

Database Name: the T\_brucei database  
Version: unknown  
Taxonomy: All Entries  
Number of Proteins: 38057

Search Engine Set: 1 Search Engine  
Search Engine: Mascot  
Version: 2.3.02  
Samples: All Samples  
Fragment Tolerance: 0,60 Da (Monoisotopic)  
Parent Tolerance: 10,0 PPM (Monoisotopic)  
Fixed Modifications:  
Variable Modifications: +16 on M (Oxidation), +57 on C (Carbamidomethyl)  
Database: the T\_brucei database (unknown version, 38057 entries)  
Digestion Enzyme: Trypsin  
Max Missed Cleavages: 2

Scaffold: Version: Scaffold\_4.4.1.1  
Modification Metadata Set: 1541 modifications  
  
Comment:  
Protein Grouping Strategy: Experiment-wide grouping with binary peptide-protein weights  
Peptide Thresholds: 95,0% minimum  
Protein Thresholds: 95,0% minimum and 3 peptides minimum  
Peptide FDR: 0,7% (Prophet)  
Protein FDR: 0,0% (Prophet)

**Displaying: Exclusive Unique Peptide Count**

#	Identified Proteins (51)	Accession Number	Molecular mass (kDa)	ctr (WT)	CPSF160 prot C experiment 1	CPSF160 prot C experiment 2	factor
1	cleavage and polyadenylation specificity factor-like protein	Tb927.11.14560	159	0	83	84	CPSF160
2	hypothetical protein	Tb927.8.7490	158	0	79	76	Symplekin
3	cleavage and polyadenylation specificity factor, putative	Tb927.11.230	91	0	45	42	CPSF100
4	cleavage and polyadenylation specificity factor subunit, putative	Tb927.4.1340	85	0	37	33	CstF50
5	hypothetical protein	Tb927.6.1830	50	0	23	25	CPSF73
6	beta tubulin	Tb927.1.2330	50	10	23	23	
7	alpha tubulin	Tb927.1.2340	50	9	20	20	
8	heat shock protein 70	Tb927.11.11330	71	2	16	19	
9	hypothetical protein	Tb927.11.13860	30	0	15	17	hyp. protein

10	cleavage and polyadenylation specificity factor 30 kDa subunit	Tb927.11.12750	32	0	15	12	CPSF30
11	hypothetical protein	Tb927.8.4480	29	0	15	18	hyp. protein
12	elongation factor 1-alpha, EF-1-alpha (TEF1)	Tb927.10.2100	49	2	13	9	
13	hypothetical protein, conserved	Tb927.5.4320	31	0	9	9	Fip1
14	unspecified product	Tb927.9.5750	22	1	5	3	
15	chaperonin Hsp60, mitochondrial precursor	Tb927.10.6400	60	1	4	5	
16	hypothetical protein	Tb927.8.7490	158	0	3	3	
17	Heat shock protein 83, putative	Tb927.10.10890	81	0	3	8	
18	heat shock 70 kDa protein, putative	Tb927.7.710	70	0	3	6	
19	60S acidic ribosomal subunit protein, putative	Tb927.11.2050	35	0	3	2	
20	heat shock 70 kDa protein, mitochondrial precursor, putative	Tb927.6.3740	72	1	2	7	
21	hypothetical protein, conserved	Tb927.8.8210	15	0	2	5	CstF64
22	actin A	Tb927.9.8850	45	0	2	4	
23	peroxidoxin (TRYP2)	Tb927.8.1990	26	0	2	4	
24	chaperone protein DnaJ, putative	Tb927.2.5160	45	0	2	3	
25	GTP-binding nuclear protein rtb2, putative	Tb927.3.1120	24	0	2	3	
26	glutamine synthetase, putative	Tb927.7.4970	47	0	1	12	
27	40S ribosomal protein S3, putative	Tb927.9.6070	30	0	1	3	
28	40S ribosomal protein S4, putative	Tb927.11.3590	31	0	1	3	
29	t-complex protein 1 gamma subunit, putative	Tb927.8.3150	61	0	1	3	
30	elongation factor 2	Tb10.70.2650	94	2	0	9	
31	glutamate dehydrogenase (GDH)	Tb927.9.5900	112	0	0	10	
32	succinyl-CoA ligase [GDP-forming] beta-chain, putative	Tb927.9.5900	55	2	0	7	
33	enolase	Tb927.10.2890	47	0	0	10	
34	T-complex protein 1, alpha subunit, putative (TCP-1-alpha)	Tb927.11.16760	53	0	0	4	
35	retrotransposon hot spot protein 5 (RHS5), putative	Tb927.2.240	95	0	0	3	
36	ATP-dependent DEAD box helicase, putative, eukaryotic initiation factor 4;	Tb927.9.4680	45	0	0	4	
37	2-amino-3-ketobutyrate coenzyme A ligase, putative	Tb927.8.6060	44	0	0	5	
38	DHH1	Tb927.10.3990	46	0	0	4	
39	hypothetical protein, conserved	Tb927.4.1300	42	0	0	5	
40	phosphoglycerate kinase	Tb927.1.710	45	0	0	5	
41	delta-1-pyrroline-5-carboxylate dehydrogenase, putative	Tb927.10.3210	62	0	0	4	
42	T-complex protein 1, beta subunit, putative	Tb927.11.1900	58	0	0	3	
43	unspecified product	Tb927.9.6230	42	0	0	4	
44	T-complex protein 1, zeta subunit, putative	Tb927.11.3240	60	0	0	3	
45	ATP-dependent DEAD/H RNA helicase, putative	Tb927.10.540	49	0	0	4	
46	cystathionine beta-synthase, putative	Tb11.02.5400	39	0	0	4	
47	Chain A, S-Adenosyl Homocysteine Hydrolase (Sahh)	Tb927.11.9590	48	0	0	3	
48	ADP-ribosylation factor-like protein 3A, putative	Tb927.3.3450	20	0	0	3	
49	prostaglandin f synthase	Tb927.11.4700	32	0	0	3	

50	L-threonine 3-dehydrogenase, putative	Tb927.6.2790	37	0	0	3
51	malic enzyme	Tb927.11.5440	62	0	0	3

*T.brucei* proteins were identified by mass spectroscopy as described under “Materials and Methods.”

Each protein is described by the systematic TriTrypDB annotation, TriTrypDB accession number, molecular mass (kDa).