTGCATCTTCTAATGAATTAAGCTTGAAACTTCTT CGTATATGTAGAAATAGCACACCAGAAGCGAATCTATTTTATTCGCC AGCCAGTATTACGATATGTTTGTCTATGCTGAAAACTGGTGCAAAAG AAGAAACGCTAAAGCAAATCGAAGAGATTCTAAGTATTGGAGAAGA TCAGTGCAAGGATGATGGATTCGGAGTTCTTTCGAGATATTTGCAAG AATCAAAAGGTCCTATTACTTTGAAGATATCAAACATACTCGCTGTT GATCAGCAGTTTGCGATAGAACCAGAATTCGTTAATAATTTAAAATT AAATTATAACTCTGAGATGAAAGAGCTTCCATTTCAGTCCGATCCGG AAAAGTCCAGGAAAGAAATAAATCGTTTGGTAGAAGAAGGCACGAA TGGAAAAATTAAAGACATGCTTGTACCAGGATCGATCTCTTCAGATT CCAGACTCGTTTTGGCCAATGCTATTTATTTTATGGGGAAATGGCAA ACTAGATTTAAGCGATATGAAACAAGAAAAGTTCCCTTCTATACAAT TAATGAAGAGAACTCTATGGTAGATATGATGTTTAAAATGGAGTCTT ATAAATATATCCATAGTAAGGATTTAAATGCAGACATAATCGAAGTA CCATATCTAGGAGAAACAGTTAGTTTGATCATATTACTTCCATTTGAA AGATTTGGTCTCCCTCTTCTTGAAAAGAATATTTCTGTACAGAAGTTG AACCACGCAGTTGGGCAAATGCAGATGGAAAACTATGTAGAACTTG GACTTCCAAAGTTTAAACTGGAGGAGAAAATCTCTCTCGAAGAACAT CTACAGAATATGGGAATGACAGAAGCATTCATTAAAGGAGCAGCTA ACTTTTCAGGGATTTCTGGTGAAGGAAACCTATGTCTCTCATCCGCTA TCCATAAAACATTCCTTGATATCAACGAAGAGGGCACAGAAGCAGCT GCAGCCACTGGATTAGAAATTATGCTGTGTTGTTTACCTCCACCTCCT CGTTTTCACTTTACCGTGGATCATCCTTTCATGCTGTTGATCCGCGAA TCAACTACTGGACTAATCCTATTTCTTGGAAGTGTTAACAACTTATAG

TatPInSrp08	XP_015915292.1	7 e-120	PF00079	--		Serpin like	MQKIVLILAGIIAVSSSRCIQTNNTIDTTDIERSLPSLQYGS TNFALEMFRVLHSESSIPDNLFFSPVSIWTALVTIFEGAR QQTEKELASVLGLTNISPALLPAALDAFLQSCSSCQEGD KPNVKIANRIYFQDGLEFKLCNQQLEKIIHKIDFESDPEK ARDTINNFVESVTNGKIQELIPPNSVGPLTQMIIANAVYF KGTWKNQFPPSMTRQVRFNVDRDSTVTVSMMNTIGTY FYGVSDQMDCQALEIPYNDDRVSMLILLPKHSFRGLDTL ARTISPERLKALLNSMVSREVLVSIPKFKVEQEYEMSKP LQKMGLRNLFDPRFSDLSGFTGARRLNLDAIHHKSYIKV NEEGTEAAAATAFVISRTGTQDSGITRFYADRPFLYFIRD SYSGSMLFMGTVRSPRYDEN

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TatPInSrp09	XP_002407493.1	1 e-90	PF00079	--		Serpin-like	MEIAVSSSNQFNLKLLKIYQDEKKEGNTFYSPASITIALA MLYTGAQEKTRKQMEHILSIEGQHSIHEGFSSVFSLFQD LPSETVLNITNMLAIDQKYNILPEFSNDLKSYYNTQTRLY DFEFQSSKALAEINQLIEVATNGKIKDFFPNESIASDTILV LANAIYFKGLWSISFDEKNTSKKPFYTITNEERMVDMMF RRASFRISDSPNLNARLLEMPYIGNRLRMILILPTEKDGIS FVENNITVDNLNNAIKNLQKANDVRLSLPRFKLEESLPL KDCLIKMGMKDAFTDNADFSGITGNKDTLISAAFHKAFI DVNEEGTEASAVTGMVKIAKCSRPPPPPVLFIVDHPFMFI IQEIGTGLILFTGSIRSL

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TGGCACAGGGCTTATTCTTTTCACTGGAAGTATTCGATCATTGTAA

TatPInSrp10	JAT91131.1	2 e-105	PF00079	--		Serpin-like	MIKMNFFVLPLLLSFIDSEQLVISGETSVKELAVANNKFA FKLYKTFNSDGNAFWSPISVLTAIGTLYTGARLKTAEEIR HAVLNTVAGLSDEQINKAFHALIRSLSGGSDEGRLDIAN AVIIRRNSNPILREYKQNLRYFYSSIVKEMNPEIDSEELIRDI NSWIRKRTYGKITELLESIDYDTVLVLLNAVYFKGKWK KPFLDILTEKEPFYNKGIHATTVSMMIQENHFFYGNFPE YDIHALKMPYLGDKFSMIILLPFQRNGLWRLEENLTPNM FDHIVANLKNQNVIVKLPKFKLEDSRDIKRSLKMLGMK SAFTDKADFGGINKDANLKISKIIHKAVIEVNEAGTEVA GATGVVAIPRMFQEARYFLVEHPFLFFIRNEVTGAIVFFG RLNEL	ATGATAAAAATGAACTTCTTCGTATTACCATTGCTGCTGTCGTTCATT GATAGTGAACAGCTAGTTATATCTGGAGAAACTAGCGTAAAAGAAC TAGCAGTAGCTAATAACAAGTTTGCCTTCAAACTGTACAAAACTTTT AACTCCGACGGAAATGCTTTTTGGTCTCCAATTAGTGTTCTTACTGCC ATTGGAACGCTATATACAGGAGCCAGATTGAAAACAGCGGAAGAAA TTCGTCATGCCGTTTTAAATACCGTTGCAGGATTAAGTGATGAACAG ATAAACAAAGCCTTTCACGCTTTGATTCGTTCCCTTTCAGGAGGATCT GATGAGGGGAGATTAGACATTGCTAATGCTGTAATCATTCGTAATAG TAACCCAATATTGAGAGAATACAAACAGAATTTGAGATACTTTTATA GCTCCATAGTGAAAGAAATGAATCCCGAGATCGACTCTGAGGAGCT GATTCGTGATATCAACAGCTGGATTAGAAAGAGAACTTATGGAAAA ATAACAGAGTTGCTAGAATCTATAGATTATGATACAGTGCTAGTGCT TCTGAACGCAGTTTATTTCAAGGGTAAGTGGAAAAAGCCATTTCTAG ATATCCTCACTGAAAAAGAACCGTTTTATAATAAAGGAATTCACGCT ACTACTGTATCCATGATGATTCAAGAGAATCATTTCTTCTATGGAAAT TTTCCTGAATATGACATTCACGCTTTAAAGATGCCTTACTTAGGTGAT AAATTCAGCATGATTATACTTCTGCCCTTTCAAAGAAATGGTCTTTGG CGATTAGAAGAAAACTTAACTCCTAATATGTTCGATCATATTGTTGC GAATTTAAAAAATCAAATGTCATAGTTAAATTGCCTAAGTTCAAAC TGGAAGATTCTAGAGACATAAAGCGTAGTTTGAAAATGTTAGGAATG AAAAGCGCTTTTACAGATAAAGCTGATTTTGGTGGTATTAATAAAGA CGCCAATCTGAAAATATCCAAGATCATTCACAAAGCAGTGATAGAA GTAAATGAAGCGGGAACCGAAGTGGCTGGTGCGACTGGTGTAGTTG CTATTCCAAGGATGTTTCAAGAGGCAAGATATTTCCTCGTAGAGCAT CCCTTTTTGTTTTTCATTAGAAATGAAGTAACGGGAGCGATCGTGTTT TTTGGACGCCTCAATGAATTATAA
TatPInSrp11	XP_014715077.1	1 e-83	PF00079	--		Serpin-like	MGIPAMDSAVASSNELSLKLLRICRNSTPEANLFYSPASI TICLSMLKTGAKEETLKQIEEILSIGEDQCKDDGFGVLSR YLQESKGPITLKISNILAVDQQFAIEPEFVNNLKLNYNSE MKELPFQSDPEKSRKEINRLVEEGTNGKIKDMLVPGSISS DSRLVLANAIYFMGKWQTRFKRYETRKVPFYTINEENS MVDMMFKMESYKYIHSKDLNADIIEVPYLGETVSLIILL PFERFGLPLLEKNISVQKLNHAVGQMQMENYVELGLPK FKLEEKISLEEHLQNMGMTEAFIKGAANFSGISGEGNLC LSSAIHKTFLDINEEGTEAAAATALEITLYCLPPPPRFHFT VDHPFMMLIRESTTGLILFLGSVNNL	ATGGGTATACCAGCGATGGATTCTGCAGTTGCATCTTCTAATGAATT AAGCTTGAAACTTCTTCGTATATGTAGAAATAGCACACCAGAAGCGA ATCTATTTTATTCGCCAGCCAGTATTACGATATGTTTGTCTATGCTGA AAACTGGTGCAAAAGAAGAAACGCTAAAGCAAATCGAAGAGATTCT AAGTATTGGAGAAGATCAGTGCAAGGATGATGGATTCGGAGTTCTTT CGAGATATTTGCAAGAATCAAAAGGTCCTATTACTTTGAAGATATCA AACATACTCGCTGTTGATCAGCAGTTTGCGATAGAACCAGAATTCGT TAATAATTTAAAATTAAATTATAACTCTGAGATGAAAGAGCTTCCAT TTCAGTCCGATCCGGAAAAGTCCAGGAAAGAAATAAATCGTTTGGTA GAAGAAGGCACGAATGGAAAAATTAAAGACATGCTTGTACCAGGAT CGATCTCTTCAGATTCCAGACTCGTTTTGGCCAATGCTATTTATTTTA TGGGGAAATGGCAAACTAGATTTAAGCGATATGAAACAAGAAAAGT TCCCTTCTATACAATTAATGAAGAGAACTCTATGGTAGATATGATGT TTAAAATGGAGTCTTATAAATATATCCATAGTAAGGATTTAAATGCA GACATAATCGAAGTACCATATCTAGGAGAAACAGTTAGTTTGATCAT ATTACTTCCATTTGAAAGATTTGGTCTCCCTCTTCTTGAAAAGAATAT TTCTGTACAGAAGTTGAACCACGCAGTTGGGCAAATGCAGATGGAA AACTATGTAGAACTTGGACTTCCAAAGTTTAAACTGGAGGAGAAAAT CTCTCTCGAAGAACATCTACAGAATATGGGAATGACAGAAGCATTCA TTAAAGGAGCAGCTAACTTTTCAGGGATTTCTGGTGAAGGAAACCTA TGTCTCTCATCCGCTATCCATAAAACATTCCTTGATATCAACGAAGA GGGCACAGAAGCAGCTGCAGCCACTGCATTAGAAATTACGCTGTATT GTTTACCTCCACCTCCTCGTTTTCACTTTACCGTGGATCACCCTTTCAT GATGTTGATCCGCGAATCAACTACTGGACTAATCCTATTTCTTGGAA GTGTTAACAACTTATAG

TatPInSrp12	JAT91131.1	4 e-140	PF00079	--	Serpin-like	MKEKMIALMVLFLGGLLTSQASSELKNLGKANNDFSIKI YKSLPSTGNAFFCPASVFTALGMLFKGAGGNTAEEMRE ALSYKTAGLTDETVHQKFKDVMELFGNPSNEYALEIAN AIVTSDGFEISEEYKEALKTFYKAITKKVSFKGAEKAAA LNEINGWVSEKTHGKIAKLLEDLDEDTVMVLLNAVYFK GTWESEFNANLTKDDVFYANGKDPKTVRMMNKRNFFL YNEFDKDNFKALKLPYKGEHLSMVILLPNERDGLKQLE ESLTLQKLTEVMSSLGDRERKVKVSIPKFKLEDSRKLVE NLKQLGMKDAFKGGAADFTGIDKSGRLVVSDVVHKAV IDVNEEGTEAAGATAVIGIVRSSRPLRQLEFKADHPFLFF IHDQRTEMILFMGRVNEL	ATGAAAGAAAAGATGATTGCTTTAATGGTGTTATTTCTCGGTGGTCT CCTTACAAGTCAAGCATCCTCTGAGTTAAAGAACTTAGGAAAAGCGA ATAATGACTTCTCTATAAAGATATACAAATCATTACCATCAACAGGA AATGCCTTCTTTTGTCCAGCTAGCGTCTTTACCGCTCTGGGAATGCTG TTTAAAGGAGCAGGAGGAAATACCGCTGAAGAAATGCGAGAAGCGT TATCCTACAAGACAGCTGGATTAACTGACGAAACGGTACATCAGAA ATTCAAAGATGTCATGGAATTATTTGGAAACCCTTCTAACGAGTACG CACTAGAAATTGCAAATGCTATAGTGACGTCTGATGGATTCGAGATA TCCGAGGAGTATAAGGAAGCATTGAAAACGTTCTACAAGGCAATAA CAAAAAAGGTTAGTTTTAAAGGGGCTGAGAAGGCGGCTGCCCTTAAT GAAATCAATGGCTGGGTTAGTGAGAAAACTCATGGAAAAATTGCCA AACTTTTAGAAGATTTAGATGAGGATACCGTGATGGTACTGCTGAAT GCTGTTTACTTTAAAGGAACATGGGAATCTGAATTCAATGCAAATCT TACAAAGATGATGTATTTTATGCTAATGGAAAAGATCCCAAAACGG TACGAATGATGAACAAACGAAATTTTTTCTTGTACAATGAATTTGAT AAAGACAATTTCAAAGCACTTAAACTGCCTTATAAAGGGGAACATCT GAGTATGGTAATACTTCTGCCAAACGAAAGAGATGGATTGAAGCAA TTAGAAGAATCTCTGACATTACAGAAGCTTACCGAGGTCATGTCTAG TTTAGGCGACCGTGAACGAAAAGTAAAAGTGTCCATTCCCAAATTTA AACTTGAGGACAGCAGGAAGTTAGTGGAAAACTTGAAGCAGCTGGG TATGAAAGATGCGTTTAAAGGTGGAGCAGCAGATTTTACTGGCATTG ACAAAAGTGGACGATTAGTTGTTTCGGATGTTGTACACAAAGCTGTA ATAGATGTTAACGAAGAAGGAACTGAAGCTGCAGGTGCTACAGCTG TTATTGGCATTGTGCGATCCAGCAGACCTCTTCGTCAACTTGAATTTA AGGCTGATCATCCGTTCTTATTTTTTATTCATGACCAGAGAACAGAA ATGATTCTTTTTATGGGACGAGTTAATGAACTATAA
TatPInSrp13	JAT91131.1	8 e-121	PF00079	--	Serpin-like	MLSKGAGGNTAEEMREVLSYKTAELTDETIHQQFKDLL QLIEKSSNEYVLEIANAIITSDEYAISEEYKGALKTFYSA MSKEVNFKGSEKAAALAEINGWVSEKTHGKIAKLLEDL DEDTVMVLLNAIYFKGMWKSEFNANRTKDDVFYANGK DPKTVRMMNKRNFFLYNEFDKDNFKALKLPYKGEHLS MVILLPNERDGLKQLEESLTLQKLTEVMSSLGDRERKV KVSIPKFKLEDSRKLVENLKQLGMKDAFKGGAADFTGI DKSGRLVVSDVVHKAVIDVNEEGTEAAGATAVIGIVRS SRPLRQLEFKADHPFLFFIHDQRTEMILFMGRVNEL	ATGCTGTCTAAAGGTGCAGGAGGAAATACTGCTGAAGAAATGCGAG AAGTTTTATCCTACAAGACAGCTGAATTAACTGACGAAACAATACAT CAACAATTCAAAGATCTCCTCCAACTGATCGAAAAATCTTCTAACGA ATATGTCCTGGAAATTGCAAATGCCATAATAACATCTGATGAATATG CAATATCCGAAGAGTACAAGGGAGCACTGAAAACTTTTTACAGCGC AATGAGTAAAGAAGTTAATTTTAAAGGAAGTGAAAAAGCTGCTGCC CTTGCAGAAATCAATGGCTGGGTTAGTGAGAAAACTCATGGAAAAA TTGCCAAACTTTTAGAAGATTTAGATGAGGATACCGTGATGGTATTG CTGAATGCTATTTACTTTAAAGGAATGTGGAAATCGGAATTCAATGC AAATCGTACAAAAGATGATGTATTTTATGCTAATGGAAAAGATCCCA AAACGGTACGAATGATGAACAAACGAAATTTTTTCTTGTACAATGAA TTTGATAAAGACAATTTCAAAGCACTTAAACTGCCTTATAAAGGGGA ACATCTGAGTATGGTAATACTTCTGCCAAACGAAAGAGATGGATTGA AGCAATTAGAAGAATCTCTGACATTACAGAAGCTTACCGAGGTCATG TCTAGTTTAGGCGACCGTGAACGAAAAGTAAAAGTGTCCATTCCCAA ATTTAAACTTGAGGACAGCAGGAAGTTAGTGGAAAACTTGAAGCAG CTGGGTATGAAAGATGCGTTTAAAGGTGGAGCAGCAGATTTTACTGG CATTGACAAAAGTGGACGATTAGTTGTTTCGGATGTTGTACACAAAG CTGTAATAGATGTTAACGAAGAAGGAACTGAAGCTGCAGGTGCTAC AGCTGTTATTGGCATTGTGCGATCCAGCAGACCTCTTCGTCAACTTGA ATTTAAGGCTGATCATCCGTTCTTATTTTTTATTCATGACCAGAGAAC AGAAATGATTCTTTTTATGGGACGAGTTAATGAACTATAA

TatPInSrp14	XP_005307140.1	1 e-101	PF00079	--	Serpin-like	MFSCYRLRSSRTNCSCWFNLLLGVVTLNVLATSMATSP KNLLSKAFSEFAVKLYRSVSEQQDNVLVSPISISTVLSMV LVGAKGSTSDQMKKVLSIDSIEETIPGFSDLISHLNSGNIS DKMSIGNRVFLEEGLPIVNDFTFLMKDVFKAEYGKVSFS TQPLAAKEAINSWVSAITNEKIKELITDDIDPLTKLVLVS AIYFKGFWAEQFLKDSTEIAPFHLNSKQSINIEMMYQKK KFGFAYDSELKVKIIDLPYEQLAVSMIIILPDEYEGLSTIE RQLDSDKLNKLLLEVRKHQTKLDVFLPKFKLEESLSLKP ILSAMGMVDMFCSDKADLSGIVEGKDLYVESVIHKACI DVNEEGTEAAAATAVRIMARSIHIIPEFRADHPFLFLIVE NSHNLILFFGALKTPKAVESRDHEEL	ATGTTTTCATGTTATCGATTACGGTCTTCGAGGACAAATTGTAGTTGC TGGTTTAATTTGTTGTTAGGCGTAGTTACTCTCAACGTTTTAGCTACT AGTATGGCTACATCACCCAAAAATCTACTATCCAAGGCATTTTCAGA GTTTGCAGTGAAACTGTACAGATCAGTTTCTGAACAACAAGACAATG TTTTAGTATCCCCTATAAGTATTTCTACTGTGTTGAGCATGGTTTTGG TAGGAGCAAAAGGAAGTACTTCAGACCAGATGAAGAAAGTGCTCAG CATTGATAGCATTGAAGAAACAATACCTGGTTTTTCTGATTTAATCTC TCACTTAAATTCTGGCAACATTTCTGACAAAATGAGCATTGGAAATA GGGTGTTTTGGAGGAAGGACTGCCAATTGTAAATGATTTTACATTT CTGATGAAAGATGTATTTAAAGCTGAATATGGGAAAGTCAGCTTTTC CACTCAGCCATTGGCTGCTAAAGAAGCTATCAATTCTTGGGTTTCAG CAATCACAAATGAAAAGATAAAAGAATTAATCACTGATGACATCGA TCCATTGACAAAACTTGTGCTTGTCAGTGCAATTTACTTTAAAGGCTT TTGGGCAGAACAGTTTTTGAAGGATTCAACCGAGATTGCTCCATTCC ATTTAAACTCCAAACAATCTATTAATATTGAAATGATGTATCAGAAG AAAAAATTTGGATTTGCCTATGATAGTGAATTGAAAGTTAAGATTAT TGATTTGCCTTATGAACAACTTGCCGTTAGCATGATTATTATATTGCC CGATGAGTATGAAGGACTGAGTACTATTGAGCGGCAGCTTGATTCAG ATAAGCTAAATAAGCTTCTTCTTGAAGTTAGAAAGCATCAGACTAAG TTAGATGTTTTCTTGCCAAAATTTAAATTGGAGGAATCATTGAGCCTA AAGCCCATTCTTTCTGCAATGGGTATGGTGGATATGTTCTGTTCAGAC AAAGCAGACTTATCTGGTATTGTAGAAGGTAAAGATTTGTATGTTGA ATCAGTAATTCACAAAGCATGTATCGATGTAAATGAGGAAGGCACTG AGGCTGCTGCAGCTACTGCCGTTCGTATTATGGCAAGAAGCATTCAT ATTATACCAGAGTTTCGTGCTGATCATCCATTCCTATTTCTTATTGTT GAAAATTCACATAATTTGATTCTTTTCTTTGGTGCTTTGAAAACCCCA AAAGCTGTTGAGAGCAGAGATCATGAAGAATTATAA
TatPInSrp15	XP_013779833.1	6 e-116	PF00079	--	Serpin-like	MQKILLVLICSFAAAVSSCIPENGTTNVTNIQNNLLSFQY GSIDFALDMFRGLYNDTVNLFFSPLSVWVTLVTIYTGSR HQTAKELSSVLGITDTDLTLLPETLSAFIEICSGCKQDNK STVKIANRIYFQEDLELKLCGREVEKMFHKIDFKTNPEG ARDTINDFIKNETNGKILELIPPLSVSPLTQMVIANAVYF KGIWRNKFNKTMTRPLRFYPDRETTLTVDMMNTIGTYI YGVSDQMDCQALEIPYEGGSINMLILLPRHSFRGLDILAS TITPERLENLLNSMASQDVLITLPKFKVEQQYELSKTLRK LGLRNLFDPRFSDLSGFTGIRGLSIDAIHHKSYIKVNEEG TEAAGATGSLLSRDSHPLGVTRFYANRPFVYFIRDTYSD ELLFMGTIRVPQYNKQQ	ATGCAGAAGATATTATTGGTATTAATCTGTAGTTTTGCTGCTGCCGTT TCAAGCTGCATACCAGAAATGGTACAACAAATGTCACCAATATTCA AAACAATTTACTTTCCTTCCAGTATGGCAGCATAGATTTCGCCCTGGA TATGTTTCGTGGTCTTTATAATGATACCGTAAACTTATTTTTTAGCCC GCTTAGTGTGTGGGTAACTCTCGTTACCATTTATACAGGCTCAAGAC ATCAAACGGCCAAAGAACTTTCCAGTGTTTTAGGGATAACTGATACT GATCTAACATTGCTGCCCGAAACACTAAGTGCCTTTATAGAAATCTG CAGTGGCTGCAAACAGGATAATAAATCAACTGTTAAAATAGCAAAT AGAATTTACTTTCAGGAAGATCTTGAATTAAAACTCTGCGGAAGGGA AGTGGAGAAAATGTTTCATAAAATTGACTTCAAAACTAATCCCGAAG GAGCGAGGGACACTATTAATGATTTCATAAAAAATGAAACAAATGG AAAAATATTGGAATTAATCCCTCCTCTGTCTGTTGTTAGCCCTCTAACTCA AATGGTAATTGCTAATGCAGTTTATTTTAAAGGAATTTGGCGGAATA AATTCAACAAAACAATGACTCGTCCACTTCGTTTCTATCCAGATCGT GAAACCACTTTAACGGTGGACATGATGAATACAATAGGAACGTATAT TTATGGAGTTAGCGACCAAATGGATTGCCAAGCTCTAGAGATTCCTT ACGAAGGTGGAAGCATAAACATGCTGATATTATTACCGAGACATTCC TTCCGAGGATTGGACATCCTCGCAAGTACGATTACTCCAGAACGTCT AGAGAACCTCCTCAACTCTATGGCTTCCCAAGACGTTTTAATTACTCT ACCCAAATTTAAAGTTGAACAACAGTATGAACTATCAAAGACTCTCC GGGAAACTTGGATTGCGTAATCTGTTTGATCCTCGTTTTTCCGATCTCT CAGGCTTCACAGGAATTAGAGGCTTAAGCATAGATGCCATACATCAT AAATCTTACATTAAAGTCAATGAAGAAGGAACAGAAGCTGCTGGAG CAACGGGTTCCCTGTTGTCCAGGGATTCTCATCCACTGGGAGTTACA CGATTTTATGCAAATAGACCTTTCGTGTACTTTATTCGTGACACTTAT TCTGACGAACTACTCTTTATGGGCACAATAAGGGGTTCCTCAATATAA TAAACAGCAATAA

TatPInSrp16	JAT91131.1	5 e-133	PF00079	--		Serpin-like	MIPLTSAFLLALVVTQQASSEYDDIKNLALANNELAFKL HKTFNLQGNAFTSPASIFTALAMLYQGARGVTAEEMRE VLSFSVAGLTDRNINQHFQELLSLLGRSSGEYKLNIANAI LSQSRSPVLKNYKDVLEKYYHAKLKEVDFARENAKAV EEVNNWVSDKTNNKITNLLDAIPSDTVLLLLNAVYFKG TWKTQFSPRTTREAPFYNDGINEVSVQMMGAKNKFFYG DFNDYGVQAVKLPYNGEDMSMVVLLPYKRDGLQKVE QQLNPNKLDDIISKMELETVIVNIPKFKLEDKKELKLNLT NLGMRSAFVNGANFAGITNEGNLKVSEIVHKAVVEVNE EGSEAAGASAVLIVPYSSGNVVQYFGANHPFIFFIRDDRT GMILFYGRVNNL	ATGATTCCTTTAACATCAGCATTCCTCTTAGCTCTGGTTGTTACCCAA CAAGCCTCCTCAGAATACGATGACATTAAGAATCTAGCATTGGCCAA TAACGAACTAGCTTTCAAACTGCACAAAACATTTAATTTGCAAGGAA ATGCCTTTACCTCACCGGCAAGTATCTTCACTGCTCTGGCTATGCTCT ATCAAGGTGCAAGAGGTGTTACAGCTGAGGAGATGCGTGAAGTATT GTCTTTCAGTGTTGCCGGTTTGACTGACAGAAACATCAACCAACATT TCCAAGAATTACTTTCCCTTCTGGGGAGATCTTCTGGAGAATACAAA CTTAATATTGCCAATGCTATTTTGTCGCAGTCTAGGAGTCCAGTACTG AAGAATTACAAAGATGTCCTGGAGAAGTACTACCATGCCAAGTTGA AAGAAGTTGATTTTGCAAGAGAGAACGCAAAGGCTGTTGAAGAAGT TAATAACTGGGTTAGTGATAAAACAAACAACCAAAATCACCAATTTGT TGGATGCAATACCTTCCGATACAGTTTTGTTACTGCTGAATGCTGTTT ATTTCAAAGGTACATGGAAAACTCAGTTCTCTCCACGTACCACTAGA GAGGCACCATTCTACAATGATGGCATCAATGAAGTTTCAGTTCAAAT GATGGGAGCAAAGAATAAGTTCTTTTATGGTGATTTCAATGACTATG GTGTCCAGGCTGTGAAACTGCCATACAATGGTGAAGATATGAGCATG GTAGTACTTCTACCATATAAAAGAGATGGTTTACAAAAAGTAGAACA ACAGCTCAATCCAAATAAAATTAGACGACATTATTTCCAAAATGGAGT TGGAAACCGTTATCGTCAACATACCTAAGTTTAAATTGGAAGATAAG AAGGAATTAAAACTTAATCTAACCAATTTAGGAATGAGAAGTGCTTT TGTTAATGGAGCAAATTTCGCCGGTATTACAAATGAAGGAAACCTTA AAGTATCAGAAATTGTTCACAAAGCTGTGGTTGAAGTAAATGAGGA AGGAAGTGAAGCAGCTGGTGCAAGTGCTGTTTTAATAGTACCATATT CCTCAGGGAATGTTGTACAATACTTTGGAGCCAACCATCCTTTTATCT TCTTCATCAGAGACGATAGGACTGGAATGATACTTTTCTATGGAAGA GTCAATAATTTGTAA
TatPInSrp17	JAT91131.1	7 e-139	PF00079	--		Serpin-like	MIGKMIVLMVMFLAGLLTSQASTDLKNLAKANNDFCIK IYKSLPSTGNAFFCPASVFTALGMLFKGAGGNTAEEMRE ALSYKTAGLTDETVHQKFKDVMELFGNPSNEYALEIAN AIVTSDGFEISEEYKEALKTFYKAITKKVSFKGAEKAAA LNEINGWVSEKTHGKIAKLLEDLDEDTVMVLLNAVYFK GTWESEFNANLTKDDVFYANGKDPKTVRMMNKRNFFL YNEFDKDNFKALKLPYKGEHLSMVILLPNERDGLKQLE ESLTLQKLTEVMSSLGDRERKVKVSIPKFKLEDSRKLVE NLKQLGMKDAFKGGAADFTGIDKSGRLFVSDIVHKAIIE INEEGAEAAGVTGVVIVPLSARPPQQLKFNADHPFLFFIQ DDRTNMILFMGRVNDI	ATGATAGGCAAGATGATTGTTTTAATGGTGATGTTTCTTGCTGGTCTT CTAACAAGTCAAGCTTCTACAGATTTAAAGAATTTAGCAAAAGCGAA TAACGACTTCTGTATAAAGATATACAAATCATTACCATCAACAGGAA ATGCCTTCTTTTGTCCAGCTAGCGTCTTTACCGCTCTGGGAATGCTGT TTAAAGGAGCAGGAGGAAATACCGCTGAAGAAATGCGAGAAGCGTT ATCCTACAAGACAGCTGGATTAACTGACGAAACGGTACATCAGAAA TTCAAAGATGTCATGGAATTATTTGGAAACCCTTCTAACGAGTACGC ACTAGAAATTGCAAATGCTATAGTGACGTCTGATGGATTCGAGATAT CCGAGGAGTATAAGGAAGCATTGAAAACGTTCTACAAGGCAATAAC AAAAAAGGTTAGTTTTAAAGGGGCTGAGAAGGCGGCTGCCCTTAAT GAAATCAATGGCTGGGTTAGTGAGAAAACTCATGGAAAAATTGCCA AACTTTTAGAAGATTTAGATGAGGATACCGTGATGGTACTGCTGAAT GCTGTTTACTTTAAAGGAACATGGGAATCTGAATTCAATGCAAATCT TACAAAAGATGATGTATTTTATGCTAATGGAAAAGATCCCAAAACGG TACGAATGATGAACAAACGAAATTTTTTCTTGTACAATGAATTTGAT AAAGACAATTTCAAAGCACTTAAACTGCCTTATAAAGGGGAACATCT GAGTATGGTAATACTTCTGCCAAACGAAAGAGATGGATTGAAGCAA TTAGAAGAATCTCTGACATTACAGAAGCTTACCGAGGTCATGTCTAG TTTAGGCGACCGTGAACGAAAAGTAAAAGTGTCCATTCCCAAATTTA AACTTGAGGACAGCAGGAAGTTAGTGGAAAACTTGAAGCAGCTGGG TATGAAAGATGCGTTTAAAGGTGGAGCAGCAGATTTTACTGGCATTG ACAAAAGTGGACGCCTATTTGTTTCGGACATTGTACACAAAGCTATA ATAGAAATTAATGAGGAGGGAGCAGAAGCAGCAGGTGTGACAGGTG TTGTTATTGTTCCTTTATCCGCAAGACCTCCTCAACAGTTGAAGTTCA ATGCTGACCATCCTTTCTTATTTTTCATTCAGGATGACAGAACAAATA TGATTCTTTTTATGGGTAGAGTTAATGACATATAA

TatPInSrp18	XP_013786963.1	9 e-144	PF00079	--	Serpin like	MYPVVISVFFYISAFLYLQGNAETVNSPFNHLVEANLDF SSDLYNEISKRKGYQDNIMFSPFGLYTVLLMTELGSRGQ TAQELCQLLHLCRVNISYIHDAYGRIVTDLLTDASIRQSL SIANRLYVQKGLEISKFYDYALRYYYNTTIRQVDFQNNS AQVREEINNWVHGQTSGRILHFLSRPPSQATKMMTINAL YFDSDWLWKFDPAMTEPKARFYVTPHFHAVVPMMVG KLNLAIGHCSSLDASILELPFKSNRISMFLVLPDQLEGLGI LQKQLNSTTMKQLISTMKKGEVNVRIPRFYVESQPLITE LLRNLGVHHLFSPSANLKGITTSSDIYIGDMIHWAVINLD ERGSMAVSATATVVERIGTFNGQYFEADHPFLFFIMDKQ TGLVLFMGRIAGP	ATGTATCCTGTGGTCATTTCAGTGTTTTTCTACATATCAGCCTTTTTGT ACCTCCAAGGCAATGCCGAGACAGTGAACTCACCTTTTAACCATTTA GTAGAAGCTAATTTAGACTTCAGTTCTGATTTGTACAATGAAATATC GAAGCGCAAAGGTTATCAAGACAACATCATGTTTTCTCCTTTTGGTTT ATACACGGTACTACTAATGACAGAATTAGGCTCGAGAGGGCAGACC GCACAAGAACTCTGTCAGTTACTCCACTTGTGTCGGGTTAATATTTCG TACATTCACGACGCTTATGGTCGTATAGTGACAGATTTACTCACCGA CGCATCAATTCGTCAATCATTATCAATAGCCAACCGTTTGTACGTTCA GAAGGGGTTAGAAATATCGAAATTTTACGACTACGCACTACGGTATT ACTACAACACAACAATACGACAAGTAGATTTTCAAAATAACAGTGC GCAAGTACGAGAGGAGATAAATAACTGGGTTCACGGACAAACTTCT GGAAGGATTCTACATTTCTTTCCTCGTCCTCCATCGCAGGCTACTAAA ATGATGACTATTAATGCACTTTATTTCGATTCAGATTGGTTGTGGAAG TTTGATCCAGCTATGACTGAACCGAAAGCTCGCTTTTACGTCACCCC ACACTTCCATGCCGTAGTTCCAATGATGGTAGGTAAGCTGAACCTCG CTATTGGACATTGCTCGTCGCTAGATGCAAGTATTTTAGAATTACCTT TCAAATCGAACCGAATCAGTATGTTCCTAGTTTTACCCGATCAACTA GAAGGACTCGGTATTCTACAGAAACAGCTAAACTCAACGACGATGA AACAACTCATATCAACTATGAAGAAAGTGAAGTGAATGTGCGAAT TCCCAGATTTTATGTCGAATCTCAACCGCTAATCACCGAACTTCTACG GAATCTCGGTGTACATCATCTATTCTCTCCATCTGCTAATCTAAAAGG AATAACAACATCCAGTGACATTTATATCGGCGATATGATCCATTGGG CGGTGATTAATTTAGACGAAAGAGGCAGCATGGCCGTATCTGCAACA GCAACCGTAGTTGAACGGATAGGAACTTTCAATGGACAATATTTCGA AGCTGATCATCCTTTCTTATTCTTTATAATGGACAAACAAACCGGATT AGTGCTGTTTATGGGAAGGATAGCTGGTCCTTAA
TatPInSrp19	JAT91123.1	4 e-45	PF00079	--	Serpin-like	MVISLILTMLLILDVTRQGSSEFDNIKKIALANNEFTFKLS GAFDSQENVIISPANIFIALAMLYQGARGITAEELRELLSF NATGLSDEDMNQQFLELLTFLGNSSDDYNLYIANAVVS QYQYPVLKEYKDVLKYYDATLKESNISEDHTKAVEEVN DWVKNKTMGRIQYLSKSILNDTALVLLNTAYFKGTWK	ATGGTGATATCATTGATCCTAACAATGTTATTGATTCTGGATGTTACC AGACAAGGATCCTCCGAATTTGATAACATTAAGAAAATTGCACTAGC TAATAACGAATTTACTTTCAAATTAAGTGGGGCATTTGATTCTCAGG AAAATGTCATAATTTCACCAGCGAATATTTTCATTGCTCTGGCAATGC TGTATCAAGGTGCAAGAGGTATTACTGCCGAGGAACTGCGTGAATTG TTGTCTTTCAATGCTACTGGATTGAGTGACGAAGACATGAATCAGCA ATTTCTAGAATTGCTCACTTTCTTGGGAAACAGCTCTGATGATTACAA TCTGTATATTGCTAACGCTGTTGTATCACAATATCAGTATCCGGTACT AAAGGAATACAAAGATGTACTGAAGTACTACGATGCTACATTGAAA GAATCTAATATTTCCGAAGACCATACAAAGGCAGTCGAAGAGGTAA ACGATTGGGTCAAGAATAAAACAATGGGTAGGATCCAGTACTTGTCA AAATCAATACTTAATGATACAGCTTTAGTATTGTTGAATACAGCTTAT TTCAAAGGTACATGGAAA
TatPInKun01	XP_008472165.1	2 e-18	PF00014	--	Kunitz-type like	SFKISVLPKPYCRMLFSISVVSFVLFVLHPNGWTKEMDQ CSLQPEGGNCRGIFQKFYYNETTGSCFPFFYGGCGGNEN RFETEEDCMKTCKAEEIEIRIFRILPKQRKGIEKVTEKPQ	TCGTTTAAAATTTCCGTTCTCCCTAAGCCTTACTGCAGAATGCTATTC TCAATTTCTGTTGTTTCCTTTGTTCTATTTGTTTTTGCACCCTAACGGAT GGACTAAAGAGATGGACCAATGTTCTCTTCAACCAGAGGGAGGCAA TTGCAGAGGGATTTTCCAGAAATTTTATTACAACGAAACGACAGGTA GCTGCTTCCCCTTTTTCTACGGTGGATGGTGGTGGAAACGAAAATCGC TTTGAAACAGAAGAAGATTGCATGAAAACCTGCAAAGCAGAAGAAA TTGAAATTAGGATTTTCCGAATTCTTCCAAAGCAAAGAAAAGGAATT GAAAAGGTTACAGAGAAACCTCAG
TatPInKun02	XP_015905520.1	1 e-109	PF00014	--	Kunitz-type like	VTQWSEWSPCTVTCGKGMKIRTRLYFDSSSLDTCNVELI QKMLCMADRTDCSIDPAEAKEICMQPKETGACRGYFPR WHYDLSRRECVQFIYGGCRGNRNNFERYSDCSQMCSMI FKGPPSTIATLAASPIQVPNITEAPPVNCMVTPWSPWTAC SRSCGNGRKERRRMIKVAPLNGGKPCPRRLTQRRKCKD LPACSVDCMVTPWGEWSTCSTTCGQSSTQQRTREIKRP AKHGGIPCGPRVERRFCTIPLCTY	GTTACACAGTGGTCTGAGTGGTCACCATGCACAGTTACTTGTGGTAA GGGGATGAAAATCCGTACCCGCCTGTACTTTGATTCATCCTCTCTAG ATACATGTAATGTGGAACTAATACAGAAAATGCTTTGTATGGCTGAT AGAACCGATTGCAGTATCGACCCAGCCGAAGCCAAAGAAATCTGTA TGCAGCCTAAGGAAACAGGAGCTTGCAGAGGGATATTTTCCAAGGTG GCACTACGATTTATCCAGAAGAGAATGCGTTCAATTTATATACGGAG GATGCCGAGGGAACAGAAATAATTTTGAACGCTATTCAGACTGTAGT CAGATGTGCTCGATGATATTTAAAGGTCCACCTAGCACTATAGCTAC CTTAGCTGCATCCCCTATACAAGTCCCCAACATTACAGAAGCCCCAC CTGTTAATTGTATGGTTACACCTTGGTCACCATGGACAGCATGTTCTC GTTCCTGTGGTAATGGCCGTAAAGAAGGAAGAAGAATGATCAAAGT TGCACCTCTTAATGGCGGGAAACCATGTCCCCGTAGGCTAACCCAGA GAAGGAAGTGTAAAGATTTACCTGCCTGCTCTGTTGATTGTATGGTT ACCCCATGGGGAGAATGGTCAACATGTTCAACAACGTGCGGTCAAA GTAGTACTCAACAAAGAACAAGGGAAATTAAACGTCCAGCCAAGCA TGGTGGTATACCTTGTGGACCAAGAGTGGAACGTAGGTTCTGTACAA TTCCTCTTTGCACTTAT

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatPInKun03	ADV40356.1	9 e-16	PF00014	--	Kunitz-type like	CETGQDRKTVRDKRIFNNMASSLLLFLILTNLVIAVVSS KDVCELPPERGPCKARKTMFYYNSRCKCCKVFTYGGCR GNGNKFKTVDKCLDECAQD	TGCGAAACGGGACAAGACAGAAAGACAGTTCGCGATAAACGTATCT TCAACAACATGGCCTCATCGCTTCTGCTATTTTTAATCTTGACGAATC TAGTAAATAGCGGTAGTTTCTTCTAAAGATGTCTGCGAACTTCCTCCGG AAAGAGGACCTTGCAAGGCACGTAAGACAATGTTTTATTACAACTCT AGATGCAAATGTTGCAAAGTCTTCACTTATGGAGGATGCAGAGGAA ATGGCAATAAATTCAAAACGGTTGATAAGTGCTTAGATGAATGTGCA CAAGATTAG
TatPInKun04	KFM77843.1	2 e-58	PF00014	--	Kunitz-type like	TSLLPIDRSFEDSLRFLVILRGMPSLNGGCGVTAWSDWS PCNATCEMTMGMRLRTRLFLNPAINISSCNIHTIETEPCR SERTDCNGAPKEICFEPKEEGPCRSYFVRWYYNVQEGR CLQFVYGGCRGNRNNFKSFSECHRICNNVLREPPYNMPI PLSPDDPTLVIDCRLTQWAPWSECSNTCGVAWKDRRRT VEINAQNGGKPCDSKLYQRKRCKSQPPCEPIY	ACATCGTTGCTGCCCATCGACCGTTCGTTTGAAGATTCTTTAAGGTTT TTGGTGATTTTGAGAGGAATGCCTTCACTGAACGGTGGATGTGGAGT TACAGCATGGTCAGATTGGTCACCATGCAACGCAACATGCGAAATGA CAATGGGAATGAGATTGAGGACACGTTTATTCTTGAACCCCGCAATA AATATTAGCAGCTGCAACATCCATACTATTGAAACTGAACCATGTCG TTCTGAAAGAACAGATTGCAATGGAGCTCCTAAAGAAATATGTTTCG AACCAAAAGAAGAAGGTCCTTGCCGTAGTTACTTTGTGCGCTGGTAC TATAACGTTCAAGAAGGAAGATGTCTACAGTTTGTTTATGGTGGATG CCGTGGAAATAGAAATAACTTCAAAAGTTTTTCCGAATGTCATAGGA TATGTAACAATGTTCTGAGAGAGCCTCCATACAACATGCCAATCCCT TTGTCTCCTGATGATCCAACTCTAGTTATTGACTGTAGATTAACGCAG TGGGCTCCATGGTCAGAATGTTCTAATACCTGTGGCGTTGCGTGGAA GGACAGAAGACGCACAGTTGAAATAAATGCACAGAATGGTGGAAAA CCATGCGATAGTAAATTATACCAAAGAAAAAGATGTAAAAGTCAAC CACCTTGTGAACCAATCTAT
TatPInKun05	XP_013169137.1	3 e-22	PF00014	--	Kunitz-type like	IKVQKRSSVIFIKRSEGLLVIMFGSWLACSITIMIMLFNNV VYSWDDCDLIPSSEDCGKRTQMYYYDMRSDTCKEFTDF GCPGNKNKFKDKERCIKTCGNDCSLFPDSGVCFEDHRL YYYNPETNKCKIFSYGGCGGNRNKFVTEAECLKTCERT WMNDNKE	ATCAAAGTACAAAAACGAAGTTCTGTCATTTTCATTAAACGGAGTGA GGGATTGTTAGTCATAATGTTTGGATCATGGCTCGCATGTTCGATTAC AATAATGATAATGTTATTCAACAATGTTGTTTATTCCTGGGATGATTG TGACCTGATACCAAGCTCAGAAGACTGCGGGAAAACGCACACAGATG TACTACTATGATATGCGATCCGACACCTGTAAAGAGTTTACCGACTT TGGATGTCCAGGGAATAAAAATAAATTTAAAGATAAAGAAAGGTGT ATCAAGACTTGTGGAAATGACTGCAGCTTATTTCCCGATTCTGGAGT ATGCTTTGAAGATCATCGATTATATTACTACAATCCAGAAACCAACA AGTGTAAAGATATTCTCATATGGTGGATGTGGAGGGAAACAGAACAA GTTCGTCACTGAAGCTGAATGCCTTAAAACATGCGAAAGAACTTGGA TGAACGACAACAAAGAA

<p style="text-align:center">Venom components</p>

ID	ID/Reference protein	e-value	PFAM domain	MW (Da)	Sub-classification	Amino acid sequence	Nucleotide sequence
TatVeCOth01	ABR21061.1	3 e-29	PF15430	12495.38	Venom protein-7	MAWKLLFLFVLPCIVFGTDEPAR**FIAYKNDVVSPLTAG KCKIGEDKMIEQGETWYREDFCEKVYCLRTGNLGH MEVRGCTPIAPTNPNCTVVYHKGLYPDCCSGDIVCN QPPPEPKSDVEMAELFRSLLQNKKK**	ATGGCGTGGAAATTACTGTTCCTGTTTGTTTTTACCTTGTATCGTTTTTG GAACCGATGAACCTGCGAGATTCATTGCATATAAAAATGATGTAGTT TCTCCACTGACAGCAGGAAAATGCAAAATTGGTGAAGATAAAATGA TTGAACAGGGTGAGACTTGGTACAGAGAGGACTTCTGCGAAAAAGT ATACTGTCTCCGTACTGGAAATCTGGGCCATATGGAAGTAAGAGGAT GTACTCCTATTGCGCCCACTAACCCTAATTGCACTGTCGTCTACCATA AGGGGCTATATCCTGACTGCTGTAGCGGTGATATCGTTTGTAATCAA CCTCCTCCTGAGCCAAAATCAGATGTGGAAATGGCCGAGCTGTTTAG ATCCCTACTACAAAATAAGAAGAAATGA
TatVeCOth02	AOF40196.1	2 e-8	PF15430	--	Venom peptide HtfTx2	MENNKGRKCSYASELKENDEIWYNPNFCEQLTCQIEGD KAYIVIIDCGVPAVPHRSCTVSVGKGNYPDCCPKINCNEI MNTAE	ATGGAGAATAACAAAGGAAGAAAATGTTCCTACGCATCAGAATTGA AAGAGAATGATGAGATATGGTATAATCCTAATTTCTGCGAGCAACTG ACTTGTCAAATAGAGGGGGATAAAGCCTACATTGTCATAATTGATTG CGGAGTACCAGCAGTGCCACATCGAAGCTGCACAGTATCTGTAGGA AAAGGAAATTATCCAGATTGTTGCCCAAAAATAAACTGTAACGAAAT TATGAATACAGCAGAATAA
TatVeCOth03	API81329.1	4 e-32	PF15430	8721.03	Toxin protein	MKSTAVVFFSLYAATYLIFSQA**RQEICMAGEELTLYLG EEKQDPNACALYKCERYFSRIVLHTLTCAPQELSSGC RNVDGPIDAPFPDCCPMVVCNAPVFG**	ATGAAATCGACCGCTGTGTGGTATTTTTCAGCCTGTATGCCGCTACCTAC CTCATCTTTTCCCAAGCTCGGCAAGAAATTTGCATGGCTGGGGAGGA GTTGACCCTATATCTCGGCGAAGAAAAACAAGATCCTAACGCATGCG CATTGTATAAATGCGAAAGATATTTTTCGAGGATCGTTCTTCATCAC TGACCTGCGCACCTCAGGAACTGAGTAGTGGATGCCGAAATGTTGAT GGACCAATTGACGCTCCTTTTTCCAGATTGCTGTCCAATGGTAGTATGC AACGCCCCTGTGTTTGGA

TatVeCOth04	AOF40196.1	3 e-9	PF15430	9766.03	Venom peptide HtfTx2	MMLLCCLITAFALTFSASG**YVFNSTVSLIDGKCSYASEL KENDEIWYNPNFCEQLTCQIEGDKAYIVIIDCGVPAV PHRSCTVSVGKGNYPDCCPKINCNEIMNTAE**	ATGATGCTCTTGTGCTGTCTAATAACCGCATTTGCCTTGACGTTTTCA GCGAGTGGCTACGTTTTTAATAGTACAGTTTCATTAATAGATGGAAA ATGTTCCTACGCATCAGAATTGAAAGAGAATGATGAGATATGGTATA ATCCTAATTTCTGCGAGCAACTGACTTGTCAAATAGAGGGGGGATAAA GCCTACATTGTCATAATTGATTGCGGAGTACCAGCAGTGCCACATCG AAGCTGCACAGTATCTGTAGGAAAAGGAAATTATCCAGATTGTTGCC CAAAAATAAACTGTAACGAAATTATGAATACAGCAGAA
TatVeCOth05	C5J895.1	1 e-28	PF15430	--	Venom toxin OcyC11	MKATCFLLISLVVFYTANA**AMIPKGFCRTRTGELLRD GQEWKDPHQCAIYKCSIYDGESELNGMICAVFQVPP NCREVPGRGRLYPECCPTVVC**	ATGAAAGCAACGTGTTTCCTTTTAATATCCTTGGTGGTCTTTTATACT GCAAATGCAGCTATGATCCCGAAAGGATTCTGCAGAACAAGAACAG GAGAACTTTTACGAGATGGTCAAGAATGGAAGGACCCCCCATCAATGT GCTATATATAAATGCAGTATTTACGATGGTGAATCTGAACTTAATGG CATGATATGCGCAGTATTTCAGGTCCCGCCTAATTGCAGAGAAGTTC CAGGTAGAGGAAGGCTTTATCCAGAATGCTGCCCCACCGTAGTGTGC
TatVeCOth06	CAX51433.1	1 e-19	N/D	6768.55	Venom component	MWKIVFVCFAVLVSTICKG**DESMEEGRTINLLFSEDGR RTLGCWFTYAFSYNPTADIPTKTEGQKKLCECMQKA LSGSN**	ATGTGGAAGATTGTCTTTGTTTGTTTCGCAGTTTTAGTATCTACTATTT GCAAAGGAGATGAGAGTATGGAAGAAGGAAGAACAATTAATCTCTT GTTTTCGGAAGATGGTAGAAGGACATTAGGGTGCTGGTTCACTTACG CCTTTTCTTATAATCCCACTGCTGATATTCCTACAAAGACAGAGGGCC AGAAAAAGCTGTGTGAGTGTATGCAAAAGGCACTATCTGGAAGTAA TTGA
TatVeCOth07	JAV47658.1	2 e-46	N/D	--	Venom protein	LLMMYALYLLLLFGFMHVAIIKTKESFPYHAAKVGRDC DFKIFPPLKCNEQCWREGYNWGTCVGLLEGLCWHQKC CCFTKPIQELEIDDDPYVDMTIQVEDPNVKTNPDERICQ	TTGCTGATGATGTATGCTCTTTATTTGCTGCTTTTATTTGGATTCATGC ATGTGGCGATCATAAAAACAAAGGAATCATTTCCATATCATGCAGCA AAAGTTGGAAGGGACTGTGACTTTAAAATCTTCCCTCCCCTGAAATG CAATGAACAATGTTGGCGCGAAGGGTACAATTGGGGTACTTGTGTTG GTTTATTAGAAGGTCTATGTTGGCATCAAAAGTGTTGTTGCTTCACTA AGCCAATACAGGAATTAGAAATCGATGACGATCCATACGTGGACAT GACAATACAAGTTGAGGATCCCAATGTAAAGACAAATCCAGACGAA AGAATTTGCCAA
TatVeCOth08	JAV47706.1	6 e-23	N/D	--	Venom protein	MYALRIAVLSLLVYGVICELKMLTASRRYCAKTCDKKS ARHCAEDIMPGFLGLYVKCVQSIRPEANTWDEINDVYC SQVSQEEFLHQVMCFNLELNTRFKDGNHGDVCLKCLDE AGC	ATGTACGCTTTACGAATAGCTGTCCTGTCTCTACTGGTATATGGCGTT ATTTGCGAGCTAAAAATGCTGACTGCTTCACGTAGATATTGTGCAAA AACCTGTGACAAGAAAAGTGCTCGACATTGTGCAGAAGACATTATGC CAGGGTTTTTAGGTTTATACGTGAAATGTGTTCAGTCCATACGACCA GAAGCAAACACATGGGACGAAATCAATGATGTTTATTGTAGCCAGGT CTCCCAAGAAGAATTTTTGCATCAGGTAATGTGTTTCAATCTTGAGCT GAATACAAGATTCAAAGATGGCAACCATGGTGACGTGTGCTTGAAAT GCTTGGATGAAGCTGGTTGT