

Table S2. Sequences identified with the Proteome Discoverer software. Transcriptome ID corresponds to the identifier of the transcript. Fragments with a good Xcorr value (above 1) are highlighted in green in the corresponding protein/peptide.

Transcriptome ID	Transcript-derived mature aa sequence	Peptide fragments	Xcorr
comp8310_c0_seq1	DQDTSTADRDKRAPQMYSFGLGKKSYD LPLEDSDRDKRAPQLYNFGLGK KSYDLP LDDSTAPDDYMIGEPGVK KDQRFSGLG	KSYDLPDDSTAPDDYMIGEPGVK	4.34
	KRQDHRFAFGLGKRDPSSGRYSFGLGKRE PNRFAFGLGKREPSRFAFGLGKRQITEDF DDYMKRRFSFGLGKRSDNRFSGFLGKRP ENRFSFGLGKRPDNRFSGFLGRRKRFSDD SDSYSEEDYNLSQ		
comp32030_c1_seq1	RWDLFNGTINVDDMNSKWWEYRLKYQ GNCPSVKRTEK DLDPASLYHVPADISYA	DLDPASLYHVPADISYAR	4.67
	R YFTALILQFQHKALCDAAGHSGPLHK CDIYGSSEAGERLK AMMSLGISKWPPEA LK ILTNGEVDDLDVAPMLEYFQPLQEWL EKENKDEVIGWNSDDATICP	AMMSLGISKWPPEALK	4.1
comp32030_c2_seq1	IYQVLEEKIFAMQAGVVCFLLLSSVSISYS AKFCNGGSCEEEQGIRLLEHYNAGEEDI CSRHTLSIWYYVNITDENQERESK LQEE YDKFITDIVK EASQCGWSSFSDPMIRRF KFLVEKSSKQLSPEESKQEETLKYQMQG LFGTAKVCPYDSNGTEKDNCTMTLDDGI QQILESSTNFDELLYYWKAW	LQEEYDKFITDIVK	4.91
comp33161_c0_seq1	MCRFREASKQTSTSSSRMTTFLTLVLVE LFLNYEIHVLSSLISDEGKAEEFLDDVDQ QHREWCLDNTKELDYR QIWSFDWQHFS NPEL RAFKLLSRTEPASMNEPNQDDKS	TADLSAWTESYLR	3.87
	KYEELEETLISGILGGSVCYPDQMCSKKL	SIGTPELDAAFWR	3.46
	KYSGINREVDPSIDYQKRLYYWKEWRD	YNGPIPEHLIGLIPQK	3.16
	ATGKSLKSTYSDFVDIANKINNGYESYG DYWLREYDVSADEFLQELETLSQQLPL	ATSNLHYPFQGAANPGFLVAIGR	5.48
	YQQLHAYVRRRLIDVYGEDKIK YNGPIP EHLIGLIPQK WKNIMK IINPFENDFDVSIK	IINPFENDFDVSIK	4.26
	MKQKGMTVSEMVDLAEEFYK SIGTPELD AAFWR DSVFEKSPQMESCNEIREGCAG	SVGLFDESYGDDRDISVLLR	3.84
	NGARIRMCTNATEYYLHLLQLLGDAH QEK ATSNLHYPFQGAANPGFLVAIGRTA DLSAWTESYLR SVGLFDESYGDDRDISV LLRIALENIPIIFSSLSMEK WRLDVFDKITP	QIWSFDWQHFSNPELR	3.99
	FSSMNSKYWEKRVKKEGLCPPVRRTEN	SKPWPEVLSLLTSGR	3.13
	DFDPGAHIHISTHSPVIEYFVGGILQFQFH KALSEAAGCSDPLHKCSIYQSSAAGRIFN	IALENIPIIFSSLSmEK	4.8
	EVMEELGK SKPWPEVLSLLTSGR TNSLDT GALLEYFRPLYEWLQQQNELEYIGWVA DDSLQC	YnGPIPEHLIGLIPQK	3.9

comp33725_c0_seq1	FLDHLVSWNVIIHQVINLLYMTIPLEFSV HFGYPSIRRMRSILFHSVVLIFSFFIRHNLS TLITDEKEAWELLAEDEKMYNNCLKGE YSLSDTTIDTVAWQNFTDPLVKRAFELN AQKHYYVGSTLRISNTSDGQRRGEIWNE KRNILSNTKVCTYETKMDMGNCTMERIF DILRNYDKSENNDERKYYWVAWHNAIG KMRGIYDEDLQILKRLNLPDYNDWWL YFYEEPTSHIREEMERVMQEILPLHKELH AYIRRRRLINQYSGSVITSBGPIPSQLLGLW EYNGWRITFVPYPEKALNITEKLKEKNIT PVGMLKLAEDFYHSLGLPYIDAEFWDNI DLSTKELCYYNFRYTCKPIISGASGCMPI AGSLHKLIGAAIDHWLKLRLQTEMWPNV LIDVPPNPAFRMAFRHALELPTWTVDYLS QIGLIEHIPMDSDEVTEFDINQLMEVAIRF FTLLPSLLQTAKWKWDSLDFVLSNDNYN RRWWEYSKYQGVCPPVRRTEENFDPA SSMHLANGLQLVRDFIGVIYGFQFYEA CKEAGHTDLLHRCNLYGARTFGDKIREV YTLGKSINGSQGIAIMTNGESDKMDTKPL LEYFRPLYEWLKNENEGETVGWKSDDP MICP	LIGAAIDHWLK	3.23
	TEENFDPASSMHLANGLQLVR	4.17	
	FFTLPSLLQTAK	3.39	
comp33936_c0_seq1	NTGSRRLOKSHAYSGVRYILLESFITTDY TKQLLNLRVSKPSSEGGRFVMQAEVIW SFFLCSFSFSVYCNAISHEEEEGIQLLERY NSRRLDVCRRRSLVIWNSYVDSSQRNPT MASKLSEESNNLTTEFVKKASQYDWTSE SDPLIRROQFKFLVEKLSKQLSPEESEKEET LRRQMGRFTFRVATVCPYGINATEKQNC MTLDNGIESIIGSSTNFDELLYYWKA DETGGKMRDLYAKFIPLANKEAVINGFP DHGAQWRSVYEVDNLSNRVDELFNQVL PLYKQLHAYVRNKLIGIYGEDHICTDGPI PAHLLGHMMGESWANLENLTRYPNKP LVDITPVMQERNMTMLDIVKISEDFFESL GLPPMTNEFWNHSIFERIPGRKMSCHPISF DLCNGEDFRILMCGRVDMNSLKIVHHE MGHIHYMQYVHQPHLFRKGANEGFHE AIGDTIALSVFTPTHWKALGFIQNETDDE EQDINALFSTAMDKLPLPHAYVVDWRWR WDLFNGTINVSNMNSEWWEYRLKYQG NCPSIRRTENDLDPASLYHVPVDSSYVRY FVALILQFQFHKALCNAAGYTGPLHKCD IYGSHEAGERLKAMMSLGISKPWPEALK VLTNGEVDDLVDVSPLEEFQPLQEWLEN ENKDEVIGWSSDDATICP	AMMSLGISKPWPEALK	4.1
	ASQYDWTSESDPLIR	4.08	
	VDELfNQLPLYK	4.36	
	KGANEGFHEAIGDTIALSVFTPTHWK	5.67	
	GANEGFHEAIGDTIALSVFTPTHWK	7.32	
	SVYEVDNLSNRVDELFNQVLPLYK	5.37	
TatCaTClc01	ADCLAHLKLCKKNKDCCSKKCSRRGTN PEQRCR	ADcLAHLK	2.19
comp32319_c0_seq1	MRSMDVKILAGIFLVLGISDVITVSLAYK LTGWKIPFYGIILDAGSSKTQVTLYKWE AHKDKGTGIVEQVDTCKVKGGLHNRNS TIHAGEELLPCMLKISASIEGQQENTPLY LGATAGMRLRLGNPLLAAGIILEVKYSL LRNTNFLIRDVRILNGRDEGIFAWVTGNY	LGNPLLAAGIILEVK	4.36

	LLDTLHDGVNDHDPATYGALDMGGAS TQISFELPPRKIAKIDNATTVNMTLFGQN YLVFGESYLCFGINEAMRRHRARLTIGK DPEGEITDPCGFKDDIVEYSVKDLFGHQ TRSLTPTLNKDGVIKFRGTGDSKLSIEV EKLTDQEECKVFKKPCFAEPKEKLSNV KYMAVSTFYFTASALNITNTSLQNYKNA IDYYCGLSKDEAHRRLKPEESQYVRDYC LEAHYVHHILTK EYGF DENTWQNIMFV MKVR GSDLGWSLGYMINATNTIP	EYGF DENTWQNIMFVMKVR	1.4
comp881_c0_seq1	YPASLLEDEDEYENS RVFRGRFAK QGEL P WMIQLQVSK GNGKAGMCGGSIISKRHV	TPLTNYDNNIQNIcLPK	5.71
	LTAAHCVCSNATTKAYANVNDITGRIGH INRADATPVKFK RL VVHPGYDADYNADI ALIEFK TPLTNYDNNIQNICLPK KGKSY	RLVVHPGYDADYNADIALIEFK	7.22
	NRQPV LQMGWGRFDNGSVGTSPTLKITN VG TILDR TTCIREMRSYAEPGQLCISNAG	QGELP WMIQLQVSK	4.69
	GEKICGGDSGGPLVLVNGV NKMAIGIVS FDYFDWCVEDTEGPAIYTDASYA EWIK	LVVHPGYDADYNADIALIEFK	6.64
	TNTNDNGICWKD		
TatHDPND201	GIWSTIKK YASK A WNSDIGK SLRNKAAG	AWNSDIGK	3.03
	AINKFVADKIGVTPSQAASMTLDQIVDA	GIWSTIK	2.65
	MY YD	GIWSTIKK	2.02
TatHDPND301	LPFFLLSLVPTAISAIKKL	LPFFLLSLVPTAISAIKK	5.94
ViVlp1	GIFSWVKKA WNSGVGK SLRKQAVKAAK	KAWNSGVGK	3.27
	NYVANKLGGTPEEAGAMPFDEFMDVLH	GIFSWVK	2.5
	YN	AWNSGVGK	2.1
ViAMP1	FWGFLGK LAMK AIPSLIGGNK	AIPSLIGGNK	3.01
		FWGFLGK	2.79
TatHDPND401	FLK GIIDTVGK WL	GIIDTVGK	2.31
TatHDPND403	FWNTLLSVGK SLL	FWNTLLSVGK	
ViCT2	FWGAVWNAAKSIL	FWGAVWNAAK	2.06
TatEnzHya01	NFEVFWNVPSLLCSIKFGVNLTQTLLKY	WcYYLFPDcYNYFGK	4.84
	K ILVNNGESFIGDKIALIYENGIGKYPHID PK KGDINGGIPQLDKLNEHLKLAENDIQK	ILVNNGESFIGDKIALIYENGIGKYPHIDPK	4.26
	LIPNPDFNGLGIIDWEAWRPIWEYHWGS	IYPYINYMVHVS	4.22
	LGIYKNRTLEMVKKDHPTWSEQLVQSTA	cTWPNDPFTSWK	3.38
	KNIWENSAKQWMLKTLELAKKL RPHGR		
	WCYYLFPDCYNYFGK DQPSQFFCSAMIQ		
	NNNDRLSWMWDASTALCPSIYFIENQM		
	KYNGSQR TWFLYGKLA EAVRVARPHTR YPYINYMVHVS R IPVPE DHFWKMLS LIA	YLT DINSDFDSK	2.29
	LGLDGAHWGSSSYLS DITSCQDLETYVN		
	NVIGPAVTTVSSNVERCSQMCN GRGKC TWPNDPFTSWK YLT DINSDFDSK EITCRC QTHKG RYCD		
comp15335_c0_seq1	LQTVSSTEMKSIILAVVVVAVASQQLGE DPLCRAPESVVNRYIECMRSNYKPAFDY ALTCSR ELGAGALADFIK FSCGKL RATKE QETKYGNCLTRAIDPSNALSEEDLSKVVE SCRQQALASQ	ELGAGALADFIK	3.27
comp30560_c0_seq1	NMNVINVTFTFVVVFTSPYLHIHVFAE NLSVDHWEFVCSSEETILGLLDCSMPEE TKDSLKRINGLMECTK MPQIEIIQSLCK ID SLPEAKVN LIDSCLEKHFADVDESQPNPV	MPQIEIIQSLcK	4.02

	VKCIEQKPEFHSMRAEK		
comp31101_c0_seq1	EQELRINLYRRMLTCITIGSFILITSVTSIQ		
	CCHHTTTLNNTDVENTNTTSDAFQDSCIL	TIDTIPLPDDPGSTSLK	3.44
	ADPNDYVDDLISKLNK TIDTIPLPDDPG		
	STSLK EGQLWGLSSLKRVGNATIIYCNET	TFSGQVFNADTADILFR	6.03
	LTSVEVLISFEELRGRYNWERKVLLK TFS		
	GQVFNADTADILFR VSQEHANSTGIVLE		
	ELSIKNLSGIHTKVTGLGVVTW AISVITDP	TLSTAVEGPLKDAIGLALR	5.01
	VANLFKK TLSTAVEGPLKDAIGLALR DL		
	DVPLY		
	VLTSSTMSRQEFVIVFLALYCISSFSVIKV		
	SATSSIIYAPLVKVSYYETLCPDSRDYIT		
	KQVWPTYQKVSDIMELELIPFGIATETPL		
comp30730_c0_seq1	NSTHYIYTCHHGKDECYGNAVHTCAIHL	ATDNLLSVVcTLYK	4.28
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	TDLEINYLSIEACANARLGNELQHEMAT		
	KTKNLNPPMDFVPWNVINGNSDSGMQK		
	R ATDNLLSVVCTLYK GEKPKPCSSA		
	GLIRE EKYFHQGV DALTPLIPVPVVGGVV	YFHQGV DALTPLIPVPVVGGVVNK	7.67
	NKVAK QMIHKIGK IQSLCAFNK DMAGLC	EKYFHQGV DALTPLIPVPVVGGVVNK	6.73
	EK KCQETEKVK GYCHGKCKCGKPLSY	YFHQGV DALTPLIPVPVVGGVVNKVAK	4.51
TatKTxScr02	K	IQSLcAFNK	1.96
		KcQETEKVK	1.48
	GLIKEKHVQK GVDALTNLIPAPVVGGIIN	GVDALTNLIPAPVVGGIINK	5.76
	KVAKQ VMVHKMGK VQELCAFNKDVMG		
TatKTxScr01	WCDK ACLEKEQTNGFCHGKCKCGKPL	VQELcAFNKDVMGWcDK	3.94
	SY		
ViLa1lp1	VGEICQVGSMSINVGKKMQDPKSCVIYE		
	CVEQNYRILLSKMSCSPQVPKRGCR NVP	NVPGPVDAPFPDccPTSLcR	3.87
	GPVDAPFPDCCPTSLCR GKQWDE		
	FGETCQAGGKYNVRVGQPIQDPNSCVLY	FAAAAPGTPFPNccPMVIcK	4.67
TatOthLa101	KCLNYNRR YVLQTLSCATQTLK SGCRFA	YVLQTLScATQTLK	5.89
	AAAPGTPFPNCCPMVICK GSG		
	MTTEEGKVVDVLDTEPF AEQKSGCGNGI		
	TSSREKNLVIIAFVFGLLVLCLLCAIIMTV	NKATIDAVLG VVEYNKDLR	5.96
	VIGLLFPKREFCLTDHCVKKAGSILRIMD		
	TTVDPCVDFFRFACGGWMDEYD VDENS		
	ETAILGKMQLKIYRKLDKIIERVKSSLPTL		
	NLTDPKQIAEAGLKAIDSYDACNQLSTA		
	YDPENIIPFMASFGGWPMVDDKWKEDP		
	NMKIETKISSLISEFGVAPLFIITINPLEDDP	ATIDAVLG VVEYNKDLR	4.9
	TRNVLVIAPPSLSTSFVYLNASAIARKM		
	KKVAEEDIDEDVKNVIKLRDEINKTLTAS		
	IEDDSSELT VADLKLHLKNMDINWEKVF		
	ASLLKSGKLA AEDTVKDLPVIVR NKAT		
comp34524_c0_seq1	IDAVLG VVEYNKDLR ALSNYFAIEVLLN		
	HPLL VVNVTDGSSNNQAKALKNNNILT N		
	MKENCLATVSEYLN FAMDHV FVYNEPIS	NKWPEIVSFSVSSVNAFYIPHQNNFVLPR	6.26
	TGKAGEFIKYIREAFKQLIRKYDWIDDIT		
	RRALLKKLEKMNNFIDHPPWIIDKEKLN		
	AYYQDYTYTKGNPVATYFSMVAFGVHK		
	SLETYNQISNR NKWPEIVSFSVSSVNAFYI		
	PHQNNFVLPR SILHPPIYDENNP NYLSFGS	SILHPPIYDENNP NYLSFGSIGAVIGHEITHG	5.72
	IGAVIGHEITHG FDSEGRNYDEIGKVSSSL	FDSEGR	
	WTP TSTKEYNKLSQCFVTQYSNYSFGGN		

	VTVNGKTTLAENIADNGGLRQALRAYRL WLKRNERELPLPGLAKYTPEQMFFISYG QSWCISAGKKFLKKQVKTDEHTPNTYRV IGTLSNMEEFAKEFQCKKATPMNPVNKC VLW		
TatEnzMtp04	LKGCFTepQDAICGNEVVEKGEEDCGW EEDCEEPCCFPMRSNPPRDEPPCHLRPNV VCSPSQGPCCTHDCRIKVGEECRGDNGC RSASYRDGQGPHCPSSSTNKPNTVCNDE FVCYMGECTGSICMAYGLESCQCKRGLH DPLTKACELCCKLPRD	LKGcFTepQDAIcGNEVVEK	1.61
comp32637_c0_seq1	FNLTLHTNDVHSRFEQFNTFGSRCTESS	LVFTDEIEcLK	3.08
	AEKGECFGGVARQYTKLKELREKYPNSL	AEFPILcNLDVSR	4.33
	FLSAGDYYQGTFMYTLHKWKIVADFMN	KVGIIGYTTPDTMFLSR	4.61
	RLGHDVMAIGNHELDGVAAGLVPLIEKA	VGIIGYTTPDTmFLSR	4.56
	EFPIICCNLDVSRSPSMKGKVSPFVIKEVD	AEKLVFTDEIEcLKDAVK	4.89
	GRKVGIIGYTTPDTMFLSRAEKL VFTDEI	SLKGSVDIII ALGHSGFPK	5.2
	ECLKDAVKS LKGSVDIII ALGHSGFPK D	VGIIGYTTPDTMFLSR	4.94
	VEIAEAVEGV DIVVGGHTDTFLYSGDPPS	GSVDIII ALGHSGFPK	4.79
	VEEPQGEYPTVVSHADG TKLVVQDYTF	LVFTDEIEcLKDAVK	4.63
	GKYIGFLKVKFDDKGNVKS WEGNPILLD	EKYPNSLFLSAGDYYQGTFmYTLHK	7.05
	NSVEQDPEILGALQPYVDAVSSIAKETVG	LGHdVmAIGNHELDGVAAGLVPLIEK	7.12
	NTKVLLRGDRTVCRMEECNLGNMLADA	QYGWTSAAISIWNSSGIR	5.6
	LVDYFTDSPKQYGWTSAAISIWNSSGIRS	IVVPAYILGGGDGITVFKEK	4.78
	SIDETA AEGNITVEDIMNVAPFSNTFSLAE	TLVVQDYTFGKYIGFLK	4.29
	LRGEDLYTLMEESVSEYDASAIDPPGKLL	IVVPAYILGGGDGITVFK	5.39
	QVSGLKVG YKMDQPPFHRVSELQVRCA	LGHdVMAIGNHELDGVAAGLVPLIEK	7.05
	KCRVPKYEKVDKKVVYRIVVPAYILGGG	AVTVFNTGVLDSDVIQTYLSR	5.81
	DGITVFKEKAVTVFNTGVLDSDVIQTYLS	mEEcNLGNmLADALVDYFTDSPK	4.34
	RHSSITTGVEGRIYFITPPAQSNSTSKRYIR		
	SFRFNK		
comp26928_c1_seq1	LLMMYALYLLLLFGFMHVAIKTKESFP YHAAKVGRDCDFKIFPLKCNEQCWR EG YNWGTCVGLLEGLCWHQKCCCFTKPIQ ELEIDDDPYVDMTIQVEDPNVKTNPDERI CQ	EGYNWGTeVGLLEGLcWHQK	4.98
comp27809_c1_seq1	EQTMA YRCLHIVLLFLAVLGTVRTQLID	IVSTcEGcAPIILR	4.05
	QCSAVKLTVDKDMYEVNERIVSTCEGCA PIILRMRSAGEVKVRDRNFNVGMVKIK QAYEATSDLEILCYSDRIGELKEMTLVKC ASNNDLLCPFQGHNKNG	QAYEATSDLEILcYSDR	6.08
comp30392_c0_seq1	DESMEEGR TINLLFSEDGRR TLGCWFTY AFSYNPTADIPTKTEGQK KLCECMQKAL SGSN	TLGcWFTYAFSYNPTADIPTKTEGQK	6.77
comp32982_c0_seq3	ELKMLTASRRYCAKTCDKKSARHCAEDI MPGFLGLYVKCVQSIRPEANTWDEINDV YCSQVSQEEFLHQVMCFNLELNTRFKDG NHGDVCLKCLDEAGC	HcAEDIMPGFLGLYVK	4.95
comp43100_c0_seq1	MLNIHFHKLSVNINQCSAFIRCTLLFVSH QRSVHIFAVMMLTYLSVVMCITMLSLSA RSQR CVDGCPVPNGVIETALVGTGK SC EDVTDATVRCGCTSTCEMKETFTGCTK ACHCEDIDLFFDKNLLSCVSVNDCTH	cVDGcPEVPNGVIETALVGTGK	5.25
comp31198_c0_seq1	MESKQYFVISVYIMGFAELIISTNVYCPD DQLCDCTPESIKCICLQRENIFFQKGETFM GEKIIVKGCGEVK IATSFTK NLVVESFLIS	NLVVESFLISDVLK	5.3

DVLK L HIAQYAFKGSSIRKLSIGNISDFTL
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 MESFLENN TVDDLSGSIEISNIKNFSFIR
 NVVKNSGFYISLYMADKVEFAYCHFLQ
 INSSMIYTHDIELFSFHDNHVESCEKKAF
 WHVQANTKVTFVNNQIISANNDSLIPNFS
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 INNVGTCISVEKVS VSSAMPKITKLKYILE
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 EISTNQKTVASISPKAEAIHETDLSINPKSE
 TLPSRKIVTPISPKTMT PASHSAHNEKRL
 KQNLNSTSADMSTNIKSERPKSSKIMIPT
 NSKADTSKESSKIDISRI PKSAVSTIQKSDI
 SINPKMETPKQSKAEISAKFKRNAETSTE
 TESSQTN TAVTQKTD PKADVSVTPETDS
 KVQNSESSTTDKSITTEPKSSESSKENTPT
 SLKEATPGNPKTDLLTPKSEISASTKPKT
 TINSKAETATNSKTETTTSPKTETTTSSKT
 ATTTSPKSQTVTSSKMETTNPKTETA

TatEnzPA201	TLRTFHGCQILQSLTDIAREVSILPKYAIR	ALcANPTAEYTGESGFAK	5.74
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	CGAGNESSGYEDLG YFYNVDSCCRHDH		
	HCDSIPSGGTKYSLKNEGKFTMMNCECE	VVEGTSWYDYLATLGLIK	6.67
	DAFAK CLDKVVEGTSWYDYLATLGLIKS FKGVYFNLYGNGCFHV KCNSGRSERRAL CANPTAEYTGESGFAKLLNG	cLDKVVEGTSWYDYLATLGLIK	5.66
TatEnzPA213	AERELHVNFD PWPVARAAIVNF DYNSET RREFSDCRMITSLDEITREGLDLPEHLIKR VSKEEMDALEKRCSGSAEMERFGMIYPG TKWCGPGNISSYS DLGELEADKCCRDH DHCD SIPAGQTKYGLSNTGEYTL MNCDCE EK AFDSCLGDAADKEYLWNSMR TKTLR WTYFSAYSPK CYSVSCSAKRLDMEARC ANGIGEWKSSYNV	WTYFSAYSPK	2.95
		AFDS cLGDAADKEYLWNSMR	5.85
TatEnzPA215	MYLAVFTALLSLCCSRAAQRELYINFEPL PGQRDSWPIARAAIVNFEEKSEMGREFSG CRMISSVDELAREGTDLPEHLIKRASKEE MDALQERCSGSAEMERFTMIYPGTKWC GPGNKAKNESDLGSLEADKCCRAHDHC DNIGAGK SKYGLTNTGSFTLLNCDCE NT FDRCLSDAAEKEGWFKKQGTKALR WTY FTAYSPKCYLSLSCNKKRSILEARCANPVG KWKENYKL	YGLTNTGSFTLLNcDcENTFDR	7.49
		WTYFTAYSPK	3.08
		FTMIYPGTK	3.22
		WKENYKL	2.31
		cLSDAAEKEGWFK	3.18
		SKYGLTNTGSFTLLNcDcENTFDR	7.98
TatEnzPA202	TFSKCRMLNSTKEAAREVSKFPQH LIKR VSKEEMDNLERRCSGPLETRGFTDNFAF KGTKWCGPGTMAENEDDLGPLEADKCC RAHDHCD SIESGGFKYNLKNNAYRTLLN CECEEA FDRCLQATADRVEGTEKEETKM LR NYFFNILHVQCYRLYCRNGGPASENN CTDKFGVWMENYYEENFERKDITFY	NYFFNILHVQcYR	5.16
comp20627_c0_seq1	IQIDKAYQVELIEGLNLFNASYRGVALVD GYHHWSPA VLLRGELRRQLPIEVCR KA SEILSKSNEFTLMATLRQEQRNAGTILSFS EGNNRFLELQSSGRKHEIRLHYNHNNMV	KASEILSK	2.82

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MDRFSCIEHDECRSNDHNCDENAICANT
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ETIPIVQDPCASCKCQVPHCEHSVSNTGY
SSHRMDSSAARTVPFVWTILLSLLLTCPY
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LHYLYICFLPLLQCPLWRMGSYFNCFP
CQRTSQLKIASKVNLAAGSLNTQKIPI

TatOthCRI06

MASVIITILVLWVTTIQSFEANDECDERY
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QLLRTHNLIRNSIWKYVGKNYPLATNME
IMQWDEL YEIAR **MHSLQCVEQPDCLC**
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KRFQTVIKEWAAELKQYDPSIVNDFVT
EELPTNWTNLRANTSFVGCASMNFYTD
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GKPCSDCEDDGICDEEFKNLCVPADLEL
NITIVIEEEDTEIWLGEKNYNGTSLSEEIE
GTTSPNEFTTAESAFTLYRQTGTPEETH
TAIGEENS SVFTETAPEETSIVEFTTELS
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MHSLQcVEQPDcDLcHQIGYFPVEQNFAVK

4.59

TatOthCRI07

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SFGFSAPGIIFGDPIK IEQGGS AFWTIGMH
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5.75

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