TABLE S1 (BANDS 1-7): COMPLETE PEPTIDE LIST

Note: Table S1 shows the list of hits extracted from the Mascot html output results for bands 1 to 7 of the 1DGE. Mr indicates the theoretical molecular weight of the protein; Score refers to the Mascot protein score; # Pept refers to the number of peptides matched to each hit with the respective peptide e-value. Only unique peptides to each hit are indicated, not the ones shared with the previous hit. Additional gene copies column, indicates how many other annotated proteins are matched to the same set of peptides; meaning copies of the same gene product. This table is not filtered, meaning several proteins appear in more than one band; either due to proteolysis or carry over during the mass spectrometry analysis from one sample to the other one.

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Mascot Sequence	Additional gene copies under same match
Band 1	EAN87014.1	kinetoplastid membrane protein KMP-11	10876	46	1	8.20E-05	K.FAELLEQQK.N	3
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	21	1	3.40E-02	K.VAISLPSR.M	1
Band 2	EAN81533.1	histone H4, putative	11163	609	15	4.00E-01	R.GITRGSIR.R	10
						1.20E-03	R.GKILYGYA.-	
						2.20E-03	K.SFVEGVVR.D	
						5.00E-03	K.ILRENVR.G	
						1.20E-01	R.ENVRGITR.G	
						1.30E-05	R.ISGVIYDEVR.G	
						4.20E-05	R.DATAYTEYSR.K	
						7.50E-07	K.TVTAVDVVNALR.K	
						5.40E-04	R.GVIKSFVEGVVR.D	
						1.80E-04	R.DATAYTEYSRK.K	
						1.10E-02	K.RISGVIYDEVR.G	
						5.00E-04	K.TVTAVDVVNALRK.R	
						1.40E-07	K.KTVTAVDVVNALR.K	
						9.10E-07	R.ISGVIYDEVRGVIK.S	
						7.20E-05	K.SFVEGVVRDATAYTEYSR.K	
	EAN85055.1	histone H4, putative	11177	608	15	3.80E-06	R.ISGIIYDEVR.G	6
						1.80E-03	K.RISGIIYDEVR.G	
						2.00E-05	R.ISGIIYDEVRGVIK.S	
	EAN81454.1	histone H4, putative	11280	429	11	1.00E-02	K.FVEGVVR.D	1
						1.70E-03	R.GKILYGYE.-	
						9.90E-06	R.ISGVMYDEVR.G + Oxidation	
						1.50E-03	R.ISGVMYDEVR.G	
	EAN83533.1	histone H2B, putative	12353	189	4	2.70E-02	R.ELQTAVR.L	1
						1.90E-03	R.LVLPADLAK.H	
						2.70E-07	R.IASEAATVVR.V	
						2.30E-07	K.IVNSFVNDLFER.I	
	EAN85330.1	histone H2A, putative	14385	103	3	3.70E-03	R.VGSLLRR.G	13
						1.10E-02	R.GGVMPSLNK.A + Oxidation (M)	
						3.10E-05	K.AGLIFPVGR.V	
	EAN98366.1	40S ribosomal protein S15a, putative	14935	61	1	2.50E-06	M.TMMSVLANALR.C + 2 Oxidation (M)	0
	EAN90233.1	hypothetical protein, conserved	14887	46	1	9.50E-05	R.RLEYETVESK.Y	1

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 2 cont.	EAN83566.1	60S ribosomal protein l36, putative	13040	44	2	1.20E-03	R.RVQELLR.V	2
						2.80E-01	K.AIITDLVGLSPMER.R + Oxidation	
	EAN84604.1	histone H3, putative	21714	44	1	1.40E-04	R.STDLLLQK.A	7
Band 3	EAN83533.1	histone H2B, putative	12353	532	12	9.80E-03	R.ELQTAVR.L	1
						9.10E-05	R.LVLPADLAK.H	
						6.70E-08	R.IASEAATVVR.V	
						5.80E-03	R.TWNVYISR.S	
						1.10E-04	K.RTWNVYISR.S	
						6.50E-07	K.SINNHMSMSGR.T	
						1.30E-03	K.SINNHMSMSGR.T + Oxidation (M)	
						2.00E-03	R.TLGARELQTAVR.L	
						4.00E-07	R.IASEAATVVRVNK.K	
						3.10E-06	K.IVNSFVNDLFER.I	
						4.60E-02	K.HAMAEGTKAVSHASS.- + Oxidation (M)	
						1.60E-01	R.SLKSINNHMSMSGR.T + Oxidation (M)	
						2.70E-02	R.SLKSINNHMSMSGR.T + 2 Oxidation (M)	
						3.30E-07	R.TMKIVNSFVNDLFER.I + Oxidation	
	EAN85055.1	histone H4, putative	11177	237	6	4.60E-04	R.GKILYGYA.-	7
						2.80E-02	K.SFVEGVVR.D	
						4.10E-05	R.ISGIIYDEVR.G	
						4.00E-05	R.DATAYTEYSR.K	
						4.40E-06	K.TVTAVDVVNALR.K	
						7.70E-03	R.ISGIIYDEVRGVIK.S	
	EAN81533.1	histone H4, putative	11163	209	5	1.50E-04	R.ISGVIYDEVR.G	10
	EAN85330.1	histone H2A, putative	14385	96	3	3.30E-02	R.VGSLLRR.G	13
						9.10E-03	R.GGVMPSLNK.A + Oxidation (M)	
						2.00E-05	K.AGLIFPVGR.V	
						8.90E-03	K.AGLIFPVGR.V	
	EAN84604.1	histone H3, putative	21714	92	2	2.00E-05	R.STDLLLQK.A	7
						4.90E-04	R.EVSGAQKEGLR.F	
	EAN81492.1	40S ribosomal protein S14, putative	15771	57	1	9.80E-06	R.IEDVTPIPTDSTR.R	2
	EAN98366.1	40S ribosomal protein S15a, putative	14935	54	1	1.60E-05	M.TMMSVLANALR.C + 2 Oxidation	0
	EAN85291.1	ribosomal protein S26, putative	13109	41	1	4.20E-04	R.MLDQASAR.D + Oxidation (M)	1
	EAN83385.1	cytochrome c oxidase VIII (COX VIII), putative	18658	39	1	3.90E-04	K.GSDVWAADGK.F	1
	EAN84245.1	histone H3 variant, putative	17193	35	1	1.20E-01	K.DIQLALK.L	1
						2.90E-02	R.YQSSTEFLIAK.A	
	EAN89722.1	60S ribosomal protein L34, putative	19668	34	1	2.70E-03	R.AFLIEEQR.I	3
	EAN83566.1	60S ribosomal protein l36, putative	13040	33	1	2.00E-03	R.RVQELLR.V	2

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 3 cont.	EAN82747.1	Gim5A protein, putative	27268	31	1	3.20E-03	R.GVLNSGLTR.F	3
	EAN92211.1	hypothetical protein, conserved	161130	25	1	1.80E-02	R.AVVMAADAIR.T + Oxidation	1
	EAO00223.1	Heat shock protein 20, putative	15973	20	1	2.80E-02	R.MQSVTGTSFLSTSAR.G + Oxidation	1
	EAN84514.1	calpain-like cysteine peptidase, p	15077	19	1	4.40E-02	K.VKMDAVPTEK.N + Oxidation	0
Band 4	EAN84604.1	histone H3, putative	21714	412	12	2.80E-05	R.STDLLLQK.A	7
						1.40E-02	R.EIRQFQR.S	
						3.80E-03	R.WRPGTVALR.E	
						1.40E-03	K.APKAPGAATGVK.H	
						1.90E-02	R.LVREVSGAQK.E	
						3.20E-03	K.DIHLALCLR.G	
						9.90E-06	R.EVSGAQKEGLR.F	
						4.80E-04	R.RWRPGTVALR.E	
						1.10E-03	K.APGAATGVKHAQR.R	
						2.60E+00	K.DIHLALCLRGER.A	
						7.80E-04	R.STDLLLQKAPFQR.L	
						5.70E-07	R.FQSSAILAAQEATESYVVSLLADTNR.A	
	EAN85330.1	histone H2A, putative	14385	283	10	3.70E-03	R.VGSLLRR.G	9
						6.70E-03	R.GGVMPSLNK.A + Oxidation	
						9.10E-06	K.AGLIFPVGR.V	
						3.30E-07	R.HDDDLGMLLK.D	
						1.10E-04	R.HDDDLGMLLK.D + Oxidation	
						1.80E-04	R.SAKAGLIFPVGR.V	
						3.30E-03	R.HDDDLGMLLKDVTLSR.G	
						2.40E-04	R.HDDDLGMLLKDVTLSR.G + Oxidation	
						1.20E-02	R.TVTLAVRHDDDLGMLLK.D	
						4.50E-02	R.TVTLAVRHDDDLGMLLK.D + Oxidation	
	EAN83533.1	histone H2B, putative	12353	274	8	2.80E-02	R.ELQTAVR.L	1
						1.90E-03	R.LVLPADLAK.H	
						6.50E-08	R.IASEAATVVR.V	
						6.50E-03	R.TWNVYISR.S	
						1.50E-04	K.RTWNVYISR.S	
						2.00E-01	K.SINNHMSMSGR.T	
						4.50E-02	K.SINNHMSMSGR.T + Oxidation (M)	
						1.90E-07	K.IVNSFVNDLFER.I	
	EAN88264.1	histone H2A, putative	14345	238	6	7.10E-05	R.HDDDLGTLLK.D	3
						9.60E-05	R.HDDDLGTLLKDVTLSR.G	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 4 cont.	EAN81533.1	histone H4, putative **carry over**	11163	197	5	1.30E-02	R.GKILYGYA.-	10
						2.40E-02	K.SFVEGVVR.D	
						3.70E-05	R.ISGVIYDEVR.G	
						4.00E-05	R.DATAYTEYSR.K	
						1.40E-05	K.TVTAVDVVNALR.K	
	EAN85055.1	histone H4, putative **carry over**	11177	195	5	5.10E-05	R.ISGIIYDEVR.G	7
	EAN94839.1	beta tubulin, putative	50520	186	4	1.70E-04	K.LAVNLVPFPR.L	4
						4.30E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						7.70E-06	R.INVYFDEATGGR.Y	
						5.90E-04	R.AVLIDLEPGTMDSVR.A + Oxidation	
	EAN83566.1	60S ribosomal protein l36, putative	13040	120	4	3.40E-04	R.RVQELLR.V	2
						4.20E-03	K.EVPKAEAPAPR.T	
						3.50E-03	K.AIITDLVGLSPMER.R	
						1.40E-05	K.AIITDLVGLSPMER.R + Oxidation (M)	
	EAN99789.1	60S ribosomal protein L23, putative	15063	102	4	2.60E-01	K.ISSHAPAIV.-	1
						5.00E-06	K.VLNAVIIR.Q	
						4.00E-03	K.NLYIISVK.G	
						1.70E-01	K.GEMKGSGIAGPVAK.E + Oxidation	
	EAN85296.1	hypothetical protein, conserved	11324	68	1	4.30E-07	R.ANYASAVESR.M	1
	EAN84514.1	calpain-like cysteine peptidase, putative	15077	66	2	1.40E-02	K.MDAVPTEK.N + Oxidation	0
						1.60E-04	R.GFDEGNGLLFR.I	
	EAN98366.1	40S ribosomal protein S15a, putative	14935	61	1	2.60E-06	M.TMMSVLANALR.C + 2 Oxidation	0
	EAN82862.1	ribosomal protein L24, putative	14735	59	2	5.20E-01	R.FVPWTR.T	3
						2.80E-05	R.GIVGADLSYIQEVR.A	
	EAN82857.1	elongation factor 1-alpha (EF-1-alpha), putative	48884	59	2	5.20E-03	R.QTVAVGIIK.A	4
						1.70E-03	K.STATGHLIYK.C	
	EAN89019.1	40S ribosomal protein S16, putative	16930	58	1	5.20E-06	R.GAGQVAQAYATR.Q	3
	EAN86373.1	vacuolar ATP synthase, putative	19981	56	1	4.90E-06	K.SGVGVAHLGILHSER.I	1
	EAN82747.1	Gim5A protein, putative	27268	54	2	2.40E+00	K.ALLPEDAEK.K	2
						2.60E-06	R.LSLLLNALSSK.T	
	EAN81492.1	40S ribosomal protein S14, putative	15771	53	1	1.20E-05	R.SPGPGAQAALR.A	2
	EAN85210.1	kinetoplast DNA-associated protein, putative	14529	53	1	4.10E-06	K.NNPALSGLPVAK.R	1
	EAN94958.1	hypothetical protein, conserved	17131	50	2	1.70E+00	K.LYSAYGPK.D	1
						6.80E-05	R.ALGEYYFQR.A	
	EAN84418.1	60S ribosomal protein L13a, putative	32939	49	1	8.20E-05	R.SPSDIFLR.T	3
	EAN80947.1	tryparedoxin peroxidase, putative	22886	39	1	2.60E-04	R.QITVNDLPVGR.D	5
	EAN89722.1	60S ribosomal protein L34, putative	19668	39	1	7.40E-04	R.AFLIEEQR.I	3
	EAN85291.1	ribosomal protein S26, putative	13109	38	1	8.60E-04	R.MLDQASAR.D + Oxidation	1

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 4 cont.	EAN85212.1	kinetoplast DNA-associated protein, putative	14224	36	1	6.30E-04	K.NNPALSGLPISER.G	1
	EAN96914.1	mitochondrial import inner membrane translocase subunit Tim17, putative	16142	28	1	5.10E-03	R.IIDALGFAQH.-	1
	EAN91849.1	small nuclear ribonucleoprotein Sm-F, putative	8736	21	1	3.90E-02	R.CNNVLYIR.E	1
Band 5	EAN90899.1	ribosomal protein L21E (60S), putative	18271	346	8	4.80E-04	K.RVEVLAR.R	0
						1.20E-04	K.DFLAFQAAK.K	
						7.60E-07	R.GVGVIVNKPVR.N	
						2.30E-04	R.TGIVWNVTPR.G	
						4.20E-04	R.AAEYEAMIPY.- + Oxidation (M)	
						1.80E-02	K.QKDFLAFQAAK.K	
						7.60E-03	R.RAAEYEAMIPY.- + Oxidation (M)	
						1.90E-08	K.VGDYVDVVADSAVR.A	
	EAN82549.1	ribosomal protein L21E (60S), putative	18285	336	8	3.60E-03	K.RVELLAR.R	0
	EAN94839.1	beta tubulin, putative	50520	311	8	5.70E-02	R.YLTASALFR.G	0
						2.00E-05	K.LAVNLVPFPR.L	
						3.00E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						3.40E-05	R.INVYFDEATGGR.Y	
						2.60E-01	K.EVDEQMLNVQNK.N	
						6.70E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						9.90E-05	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						1.30E-05	K.NSSYFIEWIPNNIK.S	
	EAN83533.1	histone H2B, putative	12353	175	4	2.80E-02	R.ELQTAVR.L	1
						2.50E-03	R.LVLPADLAK.H	
						6.00E-07	R.IASEAATVVR.V	
						1.80E-06	K.IVNSFVNDLFER.I	
	EAN84275.1	succinate dehydrogenase, putative	21862	169	6	1.00E-01	R.VPPPLDAK.I	0
						7.60E-04	R.MSSPVTPR.V + Oxidation (M)	
						1.40E-01	K.FLNPAYASK.E	
						7.90E-06	M.PSAPLTGEVAR.Y	
						3.40E-03	R.YSSPLFMYR.R + Oxidation (M)	
						6.90E-02	K.NAAPKPETVFTAK.D	
	EAN85055.1	histone H4, putative	11177	166	4	3.00E-02	K.SFVEGVVR.D	7
						9.20E-05	R.ISGIIYDEVR.G	
						4.10E-05	R.DATAYTEYSR.K	
						2.90E-05	K.TVTAVDVVNALR.K	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 5 cont.	EAN83814.1	COP-coated vesicle membrane protein gp25L precursor, putative	36993	162	5	2.70E-02	R.VLEDAVR.S	1
						5.30E-02	R.NANEAMTFK.V + Oxidation (M)	
						2.10E-03	K.LRPIEVELR.V	
						9.90E-10	R.VGSENNDYSELATK.E	
						1.10E+00	R.SIHSEYLYYKEK.E	
	EAN81533.1	histone H4, putative	11163	160	4	4.30E-04	R.ISGVIYDEVR.G	10
	EAN83023.1	60S ribosomal protein L17, putative	19386	155	5	3.00E-03	K.NAEANAIEK.G	3
						8.70E-04	K.HVQVDQAAR.M	
						5.00E-03	K.SVVAMLSLLK.N + Oxidation (M)	
						7.00E-01	K.GLDPNKMVIK.H + Oxidation (M)	
						8.20E-06	K.NTFETANVINGMPLR.K + Oxidation	
	EAN92891.1	40S ribosomal protein S17, putative	23047	145	3	1.20E-01	R.METGVPR.H + Oxidation	1
						1.10E-05	R.VVMDVTIAR.S + Oxidation	
						1.70E-08	R.HVALTTVVAPVTK.K	
	EAN88197.1	ribosomal protein S19, putative	19134	138	4	7.80E-05	K.LADAIAFK.V	1
						1.60E-04	R.KLADAIAFK.V	
						1.20E-02	R.GSRPEITVR.A	
						5.70E-03	R.AVYMRPGVGYGGLSK.R + Oxidation	
	EAN82577.1	ADP-ribosylation factor 1, putative	20806	136	4	4.40E-03	K.MFTEDELR.N + Oxidation (M)	3
						3.60E-04	R.ILMVGLDAAGK.T	
						2.70E-06	R.ILMVGLDAAGK.T + Oxidation (M)	
						1.40E-05	K.QDLPNAMSTTEVTEK.L + Oxidation (M)	
	EAN81803.1	60S ribosomal protein L11, putative	22600	119	3	3.30E-02	K.VKEFELK.S	0
						5.60E-05	K.KAEELLEK.G	
						1.90E-05	R.TYDGIIFQAK.K	
	EAN99605.1	hypothetical protein, conserved	19732	115	5	2.40E-01	R.ALMEQER.C + Oxidation (M)	0
						2.30E-03	R.IEEENLR.I	
						2.20E-03	R.YTYEPMGSR.R + Oxidation (M)	
						3.10E-03	R.LQNEEYIAR.L	
						1.40E-01	R.IVHNMTIIMKR.G + 2 Oxidation	
	EAN81053.1	alpha tubulin, putative	50549	112	3	1.10E-02	R.LSVDYGKK.S	0
						3.30E-04	K.DVNAAVATIK.T	
						4.20E-05	R.AVFLDLEPTVVDEIR.T	
	EAN89208.1	60S ribosomal protein L35, putative	15310	109	4	7.40E-01	R.ILTVLNR.N	2
						5.50E-04	R.LALKDNEK.N	
						2.80E+00	K.QLMEFKK.E + Oxidation (M)	
						4.20E-06	R.VAQQLNSAGTR.L	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 5 cont.	EAN90616.1	glycosomal malate dehydrogenase, putative	34347	107	2	1.50E-03	R.VQVAGTEVVK.A	1
						1.60E-07	R.GSATLSMAEAGAR.F + Oxidation	
	EAN96121.1	RNA-binding protein, putative	17759	106	3	2.00E-04	R.VYVGNIDKR.A	0
						4.50E-02	K.TIEDSWLAR.R	
						6.60E-05	R.VLVVETSTTTTLPK.E	
	EAN80947.1	tryparedoxin peroxidase, putative	22886	103	3	6.60E-03	K.AFQFVEK.H	3
						1.40E-03	R.GLFIIDPK.Q	
						3.80E-05	R.QITVNDLPVGR.D	
	EAN99961.1	ribosomal protein L35A, putative	17023	96	5	2.50E-01	R.IENVNTK.E	0
						1.30E-04	K.AVLAGYTR.G	
						3.90E-01	R.VYLYPSR.I	
						4.00E-03	R.VYLYPSRI.-	
						2.90E+00	R.KFHGSLAANR.S	
	EAN87953.1	ribosomal protein L27, putative	15503	87	3	2.60E-03	K.VVIVTSGR.Y	2
						7.60E-02	R.INVSDASK.K	
						9.00E-04	K.AVIVQNTDSK.S	
	EAN98360.1	60S ribosomal protein L28, putative	16372	79	1	5.30E-08	K.AVMDAGVEASVVSK.A + Oxidation	2
	EAN87059.1	hypothetical protein, conserved	21263	77	3	3.40E-03	K.KAAALYVR.F	0
						2.10E-01	R.FYHALKK.S	
						6.70E-04	K.SVGLTAALSPK.Q	
	EAN90740.1	vacuolar transporter chaperone, putative	20216	75	3	1.50E-01	K.TFFANER.T	0
						3.70E-04	K.YMNLQGPGVR.N + Oxidation (M)	
						1.50E-02	K.AMTPTIHGGAIFS.- + Oxidation (M)	
	EAN89163.1	hypothetical protein, conserved	25313	74	3	1.90E-03	R.RLNEGGLR.F	1
						3.30E-02	R.LRDLYER.N	
						4.30E-02	R.SGRDDDIAAPR.R	
	EAN82199.1	hypothetical protein, conserved	23072	72	2	5.30E-04	R.GVVSVVTR.E	1
						3.70E-03	R.AYSNVIR.E	
	EAN89722.1	60S ribosomal protein L34, putative	19668	71	3	4.10E-03	R.AFLIEEQR.I	3
						2.80E-04	K.STSRPYGGVLSHEQVR.D	
	EAN87271.1	glycosomal membrane protein, putative	24137	70	2	4.80E-05	K.SVSSSITDGR.S	1
						1.50E-02	R.YKLVPGQPK.R	
	EAN85214.1	hypothetical protein, conserved	21287	68	3	4.30E-01	R.FYYALKK.S	0
						4.60E-03	K.SVGLTAALSPR.Q	
	EAN99158.1	hypothetical protein, conserved	17771	67	2	2.60E-03	R.LGIGFDDR.R	0
						1.00E-03	R.NALDLGDDRR.D	
	EAN98186.1	40S ribosomal protein S18, putative	17679	62	2	1.50E-03	R.LLNTNVEGK.R	1
						8.70E-03	K.TGKTEHLTSAMVDTR.L + Oxidation	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 5 cont.	EAN87824.1	hypothetical protein, conserved	29236	61	2	3.80E-03	K.VIANLLNR.-	1
						7.10E-04	K.IINLSAEEIR.A	
	EAN81251.1	40S ribosomal protein S8, putative	30143	60	1	3.80E-06	K.AVADQLKEGR.L	2
	EAN95668.1	hypothetical protein, conserved	17874	49	2	6.40E-02	R.LGLDFDDRR.G	0
	EAN82857.1	elongation factor 1-alpha (EF-1-alpha), putative	48884	49	2	2.20E-02	K.SVNFAQER.Y	6
						1.10E-02	K.STATGHLIYK.C	
	EAN97136.1	ATP synthase, epsilon chain, putative	20447	47	1	6.50E-05	K.ALAAQQASLGSAK.D	0
	EAN83270.1	hypothetical protein, conserved	25371	46	2	1.40E-01	R.EVVPPQSR.V	0
						1.10E-03	R.ATVEESSER.L	
	EAN86269.1	60S ribosomal protein L19, putative	37755	42	1	2.80E-04	R.QLAEQLAAK.R	3
	EAN91609.1	vacuolar-type proton translocating pyrophosphatase 1, putative	86135	41	1	7.90E-05	R.VGIPTINILDAR.V	1
	EAN82898.1	hypothetical protein, conserved	23348	41	1	1.50E-04	R.EVEEYDAAVER.V	2
	EAO00224.1	60S ribosomal protein L13, putative	25420	40	1	4.00E-04	R.FAPTIGIR.V	2
	EAN82879.1	40S ribosomal protein S11, putative	20229	40	1	2.30E-04	R.YNVLEVVSK.S	3
	EAN82694.1	40S ribosomal protein S13, putative	17431	37	1	9.10E-04	R.DSMGIAQVK.N + Oxidation	3
	EAN92417.1	signal peptidase type I, putative	22932	36	2	6.30E-01	R.TVPIVHR.V	1
						6.60E-04	R.LMELQFSQMGR.I + 2 Oxidation	
	EAN86445.1	hypothetical protein, conserved	22586	36	1	8.90E-04	R.ILYNTTNVDR.T	1
	EAN98272.1	eukaryotic initiation factor 4a, putative	49984	31	1	1.20E-03	R.VLVTTDLVAR.G	1
	EAN89019.1	40S ribosomal protein S16, putative	16930	29	1	7.80E-03	K.IMEAVNVVGSR.Q + Oxidation	3
	EAN93852.1	reticulon domain protein, p	21286	25	1	5.90E-03	R.LVTALESMHQLVTWR.D + Oxidation	0
	EAN87937.1	hypothetical protein, conserved	21881	18	1	7.80E-02	K.STAAFTPTGPK.R	1
Band 6	EAN82805.1	40S ribosomal protein L14, putative	20789	277	8	0.006	K.FSVELSR.N	2
						0.00034	M.VKANYIR.A	
						0.059	R.VLVENPADK.K	
						4.1e-005	R.KVFDENDK.K	
						0.00011	R.TLKNVLAEK.K	
						7.6e-005	R.VLVENPADKK.M	
						8.2e-006	R.VGVVVDIIDGNR.V	
						0.13	R.STDFERYQLR.V	
	EAN94839.1	beta tubulin, putative	50520	228	7	1.50E-01	R.YLTASALFR.G	0
						2.70E-02	K.NMMQAADPR.H + 2 Oxidation (M)	
						2.00E-02	K.LAVNLVPFPR.L	
						1.50E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						7.20E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						6.80E-04	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						1.40E-04	R.GLSVPELTQQMFDAK.N + Oxidation (M)	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 6 cont.	EAN80947.1	tryparedoxin peroxidase, putative	22886	217	6	7.10E-03	R.DVDEALR.L	3
						1.00E-03	K.AFQFVEK.H	
						1.70E-05	R.GLFIIDPK.Q	
						8.90E-04	K.SKEYFGAVA.-	
						1.40E-04	R.QITVNDLPVGR.D	
						1.80E-03	K.SYGVLKEEDGVAYR.G	
	EAN87271.1	glycosomal membrane protein, putative	24137	213	6	5.10E-03	K.LLGQTDGR.D	1
						9.20E-04	K.SALINLTK.D	
						1.30E-01	K.WMGDIPK.M + Oxidation (M)	
						1.30E-04	K.SVSSSITDGR.S	
						1.50E-03	R.YKLVPGQPK.R	
						4.40E-06	R.SAYKSVSSSITDGR.S	
	EAN89424.1	hypothetical protein, conserved	23550	166	8	3.40E-01	K.DEYEVR.R	1
						4.20E-03	R.FNEIVKR.Y	
						8.80E-01	R.LTSYMTSK.K + Oxidation (M)	
						6.00E-03	K.VYYPLRR.H	
						3.10E-01	K.FVYKEMGK.V + Oxidation (M)	
						1.50E-02	K.HIQDLWTR.V	
						2.40E-02	R.RLTSYMTSK.K	
						3.20E-04	R.YGQAPQYAEVK.-	
	EAN87517.1	40S ribosomal protein S9, putative	22333	147	7	8.10E-03	R.VNMTLSK.M + Oxidation (M)	2
						8.50E-02	K.LCGQYGLR.C	
						4.80E-02	R.RLQTVVFK.H	
						5.20E-03	R.QLEGSAIMR.R + Oxidation (M)	
						6.60E-01	R.RQLEGSAIMR.R + Oxidation (M)	
						2.00E-02	K.QIVTIPSFIVR.V	
						1.80E-04	R.LLLTLPENHPR.R	
	EAN85226.1	histone H2A, putative	18753	137	3	1.50E-03	R.GGVVPFVHK.S	0
						1.70E-05	R.ADLNFPVGR.I	
						5.50E-06	R.GDEELNQIVNATIAR.G	
	EAN81803.1	60S ribosomal protein L11, putative	22600	136	5	3.60E-03	K.AEELLEK.G	0
						1.30E-02	K.VKEFELK.S	
						8.00E-05	K.KAEELLEK.G	
						3.10E-02	R.TYDGIIFQAK.K	
						9.80E-02	K.ATNPMREIVVK.K + Oxidation (M)	
	EAN83533.1	histone H2B, putative	12353	136	3	1.50E-03	R.LVLPADLAK.H	1
						1.40E-05	R.IASEAATVVR.V	
						1.70E-06	K.IVNSFVNDLFER.I	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 6 cont.	EAN97975.1	60S ribosomal protein L18, putative	21876	118	4	6.30E-04	M.GVDLTGVQK.K	0
						2.10E-02	M.GVDLTGVQKK.K	
						1.60E-03	R.SNRAPISLSR.I	
						3.70E-02	R.HHTYSTNPYIK.L	
	EAN84950.1	kinetoplast DNA-associated protein, putative	21340	116	5	9.70E-03	R.EEAASLAR.S	1
						2.90E-01	K.FVRENYHK.V	
						1.30E-02	K.QREEAASLAR.S	
						1.10E-03	K.MYKELSQNQR.R + Oxidation (M)	
						6.10E-02	R.FGALSQLYDVSKPLDVEK.E	
	EAN86177.1	60S ribosomal subunit protein L31, putative	21575	88	2	2.60E-04	R.KQALLDAR.K	3
						7.40E-05	R.KPDNITMEATIHLSK.L + Oxidation (M)	
	EAN83877.1	ribosomal protein S7, putative	24970	77	3	1.30E-01	R.FHINTVR.T	3
						6.30E-04	R.TATVVFYPLR.F	
						3.10E-03	K.RPNPSEDEDSVAK.A	
	EAN81053.1	alpha tubulin, putative	50549	72	4	3.10E-01	R.LSVDYGKK.S	0
						1.20E-01	R.IDHKFDLMYSK.R + Oxidation (M)	
						2.80E-01	R.TIQFVDWSPTGFK.C	
						2.40E-04	R.AVFLDLEPTVVDEIR.T	
	EAN82879.1	40S ribosomal protein S11, putative	20229	71	2	2.40E-02	R.DYLHFIR.K	3
						2.60E-05	R.YNVLEVVSK.S	
	EAN84629.1	hypothetical protein, conserved	20294	59	2	2.40E-02	K.FASTATSLR.S	0
						3.60E-04	R.GQVRPVQLASGEGK.K	
	EAN82747.1	Gim5A protein, putative	27268	51	1	5.10E-06	R.LSLLLNALSSK.T	2
	EAN87059.1	hypothetical protein, conserved	21263	49	3	2.20E-03	K.KAAALYVR.F	0
						1.10E-02	R.FYHALKK.S	
						1.20E+00	K.TVTSTVPPLP.-	
	EAN90235.1	hypothetical protein, conserved	24533	48	2	1.90E-01	K.YIYEPK.S	1
						4.40E-04	R.EFLSVQNAHK.V	
	EAN86445.1	hypothetical protein, conserved	22586	46	1	1.00E-04	R.ILYNTTNVDR.T	1
	EAN81438.1	ADP-ribosylation factor, putative	18405	45	1	7.10E-05	R.TPFIILGNK.I	1
	EAN86269.1	60S ribosomal protein L19, putative	37755	43	1	2.30E-04	R.QLAEQLAAK.R	3
	EAN91922.1	hypothetical protein, conserved	23735	42	2	6.00E-03	R.YDAMSVER.R + Oxidation (M)	0
						3.80E-02	R.GGFTSPSFLR.A	
	EAN97577.1	hypothetical protein, conserved	56966	39	1	4.90E-04	R.LQQLEEAAR.R	0
	EAN93193.1	60S ribosomal protein L18a, putative	20978	37	2	1.50E+00	K.SIPNHQVK.R	2
						7.40E-04	K.AGAVSQAYHDLASR.H	
	EAN89163.1	hypothetical protein, conserved	25313	35	1	1.30E-03	R.RLNEGGLR.F	1
	EAN83023.1	60S ribosomal protein L17, putative	19386	33	1	2.00E-03	K.HVQVDQAAR.M	3

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 6 cont.	EAN82173.1	hypothetical protein, conserved	23907	33	1	1.40E-03	R.SSLADYVLR.A	1
	EAN82317.1	glutamamyl carboxypeptidase, putative	44248	33	1	1.30E-03	K.LVAFDTTSR.N	5
	EAN85542.1	COP-coated vesicle membrane protein p24 precursor, puta	25156	30	1	4.60E-03	R.ATTEVANTR.V	1
	EAN85405.1	hypothetical protein, conserved	98633	22	1	4.30E-02	R.ELEDLSAK.K	1
	EAN90473.1	hypothetical protein, conserved	22542	20	1	3.90E-03	R.QNILLLPR.S	1
	EAN99961.1	ribosomal protein L35A, putative	17023	20	1	2.40E-02	R.VYLYPSRI.-	0
	EAN84470.1	60S ribosomal protein L26, putative	16431	20	1	2.30E-02	R.ILMSAPLSK.E + Oxidation (M)	2
	EAN89722.1	60S ribosomal protein L34, putative	19668	20	1	2.30E-02	K.AASRVPVGAK.V	3
Band 7	EAN87845.1	40S ribosomal protein S4, putative	30998	658	17	0.00016	K.KVVDLIK.S	2
						5.00E-05	R.INVIQER.E	
						0.00034	K.LIAAEARK.N	
						0.00038	K.VGEAEGNIK.L	
						2.3	R.IRYPDPR.T	
						0.00017	R.ASNIFVIGK.D	
						5.20E-05	K.VVMVTGGANR.G	
						0.00056	K.VVMVTGGANR.G + Oxidation (M)	
						0.011	R.IGEIMSIER.H	
						2.70E-05	K.VENVYTSTGR.I	
						0.019	R.IPVAMTHDGHR.I + Oxidation (M)	
						0.00053	R.INVIQEREEK.L	
						6.50E-08	R.LKDAAGHEFATR.A	
						0.00033	R.THRGDTLVYNLK.E	
						7.60E-05	K.LLKVENVYTSTGR.I	
						4.40E-06	K.YPVGFMDVVEIPR.T + Oxidation (M)	
						0.00016	R.ASNIFVIGKDMQSVPVTLPK.Q + Oxidation (M)	
	EAN83261.1	hypothetical protein, conserved	30260	524	16	0.00055	M.PPMLAAAK.S + Oxidation (M)	0
						0.0085	K.FKGPEDK.L	
						0.21	K.DFNKDVK.D	
						0.0012	K.DVKDMLTK.S + Oxidation (M)	
						0.048	K.EWAVVYIAK.L	
						0.0015	K.SYSDAQKWK.L	
						0.013	K.NLKPGVLLTHS.-	
						4.80E-06	K.FSVDVEYAPR.C	
						6.40E-05	R.YAHAGYALAVR.T	
						0.024	K.SLTLYKDFNK.D	
						6.10E-05	K.LFVNPMATSDGK.F	
						1.60E-06	K.LFVNPMATSDGK.F + Oxidation (M)	
						0.00021	K.NKEWAVVYIAK.L	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 7 cont.						0.00015	R.SYTTSFVTPIPK.C	
						0.00088	K.NGEYELSHEFVMPSR.M	
						8.20E-05	K.LVDNWTAAVTLDKNLKPGVLLTHS.-	
	EAN81197.1	hypothetical protein, conserved	30269	497	15	0.8	K.SYSDAHKWK.L	0
	EAN95832.1	hypothetical protein, conserved	30333	496	14	9.30E-06	R.YAYAGYALAVR.T	1
	EAN82858.1	elongation factor 1-alpha (EF-1-alpha), putative	49694	327	10	0.0022	K.VGYNVEK.V	4
						0.028	K.YAWVLDK.L	
						0.089	R.TIEKFEK.E	
						0.002	K.SVNFAQER.Y	
						1.50E-06	K.IGGIGTVPVGR.V	
						0.0017	K.STATGHLIYK.C	
						0.098	R.GITIDIALWK.F	
						0.021	K.YAWVLDKLK.A	
						0.0001	K.VHMNLVVVGHVDAGK.S + Oxidation (M)	
						1.90E-05	R.FIPISGWQGDNMIDK.S + Oxidation (M)	
	EAN97607.1	ADP,ATP carrier protein 1, mitochondrial precursor, putative	35287	294	8	0.026	K.TVAAPIER.V	0
						8.50E-05	K.TEGAASLMR.G + Oxidation (M)	
						0.11	K.TEGLYSLWR.G	
						2.40E-06	R.YFPTQALNFAFK.D	
						0.0023	R.VKLLVQNQGEMIK.Q + Oxidation (M)	
						0.072	K.LLVQNQGEMIKQGR.L + Oxidation (M)	
						1.60E-09	K.LGFFEEFMVGGVAAGVSK.T + Oxidation (M)	
						0.044	R.GIAGAGVLSGVDALKPIYVR.W	
	EAN86006.1	glucosamine-6-phosphate isomerase, putative	31635	278	8	0.00042	R.FFNNDIR.K	0
						0.28	R.IHDFSPSK.E	
						0.00023	K.SVLVIATGSKK.A	
						0.015	R.LIQAYREGR.V	
						0.00018	K.VPTMALTVGIR.T + Oxidation (M)	
						4.30E-07	K.SLNDETIASNAR.F	
						0.002	R.VKSLNDETIASNAR.F	
						0.002	K.ERPFVLGLPTGGTPVR.T	
	EAN90413.1	ADP,ATP carrier protein 1, mitochondrial precursor, putative	35303	271	7	0.00044	R.GIAGAGVLSGVDALKPMYVR.W	0
						0.22	R.GIAGAGVLSGVDALKPMYVR.W + Oxidation (M)	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 7 cont.	EAN94839.1	beta tubulin, putative	50520	234	8	0.099	R.YLTASALFR.G	0
						0.051	K.NMMQAADPR.H + 2 Oxidation (M)	
						6.60E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						0.014	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						1.50E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						1.10E-05	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						0.037	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
						0.43	R.LHFFMMGFAPLTSR.G + 2 Oxidation (M)	
	EAN90437.1	glucosamine-6-phosphate isomerase, putative	31635	228	7	1.30E-05	K.SLNDETVASNAR.F	0
	EAN81873.1	hypothetical protein, conserved	30818	222	7	0.015	R.VIIGTEAR.S	0
						0.016	R.GRVIIGTEAR.S	
						0.00056	K.FTTSTQLSMR.N + Oxidation (M)	
						0.17	R.RFGLVFTSQDAP.-	
						0.0043	R.KGDITLSADVSSNPK.A	
						2.10E-08	M.APNQFVELVDTVEK.Y	
						0.058	R.IPVKPLMGAVALVER.G + Oxidation (M)	
	EAN83852.1	heat shock 70 kDa protein, putative	41044	217	5	0.012	R.GTLQPVER.V	0
						3.20E-05	R.VEIIANDQGNR.T	
						6.90E-07	R.TTPSYVAFTDTER.L	
						0.012	K.AVVTVPAYFNDSQR.Q	
						2.10E-05	K.TFNPEEVSSMVLSK.M + Oxidation (M)	
	EAN99433.1	60S ribosomal protein L7a, putative	34992	151	7	3.1	K.ARLGDAVGR.K	0
						0.2	R.LFDVATEK.K	
						0.028	R.SSRNELLK.L	
						0.023	R.NAGKDAAAVM.- + Oxidation (M)	
						0.019	K.NFGIGHDVPYAR.D	
						5.80E-05	K.APLSVVTGLQEVTR.T	
						0.0042	K.KAPLSVVTGLQEVTR.T	
	EAN95595.1	40S ribosomal protein S6, putative	28333	147	3	0.041	R.AYLHLIGTR.R	0
						5.00E-07	K.QFEITEEVLR.R	
						4.90E-06	R.LGNEVDGAIFGDAFR.G	
	EAO00224.1	60S ribosomal protein L13, putative	25420	136	5	0.43	R.FAPTIGIR.V	2
						0.039	R.GFTVEELK.A	
						0.14	K.VFLNQPAQK.L	
						0.0038	K.LVLFPMSYK.N + Oxidation (M)	
						2.10E-06	R.FGTAAVGGFVTPAPEAPR.K	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 7 cont.	EAN87804.1	60S ribosomal protein L2, putative	28854	135	7	0.0044	R.IEKPVLK.A	2
						0.24	R.LKLPSGQK.K	
						0.036	R.ILDYAER.H	
						0.024	K.TIEHEPGR.G	
						4.40E-05	R.AMIGIIAGGGR.I	
						1.80E-05	R.AMIGIIAGGGR.I + Oxidation (M)	
						0.67	K.TIEHEPGRGAPLAR.V	
	EAN85055.1	histone H4, putative	11177	117	3	0.0004	R.ISGIIYDEVR.G	7
						0.0019	R.DATAYTEYSR.K	
						4.40E-05	K.TVTAVDVVNALR.K	
	EAN97448.1	RNA-binding protein, putative	27602	114	3	0.0075	K.QILELFSGMK.V + Oxidation (M)	1
						0.00022	K.EFMGNVLSVVPAK.T + Oxidation (M)	
						6.5e-005	R.YAIIFFENAAAVK.K	
	EAN90286.1	glyceraldehyde 3-phosphate dehydrogenase, putative	39292	106	4	0.0039	K.ATLQNNLPK.E	3
						0.11	K.VVISAPASGGAK.T	
						0.00073	R.KVVISAPASGGAK.T	
						0.0039	K.AVGMVIPSTQGK.L + Oxidation (M)	
	EAN95952.1	hypothetical protein, conserved	43691	105	3	5.00E-06	K.VIANLLNR.-	0
						1.50E-05	R.FVFTAVLPR.F	
						9.30E-01	R.LIFLYPMSK.L + Oxidation (M)	
	EAN84522.1	hypothetical protein, conserved	29041	105	3	0.0015	K.QVVQLLFPR.M	1
						0.00054	K.GALLPALVELSK.A	
						0.00013	R.MLAQDVPSTGASK.E + Oxidation (M)	
	EAN88964.1	glycosomal phosphoenolpyruvate carboxykinase, putative	59404	103	3	0.097	R.YVEFAHL.-	0
						0.00036	K.LSEESFAR.V	
						7.30E-05	R.VWLLNTGYAGGR.A	
	EAN83533.1	histone H2B, putative	12353	97	3	0.026	R.ELQTAVR.L	1
						0.016	R.LVLPADLAK.H	
						2.20E-06	K.IVNSFVNDLFER.I	
	EAN82747.1	Gim5A protein, putative	27268	88	3	0.0024	R.GVLNSGLTR.F	2
						1.60E-05	R.LSLLLNALSSK.T	
						0.1	R.AIAPNKLHLSDTVR.G	
	EAN88839.1	prohibitin, putative	31036	86	4	0.017	R.SGQGLLELR.R	1
						1.6	K.DLQMVNIR.L + Oxidation (M)	
						0.0014	R.YVVQENEQK.K	
						0.0088	R.ILPSISNEILK.A	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 7 cont.	EAN96063.1	cytochrome c1, heme protein, mitochondrial precursor, putative	30202	86	3	0.015	K.DVVNFLR.W	0
						0.0045	R.MTFTHFQGFMTR.E + 2 Oxidation (M)	
						0.0016	R.AAQFANNGSEPPDLQHSVFGK.E	
	EAN85170.1	dolichyl-phosphate beta-D-mannosyltransferase precursor, putative	29445	83	4	0.29	R.DLSPIGYK.I	0
						0.11	R.GLSSAVIHGISNSK.G	
						0.0085	K.YILVMDADLQHPPEAVPR.L + Oxidation (M)	
						0.00067	R.VLARPLTPLSDPMSGFFGLPK.E + Oxidation (M)	
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	81	3	0.0038	R.ALPNETVSK.M	3
						0.023	K.LVAFDTTSR.N	
						0.0025	R.EIAEEYRR.N	
	EAN97655.1	chaperonin HSP60, mitochondrial precursor	59991	76	1	3.70E-08	R.AVGVILQSVAEQSR.K	2
	EAN81053.1	alpha tubulin, putative	50549	74	2	0.014	R.LSVDYGKK.S	0
						1.30E-05	R.AVFLDLEPTVVDEIR.T	
	EAN94248.1	60S ribosomal protein L7, putative	27987	67	2	0.00045	R.QIFNTVFVR.L	2
						0.0033	R.AVEPYIAYGYPSLR.T	
	EAN92689.1	mitochondrial phosphate transporter, putative	34906	65	3	0.038	K.SLVPLWSR.Q	0
						0.0013	K.STLGLGTSGGTGK.K	
						0.15	R.YLNPDIPHTNSYYLK.C	
	EAN81757.1	mitochondrial processing peptidase, beta subunit, putative	31341	65	1	1.70E-06	R.AAASNFGDLVAASTK.S	0
	EAN87966.1	glucose-regulated protein 78, putative	71414	62	2	0.012	R.NSLESVAYSLR.N	0
						0.00043	R.ITPSVVAFTETER.L	
	EAN80947.1	tryparedoxin peroxidase, putative	22886	55	2	0.0078	K.AFQFVEK.H	3
						0.0012	R.GLFIIDPK.Q	
	EAN81369.1	3-oxo-5-alpha-steroid 4-dehydrogenase, putative	29941	54	3	0.008	K.GYVNSDPK.V	0
						0.4	K.DLGPQVGYR.T	
						0.096	R.ELESLFVHK.F	
	EAN80692.1	farnesyl synthetase, putative	32609	53	1	1.10E-05	R.AVLAGDFLLAR.A	1
	EAN83495.1	40S ribosomal protein S3a, putative	28554	51	1	3.70E-05	K.FVVQEVQGR.N	4
	EAN94685.1	methylthioadenosine phosphorylase, putative	33600	49	1	4.80E-05	R.LHEQGTSVTMEGPQFSTK.A + Oxidation (M)	1
	EAN91936.1	14-3-3 protein, putative	29450	48	1	5.60E-05	K.LNPVLSSEER.N	1
	EAN81327.1	cytochrome-B5 reductase, putative	34753	45	3	0.086	R.FYTPVTR.N	1
						0.0073	K.LVGAPPSVLK.A	
						0.12	K.MLQETMPKPAPK.N + 2 Oxidation (M)	
	EAN99627.1	hypothetical protein, conserved	35045	43	1	0.00014	R.SAETASELVSK.L	0

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 7 cont.	EAN87577.1	hypothetical protein, conserved	40702	42	2	2	K.LMSTMLR.E + 2 Oxidation (M)	1
						0.00015	K.SIFDKLDTLR.W	
	EAN82896.1	hypothetical protein, conserved	29537	42	2	0.017	M.VFLTLLR.T	1
						0.0054	R.YLVTTEVLR.F	
	EAN92511.1	prostaglandin F synthase, putative	32845	41	1	0.00022	R.AQDGAETANAVR.W	0
	EAN91318.1	I/6 autoantigen, putative	23495	40	1	0.00035	R.VSLQEIAAK.T	1
	EAN90694.1	serine/threonine protein kinase, putative	34153	38	1	0.00051	K.IIDKEQLVR.E	1
	EAN83816.1	60S ribosomal protein L5, putative	34902	37	1	0.00022	K.EADGSYSAVR.T	2
	EAN87359.1	mitochondrial malate dehydrogenase, putative	31921	33	1	0.00086	R.LFGVTTLDLVR.A	1
	EAN89428.1	mitochondrial carrier protein, putative	32010	32	1	0.0022	K.GFYAGIIPR.M	1
	EAN84418.1	60S ribosomal protein L13a, putative	32939	29	1	0.0068	R.SPSDIFLR.T	3
	EAN99701.1	hypothetical protein, conserved	31603	29	1	0.0036	R.IADSGAFIIR.A	0
	EAN88665.1	60S ribosomal protein L10, putative	25170	29	1	0.0036	R.ELEQISSEALEAAR.I	3
	EAN81251.1	40S ribosomal protein S8, putative	30143	25	1	0.0049	R.ILDVVYNATSNELVR.T	2
	EAN85113.1	elongation factor 1-gamma (EF-1-gamma), putative	47053	24	1	0.0069	K.AAAAAADGAEEEDEAPREK.K	0
	EAN99763.1	hypothetical protein, conserved	30157	23	1	0.0091	R.LLFIETAR.N	0
	EAN98359.1	lanosterol 14-alpha-demethylase, putative	55343	20	1	0.0024	K.ILGEIIVAR.E	1

TABLE S2 (BANDS 8-10): COMPLETE PEPTIDE LIST

Note: Table S2 shows the list of hits extracted from the Mascot html output results for the 1DGE bands. Mr indicates the theoretical molecular weight of the protein; Score refers to the Mascot protein score; # Pept refers to the number of peptides matched to each hit with the respective peptide e-value. Only unique peptides to each hit are indicated, not the ones shared with the previous hit. Additional gene copies column, indicates how many other annotated proteins are matched to the same set of peptides; meaning copies of the same gene product. This table is not filtered, meaning several proteins appear in more than one band; either due to proteolysis or carry over during the mass spectrometry analysis from one sample to the other one.

						Mascot		
Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies under same match**
Band 8	EAN94839.1	beta tubulin, putative	50520	536	17	7.2E-03	R.YLTASALFR.G	0
						7.3E-03	K.NMMQAADPR.H + Oxidation (M)	
						3.0E-04	K.NMMQAADPR.H + 2 Oxidation (M)	
						7.5E-03	K.LREEYPDR.I	
						6.0E-05	K.LAVNLVPFPR.L	
						7.6E-04	R.FPGQLNSDLR.K	
						7.4E-05	R.VGEQFTAMFR.R + Oxidation (M)	
						3.8E-05	R.KLAVNLVPFPR.L	
						1.6E-02	R.FPGQLNSDLRK.L	
						9.0E-08	R.INVYFDEATGGR.Y	
						2.7E-03	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						1.5E-04	K.EVDEQMLNVQNK.N + Oxidation (M)	
						9.2E-05	R.AVLIDLEPGTMDSVR.A	
						9.7E-06	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						5.4E-03	R.GLSVPELTQQMFDAK.N	
						1.8E-04	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
						2.9E-02	R.LHFFMMGFAPLTSR.G + 2 Oxidation (M)	
	EAN91944.1	glyceraldehyde 3-phosphate dehydrogenase, putative	39277	480	12	6.9E-02	K.TVDGVSVK.D	1
						7.6E-04	K.YNVTTTK.S	
						5.6E-02	R.NPADLPWGK.L	
						2.4E-04	K.ATLQNNLPK.E	
						3.1E-03	K.VVISAPASGGAK.T	
						2.9E-02	K.FKYNVTTTK.S	
						2.2E-03	R.KVVISAPASGGAK.T	
						9.2E-03	K.AVGMVIPSTQGK.L + Oxidation (M)	
						8.1E-04	R.AAAVNIIPSTTGAAK.A	
						3.9E-07	R.DTSIQEIDAALKR.A	
						4.7E-07	K.LGVEYVIESTGLFTAK.A	
						7.2E-10	R.VPTPDVSVVDLTFTAAR.D	
	EAN90286.1	glyceraldehyde 3-phosphate dehydrogenase, putative	39292	431	12	5.2E-01	K.YTVTTTK.S	1
	EAN83816.1	60S ribosomal protein L5, putative	34902	385	12	2.8E-03	R.QMVLQDK.T + Oxidation (M)	1
						1.8E-03	K.AILDVGLAR.T	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Mascot E-value	Sequence	Additional copies
8 cont.	EAN83816.1	cont.				1.8E-08	K.IAFLVASIR.E	
						9.4E-01	R.RQMVLQDK.T + Oxidation (M)	
						6.1E-05	K.EADGSYSAVR.T	
						9.5E-05	K.LGLANKFEGTK.E	
						9.2E-04	K.EKIAFLVASIR.E	
						3.5E-03	R.ILGLHVAEYLK.Q	
						6.0E-01	K.VVPNELEGMYK.K	
						4.7E-01	K.VVPNELEGMYK.K + Oxidation (M)	
						8.3E-03	K.VVPNELEGMYKK.A + Oxidation (M)	
						2.1E-06	R.ITNRDIIAQVVQAK.V	
	EAN82497.1	casein kinase, putative	38355	328	11	5.4E-02	R.IEFVHSK.S	1
						4.4E+00	R.ERGDVEQA.-	
						1.3E-03	R.GSLPWQGLK.A	
						3.4E-02	R.HPQLAFEAR.F	
						2.0E-06	K.IGAGSFGEIFR.G	
						1.4E-03	K.TRHPQLAFEAR.F	
						3.4E-03	R.GTNMQTGETVAIK.L + Oxidation (M)	
						1.6E-05	K.TTLMLAEQMIAR.I + Oxidation (M)	
						9.7E-08	K.TTLMLAEQMIAR.I + 2 Oxidation (M)	
						1.1E-02	R.DMKPDNFLMGTGK.K + 2 Oxidation (M)	
						1.2E-02	R.FEDKPDYSYLKR.L	
	EAN89795.1	pyruvate dehydrogenase E1 beta subunit, putative	38411	320	8	3.4E-02	R.TIIESIMK.T	0
						1.1E-03	R.TIIESIMK.T + Oxidation (M)	
						3.8E-03	K.GLLDKYGTSR.V	
						3.0E-03	K.EGIEAEVINLR.S	
						8.7E-05	K.VFAPYNSEDAR.G	
						1.0E-03	R.VGQHISMIGFSR.G + Oxidation (M)	
						1.1E-07	K.VFILGEEVGQYQGAYK.V	
						7.7E-08	K.DLEVASQPQVSDVLAVAR.R	
	EAN87359.1	mitochondrial malate dehydrogenase, putative	31921	302	7	3.6E-03	R.TFVAEAGGK.S	1
						3.7E-03	K.FEESLMEK.A + Oxidation (M)	
						1.6E-05	R.LFGVTTLDLVR.A	
						6.2E-05	K.VTGYTKEEINK.A	
						2.5E-05	R.VQYGGDEVVQAK.D	
						8.9E-06	R.DDLFNTNASIVR.D	
						6.6E-05	K.ALDGAELVLIPAGVPR.K	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
8 cont.	EAN82858.1	elongation factor 1-alpha (EF-1-alpha), putative	49694	285	10	1.7E-03	K.VGYNVEK.V	3
						1.2E-02	K.FAEIESK.I	
						7.0E-01	R.TIEKFEK.E	
						1.1E-02	R.QTVAVGIIK.A	
						4.8E-03	K.SVNFAQER.Y	
						3.5E-02	R.LPLQDVYK.I	
						2.4E-06	K.IGGIGTVPVGR.V	
						1.1E-02	K.STATGHLIYK.C	
						2.4E-02	R.EHALLAFTLGVK.Q	
						2.3E-04	K.VHMNLVVVGHVDAGK.S + Oxidation (M)	
	EAN82496.1	casein kinase, putative	38351	273	9	2.7E-03	K.TRHPQLAFEVR.F	0
	EAN97324.1	pyruvate dehydrogenase E1 beta subunit, putative	38393	266	8	1.3E-02	K.DLELASQPQVSDVLAVAHR.V	0
	EAN86374.1	ATP synthase F1 subunit gamma protein, putative	34733	250	8	6.3E-02	R.TSSLYNK.T	1
						6.6E-03	R.FVSAGVQK.H	
						2.6E+00	K.LYPNEFK.Y	
						4.9E-02	K.MVLMPIGK.R + 2 Oxidation (M)	
						1.2E-03	K.HAVYNIPSFEK.W	
						3.1E-04	K.NALVYIPITTNR.G	
						2.6E-10	R.LVAVEGQLTNISTLK.Q	
						2.2E-02	R.LVAVEGQLTNISTLKQR.T	
	EAN81053.1	alpha tubulin, putative	50549	229	6	1.1E-02	R.LSVDYGKK.S	0
						3.7E-04	K.DVNAAVATIK.T	
						3.6E-03	R.IDHKFDLMYSK.R + Oxidation (M)	
						5.8E-10	R.LIGQVVSALTASLR.F	
						1.8E-02	R.NLDIERPTYTNLNR.L	
						6.2E-03	R.IHFVLTSYAPVISAEK.A	
	EAN94545.1	hypothetical protein, conserved	24439	193	4	1.6E-03	K.ENVKVER.K	0
						2.2E-04	R.SYITYAIALLR.G	
						2.5E-05	R.GEDGKVQNDTIK.I	
						7.8E-08	K.EQDDPEPGESAGENR.N	
	EAN81197.1	hypothetical protein, conserved	30269	148	4	1.0E-02	K.NLKPGVLLTHS.-	1
						3.0E-08	K.FSVDVEYAPR.C	
						5.1E-04	R.YAHAGYALAVR.T	
						4.6E-01	K.SLTLYKDFNK.D	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
8 cont.	EAN95595.1	40S ribosomal protein S6, putative	28333	147	3	1.1E-03	R.GAVGFNTFR.G	1
						1.2E-05	R.LGNEVDGAIFGDAFR.G	
						4.9E-06	K.TGEQPIEGVTDVSVPR.R	
	EAN83533.1	histone H2B, putative	12353	139	3	2.0E-03	R.LVLPADLAK.H	1
						3.1E-06	R.IASEAATVVR.V	
						4.1E-06	K.IVNSFVNDLFER.I	
	EAN87011.1	RNA-binding protein, putative	31148	136	4	2.1E-03	R.YTDLIADR.M	1
						1.1E-04	R.SQQVNEFGR.K	
						1.2E-04	R.ETFQQVGNVER.A	
						9.1E-02	R.LFDDGPRPPIVQR.G	
	EAN91782.1	hypothetical protein, conserved	36162	134	4	5.9E-03	K.LSTIEATR.R	0
						1.2E+00	K.LSTIEATRR.L	
						1.5E-04	K.VAVDLGGEGMR.Y + Oxidation (M)	
						4.2E-06	R.LVAPPSYIADQLFASAGR.L	
	EAN87428.1	hypothetical protein, conserved	37186	134	5	1.7E-01	K.EYLVEPK.M	0
						1.9E-01	R.VSFPATEEK.A	
						7.4E-06	R.LDDGLTPEDR.A	
						1.1E-03	K.SNVLSEYITR.M	
						2.3E-02	R.RMVETSLNYGLQR.S + Oxidation (M)	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	114	3	7.7E-04	R.SATGVAFSR.S	1
						2.4E-03	R.GTKFDTDLTAK.D	
						3.4E-05	R.TPQQIGQSLSLR.W	
	EAN94284.1	reiske iron-sulfur protein precursor, putative	34159	112	4	8.0E-03	R.GRPVFVYK.R	1
						3.9E-05	K.LPEELEDR.A	
						5.3E-03	R.IETTAGVALK.D	
						5.3E-02	R.QGPAPLNLEVPPYK.W	
	EAN81270.1	sterol 24-c-methyltransferase, putative	41138	112	3	2.4E-02	K.GQVIEALK.A	1
						3.9E-06	K.GAEILEEAAR.S	
						3.0E-03	R.VLEFAGLAPSGTHK.G	
	EAN83495.1	40S ribosomal protein S3a, putative	28554	107	2	1.5E-03	K.FVVQEVQGR.N	4
						1.6E-07	K.VNINEAVTLLTR.N	
	EAN90616.1	glycosomal malate dehydrogenase, putative	34347	105	2	2.6E-05	K.LLGVSLLDGLR.A	1
						3.0E-06	R.GSATLSMAEAGAR.F + Oxidation (M)	
	EAN92511.1	prostaglandin F synthase, putative	32845	100	2	2.2E-03	K.SPAQVVIR.W	0
						2.0E-07	R.AQDGAETANAVR.W	
	EAN87575.1	hypothetical protein, conserved	37110	100	4	2.7E-01	R.VSFPATEK.A	0

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
8 cont.	EAN90238.1	prohibitin, putative	33115	98	3	6.8E-02	K.EYTSAVEAK.Q	1
						4.7E-04	R.DLQTVNLAVR.V	
						9.3E-05	K.GAILLAEGEAEAAK.L	
	EAN83852.1	heat shock 70 kDa protein, putative	41044	90	3	9.4E-03	R.GTLQPVER.V	1
						3.0E-03	K.DAGTIAGMEVLR.I + Oxidation (M)	
						1.2E-03	R.AVHDVVLVGGSTR.I	
	EAN85971.1	NADH-cytochrome B5 reductase, putative	34825	88	2	5.2E-04	R.GPVGNFEYLGK.G	1
						3.8E-05	K.YGTGYVDEATLR.A	
	EAN85276.1	hypothetical protein	52756	87	1	3.9E-09	R.FADANEENVPAAQVNR.V	1
	EAN92507.1	fibrillarin, putative	30769	82	3	5.6E-01	K.EQASLEPFER.D	1
						1.2E-01	R.NNIVPILEDAR.Y	
						8.4E-06	R.VSGTIAGETESTEFR.V	
	EAN95882.1	activated protein kinase C receptor, putative	35649	82	2	8.0E-05	K.DVLSVTFSPDNR.Q	1
						8.2E-04	R.DNTLIAWGSNMDR.N + Oxidation (M)	
	EAN98272.1	eukaryotic initiation factor 4a, putative	49984	74	2	8.8E-04	R.VLVTTDLVAR.G	1
						1.2E-04	K.LQAGSIVAVGTPGR.V	
	EAN80947.1	tryparedoxin peroxidase, putative	22886	66	3	5.7E-01	K.AFQFVEK.H	3
						3.7E-04	R.GLFIIDPK.Q	
						2.0E-03	R.QITVNDLPVGR.D	
	EAN88371.1	glutathione-S-transferase/glutaredoxin, putative	35538	66	4	2.6E-02	K.EISSFAYK.K	1
						1.3E-02	K.EHPQILLYR.Y	
						4.4E-02	R.LHGEINTFIEK.A	
						7.4E-01	R.LLTLEFNSSLYR.A	
	EAN87824.1	hypothetical protein, conserved	29236	65	2	2.5E-02	R.FVFTAVLPR.F	1
						9.0E-05	K.IINLSAEEIR.A	
	EAN87301.1	hypothetical protein, conserved	33827	63	2	9.5E-03	R.LATSYGVLR.Y	1
						3.7E-04	R.YAYLSAAVR.A	
	EAN88964.1	Glycosomal phosphoenolpyruvate carboxykinase, putative	59404	59	2	1.5E-03	K.TTLSADPHR.N	1
						1.3E-02	K.TEKDIYDAVR.F	
	EAN97655.1	chaperonin HSP60, mitochondrial precursor	59991	58	1	2.7E-06	R.AVGVILQSVAEQSR.K	2
	EAN84262.1	tricarboxylate carrier, putative	36312	57	2	9.2E-01	K.VVDEDGEVR.G	0
						1.3E-05	R.VPSGTLQATVIR.A	
	EAN99701.1	hypothetical protein, conserved	31603	57	1	7.3E-06	R.IADSGAFIIR.A	0
	EAN93401.1	hypothetical protein, conserved	36346	54	3	2.6E-01	R.QVVYAPAR.L	1
						4.8E-01	K.LPSGQAAELK.Y	
						1.2E-03	K.GASPETAPSIADR.A	
	EAN98983.1	succinyl-CoA synthetase alpha subunit, putative	32274	52	1	1.9E-05	R.SGTLTYEAVAQTTAK.S	0

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
8 cont.	EAN85330.1	histone H2A, putative	14385	49	2	1.4E-02	R.GGVMPSLNK.A + Oxidation (M)	13
						5.7E-03	K.AGLIFPVGR.V	
	EAN87340.1	RNA-binding protein, putative	50174	49	1	4.6E-05	R.NIAENTTEQQLR.E	1
	EAN85190.1	hypothetical protein, conserved	43072	47	1	8.2E-05	K.AILEYNATLAER.E	1
	EAN87214.1	hypothetical protein, conserved	36338	47	2	1.7E-02	R.HQTPLDDGVK.L	3
						1.5E-02	R.LAHQEYTVYELK.S	
	EAN83925.1	40S ribosomal protein S2, putative	28727	45	1	1.8E-05	R.GAGIVAAPVPK.K	3
	EAN82415.1	40S ribosomal protein SA, putative	28114	45	2	2.7E-03	R.VLLVTDPR.T	2
						3.3E-02	R.FIPGTFTNQIQK.K	
	EAN88258.1	hypothetical protein, conserved	32143	45	1	9.9E-05	R.ALEIAQQGAEAK.G	1
	EAN90413.1	ADP,ATP carrier protein 1, mitochondrial precursor, putative	35303	43	1	1.5E-04	K.LLVQNQGEMIK.Q + Oxidation (M)	1
	EAN84604.1	histone H3, putative	21714	38	1	5.1E-04	R.STDLLLQK.A	7
	EAN98396.1	hypothetical protein, conserved	64335	38	2	3.2E-03	K.AANDAVEAALK.K	0
						2.2E-01	K.LSTATPHFSAAPPELK.E	
	EAN87271.1	glycosomal membrane protein, putative	24137	38	1	6.5E-04	K.SVSSSITDGR.S	1
	EAN87634.1	60S ribosomal protein L7a, putative	34671	38	1	2.3E-04	K.KAPLSVVTGLQEVTR.T	1
	EAN86269.1	60S ribosomal protein L19, putative	37755	35	1	1.5E-03	R.QLAEQLAAK.R	3
	EAN99009.1	peroxin-2, putative	37929	34	1	1.0E-03	R.LVYGSQSTQR.V	0
	EAN85108.1	hypothetical protein, conserved	45955	34	1	9.0E-04	R.STAENVSSDAMGNLR.G + Oxidation (M)	1
	EAO00202.1	6-phospho-1-fructokinase, putative	54100	34	1	1.2E-03	R.ELEAISLVR.E	0
	EAN87845.1	40S ribosomal protein S4, putative	30998	31	1	1.9E-03	R.ASNIFVIGK.D	2
	EAN89722.1	60S ribosomal protein L34, putative	19668	30	1	6.2E-03	R.AFLIEEQR.I	3
	EAN94586.1	hypothetical protein, conserved	30181	29	1	2.2E-03	R.VLEATLSPLEK.A	1
	EAN87063.1	hypothetical protein, conserved	44364	21	1	1.5E-02	R.EDLNEVER.K	0
	EAN86096.1	fructose-bisphosphate aldolase, glycosomal, putative	23483	26	1	1.3E-02	R.FNAETLAR.Y	3
	EAN87418.1	heat shock protein-like protein, putative	36225	24	1	6.6E-03	R.NEDLSNPR.G	1
	EAN82309.1	hypothetical protein, conserved	26480	23	2	1.5E+00	R.MLTTNPLR.Y + Oxidation (M)	1
						8.4E-02	R.ELEVSTLAEK.N	
	EAN82747.1	Gim5A protein, putative	27268	21	1	3.7E-02	R.GVLNSGLTR.F	3
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	20	1	4.3E-02	K.VAISLPSR.M	1
	EAN97099.1	hypothetical protein, conserved	34072	20	1	2.8E-02	R.AFLYEAEVK.T	0
	EAN93711.1	dihydrolipoamide acetyltransferase precursor, putative	49984	19	1	3.6E-02	K.ITVNDYTIK.A	1
	EAN85329.1	hypothetical protein, conserved	72639	19	1	3.9E-02	R.EIESSISALRNDILR.Q	0
	EAN97577.1	hypothetical protein, conserved	56966	18	1	4.2E-02	R.QQAAAEALR.L	0
	EAN88802.1	hypothetical protein, conserved	28041	18	1	8.1E-02	R.LPSETADKK.G	1
	EAN94012.1	hypothetical protein, conserved	30503	17	1	5.4E-02	R.FLSVSYGSPETR.M	1

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
Band 9	EAN91944.1	glyceraldehyde 3-phosphate dehydrogenase, putative	39277	779	22	1.3E-01	K.TVDGVSVK.D	1
						1.2E-01	K.LTGMSFR.V	
						1.1E-05	K.VGINGFGR.I	
						1.8E-04	K.YNVTTTK.S	
						1.1E-02	R.NPADLPWGK.L	
						2.1E-04	K.ATLQNNLPK.E	
						1.1E-02	K.VVISAPASGGAK.T	
						1.2E-02	K.FKYNVTTTK.S	
						6.0E-04	K.DDTLVVNGHR.I	
						4.2E-04	R.KVVISAPASGGAK.T	
						1.1E-03	K.AVGMVIPSTQGK.L	
						6.0E-04	K.AVGMVIPSTQGK.L + Oxidation (M)	
						5.2E-02	K.TVDGVSVKDWR.G	
						2.0E-06	R.DTSIQEIDAALK.R	
						7.9E-06	R.AAAVNIIPSTTGAAK.A	
						3.1E-07	R.DTSIQEIDAALKR.A	
						1.1E-06	K.LGVEYVIESTGLFTAK.A	
						1.2E-04	K.SSPSVAKDDTLVVNGHR.I	
						1.2E-05	R.VPTPDVSVVDLTFTAAR.D	
						4.4E-04	K.IVSWYDNEWGYSHR.V	
						2.3E-02	K.EGFGVQTGLMTTIHSYTATQK.T	
						1.6E-02	K.EGFGVQTGLMTTIHSYTATQK.T + Oxidation (M)	
	EAN90286.1	glyceraldehyde 3-phosphate dehydrogenase, putative	39292	740	21	7.3E-03	K.FKYTVTTTK.S	1
	EAN82665.1	60S ribosomal protein L4, putative	41429	488	18	8.1E-02	K.EAMAFLK.A	0
						2.7E-01	K.EAMAFLK.A + Oxidation (M)	
						1.1E-03	R.IMQSEEVR.R + Oxidation (M)	
						5.8E-01	R.LRLNPFQK.K	
						8.5E-06	K.AIGAVDDVNR.V	
						1.1E-02	R.LTQPTNGFR.N	
						1.7E-03	K.TKEAMAFLK.A	
						1.2E-05	R.GPMLVMPDNK.G + 2 Oxidation (M)	
						3.2E-01	R.IMQSEEVRR.V	
						4.4E-01	R.IMQSEEVRR.V + Oxidation (M)	
						5.7E-02	R.RGPMLVMPDNK.G + 2 Oxidation (M)	
						6.9E-02	R.HDIVQFVHTNMAK.N + Oxidation (M)	
						9.3E-05	K.AIGAVDDVNRVNDSR.E	
						3.1E-05	R.LSGMNHSAESWGTGR.A + Oxidation (M)	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
9 cont.	EAN82665.1	cont.				2.2E-03	K.GFMLPAPMLTNTDVTR.I + Oxidation (M)	
						1.5E-01	K.GFMLPAPMLTNTDVTR.I + 2 Oxidation (M)	
						1.3E-03	K.KGFMLPAPMLTNTDVTR.I + 2 Oxidation (M)	
						3.1E-06	K.IENVAEVPLVVEDAVQGYEK.T	
	EAN94839.1	beta tubulin, putative	50520	458	14	3.2E-01	R.YLTASALFR.G	0
						2.6E-02	K.LREEYPDR.I	
						1.7E-06	K.LAVNLVPFPR.L	
						8.1E-03	R.FPGQLNSDLR.K	
						3.2E-02	R.VGEQFTAMFR.R	
						9.0E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						8.4E-07	R.KLAVNLVPFPR.L	
						1.1E-07	R.INVYFDEATGGR.Y	
						9.4E-04	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						1.6E-05	K.EVDEQMLNVQNK.N	
						5.2E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						1.3E-05	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						8.2E-01	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
						3.2E-01	R.LHFFMMGFAPLTSR.G + 2 Oxidation	
	EAN86462.1	aspartate aminotransferase, mitochondrial, putative	46511	399	11	6.9E-03	K.NFGLYGLR.C	0
						1.6E-01	K.GIDLPGMLK.S	
						1.4E-02	K.SLEAMPER.S + Oxidation (M)	
						5.4E-02	K.GIDLPGMLK.S + Oxidation (M)	
						1.4E-03	K.VNLAVGVYR.D	
						6.7E-07	R.VLSQYALLIR.T	
						4.2E-02	R.QIGMMSYTGLTK.E + Oxidation (M)	
						1.2E-04	R.DDANRPFVLESVK.R	
						8.2E-08	R.AAISGLNSTNVSYVAK.A	
						1.7E-05	R.DDANRPFVLESVKR.S	
						1.3E-05	R.SDTGSDMEYAPINGMR.S + 2 Oxidation (M)	
	EAN87634.1	60S ribosomal protein L7a, putative	34671	295	8	4.9E-01	R.LFDVATEK.K	1
						4.2E-03	R.NAGKDAAAVM.- + Oxidation (M)	
						3.4E-03	R.ANKVPYAIVK.D	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
9 cont.	EAN87634.1	cont.				7.2E-04	R.QWGGLQLSLR.S	
						4.1E-03	R.WPTFVTMQR.K + Oxidation (M)	
						7.3E-03	K.NFGIGHDVPYAR.D	
						5.8E-10	K.APLSVVTGLQEVTR.T	
						3.4E-05	K.KAPLSVVTGLQEVTR.T	
	EAN83852.1	heat shock 70 kDa protein, putative	41044	243	8	2.3E-02	R.GTLQPVER.V	0
						1.1E-04	R.VEIIANDQGNR.T	
						7.5E-05	K.DAGTIAGMEVLR.I	
						8.7E-03	K.DAGTIAGMEVLR.I + Oxidation (M)	
						5.7E-02	R.AVHDVVLVGGSTR.I	
						7.6E-04	K.VMQLVSDFFGGK.E + Oxidation (M)	
						4.4E-04	R.TTPSYVAFTDTER.L	
						2.3E-04	K.NQVAMNPTNTVFDAK.R + Oxidation	
	EAN82857.1	elongation factor 1-alpha (EF-1-alpha), putative	48884	234	6	9.3E-04	K.SVNFAQER.Y	5
						8.7E-03	R.LPLQDVYK.I	
						1.4E-06	K.IGGIGTVPVGR.V	
						6.5E-03	K.STATGHLIYK.C	
						2.0E-05	R.FIPISGWQGDNMIDK.S + Oxidation (M)	
						4.1E-03	R.VETGTMKPGDVVTFAPANVTTEVK.S + Oxidation (M)	
	EAN92220.1	pyruvate dehydrogenase E1 component alpha subunit, putative	43381	222	7	4.2E-05	K.SDIQDVR.K	0
						5.0E-02	K.SDIQDVRK.T	
						4.9E-02	R.TTQGTVYAKP.-	
						1.5E-02	R.AAYQPEMYR.R + Oxidation (M)	
						4.1E-03	K.TIPINPQKPFK.L	
						2.4E-03	K.EVDQQLQPAEK.Q	
						1.3E-05	K.GPIVLEFDSYR.Y	
	EAN99952.1	hypothetical protein, conserved	42578	220	7	4.8E-03	K.IIQAPLR.S	0
						1.7E-05	R.ISLLYNAR.R	
						6.3E-05	R.EVISMDALR.S + Oxidation (M)	
						5.5E-03	K.AIAMLGTSPGVLPVR.E	
						4.3E-04	K.AIAMLGTSPGVLPVR.E + Oxidation (M)	
						6.7E-04	R.SLPNPPSNSGADATER.H	
						6.7E-03	R.LELDSPHNTMLAQLR.E + Oxidation (M)	
	EAN86097.1	fructose-bisphosphate aldolase, glycosomal, putative	41279	216	4	8.9E-05	R.FNAETLAR.Y	2
						5.0E-05	K.IQNGTVSEAAVR.F	
						2.2E-06	K.ASTGETFVQLLQR.K	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
9 cont.	EAN86097.1	cont.				2.8E-06	R.ATPGQVAQYTVSTLAR.V	
	EAO00025.1	alcohol dehydrogenase, putative	42442	200	4	3.2E-08	K.NAAAAAIDAIR.A	1
						2.2E-04	R.FAVITDEKR.H	
						1.3E-02	K.DIPALAESALK.D	
						5.0E-06	K.VSYLGVGALDSATSK.M	
	EAN93231.1	pyruvate dehydrogenase E1 component alpha subunit, putative	22293	183	6	9.4E-02	K.EVDQQLLPAEK.Q	0
	EAN97551.1	hypothetical protein, conserved	43296	180	7	3.2E-04	K.EVLALQAR.I	0
						2.5E-04	K.EIDALLGGAEK.M	
						7.7E-04	R.NTSIAIEMIK.R + Oxidation (M)	
						1.1E-01	R.AEQGLPSALLPK.N	
						2.2E-01	R.LLKEVLALQAR.I	
						2.2E-04	K.WVVYTPEDEVK.L	
	EAN80947.1	tryparedoxin peroxidase, putative	22886	179	5	4.1E-02	R.DVDEALR.L	3
						1.1E-02	K.AFQFVEK.H	
						7.1E-04	R.GLFIIDPK.Q	
						3.6E-04	R.QITVNDLPVGR.D	
						1.1E-06	R.GGLGQMNIPILADK.T + Oxidation	
	EAN90786.1	RNA-binding protein, putative	36346	168	4	2.1E-03	R.NNEIGEVSR.V	0
						1.2E-04	R.VQALVQFDSK.V	
						6.7E-05	K.SAQQLVDFFR.Q	
						6.9E-05	R.QMNQALVEMESTK.S + 2 Oxidation	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	163	4	2.3E-04	R.SATGVAFSR.S	1
						3.4E-04	K.GLPQEVVEQVK.A	
						1.8E-04	R.EMILADTLEGR.K	
						1.3E-04	R.TPQQIGQSLSLR.W	
	EAN91216.1	protein disulfide isomerase, putative	42060	159	4	4.1E-03	K.VGVNDELSK.V	0
						3.9E-05	R.NNILASLKDE.-	
						8.0E-05	K.NRLPSGDLSEK.V	
						3.0E-03	R.NFDAVVMDEAK.D + Oxidation	
	EAN92109.1	hypothetical protein, conserved	38049	156	4	1.8E-03	K.FMIIAVPETVR.L + Oxidation (M)	1
						4.3E-04	R.AALQSSIPLLSAR.Y	
						5.5E-04	R.GQYVFTPSGSGVSK.N	
						1.3E-05	R.ILYGPTYSSVTDR.L	
	EAN85055.1	histone H4, putative	11177	146	3	3.9E-04	R.ISGIIYDEVR.G	7
						4.9E-05	R.DATAYTEYSR.K	
						2.7E-06	K.TVTAVDVVNALR.K	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
9 cont.	EAN95952.1	hypothetical protein, conserved	43691	144	3	1.8E-04	R.FVFTAVLPR.F	0
						7.9E-05	K.IINLSAEEIR.A	
						8.5E-06	R.VIYLNLNEEPR.T	
	EAN81533.1	histone H4, putative	11163	143	3	7.4E-04	R.ISGVIYDEVR.G	10
	EAN84988.1	hypothetical protein, conserved	43368	136	3	1.3E-05	K.VGPWAIAGR.N	1
						1.1E-04	R.QGLGSEVAEVK.A	
						1.3E-04	R.THYVDSTGEYNFVR.Q	
	EAN81053.1	alpha tubulin, putative	50549	128	6	9.0E-03	R.LSVDYGKK.S	0
						9.2E-05	K.EDAANNYAR.G	
						2.2E-01	R.QLFHPEQLISGK.E	
						3.7E-01	R.TIQFVDWSPTGFK.C	
						1.1E-01	R.NLDIERPTYTNLNR.L	
						2.0E-03	K.AYHEQLSVSEISNAVFEPASMMTK.C + 2 Oxidat	
	EAN98272.1	eukaryotic initiation factor 4a, putative	49984	120	3	2.3E-05	R.VLVTTDLVAR.G	1
						3.2E-03	K.TGAFSIGLLQR.L	
						9.8E-05	K.LQAGSIVAVGTPGR.V	
	EAN89624.1	oxidoreductase, putative	36790	112	2	4.5E-05	K.VVLLAFMGGAK.V + Oxidation (M)	0
						6.8E-07	K.GSSEILGMEVSGVVEK.V + Oxidation	
	EAN83800.1	D-isomer specific 2-hydroxyacid dehydrogenase-protein, putative	28659	112	2	9.5E-04	R.FIGLVNEYAK.T	1
						8.7E-08	K.VGIIGYGDIGQASAK.L	
	EAN81197.1	hypothetical protein, conserved	30269	110	3	5.0E-05	K.FSVDVEYAPR.C	3
						3.6E-03	K.LFVNPMATSDGK.F + Oxidation (M)	
						1.3E-03	R.SYTTSFVTPIPK.C	
	EAN97019.1	hypothetical protein, conserved	38819	107	4	3.5E-03	K.AAVGLPFGGER.I	1
						6.8E-01	R.NAQNVMISSK.C + Oxidation (M)	
						7.9E-05	K.LVSYESMFR.G	
						2.8E-02	K.GTSLSHGFTAVNSLKK.G	
	EAN95492.1	vacuolar-type Ca2+-ATPase, putative	123386	92	2	1.2E-03	R.LDELAGLIGR.F	1
						3.1E-06	R.QLMEENSAQPIAVIR.D + Oxidation	
	EAN82629.1	heat shock protein 85, putative	81244	92	2	4.3E-05	K.AELVNNLGTIAR.S	2
						1.6E-04	R.GVVDSEDLPLNISR.E	
	EAN83191.1	eukaryotic translation initiation factor 5, putative	43635	91	2	4.0E-04	K.FFQSEIGAQR.T	1
						3.0E-05	R.VTGTALLDAATDEATK.S	
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	88	5	1.3E+00	R.ALPNETVSK.M	3
						2.1E-02	K.LVAFDTTSR.N	
						1.8E-01	R.EIAEEYRR.N	
						2.0E-02	R.SYVETQLLPAMK.A + Oxidation (M)	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
9 cont.	EAN82710.1	cont.				5.4E-03	K.ANLWATLPGDGGVTK.G	
	EAN86484.1	hypothetical protein, conserved	50613	86	4	2.2E-03	R.AELNEAR.S	1
						4.7E-01	R.LYGETLR.G	
						1.3E+00	R.ARAELNEAR.S	
						2.1E-03	K.FDAAVLNSHGK.L	
	EAN85108.1	hypothetical protein, conserved	45955	85	2	1.5E-03	R.VLAFSLR.S	1
						2.1E-05	R.AAFATPAEFK.V	
	EAN87049.1	vacuolar ATP synthase, putative	41526	81	2	5.7E-05	R.FFSADGDFAR.D	0
						3.7E-04	R.TVLTFAANTMGMR.E + 2 Oxidation	
	EAN95821.1	fatty acid desaturase, putative	47196	77	2	6.3E-02	R.EIQEKIPVK.Y	0
						1.3E-06	R.EILGATYITDER.S	
	EAN88264.1	histone H2A, putative	14345	69	3	3.0E-01	R.GGVMPSLNK.A + Oxidation (M)	3
						8.7E-04	K.AGLIFPVGR.V	
						1.1E-02	R.HDDDLGTLLK.D	
	EAN83816.1	60S ribosomal protein L5, putative	34902	68	2	3.3E-03	K.AILDVGLAR.T	2
						1.1E-04	R.DIIAQVVQAK.V	
	EAN83988.1	fructose-1,6-bisphosphatase, cytosolic, putative	38159	68	2	2.6E-03	R.LDVIANNAFK.A	1
						6.7E-04	R.LLYEAAPLAMLVEQAGGK.A + Oxidation	
	EAN81547.1	NAD(P)-dependent steroid dehydrogenase protein, putative	26207	68	2	2.4E-03	K.FYIVTDGR.T	0
						9.2E-04	R.DNLFLPNMLEAAGTGK.L + Oxidation	
	EAN87340.1	RNA-binding protein, putative	50174	65	1	9.3E-07	R.NIAENTTEQQLR.E	1
	EAN91740.1	hypothetical protein, conserved	40379	65	2	7.7E-03	R.LVQNAYK.I	0
						1.4E-03	K.VAYIDPQR.V	
	EAN85330.1	histone H2A, putative	14385	65	3	2.5E-02	R.HDDDLGMLLK.D	9
	EAN84095.1	hypothetical protein, conserved	33996	64	2	1.6E-03	R.WVAAEFIAR.T	3
						4.2E-03	R.QEPFLLGTLR.S	
	EAN95983.1	ATPase beta subunit, putative	55980	60	1	1.9E-06	K.LADQAAEDTILTTGIK.V	0
	EAN85276.1	hypothetical protein	52756	60	1	3.0E-06	R.FADANEENVPAAQVNR.V	1
	EAN84918.1	ATPase alpha subunit, putative	24506	59	2	8.4E-02	R.FVALFNQK.Q	0
						1.6E-04	R.VGSSAQNVAMK.G + Oxidation	
	EAN82747.1	Gim5A protein, putative	27268	58	1	1.1E-06	R.LSLLLNALSSK.T	2
	EAN98983.1	succinyl-CoA synthetase alpha subunit, putative	32274	53	1	1.4E-05	R.SGTLTYEAVAQTTAK.S	0
	EAN95493.1	hypothetical protein, conserved	38907	51	3	2.1E-03	R.EYVEFYTR.L	1
						8.1E-01	R.MGTLLQPMAQR.M + 2 Oxidation (M)	
						1.0E-01	R.DTVISEEFHLHDKEGR.M	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
9 cont.	EAN85190.1	hypothetical protein, conserved	43072	51	3	5.6E-04	K.AAAALALIK.Q	1
						1.1E+00	K.ELEEEDIR.M	
						1.6E-01	M.PLPPLEEAPR.S	
	EAN99001.1	serine/threonine protein kinase, putative	55378	48	2	1.8E-01	R.YRDVFVER.N	0
						6.4E-04	K.GSFAYVVLVR.R	
	EAN98359.1	lanosterol 14-alpha-demethylase, putative	55343	45	1	7.9E-06	K.ILGEIIVAR.E	1
	EAN92822.1	ribosomal protein L3, putative	48865	43	1	1.4E-04	K.SITPMGGFVGYGTVR.N + Oxidation	1
	EAN81270.1	sterol 24-c-methyltransferase, putative	41138	42	1	1.9E-04	K.GAEILEEAAR.S	1
	EAN84370.1	heat shock 70 kDa protein, mitochondrial precursor, putative	71585	41	2	1.7E+00	R.SKFESLAEK.L	0
						4.8E-04	K.DAGTIAGLNVIR.V	
	EAN81497.1	retrotransposon hot spot (RHS) protein, putative	91127	41	3	2.6E-01	R.LMVLTSDK.G + Oxidation (M) not unique	4
						7.7E-02	R.VLIGTPGIGK.S	
						3.6E-01	K.GYIIYDVAK.K	
	EAN89176.1	NADH dehydrogenase, putative	56934	41	1	4.4E-05	K.LPLPTLAAVASR.Q	1
	EAN88252.1	ribonucleoside-diphosphate reductase small chain, putative	39426	40	1	1.8E-04	R.LLVALGNER.H	1
	EAN81916.1	ATP synthase, alpha chain, mitochondrial precursor, putative	25912	40	1	1.4E-04	K.TSIAVSTIINQVR.I	0
	EAN89677.1	hypothetical protein, conserved	34143	39	1	3.0E-04	K.NGDLLVLSPTTR.H	0
	EAN90413.1	ADP,ATP carrier protein 1, mitochondrial precursor, putative	35303	38	1	4.1E-04	K.LLVQNQGEMIK.Q + Oxidation	1
	EAN84604.1	histone H3, putative	21714	38	1	5.9E-04	R.STDLLLQK.A	7
	EAN87271.1	glycosomal membrane protein, putative	24137	37	1	8.5E-04	K.SVSSSITDGR.S	1
	EAN97655.1	chaperonin HSP60, mitochondrial precursor	59991	37	2	4.8E-01	R.AVSAVATTLGPK.G	2
						2.0E-03	R.AVGVILQSVAEQSR.K	
	EAO00075.1	cytochrome C oxidase subunit IV, putative	39137	37	2	2.7E-02	R.ILDIYAR.A	1
						7.6E-02	R.TEEETAFAK.S	
	EAN95757.1	prostaglandin F2alpha synthase, putative	14719	36	1	1.3E-03	K.FIANPDLVER.A	1
	EAN85971.1	NADH-cytochrome B5 reductase, putative	34825	33	1	2.1E-03	R.GPVGNFEYLGK.G	1
	EAN98357.1	pretranslocation protein, alpha subunit, putative	53952	32	2	1.2E-01	R.AVFEGIQK.I	1
						4.1E-02	K.DLGYGFLK.Q	
	EAN98716.1	hypothetical protein, conserved	125785	31	1	2.2E-03	K.NELDDIER.K	0
	EAN80688.1	heat shock protein 70 (HSP70), putative	15424	31	1	2.4E-03	K.DAGTIAGLNVVR.I	1
	EAN97971.1	hypothetical protein, conserved	39401	31	1	1.4E-03	R.ELELQQNIIR.S	0
	EAN89722.1	60S ribosomal protein L34, putative	19668	30	1	5.0E-03	R.AFLIEEQR.I	3
	EAN83495.1	40S ribosomal protein S3a, putative	28554	30	1	4.7E-03	K.FVVQEVQGR.N	4

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
9 cont.	EAN84364.1	nucleosome assembly protein-like protein, putative	51024	28	1	2.9E-03	R.VVTPQEEK.S	1
	EAN81827.1	hypothetical protein, conserved	39880	28	1	3.1E-03	R.DAPLPVALEVPTR.D	1
	EAN94487.1	50S ribosomal protein L17, putative	35432	28	1	2.3E-03	R.ILADHVVDLAK.A	0
	EAN89399.1	nitrate reductase, putative	52680	27	1	5.8E-03	K.LGEEVGEVFER.I	0
	EAN91887.1	mitochondrial DNA polymerase beta, putative	45752	27	1	4.1E-03	R.SVPTALLTFTGSK.N	1
	EAN99050.1	phosphoglycerate kinase, putative	100682	25	1	7.6E-03	K.TLVFSQLENAAK.F	0
	EAN87059.1	hypothetical protein, conserved	21263	24	2	2.2E+00	K.HVPSSFLLK.D	0
						1.3E-02	K.SVGLTAALSPK.Q	
	EAN87305.1	eukaryotic translation initiation factor 3 subunit, putative	38050	24	2	4.8E-01	R.EGDLLFSTAK.E	1
						6.5E-02	R.GFASGAFDGLVK.L	
	EAN83529.1	hypothetical protein, conserved	93603	23	1	9.1E-03	R.SSVLVVFGAK.K	1
	EAN87488.1	hypothetical protein, conserved	38355	21	1	1.5E-02	R.IPAQQPASK.-	1
	EAN97370.1	isopentenyl-diphosphate delta-isomerase, putative	19746	20	1	2.4E-02	K.AALESPER.V	0
	EAN87190.1	elongation factor 2, putative	95336	20	1	3.5E-02	K.SQANTLTLSVR.Q	2
	EAN88283.1	hypothetical protein, conserved	46409	18	1	2.6E-02	R.TLLTTLSEAHR.Q	0
	EAN97099.1	hypothetical protein, conserved	34072	18	1	3.1E-02	R.AFLYEAEVK.T	0
	EAN84096.1	hypothetical protein, conserved	38584	17	1	1.8E-02	R.EAVLQDPLGLK.V	3
Band 10	EAN99374.1	pyruvate phosphate dikinase, putative	101851	714	23	6.2E-03	K.LQSPDLK.G	0
						7.0E-02	R.VAIDMVR.E	
						1.1E-01	R.VAIDMVR.E + Oxidation (M)	
						6.1E-03	R.DDAGSFLR.H	
						1.2E-04	R.SATGVAFSR.S	
						7.3E-03	K.FDTDLTAK.D	
						6.3E-03	K.ATAEAWIR.R	
						3.0E-03	R.GDFLGIFR.T	
						2.0E-03	K.GLIYAGQLK.L	
						1.7E-02	R.GGMTSHAAVVAR.G + Oxidation (M)	
						1.6E-02	R.GTKFDTDLTAK.D	
						9.8E-03	R.EGDYITLDGSK.G	
						7.6E-06	K.TAEETLAAAGQR.V	
						6.5E-04	K.GLPQEVVEQVK.A	
						1.2E-02	K.KFVYYFGGQK.A	
						2.6E-05	R.EMILADTLEGR.K	
						2.4E-05	R.EMILADTLEGR.K + Oxidation (M)	
						2.9E-02	K.VIPEIMIPLVGK.K + Oxidation (M)	
						2.2E-05	R.TPQQIGQSLSLR.W	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
10 cont.	EAN99374.1	cont.				3.5E-02	K.SLHEMNPMLGHR.G + 2 Oxidation (M)	
						4.2E-04	R.VDYIVGTMIEVPR.A + Oxidation (M)	
						1.8E-07	R.LETSPEDLAGMDAAR.G + Oxidation (M)	
						3.6E-05	R.RVEADMGTNFGDVENPLLFSVR.S + Oxidat	
	EAN85190.1	hypothetical protein, conserved	43072	572	18	1.1E-04	K.AAAALALIK.Q	0
						7.2E-04	R.VSAYAPTR.K	
						3.5E-04	R.ADVLQQLK.D	
						4.3E-01	K.AREEAELK.A	
						1.0E-01	R.RNYLVER.N	
						3.0E-02	K.DREEYLR.K	
						5.8E-05	R.VSAYAPTRK.E	
						5.0E-05	K.ELEEEDIR.M	
						4.7E-03	K.AEFEETIEK.Q	
						2.1E-02	M.PLPPLEEAPR.S	
						1.5E-03	K.IVKEEEAQLK.A	
						1.6E-04	K.AYISSLVESNK.E	
						6.7E-06	K.AILEYNATLAER.E	
						1.2E-04	R.EREEYELSLIR.T	
						2.9E-01	R.IHNYDEPPESIR.E	
						8.3E-03	R.EKQEWQLTHIDGV.-	
						1.3E-02	R.DQYKAEFEETIEK.Q	
						2.9E-02	K.SQSMYNPDLTRPLPGGGPR.S + Oxidation	
	EAN88063.1	hypothetical protein, conserved	43064	562	18	5.3E-02	R.VSAYAPTRR.E	0
						3.1E-03	K.AYVSSLVESNK.E	
						3.8E-04	K.AYVSSLVESNKEQAR.K	
	EAN95952.1	hypothetical protein, conserved	43691	514	13	3.5E-06	K.VIANLLNR.-	0
						6.5E-05	R.FVFTAVLPR.F	
						6.9E-03	R.LIFLYPMSK.L	
						4.1E-02	R.LIFLYPMSK.L + Oxidation (M)	
						6.1E-06	K.IINLSAEEIR.A	
						1.7E-05	K.RFVFTAVLPR.F	
						6.5E-04	R.RLIFLYPMSK.L	
						9.3E-02	R.RLIFLYPMSK.L + Oxidation (M)	
						4.6E-04	K.KIINLSAEEIR.A	
						3.2E-06	R.VIYLNLNEEPR.T	
						1.3E-06	K.SEEPSGLELVDLR.D	
						8.4E-07	R.NYQILEEWYGR.E	
						2.4E-03	K.LLDVVCSPENLNIPK.E	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
10 cont.	EAN94839.1	beta tubulin, putative	50520	486	17	1.4E-01	R.YLTASALFR.G	0
						8.9E-03	K.NMMQAADPR.H + Oxidation (M)	
						2.3E-02	K.NMMQAADPR.H + 2 Oxidation (M)	
						7.5E-02	K.LREEYPDR.I	
						2.8E-05	K.LAVNLVPFPR.L	
						4.0E-03	R.FPGQLNSDLR.K	
						5.8E-05	R.VGEQFTAMFR.R	
						5.8E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						4.6E-05	R.KLAVNLVPFPR.L	
						5.0E-08	R.INVYFDEATGGR.Y	
						3.8E-04	R.IMMTFSIIPSPK.V + Oxidation (M)	
						4.8E-04	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						1.4E-04	K.EVDEQMLNVQNK.N	
						9.1E-06	K.EVDEQMLNVQNK.N + Oxidation (M)	
						2.6E-06	R.AVLIDLEPGTMDSVR.A	
						1.9E-04	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						1.9E-04	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
	EAN94612.1	hexokinase, putative	52802	448	15	1.9E-01	K.DVVELLQK.A	0
						1.4E-04	R.MPGLQFTR.Q	
						2.9E-03	R.MPGLQFTR.Q + Oxidation (M)	
						9.3E-03	K.GVDHGFLIK.W	
						1.2E+00	R.MLPSYVYK.T	
						6.9E-01	R.MLPSYVYK.T + Oxidation (M)	
						2.5E-05	K.FMGMISADR.M + 2 Oxidation (M)	
						6.3E-04	R.ATVAIDGSVFEK.T	
						7.5E-02	R.LNNLLQHIAVK.D	
						1.9E-04	K.MVSGMYLGEISR.R	
						2.2E-05	K.MVSGMYLGEISR.R + 2 Oxidation (M)	
						3.1E-03	R.GVEGKDVVELLQK.A	
						1.5E-03	R.TVPLGFTFSFPTEQK.G	
						1.1E-08	K.ATGVFYALDLGGTNFR.V	
						3.8E-08	K.FVLPVTAYDEAMDAVTPNR.N + Oxidation	
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	425	14	1.9E-01	R.ALPNETVSK.M	0
						2.6E-02	K.DYLEGLGVK.C	
						2.1E-04	K.LVAFDTTSR.N	
						2.0E-02	K.LREIAEEYR.R	
						2.6E-04	R.SMDHTQWLAK.L	
						4.7E-03	R.SMDHTQWLAK.L + Oxidation (M)	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
10 cont.	EAN82710.1	cont.				5.8E-05	K.WDSDPFTLTER.D	
						3.0E-05	R.SYVETQLLPAMK.A	
						9.9E-02	R.SYVETQLLPAMK.A + Oxidation (M)	
						2.4E-02	K.AEFEDAEIVITPR.D	
						8.6E-04	K.ANLWATLPGDGGVTK.G	
						3.0E-05	R.DETPSFEGSEEAPITK.L	
						2.4E-05	K.GGIILSGHTDVVPVDGQK.W	
						9.7E-04	R.AEGCIIGEPTGMTVVIAHK.G + Oxidation	
	EAN87141.1	hexokinase, putative	52750	425	15	1.7E-01	K.GVDNGFLIK.W	0
						2.9E-01	R.MIAHLAELR.C + Oxidation	
						1.5E-02	K.DVVELLQNALKR.M	
	EAN85498.1	glutamamyl carboxypeptidase, putative	44258	424	15	2.6E-05	R.NETPSFEGSEEAPFTK.L	0
	EAN85497.1	glutamamyl carboxypeptidase, putative	44390	419	14	6.9E-05	R.DETPSFEGSEEAPFTK.L	0
	EAN82857.1	elongation factor 1-alpha (EF-1-alpha), putative	48884	351	11	5.6E-04	K.VGYNVEK.V	4
						1.9E-02	K.FAEIESK.I	
						1.3E-02	K.YAWVLDK.L	
						3.6E-01	R.TIEKFEK.E	
						3.8E-03	R.QTVAVGIIK.A	
						4.2E-03	K.SVNFAQER.Y	
						1.8E-03	R.LPLQDVYK.I	
						1.8E-05	K.IGGIGTVPVGR.V	
						2.8E-02	K.STATGHLIYK.C	
						8.5E-07	R.FIPISGWQGDNMIDK.S + Oxidation (M)	
						3.2E-03	R.VETGTMKPGDVVTFAPANVTTEVK.S + Oxidation (M)	
	EAN91887.1	mitochondrial DNA polymerase beta, putative	45752	329	8	1.5E-02	K.LGSPEEVK.A	1
						1.9E-05	K.TNLDLPLR.T	
						1.1E-02	R.IQLTDQQR.V	
						8.2E-05	K.GYLLNEYGLFK.L	
						3.7E-06	R.SVPTALLTFTGSK.N	
						4.7E-05	R.EGIFTVEELIEK.A	
						4.9E-06	R.NYLEATMAQGPLK.Y + Oxidation (M)	
						6.6E-02	K.AIQELTQVHGFGPR.A	
	EAN81053.1	alpha tubulin, putative	50549	303	8	2.9E-02	R.LSVDYGKK.S	0
						8.3E-01	K.DVNAAVATIK.T	
						3.6E-02	R.QLFHPEQLISGK.E	
						1.2E-05	R.TIQFVDWSPTGFK.C	
						4.8E-07	R.AVFLDLEPTVVDEIR.T	

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10 cont.	EAN81053.1	cont.				7.0E-03	R.NLDIERPTYTNLNR.L	
						4.0E-07	R.IHFVLTSYAPVISAEK.A	
						5.0E-05	K.AYHEQLSVSEISNAVFEPASMMTK.C + 2 Oxidation (M)	
	EAN95886.1	heat shock protein 70 (HSP70), putative	71171	293	8	7.4E-02	R.NQIVITNDK.G	1
						2.8E-03	K.DAGTIAGMEVLR.I	
						2.8E-04	R.AVHDVVLVGGSTR.I	
						1.2E-04	K.VMQLVSDFFGGK.E	
						3.6E-04	K.VMQLVSDFFGGK.E + Oxidation (M)	
						2.4E-05	R.TTPSYVAFTDTER.L	
						5.6E-03	K.TFNPEEVSSMVLSK.M + Oxidation (M)	
						2.4E-08	K.NQVAMNPTNTVFDAK.R + Oxidation	
	EAN96060.1	glutamamyl carboxypeptidase, putative	44531	274	10	2.6E-02	K.DYLEGLGVK.C only shared	0
						2.0E-02	K.LVSFDTTSR.N	
						1.0E-02	K.INEIAENIK.F	
						1.8E-01	K.AIQGDGAVARPHL.-	
						7.2E-06	K.AYVNDTLLPSMK.K	
						4.2E-04	K.WNSDPFTLTER.D	
						5.8E-04	K.AYVNDTLLPSMK.K + Oxidation (M)	
						5.4E-02	K.AYVNDTLLPSMKK.A + Oxidation (M)	
						3.7E-04	K.DANEKDPFTLLMR.Q + Oxidation (M)	
						1.7E-04	R.YLPEAEAEKFEER.I	
	EAN84918.1	ATPase alpha subunit, putative	24506	243	9	2.0E-01	K.GILAEYRK.L	0
						7.0E-04	R.FVALFNQK.Q	
						1.8E-01	K.DLSIMYGSAK.N	
						4.8E-04	K.DLSIMYGSAK.N + Oxidation (M)	
						2.0E-06	R.VGSSAQNVAMK.G + Oxidation (M)	
						2.6E-03	K.FYEYLLVHK.D	
						1.4E-02	K.QHTQLFLQHYQSK.M	
						1.7E-04	K.LAADSVGGQQVQTIPMIR.G	
						8.6E-05	K.LAADSVGGQQVQTIPMIR.G + Oxidation (M)	
	EAN90286.1	glyceraldehyde 3-phosphate dehydrogenase, putative	39292	233	7	1.1E-01	K.LTGMSFR.V + Oxidation (M)	3
						1.0E-03	R.NPADLPWGK.L	
						2.7E-03	K.ATLQNNLPK.E	
						1.1E-03	K.AVGMVIPSTQGK.L + Oxidation (M)	
						3.8E-04	R.AAAVNIIPSTTGAAK.A	
						3.5E-03	R.DTSIQEIDAALKR.A	
						7.8E-06	R.VPTPDVSVVDLTFTAAR.D	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
10 cont.	EAO00202.1	6-phospho-1-fructokinase, putative	54100	229	6	8.0E-02	R.FGYWGLSK.K	0
						8.7E-05	R.ELEAISLVR.E	
						1.8E-03	R.TFGFETAVDK.A	
						1.9E-07	R.SLTLTAVNAYR.V	
						2.6E-03	R.YNSYILVPIK.V	
						8.4E-05	R.GPQDTSEMVDTLER.L + Oxidation (M)	
	EAN81916.1	ATP synthase, alpha chain, mitochondrial precursor, putative	25912	224	6	1.2E-03	R.INQQILSK.D	0
						2.7E-04	K.AVDTMIPIGR.G	
						8.5E-06	K.AVDTMIPIGR.G + Oxidation (M)	
						4.7E-03	K.VDTGAPNIVSR.S	
						3.3E-05	R.SPVNYNLLTGFK.A	
						7.2E-06	K.TSIAVSTIINQVR.I	
	EAN97655.1	chaperonin HSP60, mitochondrial precursor	59991	223	4	6.0E-05	R.GYISPYFVTDAK.A	1
						1.5E-07	K.AELEDAFVLVSAK.K	
						8.5E-08	R.AVGVILQSVAEQSR.K	
						3.6E-04	R.AAVQEGIVPGGGVALLR.A	
	EAN98272.1	eukaryotic initiation factor 4a, putative	49984	220	5	6.6E-04	R.VLVTTDLVAR.G	1
						4.8E-06	K.TGAFSIGLLQR.L	
						2.7E-06	R.GGDIIAQAQSGTGK.T	
						7.0E-06	R.ELALQTAEVITR.I	
						3.8E-02	R.HNVLQGLVLSPTR.E	
	EAN86150.1	hypothetical protein, conserved	47419	202	9	1.2E-02	R.EQLMER.V + Oxidation (M)	0
						1.4E+00	R.FLAPYDK.N	
						2.4E-02	K.AASSADPVKTG.-	
						5.5E-02	R.AWDDLFEK.N	
						5.0E-02	K.EVSQEEIAK.L	
						6.3E-02	R.SIPSYLTDTK.W	
						5.9E-04	R.HAADMYDGFIK.F	
						2.6E-05	K.QTQEAVDIWLR.I	
						3.2E-02	K.DFVEQSETFSPDYHKR.F	
	EAN87966.1	glucose-regulated protein 78, putative	71414	201	3	1.5E-05	K.DAGTIAGLNVVR.I	0
						5.8E-08	R.ITPSVVAFTETER.L	
						1.4E-07	R.IINEPTAAAIAYGLNK.A	
	EAN88964.1	glycosomal phosphoenolpyruvate carboxykinase, putative	59404	200	5	8.5E-04	K.LSEESFAR.V	1
						2.9E-04	K.TTLSADPHR.N	
						1.1E+00	K.IAKEFLDTR.E	
						2.2E-05	K.TEKDIYDAVR.F	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
10 cont.	EAN88964.1	cont.				8.1E-07	K.NVIFLTNDAFGVMPPVAR.L + Oxidation (M)	
	EAN95983.1	ATPase beta subunit, putative	55980	198	4	1.5E-03	K.IGLFGGAGVGK.T	0
						2.6E-06	R.IFNVLGDAIDQR.G	
						7.0E-08	R.FTQANSEVSALLGR.I	
						5.7E-03	R.VAQSALTMAEYFR.D + Oxidation	
	EAN89176.1	NADH dehydrogenase, putative	56934	197	5	3.7E-02	K.GAVVAVNNK.E	1
						1.7E-06	K.LANLQVLSVR.N	
						1.3E-02	R.IQPALATLPNR.F	
						1.5E-07	K.LPLPTLAAVASR.Q	
						3.6E-04	R.DTTFIGDLSEDR.V	
	EAN96732.1	succinyl-CoA ligase [GDP-forming] beta-chain, putative	46089	195	4	3.2E-06	R.TLEEVEAALGK.I	0
						2.9E-06	K.LSFDDNAEFR.Q	
						1.0E-03	R.ILQESGLPLHPAR.N	
						5.0E-05	K.EQIVAAFQIITGDEK.V	
	EAN86097.1	fructose-bisphosphate aldolase, glycosomal, putative	41279	192	5	5.7E-04	R.FNAETLAR.Y	2
						4.0E-06	K.IQNGTVSEAAVR.F	
						6.0E-06	K.ASTGETFVQLLQR.K	
						4.1E-01	R.FAPLGLSNTEEHRR.Q	
						2.1E-03	R.ATPGQVAQYTVSTLAR.V	
	EAN92280.1	ATP-dependent DEAD/H RNA helicase, putative	47149	191	5	3.8E-02	R.VVDLASKR.T	0
						1.1E-02	K.YAETYLHR.I	
						8.9E-07	R.ELALQTAQVTK.E	
						5.3E-04	K.TASFVIPVLEK.V	
						2.1E-05	R.QSLLFSATFPVTVK.D	
	EAN88162.1	hypothetical protein, conserved	39057	187	6	1.6E-03	K.SNSTIVGR.R	0
						2.3E-04	R.ATDVVNQR.N	
						4.8E-02	R.TFAPQLLYK.E	
						2.1E-04	R.MEEINTTSTR.D + Oxidation (M)	
						8.1E-04	R.DALDVIEEANKK.S	
						1.1E-02	R.LFPLLKPLVDER.G	
	EAN88387.1	hypothetical protein, conserved	39017	180	5	3.6E-05	R.IEEINTTSTR.D	0
	EAN86269.1	60S ribosomal protein L19, putative	37755	175	5	4.4E-03	R.EDAAAAAAAK.Q	3
						2.9E-03	R.QLAEQLAAK.R	
						8.9E-01	R.NLMEHIHK.V + Oxidation (M)	
						2.7E-03	R.REDAAAAAAAK.Q	
						3.4E-07	R.VWLDPNEASEISNANSR.K	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
10 cont.	EAN89593.1	hypothetical protein, conserved	52619	162	4	9.8E-04	R.DADLSLPGR.S	0
						2.4E-01	R.HIDASLLSR.L	
						4.3E-05	R.VQTALSMLVLMR.Q + 2 Oxidation (M)	
						7.3E-07	R.FADANEENVPAAQVNR.V	
	EAN87378.1	3-hydroxy-3-methylglutaryl-CoA reductase, putative	46865	128	4	6.6E-04	K.TLLLGEGMTR.A + Oxidation (M)	1
						5.3E-03	K.EAFESTTQYGK.L	
						2.1E-02	R.APVVELPSLEEAGR.L	
						3.5E-05	R.EVVSEIASQQPEAK.K	
	EAN83022.1	hypothetical protein, conserved	37536	114	5	6.5E-04	R.VFLSDTR.D	2
						1.1E-04	K.VGPWAIAGR.N	
						1.7E+00	R.RVFLSDTR.D	
						1.0E-02	R.QGLGSEVAEVK.A	
						2.1E-01	R.GVWYDFSER.R	
	EAN84370.1	heat shock 70 kDa protein, mitochondrial precursor, putative	71585	103	4	2.0E+00	R.TTPSVVAFK.G	0
						8.6E-02	R.SKFESLAEK.L	
						4.9E-04	R.VLENTEGFR.T	
						8.3E-05	K.DAGTIAGLNVIR.V	
	EAN97592.1	chaperone DnaJ protein, putative	47563	102	4	2.2E-01	K.ILEVHIEK.G	0
						1.0E-03	K.ALGVTESFPR.V	
						1.3E-03	R.VSLEDMYNGK.T + Oxidation (M)	
						6.0E-03	R.GEGMPLPNTGGLDR.G + Oxidation (M)	
	EAN87051.1	SPFH domain / Band 7 family protein, putative	44546	100	2	7.9E-03	R.NTIFNIVPQGR.Q	0
						1.3E-07	R.AEAEAEATGVMAAAISK.S + Oxidation	
	EAN88283.1	hypothetical protein, conserved	46409	99	4	4.6E-05	R.SGMSYFLR.L	0
						1.5E-01	R.AEMLVQLLAR.V	
						3.0E-04	R.TLLTTLSEAHR.Q	
						2.6E+00	R.DRAEMLVQLLAR.V + Oxidation (M)	
	EAN98485.1	histidine ammonia-lyase, putative	58685	99	3	9.6E-03	K.VVENVER.I	0
						1.1E-05	K.GQQLVAQR.L	
						1.9E-02	R.ELGVEPITLAAK.E	
	EAN81454.1	histone H4, putative	11280	99	2	7.0E-05	R.DATAYTEYSR.K	20
						1.2E-05	K.TVTAVDVVNALR.K	
	EAN88684.1	heat shock protein DnaJ, putative	45029	99	4	7.1E-03	R.YDQFGEK.G	0
						1.9E-03	K.IFEIFVEK.G	
						4.4E-03	R.GEGDQIPGVR.L	
						3.2E-02	R.EGMPIPNTGGVER.G + Oxidation	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
10 cont.	EAN85113.1	elongation factor 1-gamma (EF-1-gamma), putative	47053	98	3	3.3E-02	R.EYSNTDTR.T	0
						3.3E-05	R.ALEAWLETR.T	
						2.4E-03	R.LYNTVMQQPK.T + Oxidation	
	EAN99629.1	developmentally regulated GTP-binding protein, putative	41922	96	2	6.5E-06	R.IGFIGFPSVGK.S	0
						1.5E-04	K.INDIEAEIAR.T	
	EAN83019.1	cystathionine beta-synthase	44273	95	2	2.0E-03	K.GYVLLDQYR.N	7
						1.2E-06	K.EVTLQALGAEVIR.T	
	EAN83533.1	histone H2B, putative	12353	95	3	3.3E-02	R.ELQTAVR.L	1
						2.0E-03	R.LVLPADLAK.H	
						1.8E-05	K.IVNSFVNDLFER.I	
	EAN85464.1	N-acetylglucosamine-6-phosphate deacetylase-like protein, putative	30949	94	2	2.1E-03	R.LDGVGSIER.G	1
						1.5E-06	K.ANILILNSELNTITK.R	
	EAN92822.1	ribosomal protein L3, putative	48865	91	4	6.5E-01	R.VMYTVAR.A + Oxidation (M)	1
						1.3E-03	R.VVAHTQLR.K	
						8.6E-02	R.KLTEQITLK.F	
						6.3E-05	K.SITPMGGFVGYGTVR.N + Oxidation	
	EAN86592.1	nucleolar RNA-binding protein, putative	38208	88	2	9.6E-04	K.IPEEHALR.L	2
						2.6E-05	K.QFTIATLDPK.K	
	EAN89594.1	metal-ion transporter, putative	50934	82	2	1.5E-03	R.MPAAVAAITR.Q + Oxidation	0
						6.3E-05	R.GGSGGEVVADAVLASSR.R	
	EAN80947.1	tryparedoxin peroxidase, putative	22886	82	3	9.5E-02	R.DVDEALR.L	5
						4.1E-04	R.GLFIIDPK.Q	
						8.4E-04	R.QITVNDLPVGR.D	
	EAN91430.1	hypothetical protein, conserved	48635	81	3	3.3E-01	R.HSLIEDPR.A	0
						1.3E-03	K.FVQLTGSMNPK.F + Oxidation (M)	
						4.4E-04	R.ELIDGTAEYLAYR.H	
	EAN87724.1	glutamate dehydrogenase, putative	45525	79	3	6.2E-03	K.HGTVEEYAK.G	1
						8.1E-03	K.GLGLQYYAGK.R	
						1.2E-02	K.FLGFEQTFK.N	
	EAN82747.1	Gim5A protein, putative	27268	77	2	5.5E-01	K.ALLPEDAEK.K	2
						7.0E-08	R.LSLLLNALSSK.T	
	EAN83495.1	40S ribosomal protein S3a, putative	28554	74	1	1.1E-07	K.VNINEAVTLLTR.N	4
	EAN99758.1	poly(A)-binding protein, putative	61726	74	4	9.3E-05	R.SGVTNIVVK.K	0
						1.7E+00	K.QFTNLYVK.N	
						2.1E-02	K.NFDDTVTSER.L	
						8.4E-01	K.AVEELDEKESPLAK.E	

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
10 cont.	EAN81757.1	mitochondrial processing peptidase, beta subunit, putative	31341	72	1	2.2E-07	R.AAASNFGDLVAASTK.S	0
	EAN95481.1	retrotransposon hot spot (RHS) protein, putative	108368	70	2	8.9E-02	R.VLIGTPGIGK.S	0
						1.5E-04	K.GYIIYDVAK.K	
	EAN90055.1	galactokinase, putative	52393	69	1	5.3E-07	R.GIFNIAEQIR.T	1
	EAN81197.1	hypothetical protein, conserved	30269	68	4	3.9E-02	K.NLKPGVLLTHS.-	2
						1.3E-02	K.LFVNPMATSDGK.F	
						1.4E-02	K.LFVNPMATSDGK.F + Oxidation (M)	
						3.5E-03	R.SYTTSFVTPIPK.C	
	EAN81408.1	retrotransposon hot spot (RHS) protein, putative	103887	66	3	2.1E+00	K.ELEGGVTR.I	0
	EAN99391.1	hypothetical protein, conserved	48903	66	2	1.5E-04	R.EGFFVGVLNAR.G	0
						1.3E-02	R.LPGVDTQLLFK.G	
	EAN92220.1	pyruvate dehydrogenase E1 component alpha subunit, putative	43381	65	2	4.5E-03	K.SDIQDVR.K	0
						7.7E-04	R.GGTPGEVFAEMFGK.E + Oxidation	
	EAN87063.1	hypothetical protein, conserved	44364	63	2	2.7E-03	K.ALTEEWILGR.K	0
						2.5E-03	K.ANESLDVLNLGQYTR.E	
	EAN82629.1	heat shock protein 85, putative	81244	63	2	8.9E-05	R.GVVDSEDLPLNISR.E	2
						6.7E-02	R.YQSLTNQAVLGDESHLR.I	
	EAN86151.1	RNA helicase, putative	49885	62	2	1.2E+00	R.DVQTVFLK.T	0
						3.0E-06	R.IIVATDLFGR.G	
	EAN85330.1	histone H2A, putative	14385	61	2	1.2E-04	K.AGLIFPVGR.V	10
						2.2E-02	R.HDDDLGMLLK.D + Oxidation (M)	
	EAN87340.1	RNA-binding protein, putative	50174	61	1	2.3E-06	R.NIAENTTEQQLR.E	1
	EAN95438.1	hypothetical protein, conserved	55839	60	2	2.8E-03	R.DVAEAHVR.A	0
						1.2E-01	R.AGEVPAPNAPR.A	
	EAN85411.1	actin, putative	42296	60	1	2.2E-06	K.AGFSGDDAPR.H	2
	EAN80692.1	farnesyl synthetase, putative	32609	55	1	8.1E-06	R.AVLAGDFLLAR.A	1
	EAN97586.1	mitochondrial processing peptidase alpha subunit, putative	53421	53	2	8.5E-03	K.VKDDEVAAGR.A	0
						1.8E-02	K.EIAGFLDAAR.G	
	EAN91961.1	actin-like protein, putative	35384	51	1	2.9E-05	K.VAISSGNSDGITSK.Y	1
	EAO00026.1	elongation factor TU, putative	52462	49	1	3.2E-05	K.IVGSGETVNLSK.E	1
	EAN97520.1	hypothetical protein, conserved	42890	49	2	4.6E-03	R.NIGAVAFSTR.R	0
						2.7E-02	R.LSHSANEIAR.S	
	EAN83372.1	casein kinase II, alpha chain, putative	48379	47	1	2.0E-05	K.APELLLGLR.L	1
	EAN85286.1	hypothetical protein, conserved	50456	45	1	7.1E-05	K.GTTTLNLFR.N	0
	EAN87845.1	40S ribosomal protein S4, putative	30998	44	1	1.0E-03	K.VENVYTSTGR.I	2

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
10 cont.	EAN97374.1	CAAX prenyl protease 1, putative	49012	44	2	2.0E-03	K.LYQVDGSR.R	0
						1.2E-01	R.VAAIDAEIKK.S	
	EAN91964.1	mitochondrial DNA topoisomerase II, putative	138876	43	1	1.1E-04	R.NLGLLEAELAR.E	1
	EAN84604.1	histone H3, putative	21714	43	1	2.0E-04	R.STDLLLQK.A	7
	EAN86114.1	cysteine desulfurase, putative	49300	39	1	3.4E-04	R.AEVADLIGTSPK.G	1
	EAN83160.1	phosphomannose isomerase, putative	46214	38	2	1.2E+00	R.NNVPFLLK.V	0
						8.8E-04	K.TLLGNVAVVSAK.E	
	EAN81270.1	sterol 24-c-methyltransferase, putative	41138	38	1	4.9E-04	K.GAEILEEAAR.S	1
	EAN92318.1	69 kDa paraflagellar rod protein, putative	70087	37	1	4.9E-04	R.TVSFTGTIDNAIAK.L	0
	EAN94531.1	hypothetical protein, conserved	57858	37	1	4.9E-04	K.AIEAFALLR.E	1
	EAN91609.1	vacuolar-type proton translocating pyrophosphatase 1, putative	86135	36	1	3.1E-04	R.VGIPTINILDAR.V	1
	EAN85233.1	axoneme central apparatus protein, putative	34377	35	1	1.1E-03	R.TAASTLSDIAK.H	1
	EAN86963.1	calcium-binding protein, putative	59793	34	1	5.4E-04	R.VPGEVIDLLR.E	1
	EAN92888.1	acyl-CoA dehydrogenase, putative	69549	33	1	3.2E-04	K.GISLFLVPR.H	0
	EAN99748.1	isocitrate dehydrogenase, putative	47184	33	2	3.7E-02	R.HAFGDQYR.A	0
						8.6E-02	K.LVQFSMLLEK.V + Oxidation	
	EAN90413.1	ADP,ATP carrier protein 1, mitochondrial precursor, putative	35303	32	1	2.1E-03	K.LLVQNQGEMIK.Q + Oxidation	1
	EAN95451.1	hypothetical protein, conserved	40559	32	1	1.1E-03	R.DFYTTLGYQR.N	0
	EAN98359.1	lanosterol 14-alpha-demethylase, putative	55343	30	1	2.4E-04	K.ILGEIIVAR.E	1
	EAN83529.1	hypothetical protein, conserved	93603	30	1	5.1E-03	K.SYPLNTPSQR.L	1
	EAN88449.1	eukaryotic translation initiation factor, putative	46736	30	1	4.7E-03	K.LTGSEIDALR.S	1
	EAN81839.1	hypothetical protein, conserved	57315	29	1	2.6E-03	R.TTSYGVGQIIK.Y	1
	EAN87580.1	cytosolic leucyl aminopeptidase, putative	62519	28	1	4.6E-03	R.HSDEATALVGK.G	1
	EAN86158.1	hexose transporter, putative	59892	28	1	5.1E-03	R.QSPIEVATPGNR.Q	1
	EAN83996.1	retrotransposon hot spot (RHS) protein, putative	70492	28	2	5.5E-04	R.LLLIGTPGIGK.S	0
						1.1E+00	K.AGTGMGMKVEK.G	
	EAN82723.1	glutamate dehydrogenase, putative	43888	27	1	4.4E-03	R.GYTTDDGTTSVYTAK.W	0
	EAO00208.1	hypothetical protein, conserved	38955	27	1	2.6E-03	K.VFLLPSYPK.W	1
	EAN87059.1	hypothetical protein, conserved	21263	26	1	8.6E-03	K.SVGLTAALSPK.Q	0
	EAN84271.1	glutamate dehydrogenase, putative	24319	26	1	7.0E-03	R.ANILASDVFK.N	0
	EAO00224.1	60S ribosomal protein L13, putative	25420	24	1	7.0E-03	K.LVLFPMSYK.N + Oxidation	2
	EAN99098.1	hypothetical protein, conserved	62079	22	1	3.6E-03	K.AALLAYLEK.K	0
	EAO00215.1	hypothetical protein, conserved	49404	22	1	8.5E-03	R.ALTGALSAVYK.L	1
	EAN84761.1	mitochondrial processing peptidase, beta subunit, putative	15529	22	1	1.1E-02	R.AVGLLADVVR.N	1

Band no.	Accession no.	Protein Identity	Mr	Mascot SCORE	# PEPT.	E-value	Sequence	Additional copies
10 cont.	EAN81429.1	hypothetical protein, conserved	69263	20	1	2.9E-02	R.LLYGEWYTR.E	9
	EAN88664.1	chaperone DnaJ protein, putative	51044	20	1	2.5E-02	K.VPVGTQQGDK.L	1
	EAN93181.1	hypothetical protein, conserved	40812	19	1	8.5E-03	K.MVLLTVK.G + Oxidation	0
	EAN85214.1	hypothetical protein, conserved	21287	19	1	1.4E-02	K.HALSSFLLK.D	0
	EAN87862.1	vesicle-fusing ATPase, putative	80311	17	1	4.1E-02	K.GVLLYGPPGTGK.T	11

TABLE S3 (BANDS 11-12): COMPLETE PEPTIDE LIST

Note: Table S3 shows the list of hits extracted from the Mascot html output results for the 1DGE bands. Mr indicates the theoretical molecular weight of the protein; Score refers to the Mascot protein score; # Pept refers to the number of peptides matched to each hit with the respective peptide e-value. Only unique peptides to each hit are indicated, not the ones shared with the previous hit. Additional gene copies column, indicates how many other annotated proteins are matched to the same set of peptides; meaning copies of the same gene product. This table is not filtered, meaning several proteins appear in more than one band; either due to proteolysis or carry over during the mass spectrometry analysis from one sample to the other one.

			Mascot					
Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies under same match**
Band 11	EAN99374.1	pyruvate phosphate dikinase, putative	101851	722	21	1.3E-02	K.LQSPDLK.G	0
						1.0E-02	R.DDAGSFLR.H	
						1.2E-04	R.SATGVAFSR.S	
						6.3E-03	K.ATAEAWIR.R	
						1.2E-02	R.GDFLGIFR.T	
						2.5E-01	R.FVYDSYR.R	
						4.2E-04	K.GLIYAGQLK.L	
						3.4E-01	K.KEELTFTK.Q	
						7.5E-04	R.ANADTPNDAAK.A	
						1.0E-04	R.GGMTSHAAVVAR.G + Oxidation (M)	
						8.5E-06	K.TAEETLAAAGQR.V	
						8.4E-05	K.GLPQEVVEQVK.A	
						2.5E-05	R.EMILADTLEGR.K	
						4.5E-02	R.TEHMFFEGSR.I + Oxidation (M)	
						1.2E-04	R.EMILADTLEGR.K + Oxidation (M)	
						8.1E-02	K.VIPEIMIPLVGK.K + Oxidation (M)	
						3.8E-06	R.TPQQIGQSLSLR.W	
						8.5E-06	R.EGLITKEEAVLR.I	
						4.0E-02	K.SLHEMNPMLGHR.G + 2 Oxidation (M)	
						1.8E-07	R.LETSPEDLAGMDAAR.G + Oxidation (M)	
						3.5E-07	K.GLAASPGAAVGQIVFDADSAK.E	
	EAN85498.1	glutamamyl carboxypeptidase, putative	44258	635	19	7.0E-03	R.EIAEEYR.R	0
						3.3E-01	K.GGSHFWVR.V	
						6.0E-01	R.ALPNETVSK.M	
						3.3E-02	K.DYLEGLGVK.C	
						4.8E-06	K.LVAFDTTSR.N	
						4.7E-03	R.EIAEEYRR.N	
						1.9E-05	K.CTLLHNAER.N	
						1.5E-02	K.LREIAEEYR.R	
						2.6E-04	R.SMDHTQWLAK.L	
						2.9E-02	R.SMDHTQWLAK.L + Oxidation (M)	
						5.7E-06	K.WDSDPFTLTER.D	
						2.8E-06	R.SYVETQLLPAMK.A	
						4.8E-03	R.SYVETQLLPAMK.A + Oxidation (M)	
						1.8E-05	K.AEFEDAEIVITPR.N	
						2.0E-05	K.ANLWATLPGDGGVTK.G	
						3.9E-06	R.NETPSFEGSEEAPFTK.L	

							Mascot	
Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
11 cont.	EAN85498.1	cont.				5.0E-03	K.GGIILSGHTDVVPVDGQK.W	
						2.5E-04	R.AEGCIIGEPTGMTVVIAHK.G + Oxidation (M)	
						4.6E-03	R.SYVETQLLPAMKAEFEDAEIVITPR.N + Oxidation (M)	
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	625	18	1.4E-05	R.DETPSFEGSEEAPITK.L	0
	EAN82317.1	glutamamyl carboxypeptidase, putative	44248	567	16	7.0E-03	R.EIAEEYR.R	1
						3.3E-02	K.DYLEGLGVK.C	
						4.8E-06	K.LVAFDTTSR.N	
						4.7E-03	R.EIAEEYRR.N	
						1.9E-05	K.CTLIHNAER.N	
						1.5E-02	K.LREIAEEYR.R	
						2.6E-04	R.SMDHTQWLAK.L	
						2.9E-02	R.SMDHTQWLAK.L + Oxidation (M)	
						5.7E-06	K.WDSDPFTLTER.D	
						2.8E-06	R.SYVETQLLPAMK.A	
						4.8E-03	R.SYVETQLLPAMK.A + Oxidation (M)	
						1.8E-05	K.AEFEDAEIVITPR.N	
						2.0E-05	K.ANLWATLPGDGGVTK.G	
						5.0E-03	K.GGIILSGHTDVVPVDGQK.W	
						2.5E-04	R.AEGCIIGEPTGMTVVIAHK.G + Oxidation (M)	
						4.6E-03	R.SYVETQLLPAMKAEFEDAEIVITPR.N + Oxidation (M)	
	EAN87141.1	hexokinase, putative	52750	543	19	0.0008	R.MPGLQFTR.Q	0
						0.0014	K.GVDNGFLIK.W	
						0.00056	R.MPGLQFTR.Q + Oxidation (M)	
☐						0.97	R.MLPSYVYK.T + Oxidation (M)	
☐						0.0004	K.FMGMISADR.M	
☐						6.2e-005	R.MIAHLAELR.C	
☐						0.005	K.FMGMISADR.M + 2 Oxidation (M)	
☐						0.00099	R.ATVAIDGSVFEK.T	
☐						0.02	K.MAKPWSFETK.F + Oxidation (M)	
☐						0.0021	R.LNNLLQHIAVK.D	
☐						8.7e-005	K.MVSGMYLGEISR.R + Oxidation (M)	
☐						1.4e-005	K.MVSGMYLGEISR.R + 2 Oxidation (M)	
☐						3.7e-005	K.DVVELLQNALKR.M	
☐						0.00017	R.MALASLANQFTVGK.D	
☐						7.7e-007	R.MALASLANQFTVGK.D + Oxidation (M)	
☐						0.00044	R.TVPLGFTFSFPTEQK.G	
☐						0.71	R.DGSGIGAAFISALVVNDK.-	
☐						0.13	R.MALASLANQFTVGKDHLK.Q + Oxidation (M)	
☐						4e-009	K.FVLPVTAYDEAMDAVTPNR.N + Oxidation (M)	

						Mascot		
Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
11 cont.	EAN97657.1	chaperonin HSP60, mitochondrial precursor	59413	523	9	3.4E-06	R.AVSAVATTLGPK.G	0
						1.6E-06	K.VGGGSEVEVNEK.K	
						5.1E-06	R.NVIIEQSYGAPK.I	
						5.9E-05	R.GLIDGETSDYNR.E	
						5.9E-05	R.GYISPYFVTDAK.A	
						1.4E-07	K.AELEDAFVLVSAK.K	
						3.6E-08	R.AVGVILQSVAEQSR.K	
						1.1E-06	K.TAMMQDIAIFAGAR.L + 2 Oxidation (M)	
						1.3E-04	R.AAVQEGIVPGGGVALLR.A	
	EAN94839.1	beta tubulin, putative	50520	498	16	1.1E-02	R.YLTASALFR.G	0
						2.9E-04	K.NMMQAADPR.H + Oxidation (M)	
						3.0E-05	K.LAVNLVPFPR.L	
						2.8E-03	R.FPGQLNSDLR.K	
						3.4E-06	R.VGEQFTAMFR.R	
						7.0E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						3.6E-05	R.KLAVNLVPFPR.L	
						9.6E-08	R.INVYFDEATGGR.Y	
						1.1E-01	R.IMMTFSIIPSPK.V + Oxidation (M)	
						2.7E-02	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						1.5E-06	K.EVDEQMLNVQNK.N + Oxidation (M)	
						4.3E-05	R.AVLIDLEPGTMDSVR.A	
						3.7E-06	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						1.3E-04	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
						9.8E-02	R.LHFFMMGFAPLTSR.G + 2 Oxidation (M)	
	EAN94612.1	hexokinase, putative	52802	468	19	1.4E-02	K.DVVELLQK.A	0
						4.1E-03	K.GVDHGFLIK.W	
	EAN81053.1	alpha tubulin, putative	50549	424	10	6.2E-02	R.LSVDYGKK.S	0
						2.6E-04	K.DVNAAVATIK.T	
						2.2E-04	K.EDAANNYAR.G	
						1.0E-02	R.IDHKFDLMYSK.R	
						2.0E-03	R.QLFHPEQLISGK.E	
						3.4E-08	R.LIGQVVSALTASLR.F	
						2.5E-05	R.TIQFVDWSPTGFK.C	
						4.5E-06	R.AVFLDLEPTVVDEIR.T	
						7.8E-06	R.IHFVLTSYAPVISAEK.A	
						1.9E-04	K.AYHEQLSVSEISNAVFEPASMMTK.C + 2 Oxidation (M)	
	EAN98272.1	eukaryotic initiation factor 4a, putative	49984	370	9	2.8E-01	R.AIVPFTR.G	1
						1.5E-03	R.ESLTLEGIK.Q	
						3.9E-05	R.VLVTTDLVAR.G	
						2.6E-07	K.TGAFSIGLLQR.L	
						3.7E-03	R.KGVAINFVTQK.D	

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Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
11 cont.	EAN98272.1	cont.				1.4E-07	R.GGDIIAQAQSGTGK.T	
						1.4E-05	K.LQAGSIVAVGTPGR.V	
						1.5E-04	R.HNVLQGLVLSPTR.E	
						9.2E-03	R.GIYSHGFEKPSSIQQR.A	
	EAN87966.1	glucose-regulated protein 78, putative	71414	364	7	1.3E-03	R.LSEEEIER.M	0
						6.1E-05	K.DAGTIAGLNVVR.I	
						3.3E-03	R.NSLESVAYSLR.N	
						1.8E-02	K.LQSVTNPIIQK.V	
						4.7E-07	R.ITPSVVAFTETER.L	
						5.9E-09	R.IINEPTAAAIAYGLNK.A	
						1.9E-08	R.VEVDSLTEGFDFSEK.I	
	EAO00202.1	6-phospho-1-fructokinase, putative	54100	357	9	3.4E-02	R.FGYWGLSK.K	0
						5.1E-05	R.YGGTILGSSR.G	
						4.1E+00	R.ELEAISLVR.E	
						9.5E-06	K.LTDIGVVLTK.R	
						1.4E-06	R.GANLAVFGIPK.T	
						1.6E-03	R.TFGFETAVDK.A	
						1.0E-08	R.SLTLTAVNAYR.V	
						1.2E-03	R.YNSYILVPIK.V	
						6.8E-04	R.GPQDTSEMVDTLER.L + Oxidation (M)	
	EAN95952.1	hypothetical protein, conserved	43691	351	8	1.4E-05	K.VIANLLNR.-	0
						8.4E-05	R.FVFTAVLPR.F	
						4.1E-03	R.LIFLYPMSK.L	
						4.5E-02	R.LIFLYPMSK.L + Oxidation (M)	
						4.9E-06	K.IINLSAEEIR.A	
						5.9E-06	R.VIYLNLNEEPR.T	
						5.3E-07	K.SEEPSGLELVDLR.D	
						6.9E-06	R.NYQILEEWYGR.E	
	EAN95886.1	heat shock protein 70 (HSP70), putative	71171	330	10	1.2E+00	R.NQIVITNDK.G	0
						2.4E-03	K.NTVNEPNVAGK.I	
						2.0E-04	R.VEIIANDQGNR.T	
						5.2E-04	K.DAGTIAGMEVLR.I	
						1.1E-01	R.AVHDVVLVGGSTR.I	
						1.8E-03	K.VMQLVSDFFGGK.E + Oxidation (M)	
						1.2E-03	R.TTPSYVAFTDTER.L	
						9.9E-02	K.TFNPEEVSSMVLSK.M + Oxidation (M)	
						1.0E-03	R.IINEPTAAAIAYGLDK.V	
						6.6E-09	K.NQVAMNPTNTVFDAK.R + Oxidation (M)	
	EAN83852.1	heat shock 70 kDa protein, putative	41044	324	10	7.5E-03	R.GTLQPVER.V	0
						8.1E-01	R.LVSHFTDEFK.R	

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Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
11 cont.	EAN96732.1	succinyl-CoA ligase [GDP-forming] beta-chain, putative	46089	276	9	3.1E-01	R.NFEEAAK.L	0
						2.1E-04	R.AAENAAEQVK.A	
						2.8E-02	R.GMGTFEDGFK.G + Oxidation (M)	
						2.3E-03	R.TLEEVEAALGK.I	
						5.5E-06	K.LSFDDNAEFR.Q	
						7.3E-04	R.ILQESGLPLHPAR.N	
						5.5E-02	K.DIFSLADDTQIDPK.E	
						5.8E-07	K.EQIVAAFQIITGDEK.V	
						3.3E+00	R.QKDIFSLADDTQIDPK.E	
	EAN92822.1	ribosomal protein L3, putative	48865	264	8	5.1E-02	R.VMYTVAR.A + Oxidation (M)	1
						2.3E-03	R.VVAHTQLR.K	
						2.4E-03	K.QSAQLAFTK.R	
						1.9E-02	R.RPMAPQTSR.K	
						5.2E-03	R.KLTEQITLK.F	
						1.1E-04	K.SITPMGGFVGYGTVR.N	
						5.1E-06	K.SITPMGGFVGYGTVR.N + Oxidation (M)	
						1.1E-08	R.AVSMEPNQATTTYDLTAK.S + Oxidation (M)	
	EAN90055.1	galactokinase, putative	52393	246	5	2.2E-05	K.MNNAAFTFR.D + Oxidation (M)	0
						2.4E-05	R.SDAEGAQAVVR.K	
						5.8E-04	R.GIFNIAEQIR.T	
						3.0E-06	R.AINLEEGVSGGR.L	
						2.0E-04	K.AGELLNATHQGQR.D	
	EAN82858.1	elongation factor 1-alpha (EF-1-alpha), putative	49694	236	5	2.3E-03	K.SVNFAQER.Y	4
						8.8E-07	K.IGGIGTVPVGR.V	
						6.2E-03	K.STATGHLIYK.C	
						1.2E-03	K.VHMNLVVVGHVDAGK.S + Oxidation (M)	
						6.6E-08	R.FIPISGWQGDNMIDK.S + Oxidation (M)	
	EAN91288.1	galactokinase, putative	52368	235	5	4.3E-04	R.SDAEGAQAVVK.K	0
	EAN95983.1	ATPase beta subunit, putative	55980	233	5	1.5E-03	K.IGLFGGAGVGK.T	0
						9.6E-07	R.IFNVLGDAIDQR.G	
						8.8E-07	R.VAQSALTMAEYFR.D	
						3.6E-07	R.FTQANSEVSALLGR.I	
						9.1E-06	R.VAQSALTMAEYFR.D + Oxidation (M)	
	EAN88964.1	glycosomal phosphoenolpyruvate carboxykinase, putative	59404	223	6	2.6E-02	R.IVDTDDVR.E	1
						6.1E-04	K.LSEESFAR.V	
						3.9E-05	K.TTLSADPHR.N	
						3.1E-04	K.TEKDIYDAVR.F	
						3.0E-04	R.VWLLNTGYAGGR.A	
						1.4E-03	R.EQVILGTEYAGEMK.K	

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Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
11 cont.	EAN99758.1	poly(A)-binding protein, putative	61726	216	7	4.3E-04	K.ALDQAGVK.L	0
						1.2E+00	K.YPNLYVK.N	
						3.2E-03	R.SGVTNIVVK.K	
						5.0E-05	K.NFDDTVTSER.L	
						3.9E-07	R.LTAIGLATNENGESR.G	
						4.7E-01	K.AVEELDEKESPLAK.E	
						4.9E-02	R.DLGANQTVGFAYVAYATHEAAAK.A	
	EAN85411.1	actin, putative	42296	208	5	5.4E-05	K.AGFSGDDAPR.H	1
						6.0E-02	R.HVFPSIVGRPK.N	
						7.3E-04	K.EISNLAPSSIKPK.V	
						2.3E-09	K.LLMESGMTFTTSAEK.E + 2 Oxidation (M)	
						5.7E-03	R.VNPESHSVLLTEAPMNPK.Q + Oxidation (M)	
	EAN88605.1	acetylornithine deacetylase-like, putative	44189	187	4	4.2E-03	R.LIAFDTTSR.N	0
						2.5E-05	M.PLDSVEWLR.R	
						2.9E-05	R.IDDFVAATAQK.M	
	EAN81916.1	ATP synthase, alpha chain, mitochondrial precursor, putative	25912	182	4	5.7E-05	K.AVDTMIPIGR.G + Oxidation (M)	0
						1.3E-04	K.VDTGAPNIVSR.S	
						6.3E-04	R.SPVNYNLLTGFK.A	
						6.0E-06	K.TSIAVSTIINQVR.I	
	EAN85464.1	N-acetylglucosamine-6-phosphate deacetylase-like protein, putative	30949	182	6	3.1E-03	R.LDGVGSIER.G	1
						1.4E-01	R.LLRPSVSHM.- + Oxidation (M)	
						1.2E-01	R.IMTISPHIDAR.S	
						3.9E-02	R.IMTISPHIDAR.S + Oxidation (M)	
						8.0E-05	R.SNYELIGYLLR.L	
						5.2E-08	K.ANILILNSELNTITK.R	
	EAN97586.1	mitochondrial processing peptidase alpha subunit, putative	53421	180	4	6.2E-05	K.YATALVAR.E	0
						6.1E-05	K.FGQPSLTR.A	
						2.4E-04	K.VKDDEVAAGR.A	
						1.2E-03	K.EIAGFLDAAR.G	
	EAN99748.1	isocitrate dehydrogenase, putative	47184	164	4	5.1E-04	R.HAFGDQYR.A	0
						3.4E-02	K.LVQFSMLLEK.V + Oxidation (M)	
						5.3E-07	R.TVEAEAAHGTVTR.H	
						5.9E-04	R.DKTDDQVTVDAAHAIK.K	
	EAN96060.1	glutamamyl carboxypeptidase, putative	44531	157	4	1.3E-05	K.LVSFDTTSR.N	0
						1.3E-03	K.AYVNDTLLPSMK.K + Oxidation (M)	
						3.3E-05	R.YLPEAEAEKFEER.I	
	EAN85113.1	elongation factor 1-gamma (EF-1-gamma), putative	47053	148	5	1.3E-01	R.TFLVGER.M	0
						4.5E-01	R.SQGATFGPVK.A	
						1.2E-05	R.ALEAWLETR.T	

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Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
11 cont.	EAN85113.1	cont.				7.3E-04	R.LYNTVMQQPK.T + Oxidation (M)	
						2.8E-03	K.AAAAAADGAEEEDEAPREK.K	
	EAN85055.1	histone H4, putative	11177	142	4	5.2E-01	K.SFVEGVVR.D	7
						3.1E-03	R.ISGIIYDEVR.G	
						8.4E-05	R.DATAYTEYSR.K	
						6.8E-06	K.TVTAVDVVNALR.K	
	EAN86151.1	RNA helicase, putative	49885	121	3	3.1E-03	R.DVQTVFLK.T	0
						8.2E-06	R.IIVATDLFGR.G	
						4.9E-04	K.KFMNNPTEIYVDQR.A + Oxidation (M)	
	EAN85395.1	3-ketoacyl-CoA thiolase, putative	46802	119	4	3.5E-04	R.VGGDYLAR.A	1
						2.7E-02	K.TAVSTVIANI.-	
						9.7E-01	K.GSPLFIDKK.H	
						3.5E-05	K.MGISPNDSSLVEIK.S + Oxidation (M)	
	EAN80947.1	tryparedoxin peroxidase, putative	22886	117	5	4.3E-01	R.DVDEALR.L	3
						4.9E-02	K.AFQFVEK.H	
						3.5E-04	R.GLFIIDPK.Q	
						2.4E-04	R.QITVNDLPVGR.D	
						2.0E-02	R.GGLGQMNIPILADK.T + Oxidation (M)	
	EAN83533.1	histone H2B, putative	12353	108	3	2.9E-02	R.ELQTAVR.L	1
						4.6E-03	R.LVLPADLAK.H	
						6.6E-07	R.IASEAATVVR.V	
	EAN87724.1	glutamate dehydrogenase, putative	45525	107	4	8.2E-02	K.VLSVSDSR.G	0
						1.5E-02	K.GLGLQYYAGK.R	
						5.8E-05	K.FLGFEQTFK.N	
						3.6E-02	R.EVGYMAGMTQK.L + Oxidation (M)	
	EAN85190.1	hypothetical protein, conserved	43072	105	3	2.6E-05	R.VSAYAPTR.K	1
						2.3E-03	K.ELEEEDIR.M	
						2.0E-02	M.PLPPLEEAPR.S	
	EAN92280.1	ATP-dependent DEAD/H RNA helicase, putative	47149	103	3	1.5E-06	R.ELALQTAQVTK.E	0
						4.7E-04	K.TASFVIPVLEK.V	
						3.7E-01	R.NVTFEEYGLR.R	
	EAN87063.1	hypothetical protein, conserved	44364	102	3	4.5E-03	K.ALTEEWILGR.K	0
						2.6E-06	K.ANESLDVLNLGQYTR.E	
						2.2E-01	K.DLVEAPARPASANAAAGGSGK.K	
	EAN88162.1	hypothetical protein, conserved	39057	101	3	1.7E-01	K.SNSTIVGR.R	1
						6.7E-05	R.ATDVVNQR.N	
						9.4E-04	R.DALDVIEEANKK.S	
	EAN86150.1	hypothetical protein, conserved	47419	97	5	1.0E-02	R.EQLMER.V + Oxidation (M)	0
						5.8E-01	R.FLAPYDK.N	
						5.4E-03	R.AWDDLFEK.N	
						1.5E-03	K.EVSQEEIAK.L	

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Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
11 cont.	EAN86150.1	cont.				5.5E-01	R.SIPSYLTDTK.W	
	EAN91858.1	hypothetical protein, conserved	45957	96	1	9.6E-10	K.LAQAANTSTTATSSGTK.D	0
	EAN99391.1	hypothetical protein, conserved	48903	96	3	3.3E-01	R.NLIAYAER.H	0
						1.2E-04	R.EGFFVGVLNAR.G	
						3.1E-04	R.LPGVDTQLLFK.G	
	EAN86592.1	nucleolar RNA-binding protein, putative	38208	94	2	9.3E-04	K.IPEEHALR.L	2
						6.8E-06	K.QFTIATLDPK.K	
	EAN99098.1	hypothetical protein, conserved	62079	94	2	7.9E-04	K.AALLAYLEK.K	0
						5.0E-07	K.ALTGVTALGGFNK.E	
	EAN82747.1	Gim5A protein, putative	27268	93	3	9.3E-02	K.LHLSDTVR.G	2
						8.5E-01	K.ALLPEDAEK.K	
						3.1E-08	R.LSLLLNALSSK.T	
	EAN84918.1	ATPase alpha subunit, putative	24506	87	3	3.0E-03	R.FVALFNQK.Q	0
						9.3E-05	R.VGSSAQNVAMK.G + Oxidation (M)	
						1.5E-01	K.FYEYLLVHK.D	
	EAN91887.1	mitochondrial DNA polymerase beta, putative	45752	78	2	6.5E-04	K.LGSPEEVK.A	1
						1.0E-04	R.SVPTALLTFTGSK.N	
	EAN88244.1	phosphoinositide-binding protein, putative	48519	77	3	1.2E-03	K.IVGSGSQSASR.L	1
						2.2E-02	R.ASTTLSTYAQK.D	
						2.1E-02	R.LYIQQLEDSIK.M	
	EAN89176.1	NADH dehydrogenase, putative	56934	76	2	1.3E-01	R.IQPALATLPNR.F	1
						6.7E-08	K.LPLPTLAAVASR.Q	
	EAN84370.1	heat shock 70 kDa protein, mitochondrial precursor, putative	71585	75	3	9.3E-02	R.SKFESLAEK.L	0
						1.5E-03	R.VLENTEGFR.T	
						1.3E-02	K.DAGTIAGLNVIR.V	
	EAN90081.1	ATP-dependent RNA helicase, putative	69157	74	1	1.8E-07	R.VGSTTENITQDVR.W	1
	EAN85276.1	hypothetical protein	52756	72	2	2.8E-02	R.DADLSLPGR.S	1
						1.5E-05	R.FADANEENVPAAQVNR.V	
	EAN83474.1	retrotransposon hot spot (RHS) protein, putative	106086	72	2	3.6E-02	R.VLIGTPGIGK.S	3
						1.5E-05	K.LNDFLLLR.F	
	EAN86114.1	cysteine desulfurase, putative	49300	70	2	1.0E-04	R.AEVADLIGTSPK.G	1
						9.4E-03	R.ALGIDAENAHTSIR.F	
	EAN83019.1	cystathionine beta-synthase	44273	68	1	3.7E-07	K.EVTLQALGAEVIR.T	8
	EAN88684.1	heat shock protein DnaJ, putative	45029	67	2	4.6E-03	K.IFEIFVEK.G	0
						2.7E-04	R.GEGDQIPGVR.L	
	EAN82629.1	heat shock protein 85, putative	81244	65	2	2.5E-05	K.AISNDWEEPLSTK.H	3
						1.3E-01	R.GVVDSEDLPLNISR.E	
	EAN87340.1	RNA-binding protein, putative	50174	59	1	3.5E-06	R.NIAENTTEQQLR.E	1
	EAO00026.1	elongation factor TU, putative	52462	58	2	4.8E-02	K.ALEGDAENEGK.I	1
						1.1E-04	K.IVGSGETVNLSK.E	

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Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
11 cont.	EAN94510.1	mitochondrial processing peptidase, beta subunit, putative	55057	56	2	3.3E-04	R.AVGLLADVVR.N	1
						4.2E-02	R.LADEDIQAAK.Q	
	EAN89594.1	metal-ion transporter, putative	50934	55	2	6.0E-03	R.MPAAVAAITR.Q + Oxidation (M)	0
						8.5E-03	R.GGSGGEVVADAVLASSR.R	
	EAN86224.1	hypothetical protein, conserved	56869	53	1	5.9E-06	R.LPALEQIVVGSR.R	1
	EAN90413.1	ADP,ATP carrier protein 1, mitochondrial precursor, putative	35303	50	1	4.2E-05	K.LLVQNQGEMIK.Q + Oxidation (M)	1
	EAN86269.1	60S ribosomal protein L19, putative	37755	49	2	1.7E-01	R.EDAAAAAAAK.Q	3
						3.5E-03	R.QLAEQLAAK.R	
	EAN81976.1	elongation factor 2, putative	19244	48	1	2.7E-05	K.STLSDSLVGAAGIIK.M	3
	EAN99332.1	RAB GDP dissociation inhibitor alpha, putative	50517	47	1	9.2E-05	K.LIVGDPSYFPDR.V	0
	EAN85839.1	hypothetical protein, conserved	86830	47	1	5.0E-05	R.SVVSNALEEVALR.H	1
	EAN86428.1	hypothetical protein, conserved	50343	47	2	3.0E-01	R.VVYVSSAAHR.F	1
						1.4E-03	R.FVDQFQATYK.R	
	EAN81897.1	2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamid succinyltransferase, putative	42903	44	1	8.2E-05	R.LIDGSDAVTFLVK.V	1
	EAN97592.1	chaperone DnaJ protein, putative	47563	43	1	2.1E-04	K.ALGVTESFPR.V	0
	EAN80692.1	farnesyl synthetase, putative	32609	42	1	1.3E-04	R.AVLAGDFLLAR.A	1
	EAN87271.1	glycosomal membrane protein, putative	24137	41	1	2.9E-04	K.SVSSSITDGR.S	1
	EAN91644.1	GTP-binding protein, putative	44891	41	2	2.9E-02	K.STFFNVLSK.K	1
						5.2E-03	K.VGIVGLPNVGK.S	
	EAN92675.1	hypothetical protein, conserved	51070	40	2	1.5E-03	R.NILFSLAR.Q	1
						9.1E-01	R.DLYVTAERPK.N	
	EAN88187.1	hypothetical protein, conserved	43723	37	1	9.3E-04	R.TVTLLDFGQNK.L	1
	EAN83495.1	40S ribosomal protein S3a, putative	28554	35	1	1.1E-03	K.FVVQEVQGR.N	4
	EAO00028.1	citrate synthase, putative	53081	34	1	7.5E-04	R.TPYLAAAIYNR.L	1
	EAN87845.1	40S ribosomal protein S4, putative	30998	32	1	1.5E-03	K.VENVYTSTGR.I	2
	EAN88420.1	chaperone DnaJ protein, putative	49727	31	1	1.5E-03	R.GPAQVQPIEVK.L	1
	EAN87580.1	cytosolic leucyl aminopeptidase, putative	62519	31	1	6.5E-04	R.LILADTLTFVQR.D	1
	EAN81197.1	hypothetical protein, conserved	30269	30	1	1.7E-03	R.SYTTSFVTPIPK.C	3
	EAN86097.1	fructose-bisphosphate aldolase, glycosomal, putative	41279	27	1	3.3E-03	K.ASTGETFVQLLQR.K	2
	EAN86375.1	centromere/microtubule binding protein cbf5, putative	49155	26	1	2.2E-03	K.NYDQMNVR.S + Oxidation (M)	1
	EAN92888.1	acyl-CoA dehydrogenase, putative	69549	25	1	6.1E-03	K.GISLFLVPR.H	0
	EAN83903.1	flagellar protofilament ribbon protein, putative	46306	25	2	3.1E-01	R.IYEVER.N	1
						9.4E-02	R.DWAQQQVEEK.L	
	EAN98359.1	lanosterol 14-alpha-demethylase, putative	55343	25	1	8.8E-04	K.ILGEIIVAR.E	1
	EAN87059.1	hypothetical protein, conserved	21263	25	1	1.1E-02	K.SVGLTAALSPK.Q	0

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Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
11 cont.	EAN96768.1	hypothetical protein, conserved	26779	24	1	7.0E-03	-.MLFLYR.R + Oxidation (M)	0
	EAN90286.1	glyceraldehyde 3-phosphate dehydrogenase, putative	39292	24	2	8.3E-02	K.AVGMVIPSTQGK.L + Oxidation (M)	3
						6.5E-01	R.DTSIQEIDAALKR.A	
	EAN98432.1	nucleolar RNA binding protein, putative	55470	23	1	5.4E-03	K.IVNDNLLYAK.I	0
	EAN85214.1	hypothetical protein, conserved	21287	20	1	1.9E-02	K.HALSSFLLK.D	1
Band 12	EAN84978.1	elongation factor 1-alpha (EF-1-alpha), putative	49652	862	24	1.4E-06	K.SGDAAMVR.M	1
						1.6E-04	K.VGYNVEK.V	
						2.9E-04	K.FAEIESK.I	
						6.9E-03	K.YAWVLDK.L	
						2.6E-02	R.TIEKFEK.E	
						3.1E-04	R.QTVAVGIIK.A	
						1.6E-03	K.SVNFAQER.Y	
						7.8E-05	R.LPLQDVYK.I	
						2.5E-06	K.IGGIGTVPVGR.V	
						5.4E-04	K.SENMPWYK.G	
						3.2E-03	K.SENMPWYK.G + Oxidation (M)	
						2.8E-03	K.STATGHLIYK.C	
						6.5E-04	K.FEKEAAEIGK.S	
						1.0E-02	R.GITIDIALWK.F	
						3.7E-03	R.EHALLAFTLGVK.Q	
						4.2E-03	K.MDDKSVNFAQER.Y + Oxidation (M)	
						1.0E-04	K.VHMNLVVVGHVDAGK.S	
						2.4E-05	K.VHMNLVVVGHVDAGK.S + Oxidation (M)	
						8.3E-03	R.FIPISGWQGDNMIDK.S	
						3.1E-08	R.FIPISGWQGDNMIDK.S + Oxidation (M)	
						7.7E-03	R.VETGTMKPGDVVTFAPANVTTEVK.S	
						4.9E-03	R.VETGTMKPGDVVTFAPANVTTEVK.S + Oxidation (M)	
						7.9E-07	K.SIEMHHEQLAEATPGDNVGFNVK.N + Oxidation (M)	
						1.0E-07	K.NMITGTSQADAAVLVIASSQGEFEAGISK.D + Oxidation (M)	
	EAN82858.1	elongation factor 1-alpha (EF-1-alpha), putative	49694	843	25	3.4E-03	K.SIEMHHEQLVEATPGDNVGFNVK.N	1
						4.2E-05	K.SIEMHHEQLVEATPGDNVGFNVK.N + Oxidation (M)	
	EAN94839.1	beta tubulin, put	50520	777	24	5.7E-01	R.EEYPDR.I	0
						3.2E-05	K.NMMQAADPR.H	
						2.1E-03	R.YLTASALFR.G	
						5.6E-04	K.NMMQAADPR.H + Oxidation (M)	
						1.4E-04	K.NMMQAADPR.H + 2 Oxidation (M)	
						1.4E-06	K.LAVNLVPFPR.L	
						1.2E-05	R.FPGQLNSDLR.K	
						2.9E-07	R.VGEQFTAMFR.R + Oxidation (M)	

						Mascot		
Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
12 cont.	EAN94839.1	cont.				5.6E-06	R.KLAVNLVPFPR.L	
						6.7E-03	R.FPGQLNSDLRK.L	
						3.9E-09	R.INVYFDEATGGR.Y	
						1.0E-03	R.RVGEQFTAMFR.R + Oxidation (M)	
						3.2E-05	R.IMMTFSIIPSPK.V	
						1.3E-04	R.IMMTFSIIPSPK.V + Oxidation (M)	
						1.1E-04	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						2.7E-06	R.AVLIDLEPGTMDSVR.A	
						1.3E-05	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						3.4E-02	R.LHFFMMGFAPLTSR.G	
						6.5E-03	R.GLSVPELTQQMFDAK.N	
						5.1E-04	R.LHFFMMGFAPLTSR.G + Oxidation (M)	
						5.6E-05	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
						2.3E-06	R.LHFFMMGFAPLTSR.G + 2 Oxidation (M)	
						2.7E-04	K.NSSYFIEWIPNNIK.S	
						3.2E-06	K.FWEVISDEHGVDPTGTYQGDSDLQLER.I	
	EAN81053.1	alpha tubulin, put	50549	740	17	4.9E-04	R.EDLAALEK.D	0
						4.1E-03	R.LSVDYGKK.S	
						5.3E-06	K.DVNAAVATIK.T	
						1.2E-02	R.QLFHPEQLISGK.E	
						1.0E-03	R.IDHKFDLMYSK.R + Oxidation (M)	
						5.2E-09	R.LIGQVVSALTASLR.F	
						1.3E-05	R.TIQFVDWSPTGFK.C	
						1.4E-03	K.RTIQFVDWSPTGFK.C	
						2.6E-07	R.AVFLDLEPTVVDEIR.T	
						2.5E-03	R.NLDIERPTYTNLNR.L	
						9.0E-08	R.IHFVLTSYAPVISAEK.A	
						8.9E-04	K.CGINYQPPTVVPGGDLAK.V	
						4.3E-09	K.TIGVEDDAFNTFFSETGAGK.H	
						2.4E-05	R.QLFHPEQLISGKEDAANNYAR.G	
						3.9E-03	K.AYHEQLSVSEISNAVFEPASMMTK.C	
						7.4E-05	K.AYHEQLSVSEISNAVFEPASMMTK.C + Oxidation (M)	
						2.4E-05	K.AYHEQLSVSEISNAVFEPASMMTK.C + 2 Oxidation (M)	
	EAN95983.1	ATPase beta subunit, putative	55980	723	14	4.2E-04	R.MPIHAVAPK.L	0
						6.1E-04	K.VIDLKGDSK.C	
						3.5E-04	K.IGLFGGAGVGK.T	
						4.1E-02	R.MPIHAVAPK.L + Oxidation (M)	
						3.4E-05	K.MAEEAAELEK.L + Oxidation (M)	
						5.3E-04	K.KMAEEAAELEK.L	
						5.4E-06	K.VVSSGGNISVPVGR.E	
						4.4E-05	R.IFNVLGDAIDQR.G	
						2.5E-06	K.TVIIMELINNVAK.G + Oxidation (M)	

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Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
12 cont.	EAN95983.1	cont.				1.1E-06	R.VAQSALTMAEYFR.D	
						2.8E-11	R.FTQANSEVSALLGR.I	
						8.8E-06	R.VAQSALTMAEYFR.D + Oxidation (M)	
						4.9E-09	K.LADQAAEDTILTTGIK.V	
						3.7E-10	R.IPAAVGYQPTLAEDLGQLQER.I	
	EAO00202.1	6-phospho-1-fructokinase, putative	54100	438	11	4.7E-03	R.FGYWGLSK.K	0
						6.0E-05	R.YGGTILGSSR.G	
						9.0E-05	R.ELEAISLVR.E	
						4.9E-04	K.LTDIGVVLTK.R	
						1.6E-03	R.TFGFETAVDK.A	
						9.4E-03	K.YIDPSYMIR.A + Oxidation (M)	
						7.9E-07	R.SLTLTAVNAYR.V	
						2.3E-05	R.YNSYILVPIK.V	
						4.5E-04	R.EITVGLQDDVR.A	
						5.1E-05	R.GPQDTSEMVDTLER.L	
						9.4E-09	R.GPQDTSEMVDTLER.L + Oxidation (M)	
	EAN91609.1	vacuolar-type proton translocating pyrophosphatase 1, putative	86135	384	10	6.7E-01	K.AFQTAFR.G	1
						2.0E-02	R.NVYVISR.R	
						3.9E-01	R.NIPEDDAR.N	
						2.3E-03	K.AADVGADLVGK.V	
						1.0E-04	R.NAYLTDEVMR.N	
						2.0E-05	R.VGIPTINILDAR.V	
						7.7E-07	K.SVGLAAMDMVNEIR.R	
						7.4E-05	K.SVGLAAMDMVNEIR.R + 2 Oxidation (M)	
						3.9E-08	R.EITDALDAAGNTTAAIGK.G	
						2.6E-08	R.TAVMATEGSEEGDQSLGFAK.A + Oxidation (M)	
	EAN89593.1	hypothetical protein	52619	377	10	3.0E-03	R.LEQPSDK.H	0
						1.3E-03	R.DADLSLPGR.S	
						2.3E+00	K.YRDLWTLR.R	
						1.2E-02	K.GNMLAWYMR.T + 2 Oxidation (M)	
						1.5E-08	R.VQTALSMLVLMR.Q + Oxidation (M)	
						2.0E-05	R.VQTALSMLVLMR.Q + 2 Oxidation (M)	
						1.8E-04	R.IIAKPSVVDIDYK.A	
						1.1E-04	K.SLHYSTMEVDASK.K + Oxidation (M)	
						7.1E-08	R.FADANEENVPAAQVNR.V	
						3.5E-05	R.SNSEEYPDILFVPTLER.F	
	EAO00026.1	elongation factor TU, putative	52462	371	7	6.8E-04	K.ALDYFAIDK.S	1
						3.7E-01	K.EAELKEFEK.T	
						7.0E-06	K.ALEGDAENEGK.I	
						2.3E-06	K.IVGSGETVNLSK.E	
						1.3E-08	K.VGADAELSGFSAK.K	

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Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
12 cont.	EAO00026.1	cont.				1.2E-10	K.TTLTSAITTVLSK.H	
						2.9E-03	K.YKFPAEETPFVR.G	
	EAN90443.1	dihydrolipoyl dehydrogenase, putative	51408	339	8	5.0E-04	K.FPFNANSR.A	1
						5.5E-04	K.AVSTEDGFVK.V	
						6.8E-04	R.RPFTGGLGLDK.I	
						2.1E-03	K.GLTGGVEYLFK.K	
						4.1E-05	K.VVLSSTGALALPR.V	
						1.8E-07	K.GEGSFETAHSIR.V	
						6.9E-07	R.YGLMGGEGVTMDSAK.M + 2 Oxidation (M)	
						3.2E-02	K.TIIATGSEPTELPFLPFDEK.V	
	EAN85276.1	hypothetical protein	52756	332	10	4.3E-05	R.TDNETDFMK.I + Oxidation (M)	0
						2.6E-03	R.LSVLASQLGIK.L	
						1.4E-01	R.IIARPSVVDIDYK.A	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	302	9	4.6E-03	R.GDFLGIFR.T	1
						6.2E-03	K.GLIYAGQLK.L	
						1.7E-01	R.EGDYITLDGSK.G	
						2.7E-06	K.TAEETLAAAGQR.V	
						1.1E-03	K.GLPQEVVEQVK.A	
						2.2E-01	K.KFVYYFGGQK.A	
						7.2E-04	R.EMILADTLEGR.K	
						1.4E-04	R.EMILADTLEGR.K + Oxidation (M)	
						5.5E-09	R.LETSPEDLAGMDAAR.G + Oxidation (M)	
	EAN87141.1	hexokinase, putative **carry over**	52750	288	7	1.1E-03	K.APEDLNR.T	1
						3.0E+00	R.MLPSYVYK.T + Oxidation (M)	
						6.5E-03	K.FMGMISADR.M + 2 Oxidation (M)	
						8.6E-06	R.LNNLLQHIAVK.D	
						3.7E-05	R.TVPLGFTFSFPTEQK.G	
						6.0E-06	K.ATGVFYALDLGGTNFR.V	
						1.5E-08	R.DGSGIGAAFISALVVNDK.-	
	EAN97655.1	chaperonin HSP60, mitochondrial precursor, putative	59991	214	4	4.5E-03	R.GYISPYFVTDAK.A	1
						5.2E-07	K.AELEDAFVLVSAK.K	
						1.1E-08	R.AVGVILQSVAEQSR.K	
						1.1E-04	R.AAVQEGIVPGGGVALLR.A	
	EAN94594.1	hypothetical protein, conserved	57998	193	4	8.9E-03	R.SSPVPLLK.L	0
						3.9E-05	K.AIEAFALLR.E	
						4.5E-05	K.LIEGDILER.R	
						8.3E-08	K.SLDGQGPLLNSTNSHL.-	
	EAN94854.1	hypothetical protein, conserved	52674	190	5	1.4E-01	K.QLAEEQR.L	0
						4.6E-04	R.IAVDAVVAR.A	
						6.9E-05	R.AQLLADYLPK.L	
						1.9E-05	R.QLQAEQDEFYR.L	

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Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
12 cont.	EAN94854.1	cont.				2.5E-04	R.ALQEEEAINAYHAEQSR.R	
	EAN94510.1	mitochondrial processing peptidase, beta subunit, putative	55057	169	5	1.2E-02	K.SAGFPEAR.Y	0
						2.4E-05	R.AVGLLADVVR.N	
						1.7E-03	R.LADEDIQAAK.Q	
						9.5E-03	K.MLHQHELEQAK.V + Oxidation (M)	
						1.0E-03	R.ARPASNHATTQALR.S	
	EAN89176.1	NADH dehydrogenase, putative	56934	167	4	2.0E-05	K.LANLQVLSVR.N	1
						2.0E-01	R.IQPALATLPNR.F	
						9.3E-10	K.LPLPTLAAVASR.Q	
						2.4E-03	R.TGLVVWSTGVGPSSLTK.D	
	EAN95887.1	heat shock protein 70 (HSP70), putative	73607	158	5	1.3E-01	R.GTLQPVER.V	0
						4.5E-03	K.NTVNEPNVAGK.I	
						1.4E-01	R.LVSHFTDEFK.R	
						1.1E-05	K.VMQLVSDFFGGK.E	
						2.6E-05	R.TTPSYVAFTDTER.L	
	EAN98359.1	lanosterol 14-alpha-demethylase, putative	55343	153	7	5.0E-02	R.NEILSPR.E	1
						5.8E-05	K.VGSYVVPK.G	
						9.4E-03	R.LPLPQSAR.C	
						4.7E-02	K.TILATAFR.E	
						3.3E-03	R.DPPLLMVMR.M	
						1.5E+00	R.EYDFQLLR.D	
						1.0E-01	R.VTIVGDPHEHSR.F	
	EAN81757.1	mitochondrial processing peptidase, beta subunit, putative	31341	141	3	6.4E-09	R.AAASNFGDLVAASTK.S	0
	EAN94531.1	hypothetical protein, conserved	57858	140	4	2.3E-02	R.RVSDSAFYR.F	0
	EAN81851.1	nucleolar protein, putative	31894	140	4	2.2E-04	K.VALLIGSR.S	1
						3.0E-02	R.ESLQQYLVEK.M	
						2.2E-07	K.APASTIQILGAEK.A	
	EAN92450.1	thiolase protein-like protein, putative	48368	119	4	2.3E-02	K.GLAALPAFFK.E	0
						7.3E-01	K.QLGYPTDISVK.S	
						5.1E-03	R.ADQEALAIASHK.N	
						1.9E-07	R.LVAPATLSYGLAR.L	
	EAN97131.1	cytochrome p450-like protein, putative	58087	115	3	7.2E-06	R.ASFLNLFATK.A	0
						2.9E-04	K.FVTPLLGGLVMMMK.D + 3 Oxidation (M)	
						2.8E-02	K.AHSDFVIDGHYTVPK.G	
	EAN96277.1	hypothetical protein, conserved	54284	110	2	1.6E-04	R.AFSAALGTLR.A	0
						1.6E-06	R.LEGLDDLTDEELIK.A	
	EAN99758.1	poly(A)-binding protein, putative	61726	105	4	4.5E-04	R.SGVTNIVVK.K	0
						5.9E-01	K.QFTNLYVK.N	
						4.7E-05	K.NFDDTVTSER.L	
						1.1E-01	K.EVFSAFGEVTSAK.V	

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Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
12 cont.	EAN85055.1	histone H4, putative	11177	104	3	1.1E-01	R.ISGIIYDEVR.G	7
						1.6E-04	R.DATAYTEYSR.K	
						3.7E-05	K.TVTAVDVVNALR.K	
	EAN82747.1	Gim5A protein, putative	27268	98	3	2.4E-01	K.LHLSDTVR.G	2
						4.3E-02	K.ALLPEDAEK.K	
						7.0E-08	R.LSLLLNALSSK.T	
	EAN87824.1	hypothetical protein, conserved	29236	96	2	2.0E-05	R.FVFTAVLPR.F	1
						8.5E-05	K.IINLSAEEIR.A	
	EAN93034.1	thiol-dependent reductase 1, putative	51153	94	3	4.4E-03	K.AYFGLVR.D	0
						3.4E-05	K.DADGSYHVR.F	
						7.8E-03	R.ETVPTLLTPR.G	
	EAN80947.1	tryparedoxin peroxidase, putative	22886	90	3	4.0E-03	K.AFQFVEK.H	3
						4.2E-04	R.GLFIIDPK.Q	
						1.0E-03	R.QITVNDLPVGR.D	
	EAN87340.1	RNA-binding protein, putative	50174	89	4	2.5E-01	R.ENVLPTK.V	0
						3.1E-01	R.EFVDRR.D	
						9.4E-02	K.GMPPNTNEDDLR.A + Oxidation (M)	
						3.5E-06	R.NIAENTTEQQLR.E	
	EAN84761.1	mitochondrial processing peptidase, beta subunit, putative	15529	84	3	1.2E+00	K.IPPTNISTVGK.G	0
	EAN85113.1	elongation factor 1-gamma (EF-1-gamma), putative	47053	79	3	1.9E-03	R.EYSNTDTR.T	0
						3.6E-02	R.SQGATFGPVK.A	
						3.0E-03	R.LYNTVMQQPK.T + Oxidation (M)	
	EAN92822.1	ribosomal protein L3, putative	48865	78	3	3.4E-01	R.RPMAPQTSR.K	1
						2.6E-06	K.SITPMGGFVGYGTVR.N + Oxidation (M)	
						3.0E-01	K.TIGTVWAHHTSVEFR.R	
	EAN94343.1	eukaryotic peptide chain release factor subunit 1, putative	51251	77	3	1.1E-02	K.EQVSGMVTK.L + Oxidation (M)	0
						4.3E-03	R.SQEGTQFVR.G	
						1.0E-02	K.LGSFTVELPK.K	
	EAN87063.1	hypothetical protein, conserved	44364	75	2	5.0E-02	K.ALTEEWILGR.K	0
						7.8E-06	K.ANESLDVLNLGQYTR.E	
	EAN82629.1	heat shock protein 85, putative	81244	72	2	1.6E+00	K.DVLGDKVEK.V	3
						7.4E-07	R.GVVDSEDLPLNISR.E	
	EAN87979.1	paraflagellar rod protein 3, putative	69189	70	3	7.4E-01	R.LIDLIQDK.F	0
						4.4E-06	R.SQLDATQLAQVPTR.T	
						6.2E-01	R.VVSFTQMIDNAIAK.M + Oxidation (M)	
	EAN84157.1	hypothetical protein, conserved	55204	67	2	5.9E-04	R.VVSASDDATLR.I	1
						2.7E-03	K.SGGSGGGLSVPEAVLR.D	
	EAN83495.1	40S ribosomal protein S3a, putative	28554	67	1	5.0E-07	K.VNINEAVTLLTR.N	4

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Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
12 cont.	EAN85172.1	eukaryotic translation initiation factor 3 (eIF-3) interacting protein, putative	56637	66	2	9.6E-05	R.TAEQLYSFLR.L	1
						1.8E-02	R.GFFGVYQTTTTELVK.T	
	EAN84370.1	heat shock 70 kDa protein, mitochondrial precursor, putative	71585	64	2	2.5E-02	R.SKFESLAEK.L	0
						2.1E-04	K.STGIDLSNER.M	
	EAN85330.1	histone H2A, putative	14385	61	2	1.3E-03	K.AGLIFPVGR.V	10
						1.8E-03	R.HDDDLGMLLK.D + Oxidation (M)	
	EAO00256.1	elongation initiation factor 2 alpha subunit, putative	48311	57	1	8.9E-07	K.LLLATLEHTVR.N	0
	EAN90081.1	ATP-dependent RNA helicase, putative	69157	56	1	1.2E-05	R.VGSTTENITQDVR.W	1
	EAN82311.1	eukaryotic translation initiation factor 2 subunit, putative	53257	56	2	1.2E-01	R.LIGWGIIR.R	1
						1.1E-04	R.LANLVILQNK.I	
	EAN83533.1	histone H2B, putative	12353	55	1	9.7E-06	K.IVNSFVNDLFER.I	1
	EAN85586.1	axoneme central apparatus protein, putative	56894	55	2	6.4E-03	K.AAAAWSLGQIGR.H	0
						5.4E-03	K.IENYHVQQVQQS.-	
	EAN81839.1	hypothetical protein, conserved	57315	53	2	4.9E-02	K.YAVEYVAR.E	1
						5.3E-04	R.TTSYGVGQIIK.Y	
	EAN85727.1	peptidylprolyl isomerase-like, putative	52323	51	1	1.4E-05	K.VLLQQLQEK.R	1
	EAN90288.1	hypothetical protein, conserved	44654	50	3	6.0E-02	K.AHVETGIEK.S	0
						6.4E-01	K.GVAAFDSAWK.H	
						3.2E-03	R.ALFLENAAYK.H	
	EAN81944.1	lysosomal/endosomal membrane protein p67, putative	73065	50	2	6.3E-01	K.TVSEFLR.V	0
						1.0E-03	K.NYGPLYEYLGR.R	
	EAN84604.1	histone H3, putative	21714	48	1	6.1E-05	R.STDLLLQK.A	7
	EAN90035.1	proteasome regulatory non-ATPase subunit 5, putative	55341	48	4	9.4E-02	R.FTSIELIR.E	0
						1.8E+00	R.NAAIQGITTK.L	
						1.6E+00	R.MLHNISAAR.A + Oxidation (M)	
						4.7E-04	K.INATTIPVLLR.S	
	EAN94547.1	RuvB-like DNA helicase, putative	52952	48	2	1.5E-04	R.GLGLDDALEAR.M	0
						9.9E-01	R.MVIVTTKPYSEAELSK.I + Oxidation (M)	
	EAN87966.1	glucose-regulated protein 78, putative	71414	45	1	7.1E-05	R.LSEEEIER.M	0
	EAN92377.1	calcium-translocating P-type ATPase, putative	110858	45	1	1.3E-04	R.TGAFTEIGSIER.D	0
	EAN85669.1	hypothetical protein, conserved	50997	44	1	1.2E-04	K.QIENAIAR.R	0
	EAN86005.1	chaperonin alpha subunit, putative	59639	43	1	1.7E-04	R.ALNDALWAVAR.T	1
	EAN81197.1	hypothetical protein, conserved	30269	41	1	2.9E-04	K.LFVNPMATSDGK.F + Oxidation (M)	5
	EAN95506.1	translation initiation factor, putative	79951	38	1	4.5E-04	R.VLQAASSTTPK.S	0

							Mascot	
Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
12 cont.	EAN87391.1	acid phosphatase, putative	52707	38	2	5.9E-02	K.KLNDFVDTR.Q	1
						2.0E-02	R.NELPVASTLIVER.L	
	EAN86492.1	squalene monooxygenase, putative	64665	38	1	1.7E-04	K.YGTVFLAK.T	1
	EAO00085.1	alanine aminotransferase, putative	55168	32	1	3.1E-03	R.VVAAEYAVR.G	3
	EAN82317.1	glutamamyl carboxypeptidase, putative	44248	31	2	9.9E-01	R.SYVETQLLPAMK.A + Oxidation (M)	5
						7.0E-03	K.ANLWATLPGDGGVTK.G	
	EAN80692.1	farnesyl synthetase, putative	32609	25	1	8.3E-03	R.AVLAGDFLLAR.A	1
	EAN95652.1	hypothetical protein, conserved	182938	22	1	1.1E-02	R.LAEELEQK.A	2
	EAN83816.1	60S ribosomal protein L5, putative	34902	21	1	9.8E-03	R.DIIAQVVQAK.V	2
	EAN83893.1	hypothetical protein, conserved	107055	21	1	2.7E-02	K.LSSAVNLLR.L	1
	EAN81577.1	trichohyalin, putative	54815	21	1	1.4E-02	R.QLEQELK.A	1
	EAN89707.1	hypothetical protein, conserved	57431	19	1	1.8E-02	R.IALFDAFR.H	0
	EAO00028.1	citrate synthase, putative	53081	19	1	2.5E-02	R.TPYLAAAIYNR.L	1

TABLE S4 (BAND 13): COMPLETE PEPTIDE LIST

Note: Table S4 shows the list of hits extracted from the Mascot html output results for the 1DGE bands. Mr indicates the theoretical molecular weight of the protein; Score refers to the Mascot protein score; # Pept refers to the number of peptides matched to each hit with the respective peptide e-value. Only unique peptides to each hit are indicated, not the ones shared with the previous hit. Additional gene copies column, indicates how many other annotated proteins are matched to the same set of peptides; meaning copies of the same gene product. This table is not filtered, meaning several proteins appear in more than one band; either due to proteolysis or carry over during the mass spectrometry analysis from one sample to the other one.

						Mascot		
Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies under same match**
Band 13	EAN99374.1	pyruvate phosphate dikinase, putative	101851	2013	64	8.2E-03	K.LQSPDLK.G	0
						2.1E-03	R.VAIDMVR.E	
						9.6E-04	K.QFTLSGR.V	
						9.6E-03	R.VAIDMVR.E + Oxidation (M)	
						1.6E-02	K.EELTFTK.Q	
						2.0E-03	R.DDAGSFLR.H	
						1.1E-04	R.SATGVAFSR.S	
						4.8E-03	K.FDTDLTAK.D	
						1.8E-04	K.ATAEAWIR.R	
						1.9E-03	R.GDFLGIFR.T	
						5.1E-02	R.FVYDSYR.R	
						8.5E-04	K.GLIYAGQLK.L	
						1.4E-02	R.DMKELLGGK.G	
						7.2E-04	K.GKQFTLSGR.V	
						1.8E-01	K.KEELTFTK.Q	
						1.3E-01	R.DMKELLGGK.G + Oxidation (M)	
						7.6E-04	R.ANADTPNDAAK.A	
						1.1E+00	R.FVYDSYRR.F	
						5.0E-01	K.FVYYFGGQK.A	
						3.2E-08	R.GGMTSHAAVVAR.G	
						1.4E-05	R.SFGAEGVGLCR.T	
						3.0E-06	R.GGMTSHAAVVAR.G + Oxidation (M)	
						1.3E-04	R.GTKFDTDLTAK.D	
						2.1E-01	R.EGDYITLDGSK.G	
						1.3E-07	K.TAEETLAAAGQR.V	
						3.8E-04	K.GLPQEVVEQVK.A	
						1.5E-03	K.KFVYYFGGQK.A	
						2.0E-03	R.TEHMFFEGSR.I	
						2.2E-05	R.EMILADTLEGR.K	
						6.3E-05	R.EMILADTLEGR.K + Oxidation (M)	
						2.0E-03	K.VIPEIMIPLVGK.K	
						5.9E-08	R.VPVATVAAAHAALK.E	
						3.8E-05	K.VIPEIMIPLVGK.K + Oxidation (M)	
						5.6E-05	R.TPQQIGQSLSLR.W	
						2.0E-05	R.EGLITKEEAVLR.I	

						Mascot		
Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional gene copies
	EAN99374.1	cont.				3.1E-06	R.EMILADTLEGRK.A	
						1.8E-03	R.EMILADTLEGRK.A + Oxidation (M)	
						1.9E-02	K.SLHEMNPMLGHR.G	
						1.5E-02	K.VIPEIMIPLVGKK.E	
						2.6E-02	K.SLHEMNPMLGHR.G + 2 Oxidation (M)	
						2.6E-05	K.TKGLPQEVVEQVK.A	
						1.6E-05	R.VDYIVGTMIEVPR.A	
						4.4E-05	R.VDYIVGTMIEVPR.A + Oxidation (M)	
						1.2E-03	K.ELTEEYLVLFQR.K	
						1.2E-08	R.DMQDIEFTVQDGR.L	
						2.2E-09	R.LETSPEDLAGMDAAR.G	
						1.1E-06	R.LETSPEDLAGMDAAR.G + Oxidation (M)	
						7.1E-02	R.VFREGDYITLDGSK.G	
						1.8E-04	R.FITMYADIVMQVGR.E + Oxidation (M)	
						8.6E-06	R.YPSMEETMPENYR.L + 2 Oxidation (M)	
						2.1E-07	K.DPFESIDQEGVGELMR.I	
						7.4E-03	R.IDAIREMILADTLEGR.K + Oxidation (M)	
						2.6E-03	R.HRYPSMEETMPENYR.L	
						1.5E-08	K.GLAASPGAAVGQIVFDADSAK.E	
						2.2E-04	R.HRYPSMEETMPENYR.L + Oxidation (M)	
						6.3E-04	R.HRYPSMEETMPENYR.L + 2 Oxidation (M)	
						1.1E-05	R.SGAAASMPGMMDTVLNLGMNK.A + 3 Oxidation (M)	
						4.6E-06	R.SGAAASMPGMMDTVLNLGMNK.A + 4 Oxidation (M)	
						2.1E-03	R.IDPLQVDHLMHPNIEPGAAK.S	
						2.2E-02	R.IDPLQVDHLMHPNIEPGAAK.S + Oxidation (M)	
						8.4E-03	R.LLDPPLHEFVPHEDAAQAELAK.K	
						6.7E-06	R.RVEADMGTNFGDVENPLLFSVR.S	
						2.5E-05	R.RVEADMGTNFGDVENPLLFSVR.S + Oxidation (M)	
						1.2E-03	K.GLAASPGAAVGQIVFDADSAKEWSAR.G	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	2011	59	1.6E-03	K.VVPEIMIPLVGK.K	0
						1.6E-05	K.VVPEIMIPLVGK.K + Oxidation	
						6.1E-08	K.DPFESIDQEGVGELVR.I	
	EAN92377.1	calcium-translocating P-type ATPase, putative	110858	611	21	1.1E+00	R.AIFNNTK.Q	0
						8.5E-02	K.LNSLFVK.G	
						1.5E-03	R.AESAIEALK.S	

						Mascot		
Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional gene copies
	EAN92377.1	cont.				1.6E-02	K.NTTLEFTR.Q	
						1.8E-01	K.GAPEEVLRR.S	
						6.5E-04	R.DLPSVETLGR.C	
						9.8E-07	K.AVMSAVLFSR.T + Oxidation (M)	
						2.1E-04	R.GLSADEVEER.R	
						3.8E-04	K.LDEFGMLLSK.V	
						1.2E-03	K.LDEFGMLLSK.V + Oxidation (M)	
						3.8E-04	R.TGAFTEIGSIER.D	
						3.5E-06	K.IDAMSGSEHALR.C + Oxidation (M)	
						2.9E-02	K.MVLADDNFATVVK.A	
						2.2E-04	K.ADIGIAMGSGTQVAK.A + Oxidation (M)	
						3.1E-07	K.MVLADDNFATVVK.A + Oxidation (M)	
						9.8E-03	R.EQEEVKTPLQIK.L	
						5.4E-03	K.KADIGIAMGSGTQVAK.A	
						1.2E-07	K.IGEATEAALLVMSEK.L	
						3.9E-03	K.KADIGIAMGSGTQVAK.A + Oxidation (M)	
						6.9E-08	K.IGEATEAALLVMSEK.L + Oxidation	
	EAN87190.1	elongation factor 2, putative	95336	556	19	3.4E-01	K.MVPTADR.G + Oxidation (M)	1
						1.6E-02	K.YSVSPVVR.V	
						1.7E-02	R.GGGQIIPTAR.R	
						8.6E-04	K.VSEPVVSFR.E	
						6.4E-05	R.GPNVVVDVTK.G	
						6.7E-04	M.VNFTVDEVR.A	
						1.0E-02	R.IRPVVFINK.V	
						3.6E-03	R.IMGNNYVFGK.K + Oxidation (M)	
						2.7E-05	K.SQANTLTLSVR.Q	
						7.9E-02	R.ALMDYPEQIR.N	
						9.6E-03	R.ALMDYPEQIR.N + Oxidation (M)	
						1.0E-01	R.NMSVIAHVDHGK.S	
						4.3E-02	R.NMSVIAHVDHGK.S + Oxidation (M)	
						7.2E-07	K.STLSDSLVGAAGIIK.M	
						2.3E-04	K.KQDLYEDKPVQR.T	
						3.1E-07	K.SATITDDGESPHPLR.D	
						6.3E-02	R.FLADKFDWDVAEAR.K	
						2.9E-04	R.GVIIGEENRPGTPIYNVR.A	
	EAN94839.1	beta tubulin, putative	50520	519	20	2.8E-03	K.NMMQAADPR.H	0
						4.2E-01	R.YLTASALFR.G	
						3.2E-03	K.NMMQAADPR.H + Oxidation (M)	
						7.3E-03	K.NMMQAADPR.H + 2 Oxidation (M)	
						7.6E-03	K.LREEYPDR.I	
						3.7E-05	K.LAVNLVPFPR.L	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Mascot		Additional gene copies
						E-value	Sequence	
	EAN94839.1	cont.				8.0E-06	R.VGEQFTAMFR.R	
						1.9E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						9.2E-06	R.KLAVNLVPFPR.L	
						3.8E-01	R.FPGQLNSDLRK.L	
						9.5E-08	R.INVYFDEATGGR.Y	
						1.7E-05	R.IMMTFSIIPSPK.V + Oxidation (M)	
						7.1E-04	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						8.9E-04	K.EVDEQMLNVQNK.N	
						1.3E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						7.6E-05	R.AVLIDLEPGTMDSVR.A	
						1.3E-03	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						4.4E-05	R.GLSVPELTQQMFDAK.N	
						1.6E-04	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
						6.6E-03	R.LHFFMMGFAPLTSR.G + 2 Oxidation	
	EAN82002.1	cytoskeleton-associated protein CAP5.5, putative	82008	506	13	1.0E-01	K.LDIQFTK.L	0
						6.3E-02	R.DFTGAPSYR.F	
						1.6E-03	K.GYGGVNELLGK.L	
						6.9E-02	R.HSPLMISVSR.A	
						4.4E-04	R.ATVPEEVLER.L	
						1.2E-03	R.FDEAWVNATK.G	
						5.5E-07	K.LSATNPALHNR.V	
						3.6E-04	K.MPGEAAVTSAGSK.L + Oxidation (M)	
						3.0E-03	R.QFQNFGITMLK.I + Oxidation (M)	
						4.2E-07	R.SDVFAQALSEEYR.Q	
						1.4E-03	K.FSPDSSVIPLGSSIK.K	
						4.9E-08	R.YLEAGNIVLLNTPAGK.S	
						2.1E-04	R.VIELADGSVDEEGILSK.C	
	EAN96800.1	lipophosphoglycan biosynthetic protein, putative	86969	491	13	1.0E-01	R.LKEGLEK.E	0
						1.7E-02	R.VLELNHR.H	
						8.6E-03	K.FWAQFGK.H	
						1.8E-02	R.MLYLTAPK.E + Oxidation (M)	
						1.4E-04	R.LGILEDANNR.G	
						1.5E-02	R.RIFITDEFR.Q	
						2.2E-03	K.HIYFLTGDSVK.K	
						3.5E-05	R.KPSEVTEEEYHK.F	
						1.4E-06	R.GIVDSNDLPLNVSR.E	
						4.5E-06	K.MLDILINSLYTNR.A + Oxidation (M)	
						3.0E-08	K.AELEEHLGSLGTSGTK.R	
						2.8E-03	K.AELEEHLGSLGTSGTKR.F	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Mascot		Additional gene copies
						E-value	Sequence	
	EAN96800.1	cont.				1.7E-03	R.MVNVMNQQAISSLHTMR.Y + 3 Oxidation	
	EAN92788.1	cytoskeleton-associated protein CAP5.5, putative	89960	436	11	1.1E-04	K.NSSGDPESPSDAFTFVVAR.E	0
	EAN95481.1	retrotransposon hot spot (RHS) protein, putative	108368	398	11	4.1E-02	K.ELQGGVTR.I	0
						3.2E-03	R.VLIGTPGIGK.S	
						5.9E-03	K.SVLGGLWQR.G	
						2.2E-02	K.GYIIYDVAK.K	
						2.0E-03	K.DILLEGSTLR.T	
						1.7E-03	R.NGNVIMEAFVR.R	
						3.4E-06	R.SNLGEEWVVER.N	
						3.0E-05	R.VWQIVLDDLTK.W	
						1.1E-08	R.TLLGWSTATAEIR.A	
						7.9E-04	R.IPMEYGVLYIPK.V	
						1.8E-03	R.IPMEYGVLYIPK.V + Oxidation	
	EAN82857.1	elongation factor 1-alpha (EF-1-alpha), putative	48884	374	12	4.7E-03	K.VGYNVEK.V	4
						4.5E-04	K.FAEIESK.I	
						1.5E-02	K.YAWVLDK.L	
						7.3E-02	R.TIEKFEK.E	
						1.8E-03	R.QTVAVGIIK.A	
						1.3E-03	K.SVNFAQER.Y	
						4.9E-05	K.IGGIGTVPVGR.V	
						5.0E-01	K.SENMPWYK.G + Oxidation (M)	
						7.7E-03	K.STATGHLIYK.C	
						9.0E-04	R.GITIDIALWK.F	
						1.3E-05	R.FIPISGWQGDNMIDK.S + Oxidation (M)	
						1.4E-03	R.VETGTMKPGDVVTFAPANVTTEVK.S + Oxidation	
	EAN81053.1	alpha tubulin, putative	50549	349	9	8.6E-03	R.LSVDYGKK.S	0
						8.3E-06	K.DVNAAVATIK.T	
						9.3E-04	K.EDAANNYAR.G	
						2.7E-02	R.IDHKFDLMYSK.R + Oxidation (M)	
						7.9E-07	R.AVFLDLEPTVVDEIR.T	
						3.1E-04	R.NLDIERPTYTNLNR.L	
						1.1E-05	R.IHFVLTSYAPVISAEK.A	
						4.1E-01	R.RNLDIERPTYTNLNR.L	
						1.1E-05	K.AYHEQLSVSEISNAVFEPASMMTK.C + 2 Oxidation (M)	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Mascot		Additional gene copies
						E-value	Sequence	
	EAN91609.1	vacuolar-type proton translocating pyrophosphatase 1, putative	86135	344	11	1.3E+00	K.AFQTAFR.G	1
						4.8E-02	R.NVYVISR.R	
						2.0E-01	R.NIPEDDAR.N	
						1.4E-03	R.NAYLTDEVMR.N	
						3.8E-04	R.NAYLTDEVMR.N + Oxidation (M)	
						7.4E-03	K.AADVGADLVGKVER.N	
						9.6E-05	K.SVGLAAMDMVNEIR.R + 2 Oxidation (M)	
						1.6E-09	R.EITDALDAAGNTTAAIGK.G	
						1.1E-01	K.GSPQHAAAVIGDTVGDPLK.D	
						3.0E-10	R.TAVMATEGSEEGDQSLGFAK.A	
						9.8E-10	R.TAVMATEGSEEGDQSLGFAK.A + Oxidation	
	EAN84826.1	retrotransposon hot spot (RHS) protein, putative	104023	342	13	2.1E+00	K.DILLEGR.T	0
						8.5E-03	R.ASAVPQGDR.Q	
						9.7E-03	K.IVAFWDGK.V	
						1.9E-02	R.DFFSDPTR.Y	
						3.8E-01	R.ILTTTSAAMK.M	
						2.2E-02	*K.GYIIYDVAK.K* *not unique*	
						2.4E-01	K.LNHQGYPTR.T	
						5.1E-01	K.DILLLILGSR.G	
						2.2E-02	K.LTNYDEWEK.Q	
						4.0E-05	K.NSLDTAFEVAR.I	
						5.1E-04	R.HIFDEDKYIIR.L	
						2.4E-07	K.LNDFLTLEMEGR.G + Oxidation (M)	
						1.4E-04	R.ARPESEDVTDQPAATQIR.V	
	EAN81408.1	retrotransposon hot spot (RHS) protein, putative	103887	340	14	4.7E-04	R.ALEQLGLR.A	0
						7.9E-02	R.STVEDILLK.G	
						1.0E+00	R.LGAVNAALVAIK.D	
						4.1E-05	K.NSLDAAFEVAR.I	
						4.6E-03	R.SEFEGDTDQPAATHIR.V	
	EAN82412.1	retrotransposon hot spot (RHS) protein, putative	109652	311	10	1.4E-01	R.VWQFVK.G	0
						4.9E-03	K.AGVHDITK.Q	
						4.6E-02	R.LMVLTSDK.G + Oxidation (M)	
						3.2E-03	*R.VLIGTPGIGK.S* *not unique*	
						9.3E-06	K.LNDFLTLR.F	
						2.5E-01	R.MEDLGPLLR.Y + Oxidation (M)	
						4.5E-01	R.NDTLTPLASGK.L	
						1.2E-04	K.QTLDAALEEVR.N	

						Mascot		
Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional gene copies
	EAN82412.1	cont.				4.6E-05	R.YIGDEGVLNEIK.T	
						1.5E-05	R.IINLPAYQALEER.K	
	EAN94997.1	retrotransposon hot spot (RHS) protein, putative	126164	288	8	4.3E-03	R.LLIGTPGIGK.S	0
						3.9E-04	K.IVLGDLWQR.G	
						1.2E-04	*K.QTLDAALEEVR.N not unique*	
						1.7E-05	R.SNLGDEWVVER.N	
						3.0E-05	*R.VWQIVLDDLTK.W not unique*	
						5.7E-02	K.LEGLYESVYNAR.W	
						9.9E-01	K.LNDFLTMELDGR.G	
						4.2E-06	K.LNDFLTMELDGR.G + Oxidation (M)	
	EAN83522.1	retrotransposon hot spot (RHS) protein, putative	76947	252	8	6.7E-09	R.LGAVDVALLAIK.D	0
	EAN97655.1	chaperonin HSP60, mitochondrial precursor	59991	198	4	1.5E-04	R.AVSAVATTLGPK.G	1
						2.6E-06	K.VGGGSEVEVNEK.K	
						3.9E-07	R.AVGVILQSVAEQSR.K	
						2.4E-04	R.AAVQEGIVPGGGVALLR.A	
	EAN84956.1	retrotransposon hot spot (RHS) protein, putative	115032	197	8	2.3E-02	K.ILLEAITK.L	0
						8.4E-01	K.EFFKDPTK.Y	
						1.0E-02	K.GYIIYDVAR.K	
	EAN97710.1	retrotransposon hot spot (RHS) protein, putative	108700	192	6	4.3E-03	R.VQTSTSVVK.S	0
						2.3E-02	R.MEEVGPILR.Y + Oxidation (M) not unique	
						3.3E-03	K.GVVSLEQWR.N	
						1.4E-05	R.LLLIGTPGIGK.S	
						1.7E-01	R.NYEGKDTVSPLAK.G	
						4.3E-06	K.LNDFLLLEMEGK.G	
	EAN95887.1	heat shock protein 70 (HSP70), putative	73607	189	6	9.2E-03	R.GTLQPVER.V	0
						9.4E-02	K.NTVNEPNVAGK.I	
						1.1E-03	K.DAGTIAGMEVLR.I	
						5.2E-02	R.AVHDVVLVGGSTR.I	
						3.8E-04	K.VMQLVSDFFGGK.E + Oxidation (M)	
						2.2E-06	R.TTPSYVAFTDTER.L	
	EAN87824.1	hypothetical protein, conserved	29236	171	3	2.4E-06	R.FVFTAVLPR.F	1
						3.0E-06	K.IINLSAEEIR.A	
						1.4E-05	K.SEEPSGLELVDLR.D	
	EAN85054.1	retrotransposon hot spot (RHS) protein, putative	139992	168	5	9.7E-02	R.VLTQLLR.E	0

						Mascot		
Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies**
	EAN83533.1	histone H2B, putative	12353	161	4	3.8E-02	R.ELQTAVR.L	1
						9.5E-03	R.LVLPADLAK.H	
						2.1E-06	R.IASEAATVVR.V	
						1.2E-06	K.IVNSFVNDLFER.I	
	EAN81877.1	ATP-dependent Clp protease subunit, heat shock protein 100 (HSP100), putative	67834	157	4	7.8E-02	K.YRGEFEER.L	0
						9.5E-03	R.GDVPDTLSSSR.I	
						8.8E-06	K.VTEVEVAAVVAR.W	
						8.9E-07	K.TSIVEGIAQQIVR.G	
	EAN81660.1	retrotransposon hot spot (RHS) protein, putative	62254	149	5	2.3E-02	R.VLTQVLR.E	0
						3.4E-01	R.VLTQVLREER.R	
	EAN82470.1	retrotransposon hot spot (RHS) protein, putative	114542	142	6	3.3E-03	K.WSEAAAEVK.A	1
						2.9E-04	K.LNAVLTQVLTEEK.R	
	EAN80947.1	tryparedoxin peroxidase, putative	22886	136	4	6.2E-03	K.AFQFVEK.H	3
						1.1E-03	R.GLFIIDPK.Q	
						4.4E-04	R.QITVNDLPVGR.D	
						6.1E-04	K.SYGVLKEEDGVAYR.G	
	EAN94699.1	hypothetical protein, conserved	87437	133	4	2.2E-02	R.IVYPDGSR.Y	1
						7.1E-05	K.DAPVGAGVFLHR.L	
						1.7E-01	K.AVNFPPVQRWIK.S	
						3.6E-06	R.FINDVDDDEELER.M	
	EAN81423.1	calcium-translocating P-type ATPase, putative	19723	132	3	4.7E-06	K.LVLAQFEDTLVR.I	0
	EAN99306.1	retrotransposon hot spot (RHS) protein, putative	109235	127	5	4.8E-01	R.AQISTSVVK.S	0
						1.6E-04	R.GGVLSLEQWR.D	
						1.2E-04	R.NDSVQQSGEAR.L	
	EAN95492.1	vacuolar-type Ca2+-ATPase, putative	123386	122	3	3.6E-04	R.LDELAGLIGR.F	1
						4.2E-02	K.TDNALLDFVDR.V	
						1.4E-06	K.SSDIVLLDDNFR.S	
	EAN82723.1	glutamate dehydrogenase, putative	43888	108	3	9.8E-02	K.WQPFVNPQPK.L	1
						6.1E-04	K.GSVGPVFTLVDGK.D	
						4.2E-06	R.GYTTDDGTTSVYTAK.W	
	EAN85113.1	elongation factor 1-gamma (EF-1-gamma), putative	47053	104	3	1.0E-04	R.ALEAWLETR.T	0
						6.0E-03	R.LNGAEGEALTK.K	
						8.1E-03	R.LYNTVMQQPK.T + Oxidation	

						Mascot		
Band no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies**
	EAN97907.1	lanosterol synthase, putative	103755	102	3	7.0E-01	R.HNPFSVSR.I	1
						5.7E-04	R.RAEINAAIR.E	
						1.9E-06	R.IRDAVDEILSLR.N	
	EAN81429.1	hypothetical protein, conserved	69263	90	1	1.5E-09	K.TLLTVLNGVGSAAGR.L	7
	EAN84271.1	glutamate dehydrogenase, putative	24319	89	3	1.6E-03	R.ANILASDVFK.N	0
						3.8E-01	K.TLISDTLSEK.N	
						4.2E-05	K.TLLEVVPVDELMNR.V + Oxidation	
	EAN81982.1	plasma-membrane proton-efflux P-type ATPase, putative	54076	84	2	2.2E-07	R.SVLVLAALAAK.W	1
						6.5E-03	K.NSLKPVATVHR.D	
	EAN85055.1	histone H4, putative	11177	82	2	1.1E-02	R.ISGIIYDEVR.G	7
						2.1E-05	K.TVTAVDVVNALR.K	
	EAN81197.1	hypothetical protein, conserved	30269	77	3	1.2E-01	K.NLKPGVLLTHS.-	2
						1.8E-04	K.LFVNPMATSDGK.F + Oxidation (M)	
						6.0E-03	R.SYTTSFVTPIPK.C	
	EAN80692.1	farnesyl synthetase, putative	32609	70	1	3.0E-07	R.AVLAGDFLLAR.A	1
	EAN91538.1	hypothetical protein, conserved	97545	69	2	2.7E-03	R.LADELEQK.A	2
						3.3E-04	R.LAEELEQK.A	
	EAN92997.1	carbonic anhydrase-like protein, putative	59297	69	3	7.9E-03	R.LVEAFQR.S	0
						3.7E-01	K.DMGPLVFSR.G	
						2.0E-03	R.NSTAGENETESLFR.S	
	EAN85276.1	hypothetical protein	52756	65	2	2.7E-01	R.HIDASLLSR.L	1
						1.6E-05	R.FADANEENVPAAQVNR.V	
	EAN95173.1	ATP-dependent RNA helicase, putative	90610	65	2	6.4E-02	K.FLVLDEADR.M	1
						4.4E-05	K.LFEVIYQQK.Q	
	EAN85214.1	hypothetical protein, conserved	21287	65	2	6.9E-02	K.HALSSFLLK.D	0
						9.5E-05	K.SVGLTAALSPR.Q	
	EAN90413.1	ADP,ATP carrier protein 1, mitochondrial precursor, putative	35303	60	2	3.1E-01	K.TVAAPIER.V	1
						3.2E-05	K.LLVQNQGEMIK.Q + Oxidation	
	EAN92899.1	coatomer gamma subunit, putative	84629	58	1	8.0E-06	R.SAVLNTVAEDIGR.Q	1
	EAN81193.1	ATP-dependent Clp protease subunit, heat shock protein 100, putative	28801	58	1	6.8E-06	R.LDDIVLFR.R	0
	EAN82317.1	glutamamyl carboxypeptidase, putative	44248	57	2	9.9E-03	K.LVAFDTTSR.N	5
						1.8E-03	K.ANLWATLPGDGGVTK.G	
	EAN90819.1	DNA topoisomerase IA, putative	92252	54	1	5.8E-06	R.IFGFLGSSVVR.A	1
	EAO00045.1	aconitase, putative	99497	52	2	2.8E-01	R.YVTPELFK.S	0
						1.3E-04	K.VVIAESFER.I	

Band no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Mascot		Additional gene copies
						E-value	Sequence	
	EAN90081.1	ATP-dependent RNA helicase, putative	69517	51	2	5.2E-02	R.AISFFNEK.N	1
						1.6E-03	R.GYVTFSSIR.F	
	EAN97573.1	vacuolar protein sorting-associated protein 35, putative	102329	50	1	8.2E-05	K.AVEAQSQVQR.K	0
	EAN82045.1	hypothetical protein, conserved	101365	48	1	7.9E-05	K.ATTTATEELR.V	0
	EAN90017.1	hypothetical protein, conserved	110588	46	3	2.1E-02	R.LFIESIPR.V	1
						3.8E-01	R.HVGQYGTPK.D	
						5.6E-02	K.LFVEFSPR.I	
	EAN88964.1	glycosomal phosphoenolpyruvate carboxykinase, putative	59404	45	1	5.8E-05	R.VWLLNTGYAGGR.A	1
	EAN88665.1	60S ribosomal protein L10, putative	25170	45	1	1.0E-04	R.ELEQISSEALEAAR.I	3
	EAN87063.1	hypothetical protein, conserved	44364	41	2	1.9E-02	K.ALTEEWILGR.K	0
						6.7E-02	K.ANESLDVLNLGQYTR.E	
	EAN82747.1	Gim5A protein, putative	27268	39	1	8.9E-05	R.LSLLLNALSSK.T	2
	EAN99050.1	phosphoglycerate kinase, putative	100682	38	1	7.6E-04	R.AFATILAQER.K	0
	EAN92121.1	fatty acid elongase, putative	32936	37	1	6.1E-04	R.DGATSVAPAR.Q	1
	EAN83495.1	40S ribosomal protein S3a, putative	28554	37	1	8.2E-04	K.FVVQEVQGR.N	4
	EAN81916.1	ATP synthase, alpha chain, mitochondrial precursor, putative	25912	35	1	6.8E-04	R.SPVNYNLLTGFK.A	0
	EAN91697.1	PAS-domain containing phosphoglycerate kinase, putative	58534	33	1	7.4E-04	R.ILGAGVTGYLIDR.E	1
	EAN89775.1	NUP-1 protein, putative	88038	32	1	4.0E-03	R.VAELTAAVAR.L	0
	EAN81577.1	trichohyalin, putative	54815	31	1	1.3E-03	R.QLEQELK.A	1
	EAN83138.1	calpain cysteine peptidase, putative	146488	29	1	1.2E-03	R.AFLDQKPEGVPLR.E	1
	EAN87359.1	mitochondrial malate dehydrogenase, putative	31921	28	1	2.9E-03	R.LFGVTTLDLVR.A	1
	EAN83327.1	hypothetical protein, conserved	80349	27	1	8.4E-03	K.LTDEQLVEVR.W	0
	EAN82549.1	ribosomal protein L21E (60S), putative	18285	27	1	7.4E-03	R.TGIVWNVTPR.G	1
	EAN85088.1	RNA-binding protein, putative	18816	24	1	1.1E-02	K.SAQQLVDFFR.Q	1
	EAN91887.1	mitochondrial DNA polymerase beta, putative	45752	23	1	1.1E-02	R.SVPTALLTFTGSK.N	1
	EAN97986.1	RNA helicase, putative	98795	20	1	3.4E-02	R.VLVATDIASR.G	0
	EAN88441.1	hypothetical protein, conserved	47220	18	1	5.1E-02	R.ALLSLSPR.I	1
	EAN83893.1	hypothetical protein, conserved	107055	17	1	6.9E-02	K.LSSAVNLLR.I	1

TABLE S5 (SPOTS 1-29): COMPLETE PEPTIDE LIST

Note: The table shows the list of hits extracted from the Mascot html output results for the 2DGE spots. Mr indicates the theoretical molecular weight of the protein; Score refers to the Mascot protein score; # Pept refers to the number of peptides matched to each hit with the respective peptide e-value. Only unique peptides to each hit are indicated, not the ones shared with the previous hit. Additional gene copies column, indicates how many other annotated proteins are matched to the same set of peptides; meaning copies of the same gene product. This table is not filtered, meaning several proteins appear in more than one band; either due to proteolysis or carry over during the mass spectrometry analysis from one sample to the other one.

							Mascot	Additional gene copies under same match
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	
Spot 1	EAN83392.1	calmodulin, putative	16814	261	6	5.1E-03	K.ELGTVMR.S + Oxidation (M)	3
						1.7E-03	R.HVMTNLGEK.L + Oxidation (M)	
						1.5E-05	K.LTDEEVDEMIR.E + Oxidation (M)	
						3.3E-08	R.VFDKDGNGFISAAELR.H	
						1.5E-03	K.MQDSDSEEEIKEAFR.V + Oxidation (M)	
						5.7E-04	K.EAFSLFDKDGDGTITTK.E	
	EAN97655.1	chaperonin HSP60, mitochondrial precursor	59991	168	3	6.9E-06	R.YVNMFEAGIIDPAR.V + Oxidation (M)	2
						2.3E-07	K.VLENNDVTVGYDAQR.D	
						2.6E-04	K.VLENNDVTVGYDAQRDR.Y	
	EAN94839.1	beta tubulin, putative	50520	79	1	1.4E-08	R.INVYFDEATGGR.Y	0
	EAN89727.1	calmodulin, putative	17154	58	1	4.0E-06	K.TGFINVTDLK.F	1
	EAN88441.1	hypothetical protein, conserved	47220	19	1	3.5E-02	R.ALLSLSPR.I	1
2	EAN98394.1	p22 protein precursor, putative	26158	363	9	4.5E-04	K.LDELDER.L	0
						3.3E-03	K.HEDEEIVIR.C	
						2.7E-04	K.GPKLDELDER.L	
						2.0E-05	R.HELEEEQQR.S	
						4.0E-03	R.KPGQMLFTMR.K + 2 Oxidation (M)	
						8.7E-07	K.LALDDSVEGNQK.R	
						2.2E-04	R.LVDSLTSYLKDR.G	
						6.5E-07	K.LALDDSVEGNQKR.Q	
						8.9E-01	R.MSFESEEVIMGQVSFLDDAK.L + 2 Oxidation (M)	
	EAN91460.1	p22 protein precursor, putative	26184	323	8	9.8E-06	K.HEDEEIIIR.C	0
						3.2E-07	K.LALDDSVEGNR.K	
	EAN84508.1	IgE-dependent histamine-releasing factor, putative	19717	82	2	1.4E-04	R.VVDVVHNNR.Y	1
						2.1E-04	K.FQANAAAFVK.K	
	EAN81053.1	alpha tubulin, putative	50549	31	1	3.2E-03	K.DVNAAVATIK.T	1
	EAN88441.1	hypothetical protein, conserved	47220	19	1	3.5E-02	R.ALLSLSPR.I	1
3	EAN83132.1	hypothetical protein, conserved	26313	44	2	1.6E-03	R.LYWQEPAK.V	1
						3.4E-01	K.LMDQSLPVYDDVVTGSGR.L + Oxidation (M)	
4	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	21	1	2.8E-02	K.VAISLPSR.M	1

							Mascot	
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies**
5	EAN83132.1	hypothetical protein, conserved	26313	144	2	2.7E-03	R.LYWQEPAK.V	1
						2.8E-11	K.LMDQSLPVYDDVVTGSGR.L + Oxidation (M)	
	EAN84888.1	tryparedoxin peroxidase, putative	25774	62	2	1.1E-02	R.NVEEVLR.V	0
						9.7E-04	R.HITVNDLPVGR.N	
	EAN83371.1	hypothetical protein, conserved	30261	54	1	1.0E-05	R.TLNQSLSPEVR.D	1
	EAN82455.1	25 kDa translation elongation factor 1-beta	24437	28	1	6.9E-04	K.LVPVAFGVK.K	2
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	18	1	5.8E-02	K.VAISLPSR.M	1
	EAN91318.1	I/6 autoantigen, putative	23495	18	1	2.8E-02	K.ESVPAAAAPK.K	1
6	EAN84888.1	tryparedoxin peroxidase, putative	25774	239	6	6.7E-03	R.NVEEVLR.V	0
						7.2E-05	K.ANEYFEK.N	
						8.9E-05	R.EAAPEWAGK.A	
						9.2E-06	R.VVQAFQYVDK.N	
						2.8E-03	R.HITVNDLPVGR.N	
						9.1E-05	R.GLFIIDDKGILR.H	
	EAN83132.1	hypothetical protein, conserved	26313	124	2	8.4E-04	R.LYWQEPAK.V	1
						6.2E-09	K.LMDQSLPVYDDVVTGSGR.L + Oxidation (M)	
	EAN96820.1	translation elongation factor 1-beta, putative	21996	93	3	2.1E-03	K.LVPVAFGVK.K	0
						3.7E-05	R.MASYYQAER.E + Oxidation (M)	
						8.2E-03	R.MASYYQAEREQILK.G + Oxidation (M)	
	EAN91318.1	I/6 autoantigen, putative	23495	46	1	6.5E-05	R.EAAAAAAAAAPK.E	0
	EAN83371.1	hypothetical protein, conserved	30261	39	1	3.2E-04	R.TLNQSLSPEVR.D	1
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	20	1	3.8E-02	K.VAISLPSR.M	1
	EAN82747.1	Gim5A protein, putative	27268	17	1	8.4E-02	R.GVLNSGLTR.F	3
7		**Sample lost**						
8	EAO00075.1	cytochrome C oxidase subunit IV, putative	39137	724	23	1.5E-03	R.EYADEAK.S	0
						3.2E-04	R.ILDIYAR.A	
						5.7E-03	R.HITPEAIK.A	
						3.4E-04	R.LENTMIAR.I	
						3.8E-04	R.LTAWLPEK.Y	
						2.9E-05	R.LENTMIAR.I + Oxidation (M)	
						2.9E-03	R.TEEETAFAK.S	
						2.6E-03	K.EFGNEVTFR.L	
						9.6E-07	R.VVHEYNGDDR.I	
						4.1E-02	K.FTGEPPSWMR.Q + Oxidation (M)	
						5.5E-06	R.KEFGNEVTFR.L	

						Mascot		
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies**
8 cont.	EAO00075.1	cont.				1.8E-02	R.ERTEEETAFAK.S	
						1.8E-05	R.EMLNIVQNVER.E	
						4.2E-05	R.EMLNIVQNVER.E + Oxidation (M)	
						6.5E-04	R.WNVNTELHPADR.A	
						1.6E-03	K.EFGNEVTFRLEK.Q	
						9.1E-08	R.IFDEEHVQAEMK.Y	
						1.8E-04	R.IFDEEHVQAEMK.Y + Oxidation (M)	
						1.1E-02	R.REMLNIVQNVER.E + Oxidation (M)	
						1.7E-02	K.SSSDERLENTMIAR.I	
						9.1E-04	K.SSSDERLENTMIAR.I + Oxidation (M)	
						1.3E-03	R.WYGHALELDSHNYK.F	
						3.3E-04	R.ANELAEDNRLDILPGGSPNSLR.E	
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	123	3	1.3E-03	R.ALPNETVSK.M	0
						1.7E-04	K.LVAFDTTSR.N	
						4.4E-05	R.DETPSFEGSEEAPITK.L	
	EAN94839.1	beta tubulin, putative	50520	99	2	1.9E-06	R.INVYFDEATGGR.Y	0
						2.8E-04	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
	EAN97655.1	chaperonin HSP60, mitochondrial precursor	59991	96	2	9.6E-02	R.LIGQAMEK.V + Oxidation (M)	1
						4.5E-08	K.VGGGSEVEVNEK.K	
	EAN84370.1	heat shock 70 kDa protein, mitochondrial precursor, putative	71585	50	1	4.3E-05	K.EISEVVLVGGMTR.M + Oxidation (M)	0
	EAN90241.1	2-oxoisovalerate dehydrogenase beta subunit, mitochondrial precursor, putative	40776	46	2	6.5E-01	R.VIVTHEAPK.T	1
						2.5E-04	K.IVMPSTPSDAK.G + Oxidation (M)	
	EAN81195.1	succinyl-CoA ligase [GDP-forming] beta-chain, putative	35009	32	1	2.6E-03	R.ASENAAEQVK.A	0
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	18	1	6.0E-02	K.VAISLPSR.M	1
9	EAN99021.1	cytochrome C oxidase subunit IV, putative	39097	1038	30	5.9E-03	R.LNGHLNR.K	0
						1.5E-03	R.EYADEAK.S	
						3.2E-04	R.ILDIYAR.A	
						1.4E-03	R.HITSEAIK.A	
						9.0E-04	R.LTAWLPEK.Y	
						5.0E-06	R.LENTMIAR.I + Oxidation (M)	
						2.1E-04	K.NADHQALVK.N	
						1.8E-03	R.TEEETAFAK.S	

						Mascot		
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional gene copies
9 cont.	EAN99021.1	cont.				1.2E-05	R.ANELAEDNR.L	
						4.7E-05	K.EFGNEVTFR.L	
						3.1E-03	R.VVHEYNGDDR.I	
						8.5E-04	K.FTGEPPSWMR.Q	
						1.3E-02	K.FTGEPPSWMR.Q + Oxidation (M)	
						5.2E-03	R.KEFGNEVTFR.L	
						4.6E-06	R.ERTEEETAFAK.S	
						7.0E-06	R.EMLNIVQNVER.E	
						2.5E-05	R.EMLNIVQNVER.E + Oxidation (M)	
						1.2E-04	R.WNVNTELHPADR.A	
						3.3E-02	K.EFGNEVTFRLEK.Q	
						7.5E-04	K.EFGNEVTFRLEK.Q	
						2.4E-06	R.IFDEEHVQAEMK.Y	
						4.2E-03	R.IFDEEHVQAEMK.Y + Oxidation (M)	
						1.2E-02	R.REMLNIVQNVER.E + Oxidation (M)	
						3.4E-05	K.EVVNELLDDVDPSR.H	
						2.3E-02	K.SSSDERLENTMIAR.I	
						3.4E-04	K.SSSDERLENTMIAR.I + Oxidation (M)	
						1.9E-06	K.ACTDLNQLEEWSR.V	
						7.2E-04	R.WYGHALELDSHNYK.F	
						1.3E+00	R.VVHEYNGDDRILDIYAR.A	
						1.6E-04	K.YHIVYFDDFQTVAANDPSAR.R	
						1.6E-06	R.ANELAEDNRLDILPGGSPNSLR.E	
	EAO00075.1	cytochrome C oxidase subunit IV, putative	39137	1032	29	9.1E-03	R.HITPEAIK.A	0
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	262	7	3.3E-02	R.ALPNETVSK.M	0
						6.7E-05	K.LVAFDTTSR.N	
						3.1E-02	R.EIAEEYRR.N	
						4.4E-04	R.SYVETQLLPAMK.A + Oxidation (M)	
						7.8E-05	K.AEFEDAEIVITPR.D	
						2.5E-06	R.DETPSFEGSEEAPITK.L	
						3.9E-03	K.GGIILSGHTDVVPVDGQK.W	
	EAN97655.1	chaperonin HSP60, mitochondrial precursor	59991	138	2	7.3E-06	K.VGGGSEVEVNEK.K	1
						8.3E-09	R.AVGVILQSVAEQSR.K	

				Mascot				
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies**
9 cont.	EAN81195.1	succinyl-CoA ligase [GDP-forming] beta-chain, putative	35009	132	3	1.8E-03	R.ASENAAEQVK.A	0
						1.1E-06	K.LSFDDNAEFR.Q	
						1.9E-04	R.ILQESGLPLHPAR.N	
	EAN90241.1	2-oxoisovalerate dehydrogenase beta subunit, mitochondrial precursor, putative	40776	67	2	1.2E-04	R.VIVTHEAPK.T	1
						1.3E-02	K.IVMPSTPSDAK.G + Oxidation (M)	
	EAN85543.1	calpain-like cysteine peptidase, putative	32320	62	3	1.3E-02	K.GDAVLVIR.H	1
						1.0E-01	R.ETQLILAK.V	
						2.0E-02	R.HNHTNVPLASTK.A	
	EAN82883.1	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative	39837	53	1	2.7E-05	K.GITTVQLSR.G	1
	EAN94839.1	beta tubulin, putative	50520	49	2	9.4E-02	K.LREEYPDR.I	0
						7.7E-04	R.INVYFDEATGGR.Y	
10	EAN82883.1	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative	39837	311	7	3.8E-04	K.GLGAYLAR.L	0
						3.6E-04	K.GITTVQLSR.G	
						3.0E-03	R.FMAIPQQSR.W + Oxidation (M)	
						1.7E-04	R.QGVPSGVPPELR.A	
						1.4E-02	R.EAERFMAIPQQSR.W + Oxidation (M)	
						2.5E-06	R.MLQLGETPTADEALR.I + Oxidation (M)	
						2.3E-07	K.IDTNEKGITTVQLSR.G	
	EAN83656.1	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative	45479	298	7	6.2E-03	R.QGAPTGVPPELR.A	0
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	129	4	3.2E-03	R.ALPNETVSK.M	0
						1.1E-03	K.LVAFDTTSR.N	
						6.0E-03	R.EIAEEYRR.N	
						5.2E-04	R.DETPSFEGSEEAPITK.L	
11	EAO00025.1	alcohol dehydrogenase, putative	42442	596	14	2.3E-02	K.IYRESM.- + Oxidation (M)	0
						3.0E-02	K.DGKNLVAR.E	
						3.6E-03	R.FAVITDEK.R	
						1.9E-03	K.DVCAATNPR.Q	
						8.7E-09	K.NAAAAAIDAIR.A	
						4.9E-06	R.FAVITDEKR.H	
						3.2E-02	K.DIPALAESALK.D	
						3.0E-05	K.AGILETVMDVLK.K + Oxidation (M)	
						2.2E-05	K.EKDIPALAESALK.D	

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Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies**
11 cont.	EAO00025.1	cont.				5.7E-06	K.KPLLVCDTGIEK.A	
						1.5E-06	K.VSYLGVGALDSATSK.M	
						1.6E-06	K.ANGGTIYDYEGLDK.A	
						2.3E-05	K.EVQIPSGFEQLGMK.E + Oxidation (M)	
						2.3E+00	K.EVQIPSGFEQLGMKEK.D + Oxidation (M)	
	EAN97413.1	alcohol dehydrogenase, putative	42479	581	14	1.3E-03	K.EVQIPPGFEQLGMK.E + Oxidation (M)	0
						1.6E+00	K.EVQIPPGFEQLGMKEK.D + Oxidation (M)	
	EAN99752.1	prostaglandin F2alpha synthase	42496	424	10	9.1E-04	K.VDAVAFGAK.F	0
						6.0E-03	R.IIMAPLTR.C + Oxidation (M)	
						2.3E-05	K.SDQDPLAGR.L	
						4.3E-04	R.IPAYFAASGEK.E	
						1.0E-03	R.CQLIYDVTK.S	
						4.2E-04	K.FIANPDLVER.A	
						1.0E-04	R.QSGPYAGTTIDTR.C	
						4.3E-07	R.YDFEEADQQIR.E	
						1.0E-03	R.LLAPSAIPIKDHR.I	
						1.1E-06	R.TAVGYNDYPTYNK.-	
	EAN85497.1	glutamamyl carboxypeptidase, putative	44390	366	9	4.3E-03	R.ALPNETVSK.M	0
						8.9E-06	K.LVAFDTTSR.N	
						4.9E-03	R.EIAEEYRR.N	
						3.5E-03	R.SMDHTQWLAK.L + Oxidation (M)	
						1.4E-03	R.SYVETQLLPAMK.A + Oxidation (M)	
						1.9E-05	K.AEFEDAEIVITPR.D	
						3.3E-02	K.ANLWATLPGDGGVTK.G	
						2.1E-07	R.DETPSFEGSEEAPFTK.L	
						1.8E-05	K.GGIILSGHTDVVPVDGQK.W	
	EAN85498.1	glutamamyl carboxypeptidase, putative	44258	347	9	2.7E-05	R.NETPSFEGSEEAPFTK.L	0
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	345	9	4.9E-05	R.DETPSFEGSEEAPITK.L	0
	EAN86462.1	aspartate aminotransferase, mitochondrial, putative	46511	302	7	3.6E-01	K.EQVEMLK.K + Oxidation (M)	0
						1.1E-03	K.NFGLYGLR.C	
						8.9E-03	K.SLEAMPER.S + Oxidation (M)	
						3.8E-05	K.VNLAVGVYR.D	
						3.1E-07	R.VLSQYALLIR.T	
						3.1E-05	R.TMYSNPPITGAR.I + Oxidation (M)	
						9.2E-07	R.AAISGLNSTNVSYVAK.A	

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Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional gene copies
11 cont.	EAN92220.1	pyruvate dehydrogenase E1 component alpha subunit, putative	43381	136	5	8.2E-03	R.TTQGTVYAKP.-	0
						7.7E-01	R.AAYQPEMYR.R + Oxidation (M)	
						2.8E-05	K.GPIVLEFDSYR.Y	
						2.9E-04	R.GGTPGEVFAEMFGK.E + Oxidation (M)	
						3.9E-03	R.YVGHSMSDPDSQYR.K + Oxidation (M)	
	EAN84370.1	heat shock 70 kDa protein, mitochondrial precursor, putative	71585	108	4	1.8E-01	R.SKFESLAEK.L	0
						6.1E-05	R.VLENTEGFR.T	
						1.7E-03	K.DAGTIAGLNVIR.V	
						1.4E-01	R.VVNEPTAAALAYGLDK.T	
	EAN86096.1	fructose-bisphosphate aldolase, glycosomal, putative	23483	98	3	3.8E-03	R.ALQSSALK.A	3
						3.0E-01	R.FNAETLAR.Y	
						7.1E-06	K.IQNGTVSEAAVR.F	
	EAN84558.1	arginine kinase, putative	40528	59	1	2.3E-06	R.LVTAVGVIEEK.V	0
	EAN91548.1	2- aminoethylphosphonate: pyruvateaminotransferase-like protein, putative	44677	46	1	4.2E-05	R.EAQLDDYGSR.D	1
	EAN96060.1	glutamamyl carboxypeptidase, putative	44531	42	1	1.6E-04	K.LVSFDTTSR.N	0
	EAN90286.1	glyceraldehyde 3-phosphate dehydrogenase, putative	39292	29	1	4.6E-03	K.AVGMVIPSTQGK.L + Oxidation (M)	3
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	21	1	3.1E-02	K.VAISLPSR.M	1
	EAN96732.1	succinyl-CoA ligase [GDP-forming] beta-chain, putative	46089	21	1	3.8E-02	R.AAENAAEQVK.A	0
	EAN93479.1	acyl-CoA dehydrogenase, putative	44561	19	1	2.1E-02	R.SNTYYASSAK.L	1
	EAN87527.1	protein phosphatase 2A catalytic subunit, putative	35426	18	1	6.8E-02	R.TFLETNR.L	1
12	EAO00025.1	alcohol dehydrogenase, putative	42442	636	13	5.7E-02	K.IYRESM.- + Oxidation (M)	0
						7.2E-03	R.FAVITDEK.R	
						1.1E-03	K.DVCAATNPR.Q	
						3.8E-07	K.NAAAAAIDAIR.A	
						2.4E-05	R.FAVITDEKR.H	
						4.1E-05	K.DIPALAESALK.D	
						4.4E-06	K.AGILETVMDVLK.K + Oxidation (M)	
						1.1E-04	K.EKDIPALAESALK.D	
						2.7E-05	K.KPLLVCDTGIEK.A	
						6.5E-07	K.ANGGTIYDYEGLDK.A	

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Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies**
12 cont.	EAO00025.1	cont.				1.2E-05	K.EVQIPSGFEQLGMK.E + Oxidation (M)	
						2.6E-06	K.NACDSIIAIGGGSPQDCAK.G	
						5.8E-07	K.DVHPNPTAHNVETGLELLNK.N	
	EAN97413.1	alcohol dehydrogenase, putative	42479	616	14	4.4E-03	K.EVQIPPGFEQLGMK.E + Oxidation (M)	0
						1.2E+00	K.EVQIPPGFEQLGMKEK.D + Oxidation (M)	
	EAN99752.1	prostaglandin F2alpha synthase	42496	569	15	1.4E-03	K.VDAVAFGAK.F	0
						6.3E-03	R.IIMAPLTR.C + Oxidation (M)	
						2.5E-05	K.SDQDPLAGR.L	
						3.8E-04	R.LLAPSAIPIK.D	
						1.8E-03	K.SVCDAVGSDR.V	
						7.9E-04	R.IPAYFAASGEK.E	
						1.3E-03	R.CQLIYDVTK.S	
						4.2E-03	K.FIANPDLVER.A	
						2.2E-03	R.EGKVDAVAFGAK.F	
						3.1E-01	R.DGIIPLFVEGAK.N	
						6.3E-06	R.QSGPYAGTTIDTR.C	
						1.8E-07	R.YDFEEADQQIR.E	
						1.0E-03	R.LLAPSAIPIKDHR.I	
						3.1E-06	R.TAVGYNDYPTYNK.-	
						4.2E-05	K.ETYGVPEELTDDEVR.D	
	EAN85497.1	glutamamyl carboxypeptidase, putative	44390	332	8	5.1E-04	R.ALPNETVSK.M	0
						1.1E-06	K.LVAFDTTSR.N	
						2.5E-03	R.EIAEEYRR.N	
						1.4E-02	K.WDSDPFTLTER.D	
						7.1E-05	R.SYVETQLLPAMK.A + Oxidation (M)	
						5.0E-04	K.AEFEDAEIVITPR.D	
						5.1E-07	R.DETPSFEGSEEAPFTK.L	
						6.0E-03	K.GGIILSGHTDVVPVDGQK.W	
	EAN85498.1	glutamamyl carboxypeptidase, putative	44258	326	8	2.8E-06	R.NETPSFEGSEEAPFTK.L	0
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	304	8	5.7E-04	R.DETPSFEGSEEAPITK.L	0
	EAN86462.1	aspartate aminotransferase, mitochondrial, putative	46511	299	7	1.6E-03	K.NFGLYGLR.C	0
						6.9E-03	K.SLEAMPER.S + Oxidation (M)	
						3.6E-02	K.GIDLPGMLK.S + Oxidation (M)	
						1.0E-04	K.VNLAVGVYR.D	
						9.7E-06	R.TMYSNPPITGAR.I + Oxidation (M)	
						1.4E-03	R.QIGMMSYTGLTK.E + 2 Oxidation (M)	

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Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional gene copies
12 cont.	EAN86462.1	cont.				3.5E-08	R.AAISGLNSTNVSYVAK.A	
	EAN92220.1	pyruvate dehydrogenase E1 component alpha subunit, putative	43381	130	4	8.1E-05	K.SDIQDVR.K	0
						5.3E-03	R.TTQGTVYAKP.-	
						4.8E-02	R.AAYQPEMYR.R + Oxidation (M)	
						1.2E-03	K.EVDQQLQPAEK.Q	
	EAN84558.1	arginine kinase, putative	40528	123	3	2.0E-03	K.EVFDQLK.G	0
						1.5E-06	R.LVTAVGVIEEK.V	
						5.5E-03	R.VKGQLESMSGELR.G + Oxidation (M)	
	EAN85848.1	protein disulfide isomerase, putative	29802	21	1	5.6E-02	K.VGVNDELSK.V	1
13	EAN88322.1	hslvu complex proteolytic subunit-like, putative	23080	215	4	4.0E-03	R.QVTLGER.I	1
						3.0E-06	R.KGDTVVLIGDR.Q	
						3.3E-06	K.VGEFPQQLTR.A	
						5.4E-06	K.LENKVGEFPQQLTR.A	
	EAN91467.1	hypothetical protein, conserved	28555	72	2	9.4E-02	K.EVPREFAEK.A	1
						1.0E-05	K.AIGELETELSSVR.H	
	EAN86560.1	cytochrome c oxidase subunit V, putative	22450	59	2	8.2E-02	R.DADVLRR.L	1
						8.8E-05	R.SQYASTMDPR.D + Oxidation (M)	
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	27	1	7.3E-03	K.VAISLPSR.M	1
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	27	1	6.8E-03	R.ALPNETVSK.M	4
	EAN80947.1	tryparedoxin peroxidase, putative	22886	27	1	3.4E-03	R.GLFIIDPK.Q	5
14	EAN88322.1	hslvu complex proteolytic subunit-like, putative	23080	257	6	6.4E-03	R.QVTLGER.I	1
						1.9E-02	K.GDTVVLIGDR.Q	
						6.8E-04	R.AAVELAKDWR.T	
						3.5E-06	K.VGEFPQQLTR.A	
						6.8E-05	R.ALIDVDGYDAEK.I	
						1.0E-05	R.KPAKPADAPSEEK.K	
	EAN86560.1	cytochrome c oxidase subunit V, putative	22450	153	4	2.3E-01	R.DADVLRR.L	1
						1.1E-03	R.IDEFKDGNK.V	
						4.3E-06	R.SQYASTMDPR.D + Oxidation (M)	
						3.0E-05	R.GAASLLESLYR.G	
	EAN91467.1	hypothetical protein, conserved	28555	91	2	6.7E-02	K.EVPREFAEK.A	1
						2.4E-07	K.AIGELETELSSVR.H	

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Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies**
14 cont.	EAN80947.1	tryparedoxin peroxidase, putative	22886	69	2	4.6E-04	K.AFQFVEK.H	3
						2.5E-04	R.GLFIIDPK.Q	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	51	3	1.9E-03	R.GTKFDTDLTAK.D	1
						2.7E-02	K.GLPQEVVEQVK.A	
						2.7E+00	R.IDPLQVDHLMHPNIEPGAAK.S + Oxidation (M)	
	EAN95114.1	hypothetical protein, conserved	23669	50	1	1.7E-05	R.AGDSGISPLTTNVLR.M	0
	EAN87271.1	glycosomal membrane protein, putative	24137	27	1	9.8E-03	K.SVSSSITDGR.S	1
15	EAN86560.1	cytochrome c oxidase subunit V, putative	22450	392	12	7.1E-03	K.SLLETMK.W + Oxidation (M)	1
						9.4E-03	R.DADVLRR.L	
						4.5E-02	K.ENKTFIR.V	
						3.1E-05	R.LGEVAKENK.T	
						1.1E-02	R.IDEFKDGNK.V	
						6.0E-03	R.SQYASTMDPR.D	
						2.9E-05	R.SQYASTMDPR.D + Oxidation (M)	
						7.7E-08	R.GAASLLESLYR.G	
						4.5E-03	R.VFLPPHLGDPHR.L	
						7.0E-03	R.VRSQYASTMDPR.D + Oxidation (M)	
						2.7E-04	K.VVIPHIELVEYLAK.S	
						2.0E-04	R.GADIPDHVFQTPAVIER.I	
	EAN80947.1	tryparedoxin peroxidase, putative	22886	117	4	8.2E-02	R.DVDEALR.L	3
						6.0E-03	K.AFQFVEK.H	
						2.8E-04	R.GLFIIDPK.Q	
						3.0E-04	R.QITVNDLPVGR.D	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	59	2	3.3E-04	K.ATAEAWIR.R	1
						7.9E-02	R.FVYDSYRR.F	
	EAN81815.1	co-chaperone GrpE, putative	24421	28	2	9.9E-02	R.IGRDDVEK.A	0
						4.3E-01	K.VSTEEIESNK.N	
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	25	1	1.2E-02	R.ALPNETVSK.M	4
16	EAN82242.1	co-chaperone GrpE, putative	24363	650	16	5.6E-04	K.LLLNNLAK.H	0
						1.9E-02	R.IGRDDVEK.A	
						3.7E-02	R.SYGISSFGK.D	
						1.7E-02	R.ENISELKK.E	
						1.5E-03	R.APQVGVAGEGE.-	
						6.1E-03	K.HGIEKLDVK.V	
						2.0E-04	K.NLSSIHTGVK.L	
						2.9E-06	K.VSAEEIESNK.N	

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Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional gene copies
16 cont.	EAN82242.1	cont.				3.7E-05	K.FDPNIHEALIK.T	
						4.1E-03	K.DMLEVVDTLEK.G + Oxidation (M)	
						1.9E-05	R.ILRAPQVGVAGEGE.-	
						1.3E-08	K.ATEGSQLKEETFAK.L	
						4.3E-04	K.VGSKFDPNIHEALIK.T	
						2.7E-04	K.TPASSEFPSGHISIVLK.V	
						4.2E-05	K.VSAEEIESNKNLSSIHTGVK.L	
						5.5E-06	R.SYGISSFGKDMLEVVDTLEK.G + Oxidation (M)	
	EAN81815.1	co-chaperone GrpE, putative	24421	624	16	1.8E-05	K.VSTEEIESNK.N	0
						2.0E-03	K.VSTEEIESNKNLSSIHTGVK.L	
	EAN80947.1	tryparedoxin peroxidase, putative	22886	59	3	1.7E-02	R.DVDEALR.L	5
						3.9E-04	R.GLFIIDPK.Q	
						1.4E+00	R.QITVNDLPVGR.D	
	EAN86560.1	cytochrome c oxidase subunit V, putative	22450	35	1	2.6E-04	R.SQYASTMDPR.D + Oxidation	1
17	EAN81815.1	co-chaperone GrpE, putative	24421	777	21	1.1E-01	K.KEVLYR.A	0
						2.2E-02	K.LLLNNLAK.H	
						9.4E-03	R.IGRDDVEK.A	
						3.8E-02	R.SYGISSFGK.D	
						1.8E-02	R.ENISELKK.E	
						3.9E-06	R.APQVGVAGEGE.-	
						2.0E-03	K.HGIEKLDVK.V	
						1.9E-04	K.NLSSIHTGVK.L	
						1.8E-04	K.LERELESAR.E	
						5.8E-03	K.EETFAKLER.E	
						1.1E-06	K.VSTEEIESNK.N	
						1.2E-05	K.DMLEVVDTLEK.G	
						4.6E-02	K.FDPNIHEALIK.T	
						3.2E-05	K.DMLEVVDTLEK.G + Oxidation (M)	
						2.2E-07	R.ILRAPQVGVAGEGE.-	
						3.2E-03	R.ELESARENISELK.K	
						1.9E-06	K.ATEGSQLKEETFAK.L	
						2.2E-04	K.VGSKFDPNIHEALIK.T	
						3.5E-05	K.TPASSEFPSGHISIVLK.V	
						1.2E-04	K.VSTEEIESNKNLSSIHTGVK.L	
						4.5E-04	R.SYGISSFGKDMLEVVDTLEK.G + Oxidation	
	EAN82242.1	co-chaperone GrpE, putative	24363	742	20	2.6E-07	K.VSAEEIESNK.N	0
	EAN82317.1	glutamamyl carboxypeptidase, putative	44248	46	1	6.8E-05	K.LVAFDTTSR.N	5

						Mascot		
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies**
17 cont.	EAN94516.1	hypothetical protein, conserved	250837	17	1	8.1E-02	R.RQLTVDNNK.I	0
	EAN80947.1	tryparedoxin peroxidase, putative	22886	32	1	3.4E-04	R.GLFIIDPK.Q	5
	EAN86366.1	trans-sialidase, putative	94015	23	1	3.6E-02	K.KENGNEK.G	1
18	EAN98352.1	pyruvate phosphate dikinase, putative	101833	438	11	4.4E-04	K.FDTDLTAK.D	1
						9.8E-05	K.ATAEAWIR.R	
						5.6E-02	R.DMKELLGGK.G + Oxidation (M)	
						7.8E-02	R.FVYDSYRR.F	
						1.8E-05	R.GTKFDTDLTAK.D	
						4.9E-04	K.TAEETLAAAGQR.V	
						5.5E-06	K.GLPQEVVEQVK.A	
						4.1E-04	K.KFVYYFGGQK.A	
						2.5E-05	R.TKGLPQEVVEQVK.A	
						7.2E-05	R.SGAAASMPGMMDTVLNLGMNK.A + 4 Oxidation (M)	
						6.4E-05	R.RVEADMGTNFGDVENPLLFSVR.S + Oxidat	
	EAN85813.1	dynein light chain, putative	29682	54	1	1.3E-05	R.VVAAEEPR.V	2
	EAN87362.1	mucin-associated surface protein (MASP), putative	43226	22	1	3.9E-02	R.VTTVGEEAK.T	0
	EAN88441.1	hypothetical protein, conserved	47220	19	1	3.9E-02	R.ALLSLSPR.I	1
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	18	1	6.1E-02	K.VAISLPSR.M	1
19	EAN97136.1	ATP synthase, epsilon chain, putative	20447	248	5	2.9E-03	K.AKAVIEIR.I	0
						2.1E-07	K.ALAAQQASLGSAK.D	
						6.7E-09	K.ALAAQQASLGSAKDEK.A	
						6.2E-04	K.VVDKDIHATHENLETLR.F	
						5.2E-03	K.IVQLVPAPLTVEFTDGTTKK.Y	
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	20	1	4.3E-02	K.VAISLPSR.M	1
20	EAN85671.1	ribonucleoprotein p18, mitochondrial precursor, putative	27768	169	6	1.1E-03	R.IYEAPSK.Q	0
						3.0E-03	K.VMEAEFK.S + Oxidation (M)	
						5.9E-02	R.LGYCIQK.V	
						1.8E-01	K.SCPADLVK.Q	
						1.5E-04	K.QAQPVENESK.F	
						4.9E-04	R.IYEAPSKQAQPVENESK.F	
	EAN86067.1	succinyl-coA:3-ketoacid-coenzyme A transferase, mitochondrial precursor	53415	137	2	5.5E-09	K.GPGGAMDLVASGTR.V + Oxidation (M)	1
						6.0E-05	K.EVAEGVTVEQVKK.I	
	EAN81053.1	alpha tubulin, putative	50549	62	2	1.1E-02	R.LSVDYGKK.S	0
						3.5E-04	R.AVFLDLEPTVVDEIR.T	

Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Mascot E-value	Sequence	Additional gene copies
20 cont.	EAN86560.1	cytochrome c oxidase subunit V, putative	22450	23	1	3.8E-03	R.SQYASTMDPR.D + Oxidation	1
	EAN82317.1	glutamamyl carboxypeptidase, putative	44248	22	1	1.8E-02	K.LVAFDTTSR.N	5
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	20	1	3.6E-02	K.VAISLPSR.M	1
21	EAN85850.1	10 kDa heat shock protein, putative	10694	236	5	3.0E-02	K.LQPLGQR.V	4
						1.2E-03	K.KLQPLGQR.V	
						2.8E-05	K.AGVLIPEQVAGK.V	
						2.1E-10	K.VNEGTVVAVAAATK.D	
						3.4E-04	K.VDDTVLLPEFGGSSVK.V	
	EAN85055.1	histone H4, putative	11177	188	4	1.6E-02	K.SFVEGVVR.D	7
						5.5E-06	R.ISGIIYDEVR.G	
						5.5E-04	R.DATAYTEYSR.K	
						5.8E-07	K.TVTAVDVVNALR.K	
	EAN81533.1	histone H4, putative	11163	186	4	7.3E-06	R.ISGVIYDEVR.G	10
	EAN87418.1	heat shock protein-like protein, putative	36225	49	1	6.9E-06	R.GIYDMYGEEGVR.H + Oxidation	1
	EAO00025.1	alcohol dehydrogenase, putative	42442	37	1	4.9E-04	K.VSYLGVGALDSATSK.M	1
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	18	1	6.7E-02	K.VAISLPSR.M	1
22	EAN82097.1	hypothetical protein, conserved	14352	247	6	2.9E-04	K.LVSSTALR.T	0
						1.2E-02	R.IMGPVKEQTIDK.L + Oxidation (M)	
						7.6E-05	K.LNEVIPNATSTAR.S	
						1.2E-04	K.DYTETHVLFMNK.L + Oxidation (M)	
						2.1E-07	M.VQNLVINLLFNSPEIR.I	
						4.5E-03	R.TPVGQSSKDYTETHVLFMNK.L + Oxidation (M)	
	EAN97997.1	hypothetical protein, conserved	14334	242	6	1.4E-02	R.TPAGQSSKDYTETHVLFMNK.L + Oxidation	0
	EAN85850.1	10 kDa heat shock protein, putative	10694	125	2	6.7E-04	K.AGVLIPEQVAGK.V	5
						8.3E-10	K.VNEGTVVAVAAATK.D	
23	EAN93009.1	hypothetical protein, conserved	13620	136	6	2.5E-02	K.SIINKMR.N + Oxidation (M)	1
						1.5E-02	K.IRTPEER.Y	
						1.5E-02	K.AQMASLEEK.L + Oxidation (M)	
						2.8E-02	K.HNEKIDAIK.A	
						4.3E-02	R.ELMKSIINK.M + Oxidation (M)	
						8.1E-03	R.NEHDEKLGAAVAK.H	
	EAN85850.1	10 kDa heat shock protein, putative	10694	34	1	2.9E-04	K.AGVLIPEQVAGK.V	5
24	EAN93009.1	hypothetical protein, conserved	13620	114	4	1.4E-02	K.IRTPEER.Y	1
						2.2E-03	K.AQMASLEEK.L + Oxidation (M)	
						9.2E-05	K.HNEKIDAIK.A	

							Mascot	
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional gene copies
24 cont.	EAN93009.1	cont.				1.5E-01	R.ELMKSIINK.M + Oxidation (M)	
	EAN81211.1	cytochrome c oxidase subunit 10, putative	13942	38	1	5.6E-04	R.INNNPTVGQFR.T	3
	EAN85850.1	10 kDa heat shock protein, putative	10694	20	1	6.7E-03	K.AGVLIPEQVAGK.V	5
25	EAN81211.1	cytochrome c oxidase subunit 10, putative	13942	158	5	5.7E-03	R.NLFWGSDR.Q	3
						1.1E-04	R.RNLFWGSDR.Q	
						2.6E-05	R.INNNPTVGQFR.T	
						1.4E-02	R.KWGFDDMSYMR.E + 2 Oxidation (M)	
						2.4E-02	R.NLFWGSDRQDFFR.H	
	EAN89189.1	hypothetical protein, conserved	11216	53	2	4.4E-02	R.HFEVMK.L + Oxidation (M)	1
						6.0E-04	K.ELVEGDLPDSK.L	
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	21	1	3.3E-02	K.VAISLPSR.M	1
	EAN90963.1	hypothetical protein, conserved	81004	18	1	4.5E-02	K.TAEHSALRPASVAEAADVMLR.V + Oxidat	0
	EAN98338.1	hypothetical protein, conserved	156352	17	1	9.3E-02	R.AEVRNTDLK.S	0
26	EAN85850.1	10 kDa heat shock protein, putative	10694	290	6	1.5E-02	K.LQPLGQR.V	4
						5.9E-03	K.DWTPTVK.V	
						4.6E-04	K.KLQPLGQR.V	
						4.6E-06	K.AGVLIPEQVAGK.V	
						4.4E-11	K.VNEGTVVAVAAATK.D	
						8.0E-05	K.VDDTVLLPEFGGSSVK.V	
	EAN85055.1	histone H4, putative	11177	213	5	5.7E-03	K.SFVEGVVR.D	6
						8.5E-03	K.ILRENVR.G	
						5.6E-06	R.ISGIIYDEVR.G	
						4.0E-05	R.DATAYTEYSR.K	
						2.0E-05	K.TVTAVDVVNALR.K	
	EAN81533.1	histone H4, putative	11163	207	5	2.8E-05	R.ISGVIYDEVR.G	10
	EAN81211.1	cytochrome c oxidase subunit 10, putative	13942	48	1	4.3E-05	R.INNNPTVGQFR.T	3
	EAN92546.1	adenosine 5'-monophosphoramidase, putative	15760	30	1	1.6E-03	R.VVAGEGEPK.T	1
	EAN82295.1	hypothetical protein, conserved	13703	22	1	8.4E-03	R.TTDSHESDNGKDITR.L	1
	EAN88441.1	hypothetical protein, conserved	47220	19	1	3.6E-02	R.ALLSLSPR.I	1
27	EAN85850.1	10 kDa heat shock protein, putative	10694	170	3	1.8E-05	K.AGVLIPEQVAGK.V	4
						4.4E-09	K.VNEGTVVAVAAATK.D	
						9.0E-04	K.VDDTVLLPEFGGSSVK.V	

							Mascot	
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional gene copies
27 cont.	EAN89655.1	cytochrome C oxidase subunit VI, putative	19230	139	4	7.0E-03	R.FSYTANK.Q	0
						6.8E-05	R.FSYTANKQK.N	
						2.2E-06	K.APILHDVFVNGK.K	
						4.2E-02	R.EEMPAVPHFSDFSDPR.F + Oxidation	
	EAN85330.1	histone H2A, putative	14385	33	2	1.0E-01	R.GGVMPSLNK.A + Oxidation	13
						4.5E-02	K.AGLIFPVGR.V	
28	EAN89116.1	heat shock protein 20, putative	16000	269	7	7.0E-05	R.SGISVKIN.-	0
						1.6E-02	K.NVVMAER.G + Oxidation (M)	
						1.3E-04	K.ILADLPGMNR.N + Oxidation (M)	
						1.3E-02	R.DSVLLVEVKK.V	
						1.0E-04	R.LPSPLEEGSVK.A	
						3.3E-07	R.MQSVTGTSFLSTSAR.G + Oxidation (M)	
						2.3E-02	K.SMLSEEEHKNVVMAER.G + 2 Oxidation	
	EAO00223.1	heat shock protein 20, putative	15973	266	7	3.5E-04	K.ILADLPGMSR.N + Oxidation	0
	EAN85850.1	10 kDa heat shock protein, putative	10694	75	2	9.2E-05	K.AGVLIPEQVAGK.V	5
						5.8E-04	K.VNEGTVVAVAAATK.D	
	EAN81492.1	40S ribosomal protein S14, putative	15771	55	1	5.0E-06	R.SPGPGAQAALR.A	2
	EAN83533.1	histone H2B, putative	12353	29	1	6.0E-03	R.IASEAATVVR.V	1
29	EAN85850.1	10 kDa heat shock protein, putative	10694	84	3	8.5E-03	K.LQPLGQR.V	5
						3.9E-04	K.AGVLIPEQVAGK.V	
						3.1E-03	K.VNEGTVVAVAAATK.D	
	EAN81916.1	ATP synthase, alpha chain, mitochondrial precursor, putative	25912	30	1	5.4E-04	K.VMATGQLLHIPVGAGVLGK.V + Oxidation	0
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	23	1	1.8E-02	K.VAISLPSR.M	1

TABLE S5 (SPOTS 30-34): COMPLETE PEPTIDE LIST

Note: The table shows the list of hits extracted from the Mascot html output results for the 2DGE spots. Mr indicates the theoretical molecular weight of the protein; Score refers to the Mascot protein score; # Pept refers to the number of peptides matched to each hit with the respective peptide e-value. Only unique peptides to each hit are indicated, not the ones shared with the previous hit. Additional gene copies column, indicates how many other annotated proteins are matched to the same set of peptides; meaning copies of the same gene product. This table is not filtered, meaning several proteins appear in more than one band; either due to proteolysis or carry over during the mass spectrometry analysis from one sample to the other one.

							Mascot	
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional gene copies under same match**
Spot 30	EAN85498.1	gamma-glutamyl carboxypeptidase, putative	44258	714	20	3.5E-03	K.MMQQVR.S + Oxidation (M)	0
						6.6E-03	R.EIAEEYR.R	
						3.2E-03	K.GGSHFWVR.V	
						9.4E-04	R.ALPNETVSK.M	
						3.5E-03	K.DYLEGLGVK.C	
						2.2E-05	K.LVAFDTTSR.N	
						4.6E-03	R.EIAEEYRR.N	
						2.6E-04	K.LREIAEEYR.R	
						1.1E-03	R.SMDHTQWLAK.L	
						1.6E-03	R.SMDHTQWLAK.L + Oxidation (M)	
						1.7E-05	K.WDSDPFTLTER.D	
						3.0E-05	R.SYVETQLLPAMK.A	
						1.9E-04	R.SYVETQLLPAMK.A + Oxidation (M)	
						2.8E-04	K.AEFEDAEIVITPR.N	
						2.2E-05	K.ANLWATLPGDGGVTK.G	
						2.0E-02	R.NKANLWATLPGDGGVTK.G	
						7.6E-08	R.NETPSFEGSEEAPFTK.L	
						3.7E-06	K.GGIILSGHTDVVPVDGQK.W	
						1.7E-02	K.AAHSSLALTGESCNAIDYATK.L	
						3.1E-04	R.SYVETQLLPAMKAEFEDAEIVITPR.N + Oxidation (M)	
	EAN85497.1	gamma-glutamyl carboxypeptidase, putative	44390	707	20	2.3E-04	K.GTSHFWVR.V	0
						4.3E-06	R.DETPSFEGSEEAPFTK.L	
	EAN82710.1	gamma-glutamyl carboxypeptidase, putative	44359	701	20	5.2E-05	R.DETPSFEGSEEAPITK.L	0
	EAN82318.1	gamma-glutamyl carboxypeptidase, putative	44366	645	18	8.7E-06	R.NETPSFEGSEEAPLTK.L	0
	EAN96732.1	succinyl-CoA ligase [GDP-forming] beta-chain, putative	46089	441	9	3.8E-02	K.SQILAGGR.G	0
						8.7E-07	R.AAENAAEQVK.A	
						1.2E-03	R.GMGTFEDGFK.G + Oxidation (M)	
						1.3E-05	R.TLEEVEAALGK.I	
						1.7E-06	K.LSFDDNAEFR.Q	
						4.7E-06	R.ILQESGLPLHPAR.N	

						Mascot		
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
30 cont.	EAN96732.1	cont.				8.9E-08	R.VNLLYVTEAVTGIK.R	
						2.9E-02	K.DIFSLADDTQIDPK.E	
						1.9E-06	K.EQIVAAFQIITGDEK.V	
	EAN97657.1	chaperonin HSP60, mitochondrial precursor	59413	398	6	8.0E-05	R.AVSAVATTLGPK.G	0
						9.0E-08	K.VGGGSEVEVNEK.K	
						1.1E-06	R.NVIIEQSYGAPK.I	
						2.5E-07	K.AELEDAFVLVSAK.K	
						3.7E-08	R.AVGVILQSVAEQSR.K	
						8.4E-07	K.TAMMQDIAIFAGAR.L + 2 Oxidation (M)	
	EAN81053.1	alpha tubulin, putative	50549	389	7	7.1E-03	R.LSVDYGKK.S	0
						2.1E-05	K.DVNAAVATIK.T	
						1.5E-08	R.LIGQVVSALTASLR.F	
						4.6E-06	R.TIQFVDWSPTGFK.C	
						1.6E-08	R.AVFLDLEPTVVDEIR.T	
						3.8E-03	R.NLDIERPTYTNLNR.L	
						5.4E-07	R.IHFVLTSYAPVISAEK.A	
	EAN98272.1	eukaryotic initiation factor 4a, putative	49984	369	7	1.5E-03	R.ESLTLEGIK.Q	1
						2.0E-03	K.GVAINFVTQK.D	
						2.6E-05	R.VLVTTDLVAR.G	
						3.1E-06	K.TGAFSIGLLQR.L	
						7.0E-08	R.GGDIIAQAQSGTGK.T	
						2.0E-05	K.LQAGSIVAVGTPGR.V	
						1.6E-07	R.ELALQTAEVITR.I	
	EAN94839.1	beta tubulin, putative	50520	352	10	2.3E-01	R.YLTASALFR.G	0
						5.4E-05	K.LAVNLVPFPR.L	
						2.9E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						2.6E-07	R.INVYFDEATGGR.Y	
						1.3E-01	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						5.4E-06	K.EVDEQMLNVQNK.N	
						1.1E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						3.6E-04	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						2.6E-04	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
						3.6E-02	K.NSSYFIEWIPNNIK.S	
	EAN95952.1	hypothetical protein, conserved	43691	331	6	1.6E-05	K.VIANLLNR.-	0
						1.3E-06	R.FVFTAVLPR.F	
						6.8E-03	R.LIFLYPMSK.L + Oxidation (M)	
						1.4E-06	K.IINLSAEEIR.A	
						2.9E-06	R.VIYLNLNEEPR.T	

						Mascot		
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
30 cont.	EAN95952.1	cont.				2.0E-07	K.SEEPSGLELVDLR.D	
	EAN86150.1	hypothetical protein, conserved	47419	231	8	1.7E-02	R.QLNYGPK.D	0
						1.1E-02	R.FLAPYDK.N	
						1.1E-03	R.AWDDLFEK.N	
						1.8E-03	K.EVSQEEIAK.L	
						1.8E-04	R.SIPSYLTDTK.W	
						2.8E-02	R.NFFPGLALFAK.Q	
						2.7E-01	R.HAADMYDGFIK.F + Oxidation (M)	
						2.6E-05	K.QTQEAVDIWLR.I	
	EAN96060.1	gamma-glutamyl carboxypeptidase, putative	44531	210	5	*3.5E-03*	*K.DYLEGLGVK.C not unique*	0
						1.1E-04	K.LVSFDTTSR.N	
						5.1E-03	K.INEIAENIK.F	
						1.4E-05	K.AYVNDTLLPSMK.K + Oxidation (M)	
						1.3E-05	R.YLPEAEAEKFEER.I	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	196	4	1.1E-05	K.TAEETLAAAGQR.V	1
						1.0E-04	K.GLPQEVVEQVK.A	
						2.0E-04	R.EMILADTLEGR.K + Oxidation (M)	
						6.9E-06	R.TPQQIGQSLSLR.W	
	EAN92220.1	pyruvate dehydrogenase E1 component alpha subunit, putative	43381	147	4	1.1E-04	K.SDIQDVR.K	0
						1.6E-02	R.AAYQPEMYR.R + Oxidation (M)	
						3.0E-05	K.GPIVLEFDSYR.Y	
						4.1E-03	R.GGTPGEVFAEMFGK.E + Oxidation (M)	
	EAN83160.1	phosphomannose isomerase, putative	46214	141	4	1.9E-02	K.VAAESFVAK.M	0
						3.1E-03	R.FTEFSLYR.M	
						2.8E-05	K.TLLGNVAVVSAK.E	
						2.9E-04	R.AAEGEAWEVQR.Y	
	EAN98440.1	actin-like protein, putative	47418	136	3	1.4E-04	K.EVQTPLLLTEK.M	0
						5.8E-05	R.QAAIVDIGSYTTR.I	
						6.1E-05	K.LDYEESGPSAVLR.R	
	EAN85395.1	3-ketoacyl-CoA thiolase, putative	46802	130	2	3.3E-05	K.MGISPNDSSLVEIK.S + Oxidation (M)	1
						2.9E-08	K.SLAAASGNLYEDPPDATR.M	
	EAN86097.1	fructose-bisphosphate aldolase, glycosomal, putative	41279	103	2	9.1E-07	R.VEVLQTQLPAYNR.L	2
						3.6E-04	R.ATPGQVAQYTVSTLAR.V	
	EAN81757.1	mitochondrial processing peptidase, beta subunit, putative	31341	87	1	6.3E-09	R.AAASNFGDLVAASTK.S	1
	EAN92798.1	phosphomannose isomerase, putative	46092	87	3	*1.9E-02*	K.VAAESFVAK.M not unique	0
						3.1E-03	R.FTEFSLYR.L not unique	

							Mascot	
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
30 cont.	EAN92798.1	cont.				8.3E-04	K.TLLGNTAVVSAK.E	
	EAN82857.1	elongation factor 1-alpha (EF-1-alpha), putative	48884	86	2	2.8E-03	K.SVNFAQER.Y	5
						8.0E-06	K.IGGIGTVPVGR.V	
	EAN88964.1	glycosomal phosphoenolpyruvate carboxykinase, putative	59404	74	2	1.8E-03	K.TTLSADPHR.N	1
						1.9E-04	K.TEKDIYDAVR.F	
	EAN85276.1	hypothetical protein	52756	60	1	1.7E-06	R.FADANEENVPAAQVNR.V	1
	EAN87042.1	SPFH domain / Band 7 family protein, putative	44380	54	1	1.3E-05	R.AEAEAEATGVMAAAISK.S + Oxidation	1
	EAN92318.1	69 kDa paraflagellar rod protein, putative	70087	53	1	1.2E-05	R.TVSFTGTIDNAIAK.L	0
	EAO00025.1	alcohol dehydrogenase, putative	42442	53	1	1.3E-05	K.VSYLGVGALDSATSK.M	1
	EAO00026.1	elongation factor TU, putative	52462	40	1	2.5E-04	K.IVGSGETVNLSK.E	1
	EAN87141.1	hexokinase, putative	52750	29	1	5.1E-03	R.ATVAIDGSVFEK.T	1
	EAN83852.1	heat shock 70 kDa protein, putative	41044	28	1	5.7E-03	R.VEIIANDQGNR.T	1
	EAN95757.1	prostaglandin F2alpha synthase	14719	26	1	1.2E-02	K.FIANPDLVER.A	1
	EAN86294.1	phosphoglycerate kinase, putative	44867	19	1	3.2E-02	K.TLPGVAVLDDKE.-	3
	EAN85233.1	axoneme central apparatus protein, putative	34377	19	1	5.2E-02	R.TAASTLSDIAK.H	1
Spot 31	EAN85497.1	gamma-glutamyl carboxypeptidase, putative	44390	778	21	2.7E-02	K.MMQQVR.S + Oxidation (M)	0
						3.7E-03	R.EIAEEYR.R	
						7.7E-04	R.ALPNETVSK.M	
						8.4E-04	K.GTSHFWVR.V	
						2.6E-03	K.DYLEGLGVK.C	
						7.1E-05	K.LVAFDTTSR.N	
						4.6E-03	R.EIAEEYRR.N	
						1.8E-04	K.LREIAEEYR.R	
						1.8E-04	R.SMDHTQWLAK.L	
						2.1E-03	R.SMDHTQWLAK.L + Oxidation (M)	
						1.5E-05	K.WDSDPFTLTER.D	
						1.5E-06	R.SYVETQLLPAMK.A	
						1.4E-02	R.SYVETQLLPAMK.A + Oxidation (M)	
						2.6E-04	K.AEFEDAEIVITPR.D	
						1.4E-04	K.ANLWATLPGDGGVTK.G	
						1.1E-02	K.WDSDPFTLTERDGK.L	
						1.7E-06	R.NKANLWATLPGDGGVTK.G	
						4.0E-08	R.DETPSFEGSEEAPFTK.L	
						4.1E-05	K.GGIILSGHTDVVPVDGQK.W	

						Mascot		
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
31 cont.	EAN85497.1	cont.				7.7E-03	K.AAHSSLALTGESCNAIDYATK.L	
						2.8E-03	R.SYVETQLLPAMKAEFEDAEIVITPR.D + Oxidat	
	EAN82710.1	gamma-glutamyl carboxypeptidase, putative	44359	750	21	5.3E-05	R.DETPSFEGSEEAPITK.L	0
	EAN85498.1	gamma-glutamyl carboxypeptidase, putative	44258	748	21	3.1E-03	K.GGSHFWVR.V	0
						1.1E-05	R.NETPSFEGSEEAPFTK.L	
	EAN82318.1	gamma-glutamyl carboxypeptidase, putative	44366	701	19	7.8E-06	R.NETPSFEGSEEAPLTK.L	0
	EAN98272.1	eukaryotic initiation factor 4a, putative	49984	374	7	5.4E-04	R.ESLTLEGIK.Q	1
						3.8E-05	R.VLVTTDLVAR.G	
						1.2E-06	K.TGAFSIGLLQR.L	
						4.7E-04	R.KGVAINFVTQK.D	
						2.1E-06	R.GGDIIAQAQSGTGK.T	
						2.2E-06	K.LQAGSIVAVGTPGR.V	
						1.5E-07	R.ELALQTAEVITR.I	
	EAN96060.1	gamma-glutamyl carboxypeptidase, putative	44531	248	6	2.6E-03	K.DYLEGLGVK.C not unique	0
						2.2E-05	K.LVSFDTTSR.N	
						4.3E-03	K.INEIAENIK.F	
						1.5E-04	K.AYVNDTLLPSMK.K	
						1.4E-05	K.AYVNDTLLPSMK.K + Oxidation (M)	
						1.9E-02	K.AYVNDTLLPSMKK.A + Oxidation (M)	
						2.3E-06	R.YLPEAEAEKFEER.I	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	247	5	1.5E-04	R.SATGVAFSR.S	1
						6.7E-06	K.TAEETLAAAGQR.V	
						4.8E-03	K.GLPQEVVEQVK.A	
						4.6E-05	R.EMILADTLEGR.K	
						7.5E-06	R.EMILADTLEGR.K + Oxidation (M)	
						5.2E-07	R.TPQQIGQSLSLR.W	
	EAN88964.1	glycosomal phosphoenolpyruvate carboxykinase, putative	59404	197	4	1.5E-04	K.LSEESFAR.V	1
						6.4E-05	K.TTLSADPHR.N	
						2.3E-04	K.TEKDIYDAVR.F	
						1.5E-06	R.HATFYGEQLAEK.M	
	EAN95952.1	hypothetical protein, conserved	43691	196	4	4.0E-05	K.VIANLLNR.-	0
						2.3E-04	R.FVFTAVLPR.F	
						2.0E-05	K.IINLSAEEIR.A	
						3.1E-06	R.VIYLNLNEEPR.T	

						Mascot		
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
31 cont.	EAN94510.1	mitochondrial processing peptidase, beta subunit, putative	55057	190	3	3.6E-07	R.AVGLLADVVR.N	0
						1.1E-03	R.LADEDIQAAK.Q	
						3.4E-09	R.VVVVGSGAVDHTALER.A	
	EAN96732.1	succinyl-CoA ligase [GDP-forming] beta-chain, putative	46089	178	3	2.6E-05	R.AAENAAEQVK.A	0
						1.1E-05	R.TLEEVEAALGK.I	
						2.4E-07	K.LSFDDNAEFR.Q	
	EAN86097.1	fructose-bisphosphate aldolase, glycosomal, putative	41279	174	3	8.7E-06	K.IQNGTVSEAAVR.F	2
						2.1E-06	K.ASTGETFVQLLQR.K	
						2.3E-06	R.VEVLQTQLPAYNR.L	
	EAN81757.1	mitochondrial processing peptidase, beta subunit, putative	31341	162	2	1.2E-07	R.AAASNFGDLVAASTK.S	0
						3.4E-09	*.VVVVGSGAVDHTALER.A not unique*	
	EAN94839.1	beta tubulin, putative	50520	161	3	1.4E-07	R.INVYFDEATGGR.Y	0
						1.5E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						4.2E-04	R.AVLIDLEPGTMDSVR.A + Oxidation	
	EAN85395.1	3-ketoacyl-CoA thiolase, putative	46802	161	3	6.8E-06	K.MGISPNDSSLVEIK.S + Oxidation (M)	1
						4.9E-03	K.AIQESQHFTMEDTAR.V + Oxidation (M)	
						3.5E-08	K.SLAAASGNLYEDPPDATR.M	
	EAN82857.1	elongation factor 1-alpha (EF-1-alpha), putative	48884	118	3	4.7E-03	K.SVNFAQER.Y	5
						2.8E-04	R.LPLQDVYK.I	
						2.5E-05	K.IGGIGTVPVGR.V	
	EAN81053.1	alpha tubulin, putative	50549	106	2	1.4E-05	K.DVNAAVATIK.T	0
						2.1E-05	R.AVFLDLEPTVVDEIR.T	
	EAN80998.1	hypothetical protein, conserved	39206	99	2	2.7E-06	K.ATADAEILSLR.Q	1
						2.3E-03	R.SSQIGGVGGTTTR.Q	
	EAN92220.1	pyruvate dehydrogenase E1 component alpha subunit, putative	43381	94	1	3.9E-04	K.EVDQQLQPAEK.Q	0
						1.0E-05	K.GPIVLEFDSYR.Y	
	EAN93231.1	pyruvate dehydrogenase E1 component alpha subunit, putative	22293	88	2	1.6E-03	K.EVDQQLLPAEK.Q	0
						1.0E-05	*K.GPIVLEFDSYR.Y not unique*	
	EAN81897.1	2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide succinyltransferase, putative	42903	58	1	3.0E-06	R.LIDGSDAVTFLVK.V	1
	EAN87141.1	hexokinase, putative	52750	58	1	2.4E-01	R.MLPSYVYK.T + Oxidation (M)	1
						7.7E-05	R.ATVAIDGSVFEK.T	

						Mascot		
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
31 cont.	EAN83022.1	hypothetical protein, conserved	37536	57	1	9.5E-06	R.QGLGSEVAEVK.A	3
	EAN81715.1	hypothetical protein, conserved	41759	55	1	2.1E-05	K.GVIAELDLSGR.L	1
	EAN82747.1	Gim5A protein, putative	27268	44	1	2.9E-05	R.LSLLLNALSSK.T	2
	EAN88684.1	heat shock protein DnaJ, putative	45029	41	1	3.4E-04	R.GEGDQIPGVR.L	0
	EAN87378.1	3-hydroxy-3-methylglutaryl-CoA reductase, putative	46865	36	1	8.4E-04	K.ESPGTNAQLLSR.V	1
	EAN87724.1	glutamate dehydrogenase, putative	45525	33	1	1.5E-03	R.VQFNSSIGPYK.G	0
	EAO00026.1	elongation factor TU, putative	52462	28	2	9.4E-03	K.IVGSGETVNLSK.E	1
						7.9E-01	R.AQVYVLTKEEGGR.H	
	EAN90286.1	glyceraldehyde 3-phosphate dehydrogenase, putative	39292	22	1	9.6E-03	R.AAAVNIIPSTTGAAK.A	3
	EAN99859.1	hypothetical protein, conserved	13236	18	1	6.1E-02	R.YYAMNSLTAIASVK.V	0
32	EAN92318.1	69 kDa paraflagellar rod protein, putative	70087	1273	31	8.0E-03	K.TVQQITQ.-	0
						1.2E-03	K.AQLAAIEK.A	
						1.6E-04	K.TLGQLVYK.K	
						5.7E-03	K.RLEEIDR.N	
						5.9E-04	R.RIQELER.V	
						5.0E-05	R.GKTVQQITQ.-	
						3.7E-04	K.SFQETSAIK.D	
						3.4E-04	K.TLQSQQYR.G	
						7.2E-03	K.FIQENLDR.Q	
						8.7E-04	K.TLGQLVYKK.E	
						5.8E-06	K.TNEELADLR.L	
						1.6E-02	K.KSFQETSAIK.D	
						8.6E-02	R.LEEIDRNIR.T	
						1.6E-02	R.LGTERFEEVK.R	
						9.4E-05	R.SKTLQSQQYR.G	
						9.5E-06	K.WNLTEAYDIK.K	
						3.5E-07	K.AQELLSSVEGGTK.W	
						3.6E-06	K.SFQETSAIKDAK.R	
						2.8E-03	R.AQVEEELEMLK.D + Oxidation (M)	
						7.5E-03	K.WNLTEAYDIKK.L	
						2.1E-06	R.TVSFTGTIDNAIAK.L	
						4.2E-05	R.LQVHQEYLEAFR.R	
						1.5E-04	R.AQVEEELEMLKDK.M + Oxidation (M)	
						3.1E-06	R.IIGQTEDENKPFGR.I	
						8.4E-07	R.SQLDASEMAQVPVAVLK.N	
						4.4E-07	R.SQLDASEMAQVPVAVLK.N + Oxidation (M)	
						2.5E-03	R.TVSFTGTIDNAIAKLEK.I	

						Mascot		
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
32 cont.	EAN92318.1	cont.				9.6E-04	K.FIQENLDRQDEAWR.R	
						2.2E-03	R.TTHIQLEFAIETFDPNAK.K	
						1.4E-08	R.NVAIADGEMAIAEEQYYIK.A + Oxidation (M)	
						9.0E-04	K.EASGAVGPADQQQPAVPEVTDVTLEAAR.K	
	EAN81200.1	paraxonemal rod protein PAR2, putative	31620	554	15	1.4E-04	K.TNEELGDLR.L	0
	EAN87979.1	paraflagellar rod protein 3, putative	69189	493	12	1.0E+00	K.VEEELRR.S	0
						3.9E-02	K.TQLAQLEK.T	
						5.1E-05	R.LIDLIQDK.F	
						4.4E-05	K.TSQDLAALR.L	
						1.3E-04	K.AQFMDIIGVK.K + Oxidation (M)	
						2.3E-03	R.IEEVDREEK.R	
						1.6E-02	*K.LGTERFEEVK.R not unique*	
						5.6E-06	R.LIDLIQDKFR.L	
						2.7E-05	R.QGVEEELAMLK.E + Oxidation (M)	
						3.5E-03	K.ADLEDAEAMKR.H + Oxidation (M)	
						4.3E-06	R.SQLDATQLAQVPTR.T	
						8.9E-08	R.VVSFTQMIDNAIAK.M + Oxidation (M)	
	EAN96800.1	lipophosphoglycan biosynthetic protein, putative	86969	107	2	2.6E-02	R.EVLQESR.I	0
						1.5E-08	R.GIVDSNDLPLNVSR.E	
	EAN94839.1	beta tubulin, putative	50520	92	2	1.1E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	0
						4.2E-04	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
	EAN96878.1	dynein, putative	69173	60	1	5.1E-06	K.AAIGQMLENQSIR.D + Oxidation (M)	0
	EAN81053.1	alpha tubulin, putative	50549	53	1	2.0E-05	K.DVNAAVATIK.T	0
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	49	1	4.6E-05	K.TAEETLAAAGQR.V	1
	EAN82747.1	Gim5A protein, putative	27268	40	1	7.5E-05	R.LSLLLNALSSK.T	2
	EAN87573.1	succinate dehydrogenase flavoprotein, putative	67998	21	1	1.5E-02	R.AITLEVLAGR.G	0
Spot 33	EAN92318.1	69 kDa paraflagellar rod protein, putative	70087	1430	36	2.9E-05	R.QDEAWR.R	0
						2.8E-03	K.TVQQITQ.-	
						7.9E-05	K.AQLAAIEK.A	
						3.1E-03	K.TLGQLVYK.K	
						3.8E-03	K.RLEEIDR.N	
						1.0E-03	K.NLHDAIQK.A	
						3.1E-03	R.RIQELER.V	
						1.1E-01	R.QDEAWRR.I	
						4.5E-04	K.SFQETSAIK.D	
						1.0E-02	K.FIQENLDR.Q	

						Mascot		
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
33 cont.	EAN92318.1	cont.				7.9E-04	K.TLGQLVYKK.E	
						5.5E-03	K.IAAEREELK.R	
						1.1E-06	K.TNEELADLR.L	
						9.5E-03	K.KSFQETSAIK.D	
						2.0E-03	R.LGTERFEEVK.R	
						4.4E-04	R.SKTLQSQQYR.G	
						1.2E-04	K.WNLTEAYDIK.K	
						7.0E-03	K.ADMEDAEAMKR.F + Oxidation (M)	
						1.7E-05	K.AQELLSSVEGGTK.W	
						1.5E-06	K.SFQETSAIKDAK.R	
						2.3E-04	R.AQVEEELEMLK.D + Oxidation (M)	
						4.1E-05	K.WNLTEAYDIKK.L	
						6.6E-08	R.TVSFTGTIDNAIAK.L	
						2.1E-05	R.LQVHQEYLEAFR.R	
						5.4E-04	R.AQVEEELEMLKDK.M	
						6.7E-06	R.AQVEEELEMLKDK.M + Oxidation (M)	
						1.2E-07	R.IIGQTEDENKPFGR.I	
						3.1E-03	R.LQVHQEYLEAFRR.L	
						2.7E-08	R.SQLDASEMAQVPVAVLK.N	
						5.0E-07	R.SQLDASEMAQVPVAVLK.N + Oxidation (M)	
						3.2E-03	K.FIQENLDRQDEAWR.R	
						2.7E-03	R.TTHIQLEFAIETFDPNAK.K	
						1.6E-09	R.NVAIADGEMAIAEEQYYIK.A	
						6.5E-08	R.NVAIADGEMAIAEEQYYIK.A + Oxidation (M)	
						8.8E-04	R.TTHIQLEFAIETFDPNAKK.H	
						1.1E-04	K.EASGAVGPADQQQPAVPEVTDVTLEAAR.K	
	EAN87979.1	paraflagellar rod protein 3, putative	69189	1135	31	2.0E-01	R.QEEAWNK.I	0
						1.2E-01	K.VEEELRR.S	
						2.1E-03	K.TQLAQLEK.T	
						1.6E-05	R.LIDLIQDK.F	
						3.3E-07	K.TSQDLAALR.L	
						2.5E-02	K.EHLEYFR.M	
						5.5E-03	*K.IAAEREEIK.R not unique*	
						1.0E-03	K.AQFMDIIGVK.K	
						2.0E-04	K.AQFMDIIGVK.K + Oxidation (M)	
						1.8E-03	R.IEEVDREEK.R	
						9.1E-06	R.IGNNTAPARLE.-	
						1.2E-03	K.MEKVEEELR.R + Oxidation (M)	
						2.0E-03	*K.LGTERFEEVK.R not unique*	

						Mascot		
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
33 cont.	EAN87979.1	cont.				2.3E-05	K.ADLEDAEAMKR.H	
						1.7E-05	R.LIDLIQDKFR.L	
						1.4E-05	R.QGVEEELAMLK.E + Oxidation (M)	
						1.2E-03	K.ADLEDAEAMKR.H + Oxidation (M)	
						2.7E-03	K.AQFMDIIGVKK.V + Oxidation (M)	
						4.3E-05	K.AEELVASVDVGTK.W	
						2.1E-05	K.WNLTEAYDLAK.L	
						1.6E-06	R.MLYLTLGSLIYK.K + Oxidation (M)	
						2.3E-06	R.SQLDATQLAQVPTR.T	
						2.4E-02	K.LRQGVEEELAMLK.E + Oxidation (M)	
						4.4E-05	R.VVSFTQMIDNAIAK.M	
						7.5E-09	R.VVSFTQMIDNAIAK.M + Oxidation (M)	
						5.1E-02	R.ENEERQEEAWNK.I	
						2.0E-02	R.VEYSQFLEVASQHK.K	
						5.0E-05	R.RSQLDATQLAQVPTR.T	
						1.3E-01	R.VEYSQFLEVASQHKK.L	
						1.3E-05	R.GAHLKAEELVASVDVGTK.W	
						1.3E-04	K.QIEDIMNATQIQNALASTDDQIK.T + Oxidat	
	EAN81200.1	paraxonemal rod protein PAR2, putative	31620	652	19	8.1E-05	K.TNEELGDLR.L	0
						1.5E-03	R.HDKTNEELGDLR.L	
	EAN96800.1	lipophosphoglycan biosynthetic protein, putative	86969	382	9	2.6E-03	R.MLYLTAPK.E + Oxidation (M)	0
						4.0E-02	R.VIIDNERK.T	
						5.7E-05	R.LGILEDANNR.G	
						6.7E-05	K.ALSMISEIAEK.D + Oxidation (M)	
						3.9E-05	K.HIYFLTGDSVK.K	
						7.0E-02	K.GRPISFQAEVSK.M	
						1.0E-09	R.GIVDSNDLPLNVSR.E	
						3.2E-05	K.MLDILINSLYTNR.A + Oxidation (M)	
						9.7E-03	K.AELEEHLGSLGTSGTK.R	
	EAN94839.1	beta tubulin, putative	50520	333	7	1.1E-06	K.LAVNLVPFPR.L	0
						3.5E-05	R.VGEQFTAMFR.R + Oxidation (M)	
						1.6E-07	R.INVYFDEATGGR.Y	
						6.6E-03	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						4.6E-04	K.EVDEQMLNVQNK.N + Oxidation (M)	
						1.2E-05	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						8.9E-04	R.GLSVPELTQQMFDAK.N + Oxidation (M)	

							Mascot	
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
33 cont.	EAN87573.1	succinate dehydrogenase flavoprotein, putative	67998	286	6	5.3E-03	R.AITLEVLAGR.G	0
						1.0E-04	R.TKDGFIYQR.A	
						5.0E-05	K.YTILATGGYGR.C	
						9.0E-06	R.AFGGQSIHFGGK.Q	
						3.8E-05	R.GEGGYLVNSEGER.F	
						3.7E-07	R.LGANSLLDIVVFGK.S	
	EAN95887.1	heat shock protein 70 (HSP70), putative	73607	204	5	3.7E-03	R.GTLQPVER.V	0
						3.4E-04	K.NTVNEPNVAGK.I	
						1.0E-02	K.VMQLVSDFFGGK.E + Oxidation (M)	
						4.3E-04	R.TTPSYVAFTDTER.L	
						8.8E-08	K.NQVAMNPTNTVFDAK.R + Oxidation (M)	
	EAN95886.1	heat shock protein 70 (HSP70), putative	71171	202	5	7.1E-03	R.VEIIANDQGNR.T	0
	EAN96878.1	dynein, putative	69173	175	3	2.5E-06	R.LQEELEVQR.R	0
						1.3E-05	K.LPEDSLTLLPK.S	
						1.8E-06	K.AAIGQMLENQSIR.D + Oxidation	
	EAN82857.1	elongation factor 1-alpha (EF-1-alpha), putative	48884	119	3	3.1E-03	K.SVNFAQER.Y	5
						1.2E-06	K.IGGIGTVPVGR.V	
						1.0E-02	R.VETGTMKPGDVVTFAPANVTTEVK.S + Oxidation (M)	
	EAN84370.1	heat shock 70 kDa protein, mitochondrial precursor, putative	71585	104	2	7.3E-05	K.STGIDLSNER.M	0
						9.4E-06	K.DAGTIAGLNVIR.V	
	EAN97980.1	mitochondrial intermediate peptidase, putative	77969	103	3	1.2E-02	K.HAAYAFQK.G	0
						7.3E-05	K.ELVQEVMR.H + Oxidation (M)	
						1.5E-03	R.TLGDSSDYGR.G	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	96	3	2.1E-05	K.TAEETLAAAGQR.V	1
						2.8E-04	R.EMILADTLEGR.K + Oxidation (M)	
						3.2E+00	R.VKSLHEMNPMLGHR.G + Oxidation (M	
	EAN81053.1	alpha tubulin, putative	50549	86	2	2.4E-03	K.EDAANNYAR.G	0
						3.8E-06	R.AVFLDLEPTVVDEIR.T	
	EAN82747.1	Gim5A protein, putative	27268	63	1	3.7E-07	R.LSLLLNALSSK.T	2
	EAN80947.1	tryparedoxin peroxidase, putative	22886	30	1	2.2E-03	R.QITVNDLPVGR.D	5
Spot 34	EAN87979.1	paraflagellar rod protein 3, putative	69189	1246	39	8.0E-02	R.QEEAWNK.I	0
						9.0E-04	K.KIYEVQK.Q	
						2.5E-06	R.IGNNTAPAR.L	

Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
34 cont.	EAN87979.1	cont.				1.8E-01	K.VEEELRR.S	
						1.0E-02	K.TQLAQLEK.T	
						6.6E-03	R.EKSDGFVR.E	
						1.7E-02	K.RMEEIDR.N	
						3.1E-05	R.LIDLIQDK.F	
						3.8E-06	K.TSQDLAALR.L	
						2.0E-01	K.EHLEYFR.M	
						3.2E-02	R.ELYRPEDK.A	
						8.8E-03	K.IAAEREEIK.R	
						9.0E-06	K.ADLEDAEAMK.R + Oxidation (M)	
						2.5E-04	K.AQFMDIIGVK.K	
						2.1E-04	K.AQFMDIIGVK.K + Oxidation (M)	
						3.0E-03	R.IEEVDREEK.R	
						4.9E-04	R.IGNNTAPARLE.-	
						1.6E-03	K.MEKVEEELR.R + Oxidation (M)	
						1.1E-02	K.LGTERFEEVK.R	
						2.5E-04	R.QGVEEELAMLK.E	
						3.6E-05	K.ADLEDAEAMKR.H	
						3.2E-05	R.LIDLIQDKFR.L	
						2.0E-05	R.QGVEEELAMLK.E + Oxidation (M)	
						2.2E-03	K.ADLEDAEAMKR.H + Oxidation (M)	
						5.6E-03	K.AQFMDIIGVKK.V + Oxidation (M)	
						1.4E-06	K.WNLTEAYDLAK.L	
						2.7E-07	R.MLYLTLGSLIYK.K + Oxidation (M)	
						1.2E+00	R.QGVEEELAMLKEK.Q + Oxidation (M)	
						4.6E-06	R.SQLDATQLAQVPTR.T	
						1.6E-05	K.LRQGVEEELAMLK.E + Oxidation (M)	
						7.3E-07	R.VVSFTQMIDNAIAK.M	
						1.7E-07	R.VVSFTQMIDNAIAK.M + Oxidation (M)	
						1.0E-02	R.ENEERQEEAWNK.I	
						1.8E-05	R.VEYSQFLEVASQHK.K	
						2.2E-05	R.RSQLDATQLAQVPTR.T	
						4.9E-02	R.VEYSQFLEVASQHKK.L	
						4.6E-05	R.RVEYSQFLEVASQHK.K	
						8.6E-10	R.GAHLKAEELVASVDVGTK.W	
						9.2E-06	K.QIEDIMNATQIQNALASTDDQIK.T + Oxidat	
	EAN92318.1	69 kDa paraflagellar rod protein, putative	70087	955	23	7.7E-03	K.TVQQITQ.-	0
						1.1E-03	K.AQLAAIEK.A	
						2.6E-03	K.TLGQLVYK.K	

Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
34 cont.	EAN92318.1	cont.				1.6E-02	K.RLEEIDR.N	
						9.3E-03	K.NLHDAIQK.A	
						1.6E-03	R.RIQELER.V	
						4.4E-04	K.SFQETSAIK.D	
						3.3E-04	K.TLQSQQYR.G	
						1.2E-02	K.FIQENLDR.Q	
						8.8E-03	*K.IAAEREELK.R not unique*	
						3.5E-07	K.TNEELADLR.L	
						1.1E-02	K.KSFQETSAIK.D	
						1.1E-02	*R.LGTERFEEVK.R not unique*	
						7.2E-05	K.WNLTEAYDIK.K	
						2.7E-06	K.AQELLSSVEGGTK.W	
						8.5E-06	K.SFQETSAIKDAK.R	
						1.2E-02	R.AQVEEELEMLK.D + Oxidation (M)	
						8.4E-08	R.TVSFTGTIDNAIAK.L	
						6.2E-06	R.AQVEEELEMLKDK.M + Oxidation (M)	
						7.7E-05	R.IIGQTEDENKPFGR.I	
						7.9E-07	R.SQLDASEMAQVPVAVLK.N + Oxidation (M)	
						1.4E-04	R.NVAIADGEMAIAEEQYYIK.A + Oxidation (M)	
						2.7E-04	K.EASGAVGPADQQQPAVPEVTDVTLEAAR.K	
	EAN81200.1	paraxonemal rod protein PAR2, putative	31620	350	10	7.7E-05	K.TNEELGDLR.L	0
	EAN94839.1	beta tubulin, putative	50520	218	4	3.4E-05	K.LAVNLVPFPR.L	0
						5.2E-07	R.INVYFDEATGGR.Y	
						3.9E-06	K.EVDEQMLNVQNK.N + Oxidation (M)	
						3.1E-05	R.AVLIDLEPGTMDSVR.A + Oxidation	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	193	4	5.3E-05	K.TAEETLAAAGQR.V	1
						8.6E-07	R.TPQQIGQSLSLR.W	
						3.7E-08	R.LETSPEDLAGMDAAR.G + Oxidation (M)	
						2.2E+00	R.VKSLHEMNPMLGHR.G + Oxidation (M	
	EAN87573.1	succinate dehydrogenase flavoprotein, putative	67998	55	2	6.6E-02	R.AITLEVLAGR.G	0
						2.0E-04	R.GEGGYLVNSEGER.F	
	EAN82747.1	Gim5A protein, putative	27268	52	1	4.0E-06	R.LSLLLNALSSK.T	2
	EAN81053.1	alpha tubulin, putative	50549	51	1	3.3E-05	K.DVNAAVATIK.T	0
	EAN87966.1	glucose-regulated protein 78, putative	71414	48	1	4.7E-05	R.NSLESVAYSLR.N	0
	EAN96060.1	glutamamyl carboxypeptidase, putative	44531	32	1	1.8E-03	K.LVSFDTTSR.N	0
	EAN82857.1	elongation factor 1-alpha (EF-1-alpha), putative	48884	29	1	6.5E-03	K.SVNFAQER.Y	6
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	21	1	2.9E-02	K.VAISLPSR.M	1

TABLE S5 (SPOTS 35-39): COMPLETE PEPTIDE LIST

Note: The table shows the list of hits extracted from the Mascot html output results for the 2DGE spots. Mr indicates the theoretical molecular weight of the protein; Score refers to the Mascot protein score; # Pept refers to the number of peptides matched to each hit with the respective peptide e-value. Only unique peptides to each hit are indicated, not the ones shared with the previous hit. Additional gene copies column, indicates how many other annotated proteins are matched to the same set of peptides; meaning copies of the same gene product. This table is not filtered, meaning several proteins appear in more than one band; either due to proteolysis or carry over during the mass spectrometry analysis from one sample to the other one.

							Mascot	Additional gene copies under same match
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	
Spot 35	EAN87979.1	paraflagellar rod protein 3, putative	69189	1219	34	5.3E-02	R.QEEAWNK.I	0
						1.0E-03	K.KIYEVQK.Q	
						1.4E-06	R.IGNNTAPAR.L	
						1.1E-01	K.VEEELRR.S	
						4.0E-02	K.TQLAQLEK.T	
						1.5E-05	R.LIDLIQDK.F	
						2.3E-02	K.EHLEYFR.M	
						5.1E-03	K.IAAEREEIK.R	
						2.9E-06	K.ADLEDAEAMK.R + Oxidation (M)	
						3.9E-04	K.AQFMDIIGVK.K	
						1.3E-04	K.AQFMDIIGVK.K + Oxidation (M)	
						4.6E-03	R.IEEVDREEK.R	
						1.2E-03	R.IGNNTAPARLE.-	
						8.6E-03	K.MEKVEEELR.R + Oxidation (M)	
						4.0E-01	K.LGTERFEEVK.R	
						1.3E-06	R.QGVEEELAMLK.E	
						4.7E-05	K.ADLEDAEAMKR.H	
						4.5E-04	R.LIDLIQDKFR.L	
						2.3E-05	R.QGVEEELAMLK.E + Oxidation (M)	
						6.9E-04	K.ADLEDAEAMKR.H + Oxidation (M)	
						3.4E-05	K.WNLTEAYDLAK.L	
						7.4E-07	R.MLYLTLGSLIYK.K + Oxidation (M)	
						4.6E-06	R.SQLDATQLAQVPTR.T	
						4.7E-04	K.LRQGVEEELAMLK.E + Oxidation (M)	
						2.1E-06	R.VVSFTQMIDNAIAK.M	
						7.0E-09	R.VVSFTQMIDNAIAK.M + Oxidation (M)	
						7.2E-02	R.ENEERQEEAWNK.I	
						1.6E-05	R.VEYSQFLEVASQHK.K	
						2.1E-06	R.RSQLDATQLAQVPTR.T	
						3.4E-01	R.VEYSQFLEVASQHKK.L	
						1.4E-04	R.RVEYSQFLEVASQHK.K	
						1.6E-04	R.GAHLKAEELVASVDVGTK.W	
						1.2E-06	K.QIEDIMNATQIQNALASTDDQIK.T + Oxidation (M)	

Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Mascot Sequence	Additional copies
35 cont.	EAN87979.1	cont.				8.0E-06	K.TNEIQNVAMHDGEMQVAEEQMWTK.V + 3 Oxidation (M)	
	EAN92318.1	69 kDa paraflagellar rod protein, putative	70087	953	21	1.6E-02	K.TVQQITQ.-	0
						1.4E-04	K.AQLAAIEK.A	
						2.6E-04	K.TLGQLVYK.K	
						3.5E-03	K.RLEEIDR.N	
						2.2E-03	R.RIQELER.V	
						4.9E-04	K.SFQETSAIK.D	
						5.0E-03	K.FIQENLDR.Q	
						5.1E-03	*K.IAAEREELK.R not unique*	
						8.5E-08	K.TNEELADLR.L	
						1.4E-03	K.KSFQETSAIK.D	
						4.0E-01	*R.LGTERFEEVK.R not unique*	
						7.2E-05	K.WNLTEAYDIK.K	
						9.1E-07	K.AQELLSSVEGGTK.W	
						6.0E-05	K.SFQETSAIKDAK.R	
						3.0E-03	R.AQVEEELEMLK.D + Oxidation (M)	
						9.4E-07	R.TVSFTGTIDNAIAK.L	
						1.4E-04	R.AQVEEELEMLKDK.M + Oxidation (M)	
						1.9E-08	R.IIGQTEDENKPFGR.I	
						8.9E-07	R.SQLDASEMAQVPVAVLK.N + Oxidation (M)	
						1.2E-05	R.NVAIADGEMAIAEEQYYIK.A + Oxidation (M)	
						9.0E-06	K.EASGAVGPADQQQPAVPEVTDVTLEAAR.K	
	EAN81200.1	paraxonemal rod protein PAR2, putative	31620	297	9	2.0E-04	K.TNEELGDLR.L only unique	0
	EAN94839.1	beta tubulin, putative	50520	279	6	2.8E-05	K.LAVNLVPFPR.L	0
						4.3E-05	R.VGEQFTAMFR.R + Oxidation (M)	
						4.2E-06	R.INVYFDEATGGR.Y	
						1.2E-02	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						1.2E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						2.5E-05	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
	EAN81053.1	alpha tubulin, putative	50549	155	3	3.1E-05	K.DVNAAVATIK.T	0
						5.6E-04	K.EDAANNYAR.G	
						2.5E-07	R.AVFLDLEPTVVDEIR.T	
	EAN96878.1	dynein, putative	69173	83	2	1.3E-03	R.LQEELEVQR.R	0
						5.1E-05	K.AAIGQMLENQSIR.D + Oxidation (M)	

Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Mascot Sequence	Additional copies
35 cont.	EAN82857.1	elongation factor 1-alpha (EF-1-alpha), putative	48884	81	2	2.0E-06	K.IGGIGTVPVGR.V	5
						3.0E-02	K.STATGHLIYK.C	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	66	2	9.4E-07	R.TPQQIGQSLSLR.W	1
						3.2E+00	R.VKSLHEMNPMLGHR.G + Oxidation (M)	
	EAN98272.1	eukaryotic initiation factor 4a, putative	49984	66	1	7.6E-07	R.ELALQTAEVITR.I	1
	EAN87966.1	glucose-regulated protein 78, putative	71414	65	2	1.2E-04	R.NSLESVAYSLR.N	0
						1.3E-02	K.LQSVTNPIIQK.V	
	EAN82747.1	Gim5A protein, putative	27268	61	1	5.7E-07	R.LSLLLNALSSK.T	2
	EAN96800.1	lipophosphoglycan biosynthetic protein, putative	86969	61	1	1.8E-06	R.GIVDSNDLPLNVSR.E	0
	EAN87573.1	succinate dehydrogenase flavoprotein, putative	67998	50	1	2.6E-05	R.GEGGYLVNSEGER.F	0
	EAN83852.1	heat shock 70 kDa protein, putative	41044	50	1	4.1E-05	K.NQVAMNPTNTVFDAK.R + Oxidation (M)	4
	EAN80947.1	tryparedoxin peroxidase, putative	22886	43	1	1.2E-04	R.QITVNDLPVGR.D	5
	EAN95112.1	hypothetical protein, conserved	90858	40	1	2.3E-04	R.EALSSIEQTLR.L	0
	EAN87401.1	dynein intermediate chain, putative	75900	35	2	2.6E-01	R.AVTSISLNNR.Y	1
						1.6E-02	R.HFSQDGSTVR.K	
	EAN85221.1	hypothetical protein, conserved	84600	21	1	4.8E-02	R.STVAALEER.L	0
	EAN81833.1	prostaglandin F2alpha synthase	28479	17	1	4.6E-02	R.CQLIYDVTK.S	1
Spot 36	EAN94839.1	beta tubulin, putative	50520	912	27	2.1E-01	R.EEYPDR.I	0
						1.4E-01	K.SSICDIPPK.G	
						1.8E-05	K.NMMQAADPR.H	
						6.8E-05	R.YLTASALFR.G	
						7.4E-05	K.NMMQAADPR.H + Oxidation (M)	
						6.9E-06	K.NMMQAADPR.H + 2 Oxidation (M)	
						3.3E-03	K.LREEYPDR.I	
						1.5E-06	K.LAVNLVPFPR.L	
						3.0E-05	R.FPGQLNSDLR.K	
						7.1E-07	R.VGEQFTAMFR.R	
						9.2E-07	R.VGEQFTAMFR.R + Oxidation (M)	
						7.4E-03	R.KLAVNLVPFPR.L	
						1.6E-03	R.FPGQLNSDLRK.L	
						3.8E-08	R.INVYFDEATGGR.Y	
						1.2E-03	R.RVGEQFTAMFR.R	
						1.8E-07	R.IMMTFSIIPSPK.V	
						1.4E-05	K.EVDEQMLNVQNK.N	
						2.4E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						1.2E-06	R.AVLIDLEPGTMDSVR.A	
						2.9E-06	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	

Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Mascot E-value	Sequence	Additional copies
36 cont.	EAN94839.1	cont.				1.5E-06	R.LHFFMMGFAPLTSR.G	
						5.3E-04	R.LHFFMMGFAPLTSR.G + Oxidation (M)	
						1.2E-05	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
						6.8E-06	R.LHFFMMGFAPLTSR.G + 2 Oxidation (M)	
						1.2E-04	K.NSSYFIEWIPNNIK.S	
						1.6E+00	K.MAVTFVGNNTCIQEMFR.R + Oxidation (M)	
						9.4E-08	K.FWEVISDEHGVDPTGTYQGDSDLQLER.I	
	EAN81053.1	alpha tubulin, putative	50549	632	13	3.4E-04	R.EDLAALEK.D	0
						7.6E-03	R.LSVDYGKK.S	
						3.3E-05	K.DVNAAVATIK.T	
						8.0E-04	K.EDAANNYAR.G	
						1.7E-01	R.IDHKFDLMYSK.R	
						1.3E-02	R.QLFHPEQLISGK.E	
						4.1E-03	R.IDHKFDLMYSK.R + Oxidation (M)	
						1.9E-09	R.LIGQVVSALTASLR.F	
						1.9E-05	R.TIQFVDWSPTGFK.C	
						6.6E-07	R.AVFLDLEPTVVDEIR.T	
						1.5E-03	R.NLDIERPTYTNLNR.L	
						3.4E-08	R.IHFVLTSYAPVISAEK.A	
						6.3E-12	R.FDGALNVDLTEFQTNLVPYPR.I	
	EAN95983.1	ATPase beta subunit, putative	55980	299	6	6.3E-04	K.IGLFGGAGVGK.T	0
						8.1E-04	K.MAEEAAELEK.L + Oxidation (M)	
						2.5E-03	K.VVSSGGNISVPVGR.E	
						2.4E-06	K.TVIIMELINNVAK.G + Oxidation (M)	
						3.2E-06	R.VAQSALTMAEYFR.D + Oxidation (M)	
						1.7E-08	K.LADQAAEDTILTTGIK.V	
	EAN97655.1	chaperonin HSP60, mitochondrial precursor	59991	262	4	8.4E-08	K.VGGGSEVEVNEK.K	1
						9.2E-09	R.AVGVILQSVAEQSR.K	
						1.5E-04	R.AAVQEGIVPGGGVALLR.A	
						2.3E-07	K.ALDSLLGDSSLTADQR.T	
	EAN87966.1	glucose-regulated protein 78, putative	71414	166	5	1.4E-02	K.GTLVPVQR.V	0
						6.6E-03	K.KEEITITNDK.G	
						1.8E-05	R.EAAEFEDEDR.K	
						6.6E-05	R.NSLESVAYSLR.N	
						1.9E-03	K.LQSVTNPIIQK.V	
	EAN82340.1	calreticulin, putative	46419	160	5	7.4E-04	K.FYADAEK.S	0
						6.6E-02	R.IRFPEDK.L	
						1.5E-01	R.QIPNPAYK.G	

						Mascot		Additional copies
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	
36 cont.	EAN82340.1	cont.				5.5E-04	K.SMEHWTTSK.H	
						3.3E-06	K.GQLEEDWSLLLPR.E	
	EAN90720.1	calreticulin, putative	46396	139	5	3.1E-04	R.FYALSTAFPTPITNEK.K	0
	EAN98377.1	importin alpha, putative	58727	67	1	3.9E-07	R.VQAVVDAGVVPR.M	0
	EAN99322.1	protein disulfide isomerase, putative	54011	47	2	3.8E-02	K.FIIEYSEK.K	0
						4.7E-04	K.GFPTIILFR.D	
	EAN81110.1	calpain-like cysteine peptidase, putative	72116	33	1	1.4E-03	R.EIAALEESMNAR.A	2
	EAO00045.1	aconitase, putative	99497	28	1	1.3E-02	R.SVEQLER.I	0
	EAN83235.1	hypothetical protein, conserved	124306	18	1	4.4E-02	K.NLQADPHDPTSILVR.C	1
	EAN91861.1	pyrroline-5-carboxylate reductase, putative	29137	18	1	7.4E-02	K.IRDAVTEDK.I	0
Spot 37	EAN81053.1	alpha tubulin, putative	50549	1122	26	3.9E-04	R.EDLAALEK.D	0
						3.5E-04	K.FDLMYSK.R	
						1.9E-03	R.LSVDYGKK.S	
						2.2E-04	K.FDLMYSK.R + Oxidation (M)	
						1.7E-06	K.DVNAAVATIK.T	
						6.3E-04	K.EDAANNYAR.G	
						4.3E-01	K.EIVDLCLDR.I	
						1.8E-05	K.DVNAAVATIKTK.R	
						8.4E-05	R.IDHKFDLMYSK.R	
						4.8E-05	R.QLFHPEQLISGK.E	
						1.3E-02	R.IDHKFDLMYSK.R + Oxidation (M)	
						8.7E-11	R.LIGQVVSALTASLR.F	
						4.8E-06	R.TIQFVDWSPTGFK.C	
						1.1E-03	R.GDVVPKDVNAAVATIK.T	
						5.8E-04	K.RTIQFVDWSPTGFK.C	
						6.7E-07	R.AVFLDLEPTVVDEIR.T	
						4.5E-04	R.NLDIERPTYTNLNR.L	
						1.1E-08	R.IHFVLTSYAPVISAEK.A	
						1.8E-01	R.RNLDIERPTYTNLNR.L	
						1.2E-08	K.TIGVEDDAFNTFFSETGAGK.H	
						3.0E-05	R.AFVHWYVGEGMEEGEFSEAR.E	
						8.6E-06	R.AFVHWYVGEGMEEGEFSEAR.E + Oxidation (M)	
						4.8E-05	R.QLFHPEQLISGKEDAANNYAR.G	
						2.1E-11	R.FDGALNVDLTEFQTNLVPYPR.I	
						3.6E-05	K.AYHEQLSVSEISNAVFEPASMMTK.C	
						1.5E-05	K.AYHEQLSVSEISNAVFEPASMMTK.C + Oxidation (M)	
	EAN95983.1	ATPase beta subunit, putative	55980	1073	23	1.7E-03	K.VIDLKGDSK.C	0
						8.0E-04	K.IGLFGGAGVGK.T	

Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Mascot E-value	Sequence	Additional copies
37 cont.	EAN95983.1	cont.				7.1E-04	R.MPIHAVAPK.L + Oxidation (M)	
						1.0E-06	K.MAEEAAELEK.L	
						3.2E-04	K.MAEEAAELEK.L + Oxidation (M)	
						1.1E-04	K.KMAEEAAELEK.L + Oxidation (M)	
						7.6E-07	K.VVSSGGNISVPVGR.E	
						6.4E-06	R.IFNVLGDAIDQR.G	
						4.7E-05	K.GHGGFSVFAGVGER.T	
						7.6E-09	K.TVIIMELINNVAK.G	
						3.3E-08	K.TVIIMELINNVAK.G + Oxidation (M)	
						4.6E-08	R.VAQSALTMAEYFR.D	
						2.9E-11	R.FTQANSEVSALLGR.I	
						3.7E-06	R.VAQSALTMAEYFR.D + Oxidation (M)	
						7.9E-05	K.SKVVSSGGNISVPVGR.E	
						4.7E-04	R.EGTDLYLEMMQSK.V + Oxidation (M)	
						4.1E-09	K.LADQAAEDTILTTGIK.V	
						2.6E-03	R.TREGTDLYLEMMQSK.V + 2 Oxidation (M)	
						3.1E-04	R.DEPLTLEIVQHLDAHTGR.C	
						5.8E-09	R.IPAAVGYQPTLAEDLGQLQER.I	
						4.4E-05	K.ELQDIIAVLGIDELSEEDKLIVDR.A	
						3.7E-02	R.IMDPDVISVDHYNVAQDVVQMLTK.Y	
						4.1E-06	R.IMDPDVISVDHYNVAQDVVQMLTK.Y + Oxidation (M)	
	EAN94839.1	beta tubulin, putative	50520	844	25	4.9E-01	R.EEYPDR.I	0
						1.5E-05	K.NMMQAADPR.H	
						1.0E-03	R.YLTASALFR.G	
						2.1E-03	K.NMMQAADPR.H + 2 Oxidation (M)	
						5.7E-07	K.LAVNLVPFPR.L	
						1.1E-04	R.FPGQLNSDLR.K	
						1.2E-06	R.VGEQFTAMFR.R	
						2.8E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						2.4E-06	R.KLAVNLVPFPR.L	
						3.5E-04	R.FPGQLNSDLRK.L	
						1.3E-07	R.INVYFDEATGGR.Y	
						4.7E-04	R.RVGEQFTAMFR.R	
						1.8E-03	R.RVGEQFTAMFR.R + Oxidation (M)	
						3.0E-04	R.IMMTFSIIPSPK.V	
						1.5E-05	R.IMMTFSIIPSPK.V + Oxidation (M)	
						6.6E-05	K.EVDEQMLNVQNK.N	
						1.1E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						9.2E-05	R.AVLIDLEPGTMDSVR.A	

Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Mascot E-value	Sequence	Additional copies
37 cont.	EAN94839.1	cont.				1.1E-06	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						3.4E-04	R.GLSVPELTQQMFDAK.N	
						5.5E-04	R.LHFFMMGFAPLTSR.G + Oxidation (M)	
						2.0E-05	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
						1.6E-05	R.LHFFMMGFAPLTSR.G + 2 Oxidation (M)	
						5.4E-04	K.NSSYFIEWIPNNIK.S	
						2.5E-07	K.FWEVISDEHGVDPTGTYQGDSDLQLER.I	
	EAN97657.1	chaperonin HSP60, mitochondrial precursor	59413	787	14	9.9E-04	K.APGFGDNK.T	0
						1.4E-03	K.EGAVVVEK.V	
						1.4E-05	K.LSGGVAVIK.V	
						5.2E-03	R.LIGQAMEK.V + Oxidation (M)	
						7.8E-04	K.DGVITTQDGK.T	
						8.2E-08	K.VGGGSEVEVNEK.K	
						3.9E-07	R.GLIDGETSDYNR.E	
						1.3E-05	R.GYISPYFVTDAK.A	
						1.4E-07	K.AELEDAFVLVSAK.K	
						3.6E-08	R.AVGVILQSVAEQSR.K	
						4.8E-06	R.AAVQEGIVPGGGVALLR.A	
						1.3E-08	K.ALDSLLGDSSLTADQR.T	
						6.1E-07	K.VLENNDVTVGYDAQR.D	
						6.3E-06	K.VSSIHTILPALNHVVR.T	
	EAN84370.1	heat shock 70 kDa protein, mitochondrial precursor, putative	71585	566	12	1.0E-01	R.TLLAELR.K	0
						6.3E-03	R.SKFESLAEK.L	
						2.8E-05	K.DAGTIAGLNVIR.V	
						1.5E-05	K.YVSDAEKENVR.T	
						5.9E-06	R.NNAETQANTAER.Q	
						2.5E-06	K.EISEVVLVGGMTR.M	
						1.3E-06	K.TQNITITASGGLSK.E	
						2.1E-05	K.EISEVVLVGGMTR.M + Oxidation (M)	
						9.6E-08	K.SQTFSTAADNQTQVGIK.V	
						1.8E-10	R.GVNPDEAVALGAATLGGVLR.G	
						4.1E-03	K.KSQTFSTAADNQTQVGIK.V	
						5.3E-04	K.SMENPNVTKDELSAATDK.L + Oxidation (M)	
	EAN94132.1	hypothetical protein, conserved	44487	300	9	7.3E-04	K.WTLLYER.Y	0
						6.3E-04	R.YFVAEVPHDVR.V	
						2.2E-04	R.FDLLTNSFVYK.W	
						2.6E-04	R.VEGPQVVPTQYMR.N	
						2.8E-01	R.EMRPPDIPPISLK.L + Oxidation (M)	

						Mascot		
Spot no.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**E-value**	**Sequence**	**Additional copies**
37 cont.	EAN94132.1	cont.				5.3E-02	R.VEGPQVVPTQYMR.N + Oxidation (M)	
						6.9E-07	R.SGDSSAFLSDDEALR.G	
						4.5E-07	K.LMETAIQQDPVYVR.L	
						1.6E-06	K.LMETAIQQDPVYVR.L + Oxidation (M)	
	EAN99322.1	protein disulfide isomerase, putative	54011	178	6	9.1E-05	K.SSDIVNYVK.A	0
						1.8E-02	K.FIIEYSEK.K	
						1.0E-04	K.GFPTIILFR.D	
						3.5E-01	K.DVPIPEEVKR.E	
						5.5E-06	K.EVFDGAMETADLK.S + Oxidation (M)	
						4.0E-02	K.ANLGTAVVHVETAEELEK.L	
	EAN89640.1	Hsc70-interacting protein (Hip), putative	48275	149	3	5.7E-04	R.ALDLNPENVR.A	1
						2.4E-07	R.VLSGVELEAVNR.V	
						6.8E-05	R.SNPMAALQMMGDPK.V + 3 Oxidation (M)	
	EAN90182.1	intraflagellar transport protein component, putative	72460	73	2	9.0E-03	R.ALLDYVFR.Q	1
						1.2E-05	R.VAVEQQEELPR.D	
	EAN87966.1	glucose-regulated protein 78, putative	71414	63	2	1.4E-02	K.KEEITITNDK.G	0
						1.9E-04	K.LQSVTNPIIQK.V	
	EAN83974.1	paraflagellar rod component Par4, putative	68470	58	2	4.0E-02	R.TIISQLQQK.L	0
						2.5E-04	K.AIQETEATQTAK.I	
	EAN88605.1	acetylornithine deacetylase-like, putative	44189	43	1	1.9E-04	R.ALAQLTGSAVGSR.L	0
	EAN88008.1	hypothetical protein, conserved	110934	40	1	2.9E-04	K.QEKILLER.V	0
	EAN81557.1	serine carboxypeptidase (CBP1), putative	60759	27	1	8.2E-03	R.EDVQSSLGAK.R	2
	EAN89795.1	pyruvate dehydrogenase E1 beta subunit, putative	38411	26	1	7.0E-03	K.EGIEAEVINLR.S	1
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	23	1	1.8E-02	K.VAISLPSR.M	1
	EAN83367.1	hypothetical protein, conserved	119453	22	1	2.1E-02	K.TLQVYDAVAR.V	1
	EAN89431.1	hypothetical protein, conserved	92676	17	1	3.6E-02	K.SEGADAAPMQAPPSVK.D + Oxidation (M)	0
Spot 38	EAN87966.1	glucose-regulated protein 78, putative	71414	2323	55	7.4E-03	R.NTQIPTK.K	0
						4.8E-03	K.VQVEVGGK.K	
						7.7E-04	K.GTLVPVQR.V	
						6.0E-04	R.YFVDMLK.K	
						1.5E-03	R.YFVDMLK.K + Oxidation (M)	
						1.6E-06	R.LSEEEIER.M	
						3.0E-02	R.YFVDMLKK.K	
						2.6E-02	R.YFVDMLKK.K + Oxidation (M)	
						5.6E-03	K.EEITITNDK.G	

							Mascot	
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
38 cont.	EAN87966.1	cont.				7.2E-07	K.YSDATVQTDK.K	
						7.2E-07	K.LLSYEVVADK.D	
						7.3E-05	K.EIAETYLGEK.V	
						8.4E-05	R.DFFGGKEPNR.G	
						1.2E-05	K.FELSGIPPAPR.G	
						1.2E-05	K.DAGTIAGLNVVR.I	
						9.4E-05	K.KEEITITNDK.G	
						2.8E-08	R.EAAEFEDEDR.K	
						3.4E-05	R.NSLESVAYSLR.N	
						2.9E-04	K.LQSVTNPIIQK.V	
						3.9E-05	K.YSDATVQTDKK.L	
						2.6E-07	K.KLLSYEVVADK.D	
						3.6E-05	K.EEITITNDKGR.L	
						2.5E-06	K.FEELNMELFK.G	
						9.0E-06	K.FEELNMELFK.G + Oxidation (M)	
						1.7E-05	R.EAAEFEDEDRK.V	
						1.1E-07	K.LSADDKSAVEAAVK.E	
						3.3E-05	K.MKEIAETYLGEK.V	
						1.5E-05	K.MKEIAETYLGEK.V + Oxidation (M)	
						6.1E-04	K.GDVHIIPNDMGNR.I	
						3.9E-08	R.ITPSVVAFTETER.L	
						1.6E-03	K.GDVHIIPNDMGNR.I + Oxidation (M)	
						3.1E-05	K.SDIHEIVLVGGSTR.V	
						5.6E-05	R.DKLQSVTNPIIQK.V	
						5.3E-07	R.AKFEELNMELFK.G	
						5.4E-04	R.AKFEELNMELFK.G	
						4.4E-04	R.AKFEELNMELFK.G + Oxidation (M)	
						1.7E-06	K.QFTPEEVSAMVLQK.M	
						2.3E-07	K.KSDIHEIVLVGGSTR.V	
						2.4E-04	K.QFTPEEVSAMVLQK.M + Oxidation (M)	
						1.2E-08	R.IINEPTAAAIAYGLNK.A	
						2.6E-07	K.LLSYEVVADKDGKPK.V	
						1.1E-07	K.NAVVTVPAYFNDAQR.Q	
						3.3E-08	R.VEVDSLTEGFDFSEK.I	
						6.0E-05	K.KQFTPEEVSAMVLQK.M	
						4.3E-05	K.KQFTPEEVSAMVLQK.M + Oxidation (M)	
						2.8E-04	K.NQLPQNPHNTIYAIK.R	
						8.1E-07	K.VYQSGGGADGDERPEPMDDL.-	

						Mascot		
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
38 cont.	EAN87966.1	cont.				2.5E-05	K.VYQSGGGADGDERPEPMDDL.- + Oxidation (M)	
						2.7E-10	R.VVLVDVIPLSLGIETVGGVMTK.L	
						6.9E-11	R.VVLVDVIPLSLGIETVGGVMTK.L + Oxidation (M)	
						2.5E-04	K.EAMQFLDDNPNADKEEYDEAR.D	
						8.4E-05	K.EAMQFLDDNPNADKEEYDEAR.D + Oxidation (M)	
						1.1E-06	K.SQVFSTYQDNQPGVLIQVYEGER.Q	
						1.9E-06	R.GINPDEAVAYGAAVQAAVLTGESEVGGR.V	
						4.3E-04	K.KSQVFSTYQDNQPGVLIQVYEGER.Q	
	EAN95887.1	heat shock protein 70 (HSP70), putative	73607	1070	31	4.0E-01	K.DLTTSQR.A	1
						1.7E-03	R.GTLQPVER.V	
						1.8E-03	K.EIAESYLGK.Q	
						6.0E-03	R.NQIVITNDK.G	
						7.6E-04	K.NTVNEPNVAGK.I	
						1.3E-02	K.RNQIVITNDK.G	
						8.2E-04	R.LVSHFTDEFK.R	
						1.1E-06	K.DAGTIAGMEVLR.I	
						7.6E-05	K.DAGTIAGMEVLR.I + Oxidation (M)	
						1.3E-05	K.FSDPVVQSDMK.H	
						6.1E-05	R.NQIVITNDKGR.L	
						6.1E-06	K.FSDPVVQSDMK.H + Oxidation (M)	
						1.2E-04	K.MKEIAESYLGK.Q	
						4.2E-05	K.MKEIAESYLGK.Q + Oxidation (M)	
						8.3E-06	K.NGLENYAFSMK.N + Oxidation (M)	
						1.3E-05	R.AVHDVVLVGGSTR.I	
						4.3E-07	K.VMQLVSDFFGGK.E	
						3.0E-04	K.VMQLVSDFFGGK.E + Oxidation (M)	
						1.1E-04	R.KFSDPVVQSDMK.H	
						3.4E-04	K.GDDKPVIQVQFR.G	
						3.5E-05	R.TTPSYVAFTDTER.L	
						3.7E-02	K.AVVTVPAYFNDSQR.Q	
						7.3E-07	K.TFNPEEVSSMVLSK.M	
						1.6E-05	K.TFNPEEVSSMVLSK.M + Oxidation (M)	
						3.1E-06	K.NQVAMNPTNTVFDAK.R	
						3.3E-04	R.IINEPTAAAIAYGLDK.V	
						6.0E-09	K.NQVAMNPTNTVFDAK.R + Oxidation (M)	

							Mascot	
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
38 cont.	EAN95887.1	cont.				1.5E-04	K.KAVVTVPAYFNDSQR.Q	
						4.3E-05	K.ATNGDTHLGGEDFDNR.L	
						3.2E-02	R.IINEPTAAAIAYGLDKVEDGK.E	
						3.7E-03	K.SQIFSTYADNQPGVHIQVFEGER.A	
	EAN95886.1	heat shock protein 70 (HSP70), putative	71171	1053	30	3.4E-05	R.VEIIANDQGNR.T	0
	EAN99876.1	paraflagellar rod component, putative	69022	788	18	1.2E-03	R.DATDSISR.F	0
						2.6E-04	R.IPQQNLR.Q	
						4.4E-07	R.GSELLAASK.E	
						7.4E-04	K.EMVEAQVR.A	
						1.8E-02	K.EMVEAQVR.A + Oxidation (M)	
						6.7E-05	R.SYVDEMVTR.I	
						1.3E-03	R.SYVDEMVTR.I + Oxidation (M)	
						3.8E-06	R.AELSELDGER.D	
						2.5E-04	K.LKDAIHLYER.A	
						5.7E-06	R.AELSELDGERDK.V	
						4.2E-05	R.LELDDIIEQMK.G + Oxidation (M)	
						3.6E-06	R.ETAAQIGQIVEQK.K	
						1.5E-10	R.QAVEEDEAATESAIR.N	
						7.2E-03	R.SGTPFVHPLQEYGIK.S	
						1.2E-07	R.DSAMESLDPNMSNYR.L + 2 Oxidation (M)	
						3.6E-07	R.VTAYNEFVNMEEQQK.H	
						2.5E-05	R.VTAYNEFVNMEEQQK.H + Oxidation (M)	
						1.3E-04	K.GVSGVINALNATQDAGEQLFQSVEK.G	
	EAN83974.1	paraflagellar rod component Par4, putative	68470	770	15	2.3E-04	R.TIISQLQQK.L	0
						9.1E-05	R.SLQEVVETR.E	
						1.3E-02	K.EEVLQLETK.C	
						2.6E-06	R.SDSAYLAAELR.A	
						4.1E-04	R.DSLLNEVSLLR.V	
						2.0E-07	K.AIQETEATQTAK.I	
						4.9E-05	R.EAQLLSEVAVLK.A	
						8.2E-04	R.EYQQQIEQVR.S	
						2.7E-06	K.ITFLNAQVSNNR.T	
						8.4E-07	R.IANQEEVIEALR.E	
						1.1E-05	R.EQLALENETQLK.A	
						2.6E-06	K.VEQLTTSLHDER.V	
						1.2E-05	R.VASEAQVEQLVLMR.D + Oxidation (M)	
						2.3E-06	K.QLYALESEAEELQK.R	

Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Mascot Sequence	Additional copies
38 cont.	EAN83974.1	cont.				6.8E-05	K.ATTFHVQTALQDTQR.N	
	EAN81053.1	alpha tubulin, putative	50549	606	13	5.6E-05	K.DVNAAVATIK.T	0
						1.1E-04	K.EDAANNYAR.G	
						6.4E-05	R.IDHKFDLMYSK.R	
						1.3E-03	R.QLFHPEQLISGK.E	
						6.1E-02	R.IDHKFDLMYSK.R + Oxidation (M)	
						6.3E-09	R.LIGQVVSALTASLR.F	
						2.8E-07	R.TIQFVDWSPTGFK.C	
						8.6E-06	R.AVFLDLEPTVVDEIR.T	
						7.6E-03	R.NLDIERPTYTNLNR.L	
						4.1E-07	R.IHFVLTSYAPVISAEK.A	
						1.5E-07	K.TIGVEDDAFNTFFSETGAGK.H	
						8.5E-02	R.FDGALNVDLTEFQTNLVPYPR.I	
						1.0E-05	K.AYHEQLSVSEISNAVFEPASMMTK.C + 2 Oxidat	
	EAN84370.1	heat shock 70 kDa protein, mitochondrial precursor, putative	71585	594	13	9.5E-04	R.TLLAELR.K	0
						1.6E+00	R.TTPSVVAFK.G	
						5.8E-02	R.SKFESLAEK.L	
						6.7E-06	R.VLENTEGFR.T	
						5.9E-05	K.STGIDLSNER.M	
						5.3E-05	K.DAGTIAGLNVIR.V	
						3.0E-04	K.YVSDAEKENVR.T	
						3.7E-06	R.NNAETQANTAER.Q	
						9.7E-07	K.TQNITITASGGLSK.E	
						4.3E-06	K.EISEVVLVGGMTR.M + Oxidation (M)	
						3.1E-06	R.QAITNPQSTFFAVK.R	
						2.2E-06	K.SQTFSTAADNQTQVGIK.V	
						2.0E-04	R.GVNPDEAVALGAATLGGVLR.G	
	EAN94839.1	beta tubulin, putative	50520	483	15	2.0E-02	R.YLTASALFR.G	0
						1.6E-02	K.NMMQAADPR.H + Oxidation (M)	
						2.0E-01	K.LREEYPDR.I	
						2.8E-05	K.LAVNLVPFPR.L	
						6.4E-03	R.FPGQLNSDLR.K	
						2.8E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						1.1E-07	R.INVYFDEATGGR.Y	
						7.7E-04	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						7.5E-05	K.EVDEQMLNVQNK.N	
						5.6E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						3.0E-06	R.AVLIDLEPGTMDSVR.A	

Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Mascot E-value	Sequence	Additional copies
38 cont.	EAN94839.1	cont.				1.2E-04	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						5.1E-02	R.GLSVPELTQQMFDAK.N	
						2.1E-04	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
						1.2E-04	K.NSSYFIEWIPNNIK.S	
	EAN97655.1	chaperonin HSP60, mitochondrial precursor, putative	59991	454	9	1.3E-01	K.EGAVVVEK.V	1
						4.1E-03	R.LIGQAMEK.V + Oxidation (M)	
						2.0E-10	K.VGGGSEVEVNEK.K	
						2.9E-02	R.LPAHTIVLNAGK.E	
						2.1E-06	R.NVIIEQSYGAPK.I	
						1.3E-05	R.GLIDGETSDYNR.E	
						1.9E-06	K.AELEDAFVLVSAK.K	
						3.7E-08	R.AVGVILQSVAEQSR.K	
						3.8E-05	R.AAVQEGIVPGGGVALLR.A	
	EAN95983.1	ATPase beta subunit, putative	55980	396	7	6.9E-05	K.VVSSGGNISVPVGR.E	0
						1.1E-07	R.IFNVLGDAIDQR.G	
						3.1E-04	K.TVIIMELINNVAK.G + Oxidation (M)	
						1.6E-03	R.VAQSALTMAEYFR.D	
						1.2E-09	R.FTQANSEVSALLGR.I	
						9.7E-07	R.VAQSALTMAEYFR.D + Oxidation (M)	
						2.2E-08	K.LADQAAEDTILTTGIK.V	
	EAN83529.1	hypothetical protein, conserved	93603	266	7	1.2E-02	R.QQNFTER.L	1
						9.3E-07	K.IVAELGVFR.R	
						3.0E-05	R.SSVLVVFGAK.K	
						1.2E-04	K.LQEMATDTGK.L	
						1.8E-05	K.LQEMATDTGK.L + Oxidation (M)	
						1.7E-05	R.AVMLALQEDR.V	
						3.6E-03	R.EEEEMQELK.T	
	EAN84609.1	heat shock 70 kDa protein, putative	24348	205	5	2.2E-05	R.TTPSYVAFTETER.L	1
	EAN91609.1	vacuolar-type proton translocating pyrophosphatase 1, putative	86135	143	4	2.0E-02	R.NAYLTDEVMR.N	1
						9.6E-03	R.NAYLTDEVMR.N + Oxidation (M)	
						2.2E-05	K.SVGLAAMDMVNEIR.R + 2 Oxidation (M)	
						3.8E-07	R.EITDALDAAGNTTAAIGK.G	
	EAN89518.1	hypothetical protein, conserved	68407	114	3	2.2E-03	K.LFLASIEQR.L	1
						1.9E-05	R.GAGITLVESLR.R	
						2.8E-03	R.LAEMAGSESLPDIER.Y + Oxidation	
	EAN95112.1	hypothetical protein, conserved	90858	101	2	1.5E-05	R.EALSSIEQTLR.L	0
						4.4E-05	K.YLQQVDSDANK.N	

						Mascot		
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	Additional copies
38 cont.	EAN92318.1	69 kDa paraflagellar rod protein, putative	70087	69	2	1.3E+00	K.SFQETSAIK.D	0
						5.8E-07	R.TVSFTGTIDNAIAK.L	
	EAN82629.1	heat shock protein 85, putative	81244	64	1	1.5E-06	R.GVVDSEDLPLNISR.E	1
	EAN90182.1	intraflagellar transport protein component, putative	72460	63	1	8.6E-07	R.VAVEQQEELPR.D	3
	EAN82710.1	gamma-glutamyl carboxypeptidase, putative	44359	55	1	7.9E-06	R.DETPSFEGSEEAPITK.L	0
	EAN87979.1	paraflagellar rod protein 3, putative	69189	45	1	8.3E-05	R.SQLDATQLAQVPTR.T	0
	EAN85497.1	glutamamyl carboxypeptidase, putative	44390	37	1	1.8E-04	R.DETPSFEGSEEAPFTK.L	1
	EAN84397.1	hypothetical protein, conserved	69890	33	1	7.2E-04	R.SVLQPEPLPR.R	1
	EAN81302.1	hypothetical protein, conserved	20849	31	1	1.8E-03	K.DLVTSPVTELNFVR.D	1
	EAN84897.1	hypothetical protein, conserved	62372	25	1	2.9E-02	R.EERALAR.E	0
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	21	1	3.1E-02	K.VAISLPSR.M	1
Spot 39	EAN90720.1	calreticulin, putative	46396	906	27	1.6E-03	K.FYADAEK.S	0
						5.1E-03	K.GDGDKEDL.-	
						5.2E-04	K.VMEDMEK.E	
						1.6E-02	R.IRFPEDK.L	
						3.9E-02	R.QIPNPAYK.G	
						2.3E-02	R.EIVDETDK.K	
						1.1E-02	K.EVLELVEK.T	
						8.9E-04	K.SLVVSFSVK.H	
						9.4E-02	K.LLPSMDPEK.F	
						1.9E-03	K.DIMIGDDLK.E + Oxidation (M)	
						7.4E-04	K.LLPSMDPEK.F + Oxidation (M)	
						7.8E-05	K.KSLVVSFSVK.H	
						2.4E-04	K.SMEHWTTSK.H	
						3.0E-06	K.SMEHWTTSK.H + Oxidation (M)	
						1.5E-04	K.VMEDMEKEK.R	
						2.1E-03	K.YWLMFGPDR.C + Oxidation (M)	
						2.4E-07	R.DDFGKVEISAGK.F	
						1.4E-02	R.VHIILHYNGENR.E	
						1.3E-06	K.GQLDGDWTLLPPR.E	
						8.9E-06	K.AEEEKDEEELEEK.G	
						7.4E-04	K.IPNPDFVEDSELHK.V	
						2.4E-01	K.LLPSMDPEKFHGETK.Y + Oxidation (M)	
						7.9E-05	R.FYALSTAFPTPITNEK.K	
						9.5E-05	R.FYALSTAFPTPITNEKK.S	
						8.0E-04	K.KPEDWDNEPAMIPDADAK.K + Oxidation (M)	

						Mascot		Additional copies
Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	E-value	Sequence	
39 cont.	EAN90720.1	cont.				2.4E-06	K.VPEPLTHVGIDVWQVESGSIFK.D	
						1.3E-03	K.KPDDWDDAEDGPWEAPMIPNPK.S + Oxidation (M)	
	EAN82340.1	calreticulin, putative	46419	894	27	3.0E-02	K.EVLDLVEK.T	0
						7.7E-03	K.DIVIGDDLK.E	
						5.3E-06	K.GQLEEDWSLLLPR.E	
						3.8E-06	R.FYALSTAFPTPINNEK.K	
						6.7E-04	R.FYALSTAFPTPINNEKK.S	
	EAN87966.1	glucose-regulated protein 78, putative	71414	760	16	1.3E-03	K.GTLVPVQR.V	0
						1.7E-05	R.LSEEEIER.M	
						7.9E-05	R.DFFGGKEPNR.G	
						4.3E-04	K.FELSGIPPAPR.G	
						7.1E-07	K.DAGTIAGLNVVR.I	
						4.2E-04	K.KEEITITNDK.G	
						1.5E-06	R.EAAEFEDEDR.K	
						2.2E-06	R.NSLESVAYSLR.N	
						5.0E-04	K.LQSVTNPIIQK.V	
						2.1E-05	K.LSADDKSAVEAAVK.E	
						5.0E-06	R.ITPSVVAFTETER.L	
						6.8E-05	K.SDIHEIVLVGGSTR.V	
						4.9E-08	R.IINEPTAAAIAYGLNK.A	
						2.9E+00	K.NAVVTVPAYFNDAQR.Q	
						5.3E-09	R.VEVDSLTEGFDFSEK.I	
						3.3E-02	K.NQLPQNPHNTIYAIK.R	
	EAN97657.1	chaperonin HSP60, mitochondrial precursor, putative	59413	641	12	3.8E-03	K.EGAVVVEK.V	0
						1.4E-04	K.LSGGVAVIK.V	
						7.6E-04	R.LIGQAMEK.V + Oxidation (M)	
						7.4E-04	K.DGVITTQDGK.T	
						8.0E-08	K.VGGGSEVEVNEK.K	
						4.3E-06	R.LPAHTIVLNAGK.E	
						2.3E-05	R.GLIDGETSDYNR.E	
						1.9E-04	R.GYISPYFVTDAK.A	
						1.0E-07	K.AELEDAFVLVSAK.K	
						6.6E-06	K.TAMMQDIAIFAGAR.L + 2 Oxidation (M)	
						9.8E-07	R.AAVQEGIVPGGGVALLR.A	
						9.0E-09	K.VLENNDVTVGYDAQR.D	
	EAN94839.1	beta tubulin, putative	50520	562	16	4.5E-05	K.NMMQAADPR.H	0
						3.0E-02	R.YLTASALFR.G	

Spot no.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Mascot E-value	Sequence	Additional copies
39 cont.	EAN94839.1	cont.				7.9E-05	K.NMMQAADPR.H + Oxidation (M)	
						7.4E-05	K.LAVNLVPFPR.L	
						3.0E-05	R.FPGQLNSDLR.K	
						3.2E-05	R.VGEQFTAMFR.R	
						1.0E-06	R.VGEQFTAMFR.R + Oxidation (M)	
						1.0E-01	R.FPGQLNSDLRK.L	
						9.4E-08	R.INVYFDEATGGR.Y	
						8.6E-04	R.IMMTFSIIPSPK.V + 2 Oxidation (M)	
						4.6E-06	K.EVDEQMLNVQNK.N	
						6.1E-05	K.EVDEQMLNVQNK.N + Oxidation (M)	
						4.9E-07	R.AVLIDLEPGTMDSVR.A	
						4.4E-05	R.AVLIDLEPGTMDSVR.A + Oxidation (M)	
						4.8E-05	R.GLSVPELTQQMFDAK.N + Oxidation (M)	
						2.9E-04	K.NSSYFIEWIPNNIK.S	
	EAN81053.1	alpha tubulin, putative	50549	269	6	3.9E-05	K.DVNAAVATIK.T	0
						4.2E-04	K.EDAANNYAR.G	
						4.6E-06	R.TIQFVDWSPTGFK.C	
						9.2E-08	R.AVFLDLEPTVVDEIR.T	
						1.4E-02	R.NLDIERPTYTNLNR.L	
						4.9E-03	R.IHFVLTSYAPVISAEK.A	
	EAN88187.1	hypothetical protein, conserved	43723	227	5	2.4E-04	R.VAAEASSLK.H	1
						6.1E-06	R.GGAVVAELLR.A	
						8.2E-05	R.IGPIGAEAIAK.G	
						2.7E-03	K.EGLLMNNTIK.R + Oxidation (M)	
						8.4E-06	R.TVTLLDFGQNK.L	
	EAN95983.1	ATPase beta subunit, putative	55980	181	3	8.6E-06	R.IFNVLGDAIDQR.G	0
						1.5E-05	R.VAQSALTMAEYFR.D + Oxidation (M)	
						1.1E-07	K.LADQAAEDTILTTGIK.V	
	EAN85497.1	glutamamyl carboxypeptidase, putative	44390	64	1	3.4E-07	R.DETPSFEGSEEAPFTK.L	1
	EAN81110.1	calpain-like cysteine peptidase, putative	72116	55	1	9.8E-06	R.EIAALEESMNAR.A + Oxidation	2
	EAN82710.1	gamma-glutamyl carboxypeptidase, putative	44359	47	1	4.9E-05	R.DETPSFEGSEEAPITK.L	0
	EAN83379.1	proteasome regulatory non-ATPase subunit, putative	37481	37	1	2.3E-04	R.MSLEEEQQR.Q + Oxidation (M)	1
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	21	1	3.1E-02	K.VAISLPSR.M	1

TABLE S6: PROTEIN ISOFORMS

(*) In **bold** are shown the peptides shared between the isoforms, that carry the sequence difference. In *italics* are the peptides present in one isoform but it does not match to the others. (#) In additional gene copies, we list the other genomic versions that match to the specific isoform. It shows how represented it is each protein group in the genome.

				Mascot			
Band / Spot No.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**Sequence (*)**	**Additional gene copies under same match (#)**
Band 2	EAN81533.1	histone H4, putative	11163	609	15	**R.GKILYGYA.-** **K.SFVEGVVR.D** **R.ISGVIYDEVR.G** **K.RISGVIYDEVR.G** **R.ISGVIYDEVRGVIK.S**	EAN81534.1; EAN81535.1; EAN81536.1; EAN81537.1; EAN88987.1; EAN89000.1; EAN89001.1; EAN90974.1; EAN90975.1; EAN90976.1
	EAN85055.1	histone H4, putative	11177	608	15	**R.ISGIIYDEVR.G** **K.RISGIIYDEVR.G** **R.ISGIIYDEVRGVIK.S**	EAN85056.1 EAN85057.1 EAN85058.1 EAN90629.1 EAN90630.1 EAN90631.1
	EAN81454.1	histone H4, putative	11280	429	18	**K.FVEGVVR.D** **R.GKILYGYE.-** R.ISGVMYDEVR.G + Oxidation **R.ISGVMYDEVR.G**	EAN94076.1
Band 4	EAN85330.1	histone H2A, putative	14385	283	10	**R.HDDDLGMLLK.D** **R.HDDDLGMLLKDVTLSR.G**	EAN91807.1; EAN91809.1; EAN91855.1; EAN91869.1; EAN97510.1; EAN97511.1; EAN97526.1; EAN97527.1; EAN97528.1
	EAN88264.1	histone H2A, putative	14345	238	6	**R.HDDDLGTLLK.D** **R.HDDDLGTLLKDVTLSR.G**	EAN88265.1 EAN88266.1 EAN88267.1
Band 4	EAN85210.1	kinetoplast DNA-associated protein, putative	14529	53	1	**K.NNPALSGLPVAK.R**	EAN87062.1
	EAN85212.1	kinetoplast DNA-associated protein, putative	14224	36	1	**K.NNPALSGLPISER.G**	EAN87060.1
Band 5	EAN87059.1	hypothetical protein, conserved	21263	77	3	K.KAAALYVR.F **R.FYHALKK.S** **K.SVGLTAALSPK.Q**	
	EAN85214.1	hypothetical protein, conserved	21287	68	3	**R.FYYALKK.S** **K.SVGLTAALSPR.Q**	
Band 5	EAN99158.1	hypothetical protein, conserved	17771	67	2	**R.LGIGFDDR.R** R.NALDLGDDRR.D	
	EAN95668.1	hypothetical protein, conserved	17874	49	2	R.LGLDFDDRR.G	

Band / Spot No.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Sequence (*)	Additional gene copies (#)
Band 7	EAN83261.1	hypothetical protein, conserved	30260	524	16	**K.SYSDAQKWK.L** **R.YAHAGYALAVR.T**	Localized by us to the Mitochondria
	EAN81197.1	hypothetical protein, conserved	30269	497	15	**K.SYSDAHKWK.L**	
	EAN95832.1	hypothetical protein, conserved	30333	496	14	**R.YAYAGYALAVR.T**	EAN99221.1
Band 7	EAN97607.1	ADP,ATP carrier protein 1, mitochondrial precursor, putative	35287	294	8	**R.GIAGAGVLSGVDALKPIYVR.W**	
	EAN90413.1	ADP,ATP carrier protein 1, mitochondrial precursor, putative	35303	271	7	**R.GIAGAGVLSGVDALKPMYVR.W** R.GIAGAGVLSGVDALKPMYVR.W + Oxidation (M)	
Band 7	EAN86006.1	glucosamine-6-phosphate isomerase, putative	31635	278	8	**K.SLNDETIASNAR.F**	
	EAN90437.1	glucosamine-6-phosphate isomerase, putative	31635	228	7	K.SLNDETVASNAR.F	
Band 8-9	EAN91944.1	glyceraldehyde 3-phosphate dehydrogenase, putative	39277	779	22	**K.FKYNVTTTK.S**	EAN91945.1
	EAN90286.1	glyceraldehyde 3-phosphate dehydrogenase, putative	39292	740	21	**K.FKYTVTTTK.S**	EAN90287.1
Band 8	EAN82497.1	casein kinase, putative	38355	328	11	**K.TRHPQLAFEAR.F**	EAN83293.1
	EAN82496.1	casein kinase, putative	38351	273	9	K.TRHPQLAFEVR.F	
Band 8	EAN89795.1	pyruvate dehydrogenase E1 beta subunit, putative	38411	320	8	**K.DLEVASQPQVSDVLAVAR.R**	
	EAN97324.1	pyruvate dehydrogenase E1 beta subunit, putative	38393	266	8	**K.DLELASQPQVSDVLAVAHR.V**	
Band 8	EAN87428.1	hypothetical protein, conserved	37186	134	5	**R.VSFPATEEK.A**	
	EAN87575.1	hypothetical protein, conserved	37110	100	4	**R.VSFPATEK.A**	
Band 9	EAN92220.1	pyruvate dehydrogenase E1 component alpha subunit, putative	43381	222	7	**K.EVDQQLQPAEK.Q**	
	EAN93231.1	pyruvate dehydrogenase E1 component alpha subunit, putative	22293	183	6	**K.EVDQQLLPAEK.Q**	
Band 10	EAN85190.1	hypothetical protein, conserved	43072	572	18	**R.VSAYAPTR.K** **K.AYISSLVESNK.E**	
	EAN88063.1	hypothetical protein, conserved	43064	562	18	**R.VSAYAPTRR.E** **K.AYVSSLVESNK.E** K.AYVSSLVESNKEQAR.K	
Band 10	EAN88162.1	hypothetical protein, conserved	39057	187	6	**R.MEEINTTSTR.D + Oxidation (M)**	
	EAN88387.1	hypothetical protein, conserved	39017	180	5	**R.IEEINTTSTR.D**	

Band / Spot No.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**Sequence (*)**	**Additional gene copies (#)**
Band 10	EAN97592.1	chaperone DnaJ protein, putative	47563	102	4	***K.ILEVHIEK.G***	
						K.ALGVTESFPR.V	
						R.VSLEDMYNGK.T + Oxidation (M)	
						R.GEGMPLPNTGGLDR.G + Oxidation (M)	
	EAN88684.1	heat shock protein DnaJ, putative	45029	99	4	***R.YDQFGEK.G***	
						K.IFEIFVEK.G	
						R.GEGDQIPGVR.L	
						R.EGMPIPNTGGVER.G + Oxidation	
	EAN88664.1	chaperone DnaJ protein, putative	51044	20	1	***K.VPVGTQQGDK.L***	EAN93511.1
Band 10	EAN82723.1	glutamate dehydrogenase, putative	43888	27	1	***R.GYTTDDGTTSVYTAK.W***	
	EAN84271.1	glutamate dehydrogenase, putative	24319	26	1	***R.ANILASDVFK.N***	
Band 10-11 Spot 11-12 Spot 30-31	EAN85498.1	glutamamyl carboxypeptidase, putative	44258	635	19	R.EIAEEYR.R	
						K.GGSHFWVR.V	
						R.ALPNETVSK.M	
						K.DYLEGLGVK.C	
						K.LVAFDTTSR.N	
						R.EIAEEYRR.N	
						K.CTLLHNAER.N	
						K.LREIAEEYR.R	
						R.SMDHTQWLAK.L	
						R.SMDHTQWLAK.L + Oxidation (M)	
						K.WDSDPFTLTER.D	
						R.SYVETQLLPAMK.A	
						R.SYVETQLLPAMK.A + Oxidation (M)	
						K.AEFEDAEIVITPR.N	
						K.ANLWATLPGDGGVTK.G	
						R.NETPSFEGSEEAPFTK.L	
						K.GGIILSGHTDVVPVDGQK.W	
						R.AEGCIIGEPTGMTVVIAHK.G + Oxidation (M)	
						R.SYVETQLLPAMKAEFEDAEIVITPR.N + Oxidation (M)	
	EAN82710.1	glutamamyl carboxypeptidase, putative	44359	625	18	**R.DETPSFEGSEEAPITK.L**	
	EAN82317.1	glutamamyl carboxypeptidase, putative	44248	567	16	*R.EIAEEYR.R*	EAN82318.1
						K.DYLEGLGVK.C	
						K.LVAFDTTSR.N	
						R.EIAEEYRR.N	
						K.CTLIHNAER.N	
						K.LREIAEEYR.R	

Band / Spot No.	**Accession no.**	**Protein Identity**	**Mr**	**SCORE**	**# PEPT.**	**Sequence (*)**	**Additional gene copies (#)**
cont. Band 10-11 Spot 11-12 Spot 30-31	EAN82317.1	cont.				*R.SMDHTQWLAK.L* *R.SMDHTQWLAK.L + Oxidation (M)* *K.WDSDPFTLTER.D* *R.SYVETQLLPAMK.A* *R.SYVETQLLPAMK.A + Oxidation (M)* *K.AEFEDAEIVITPR.N* *K.ANLWATLPGDGGVTK.G* *K.GGIILSGHTDVVPVDGQK.W* *R.AEGCIIGEPTGMTVVIAHK.G + Oxidation (M)* *R.SYVETQLLPAMKAEFEDAEIVITPR.N + Oxidation (M)*	
	EAN88605.1	acetylornithine deacetylase-like, putative	44189	187	4	**R.LIAFDTTSR.N** **M.PLDSVEWLR.R** **R.IDDFVAATAQK.M** *K.WDSDPFTLTER.D*	Shares 1 peptide with glutamamyl carboxypeptidases
	EAN96060.1	glutamamyl carboxypeptidase, putative	44531	157	4	**K.LVSFDTTSR.N** **K.AYVNDTLLPSMK.K + Oxidation (M)** **R.YLPEAEAEKFEER.I** *K.DYLEGLGVK.C*	Shares this peptide with EAN82317.1
Band 11-12	EAN94612.1	hexokinase, putative	52802	448	15	**K.DVVELLQK.A** **K.GVDHGFLIK.W**	
	EAN87141.1	hexokinase, putative	52750	425	15	**K.GVDNGFLIK.W** ***R.MIAHLAELR.C + Oxidation*** **K.DVVELLQNALKR.M**	
Band 11	EAN95886.1	heat shock protein 70 (HSP70), putative	71171	330	10	R.NQIVITNDK.G K.NTVNEPNVAGK.I R.VEIIANDQGNR.T K.DAGTIAGMEVLR.I R.AVHDVVLVGGSTR.I K.VMQLVSDFFGGK.E + Oxidation (M) R.TTPSYVAFTDTER.L K.TFNPEEVSSMVLSK.M + Oxidation (M) R.IINEPTAAAIAYGLDK.V K.NQVAMNPTNTVFDAK.R + Oxidation (M)	

Band / Spot No.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Sequence (*)	Additional gene copies (#)
cont. Band 11	EAN83852.1	heat shock 70 kDa protein, putative	41044	324	10	***R.GTLQPVER.V*** ***R.LVSHFTDEFK.R***	
	EAN95887.1	heat shock protein 70 (HSP70), putative	73607	319	11	*R.GTLQPVER.V* *R.NQIVITNDK.G* *K.NTVNEPNVAGK.I* *R.LVSHFTDEFK.R* *K.DAGTIAGMEVLR.I* *R.AVHDVVLVGGSTR.I* *K.VMQLVSDFFGGK.E + Oxidation (M)* *R.TTPSYVAFTDTER.L* *K.TFNPEEVSSMVLSK.M + Oxidation (M)* *R.IINEPTAAAIAYGLDK.V* *K.NQVAMNPTNTVFDAK.R + Oxidation (M)*	No unique peptides in sequences, shares different with prevoius both.
Band 11	EAN90055.1	galactokinase, putative	52393	246	5	**R.SDAEGAQAVVR.K**	
	EAN91288.1	galactokinase, putative	52368	235	5	**R.SDAEGAQAVVK.K**	
Band 12	EAN84978.1	elongation factor 1-alpha (EF-1-alpha), putative	49652	862	24	**K.SIEMHHEQLAEATPGDNVGFNVK.N + Oxidation (M)**	EAN97588.1
	EAN82858.1	elongation factor 1-alpha (EF-1-alpha), putative	49694	843	25	***K.SIEMHHEQLVEATPGDNVGFNVK.N*** **K.SIEMHHEQLVEATPGDNVGFNVK.N + Oxidation (M)**	EAN97589.1
Band 12	EAN89593.1	hypothetical protein	52619	377	10	**R.IIAKPSVVDIDYK.A**	
	EAN85276.1	hypothetical protein	52756	332	10	***R.TDNETDFMK.I + Oxidation (M)*** ***R.LSVLASQLGIK.L*** **R.IIARPSVVDIDYK.A**	
Band 12	EAN94510.1	mitochondrial processing peptidase, beta subunit, putative	55057	169	5	**R.ARPASNHATTQALR.S**	
Spot 31	EAN81757.1	mitochondrial processing peptidase, beta subunit, putative	31341	141	3	**R.AAASNFGDLVAASTK.S**	Shares 2 peptides to EAN94510.1
	EAN84761.1	mitochondrial processing peptidase, beta subunit, putative	15529	84	3	***K.IPPTNISTVGK.G***	Shares 1 peptide to EAN94510.1
Band 12	EAN94594.1	hypothetical protein, conserved	57998	193	4	R.SSPVPLLK.L K.AIEAFALLR.E K.LIEGDILER.R K.SLDGQGPLLNSTNSHL.-	
	EAN94531.1	hypothetical protein, conserved	57858	140	4	***R.RVSDSAFYR.F***	

Band / Spot No.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Sequence (*)	Additional gene copies (#)
Band 13	EAN99374.1	pyruvate phosphate dikinase, putative	101851	2013	64	**K.VIPEIMIPLVGK.K** **K.VIPEIMIPLVGK.K + Oxidation (M)** **K.DPFESIDQEGVGELMR.I**	
	EAN98352.1	pyruvate phosphate dikinase, putative	101833	2011	59	**K.VVPEIMIPLVGK.K** **K.VVPEIMIPLVGK.K + Oxidation** **K.DPFESIDQEGVGELVR.I**	
Band 13	EAN82002.1	cytoskeleton-associated protein CAP5.5, putative	82008	506	13	K.LDIQFTK.L R.DFTGAPSYR.F K.GYGGVNELLGK.L R.HSPLMISVSR.A R.ATVPEEVLER.L R.FDEAWVNATK.G K.LSATNPALHNR.V K.MPGEAAVTSAGSK.L + Oxidation (M) R.QFQNFGITMLK.I + Oxidation (M) R.SDVFAQALSEEYR.Q K.FSPDSSVIPLGSSIK.K R.YLEAGNIVLLNTPAGK.S R.VIELADGSVDEEGILSK.C	
	EAN92788.1	cytoskeleton-associated protein CAP5.5, putative	89960	436	11	***K.NSSGDPESPSDAFTFVVAR.E***	
Band 13	EAN95481.1	retrotransposon hot spot (RHS) protein, putative	108368	398	11	**R.VLIGTPGIGK.S** **K.GYIIYDVAK.K** **R.VWQIVLDDLTK.W**	
	EAN84826.1	retrotransposon hot spot (RHS) protein, putative	104023	342	13	**K.GYIIYDVAK.K** **K.NSLDTAFEVAR.I**	
	EAN81408.1	retrotransposon hot spot (RHS) protein, putative	103887	340	14	***R.ALEQLGLR.A*** **R.STVEDILLK.G** ***R.LGAVNAALVAIK.D*** **K.NSLDAAFEVAR.I** **R.SEFEGDTDQPAATHIR.V**	
	EAN82412.1	retrotransposon hot spot (RHS) protein, putative	109652	311	10	**R.VLIGTPGIGK.S** **R.MEDLGPLLR.Y + Oxidation (M)** **K.QTLDAALEEVR.N**	

Band / Spot No.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Sequence (*)	Additional gene copies (#)
cont.	EAN94997.1	retrotransposon hot spot (RHS) protein, putative	126164	288	8	**R.LLIGTPGIGK.S** **K.QTLDAALEEVR.N not unique** **R.VWQIVLDDLTK.W not unique**	
	EAN83522.1	retrotransposon hot spot (RHS) protein, putative	76947	252	8	***R.LGAVDVALLAIK.D***	
	EAN84956.1	retrotransposon hot spot (RHS) protein, putative	115032	197	8	***K.ILLEAITK.L***	
						K.EFFKDPTK.Y **K.GYIIYDVAR.K**	
	EAN97710.1	retrotransposon hot spot (RHS) protein, putative	108700	192	6	***R.VQTSTSVVK.S*** **R.MEEVGPILR.Y + Oxidation (M)** ***K.GVVSLEQWR.N*** ***R.LLLIGTPGIGK.S*** ***R.NYEGKDTVSPLAK.G*** ***K.LNDFLLLEMEGK.G***	
	EAN85054.1	retrotransposon hot spot (RHS) protein, putative	139992	168	5	***R.VLTQLLR.E***	
	EAN81660.1	retrotransposon hot spot (RHS) protein, putative	62254	149	5	**R.VLTQVLR.E** ***R.VLTQVLREER.R***	
	EAN82470.1	retrotransposon hot spot (RHS) protein, putative	114542	142	6	***K.WSEAAAEVK.A*** ***K.LNAVLTQVLTEEK.R***	EAN98283.1
	EAN99306.1	retrotransposon hot spot (RHS) protein, putative	109235	127	5	***R.AQISTSVVK.S*** ***R.GGVLSLEQWR.D*** ***R.NDSVQQSGEAR.L***	

The following appear on the list but no unique peptides to them; all shared to previous reported above: EAN84856.1;EAN87824.1;EAN86507.1;EAN90067.1;EAN90465.1;EAN88911.1;EAN94539.1;EAN98325.1;EAN86737.1;EAN83818.1;EAN93613.1;EAN91620.1;EAN94122.1;EAN97715.1;EAN86249.1;EAN99309.1;EAN86534.1;EAN83062.1;EAN96809.1;EAN85806.1;EAN94683.1;EAN93071.1;EAN91733.1;EAN96808.1;EAN84415.1;EAN88539.1;EAN81681.1;EAN82927.1;EAN94606.1;EAN85486.1;EAN93121.1

Band / Spot No.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Sequence (*)	Additional gene copies (#)
Band 13	EAN92377.1	calcium-translocating P-type ATPase, putative	110858	611	21	R.AIFNNTK.Q	
						K.LNSLFVK.G	
						R.AESAIEALK.S	
						K.NTTLEFTR.Q	
						K.GAPEEVLRR.S	
						R.DLPSVETLGR.C	
						K.AVMSAVLFSR.T + Oxidation (M)	
						R.GLSADEVEER.R	
						K.LDEFGMLLSK.V	
						K.LDEFGMLLSK.V + Oxidation (M)	
						R.TGAFTEIGSIER.D	
						K.IDAMSGSEHALR.C + Oxidation (M)	
						K.MVLADDNFATVVK.A	
						K.ADIGIAMGSGTQVAK.A + Oxidation (M)	
						K.MVLADDNFATVVK.A + Oxidation (M)	
						R.EQEEVKTPLQIK.L	
						K.KADIGIAMGSGTQVAK.A	
						K.IGEATEAALLVMSEK.L	
						K.KADIGIAMGSGTQVAK.A + Oxidation (M)	
						K.IGEATEAALLVMSEK.L + Oxidation	
	EAN81423.1	calcium-translocating P-type ATPase, putative	19723	132	3	**K.LVLAQFEDTLVR.I**	
Spot 1	EAN83392.1	calmodulin, putative	16814	261	6	K.ELGTVMR.S + Oxidation (M)	EAN83393.1
						R.HVMTNLGEK.L + Oxidation (M)	EAN86238.1
						K.LTDEEVDEMIR.E + Oxidation (M)	EAN86242.1
						R.VFDKDGNGFISAAELR.H	
						K.MQDSDSEEEIKEAFR.V + Oxidation (M)	
						K.EAFSLFDKDGDGTITTK.E	
	EAN89727.1	calmodulin, putative	17154	58	1	**K.TGFINVTDLK.F**	EAN93967.1
Spot 2	EAN98394.1	p22 protein precursor, putative	26158	363	9	**K.HEDEEIVIR.C**	
						K.LALDDSVEGNQK.R	
	EAN91460.1	p22 protein precursor, putative	26184	323	8	**K.HEDEEIIIR.C**	
						K.LALDDSVEGNR.K	
Spot 8-9	EAN99021.1	cytochrome C oxidase subunit IV, putative	39097	1038	30	**R.HITSEAIK.A**	
	EAO00075.1	cytochrome C oxidase subunit IV, putative	39137	1032	29	**R.HITPEAIK.A**	

Band / Spot No.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Sequence (*)	Additional gene copies (#)
Spot 10	EAN82883.1	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative	39837	311	7	**R.QGVPSGVPPELR.A**	
	EAN83656.1	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative	45479	298	7	**R.QGAPTGVPPELR.A**	
Spot 11-12	EAO00025.1	alcohol dehydrogenase, putative	42442	596	14	**K.EVQIPSGFEQLGMK.E + Oxidation (M)** **K.EVQIPSGFEQLGMKEK.D + Oxidation (M)**	
	EAN97413.1	alcohol dehydrogenase, putative	42479	581	14	**K.EVQIPPGFEQLGMK.E + Oxidation (M)** **K.EVQIPPGFEQLGMKEK.D + Oxidation (M)**	
Spot 16-17	EAN82242.1	co-chaperone GrpE, putative	24363	650	16	**K.VSAEEIESNK.N** **K.VSAEEIESNKNLSSIHTGVK.L**	In spot 17 first is EAN81815.1 then EAN82242.1
	EAN81815.1	co-chaperone GrpE, putative	24421	624	16	**K.VSTEEIESNK.N** **K.VSTEEIESNKNLSSIHTGVK.L**	
Spot 18	EAN87362.1	mucin-associated surface protein (MASP), putative	43226	22	1	***R.VTTVGEEAK.T***	
	EAN84330.1	mucin-associated surface protein (MASP), putative	44673	18	1	***K.VAISLPSR.M***	EAN86283.1
Spot 22	EAN82097.1	hypothetical protein, conserved	14352	247	6	**R.TPVGQSSKDYTETHVLFMNK.L + Oxidation (M)**	
	EAN97997.1	hypothetical protein, conserved	14334	242	6	**R.TPAGQSSKDYTETHVLFMNK.L + Oxidation**	
Spot 28	EAN89116.1	heat shock protein 20, putative	16000	269	7	**K.ILADLPGMNR.N + Oxidation (M)**	
	EAO00223.1	heat shock protein 20, putative	15973	266	7	**K.ILADLPGMSR.N + Oxidation**	
Spot 30	EAN83160.1	phosphomannose isomerase, putative	46214	141	4	**K.VAAESFVAK.M** **R.FTEFSLYR.M** **K.TLLGNVAVVSAK.E** R.AAEGEAWEVQR.Y	
	EAN92798.1	phosphomannose isomerase, putative	46092	87	3	**K.VAAESFVAK.M not unique** **R.FTEFSLYR.L not unique** ***K.TLLGNTAVVSAK.E***	

Band / Spot No.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Sequence (*)	Additional gene copies (#)
Spot 32-33	EAN92318.1	69 kDa paraflagellar rod protein, putative	70087	1273	31	K.TVQQITQ.-	
Spot 34-35						K.AQLAAIEK.A	
						K.TLGQLVYK.K	
						K.RLEEIDR.N	
						R.RIQELER.V	
						R.GKTVQQITQ.-	
						K.SFQETSAIK.D	
						K.TLQSQQYR.G	
						K.FIQENLDR.Q	
						K.TLGQLVYKK.E	
						K.TNEELADLR.L	
						K.KSFQETSAIK.D	
						R.LEEIDRNIR.T	
						R.LGTERFEEVK.R	
						R.SKTLQSQQYR.G	
						K.WNLTEAYDIK.K	
						K.AQELLSSVEGGTK.W	
						K.SFQETSAIKDAK.R	
						R.AQVEEELEMLK.D + Oxidation (M)	
						K.WNLTEAYDIKK.L	
						R.TVSFTGTIDNAIAK.L	
						R.LQVHQEYLEAFR.R	
						R.AQVEEELEMLKDK.M + Oxidation (M)	
						R.IIGQTEDENKPFGR.I	
						R.SQLDASEMAQVPVAVLK.N	
						R.SQLDASEMAQVPVAVLK.N + Oxidation (M)	
						R.TVSFTGTIDNAIAKLEK.I	
						K.FIQENLDRQDEAWR.R	
						R.TTHIQLEFAIETFDPNAK.K	
						R.NVAIADGEMAIAEEQYYIK.A + Oxidation (M)	
						K.EASGAVGPADQQQPAVPEVTDVTLEAARK	
	EAN81200.1	paraxonemal rod protein PAR2, putative	31620	554	15	**K.TNEELGDLR.L**	
	EAN87979.1	paraflagellar rod protein 3, putative	69189	493	12	K.VEEELRR.S	
						K.TQLAQLEK.T	
						R.LIDLIQDK.F	

Band / Spot No.	Accession no.	Protein Identity	Mr	SCORE	# PEPT.	Sequence (*)	Additional gene copies (#)
cont.	EAN87979.1	cont.				K.TSQDLAALR.L	
						K.AQFMDIIGVK.K + Oxidation (M)	
						R.IEEVDREEK.R	
						K.LGTERFEEVK.R not unique	
						R.LIDLIQDKFR.L	
						R.QGVEEELAMLK.E + Oxidation (M)	
						K.ADLEDAEAMKR.H + Oxidation (M)	
						R.SQLDATQLAQVPTR.T	
						R.VVSFTQMIDNAIAK.M + Oxidation (M)	
Spot 33	EAN95887.1	heat shock protein 70 (HSP70), putative	73607	204	5	R.GTLQPVER.V	EAN83852.1 no unique peptides but shares with both…
						K.NTVNEPNVAGK.I	
						K.VMQLVSDFFGGK.E + Oxidation (M)	
						R.TTPSYVAFTDTER.L	
						K.NQVAMNPTNTVFDAK.R + Oxidation (M)	
	EAN95886.1	heat shock protein 70 (HSP70), putative	71171	202	5	**R.VEIIANDQGNR.T**	
Spot 38	EAN95887.1	heat shock protein 70 (HSP70), putative	73607	1070	31	**R.TTPSYVAFTDTER.L**	EAN83852.1
	EAN95886.1	heat shock protein 70 (HSP70), putative	71171	1053	30	***R.VEIIANDQGNR.T***	
	EAN84609.1	heat shock 70 kDa protein, putative	24348	205	5	**R.TTPSYVAFTETER.L**	EAN89698.1
Spot 36-39	EAN90720.1	calreticulin, putative	46396	906	27	**K.EVLELVEK.T**	
						K.DIMIGDDLK.E + Oxidation (M)	
						K.GQLDGDWTLLPPR.E	
						R.FYALSTAFPTPITNEK.K	
						R.FYALSTAFPTPITNEKK.S	
	EAN82340.1	calreticulin, putative	46419	894	27	**K.EVLDLVEK.T**	
						K.DIVIGDDLK.E	
						K.GQLEEDWSLLLPR.E	
						R.FYALSTAFPTPINNEK.K	
						R.FYALSTAFPTPINNEKK.S	

TABLE S7: PROTEINS FUNCTIONAL GROUPS - CELLULAR LOCATION - COMPARATIVE EXPRESSION DATA

Notes: (*) The assignment of the protein cellular location is based on: a. publications describing the location of the protein in *T cruzi;* b. publications describing the location of conserved pathways in trypanosomatids or in other eukaryotes; c. gene ontology annotation found in GeneBank. d. in silico prediction based in targeting signals. When the location is unknown or uncertain, an **X** is displayed in the table. An asterisk indicates when the location of the protein in T. cruzi has been experimentally demonstrated.

Numbers is brackets denote: (1) No previous expression data in *T. cruzi* proteome (Atwood et al, 2005), **(2)** Not previously found in the epimastigote stage whole cell proteomic study (Atwood et al, 2005) (3) Not previously found in the epimastigote stage whole cell proteomic study but evidence available indicating the expression of the protein in the epimastigote stage.

PubMed Reference: The references correspond to work in which the gene, protein, or activity of the protein has been described either in *T. cruzi* or in other trypanosomatids. When no reference in trypanosomatids is available, the reference corresponds to the identification of the gene, protein or activity in other species. N/A : references not available in trypanosomatids

ACC No.	METABOLISM	Predicted Location	PubMed REFERENCE
	AMINOACID MET.	**8**	
EAN98485.1	histidine ammonia-lyase, putative	X	Important for conversion of histidine to glutamate. The *Trypanosoma cruzi* proteome. Science. 2005 Jul 15;309(5733):473-6. Atwood JA 3rd, Weatherly DB, Minning TA, Bundy B, Cavola C, Opperdoes FR, Orlando R, Tarleton RL.
EAN87724.1	glutamate dehydrogenase, putative	cytoplasm/ mitochondrion*	The NADP+-linked glutamate dehydrogenase from *Trypanosoma cruzi*: sequence, genomic organization and expression. Biochem J. 1998 March 1; 330(Pt 2): 951–958. P Barderi, O Campetella, A C Frasch, J A Santomé, U Hellman, U Pettersson, and J J Cazzulo
EAN86114.1	cysteine desulfurase, putative (1)	mitochondrion	Important for Fe-S cluster biogenesis (IscS). // Knock-downs of iron-sulfur cluster assembly proteins IscS and IscU down-regulate the active mitochondrion of procyclic *Trypanosoma brucei*. J Biol Chem. 2006 Sep 29;281(39):28679-86. Smíd O, Horáková E, Vilímová V, Hrdy I, Cammack R, Horváth A, Lukes J, Tachezy J.
EAN88605.1	acetylornithine deacetylase-like, putative	X	N/A. In bacteria is important for synthesis or arginine. The sequence has similarities to those of metallopeptidases // Mechanistic analysis of the argE-encoded N-acetylornithine deacetylase. Biochemistry, 39 (6), 1285 -1293, 2000. // Farah Javid-Majd and John S. Blanchard //Sequence analysis of the aminoacylase-1 family. A new proposed signature for metalloexopeptidases. Comp Biochem Physiol B Biochem Mol Biol. 2001 Mar;128(3):469-81. Biagini A, Puigserver A.
EAN83019.1	cystathionine beta-synthase	X	Characterization of transsulfuration and cysteine biosynthetic pathways in the protozoan hemoflagellate, *Trypanosoma cruzi.* Isolation and molecular characterization of cystathionine beta-synthase and serine acetyltransferase from *Trypanosoma*. J Biol Chem. 2001 Mar 2;276(9):6516-23. Nozaki T, Shigeta Y, Saito-Nakano Y, Imada M, Kruger WD.
EAN91861.1	pyrroline-5-carboxylate reductase, putative (1)	X	Important for oxidation of proline (proline oxidase) // Differentiation of *Trypanosoma brucei* bloodstream trypomastigotes from long slender to short stumpy-like forms in axenic culture. Mol Biochem Parasitol. 1990 Apr;40(1):13-22. Hamm B, Schindler A, Mecke D, Duszenko M.
EAN86462.1	aspartate aminotransferase, mitochondrial, putative	mitochondrion / cytoplasm*	Glutamate dehydrogenase and aspartate aminotransferase in *Trypanosoma cruzi*. Comp Biochem Physiol B. 1977;56(3):301-3. Cazzulo JJ, Juan SM, Segura EL.
EAO00085.1	alanine aminotransferase, putative	mitochondrion / cytoplasm*	Subcellular localization of glutamate dehydrogenases and alanine aminotransferase in epimastigotes of *Trypanosoma cruzi*. FEMS Microbiol Lett. 1991 Oct 1;67(2):131-5. Duschak VG,
	NUCLEOSIDE, NUCLEOTIDE & NUCLEIC ACID MET.	**3**	
EAN88252.1	ribonucleoside-diphosphate reductase small chain, putative	X	Cloning, sequencing and expression of ribonucleotide reductase R2 from *Trypanosoma brucei*. FEBS Lett. 1997 Sep 8;414(2):449-53. Dormeyer M, Schöneck R, Dittmar GA, Krauth-Siegel RL.
EAN92546.1	adenosine 5'-monophosphoramidase, putative	nucleus / cytoplasm	N/A. Nucleoside monophosphoramidate hydrolase from rat liver: purification and characterization. Int J Biochem. 1994 Feb;26(2):235-45. Kuba M, Okizaki T, Ohmori H, Kumon A.
EAN94685.1	methylthioadenosine phosphorylase, putative	X	*Trypanosoma cruzi* adenine nucleoside phosphorylase. Purification and substrate specificity. Biochem Pharmacol. 1987 Feb 15;36(4):553-60. Miller Rl, Sabourin CL, Krenitsky TA.
	CARBOHYDRATE MET.	**9**	
EAN86006.1	glucosamine-6-phosphate isomerase, putative	glycosome	N/A. Molecular cloning and analysis of the NAG1 cDNA coding for glucosamine-6-phosphate deaminase from *Candida albicans*. J Biol Chem. 1993 May 5;268(13):9206-14. Natarajan K, Datta A.// In silico prediction of the glycosomal enzymes of *Leishmania major* and trypanosomes. Mol Biochem Parasitol. 2006 Jun;147(2):193-206. Opperdoes FR, Szikora JP.
EAO00025.1	alcohol dehydrogenase, putative	X	Characterization by electrophoretic zymograms of 19 *Trypanosoma cruzi* clones derived from two chronic chagasic patients. Comp Biochem Physiol B. 1987;87(2):417-22. Montamat EE, Arauzo S, Cazzulo JJ, Subías E.
EAN85464.1	N-acetylglucosamine-6-phosphate deacetylase-like protein, putative	X	N/A. Identification and characterization of the genes for N-acetylglucosamine kinase and N-acetylglucosamine-phosphate deacetylase in the pathogenic fungus *Candida albicans*. Eur J Biochem. 2001 Apr;268(8):2498-505. Yamada-Okabe T, Sakamori Y, Mio T, Yamada-Okabe H.
EAN90055.1	galactokinase, putative	glycosome	Putative galactokinase genes exist in *T. cruzi*, even though this organism cannot take up galactose. It is possible that one or more of these enzymes may be involved in salvage pathways for other sugars in this organism. /// Plant-like traits associated with metabolism of *Trypanosoma* parasites.Proc Natl Acad Sci U S A. 2003 Feb 4;100(3):1067-71. Hannaert V, Saavedra E, Duffieux F, Szikora JP, Rigden DJ, Michels PA, Opperdoes FR. // Sugar nucleotide pools of *Trypanosoma brucei, Trypanosoma cruzi,* and *Leishmania major.* Eukaryot Cell. 2007 Aug;6(8):1450-63. Turnock DC, Ferguson MA. // In silico prediction of the glycosomal enzymes of Leishmania major and trypanosomes. Mol Biochem Parasitol. 2006 Jun;147(2):193-206. Opperdoes FR, Szikora JP.
EAN83988.1	fructose-1,6-bisphosphatase, cytosolic, putative (2)	cytoplasm / glycosome	Plant-like traits associated with metabolism of *Trypanosoma* parasites.Proc Natl Acad Sci U S A. 2003 Feb 4;100(3):1067-71. Hannaert V, Saavedra E, Duffieux F, Szikora JP, Rigden DJ, Michels PA, Opperdoes FR. // In silico prediction of the glycosomal enzymes of *Leishmania major* and trypanosomes. Mol Biochem Parasitol. 2006 Jun;147(2):193-206. Opperdoes FR, Szikora JP.
EAN90241.1	2-oxoisovalerate dehydrogenase beta subunit, mitochondrial precursor (1)	mitochondrion	2-oxoglutarate dehydrogenase complex catalyzes a step within the citric acid cycle, the branched-chain 2-oxo acid dehydrogenase complex is involved in amino acid degradation /// A family of highly conserved glycosomal 2-hydroxyacid dehydrogenases from *Phytomonas* sp. J Biol Chem. 2000 Oct 13;275(41):31833-7. Uttaro AD, Altabe SG, Rider MH, Michels PA, Opperdoes FR.//Crystal structure of 2-oxoisovalerate dehydrogenase and the architecture of 2-oxo acid dehydrogenase multienzyme complexes. Nat Struct Biol. 1999 Aug;6(8):785-92. Aevarsson A, Seger K, Turley S, Sokatch JR, Hol WG.
EAN83800.1	D-isomer specific 2-hydroxyacid dehydrogenase-protein, putative	X	The NAD-linked aromatic alpha-hydroxy acid dehydrogenase from *Trypanosoma cruzi.* A new member of the cytosolic malate dehydrogenases group without malate dehydrogenase activity. Eur J Biochem. 1999 Dec;266(3):903-10. Cazzulo Franke MC, Vernal J, Cazzulo JJ, Nowicki C.
EAN91548.1	2- aminoethylphosphonate:pyruvateaminotransferase-like protein, putative (3)	cytoplasmic vesicles*	Properties of phosphoenolpyruvate mutase, the first enzyme in the aminoethylphosphonate biosynthetic pathway in *Trypanosoma cruzi.* J Biol Chem. 2003 Jun 20;278(25):22703-8. Sarkar M, Hamilton CJ, Fairlamb AH.
EAN83160.1	phosphomannose isomerase, putative (1)	glycosome	The role of phosphomannose isomerase in *Leishmania mexican*a glycoconjugate synthesis and virulence. J Biol Chem. 2001 Mar 2;276(9):6566-75. Garami A, Ilg T. // In silico prediction of the glycosomal enzymes of Leishmania major and trypanosomes. Mol Biochem Parasitol. 2006 Jun;147(2):193-206. Opperdoes FR, Szikora JP.
	LIPID, FATTY ACID AND STEROL MET.	**17**	
EAN87378.1	3-hydroxy-3-methylglutaryl-CoA reductase, putative	X	Mitochondrial localization of the mevalonate pathway enzyme 3-Hydroxy-3-methyl-glutaryl-CoA reductase in the Trypanosomatidae. Mol Biol Cell. 2004 Mar;15(3):1356-63. Peña-Diaz J, Montalvetti A, Flores CL, Constán A, Hurtado-Guerrero R, De Souza W, Gancedo C, Ruiz-Perez LM, Gonzalez-Pacanowska D.
EAN97370.1	isopentenyl-diphosphate delta-isomerase,putative (1)	glycosome	N/A although necessary for the next step of isoprenoid sythesis, which has been described in *T. cruzi* /// Bisphosphonates are potent inhibitors of *Trypanosoma cruzi* farnesyl pyrophosphate synthase. J Biol Chem. 2001 Sep 7;276(36):33930-7. Montalvetti A, Bailey BN, Martin MB, Severin GW, Oldfield E, Docampo R. // In silico prediction of the glycosomal enzymes of *Leishmania major* and trypanosomes. Mol Biochem Parasitol. 2006 Jun;147(2):193-206. Opperdoes FR, Szikora JP.
EAN86492.1	squalene monooxygenase, putative (3)	X	Squalene epoxidase. Nor studied in trypanosomatids althought sterol biosynthesis occurs through the mevalonate pathway/// Lipid biosynthesis pathways as chemotherapeutic targets in kinetoplastid parasites.Parasitology. 1997;114 Suppl:S91-9. Urbina JA.
EAN97907.1	lanosterol synthase, putative (2)	X	Cloning and heterologous expression of the *Trypanosoma brucei* lanosterol synthase gene. Mol Biochem Parasitol. 2000 Oct;110(2):399-403. Buckner FS, Nguyen LN, Joubert BM, Matsuda SP.

EAN98359.1	lanosterol 14-alpha-demethylase, putative (3)	X	Cloning and analysis of *Trypanosoma cruzi* lanosterol 14alpha-demethylase. Mol Biochem Parasitol. 2003 Dec;132(2):75-81. Buckner FS, Joubert BM, Boyle SM, Eastman RT, Verlinde CL, Matsuda SP.
EAN81270.1	sterol 24-c-methyltransferase, putative	X	Modification of the sterol composition of *Trypanosoma (Schizotrypanum) cruzi* epimastigotes by delta 24(25)-sterol methyl transferase inhibitors and their combinations with ketoconazole. Mol Biochem Parasitol. 1995 Jul;73(1-2):199-210. Urbina JA, Vivas J, Visbal G, Contreras LM.
EAN80692.1	solanesyl diphosphate synthase (annotation: farnesyl synthetase) (3)	glycosome*	A solanesyl-diphosphate synthase localizes in glycosomes of Trypanosoma cruzi. J Biol Chem. 2006 Dec 22;281(51):39339-48. Ferella M, Montalvetti A, Rohloff P, Miranda K, Fang J, Reina S, Kawamukai M, Búa J, Nilsson D, Pravia C, Katzin A, Cassera MB, Aslund L, Andersson B, Docampo R, Bontempi EJ.
EAN95821.1	fatty acid desaturase, putative (1)	X	*Trypanosoma brucei* oleate desaturase may use a cytochrome b5-like domain in another desaturase as an electron donor. J Parasitol. 2006 Oct;92(5):1064-74.Guillermo A. Petrini, Silvia G. Altabe and Antonio D. Uttaro
EAN92121.1	fatty acid elongase, putative (3)	ER	Fatty acid synthesis by elongases in trypanosomes. Cell. 2006 Aug 25;126(4):691-9. Lee SH, Stephens JL, Paul KS, Englund PT. Elongation of polyunsaturated fatty acids in trypanosomatids. FEBS J. 2007 Jan;274(1):264-74. Livore VI, Tripodi KE, Uttaro AD.
EAN85395.1	3-ketoacyl-CoA thiolase, putative	glycosome	In silico prediction of the glycosomal enzymes of *Leishmania major* and trypanosomes. Mol Biochem Parasitol. 2006 Jun;147(2):193-206. Opperdoes FR, Szikora JP.
EAN92450.1	thiolase protein-like protein, putative	glycosome	same as previous
EAN81547.1	NAD(P)-dependent steroid dehydrogenase protein, putative (1)	ER/mitochondria	N/A, although NADPH cytochrome P450 reductase activities are present. NADPH-cytochrome c reductases of *Trypanosoma cruzi.* Biochem Biophys Res Commun. 1984 Oct 15;124(1):121-4. Kuwahara T, White RA Jr, Agosin M.
EAN82883.1	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative	mitochondria	N/A /// Crystallization and X-ray diffraction analysis of peroxisomal Delta3-Delta2-enoyl-CoA isomerase from *Saccharomyces cerevisiae*. Acta Crystallogr D Biol Crystallogr. 2000 Aug;56(Pt 8):1020-3. Mursula AM, van Aalten DM, Modis Y, Hiltunen JK, Wierenga RK.
EAN81369.1	3-oxo-5-alpha-steroid 4-dehydrogenase, putative	ER/mitochondria	Not studied in trypanosomatids, altough NADPH cytochrome c reductase activities are present. NADPH-cytochrome c reductases of *Trypanosoma cruzi*. Biochem Biophys Res Commun. 1984 Oct 15;124(1):121-4. Kuwahara T, White RA Jr, Agosin M.
EAN95757.1	prostaglandin F2alpha synthase	mitocondrion	Identification of a novel prostaglandin f(2alpha) synthase in *Trypanosoma brucei.* J Exp Med. 2000 Nov 6;192(9):1327-38. Kubata BK, Duszenko M, Kabututu Z, Rawer M, Szallies A, Fujimori K, Inui T, Nozaki T, Yamashita K, Horii T, Urade Y, Hayaishi O. // Thromboxane A2 is a key regulator of pathogenesis during *Trypanosoma cruzi* infection. J Exp Med. 2007 Apr 16;204(4):929-40. Ashton AW, Mukherjee S, Nagajyothi FN, Huang H, Braunstein VL, Desruisseaux MS, Factor SM, Lopez L, Berman JW, Wittner M, Scherer PE, Capra V, Coffman TM, Serhan CN, Gotlinger K, Wu KK, Weiss LM, Tanowitz HB.
EAN92511.1	prostaglandin F synthase, putative	X	N/A. Aldo/Keto reductase conserved domain. /// Human aldo-keto reductases: Function, gene regulation, and single nucleotide polymorphisms. Arch Biochem Biophys. 2007 Aug 15;464(2):241-50. Penning TM, Drury JE.// Thromboxane A2 is a key regulator of pathogenesis during *Trypanosoma cruzi* infection. J Exp Med. 2007 Apr 16;204(4):929-40. Ashton AW, Mukherjee S, Nagajyothi FN, Huang H, Braunstein VL, Desruisseaux MS, Factor SM, Lopez L, Berman JW, Wittner M, Scherer PE, Capra V, Coffman TM, Serhan CN, Gotlinger K, Wu KK, Weiss LM, Tanowitz HB.
EAN92888.1	acyl-CoA dehydrogenase, putative	cytoplasm/ mitochondrion	N/A /// Thia fatty acids, metabolism and metabolic effects. Biochim Biophys Acta. 1997 Jan 21;1344(2):115-31. Skrede S, Sørensen HN, Larsen LN, Steineger HH, Høvik K, Spydevold OS, Horn R, Bremer J.
	THIOL METABOLISM	**2**	
EAN80947.1	tryparedoxin peroxidase, putative	cytoplasm/ mitochondrion	Evidence for a trypanothione-dependent peroxidase system in *Trypanosoma cruzi.* Free Radic Biol Med. 2000 Mar 1;28(5):767-72. Lopez JA, Carvalho TU, de Souza W, Flohé L, Guerrero SA, Montemartini M, Kalisz HM, Nogoceke E, Singh M, Alves MJ, Colli W.
EAN93034.1	thiol-dependent reductase 1, putative	X	Reduction of anti-leishmanial pentavalent antimonial drugs by a parasite-specific thiol-dependent reductase, TDR1. Biochem J. 2004 Jul 15;381(Pt 2):405-12. Denton H, McGregor JC, Coombs GH.
	ENERGY METABOLISM	**9**	
EAO00028.1	citrate synthase, putative (3)	mitochondrion	The citrate synthase from *Trypanosoma cruzi*. J Parasitol. 1977 Oct;63(5):921-2.Juan SM, Cazzulo JJ, Segura EL.
EAO00045.1	aconitase, putative	mitochondrion	Mitochondrial superoxide radicals mediate programmed cell death in *Trypanosoma cruzi:* cytoprotective action of mitochondrial iron superoxide dismutase overexpression. Biochem J. 2007 Apr 15;403(2):323-34. Piacenza L, Irigoín F, Alvarez MN, Peluffo G, Taylor MC, Kelly JM, Wilkinson SR, Radi R.
EAN99748.1	isocitrate dehydrogenase, putative	mitochondrion	Differential energetic metabolism during *Trypanosoma cruzi* differentiation. I. Citrate synthase, NADP-isocitrate dehydrogenase, and succinate dehydrogenase. Arch Biochem Biophys. 1988 Nov 15;267(1):252-61. Adroher FJ, Osuna A, Lupiañez JA.
EAN96732.1	succinyl-CoA ligase [GDP-forming] beta-chain, putative	mitochondrion	Porphyrin biosynthesis in parasitic hemoflagellates: functional and defective enzymes in *Trypanosoma cruzi.* Comp Biochem Physiol B. 1982;72(4):663-7. Salzman TA, Stella AM, Wider de Xifra EA, Batlle AM, Docampo R, Stoppani AO.
EAN98983.1	succinyl-CoA synthetase alpha subunit, putative	mitochondrion	same as previous
EAN86067.1	acetyl:succinate CoA-transferase	mitochondrion	Annotated as succinyl-CaO:3-ketoacid-coenzyme A transferase.// Acetyl:succinate CoA-transferase in procyclic *Trypanosoma brucei.* Gene identification and role in in carbohydrate metabolism. J Biol Chem. 2004 Oct 29;279(44):45337-46. Rivière L, van Weelden SW, Glass P, Vegh P, Coustou V, Biran M, van Hellemond JJ, Bringaud F, Tielens AG, Boshart M.
EAN84275.1	succinate dehydrogenase, putative (iron-sulfur subunit) (3)	mitochondrion	Differential energetic metabolism during *Trypanosoma cruzi* differentiation. I. Citrate synthase, NADP-isocitrate dehydrogenase, and succinate dehydrogenase. Arch Biochem Biophys. 1988 Nov 15;267(1):252-61. Adroher FJ, Osuna A, Lupiañez JA.
EAN87573.1	succinate dehydrogenase flavoprotein, putative	mitochondrion	same as previous
EAN87359.1	mitochondrial malate dehydrogenase, putative	mitochondrion*	Glycosomal and mitochondrial malate dehydrogenases in epimastigotes of *Trypanosoma cruzi.* Mol Biochem Parasitol. 1984 Apr;11:37-49. Cannata JJ, Cazzulo JJ.
	ELECTRON CARRIERS & TRANSPORT	**14**	
EAN85971.1	NADH-cytochrome b5 reductase, putative	mitochondrion	Overexpression of a cytochrome b5 reductase-like protein causes kinetoplast DNA loss in *Trypanosoma brucei.* J Biol Chem. 2006 Jul 7;281(27):18499-506. Motyka SA, Drew ME, Yildirir G, Englund PT.
EAN81327.1	cytochrome-b5 reductase, putative	mitochondrion	same as previous
EAN97131.1	cytochrome p450-like protein, putative (3)	X	CYP51 from *Trypanosoma cruzi:* a phyla-specific residue in the B' helix defines substrate preferences of sterol 14alpha-demethylase. J Biol Chem. 2006 Feb 10;281(6):3577-85. Lepesheva GI, Zaitseva NG, Nes WD, Zhou W, Arase M, Liu J, Hill GC, Waterman MR.
EAN89176.1	NADH dehydrogenase, putative (2)	mitochondrion	Identification of a gene encoding a 54 kDa alternative NADH dehydrogenase in *Trypanosoma brucei.* Mol Biochem Parasitol. 2003 Mar;127(1):73-7. Fang J, Beattie DS.
EAN94284.1	reiske iron-sulfur protein precursor, putative (2)	mitochondrion	The trypanosomatid Rieske iron-sulfur proteins have a cleaved presequence that may direct mitochondrial import. Biochim Biophys Acta. 1995 Nov 30;1269(3):201-4. Priest JW, Hajduk SL.
EAN83385.1	cytochrome c oxidase VIII (COX VIII), putative (1)	mitochondrion	Post-transcriptional control of nuclear-encoded cytochrome oxidase subunits in *Trypanosoma brucei*: evidence for genome-wide conservation of life-cycle stage-specific regulatory elements. Nucleic Acids Res. 2006;34(18):5312-24. Mayho M, Fenn K, Craddy P, Crosthwaite S, Matthews K.
EAN96063.1	cytochrome c1, heme protein, mitochondrial precursor, putative (2)	mitochondrion	*Trypanosoma brucei* cytochrome c1 is imported into mitochondria along an unusual pathway. J Biol Chem. 2003 Apr 25;278(17):15084-94. Priest JW, Hajduk SL.
EAO00075.1	cytochrome c oxidase subunit IV, putative	mitochondrion	Post-transcriptional control of nuclear-encoded cytochrome oxidase subunits in *Trypanosoma brucei*: evidence for genome-wide conservation of life-cycle stage-specific regulatory elements. Nucleic Acids Res. 2006;34(18):5312-24. Mayho M, Fenn K, Craddy P, Crosthwaite S, Matthews K.
EAN86560.1	cytochrome c oxidase subunit V, putative	mitochondrion	Same as previous
EAN81211.1	cytochrome c oxidase subunit 10, putative	mitochondrion	Same as previous
EAN89655.1	cytochrome c oxidase subunit VI, putative (2)	mitochondrion	Same as previous
EAN88371.1	glutathione-S-transferase/glutaredoxin, putative	reservosome*	*Trypanosoma cruzi*: a 52-kDa protein sharing sequence homology with glutathione S-transferase is localized in parasite organelles morphologically resembling reservosomes. Exp Parasitol. 1995 Dec;81(4):453-61. Ouaissi MA, Dubremetz JF, Schöneck R, Fernandez-Gomez R, Gomez-Corvera R, Billaut-Mulot O, Taibi A, Loyens M, Tartar A, Sergheraert C, et al.

EAN89624.1	oxidoreductase, putative	mitochondrion	Not described as such but as part of a pathway or complex /// Mitochondrial complexes in *Trypanosoma brucei*: a novel complex and a unique oxidoreductase complex. Mol Cell Proteomics. 2007 Dec 11 Panigrahi AK, Zíková A, Dalley RA, Acestor N, Ogata Y, Anupama A, Myler PJ, Stuart KD.
EAN89399.1	nitrate reductase, putative (1)	X	N/A. Identification and localization of enzymes of the fumarate reductase and nitrate respiration systems of *Escherichia coli* by crossed immunoelectrophoresis. J Bacteriol. 1983 Feb;153(2):1027-37. van der Plas J, Hellingwerf KJ, Seijen HG, Guest JR, Weiner JH, Konings WN.
	ATP-PROTON MOTIF FORCE INTERCONVERSION	**7**	
EAN86374.1	ATP synthase F1 subunit gamma protein, putative	mitochondrion	Influence of efrapeptin, aurovertin and citreoviridin on the mitochondrial adenosine triphosphatase from *Trypanosoma cruzi.* Mol Biochem Parasitol. 1981 Jul;3(3):143-55. Cataldi de Flombaum MA, Stoppani AO. // Cloning and characterization of the subunits comprising the catalytic core of the *Trypanosoma brucei* mitochondrial ATP synthase. Mol Biochem Parasitol. 2001 Apr 6;113(2):289-301. Brown B SV, Stanislawski A, Perry QL, Williams N.
EAN97136.1	ATP synthase, epsilon chain, putative	mitochondrion	same as previous
EAN81916.1	ATP synthase, alpha chain, mitochondrial precursor, putative	mitochondrion	same as previous
EAN84918.	ATPase alpha subunit, putative (2)	mitochondrion	same as previous
EAN95983.1	ATPase beta subunit, putative	mitochondrion	same as previous
EAN86373.1	vacuolar ATP synthase, putative (1)	acidocalcisome*	Similar to subunit C of the vacuolar H+-ATPase.//Ca2+ content and expression of an acidocalcisomal calcium pump are elevated in intracellular forms of *Trypanosoma cruzi.* Mol Cell Biol. 1998 Apr;18(4):2309-23. Zhong L, Lu HG, Moreno SN, Docampo R.
1EAN91609.1	vacuolar-type proton translocating pyrophosphatase 1, putative	acidocalcisome/CV*	Presence of a plant-like proton-pumping pyrophosphatase in acidocalcisomes of *Trypanosoma cruzi*. J Biol Chem. 1998 Aug 21;273(34):22151-8. Scott DA, de Souza W, Benchimol M, Zhong L, Lu HG, Moreno SN, Docampo R. Cloning and functional expression of a gene encoding a vacuolar-type proton-translocating pyrophosphatase from *Trypanosoma cruzi.* Biochem J. 2000 Oct 1;351(Pt 1):281-8. Hill JE, Scott DA, Luo S, Docampo R.
	GLYCOLISIS/GLYCONEOGENESIS	**9**	
EAN94612.1	hexokinase, putative	glycosome*	Molecular and biochemical characterization of hexokinase from *Trypanosoma cruzi.* Mol Biochem Parasitol. 2003 Feb;126(2):251-62. Cáceres AJ, Portillo R, Acosta H, Rosales D, Quiñones W, Avilan L, Salazar L, Dubourdieu M, Michels PA, Concepción JL.
EAO00202.1	6-phospho-1-fructokinase, putative	glycosome	6-Phosphofructo-2-kinase and fructose-2,6-bisphosphatase in Trypanosomatidae. Molecular characterization, database searches, modelling studies and evolutionary analysis. FEBS J. 2005 Jul;272(14):3542-60. Chevalier N, Bertrand L, Rider MH, Opperdoes FR, Rigden DJ, Michels PA.
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EAN98352.1	glyceraldehyde 3-phosphate dehydrogenase, putative	glycosome	*Trypanosoma cruzi* glycosomal glyceraldehyde-3-phosphate dehydrogenase does not conform to the 'hotspot' topogenic signal model. EMBO J. 1990 Sep;9(9):2751-8. Kendall G, Wilderspin AF, Ashall F, Miles MA, Kelly JM.
EAN99050.1	phosphoglycerate kinase, putative (1)	glycosome/cytoplasm*	The expression and intracellular distribution of phosphoglycerate kinase isoenzymes in *Trypanosoma cruzi.* Mol Biochem Parasitol. 2001 Nov;118(1):111-21. Concepción JL, Adjé CA, Quiñones W, Chevalier N, Dubourdieu M, Michels PA.
EAN91697.1	PAS-domain containing phosphoglycerate kinase, putative (PAS domain could be a miss-assembly) (2)	glycosome/cytoplasm*	same as previous
EAN86096.1	pyruvate phosphate dikinase, putative	glycosome*	Cloning of a pyruvate phosphate dikinase from *Trypanosoma cruzi*. Mol Biochem Parasitol. 2001 Feb;112(2):183-91. Maldonado RA, Fairlamb AH.
EAN88964.1	glycosomal phosphoenolpyruvate carboxykinase, putative	glycosome*	Cloning and characterization of the gene encoding ATP-dependent phospho-enol-pyruvate carboxykinase in *Trypanosoma cruzi:* comparison of primary and predicted secondary structure with host GTP-dependent enzyme. Gene. 1993 Dec 22;136(1-2):69-77. Linss J, Goldenberg S, Urbina JA, Amzel LM.
EAN90616.1	glycosomal malate dehydrogenase, putative	glycosome*	Glycosomal and mitochondrial malate dehydrogenases in epimastigotes of *Trypanosoma cruzi.* Mol Biochem Parasitol. 1984 Apr;11:37-49. Cannata JJ, Cazzulo JJ.
	PYRUVATE DEHYDROGENASE COMPLEX	**5**	
EAN92220.1	pyruvate dehydrogenase E1 component alpha subunit, putative	mitochondrion	A putative pyruvate dehydrogenase alpha subunit gene from *Trypanosoma cruzi.* Biochim Biophys Acta. 1996 Nov 11;1309(1-2):53-7. Buscaglia CA, Pollevick GD, Veloso C, Lorca M, Frasch AC, Sánchez DO.
EAN89795.1	pyruvate dehydrogenase E1 beta subunit, putative	mitochondrion	Same as previous
EAN90443.1	dihydrolipoyl dehydrogenase, putative	mitochondrion	Cloning, sequencing and functional expression of dihydrolipoamide dehydrogenase from the human pathogen *Trypanosoma cruzi*. Eur J Biochem. 1997 Feb 1;243(3):739-47. Schöneck R, Billaut-Mulot O, Numrich P, Ouaissi MA, Krauth-Siegel RL. /// Lipoamide dehydrogenase from *Trypanosoma cruzi:* some properties and cellular localization. Biochem Int. 1991 May;24(1):147-55. Portela MP, Stopopani AO.
EAN93711.1	dihydrolipoamide acetyltransferase precursor, putative	mitochondrion	N/A. Cloning and characterization of the dihydrolipoamide S-acetyltransferase subunit of the plastid pyruvate dehydrogenase complex (E2) from *Arabidopsis.* Plant Physiol. 1999 Jun;120(2):443-52. Mooney BP, Miernyk JA, Randall DD.
EAN81897.1	2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide succinyltransferase	mitochondrion	Dihydrolipoamide dehydrogenase from *Trypanosoma brucei.* Characterization and cellular location.Biochem J. 1987 May 1; 243(3): 661–665. M J Danson, K Conroy, A McQuattie, and K J Stevenson.
	CELL STRUCTURE & MOTILITY		
	CELLULAR ORGANIZATION	**18**	
EAN94839.1	beta tubulin, putative	cytoskeleton/ flagellar and sub-pellicular microtubules*	Tight binding between a pool of the heterodimeric alpha/beta tubulin and a protein kinase CK2 in *Trypanosoma cruzi* epimastigotes. Parasitology. 2006 Apr;132(Pt 4):511-23. De Lima AR, Medina R, Uzcanga GL, Noris Suárez K, Contreras VT, Navarro MC, Arteaga R, Bubis J.// New tubulins in protozoal parasites.Curr Biol. 2000 Apr 6;10(7):R258-9. Vaughan S, Attwood T, Navarro M, Scott V, McKean P, Gull K.
EAN81053.1	alpha tubulin, putative	cytoskeleton/ flagellar and sub-pellicular microtubules*	same as previous /// Acetylated alpha-tubulin in *Trypanosoma cruzi*: immunocytochemical localization. Mem Inst Oswaldo Cruz. 1993 88(4):517-28. Souto-Padron T, Cunha e Silva NL, de Souza W.
EAN85411.1	actin, putative	cytoskeleton*	*Trypanosoma cruzi:* allelic comparisons of the actin genes and analysis of their transcripts. Exp Parasitol. 2003 Jan-Feb;103(1-2):27-34. Cevallos AM, López-Villaseñor I, Espinosa N, Herrera J, Hernández R. *Trypanosoma cruzi:* distribution of fluorescently labeled tubulin and actin in epimastigotes. J Parasitol. 1983 Feb;69(1):138-42. de Souza W, Meza I, Martinez-Palomo A, Sabanero M, Souto-Padrón T, Meirelles MN.
EAN91961.1	actin-like protein, putative (1)	cytoskeleton	Studies on trypanosomatid actin. I. Immunochemical and biochemical identification. J Protozool. 1989 Jan-Feb;36(1):8-13. Mortara RA.
EAN82002.1	cytoskeleton-associated protein CAP5.5, putative	cytoskeleton	CAP5.5, a life-cycle-regulated, cytoskeleton-associated protein is a member of a novel family of calpain-related proteins in *Trypanosoma brucei*. Mol Biochem Parasitol. 2001 Aug;116(1):25-34. Erratum in: Mol Biochem Parasitol 2001 Sep 28;117(1):119. Hertz-Fowler C, Ersfeld K, Gull K.
EAN96878.1	dynein, putative	cytoskeleton/ flagellum	Stuck in reverse: loss of LC1 in Trypanosoma brucei disrupts outer dynein arms and leads to reverse flagellar beat and backward movement. Journal of Cell Science 120, 1513-1520 (2007) Desiree M. Baron, Zakayi P. Kabututu and Kent L.Hill
EAN85813.1	dynein light chain, putative (2)	cytoskeleton/flagellum	same as previous
EAN87401.1	dynein intermediate chain, putative	cytoskeleton/flagellum	same as previous
EAN92318.1	69 kDa paraflagellar rod protein, putative	flagellum*	Evidence for two distinct major protein components, PAR 1 and PAR 2, in the paraflagellar rod of *Trypanosoma cruzi.* Complete nucleotide sequence of PAR.. Beard, C. A,, Sahorio, J. L., Tewari, D., Krieglstein, K. G., Henschen,A. H., andManning, J. E. (1992) J. Biol. Chem. 267,21656-21662 // Evidence for four distinct major protein components in the paraflagellar rod of *Trypanosoma cruzi*. J Biol Chem. 1998 Aug 21;273(34):21846-55. Fouts DL, Stryker GA, Gorski KS, Miller MJ, Nguyen TV, Wrightsman RA, Manning JE.
EAN87979.1	paraflagellar rod protein 3, putative	flagellum*	same as previous
EAN81200.1	paraxonemal rod protein PAR2, putative	flagellum*	same as previous
EAN83974.1	paraflagellar rod component Par4, putative	flagellum*	same as previous
EAN99876.1	paraflagellar rod component, putative	flagellum*	same as previous
EAN85233.1	axoneme central apparatus protein, putative	flagellum	N/A. The Parkin co-regulated gene product, PACRG, is an evolutionarily conserved axonemal protein that functions in outer-doublet microtubule morphogenesis. J Cell Sci. 2005 Dec 1;118(Pt 23):5421-30. Dawe HR, Farr H, Portman N, Shaw MK, Gull K.

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EAN87014.1	kinetoplastid membrane protein KMP-11	flagellum/ flagellar pocket/ cytoskeleton*	Molecular characterization of KMP11 from *Trypanosoma cruzi:* a cytoskeleton-associated protein regulated at the translational level. DNA Cell Biol. 2000 19 (1):47-57. M C Thomas , J L García-Pérez , C Alonso , M C López
EAN91318.1	I/6 autoantigen, putative	cytoskeleton	The *Trypanosoma brucei* autoantigen I/6 is an internally repetitive cytoskeletal protein. Eur J Cell Biol. 1997 Apr;72(4):378-84. Detmer E, Hemphill A, Müller N, Seebeck T.
EAN89775.1	NUP-1 protein, putative (2)	cytoskeleton/ nucleus	Isolation and characterization of subnuclear compartments from *Trypanosoma brucei.* Identification of a major repetitive nuclear lamina component. J Biol Chem. 2001 Oct 12;276(41):38261-71. Rout MP, Field MC.
	CELL ADHESION	**2**	
EAN84330.1	mucin-associated surface protein (MASP), putative (1)	PM	Glycoproteomics of *Trypanosoma cruzi* trypomastigotes using subcellular fractionation, lectin affinity, and stable isotope labeling. J Proteome Res. 2006 Dec;5(12):3376-84. Atwood JA 3rd, Minning T, Ludolf F, Nuccio A, Weatherly DB, Alvarez-Manilla G, Tarleton R, Orlando R.
EAN86366.1	trans-sialidase, putative (1)	PM*	Incorporation of sialic acid into *Trypanosoma cruzi* macromolecules. A proposal for a new metabolic route. Mol Biochem Parasitol. 1985 Jun;16(1):85-96. Previato JO, Andrade AF, Pessolani MC, Mendonça-Previato L.// Functional diversity in the trans-sialidase and mucin families in *Trypanosoma cruzi*. Parasitol Today. 2000 Jul;16(7):282-6. Frasch AC.
	CELL CYCLE AND DIVISION	**5**	
EAN88839.1	prohibitin, putative (1)	mitochondrion	Prohibitin and RACK homologues are up-regulated in trypanosomes induced to undergo apoptosis and in naturally occurring terminally differentiated forms. Cell Death Differ. 1998 Jul;5(7):615-22. Welburn SC, Murphy NB.
EAN86375.1	centromere/microtubule binding protein cbf5, putative	cytoskeleton/ Nucleus, nucleolus	Elucidating the role of H/ACA-like RNAs in trans-splicing and rRNA processing via RNA interference silencing of the *Trypanosoma brucei* CBF5 pseudouridine synthase. J Biol Chem. 2005 Oct 14;280(41):34558-68. Barth S, Hury A, Liang XH, Michaeli S.
EAN87051.1	SPFH domain / Band 7 family protein, putative (1)	X	PF01145: The band 7 protein is an integral membrane protein which is thought to regulate cation conductance. A variety of proteins belong to this family. These include the **prohibitins**, cytoplasmic anti-proliferative proteins and stomatin, an erythrocyte membrane protein. Bacterial HflC protein also belongs to this family. **cd03403: Band_7_stomatin_like //** The SPFH domain-containing proteins: more than lipid raft markers.Trends Cell Biol. 2007 Aug;17(8):394-402. Epub 2007 Sep 4. Review. Browman DT, Hoegg MB, Robbins SM.
EAN91936.1	14-3-3 protein, putative	X	The 14-3-3 proteins of *Trypanosoma brucei* function in motility, cytokinesis, and cell cycle. J Biol Chem. 2005 Apr 8;280(14):14085-96. Inoue M, Nakamura Y, Yasuda K, Yasaka N, Hara T, Schnaufer A, Stuart K, Fukuma T.
EAN99629.1	developmentally regulated GTP-binding protein, putative (1)	cytoplasm / endosomes	Identification of guanine nucleotide binding proteins from *Trypanosoma cruzi.* Biol Res. 1993;26(1 2):177-88. Bubis J, Millan EJ, Martinez R.
	REPLICATION / TRANSCRIPTION		
	REPLICATION / DNA REPAIR / DNA BINDING	**10**	
EAN81533.1	histone H4, putative	nucleus*	Trypanosomatid histones.Mol Microbiol. 2004 Jul;53(2):365-72. Alsford S, Horn D. /// Post-translational modifications of *Trypanosoma cruzi* histone H4. Mol Biochem Parasitol. 2006 Dec;150(2):268-77. da Cunha JP, Nakayasu ES, de Almeida IC, Schenkman S.
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EAN85330.1	histone H2A, putative	nucleus*	Same as previous /// Control mechanisms of the H2A genes expression in *Trypanosoma cruzi*. Mol Biochem Parasitol. 1998 May 1;92(2):313-24. Marañón C, Puerta C, Alonso C, López MC.
EAN84604.1	histone H3, putative	nucleus*	Same as previous /// Genes for histone H3 in *Trypanosoma cruzi.* Mol Biochem Parasitol. 1994 Jul;66(1):147-51. Bontempi EJ, Porcel BM, Henriksson J, Carlsson L, Rydåker M, Segura EL, Ruiz AM, Pettersson U. /// A variant histone H3 is enriched at telomeres in *Trypanosoma brucei*. J Cell Sci. 2004 Nov 15;117(Pt 24):5937-47. Lowell JE, Cross GA.
EAN85210.1	kinetoplast DNA-associated protein, putative (2)	kinetoplast*	Stage specific kinetoplast DNA-binding proteins in *Trypanosoma cruzi*. Acta Trop. 2000 Sep 18;76(2):139-46. Zavala-Castro JE, Acosta-Viana K, Guzmán-Marín E, Rosado-Barrera ME, Rosales-Encina JL. /// Kinetoplast DNA-binding protein profile in the epimastigote form of *Trypanosoma cruzi.* Arch Med Res. 2002 May-Jun;33(3):250-6. Zavala-Castro JE, Acosta-Viana K, Baylon-Pacheco L, González-Robles A, Guzmán-Marín E, Rosales-Encina JL.
EAN91887.1	mitochondrial DNA polymerase beta, putative	mitochondrion	In situ hybridization to the *Crithidia fasciculata* kinetoplast reveals two antipodal sites involved in kinetoplast DNA replication. Cell 70:621-629 , 1992. Ferguson, M., Torri, A.F., Ward, D.C., and Englund, P.T. /// *Trypanosoma brucei* has two distinct mitochondrial DNA polymerase enzymes. Biol. Chem., Vol. 278, Issue 49, 49095-49101, 2003 Tina T. Saxowsky, Gunjan Choudhary, Michele M. Klingbeil, and Paul T. EnglundJ.
EAN91964.1	mitochondrial DNA topoisomerase II, putative (1)	mitochondrion	Localization of a type II DNA topoisomerase to two sites at the periphery of the kinetoplast DNA of *Crithidia fasciculata.* Cell 55:1083-1088, 1988.Melendy, T., Sheline, C., and Ray, D.S.
EAN94547.1	RuvB-like DNA helicase, putative (1)	nucleus	N/A. The RuvABC resolvasome. Eur J Biochem. 2002 Nov;269(22):5492-501. Dickman MJ, Ingleston SM, Sedelnikova SE, Rafferty JB, Lloyd RG, Grasby JA, Hornby DP.
EAN90819.1	DNA topoisomerase IA, putative (1)	nucleus*	A type I DNA topoisomerase from *Trypanosoma cruzi.* Eur J Biochem. 1983 Aug 15;134(3):479-84. Riou GF, Gabillot M, Douc-Rasy S, Kayser A, Barrois M. /// Purification and nuclear localization of a type I topoisomerase from *Crithidia fasciculata*. Mol Biochem Parasitol. 1987 Jun;24(2):215-25. Melendy T, Ray DS.
EAN84364.1	nucleosome assembly protein-like protein, putative	nucleus	N/A /// The compaction pattern of the chromatin of trypanosomes. Biol Cell. 1985;53(3):199-208. Hecker H, Gander ES.
	TRANSCRIPTION /RNA PROCESSING/ RNA BINDING	**11**	
EAN92280.1	ATP-dependent DEAD/H RNA helicase, putative	nucleus / cytoplasm	DEAD-box protein HEL64 from *Trypanosoma brucei*: subcellular localization and gene knockout analysis. Parasitol Res. 1999 85(4):324-30. Missel A, Lambert L, Nörskau G, Göringer HU. /// An unusual Dicer-like1 protein fuels the RNA interference pathway in *Trypanosoma brucei*. RNA. 2006 Dec;12(12):2063-72. Shi H, Tschudi C, Ullu E.
EAN99758.1	poly(A)-binding protein, putative	cytoplasm / nucleus	Poly(A)-binding protein I of *Leishmania*: functional analysis and localisation in trypanosomatid parasites. Nucleic Acids Res. 2000 Mar 1;28(5):1211-20. Bates EJ, Knuepfer E, Smith DF.
EAN86151.1	RNA helicase, putative	X	*Trypanosoma brucei* mitochondria contain RNA helicase activity.Nucleic Acids Res. 1994 Oct 11;22(20):4050-6. Missel A, Göringer HU. /// Purification of a functional enzymatic editing complex from *Trypanosoma brucei* mitochondria. EMBO J. 1997 Jul 1;16(13):4069-81. Rusché LN, Cruz-Reyes J, Piller KJ, Sollner-Webb B.
EAN92507.1	fibrillarin, putative (1)	nucleus	RNA B is the major nucleolar trimethylguanosine-capped small nuclear RNA associated with fibrillarin and pre-rRNAs in *Trypanosoma brucei.* Mol Cell Biol. 1993 Jan;13(1):144-54. Hartshorne T, Agabian N. /// Fibrillarin-associated box C/D small nucleolar RNAs in *Trypanosoma brucei*. Sequence conservation and implications for 2'-O-ribose methylation of rRNA.J Biol Chem. 2000 May 12;275(19):14767-76. Dunbar DA, Wormsley S, Lowe TM, Baserga SJ.
EAN96121.1	RNA-binding protein, putative	nucleus / cytoplasm	No specific reference. /// In vivo UV-cross-linking hybridization: a powerful technique for isolating RNA binding proteins. Application to trypanosome mini-exon derived RNA. Nucleic Acids Res. 1993 May 25;21(10):2453-8. Pellé R, Murphy NB.
EAN86592.1	nucleolar RNA-binding protein, putative (2)	nucleus	N/A /// A major tyrosine-phosphorylated protein of *Trypanosoma brucei* is a nucleolar RNA-binding protein.J Biol Chem. 1996 Jun 28;271(26):15675-81. Das A, Peterson GC, Kanner SB, Frevert U, Parsons M. /// Developmental regulation of two nuclear RNA binding proteins, p34 and p37, from *Trypanosoma brucei.*Mol Biochem Parasitol. 1998 Apr 1;92(1):79-88. Zhang J, Ruyechan W, Williams N.
EAN90081.1	ATP-dependent RNA helicase, putative	X	N/A /// Only 32 % homology to EAN92281.1 /// *Trypanosoma brucei* mitochondria contain RNA helicase activity.Nucleic Acids Res. 1994 Oct 11;22(20):4050-6. Missel A, Göringer HU.
EAN98394.1	p22 protein precursor, putative	mitochondrion	The trypanosome homolog of human p32 interacts with RBP16 and stimulates its gRNA binding activity. Nucleic Acids Res. 2001 Dec 15;29(24):5216-25. Hayman ML, Miller MM, Chandler DM, Goulah CC, Read LK. /// UniProtKB/Swiss-Prot entry P61023 Calcium-binding protein p22

EAN91849.1	small nuclear ribonucleoprotein Sm-F, putative (1)	nucleus	The spliceosomal snRNP core complex of *Trypanosoma brucei:* cloning and functional analysis reveals seven Sm protein constituents. Proc Natl Acad Sci U S A. 2000 Aug 1;97(16):8967-72.Palfi Z, Lücke S, Lahm HW, Lane WS, Kruft V, Bragado-Nilsson E, Séraphin B, Bindereif A. /// Sm core variation in spliceosomal small nuclear ribonucleoproteins from *Trypanosoma brucei*.EMBO J. 2006 Oct 4;25(19):4513-23. Wang P, Palfi Z, Preusser C, Lücke S, Lane WS, Kambach C, Bindereif A.
EAN81851.1	nucleolar protein, putative	nucleus	N/A /// Characterization and differential nuclear localization of Nopp140 and a novel Nopp140-like protein in trypanosomes. Eukaryot Cell. 2006 May;5(5):876-9. Kelly S, Singleton W, Wickstead B, Ersfeld K, Gull K.
EAN85671.1	ribonucleoprotein p18, mitochondrial precursor, putative	mitochondrion	Characterization of two nuclear-encoded protein components of mitochondrial ribonucleoprotein complexes from *Leishmania tarentolae*. Mol Biochem Parasitol. 1995 Apr;71(1):65-79. Bringaud F, Peris M, Zen KH, Simpson L.
	PROTEIN SYNTHESIS		
	TRANSLATION	**44**	
EAN98366.1	40S ribosomal protein S15a, putative	cytoplasm / rough ER	Molecular Biology of the Cell. Third edition. Alberts et al. /// Isolation and characterization of polysomes from *Trypanosoma brucei*. Parasitology. 1980 Dec;81(Pt 3):537-51. Cordingley JS, Turner MJ. /// Species specificity in ribosome biogenesis: a nonconserved phosphoprotein is required for formation of the large ribosomal subunit in *Trypanosoma brucei*. Eukaryot Cell. 2005 Jan;4(1):30-5. Jensen BC, Brekken DL, Randall AC, Kifer CT, Parsons M.
EAN83566.1	60S ribosomal protein l36, putative	"	N/A
EAN81492.1	40S ribosomal protein S14, putative	"	N/A
EAN85291.1	ribosomal protein S26, putative	"	N/A
EAN89722.1	60S ribosomal protein L34, putative	"	N/A
EAN99789.1	60S ribosomal protein L23, putative	"	N/A
EAN82862.1	ribosomal protein L24, putative	"	Cloning and characterisation of cDNA encoding the *Trypanosoma brucei* ribosomal protein L24. Int J Parasitol. 1999 Apr;29(4):601-5. Read LK, Militello KT, Nerantzakis GE.
EAN89019.1	40S ribosomal protein S16, putative	"	N/A
EAN84418.1	60S ribosomal protein L13a, putative	"	N/A
EAN90899.1	ribosomal protein L21E (60S), putative	"	N/A
EAN83023.1	60S ribosomal protein L17, putative	"	N/A
EAN92891.1	40S ribosomal protein S17, putative	"	N/A
EAN88197.1	ribosomal protein S19, putative	"	N/A
EAN81803.1	60S ribosomal protein L11, putative	"	N/A
EAN89208.1	60S ribosomal protein L35, putative	"	N/A
EAN99961.1	ribosomal protein L35A, putative	"	N/A
EAN87953.1	ribosomal protein L27, putative	"	Analysis of the 60 S ribosomal protein L27a (L29) gene of *Trypanosoma brucei*. Int J Parasitol. 1999 May;29(5):731-6. Brown SV, Williams N.
EAN98360.1	60S ribosomal protein L28, putative	"	N/A
EAN98186.1	40S ribosomal protein S18, putative	"	The cloning and sequencing of ribosomal protein S18 of parasitic protozoa, *Entamoeba histolytica.*DNA Seq. 1998 Mar;8(4):267-70. Tanaka T, Tanaka M, Mitsui Y.
EAN81251.1	40S ribosomal protein S8, putative	"	N/A
EAN86269.1	60S ribosomal protein L19, putative	"	N/A
EAO00224.1	60S ribosomal protein L13, putative	"	N/A
EAN82879.1	40S ribosomal protein S11, putative	"	N/A
EAN82694.1	40S ribosomal protein S13, putative (1)	"	N/A
EAN82805.1	40S ribosomal protein L14, putative	"	N/A
EAN87517.1	40S ribosomal protein S9, putative	"	N/A
EAN97975.1	60S ribosomal protein L18, putative	"	The cloning and sequencing of a ribosomal L18 protein from an evolutionary divergent eukaryote, *Trypanosoma brucei.* Biochim Biophys Acta. 1996 Nov 11;1309(1-2):69-72. Coulter LJ, Hide G.
EAN86177.1	60S ribosomal subunit protein L31, putative	"	N/A
EAN83877.1	ribosomal protein S7, putative	"	N/A
EAN93193.1	60S ribosomal protein L18a, putative	"	N/A
EAN84470.1	60S ribosomal protein L26, putative	"	N/A
EAN87845.1	40S ribosomal protein S4, putative	"*	The deduced primary structure of a ribosomal protein S4 from *Trypanosoma cruzi.* Biochim Biophys Acta. 1998 Feb 11;1395(3):321-5. Hernández R, Palacios S, Herrera J, Martínez-Calvillo S, López I.
EAN99433.1	60S ribosomal protein L7a, putative	"	N/A
EAN95595.1	40S ribosomal protein S6, putative	"	N/A
EAN87804.1	60S ribosomal protein L2, putative	"	N/A
EAN94248.1	60S ribosomal protein L7, putative	"	N/A
EAN83495.1	40S ribosomal protein S3a, putative	"	N/A
EAN83816.1	60S ribosomal protein L5, putative	"	N/A
EAN88665.1	60S ribosomal protein L10, putative	"	N/A
EAN83925.1	40S ribosomal protein S2, putative	"	N/A
EAN82415.1	40S ribosomal protein SA, putative	"	N/A
EAN82665.1	60S ribosomal protein L4, putative	"	N/A
EAN92822.1	ribosomal protein L3, putative	"	N/A
EAN94487.1	50S ribosomal protein L17, putative (1)	"	N/A
	TRANSLATION FACTORS	**14**	
EAN82857.1	elongation factor 1-alpha (EF-1-alpha), putative	cytoplasm, nucleus*	*Trypanosoma cruzi* elongation factor 1-alpha: nuclear localization in parasites undergoing apoptosis. Gene. 1996 Sep 26;174(1):19-26. Billaut-Mulot O, Fernandez-Gomez R, Loyens M, Ouaissi A.
EAN85113.1	elongation factor 1-gamma (EF-1-gamma), putative	cytoplasm	Molecular and immunological characterization of a *Trypanosoma cruzi* protein homologous to mammalian elongation factor 1 gamma. Biol Cell. 1994;82(1):39-44. Billaut-Mulot O, Schöneck R, Fernandez-Gomez R, Taibi A, Capron A, Pommier V, Plumas-Marty B, Loyens M, Ouaissi A. /// Phenotype of recombinant *Trypanosoma cruzi* which overexpress elongation factor 1-gamma: possible involvement of EF-1gamma GST-like domain in the resistance to clomipramine. Gene. 1997 Oct 1;198(1-2):259-67. Billaut-Mulot O, Fernandez-Gomez R, Ouaissi A.
EAN87190.1	elongation factor 2, putative	cytoplasm	N/A. Part of the translation complex in eukaryotes /// Phylogenetic position of kinetoplastid protozoa inferred from the protein phylogenies of elongation factors 1alpha and 2. J Biochem. 1996 Jan;119(1):70-9.Nakamura Y, Hashimoto T, Kamaishi T, Adachi J, Nakamura F, Okamoto K, Hasegawa M.
EAO00026.1	elongation factor TU, putative	cytoplasm	N/A /// Identification of the elongation factor Tu binding site on 70S E. coli ribosomes by chemical crosslinking. Indian J Biochem Biophys. 1995 Dec;32(6):343-50.Nag B, Johnson AE, Traut RR.
EAO00256.1	elongation initiation factor 2 alpha subunit, putative	cytoplasm	N/A /// Mechanism of polypeptide chain initiation in eukaryotes and its control by phosphorylation of the alpha subunit of initiation factor 2.Proc Natl Acad Sci U S A. 1982 Apr;79(8):2537-40. Siekierka J, Mauser L, Ochoa S.
EAN82455.1	25 kDa translation elongation factor 1-beta	cytoplasm	*Leishmania major* elongation factor 1B complex has trypanothione S-transferase and peroxidase activity. J Biol Chem. 2004 Nov 19;279(47):49003-9. Vickers TJ, Wyllie S, Fairlamb AH. /// The cloning and characterization of *Tetrahymena pyriformi*s translation elongation factor 1b alpha and gamma subunits. Cell Mol Biol Lett. 2005;10(4):689-96. Jonusiene V, Sasnauskiene S, Juodka B.
EAN96820.1	translation elongation factor 1-beta, putative	cytoplasm	Difference at the N-terminal with previous one. /// *Leishmania major* elongation factor 1B complex has trypanothione S-transferase and peroxidase activity. J Biol Chem. 2004 Nov 19;279(47):49003-9Vickers TJ, Wyllie S, Fairlamb AH.
EAN98272.1	eukaryotic initiation factor 4a, putative	cytoplasm	The two eIF4A helicases in *Trypanosoma brucei* are functionally distinct. Nucleic Acids Res. 2006 May 10;34(9):2495-507. Dhalia R, Marinsek N, Reis CR, Katz R, Muniz JR, Standart N, Carrington M, de Melo Neto OP.
EAN83191.1	eukaryotic translation initiation factor 5, putative (1)	cytoplasm	Not found in trypanosomatids /// Interactions of eukaryotic translation initiation factor 3 (eIF3) subunit NIP1/c with eIF1 and eIF5 promote preinitiation complex assembly and regulate start codon selection. Mol Cell Biol. 2004 Nov;24(21):9437-55. Valásek L, Nielsen KH, Zhang F, Fekete CA, Hinnebusch AG.
EAN87305.1	eukaryotic translation initiation factor 3 subunit, putative (1)	cytoplasm	N/A /// Interactions of eukaryotic translation initiation factor 3 (eIF3) subunit NIP1/c with eIF1 and eIF5 promote preinitiation complex assembly and regulate start codon selection.Mol Cell Biol. 2004 Nov;24(21):9437-55. Valásek L, Nielsen KH, Zhang F, Fekete CA, Hinnebusch AG.
EAN88449.1	eukaryotic translation initiation factor, putative (1)	cytoplasm	N/A

EAN94343.1	eukaryotic peptide chain release factor subunit 1, putative (1)	cytoplasm	N/A. Recycling of eukaryotic posttermination ribosomal complexes.Cell. 2007 Oct 19;131(2):286-99. Pisarev AV, Hellen CU, Pestova TV.
EAN85172.1	eukaryotic translation initiation factor 3 (eIF-3) interacting protein, putative (1)	cytoplasm	Same as previous.
EAN82311.1	eukaryotic translation initiation factor 2 subunit, putative (2)	cytoplasm	N/A. No similarity found to EAO00256.1 /// Ribosomal localization of translation initiation factor IF2. RNA. 2003 Aug;9(8):958-69. Marzi S, Knight W, Brandi L, Caserta E, Soboleva N, Hill WE, Gualerzi CO, Lodmell JS.
	PROTEIN DESTINATION		
	PROTEIN MODIFICATION	**2**	
EAN85170.1	dolichyl-phosphate beta-D-mannosyltransferase precursor, putative (2)	ER	Possible localisation of dolichol-dependent mannosyltransferase of *Trypanosoma brucei* to the rough endoplasmic reticulum. Mol Biochem Parasitol. 1994 Feb;63(2):255-64. Prado-Figueroa M, Raper J, Opperdoes FR. /// Cloning and functional expression of glycosyltransferases from parasitic protozoans by heterologous complementation in yeast: the dolichol phosphate mannose synthase from *Trypanosoma brucei brucei*. Biochem J. 1996 Jun 15;316 (Pt 3):853-8. Mazhari-Tabrizi R, Eckert V, Blank M, Müller R, Mumberg D, Funk M, Schwarz RT.
EAN85727.1	peptidylprolyl isomerase-like, putative (2)	X	The *Trypanosoma cruzi* PIN1 gene encodes a parvulin peptidyl-prolyl cis/trans isomerase able to replace the essential ESS1 in Saccharomyces cerevisiae. Mol Biochem Parasitol. 2007 Jun;153(2):186-93. Erben ED, Daum S, Tellez-Inon MT.
	PROTEIN FOLDING AND STABILIZATION	**17**	
EAO00223.1	Heat shock protein 20, putative	Several compartments	N/A. Chloroplasts have a novel Cpn10 in addition to Cpn20 as co-chaperonins in *Arabidopsis thaliana*. J Biol Chem. 2001 Aug 10;276(32):29688-94. Koumoto Y, Shimada T, Kondo M, Hara-Nishimura I, Nishimura M.
EAN83852.1	heat shock 70 kDa protein, putative	cytoplasm	Heat shock proteins in *Trypanosoma cruzi*: identification and localization of HSP70 and HSP60 proteins and structure of HSP60 genes (brief report). Biol Res. 1993;26(1-2):313-4. de Marval MG, Souto-Padron T, Gottesdiener K, Silva R, van der Ploeg LH, Rondinelli E.
EAN87418.1	heat shock protein-like protein, putative (1)	Several compartments	N/A
EAN82629.1	heat shock protein 85, putative	Several compartments	Heat-shock disruption of *trans*-splicing in trypanosomes: effect on Hsp70, Hsp85 and tubulin mRNA synthesis.Gene. 1989 Oct 15;82(1):169-75 Muhich ML, Hsu MP, Boothroyd JC.Heat-shock
EAN84370.1	heat shock 70 kDa protein, mitochondrial precursor, putative	kinetoplast	Expression and localization of *Trypanosoma cruzi* hsp60. Mol Biochem Parasitol. 1994 Dec;68(2):197-208. Sullivan MA, Olson CL, Winquist AG, Engman DM.
EAN81877.1	ATP-dependent Clp protease subunit, heat shock protein 100 (HSP100)	X	N/A. Conservation of the regulatory subunit for the Clp ATP-dependent protease in prokaryotes and eukaryotes. Proc Natl Acad Sci U S A. 1990 May;87(9):3513-7. Gottesman S, Squires C, Pichersky E, Carrington M, Hobbs M, Mattick JS, Dalrymple B, Kuramitsu H, Shiroza T, Foster T, et al.
EAN85850.1	10 kDa heat shock protein, putative	mitochondrion	Stage-specific expression of the mitochondrial co-chaperonin of *Leishmania donovani*, CPN10. Kinetoplastid Biol Dis. 2005 Apr 29;4(1):3. Zamora-Veyl FB, Kroemer M, Zander D, Clos J.
EAN87966.1	glucose-regulated protein 78, putative (BiP)	ER	Molecular cloning and characterization of the 78-kilodalton glucose-regulated protein of *Trypanosoma cruzi*. Infect Immun. 1994 Jun;62(6):2499-507. Tibbetts RS, Kim IY, Olson CL, Barthel LM, Sullivan MA, Winquist AG, Miller SD, Engman DM.
EAN97655.1	chaperonin HSP60, mitochondrial precursor	mitocondrion	Expression and localization of *Trypanosoma cruz*i hsp60. Mol Biochem Parasitol. 1994 Dec;68(2):197-208. Sullivan MA, Olson CL, Winquist AG, Engman DM.
EAN96800.1	lipophosphoglycan biosynthetic protein, putative (HSP90)	cytoplasm/ ER	Stage-specific expression of the mitochondrial co-chaperonin of *Leishmania donovani*, CPN10. Kinetoplastid Biol Dis. 2005 Apr 29;4(1):3. Zamora-Veyl FB, Kroemer M, Zander D, Clos J.
EAN91216.1	protein disulfide isomerase, putative	ER	Characterization of two protein disulfide isomerases from the endocytic pathway of bloodstream forms of *Trypanosoma brucei*. J Biol Chem. 2005 Mar 18;280(11):10410-8. Rubotham J, Woods K, Garcia-Salcedo JA, Pays E, Nolan DP.
EAN97592.1	chaperone DnaJ protein, putative (HSP 40) (1)	mitochondrion	The DnaJ family of protein chaperones in *Trypanosoma cruzi.* Mol Biochem Parasitol. 1998 Mar 15;91(2):319-26. Tibbetts RS, Jensen JL, Olson CL, Wang FD, Engman DM.
EAN82340.1	calreticulin, putative	ER*	The Interplay between folding facilitating mechanisms in *Trypanosoma cruzi* endoplasmic reticulum. Mol. Biol. Cell 2003 September 14, 3529–40, 2003. Conte I, Labriola C, Cazzulo JJ, Docampo R, Parodi AJ.
EAN90740.1	vacuolar transporter chaperone, putative (1)	acidocalcisoma	Ablation of a small transmembrane protein of *Trypanosoma brucei* (TbVTC1) involved in the synthesis of polyphosphate alters acidocalcisome biogenesis and function, and leads to a cytokinesis defect. Biochem J. 2007 Oct 15;407(2):161-70. Fang J, Rohloff P, Miranda K, Docampo R.
EAN86005.1	chaperonin alpha subunit, putative (HSP60 family)	mitochondrion/ other compartments	N/A. General to HSP60 family.
EAN81815.1	co-chaperone GrpE, putative	mitochondrion	N/A. GrpE N-terminal domain contributes to the interaction with Dnak and modulates the dynamics of the chaperone substrate binding domain.J Mol Biol. 2007 Dec 7;374(4):1054-64. Moro F, Taneva SG, Velázquez-Campoy A, Muga A.
EAN89640.1	Hsc70-interacting protein (Hip), putative	cytoplasm/ nucleus	Stage-specific expression of the mitochondrial co-chaperonin of *Leishmania donovani*, CPN10. Kinetoplastid Biol Dis. 2005 Apr 29;4(1):3. Zamora-Veyl FB, Kroemer M, Zander D, Clos J.
	PROTEOLISIS	**12**	
EAN82317.1	gamma glutamyl carboxypeptidase, putative	X	N/A. Gamma-glutamyl hydrolase conjugase. Purification and properties of the bovine hepatic enzyme. J Biol Chem. 1975 Aug 10;250(15):5982-94. Silink M, Reddel R, Bethel M, Rowe PB.
EAN92417.1	signal peptidase type I, putative (1)	X	N/A /// The role of the membrane-spanning domain of type I signal peptidases in substrate cleavage site selection. J Biol Chem. 2000 Dec 8;275(49):38813-22. Carlos JL, Paetzel M, Brubaker G, Karla A, Ashwell CM, Lively MO, Cao G, Bullinger P, Dalbey RE.
EAN81757.1	mitochondrial processing peptidase, beta subunit, putative	mitochondrion	N/A. /// Isolation, characterization, and expression of the gene encoding the beta subunit of the mitochondrial processing peptidase from *Blastocladiella emersonii.* J Bacteriol. 1998 Aug;180(15):3967-72. Costa Rocha CR, Lopes Gomes S.
EAN97586.1	mitochondrial processing peptidase alpha subunit, putative	mitochondrion	N/A. Role of alpha-subunit of mitochondrial processing peptidase in substrate recognition. J Biol Chem. 1998 Sep 25;273(39):25158-63. Shimokata K, Kitada S, Ogishima T, Ito A.
EAN87580.1	cytosolic leucyl aminopeptidase, putative (1)	cytoplasm	N/A /// Biochemical characterization and structural prediction of a novel cytosolic leucyl aminopeptidase of the M17 family from *Schizosaccharomyces pombe*. FEBS J. 2007 Dec;274(23):6228-6240. Herrera-Camacho I, Rosas-Murrieta NH, Rojo-Domínguez A, Millán L, Reyes-Leyva J, Santos-López G, Suárez-Rendueles P.
EAN83138.1	calpain cysteine peptidase, putative	reservosome, PM*	Subcellular localization of a cysteine proteinase from *Trypanosoma cruzi*.Mol Biochem Parasitol. 1989 Feb;33(1):43-7. Bontempi E, Martinez J, Cazzulo JJ. /// Cysteine proteinase in *Trypanosoma cruzi:* immunocytochemical localization and involvement in parasite-host cell interaction.J Cell Sci. 1990 Jul;96 (Pt 3):485-90. Souto-Padrón T, Campetella OE, Cazzulo JJ, de Souza W.
EAN97980.1	mitochondrial intermediate peptidase, putative (1)	mitochondrion	N/A
EAN81557.1	serine carboxypeptidase (CBP1), putative	reservosome*	Characterization of a lysosomal serine carboxypeptidase from *Trypanosoma cruzi.* Mol Biochem Parasitol. 2003 Sep;131(1):11-23. Parussini F, García M, Mucci J, Agüero F, Sánchez D, Hellman U, Aslund L, Cazzulo JJ.
EAN90035.1	proteasome regulatory non-ATPase subunit 5, putative (2)	cytoplasm	Functional characterization of the 11 non-ATPase subunit proteins in the trypanosome 19 S proteasomal regulatory complex. J Biol Chem. 2002 Nov 8;277(45):42686-93. Li Z, Wang CC.
EAN83379.1	proteasome regulatory non-ATPase subunit, putative	cytoplasm	Same as previous.
EAN88322.1	hslvu complex proteolytic subunit-like, putative	mitochondrion	N/A. Eubacterial HslV and HslU subunits homologs in primordial eukaryotes. Mol Biol Evol. 2002 Dec;19(12):2110-7. Couvreur B, Wattiez R, Bollen A, Falmagne P, Le Ray D, Dujardin JC.
EAN97374.1	CAAX prenyl protease 1, putative (1)	ER	C-terminal proteolysis of prenylated proteins in trypanosomatids and RNA interference of enzymes required for the post-translational processing pathway of farnesylated proteins. Mol Biochem Parasitol. 2007 Jun;153(2):115-24. Gillespie JR, Yokoyama K, Lu K, Eastman RT, Bollinger JG, Van Voorhis WC, Gelb MH, Buckner FS.
	TRANSPORT PROTEINS - INTRACELLULAR TRAFFIC	**24**	
EAN95492.1	vacuolar-type Ca2+-ATPase, putative (1)	acidocalcisoma*	Ca2+ content and expression of an acidocalcisomal calcium pump are elevated in intracellular forms of Trypanosoma cruzi. Mol Cell Biol. 1998 Apr;18(4):2309-23. Lu HG, Zhong L, de Souza W, Benchimol M, Moreno S, Docampo R.
EAN92377.1	calcium-translocating P-type ATPase, putative (1)	PM*	Characterization of the plasma-membrane calcium pump from *Trypanosoma cruzi*. Biochem J. 1995 Feb 15;306 (Pt 1):299-303. Benaim G, Moreno SN, Hutchinson G, Cervino V, Hermoso T, Romero PJ, Ruiz F, de Souza W, Docampo R.
EAN81982.1	plasma-membrane proton-efflux P-type ATPase, putative	PM*	*Trypanosoma cruzi* H+-ATPase 1 (TcHA1) and 2 (TcHA2) genes complement yeast mutants defective in H+ pumps and encode plasma membrane P-type H+-ATPases with different enzymatic properties.J Biol Chem. 2002 Nov 15;277(46):44497-506. Luo S, Scott DA, Docampo R.
EAN89594.1	metal-ion transporter, putative (1)	acidocalcisoma*	N/A. /// Its localization to the acidocalcisome was studied in this work. See paper section 3.6.2

EAN89428.1	mitochondrial carrier protein, putative (1)	mitochondrion	Characterization and developmentally regulated localization of the mitochondrial carrier protein homologue MCP6 from *Trypanosoma brucei*. Eukaryot Cell. 2006 Aug;5(8):1194-205. Colasante C, Alibu VP, Kirchberger S, Tjaden J, Clayton C, Voncken F.
EAN84262.1	tricarboxylate carrier, putative (1)	mitochondrion	N/A. Identification of the substrate binding sites within the yeast mitochondrial citrate transport protein. J Biol Chem. 2007 Jun 8;282(23):17210-20. Ma C, Remani S, Sun J, Kotaria R, Mayor JA, Walters DE, Kaplan RS.
EAN92689.1	mitochondrial phosphate transporter, putative	mitochondrion	N/A
EAN86158.1	hexose transporter, putative	PM*	Characterization of glucose transport and cloning of a hexose transporter gene in *Trypanosoma cruzi*. Proc Natl Acad Sci U S A. 1994 Aug 16;91(17):8278-82. Tetaud E, Bringaud F, Chabas S, Barrett MP, Baltz T. /// Kinetoplastid glucose transporters. Biochem J. 1997 Aug 1;325 (Pt 3):569-80. Tetaud E, Barrett MP, Bringaud F, Baltz T.
EAN90182.1	intraflagellar transport protein component, putative (1)	flagellum	Intraflagellar transport and functional analysis of genes required for flagellum formation in trypanosomes. Mol Biol Cell. 2007 Dec 19 2007. Absalon S, Blisnick T, Kohl L, Toutirais G, Doré G, Julkowska D, Tavenet A, Bastin P.
EAN83814.1	COP-coated vesicle membrane protein gp25L precursor, putative (1)	cytoplasm	The coatomer of *Trypanosoma brucei.* Mol Biochem Parasitol. 2001 Jun;115(1):55-61. Maier AG, Webb H, Ding M, Bremser M, Carrington M, Clayton C.
EAN82747.1	Gim5A protein, putative	glycosome	An essential dimeric membrane protein of trypanosome glycosomes. Mol Microbiol. 2001 Mar;39(6):1443-51. Maier A, Lorenz P, Voncken F, Clayton C.
EAN90413.1	ADP,ATP carrier protein 1, mitochondrial precursor, putative	mitochondrion	Reactions involved in energy transfer in trypanosomes-I. Characterization of the mitochondrial adenine nucleotide translocator and the ATPase of *Crithidia luciliae*.Comp Biochem Physiol B. **1976**;54(1):7-12. Opperdoes FR, Rijke DD, Borst P. /// Characterization and developmentally regulated localization of the mitochondrial carrier protein homologue MCP6 from *Trypanosoma brucei*. Eukaryot Cell. 2006 Aug;5(8):1194-205. Colasante C, Alibu VP, Kirchberger S, Tjaden J, Clayton C, Voncken F.
EAN99009.1	peroxin-2, putative (1)	glycosome	Functional identification of a *Leishmania* gene related to the peroxin 2 gene reveals common ancestry of glycosomes and peroxisomes. Mol Cell Biol. 1997 Mar;17(3):1093-101. Flaspohler JA, Rickoll WL, Beverley SM, Parsons M.
EAN81944.1	lysosomal/endosomal membrane protein p67, putative (1)	lysosome	Molecular cloning of p67, a lysosomal membrane glycoprotein from *Trypanosoma brucei*. Mol Biochem Parasitol. 1999 Jan 5;98(1):17-28. Kelley RJ, Alexander DL, Cowan C, Balber AE, Bangs JD.
EAN97573.1	vacuolar protein sorting-associated protein 35, putative (2)	cytoplasm	*Trypanosoma brucei* vacuolar protein sorting 41 (VPS41) is required for intracellular iron utilization and maintenance of normal cellular morphology. Parasitology. 2007 Oct;134(Pt 11):1639-47. Lu S, Suzuki T, Iizuka N, Ohshima S, Yabu Y, Suzuki M, Wen L, Ohta N.
EAN98377.1	importin alpha, putative (2)	nucleus	Novel and essential subunits in the 300-kilodalton nuclear cap binding complex of *Trypanosoma brucei*. Mol Cell Biol. 2005 Mar;25(6):2216-26. Li H, Tschudi C.
EAN85542.1	COP-coated vesicle membrane protein p24 precursor, putative	cytoplasm	The coatomer of *Trypanosoma brucei.* Mol Biochem Parasitol. 2001 Jun;115(1):55-61. Maier AG, Webb H, Ding M, Bremser M, Carrington M, Clayton C.
EAN96914.1	mitochondrial import inner membrane translocase subunit Tim17, putative (1)	mitochondrion	The direct route: a simplified pathway for protein import into the mitochondrion of trypanosomes. Trends Cell Biol. 2008 Jan;18(1):12-8. Schneider A, Bursać D, Lithgow T.
EAN87271.1	glycosomal membrane protein, putative	glycosome	Identification of two integral glycosomal membrane proteins in *Trypanosoma brucei.* Mol Biochem Parasitol. 1987 Aug;25(1):83-92. Aman RA, Wang CC.
EAN98357.1	pretranslocation protein, alpha subunit, putative (1)	cytoplasm/ ER	N/A. Kinetic determination of the effects of ADP-ribosylation on the interaction of eukaryotic elongation factor 2 with ribosomes. J Biol Chem. 1990 Apr 15;265(11):6030-4. Nygård O, Nilsson L.
EAN92899.1	coatomer gamma subunit, putative (1)	cytoplasm	Binding of coatomer by the PEX11 C-terminus is not required for function. FEBS Lett. 2000 Nov 3;484(2):82-6. Maier AG, Schulreich S, Bremser M, Clayton C
EAN82577.1	ADP-ribosylation factor 1, putative (1)	cytoplasm	TcArf1: a *Trypanosoma cruzi* ADP-ribosylation factor. Parasitol Res. 2003 Sep;91(2):166-70. de Sá-Freire A, Nepomuceno-Silva JL, da Paixão JC, de Mendonça SM, de Melo LD, Lopes UG.
EAN81438.1	ADP-ribosylation factor, putative (ER to Golgi)	cytoplasm	same as previous.
EAN99332.1	RAB GDP dissociation inhibitor alpha, putative (2)	cytoplasm	A bioinformatic analysis of the RAB genes of *Trypanosoma brucei*. Mol Biochem Parasitol. 2005 May;141(1):89-97. Ackers JP, Dhir V, Field MC.
	SIGNAL TRANSDUCTION	**11**	
EAN82497.1	casein kinase, putative (2)	Several compartments	Two casein kinase 1 isoforms are differentially expressed in *Trypanosoma cruzi.* Mol Biochem Parasitol. 2002 Sep-Oct;124(1-2):23-36. Spadafora C, Repetto Y, Torres C, Pino L, Robello C, Morello A, Gamarro F, Castanys S. /// Protein kinase CK1 from *Trypanosoma cruzi.* J Protein Chem. 2003 Aug;22(6):591-9. Calabokis M, Kurz L, Gonzatti MI, Bubis J.
EAN83372.1	casein kinase II, alpha chain, putative (1)	nucleus	Molecular cloning of *Trypanosoma brucei* CK2 catalytic subunits: the alpha isoform is nucleolar and phosphorylates the nucleolar protein Nopp44/46. Mol Biochem Parasitol. 2002 Jan;119(1):97-106. Park JH, Brekken DL, Randall AC, Parsons M.
EAN90694.1	serine/threonine protein kinase, putative (1)	Several compartments	Cell cycle-specific induction of an 89 kDa serine/threonine protein kinase activity in *Trypanosoma brucei*. J Cell Sci. 1994 Jul;107 (Pt 7):1825-32. Gale M Jr, Carter V, Parsons M.
EAN95882.1	activated protein kinase C receptor, putative	cytoplasm	The RACK1 homologue from *Trypanosoma brucei* is required for the onset and progression of cytokinesis. J Biol Chem. 2006 Apr 7;281(14):9781-90. Rothberg KG, Burdette DL, Pfannstiel J, Jetton N, Singh R, Ruben L.
EAN84558.1	arginine kinase, putative	X	*Trypanosoma cruzi* arginine kinase characterization and cloning. A novel energetic pathway in protozoan parasites. J Biol Chem. 2000 Jan 14;275(2):1495-501. Pereira CA, Alonso GD, Paveto MC, Iribarren A, Cabanas ML, Torres HN, Flawiá MM.
EAN88244.1	phosphoinositide-binding protein, putative (1)	X	N/A. Phosphoinositides: regulators of membrane traffic and protein function. FEBS Lett. 2007 May 22;581(11):2105-11. Krauss M, Haucke V.
EAN87527.1	protein phosphatase 2A catalytic subunit, putative (1)	Several compartments	A novel protein phosphatase 2A (PP2A) is involved in the transformation of human protozoan parasite *Trypanosoma cruzi*. Biochem J. 2003 Sep 15;374(Pt 3):647-56. González J, Cornejo A, Santos MR, Cordero EM, Gutiérrez B, Porcile P, Mortara RA, Sagua H, Da Silveira JF, Araya JE.
EAN83392.1	calmodulin	CV*	Linkage of the calmodulin and ubiquitin loci in *Trypanosoma cruzi.* Nucleic Acids Res. 1990 Aug 11;18(15):4561-9. Chung SH, Swindle J.
EAN84508.1	IgE-dependent histamine-releasing factor, putative	cytoplasm	N/A. Histamine-releasing factors, a heterogeneous group of different activities. Clin Exp Allergy. 2003 Sep;33(9):1175-82. Budde IK, Aalberse RC.
EAN86963.1	calcium-binding protein, putative (1)	flagellum*	A novel flagellar Ca2+-binding protein in trypanosomes. J Biol Chem. 1989 Nov 5;264(31):18627-31. Engman DM, Krause KH, Blumin JH, Kim KS, Kirchhoff LV, Donelson JE. /// A flagellum-specific calcium sensor. J Biol Chem. 2005 Dec 2;280(48):40104-11. Buchanan KT, Ames JB, Asfaw SH, Wingard JN, Olson CL, Campana PT, Araújo AP, Engman DM.
EAN91644.1	GTP-binding protein, putative	X	Signalling the genome: the Ras-like small GTPase family of trypanosomatids. Trends Parasitol. 2005 Oct;21(10):447-50. Field MC.
	OTHERS	**5**	
EAN87391.1	acid phosphatase, putative (1)	X	Localisation of acid phosphatase activity on the surface of bloodstream forms of *Trypanosoma congolense.* Exp Parasitol. 1996 Dec;84(3):429-38. Tosomba OM, Coetzer TH, Lonsdale-Eccles JD. /// Cytochemical localization of acid phosphatase in *Leishmania mexicana amazonensis.* J Submicrosc Cytol. 1986 Jan;18(1):127-32. Pimenta PF, De Souza W.
EAN93852.1	reticulon domain protein, putative (2)	ER	N/A. Nogo and its paRTNers. Trends Cell Biol. 2003 Apr;13(4):187-94. Oertle T, Schwab ME.
EAN81497.1	retrotransposon hot spot (RHS) protein, putative	nucleus	A new, expressed multigene family containing a hot spot for insertion of retroelements is associated with polymorphic subtelomeric regions of *Trypanosoma brucei*. Eukaryot Cell. 2002 Feb;1(1):137-51. Erratum in: Eukaryot Cell 2002 Apr;1(2):305. Bringaud F, Biteau N, Melville SE, Hez S, El-Sayed NM, Leech V, Berriman M, Hall N, Donelson JE, Baltz T.
EAN81577.1	trichohyalin, putative (1)	X	N/A. Trichohyalin mechanically strengthens the hair follicle: multiple cross-bridging roles in the inner root shealth. J Biol Chem. 2003 Oct 17;278(42):41409-19. Steinert PM, Parry DA, Marekov LN.
EAN92997.1	carbonic anhydrase-like protein, putative (1)	X	N/A. Acidocalcisomes are functionally linked to the contractile vacuole of *Dictyostelium discoideum*. J Biol Chem. 2002 Mar 8;277(10):8146-53. Marchesini N, Ruiz FA, Vieira M, Docampo R.

Abbreviations used: PM: plasma membrane, ER, endoplasmic reticulum, CV, contractile vacuole

TABLE S8 A: SIGNAL PEPT. & TM:

PROTEIN ID	Gene Copy #	PolyPhobius TM - SP	HMMTOP TM	TMHMM TM	SignalP SP	Final Prediction SP - TM
EAN90233.1	1	1 - 0	1	1	N	N - 1
EAN92211.1	2	6 - 0	4	0	N	**N - 4/6**
EAN85296.1	1	0 - 0	0	0	N	N - 0
EAN94958.1	2	0 - 0	1	0	N	N - 0
EAN99605.1	1	0 - 0	0	0	N	N - 0
EAN87059.1	2	**0 - Y**	0	0	N-Y	**Y*** - 0
EAN89163.1	1	0 - 0	0	0	N	N - 0
EAN82199.1	1	**1 - Y**	2	2	**Y**	Y - 1
EAN99158.1	1	0 - 0	0	0	N	N - 0
EAN87824.1	2	0 - 0	0	0	N	N - 0
EAN83270.1	3	**1 - Y**	2	2	**Y**	Y - 1
EAN82898.1	9	4 - 0	3	1	N	**N - 3/4**
EAN86445.1	2	0 - 0	0	0	N	N - 0
EAN87937.1	1	2 - 0	2	2	N	**N - 2**
EAN89424.1	2	**1 - Y**	1	1	N	N - 1
EAN84629.1	2	0 - 0	0	0	N	N - 0
EAN90235.1	1	0 - 0	0	0	N	N - 0
EAN91922.1	3	4 - 0	4	3 (but 4)	N	**N - 4**
EAN97577.1	2	0 - 0	1	0	N	N - 0
EAN82173.1	10	0 - 0	0	0	N	N - 0
EAN85405.1	1	0 - 0	0	0	N	N - 0
EAN90473.1	1	0 - 0	0	0	N	N - 0
EAN83261.1	13	0 - 0	0	0	N	N - 0
EAN81197.1	13	0 - 0	0	0	N	N - 0
EAN95832.1	13	0 - 0	0	0	N	N - 0
EAN81873.1	1	0 - 0	0	0	N	N - 0
EAN95952.1	2	0 - 0	0	0	N	N - 0
EAN84522.1	2	0 - 0	0	0	N	N - 0
EAN99627.1	2	0 - 0	0	0	N	N - 0
EAN87577.1	2	0 - 0	0	0	N	N - 0
EAN82896.1	3	**0 - Y**	1	0	Y-N	**Y*** - 0
EAN99701.1	1	0 - 0	0	0	N	N - 0
EAN99763.1	1	0 - 0	0	0	N	N - 0
EAN94545.1	3	0 - 0	0	0	N	N - 0
EAN91782.1	2	1 - 0	2	1	**Y**	Y - 1
EAN87428.1	3	1 - 0	1	1	Y-N	N - 1
EAN85276.1	2	0 - 0	0	0	N	N - 0
EAN87301.1	2	2 - 0	3	2	N	**N - 2**
EAN93401.1	2	3 - 0	3	1 (but3)	Y-N	**N - 3**
EAN85190.1	1	0 - 0	0	0	N	N - 0
EAN87214.1	5	**0 - Y**	0	0	**Y**	Y - 0
EAN88258.1	2	0 - 0	0	0	N	N - 0
EAN98396.1	2	0 - 0	1	0	N	N - 0
EAN85108.1	2	0 - 0	1	0 (but 1)	N-Y	N - 1
EAN94586.1	2	0 - 0	1	0	N	N - 0
EAN87063.1	2	0 - 0	0	0	N	N - 0
EAN82309.1	1	1 - 0	2	1	N	N - 1
EAN97099.1	2	1 - 0	1	1	N-Y	N - 1
EAN85329.1	2	3 - 0	4	3	N-Y	**N - 3**

		PolyPhobius	**HMMTOP**	**TMHMM**	**SignalP**	**Final Prediction**
PROTEIN ID	**Gene Copy #**	**TM - SP**	**TM**	**TM**	**SP**	**SP - TM**
EAN88802.1	2	0 - 0	0	0	N	N - 0
EAN94012.1	1	0 - 0	0	0	N	N - 0
EAN99952.1	2	0 - 0	0	0	N	N - 0
EAN97551.1	2	0 - 0	0	0	N	N - 0
EAN92109.1	2	0 - 0	1	0	N	N - 0
EAN84988.1	4	1 - 0	0	0	N	N - 0
EAN97019.1	2	0 - 0	1	0	N	N - 0
EAN86484.1	3	**3 - Y**	3	4	**Y**	Y - 3
EAN91740.1	1	0 - 0	0	0	N	N - 0
EAN84095.1	9	1 - 0	1	1	**Y**	Y - 0
EAN95493.1	2	0 - 0	0	0	N	N - 0
EAN89677.1	12	0 - 0	0	0	N	N - 0
EAN98716.1	3	0 - 0	0	0	N	N - 0
EAN97971.1	2	0 - 0	0	0	N	N - 0
EAN81827.1	2	1 - 0	1	0 (but 1)	N	N - 1
EAN83529.1	2	0 - 0	0	0	N	N - 0
EAN87488.1	2	3 - 0	3	2	N	**N - 3**
EAN88283.1	3	3 - 0	2	0 (but 1)	**Y**	Y - 1
EAN84096.1	7	2 - 0	2	2	Y-N	**N - 2**
EAN88063.1	2	0 - 0	0	0	N	N - 0
EAN86150.1	3	1 - 0	0	1	N	N - 1
EAN88162.1	3	0 - 0	0	0	N	N - 0
EAN88387.1	2	0 - 0	0	0	N	N - 0
EAN89593.1	12	0 - 0	0	0	N	N - 0
EAN83022.1	5	1 - 0	0	0	N	N - 0
EAN91430.1	3	0 - 0	0	0	N	N - 0
EAN99391.1	2	2 - 0	1	1	N-Y	N - 1
EAN95438.1	1	2 - 0	3	0 (but 1/2)	N	**N - 2**
EAN97520.1	2	0 - 0	1	0	N	N - 0
EAN85286.1	2	**0 - Y**	2	0	N	**N/Y - 0/1**
EAN95451.1	2	0 - 0	0	0	N	N - 0
EAN81839.1	23	0 - 0	0	0	N	N - 0
EAO00208.1	1	0 - 0	0	0	N	N - 0
EAN99098.1	2	0 - 0	0	0	N	N - 0
EAO00215.1	2	0 - 0	1	0	N	N - 0
EAN81429.1	29	14 - 0	14	14	N	**N - 14**
EAN93181.1	2	**2 - Y**	2	2	**Y**	Y - 2
EAN91858.1	2	0 - 0	1	0	N	N - 0
EAN86224.1	2	2 - 0	2	2	**Y**	**N - 2**
EAN85839.1	3	0 - 0	0	0	N	N - 0
EAN86428.1	5	**0 - Y**	2	1	Y-N	Y - 1
EAN92675.1	2	0 - 0	0	0	N	N - 0
EAN88187.1	2	0 - 0	0	0	N	N - 0
EAN96768.1	1	**0 - Y**	1	1	Y-N	Y - 0
EAN94594.1	3	0 - 0	0	0	N	N - 0
EAN94854.1	2	0 - 0	0	0	N	N - 0
EAN96277.1	2	1 - 0	3	1	N	N - 1
EAN84157.1	3	0 - 0	0	0	N	N - 0
EAN90288.1	3	1 - 0	1	0 (but 1)	**Y**	N - 1
EAN85669.1	3	0 - 0	0	0	N	N - 0

PROTEIN ID	Gene Copy #	PolyPhobius TM - SP	HMMTOP TM	TMHMM TM	SignalP SP	Final Prediction SP - TM
EAN95652.1	2	0 - 0	1	0	N	N - 0
EAN83893.1	2	0 - 0	1	0	**Y***	N - 0
EAN89707.1	6	0 - 0	0	0	N	N - 0
EAN94699.1	2	0 - 0	0	0	N	N - 0
EAN91538.1	1	0 - 0	0	0	N	N - 0
EAN82045.1	3	0 - 0	1	0	N	N - 0
EAN90017.1	2	**2 - Y**	5	0	N*	Y - 2/5
EAN83327.1	2	**1 - Y**	2	2	**Y**	Y - 2
EAN88441.1	3	0 - 0	0	0	N	N - 0
EAN83132.1	2	**0 - Y**	1	0	**Y**	Y - 0
EAN83371.1	1	2 - 0	1	1	N-Y	N - 1
EAN91467.1	2	**0 - Y**	1	0	**Y**	Y - 0
EAN95114.1	2	0 - 0	0	0	N	N - 0
EAN94516.1	x	**0 - Y**	0	0	N	N - 0
EAN82097.1	1	0 - 0	0	0	N	N - 0
EAN97997.1	1	0 - 0	0	0	N	N - 0
EAN93009.1	1	**0 - Y**	0	0	N	N - 0
EAN89189.1	1	0 - 0	0	0	N	N - 0
EAN90963.1	2	**1 - Y**	2	1 (but 2)	**Y**	Y - 1
EAN98338.1	3	0 - 0	1	0	N	N - 0
EAN82295.1	1	0 - 0	0	0	N	N - 0
EAN80998.1	2	0 - 0	0	0	N	N - 0
EAN81715.1	3	0 - 0	0	0	**Y**	N - 0
EAN99859.1	36	**0 - Y**	0	0	**Y**	Y - 0
EAN95112.1	3	0 - 0	0	0	N	N - 0
EAN85221.1	3	0 - 0	0	0	N	N - 0
EAN83235.1	2	0 - 0	0	0	N	N - 0
EAN94132.1	2	**0 - Y**	0	0	**Y**	Y - 0
EAN88008.1	2	0 - 0	0	0	N	N - 0
EAN83367.1	3	0 - 0	1	0	N	N - 0
EAN89431.1	2	0 - 0	0	0	N	N - 0
EAN89518.1	3	0 - 0	0	0	N	N - 0
EAN84397.1	3	0 - 0	2	0	N	N - 0
EAN81302.1	1	0 - 0	0	0	N	N - 0
EAN84897.1	4	1 - 0	1	1	Y-N	N - 1
EAN85214.1	2	**0 - Y**	0	0	Y	Y - 0
EAN95668.1	1	0 - 0	0	0	N	N - 0
EAN87575.1	3	1 - 0	1	1	Y-N	N - 1
EAN94531.1	3	0 - 0	1	0	N	N - 0

Summary	SP - TM	Total	% of total
	N - 0	91	66%
	N - 1	14	10%
	N - >1	12	8.60%
	Y - 0	10	7.20%
	Y - =/>1	10	7.20%
	Not Defined	1	0.72%

Note: N: no signal peptide, non-secretory protein; Y: signal peptide, secreted protein; Y-N: signal anchor (looks like a signal peptide but the cleavage probability is not significant enough). For THMMH those cases were we indicate a '(but #)' refers to the possibility of an extra transmembrane as by indicated in the graphic output from the server (not shown here).

TABLE S8 B: TARGET SIGNAL & LOCALIZATION PREDICTIONS

The TABLA S8B shows the results form six target signal prediction servers. The final prediction is the putative location of the hypothetical protein, considering at least two or more servers agreed in the same prediction. When no agreement was observed, no location is inferred.

Abbreviations: M or m: mitochondrion; N: nucleus; PM: plasma membrane; C or cytop: cytoplasm; ER: endoplasmic reticulum; G: golgi; EXTR: extracellular-secreted; CYTOSK: cytoskeleton; Glyc: glycosome-peroxisome; SEC or s: secretory pathway.

	PENCE	pTARGET	PeroxiP	SPL-Loc	WOLF pSORT	TargetP	FINAL PREDICTION
PROTEIN ID	Location	Location	PTS1	Location	Location	Location	
EAN90233.1	-	mitochondrion		mitochondria	M	m	**M**
EAN92211.1	-	nucleus		nucleus_or_cytosol	PM / ER	-	
EAN85296.1	-	nucleus	x	nucleus_or_cytosol	N	-	**N**
EAN94958.1	-	mitochondrion		mitochondria	M	m	**M**
EAN99605.1	cytoplasm	nucleus		nucleus_or_cytosol	N / M / C	-	**N-C**
EAN87059.1	nucleus	nucleus		mitochondria	N /M	m	**N-M**
EAN89163.1	cytop/nucleus	nucleus		nucleus_or_cytosol	N	m	**N**
EAN82199.1	-	ER		secretory_pathway	EXTR / ER	s	**SEC-ER**
EAN99158.1	nucleus	nucleus		nucleus_or_cytosol	N/C	-	**N**
EAN87824.1	-	cytoplasm		nucleus_or_cytosol	N / C	-	**C**
EAN83270.1	ER / Golgi	Golgi		nucleus_or_cytosol	EXTR	s	**SEC-ER-G**
EAN82898.1	-	PM		nucleus_or_cytosol	PM	-	**PM**
EAN86445.1	-	Golgi		nucleus_or_cytosol	C/N	-	
EAN87937.1	-	mitochondrion		mitochondria	PM / EXTR / G	m	**M**
EAN89424.1	-	mitochondrion		secretory_pathway	C / EXTR	-	
EAN84629.1	-	mitochondrion		mitochondria	N / M	m	**M**
EAN90235.1	mitochondrion	mitochondrion		mitochondria	C /M /N	m	**M**
EAN91922.1	-	PM		nucleus_or_cytosol	PM	s	**PM**
EAN97577.1	cytoplasm	cytoplasm		nucleus_or_cytosol	N	-	**C**
EAN82173.1	-	Extrac/Secret		secretory_pathway	EXTR	-	**SEC-EXT**
EAN85405.1	-	nucleus		nucleus_or_cytosol	N	m	**N**
EAN90473.1	-	Golgi		mitochondria	M	m	**M**
EAN83261.1	-	peroxysomes		nucleus_or_cytosol	EXTR	-	
EAN81197.1	-	peroxysomes		nucleus_or_cytosol	EXTR	-	
EAN95832.1	-	peroxysomes		nucleus_or_cytosol	EXTR	-	
EAN81873.1	-	PM		nucleus_or_cytosol	N / C	-	**N-C**

	PENCE	pTARGET	PeroxiP	SPL-Loc	WOLF pSORT	TargetP	FINAL
PROTEIN ID	**Location**	**Location**	**PTS1**	**Location**	**Location**	**Location**	**PREDICTION**
EAN95952.1	-	Golgi		nucleus_or_cytosol	C / M / N	m	
EAN84522.1	-	nucleus		nucleus_or_cytosol	M / ER	m	**N**
EAN99627.1	-	cytoplasm		nucleus_or_cytosol	PM	-	
EAN87577.1	-	nucleus	x	nucleus_or_cytosol	N	-	**N**
EAN82896.1	-	mitochondrion		mitochondria	M / P	m	**M**
EAN99701.1	-	nucleus		nucleus_or_cytosol	N/C	m	**N**
EAN99763.1	cytoplasm	cytoplasm		nucleus_or_cytosol	EXTR / C / N	-	**C**
EAN94545.1	nucleus	nucleus		nucleus_or_cytosol	C / N	-	**N**
EAN91782.1	cytop / ER	ER		secretory_pathway	ER	s	**SEC-ER**
EAN87428.1	mitochondrion	Golgi		nucleus_or_cytosol	C / N	-	
EAN85276.1	-	cytoplasm		nucleus_or_cytosol	C / N	-	**N-C**
EAN87301.1	-	peroxysomes		nucleus_or_cytosol	C / N	-	**N-C**
EAN93401.1	mitochondrion	mitochondrion		nucleus_or_cytosol	M	-	**M**
EAN85190.1	cytoplasm	nucleus		nucleus_or_cytosol	N / C	m	**N-C**
EAN87214.1	-	mitochondrion		mitochondria	M	m	**M**
EAN88258.1	cytoplasm	mitochondrion		nucleus_or_cytosol	C/N	m	
EAN98396.1	-	cytoplasm		nucleus_or_cytosol	N / C	-	**N-C**
EAN85108.1	nucleus	nucleus		nucleus_or_cytosol	EXTR / C/N	s	**N**
EAN94586.1	-	nucleus		nucleus_or_cytosol	C/N	-	**N-C**
EAN87063.1	-	nucleus		nucleus_or_cytosol	C / N	-	**N-C**
EAN82309.1	-	ER		nucleus_or_cytosol	C	-	
EAN97099.1	-	peroxysomes		nucleus_or_cytosol	PM	-	
EAN85329.1	cytoplasm	mitochondrion		secretory_pathway	PM	s	**SEC**
EAN88802.1	cytoplasm	cytoplasm	xx	nucleus_or_cytosol	C/N	-	**C**
EAN94012.1	-	cytoplasm		nucleus_or_cytosol	C/N	-	**C**
EAN99952.1	cytoplasm	ER		nucleus_or_cytosol	C / P	-	**C**
EAN97551.1	cytoplasm	nucleus		mitochondria	N	m	
EAN92109.1	nucleus	peroxysomes		secretory_pathway	N / C	-	
EAN84988.1	-	mitochondrion		secretory_pathway	N / M / EXTR	-	**SEC**
EAN97019.1	-	Golgi		nucleus_or_cytosol	C / N	-	**N-C**
EAN86484.1	-	mitochondrion		mitochondria	PM / EXTR / M	m	**M**

	PENCE	pTARGET	PeroxiP	SPL-Loc	WOLF pSORT	TargetP	FINAL
PROTEIN ID	**Location**	**Location**	**PTS1**	**Location**	**Location**	**Location**	**PREDICTION**
EAN91740.1	mitochondrion	cytoplasm		nucleus_or_cytosol	C / M	-	**C**
EAN84095.1	-	Golgi		mitochondria	N / EXTR	s	
EAN95493.1	-	nucleus		nucleus_or_cytosol	C / N	-	**N**
EAN89677.1	PM	nucleus		nucleus_or_cytosol	N	m	**N**
EAN98716.1	ER / extracellular	nucleus		nucleus_or_cytosol	C/N	-	**N**
EAN97971.1	cytoplasm	nucleus		nucleus_or_cytosol	N	-	**N-C**
EAN81827.1	-	cytoplasm		nucleus_or_cytosol	EXTR/ PM	-	
EAN83529.1	cytoplasm	cytoplasm		nucleus_or_cytosol	C / N	-	**C**
EAN87488.1	mitochondrion	mitochondrion		nucleus_or_cytosol	C / N / M	s	
EAN88283.1	-	Golgi		nucleus_or_cytosol	PM / EXTR / M	s	
EAN84096.1	-	Golgi		secretory_pathway	PM	s	**SEC**
EAN88063.1	cytoplasm	nucleus		nucleus_or_cytosol	N	m	**N**
EAN86150.1	-	Golgi		nucleus_or_cytosol	M / C	-	
EAN88162.1	-	nucleus		nucleus_or_cytosol	C / N	-	**N-C**
EAN88387.1	-	nucleus		nucleus_or_cytosol	C / N	-	**N-C**
EAN89593.1	-	cytoplasm		nucleus_or_cytosol	N / C	-	**N-C**
EAN83022.1	-	mitochondrion		secretory_pathway	EXTR	-	**SEC**
EAN91430.1	-	peroxysomes		nucleus_or_cytosol	C / N	-	**N-C**
EAN99391.1	-	Golgi		secretory_pathway	PM / M / C	s	**SEC**
EAN95438.1	-	mitochondrion		nucleus_or_cytosol	ER / M / PM	-	
EAN97520.1	-	ER		nucleus_or_cytosol	N / C	-	**N-C**
EAN85286.1	cytoplasm	mitochondrion		mitochondria	M	m	**M**
EAN95451.1	-	peroxysomes		nucleus_or_cytosol	C/N/er/M	-	
EAN81839.1	cytoplasm	Golgi	xx	nucleus_or_cytosol	C / N	-	**C**
EAO00208.1	-	nucleus		nucleus_or_cytosol	N	-	**N**
EAN99098.1	nucleus	nucleus		nucleus_or_cytosol	N / C	-	**N**
EAO00215.1	-	peroxysomes	x	nucleus_or_cytosol	PM /C /N	-	
EAN81429.1	-	PM		nucleus_or_cytosol	PM	-	**PM**
EAN93181.1	-	ER		secretory_pathway	EXTR	s	**SEC-ER**
EAN91858.1	cytoplasm	cytoplasm		nucleus_or_cytosol	M /C	s	**C**
EAN86224.1	-	Golgi		secretory_pathway	PM	s	**SEC**

	PENCE	**pTARGET**	**PeroxiP**	**SPL-Loc**	**WOLF pSORT**	**TargetP**	**FINAL**
PROTEIN ID	**Location**	**Location**	**PTS1**	**Location**	**Location**	**Location**	**PREDICTION**
EAN85839.1	cytoplasm	nucleus		mitochondria	N	m	
EAN86428.1	ER	Golgi		mitochondria	PM / M / P	s	
EAN92675.1	-	mitochondrion	xxxx	nucleus_or_cytosol	M / C / N	m	**M**
EAN88187.1	cytoplasm	cytoplasm		nucleus_or_cytosol	CYTOSK	-	**C**
EAN96768.1	-	Golgi		secretory_pathway	EXTR / LYSO	s	**SEC**
EAN94594.1	ER	mitochondrion	xxxx	nucleus_or_cytosol	N / C	-	
EAN94854.1	cytoplasm	nucleus		nucleus_or_cytosol	N	m	**N**
EAN96277.1	mitochondrion	mitochondrion		mitochondria	M	m	**M**
EAN84157.1	nucleus	PM		nucleus_or_cytosol	PM / N / C	-	
EAN90288.1	-	ER		secretory_pathway	EXTR	s	**SEC-ER**
EAN85669.1	nucleus	nucleus		nucleus_or_cytosol	N/C	-	**N**
EAN95652.1	cytop / Golgi	peroxysomes		nucleus_or_cytosol	C / P	-	**C-GLYC**
EAN83893.1	cytop / Golgi / PM	Golgi		nucleus_or_cytosol	C/N	s	**G**
EAN89707.1	nucleus	nucleus		secretory_pathway	C / N	-	**N**
EAN94699.1	cytoplasm	cytoplasm		nucleus_or_cytosol	N / C	-	**N-C**
EAN91538.1	cytoplasm	nucleus		nucleus_or_cytosol	C / N	-	**N-C**
EAN82045.1	nucleus	cytoplasm		nucleus_or_cytosol	C/N	-	**N-C**
EAN90017.1	-	Golgi		mitochondria	M / C	m	**M**
EAN83327.1	-	mitochondrion		secretory_pathway	PM	s	
EAN88441.1	-	nucleus		nucleus_or_cytosol	N / M / C	m	
EAN83132.1	-	lysosomes		mitochondria	M	m	**M**
EAN83371.1	-	ER		secretory_pathway	M/ EXTR	s	**SEC**
EAN91467.1	-	peroxysomes		mitochondria	M	m	**M**
EAN95114.1	-	peroxysomes		nucleus_or_cytosol	C/N	-	
EAN94516.1	cytoplasm	nucleus		nucleus_or_cytosol	N/C	s	**N-C**
EAN82097.1	-	Golgi		nucleus_or_cytosol	C / N	-	**N-C**
EAN97997.1	-	Golgi		nucleus_or_cytosol	C / N	-	**N-C**
EAN93009.1	-	mitochondrion		mitochondria	M / C	m	**M**
EAN89189.1	-	nucleus		nucleus_or_cytosol	EXTR	-	**N**
EAN90963.1	-	lysosomes		secretory_pathway	PM	s	**SEC**
EAN98338.1	nucleus	cytoplasm		nucleus_or_cytosol	N/C	m	**N-C**

PROTEIN ID	PENCE Location	pTARGET Location	PeroxiP PTS1	SPL-Loc Location	WOLF pSORT Location	TargetP Location	FINAL PREDICTION
EAN82295.1	-	PM		nucleus_or_cytosol	EXTR / C/N	-	
EAN80998.1	-	nucleus		nucleus_or_cytosol	C	-	
EAN81715.1	-	Golgi		mitochondria	N/C	m	
EAN99859.1	-	PM		secretory_pathway	EXTR	s	**SEC**
EAN95112.1	cytop / Golgi	nucleus		nucleus_or_cytosol	M	-	
EAN85221.1	cytoplasm	nucleus		nucleus_or_cytosol	N / M / C	m	**N-C**
EAN83235.1	cytoplasm	nucleus		nucleus_or_cytosol	N	-	**N-C**
EAN94132.1	-	Golgi	x	nucleus_or_cytosol	M	m	
EAN88008.1	cytop / Golgi	cytoplasm		nucleus_or_cytosol	N/C	-	**C**
EAN83367.1	cytop / Golgi	nucleus	x	nucleus_or_cytosol	N	-	**N**
EAN89431.1	cytoplasm	cytoplasm		nucleus_or_cytosol	N	-	**C**
EAN89518.1	cytoplasm	nucleus		nucleus_or_cytosol	C / N	-	**N-C**
EAN84397.1	-	peroxysomes		nucleus_or_cytosol	C/N	-	
EAN81302.1	-	mitochondrion		mitochondria	M	m	**M**
EAN84897.1	cytoplasm	Golgi		secretory_pathway	ER / PM /C	s	**SEC**
EAN85214.1	nucleus	mitochondrion		mitochondria	M / N	m	**M**
EAN95668.1	cytop / nucleus	mitochondrion		nucleus_or_cytosol	N / C	-	**N-C**
EAN87575.1	mitochondrion	nucleus		mitochondria	C / M	m	**M**
EAN94531.1	ER	mitochondrion	xx	nucleus_or_cytosol	M / C / N	-	

SUMMARY

LOCATION	TOTAL #	LOCATION	TOTAL #	LOCATION	TOTAL #	LOCATION	TOTAL #
Undefined	**36**	**Cytoplasm**	**13**	**PM**	**3**	**Cyt-Glyc**	**1**
N-C	**26**	**Mitochondrion**	**20**	**Glycosome**	**1**	**N-M**	**1**
Nucleus	**20**	**Secretory Pathway**	**17**				

TABLE S8C: PROTEIN BLAST & COMPARATIVE EXPRESSION DATA

Numbers in brackets beside the accession numbers, indicate (1) no expression data found previously in whole cellular Tcruzi proteome and (2) no expression data found previously in epimastigote stage from whole cell proteomic analysis (Atwood et al, 2005). In light background are shown those hits with other Tryp proteins with ID.

	BLASTP RESULTS (310108)	
PROTEIN ID	**Sequences with E-value BETTER than threshold**	**Sequences with E-value WORSE than threshold**
EAN90233.1 (2)	Hypothetical proteins Tryps	ref|ZP_01041026.1| putative peptidase precursor [Erythrobacter sp. NAP1]
EAN92211.1	Hypothetical proteins Tryps	ref|ZP_02122410.1| peptide chain release factor 2 protein [Methylobacterium nodulans ORS 2060]
EAN85296.1 (1)	Hypothetical proteins Tryps	
EAN94958.1	Hypothetical proteins Tryps	ref|YP_001428058.1| dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. holarctica FTA]
EAN99605.1 (2)	Hypothetical proteins Tryps plus over 50 hits hypothetical proteins from other species	Hypothetical proteins from other species
EAN87059.1	Hypothetical protein only in Tcruzi	dbj|BAA22067.1| myosin heavy chain [Cyprinus carpio]
EAN89163.1 (1)	Hypothetical proteins Tryps	
EAN82199.1 (1)	Hypothetical proteins Tryps plus over 100 hits. Best ones other species gb|ABM55602.1| putative signal sequence receptor beta subunit [Maconellicoccus hirsutus] orref|YP_001274107.1| adhesin-like protein [Methanobrevibacter smithii ATCC 35061].	
EAN99158.1	Hypothetical protein only in Tcruzi and Tbrucei	
EAN87824.1	Hypothetical proteins Tryps plus best next hits ref|ZP_00994854.1| amidinotransferase family protein [Janibacter sp. TCC2649] /// ref|ZP_01130782.1| Amidinotransferase [marine actinobacterium PHSC20C1]	
EAN83270.1 (2)	Hypothetical proteins Tryps plus ref|XP_001354671.1| GA17526-PA [Drosophila pseudoobscura] = emp24/gp25L/p24 family/GOLD. Members of this family are implicated in bringing cargo forward from the ER and binding to coat proteins by their cytoplasmic domains. /// ref|XP_566482.1| COPII-coated vesicle protein [Cryptococcus neoformans var. neoformans JEC21].	
EAN82898.1 (1)	Hypothetical proteins Tryps plus over 50 hits hypothetical proteins from other species	
EAN86445.1	Hypothetical proteins Tryps	Hypothetical proteins or unrelated products from other species
EAN87937.1 (1)	Hypothetical proteins Tryps plus hits hypothetical proteins from other species	
EAN89424.1	Hypothetical proteins Tryps	Hypothetical proteins or unrelated products from other species
EAN84629.1	Hypothetical protein only in Tcruzi and Tbrucei	
EAN90235.1	Hypothetical proteins Tryps plus next best hit: sp|O01369.2|QCR7_FASHE Cytochrome b-c1 complex subunit 7 (Ubiquinol-cytochrome c reductase complex 14 kDa protein) (Complex III subunit 7) (Complex III subunit VII) [Fasciola hepatica] and similar others.	
EAN91922.1	Hypothetical proteins Tryps	Hypothetical proteins or unrelated products from other species
EAN97577.1	Hypothetical proteins Tryps	
EAN82173.1	Hypothetical proteins Tryps	
EAN85405.1	Hypothetical proteins Tryps plus hits hypothetical proteins from other species	
EAN90473.1	Hypothetical proteins Tryps	ref|XP_001689789.1| mitochondrial ribosomal protein L20 [Chlamydomonas reinhardtii]

PROTEIN ID	BLASTP RESULTS (310108)	
	Sequences with E-value BETTER than threshold	Sequences with E-value WORSE than threshold
EAN83261.1	Hypothetical proteins Tryps	Hypothetical proteins or unrelated products from other species
EAN81197.1	Hypothetical proteins Tryps	Various unrelated proteins from other species.
EAN95832.1	Hypothetical proteins Tryps	Various unrelated proteins from other species.
EAN81873.1	Hypothetical proteins Tryps	Various unrelated proteins from other species.
EAN95952.1	Hypothetical proteins Tryps plus next best hits several amidinotransferases: ref|YP_923220.1| amidinotransferase family protein [Nocardioides sp. JS614] plus other hypothetical products.	
EAN84522.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN99627.1 (1)	Hypothetical protein only in Tcruzi and Tbrucei	Various unrelated proteins from other species.
EAN87577.1 (1)	Hypothetical protein only in Tcruzi and Leishmania sp.	
EAN82896.1 (1)	Hypothetical protein only in Tcruzi and Leishmania sp plus several other hypothetical and unrelated proteins from other species: ref|YP_001175645.1| thioesterase superfamily protein [Enterobacter sp. 638]	
EAN99701.1 (2)	Hypothetical proteins Tryps plus hits hypothetical proteins from other species	
EAN99763.1 (2)	Hypothetical proteins Tryps plus several similar hits: gb|ABC02026.1| radial spoke protein 7 [Chlamydomonas reinhardtii]/// ref|NP_060048.2| ropporin [Homo sapiens]. These proteins are flagellar/axoneme related, calcium binding and kinase activity related.	
EAN94545.1	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN91782.1 (2)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species. Best next hit: emb|CAL52554.1| 17 beta-hydroxysteroid dehydrogenase type 3, HSD17B3 (ISS) [Ostreococcus tauri]	
EAN87428.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species. Best next hit:ref|YP_001516929.1| glutathione S-transferase, putative [Acaryochloris marina MBIC11017] /// gb|AAD03559.1| failed axon connections protein [Drosophila virilis]	
EAN85276.1	Hypothetical proteins from Tcruzi and Leishmania sp plus hits hypothetical or unrelated proteins from other species	
EAN87301.1 (1)	Hypothetical proteins Tryps plus hits of immunoglobulins from other species: gb|AAT65112.1| immunoglobulin E variable region [Homo sapiens]	
EAN93401.1 (1)	Hypothetical proteins Tryps plus several species similar hits: ref|NP_001090497.1| solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 [Xenopus laevis]	
EAN85190.1	Hypothetical proteins Tryps	
EAN87214.1 (2)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN88258.1 (1)	Hypothetical proteins Tryps plus several species similar hits: ref|YP_001002431.1| ribosomal protein L22 [Halorhodospira halophila SL1]	
EAN98396.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN85108.1 (1)	Hypothetical protein in Tcruzi but ref|XP_845651.1| ribosome biogenesis protein, putative [Trypanosoma brucei TREU927] /// ref|XP_001562230.1| brix domain containing-like protein [Leishmania braziliensis MHOM/BR/75/M2904] /// ref|NP_075812.3| brix domain containing 1 isoform 1 [Mus musculus]	
EAN94586.1	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN87063.1	Hypothetical proteins Tryps	

<table>
<tr><th rowspan="2">PROTEIN ID</th><th colspan="2">BLASTP RESULTS (310108)</th></tr>
<tr><th>Sequences with E-value BETTER than threshold</th><th>Sequences with E-value WORSE than threshold</th></tr>
<tr><td>EAN82309.1</td><td colspan="2">Hypothetical proteins Tryps plus several species similar hits: gb|AAF72105.1|AF154847_1 33 kDa Vamp-(vesicle-associated membrane protein)-associated protein [Homo sapiens]</td></tr>
<tr><td>EAN97099.1 (1)</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species</td></tr>
<tr><td>EAN85329.1 (1)</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species</td></tr>
<tr><td>EAN88802.1 (2)</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species</td></tr>
<tr><td>EAN94012.1 (1)</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species</td></tr>
<tr><td>EAN99952.1</td><td colspan="2">Hypothetical proteins Tryps plus hits from other species aminotransferases: ref|YP_001311379.1| aminotransferase, class IV [Clostridium beijerinckii NCIMB 8052]</td></tr>
<tr><td>EAN97551.1</td><td>Hypothetical proteins Tryps</td><td></td></tr>
<tr><td>EAN92109.1 (2)</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species</td></tr>
<tr><td>EAN84988.1</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical proteins from other species plus several Saccharopine dehydrogenase: ref|YP_958739.1| Saccharopine dehydrogenase [Marinobacter aquaeolei VT8]. Lysine metabolism.</td></tr>
<tr><td>EAN97019.1</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species</td></tr>
<tr><td>EAN86484.1</td><td>Hypothetical proteins Tryps</td><td></td></tr>
<tr><td>EAN91740.1 (2)</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species</td></tr>
<tr><td>EAN84095.1 (1)</td><td colspan="2">Hypothetical proteins Tryps plus hits of ref|XP_812721.1| D-alanyl-glycyl endopeptidase-like protein, putative [Trypanosoma cruzi strain CL Brener]; also from Tbrucei and Leishmania, among other proteins of other species.</td></tr>
<tr><td>EAN95493.1 (1)</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species</td></tr>
<tr><td>EAN89677.1 (1)</td><td>Hypothetical protein only in Tcruzi and Tbrucei</td><td></td></tr>
<tr><td>EAN98716.1 (1)</td><td>Hypothetical proteins Tryps</td><td></td></tr>
<tr><td>EAN97971.1 (1)</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species</td></tr>
<tr><td>EAN81827.1 (1)</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical proteins from other species and several like this: ref|YP_725824.1| Glutathione S-transferase-like protein [Ralstonia eutropha H16]</td></tr>
<tr><td>EAN83529.1</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical proteins from other species and several like this: ref|XP_817487.1| mitotubule-associated protein Gb4, putative [Trypanosoma cruzi strain CL Brener] and ref|XP_804415.1| dynein heavy chain, cytosolic [Trypanosoma cruzi strain CL Brener] Lower expected value.</td></tr>
<tr><td>EAN87488.1 (1)</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species</td></tr>
<tr><td>EAN88283.1</td><td>Hypothetical proteins Tryps</td><td>A few like this: sp|Q41594|TASY_TAXBR Taxadiene synthase (Taxa-4(5),11(12)-diene synthase). Diterpenoid biosynthesis.</td></tr>
<tr><td>EAN84096.1 (1)</td><td colspan="2">Hypothetical proteins Tryps plus hits of ref|XP_812721.1| D-alanyl-glycyl endopeptidase-like protein, putative [Trypanosoma cruzi strain CL Brener]; also from Tbrucei and Leishmania, among other proteins of other species.</td></tr>
<tr><td>EAN88063.1</td><td colspan="2">Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species</td></tr>
</table>

PROTEIN ID	BLASTP RESULTS (310108)	
	Sequences with E-value BETTER than threshold	Sequences with E-value WORSE than threshold
EAN86150.1 (2)	Hypothetical proteins Tryps	A few like this: ref|YP_001502637.1| methylmalonate-semialdehyde dehydrogenase [Shewanella pealeana ATCC 00345]. Participates in 3 metabolisms: inositol metabolism, valine-leucine-isoleucine degradation and propanoate metabolism.
EAN88162.1 (2)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN88387.1	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN89593.1	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN83022.1	Hypothetical proteins Tryps plus hits hypothetical proteins from other species plus several Saccharopine dehydrogenase: ref|YP_958739.1| Saccharopine dehydrogenase [Marinobacter aquaeolei VT8]. Lysine metabolism.	
EAN91430.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN99391.1 (2)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN95438.1 (1)	Hypothetical proteins Tryps plus hits hypothetical proteins from other species plus several cinnamyl-alcohol dehydrogenase: ref|ZP_00592614.1| cinnamyl-alcohol dehydrogenase (CAD), putative [Prosthecochloris aestuarii DSM 271]. Phenylpropanoid biosynthesis. Oxidoreductase family.	
EAN97520.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN85286.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN95451.1 (2)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN81839.1	Hypothetical protein only in Tcruzi. Then over 40 hits to Glycerate kinases from different species.	
EAO00208.1	Hypothetical proteins Tryps	
EAN99098.1 (1)	Hypothetical proteins Tryps plus over 30 hits like this: ref|NP_491688.1| HMG family member (hmg-3) [Caenorhabditis elegans] sp|O01683.1|SSP1B_CAEEL FACT complex subunit ssrp1-B (Facilitates chromatin transcription complex subunit ssrp1-B) (Structure-specific recognition protein 1-B) (HMG box-containing protein 3) - Interacts with histones H2A/B to effect nucleosome disassembly and transcription elongation.	
EAO00215.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN81429.1	Hypothetical proteins Tryps - 50 hits. Several copies in all three Tryps.	
EAN93181.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN91858.1 (1)	Hypothetical proteins Tcruzi and Lm, but ref|XP_845863.1| tyrosyl-tRNA synthetase, putative [Trypanosoma brucei TREU927]. Plus other species hypothetical or unrelated proteins.	
EAN86224.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN85839.1	Hypothetical proteins Tryps	
EAN86428.1 (1)	Hypothetical proteins Tcruzi and Lm, but ref|XP_827602.1| short-chain dehydrogenase [Trypanosoma brucei TREU927]. Plus other species hypothetical or short-chain dh proteins.	
EAN92675.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN88187.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN96768.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	

PROTEIN ID	BLASTP RESULTS (310108)	
	Sequences with E-value BETTER than threshold	Sequences with E-value WORSE than threshold
EAN94594.1 (1)	Hypothetical proteins Tcruzi and Tbrucei, but ref|XP_001464804.1| L-gulonolactone oxidase, putative [Leishmania infantum JPCM5] and other species hypothetical or L-gulonolactone oxidase proteins.	
EAN94854.1 (1)	Hypothetical proteins Tryps	
EAN96277.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN84157.1 (1)	Hypothetical proteins Tcruzi and Tbrucei plus hits hypothetical or unrelated proteins from other species, but gb|AAQ10955.1| putative splicing factor XB2 [Trypanosoma cruzi] and ref|XP_848208.1| WD-repeat protein [Leishmania major strain Friedlin]	
EAN90288.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN85669.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN95652.1	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species, but ref|XP_808187.1| myosin heavy chain, putative [Trypanosoma cruzi strain CL Brener] and ref|XP_001687712.1| kinesin K39, putative [Leishmania major]	
EAN83893.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN89707.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN94699.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN91538.1	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species, but ref|XP_808187.1| myosin heavy chain, putative [Trypanosoma cruzi strain CL Brener] and ref|XP_001687712.1| kinesin K39, putative [Leishmania major]	
EAN82045.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN90017.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN83327.1 (1)	Hypothetical proteins Tryps	Hypothetical proteins from other species
EAN88441.1 (1)	Hypothetical protein only in Tcruzi and Tbrucei	Hypothetical proteins or unrelated products from other species
EAN83132.1 (2)	Hypothetical proteins Tryps	
EAN83371.1 (1)	Hypothetical proteins Tryps	Hypothetical proteins or unrelated products from other species
EAN91467.1	Hypothetical proteins Tryps	
EAN95114.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN94516.1 (1)	Hypothetical proteins Tryps, but ref|XP_001563398.1| kinesin K39, putative [Leishmania braziliensis MHOM/BR/75/M2904]	
EAN82097.1	Hypothetical proteins Tryps	
EAN97997.1	Hypothetical proteins Tryps	Hypothetical proteins or unrelated products from other species
EAN93009.1 (2)	Hypothetical proteins Tryps	Hypothetical proteins from other species
EAN89189.1 (1)	Hypothetical proteins Tryps	Only 2 unrelated products from other species
EAN90963.1 (1)	Hypothetical protein only in Tcruzi and Tbrucei plus hits of other species hypothetical proteins and several like this: ref|NP_974419.1| nicastrin-related [Arabidopsis thaliana]. Part of the gamma-secretase complex; proteases involved in the processing of amyloid beta.	
EAN98338.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN82295.1	Hypothetical proteins Tryps	
EAN80998.1	Hypothetical proteins Tryps	Hypothetical proteins or unrelated products from other species

PROTEIN ID	BLASTP RESULTS (310108)	
	Sequences with E-value BETTER than threshold	Sequences with E-value WORSE than threshold
EAN81715.1 (1)	Hypothetical proteins Tryps	Hypothetical proteins or unrelated products from other species
EAN99859.1 (1)	Hypothetical proteins only in Tcruzi but also ref|XP_812770.1| surface protease GP63, putative [Trypanosoma cruzi strain CL Brener]	
EAN95112.1	Hypothetical proteins Tryps but also ref|XP_001463596.1| paraflagellar rod component, putative [Leishmania infantum JPCM5] and gb|AAQ55490.1| paraflagellar rod protein 1 [Trypanosoma brucei]	
EAN85221.1 (1)	Only two hypothetical proteins in Tcruzi.	
EAN83235.1	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN94132.1 (1)	Hypothetical proteins in Tcruzi and Lm but ref|XP_829621.1| NUDIX hydrolase [Trypanosoma brucei TREU927] plus other hydrolases from other species.	
EAN88008.1 (1)	Hypothetical proteins Tryps	
EAN83367.1 (1)	Hypothetical proteins Tryps	Hypothetical proteins or unrelated products from other species
EAN89431.1	Hypothetical proteins Tryps	
EAN89518.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN84397.1	Hypothetical proteins Tryps, but ref|XP_812111.1| calpain-like cysteine peptidase, putative [Trypanosoma cruzi strain CL Brener] plus hits hypothetical or unrelated proteins from other species	
EAN81302.1 (1)	Hypothetical proteins Tryps	
EAN84897.1 (1)	Only one copy from Tcruzi, hypothetical plus two more hits like this: gb|AAK19244.1|AF312916_1 reticulocyte binding protein 2 homolog A [Plasmodium falciparum]	
EAN85214.1	Hypothetical protein only in Tcruzi.	Five hits from other species, similar to this: dbj|BAA22067.1| myosin heavy chain [Cyprinus carpio]
EAN95668.1 (1)	Hypothetical protein only in Tcruzi and Tbrucei	
EAN87575.1 (1)	Hypothetical proteins Tryps plus hits hypothetical or unrelated proteins from other species	
EAN94531.1 (1)	Hypothetical protein only in Tcruzi and Tbrucei but : ref|XP_001464804.1| L-gulonolactone oxidase, putative Leishmania infantum JPCM5] plus same in other species.	