

Additional file 2. Additional information for peptides and proteins identified in the DIGE ana

Spot #	Protein Name	Accession #	Protein M.W.	Protein Identification Probability	Exclusive unique peptide count	Percentage Sequence Coverage	Peptide Sequence <sup>a</sup>	Best Peptide Identification Probability	Best Mascot Ion Score	Best Mascot Identity Score	Best Mascot Delta Ion Score	Number of Identified +1H spectra	Number of Identified +2H spectra	Number of Identified +3H spectra	Number of Identified +4H spectra							
664	V-ATPase A subunit	gi 13235340	68900	100.00%	12	22.90%	K.EFTMLQSWPVR.T	97.50%	45.4	43.4	23.4	0	1	0	0							
							K.KIGEGDLLTGGDLYAK.V	99.70%	78.1	42.1	61.9	0	1	0	0							
							K.LAADTPLLTGQR.V	99.70%	76.7	39.2	53	0	3	0	0							
							R.LAEMPADSGYPAYLAAR.L	99.70%	64.4	44.1	40.5	0	1	0	0							
							R.LASFYER.A	95.80%	44.5	40.7	15.5	0	1	0	0							
							R.LGDLFYR.L	99.30%	45.2	40.8	14.6	0	2	0	0							
							R.LVSQKFEDPAEGEDTLVAK.F	99.70%	57.3	44.5	21.2	0	0	2	0							
							K.LYEDLSAAFR.N	99.70%	72.1	41.9	31.1	0	2	0	0							
							R.SGDVYIPR.G	99.60%	49.3	41	18.3	0	2	0	0							
							R.TTLVANTSNMPVAAR.E	99.70%	104	43.4	75.6	0	1	0	0							
							K.TVISQALSK.Y	98.70%	47.2	39.5	18	0	2	0	0							
							R.VGYDNLIGEIIIR.L	99.70%	76.3	41.3	46.8	0	2	0	0							
							740a	Ferredoxin--nitrite reductase	gi 255555453	65991	100.00%	4	7.84%	R.AMKVTEEVQR.L	98.20%	39	42.2	19.2	0	0	1	0
														R.GVVLSDPDILK.G	99.70%	63.6	38.6	47.5	0	2	0	0
R.IGSDSHLGDVYKK.S	95.70%	43.3	42.6	22.4	0	1								0	0							
R.VQADDMDDELAR.L	99.70%	55.8	41.9	27.1	0	2								0	0							
740b	Beta-hexosaminidase 1	gi 110742769	61231	100.00%	3	3.14%	R.GLLIDTSR.H	98.30%	47.7	42.3	0	0	3	0	0							
							R.GLLIDTSRHYLPIDVIK.Q	99.40%	40.8	36.6	27	0	0	3	0							
							R.HYLPIDVIK.Q	97.40%	31.6	37.2	11.5	0	0	2	0							
760	V-ATPase B subunit	gi 26986106	54129	100.00%	31	73.90%	K.AVVGEEALSSDLLYLEFLDKFER.K	95.10%	41.1	43.8	30.8	0	0	1	0							
							K.AVVGEEALSSDLLYLEFLDKFERK.F	99.70%	44.7	43	33.1	0	0	0	2							
							K.AVVQVFEGTSGIDNK.Y	99.70%	104	42.9	81.2	0	1	0	0							
							R.DFEENGSMER.V	99.00%	46.4	39	32.1	0	2	0	0							
							R.DHSDVSNQLYANYAIGK.D	99.70%	90.7	45	72.3	0	1	0	0							
							R.DHSDVSNQLYANYAIGKDVQAMK.A	99.70%	66.9	45.9	59	0	0	2	0							
							R.ELLHRIPAK.T	98.80%	40	34.8	17.1	0	3	0	0							
							K.FVAQGAYDTR.T	98.60%	56	44.3	32	0	3	0	0							
							M.GAPNNLEMDEGNLEIGMEYR.T	99.70%	53	45	30.1	0	0	1	0							
							R.GQKIPFSAAGLPHNEIAAQICR.Q	99.70%	60.5	42.1	46.6	0	0	3	3							
							R.GQVLEVDGEKAVVQVFEGTSGIDNK.Y	99.70%	69.2	43.6	0	0	0	1	0							
							R.GYPGYMYTDLATIYER.A	99.70%	101	44.6	85.9	0	3	0	0							
							K.HVLVILTMSSYADALREVSAAAR.E	99.70%	52.2	43.4	43	0	0	2	1							
							R.IALTTAEYLAYECGK.H	99.70%	107	44.1	83.7	0	3	1	0							
							R.IFNGSGKPIDNGPPILPEAYLDISGSSINPSER.T	98.90%	44.6	43.6	30.2	0	0	1	0							
							K.IPLFSAAGLPHNEIAAQICR.Q	99.70%	69.1	42.3	59.3	0	0	3	0							
							R.KFVAQGAYDTR.T	99.70%	56.3	44.3	30.4	0	1	3	0							
							R.QYPPINVLPLSLR.L	99.40%	50.1	38.4	34.8	0	3	0	0							
							R.RDHSDVSNQLYANYAIGKDVQAMK.A	96.90%	41.8	45.6	23.5	0	0	0	2							
							R.RGQVLEVDGEK.A	99.70%	76.3	41.6	0	0	2	0	0							
							R.RGQVLEVDGEKAVVQVFEGTSGIDNK.Y	99.70%	67.2	42.9	0	0	0	2	2							
							K.SAIGGMTR.R	97.60%	48.7	42.2	27	0	2	0	0							
							R.TIFQSLDLAWTLR.I	99.70%	103	39	87.5	0	3	1	0							
							K.TLDQYYSR.D	97.80%	42.6	42.1	19.7	0	3	0	0							
							K.TPVSLDMLGR.I	98.80%	54.7	41.9	0	0	1	0	0							
							R.TVSGVAGPLVILEK.V	99.70%	76.5	36.8	58.8	0	3	0	0							
							R.TYPEEMIQTGISTIDVMNSIAR.G	99.70%	70.9	45.9	55.9	0	3	3	0							
							R.VTLFLNLANDPPTIER.I	99.70%	95.3	41	13.6	0	3	1	0							
							K.YQEIVNIR.L	99.70%	60.1	41.2	0	0	3	0	0							
							K.YTTVQFTGEVLK.T	99.70%	83	42.1	62.2	0	1	0	0							

						K.YTTVQFTGEVLKTPVSLDMLGR.I	99.70%	68.5	42.7	64.7	0	0	3	0	
765	NADP-dependent malic enzyme	gi 585453	64360	100.00%	46	70.60%	K.APVEQMR.K	99.20%	46.5	38.9	25	0	3	0	0
						R.ATGEEYAEFVQEFMSAVK.Q	99.70%	102	45	91	0	4	3	0	
						R.ATGEEYAEFVQEFMSAVKQNYGEK.I	99.70%	86.8	46.5	74.6	0	0	2	0	
						K.AYELGLASR.L	99.70%	63.7	41	29.9	0	1	0	0	
						K.AYELGLASRLPQPADLVK.F	99.70%	47.4	39.5	38.7	0	1	3	0	
						R.DAHFLR.G	97.30%	38.2	39	2.55	0	2	0	0	
						K.ERDAHFLR.G	97.10%	35.3	43.3	0	0	1	0	0	
						K.FAESCMYNPTYR.S	99.70%	79.1	42.2	60.7	0	6	2	0	
						K.FLFLGAGEAGTGIAELIALEMSKK.T	97.50%	38.8	40	27.3	0	0	1	0	
						K.FLTTLR.Q	99.30%	35.9	35.5	0	0	3	0	0	
						K.GLAFTEK.E	98.20%	35.8	41	17.5	0	2	0	0	
						K.GLAFTEKER.D	99.70%	61.8	41.7	33.3	0	2	0	0	
						K.GLIYPPFKDIR.K	96.10%	35.8	39.1	0	0	1	0	0	
						K.GLIYPPFKDIR.I	94.70%	22.6	37.1	0	0	0	1	0	
						R.GLLPPVLSQELQEK.K	99.70%	95.5	36.6	81.2	0	5	2	0	
						R.GLLPPVLSQELQEKK.F	99.70%	72	34.1	44.8	0	3	0	0	
						K.GLVVSSRK.E	96.70%	31.1	39.9	11.8	0	1	0	0	
						R.ILGLDGLGCQGMGIPVGK.L	99.70%	66.5	42.8	28.6	0	3	3	0	
						K.ILVQFEDFANHNAFELLEK.Y	99.70%	83.5	44	4.96	0	2	3	0	
						K.ILVQFEDFANHNAFELLEKYR.T	99.70%	71.4	43.4	11.1	0	0	2	0	
						K.IQVIVVTDGER.I	99.50%	43	40.3	32.9	0	3	0	0	
						K.ISAHIAAGVAAK.A	99.70%	42.9	37.7	18.6	0	0	3	0	
						K.IWLVDK.G	98.60%	37.7	41.3	9.39	0	2	0	0	
						R.KETLQQFK.L	95.70%	43.9	41.5	21.4	0	1	0	0	
						K.KIQVIVVTDGER.I	99.70%	71.7	38.6	50.4	0	2	0	0	
						R.KISAHIAAGVAAK.A	99.70%	56.3	34.1	10.9	0	3	3	0	
						K.KIWLVDK.G	98.30%	35.1	39.9	17.6	0	2	0	0	
						R.KIWLVDK.G	97.40%	29.8	37.1	10.4	0	1	0	0	
						K.LLDDEFYIGLK.Q	99.70%	87.7	45.4	57.5	0	3	0	0	
						K.LLVDHVEELLPLVYTPTVGEGCQK.Y	99.70%	78.3	41.8	66.2	0	0	2	2	
						R.LPQPADLVK.F	99.70%	61.8	36.9	37.8	0	5	0	0	
						K.LPWAHEHEPITTLIDAVQAIKPTVLIGTSGK.G	99.70%	66.2	35.9	50.8	0	0	0	2	
						K.LSLYSALGGVCPASACLPTLDVGTNNQK.L	99.70%	52	44.2	37.2	0	0	2	0	
						R.NEKL FYK.L	97.30%	37.6	38.5	8.72	0	1	0	0	
						R.QYQVPLQK.Y	99.40%	51.4	41.8	22.8	0	3	0	0	
						K.RATGEEYAEFVQEFMSAVK.Q	99.70%	71.5	45.3	55.5	0	0	3	0	
						R.RPQGLFISLK.D	99.60%	41.7	37.5	7.84	0	3	0	0	
						R.RPQGLFISLKDK.G	99.70%	56.9	37.3	39	0	1	3	0	
						R.RPQGLFISLKDKGR.I	99.70%	38.6	35.8	30.4	0	0	2	2	
						K.TKAPVEQMR.K	98.50%	37.3	41.3	20.4	0	1	0	0	
						R.TTHLVFNDDIQGTASVVLAGLIASLK.L	99.70%	62.4	37.5	13.8	0	0	1	0	
						R.VHDDMLLAASEALASQVTGEHFIK.G	99.70%	87.1	44.6	78.2	0	3	4	5	
						K.YGSIFR.R	99.30%	38.5	37.4	0	0	3	0	0	
						K.YMAMMDLQER.N	99.40%	43.2	41.6	1.11	0	4	0	0	
						K.YMAMMDLQERNEK.L	95.70%	29.7	43.4	18	0	1	1	0	
						K.YMAMMDLQERNEKLFYK.L	95.40%	31.6	45.2	22.4	0	0	0	1	
767	NADP-dependent malic enzyme	gi 585453	64360	100.00%	49	76.90%	K.APVEQMR.K	99.60%	44.5	38.9	22.9	0	3	0	0
						R.ATGEEYAEFVQEFMSAVK.Q	99.70%	77.4	45	60.5	0	3	4	0	
						R.ATGEEYAEFVQEFMSAVKQNYGEK.I	99.70%	73.8	46.5	63.1	0	0	2	0	
						K.AYELGLASR.L	99.70%	62.1	41.1	29	0	1	0	0	
						K.AYELGLASRLPQPADLVK.F	99.70%	52.5	39.6	41.9	0	0	3	0	
						K.ERDAHFLR.G	97.50%	36.5	43.3	7.39	0	2	0	0	
						K.ETLQQFK.L	99.30%	42.4	41.2	14.6	0	3	0	0	
						K.ETLQQFKLPWAHEHEPITTLIDAVQAIKPTVLIGTSGK.L	99.30%	35.8	37.5	20.4	0	0	0	1	

							K.FAESCMYNPTYR.S	99.70%	83.4	42.1	61.4	0	6	1	0
							K.FLFLGAGEAGTGIAELIALEMSK.K	99.70%	87.6	42.3	74.1	0	0	3	0
							K.FLFLGAGEAGTGIAELIALEMSK.K.T	99.70%	48.5	40	29.1	0	0	3	0
							K.FLTTLR.Q	97.80%	36.7	36	0	0	3	0	0
							K.GLAFTEKER.D	99.50%	53.8	41.6	26.1	0	1	0	0
							K.GLIYPPFKDIR.K	98.10%	40.8	39.3	0	0	1	0	0
							R.GLLPPVLSQELQEK.K	99.70%	81.7	36.7	67.2	0	4	3	0
							R.GLLPPVLSQELQEK.K.F	99.70%	88.4	34.1	54.5	0	3	0	0
							K.GLVSSRK.E	98.80%	38	39.9	20.4	0	3	0	0
							R.ILGLDGLGCGMGIPVKG.L	99.70%	67.2	42.9	37.3	0	3	3	0
							K.ILVQFEDFANHNAFELLEK.Y	99.70%	68.5	44.1	2.78	0	1	3	0
							K.ILVQFEDFANHNAFELLEKYR.T	99.70%	56.1	43.4	9.08	0	0	3	1
							K.IQVIVVTDGER.I	98.10%	41.9	40.4	31.8	0	2	0	0
							K.IQVIVVTDGERILGLDGLGCGMGIPVKG.L	99.50%	34.5	39.8	21.1	0	0	1	0
							K.ISAHIAAGVAAK.A	99.70%	43.5	37.7	19.3	0	0	3	0
							K.IWLVDSK.G	97.00%	39.8	41.3	6.47	0	2	0	0
							K.KIQVIVVTDGER.I	99.60%	58.8	38.8	34.6	0	1	1	0
							R.KISAHIAAGVAAK.A	99.70%	83.6	34.1	37.8	0	3	3	0
							K.KIWLVDK.G	99.50%	51.5	40.2	27.2	0	2	0	0
							R.KIWLVDK.G	98.60%	34	37.1	11.2	0	3	0	0
							K.LLDDEFYGLK.Q	99.70%	87.6	45.4	57.6	0	3	0	0
							K.LLGGTLADHKFLFLGAGEAGTGIAELIALEMSK.K	99.70%	41.5	39	5.2	0	0	0	1
							K.LLGGTLADHKFLFLGAGEAGTGIAELIALEMSK.K.T	99.70%	57.5	38.7	47	0	0	0	3
							K.LLVDHVEELLPLVYPTVGEQK.Y	99.70%	58.8	41.9	46.1	0	0	0	1
							R.LPQPADLVK.F	99.70%	65.3	38.2	41	0	5	0	0
							K.LPWAHEHEPITLIDAVQAIKPTVLIGTSGK.G	99.70%	66.2	35.8	59	0	0	0	2
							K.LSLYSALGGVCPACLITLDVGTNNQK.L	99.70%	51.9	44.3	46.6	0	0	2	0
							R.NEKLKY.L	99.00%	37.9	38.5	6.86	0	3	0	0
							R.QYQVPLQK.Y	98.30%	37.3	41.8	12.4	0	3	0	0
							K.RATGEEYAEFVQEFMSAVK.Q	99.70%	68.4	45.2	48.3	0	0	3	0
							R.RPQGLFISLK.D	99.70%	39.7	37.6	29.5	0	3	1	0
							R.RPQGLFISLKDK.G	99.70%	55.6	37.7	38.6	0	1	3	0
							R.RPQGLFISLKDKGR.I	99.70%	65.9	36.4	43.3	0	0	3	3
							R.TFVPGQANNAYIFPGFGLIMCGAIR.V	99.70%	71.5	44.1	57	0	0	6	0
							K.TKAPVEQMR.K	99.00%	40.5	41.3	22	0	1	0	0
							R.TTHLVFNDDIQGTASVVLGLIASLK.L	99.70%	111	37.8	0	0	1	3	2
							R.VHDDMLLAASEALASQVTGEHF.K.G	99.70%	96	44.5	82.7	0	2	3	3
							K.YGSIFR.R	98.60%	34.2	37.5	0	0	3	0	0
							K.YMAMMDLQER.N	99.60%	46	41.2	30.2	0	4	0	0
							K.YMAMMDLQERNEK.L	99.20%	36.3	43.5	24	0	1	1	0
							K.YRTTHLVFNDDIQGTASVVLGLIASLK.L	99.70%	42.2	40.3	7.13	0	0	0	1
774	NADP-dependent malic enzyme	gi 585453	64360	100.00%	48	75.90%	K.APVEQMR.K	99.30%	43.8	38.9	21.6	0	3	0	0
							R.ATGEEYAEFVQEFMSAVK.Q	99.70%	107	44.9	97.5	0	3	3	0
							R.ATGEEYAEFVQEFMSAVKQNYGEK.I	99.70%	71.9	46.5	61.8	0	0	3	0
							K.AYELGLASR.L	99.70%	70.4	40.5	36.2	0	2	0	0
							K.AYELGLASRLPQPADLVK.F	99.70%	44.7	40.2	31.9	0	1	3	0
							R.DAHFLR.G	95.40%	31	39.3	0.07	0	1	0	0
							K.ERDAHFLR.G	96.20%	35.9	43.3	7.07	0	2	0	0
							K.ETLQQFK.L	99.30%	42.8	41.2	14.6	0	1	0	0
							K.ETLQQFKLPWAHEHEPITLIDAVQAIKPTVLIGTSGK.G	99.00%	34.8	37.7	24.6	0	0	0	0
							K.FAESCMYNPTYR.S	99.70%	72.1	42	54.1	0	6	1	0
							K.FLFLGAGEAGTGIAELIALEMSK.K.T	98.70%	36.2	41.2	17.2	0	0	1	0
							K.GLAFTEKER.D	99.70%	57.5	41.6	37	0	1	0	0
							K.GLAFTEKERDAHFLR.G	98.90%	35.3	42.6	29.4	0	0	2	0
							K.GLIYPPFKDIR.K	96.60%	37.1	39.4	0	0	2	0	0
							R.GLLPPVLSQELQEK.K	99.70%	88.8	37.1	60.2	0	5	3	0

						R.GLLPPVLSQELQEKK.F	99.70%	81.6	34.6	52.1	0	3	0	0	
						K.GLVVSSRK.E	95.80%	39	39.9	21.3	0	1	0	0	
						R.ILGLDGLGCQGMGIPVGK.L	99.70%	68.8	43	27	0	3	3	0	
						K.ILVQFEDFANHNAFELLEK.Y	99.70%	64.3	43.8	2.15	0	2	3	0	
						K.ILVQFEDFANHNAFELLEKYR.T	99.70%	62.6	43.7	10.9	0	0	3	0	
						K.IQVIVVDGER.I	99.70%	62.8	40.9	43.8	0	1	0	0	
						K.ISAHIAAGVAAK.A	99.70%	74.2	37.7	32.3	0	3	3	0	
						K.IWLVDK.G	97.50%	41.7	42.1	0	0	1	0	0	
						R.KETLQQFK.L	98.00%	40.4	41.5	15.2	0	1	0	0	
						K.KIQVIVVDGER.I	99.70%	59.2	39.4	31.5	0	3	1	0	
						R.KISAHIAAGVAAK.A	99.70%	85.3	34.1	36.3	0	3	3	0	
						K.KIWLVDK.G	98.30%	42.8	40.1	22.6	0	2	0	0	
						R.KKIWLVDK.G	99.00%	37.2	37.1	14.2	0	2	0	0	
						K.LLDDEFYGLK.Q	99.70%	87.7	45.5	57.6	0	3	0	0	
						K.LLGGTLADHKFLFGAGEAGTGIAELIALEMSK.K	99.70%	46	39.4	15.6	0	0	0	1	
						K.LLVDHVEELLPLVYPTVGECCQK.Y	98.00%	33	42.2	21.8	0	0	0	1	
						R.LPQPADLVK.F	99.70%	64	37.3	41.2	0	6	0	0	
						K.LPWAHEHEPITLIDAVQAIKPTVLIGTSGK.G	99.70%	69.3	37.1	61.8	0	0	0	2	
						K.LSLYSALGVCPAACLPTLDVGTNNQK.L	99.70%	54.2	44.5	45.2	0	0	3	0	
						R.NEKLKYK.L	97.70%	36.5	38.5	5.39	0	1	0	0	
						R.QYQVPLQK.Y	98.90%	41	41.7	5.32	0	3	0	0	
						K.RATGEEYAEFVQEFMSAVK.Q	99.70%	63.8	45.2	45.4	0	0	3	0	
						K.RATGEEYAEFVQEFMSAVKQNYGEK.I	97.30%	35.7	46.2	17.5	0	0	0	1	
						R.RPQGLFISLK.D	98.70%	41.3	37.5	12.3	0	3	0	0	
						R.RPQGLFISLKD.K.G	99.70%	43.5	38.5	25.9	0	2	3	0	
						R.RPQGLFISLKD.KGR.I	99.50%	54.2	36.8	35.4	0	1	1	3	
						R.TFVPGQANNAYIFPGFGLGIMCGAIR.V	99.70%	64.8	44.3	52.5	0	0	3	0	
						K.KTAPVEQMR.K	96.10%	37.1	42	26.2	0	1	0	0	
						R.TTHLVFNDDIQGTASVVLAGLIASLK.L	99.70%	46	38.6	9.17	0	0	3	0	
						R.VHDDMLLAASEALASQVTGEHFIK.G	99.70%	90.5	44.5	82.9	0	2	5	4	
						K.YGSIFR.R	98.00%	38.5	37.7	0	0	3	0	0	
						K.YMAMMDLQER.N	99.30%	43.4	41.2	31.1	0	5	0	0	
						K.YMAMMDLQERNEK.L	99.20%	44.7	43.5	33.5	0	2	0	0	
775	NADP-dependent malic enzyme	gi 585453	64360	100.00%	54	76.90%	K.APVEQMR.K	99.60%	47.1	38.9	25.6	0	3	0	0
							R.ATGEEYAEFVQEFMSAVK.Q	99.70%	108	45	98	0	3	5	0
							R.ATGEEYAEFVQEFMSAVKQNYGEK.I	99.70%	82.7	46.5	75.8	0	0	4	0
							K.AYELGLASR.L	99.70%	61.7	41.1	30.9	0	3	0	0
							K.AYELGLASRLPQPADLVK.F	99.70%	50	39.4	40.6	0	0	3	0
							R.DAHFLR.G	97.00%	33.6	39.3	0.07	0	1	0	0
							K.ERDAHFLR.G	96.40%	36.4	43.4	14	0	1	0	0
							K.ETLQQFK.L	99.10%	43.5	41.2	9.38	0	2	0	0
							K.ETLQQFKLPWAHEHEPITLIDAVQAIKPTVLIGTSGK.G	99.70%	40.1	37.3	33.6	0	0	0	0
							K.FAESCMIYNTYR.S	99.70%	81	42.2	63	0	6	1	0
							K.FLFLGAGEAGTGIAELIALEMSK.K	99.00%	40.4	42.1	27.9	0	0	1	0
							K.FLFLGAGEAGTGIAELIALEMSK.T	99.60%	47.3	40	24.9	0	0	2	0
							K.FLTTLR.Q	98.80%	36.2	36	0	0	1	0	0
							K.FLTTLRQYQVPLQK.Y	96.20%	25.6	37.6	17.2	0	0	1	0
							K.GLAFTEKER.D	99.70%	61.3	41.7	41	0	1	0	0
							K.GLAFTEKERDAHFLR.G	98.20%	33.2	42.5	24.1	0	0	1	0
							K.GLIYPPFK.D	98.10%	36.5	39.1	0	0	1	0	0
							K.GLIYPPFKDIR.K	99.20%	42.6	39.3	0	0	3	0	0
							R.GLLPPVLSQELQEKK.K	99.70%	62.1	36.7	46.7	0	5	3	0
							R.GLLPPVLSQELQEKK.F	99.70%	77.2	33.7	67.1	0	3	0	0
							K.GLVVSSRK.E	96.60%	38.2	39.9	16.6	0	1	0	0
							R.ILGLDGLGCQGMGIPVGK.L	99.70%	76.5	42.8	54.3	0	3	3	0
							K.ILVQFEDFANHNAFELLEK.Y	99.70%	82.8	44	2.87	0	1	1	0

						K.ILVQFEDFANHNAFELLEKYR.T	99.70%	61.7	43.3	14.9	0	0	3	0	
						K.IQVIVVTDGER.I	99.70%	75.2	40.4	49.6	0	2	0	0	
						K.IQVIVVTDGERILGLDLCQGMGIPVGK.L	99.70%	52.9	39.8	34.1	0	0	1	0	
						K.ISAHIAAGVAAK.A	99.70%	45.5	37.7	17.8	0	0	3	0	
						K.IWLVDK.G	96.60%	39.7	41.3	11.9	0	2	0	0	
						R.KETLQQFK.L	98.80%	42.1	41.5	24.5	0	1	0	0	
						R.KETLQQFKLPWAHEHEPITTLIDAVQAIKPTVLIGTSGK.G	98.40%	30.8	38.5	21	0	0	0	0	
						K.KIQVIVVTDGER.I	99.70%	71.9	38.6	50.3	0	2	2	0	
						R.KISAHIAAGVAAK.A	99.70%	85.2	34.1	33.9	0	3	3	0	
						K.KIWLVDK.G	99.70%	50.2	39.9	28.7	0	3	0	0	
						R.KKIWLVDK.G	97.00%	36.5	37.1	10.6	0	1	0	0	
						K.LLDDEFYIGLK.Q	99.70%	87.7	45.4	57.6	0	3	0	0	
						K.LLGGTLADHKFLFLGAGEAGTGIAELIALEMSK.K	99.70%	50.4	38.8	4.87	0	0	0	1	
						K.LLGGTLADHKFLFLGAGEAGTGIAELIALEMSK.T	99.70%	66.8	38.5	60	0	0	0	4	
						K.LLVDHVEELLPLVYTPVTGEGCQK.Y	99.70%	50.2	41.8	39	0	0	0	1	
						R.LPQPADLVK.F	99.70%	57.3	38.2	35	0	4	0	0	
						K.LPWAHEHEPITTLIDAVQAIKPTVLIGTSGK.G	99.70%	78.3	35.8	75.1	0	0	0	2	
						K.LSLYSALGGVCPACSACLPITLDVGTNNQK.L	99.70%	66.6	44.1	59.2	0	0	3	0	
						R.NEKLQK.L	98.30%	36.3	38.5	5.51	0	1	0	0	
						R.QYQVPLQK.Y	98.90%	42.7	41.8	19.2	0	3	0	0	
						K.RATGEEYAEFVQEFMSAVK.Q	99.70%	68.7	45.3	48.6	0	0	3	0	
						R.RPQGLFISLK.D	98.50%	42	37.5	12.7	0	3	0	0	
						R.RPQGLFISLKDK.G	99.70%	47.7	37.7	31	0	3	3	0	
						R.RPQGLFISLKDKGR.I	99.70%	63.8	35.9	47.8	0	0	3	3	
						R.TFVPGQANNAYIFPGFGLIMCGAIR.V	99.70%	67.7	43.8	58.8	0	0	2	0	
						K.TKAPVEQMR.K	97.00%	35.3	41.3	17.4	0	1	0	0	
						R.TTHLVFNDDIQGTASVVLGLIASLK.L	99.70%	57.5	37.7	13.5	0	1	3	2	
						R.VHDDMLLAASEALASQVTGEHFIK.G	99.70%	76.5	44.5	62.2	0	2	3	5	
						K.YGSIFR.R	98.20%	40.5	37.4	0	0	3	0	0	
						K.YMAMMDLQER.N	99.20%	45.5	41.6	10.2	0	7	0	0	
						K.YMAMMDLQERNEK.L	96.80%	37.1	43.4	25.3	0	1	0	0	
1062	Alpha-1,4-glucan-protein synthase	gi 356495127	41713	100.00%	16	41.80%	K.ASCISFK.D	99.10%	46.8	41.7	15.2	0	3	0	0
						K.ASCISFKDSACR.C	99.50%	52.8	43	35	0	3	1	0	
						K.ASNPFVNLK.K	99.20%	59.5	41.5	35.7	0	3	0	0	
						R.CFGYMVSK.K	97.60%	37.9	40.9	18.7	0	2	0	0	
						R.CFGYMVSKK.K	95.70%	34.2	41.7	22.8	0	1	0	0	
						K.ECTSVQK.C	99.00%	43.5	39.7	14.1	0	12	0	0	
						R.EGAPTAVSHGLWLNIPDYDAPTQLVKPLER.N	99.70%	116	41.8	33.2	0	0	3	3	
						K.GTLFPMCGMNLAFDR.Q	99.70%	87	44	25.6	0	6	3	0	
						R.GYPFSLREGAPTAVSHGLWLNIPDYDAPTQLVKPLER.N	99.70%	58.5	40.9	4.09	0	0	0	2	
						K.KYIYTIDDDCFVAK.D	97.60%	35.3	44.1	21.3	0	0	2	0	
						K.KYIYTIDDDCFVAK.D	99.60%	73.4	44	56.3	0	1	0	0	
						K.NLLCPSTPFFNTLYDPYR.E	99.70%	85	45.4	69.9	0	3	0	0	
						K.VICDHLGLGVK.T	99.70%	76.6	41.8	56.6	0	3	3	0	
						R.YDDMWAGWCVK.V	99.70%	60.9	41.3	39.8	0	6	0	0	
						K.YIYTIDDDCFVAK.D	99.70%	78.3	44.2	58	0	3	0	0	
						R.YVDAVLTIPK.G	99.70%	65.5	39.5	44.2	0	3	0	0	
1065	Beta-D-galactosidase	gi 61162194	100047	100.00%	3	3.65%	K.DLHAAIK.L	96.40%	31	38.2	0	0	1	0	0
						K.LGPKQEAHVYR.M	99.70%	44.6	41.5	34.4	0	2	3	0	
						R.LPHRPVEDLAFAVAR.F	99.70%	47.2	39.7	37.9	0	0	3	0	
1071a	2-Phospho-D-glycerate hydrolase	gi 533474	48340	100.00%	12	34.50%	K.AIDENSCNALLK.V	99.70%	74.4	43	48.2	0	3	0	0
						R.IEEELGDKAVYAGANFR.R	99.70%	48	44.2	27.6	0	0	2	0	
						R.ISGEALKDLYK.S	99.70%	71.6	40.7	34	0	3	3	0	
						K.KAGWGVMAHR.S	99.70%	50.1	41.4	25	0	1	3	0	

						K.KAIDENSCNALLK.V	99.70%	103	42.4	78	0	1	2	0	
						K.KIPLYQHIAEIAGNK.N	99.70%	42.9	37.3	24.5	0	0	1	0	
						K.MGSEVYHNLK.S	99.70%	59.4	41.7	40.8	0	3	0	0	
						K.SYDLNFKEENNDGSQR.I	99.70%	48	44.5	34.3	0	0	2	0	
						K.VNQIGSVTESIEAVK.M	99.70%	91.9	41.6	72.2	0	2	0	0	
						K.VQIVGDDLLVTNPK.R	99.70%	95	38.7	63.8	0	3	0	0	
						K.VQIVGDDLLVTNPKR.V	98.70%	30.5	37.4	9.52	0	0	1	0	
						K.YGQDATNVGDEGGFAPNIQENKEGLELLK.T	99.70%	87.7	45.5	0	0	0	2	0	
1071b	Alpha-1,4-glucan-protein synthase	gi 356495127	41712	100.00%	9	27.40%	K.ASCISFK.D	98.90%	42	41.7	13.7	0	3	0	0
						K.ASCISFKDSACR.C	99.70%	49.2	43	27.7	0	1	3	0	
						K.ASNPFVNLK.K	98.90%	41.5	41.7	18.2	0	1	0	0	
						R.CFGYMVSK.K	98.60%	39.1	40.9	18.3	0	3	0	0	
						R.EGAPTAVSHGLWLNIPDYDAPTQLVKPLER.N	99.70%	114	41.7	32.1	0	0	3	3	
						R.GYPFSLR.E	94.90%	31.2	41.5	11.7	0	1	0	0	
						K.VICDHLGLGVK.T	99.70%	76.6	41.8	57	0	3	3	0	
						R.YDDMWAGWCVK.V	99.70%	60.4	40.9	41.5	0	3	0	0	
						K.YIYTIDDDCFVAK.D	99.70%	56.7	44.2	43.2	0	2	0	0	
1095	Malate dehydrogenase	gi 350536645	36152	100.00%	4	15.00%	R.DDLFNINAGIVK.S	99.70%	57.4	42.3	36.9	0	1	0	0
						K.RTQDGGTEVVEAK.A	97.80%	56.4	42.7	23.3	0	1	0	0	
						R.TQDGGTEVVEAK.A	99.70%	86.1	42.8	60.1	0	1	0	0	
						K.YCPNALVMISNPVNSTVPIAAEVFKK.A	99.70%	62.3	43.4	46.7	0	0	1	0	
1123a	Malate dehydrogenase	gi 350536645	36152	100.00%	5	21.70%	K.AGKGSMTLSIAYAGAIFADACLK.G	99.70%	74.9	45.8	60.2	0	0	1	0
						R.DDLFNINAGIVK.S	99.70%	71.5	42.3	49.7	0	3	0	0	
						RTQDGGTEVVEAK.A	99.70%	53.5	43.1	19.7	0	1	0	0	
						R.TQDGGTEVVEAK.A	99.70%	85.4	42.8	56.7	0	2	0	0	
						K.YCPNALVMISNPVNSTVPIAAEVFKK.A	99.70%	55.3	43.3	44.1	0	0	3	0	
1123b	Proline iminopeptidase	gi 224060965	37404	100.00%	4	11.50%	K.GFFPSDSFLENVDK.I	99.70%	65.6	44.3	46.8	0	3	0	0
						R.IENHYFVNK.G	99.70%	49.1	42.3	21.8	0	2	0	0	
						R.IILFDQR.G	98.60%	35.5	39.3	0	0	1	0	0	
						K.VTGLVLR.G	96.00%	27.9	38.4	0	0	1	0	0	
1153	V-ATPase E subunit	gi 3334410	26163	100.00%	26	88.90%	K.ACVSHPDIVDDIHLPPAPTSYDSHELSCSGGVVMASR.D	98.50%	33.5	46.5	18.2	0	0	0	2
						K.AKQVDVRR.K	96.40%	30.2	39.6	8.56	0	1	0	0	
						K.ANEISVSAAEEFNIEKLQVVEAK.K	99.70%	49.3	44.3	0	0	0	1	0	
						R.CREEDKHHVHR.V	99.70%	42.3	44.2	29	0	0	3	16	
						R.DGKIVFENTLDAR.L	99.70%	64.6	43.4	36.9	0	3	2	0	
						R.DGKIVFENTLDARLEVAFR.K	99.50%	38.5	41.9	24.2	0	0	1	0	
						K.EAASKELLVSGDHHQYR.N	99.70%	54.3	43.9	44.3	0	0	1	0	
						K.ELIVQSLLR.L	99.70%	55.8	38.5	18.3	0	3	0	0	
						K.ELLVSGDHHQYR.N	99.70%	77.4	43.7	43.9	0	3	2	0	
						K.ELLVSGDHHQYRNLLKELIVQSLLR.L	97.40%	25.5	32.8	17.5	0	0	0	2	
						K.IEYSMQLNASR.I	99.70%	72.9	43	41.7	0	3	0	0	
						R.IKVLAQDDLVNAMK.E	99.70%	100	40.6	0	0	5	3	0	
						R.IKVLAQDDLVNAMKEAASK.E	99.70%	65.5	40.7	26.4	0	0	5	1	
						K.IRQEYERK.A	99.30%	35.8	41.3	14.3	0	0	1	0	
						K.IVFENTLDAR.L	99.70%	68	42.1	34.3	0	3	0	0	
						R.KIEYSMQLNASR.I	99.70%	97.8	43.1	81.6	0	3	3	0	
						R.KKLPQIR.K	99.00%	28.7	30.1	0	0	2	0	0	
						R.LEVAFR.K	98.40%	35.4	39.7	0	0	2	0	0	
						R.LEVAFRK.K	99.00%	37.6	39.4	14.1	0	3	0	0	
						R.LKEPAVLLR.C	99.70%	50.2	30.5	0	0	2	0	0	
						K.LQLVEAEKK.K	98.40%	35.8	40.1	0	0	1	0	0	
						R.NLLKELIVQSLLR.L	99.70%	69.8	31.8	33.8	0	3	3	0	
						R.QEAEEKANEISVSAAEEFNIEKLQVVEAK.K	99.70%	49.7	45.3	0	0	0	0	2	
						R.RKIEYSMQLNASR.I	99.70%	60.4	42.6	41.3	0	1	5	2	

						R.VLHSAREEYGEK.A	99.70%	57.8	43.1	42.5	0	3	0	0	
						K.VLQAQDDLNVAMK.E	99.70%	90.6	42.9	0	0	6	0	0	
1307	Ascorbate peroxidase	gi 239586448	18421	100.00%	5	41.10%	K.ALLSDPAFRPLVEK.Y	99.70%	63	39.2	38.6	0	2	0	0
						K.ELLSGEKEGLQLPSDK.A	99.70%	51.4	41.3	0	0	0	2	0	
						K.ELLSGEKEGLQLPSDKALLSDPAFRPLVEK.Y	99.70%	42.2	36.4	0.88	0	0	0	1	
						K.QMGLSDKDIVALSAGHTLGR.C	99.70%	59.8	43.6	28.6	0	0	3	2	
						K.YAADEDAFFADYAEHLK.L	99.70%	64.6	47.2	51.1	0	1	3	0	
1325	Fructose-biphosphate aldolase	gi 2213867	38158	100.00%	8	20.70%	K.ALNDHHVLEGTLLKPNMVTGSESK.K	99.70%	62.1	42.3	49	0	0	0	3
						K.ALNDHHVLEGTLLKPNMVTGSESK.V	99.30%	37	40.9	29.3	0	0	0	0	
						R.CAEVTER.V	96.80%	30.6	39.2	5.56	0	3	0	0	
						R.CAQYAAAGAR.F	99.70%	67.6	42	44	0	3	0	0	
						K.KPWTLFSYGR.A	98.80%	42.9	44.2	21.2	0	1	3	0	
						K.KVAPEVIAEYTVR.A	99.70%	54.6	40.8	35	0	2	3	0	
						K.VAPEVIAEYTVR.A	99.70%	61.7	41.7	36.9	0	2	0	0	
						R.VLAACYK.A	98.70%	40	42.1	0	0	2	0	0	
1501	Alpha-galactosidase-like protein	gi 297816956	47551	100.00%	3	10.70%	K.APLIGCDVR.N	99.70%	52.7	39.6	0	0	2	0	0
						K.EVIAVNQDPLGVQGR.K	99.70%	82.9	41.4	67.3	0	1	1	0	
						R.TTDDINDTWASMTTIADLNK.W	99.50%	53.6	45.8	0	0	0	1	0	
1502	5-Methyltetrahydropteroyltri-glutamyl-homocysteine methyltransferase	gi 8134568	84824	100.00%	62	66.10%	K.AATALKGSDHR.R	97.40%	39	40.3	17.3	0	1	0	0
						K.AGINVIQIDEAALR.E	99.70%	73.4	39	45.4	0	3	3	0	
						K.AGINVIQIDEAALREGLPLR.K	99.70%	47.4	37	33.7	0	0	3	0	
						K.AGINVIQIDEAALREGLPLR.K.S	99.70%	56.2	33.5	52	0	0	2	3	
						K.AIKEEISKVVK.L	99.70%	44.4	34.2	31.6	0	3	3	0	
						K.AKKISEEEYVK.A	99.70%	52.4	41.1	39.7	0	0	2	0	
						K.ALGVDTVPVLVGPVSYLLSK.Q	99.70%	63.2	31.2	48.7	0	3	6	0	
						K.ALSGQKDEAFFSANAAALASR.K	99.70%	112	44.4	97.7	0	3	2	1	
						K.ALSGQKDEAFFSANAAALASR.K.S	99.70%	82.5	43.1	68.7	0	0	3	1	
						R.ATTVSSRLDAQQK.K	98.60%	48.3	42.3	19.2	0	2	0	0	
						K.AVLEYK.E	99.20%	43.5	36.4	0	0	3	0	0	
						K.AVLEYKEAK.A	99.70%	64.4	40.5	0	0	3	0	0	
						K.DEAFFSANAAALASR.K	99.70%	89.5	44.9	0	0	1	0	0	
						R.EGLPLR.K.S	96.70%	33.5	36.4	10.9	0	2	0	0	
						R.EGVKYGAGIGPGVYDIHSPR.I	99.70%	65.5	44.2	58	0	0	3	0	
						K.FALESFWDGK.S	99.70%	57	42.4	37.2	0	3	0	0	
						K.FALESFWDGKSTAEDLK.K	99.70%	43.2	44.9	2.02	0	0	1	0	
						K.FALESFWDGKSTAEDLKK.V	99.70%	87.2	44.4	72.4	0	1	3	1	
						K.GMLTGPVTILNWSFVR.N	99.70%	111	41.8	0	0	6	1	0	
						R.GNASVPAMEMTK.W	99.70%	72.4	42	24.2	0	10	0	0	
						R.GTKTLDLVKAEFPGK.Y	99.70%	39.7	40	20.6	0	0	1	0	
						K.GVDKSFDLLSLPK.I	99.70%	55.8	38.3	12.6	0	2	3	0	
						K.GVTGYGFDLVR.G	99.70%	79.1	41.6	57.2	0	3	0	0	
						R.HETCYQJALAIKNEVEDLEK.A	99.70%	71	44.6	58.4	0	1	3	3	
						R.HETCYQJALAIKNEVEDLEKAGINVIQIDEAALR.E	99.70%	71.3	41.8	62.8	0	0	0	2	
						K.ILPIYKEVVAELK.E	99.70%	50.2	32.7	34.5	0	3	3	0	
						R.IPTEELADR.I	99.70%	77	41.2	0	0	4	0	0	
						R.IPTEELADR.I.K	99.30%	48	40.1	0	0	3	0	0	
						K.ISEEEYVK.A	99.70%	59.1	43	36.9	0	3	0	0	
						K.KISEEEYVK.A	99.70%	51.6	42.2	17.9	0	3	3	0	
						K.KLNLPILPPTTTIGSFQTVELR.R	99.70%	68.9	33.4	11.8	0	3	1	0	
						K.KLNLPILPPTTTIGSFQTVELRR.V	99.70%	35.6	31.1	0	0	0	3	0	
						R.KMLAVLESNVLWVNPDCGLK.T	99.70%	81.6	42.9	69.6	0	3	3	0	

						R.KSEHDFYLK.W	99.70%	58.7	43.3	28.5	0	3	0	0	
						R.KYGEVNPALSNMVAQK.Q	99.70%	106	42.7	82	0	6	6	0	
						K.LDDEIKSWLAFQK.V	99.70%	44.1	43.1	0	0	0	1	0	
						K.LLSVFR.E	99.00%	40.7	35.4	0	0	3	0	0	
						K.LLSVFREGVK.Y	99.70%	60.2	37	0	0	1	0	0	
						K.LNLPILPTTTIGSFQTVLR.R	99.70%	66.5	35.5	10.4	0	0	2	0	
						K.LNLPILPTTTIGSFQTVLRR.V	99.70%	41.6	33.9	0.99	0	0	2	0	
						K.LQEELDIDVLVHGEPEP.N	99.70%	69.3	44.1	0	0	0	3	0	
						K.MLAVLESNVLWVNPDCGLK.T	99.70%	65.4	44	45.9	0	3	3	0	
						R.NDQPRHETCYQJALAIK.N	99.70%	62.7	44.8	46.9	0	0	3	0	
						R.NDQPRHETCYQJALAIKNEVEDLEK.A	99.70%	74.6	45.8	49.3	0	0	2	3	
						R.NIWANDLAASLATLEALEGVVGK.D	99.70%	52.4	40.8	43.6	0	0	1	0	
						R.NIWANDLAASLATLEALEGVVGKDK.L	99.70%	130	40.4	90.6	0	2	3	0	
						K.QLRQELASAK	99.70%	61	40.9	37	0	3	3	0	
						K.QMADAGIK.Y	99.60%	59.2	41	18.6	0	6	0	0	
						R.RATTVSSR.L	96.00%	31.7	40.6	7.64	0	6	0	0	
						R.SDEKLLSVFR.E	99.70%	64	41.6	0	0	3	3	0	
						K.SEHDFYLK.W	97.90%	41.7	41.5	24.5	0	3	0	0	
						K.SFDLLSLPK.I	99.70%	68.2	39.3	40	0	3	0	0	
						K.SWLAFQK.V	99.70%	55.9	46	0	0	2	0	0	
						K.TLDLVKAEFPGK.Y	99.70%	83.5	43.7	65.9	0	3	3	0	
						K.TLDLVKAEFPGKYLFGVVDGR.N	99.70%	53.1	40.1	29.9	0	0	0	1	
						K.TLISLKGVTGYGFDLVR.G	99.70%	76.3	37.9	63.4	0	1	3	0	
						K.VLEVNALAK.A	99.70%	54.8	40.2	5.3	0	2	0	0	
						K.WFDTNHYFIVPELGPVNFYASHK.A	99.70%	75.4	45.9	19.2	0	0	3	0	
						K.YGAGIGPGVYDIHSPR.I	99.70%	105	44	85.7	0	3	3	0	
						K.YGEVNPALSNMVAQK.Q	99.70%	90.5	43.6	76.2	0	6	0	0	
						K.YIPSNFYSYDQVLDTTAMLGAVPPR.Y	99.00%	47.8	45.4	3.41	0	0	1	0	
						K.YLFGVVDGR.N	99.70%	55.1	42.2	24.6	0	3	0	0	
1503	Triosephosphate isomerase	gi 388507284	33452	100.00%	5	23.10%	K.FFVGGNWK.C	95.50%	31.9	41.3	12.9	0	3	0	0
						R.HVIGKDEFIGK.K	99.70%	47.1	41.7	35.3	0	1	2	0	
						R.HVIGKDEFIGK.K.A	99.70%	47	40.7	32.9	0	1	3	3	
						K.KAAYALSEGLGVIAICIGELLEER.E	99.70%	67.9	41.2	54.3	0	0	1	0	
						K.KEDIDGFLVGGASLKGPEFATVNSVTSK.K	99.70%	46.4	41	1.71	0	0	0	3	
1508	V-ATPase A subunit	gi 13235340	68900	100.00%	54	85.90%	K.AREVLQREDDLNEIVQLVGK.D	99.70%	70.2	39.5	53.1	0	0	3	2
						R.DMGYNVSMMDSTSR.W	99.70%	107	41.6	14.4	0	14	4	0	
						R.EASIYTGITIAEYFR.D	99.70%	106	42.8	0	0	3	3	0	
						R.EASIYTGITIAEYFRDMGYNVSMMDSTSR.W	99.70%	70.6	46.9	0	0	0	4	2	
						R.EDDLNEIVQLVGK.D	99.70%	88.4	43.6	69.4	0	2	0	0	
						K.EFTMLQSWPVR.T	99.20%	53.7	42.7	33.3	0	5	0	0	
						R.EVLQREDDLNEIVQLVGK.D	99.70%	56.2	45.4	35.8	0	3	3	0	
						K.FDPDFINIR.T	99.40%	54.7	41.9	32.1	0	3	0	0	
						K.FEDPAEGEDTLVAK.F	99.70%	96.2	43.2	44.3	0	3	0	0	
						K.FQKLYEDLSAAR.N	99.70%	47.8	42.5	23.4	0	3	3	0	
						R.GAGSDGQKITYSLIK.L	99.70%	75	40.6	20.7	0	3	3	0	
						R.GAGSDGQKITYSLIKR.L	99.70%	45.4	37.4	31.5	0	0	1	0	
						R.GNEMAEVLMDFPQLTMTLPDGR.E	99.70%	90.5	46.2	77.7	0	2	0	0	
						R.GNEMAEVLMDFPQLTMTLPDGREESVMK.R	99.70%	74.2	46.4	57.7	0	0	3	0	
						R.GNEMAEVLMDFPQLTMTLPDGREESVMKR.T	99.70%	63.8	46.3	37	0	0	4	2	
						R.GVAVPPLDKDALWFEFEPK.K	99.70%	44.4	41.4	32.4	0	3	3	0	
						R.GVAVPPLDKDALWFEFEPK.I	98.50%	30.2	39.3	17	0	0	2	0	
						K.HFPSVNWLSYSK.Y	99.70%	48.8	42.4	21.5	0	3	3	0	
						K.ITYIAPPGQYSIQDTVLELEFQGVK.K	99.70%	49.3	40.1	0	0	0	2	0	
						K.ITYIAPPGQYSIQDTVLELEFQGVK.E	99.70%	48.5	38.5	0	0	0	2	1	
						K.KEFTMLQSWPVR.T	99.70%	71.6	42.7	55.1	0	2	2	0	



R.KHFPSVNWLSYSK.Y	99.70%	76.7	41	53.4	0	3	3	1
K.KIGEDLLTGGDLYAK.V	99.70%	75.3	41.2	57.4	0	3	3	0
R.KVSGPVVADGMNGAAMYELVR.V	99.70%	66.9	43.8	32.2	0	1	7	0
K.LAADTPLLTGQR.V	99.70%	83.1	38.9	60.9	0	3	3	0
R.LAEMPADSGYPAYLAAR.L	99.70%	104	44	80.6	0	3	2	0
R.LASFYER.A	99.10%	49.7	40.5	16.9	0	2	0	0
R.LEGDSATIQQVYEETAGLMVNDPVL.R.T	99.70%	75.6	44.5	63.4	0	1	3	0
R.LGDLFYR.L	99.40%	53.5	40.9	15.5	0	3	0	0
K.LLREDYLAQNAFTPYDK.F	99.70%	44.5	43.9	29.1	0	0	1	0
K.LRLGDLFYR.L	99.70%	34.4	37.8	9.32	0	1	3	0
R.LTTFEDSEKESEGYIR.K	99.70%	76.8	45	67.5	0	3	1	0
R.LTTFEDSEKESEGYIRK.V	99.40%	49	45.5	38.7	0	0	3	0
R.LVSQKFEDPAEGEDTLVAK.F	99.70%	53.5	43.2	21.9	0	3	3	0
K.LYEDLSAAFR.N	99.70%	76.4	45.5	34	0	3	0	0
M.PAVYGDRLTTFEDSEKESEGYIR.K	99.40%	42.5	45.6	30.1	0	0	0	2
K.RSGDVYIPR.G	98.90%	45.2	41.5	20.7	0	3	0	0
K.RTTLVANTSNMPVAAR.E	99.70%	83.7	42.4	63	0	1	4	0
R.SGDVYIPR.G	99.10%	55.1	40.5	21.5	0	3	0	0
R.TGSVTIVGAVSPPGGDFSDPVTSATLSIVQVFWGLDKK.L	99.70%	68.9	38.4	58.2	0	0	1	0
R.THKPLSVELGPGILGNIFDGIQRPLK.T	99.70%	63.6	30.9	62	0	0	2	4
R.THKPLSVELGPGILGNIFDGIQRPLKTIAK.R	99.70%	56.6	31.9	45.8	0	0	0	2
R.THKPLSVELGPGILGNIFDGIQRPLKTIAKR.S	99.70%	56.1	34.3	52.6	0	0	0	3
R.TTLVANTSNMPVAAR.E	99.70%	101	42.9	76	0	6	6	0
K.TVISQALS.K.Y	99.70%	61	39.4	31.3	0	3	0	0
K.TVISQALS.KYSNSDAVVYVGCGER.G	99.70%	56.2	44.2	8.33	0	0	2	0
R.VGYDNLIGEII.R.L	99.70%	84.9	40.3	57.7	0	3	2	0
R.VGYDNLIGEIIIRLEGDSATIQQVYEETAGLMVNDPVL.R.T	99.70%	82.3	40.9	70.1	0	0	0	1
K.VKCLGGPER.T	96.60%	39.1	42.2	5.59	0	1	0	0
R.VLDALFPSVLGGTCAIPGAFGCGK.T	99.70%	104	43.3	90.1	0	3	3	0
K.VSGPVVADGMNGAAMYELVR.V	99.70%	117	43.7	98.7	0	3	5	0
R.WAEALREISGR.L	98.00%	46.6	41.6	23.1	0	3	0	0
K.YSNSDAVVYVGCGER.G	99.70%	84.1	43.5	11.8	0	3	0	0
K.YTSALETFYEKFDPDFINIR.T	99.70%	67.1	44.5	59.7	0	1	3	0