

Peptides

Accession	Protein	Start	End	Modifications	Score	Accession	Protein	Start	End	Modifications	Score							
10	T0927.6.4380 T0927.6.4300	glyceroldehyde 3-phosphate dehydrogenase, glycosomal glyceroldehyde 3-phosphate dehydrogenase, glycosomal	1.00	2540	405	52	35	88.3	AAALNIPSTTGAAK	34.4	1.00	2259	402	48	27	80.5	AAALNIPSTTGAAK	34.4
			AAALNIPSTTGAAK Deamidated (N5)	25.8	AAALNIPSTTGAAK Deamidated (N5)	37.8												
			AAALNIPSTTGAAK/GMVPSTGK Oxidation (M19)	29.3	AQRNPADLPWGK	24.6												
			AQRNPADLPWGK	39.2	AQRNPADLPWGK/GVEYVIESTGLFTVK	25.3												
			AQRNPADLPWGK/GVEYVIESTGLFTVK	12.9	AQRNPADLPWGK/GVEYVIESTGLFTVK Deamidated (N4)	24.9												
			AQRNPADLPWGK/GVEYVIESTGLFTVK Deamidated (N4)	7.6	AQRNPADLPWGK/GVEYVIESTGLFTVK Deamidated (G2)	17.0												
			AQRNPADLPWGK/GVEYVIESTGLFTVK Deamidated (G2)	7.3	ATLQNNLPNER	41.4												
			ATLQNNLPNER	31.5	ATLQNNLPNER Deamidated (N5)	52.5												
			ATLQNNLPNER Deamidated (N5)	39.0	ATLQNNLPNER Deamidated (N6)	42.5												
			ATLQNNLPNER Deamidated (N6)	25.0	ATLQNNLPNER Deamidated (N9)	35.4												
			ATLQNNLPNER Deamidated (N5)	18.7	ATLQNNLPNER	18.3												
			AVGMVFPSTGK	35.4	ATLQNNLPNER Deamidated (N5)	16.0												
			AVGMVFPSTGK Oxidation (M4)	37.3	AVGMVFPSTGK	28.1												
			AVGMVFPSTGK Oxidation (M4)- Deamidated (O10)	43.9	AVGMVFPSTGK Oxidation (M4)	37.1												
			DTSKEDAAAK	45.5	DTSKEDAAAK	44.6												
			DTSKEDAAAKR	46.4	DTSKEDAAAKR	38.9												
			EHHVSNASCTTNCLAPLVHLVK Carbamidomethyl (C10)- Carbamidomethyl (C14)	31.5	EGFGISGLMTTYSYATQK	41.8												
			EHHVSNASCTTNCLAPLVHLVK Carbamidomethyl (C10)- Carbamidomethyl (C14)- Deamidated (N13)	23.7	EHHVSNASCTTNCLAPLVHLVK Carbamidomethyl (C10)- Carbamidomethyl (C14)	46.0												
			FKHVSSTIK	28.2	EHHVSNASCTTNCLAPLVHLVK Carbamidomethyl (C10)- Carbamidomethyl (C14)- Deamidated (N13)	33.9												
			GGRAALNIPSTTGAAK	44.1	EHHVSNASCTTNCLAPLVHLVK Deamidated (N7)- Carbamidomethyl (C10)- Carbamidomethyl (C14)	44.6												
			GGRAALNIPSTTGAAK	45.1	IVSWYDNEWGYSYR	46.0												
			LCVKAQR Carbamidomethyl (C3)	25.3	IVSWYDNEWGYSYR Deamidated (N7)	45.4												
			LCVKAQRNADLPWGK Carbamidomethyl (C3)	25.0	KVVSAPASGGAK	34.1												
			IVSWYDNEWGYSYR	49.3	LGVEYVIESTGLFTVK	8.5												
			IVSWYDNEWGYSYR Deamidated (N7)	19.9	LTGMARVPTADSVVDTFIATR	16.5												
			IVSWYDNEWGYSYR/VLVR	35.4	LTGMARVPTADSVVDTFIATR Oxidation (M4)	20.4												
			KVVSAPASGGAK	43.4	MPFGALCGDGLGNEIWDVDMNTDAR Carbamidomethyl (C7)- Deamidated (N14)	9.9												
			LGVEYVIESTGLFTVK	12.3	NILGYDEELVSDIFSISR	43.8												
			LTGMARVPTADSVVDTFIATR Oxidation (M4)	38.3	NILGYDEELVSDIFSISR Deamidated (N1)	7.3												
			MPFGALCGDGLGNEIWDVDMNTDAR Oxidation (M1)- Oxidation (M24)- Carbamidomethyl (C7)	16.4	NPADLPWGK	30.4												
			NILGYDEELVSDIFSISR	47.5	NPADLPWGK/GVEYVIESTGLFTVK	30.5												
			SAEGHLRGGAR	24.6	NPADLPWGK/GVEYVIESTGLFTVK Deamidated (N1)	45.7												
			SKPSVAKDITLVNGHNR	70.9	NPADLPWGK/GVEYVIESTGLFTVK Deamidated (N1)	21.0												
			SKPSVAKDITLVNGHNR Deamidated (N14)	48.3	SKPSVAKDITLVNGHNR	35.4												
			SKPSVAKDITLVNGHNR/LCVK Carbamidomethyl (C20)	22.3	SKPSVAKDITLVNGHNR Deamidated (N14)	57.1												
			SSVDSK	30.7	SSVDSKATLQNNLPNER	4.0												
			SSVDSKATLQNNLPNER	75.3	SSVDSKATLQNNLPNER Deamidated (N12)	42.8												
			SSVDSKATLQNNLPNER Deamidated (N12)	51.7	SSVDSKATLQNNLPNER Deamidated (N16)	44.4												
			SSVDSKATLQNNLPNER Deamidated (N13)	76.7	SSVDSKATLQNNLPNER Deamidated (Q11)	31.4												
			SSVDSKATLQNNLPNER	41.0	SSVDSKATLQNNLPNER	31.8												
			SSVDSKATLQNNLPNER Deamidated (N12)	45.3	SSVDSKATLQNNLPNER Deamidated (N12)	35.1												
			SSVDSKATLQNNLPNER Deamidated (N13)	71.5	SSVDSKATLQNNLPNER Deamidated (N13)	51.2												
			TFVAGVINDYVNR	44.9	SSVDSKATLQNNLPNER Deamidated (Q11)	43.5												
			TFVAGVINDYVNR Oxidation (M4)	32.9	TIKVINGFGR Deamidated (N7)	38.8												
			TFVAGVINDYVNR Oxidation (M4)- Deamidated (N7)	33.5	TYMKNLGYDEELVSDIFSISR Oxidation (M3)	39.9												
TIKVINGFGR	22.0	VPTADSVVDTFIATR	54.6															
TIKVINGFGR Deamidated (N7)	48.6	VVSAPASGGAK	36.3															
TYDGVSKDWR	31.7	YFVGMKYDSVHGK Oxidation (M8)	5.8															
TYDGVSKDWR/GGR	23.3																	
TYMKNLGYDEELVSDIFSISR Oxidation (M3)	25.1																	
VVSAPASGGAK	40.6																	
YFVGMKYDSVHGK Oxidation (M8)	22.6																	
11	T0927.8.3530	glycerol 3-phosphate dehydrogenase [NAD] glycosomal	1.00	2050	283	39	31	86.7	AAEAGVTAEPLEER	40.6	1.00	2514	300	46	25	83.6	AALISR	15.2
			AAEAGVTAEPLEER	51.9	AAEAGVTAEPLEER	32.8												
			CWATTDVIGGEIASAMKNVLAASGALKGLGTENNAR Carbamidomethyl (C1)- Carbamidomethyl (C10)- Deamidated (N5)	10.3	CWATTDVIGGEIASAMK Carbamidomethyl (C1)- Carbamidomethyl (C10)	81.8												
			GAELVLPVPTQFLR	32.6	CWATTDVIGGEIASAMKNVLAASGALK Carbamidomethyl (C1)- Carbamidomethyl (C10)	41.8												
			GAVFSSGAFGTALACVLAK Carbamidomethyl (C15)	37.9	CWATTDVIGGEIASAMKNVLAASGALKGLGTENNAR Carbamidomethyl (C1)- Carbamidomethyl (C10)	68.5												
			GAVFSSGAFGTALACVLAK Carbamidomethyl (C15)	55.8	GAELVLPVPTQFLR	17.0												
			GLQKNSHLR Deamidated (N6)	41.6	GAELVLPVPTQFLR Deamidated (Q12)	25.5												
			GIERSLLFPAQILEELFNPYPIGVAGPSFAIEVAK	28.3	GAVFSSGAFGTALACVLAK Carbamidomethyl (C15)	59.0												
			GLIERDLTLAAGTGEAVFQLPGLDGLLTCSSLSLR Carbamidomethyl (C32)	17.8	GAVFSSGAFGTALACVLAK Carbamidomethyl (C15)	35.3												
			GLMTNVTAAADINMAR Oxidation (M2)- Oxidation (M15)- Carbamidomethyl (C7)	49.1	GIERSLLFPAQILEELFNPYPIGVAGPSFAIEVAK	33.6												
			IMTSDGSR Oxidation (M2)	20.6	GIERSLLFPAQILEELFNPYPIGVAGPSFAIEVAK Deamidated (N20)	35.5												
			KCESVSVHNNANEAR Carbamidomethyl (C2)- Oxidation (M10)	33.1	GLIERDLTLAAGTGEAVFQLPGLDGLLTCSSLSLR Carbamidomethyl (C32)	30.8												
			KHNHLPHICHEVYVNLVANGCAK Carbamidomethyl (C9)- Carbamidomethyl (C21)	32.1	GLMTNVTAAADINMAR Carbamidomethyl (C7)	16.0												
			KHNHLPHICHEVYVNLVANGCAK Carbamidomethyl (C9)- Carbamidomethyl (C21)- Deamidated (N14)	21.0	GLMTNVTAAADINMAR Carbamidomethyl (C7)- Deamidated (N14)	58.4												
			KHNHLPHICHEVYVNLVANGCAK Carbamidomethyl (C9)- Carbamidomethyl (C21)- Deamidated (N19)	25.6	GLMTNVTAAADINMAR Deamidated (N5)- Carbamidomethyl (C7)	70.4												
			KHNHLPHICHEVYVNLVANGCAK Deamidated (N3)- Deamidated (N19)- Carbamidomethyl (C9)- Carbamidomethyl (C21)	15.7	GLMTNVTAAADINMAR Oxidation (M2)- Deamidated (N5)- Carbamidomethyl (C7)	9.0												
			KHNHLPHICHEVYVNLVANGCAK Carbamidomethyl (C9)- Carbamidomethyl (C21)- Deamidated (N19)	11.7	GLMTNVTAAADINMAR Oxidation (M2)- Oxidation (M15)- Carbamidomethyl (C7)	17.1												
			KLNSKLADEGLPALPR Carbamidomethyl (C5)	66.4	KCESVSVHNNANEAR Carbamidomethyl (C2)- Deamidated (N11)	63.4												
			KLNSKLADEGLPALPR Deamidated (N3)- Carbamidomethyl (C5)	86.4	KHNHLPHICHEVYVNLVANGCAK Carbamidomethyl (C9)- Carbamidomethyl (C21)	35.6												
			LADEGLPALPR	42.0	KHNHLPHICHEVYVNLVANGCAK Carbamidomethyl (C9)- Carbamidomethyl (C21)- Deamidated (N14)	11.1												
			LAKHNHLPHICHEVYVNLVANGCAK Carbamidomethyl (C12)- Carbamidomethyl (C24)- Deamidated (N22)	11.4	KHNHLPHICHEVYVNLVANGCAK Carbamidomethyl (C9)- Carbamidomethyl (C21)- Deamidated (N19)	18.8												
			LGGSISLEEKR	45.7	KHNHLPHICHEVYVNLVANGCAK Deamidated (N3)- Carbamidomethyl (C9)- Carbamidomethyl (C21)	28.0												
			LGGSISLEEKR Deamidated (Q3)	60.3	KHNHLPHICHEVYVNLVANGCAK Deamidated (N3)- Deamidated (N19)- Carbamidomethyl (C9)- Carbamidomethyl (C21)	42.5												
			LGGSISLEEKRSY Deamidated (Q3)	29.7	KHNHLPHICHEVYVNLVANGCAK Carbamidomethyl (C9)- Carbamidomethyl (C21)- Deamidated (N14)	21.6												
			LNSKLADEGLPALPR Carbamidomethyl (C4)	48.5	KHNHLPHICHEVYVNLVANGCAK Carbamidomethyl (C9)- Carbamidomethyl (C21)- Deamidated (N19)	25.3												
			NFTVGMKLGGSISLEEKR Oxidation (M6)	8.7	KLNSKLADEGLPALPR Carbamidomethyl (C5)	42.7												
			NHVSIR	24.0	KLNSKLADEGLPALPR Deamidated (N3)- Carbamidomethyl (C5)	49.8												
			NVLAASGALK	51.0	LADEGLPALPR	43.4												
			NVLAASGALKGLGTENNAR	66.9	LGGSISLEEKR	34.4												
			NVLAASGALKGLGTENNAR	84.1	LGGSISLEEKR Deamidated (Q3)	47.2												
			NVPVVMCSKIGIER Carbamidomethyl (C7)	32.1	LNSKLADEGLPALPR Carbamidomethyl (C4)	74.8												
			NVPVVMCSKIGIER Oxidation (M8)- Carbamidomethyl (C7)	38.7	LNSKLADEGLPALPR Deamidated (N2)- Carbamidomethyl (C4)	13.4												
			RGAVFGSAGFATALACVLAK Carbamidomethyl (C16)	37.4	NVLAASGALK	34.7												
			SFKNLNSCK Carbamidomethyl (C9)	18.7	NVLAASGALKGLGTENNAR	24.2												
			SLLFPAQILEELFNPYPIGVAGPSFAIEVAK	24.9	NVLAASGALKGLGTENNAR Deamidated (N1)	37.5												
			SLLFPAQILEELFNPYPIGVAGPSFAIEVAK Deamidated (N16)	26.9	NVLAASGALKGLGTENNAR Deamidated (N1)- Deamidated (N17)- Deamidated (N18)	49.5												
			TSKAVAEQVTAEPLEER	55.6	NVLAASGALKGLGTENNAR Deamidated (N17)	43.9												
			TSKAVAEQVTAEPLEER	49.6	NVLAASGALKGLGTENNAR Deamidated (N18)	62.4												
			YSGVITYLKR	55.3	RGAVFGSAGFATALACVLAK Carbamidomethyl (C16)	50.3												
					SLLFPAQILEELFNPYPIGVAGPSFAIEVAK	28.6												
					SLLFPAQILEELFNPYPIGVAGPSFAIEVAK Deamidated (N16)	13.8												
					SLLFPAQILEELFNPYPIGVAGPSFAIEVAK Deamidated (Q8)- Deamidated (N16)	28.2												
					TSKAVAEQVTAEPLEER	29.0												
					YSGVITYLKR	53.2												
					VVNGKHENVYFLPGAPLPHLTTADAECAK Carbamidomethyl (C30)	44.8												
		VVNGKHENVYFLPGAPLPHLTTADAECAK Deamidated (Q4)- Carbamidomethyl (C30)	33.9															
12	T0927.11.11330	heat shock protein 70	1.00	1306	63	28	21	39.9	ARFEEELCGDIFR Carbamidomethyl (C7)	37.4	1.00	1063	55	25	21	48.8	ARFEEELCGDIFR Carbamidomethyl (C7)	43.5
			ARFEEELCGDIFR/DLQVPER Carbamidomethyl (C7)	22.1	ATNGDTHLGGEDFDRVWVH#TEEKR Deamidated (N3)	29.9												
			AHHDVLLVGSTR	51.5	AHHDVLLVGSTR	59.8												
			AVTVVRYFNDISOR	28.1	AVTVVRYFNDISOR	33.2												
			AVTVVRYFNDISOR Deamidated (Q13)	18.6	AVTVVRYFNDISOR Deamidated (Q13)	32.3												
			AVTVVRYFNDISOR/QAKDAGTAGLEVLR Deamidated (N10)	28.9	DAGTAGLEVLR	64.6												
			DAGTAGLEVLR	74.8	DCHLLGTFDLGPPAPR Carbamidomethyl (C2)	16.4												
			INEPFAAAVYGLDKADEGKER	31.7	INEPFAAAVYGLDKADEGKER	54.0												
			INEPFAAAVYGLDKADEGKER Deamidated (N3)	37.8	LQADKNVATVWEALR	28.1												
			LIGDAKKNQVMMNPTVFDKAR Oxidation (M12)	46.0	LIGDAKKNQVMMNPTVFDKAR Oxidation (M12)	11.2												
			LSKADDER	40.7	MVSDAAKAYAEKQAR	24.4												
			MKEWIESTLQK Oxidation (M1)	23.1	MKGKLSLSNR	7.3												
			MKGKLSLSNR	27.8	NOVITNDKGR	14.1												
			NOVITNDKGR	44.9	NTINDPNVAGKLDADKNVATVWEALR	61.4												
			NOVITNDKGR Deamidated (N1)- Deamidated (N7)	44.9	NTINDPNVAGKLDADKNVATVWEALR Deamidated (N1)- Deamidated (N8)	55.0												

Peptides

Accession	Protein	Start	End	Modifications	Score	Accession	Protein	Start	End	Modifications	Score						
13	Tb927.11.9980 2-oxoglutarate dehydrogenase E1 component, putative	1560	116	41	33	44.0	NIQVINDKGR Deamidated (N7)	32.6	NTINDPNAVKLDDADKNAVTTAVEEARL Deamidated (N18)	14.9							
							NDVAMNFTVTPDAKR Oxidation (M5)	32.2	QATKDGATGLEVLK	20.1							
							NTKDPNNAVKLDDADKNAVTTAVEEARL	66.6	QKLEIGVCAPIK Carbamidomethyl (C8)	23.5							
							QATKDAGTAGLEVLK	66.2	QTEGLLLDAPLTLGETAGVMTALKR	27.0							
							SNPDEAWYGAADAFLTGK	32.3	SNPDEAWYGAADAFLTGK	37.4							
							TWPEEISSMLK Oxidation (M10)	16.0	SKGTGELLDDAPLTLGETAGVMTALKR	62.3							
							TTPSYAFDSEK	48.1	SKQSTYSDNGPQVHGVFEGER	44.3							
							VMQLVSDFGGKELNK	65.3	SKQSTYSDNGPQVHGVFEGER Deamidated (Q2)	44.6							
							VMQLVSDFGGKELNK Oxidation (M2)	29.7	VMQLVSDFGGKELNK	48.7							
							WLNNDGEASLDEYNHR	62.1	WLNNDGEASLDEYNHR	34.8							
							WLNNDGEASLDEYNHR Deamidated (Q6)	39.4									
							WLNNDGEASLDEYNHRKLELGVCAPIK Carbamidomethyl (C24)	37.1									
							WLNNDGEASLDEYNHRKLELGVCAPIK Deamidated (N3) Carbamidomethyl (C24)	28.8									
							AFQCFPHVNGDQPEDVAR Carbamidomethyl (C4) Carbamidomethyl (C13)	15.5	AFQCFPHVNGDQPEDVAR Carbamidomethyl (C4) Carbamidomethyl (C13)	27.7							
							AFQCFPHVNGDQPEDVAR Carbamidomethyl (C4) Carbamidomethyl (C13) Deamidated (N10)	15.5	AFQCFPHVNGDQPEDVAR Carbamidomethyl (C4) Carbamidomethyl (C13) Deamidated (N10)	33.6							
							AFQCFPHVNGDQPEDVAR Deamidated (Q2) Carbamidomethyl (C4) Carbamidomethyl (C13)	39.4	AFQCFPHVNGDQPEDVAR Deamidated (Q2) Carbamidomethyl (C4) Carbamidomethyl (C13)	13.6							
							ASAAPSTAYK	24.5	ASAAPSTAYK	57.1							
							ASAAPSTAYKTHDAEERYCECVFS Carbamidomethyl (C22) Carbamidomethyl (C24)	23.6	ASAAPSTAYKTHDAEERYCECVFS Carbamidomethyl (C22) Carbamidomethyl (C24)	17.1							
							AMTKELHDLTK	27.5	AMTKELHDLTK	65.2							
							AMTKELHDLTK Oxidation (M2)	27.5	AMTKELHDLTK Oxidation (M2)	31.3							
							DLSQFERPLTSPK	40.9	DLSQFERPLTSPK Deamidated (N4)	26.8							
							ESLQPVWDLK	25.3	ESLQPVWDLK	43.9							
							FSDGDSLNLVLR Carbamidomethyl (C3)	41.8	FSDGDSLNLVLR Carbamidomethyl (C3)	45.4							
							FLQVAEDVTPVSPER	79.9	FLQVAEDVTPVSPER	43.3							
							GMKYSELGEVLEPTAVAR Oxidation (M2)	57.2	GMKYSELGEVLEPTAVAR Oxidation (M2)	32.9							
							GRLLTYNWK Oxidation (N4)	9.1	GRLLTYNWK Oxidation (N4)	48.9							
							IELSPFVAEVK	27.8	IELSPFVAEVK	11.5							
							LKAVLEGR	35.9	LKAVLEGR	39.3							
							LLYENDSFLGTSAR	60.1	LLYENDSFLGTSAR	28.6							
							LLYENDSFLGTSAR Deamidated (N6)	56.1	LLYENDSFLGTSAR Deamidated (N6)	17.3							
							LMFTLLANPSHLEAVNPVQGYTR	26.5	LMFTLLANPSHLEAVNPVQGYTR	43.4							
							LTLMIQAFEDYHLLAR	5.1	LTLMIQAFEDYHLLAR	14.7							
							LVEEGVTKEQTK	18.6	LVEEGVTKEQTK	10.0							
							LVMKGTGYYLNR Oxidation (M3) Carbamidomethyl (C4)	32.3	LVMKGTGYYLNR Oxidation (M3) Carbamidomethyl (C4)	31.1							
							MRNGKLMFTLLANPSHLEAVNPVQGYTR Oxidation (M1) Oxidation (M7) Deamidated (N3)	18.1	MRNGKLMFTLLANPSHLEAVNPVQGYTR Oxidation (M1) Oxidation (M7) Deamidated (N3)	49.7							
							NGKLMFTLLANPSHLEAVNPVQGYTR	14.1	NGKLMFTLLANPSHLEAVNPVQGYTR	35.1							
							NGKLMFTLLANPSHLEAVNPVQGYTR Deamidated (N1)	5.8	NGKLMFTLLANPSHLEAVNPVQGYTR Deamidated (N1)	37.0							
							NGKLMFTLLANPSHLEAVNPVQGYTR Oxidation (M8)	48.0	NGKLMFTLLANPSHLEAVNPVQGYTR Oxidation (M8)	33.4							
							NGGAFYHVESR	30.8	NGGAFYHVESR	29.8							
							RHWATPDVFR	28.1	RHWATPDVFR	28.6							
							SFPVILKEFVGTARELPEFK	22.5	SFPVILKEFVGTARELPEFK	17.3							
							SSPYCSDLGR Carbamidomethyl (C5)	37.0	SSPYCSDLGR Carbamidomethyl (C5)	43.4							
							STHDAERYICECVFS Carbamidomethyl (C11) Carbamidomethyl (C13)	7.5	STHDAERYICECVFS Carbamidomethyl (C11) Carbamidomethyl (C13)	14.7							
							TDPLDAEDDSLRSPQVPR	58.8	TDPLDAEDDSLRSPQVPR	10.0							
							VGFMDQLGGMSSSR Oxidation (M4) Oxidation (M11)	39.3	VGFMDQLGGMSSSR Oxidation (M4) Oxidation (M11)	10.0							
VGFMDQLGGMSSSR Oxidation (M4) Oxidation (M11) Deamidated (Q6)	13.1	VGFMDQLGGMSSSR Oxidation (M4) Oxidation (M11) Deamidated (Q6)	10.0														
VHATPDVFR	41.0	VHATPDVFR	31.1														
VREGFVANK	18.7	VREGFVANK	49.7														
VQSLEKGEKDWGAALAFGLLLEGTAVR	17.9	VQSLEKGEKDWGAALAFGLLLEGTAVR	35.1														
VQSLEKGEKDWGAALAFGLLLEGTAVR Deamidated (Q2)	23.5	VQSLEKGEKDWGAALAFGLLLEGTAVR Deamidated (Q2)	37.0														
VVPSADMDNVEQSDICAR Oxidation (M10) Carbamidomethyl (C19)	25.0	VVPSADMDNVEQSDICAR Oxidation (M10) Carbamidomethyl (C19)	33.4														
YGHNEQDITTPQLYR	35.9	YGHNEQDITTPQLYR	29.8														
YSELGEVLEPTAVAR	41.1	YSELGEVLEPTAVAR	29.8														
YSEKLVEEGVTKEQTK	51.0	YSEKLVEEGVTKEQTK	29.8														
14	Tb927.10.15410 glycosomal malate dehydrogenase	1708	163	35	24	68.4	AGRGSATLSMAEAGAR	34.0	AGRGSATLSMAEAGAR	19.5							
							AGRGSATLSMAEAGAR Oxidation (M10)	24.4	AGRGSATLSMAEAGAR Oxidation (M10)	3.6							
							ANIEKGMNFR	28.2	ANIEKGMNFR	23.7							
							ANIEKGMNFR Oxidation (M7)	17.0	ANIEKGMNFR Oxidation (M7)	20.0							
							ANIEKGMNFR Oxidation (M7) Deamidated (N8)	23.9	ANIEKGMNFR Oxidation (M7) Deamidated (N8)	21.1							
							FINNARHPLAVASVPPVGGHSDVTPVFLFSQLPGLPEEGELTOR	50.0	FINNARHPLAVASVPPVGGHSDVTPVFLFSQLPGLPEEGELTOR	49.7							
							GSATLSMAEAGAR Oxidation (M7)	37.4	GSATLSMAEAGAR Oxidation (M7)	27.7							
							GVDFVAVGVR	30.1	GVDFVAVGVR	66.3							
							HPLAVASVPPVGGHSDVTPVFLFSQLPGLPEEGELTOR	67.2	HPLAVASVPPVGGHSDVTPVFLFSQLPGLPEEGELTOR	42.5							
							HPLAVASVPPVGGHSDVTPVFLFSQLPGLPEEGELTOR	34.2	HPLAVASVPPVGGHSDVTPVFLFSQLPGLPEEGELTOR	68.1							
							KRVQDQTEVVK	24.4	KRVQDQTEVVK	13.8							
							LGYYNKKLLGVTLDDGLR	33.1	LGYYNKKLLGVTLDDGLR	74.8							
							LGYYNKKLLGVTLDDGLR Deamidated (N7)	33.4	LGYYNKKLLGVTLDDGLR Deamidated (N7)	62.8							
							LLGVTLDDGLR	78.7	LLGVTLDDGLR	36.8							
							LLGVTLDDGLR	43.6	LLGVTLDDGLR	41.1							
							LPFGPMNAVEKEMKQISIVK Oxidation (M6) Oxidation (M13)	31.4	LPFGPMNAVEKEMKQISIVK Oxidation (M6) Oxidation (M13)	18.7							
							LPFGPMNAVEKEMKQISIVK Oxidation (M6) Oxidation (M13) Deamidated (N7)	19.7	LPFGPMNAVEKEMKQISIVK Oxidation (M6) Oxidation (M13) Deamidated (N7)	50.6							
							LPFWRPALAEAR	15.4	LPFWRPALAEAR	41.1							
							NKLLGVTLDDGLR	70.0	NKLLGVTLDDGLR	35.6							
							NKLLGVTLDDGLR Deamidated (N1)	50.5	NKLLGVTLDDGLR Deamidated (N1)	38.6							
							QLPYGSTLSLYDAGAPGVAADLSHVDR	76.8	QLPYGSTLSLYDAGAPGVAADLSHVDR	34.2							
							QLPYGSTLSLYDAGAPGVAADLSHVDR Deamidated (Q1)	60.3	QLPYGSTLSLYDAGAPGVAADLSHVDR Deamidated (Q1)	39.9							
							QLPYGSTLSLYDAGAPGVAADLSHVDRAGVTVK	71.4	QLPYGSTLSLYDAGAPGVAADLSHVDRAGVTVK	73.9							
							QLPYGSTLSLYDAGAPGVAADLSHVDRAGVTVK Deamidated (Q1)	56.1	QLPYGSTLSLYDAGAPGVAADLSHVDRAGVTVK Deamidated (Q1)	58.7							
							QSIIVKANIEK	48.5	QSIIVKANIEK	64.2							
							QSIIVKANIEK Oxidation (M14)	30.4	QSIIVKANIEK Oxidation (M14)	48.8							
							QSIIVKANIEK Oxidation (M14)	48.7	QSIIVKANIEK Oxidation (M14)	75.8							
							RLPGPMNAVEKEMK Oxidation (M14)	6.2	RLPGPMNAVEKEMK Oxidation (M14)	72.5							
							RLPGPMNAVEKEMK Oxidation (M7)	33.2	RLPGPMNAVEKEMK Oxidation (M7)	29.0							
							RVDVAGTEVVK	33.6	RVDVAGTEVVK	42.0							
							VQVAGTEVVK	30.5	VQVAGTEVVK	33.0							
							VQVAGTEVVK	22.7	VQVAGTEVVK	8.7							
							VSWVGAAGGIGQSLLLLR	22.8	VSWVGAAGGIGQSLLLLR	53.2							
							VSWVGAAGGIGQSLLLLR Deamidated (Q14)	27.9	VSWVGAAGGIGQSLLLLR Deamidated (Q14)	25.1							
							YAAGKLPVVKR	23.6	YAAGKLPVVKR	17.4							
										45.8							
										26.7							
										15.2							
							15	Tb927.9.12870 glycerol kinase, glycosomal	1499	102	30	24	55.1	AALQAIQLQNDVGSMKR	62.6	AALQAIQLQNDVGSMKR	39.5
														AALQAIQLQNDVGSMKR Deamidated (N11)	51.4	AALQAIQLQNDVGSMKR Deamidated (N11)	51.4
														AALQAIQLQNDVGSMKR Oxidation (M17)	53.3	AALQAIQLQNDVGSMKR Oxidation (M17)	17.6
														DAGLNLSSLRVGGSLK	53.6	DAGLNLSSLRVGGSLK	65.2
														FIFDER	22.9	FIFDER	23.0
														GTIVGMLKTR Oxidation (M8)	41.3	GTIVGMLKTR Oxidation (M8)	38.3
														KIAGITNQR	51.1	KIAGITNQR	32.3
KIAGITNQR Deamidated (Q10) Deamidated (N9)	4.7	KIAGITNQR Deamidated (Q10) Deamidated (N9)	38.1														
KVTAELGGGDMFAK Oxidation (M12)	36.2	KVTAELGGGDMFAK Oxidation (M12)	61.9														
KWSPLECEK Carbamidomethyl (C7)	36.0	KWSPLECEK Carbamidomethyl (C7)	32.7														
LKIPMETPEIR	43.3	LKIPMETPEIR	36.1														
LKIPMETPEIR Oxidation (M5)	38.0	LKIPMETPEIR Oxidation (M5)	16.0														
LROKASFR	22.9	LROKASFR	39.5														
LSGKAPVTDVNASR	66.7	LSGKAPVTDVNASR	54.7														
MKYVSSDQSTSTR	60.9	MKYVSSDQSTSTR	51.3														
MKYVSSDQSTSTR Oxidation (M1)	67.1	MKYVSSDQSTSTR Oxidation (M1)	50.7														
MNLFSHITECEK Oxidation (M2) Carbamidomethyl (C11)	54.7	MNLFSHITECEK Oxidation (M2) Carbamidomethyl (C11)	81.2														
MNLFSHITECEK Oxidation (M2) Carbamidomethyl (C11)	38.8	MNLFSHITECEK Oxidation (M2) Carbamidomethyl (C11)	23.7														
NTYGTGCLLMNVGEEAR Carbamidomethyl (C7) Oxidation (M11)	49.6	NTYGTGCLLMNVGEEAR Carbamidomethyl (C7) Oxidation (M11)	14.8														
SNSELFYVETDECGVAALNER Deamidated (N2) Carbamidomethyl (C14)	7.0	SNSELFYVETDECGVAALNER Deamidated (N2) Carbamidomethyl (C14)	51.7														
SNSELFYVETDECGVAALNER Deamidated (N2) Carbamidomethyl (C14)	26.0	SNSELFYVETDECGVAALNER Deamidated (N2) Carbamidomethyl (C14)	47.6														

Peptides

Accession	Gene	Protein	Start	End	Length	Peptide	Score	Modifications	Peptide	Score	Modifications											
20	Tb927.5.1060	mitochondrial processing peptidase, beta subunit, putative, metallo-peptidase, Clan ME, Family M16	1.00	1466	156	26	24	52.8	AATSAFGDLQK	33.0	1.00	818	66	17	15	36.6	AATSAFGDLQK	24.3				
										AATSAFGDLQKGTVLGAPPEAR	62.9							AATSAFGDLQKGTVLGAPPEAR	47.2			
										AVSLADVVR	51.0							AVSLADVVR	33.0			
										AVSLADVVRNAR Deamidated (N11)	16.1							AVSLADVVRNAR Deamidated (N11)	23.7			
										CAFDSITHGPGTFLYGVETGTR Carbamidomethyl (C1)	69.7							EDTERAVSLADVVR	12.1			
										EDTERAVSLADVVR	33.8							FVGGYKLVNLR	45.4			
										FVGGYKLVNLR	55.4							GTVLGAPPEAR	51.1			
										GTVLGAPPEAR	59.6							IDVPTFNQEVLYQHYFYGR	69.3			
										HEPAQYAGTAR	9.2							ILHEGELAQAK	42.6			
										IDVPTFNQEVLYQHYFYGR	45.0							IPPTTLSTVGSQVR	47.3			
										ILHEGELAQAK	56.3							RIPLEEMNAR	14.8			
										IPPTTLSTVGSQVR	60.0							TFSSLDHSTPTNTHFNEK	33.5			
										LLSNVLAKIPPTTLSTVGSQVR	52.8							TFSSLDHSTPTNTHFNEK Deamidated (N12)	34.4			
										LSDEDELVAK	41.8							VCEENPNSLAVTGVWLDAGTRHEPNQYAGTAR Carbamidomethyl (C2)	56.3			
										LSDEDEVWQMLR	32.6							VCEENPNSLAVTGVWLDAGTRHEPNQYAGTAR Carbamidomethyl (C2) Deamidated (N6)	49.4			
										QAVLRDQHFQEPDQDIDMNLHR Carbamidomethyl (C18); Oxidation (M19)	19.1							VARETERAVSLADVVR	23.7			
										RIPLEEMNAR	31.7							VVVVSGAVNHTALER Deamidated (N10)	17.1			
										SRPSSNHATK	21.5											
										SRPSSNHATKLLSNLAK	45.0											
							SRPSSNHATKLLSNLAK Deamidated (N15)	33.7														
							TFSSLDHSTPTNTHFNEK	45.6														
							VCEENPNSLAVTGVWLDAGTRHEPNQYAGTAR Carbamidomethyl (C3)	79.9														
							VARETERAVSLADVVR	33.5														
							VKLTSSLDHSTPTNTHFNEK	37.8														
							VVVVSGAVNHTALER	70.7														
							VVVVSGAVNHTALER Deamidated (N10)	46.7														
21	Tb927.11.5520	triosephosphate isomerase	1.00	1196	128	26	13	47.2	DVNGFLVGGASLKPEFVDIK	43.8	1.00	1016	134	28	14	51.2	DVNGFLVGGASLKPEFVDIK	51.3				
										DVNGFLVGGASLKPEFVDIK Deamidated (N3)	44.8							DVNGFLVGGASLKPEFVDIK Deamidated (N3)	47.7			
										DVNGFLVGGASLKPEFVDIKATQ	38.9							DVNGFLVGGASLKPEFVDIKATQ	39.9			
										DVNGFLVGGASLKPEFVDIKATQ Deamidated (N3)	38.8							DVNGFLVGGASLKPEFVDIKATQ Deamidated (N3)	32.3			
										FVIAAQNAIK	61.0							FVIAAQNAIK	47.8			
										FVIAAQNAIK Deamidated (N7)	41.9							FVIAAQNAIK Deamidated (G6)	57.2			
										FVIAAQNAIK Deamidated (G6)	42.0							IGADVAGELR	77.9			
										ILYGSVNGIK Deamidated (N8)	10.7							ILYGSVNGIK Deamidated (N8)	23.6			
										ILYGSVNGIKNAR Deamidated (N8)	15.0							ILYGSVNGIKNAR	66.1			
										ILYGSVNGIKNAR Deamidated (N8); Deamidated (N11)	41.7							ILYGSVNGIKNAR Deamidated (N11)	46.8			
										LSHPKFVIAAQNAIK	49.3							ILYGSVNGIKNAR Deamidated (N8)	43.0			
										LSHPKFVIAAQNAIK Deamidated (N12)	53.7							ILYGSVNGIKNAR Deamidated (N8); Deamidated (N11)	19.6			
										SGAFTGEVLSPLKDFGVNVLGHSERR	11.2							LSHPKFVIAAQNAIK	43.4			
										SGAFTGEVLSPLKDFGVNVLGHSERR	9.8							LSHPKFVIAAQNAIK Deamidated (G11)	19.3			
										TLYQQRDVNGLVGGASLKPEFVDIK	32.9							SGAFTGEVLSPLKDFGVNVLGHSERR	40.3			
										TLYQQRDVNGLVGGASLKPEFVDIK Deamidated (N9)	42.1							SGAFTGEVLSPLKDFGVNVLGHSERR	34.4			
										TLYQQRDVNGLVGGASLKPEFVDIK Deamidated (G5)	17.3							TLYQQRDVNGLVGGASLKPEFVDIK	22.6			
										TLYQQRDVNGLVGGASLKPEFVDIK Deamidated (G5); Deamidated (N6)	19.3							TLYQQRDVNGLVGGASLKPEFVDIK Deamidated (N9)	30.8			
										TLYQQRDVNGLVGGASLKPEFVDIKATQ	48.3							TLYQQRDVNGLVGGASLKPEFVDIK Deamidated (G5)	42.4			
										TLYQQRDVNGLVGGASLKPEFVDIKATQ Deamidated (N6)	32.4							TLYQQRDVNGLVGGASLKPEFVDIKATQ	60.0			
										TLYQQRDVNGLVGGASLKPEFVDIKATQ Deamidated (G30)	31.7							TLYQQRDVNGLVGGASLKPEFVDIKATQ Deamidated (N9)	32.3			
										TLYQQRDVNGLVGGASLKPEFVDIKATQ Deamidated (G30); Deamidated (G30)	33.3							TLYQQRDVNGLVGGASLKPEFVDIKATQ Deamidated (G30)	50.4			
										WATPQQAQEAHALR	54.3							TLYQQRDVNGLVGGASLKPEFVDIKATQ Deamidated (G5); Deamidated (G30)	30.5			
										WATPQQAQEAHALR Deamidated (G8)	19.0							TLYQQRDVNGLVGGASLKPEFVDIKATQ Deamidated (G5); Deamidated (G30)	21.4			
										VVAEYEPVWAGTQK	53.1							WATPQQAQEAHALR Deamidated (G6)	65.7			
										VVAEYEPVWAGTQK Deamidated (G8)	23.0							WATPQQAQEAHALR Deamidated (G8)	60.8			
										VVAEYEPVWAGTQK Deamidated (G8); Deamidated (G30)	56.3							WVAIEYEPVWAGTQK	33.7			
							VVAEYEPVWAGTQK Deamidated (G8); Deamidated (G30)	26.0							WVAIEYEPVWAGTQK Deamidated (G8)	48.3						
22	Tb927.4.2070	antigenic protein, putative	1.00	1118	66	25	13	4.6	ALNEQYETLQR Deamidated (G5)	33.3	1.00	221	14	6	4	1.0	ALNEQYETLQR Deamidated (G5)	17.1				
										ALNEQYETLQR	49.3							ALNEQYETLQR	48.4			
										AVNEQYETLQR	45.7							ALNEQYETLQR Deamidated (N3)	38.9			
										TNAAMEELDSLRL Deamidated (N2); Oxidation (M5)	44.8							AVNEQYETLQR	45.0			
										TNAAMEELDSLRLRAINEQYETLQR Deamidated (N2); Oxidation (M5)	12.2							TNAAMEELDSLRL	19.9			
										TNAAMEELDSLRLRAINEQYETLQR Oxidation (M5); Deamidated (G18)	41.8							TNAAMEELDSLRL Deamidated (N2)	30.5			
										TNAAMEELDSLRLRAINEQYETLQR	60.2											
										TNAAMEELDSLRLRAINEQYETLQR Deamidated (N2)	18.2											
										TNAAMEELDSLRLRAINEQYETLQR Deamidated (N2); Oxidation (M5)	59.5											
										TNAAMEELDSLRLRAINEQYETLQR Deamidated (N2); Deamidated (N2)	42.7											
										TNAAMEELDSLRLRAINEQYETLQR Oxidation (M5)	36.0											
										TNAAMEELDSLRLRAINEQYETLQR Oxidation (M5); Deamidated (G18)	33.6											
										TNAAMEELDSLRLRAINEQYETLQR	17.7											
										TNAAMEELDSLRLRAINEQYETLQR Deamidated (N2)	22.6											
										TNAAMEELDSLRLRAINEQYETLQR Deamidated (N2); Oxidation (M5)	32.3											
										TNAAMEELDSLRLRAINEQYETLQR Oxidation (M5)	39.2											
										TNAAMEELDSLRL Deamidated (N2); Oxidation (M5)	26.4											
										TNAAMEELDSLRLRAINEQYETLQR Oxidation (M5)	28.6											
										TNAAMEELDSLRLRAINEQYETLQR	57.2											
										TNAAMEELDSLRLRAINEQYETLQR Deamidated (N2)	27.8											
										TNAAMEELDSLRLRAINEQYETLQR Deamidated (G23)	39.7											
										TNAAMEELDSLRLRAINEQYETLQR Oxidation (M5)	29.7											
										TNAAMEELDSLRLRAINEQYETLQR	14.3											
										TNAAMEELDSLRLRAINEQYETLQR Deamidated (N2)	28.7											
										TNAAMEELDSLRLRAINEQYETLQR	49.3											
			23	Tb927.11.11880	2-oxoglutarate dehydrogenase E2 component, putative	1.00	1416	89	29	21	43.1	AETADKPKQNAFAAAPPK	26.7	1.00	633	38	17	13	31.6	AETADKPKQNAFAAAPPK	1.9	
													AETADKPKQNAFAAAPPK	78.0							ASPTAAPPKPAFAAAPPVTSR	35.8
													APRAGVYIK	30.9							DIMAAVLYDHR	54.2
													ASPTAAPPKPAFAAAPPVTSR	46.9							DVQNSNFAGIEK	49.6
													DIMAAVLYDHR Oxidation (M3)	53.4							DVQNSNFAGIEKQIADFGER	16.9
													DIMAAVLYDHRLDGSDAVFLVK Oxidation (M3)	27.1							GLVVPVLRDVQNSNFAGIEK	36.7
													DVQNSNFAGIEK	61.5							GLVVPVLRDVQNSNFAGIEK Deamidated (N14)	22.0
													DVQNSNFAGIEKQIADFGER	65.3							GLVVPVLRDVQNSNFAGIEK Deamidated (G17)	22.2
										DVQNSNFAGIEKQIADFGER Deamidated (N6)	41.6							GLVVPVLRDVQNSNFAGIEKQIADFGER	23.0			
										GLVVPVLRDVQNSNFAGIEK	66.9							GLVVPVLRDVQNSNFAGIEKQIADFGER Deamidated (N12); Deamidated (N14)	11.2			
										GLVVPVLRDVQNSNFAGIEK Deamidated (N12)	44.1							RLDLA	19.7			
										GLVVPVLRDVQNSNFAGIEK Deamidated (N14)	43.8							KKPVVVGNVSVPR Deamidated (N8)	13.2			
										GLVVPVLRDVQNSNFAGIEKQIADFGER	32.9							LDGSDAVFLVK	57.9			
										GLVVPVLRDVQNSNFAGIEKQIADFGER Deamidated (N12)	31.0							NLEDIPARVLDLA	49.6			
										GLVVPVLRDVQNSNFAGIEKQIADFGER Deamidated (N12); Deamidated (N14)	39.9							QNAFAAAPPKASPTAAPPKPAFAAAPPVTSR	35.4			

Peptides

Index	Accession	Protein Name	Start	End	Score	Modifications	Peptide Sequence	Score	Modifications	Peptide Sequence								
29	Tb927.9.5320	nucleolar RNA binding protein, putative	1.00	953	47	19	13	28.9	MTGAGLRRESGSHVAKL Oxidation (M1)	25.0	1.00	704	26	12	9	28.6	AIKDALAQCVHGGDTLATFR Carbamidomethyl (C10)	48.1
									RAQSFLEIPR	26.0							AIKDALAQCVHGGDTLATFR Deamidated (D9)- Carbamidomethyl (C10)	42.0
									RRRQVQADGELR Carbamidomethyl (C6)	39.6							ALRANLLEDVSTEGNLQALGLAHNLNR	75.6
									TASVDIAGNIASAEAEALDAGADLQVGVGSGICTR Carbamidomethyl (C38)	34.8							ANLDDLEDVSTEGNLQALGLAHNLNR	100.7
									TQDEDVSSLLVPEGVGACKVGPVIVR Carbamidomethyl (C21)	57.5							ANLDDLEDVSTEGNLQALGLAHNLNR Deamidated (Q17)	67.1
									AGSLLSLAKYPSSTLQLGAEK	29.3							ANLDDLEDVSTEGNLQALGLAHNLNR Deamidated (N2)	60.9
									AIKDALAQCVHGGDTLATFR Carbamidomethyl (C10)	27.9							LRQFEEVTVGR	41.5
									AIKDALAQCVHGGDTLATFR Deamidated (D9)- Carbamidomethyl (C10)	52.4							NFVEKQTEELAVADAK	42.9
									ALRANLLEDVSTEGNLQALGLAHNLNR	51.8							RGPPNGGGGAPFKR Deamidated (N5)- Deamidated (N7)	18.9
									ANLDDLEDVSTEGNLQALGLAHNLNR	66.5							RGPPNGGGGAPFKR Deamidated (N7)	42.2
									ANLDDLEDVSTEGNLQALGLAHNLNRK	45.8							STADALATTTQVWNGELAKPKRK	31.9
									ANLDDLEDVSTEGNLQALGLAHNLNRK Deamidated (G14)	32.0							YPSSTLQLGAEK	47.5
									GPNGNGGGAPFKR Deamidated (N4)	21.4								
									GPNGNGGGAPFKR Deamidated (N6)	28.8								
									LQKAGSLLSLAK	52.0								
LQKAGSLLSLAKYPSSTLQLGAEK	22.2																	
LRQFEEVTVGR	55.5																	
QTEELAVADAKLAK	41.0																	
RGPPNGGGGAPFKR Deamidated (N5)	22.7																	
RGPPNGGGGAPFKR Deamidated (N6)- Deamidated (N7)	29.5																	
RGPPNGGGGAPFKR Deamidated (N7)	33.7																	
STADALATTTQVWNGELAKPKRK	55.6																	
STADALATTTQVWNGELAKPKRK Deamidated (N14)	58.7																	
YPSSTLQLGAEK	31.1																	
30	Tb927.8.2770	inositol 1,4,5-trisphosphate receptor	1.00	636	71	18	15	8.4	EAVSALAR	14.3	1.00	1308	97	26	22	12.9	ALLVFDGKHQR	36.7
									GVVVPVNSAHEFTR	45.6							ALVIVVER	13.4
									GSNVGTGYALLPVCACQR Carbamidomethyl (C16)- Carbamidomethyl (C18)	1.5							APNSNPLSDGVSNSYDQVTFQGLFVLVHWSR	74.6
									LHWALPSEPERDPCAR Carbamidomethyl (C17)	8.3							GVVVPVNSAHEFTR	55.4
									LHWASANSVTDFTVR	2.8							GVVVPVNSAHEFTR Deamidated (N6)	17.9
									LQTFSSDLGATR	57.4							GSNVGTGYALLPVCACQR Carbamidomethyl (C16)- Carbamidomethyl (C18)	47.9
									LVLAPGEEQTCQGFITPR Carbamidomethyl (C14)	33.2							HVSAENSSVTDFTVR	79.7
									LVLKELAVR	32.9							KGPSYDQVWAGSAVTLQSGTKDVAFLDYVK	54.8
									MALSAVGAPEVNSEAK	23.4							LGHWTK	65.8
									MALSAVGAPEVNSEAK Oxidation (M1)	57.3							LHWALPSEPERDPCAR Carbamidomethyl (C17)	12.5
									MALSAVGAPEVNSEAK Oxidation (M1)- Deamidated (N13)	69.7							LHWASANSVTDFTVR	86.4
									MLTNLTPRPSLSLK Oxidation (M1)	10.7							LQTFSSDLGATR	61.9
									MLTNLTPRPSLSLKV Oxidation (M1)	39.3							LVLAPGEEQTCQGFITPR Carbamidomethyl (C14)	47.3
									KNELSDDAEPLPLFGFETSVQILPPTVAK	24.0							MALSAVGAPEVNSEAK	56.9
									KNELSDDAEPLPLFGFETSVQILPPTVAK Deamidated (G23)	13.4							MALSAVGAPEVNSEAK Oxidation (M1)	17.9
RADVSTGDPFVTSPTERDALLWHK	9.3	MALSAVGAPEVNSEAK Oxidation (M1)- Deamidated (N13)	46.0															
SALPVTHLELTSYGTSTYPLVEVPRPR	9.9	MLTNLTPRPSLSLK Oxidation (M1)	48.0															
SFETYAKENAGR	52.9	KNELSDDAEPLPLFGFETSVQILPPTVAK	34.8															
		KNELSDDAEPLPLFGFETSVQILPPTVAK Deamidated (G23)	23.8															
		RADVSTGDPFVTSPTER	30.7															
		RADVSTGDPFVTSPTERDALLWHK	28.6															
		SALPVTHLELTSYGTSTYPLVEVPRPR	52.6															
		SFETYAKENAGR	52.6															
		SLVNRDLQITMEDSTLGEPAQIMNALLSCR Carbamidomethyl (C31)	33.0															
		VAAEGLSKGNR	35.2															
		YDEGIAALHPDGEFATK	27.5															
31	Tb927.10.3210	delta-1-pyrroline-5-carboxylate dehydrogenase, putative	1.00	827	69	19	14	31.4	AIRDATEHLR	21.2	1.00	650	33	16	11	24.6	AAFLHAAHLSTK	57.6
									ASSNDKPSGSAFLTR	56.6							ADTALGAAK	31.7
									ASSNDKPSGSAFLTR Deamidated (N5)	58.5							CTGMVGGQPFQGAR Carbamidomethyl (C1)	62.8
									CGATDPIVGGKEVYR Carbamidomethyl (C1)- Carbamidomethyl (C6)	25.0							GLEAQR Carbamidomethyl (C6)	21.4
									CGATDPIVGGKEVYRDNAINR Carbamidomethyl (C1)- Carbamidomethyl (C6)	44.3							GYNATPELAK Deamidated (N3)	28.3
									GAFEYQKQCSATSR Carbamidomethyl (C10)	49.3							MIPSSHQDQVAK	39.1
									GTLCAQR Carbamidomethyl (C6)	24.9							MIPSSHQDQVAK Oxidation (M1)	31.2
									GYNATPELAK	57.1							SPVWNERMDSFQPGSDAR Oxidation (M9)	9.7
									LRCGATDPIVGGK Carbamidomethyl (C3)- Carbamidomethyl (C8)	35.7							TIKENFDHSAQVSYPHQLPDPVTL	23.2
									MIPSSHQDQVAK	28.9							TIKENFDHSAQVSYPHQLPDPVTL Deamidated (Q17)	4.3
									MIPSSHQDQVAK Oxidation (M1)	25.4							YAAGNYNDKCTGAVGGQPFQGAR Carbamidomethyl (C12)	34.9
									MIPSSHQDQVAK Oxidation (M1)	13.2							YAAGNYNDKCTGAVGGQPFQGAR Deamidated (N6)- Carbamidomethyl (C12)	25.9
									MTALTYRGAFYQKQCSATSR Carbamidomethyl (C18)	35.6							YAAGNYNDKCTGAVGGQPFQGAR Deamidated (Q19)- Deamidated (N5)- Carbamidomethyl (C12)	55.0
									SPVWNERMDSFQPGSDAR Oxidation (M9)	24.9							YAAGNYNDKCTGAVGGQPFQGAR Deamidated (Q19)- Deamidated (N5)- Carbamidomethyl (C12)	31.1
									TIKENFDHSAQVSYPHQLPDPVTL	29.6							YALTGSIFAQDR	71.2
YAAGNYNDKCTGAVGGQPFQGAR Carbamidomethyl (C12)	42.5	YALTGSIFAQDRK	75.7															
YAAGNYNDKCTGAVGGQPFQGAR Deamidated (C19)	42.8																	
YAAGNYNDKCTGAVGGQPFQGAR Deamidated (N5)- Carbamidomethyl (C12)	38.1																	
YAAGNYNDKCTGAVGGQPFQGAR Deamidated (N6)- Carbamidomethyl (C12)	38.9																	
32	Tb927.11.1020	ribokinase, putative	1.00	1213	62	20	10	39.3	ANMAAISVQRPTGSSYPTLDELPAEVEKIKI Carbamidomethyl (C31)	75.1	1.00	1270	94	21	10	38.9	ANMAAISVQRPTGSSYPTLDELPAEVEKIKI Carbamidomethyl (C31)	62.7
									ANMAAISVQRPTGSSYPTLDELPAEVEKIKI Deamidated (Q10)- Carbamidomethyl (C31)	56.4							ANMAAISVQRPTGSSYPTLDELPAEVEKIKI Deamidated (Q10)- Carbamidomethyl (C31)	62.7
									ANMAAISVQRPTGSSYPTLDELPAEVEKIKI Oxidation (M3)- Carbamidomethyl (C31)	48.9							ANMAAISVQRPTGSSYPTLDELPAEVEKIKI Deamidated (Q15)- Carbamidomethyl (C31)	62.0
									ANMAAISVQRPTGSSYPTLDELPAEVEKIKI Oxidation (M3)- Deamidated (Q15)- Carbamidomethyl (C31)	45.3							ANMAAISVQRPTGSSYPTLDELPAEVEKIKI Deamidated (Q16)- Deamidated (N2)- Oxidation (M3)- Carbamidomethyl (C31)	6.3
									GFSGKSNQAVCAGR Carbamidomethyl (C12)	69.6							ANMAAISVQRPTGSSYPTLDELPAEVEKIKI Oxidation (M3)- Carbamidomethyl (C31)	59.5
									GKPRRHLPSTVYK	25.2							GFSGKSNQAVCAGR Carbamidomethyl (C12)	67.2
									KQSDNYNFFGPK	63.4							KQSDNYNFFGPK	61.6
									KQSDNYNFFGPK Deamidated (N7)	59.2							KQSDNYNFFGPK Deamidated (N5)	57.0
									KQSDNYNFFGPK Deamidated (Q2)	10.5							KQSDNYNFFGPK Deamidated (Q2)- Deamidated (N5)	32.4
									LGHSVVTLLGGNGYVGEK	80.0							LGHSVVTLLGGNGYVGEK	51.3
									LGHSVVTLLGGNGYVGEK Deamidated (N13)	61.0							LGHSVVTLLGGNGYVGEK Deamidated (N13)	48.9
									LGHSVVTLLGGNGYVGEKQKPRR	82.0							LGHSVVTLLGGNGYVGEKQKPRR	71.0
									LGHSVVTLLGGNGYVGEKQKPRR Deamidated (N13)	67.8							LGHSVVTLLGGNGYVGEKQKPRR Deamidated (N13)	57.5
									NGVQVSNVYR	39.0							NGVQVSNVYR Deamidated (N1)	59.7
									NGVQVSNVYR Deamidated (N1)	38.8							QSDNYNFFGPK	20.8
NGVQVSNVYR Deamidated (Q4)	50.0	QSDNYNFFGPK Deamidated (N4)- Deamidated (N6)- Deamidated (N7)	47.0															
QSDNYNFFGPK	47.8	SFSKGFQKSNQAVCAGR Carbamidomethyl (C16)	21.7															
SFSKGFQKSNQAVCAGR Carbamidomethyl (C16)	47.2	YILQNEPVETLLDLKKAHTR	44.5															
YILQNEPVETLLDLKKAHTR	32.2	YILQNEPVETLLDLKKAHTR Deamidated (Q5)	48.7															
YILQNEPVETLLDLKKAHTR Deamidated (Q5)	29.8	YILQNEPVETLLDLKKAHTR	43.3															
		YILQNEPVETLLDLKKAHTR Deamidated (Q5)	30.0															
33	Tb927.11.2690	succinyl-coA:3-ketoadid-coenzyme A transferase, mitochondrial precursor, putative	1.00	583	20	9	4	13.8	GPFGAMDVLSGTR Oxidation (M6)- Carbamidomethyl (C11)	69.7	1.00	766	21	12	6	17.2	GPFGAMDVLSGTR Carbamidomethyl (C11)	18.4
									NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Carbamidomethyl (C9)	57.1							NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Carbamidomethyl (C9)	56.2
									NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Deamidated (O11)	91.4							LLKIAEDTVDVQK	54.6
									NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Deamidated (O11)- Deamidated (N1)- Deamidated (N2)- Carbamidomethyl (C9)	71.42							NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Carbamidomethyl (C9)	70.0
									NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Deamidated (O8)- Carbamidomethyl (C9)	50.3							NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Carbamidomethyl (C9)- Deamidated (N19)	119.5
									NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Deamidated (O8)- Deamidated (N1)- Deamidated (N2)- Carbamidomethyl (C9)	95.8							NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Carbamidomethyl (C9)- Deamidated (N23)	186.0
									VVYPERVQLEHR	20.6							NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Deamidated (N3)- Carbamidomethyl (C9)	63.5
									VVYPERVQLEHR Deamidated (Q8)	27.5							NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Deamidated (Q8)- Deamidated (N1)- Deamidated (N3)- Deamidated (N19)- Carbamidomethyl (C9)	36.4
									YQTLIEHR	39.9							NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Deamidated (Q8)- Deamidated (N1)- Deamidated (N3)- Deamidated (N23)- Carbamidomethyl (C9)	42.2
																	NFNVPVGGCGQTVIAEVENLNGDIDPEVHLPVYVDR Deamidated (Q8)- Deamidated (G11)- Deamidated (N3)- Deamidated (N23)- Carbamidomethyl (C9)	21.3
																	YQTLIEHR	37.4
																		32.4
34	Tb927.11.1450	2-oxoglutarate dehydrogenase E1 component, putative	1.00	813	75	23	21	30.9	AESSEGAEWCLAEMAFGATALEGTHVR Carbamidomethyl (C11)	5.8	1.00	1034	59	24	22	34.2	AESSEGAEWCLAEMAFGATALEGTHVR Carbamidomethyl (C11)	34.7
									FSLDCAELVWMLMGEASDLGVTSFVQGMFHR	61.3							FSLDCAELVWMLMGEASDLGVTSFVQGMFHR	48.1
									GRNLNLANVK	31.1							GRNLNLANVK	23.3
									HAAYDLLETNRK	38.7							HAAYDLLETNRK	37.2
									HAAYDLLETNRK Deamidated (N10)	34.7							KVLFCTGQIESVDDR Carbamidomethyl (C5)	58.8
									HLGMAGSSDFLPVYGR	1.3							KVLFCTGQIESVDDR Carbamidomethyl (C5)	29.5
									HLGMAGSSDFLPVYGR Oxidation (M4)	39.1							LGDNHYLGADR	41.9
									KVLFCTGQIESVDDR Carbamidomethyl (C5)	60.4							LREAYTAGSCEPYTK Carbamidomethyl (C11)	47.6

Peptides

Accession	Protein	Start	End	Modifications	Peptide	Score	Accession	Protein	Start	End	Modifications	Peptide	Score																		
35	Tb927.10.14820 mitochondrial carrier protein, putative, ADP/ATP translocase 1, putative Tb927.10.14830 mitochondrial carrier protein, putative, ADP/ATP translocase 1, putative Tb927.10.14840 mitochondrial carrier protein, putative, ADP/ATP translocase 1, putative	1.00	990	216	21	15	45.6	LAGEDVERSTFTGR	35.3	0.99	737	148	13	9	38.2	NGKVINFDLLCNPSHLEAMNPLVLGK Deamidated (N1); Carbamidomethyl (C11)	50.8														
								LDGNYHGLADR	32.6							NGKVINFDLLCNPSHLEAMNPLVLGK Deamidated (N1); Deamidated (N6); Deamidated (N12); Carbamidomethyl (C11)	31.5														
								LRGAEVTDQSPKTYK Carbamidomethyl (C11)	54.0							RGDPKPLVFFSK	29.8														
								RGDPKPLVFFSK	25.1							SGSPDAPLVQDFTRPK	34.8														
								RVGLHVTTPSEVK	32.8							SLRRLVDVYSLVEEGVLTKEVDK	42.8														
								SLRRLVDVYSLVEEGVLTKEVDK	21.0							SLRRLVDVYSLVEEGVLTKEVDKAK	33.3														
								SLRFLVDVYSLVEEGVLTKEVDKAK	26.3							TLPIAHGDAAASGLMGCHETMGLVLDNVR	14.4														
								VGLHVTTPSEVK	31.3							TVRQPHRYDAITAENEVYIEQLK	31.6														
								VGLHVTTPSEVK	34.4							TVRQPHRYDAITAENEVYIEQLK Deamidated (Q22)	31.1														
								VGLHVTTPSEVKWHPVIER	32.5							VGLHVTTPSEVK	49.6														
								VIPNLREDAGNASEGYDLAEKEANLPK	26.4							VGLHVTTPSEVK	24.2														
								VKPLTDLAEFEQK	21.5							VIPNLREDAGNASEGYDLAEKEANLPK Carbamidomethyl (C8)	25.1														
								VKPLTDLAEFEQKTHR	30.6							VIPNLREDAGNASEGYDLAEKEANLPK	43.4														
								VTAASPTGVATVHAEEAEIRQALA	11.7							VKPLTDLAEFEQK	38.6														
								YLGQCSDTDVVPHNFR Carbamidomethyl (C5)	28.2							VKPLTDLAEFEQKTHR	15.9														
						YLGQCSDTDVVPHNFR Carbamidomethyl (C5)	46.1																								
36	Tb927.10.14550 ATP-dependent DEAD/H RNA helicase, putative	1.00	836	50	16	10	19.6	GAGANILRGIAGAGVLSGDVDAKPIYVEWR	44.8	1.00	687	52	13	10	23.8	GLDIPNVGVVQYDMPNDDVYHR	27.6														
								GIAGAGVLSGDVDAKPIYVEWR	65.4							HSLFQVGR	30.5														
								GIAGAGVLSGDVDAKPIYVEWR	35.5							KFTYVTVR	33.9														
								LDKPYNGVDFCFRR Carbamidomethyl (C11)	20.8							NIVDOLPLLNQVSPVPR	52.3														
								LDKPYNGVDFCFRR Deamidated (N6); Carbamidomethyl (C11)	23.7							NIVDOLPLLNQVSPVPR Deamidated (Q15)	19.2														
								LGFLPEEMIGVAAAGLSK	30.6							QALLTLLENQK	29.1														
								LGFLPEEMIGVAAAGLSK Oxidation (M8)	26.4							SGAGQVATDVAWR Carbamidomethyl (C4)	55.4														
								LLVQNGEMMK Oxidation (M10)	12.1							TASYLIPANELLNENRPPYSPGSHSPQALLAPTR	50.4														
								LLVQNGEMMK Oxidation (M9); Oxidation (M10)	45.5							TASYLIPANELLNENRPPYSPGSHSPQALLAPTR Deamidated (N10)	59.5														
								RTISTEGVPLWR	23.8							TASYLIPANELLNENRPPYSPGSHSPQALLAPTR Deamidated (Q31)	42.8														
								TAAPIER	22.3							VGISTENTQDVR	55.0														
								TAAPIERVK	27.0							VGVASFFNEK	54.1														
								TISTEGVPLWR	53.7							VGVASFFNEK Deamidated (N9)	46.4														
								TISTEGVPLWRHLSVLR	15.8																						
								VKLLVQNGEMMK Oxidation (M11); Oxidation (M12)	31.8																						
								VKLLVQNGEMMK Oxidation (M12)	13.6																						
								YFPTQALNFAFK	47.3																						
								YFPTQALNFAFK Deamidated (Q5)	25.7																						
								YFPTQALNFAFKK	59.9																						
								YKNSMDCMLQVKGGAASLMR Oxidation (M5); Oxidation (M8); Oxidation (M21); Carbamidomethyl (C7)	26.6																						
								YKNSMDCMLQVKGGAASLMR Oxidation (M5); Oxidation (M8); Oxidation (M21); Carbamidomethyl (C7); Deamidated (Q10)	22.3																						
								37	Tb927.10.2090 elongation factor 1-alpha, EF-1-alpha Tb927.10.2100 elongation factor 1-alpha, EF-1-alpha Tb927.10.2110 elongation factor 1-alpha							1.00	1018	179	22	12	43.4	APAFGEAGHQVGNVYGGYQQRPR	51.5	0.97	591	54	15	10	42.5	GPTLEALDMLPEPPRSDKPLRLPLQDVYK	25.9
																						APAFGEAGHQVGNVYGGYQQRPR Deamidated (N14)	62.4							IGSGIVPVGR	57.5
																						APAFGEAGHQVGNVYGGYQQRPR Deamidated (Q10)	65.8							IGSGIVPVGR	34.9
																						APAFGEAGHQVGNVYGGYQQRPR Deamidated (Q20)	31.0							IGSGIVPVGRVETGVMPKGDVTFAPANVTEVK Deamidated (N29)	37.6
																						FLLDDEADRLDMGFEPQIR Oxidation (M10); Oxidation (M13)	23.5							IGSGIVPVGRVETGVMPKGDVTFAPANVTEVK Oxidation (M17)	18.6
																						HRLQLVGR	38.3							IGSGIVPVGRVETGVMPKGDVTFAPANVTEVK Oxidation (M17); Deamidated (N29)	17.0
																						MIVQGPSDMR Oxidation (M10); Oxidation (M10)	39.8							MVPQKMCVEFVNDVAPLGR Carbamidomethyl (C8)	12.2
																						MIVQGPSDMR Oxidation (M10)	6.0							MVPQKMCVEFVNDVAPLGR Oxidation (M1); Carbamidomethyl (C8)	35.8
																						NIVDOLPLLNQVSPVPR	37.8							MVPQKMCVEFVNDVAPLGR Oxidation (M7); Carbamidomethyl (C8)	40.0
																						NIVDOLPLLNQVSPVPR Deamidated (Q15)	26.2							MVPQKMCVEFVNDVAPLGR Oxidation (M7); Carbamidomethyl (C8)	40.4
																						NRNVDLPLLNQVSPVPR Deamidated (N13)	31.2							OTVAVGIK	43.5
																						QTLYSATPVEIGR	56.5							SGDAAVR	33.8
																						SGAGQVATDVAWR Carbamidomethyl (C4)	63.0							SGKELEKAPK	40.4
																						VGVASFFNEK	48.7							SIEMHHEQLAEATPGDVGFNWK	40.4
VGVASFFNEK Deamidated (N9)	43.4	SIEMHHEQLAEATPGDVGFNWK Oxidation (M4)	47.7																												
VGVASFFNEKRNIVDOLPLLNQVSPVPR	25.0	SIEMHHEQLAEATPGDVGFNWK Oxidation (M4); Deamidated (N17)	34.0																												
		SIEMHHEQLAEATPGDVGFNWK Oxidation (M4); Deamidated (N21)	29.1																												
		SIKSDAVIR	44.1																												
		VETGMKPGDVTTFAPANVTEVK	26.9																												
		VETGMKPGDVTTFAPANVTEVK Oxidation (M6)	41.6																												
		VETGMKPGDVTTFAPANVTEVK Oxidation (M6); Deamidated (N18)	30.1																												
		VGVNEKVR	46.0																												
38	Tb927.7.7420 ATP synthase alpha chain, mitochondrial precursor, ATP synthase F1, alpha subunit Tb927.7.7430 ATP synthase alpha chain, mitochondrial precursor, ATP synthase F1, alpha subunit	1.00	1032	79	25	16	23.5			ALKNLLYSCK Carbamidomethyl (C9)	47.6	0.84	247	24	10							8	16.1							ALKNLLYSCKR Carbamidomethyl (C9)	25.9
										ALKNLLYSCKR Carbamidomethyl (C9)	15.5																			AQDTMIPGR	19.1
										AVDTMIPGR Oxidation (M5)	53.0																			EAYPGDFVYLSR	14.7
										EAYPGDFVYLSR	24.9																			LAADSVGGQVQVTPIMR	11.2
										ELIVGDRGQTK	26.3																			LAADSVGGQVQVTPIMR Oxidation (M16)	8.9
										GLAEYK	36.0																			LAADSVGGQVQVTPIMRGR Oxidation (M16)	1.8
										LAADSVGGQVQVTPIMR	17.7																			LAADSVGGQVQVTPIMRGR Oxidation (M17)	52.1
										LAADSVGGQVQVTPIMR Oxidation (M16)	41.6																			SPVNYLLTGFK Deamidated (N6)	19.2
										LAADSVGGQVQVTPIMRGR Oxidation (M16)	26.9																			VDTGAPNISR	50.0
										LKGLAEYK	29.5																			VSSAQAAMKGVAGK	13.6
										SPVNYLLTGFK	51.1																				
										SPVNYLLTGFK Deamidated (N4)	22.2																				
										SPVNYLLTGFKVDTMIPGR	41.6																				
								SPVNYLLTGFKVDTMIPGR Deamidated (N4); Deamidated (N6)	25.3																						
								SPVNYLLTGFKVDTMIPGR Deamidated (N4); Oxidation (M17)	33.6																						
								SPVNYLLTGFKVDTMIPGR Deamidated (N6); Oxidation (M17)	25.1																						
								SPVNYLLTGFKVDTMIPGR Oxidation (M17)	45.8																						
								SPVNYLLTGFKVDTMIPGRGR	44.9																						
								SPVNYLLTGFKVDTMIPGRGR Deamidated (Q24); Deamidated (N6)	35.4																						
								SPVNYLLTGFKVDTMIPGRGR Oxidation (M17)	44.7																						
								VDTGAPNISR	38.3																						
								VSSAQAAMKGVAGK Oxidation (M10)	24.2																						
								VSSAQAAMKGVAGLK Oxidation (M10)	43.0																						
								VMATGQLLHPVAVKDLK	23.7																						
								VMATGQLLHPVAVKDLK Oxidation (M2)	43.0																						
								39	Tb927.10.2020 hexokinase	1.00	534					27	12	11	34.8	AAQLSAGFCCAPLVK Carbamidomethyl (C9); Carbamidomethyl (C10)	58.3			1.00	618	38	15	13	42.3	ATIADSVFEKIPFRR	4.2
																				FAGMISADRMPLQDFTR Oxidation (M4); Oxidation (M10)	21.9									ATIADSVFEKIPFRR	37.1
																				FVLPFTKFDLDDASLNKGGQALEK Deamidated (Q21)	37.9									FVLPFTKFDLDDASLNKGGQALEK	68.8
																				FVLPFTKFDLDDASLNKGGQALEK Deamidated (Q22)	53.5									GSALTPIHMEISGNFDSKVR Deamidated (N13)	2.2
																				GSALTPIHMEISGNFDSKVR Oxidation (M9)	47.2									GIMTYLVMREGLGR	39.9
																				IRRDVCR Carbamidomethyl (C6)	20.2									RLNLEHISQGNQDQVTR	29.3
																				RLNLEHISQGNQDQVTR	20.4									TVRLDFVFFPEQTK	34.2
																				RIVHLSINCLPAALQALGNR Carbamidomethyl (C11)	55.2									WCKEGAVVDSSTAFKIPK Carbamidomethyl (C3)	25.3
																				RIVHLSINCLPAALQALGNR Carbamidomethyl (C10)	29.2									VGVVDVQSDLR Carbamidomethyl (C2); Deamidated (Q7)	13.2
																				VLDQNNRILGPECDVR Carbamidomethyl (C14)	25.5									VHLLSINCLPAALQALGNR Carbamidomethyl (C10)	65.3
YALEGNATLDFDIASVVK	72.7																														

Peptides

Index	Accession	Protein Name	Score	Length	Start	End	Modifications	Peptide Sequence	Score	Length	Start	End	Modifications	Peptide Sequence	Score	Length	Start	End	Modifications	
								VALEGNATLDFDIASNVKK	26.1					VALEGNATLDFDIASNVKK	57.6					
								VALEGNATLDFDIASNVK Deamidated (N6)						VALEGNATLDFDIASNVK Deamidated (N6)	12.5					
								VALEGNATLDFDIASNVKK Deamidated (N6)						VALEGNATLDFDIASNVKK Deamidated (N6)	63.2					
								VALEGNATLDFDIASNVKK Deamidated (N6)						VALEGNATLDFDIASNVKK Deamidated (N6)	40.9					
40	Tb927.10.1510	NOT1	1.00	661	42	18	15	11.0	4FLAVGQNP	32.1	1.00	601	30	13	12	10.2	ADPPTISALAFIEQLLK	34.9		
								ANRPLGANNPEPKPKDMSVSGGALAFEAQPR Oxidation (M18)	19.9								ALEWDAEEGAK	8.5		
								ASPSALNLVEQHR	58.4								ATAALNTFLASSLKDLLR	86.3		
								AVYEFEFNSVPPVGLLIAYVR	32.8								AVYEFEFNSVPPVGLLIAYVR	27.7		
								NAQQQVQGSSTGASASTATQGK	45.1								AWTLPLAPKQFDTLVEVYGALEQKQPR	37.4		
								NAQQQVQGSSTGASASTATQGK Deamidated (N1)	32.7								FAWATSIVEAEQLDKQK	56.2		
								QGVVDFAGALS	18.7								NAQQQVQGSSTGASASTATQGK Deamidated (N1)	9.7		
								RLVPTLAPKQGEAEKIR	31.7								RLVPTLAPKQGEAEKIR	37.4		
								RPPVITPETVIR	24.8								RPPVITPETVIR	17.1		
								RPPVITPETVIRVSEEAELFGER	28.4								RPPVITPETVIRVSEEAELFGER	49.9		
								SLASNLCTVARDALPEFPN/QVQDLISR Carbamidomethyl (C7)	47.8								SLASNLCTVARDALPEFPN/QVQDLISR Carbamidomethyl (C7)	69.3		
								SLASNLCTVARDALPEFPN/QVQDLISR Carbamidomethyl (C7) Deamidated (N20)	44.9								SLASNLCTVARDALPEFPN/QVQDLISR Carbamidomethyl (C7) Deamidated (N20)	34.9		
								SLASNLCTVARDALPEFPN/QVQDLISR Deamidated (N5) Carbamidomethyl (C7)	45.2								SLASNLCTVARDALPEFPN/QVQDLISR Deamidated (N5) Carbamidomethyl (C7)	15.6		
								TLEDATVQHYSTGDAK	18.3								TLEDATVQHYSTGDAK			
								TTQQQKEVESLSDPWALSTERR	7.9								TTQQQKEVESLSDPWALSTERR			
								VAAATLHQHDIGTLSSK	38.2								VAAATLHQHDIGTLSSK			
								VAAATLHQHDIGTLSSK	24.6								VAAATLHQHDIGTLSSK			
								VTQELKPTVGR	29.3								VTQELKPTVGR			
41	Tb927.2.1560 Tb927.2.1680	cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative	0.98	742	20	10	6	66.8	AGKHFGPGLTSMANAGR Oxidation (M12)	9.7	0.00	0	0	0	0	0.0				
								AGRVEMELFKDVPK Oxidation (M6)	24.5											
								ALCTYGEKGLGR Carbamidomethyl (C3)	39.4											
								RPIYVWNSVLYVDSIGSK	49.2											
								NTNGSFFICTAATPWLDGKHVFGQVTK Deamidated (N3) Carbamidomethyl (C10)	69.7											
								VIPQFMCGGDDFTSGNGTGGESYGLKFPDEFAGR Carbamidomethyl (C7) Deamidated (Q8)	110.5											
								VIPQFMCGGDDFTSGNGTGGESYGLKFPDEFAGR Carbamidomethyl (C7) Deamidated (Q8) Deamidated (N16)	122.3											
								VIPQFMCGGDDFTSGNGTGGESYGLKFPDEFAGR Deamidated (Q4) Deamidated (Q8) Oxidation (M6) Carbamidomethyl (C7)	97.2											
								VIPQFMCGGDDFTSGNGTGGESYGLKFPDEFAGR Oxidation (M6) Carbamidomethyl (C7)	102.3											
								VIPQFMCGGDDFTSGNGTGGESYGLKFPDEFAGR Oxidation (M6) Carbamidomethyl (C7) Deamidated (N16)	56.9											
42	Tb927.3.3580	lipophosphoglycan biosynthetic protein, putative	1.00	680	58	14	12	21.9	AVFLRELISNGSDALDKR	62.8	1.00	798	62	19	15	22.3	AVFLRELISNGSDALDKR	0.3		
								AVFLRELISNGSDALDKR Deamidated (N10)	52.4								AVFLRELISNGSDALDKR Deamidated (N10)	17.6		
								IGQVIMTRIELEANLSSLGSSGTR Oxidation (M6)	11.1								ELISNGSDALDKR	60.8		
								ELISNGSDALDKR	30.4								ELISNGSDALDKR Deamidated (N5)	41.9		
								FRPLTDALTR	39.2								FRPLTDALTR	35.2		
								GVEVLLMTDADEYVGGVDFANK Oxidation (M7)	15.8								GKSPYQAEVSK	11.5		
								HPVVQQLAR	17.1								GTETLELFPDLNLSPETVR	43.8		
								KLINATDSAGLDDVTDKQK	43.9								GVEVLLMTDADEYVGGVDFANK	47.1		
								KLINATDSAGLDDVTDKQK	48.9								GVEVLLMTDADEYVGGVDFANK	57.8		
								LSVPEKTLTLR	49.2								HPVVQQLAR	24.7		
								MLDLHSLYTNR	59.8								HPVVQQLAR Deamidated (Q6)	14.5		
								MLDLHSLYTNR Oxidation (M1)	47.6								KLINATDSAGLDDVTDKQK	33.2		
								MLYLLTPKEPKVKGGEAPTMDIR Oxidation (M1) Oxidation (M20)	20.5								KLINATDSAGLDDVTDKQK	58.3		
								QYSEFVHPFR	30.8								LSVPEK	21.0		
																	LSVPEKTLTLR	1.1		
																	MLDLHSLYTNR	49.0		
																	QYSEFVHPFR	33.7		
																	QYSEFVHPFR Deamidated (Q1)	32.6		
																	RGEEDVLENENQPIWTR	32.1		
43	Tb927.1.1790	pyruvate dehydrogenase E1 beta subunit, putative	1.00	881	70	17	16	40.8	AAEQLKSSIEAEVNL	35.0	1.00	567	35	13	11	46.0	AARDNPVVALEHLYMGETFKVSEAMGEDVFPFGK	60.8		
								AKIERPGKDTMIGFSR Oxidation (M12)	25.1								AARDNPVVALEHLYMGETFKVSEAMGEDVFPFGK Oxidation (M29)	37.1		
								ATIQSVK	47.9								AKIERPGKDTMIGFSR Oxidation (M12)	6.7		
								ATIQSVKTR	36.0								ATIQSVK	29.5		
								DALNSAEELSRDKTVLVEEVQVGGYK	24.2								DALNSAEELSRDKTVLVEEVQVGGYK	52.7		
								GLVDKYGTSR	27.6								GLVDKYGTSR	49.6		
								NLEVASQVSDVLDWAR	62.5								NLEVASQVSDVLDWAR	44.6		
								NLEVASQVSDVLDWARR	27.6								NLEVASQVSDVLDWARR	35.0		
								SGIEAEVNL	73.7								NLEVASQVSDVLDWARR Deamidated (Q9)	17.3		
								SGIEAEVNLR Deamidated (N9)	56.8								SGIEAEVNL	54.0		
								SLRPLDRATHQGVK	24.2								VFSPIYSEEDAR	16.0		
								SLRPLDRATHQGVK	29.4								VSCADCFPYSKNLEVASQVSDVLDWARR Carbamidomethyl (C3) Carbamidomethyl (C6)	28.2		
								VFSPIYSEEDAR	23.9								VSCADCFPYSKNLEVASQVSDVLDWARR Carbamidomethyl (C3) Carbamidomethyl (C6)	20.9		
								VFSPIYSEEDARGLK Oxidation (M13)	28.3								VSCADCFPYSKNLEVASQVSDVLDWARR Carbamidomethyl (C3) Carbamidomethyl (C6)	16.0		
								VSCADCFPYSK Carbamidomethyl (C3) Carbamidomethyl (C6)	37.0								VSCADCFPYSK Carbamidomethyl (C3) Carbamidomethyl (C6)	28.2		
								VSCADCFPYSKNLEVASQVSDVLDWAR Carbamidomethyl (C3) Carbamidomethyl (C6)	59.5								VSCADCFPYSKNLEVASQVSDVLDWAR Carbamidomethyl (C3) Carbamidomethyl (C6)	20.9		
								VSCADCFPYSKNLEVASQVSDVLDWARR Carbamidomethyl (C3) Carbamidomethyl (C6)	73.9								VSCADCFPYSKNLEVASQVSDVLDWARR Carbamidomethyl (C3) Carbamidomethyl (C6)	20.9		
44	Tb927.10.7570	dihydroisopimide acetyltransferase E2 subunit, putative	1.00	560	39	15	13	42.6	ANMLVFEANSSHWGDFIR Oxidation (M3)	34.9	1.00	549	27	11	10	37.7	ANMLVFEANSSHWGDFIR Oxidation (M3)	3.6		
								EHAAPAAAPAKPVVPIATPSTQNYTDPVTNMR	67.1								EHAAPAAAPAKPVVPIATPSTQNYTDPVTNMR	59.4		
								EHAAPAAAPAKPVVPIATPSTQNYTDPVTNMR Deamidated (N34)	23.5								EHAAPAAAPAKPVVPIATPSTQNYTDPVTNMR Deamidated (N26)	41.2		
								EHAAPAAAPAKPVVPIATPSTQNYTDPVTNMR Oxidation (M35)	76.4								FTASFDR	42.3		
								FTASFDR	42.9								FTASFDRVQVAGASQWCK Deamidated (C17) Carbamidomethyl (C19)	49.6		
								FTASFDRVQVAGASQWCK Deamidated (C17) Carbamidomethyl (C19)	12.2								FKDAVENLSLL	47.0		
								GRISEWVK	44.7								IKRQVEAASK	32.6		
								GLVDSNEMK Oxidation (M8)	9.2								KTAELNLSLDTDTGGQGR	36.8		
								GLVDSNEMKVLAK Oxidation (M9)	22.5								TVDSWATPTGLTIPIKQADAR	33.2		
								FKDAVENLSLL	40.2								VQEVPSPTQVAPLPAQGEAAGR	17.2		
								IKRQVEAASK	41.2								VQEVPSPTQVAPLPAQGEAAGR	52.3		
								KTAKLN												

Peptides

Accession	Protein Name	Start	End	Score	Modifications	Accession	Protein Name	Start	End	Score	Modifications	Accession	Protein Name	Start	End	Score	Modifications
54	Tb927.10.2010 hexokinase	0.99	407	21	10	9	30.6	AGLSASFCAPLVK Carbamidomethyl (C9); Carbamidomethyl (C10)	58.3	0.98	410	25	10	10	34.0	ATIADGVSFEKIPSPFR	4.2
								FRAGMISDRPFLGQIFTR Oxidation (M4); Oxidation (M10)	21.9	ATIADGVSFEKIPSPFR						27.1	
								FVLPPTKFDLDDIDASLNKGGQALEK Deamidated (Q21)	37.9	FVLPPTKFDLDDIDASLNKGGQALEK						68.8	
								FVLPPTKFDLDDIDASLNKGGQALEK Deamidated (Q22)	53.5	QIMTYLYEMVEGLEGR						35.9	
								GSALTPNMEISGNFDSKVR Oxidation (M9)	36.1	RLNLEHISGQNDGETVR						29.3	
								IRDQCR Carbamidomethyl (C9)	22.2	RLGQDNR						34.2	
								RLNLEHISGQNDGETVR	20.4	TVPLGFTTFFVEGTQ						25.3	
								RVVHLSINCLPAALQALGNR Carbamidomethyl (C11)	53.2	VACKGAVVDSSTAFKIPK Carbamidomethyl (C3)						13.2	
								RVVHLSINCLPAALQALGNR Carbamidomethyl (C10)	29.2	VCGVDVGSIEDLR Carbamidomethyl (C2); Deamidated (Q7)						65.3	
								VLDGNNRLLGPEQVVR Carbamidomethyl (C14)	25.5	VVHLSINCLPAALQALGNR Carbamidomethyl (C10)						29.3	
55	Tb927.8.1740 hypothetical protein, conserved	1.00	350	26	9	8	17.6	AELTAKSPVAPSPQR	53.7	1.00	391	15	8	5	16.0	ARPDFVALLTQGR	50.2
								AISASPSIVRR	33.4	LVDVLLFQHFGEAEPATDNDNNGIGPAATK Deamidated (N22); Deamidated (N23)						62.8	
								ARPDFVALLTQGR	50.8	LVDVLLFQHFGEAEPATDNDNNGIGPAATK Deamidated (N23)						52.5	
								LVDVLLFQHFGEAEPATDNDNNGIGPAATK Deamidated (N22); Deamidated (N23)	7.5	LVDVLLFQHFGEAEPATDNDNNGIGPAATK Deamidated (N20)						55.9	
								LVDVLLFQHFGEAEPATDNDNNGIGPAATK Deamidated (N20)	23.7	LVDVLLFQHFGEAEPATDNDNNGIGPAATK Deamidated (N22); Deamidated (N23)						38.3	
								LVDVLLFQHFGEAEPATDNDNNGIGPAATK Deamidated (N23)	29.5	LVDVLLFQHFGEAEPATDNDNNGIGPAATK Deamidated (N23)						18.8	
								SPVYAPSPQR	32.5	TALLSAGNSGTHPELVLMNAGPVRK Deamidated (N8)						24.6	
								SSGKAELTTAKSPVAPSPQR	39.6	YAPLLHTESLQGAAGSVSK						52.6	
								TALLSAGNSGTHPELVLMNAGPVRK Oxidation (M19)	44.5								
								56	Tb927.8.6110 hypothetical protein, conserved	1.00						414	31
DAFTMTKRVK Oxidation (M5)	25.6	ALKELGMPALSR Oxidation (M7)	12.6														
GLHTSSLDKFAAKR	22.6	CLHTSSLDKFAAKR	29.7														
HACLSGVYALKGAAR Carbamidomethyl (C3)	21.0	IGTRNEAFQDIEIYR	37.6														
IGTRNEAFQDIEIYR	49.4	ILSEALGNSILTEEQYK	64.9														
IKDTIKRMMVMVGGSDASEAIPTPKGWEEAAAK Oxidation (M9); Oxidation (M11)	47.9	LLNVYEVPSR Deamidated (N4)	7.2														
LLELNTK	25.4	STAEHTKTFEELCK Carbamidomethyl (C14)	23.1														
VLRSKVFADFLGSK	51.3																
VSNVGDSPFRVPSNENAVTMAASAVLR Oxidation (M21)	59.5																
YAEVGGDDKLAHVAASDAEVALGSGTEGTGGAGSVMVLYOK Oxidation (M39)	19.2																
57	Tb927.10.2960 mitochondrial malate dehydrogenase	1.00	521	37	12	10	44.0	AGVDFARLFGITLDVVR	35.2	1.00	737	69	16	10	51.3	AGVDFARLFGITLDVVR	25.8
								ALIGVSNPNSVPIASEVKK	38.2	ALIGVSNPNSVPIASEVKK						6.5	
								ALIGVSNPNSVPIASEVKK Deamidated (N8)	34.8	ALIGVSNPNSVPIASEVKK Deamidated (N11)						28.2	
								ALIGVSNPNSVPIASEVKK	28.7	ALIGVSNPNSVPIASEVKK Deamidated (N8)						8.8	
								ALIGVSNPNSVPIASEVKK Deamidated (N11)	47.4	ALIGVSNPNSVPIASEVKK						32.7	
								ARTYVAEAAIK	34.8	IRKPDFVDESLLEK						34.9	
								AVDQADVIRPAGTFR	27.3	LFGITLDVVR						41.2	
								GGVEKHPVFDAYEQLLEK	13.2	SPYDNNVQVGGHSGPTIPLLSQAGVSLTEEQVK						60.1	
								HRPFDVYEGSLLEK	32.7	SPYDNNVQVGGHSGPTIPLLSQAGVSLTEEQVK Deamidated (Q8)						28.4	
								LFGITLDVVR	33.1	TFVAEAAKSPYDNNVQVGGHSGPTIPLLSQAGVSLTEEQVK						49.7	
58	Tb927.10.4560 elongation factor 2 Tb927.10.4570 elongation factor 2	1.00	506	58	14	12	20.3	AYLPVAESFGTADLR	16.4	0.99	444	20	10	9	16.9	ETVTDVSSIQGLSK Carbamidomethyl (C11)	47.4
								FLADKFEVDVAEAR	9.1	FLADKFEVDVAEAR						47.4	
								FLPAMEILLQRIWHLRPSK Oxidation (M11)	30.0	GTWASISSLQANWVSVTRFAKMAK Oxidation (M22)						40.4	
								GLKPDQLDITLQDK	19.8	GVIGEENRPGTTRVNR						20.8	
								GVIGEENRPGTTRVNR	24.4	GVIGEENRPGTTRVNR Deamidated (N8)						20.8	
								KGLKPDFGLDITLQDK	32.2	KGLKPDFGLDITLQDK						43.9	
								RDVIGEENRPGTTRVNR	30.4	RDVIGEENRPGTTRVNR						22.8	
								RVFYACGLTATR Carbamidomethyl (C5); Carbamidomethyl (C7)	29.8	STLSDSLVAAGIK						59.1	
								SATITDDGESPHLRDMKYSVSPVVR Oxidation (M17)	25.9	VWEAKNPISLPK						47.5	
								VWEAKNPISLPK	41.9	YGEAEDMPCGNVGLVGVDKYVK Carbamidomethyl (C10)						35.3	
VWEAKNPISLPK Deamidated (N7)	52.6																
VNFTVDEVR	48.8																
YGEAEDMPCGNVGLVGVDKYVK Carbamidomethyl (C10)	12.4																
YGEAEDMPCGNVGLVGVDKYVK Oxidation (M8); Carbamidomethyl (C10)	21.9																
59	Tb927.6.2230 hypothetical protein, conserved	1.00	315	18	8	7	12.7	ARVDPSTQDEKSVTLNCAATFR Carbamidomethyl (C19)	28.1	1.00	122	5	3	3	10.3	AATVGFHTDEIQELLEAVSYRDPQK	38.9
								KTMTNENLVAWSQPQAKVVEVLSHQTR Oxidation (M4)	30.2	ARVDPSTQDEKSVTLNCAATFR Carbamidomethyl (C19)						26.2	
								LEDVGSAPRELLK	29.0	KTMTNENLVAWSQPQAKVVEVLSHQTR						41.7	
								NRANDKIALSEQR	31.4								
								TTMENLVAWSQPQAKVVEVLSHQTR Oxidation (M3)	44.2								
								TTMENLVAWSQPQAKVVEVLSHQTR Oxidation (M3); Deamidated (N5)	39.2								
								VAPFADAASVTTMR Oxidation (M14)	42.6								
								VVEVLSHQTR	41.2								
								AYNPNVGSVAMFGFQPTGLVTAIENETGQPVVTR Deamidated (N4); Deamidated (N5); Oxidation (M13)	20.6								
								HKDSGNICPELPK Carbamidomethyl (C9)	20.3								
ILASNCPPPPPPPPSPSHR Carbamidomethyl (C6)	59.1																
KMLAPGPPFR Oxidation (M2)	36.8																
NRSNESVDNLNGVYSEQLNEVER	9.2																
SGEFDFDPTLPQQPTK	24.8																
SNEVDNLNGVYSEQLNEVER	33.7																
SSEITAHQGR Deamidated (Q2)	13.0																
VHTPMATHDFGTGGVEDIEPVIHCK Carbamidomethyl (C28)	22.7																
61	Tb927.10.7020 acid phosphatase, putative	1.00	370	31	8	8	28.5	ILSQAGAVQZLFPDQVGGVYLR	45.7	1.00	418	25	11	9	33.1	GMRVEYELSEYLR Oxidation (M2)	11.1
								LLVTRDGTATVAPHCR carbamidomethyl (C18)	42.1	BLSAQAWQGLFSDYSPSYLPR						61.4	
								LVPEKSVGEEVPSR	33.6	LILVTPDGTATVAPHCR Carbamidomethyl (C18)						28.8	
								NAYRDFGPR	45.3	NAYRDFGPR						39.6	
								QFQVVFVSDMDTHEYLLDDVPCFR Oxidation (M11); Carbamidomethyl (C23)	15.6	NAYRDFGPR Deamidated (N1)						20.7	
								RKYNVGAEDLTA	18.1	QFQVVFVSDMDTHEYLLDDVPCFR Carbamidomethyl (C23)						18.0	
								TPQLCTLKELQDYSAR Carbamidomethyl (C5)	51.1	QFQVVFVSDMDTHEYLLDDVPCFR Oxidation (M11); Carbamidomethyl (C23)						18.9	
								YNVGAEDLTA	39.8	RDKKKNLVLTK						35.7	
										RKYNVGAEDLTA						24.5	
										SVGEEVPSR						38.6	
		TPQLCTLKELQDYSAR Carbamidomethyl (C5)	68.4														
62	Tb927.6.4440 hypothetical protein, conserved	1.00	809	61	15	12	35.2	AAPFVVGASQTTVNVFR	34.9	1.00	234	18	6	6	23.0	AAPFVVGASQTTVNVFR Deamidated (Q10)	13.7
								AAPFVVGASQTTVNVFR Deamidated (N14)	28.2	AAPFVVGASQTTVNVFRQK						2.3	
								AAPFVVGASQTTVNVFRQK	38.8	TWASLASIAIK						44.5	
								APSEPVGERLMSFSDHVTDEELTALGPLAAR	29.6	TWASLASIAIKGEORPSIK						61.2	
								APSEPVGERLMSFSDHVTDEELTALGPLAAR Oxidation (M11)	56.1	VSPSTAAPVAEAVDAPTQPK						52.1	
								GRVSPSTAAPVAEAVDAPTQPK	36.8	VANESTANVAKPASPPTK Deamidated (N4)						22.9	
								LMSFSDHVTDEELTALGPLAAR	14.9								
								TWASLASIAIK	45.8								
								TWASLASIAIKGEORPSIK	34.9								
								VSPSTAAPVAEAVDAPTQPK	60.3								

Accession	Gene	Protein	Start	End	Score	Peptide	Score	Peptide	Score	Peptide									
63	Tb927.6.6060	2-amino-3-kebutyrate coenzyme A ligase, putative, glycine acetyltransferase, putative	1.00	504	31	11	10	32.4	VSPSTAAPVTEAAVDAPTGPKTWASLASIATK	32.8	1.00	462	42	10	7	26.5	ALGGASGLSSGCKEVDLQR Carbamidomethyl (C13)	67.0	52.1
									DALDSHGVLASVR	15.5							EAAAALAAKEAGTYKVER	50.2	
									EAAAMQAAHKEAGTYKVER	51.1							GRPFLFSNTIAPAAVGGTLK	39.6	
									FCGCTDTHK Carbamidomethyl (C3)	33.8							GRPFLFSNTIAPAAVGGTLK Deamidated (N8)	8.1	
									GRPYLFSNTIAPAAVGGTLK	39.7							GTALFGVDIKVDLNTLTK	50.8	
									GTALFGVDIKVDLNTLTK	49.1							GTALFGVDIKVDLNTLTK Deamidated (N16)	37.0	
									KQLGDNTHLFR	46.0							KQLGDNTHLFR	41.8	
									KQGRPYLFSNTIAPAAVGGTLK Deamidated (N10)	9.6							KQLGDNTHLFR Deamidated (Q2)	21.6	
									QLQDNTHLFR	20.1							KQGRPYLFSNTIAPAAVGGTLK Deamidated (N10)	16.6	
									QLQDNTHLFR Deamidated (Q3)	29.9							VMELGTTSSAR	60.0	
VMELGTTSSAR Oxidation (M2)	67.9																		
64	Tb927.6.2790	L-threonine 3-dehydrogenase, putative	1.00	614	47	11	10	32.2	CTDRTIEVEYVEGPAQK Carbamidomethyl (C1)	54.3	1.00	714	106	12	10	37.7	CTDRTIEVEYVEGPAQK Carbamidomethyl (C1)	42.8	
									IANSWPSLDDSNAR	49.6							IFPSTIAAFGDK	45.4	
									IFPSTIAAFGDK	42.0							IFPSTIAAFGDKGK Carbamidomethyl (C14)	60.6	
									IFPSTIAAFGDKGK Carbamidomethyl (C14)	59.3							QIPLHGLPSSL	38.4	
									IMEAPLEKLR	40.7							QIPLHGLPSSL Deamidated (Q1)	35.1	
									IMEAPLEKLR Oxidation (M2)	45.5							SIRLRFSSIAFLPGGKATDVHMYHSALLGK	23.9	
									QIPLHGLPSSL	30.9							TIEVEYVEGPAQK	43.3	
									TIEVEYVEGPAQK	42.4							TVNVTGFSFSPSELK	53.8	
									TVNVTGFSFSPSELK	71.2							VLTVALGQIGDLSLALR	42.3	
									VLTVALGQIGDLSLALR	44.0							VLTVALGQIGDLSLALR Deamidated (Q8)	42.9	
VLTVALGQIGDLSLALRDK	17.7	VLTVALGQIGDLSLALRDK	42.1																
VYTELGGTWYR		VYTELGGTWYR	41.2																
65	Tb927.4.1300	hypothetical protein, conserved	1.00	512	38	14	12	48.9	EVAIAHGNGER Deamidated (N8)	5.6	1.00	329	42	9	8	30.5	EVAIAHGNGER Deamidated (N8)	3.9	
									FVFTAVLPHR	45.2							FVFTAVLPHR	56.7	
									LLLYPMTFISR Oxidation (M7)	26.2							LLLYPMTFISR	22.7	
									QMLDQWYGLQNLFPYADLER	19.0							REIEPKQDLK	32.8	
									QMLDQWYGLQNLFPYADLER Deamidated (Q1)- Oxidation (M2)	60.4							SVGSLVSPVPHGEVLPLPGLGVIEAAK	33.4	
									REIEPKQDLK	42.2							SVGSLVSPVPHGEVLPLPGLGVIEAAK Carbamidomethyl (C37)	35.1	
									SKENGRVGEIVPHTYSLVGVGCK Carbamidomethyl (C22)	33.8							VNLDSESELRAFQGNAR Carbamidomethyl (C13)	8.5	
									SKENGRVGEIVPHTYSLVGVGCK Deamidated (N4)- Carbamidomethyl (C22)	27.5							VLCISHOALNALRPFKR Carbamidomethyl (C3)	31.2	
									SSEQVLSICAPENLIPNEKRFVFTAVLPHR Carbamidomethyl (C10)	24.1							VLCISHOALNALRPFKR Carbamidomethyl (C3)- Deamidated (Q7)	11.4	
									SVGSLVSPVPHGEVLPLPGLGVIEAAK	34.8									
SVGSLVSPVPHGEVLPLPGLGVIEAAKVDKGGC Carbamidomethyl (C37)	22.4																		
VNLDSESELRAFQGNAR Carbamidomethyl (C13)	29.2																		
VLCISHOALNALRPFKR Carbamidomethyl (C3)	36.2																		
VLCISHOALNALRPFKR Carbamidomethyl (C3)- Deamidated (Q7)	19.4																		
66	Tb927.10.4310	prohibitin 2, putative	1.00	493	24	11	9	38.0	AVIAQFNASDLLKRPVSNR	53.2	1.00	495	20	10	6	25.8	AVIAQFNASDLLK	39.7	
									AVIAQFNASDLLKRPVSNR Deamidated (N7)	32.8							AVIAQFNASDLLKRPVSNR	31.1	
									DLQDTNLAKR	24.1							AVIAQFNASDLLKRPVSNR Deamidated (G6)	54.3	
									GEAEAKLGMVQKNPAFITLR Oxidation (M11)	33.7							LIGMAVQKNPAFITLR	69.3	
									KVMAEAOxidation (M4)	39.1							LIGMAVQKNPAFITLR Oxidation (M4)	29.0	
									LIGMAVQKNPAFITLR	42.2							LIGMAVQKNPAFITLR Oxidation (M4)- Deamidated (N9)	37.4	
									LIGMAVQKNPAFITLR Oxidation (M4)	57.9							NRYEGGANPAFLETVPVDIR	29.5	
									NKPTEVALTAGSR	52.0							TYGEGANFAIFLETVPVDIR	26.4	
									NKPFITLR	28.1							VLYQPHVLSALPDYR	48.5	
									TYGEGANFAIFLETVPVDIR	28.8							VLYQPHVLSALPDYR Deamidated (Q4)	38.4	
VLYQPHVLSALPDYR	34.1																		
67	Tb927.9.14160	rieske iron-sulfur protein, mitochondrial precursor	1.00	464	47	12	9	27.6	DRPVNSWSEDFLKPVPVK	11.1	1.00	665	45	17	10	33.0	DRPVNSWSEDFLKPVPVK	23.7	
									GKPFVYR	29.1							IRQGPAPLNLEVPVYR	30.9	
									GKPFVYR	25.0							IRQGPAPLNLEVPVYR Deamidated (N9)	19.0	
									IRQGPAPLNLEVPVYR	31.5							LPNELEDRAR	27.7	
									IRQGPAPLNLEVPVYR Deamidated (N9)	40.0							OGPAPLNLEVPVYR	18.4	
									LPNELEDRAR	29.0							OGPAPLNLEVPVYR Deamidated (N7)	18.2	
									OGPAPLNLEVPVYR	27.5							OGPAPLNLEVPVYR Deamidated (Q1)	18.2	
									OGPAPLNLEVPVYR Deamidated (N7)	18.3							QLEGSNPLTVK	39.8	
									OGPAPLNLEVPVYR Deamidated (Q1)	21.9							QLEGSNPLTVKDRPVNSWSEDFLKPVPVK	21.3	
									VSLVFKQLEGSNPLTVK	62.6							QLEGSNPLTVKDRPVNSWSEDFLKPVPVK Deamidated (Q1)	20.4	
VSLVFKQLEGSNPLTVKDRPVNSWSEDFLKPVPVK	25.1	VSLVFKQLEGSNPLTVK	58.2																
VSDDKTYLQKL	51.3	VSLVFKQLEGSNPLTVK Deamidated (N12)	65.2																
		VSLVFKQLEGSNPLTVKDRPVNSWSEDFLKPVPVK	67.1																
		VSLVFKQLEGSNPLTVKDRPVNSWSEDFLKPVPVK Deamidated (Q7)	35.5																
		WDDDKTYLQKL	33.9																
		YSDPFLGSDVTSSEVLTNYPEGSR Carbamidomethyl (C7)	31.4																
		YSDPFLGSDVTSSEVLTNYPEGSR Carbamidomethyl (C7)- Deamidated (N18)	18.3																
68	Tb927.1.120	retrotransposon hot spot protein 4 (RH54), putative	1.00	406	23	13	12	15.1	AQGTAAVAIEK	20.4	1.00	332	16	8	8	10.1	AQGTAAVAIEK	35.4	
									AQGTAAVAIEKGYDYSYNAK	18.3							AQGTAAVAIEKGYDYSYNAK	60.0	
									AREVEVEGR	12.6							FVFSAPVEYHER	35.6	
									FVFSAPVEYHER	40.5							HVIVGTRGK	25.0	
									HVIVGTRGK	14.2							SLNDMASQGLR Oxidation (M6)	18.2	
									IDMVGPLR Oxidation (M3)	54.0							VFDGKQGR	32.9	
									KLVLSEEAR Carbamidomethyl (C3)	38.7							VSSGTNVDSYR	50.4	
									NAPKLMGLAGR Oxidation (M6)	32.6							WVEKAEITPR	46.9	
									SAGDKQEVVTHLKV	12.9									
									SLNDMASQGLR	52.0									
SLNDMASQGLR Oxidation (M6)	42.6																		
VFDGKQGR	21.1																		
WVEKAEITPR	22.8																		
69	Tb927.10.2350	pyruvate dehydrogenase complex E3 binding protein, putative	1.00	663	45	11	41.5	AALAEITPTGR	40.0	1.00	429	23	10	8	33.5	ADRVGQGFQYEEK	23.7		
								ADRVGQGFQYEEK	38.5							ADRVGQGFQYEEKAAAPK	34.8		
								ADRVGQGFQYEEKAAAPK	46.0							ECCAENTNGAVSSAVK Carbamidomethyl (C2)- Carbamidomethyl (C3)	65.6		
								ECCAENTNGAVSSAVK Carbamidomethyl (C2)- Carbamidomethyl (C3)	12.0							ECCAENTNGAVSSAVK Carbamidomethyl (C2)- Carbamidomethyl (C3)- Deamidated (N8)	47.6		
								ECCAENTNGAVSSAVK Carbamidomethyl (C2)- Carbamidomethyl (C3)- Deamidated (N8)	35.5							FTKADRVGQGFQYEEKAAAPK Deamidated (Q9)	5.6		
								FTKADRVGQGFQYEEKAAAPK	50.0							GSSSFTNASECCAGTAVSSAVK Deamidated (N8)- Deamidated (N19)- Carbamidomethyl (C13)- Carbamidomethyl (C14)	40.1		
								GSSSFTNASE	23.7							IARLDKAALEAITPTGR	29.7		
								IARLDKAALEAITPTGR	43.3							LDKAALEAITPTGR	52.2		
								LDKAALEAITPTGR	51.3							VSDTLLQQLNSMPTPK	35.7		
								LDKAALEAITPTGRGGR	32.3							VSDTLLQQLNSMPTPK Oxidation (M14)	18.2		
VSDTLLQQLNSMPTPK	42.5																		
VSDTLLQQLNSMPTPK Deamidated (N12)- Oxidation (M14)	38.9																		
VSDTLLQQLNSMPTPK Oxidation (M14)	19.0																		
YGGSLDEAVASGQPMR Oxidation (M17)	50.0																		
70	Tb927.10.180	ATP synthase F1 subunit gamma protein, putative	1.00	260	24	8	8	31.8	CIDSVYSSK Carbamidomethyl (C1)	36.5	1.00	155	6	3	2	19.3	LVAIEGQLNLISSQOR	45.5	
									LVAIEGQLNLISSQOR	24.5							LVAIEGQLNLISSQOR Deamidated (Q7)	46.5	
									NALVYPIITNR	43.6							YLFANALQNEEQLRDFDFHAALAVLNVAENELSEGAAR Deamidated (N5)	45.2	
									NALVYPIITNRSSCGALNSNVR Carbamidomethyl (C15)	16.5									
									RNKFWEAVTK	40.7									
									QGITAALEILSAMSSLEGNAKMGVRR Oxidation (M23)	9.4									
									RNKFWEAVTK	21.4									
									TSSLNKTNR	36.2									
71	Tb927.3.3900	carnitine O-palmitoyltransferase II, putative	1.00	508	21	11	8	17.9	IPVKDLAVNLKLR	46.1	1.00	505	25	11	10	24.5	IPVKDLAVNLKLR	43.5	
									IPVKDLAVNLKLR Deamidated (N9)	35.1							IPVKDLAVNLKLR Deamidated (N9)	34.2	

Peptides

Accession	Protein Name	Start	End	Score	Modifications	Peptide Sequence	Score	Modifications	Peptide Sequence	Score	Modifications										
81	Tb927.3.3130	hypothetical protein, conserved	1.00	438	27	13	10	9.0	AEGNKQFYQCSSSDPEPAEGFNVVGR Carbamidomethyl (C11)	14.0	AATAVANGLREGYSVALLSVHNFPEENTLLK Deamidated (N7)	39.0									
									CDDGSELWFLSLK Carbamidomethyl (C1)	13.5	AEGNKQFYQCSSSDPEPAEGFNVVGR Carbamidomethyl (C11)	60.3									
									CTFEASETPYVVR Carbamidomethyl (C1)	36.7	AEGNKQFYQCSSSDPEPAEGFNVVGR Deamidated (N6) Carbamidomethyl (C11)	61.9									
									ITGYVEAHNPVLSVPTGR	37.0	ITGYVEAHNPVLSVPTGR	52.2									
									KAATAWANGLREGYSVALLSVHNFPEENTLLK	20.8	KAATAWANGLREGYSVALLSVHNFPEENTLLK Deamidated (N8)	34.8									
									KAATAWANGLREGYSVALLSVHNFPEENTLLK Deamidated (N8)	23.7	NLVDDFLPTVGVPCYAR Carbamidomethyl (C16)	40.8									
									LDGDRFQFVEVR	24.3											
									NLVDDFLPTVGVPCYAR Carbamidomethyl (C16)	42.0											
									VLNKDGWKK	28.7											
									ANAAVSTNDVEDVRALPATLTK Deamidated (N2)	47.7	EAGEEGDRLPINLLGKLENSVDAAGSPASGGPR	27.4									
ANAAVSTNDVEDVRALPATLTKGTPPAR	20.2	EAGEEGDRLPINLLGKLENSVDAAGSPASGGPR Deamidated (N12)	40.7																		
ANAAVSTNDVEDVRALPATLTKGTPPAR Deamidated (N2)	10.1	EAGEEGDRLPINLLGKLENSVDAAGSPASGGPR Deamidated (N22)	43.3																		
ANAAVSTNDVEDVRALPATLTKGTPPAR Deamidated (N8)	11.2	KAELTLPR	39.8																		
EAGEEGDRLPINLLGKLENSVDAAGSPASGGPR	11.3	RLAALCOEKEQLPAALGAK Carbamidomethyl (C8)	31.9																		
EAGEEGDRLPINLLGKLENSVDAAGSPASGGPR Deamidated (N12)	24.8	RLAALCOEKEQLPAALGAK Carbamidomethyl (C8) - Deamidated (O11)	19.6																		
HGGYQDADVAR	47.2																				
KAELTLPR	39.1																				
LAALCOEKEQLPAALGAK Carbamidomethyl (C5)	38.0																				
NARPEWGTQVR	25.6																				
RLAALCOEKEQLPAALGAK Carbamidomethyl (C6)	38.0																				
RLPAEYGEPLLNKCEAVIQR Carbamidomethyl (C14)	49.4																				
SVADIADRLR	26.9																				
82	Tb927.9.6100	TFIIIF-stimulated CTD phosphatase, putative	1.00	354	26	9	8	19.8	ILGNVLER	51.9	IVDEVKYGQVGR	51.8									
									IVDEVKYGQVGR	62.6	LQADHALMDLIPMR	24.1									
									IVDEVKYGQVGRYEGDMAK Oxidation (M20)	15.1	NGVKEFLPNER Deamidated (N1)	33.7									
									LQADHALMDLIPMR Oxidation (M8) Oxidation (M13)	33.3	SAASSTDLHELDHWR	12.9									
									NGVKEFLPNER	35.8											
									OKLGNLTK	18.6											
									OKLGNLTKER	26.1											
									SFPLHPRNGVKIEFLPNER	29.5											
									SFPLHPRNGVKIEFLPNER Deamidated (N8)	35.2											
									AHGAPLGDDEVAR	33.2											
83	Tb927.8.6170	transketolase, putative	1.00	387	29	11	10	25.0	ATPNLLVFRSDQDTESAAWALALENTRGPSILCLSR Carbamidomethyl (C34)	26.0	ATPNLLVFRSDQDTESAAWALALENTR	18.0									
									CLAADVQQAQ Carbamidomethyl (C1)	44.4	ATPNLLVFRSDQDTESAAWALALENTRGPSILCLSR Carbamidomethyl (C34)	24.5									
									FHWQPEVYFSK	20.8	FHWQPEVYFSK	26.6									
									KYTEEFQEAALQNLDFKLPDQWK	29.1	KASENALGALLTLPALVGGSDLSPLNTRGPSAQMDVDFQK	20.2									
									KYVGGTAPAKR	38.2	KYEAALGHVIVPNSGSDFTALR	28.0									
									LASSEKHAFLPDGDEVAR	34.1	KYTEEFQEAALQNLDFKLPDQWK	28.6									
									ONTYFQTSLEQIAK	16.1	KYVGGTAPAKR	19.4									
									SKLPLNDKSIATR	17.6	LASSEKHAFLPDGDEVAR	18.5									
									SKLPLNDKSIATR Deamidated (N6)	27.6	SKLPLNDKSIATR	26.7									
									VPEEGVVISIEPFVSTGWER	18.9	SKLPLNDKSIATR Deamidated (N6)	21.5									
		VPEEGVVISIEPFVSTGWER	38.5																		
		VKEGFLDPTK	23.5																		
		YTEEFQEAALQNLDFKLPDQWK	28.8																		
84	Tb927.3.930	dynein heavy chain, putative	1.00	305	27	10	9	2.7	IYEPAPSMELQDR Oxidation (M8)	36.6	EALDESSLANMLSSRYCAFMR Deamidated (N11) Oxidation (M13) Carbamidomethyl (C19)	32.9									
									LANPALIKR	13.9	LANPALIKR	19.7									
									LALFLPTEGGGSESLTER	31.3	LRLVLEQLAEAPR	5.5									
									LRLVLEQLAEAPR	13.8	NMTPVAGASVWAR Oxidation (M2)	7.0									
									NMTPVAGASVWAR	9.2	STSKPVEVTDVTLR	64.2									
									NMTPVAGASVWAR Oxidation (M2)	26.9	VVDEVDASSVR	6.6									
									QLGEKSLGSK	35.9											
									SFKQLDLTR	7.5											
									STSKPVEVTDVTLR	31.5											
										21.5											
85	Tb927.10.14750	fibrillarin, putative	1.00	468	32	12	11	46.4	ANCIDSTADSTFAVEVQK Carbamidomethyl (C3)	70.6	ILALNAQHFLK Deamidated (N5)	36.9									
									EQASLEPFERDHAHVTVYKSPQ	36.5	SLVPGVSYGEKR	50.0									
									QNFSPNAR	18.6	SNVPLEDARYPKYR	19.9									
									ILALNAQHFLK	45.0											
									ILALNAQHFLKNGGFVISIK Deamidated (O12)	26.0											
									LVDCIFMDVAGPDQAR Carbamidomethyl (C4) Oxidation (M7)	41.2											
									LVDCIFMDVAGPDQAR Carbamidomethyl (C4) Oxidation (M7) Deamidated (O11)	33.9											
									MRGCYLLAGKOTLTK Oxidation (M1) Carbamidomethyl (C4)	21.8											
									SLVPGVSYGEKR	45.2											
									SNVPLEDARYPKK	19.5											
SNVPLEDARYPKYR	17.4																				
YRMLRPLRDLVDCIFMDVAGPDQAR Oxidation (M3) Oxidation (M14) Carbamidomethyl (C11)	19.7																				
86	Tb927.9.6090	TFIIIF-stimulated CTD phosphatase, putative	1.00	315	22	9	8	19.2	ILGNVLER	51.9	LQADHALMDLIPMR	24.1									
									LQADHALMDLIPMR Oxidation (M8) Oxidation (M13)	33.3	NGVKEFLPNER Deamidated (N1)	33.7									
									NGVKEFLPNER	35.8	SAASSTDLHELDHWR	12.9									
									OKLGNLTK	18.6	VIEGEEVVAR	30.4									
									OKLGNLTKER	26.1											
									SFPLHPRNGVKIEFLPNER	29.5											
									SFPLHPRNGVKIEFLPNER Deamidated (N8)	35.2											
									VIEGEEVVAR	26.9											
									VVIDSDVR	20.3											
									ALSDFISKR	40.7											
87	Tb927.11.2050	heat shock protein 84, putative	1.00	388	24	8	6	14.5	ELVNAQALEKR	62.1	FKKQDTEISPLNVR	34.9									
									FKKQDTEISPLNVR	72.9	FKKQDTEISPLNVR	22.4									
									FVIRDTOGIMTRELAEALNTIAGSGSK	25.1	FVIRDTOGIMTRELAEALNTIAGSGSK	38.4									
									FVIRDTOGIMTRELAEALNTIAGSGSK Oxidation (M10)	14.8	FVIRDTOGIMTRELAEALNTIAGSGSK Deamidated (N18)	47.8									
									FVIRDTOGIMTRELAEALNTIAGSGSK Oxidation (M10) - Deamidated (N18)	20.8	KYRDTQAMAGAPK Oxidation (M8)	7.4									
									HLMELSKPEEYPRGDEAPISITQSK Oxidation (M3) Carbamidomethyl (C26)	34.1	KLYTSLSPSEEVETAGLVEQMFNVAAGLDEPR	45.5									
									LHYVADPLSR	33.1	LHYVADPLSR	44.8									
											QLLDVACSLYTEKEVFR Carbamidomethyl (C8)	42.6									
									IGGGSWAYPGLDGAEGGDHPPTVTMR Oxidation (M27)	45.7	ADNWLDEFKOR	33.6									
									LLSEADDDAFTAPLSGAHEK	43.1	EPFOLGLSTVPSVWK	49.1									
SPVNDLSVENQLLAEALREIAGESPR Carbamidomethyl (C4)	38.0	IGGGSWAYPGLDGAEGGDHPPTVTMR Oxidation (M27)	10.2																		
SPVNDLSVENQLLAEALREIAGESPR Carbamidomethyl (C4) - Deamidated (O12)	37.5	LLSEADDDAFTAPLSGAHEK	39.0																		
MRDEAEEGGRIADR	29.3																				
SPVNDLSVENQLLAEALREIAGESPR Carbamidomethyl (C4)	61.8																				
SPVNDLSVENQLLAEALREIAGESPR Carbamidomethyl (C4) - Deamidated (N6)	40.3																				
SVSPSTAEPKPK	35.1																				
88	Tb927.11.13180	hypothetical protein, conserved	1.00	286	19	5	4	15.9	IGGGSWAYPGLDGAEGGDHPPTVTMR Oxidation (M27)	45.7											
									LLSEADDDAFTAPLSGAHEK	43.1											
									SPVNDLSVENQLLAEALREIAGESPR Carbamidomethyl (C4)	38.0											
									SPVNDLSVENQLLAEALREIAGESPR Carbamidomethyl (C4) - Deamidated (O12)	37.5											
									MRDEAEEGGRIADR	29.3											
									SPVNDLSVENQLLAEALREIAGESPR Carbamidomethyl (C4)	61.8											
									SPVNDLSVENQLLAEALREIAGESPR Carbamidomethyl (C4) - Deamidated (N6)	40.3											
									SVSPSTAEPKPK	35.1											
									89	Tb927.9.10770	Polyadenylate-binding protein 2 (Poly(A)-binding protein 2) (Poly(A)-binding protein II) (PABP2), putative	1.00	353	38	9	8	22.0	DLAGRPTVGFYVAYTHEAAAK	36.6	AVIELDKESPLK	12.7
																		IVYEKEEAVDAVR	21.5	DLAGRPTVGFYVAYTHEAAAK	30.3
LTAIGLATDEKGEISR	68.3	IVYEKEEAVDAVR	26.6																		
LTAIGLATDEKGEISRYAR	33.9	LTAIGLATDEKGEISR	69.8																		
NFDQVYSERLK	39.1	NLDPSVDEKKEVSPFGEVTSK	37.8																		
NLDPSVDEKKEVSPFGEVTSK	39.1	NLDPSVDEKKEVSPFGEVTSK Deamidated (N1)	26.8																		
NLDPSVDEKKEVSPFGEVTSK Deamidated (N1)	28.8	SLGYGVYVFNQNPADAEKALDDAGVK	32.2																		
SLGYGVYVFNQNPADAEKALDDAGVK	6.2																				
SLGYGVYVFNQNPADAEKALDDAGVKLTK	16.4																				
90	Tb927.8.6580	succinate dehydrogenase flavoprotein, putative	1.00	444	28	8	6	15.9										AAMGVAASYNWACVSK Oxidation (M3) Carbamidomethyl (C14)	57.5	AAMGVAASYNWACVSK Oxidation (M3) Carbamidomethyl (C14)	11.8
									AAMGVAASYNWACVSK Oxidation (M3) - Deamidated (N11) Carbamidomethyl (C14)	31.8	AFSGQSRYHYSK	51.5									
									AFSGQSRYHYSK	56.8	ATLELAGR	30.7									
									AKDLASRDVYSR	32.3	AYPVIDHTFDCVVGAGGSGLR Carbamidomethyl (C11)	62.5									
									AYPVIDHTFDCVVGAGGSGLR Carbamidomethyl (C11)	55.7	ILHNKGDIPVAR	42.6									

Peptides

Protein ID	Protein Name	Accession	Start	End	Length	Score	Modifications	Peptide	Score	Modifications	Peptide	Score
91	Tb927.11.7380	glycerol-3-phosphate dehydrogenase (FAD-dependent), mitochondrial	1.00	338	27	7	7	11.1	SDAGESSIADLDKLNKGDIPVAR	34.8	LGANSLLDIVFVGK	61.8
									TKDGFYGR	51.9	SCANTVFNLTK Carbamidomethyl (C2)	67.8
									TKDGFYGR Deamidated (Q8)	31.9		
92	Tb927.9.2470	nucleolar protein	1.00	345	24	12	11	18.5	ARKSEEVAAHAALESFHGQ	35.5	ARKSEEVAAHAALESFHGQ	43.6
									IRMSHGAPILGR Oxidation (M3)	27.4	EPSPILKLPKPEEPVADVYSAQR	35.8
									KSEEVAAHAALESFHGQ	55.0	GRVECKPGTEELGVGAHELETPEEPK Carbamidomethyl (C5)	45.9
									LITDKTSVR	36.6	KSEEVAAHAALESFHGQ	65.6
									MAPSSGTHIIDR Oxidation (M1)	38.1	MAPSSGTHIIDR Oxidation (M1)	29.1
									MAPSSGTHIIDR Oxidation (M1)	42.1	SVYNAGGPFTR	24.9
									SVYNAGGPFTR	33.6		
									AIIEQVWR	37.7	ALQDQYVQLVIEEDR	25.3
									IGGDYEWNTLAR	53.5	ENFTNLTFEYVPLEASFTEHKSTPKEELQALLER Deamidated (Q31)	39.7
									IKNELALVAESLSEK	12.1	IGGDYEWNTLAR	6.7
									KGASGALQAPLPVVR	45.5	SAGRPSSEELFSLVR	28.4
									QIAAFTTR	27.5	TLGKEPYYVQLQPEELK	45.6
									SAGRPSSEELFSLVR	38.0	YGYALLGYNEAADDFDR	50.1
									TLGKEPYYVQLQPEELK	18.1		
									TLGKEPYYVQLQPEELKMGQTVR Oxidation (M21)	24.3		
VIGLPTSQHVR	17.6											
VIGLPTSQHVR Deamidated (Q8)	8.3											
YGYALLGYNEAADDFDR	3.9											
YGYALLGYNEAADDFDRGRR	9.1											
93	Tb927.8.1160	vacuolar-type Ca2-ATPase, putative	0.65	104	7	3	3	5.4	DTSNYGTLAGR	23.8	GAEHPILLSGTVVSTAEADYILACAVGESSFGGK Carbamidomethyl (C24)	33.8
									IKTDGAWPEEPEGPFVWLLGIGDPLRPEVDAWR	43.7	GELHFLFSVGDAPKPYEELGGVGEIAR Carbamidomethyl (C3)	37.8
									LIPVSEPFER	14.9	GFAFPFTR	47.6
94	Tb927.7.2700	NADH-cytochrome b5 reductase, putative	1.00	366	29	9	9	38.0	ALLVSGPPGFMK Oxidation (M12)	55.7	NFLGRPSNTTK	42.0
									KVIEETMPSPNCVKAKLLVSGPPGFMK Oxidation (M7)	34.6	SPFSQSVYHSYK Deamidated (Q8)	29.7
									NFLGRPSNTTK	34.6	SPFSQSVYHSYK Deamidated (Q8)	47.1
									SGQYEHGMLAGGTGTPMYQIAR Oxidation (M9)	43.2	VDSIEVQSPYK Deamidated (Q8)	49.8
									SPFSQSVYHSYK	27.5		
									SGQPLSCLYK	25.7		
									SGQPLSCLYKELPEAMVYKF Oxidation (M18)	24.8		
									VDSIEVQSPYK	45.0		
									VIETMPSPNCVKAKLLVSGPPGFMK Oxidation (M6)	19.1		
									VIETMPSPNCVKAKLLVSGPPGFMK Oxidation (M6)	19.1		
									VIIEEGEDIRRRQR	49.5		
									NLACSLLSHR Carbamidomethyl (C4)	43.8		
									NLACSLLSHR Deamidated (N1)	32.2		
									NVYACDESILPSLGGSLPILALGEK Carbamidomethyl (C5)	12.6		
									SVLIGDEADWYATPWDFRGDLLPR	46.5		
VLPFSLNLFSELAEHFESAGVGGATYPAWAPETFLVK	25.8											
VLPFSLNLFSELAEHFESAGVGGATYPAWAPETFLVKGR	24.0											
VQRLNVEGAGPR	32.1											
95	Tb927.10.470	choline dehydrogenase, putative	1.00	335	22	8	7	25.1	IAVIEEGEDIRRRQR	49.5	IAVIEEGEDIRRRQR	39.6
									NLACSLLSHR Carbamidomethyl (C4)	43.8	NVTHGVGIIQLKPK	35.5
									NLACSLLSHR Deamidated (N1)	32.2	NVYACDESILPSLGGSLPILALGEK Carbamidomethyl (C5)	20.2
96	Tb927.8.1180	vacuolar-type Ca2-ATPase 1	0.60	89	6	2	2	4.3	DTSNYGTLAGR	23.8	GAEHPILLSGTVVSTAEADYILACAVGESSFGGK Carbamidomethyl (C24)	33.8
									IKTDGAWPEEPEGPFVWLLGIGDPLRPEVDAWR	43.7	GELHFLFSVGDAPKPYEELGGVGEIAR Carbamidomethyl (C3)	37.8
									LIPVSEPFER	14.9	GFAFPFTR	47.6
									IGTDGAWPEEPEGPFVWLLGIGDPLRPEVDAWR	72.9	KGAEHPILLSGTVVSTAEADYILACAVGESSFGGK Carbamidomethyl (C25)	47.0
									LGTSTDDGSEVSNR	65.1	LGTSTDDGSEVSNR	65.1
									SGDNLDDNFR	61.6	SRGFAFPFTR	31.5
									SRGFAFPFTR	31.5	TDGKNKTDQALDFVDR	49.3
									TDGKNKTDQALDFVDR	49.3		
									AGLPPAFDVAHWNDEISR	49.8		
									FLTQALHYNTGFAR	49.2		
									FLTQALHYNTGFAR Deamidated (N9)	27.1		
									FLTQALHYNTGFAR Deamidated (Q4)	37.2		
									RAQLPPAFDVAHWNDEISRGHLLR	23.0		
									RPSLAQGR	25.5		
									YTNATFTPNPAAPYFTLK	45.0		
YTNATFTPNPAAPYFTLK Deamidated (N3)	32.9											
97	Tb927.11.13280	mitochondrial RNA binding protein 2	1.00	221	18	6	6	35.7	AQLPPAFDVAHWNDEISRGHLLR	27.9	AGLPPAFDVAHWNDEISR	49.8
									FLTQALHYNTGFAR	57.4	FLTQALHYNTGFAR	49.2
									RAQLPPAFDVAHWNDEISRGHLLR	18.3	FLTQALHYNTGFAR Deamidated (N9)	6.7
									RPSLAQGR	18.3	FLTQALHYNTGFAR Deamidated (Q4)	37.2
									VLHRDTFVLDYHR	15.3	RAQLPPAFDVAHWNDEISRGHLLR	23.0
									YTNATFTPNPAAPYFTLK	42.2	RPSLAQGR	25.5
									YTNATFTPNPAAPYFTLK	42.2	YTNATFTPNPAAPYFTLK	45.0
									YTNATFTPNPAAPYFTLK Deamidated (N3)	32.9		
									AGDWWAYTCGTEGIGR	56.3		
									AWALDLNR	21.7		
									LLPESLRGEK	24.5		
									NHIEAAR	18.5		
									OTLNQGVNVR	57.8		
									OTLNQGVNVR Deamidated (Q1)	22.9		
									OTLNQGVNVR Deamidated (Q5)	43.7		
TQSKLDEVAIEK	34.7											
TQSKLDEVAIEK Deamidated (Q2)	24.1											
98	Tb927.5.1210	short-chain dehydrogenase, putative	1.00	387	29	9	6	22.5	AGDWWAYTCGTEGIGR	56.3	AGDWWAYTCGTEGIGR	64.6
									AWALDLNR	21.7	LLPESLRGEK	18.6
									LLPESLRGEK	24.5	OTLNQGVNVR	35.6
									NHIEAAR	18.5	OTLNQGVNVR Deamidated (N10)	29.6
									OTLNQGVNVR	57.8	TQSKLDEVAIEK	64.6
									OTLNQGVNVR Deamidated (Q1)	22.9		
									OTLNQGVNVR Deamidated (Q5)	43.7		
									TQSKLDEVAIEK	34.7		
									TQSKLDEVAIEK Deamidated (Q2)	24.1		
									ADAEANARRGSEDDYTK Deamidated (N6)	7.1		
									ADAEANARRGSEDDYTK Deamidated (N6)	7.1		
									ADAEANARRGSEDDYTK Deamidated (N6)	7.1		
									ADAEANARRGSEDDYTK Deamidated (N6)	7.1		
									ADAEANARRGSEDDYTK Deamidated (N6)	7.1		
									ADAEANARRGSEDDYTK Deamidated (N6)	7.1		
ADAEANARRGSEDDYTK Deamidated (N6)	7.1											
99	Tb927.6.2170	co-chaperone GrpE, putative	1.00	343	31	9	9	58.1	AYGTSFQRKMLDVEDTLER Oxidation (M11)	13.8	ADAEANARRGSEDDYTK Deamidated (N6)	7.1
									FDPNRDKALLKVPPTAEAPPGHSTYK	36.0	ARGTSEGRKLDVDTLER	29.3
									GLEATKLPQAEVGHKTLSSHTGK	16.0	FDPNRDKALLKVPPTAEAPPGHSTYK	45.3
									IAELKKEVLYR	42.1	GLEATKLPQAEVGHKTLSSHTGK Deamidated (G10)	43.8
									ISEEDVPAK	38.1		
									LSKLLLNNAK	36.5		
									TGYKIQR	28.8		
									VLRASQVGSWSD	40.4		
									VPPITAEAPPGHSTYK	21.2		
									AAADLNFPVGR	50.9		
									AAADLNFPVGR Deamidated (N7)	47.3		
									AQLEFPVGR	49.1		
									CGASAAYCAALLEYLTSEVIELAGAAK Carbamidomethyl (C1)	54.5		
									GGVVPVHK	33.9		
									HLLAIRGDEELNGVNTIAR	36.5		
HLLAIRGDEELNGVNTIAR Deamidated (N13)	25.0											
HLLAIRGDEELNGVNTIAR Deamidated (N17)	32.5											
HLLAIRGDEELNGVNTIAR Deamidated (G14)	9.1											
HLLAIRGDEELNGVNTIAR Deamidated (G14)	6.3											
100	Tb927.7.6360	histone H2A variant	1.00	459	43	10	5	40.2	AAADLNFPVGR	50.9		
									AAADLNFPVGR Deamidated (N7)	47.3		
									AQLEFPVGR	49.1		
									CGASAAYCAALLEYLTSEVIELAGAAK Carbamidomethyl (C1)	54.5		
									GGVVPVHK	33.9		
									HLLAIRGDEELNGVNTIAR	36.5		
									HLLAIRGDEELNGVNTIAR Deamidated (N13)	25.0		
									HLLAIRGDEELNGVNTIAR Deamidated (N17)	32.5		
									HLLAIRGDEELNGVNTIAR Deamidated (G14)	9.1		
									HLLAIRGDEELNGVNTIAR Deamidated (G14)	6.3		
									ASEHREGGDGSVPLVPPSKQLTSAEAEELLK	22.4		
									GAPHVIEIEMHNQDENDSVVDIKLASR Oxidation (M9)	23.4		
									GAPHVIEIEMHNQDENDSVVDIKLASR Oxidation (M9)	23.4		
									GAPHVIEIEMHNQDENDSVVDIKLASR Oxidation (M9)	47.2		
									GAPHVIEIEMHNQDENDSVVDIKLASR Deamidated (N12)	36.5		
GYPYCAMTGGDGNAPALKR Carbamidomethyl (C4)	16.4											
GYPYCAMTGGDGNAPALKR Oxidation (M6)	35.3											
GYPYCAMTGGDGNAPALKR Oxidation (M6)	35.3											
GYPYCAMTGGDGNAPALKR Oxidation (M6)	35.3											
GYPYCAMTGGDGNAPALKR Oxidation (M6)	35.3											
GYPYCAMTGGDGNAPALKR Oxidation (M6)	35.3											
GYPYCAMTGGDGNAPALKR Oxidation (M6)	35.3											
GYPYCAMTGGDGNAPALKR Oxidation (M6)	35.3											
101	Tb927.10.12500	P-type H-ATPase, putative	1.00	230	25	7	5	14.5	ASEHREGGDGSVPLVPPSKQLTSAEAEELLK	22.4	ASEHREGGDGSVPLVPPSKQLTSAEAEELLK	36.7
									GAPHVIEIEMHNQDENDSVVDIKLASR Oxidation (M9)	23.4	FOVPLVIEIEMHNQDENDSVVDIKLASR Oxidation (M9)	35.3
									GAPHVIEIEMHNQDENDSVVDIKLASR Oxidation (M9)	47.2	GAPHVIEIEMHNQDENDSVVDIKLASR Oxidation (M9)	35.3
102	Tb927.5.3810	ornithine-5-phosphate decarboxylase/ornithine decarboxylase, putative, OMPCase-OPRTase, putative	1.00	414	24	8	8	25.1	ACAPTLWILVPGVGAQGGDLK Carbamidomethyl (C2)	20.8	ACAPTLWILVPGVGAQGGDLK Carbamidomethyl (C2)	38.8
									ADTAAVALECKR Carbamidomethyl (C11)	42.6	ACAPTLWILVPGVGAQGGDLK Carbamidomethyl (C2)	24.4
									AWAQLCEDINR Carbamidomethyl (C7)	45.8	ADTAAVALECKR Carbamidomethyl (C11)	22.5
									AWAQLCEDINR Carbamidomethyl (C7)	28.6	AWAQLCEDINR Carbamidomethyl (C7)	30.8
									AWAQLCEDINR Carbamidomethyl (C7)	28.6		
									AWAQLCEDINR Carbamidomethyl (C7)	28.6		
									AWAQLCEDINR Carbamidomethyl (C7)	28.6		
									AWAQLCEDINR Carbamidomethyl (C7)	28.6		
									AWAQLCEDINR Carbamidomethyl (C7)	28.6		
									AWAQLCEDINR Carbamidomethyl (C7)	28.6		
									AWAQLCEDINR Carbamidomethyl (C7)	28.6		
									AWAQLCEDINR Carbamidomethyl (C7)	28.6		
									AWAQLCEDINR Carbamidomethyl (C7)	28.6		
									AWAQLCEDINR Carbamidomethyl (C7)	28.6		
									AWAQLCEDINR Carbamidomethyl (C7)	28.6		

Peptides

Accession	Protein Name	Start	End	Length	Score	Modifications	Peptide	Score	Modifications	Peptide	Score								
Tb927.10.14710	40S ribosomal protein S2, putative						GAGVAAPVK GAGVAAPVKK GAGVAAPVKKLEFAGVEDVYSSCGK Carbamidomethyl (C27) LSVPPVR RGRGRGR VKEVSLAIR	32.2 41.9 8.2 29.9 31.4 27.9											
129	Tb927.9.3170	cytochrome oxidase subunit V	1.00	420	36	10	9	48.0		GAASLESLYR GAEPDHFVGTWVIERPEPKDGNK Deamidated (N25) GAEPDHFVGTWVIERPEPKDGNKSN Deamidated (N25) KPEVNDRIK SLEETMWEATPR SLEETMWEATPR Oxidation (M6) SQVASTMDPRDADVLR Oxidation (M7) SQVASTMDPRDADVLR Oxidation (M7) VFLPPLGDPHR VFLPPLGDPHRLK	73.9 29.3 19.2 26.9 60.9 41.2 40.3 28.2 17.1 23.0	0.00	4	1	1	1	6.1	VFLPPLGDPHR	4.4
130	Tb927.10.520	hypothetical protein, conserved	1.00	494	49	10	7	21.0		AAAKGDNAAAVEGR AAAKGDNAAAVEGR Deamidated (N8) AAAKGDNAAAVEGRHTA AAAKGDNAAAVEGRHTA Deamidated (N8) LLAERAAAKGDNAAAVEGR MDSQSYLAK RLEFENGPLRDQVEAHTQR RLEFENGPLRDQVEAHTQR Deamidated (N6) SMNPTFPLMLAR Oxidation (M2), Oxidation (M9) YGPIDVFGSETPSPDYHKK	65.1 82.8 49.0 38.9 13.5 23.3 22.7 31.6 26.3 28.8	1.00	209	14	4	2	8.6	AAAKGDNAAAVEGR AAAKGDNAAAVEGR Deamidated (N8) RLEFENGPLRDQVEAHTQR RLEFENGPLRDQVEAHTQR Deamidated (N6)	67.8 67.1 21.9 17.3
131	Tb927.11.1090	calpain-like protein, putative, cytoskeleton associated protein, putative	1.00	248	31	8	7	2.2		ASGEVPLALTVGSPDANVR IAELEAMNEHSHKLAK Oxidation (M8) IAELEAMNEHSHKLAK Oxidation (M8) IAELEAMNEHSHKLAK Oxidation (M8), Deamidated (N9) IAELEAMNEHSHKLAK Oxidation (M8) LIAEDREGNAR LIAEDREGNAR YLNPEPEGVLELLPLNEDEVSEKEDRLR	20.3 25.6 36.8 21.3 35.9 26.1 20.9 8.5	0.39	53	5	2	2	0.4	LIAEDREGNAR LIAEDREGNAR	21.8 22.7
132	Tb927.8.7530	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative	1.00	150	7	4	4	16.8		FLSVPOGSR IGLNELKLGITPPWVWVAVYVLSGR LGITPPWVWVAVYVLSGR VGLVLDVVDGEQQLREAVLKEAER	30.7 29.4 8.6 54.4	1.00	344	13	7	6	18.4	IGLNELKLGITPPWVWVAVYVLSGR LGITPPWVWVAVYVLSGR MLQLGDTPTADEARVGLVLDVVDGEQQLR Deamidated (G28) VGLVLDVVDGEQQLR Deamidated (G12) VGLVLDVVDGEQQLREAVLKEAER VGLVLDVVDGEQQLREAVLKEAER Deamidated (G12)	23.7 36.5 42.9 62.7 35.7 65.9 47.3
133	Tb927.10.450	hypothetical protein, conserved	1.00	104	9	4	4	14.4		IVAGHEPEQTNALLQSLAALPSDKK Carbamidomethyl (C20) MFVNPDLTR Oxidation (M1) NIBSDNAAAGVWR Oxidation (M2) VIEQQARPTKDSGDTLQDGEAKYLGQQALR	11.5 18.1 35.3 29.5	0.99	41	2	1	1	4.8	IVAGHEPEQTNALLQSLAALPSDKK Carbamidomethyl (C20)	37.1
134	Tb927.11.13990 Tb927.11.13190	elongation factor 1 gamma, putative elongation factor 1 gamma, putative	0.99	342	29	9	7	21.0		ITDYLWVEGPTIPKPLEGR Carbamidomethyl (G6) KKNRDELPPSPVLDFAKR KKNRDELPPSPVLDFAKR Deamidated (N4) LDKSGFLYGR LLVVAFAFNVPTVK LLVVAFAFNVPTVK Deamidated (N8) SQGATGPKVAK TVEVLSQGATGPKV TVEVLSQGATGPKVAK	55.7 34.4 18.8 36.2 30.1 4.1 43.8 26.5 38.6	0.75	111	7	2	2	8.7	ITDYLWVEGPTIPKPLEGR Carbamidomethyl (G6) LLVVAFAFNVPTVK	36.8 49.3
135	Tb927.7.1730	60S ribosomal protein L7, putative	1.00	433	29	8	8	38.8		AAFKQQTENFRK AAANKVAAALAK AAANKVAAALAK AVEPYIAYGYSLSLTVR AVPAPESAIR HFVEGGYGRDRLNLR PKAVAPESAIR TVTNGLWPKLPPAGGMR Deamidated (N4), Oxidation (M18)	34.0 56.4 76.1 58.4 25.1 29.2 37.1 57.1	0.86	244	17	7	6	29.8	AAFKQQTENFRK AAANKVAAALAK AAANKVAAALAK AAANKVAAALAK Deamidated (N5) AVEPYIAYGYSLSLTVR AVPAPESAIR HFVEGGYGRDRLNLR	33.5 37.2 51.5 24.6 20.6 59.1 23.9
136	Tb927.6.1520	aquaporin 3, putative	1.00	173	7	3	1	10.3		SANPQEKNEVELGDNADNEAHDADVNYWAPR SANPQEKNEVELGDNADNEAHDADVNYWAPR Deamidated (N16) SANPQEKNEVELGDNADNEAHDADVNYWAPR Deamidated (G5)	56.1 52.3 50.0	1.00	243	6	5	1	10.3	SANPQEKNEVELGDNADNEAHDADVNYWAPR Deamidated (N10) SANPQEKNEVELGDNADNEAHDADVNYWAPR Deamidated (N16), Deamidated (N19) SANPQEKNEVELGDNADNEAHDADVNYWAPR Deamidated (N19) SANPQEKNEVELGDNADNEAHDADVNYWAPR Deamidated (N3) SANPQEKNEVELGDNADNEAHDADVNYWAPR Deamidated (G5)	45.2 43.5 40.2 59.1 54.7
137	Tb927.11.6250	hypothetical protein, conserved	1.00	190	20	5	4	23.1		AAQDSVLR SAQDPLFSGVSTVYVR SAQDPLFSGVSTVYVR Deamidated (G3) SVLAWAQLRELGLSSEADKVEAAASK VAGGRVQTK	15.4 64.3 36.6 8.9 27.7	1.00	237	9	3	2	16.4	SAQDPLFSGVSTVYVR SAQDPLFSGVSTVYVR Deamidated (G3) SVLAWAQLRELGLSSEADKVEAAASK	61.4 62.5 49.0
138	Tb927.11.3590 Tb927.11.3600	40S ribosomal protein S4, putative 40S ribosomal protein S4, putative	0.97	268	25	8	7	33.3		ATNIFVIGKMSVVPVTLK Deamidated (N3) ATNIFVIGKMSVVPVTLK Oxidation (M11) IRIGDVAR KIEVSIERHPGAFDIAR RVIQEREK LKDASGHEFATR LTGVFAPRR VNVVYTGTRIPVWTHDHR	22.1 25.1 21.9 42.2 8.4 27.1 44.9 30.5	0.75	115	6	2	2	11.0	KIEVSIERHPGAFDIAR LKDASGHEFATR	24.0 38.3
139	Tb927.7.3550	hypothetical protein, conserved	1.00	330	26	9	8	8.5		CGAFEGQAKVPR Carbamidomethyl (C1) DSSGRRESLFLVYR IVSSGRFELLNDSALTVK LVTWHRK LIMONIEER Oxidation (M2) SQMLQLTPK Oxidation (M3) TNSLQRVMEDEELNQPAPLPPTLDELK Oxidation (M8) VMEDEELNQPAPLPPTLDELK VMEDEELNQPAPLPPTLDELK Oxidation (M2)	29.6 34.0 32.7 18.1 27.4 30.1 23.2 27.3 47.5	0.27	33	2	2	2	2.6	AEGKPTSEASSDVGAAANTR LVTWHRK	24.1 9.2
140	Tb927.3.4760	dynamn, putative, vacuolar sortin protein 1, putative	1.00	346	17	7	7	14.7		CPVLQVQLVPR Carbamidomethyl (C1) FFDFSEINEIQNR LISVNDLHDAFANVK SATTAMTALTK Oxidation (M6), Oxidation (M7) SSVLEAVKDFLPR TVGELLAEPPOAQR TVLDSVREFALI	50.0 38.1 40.6 43.7 51.4 39.2 48.1	1.00	210	8	5	4	8.0	CPVLQVQLVPR Carbamidomethyl (C1) FFDFSEINEIQNR FFDFSEINEIQNR Deamidated (N8) SSVLEAVKDFLPR TVLDSVREFALI	46.5 62.3 38.8 31.3 33.3
141	Tb927.6.10310	mitochondrial carrier protein, putative, mitochondrial phosphate transporter, putative	1.00	219	22	4	4	23.0		ADPAAGFPKSLVLSWR CIGGVLSCGLTHTAVCLDVVK Carbamidomethyl (C1), Carbamidomethyl (C9), Carbamidomethyl (C17) SYQIANEIGYGLCTK Carbamidomethyl (C15) YANPDHNSYYLK	19.4 39.3 60.4 45.1	1.00	212	10	6	3	17.7	CIGGVLSCGLTHTAVCLDVVK Carbamidomethyl (C1), Carbamidomethyl (C9), Carbamidomethyl (C17) GIGSGFVLAEDGFYAK YANPDHNSYYLK YANPDHNSYYLK Deamidated (N10) YANPDHNSYYLK Deamidated (N3) YANPDHNSYYLK Deamidated (N3), Deamidated (N8)	36.7 32.1 33.7 31.3 24.7 29.4

Peptides

142	Tb927.9.10400	hypothetical protein, conserved	1.00	315	21	6	6	10.1	ESNYIEAADALKASNPVEIK ESNYIEAADALKASNPVEKAGR GLKFSALAKK LPKDELDQVYR YLRSNYIEAADALK YLRSNYIEAADALKASNPVEIK	55.0 47.0 31.4 52.6 25.9 36.5	1.00	111	7	2	2	4.9	ESNYIEAADALK LPKDELDQVYR	49.3 51.1
143	Tb927.10.14500	hypothetical protein, conserved	1.00	324	25	7	7	22.9	AAADAENFETLKR ATLLKNGPTTN LVLVLEKGR TGKGRPRPFDAPEEQVYR TGKGRPRPFDAPEEQVYR TIGTLNTYGRPFESAGVWVCR Carbamidomethyl (C2) VKAADAENFETLKR	42.6 33.8 34.8 31.5 31.0 26.6 46.9	0.00	20	2	2	2	12.2	TGKGRPRPFDAPEEQVYR TVARDPWRNRDAALGAVLHR	5.1 15.1
144	Tb927.7.1300	protein disulfide isomerase, putative	1.00	251	19	5	5	18.0	AAAGAKDKVLAK AFVSYLNGIK ALGEGAMHYR Oxidation (M7) IATNVLENGHEYSKEHER Deamidated (N8) YKVEGYTLVFFPK	41.6 47.1 58.7 35.2 39.6	1.00	90	6	2	2	6.1	AFVSYLNGIK LLAQIQWSPK	15.8 61.8
145	Tb927.10.3940	40S ribosomal protein S3A, putative	1.00	371	27	9	9	33.2	FTVQEVQR IADFLR IADFLRGR KEWYDVWPK LAKLNDVSLTR NEVLRQFAK TICKNTGKIAADFLR Carbamidomethyl (C3) VKFTVQEVQR VYEGNLADLNKTONEDDAYRK	44.4 28.8 23.7 45.2 18.2 30.2 30.0 30.0 24.4	0.00	0	0	0	0	0.0		
146	Tb927.2.4710	RNA binding protein, putative	1.00	257	23	6	5	17.0	FRDDYKVAWR HLPDDATEQGLR NFFAAVGEVPDIFHER NFFAAVGEVPDIFHER Deamidated (N1) NMFQSGATLDFLEPR Oxidation (M2) VAGLADGTADDVREFFTR	28.7 24.9 55.5 35.5 34.3 17.5	1.00	258	31	4	4	12.0	NFFAAVGEVPDIFHER NMFQSGATLDFLEPR VAGLADGTADDVREFFTR	66.8 52.5 40.0 26.4
147	Tb927.11.2060	60S acidic ribosomal subunit protein, putative	0.98	286	25	8	7	34.9	ATAFFQALNIATK DLRKGELVWIK Oxidation (M10) LGGGEAAPAAAAAAPAAAAAEEEEEDDDFGMGALF Oxidation (M38) SSQDHWYR TAVLEKLGSGEAAAAAAPAAAAAEEEEEDDDFGMGALF Oxidation (M45) VGAAPCDVVPAGNTGMEPK Carbamidomethyl (C7) Oxidation (M18) VFLCLMNVN Carbamidomethyl (C4) VFLCLMNVN Carbamidomethyl (C4) Oxidation (M6)	58.9 21.4 35.1 15.7 31.0 25.8 33.4 28.5	0.85	134	5	4	3	13.6	ATAFFQALNIATK ATAFFQALNIATK Deamidated (N6) VGAAPCDVVPAGNTGMEPK Carbamidomethyl (C7) Oxidation (M18) VFLCLMNVN Carbamidomethyl (C4)	57.1 36.0 5.6 31.8
148	Tb927.4.2450	thioredoxin, putative	1.00	381	16	7	5	14.8	LALPVRPLPAHGLENFCSPDAR Carbamidomethyl (C19) SAGAQSGAQLINAPGIK SAGAQSGAQLINAPGIK Deamidated (Q6) SAGAQSGAQLINAPGIK Deamidated (Q6) Deamidated (N14) SAGAQSGAQLINAPGIKTVK SRVRYVLSLSPR VPPYAVLSLSPR	46.0 80.0 74.4 7.1 32.6 35.7 59.2	1.00	64	3	1	1	4.6	SAGAQSGAQLINAPGIK	55.3
149	Tb927.4.4210	ATP-dependent zinc metallopeptidase, putative, metallo-peptidase, Clan MA(E) Family M41	1.00	292	17	7	7	11.4	ALINSYER HLENEVLTDDVYR MAMVYSSFAPRPVYAPGTGTR Oxidation (M1) Oxidation (M4) SRVLSPPER WKEHFRHLSGTASDSDNKKVNR VPTGALLGPPGTGK VPTGALLGPPGTGKTLAK	37.1 9.6 45.4 29.8 43.7 56.2 17.4	0.92	48	3	2	2	5.0	TSAGIEKGEQEHMLNELLTQLDGFSSR VPTGALLGPPGTGK	9.3 35.8
150	Tb927.10.7500	fibrillarin	1.00	238	12	5	4	21.0	GGGGGGGAGAKVVEPHLHPGVFISK ILALNAQFLK LKPLEGASLEPPERDHAHVGVYR LKPLEGASLEPPERDHAHVGVYR Deamidated (Q6) VVVEPHLHPGVFISK	27.3 37.2 43.9 33.6 42.9	1.00	160	6	3	2	13.3	LKPLEGASLEPPERDHAHVGVYR LKPLEGASLEPPERDHAHVGVYR Deamidated (Q6) VVVEPHLHPGVFISK	41.0 53.1 40.2
151	Tb927.11.3490	hypothetical protein, conserved	1.00	287	17	6	6	9.2	EADQVLLSSTPYR SAKEADQVLLSSTPYR HGGAPTQVDPDALAR NVLEQLEVDKAVDR QDASQFCETLR Carbamidomethyl (C7) SIDERVNLQK	40.8 60.6 26.5 35.9 21.0 31.7	1.00	141	6	2	2	4.4	NLEQLEVDKAVDR SVEKSEGLADTATEVYK	50.0 36.5
152	Tb927.11.2670	Nucleopoin	1.00	271	13	5	5	12.5	AGLLEWLDNDPYYR AGLLEWLDNDPYYRSGAPLTISEVLSLK IAEKQTR SSTAAGAAAAAR VVRDGHANNFLQK	15.4 70.0 31.9 74.0 40.6	1.00	125	3	3	2	5.7	AGLLEWLDNDPYYR AGLLEWLDNDPYYRSGAPLTISEVLSLK AGLLEWLDNDPYYRSGAPLTISEVLSLK Deamidated (N10)	50.1 55.3 20.0
153	Tb927.10.3650	NADH-dependent fumarate reductase, putative	0.89	242	11	6	5	5.4	ATSGINGWTR ATSGINGWTR Deamidated (N6) ELLSNSGLCGDEPTNJKLEHTPYR Carbamidomethyl (C10) FVNELDLR FVNELDLRSVSK VLRFLPGALGR	44.4 42.2 28.2 39.4 33.7 20.6	1.00	200	8	5	5	4.6	ATSGINGWTR Deamidated (N6) FVNELDLR FVNELDLR SGDAIGWLSLGVPLSVLSQLGHSFKR	32.7 42.4 29.5 29.3 34.1
154	Tb927.5.1300	vacuolar proton translocating ATPase subunit A, putative	0.48	31	2	1	1	2.7	LGQLAAFQFDLNSDVSFAQR Deamidated (Q3) Deamidated (Q8)	24.6	1.00	361	18	7	5	12.1	GNSVLHTDEITTFSEGEKER ISEVNGASLYPVAESTER ISEVNGASLYPVAESTER Deamidated (N5) LGQLAAFQFDLNSDVSFAQR LGQLAAFQFDLNSDVSFAQR Deamidated (Q8) QSPQLNLTGVPK YLHDEKGLTCTVSTEAIGR Carbamidomethyl (C13)	42.7 50.4 62.7 47.8 46.6 38.6 19.8
155	Tb927.3.4970	hypothetical protein, conserved	0.98	102	6	5	5	10.5	AANKGSVMAAPGTDRR EMRPTYPVDEWARDDAALAEQVLELKYVYR ERSPTVMSKGGTQAGSGSPGSAVESDLQK Oxidation (M7) SIAKVGGDLNVYAPK VLALEKIVESR	10.1 20.2 4.4 36.1 30.6	0.91	40	4	2	2	5.8	EMRPTYPVDEWARDDAALAEQVLELKYVYR ERSPTVMSKGGTQAGSGSPGSAVESDLQK Oxidation (M7)	24.9 6.0
156	Tb927.8.4810	prohibitin 1	1.00	245	23	5	5	17.0	AAVRAEAGEAESAR AAVRAEAGEAESARLQIAQR LISEAQR NVTFLPGSNMLLHKM Oxidation (M11) Oxidation (M15) SGGGLLELR	20.4 19.7 41.8 21.5 77.9	1.00	119	4	3	3	15.5	AAVRAEAGEAESAR ILQLEIKVFNIR NVTFLPGSNMLLHKM Deamidated (N10)	18.0 61.4 29.8
157	Tb927.10.3990	DH41	1.00	163	16	5	4	16.0	ELQMGFEKGFERSPVQEEAIPVALQKQVLYR Deamidated (Q3) Oxidation (M4) ELQMGFEKGFERSPVQEEAIPVALQKQVLYR Oxidation (M4) GFERSPVQEEAIPVALQKQVLYR NVLDEAKLLSSEFTSLMR NVTFEYGLRR	13.8 33.7 43.4 12.0 23.7	1.00	237	14	6	4	20.7	GFERSPVQEEAIPVALQKQVLYR GFERSPVQEEAIPVALQKQVLYR Deamidated (Q18) GFERSPVQEEAIPVALQKQVLYR Deamidated (Q9) NVLDEAKLLSSEFTSLMR NVTFEYGLRR TASVPIVLEKVDQLGHALLMVPTR	49.9 36.4 12.5 62.3 11.2 24.3

Peptides

158	Tb927.11.8260	carbonic anhydrase-like protein	1.00	64	4	1	1	2.6	AANFKLSQVLR	59.2	1.00	197	12	4	3	10.2	AANFKLSQVLR AANFKLSQVLR Deamidated (N4) FVIMTQISK GSVYYSGLTTPCTEGVR Carbamidomethyl (C18)	56.8 56.0 39.6 26.6
159	Tb927.8.900	splicing factor TGR1	1.00	301	35	7	7	18.6	LEQVAVPSVDR RGECAFVDVPSAHAR Carbamidomethyl (C4) RRGECAFVDVPSAHAR Carbamidomethyl (C5) SISDRRLR SKLEEAAPIGFR SKLEEAAPIGFR TALFVGLGPSGR	41.9 14.8 20.3 27.6 51.3 19.4 57.2	1.00	127	7	3	3	11.9	LTEDMDKYGEAR Oxidation (M5) SKLEEAAPIGFR TALFVGLGPSGR	9.1 41.1 57.2
160	Tb927.9.2900	hypothetical protein, conserved	1.00	212	13	6	5	3.3	HLVETVPGQR IASGGSQHAALLMNR LMAEMLPWALLETEDRDVVVEQAR Oxidation (M2) Oxidation (M5) MGADALSLVGTGGYQR MGADALSLVGTGGYQR Oxidation (M1) VLSGAGAGETPSR	39.5 8.2 29.3 29.7 19.3 67.6	0.00	14	1	1	1	0.7	MGADALSLVGTGGYQR	14.1
161	Tb927.9.4210	fatty acyl CoA synthetase 3	1.00	259	22	8	8	12.5	AFDHAFQSR ALAYRPVDRVEK ALGVAVPVPGETSDCSPIYR Carbamidomethyl (C17) ATASFQETAR GDIAEYNSLLIGVPR RVIDERYDIAPLFVEEC Carbamidomethyl (C19) VAVPVPGETSDCSPIYR Carbamidomethyl (C13) VDERYDIAPLFVEEC Carbamidomethyl (C18)	39.5 20.6 26.6 13.5 17.5 18.1 46.2 33.5	1.00	214	13	6	5	11.5	ALAYRPVDRVEK ATASFQETAR IASGGSPLSTATQDFWVVLAR IALSSGSPSTATQDFWVVLAR Deamidated (G14) VAVPVPGETSDCSPIYR Carbamidomethyl (C13) VDERYDIAPLFVEEC Carbamidomethyl (C18)	20.5 25.1 53.6 33.6 30.1 11.7
162	Tb927.3.1120	GTP-binding nuclear protein rib2, putative	1.00	211	18	4	3	31.8	KLANDPRLTVEAPMLDPNVQPLTAEQLQALQEQEAR Deamidated (N7) Oxidation (M15) KLANDPRLTVEAPMLDPNVQPLTAEQLQALQEQEAR Oxidation (M15) SNYNFEKFLWLAK VCDNIPVLVGNVDCAEER Carbamidomethyl (C2) Carbamidomethyl (C16)	55.4 59.8 22.8 36.3	1.00	57	2	1	1	8.8	VCDNIPVLVGNVDCAEER Carbamidomethyl (C2) Carbamidomethyl (C16)	39.2
163	Tb927.5.3230	hypothetical protein, conserved	1.00	218	20	4	4	4.2	AALIEACNVSMDEPELLR Carbamidomethyl (C7) Oxidation (M1) ALTQCLSTYELIAPQVLDKNVPAIQASR Carbamidomethyl (C5) SLAAWASGELSOTAACLK VLFQLLTSDHWAHETRPVVER Carbamidomethyl (C10)	32.3 31.7 50.5 35.7	0.00	12	1	1	1	0.8	STSMALGFTVPASSAR Oxidation (M4)	12.3
164	Tb927.11.1270	hypothetical protein, conserved	1.00	240	10	4	3	17.2	ATLPASQQAIFY LLSTGKIEEYLPNNK LLSTGKIEEYLPNNKATLPASQQAIFY LLSTGKIEEYLPNNKATLPASQQAIFY Deamidated (N28)	44.7 64.5 55.0 62.3	0.00	0	0	0	0	0.0		
165	Tb927.2.3780	translation initiation factor IF-2, putative	1.00	104	10	5	5	9.2	AAVFPVQLTLDANHTDRILPK AAVFPVQLTLDANHTDRILPKVK AKEHVLESVTK MAAAGFVDPVEKVR SPKCVLGHVDTGKTLSDLR Carbamidomethyl (C4) Carbamidomethyl (C5)	17.5 35.3 12.7 6.3 18.6	1.00	268	21	7	6	13.0	AAVFPVQLTLDANHTDRILPK AAVFPVQLTLDANHTDRILPKVK AKEHVLESVTK IAANILEYVPGSHLLVRRPQDKEAWK IAANILEYVPGSHLLVRRPQDKEAWK Deamidated (N4) LFDKLETTEDNLLATLK SPKCVLGHVDTGKTLSDLR Carbamidomethyl (C4) Carbamidomethyl (C5)	32.0 39.3 30.9 33.0 35.9 41.7 15.3
166	Tb927.11.13900	par1	1.00	239	18	6	6	15.7	AATPPVHRLQVHGVK ALEKYER AAWALIEAETAATAENYSGYVDSR AWEEGETELARDIPVGRA AVVGGDVEVER KAELVQLTAK	39.2 40.0 35.1 20.1 32.4 35.6	1.00	97	8	3	2	7.9	AAWALIEAETAATAENYSGYVDSR AAWALIEAETAATAENYSGYVDSR Deamidated (N18) AWEEGETELARDIPVGRA	48.7 14.0 17.6
167	Tb927.11.4480	radial spoke protein RSP4/6, putative	1.00	280	14	6	6	20.2	HSVVDGESTACNEPCVPPSELSE Carbamidomethyl (C12) Carbamidomethyl (C16) LAENERLFRAPPEIQTIEQDPYTTITTR LFRAPPEIQTIEQDPYTTITTR LSFVYVSNWAGDNTLLPVTQDQACGR Carbamidomethyl (C25) PVNPEFQDLFAFAR Oxidation (M12) SLEVPVQPEPFGVGNR	38.3 31.2 49.9 66.7 14.5 43.8	0.00	4	1	1	1	2.9	SLEVPVQPEPFGVGNR Deamidated (Q7)	3.6
168	Tb927.5.1470	NADH-cytochrome b5 reductase, putative	1.00	210	10	6	6	32.3	IKDNGSEITYYVPTPNTK ILVAGPPELKEIAGEK ILVAGPPELKEIAGEKFNEMAPPEQGLPK Oxidation (M23) LSAGYEPDTR SYGVALKSGDAPMYR Oxidation (M4) Oxidation (M14) VLGGIEINEEMR Oxidation (M12)	40.5 24.5 29.6 60.0 34.5 8.3	1.00	124	8	4	4	22.1	IKDNGSEITYYVPTPNTK ILVAGPPELKEIAGEK ILVAGPPELKEIAGEKFNEMAPPEQGLPK LSAGYEPDTR	7.3 10.8 24.5 55.3
169	Tb927.6.1890	cytochrome c1, heme protein, mitochondrial precursor	1.00	185	6	4	3	28.7	AAQFANNSEPPDLQHSVFGK Deamidated (N6) AAQFANNSEPPDLQHSVFGK Deamidated (N7) QIYTEVAPCHLGR Carbamidomethyl (C10) QLASZYEVDSAPDAGMLNRPKGFDTLPIFFNQR Oxidation (M18)	55.4 25.2 36.2 55.9	1.00	167	7	3	1	8.1	AAQFANNSEPPDLQHSVFGK Deamidated (N6) AAQFANNSEPPDLQHSVFGK Deamidated (N6) Deamidated (N7) AAQFANNSEPPDLQHSVFGK Deamidated (N7)	66.0 36.9 46.5
170	Tb927.11.2410	hypothetical protein, conserved	1.00	221	14	5	4	23.0	FKVVPSSST LYNNAVALR LYNNAVALR Deamidated (N3) QLASLRFVFGSALPK YAACSAVAGQMATELAK Carbamidomethyl (C4) Oxidation (M12)	37.6 50.9 44.4 23.9 39.8	1.00	150	8	5	5	27.9	EAGRPKIQGQEK FKVVPSSST KTLNAEIKGLASLRFVFGSALPK Deamidated (N4) TLNAEIKGLASLRFVFGSALPK YAACSAVAGQMATELAK Carbamidomethyl (C4)	33.3 14.2 34.1 28.2 28.2
171	Tb927.11.14730	metalloprotease, putative, cell division protein Flh1 homologue, putative	1.00	333	22	8	7	13.2	AVAGEANAPFLSCSGADFIFFGGSGPK Carbamidomethyl (C13) AVAGEANAPFLSCSGADFIFFGGSGPK Carbamidomethyl (C13) EAAPCVIIDEIDAGSR Carbamidomethyl (C5) EAAPCVIIDEIDAGSRNSGSR Carbamidomethyl (C5) ITGDACPKQQR Carbamidomethyl (C3) VASLTAEEAPEVK VRELFAGAR VRELFAGAR Deamidated (Q7)	39.3 55.7 41.6 24.3 13.8 27.7 33.6 34.7	1.00	201	16	5	4	9.0	AVAGEANAPFLSCSGADFIFFGGSGPK Carbamidomethyl (C13) AVAGEANAPFLSCSGADFIFFGGSGPK Carbamidomethyl (C13) EAAPCVIIDEIDAGSR Carbamidomethyl (C5) EAAPCVIIDEIDAGSR Carbamidomethyl (C5) VASLTAEEAPEVK	21.5 41.4 10.3 46.9 25.1
172	Tb927.6.4090	chaperonin HSP60, mitochondrial precursor, putative	1.00	295	17	5	3	7.6	NALAEVAGGGAALLHASK NALAEVAGGGAALLHASK Deamidated (N1) NVIKQPSGEK VIDAANAARNALAEVAGGGAALLHASK VIDAANAARNALAEVAGGGAALLHASK Deamidated (N10)	71.9 5.7 28.1 67.2 35.4	1.00	285	13	5	4	9.6	NALAEVAGGGAALLHASK NVIKQPSGEK TSLVNRNAR Deamidated (N8) VIDAANAARNALAEVAGGGAALLHASK VIDAANAARNALAEVAGGGAALLHASK Deamidated (N10)	72.4 37.2 29.5 54.8 36.5
173	Tb927.3.3490	high mobility group protein, putative	1.00	150	9	4	4	15.9	AGAAWKELGPEER AGAAWKELGPEER ANNPQGNNTALQTLGK HSDLSVEMSK Oxidation (M9)	53.8 34.5 10.7 28.5	1.00	49	3	1	1	5.2	AGAAWKELGPEER	35.8
174	Tb927.1.4310	hypothetical protein, conserved	1.00	334	18	7	6	7.3	DAPNAAGSPYNR ELVYSQAPISYTPR LLSSQKPPALEALDEADYPTAFVDRVYVYDGEWR LLSSQKPPALEALDEADYPTAFVDRVYVYDGEWR Deamidated (Q6) NLEVTCIARRLPK Carbamidomethyl (C6) GQIPQALHALFAESVSR SFVADAVQSEIDLUSDEMAR Oxidation (M19)	64.0 30.9 41.4 42.3 21.0 20.5 19.8	1.00	116	2	2	1	2.1	LLSSQKPPALEALDEADYPTAFVDRVYVYDGEWR LLSSQKPPALEALDEADYPTAFVDRVYVYDGEWR Deamidated (Q6)	67.6 48.2
175	Tb927.7.1790	Adenine phosphoribosyltransferase, putative	1.00	257	22	5	5	36.5	EAEELQEFNYSYTR GYIGAPLAWLGPVYAR RFPSSVPEGDDLKYLPMRSR Oxidation (M18) SIRNDSIPPR	48.0 65.7 27.6 22.5	1.00	142	8	2	2	15.2	EAEELQEFNYSYTR GYIGAPLAWLGPVYAR	68.7 54.4

Peptides

Accession	Protein Name	Start	End	Score	Modifications	Peptide	Score	Modifications	Peptide	Score								
198	Tb927.8.4780	hypothetical protein, conserved	1.00	199	17	6	6	2.4	ACNPFLLYEDRW Carbamidomethyl (C2) AVIEERKAEESLAAYPFLLGR ALVTGLAEENATKTDVHKQYVFLPK KAEESLAAYPFLLGR RNMIGRLGELPNDAMFSQLGOR Oxidation (M3)- Oxidation (M7) TSSDSESFAGLPGAR	24.3 17.0 20.3 47.3 29.7 21.4	0.00	8	1	1	1	0.6	ALVTGLAEENATKTDVHKQYVFLPK	8.4
199	Tb927.3.3460	hypothetical protein, conserved	1.00	233	10	5	4	14.9	GNPVGAAEDIKLPEISDALKR GNPVGAAEDIKLPEISDALKR Deamidated (N2) VDEAKGIVGEGYSTK TGAKGLAGNASVLGK TSVPHQPFVAGEDELRR	65.3 63.2 39.9 26.8 28.0	0.36	33	6	2	2	8.5	GNPVGAAEDIKLPEISDALKR TSVPHQPFVAGEDELRR	7.3 20.6
200	Tb927.11.9080	hypothetical protein, conserved	1.00	199	9	4	3	3.5	LKLGTPQK STALQEOGAGATTVAPEPR STALQEOGAGATTVAPEPR Deamidated (Q7) VKPDAATALEVVR	22.9 46.0 2.3 75.3	0.00	7	1	1	1	1.6	STALQEOGAGATTVAPEPR	6.5
201	Tb927.11.14130 Tb927.10.3840	ribosomal protein L18, putative 60S ribosomal protein L18a, putative	0.96	294	17	8	6	39.7	AGAVSDANNLQASR ARYHNIEVLGK ETPSEKNPQPTVYKFEVAFNIVAK ETPSEKNPQPTVYKFEVAFNIVAK Deamidated (N7) LNWAGFHPNLSFLLQOR LNWAGFHPNLSFLLQOR Deamidated (N10) LNWAGFHPNLSFLLQOR YHNEVLGK	81.2 19.6 29.4 29.9 29.2 17.3 17.9 41.6	0.00	0	0	0	0	0.0		
202	Tb927.10.4880	hypothetical protein, conserved	1.00	151	13	3	3	11.2	KSPFMKLDQALPVYDDVVTGSGR Oxidation (M5)- Oxidation (M9) LMDGALPVYDDVVTGSGR Oxidation (M2) SPFMKLDQALPVYDDVVTGSGR Oxidation (M4)- Oxidation (M8)	33.4 77.6 25.6	0.99	56	2	2	1	8.0	LMDGALPVYDDVVTGSGR Oxidation (M2) LMDGALPVYDDVVTGSGR Oxidation (M2)- Deamidated (D4)	44.2 11.6
203	Tb927.9.11220	hypothetical protein, conserved	1.00	195	13	6	5	17.1	AVNQFYSEELAK AVNQFYSEELAKR AVNQFYSEELAKR Deamidated (Q4) SPFEVDWTAGEAR SVPAFSLAHVAK VVDTTGSEVLVFLQTVAPR	23.3 46.7 39.8 6.7 40.6 7.4	1.00	132	10	3	3	14.0	LAAFPDIIEFLANK SVPAFSLAHVAK VVDTTGSEVLVFLQTVAPR	49.6 34.2 18.9
204	Tb927.8.3870	hypothetical protein, conserved	1.00	181	15	4	4	4.4	LYNNGETSVHTDEENERLYK PVTVEEVLR SLSHYGESEELR VEAVDSYRR	10.9 72.0 43.1 22.2	1.00	91	2	2	2	1.6	PVTVEEVLR VEAVDSYRR	71.4 20.0
205	Tb927.2.5160	chaperone protein DNAJ, putative	1.00	148	8	3	3	15.5	ILQYPKGEERPAEATEHTLAVTVLDREAR SIGRFVQMGVACPR Oxidation (M10)- Carbamidomethyl (C14) STNVDPQKLWVSR	38.3 61.6 20.3	0.00	0	0	0	0	0.0		
206	Tb927.10.240	peroxin 14, putative	1.00	177	14	7	7	23.2	AELSLTGLKR EVPALPVPVASESHVDAK HTSLLYAPQAPLPEAAATR LRGQVAVSR RHTSLLYAPQAPLPEAAATR SLVHREVPALPVPVASESHVDAK TNEKESQIKSLQEEVNR	16.8 14.6 34.0 15.5 25.9 6.6 30.8	1.00	136	8	4	3	12.8	EVPALPVPVASESHVDAK HTSLLYAPQAPLPEAAATR HTSLLYAPQAPLPEAAATR Deamidated (Q9) SLVHREVPALPVPVASESHVDAK	24.1 34.1 23.1 39.8
207	Tb927.10.8230	protein disulfide isomerase bloodstream-specific protein 2 precursor	1.00	337	20	7	7	18.7	AVNQPWTPASNAEEVTR GYPTILFRNKGAEHVGAR Deamidated (N10) LFPGRFRETIVYR SLVPEVETVDGKTTWAK TKDQIKYK VSLKFFEAEPK VSLKFFEAEPKLPDQKPTIVYR	50.0 35.2 28.8 27.8 55.1 43.6 37.7	1.00	73	5	2	2	6.0	SLVPEVETVDGKTTWAK VSLKFFEAEPK	24.2 33.3
208	Tb927.6.4210	aldehyde dehydrogenase, putative	1.00	254	15	5	4	15.6	AKHADQLVTGMTNVDFGNLYLCSLPGGK Oxidation (M12)- Carbamidomethyl (C24) ASTTDRPQVK EINWRSPTQVTPR SAAQTLTPVLELGGKDPVAVCDDADLEHVPIIMR Carbamidomethyl (C22) SAAQTLTPVLELGGKDPVAVCDDADLEHVPIIMR Carbamidomethyl (C22)- Oxidation (M35)	50.8 31.4 38.1 54.0 46.0	1.00	215	9	5	4	11.4	ASTTDRPQVK EINWRSPTQVTPR LTLTLGKR SAAQTLTPVLELGGKDPVAVCDDADLEHVPIIMR Carbamidomethyl (C22) SAAQTLTPVLELGGKDPVAVCDDADLEHVPIIMR Carbamidomethyl (C22)- Oxidation (M35)	35.4 32.2 43.7 58.3 16.6
209	Tb927.6.3150	Hydin flagellar component	1.00	218	19	8	8	3.2	ALLSVYSPFLYKEDKGNLFLPLPSGEGR ALGNVITLSPVSGTVR GAVPVASPLVEASR GRLLPESFAVSRPVK KAAVAKPTAEVAPPPADTIQMLPTVGSSTVTR Oxidation (M23) KVVGAWEAPVYR VVVVGPCCSK Carbamidomethyl (C9) VVVVGPCCSKTGTQK Carbamidomethyl (C9)	8.7 36.0 24.5 6.4 24.9 30.9 26.7 20.2	0.00	0	0	0	0	0.0		
210	Tb927.10.7090	alternative oxidase	0.75	40	2	2	2	7.3	RLQNSVNPVVLK TRTFGSEGAK	30.2 9.7	1.00	262	17	8	5	15.5	LQNSVNPVVLK LRPTNDREAVR LSFLETVPVPLR NATFRLNVR NATFRLNVR Deamidated (N1) NATFRLNVR Deamidated (N6) RLQNSVNPVVLK RLQNSVNPVVLK Deamidated (N4)	6.4 32.5 25.9 28.2 33.0 33.1 32.5 32.0
211	Tb927.11.1710	mitochondrial RNA binding protein 1_gBFP21, MRP1	1.00	210	14	5	5	30.6	AAEGGEKAAATSAEGGAR KVDPNLSPQFDADRR LLLSQYPLQVPR SISGTSRPH VAVDGLLLISQYPLQVPR Deamidated (Q15)	47.3 21.5 71.7 27.1 1.1	0.00	0	0	0	0	0.0		
212	Tb927.3.1810	hypothetical protein, conserved	1.00	63	5	2	2	15.6	LNTVLYQVNEVSPFTELGPVEEVRV SSSSPSPFEAPASSLPKDDINAR	37.5 10.8	1.00	178	5	4	2	17.5	LNTVLYQVNEVSPFTELGPVEEVRV LNTVLYQVNEVSPFTELGPVEEVRV Deamidated (Q6)- Deamidated (N10) STEGEEAVNLLLEEVQALLSRVPIGSLFR STEGEEAVNLLLEEVQALLSRVPIGSLFR Deamidated (N10)	35.0 34.2 44.0 49.5
213	Tb927.9.9450	hypothetical protein, conserved, zinc finger protein family member, putative	1.00	190	33	4	3	4.6	AAKRALQVQPR AKPNEAASPYQQQTRPTTSAR AKPNEAASPYQQQTRPTTSAR Deamidated (N4) RSEVQPTVEAKLPR	41.0 23.8 18.4 45.7	0.77	64	5	3	3	4.3	AAKRALQVQPR AKPNEAASPYQQQTRPTTSAR RSEVQPTVEAK	27.5 17.2 12.8
214	Tb927.11.8160	dynein heavy chain, putative	1.00	120	10	5	4	1.5	AVNTVISAAGLNKR AVNTVISAAGLNKR Deamidated (N3) AVNTVISAAGLNKRNPNEDLELLLR LIAGLGGKVR TKSDPSVPIGDFDAERER	35.8 20.0 9.2 18.9 14.6	0.00	14	1	1	1	0.4	TWPLLDIPGGOANSWIR	13.8
215	Tb927.4.3590	translation elongation factor 1-beta, putative	1.00	124	8	4	4	31.4	DGLLWGDHKLVPVAFGK ITPPVAAPVAAPAAAPAAATPAK	6.0 22.4	0.75	121	7	3	3	28.0	DGLLWGDHKLVPVAFGK ITPPVAAPVAAPAAAPAAATPAK	28.7 17.5

Peptides

Protein ID	Protein Name	Accession	Length	Start	End	Modifications	Score	Identified	Protein Name	Accession	Length	Start	End	Modifications	Score	Identified		
216	Tb927.9.2450	electron transport protein SCO1/SCO2, putative	1.00	149	4	3	2	11.5	LFLGGVKKPSEEDVAFNDLLGGDNTNFR TAWGAPKTFPWAAPAAAPAAAPAAATRAKK	40.5 43.5	1.00	88	4	3	3	16.4	LFLGGVKKPSEEDVAFNDLLGGDNTNFR	55.1
217	Tb927.3.2440	serine/threonine protein kinase, putative	1.00	168	6	4	2	9.4	ILGLVGTQEEVESVAR ILGLVGTQEEVESVAR Deamidated (G8) VANVATMLDENVASVQKPSSEI Oxidation (M7)	64.8 18.4 58.6	1.00	88	4	3	3	16.4	EAGASDNDGQAANIK ILGLVGTQEEVESVAR VANVATMLDENVASVQKPSSEI Deamidated (C16)	5.1 42.9 35.7
218	Tb927.9.4190	fatty acyl CoA synthetase 1	1.00	131	7	4	4	9.6	LDLKKFKPFTVGVPR LGEVPSVGGLLKGEVGR QKFGPLAHCQPAIGENCSPYVR Carbamidomethyl (C10); Carbamidomethyl (C18) TLTDDTARRP	37.8 42.9 28.3 15.3	1.00	165	13	4	4	9.0	GDLEKFKPFTVGVPR LGEVPSVGGLLK TLTDDTARRP VVFGLPLGGYQLTETCCNGSQR Deamidated (G9); Carbamidomethyl (C17); Carbamidomethyl (C18)	35.5 31.5 19.5 49.3
219	Tb927.4.4070	mevalonate kinase, putative	1.00	167	7	4	4	17.3	ALNELYSNLSEEAIVNR HLNDSKDGLLVK LTVSCPELDAATCCR Carbamidomethyl (C5); Carbamidomethyl (C14); Carbamidomethyl (C15) YVVGPSGSK	66.1 45.8 11.0 31.2	1.00	203	9	4	3	16.4	ALNELYSNLSEEAIVNR ALNELYSNLSEEAIVNR Deamidated (N8) HLNDSKDGLLVK LGGVPSGSGGASASDVLSLR	50.9 43.1 37.7 33.6
220	Tb927.10.2630	adenylate kinase, putative	1.00	223	14	6	5	32.0	GLDDVTSPELQRPDRKEVVEK MKVFLGPRQCGKGTGSPFVAK Oxidation (M1); Carbamidomethyl (C11) SVMVDVGLVSDDDVFGVKEKQKPR Oxidation (M3) SVMVDVGLVSDDDVFGVKEKQKPR Oxidation (M3); Deamidated (Q24) VFLGPRGCGK Carbamidomethyl (C9) VFLGPRGCGKGTGSPFVAK Carbamidomethyl (C9)	23.2 22.9 45.1 50.3 20.2 21.8	0.00	0	0	0	0	0.0		
221	Tb927.5.500	hypothetical protein, conserved	1.00	239	12	5	5	7.1	ASLAECNAVESTREPSGVPAGPDEAEAAKR Carbamidomethyl (C6) NVTYSALDDEFRETNVQK RVMVSVSFDTLR VQLGTATPTDAEEGEEKVGPATLSPAPYEATR VQLGTATPTDAEEGEEKVGPATLSPAPYEATRAER	67.0 15.1 28.5 28.5 54.9	0.32	42	2	2	2	2.2	NVTYSALDDEFRETNVQK RVMVSVSFDTLR	18.6 23.6
222	Tb927.2.3800	mRNA processing protein, putative	1.00	171	4	3	2	11.6	AFQLLHSETATDVGIASIDPRLPGQSK NTVWGLWNEGNLFSLVPELAFLOEHR Carbamidomethyl (C28) NTVWGLWNEGNLFSLVPELAFLOEHR Deamidated (Q25); Carbamidomethyl (C28)	62.8 59.3 43.3	1.00	61	3	1	1	5.7	AFQLLHSETATDVGIASIDPRLPGQSK	46.2
223	Tb927.7.2170	hypothetical protein, conserved	1.00	177	12	5	5	2.6	ALFQQLVAR ALLOMCLR Oxidation (M5); Carbamidomethyl (C6) LVDQVDQR Carbamidomethyl (C7) NCVIEALESSSTR Carbamidomethyl (C2) RALFQQLVAR	49.7 28.9 15.5 14.0 41.7	0.00	0	0	0	0	0.0		
224	Tb927.8.1990	peroxidase	1.00	188	12	4	4	16.4	ALFVDDKGLR ALFVDDKGLRHVTINDLPVGR HVTINDLPVGR TATVREAPEFAGK	57.9 30.5 39.6 34.1	0.25	22	1	1	1	5.3	ALFVDDKGLR	21.5
225	Tb927.10.12840	mitochondrial carrier protein, putative; mitochondrial 2-oxoglutarate/malate carrier protein, putative	1.00	153	13	4	4	16.5	AALVGAQWVHDQVLSALR GPFRLGSLTLR LGGCPFR Carbamidomethyl (C3) YKSVTQIGR	26.5 28.2 30.2 29.9	1.00	233	23	4	3	16.5	AALVGAQWVHDQVLSALR AALVGAQWVHDQVLSALR Deamidated (G8) VIREGALVYVSPYFFR YKSVTQIGR	50.1 36.1 29.9 23.6
226	Tb927.7.2390	hypothetical protein, conserved	1.00	114	3	3	2	4.1	AALVTFDSISAPLTSNGSNIPR AALVTFDSISAPLTSNGSNIPR Deamidated (N17) LPPVSAALKTHPFMK Oxidation (M14)	49.3 46.5 17.7	0.00	5	1	1	1	1.6	LPPVSAALKTHPFMK Oxidation (M14)	4.7
227	Tb927.4.1330	DNA topoisomerase II, large subunit	1.00	262	30	5	5	7.9	AVATYFDKLLR ILPEDVVLNIGK ILPEDVVLNIGKEAPVAPAGHKWK VPTALTGSASSTK VPTALTGSASSTNK	59.6 28.3 24.0 48.1 39.9	1.00	101	6	3	3	4.2	AVATYFDKLLR VPTALTGSASSTK VPTALTGSASSTNK	51.2 23.4 17.1
228	Tb927.11.12230	heat shock protein Hsc70, ATPase subunit Hsc70, putative; ATP-dependent hsc70 ATPase subunit Hsc70, putative	1.00	99	2	2	2	5.4	LVDETQSAALR VTKRWANAGNGAR	61.3 38.0	0.77	32	1	1	1	3.6	KASILDSYVGGAEGRK	32.0
229	Tb927.8.3690	isocitrate dehydrogenase [NADP], mitochondrial precursor, putative	1.00	197	10	4	4	11.2	DASNDKYTEGAAEAQR NILGCTVREPIVVK NILGCTVREPIVVKR VVPQWSEPIVGR	38.7 49.0 50.2 29.1	0.00	10	1	1	1	3.0	VVPQWSEPIVGR	10.1
230	Tb927.11.15040	chaperonin HSP60, mitochondrial precursor, putative; heat shock protein 60	1.00	229	22	5	5	10.8	HEFENSFENLGNLVR ITKDGVTYAK KLLLLGVENLVK NVLLEMPVASFQ Oxidation (M6) SVSTGTNPMDLKR Oxidation (M9)	32.5 27.8 56.3 34.4 28.3	1.00	145	7	4	4	8.8	HEFENSFENLGNLVR ITKDGVTYAK KLLLLGVENLVK SVSTGTNPMDLKR Oxidation (M9)	28.7 30.3 67.0 12.8
231	Tb927.6.3050	aldehyde dehydrogenase family, putative	1.00	118	7	4	4	10.7	EKPLALYFSNNKR SLNLVEENTDEFCK Carbamidomethyl (C14) VAEIVMAAAK Oxidation (M8) VLNLSLKPASAEVAGVGR Deamidated (N3)	18.1 47.0 34.8 12.2	1.00	52	3	1	1	2.8	SLNLVEENTDEFCK Carbamidomethyl (C14)	46.7
232	Tb927.8.5120	cytochrome c	0.99	183	8	6	5	53.5	AAQCHTGTGGSSNGVGNLYGIVGR Deamidated (G3); Carbamidomethyl (C4) AAQCHTGTGGSSNGVGNLYGIVGR Carbamidomethyl (C4); Deamidated (N13) AAQCHTGTGGSSNGVGNLYGIVGR Deamidated (G3); Carbamidomethyl (C4) ADLWLETLD MSFAGLKKPQER Oxidation (M1) SGTVEGFTYSK	35.9 34.2 33.3 22.5 20.6 27.2	0.00	0	0	0	0	0.0		
233	Tb927.6.1500	alkyl-dihydroxyacetone phosphate synthase	1.00	145	12	5	5	12.9	HNVVPFGGGTNTGGVEPNPFETR IKPTPLTKEEAK LLSPSPSEKETPK LLSPSPSEKETPKATDAR CRNSMFDKMGKPSGALQHL Oxidation (M5); Oxidation (M6); Oxidation (M10)	23.7 20.5 21.1 20.8 26.6	0.86	53	3	2	2	6.7	HNVVPFGGGTNTGGVEPNPFETR IKPTPLTKEEAK	31.9 20.3
234	Tb927.2.5660	adenylate kinase, putative	1.00	113	5	3	2	18.1	GPLQIFAGVAGSQR GIPQIFAGVAGSQR Deamidated (G6) NAQQQAQVEEGVQVFLLDLPEDLSFR Carbamidomethyl (C11)	49.1 39.1 20.2	0.00	12	1	1	1	11.5	NAQQQAQVEEGVQVFLLDLPEDLSFR Carbamidomethyl (C11)	11.7
235	Tb927.10.5770	valosin-containing protein homolog; Transitional endoplasmic reticulum ATPase, putative	1.00	184	9	4	4	9.7	AAAPCVLFFDELDSVAR Carbamidomethyl (C5) KISPLAPVDLQDLAAATHGFGADLAGICQR Carbamidomethyl (C29) KYELFATSLQGR	42.5 34.4 57.1 37.1	1.00	53	4	1	1	2.2	AAAPCVLFFDELDSVAR Carbamidomethyl (C5)	40.2
236	Tb927.11.5290	mitochondrial carrier protein, putative	1.00	146	9	3	3	14.2	AFRANAAACFAAR Carbamidomethyl (C8) DKTKSTLNLGGM Carbamidomethyl (C11); Oxidation (M13) VQASPVPLTPVAFR	59.8 6.2 54.4	0.88	39	2	2	2	9.6	VQASPVPLTPVAFR VRQGTALSSGAR	33.5 5.7
237	Tb927.9.5690	60S acidic ribosomal protein, putative	1.00	114	6	3	3	58.4	MSVSWAAAPAGGAAAPAGGAAAGAAAPAK Oxidation (M1) SVNTLAEQWAK Deamidated (N3) YLAATALASLAKPAPTADDK	27.0 31.2 16.9	0.00	13	2	1	1	29.2	MSVSWAAAPAGGAAAPAGGAAAGAAAPAK Oxidation (M1)	10.9
238	Tb927.11.6140	40S ribosomal protein S19A, putative	1.00	124	6	2	2	16.9	NTGGKLVGFY TMMSVLANLR Oxidation (M2); Oxidation (M3)	53.9 52.3	0.00	0	0	0	0	0.0		

Peptides

239	Tb927.11.600	hypothetical protein, conserved	1.00	173	10	4	3	41.5	ATTPGQLEGVPAELQQLAEFTK QQAIDSKLMQGGVR Deamidated (G2); Oxidation (M10) QQAIDSKLMQGGVR Oxidation (M10) QQNVERQAQDLSKLMQGGVR Oxidation (M16)	25.7 44.2 28.9 45.0	0.00	4	1	1	1	21.7	ATTPGQLEGVPAELQQLAEFTK	4.3
240	Tb927.2.5800	sedoheptulose-1,7-bisphosphatase	1.00	240	19	5	5	20.8	AGVPCDVVGVETVAGACR Carbamidomethyl (C5); Carbamidomethyl (C18) AAAGLRNDGVTAAK KAGVPCDVVGVETVAGACR Carbamidomethyl (C5); Carbamidomethyl (C19) LFEAPRAMELHLKAGGGR Oxidation (M8); Carbamidomethyl (C14) VYSMEGTPHALGACR Oxidation (M4); Carbamidomethyl (C14)	46.3 45.7 36.7 26.4 37.4	1.00	165	7	4	4	19.3	AGVPCDVVGVETVAGACR Carbamidomethyl (C5); Carbamidomethyl (C18) AAAGLRNDGVTAAK GNLTSDSLITDLR VYSMEGTPHALGACR Oxidation (M4); Carbamidomethyl (C14)	54.3 33.7 43.5 13.3
241	Tb927.4.2060	hypothetical protein, conserved	1.00	203	11	4	4	5.5	DKRLGELNDQLFALR KQSLVNLGNISR Deamidated (N8) LLLGNESLQGR VAWAGNPGTR	12.9 60.8 38.3 58.6	1.00	197	8	5	5	8.6	DKRLGELNDQLFALR GNSQHLGQALLKEDIAELEELKQLAEER KQSLVNLGNISR Deamidated (N8) LLLGNESLQGR Deamidated (G4) VAWAGNPGTR	32.4 29.7 36.5 35.3 45.5
242	Tb927.10.8780	hypothetical protein, conserved	1.00	114	6	3	2	2.1	QNTLVPVLVHALDNLPLSGFDLFSKXVPR Deamidated (N2) QNTLVPVLVHALDNLPLSGFDLFSKXVPR Deamidated (G1); Deamidated (N2) WVGQVTHIEPFSK Carbamidomethyl (C4)	35.0 41.5 17.0	0.00	0	0	0	0	0.0		
243	Tb927.10.15750	hypothetical protein, conserved	1.00	184	13	4	3	2.4	LFEGLMLDLARDEQGR LFEGLMLDLARDEQGR Oxidation (M6) VALESTAVETTSR VEVATWDEQQLR	23.5 38.7 69.1 25.5	0.23	22	1	1	1	0.6	QNTTEEKKEAK Deamidated (N2)	21.8
244	Tb927.9.4500	heat shock protein, putative, HSP70-like protein	1.00	91	5	2	2	3.7	AQFEAEACELFNEAVR Carbamidomethyl (C7) SGLNDVESLLHYK	63.8 11.2	0.99	56	3	2	2	4.1	FPQSGICGSLAGLVSK Carbamidomethyl (C7) SGLNDVESLLHYK	44.2 8.2
245	Tb927.9.4680	ATP-dependent DEAD box helicase, putative	1.00	102	11	3	3	10.9	GGDIAAQSQTGK GYSHGFEKPSIQGR LQSGTVAWGTGPR	34.3 41.4 9.3	0.99	80	8	3	2	7.4	GYSHGFEKPSIQGR GYSHGFEKPSIQGR Deamidated (G15) LQSGTVAWGTGPR	30.2 34.8 6.1
246	Tb927.4.870	dynein heavy chain, putative	1.00	153	13	4	4	2.1	FVAEDELFLKGLGDLFPGLDTPAQQENLNR LLPTSSLLFEVGDLYASPATYSR QLAACDDEQDLTAGLR Carbamidomethyl (C5) SITELKSFAPFASVAVVVR	25.5 40.1 47.1 18.4	0.97	42	2	1	1	0.5	LLPTSSLLFEVGDLYASPATYSR	35.5
247	Tb927.10.5780	adenylate kinase, putative	1.00	199	14	5	5	27.4	GILLDGPR GLHLLFGAPGQSK Carbamidomethyl (C12) GLHLLFGAPGQSKGTASERLVR Carbamidomethyl (C12) IYNLKSDFSPQEMGR Oxidation (M14) SWATKVDLELR	7.2 56.4 29.9 29.5 40.8	0.00	10	1	1	1	7.4	IYNLKSDFSPQEMGR Oxidation (M14)	9.9
248	Tb927.10.13180	hypothetical protein, conserved	1.00	127	6	4	4	4.4	GAICAQLSK Carbamidomethyl (C4) IYSELVEREPAAHVVR SISWITTSIAPR VHNVMKDAVAAAR Oxidation (M5)	17.5 27.5 64.6 15.9	0.00	21	1	1	1	1.4	IYSELVEREPAAHVVR	21.2
249	Tb927.11.14780	phosphomannose isomerase, putative	1.00	128	10	4	4	16.6	LKLDGQVGHYAWGKEAAESYAK Carbamidomethyl (C6) WQDVPTLLR YGTQDLGR YRAPEGSEVELQHYSPREFQDFSLYR	33.4 30.7 29.2 18.4	0.91	58	3	2	2	12.5	LKLDGQVGHYAWGKEAAESYAK Carbamidomethyl (C6) YRAPEGSEVELQHYSPREFQDFSLYR	23.8 25.0
250	Tb927.2.2940	hypothetical protein, conserved	1.00	119	9	2	2	16.1	ISEGAALFLPHADLQCGSPVSLLR Carbamidomethyl (C19) LGLLLVQLGAAKENQIFGR	25.5 53.0	1.00	148	9	4	2	16.1	ISEGAALFLPHADLQCGSPVSLLR Carbamidomethyl (C19) LGLLLVQLGAAKENQIFGR LGLLLVQLGAAKENQIFGR Deamidated (N14) LGLLLVQLGAAKENQIFGR Deamidated (G7)	30.9 56.8 41.0 3.2
251	Tb927.10.10360	microtubule-associated protein, putative	0.89	170	43	4	4	1.2	DVLRREEEVTGPR HVDPSHFR STTAESYAPIDPAAYK STTAESYAPIDPAAYK	26.2 21.6 36.6 31.1	1.00	163	17	4	4	1.9	DVLRREEEVTGPR HVDPSHFLTTHAYKPIDPSEYR HVDPSHFR STTAESYAPIDPAAYK	38.4 41.9 19.2 30.8
252	Tb927.4.1360	hypothetical protein, conserved	1.00	190	15	5	5	27.3	QIPRGGVVPVFPQGNMGPLPHFGAR Oxidation (M18) LVLVPSRM Oxidation (M9) NDDGSSILHLGGALTNWR NKEGTELLYSSK VLAGPQFEWK	20.1 28.1 49.6 41.7 12.6	0.00	0	0	0	0	0.0		
253	Tb927.11.15150	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative	1.00	98	8	3	3	10.7	AGLETVKGTVAPMEEAR Oxidation (M13); Oxidation (M14) KAGLETVKGTVAPMEEAR Oxidation (M14); Oxidation (M15) MLAVFPEGAR Oxidation (M1)	24.5 8.8 45.0	0.00	7	1	1	1	7.0	KAGLETVKGTVAPMEEAR Oxidation (M14); Oxidation (M15)	7.5
254	Tb927.10.8200	hypothetical protein, conserved	0.78	50	4	2	2	9.3	CAGLPFCHTFQIPR Carbamidomethyl (C1); Carbamidomethyl (C8) VIDSNKLSVK	23.4 19.2	1.00	195	5	4	3	20.8	CAGLPFCHTFQIPR Carbamidomethyl (C1); Carbamidomethyl (C8) EAGHSEVSDTLEDFATAPQK SFLTQLNDPQGVTHEMLR SFLTQLNDPQGVTHEMLR Deamidated (N8)	25.8 74.6 59.7 29.9
255	Tb927.7.4900	5'-3' exonuclease XRNA, putative, exonuclease 1, putative	1.00	188	11	4	4	5.9	ACGAAPFATGTVYR Carbamidomethyl (C2) SIEEFIESCGISQSVLAAQDAPFREHYR Carbamidomethyl (C9) SVTTTAAFGSGTFSVPLR VFKVPVSIHVLVDYASSR Deamidated (G3)	40.2 47.9 30.3 27.8	1.00	111	3	3	3	3.2	ACGAAPFATGTVYR Carbamidomethyl (C2) SVTTTAAFGSGTFSVPLR TLAAVETVQDR	11.1 19.1 80.7
256	Tb927.9.5960	succinate dehydrogenase, putative	1.00	221	17	5	5	33.5	AAAPKPTVFTAK AAAPKPTVFTAKDNSK PMAAPLPEWAK TAFHVYTORGFATPTVYGR VGPLEDKASKY	31.9 29.5 44.3 29.4 45.5	0.83	32	1	1	1	7.5	VGPLEDKASKY	32.2
257	Tb927.11.9400	hypothetical protein, conserved	1.00	142	7	4	2	5.3	LAQLLISGDKLEELTVGROELDELGGTLK Carbamidomethyl (C8) LAQLLISGDKLEELTVGROELDELGGTLK Carbamidomethyl (C8); Deamidated (N8) LAQLLISGDKLEELTVGROELDELGGTLK Deamidated (G3); Deamidated (N9); Carbamidomethyl (C8) VLAIQDGSNSR	46.5 20.2 41.3 24.7	1.00	170	5	3	1	3.8	LAQLLISGDKLEELTVGROELDELGGTLK Carbamidomethyl (C8) LAQLLISGDKLEELTVGROELDELGGTLK Carbamidomethyl (C8); Deamidated (N9) LAQLLISGDKLEELTVGROELDELGGTLK Carbamidomethyl (C8); Deamidated (G21); Deamidated (N9)	68.4 47.3 38.2
258	Tb927.7.210	proline dehydrogenase	0.79	32	2	1	1	3.1	TVVSEAVLALDPTPVQK	31.4	1.00	232	13	6	5	16.4	RKTVSEAVLALDPTPVQK IIDKLPK LASSQKTEDEINAVLQVLPDNEGKTYNYK LASSQKTEDEINAVLQVLPDNEGKTYNYK Deamidated (G17); Deamidated (N22) RAEAFGPFLTYNTLVK YVPYGPVKEVHLYGR	42.1 32.3 29.4 30.8 18.1 31.1
259	Tb927.11.8870	mitochondrial DEAD box protein, KRE11	1.00	109	10	3	2	6.0	GLDFPDVTCVNLIAPK Carbamidomethyl (C9) IYVLAFTRELVDQTA IYVLAFTRELVDQTA Deamidated (G12)	10.4 27.3 38.6	0.00	14	1	1	1	3.1	GLDFPDVTCVNLIAPK Carbamidomethyl (C9)	14.1
260	Tb927.11.1980	hypothetical protein, conserved, zinc finger protein family member, putative	1.00	66	4	2	2	7.7	LVYDVTDEPLTGEDADPPSNWHEQKPK TQAPASINPFR	31.6 23.3	1.00	115	4	2	2	9.1	LVYDVTDEPLTGEDADPPSNWHEQKPK NPFEELEEGNKDAVK	34.5 63.8
261	Tb927.4.4910	3,2-trans-enoil-CoA isomerase, mitochondrial precursor, putative	1.00	117	9	4	4	12.8	FLSVPOQSR KLNEMTKLGIITPRVWVAVYVLSGR LITSRIGITVLSR LGIITPRVWVAVYVLSGR	30.7 31.0 23.2 13.4	0.87	35	4	1	1	5.0	LGIITPRVWVAVYVLSGR	14.2
262	Tb927.10.16150	ATP-dependent zinc metallopeptidase, putative, metallo-peptidase, Clan MA(E) Family M41	0.62	80	1	1	1	3.0	GCLLTGQRTGKTLAK Carbamidomethyl (C2)	80.5	1.00	99	4	2	2	3.1	KVAPSVVFLDEIDAVGTR	24.4

Peptides

263	Tb927.11.8050	hypothetical protein, conserved	1.00	91	4	2	2	8.8	TPEFNTQSVAPVIEAVERDYAALTSSER TVQPEEGGFVGPLLK	29.0 41.2	1.00	158	8	5	3	12.2	VAPSVFLDEIDAVGTR AAASVLGVHEDEQDFAK TPEFNTQSVAPVIEAVERDYAALTSSER TPEFNTQSVAPVIEAVERDYAALTSSER Deamidated (N5) TPEFNTQSVAPVIEAVERDYAALTSSER Deamidated (C8) TVQPEEGGFVGPLLK	51.7 16.8 41.1 44.1 31.3 11.6
264	Tb927.10.2950	hypothetical protein, conserved	1.00	103	4	2	2	1.5	IGKSNVETTAAGTAAGSR VAGLIGQR	62.7 23.1	0.00	7	2	1	1	1.0	IGKSNVETTAAGTAAGSR	7.0
265	Tb927.8.1550	parafagellar rod component, putative	1.00	186	11	5	5	10.3	DMAAEELLAQQQYFSR LSSTVIGDQR RPVATTVPHSGVLSKPLPPVEALR SVHVDRLQTLQR TVGINHEEAFLEK	3.2 80.2 30.8 12.3 33.5	1.00	60	4	2	2	5.3	RGEVEPLGHVSYNR RPVATTVPHSGVLSKPLPPVEALR	14.4 36.5
266	Tb927.5.4420	nucleolar RNA helicase II, putative, nucleolar RNA helicase Gu, putative	1.00	135	9	3	3	7.6	GLDLPMVDLVCQAPPTDIDAFHR Oxidation (M6)- Carbamidomethyl (C13) GSATVQLGQR Oxidation (M7) SLPHTVFCSLR Carbamidomethyl (C8)	32.1 39.1 34.8	0.59	29	1	1	1	2.5	IKFEVLPAPTRREELK	28.8
267	Tb927.10.770	hypothetical protein, conserved	1.00	202	8	4	3	5.2	INLGPHEELFAELSSIR INLGPHEELFAELSSIR Deamidated (N2) ISSGAAQPTIDELKK ISSGAAQPTIDELKINLGPHEELFAELSSIR	58.8 57.9 40.8 18.6	1.00	117	5	2	1	2.9	INLGPHEELFAELSSIR INLGPHEELFAELSSIR Deamidated (N2)	60.1 45.0
268	Tb927.11.3360	hypothetical protein, conserved	1.00	99	3	2	2	1.8	AATVLSQAVQALTR AATVLSQAVQALTRK Deamidated (Q6)	65.1 19.2	1.00	60	2	2	2	1.8	AATVLSQAVQALTR AATVLSQAVQALTRK Deamidated (Q6)	54.8 5.7
269	Tb927.6.4980	40S ribosomal protein S14	1.00	226	19	6	6	29.2	AGMKIGREDVTPPTDSTR Oxidation (M3) ATGGVTKSPGQGAALR IGRIEDVTPPTDSTR IGRIEDVTPPTDSTR MRATGGVTKSPGQGAALR Oxidation (M1) SPGPGGAALR	33.8 51.8 34.5 15.4 25.5 20.5	0.00	4	1	1	1	14.6	MRATGGVTKSPGQGAALR Oxidation (M1)	3.6
270	Tb927.10.10280	microtubule-associated protein, putative	1.00	209	51	5	5	2.2	DVLRREEEATGPR DVLREEEIVTGR HVDPSHR STTAESVAPIDPAAVK STTAESVAPIDPAAVK	21.3 26.2 21.6 36.6 31.1	0.67	112	13	3	3	1.6	DVLRREEEIVTGR HVDPSHR STTAESVAPIDPAAVK	38.4 19.2 30.8
271	Tb927.3.1840	3-oxo-5-alpha-steroid 4-dehydrogenase, putative	1.00	186	12	5	5	29.9	ALTEGGVKDSEVYKDLGPOVGYR MKVTVSGSSSEVELPSNAGLTDLKK Oxidation (M1) NKKMLPFL Oxidation (M5) NKYKTSVY SGGDKNDKSAVTLDAK	32.7 23.6 25.6 33.9 48.1	0.00	18	1	1	1	9.1	MKVTVSGSSSEVELPSNAGLTDLKK Oxidation (M1)	18.0
272	Tb927.11.4450	hypothetical protein, conserved	1.00	114	5	3	3	43.6	AISDAWAEILKQGLDVK LSGGKPEVTSALGK SKDFDTYAEQQKR	34.0 11.1 42.5	0.00	0	0	0	0	0.0		
273	Tb927.7.3370	hypothetical protein, conserved	1.00	102	7	4	3	8.7	ATRDEAFNVDLWLSHQHOR ITELTTEIERLNEGEELVKGSSVLTQLQQR ITELTTEIERLNEGEELVKGSSVLTQLQQR Deamidated (N12) LNEGEELVKGSSVLTQLQQR	9.4 39.7 36.4 10.0	0.00	0	0	0	0	0.0		
274	Tb927.8.4400	hypothetical protein, conserved	1.00	189	19	5	3	7.9	ILAEVQHTDLAEQVSLYKPEVVPR ILAEVQHTDLAEQVSLYKPEVVPR Deamidated (Q15) ILAEVQHTDLAEQVSLYKPEVVPR Deamidated (Q7) TKIENVTLQLLGAK TRLPSAAAGR	30.0 16.3 42.3 35.9 23.3	1.00	64	2	1	1	4.0	ILAEVQHTDLAEQVSLYKPEVVPR	56.6
275	Tb927.11.10760	kinesin-like protein, putative	1.00	144	4	4	4	9.6	AEKEFESVHOKEGTR FTDELAAPKR ILAFUNASPEER VYSLYGNVGLLEGGLPR	35.5 71.7 8.5 28.0	0.97	62	3	2	2	4.1	FTDELAAPKR TLTLDATNEFLPR	25.6 32.0
276	Tb927.10.9780	ATP-dependent DEAD(H) RNA helicase, putative, ATP-dependent RNA helicase, putative	1.00	87	6	2	2	7.1	FTHTPTVQEEVPSVLSQNVGDR TLFAFAPILQHLVNLVNEVTGDPGKIGNEETANAAK	35.2 26.2	0.69	30	1	1	1	4.1	ELALQISEAMQQLVHAPVGVGCVGMAPEKQQR Carbamidomethyl (C24)	30.0
277	Tb927.11.16510	hypothetical protein, conserved	1.00	170	15	4	4	29.5	APPKASLPAR HHYAGPSPGSEK HHYAGPSPGSEKLTTE WASDKYAEEMVLLSR Oxidation (M10)	27.0 41.5 38.7 33.6	0.00	0	0	0	0	0.0		
278	Tb927.11.17000	hypothetical protein, conserved, leucine-rich repeat protein (LRP), putative	1.00	134	11	4	3	4.9	EVPVTEEFVDTQVR IVQVPHGDDGETTR IVQVPHGDDGETTR Deamidated (Q3) LVPDDESRNLTGVPVR	50.4 29.0 11.2 20.1	1.00	108	6	2	2	3.1	EVPVTEEFVDTQVR IVQVPHGDDGETTR	44.1 33.7
279	Tb927.9.15360	40S ribosomal protein S6, putative	1.00	156	9	3	2	9.6	MKLNIAVPR Oxidation (M1) NGTVQGFVADEVLR NGTVQGFVADEVLR Deamidated (N1)	41.0 41.8 44.1	0.00	0	0	0	0	0.0		
280	Tb927.10.170	pseudouridine synthase, Clf5p	1.00	136	11	4	4	9.6	RVLPCVYLLTNYKR Carbamidomethyl (C6) RWGLGPVAVK VILGCEVLLTNYKR Carbamidomethyl (C5) VVWQDSANAVCYGAK Carbamidomethyl (C12)	37.5 37.7 27.7 10.2	0.81	30	1	1	1	3.5	RVLPCVYLLTNYKR Carbamidomethyl (C6)	30.4
281	Tb927.3.5570	syntaxin, putative	1.00	134	5	3	2	6.9	NAVGHLOQAR NAVGHLOQAR Deamidated (N1) SCDVFYKK Carbamidomethyl (C2)	44.1 51.1 31.2	1.00	77	2	2	1	3.9	NAVGHLOQAR NAVGHLOQAR Deamidated (N1)	30.3 46.3
282	Tb927.10.6630	ATP-dependent DEAD(H) RNA helicase HEL64, putative	1.00	177	10	4	4	10.6	AGAWGDAFTLTK EAQTPSVLKEIGLER IKPVWGNVSLVPGNWK LCLVATDVAAR Carbamidomethyl (C2)	20.5 32.0 29.2 65.3	1.00	127	9	3	3	8.6	AGAWGDAFTLTK EAQTPSVLKEIGLER IKPVWGNVSLVPGNWK	13.7 53.6 43.2
283	Tb927.8.2740	mitochondrial RNA binding protein	1.00	150	6	3	2	12.4	FLIFNVEQLEDPEVALR TLDRSPVSPITFLLSGEPMOHEGVK Oxidation (M19) TLDRSPVSPITFLLSGEPMOHEGVK Oxidation (M19)- Deamidated (Q20)	62.2 29.7 27.9	1.00	127	4	2	1	5.0	FLIFNVEQLEDPEVALR FLIFNVEQLEDPEVALR Deamidated (N5)	65.5 49.1
284	Tb927.10.2770	eukaryotic translation initiation factor 5, putative	1.00	197	13	4	4	10.7	SCRNPETQLSVER Carbamidomethyl (C2) YVQSEFGAQR YVYALATHFAK YVYALATHFAKNQAAALR	31.6 21.5 57.7 39.1	0.00	0	0	0	0	0.0		
285	Tb927.7.3980	immunodominant antigen, putative, tcd4 antigen-like	1.00	105	7	3	2	2.3	RSPAGAAKPSNVLAPTTGTK RSPAGAAKPSNVLAPTTGTK Deamidated (N12) RSPAGAAKPSNVLAPTTGTK	37.7 20.3 23.6	0.52	39	2	2	1	2.3	RSPAGAAKPSNVLAPTTGTK RSPAGAAKPSNVLAPTTGTK Deamidated (N12)	24.8 14.3
286	Tb927.3.3590	U3 small nucleolar ribonucleoprotein protein MPP10, putative	1.00	83	3	2	2	5.1	FVKELEGAR LAQHLDALSNFHYTRKPVQEDLSAR	35.2 43.1	0.00	3	1	1	1	3.7	LAQHLDALSNFHYTRKPVQEDLSAR	3.3
287	Tb927.11.11540	DNA topoisomerase II, putative	1.00	155	13	4	4	3.4	FGSTCDLPSALDIOVLK Carbamidomethyl (C5)- Carbamidomethyl (C14)	18.6	0.94	36	2	1	1	0.8	LRVPLLSDAAR	32.5

Peptides

316	Tb927.6.3890	replication factor C, subunit 2, putative	1.00	121	8	4	3	3	14.1	SLDEVKSGEEVVOALR SLDEVKSGEEVVOALR Deamidated (D8) SSSIALDHWVSGDLR TTALAWAHELFGPDYK	21.0 43.5 27.5 14.1	1.00	75	3	2	2	2	9.8	SLDEVKSGEEVVOALR Deamidated (Q8) TTALAWAHELFGPDYK	19.1 46.2
317	Tb927.11.16480	enoyl-CoA hydratase/isomerase family protein, putative	1.00	88	6	2	2	2	8.0	ATDPNEVFSTDYVQAR THACGDFPEGVR Carbamidomethyl (C4)	50.7 22.4	0.73	55	5	3	3	3	16.0	ATDPNEVFSTDYVQAR TAISMEKLSPTSK Oxidation (M6) VFTLKDSTVEDVMGSLAADGGEFAR	22.2 1.8 23.3
318	Tb927.7.2190	hypothetical protein, conserved	1.00	56	4	1	1	1	8.3	RVEVGTGGDGYDPDYVSEHLR	50.1	0.76	30	2	1	1	1	5.3	VRGGSTPTFHAGSR	21.1
319	Tb927.7.3430	cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative	0.99	111	7	4	4	4	34.2	ALHTMPGKVLDLSPRY Oxidation (M5) HWITGQSSQSKLELTERALSGER Carbamidomethyl (C6) VRFQFVGGDILLKDKGR VPGFVGGDILLKDKGRNSVVFGRFPDFEFEGK	35.4 16.5 27.3 22.4	0.00	0	0	0	0	0	0.0		
320	Tb927.11.3770	hypothetical protein, conserved	1.00	122	4	3	2	2	12.2	LLNTNVRAPPLISAANGDTEVTEQ LLNTNVRAPPLISAANGDTEVTEQ Deamidated (N16) TVLLVRRR	54.8 39.0 19.4	0.00	0	0	0	0	0	0.0		
321	Tb927.7.3330	hypothetical protein, conserved	1.00	122	14	3	3	3	1.1	CAVVVDAAACR Carbamidomethyl (C1)- Carbamidomethyl (C11) VVEFDVTHPSHPSIAQR VVRDCVSNVTFPSGR Carbamidomethyl (C5)	28.3 34.1 26.9	0.90	41	2	2	2	2	1.0	ELDVQNEKLHEMEQLAEAELEER Deamidated (Q5) VVRDCVSNVTFPSGR Carbamidomethyl (C5)	34.5 6.7
322	Tb927.11.7900	mitochondrial RNA binding protein, RBP16, RNA binding protein of 16 kDa	1.00	142	7	5	3	3	51.8	GFGFIEDADKQHFVHSALOTETGGFR GFGFIEDADKQHFVHSALOTETGGFR Deamidated (Q13) GRNNGQGGQHSFSDDF GRNNGQGGQHSFSDDF Deamidated (N3) TRAENVYSPGAKLPSGRPPREGAGR	43.3 30.5 16.0 4.8 29.7	0.00	0	0	0	0	0	0.0		
323	Tb927.11.10240	hslVU complex proteolytic subunit, putative, hslVU complex proteolytic subunit, threonine peptidase, Clan T(1), family T18	1.00	153	6	2	2	2	12.0	AVELAKEWR ALIDVDGYDEKAR	53.4 68.9	0.00	0	0	0	0	0	0.0		
324	Tb927.6.2640	importin alpha subunit, putative	0.00	22	1	1	1	1	5.1	DIALQHNAPAFVNLISDPDQLSIVR	21.8	1.00	51	5	1	1	1	5.1	DIALQHNAPAFVNLISDPDQLSIVR	43.0
325	Tb927.10.4000	methylglutaconyl-CoA hydratase, mitochondrial precursor, putative	1.00	156	12	3	3	3	24.9	APLVMGSLNQLQLTADVPAERAGR Oxidation (M5) FGLPETGLAHPGAGTYR LGLVTELVKGGASEALAWAGR	36.0 23.7 42.0	1.00	96	8	2	2	2	15.2	FGLPETGLAHPGAGTYR LGLVTELVKGGASEALAWAGR	12.9 56.6
326	Tb927.4.1540	hypothetical protein, conserved	1.00	114	8	2	2	2	4.7	IAPGATVSTLSQLSSETEKER IAPGATVSTLSQLSSETEKERAK	74.7 18.9	1.00	80	6	1	1	1	4.3	IAPGATVSTLSQLSSETEKER	65.3
327	Tb927.6.4630	kinetoplastid-specific phospho-protein phosphatase, putative	0.00	7	1	1	1	1	5.2	NLLGDYSAVDPGSLAGSGVSGR	6.6	1.00	210	9	3	3	3	17.8	EAQSVGGDVIELGNHIER ITGLVDDRQHWIGDFFVOLGDFDVPDSDIVK NLLGDYSAVDPGSLAGSGVSGR	39.6 44.8 56.1
328	Tb927.11.5600	hypothetical protein, conserved	1.00	162	7	3	2	2	16.8	LLQEEASQVVR LLQEEASQVVR Deamidated (Q3) SNTEGGRKLLQEEASQVVR	30.1 40.1 40.0	0.00	9	1	1	1	1	16.8	SNTEGGRKLLQEEASQVVR	9.3
329	Tb927.10.5990	hypothetical protein, conserved	1.00	134	6	2	2	2	3.2	SIVLALQTLQEK SIVLALQTLQEKIR	44.3 72.2	1.00	56	1	1	1	1	2.7	SIVLALQTLQEK	55.6
330	Tb927.2.3610	hypothetical protein, conserved	1.00	185	10	3	3	3	10.4	KLAALTDAGIQK LAALTDAGIQK SAKGAALTDAGIQK	43.4 32.0 62.9	0.00	0	0	0	0	0	0.0		
331	Tb927.11.10150	hypothetical protein, conserved	0.97	41	1	1	1	1	1.4	LFNLTETAGTSVEPWAR	40.7	1.00	80	2	2	2	2	4.4	LFNLTETAGTSVEPWAR TLTIEQLPQSTHNTSDSHITPYTLGSAVGQR	21.1 59.3
332	Tb927.7.640	hypothetical protein, conserved	1.00	130	15	2	2	2	5.1	VKEEVAQLAEK VKEEVAQLAEKVSASR	22.8 61.3	1.00	115	5	3	2	2	5.1	VKEEVAQLAEK VKEEVAQLAEKVSASR Deamidated (Q7)	16.3 49.6 37.9
333	Tb927.7.5940	Protein Associated with Differentiation	1.00	68	4	1	1	1	6.1	IKAEADNGTNAENVCAEPTCCDNADACLEKAADSK Carbamidomethyl (C15)- Carbamidomethyl (C20)- Carbamidomethyl (C27)	57.3	0.00	0	0	0	0	0	0.0		
334	Tb927.10.7380	hypothetical protein, conserved	1.00	172	7	3	2	2	15.8	ILPAPVEGTPAHTAVEQLLAEVQCEALGASVADPVTATR Carbamidomethyl (C27) ILPAPVEGTPAHTAVEQLLAEVQCEALGASVADPVTATR Deamidated (G16)- Carbamidomethyl (C27) VLSNERPLQNVYR	63.8 56.5 25.6	1.00	100	7	1	1	1	12.0	ILPAPVEGTPAHTAVEQLLAEVQCEALGASVADPVTATR Carbamidomethyl (C27)	60.4
335	Tb927.11.4680	hypothetical protein, conserved	1.00	122	6	3	3	3	17.1	KLGTVAAPR KPPVYELPPGDATIDEFELPAFEGTFDNEGSMVGR Oxidation (M34) QMTAGTLLER Oxidation (M2)	41.8 25.8 42.1	0.00	0	0	0	0	0	0.0		
336	Tb927.9.2320	hypothetical protein, conserved	1.00	89	3	2	2	2	10.9	NVQSANLNQPKYEAPLQGDITVER TACLPGAVPQR Carbamidomethyl (C3)	65.0 18.1	1.00	142	3	3	1	7.6	NVQSANLNQPKYEAPLQGDITVER NVQSANLNQPKYEAPLQGDITVER Deamidated (N1) NVQSANLNQPKYEAPLQGDITVER Deamidated (Q4)	46.8 39.8 55.4	
337	Tb927.10.11520	hypothetical protein, conserved	1.00	134	5	3	3	3	27.4	ATQAFQSVGALR ATQAFQSVGALRQSNLHR Oxidation (M13) CLDTEELYTLR Carbamidomethyl (C1)	53.6 31.9 29.1	0.00	0	0	0	0	0	0.0		
338	Tb927.10.3040	hypothetical protein, conserved	1.00	171	18	4	4	4	20.0	APESIFKY AVLDEVREAVVDGK AVLDEVREAVVDGKK RAPESIFKY	40.9 36.7 26.2 34.8	0.00	0	0	0	0	0	0.0		
339	Tb927.10.14700	hypothetical protein, conserved	1.00	117	6	3	3	3	9.9	GGSSPSFLEMR SLRDSSTINR VROPDLGEHPLR	61.0 15.5 26.9	0.00	0	0	0	0	0	0.0		
340	Tb927.7.680	chaperone protein DNAj, putative	1.00	121	5	2	2	2	4.8	FAAQNVLDVAITEGRR SGQPOSEVADALDELSGR	33.2 68.5	1.00	117	5	2	2	2	4.8	FAAQNVLDVAITEGRR SGQPOSEVADALDELSGR	13.9 60.2
341	Tb927.5.4330	dihydroipamide branched chain transacylase, putative	1.00	112	8	4	4	4	12.3	QLVVPVROVDQK SIVELVHEVNEVTLGR VLATPAVREFAR VLREDVLSYAGK	26.4 11.3 35.3 24.9	0.99	50	3	2	2	2	6.6	SIVELVHEVNEVTLGR VLATPAVREFAR	27.7 2.1
342	Tb927.8.610	hypothetical protein, conserved	1.00	127	6	3	2	2	3.2	NEAQELRLR VAAAGVTYVKLQELQAARNEAQELR VAAAGVTYVKLQELQAARNEAQELR Deamidated (Q12)	29.7 44.7 30.7	0.00	13	1	1	1	3.0	VAAAGVTYVKLQELQAARNEAQELR	12.9	
343	Tb927.4.4700	hypothetical protein, conserved	0.96	63	3	2	2	2	7.4	HTFPAIGQPR LLAEAAAAAR	35.9 25.1	0.00	0	0	0	0	0	0.0		
344	Tb927.10.12590	hypothetical protein, conserved	1.00	131	6	2	2	2	4.6	ATTGPLGTSFAFAEDLQR TTALVAGQKTEELAAAMAENHAIR Oxidation (M17)	57.0 40.6	0.00	0	0	0	0	0	0.0		
345	Tb927.7.3500	glutathione-S-transferase:glutaredoxin, putative	1.00	67	4	2	2	2	12.5	FHGSKPOLADLTHVLSQVSR LYNEIEATTKPWLER	39.4 22.7	1.00	135	12	3	2	12.5	FHGSKPOLADLTHVLSQVSR LYNEIEATTKPWLER LYNEIEATTKPWLER Deamidated (N5)	20.0 47.0 30.4	
346	Tb927.11.900	isocitrate dehydrogenase, putative	1.00	131	14	3	3	3	13.3	HAFGDOYSADVAVKEPTEMR Oxidation (M22) LVTWKKPVIGR TILGGTVFREPICSNVR Carbamidomethyl (C14)	31.0 18.1 47.0	0.00	12	1	1	1	4.6	TILGGTVFREPICSNVR Carbamidomethyl (C14)	11.7	

347	Tb927.5.2790	mitochondrial DNA polymerase beta-PAK	1.00	143	8	5	4	9.1	AKSPAPFPALDADDAVAVPTPK QAAAAAPVSPRPVQAGTR QAAAAAPVSPRPVQAGTR Deamidated (G1) SPWVGTIEDAVDEKDGAAVGRNAK SPWVGTIEDAVDEKDGAAVGRNAK	16.8 23.3 34.6 23.7 28.4	0.00	0	0	0	0	0.0		
348	Tb927.5.4470	hypothetical protein, conserved	1.00	121	6	3	2	3.6	AVGVYGGGCGTGYLK Carbamidomethyl (C9) LVLANAASQVEVQR LVLANAASQVEVQR Deamidated (N6)	14.4 34.3 39.2	0.99	48	2	2	2	3.0	LVLANAASQVEVQR VLNERVENLTK	46.6 1.8
349	Tb927.3.5430	hypothetical protein, conserved	1.00	142	9	3	3	15.9	LKPLVYGSQR SKSLKLAIPRR SVSLGRREGQIAFVGEIEKLR	43.6 35.3 46.1	0.00	0	0	0	0	0.0		
350	Tb927.10.4080	hypothetical protein, conserved	1.00	103	20	2	2	1.7	AAPPAPELQK AAPPAPELQKAAAPPAPELQK	29.4 52.2	0.41	35	2	1	1	0.9	AAPPAPELQK	29.6
351	Tb927.10.7810	hypothetical protein, conserved	1.00	95	6	2	2	6.5	LASDAAAEADTRFGSK YVDDSEVFNPNKADRPANVYQPLAAMK	33.5 40.1	0.00	0	0	0	0	0.0		
352	Tb927.11.10680	hypothetical protein, conserved	0.78	30	1	1	1	1.7	TLVDCRR Carbamidomethyl (C5)	29.6	0.99	73	6	2	2	10.1	AVLEELLALHPEYAPLR AFVLPFDSPTPPSPDLDSAAR	21.3 24.9
353	Tb927.10.5840	translation elongation factor 1-beta, putative	0.00	17	2	2	2	17.9	DGLLWGDHKLVPVAFGK LSAQPVYSGFTPSKEDAR	6.0 11.1	1.00	135	5	4	4	44.8	AAAGDDDDILFGEATEEELAALEAK DGLLWGDHKLVPVAFGK LSAQPVYSGFTPSKEDAR SSLFDKPVWDVTVLQDLAQLKHAUKR	35.7 28.7 35.8 32.9
354	Tb927.3.750	hypothetical protein, conserved	1.00	149	6	3	2	10.2	VSPKGGTIDSPNDGIVTK VSPKGGTIDSPNDGIVTKVDKIDNPNNGGAYAR VSPKGGTIDSPNDGIVTKVDKIDNPNNGGAYAR Deamidated (D5)	43.1 44.2 48.5	0.00	0	0	0	0	0.0		
355	Tb927.8.1270	hypothetical protein, conserved	1.00	90	6	3	3	7.5	AREVIVETSPLQK CGALPFEKAEVIR TAWATAWAAGKSDGR	23.2 12.9 40.4	0.97	39	2	1	1	2.9	TAWATAWAAGKSDGR	27.9
356	Tb927.4.1920	GPI transamidase, putative	1.00	70	3	2	1	2.6	LVNPTPEVPTSGNSNTK LVNPTPEVPTSGNSNTK Deamidated (N16)	41.6 5.5	0.97	66	2	2	2	6.7	LVNPTPEVPTSGNSNTK Deamidated (N16) SGNDNQALGVETPTAQHFISAYGDR	31.7 33.8
357	Tb927.7.3050	hypothetical protein, conserved	0.00	18	1	1	1	2.3	VKDATAEAGVTHPAADFTPFCAFLR Carbamidomethyl (C23)	18.4	1.00	66	2	1	1	2.3	VKDATAEAGVTHPAADFTPFCAFLR Carbamidomethyl (C23)	43.3
358	Tb927.11.880	cyclophilin a,cyclophilin type peptidyl-prolyl cis-trans isomerase	1.00	70	3	2	2	18.6	ALCTGEGKFGYAGSFHR Carbamidomethyl (C3) SIYGEKFPDESFAK	31.2 24.9	0.00	0	0	0	0	0.0		
359	Tb927.1.2100	calpain-like cysteine peptidase, putative,cysteine peptidase, Clan CA, family C2, putative	1.00	87	6	3	3	4.0	AVPLTEEYAR HTQESVNDLTKPR VVGNSADAYHPLSKWTFYQAR	23.7 31.2 1.5	0.00	0	0	0	0	0.0		
360	Tb927.5.800	casein kinase I, isoform 2	1.00	89	4	3	3	15.4	IHDTLQEGRADQQQQQQQQQR ISDRKQTTSETLCLR Carbamidomethyl (C14) SFPAAEFAVLYNTR	35.1 12.5 39.5	0.00	0	0	0	0	0.0		
361	Tb927.10.8590	flagellum transition zone component	1.00	129	6	2	1	2.7	ESAGSASSENKLSDNVAVPPRRVSVVPAVPR ESAGSASSENKLSDNVAVPPRRVSVVPAVPR Deamidated (N17)	62.6 34.9	0.00	0	0	0	0	0.0		
362	Tb927.10.7230	hypothetical protein, conserved	0.99	60	5	2	2	1.5	ALCHVDHPTDLSEWAEPLVR Carbamidomethyl (C3) ALLVFKPHANTPETR	23.9 15.2	0.00	11	1	1	1	0.9	ALCHVDHPTDLSEWAEPLVR Carbamidomethyl (C3); Deamidated (N18)	10.9
363	Tb927.11.9530	14-3-3-1 protein	1.00	91	3	2	2	16.0	LLRDLNLVTDQPVN QAYDEAVTELETLDDEAYRESNLIVR	29.0 57.5	1.00	128	5	3	2	16.0	LLRDLNLVTDQPVN QAYDEAVTELETLDDEAYRESNLIVR QAYDEAVTELETLDDEAYRESNLIVR Deamidated (G1)	29.2 44.6 29.8
364	Tb927.4.3450	hypothetical protein, conserved	1.00	78	4	1	1	21.1	VLDETYTEWTEELDQAVTDAITR	71.4	0.00	5	1	1	1	21.1	VLDETYTEWTEELDQAVTDAITR	4.8
365	Tb927.11.2430	dynein heavy chain, putative	1.00	56	3	1	1	0.4	SGPVVIESQLLNVQR	51.0	0.00	35	2	2	2	1.3	LLSDLANSGGDLLENTALIGALNDVKVQASSITALEK Deamidated (N7) SGPVVIESQLLNVQR	31.8 3.5
366	Tb927.10.1060	hypothetical protein, conserved	0.99	63	5	2	2	11.5	DVAFGTLRELSSGNQR TVLSVSPDERHGSVFPQ	14.1 31.2	0.95	66	4	2	2	9.5	DVAFGTLRELSSGNQR RMINEDPQER Oxidation (M2)	32.2 26.2
367	Tb927.11.1620	hypothetical protein, conserved	1.00	110	3	2	2	16.7	KFELLPTSAEAEAR NLSHVVTIDSIVETR	40.8 64.1	0.00	0	0	0	0	0.0		
368	Tb927.1.2670	flagellar protein PF16	1.00	89	5	2	2	3.5	ALKNIQR VLPDIAKR	44.2 28.5	1.00	49	1	1	1	2.3	SAAAWSLQIGR	48.7
369	Tb927.11.9570	hypothetical protein, conserved	1.00	135	4	3	2	14.1	GLRDEQVWASGLPQASDVALAR LSALQVLLLESNLCEIR Carbamidomethyl (C14) LSALQVLLLESNLCEIR Deamidated (D5); Carbamidomethyl (C14)	27.4 56.3 45.5	0.44	66	2	2	1	5.7	LSALQVLLLESNLCEIR Deamidated (N12); Carbamidomethyl (C14) LSALQVLLLESNLCEIR Deamidated (D5); Carbamidomethyl (C14)	44.6 21.8
370	Tb927.10.14680	intraflagellar transport protein IFT52, putative	0.40	25	1	1	1	2.3	VAVEQEEELPRDFTK	25.4	1.00	73	5	2	2	6.3	LNQIDAEPTDITYHHPDIALSER VAVEQEEELPRDFTK	31.1 17.4
371	Tb927.11.15550	NADH-cytochrome b5 reductase, putative	1.00	63	4	1	1	6.5	FKPLALGEVNLAEVAFRR	46.8	1.00	114	7	1	1	6.5	FKPLALGEVNLAEVAFRR	72.2
372	Tb927.3.4650	C-8 sterol isomerase, putative	0.99	68	7	3	2	6.8	MPQPCFALEYAR Oxidation (M1); Carbamidomethyl (C5) CYKAMPQPCFALEYAR Deamidated (G1); Oxidation (M4); Carbamidomethyl (C9) CYKAMPQPCFALEYAR Oxidation (M4); Carbamidomethyl (C8)	33.0 34.3 16.0	0.00	0	0	0	0	0.0		
373	Tb927.7.2710	NADH-cytochrome b5 reductase, putative	1.00	88	4	1	1	6.3	IGLASDGTGIAPVYQVAR	72.5	1.00	93	3	1	1	6.3	IGLASDGTGIAPVYQVAR	78.4
374	Tb927.5.1710	ribonucleoprotein p18, mitochondrial precursor, putative	1.00	119	9	2	2	21.8	KYDLFGYEVDTNAPWIEK TEGKEHPGHLSSQAGLFDVKKVE	60.6 27.5	0.00	0	0	0	0	0.0		
375	Tb927.3.5370	hypothetical protein, conserved	1.00	87	5	2	2	12.5	RVPPEPSTPTEALTPESVKK YFVITKPEVDDDDPLAK	19.7 57.8	0.26	24	1	1	1	6.7	RVPPEPSTPTEALTPESVKK	24.1
376	Tb927.4.470	snoRNP protein GAR1, putative	0.99	59	5	2	2	17.0	FNAPFYGANKAK TVPGQAESISAGDTIYISPTQISPLR	44.3 12.4	0.96	64	7	2	2	17.0	FNAPFYGANKAK TVPGQAESISAGDTIYISPTQISPLR	26.2 28.3
377	Tb927.11.2610	hypothetical protein, conserved	0.97	85	5	3	3	8.2	AGGDENLPHLDELHLER IRGELPLAGTR VORLEGFAGR	22.1 26.5 30.9	1.00	82	3	2	2	6.1	AGGDENLPHLDELHLER IRGELPLAGTR	32.4 43.2
378	Tb927.11.4880	hypothetical protein, conserved	1.00	138	8	4	4	17.9	AHNFVYDDRN GVFVQATKVK KNEGVTASR NYVANAVENLALPTK	34.8 26.4 31.0 30.5	0.00	22	1	1	1	6.2	NYVANAVENLALPTK	21.8
379	Tb927.3.2310	flagellar component,PAICRGA	1.00	66	4	2	2	6.7	ARGDAIDFGQR FAYKGTVQR	42.2 13.9	0.00	0	0	0	0	0.0		
380	Tb927.11.5420	hypothetical protein, conserved	0.96	75	2	2	2	9.7	ELEKMAKNR Oxidation (M5) NAAAALVDPALKDEEIDLETR	29.3 45.5	0.00	0	0	0	0	0.0		

Peptides

381	Tb927.9.6870	RNA-binding protein, putative	1.00	64	6	2	2	18.9	ACEFVETFGKEFR Carbamidomethyl (C2) RPPGFARTIAPSR	12.2 35.1	0.26	22	2	1	1	9.5	RPPGFARTIAPSR	20.3
382	Tb927.10.6220	5'-3' exonuclease XRND, putative, 5'-3' exonuclease 2, putative	1.00	112	5	3	3	7.2	DVQIVCPDAAAEKTHAGAEICNAAR Carbamidomethyl (C6) HPVQQLLAVLPR SSMKRPIEVAAKFIAGR Oxidation (M3)	9.7 57.3 39.8	1.00	58	2	1	1	1.5	HPVQQLLAVLPR	57.6
383	Tb927.7.1670	hypothetical protein, conserved	1.00	87	5	2	2	18.8	TKVQATQAVPLVLAAMGEHLR Oxidation (M17) TVTDGFSHADVVR	31.7 30.1	0.00	0	0	0	0	0.0		
384	Tb927.10.11760	pumilio/PUF RNA binding protein 6	0.99	81	8	3	2	2.7	WAHLNHAWEFAQDQEGSR WAHLNHAWEFAQDQEGSR Deamidated (O15) WAHLNHAWEFAQDQEGSRFDR	10.5 34.5 22.9	0.99	43	2	1	1	2.3	WAHLNHAWEFAQDQEGSR	34.8
385	Tb927.4.560	dynein heavy chain, putative	1.00	46	7	1	1	0.7	TEANTPLILTTTGADPSQELGAHAHQK	33.5	0.00	0	0	0	0	0.0		
386	Tb927.5.2850	radial spoke protein RSP2, putative	0.99	99	6	3	2	9.9	AWAETVLAQSPNPQVEYALYLLHLVQEEQNAIAATR AWAETVLAQSPNPQVEYALYLLHLVQEEQNAIAATR Deamidated (O9) GTLPSDDAMEKLVK	36.4 31.3 29.9	1.00	126	5	2	1	7.1	AWAETVLAQSPNPQVEYALYLLHLVQEEQNAIAATR AWAETVLAQSPNPQVEYALYLLHLVQEEQNAIAATR Deamidated (O9)	44.4 54.0
387	Tb927.5.2780	mitochondrial DNA polymerase beta	1.00	119	7	2	2	11.6	AAATLFDREGIFTEVDLEKADQQLTEQQR LKAQELTQIHGFGPR	40.8 54.5	1.00	49	4	1	1	7.6	AAATLFDREGIFTEVDLEKADQQLTEQQR	38.9
388	Tb927.10.9520	hypothetical protein, conserved	1.00	138	8	4	3	12.4	GQLGGESSSPFNLSAQLAGQKR NNAGSGTKGLGGESSSPFNLSAQLAGQKR NNAGSGTKGLGGESSSPFNLSAQLAGQKR Deamidated (N2) RSTTVPPVSLVPLPSDAAR	21.0 38.6 32.0 23.1	0.00	4	1	1	1	4.9	RSTTVPPVSLVPLPSDAAR	4.4
389	Tb927.11.16830	Rab-like 5, small G protein	0.84	54	3	2	2	17.8	ALETSLDYQSDNFKEAFDALVEQIASR STVYNFLAGTR	22.5 24.5	1.00	64	2	1	1	12.8	ALETSLDYQSDNFKEAFDALVEQIASR	50.0
390	Tb927.7.920	dynein heavy chain, putative	1.00	71	2	1	1	0.5	ILHLTSTSTGNDLNEPLVR	46.9	0.00	0	0	0	0	0.0		
391	Tb927.11.5180	hypothetical protein, conserved	1.00	90	9	2	2	8.4	CSAGCAVIEHAWR Carbamidomethyl (C1) LLRPIER	51.6 27.0	0.00	0	0	0	0	0.0		
392	Tb927.10.15250	parafagellar rod component, putative	1.00	52	2	1	1	2.7	LAELDQPEVHER	39.7	0.99	45	2	1	1	2.7	LAELDQPEVHER	41.3
393	Tb927.7.6660	chaperone protein DnaJ, putative	1.00	93	7	2	2	12.1	GSGVPVSGVPADESSR KPREEDVLKNSGR	52.0 22.2	0.00	0	0	0	0	0.0		
394	Tb927.3.3330	heat shock protein 20, putative	1.00	99	4	1	1	10.6	VLPLTGAAGSFSFSR	86.5	0.00	0	0	0	0	0.0		
395	Tb927.1.3950	D-alanine aminotransferase	1.00	60	4	1	1	3.4	VLVVNPGNPTGSVLR	57.7	0.00	0	0	0	0	0.0		
396	Tb927.8.4230	hypothetical protein, conserved	0.99	48	2	1	1	1.6	TIQAAVEEFVANKGR	30.0	0.00	0	0	0	0	0.0		
397	Tb927.8.7040	hypothetical protein, conserved	1.00	128	15	3	3	24.3	ATEARVEEEAEGTLELVNTLIR ATEARVEEEAEGTLELVNTLIRK AVGKDEEKEEYSPTEILDVLR	22.2 25.0 47.2	0.00	0	0	0	0	0.0		
398	Tb927.5.550	vacuolar ATP synthase, putative	1.00	97	4	1	1	7.1	LFPSPGSLVDHDDIAEAEVQLRER	69.5	1.00	83	12	1	1	7.1	LFPSPGSLVDHDDIAEAEVQLRER	53.0
399	Tb927.2.4110	mitochondrial processing peptidase alpha subunit, putative, metallo-peptidase, Clan ME, Family M16	1.00	109	7	2	2	4.9	TVLAATGVADHK TVLAATGVADHKSFAEVEKLLR	20.6 62.2	0.00	0	0	0	0	0.0		
400	Tb927.9.10580	3-demethylubiquinone-9 3-methyltransferase, putative	0.99	68	3	2	2	9.0	GVSAAEIKFSR VLRDITPOASLAVR	38.9 26.1	0.37	44	1	1	1	3.1	FPPADLSR	43.6
401	Tb927.11.3290	hypothetical protein, conserved	0.99	58	3	2	2	2.1	LLQLEDVKKTPR QQQATQDKVDVVEALAK Deamidated (O2) Deamidated (O3) Deamidated (O6)	38.5 12.6	0.71	31	1	1	1	1.2	QQQATQDKVDVVEALAK Deamidated (O2) Deamidated (O3) Deamidated (O6)	30.9
402	Tb927.11.4000	hypothetical protein, conserved	1.00	98	5	2	2	11.2	ASSTTLAQWNAWVSYPASSLPDRAGATLPHAPR LLPLVALAQLDADVFLITGPKVPSEVK	68.5 17.0	0.00	0	0	0	0	0.0		
403	Tb927.4.590	hypothetical protein, conserved	1.00	55	7	2	1	1.6	FVGVVEGAALHPK FVGVVEGAALHPK Deamidated (O4)	34.2 7.7	1.00	102	10	3	2	5.6	FVGVVEGAALHPK FVGVVEGAALHPK Deamidated (O4) GYLASSSPSVPLVTLVQLFPIHATGEDALR	34.1 13.7 26.2
404	Tb927.4.600	hypothetical protein, conserved	0.99	56	5	2	2	7.6	FVLFEGDRGGISLQAQGPWVTR SGGISLQAQGPWVTR	17.0 13.8	0.00	14	1	1	1	7.6	FVLFEGDRGGISLQAQGPWVTR	14.3
405	Tb927.1.1580	cytochrome c oxidase assembly factor, putative, electron transport protein SCO12, putative	1.00	78	9	2	1	4.7	GLTGSKEIQAAAR GLTGSKEIQAAAR Deamidated (O11)	47.6 4.1	0.99	65	2	2	1	4.7	GLTGSKEIQAAAR GLTGSKEIQAAAR Deamidated (O11)	41.9 23.3
406	Tb927.6.2560	hypothetical protein, conserved	0.97	38	2	1	1	12.6	LITLDEKINPTVSASFPLVVTAAIPSSLSIQLAPR	27.1	1.00	65	5	1	1	12.6	LITLDEKINPTVSASFPLVVTAAIPSSLSIQLAPR	52.9
407	Tb927.11.4980	ATP-dependent DEAD/H RNA helicase, putative, ATP-dependent RNA helicase, putative	0.86	33	2	1	1	4.8	NAQNPVALLLPSELOKQTEVANALTR Carbamidomethyl (C17)	26.8	1.00	55	1	1	1	2.7	LTAAPLVSTAASLQK	54.6
408	Tb927.11.13510	hypothetical protein, conserved	0.98	63	5	2	2	21.7	SRIPTEYR VVGQTPNSVEWDRPNPDPFFFTETTAVER	24.8 34.8	0.00	0	0	0	0	0.0		
409	Tb927.11.7780	hypothetical protein, conserved	0.99	87	7	3	3	9.6	LAENFSATSDPR LSAERHGSTLVR SGGHAELAEIEENLCR Carbamidomethyl (C15)	24.9 25.2 22.6	0.00	0	0	0	0	0.0		
410	Tb927.11.7290	pantothenate kinase subunit, putative	1.00	124	8	3	3	3.1	EGEVAGEDNLSNWAK LLNDGPRSTVGLTGFPAK TLPIAMMVTGTR Oxidation (M7)	32.0 48.8 32.0	0.00	0	0	0	0	0.0		
411	Tb927.9.9860	hypothetical protein, conserved	1.00	93	3	2	2	3.1	ISPLVGGSTVSGQR RVLANEIRR Deamidated (N5)	55.7 31.9	0.00	0	0	0	0	0.0		
412	Tb927.11.2510	hypothetical protein, conserved	0.98	81	5	2	2	2.4	RVVGVQNVQVER SRNGLVHADALNEGAWQR Deamidated (N3)	21.8 49.1	0.00	0	0	0	0	0.0		
413	Tb927.7.3630	TPR-repeat-containing chaperone protein DnaJ, putative	0.93	36	57	1	1	5.5	YNMILKILLVGAAGAECSGVADDDTTK Deamidated (N2) Oxidation (M3) Carbamidomethyl (C19)	20.5	1.00	83	92	2	2	12.3	AECALCGDNGAAEELKYVQREPNLDLWALGAR Carbamidomethyl (C3) Carbamidomethyl (C7) YNMILKILLVGAAGAECSGVADDDTTK Deamidated (N2) Oxidation (M3) Carbamidomethyl (C19)	49.5 20.9
414	Tb927.3.3450	ADP-ribosylation factor-like protein 3A, putative	1.00	70	7	2	1	9.0	ILILGLDNAGKTSILR ILILGLDNAGKTSILR Deamidated (N8)	42.9 11.0	0.00	0	0	0	0	0.0		
415	Tb927.10.16000	hypothetical protein, conserved	1.00	51	7	1	1	5.0	ILANLATQGGKDVSSLTIPIK	34.8	0.00	21	2	1	1	5.0	ILANLATQGGKDVSSLTIPIK	13.6
416	Tb927.11.10140	hypothetical protein, conserved	1.00	79	4	1	1	6.7	AGSEPESTFVDPANLR	62.6	0.93	37	1	1	1	6.7	AGSEPESTFVDPANLR	36.9
417	Tb927.11.3710	hypothetical protein, conserved	1.00	120	7	3	3	7.6	SLIILDEAKDRDQALVAK VLSSTSQVGR	15.3 38.9 49.3	0.80	31	2	1	1	3.7	SULLDEAKDRDQALVAK	28.7
418	Tb927.10.11300	parafagellar rod component, putative	0.99	79	7	2	1	19.8	ILGRIKEQTEKLNVDVNPATTTSR ILGRIKEQTEKLNVDVNPATTTSR Deamidated (N14) Deamidated (N19)	32.5 36.2	0.00	0	0	0	0	0.0		
419	Tb927.7.4550	60S ribosomal protein-l1e	1.00	134	5	2	2	21.9	GLGGGGGGAAWAFVMAAAGAPSGASATEAEPKTEK GLGGGGGGAAWAFVMAAAGAPSGASATEAEPKTEK	58.8 52.2	0.00	0	0	0	0	0.0		

Peptides

420	Tb927.11.5820	hypothetical protein, conserved	1.00	80	3	2	1	3.3	IAQLGSGDR IAQLGSGDR Deamidated (Q3)	57.7 19.5	0.00	0	0	0	0	0.0		
421	Tb927.10.3500	RNA-binding protein, putative	1.00	67	6	2	2	3.1	SLYGSTVPIFTR VLPADVFPVPIK	11.3 34.8	1.00	51	5	1	1	1.6	VLPADVFPVPIK	37.9
422	Tb927.10.9810	hypothetical protein, conserved	0.99	65	6	2	2	8.6	AVENDPANLEFACR Carbamidomethyl (C13) DHWCDRLDLLQR Carbamidomethyl (C4)	31.7 16.4	0.00	0	0	0	0	0.0		
423	Tb927.10.16170	hypothetical protein, conserved	1.00	103	3	3	3	5.2	KGQLHVNALSR LLLRRPAEESPEVSPQREENG RLLLRPAEESPEVSPQREENG	16.4 47.6 38.7	0.00	0	0	0	0	0.0		
424	Tb927.9.2050	hypothetical protein, conserved	1.00	112	12	3	3	9.2	TTPGAASILDPAVYDPLDGGDVRRLQSGK Carbamidomethyl (C20) TTPGAASILDPAVYDPLDGGDVRRLQSGKWK Carbamidomethyl (C20) VGGPHTAVAGFVAPLVNTYRPR	24.0 30.3 23.5	0.00	12	1	1	1	3.8	VGGPHTAVAGFVAPLVNTYRPR	11.9
425	Tb927.11.6440	hypothetical protein, conserved	1.00	64	7	1	1	2.5	VVFEAPASHQR	41.0	0.97	39	1	1	1	2.5	VVFEAPASHQR	39.4
426	Tb927.5.1520	heat shock protein Hsp70, ATPase subunit Hsp70, putative	0.98	49	2	1	1	3.0	ALAGVSDGFREHLR	46.0	0.90	55	3	2	2	8.8	ALAGVSDGFREHLR KQDFWALQGEELDKVDTEDVSAELR	21.8 25.4
427	Tb927.4.4690	hypothetical protein, conserved	1.00	74	4	2	2	10.4	GIVDRQEQMQLR Oxidation (M10) GIVNRPLNQTNDILR	26.3 40.2	1.00	96	2	2	1	5.8	GIVNRPLNQTNDILR GIVNRPLNQTNDILR Deamidated (N11)	48.4 47.4
428	Tb927.10.13720	RNA-binding protein, putative	1.00	75	15	2	2	8.2	GYYAGGLGRAPYTRPFWNPQPEETLK GYYAGGLGRAPYTRPFWNPQPEETLKL	29.1 20.9	0.94	85	6	3	2	8.2	GYYAGGLGRAPYTRPFWNPQPEETLK GYYAGGLGRAPYTRPFWNPQPEETLK Deamidated (Q22) GYYAGGLGRAPYTRPFWNPQPEETLKL	24.6 29.9 19.9
429	Tb927.3.2660	hypothetical protein, conserved	0.97	75	4	2	2	5.9	ASSYKQQLAR GTPPIYVLAEGVYSSNAPGIYRPSFVHSLR	30.9 25.7	1.00	75	1	1	1	4.4	GTPPIYVLAEGVYSSNAPGIYRPSFVHSLR	75.4
430	Tb927.7.320	hypothetical protein, conserved	1.00	87	3	2	2	13.9	ATYSFPLKQPR SWGTEGINAPLQK	31.1 39.6	0.00	0	0	0	0	0.0		
431	Tb927.9.9060	p21 antigen protein, putative	1.00	53	1	1	1	12.6	NQLLOTDDKTPAALDTLKLER	52.8	0.00	0	0	0	0	0.0		
432	Tb927.11.10860	hypothetical protein, conserved	0.99	41	2	1	1	0.7	AQLQGIESALAVLGTTEAEMPLASAGR Carbamidomethyl (C3); Oxidation (M21)	34.0	0.00	0	0	0	0	0.0		
433	Tb927.11.14090	hypothetical protein, conserved	0.97	45	4	1	1	2.5	KVPFAGTVSAK	30.7	0.00	17	1	1	1	2.5	KVPFAGTVSAK	16.7
434	Tb927.9.8740	RNA-binding protein	1.00	114	4	2	1	4.9	GGFDAQKQQLQIGR GGFDAQKQQLQIGR Deamidated (Q11)	53.5 48.6	0.00	0	0	0	0	0.0		
435	Tb927.7.7500	thymine-7-hydroxylase, putative	0.00	14	2	1	1	5.0	TWGFHVGHPSFER	11.4	1.00	122	2	2	2	15.0	ESSBHPVCGEDTDYDITLLYQDSVGLQLR Carbamidomethyl (Q9) TWGFHVGHPSFER	79.8 41.9
436	Tb927.9.8160	chaperone protein DNAJ, putative	1.00	75	10	1	1	4.7	LALILHPDKTGGTTEGFTR	37.8	1.00	63	11	1	1	4.7	LALILHPDKTGGTTEGFTR	38.6
437	Tb927.2.190	retrotransposon hot spot protein 1 (RH51), putative	0.99	102	9	3	3	5.6	GRLDAAVAAK NDPQSVLVLQEP RRDENVPPFAAAGPPQIR	26.1 17.9 31.5	0.00	0	0	0	0	0.0		
438	Tb927.11.10780	hypothetical protein, conserved	1.00	63	3	1	1	5.4	MGPSEYDELENVER Oxidation (M1)	40.9	0.00	0	0	0	0	0.0		
439	Tb927.2.2970	mitochondrial carrier protein, putative	0.00	22	2	1	1	7.7	ATAAGIAGVMEGLFHPFDIAKR Oxidation (M10)	11.4	0.99	44	1	1	1	5.5	VQWKDPGSTLGLVFR	44.4
440	Tb927.10.4090	serine palmitoyltransferase, putative	1.00	85	6	1	1	4.7	GAVVANKAVTEAESCEAYNKQGSVR Carbamidomethyl (C15)	68.7	0.00	0	0	0	0	0.0		
441	Tb04.2AM18.150	hypothetical protein, conserved	0.99	57	5	2	2	29.6	DLRDAEHLAVLPIEDGEDHAHTESAFSQLPK VLVPAITPAKDSAR	11.8 33.8	0.00	0	0	0	0	0.0		
442	Tb927.6.4990	ATP synthase, epsilon chain, putative	1.00	58	6	1	1	7.7	ISVIEVAALKHH	36.5	0.00	0	0	0	0	0.0		
443	Tb927.10.9830	hypothetical protein, conserved	1.00	50	3	1	1	7.6	ANIEGQVAVK	46.9	0.00	0	0	0	0	0.0		
444	Tb927.10.10140	paraflagellar rod component, putative	0.00	23	3	2	1	8.8	AAESEHAAALQFLADEDFRTEKNNR AAESEHAAALQFLADEDFRTEKNNR Deamidated (N28)	8.0 11.6	0.99	113	3	3	1	8.8	AAESEHAAALQFLADEDFRTEKNNR AAESEHAAALQFLADEDFRTEKNNR Deamidated (N28) AAESEHAAALQFLADEDFRTEKNNR Deamidated (Q12)	33.0 45.4 34.4
445	Tb927.6.1570	2-hydroxy-3-oxopropionate reductase, putative	1.00	64	3	1	1	3.3	AGFLVFNRR	47.9	0.00	0	0	0	0	0.0		
446	Tb927.8.6240	hypothetical protein, conserved	0.70	37	6	2	2	7.1	IYRPAESFKPR YKQELPK	18.2 8.1	0.96	38	3	1	1	4.1	IYRPAESFKPR	27.3
447	Tb927.11.1670	cysteine desulfurase	0.99	44	1	1	1	3.2	ALGDAENHTSIR	44.3	0.00	6	1	1	1	3.2	ALGDAENHTSIR	6.5
448	Tb927.10.1100	60S ribosomal protein L9, putative	1.00	62	2	1	1	5.3	FLDGYVQTK	55.0	0.00	0	0	0	0	0.0		
449	Tb927.3.2880	hypothetical protein, conserved	1.00	65	5	2	2	15.4	WTGCSVEQLEELSR Carbamidomethyl (C4) WTGCSVEQLEELSRVY Carbamidomethyl (C4)	11.6 36.8	0.00	12	1	1	1	15.4	WTGCSVEQLEELSRVY Carbamidomethyl (C4)	12.1
450	Tb927.11.14700	hypothetical protein, conserved	0.94	37	1	1	1	2.6	SAAQVTPVIVHSGR	36.9	0.96	35	1	1	1	5.1	SGQVSTVAADGESTVPDHPGLRPTGLWK	35.5
451	Tb927.10.7350	hypothetical protein, conserved	0.98	55	5	2	2	2.2	TITGDMGAGLLGR Oxidation (M6) VLSAAAPALHSGVADHNTMSLPLKK Oxidation (M20)	30.3 11.6	0.00	0	0	0	0	0.0		
452	Tb927.2.270	retrotransposon hot spot protein (RH5, pseudogene), putative; retrotransposon hot spot protein 3 (RH53), transmembrane	1.00	71	4	2	2	6.0	EFVQPIWATLDR RRDENVPPFAAAGPPQIR	26.9 42.2	0.00	0	0	0	0	0.0		
453	Tb927.10.11390	60S ribosomal protein L6, putative	0.00	13	1	1	1	9.4	VDTGVDSATTFEKKR	12.7	1.00	68	2	2	2	21.9	GVTSDEKRAQLQNAIDALQIAKK VDTGVDSATTFEKKR	11.0 57.1
454	Tb927.8.3290	DNA polymerase zeta catalytic subunit, putative	0.98	65	8	2	1	0.8	GGSGLLGNQARGAK Deamidated (Q9) GGSGLLGNQARGAK Deamidated (Q9); Deamidated (N8)	24.3 23.8	0.00	15	1	1	1	0.8	GGSGLLGNQARGAK Deamidated (Q9)	14.8
455	Tb927.10.15360	hypothetical protein, conserved	1.00	58	4	1	1	0.7	NAVNNAPIQGR	50.9	0.00	0	0	0	0	0.0		
456	Tb927.10.8640	COP-coated vesicle membrane protein env25 precursor, putative; ER-golgi transport protein env25 precursor, putative	0.00	16	1	1	1	11.1	FLQNTQPCFVEEVEDTRFLTGYYTR Carbamidomethyl (C10)	15.7	1.00	103	4	2	1	11.1	FLQNTQPCFVEEVEDTRFLTGYYTR Carbamidomethyl (C10) FLQNTQPCFVEEVEDTRFLTGYYTR Deamidated (N5); Carbamidomethyl (C10)	43.4 35.1
457	Tb927.10.4040	3-keto-dihydroxyphosphine reductase	1.00	62	3	1	1	5.8	FQVSPDQVYTPGFEGENIR	53.6	0.96	56	2	2	1	5.8	FQVSPDQVYTPGFEGENIR FQVSPDQVYTPGFEGENIR Deamidated (N18)	15.8 40.4
458	Tb927.10.4130	NADH-ubiquinone oxidoreductase complex I subunit, putative; NDJFA6/13 subunit, putative	1.00	53	2	1	1	3.4	FAVDKDLGR	41.6	0.00	0	0	0	0	0.0		
459	Tb927.3.1410	cytochrome oxidase subunit VII	1.00	71	11	2	2	11.5	PRPFGWAWATTLAEYR PRPFGWAWATTLAEYRAR	19.8 21.0	0.00	0	0	0	0	0.0		
460	Tb927.11.4690	hypothetical protein, conserved	1.00	60	3	2	1	2.2	SNYDGTSLPWWAPGKPYPAALSELRLPQPR SNYDGTSLPWWAPGKPYPAALSELRLPQPR Deamidated (N2)	38.5 9.7	0.00	15	1	1	1	2.2	SNYDGTSLPWWAPGKPYPAALSELRLPQPR	14.7
461	Tb927.11.6230	pretranslocation protein, alpha subunit, putative; SEC01-like (pretranslocation process) protein, putative	1.00	100	4	2	1	3.3	MSPLAFLPEWATPLR MSPLAFLPEWATPLR Oxidation (M1)	40.6 44.1	0.37	24	1	1	1	3.3	MSPLAFLPEWATPLR	24.1
462	Tb927.8.2020	agmatinase, putative	1.00	56	3	1	1	4.5	LGPVALFGYAGMPR Oxidation (M13)	51.5	0.00	0	0	0	0	0.0		

463	Tb927.2.5270	dynein heavy chain, putative	1.00	47	3	1	1	0.6	STLLAQGGASAVNPDAEVEKDGRR	30.6	0.00	0	0	0	0	0.0		
464	Tb927.10.10010	60S acidic ribosomal protein, putative	1.00	99	7	2	2	9.3	RATVPLTK TGVATCPLLLR Carbamidomethyl (C7)	26.7 57.4	0.94	37	1	1	1	5.3	TGVATCPLLLR Carbamidomethyl (C7)	36.6
465	Tb927.4.3890	ATP-dependent RNA helicase, putative	1.00	68	5	2	2	3.0	LAALFPEKQVK SSAGRPAAETTSKPEVPKRR	18.7 32.0	0.00	0	0	0	0	0.0		
466	Tb927.11.10090	hypothetical protein, conserved	0.99	67	4	2	2	5.3	LHAPQIPAGR NRRGEGDAVR	34.4 29.2	0.00	0	0	0	0	0.0		
467	Tb927.4.3070	hypothetical protein, conserved	0.99	71	6	2	2	8.3	JATAAVIGMNR Oxidation (M6) WATLLPGDLGHTSTTEEDKAGQYVR	40.0 18.5	0.00	20	1	1	1	5.8	WATLLPGDLGHTSTTEEDKAGQYVR	19.9
468	Tb927.7.6350	NADH-ubiquinone oxidoreductase, mitochondrial, putative	0.99	46	1	1	1	4.4	SAIPLHLAQR	46.0	0.00	0	0	0	0	0.0		
469	Tb927.8.4930	hypothetical protein, conserved	1.00	63	4	1	1	5.3	VITALPSSHAPSGASR	45.4	0.98	43	2	1	1	5.3	VITALPSSHAPSGASR	38.8
470	Tb927.1.90	retrotransposon hot spot protein (RHS, pseudogene), putative	0.93	46	2	2	2	6.3	HVIGTFRGK RRIDENVPPPPAAAAAQPQIR VRDVLLEDALLQR	14.2 37.5 8.4	1.00	49	2	1	1	2.2	HVIGTFRGK VRDVLLEDALLQR	25.0 48.7
471	Tb927.9.6920	hypothetical protein, conserved	0.97	36	2	1	1	7.2	EGWKFFDPADPLGGAIVPEHALPKPR	36.2	0.00	8	1	1	1	7.5	REGVKFFDPADPLGGAIVPEHALPKPR	7.9
472	Tb927.6.4320	hypothetical protein, conserved	0.97	38	1	1	1	2.5	AAILENAASR	37.6	0.00	0	0	0	0	0.0		
473	Tb927.7.6260	hypothetical protein, conserved	0.00	14	1	1	1	4.4	AAYGLVWVANEIR	14.4	0.98	42	1	1	1	4.4	AAYGLVWVANEIR Deamidated (N10)	42.2
474	Tb927.11.4920	hypothetical protein, conserved	0.99	63	5	2	2	12.9	KAVTTADAPLPSCTFNTTVSR Carbamidomethyl (C13) SRFPQRPWWTSTK	15.9 34.6	0.00	0	0	0	0	0.0		
475	Tb927.11.15880	hypothetical protein, conserved	1.00	56	1	1	1	4.4	TFQPELLGQAVSVNPKLFLWGTGVSVAQQALR	56.4	0.00	0	0	0	0	0.0		
476	Tb927.10.510	hypothetical protein, conserved	0.99	54	5	2	2	11.4	DGGLPVTLEVPVQGR LTAEVVLRFVYTHSDAGILR	34.0 7.2	1.00	63	3	2	2	11.4	DGGLPVTLEVPVQGR LTAEVVLRFVYTHSDAGILR	46.1 36.6
477	Tb927.9.10520	hypothetical protein, conserved	0.98	64	6	2	2	9.9	ALAWESRNEVR TQYVQGFHQHLK	18.8 29.8	0.91	35	3	1	1	4.7	ALAWESRNEVR	29.4
478	Tb927.10.15710	mitochondrial carrier protein, putative	1.00	71	4	1	1	5.6	HAPLVDVVAGGLGSAAK	35.1	0.00	0	0	0	0	0.0		
479	Tb927.4.3840	nucleolar protein, putative	1.00	74	3	2	2	4.6	NTGVFANDSEPR TKSLNANLQR	50.2 21.4	0.00	0	0	0	0	0.0		
480	Tb927.11.13890	hypothetical protein, conserved	1.00	65	3	1	1	5.6	IAPOVTVETDVQSR	54.9	0.00	0	0	0	0	0.0		
481	Tb927.7.5790	protein disulfide isomerase, putative	1.00	50	2	1	1	7.4	GYPTELLFAR	30.8	0.00	0	0	0	0	0.0		
482	Tb927.7.7260	kinesin, putative	0.99	73	17	2	1	1.1	DALRLQLDPPQ Deamidated (G6) DALRLQLDPPQ Deamidated (G6)- Deamidated (G11)	30.0 25.6	0.92	56	9	2	1	1.1	DALRLQLDPPQ Deamidated (G6) DALRLQLDPPQ Deamidated (G6)- Deamidated (G11)	17.5 29.7
483	Tb927.4.1280	hypothetical protein, conserved	0.96	40	2	1	1	4.5	AIEATASETHPAAQLR	24.7	0.00	0	0	0	0	0.0		
484	Tb927.3.2080	hypothetical protein, conserved	0.99	67	5	2	2	5.8	AGRDPTLGL ELAERKGRDPTLGL	32.5 24.6	0.00	0	0	0	0	0.0		
485	Tb927.11.7520	hypothetical protein, conserved	0.99	46	2	1	1	3.3	EIDDTVLLQSR	33.2	0.00	0	0	0	0	0.0		
486	Tb927.5.3900	glutamine hydrolysing (not ammonia-dependent) carbonyl phosphate synthase, putative	0.97	39	2	1	1	0.5	ELVIDMVK Oxidation (M6)	32.0	0.00	0	0	0	0	0.0		
487	Tb927.11.13310	hypothetical protein, conserved	1.00	56	2	1	1	6.0	SVVNSGGGGAPASPTR	30.6	0.00	10	1	1	1	6.0	SVVNSGGGGAPASPTR	10.4
488	Tb927.7.7210	hypothetical protein, conserved	0.00	9	1	1	1	2.7	ACGPLTDELADLVDFWK Carbamidomethyl (C2)	8.7	1.00	84	4	1	1	2.7	ACGPLTDELADLVDFWK Carbamidomethyl (C2)	34.6
489	Tb927.11.16750	hypothetical protein, conserved	1.00	74	9	2	2	15.4	LGGQAMTPAQGTGVKMPGQSS Oxidation (M6)- Oxidation (M17) GGGAPLGVTDVNLK	26.2 22.7	0.00	17	1	1	1	6.0	GGGAPLGVTDVNLK	17.2
490	Tb927.10.830	adenylate kinase, putative	1.00	84	3	1	1	5.0	AVTADLVKTESR	67.9	0.00	0	0	0	0	0.0		
491	Tb927.7.6990	hypothetical protein, conserved	0.97	64	6	2	2	9.0	ELCEGRDLKAGER Carbamidomethyl (C3) KGPVAVHSLPVYK	28.4 27.7	0.00	0	0	0	0	0.0		
492	Tb927.11.5250	hypothetical protein, conserved	1.00	82	5	2	2	1.5	RQDVGWELLR	41.4	0.00	0	0	0	0	0.0		
493	Tb927.10.8980	hypothetical protein, conserved	0.97	39	5	1	1	7.1	TPLFVGNAAASR	28.8	0.00	0	0	0	0	0.0		
494	Tb927.11.12040	hypothetical protein, conserved	0.96	37	4	1	1	13.2	TGRLLMPDPLFNPPIHMANFR Oxidation (M6)- Oxidation (M17)	31.3	0.00	0	0	0	0	0.0		
495	Tb927.11.540	ABC transporter, putative	0.70	30	1	1	1	4.1	SPGILLDEATSDLDSEIVHEAVSR	30.0	1.00	80	4	1	1	4.1	SPGILLDEATSDLDSEIVHEAVSR	60.9
496	Tb927.11.6430	hypothetical protein, conserved	0.98	65	4	2	2	2.9	AVSPVGVYSSINGAGVSLPR LAPLSASTLRPAK	32.7 17.6	0.00	11	2	1	1	1.1	LAPLSASTLRPAK	9.1
497	Tb927.1.3450	hypothetical protein, conserved	1.00	79	2	1	1	1.6	ALVALQGLCNDAR Carbamidomethyl (C9)	73.9	0.00	0	0	0	0	0.0		
498	Tb927.8.6640	hypothetical protein, conserved	1.00	78	6	1	1	3.0	STAASTAQGLNPLTAAK	54.3	0.00	0	0	0	0	0.0		
499	Tb927.11.610	hypothetical protein, conserved	1.00	75	2	2	2	10.7	FLPGVGHPTYSCK Carbamidomethyl (C13) FSPESPHEVAPLPLPLTQRR	36.1 39.2	0.00	0	0	0	0	0.0		
500	Tb927.8.1870	Golgi lysosome glycoprotein 1	1.00	44	4	1	1	5.0	FVSDTEDCDASAAGVPELTALEPEDRFQPK Carbamidomethyl (C8)	37.9	0.00	9	1	1	1	5.0	FVSDTEDCDASAAGVPELTALEPEDRFQPK Carbamidomethyl (C8)	9.2
501	Tb927.8.6050	hypothetical protein, conserved	1.00	77	4	1	1	11.1	AVISPQEKPLTSSSSGALGGSGNEVKK	54.5	0.00	0	0	0	0	0.0		
502	Tb927.6.2870	hypothetical protein, conserved	0.99	67	3	2	1	2.8	GFNAEQTTDASR GFNAEQTTDASR Deamidated (N4)	18.6 34.0	0.97	41	3	1	1	2.8	GFNAEQTTDASR	29.2
503	Tb927.8.630	hypothetical protein, conserved	0.96	38	1	1	1	3.6	TGAEALFFALDPASNPGEELPLIGR	37.6	1.00	66	3	1	1	3.6	TGAEALFFALDPASNPGEELPLIGR	44.3
504	Tb927.7.4290	hypothetical protein, conserved	1.00	52	4	1	1	4.0	AAAQAAEAANKR	42.4	0.00	0	0	0	0	0.0		
505	Tb927.5.4040	hypothetical protein, conserved	0.80	29	4	1	1	2.3	RLVEPQLRPOATDALLAR	26.8	0.99	38	4	1	1	2.3	RLVEPQLRPOATDALLAR	20.4
506	Tb927.10.12960	ras-related protein rab-5 small GTPase, putative	1.00	76	2	1	1	8.7	LLLEHGLGANGSGPGLSGPR	40.5	1.00	72	2	1	1	8.7	LLLEHGLGANGSGPGLSGPR	55.7
507	Tb927.10.2950	malate dehydrogenase-related	1.00	69	7	1	1	6.2	AAPHAVGIASGPNVLSVPLAR	57.6	1.00	61	1	1	1	6.2	AAPHAVGIASGPNVLSVPLAR	60.8
508	Tb927.3.1820	hypothetical protein, conserved	0.29	24	1	1	1	7.8	ANPSDGLVYVAATPLAYOK	24.2	1.00	59	4	1	1	7.8	ANPSDGLVYVAATPLAYOK	32.6
509	Tb927.6.3670	parafagellar rod component, putative	1.00	50	3	1	1	0.6	AVPIAAHAFDPLPAPFLR	42.3	0.00	16	1	1	1	0.6	AVPIAAHAFDPLPAPFLR	15.7
510	Tb927.5.1680	hypothetical protein, conserved	1.00	72	9	1	1	1.3	AAAAAAAIVEESGIAGVEETLRR	43.0	0.00	0	0	0	0	0.0		
511	Tb927.8.4450	RNA-binding protein, putative	0.98	43	1	1	1	4.7	STVSSSSVATVPSNVSGK	42.9	0.00	0	0	0	0	0.0		

Peptides

512	Tb927.6.4080	hypothetical protein, conserved	0.99	44	1	1	1	0.8	TILGPGGGFAGEER	44.0	0.00	0	0	0	0	0.0		
513	Tb927.6.1870	eukaryotic translation initiation factor 4e, putative	1.00	71	3	1	1	3.0	AATNAAMALWKEK	51.7	0.00	0	0	0	0	0.0		
514	Tb927.11.6660	hypothetical protein, conserved	1.00	64	4	1	1	2.3	VAAASVGGATPVTSFOTPTER	51.7	0.00	0	0	0	0	0.0		
515	Tb927.9.14420	cyclophilin-like protein, putative	1.00	51	3	1	1	3.7	RLRLTLIEEVPLPR	37.9	0.00	9	1	1	1	3.7	RLRLTLIEEVPLPR	9.2
516	Tb927.10.9820	mitochondrial intermediate peptidase, putative.metallo-peptidase, Clan MA(E) Family M3	0.98	43	2	1	1	2.8	SACVTDVEEIPFLSLSK Carbamidomethyl (C3)	41.1	0.00	17	1	1	1	2.8	SACVTDVEEIPFLSLSK Carbamidomethyl (C3)	16.5
517	Tb927.11.10960	hypothetical protein, conserved	1.00	67	3	1	1	3.4	SGGLGEGELGSSPHHLSLEQYR	41.4	0.00	0	0	0	0	0.0		
518	Tb927.11.8800	hypothetical protein, conserved	1.00	57	2	1	1	5.1	TIVLIGKPEDVYVR	55.3	0.00	0	0	0	0	0.0		
519	Tb927.5.2530	hypothetical protein, conserved	0.98	39	2	1	1	1.1	PPPTSVASTAR	24.4	0.99	44	3	1	1	1.1	PPPTSVASTAR	33.1
520	Tb927.5.3390	ADG1, pseudogene	1.00	65	4	1	1	9.3	RLELQNVVEQTR	58.9	0.00	0	0	0	0	0.0		
521	Tb927.7.5680	deoxyribose-phosphate aldolase, putative	1.00	64	2	1	1	5.0	QGFTGKLDALLER	43.9	0.00	0	0	0	0	0.0		
522	Tb927.10.6610	chaperone protein DNAj, putative	1.00	58	2	1	1	4.4	NVVOQQEQLAR	54.7	0.00	0	0	0	0	0.0		
523	Tb927.11.9580	oxidoreductase, putative	1.00	63	1	1	1	2.9	LVVGLSIESPALLLR Carbamidomethyl (C4)	63.2	0.00	0	0	0	0	0.0		
524	Tb927.10.3640	hypothetical protein, conserved	1.00	62	2	1	1	3.9	YATGKPKITAK	56.6	0.76	41	2	1	1	3.9	YATGKPKITAK	36.4
525	Tb927.6.4070	hypothetical protein, conserved	1.00	56	2	1	1	7.7	DYPQVFGGSPSTSYVPATAH	50.8	0.00	0	0	0	0	0.0		
526	Tb927.11.7100	hypothetical protein, conserved	1.00	48	2	1	1	4.9	VLSSSHGAR	40.6	0.00	0	0	0	0	0.0		
527	Tb927.11.1680	vesicular-fusion protein SEC18, putative	1.00	44	2	1	1	1.0	AAVSHALLR	25.3	0.53	31	1	1	1	1.0	AAVSHALLR	30.6
528	Tb927.8.5860	50S ribosomal protein L17, putative	1.00	60	1	1	1	3.7	ILADHVVELAK	59.9	0.00	0	0	0	0	0.0		
529	Tb927.10.14770	protein kinase, putative	0.99	47	2	1	1	2.2	LANSLPVVHTSTR	30.5	0.00	0	0	0	0	0.0		
530	Tb927.7.4460	hypothetical protein, conserved	1.00	60	4	1	1	2.0	SQTIPGAADTPWAAR	42.2	0.00	0	0	0	0	0.0		
531	Tb927.2.2160	parafagellar rod component, putative	0.59	28	2	1	1	5.2	SSSTYVDVWFENLIER	23.4	0.99	47	1	1	1	5.2	SSSTYVDVWFENLIER	46.6
532	Tb927.10.360	hypothetical protein, conserved	1.00	56	2	1	1	5.0	VVPVAGQATFEAR	44.2	0.00	0	0	0	0	0.0		
533	Tb927.7.1090	hypothetical protein, conserved	1.00	56	2	1	1	1.8	FATSATNOGGLVKPSPSSVMAAQR	55.6	0.00	0	0	0	0	0.0		
534	Tb927.11.8030	hypothetical protein, conserved	1.00	56	1	1	1	2.6	ILDYSHVGLHR	55.7	0.00	0	0	0	0	0.0		
535	Tb927.8.3050	hypothetical protein, conserved	1.00	55	2	1	1	2.1	VGLGTGAQQLAR	35.6	0.00	0	0	0	0	0.0		
536	Tb927.11.10080	hypothetical protein, conserved	1.00	55	1	1	1	13.2	FRVQPLPSLHANSIADDTPLVTTTR	55.1	0.00	0	0	0	0	0.0		
537	Tb927.11.10210	hypothetical protein, conserved	0.99	45	2	1	1	1.0	LISLASSAGR	40.0	0.00	0	0	0	0	0.0		
538	Tb927.6.5090	hypothetical protein, conserved	1.00	54	2	1	1	1.7	AALGTEGVLSR	44.1	0.00	0	0	0	0	0.0		
539	Tb927.11.460	hypothetical protein, conserved,predicted WD40 repeat protein	0.99	41	5	1	1	1.0	SLVANKPR	31.7	0.00	0	0	0	0	0.0		
540	Tb927.11.11290	cytosolic malate dehydrogenase	0.99	47	1	1	1	6.7	VWVTGAAGQIGYSLPLAAGR	47.0	0.26	24	1	1	1	6.7	VWVTGAAGQIGYSLPLAAGR	23.5
541	Tb927.6.1950	hypothetical protein, conserved,leucine-rich repeat protein (LRRP), putative	0.99	45	4	1	1	2.6	ALGAHPTLR	33.9	0.00	0	0	0	0	0.0		
542	Tb927.7.540	chaperone protein DNAj, putative	1.00	46	2	1	1	5.3	AAALQNHPDHAKPEAEQAQAQR	45.2	0.00	0	0	0	0	0.0		
543	Tb927.7.5320	hypothetical protein, conserved	1.00	53	2	1	1	2.0	EAPLVLVSTWAEKLR	47.4	0.00	0	0	0	0	0.0		
544	Tb927.10.14720	peroxin 13	1.00	53	4	1	1	2.6	KGLVPGNLR	41.4	0.00	0	0	0	0	0.0		
545	Tb927.4.1600	hypothetical protein, conserved	1.00	52	1	1	1	5.1	VLLVMPGSGK Oxidation (M7)	51.6	0.00	0	0	0	0	0.0		
546	Tb927.9.3370	thioredoxin	0.98	44	1	1	1	10.3	VLQLPTFIAR	44.0	0.00	0	0	0	0	0.0		
547	Tb927.10.10800	hypothetical protein, conserved	1.00	46	2	1	1	7.7	GVCNVYHLSQVSSHVGSLLGQTFPTAVPLTSPTPV Carbamidomethyl (C3)	34.8	0.44	27	1	1	1	7.7	GVCNVYHLSQVSSHVGSLLGQTFPTAVPLTSPTPV Carbamidomethyl (C3)	26.9
548	Tb927.7.3810	hypothetical protein, conserved	1.00	49	3	1	1	3.7	ALGFAADSKPAAAR	38.8	0.00	0	0	0	0	0.0		
549	Tb927.10.7700	ABC transporter, putative	1.00	48	2	1	1	2.1	VILHLITGALPSR	32.6	0.00	0	0	0	0	0.0		
550	Tb927.8.8120	hypothetical protein, conserved	0.99	48	1	1	1	6.3	GGGPSAVCEENLCTAR Carbamidomethyl (C8)- Carbamidomethyl (C14)	47.6	0.49	27	1	1	1	6.3	GGGPSAVCEENLCTAR Carbamidomethyl (C8)- Carbamidomethyl (C14)	26.9
551	Tb927.7.2670	hypothetical protein, conserved,zinc finger protein family member, putative	0.99	44	2	1	1	2.2	FVQGHGIVPR	40.0	0.00	0	0	0	0	0.0		
552	Tb927.9.10070	hypothetical protein, conserved	1.00	48	1	1	1	4.4	CVAALEEPVFFRN Carbamidomethyl (C1)	48.3	0.00	0	0	0	0	0.0		
553	Tb927.10.15950	TFIID-like protein, putative	1.00	48	1	1	1	5.3	AAGASGVYDAAPK	48.0	0.00	0	0	0	0	0.0		
554	Tb927.5.1160	hypothetical protein, conserved	1.00	48	4	1	1	9.2	NFLIEDRGLTQGGQEKADFVR Carbamidomethyl (C10)- Carbamidomethyl (C13)	42.5	0.00	0	0	0	0	0.0		
555	Tb927.6.2720	calcium-binding protein, putative	1.00	48	1	1	1	3.1	VSGEADALKR	48.0	0.00	0	0	0	0	0.0		
556	Tb927.11.15240	small GTPase, putative,ras-related protein rab-2a, putative	1.00	46	1	1	1	14.6	TAMMIYDNVIEGVDAGAVSGKQGTGPGVAR Oxidation (M4)	46.3	0.00	0	0	0	0	0.0		
557	Tb927.10.600	hypothetical protein, conserved	0.00	0	0	0	0	0.0			1.00	90	3	2	2	7.2	APSHGALLDDVPHQEAWR FAGEANEESTLDVLENFGR	29.6 46.7
558	Tb927.9.15060	rRNA processing protein, putative	0.00	0	0	0	0	0.0			0.99	64	2	2	1	13.9	MALSTKPLPSDLNADDPKREAFIQGALLSVR MALSTKPLPSDLNADDPKREAFIQGALLSVR Oxidation (M1)	29.1 35.0
559	Tb927.9.5040	cAMP-specific phosphodiesterase	0.00	0	0	0	0	0.0			1.00	136	5	3	3	8.3	ERFPFGQGIAGTVAASGVGENIQDVAQDPR Carbamidomethyl (C8) GGIGFIDFVAAPFFOK Deamidated (O15) TYHNNPDVLAQPHDTAALIDETAIGK	52.7 30.0 35.0
560	Tb927.8.4500	eukaryotic translation initiation factor 4 gamma, putative	0.00	0	0	0	0	0.0			1.00	108	4	2	2	5.1	IQFLLNTLETDDNNVWR YSPRLLSGTVDSESDILR	36.6 37.2
561	Tb927.9.5280	hypothetical protein, conserved	0.00	0	0	0	0	0.0			1.00	73	4	1	1	18.3	LSPATESPQSGTASGDPEPTDVEGETTVDDIEIALEALEALEREQGGK	42.8
562	Tb927.2.4090	hypothetical protein, conserved	0.00	0	0	0	0	0.0			1.00	45	3	1	1	14.1	KFSANFQVVPVQVDSISFVGPEDQVYVPEVREFATS	40.0
563	Tb927.8.4890	endoplasmic reticulum oxidoreductin, putative,pol-associated gene 1	0.00	0	0	0	0	0.0			1.00	59	1	1	1	7.7	GFEDEKPIDPORDATYVDLONPEANTGYSGPK	58.6
564	Tb927.10.790	vesicle-associated membrane protein, putative,synaptobrevin, putative	0.00	0	0	0	0	0.0			1.00	56	1	1	1	6.7	KAVDEKVEIALDNVER	56.0
565	Tb927.11.3240	T-complex protein 1, zeta subunit, putative	0.00	0	0	0	0	0.0			1.00	113	5	3	3	5.7	LDTGSVDPLAAGLDNLVYK LDTGSVDPLAAGLDNLVLR YDQGLHR	39.9 35.6 34.7
566	Tb927.11.10170	hypothetical protein, conserved	0.00	0	0	0	0	0.0			1.00	49	5	1	1	12.2	RGPSGLNNNELIDAWKEFDVSPRLR	28.7

