

Subcellular (Non-plant)

Table S4. Predicted subcellular locations for high-confidence protein groups (protein probability: 1% false discovery rate, $p \geq 0.95$.) identified in the *T. brucei* acidocalcisome fractions (ACCS1 and ACCS2) from our prediction servers using non-plant based algorithms. Individual protein predictions are based upon agreement between at least two analysis packages. Consensus for identifications with multiple protein hits (see Methods for explanation of protein grouping based on degenerate peptide fingerprints) is given when prediction for a compartment agrees among two or more members of the group. S, secreted. C, cytosol. M, mitochondrion. N, nucleus. PM, plasma membrane. G, Golgi complex. ER, endoplasmic reticulum. P, peroxisome. L, lysosome. CYKS, cytoskeleton. Threshold probabilities and confidences used to screen our predictions with poor reliability: targetP (RC = 1). pTarget $\geq 80\%$, SLP-LOCAL ≥ 2 , WoLFPSort $\geq 80\%$. WoLFPSORT thresholds for each subcellular location were derived from empirical prediction confidence statistics (wolfsort.org/empiricalConfidenceByNumNeighbors/index.html, updated August 15, 2007).

Protein Group	GeneID	Description	Group Consensus	TargetP		pTARGET		SLP-LOCAL		WoLF-PSORT	Individual Consensus
				Location	Reliability	Location	Confidence	Location	Reliability	Location	
1	Tb927.6.3740	heat shock 70 kDa protein, mitochondrial precursor, putative	M			M	81.4			M	M
	Tb927.6.3750	heat shock 70 kDa protein, mitochondrial precursor, putative				M	81.4			M	M
	Tb927.6.3800	heat shock 70 kDa protein, mitochondrial precursor, putative				M	81.4			M	M
2	Tb927.11.6280	pyruvate phosphate dikinase	C			C	100	NC	4		C
3	Tb927.1.2330	beta tubulin	C			C	87.6	NC	3		C
	Tb927.1.2350	beta tubulin				C	87.6	NC	3		C
	Tb927.1.2370	beta tubulin				C	87.6	NC	3		C
	Tb927.1.2390	beta tubulin				C	87.6	NC	3		C
4	Tb927.10.6400	chaperonin HSP60, mitochondrial precursor	M			M	93.9	M	2		M
	Tb927.10.6510	chaperonin HSP60, mitochondrial precursor				M	93.9	M	2		M
5	Tb927.3.1380	ATP synthase beta chain, mitochondrial precursor,ATP synthase F1, beta subunit	M			M	93.9	M	3	M	M
6	Tb927.2.4210	glycosomal phosphoenolpyruvate carboxykinase				P	81.4				
7	Tb927.11.7460	glucose-regulated protein 78, putative,luminal binding protein 1 (BiP), putative	S	S	1	M	81.4	S	2		S
	Tb927.11.7510	glucose-regulated protein 78, putative,luminal binding protein 1 (BiP), putative		S	1	M	81.4	S	2		S
8	Tb927.10.5620	fructose-bisphosphate aldolase, glycosomal				P	81.4				
9	Tb927.1.2340	alpha tubulin	C			C	81.4	NC	2		C
	Tb927.1.2360	alpha tubulin				C	81.4	NC	2		C
	Tb927.1.2380	alpha tubulin				C	81.4	NC	2		C
	Tb927.1.2400	alpha tubulin				C	81.4	NC	2		C
10	Tb927.6.4280	glyceraldehyde 3-phosphate dehydrogenase, glycosomal				M	93.9				
	Tb927.6.4300	glyceraldehyde 3-phosphate dehydrogenase, glycosomal				M	93.9				
11	Tb927.8.3530	glycerol-3-phosphate dehydrogenase [NAD], glycosomal									
12	Tb927.11.11330	heat shock protein 70	C			C	87.6	NC	3		C
13	Tb927.11.9980	2-oxoglutarate dehydrogenase E1 component, putative				P	81.4				
14	Tb927.10.15410	glycosomal malate dehydrogenase				M	87.6				
15	Tb927.9.12570	glycerol kinase, glycosomal						NC	2		
16	Tb927.5.930	NADH-dependent fumarate reductase				P	100	NC	2		
17	Tb927.11.3980	mitochondrial processing peptidase alpha subunit, putative,metallo-peptidase, Clan ME, Family M16				P	87.6			M	
18	Tb927.2.4230	NUP-1 protein, putative	N			N	100	NC	3		N
19	Tb927.3.2230	succinyl-CoA synthetase alpha subunit, putative	M			M	100	M	2		M
20	Tb927.5.1060	mitochondrial processing peptidase, beta subunit, putative,metallo-peptidase, Clan ME, Family M16				G	81.4			M	
21	Tb927.11.5520	triosephosphate isomerase	C			C	87.6	NC	2		C
22	Tb927.4.2070	antigenic protein, putative	C			C	87.6	NC	4		C
23	Tb927.11.11680	2-oxoglutarate dehydrogenase E2 component, putative	M			M	87.6			M	M
24	Tb927.10.8030	hypothetical protein, conserved	M					M	2		M
25	Tb927.10.7410	succinyl-CoA ligase [GDP-forming] beta-chain, putative-with=GeneDB:LmjF36.2950	M			M	87.6			M	M
26	Tb927.9.5900	glutamate dehydrogenase								M	M
27	Tb927.5.2930	hypothetical protein, conserved				G	81.4			N	
28	Tb927.5.2080	guanosine monophosphate reductase, putative	C			C	100	NC	3		C
29	Tb927.9.5320	nucleolar RNA binding protein, putative				P	81.4				
30	Tb927.8.2770	inositol 1,4,5-trisphosphate receptor	C			C	81.4	NC	3	PM	C
31	Tb927.10.3210	delta-1-pyrroline-5-carboxylate dehydrogenase, putative				P	87.6				
32	Tb927.11.1020	ribokinase, putative	C			C	87.6	NC	2		C
33	Tb927.11.2690	succinyl-coA:3-ketoacid-coenzyme A transferase, mitochondrial precursor, putative				P	87.6				
34	Tb927.11.1450	2-oxoglutarate dehydrogenase E1 component, putative	M	M	1	P	81.4	M	2		M
35	Tb927.10.14820	mitochondrial carrier protein, putative,ADP/ATP translocase 1, putative						NC	3		
	Tb927.10.14830	mitochondrial carrier protein, putative,ADP/ATP translocase 1, putative						NC	3		
	Tb927.10.14840	mitochondrial carrier protein, putative,ADP/ATP translocase 1, putative						NC	3		
36	Tb927.10.14550	ATP-dependent DEAD/H RNA helicase, putative						NC	3		
37	Tb927.10.2090	elongation factor 1-alpha,EF-1-alpha	C			C	100			N	
	Tb927.10.2100	elongation factor 1-alpha,EF-1-alpha				C	93.9	NC	2	C	C
	Tb927.10.2110	elongation factor 1-alpha				C	93.9	NC	2	C	C
38	Tb927.7.7420	ATP synthase alpha chain, mitochondrial precursor,ATP synthase F1, alpha subunit	M			M	100	M	3	M	M
	Tb927.7.7430	ATP synthase alpha chain, mitochondrial precursor,ATP synthase F1, alpha subunit				M	100	M	3	M	M
39	Tb927.10.2020	hexokinase	C			C	93.9	NC	3		C
40	Tb927.10.1510	NOT1				P	93.9	NC	2		
41	Tb927.2.1560	cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative									
	Tb927.2.1680	cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative									
42	Tb927.3.3580	lipophosphoglycan biosynthetic protein, putative	S	S	1	M	87.6	S	3		S
43	Tb927.3.1790	pyruvate dehydrogenase E1 beta subunit, putative	M			M	87.6	M	3	M	M
44	Tb927.10.7570	dihydrolipoamide acetyltransferase E2 subunit, putative	M			M	93.9			M	M
45	Tb927.5.3400	calcium-translocating P-type ATPase,calcium pump				P	100	NC	3		
46	Tb927.8.3750	nucleolar protein, putative				C	87.6				
47	Tb927.1.4100	cytochrome oxidase subunit IV	M			N	81.4	M	3	M	M

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48	Tb927.8.2540	3-ketoacyl-CoA thiolase, putative	M				M	93.9				M		M
49	Tb927.8.5640	hypothetical protein, conserved	M				M					M		M
50	Tb927.10.1170	intraflagellar transport protein IFT172, putative			M	1								
51	Tb927.10.12700	pyruvate dehydrogenase E1 alpha subunit, putative	M							M	2			M
52	Tb927.10.16120	inosine-5'-monophosphate dehydrogenase,IMP dehydrogenase												
53	Tb927.9.11580	Gim5A protein,glycosomal membrane protein	PM							NC	3			
	Tb927.9.11600	Gim5B protein,glycosomal membrane protein								NC	3			
54	Tb927.10.2010	hexokinase	C							NC	3		PM	PM
55	Tb927.8.1740	hypothetical protein, conserved												
56	Tb927.8.6110	hypothetical protein, conserved	M											
57	Tb927.10.2560	mitochondrial malate dehydrogenase								P	87.6	M	2	M
58	Tb927.10.4560	elongation factor 2	C							C	100	NC	4	C
	Tb927.10.4570	elongation factor 2								C	100	NC	4	C
59	Tb927.6.2230	hypothetical protein, conserved	N							N	87.6	NC	3	N
60	Tb927.10.8940	hypothetical protein, conserved	N							N	93.9	NC	2	N
61	Tb927.10.7020	acid phosphatase, putative			S	1				G	87.6			
62	Tb927.6.4440	hypothetical protein, conserved	N							N	93.9	NC	3	N
63	Tb927.8.6060	2-amino-3-ketobutyrate coenzyme A ligase, putative,glycine acetyltransferase, putative	M							M	93.9	M	2	M
64	Tb927.6.2790	L-threonine 3-dehydrogenase, putative								M	93.9			
65	Tb927.4.1300	hypothetical protein, conserved								P	87.6	NC	2	
66	Tb927.10.4310	prohibitin 2, putative								M	87.6	NC	2	
67	Tb927.9.14160	rieske iron-sulfur protein, mitochondrial precursor								G	93.9	M	2	
68	Tb927.1.120	retrotransposon hot spot protein 4 (RHS4), putative	C							C	81.4	NC	5	C
69	Tb927.10.2350	pyruvate dehydrogenase complex E3 binding protein, putative								M	81.4			
70	Tb927.10.180	ATP synthase F1 subunit gamma protein, putative										NC	3	
71	Tb927.3.3900	carnitine O-palmitoyltransferase II, putative								G	100			M
72	Tb927.2.3030	ATP-dependent Clp protease subunit, heat shock protein 78 (HSP78), putative,serine peptidase, putative	M							M	87.6			M
73	Tb927.3.3270	ATP-dependent phosphofructokinase								P	93.9			
74	Tb927.10.2240	hypothetical protein, conserved												
75	Tb927.11.16730	dihydrolipoyl dehydrogenase								C	87.6			
76	Tb927.9.12510	ATP-dependent DEAD/H RNA helicase, putative	N							N	100	NC	3	N
77	Tb927.3.5050	60S ribosomal protein L4	N							N	93.9	NC	2	N
78	Tb927.4.4380	vacuolar-type proton translocating pyrophosphatase 1, putative	S		S	1						S	2	PM
	Tb927.8.7980	vacuolar-type proton translocating pyrophosphatase 1,V-type H(-)-translocating pyrophosphatase			S	1						S	2	PM
79	Tb927.9.5150	ribosomal protein S6, putative,NHP2/RS6-like protein	C							C	93.9	NC	4	C
80	Tb927.4.3950	cytoskeleton-associated protein CAP5.5, putative,cysteine peptidase, Clan CA, family C2, putative										NC	3	
81	Tb927.3.3130	hypothetical protein, conserved												
82	Tb927.9.6100	TFIIIF-stimulated CTD phosphatase, putative								M	100			
83	Tb927.8.6170	transketolase, putative								P	100	NC	2	
84	Tb927.3.930	dynein heavy chain, putative								P	81.4	NC	2	
85	Tb927.10.14750	fibrillarin, putative	N							N	93.9	NC	2	N
86	Tb927.9.6090	TFIIIF-stimulated CTD phosphatase, putative								M	100			
87	Tb927.11.2650	heat shock protein 84, putative								M	93.9	M	3	M
88	Tb927.11.13180	hypothetical protein, conserved	M		M	1				M	100	NC	2	
89	Tb927.9.10770	Polyadenylate-binding protein 2 (Poly(A)-binding protein 2) (Poly(A)-binding protein II) (PABII) (Polyadenylate-binding nuclear protein 1) (Nuclear poly(A)-binding protein 1) (PABP2), putative								P	81.4	NC	2	
90	Tb927.8.6580	succinate dehydrogenase flavoprotein, putative	M							P	81.4	M	2	M
91	Tb927.11.7380	glycerol-3-phosphate dehydrogenase (FAD-dependent), mitochondrial								M	81.4			
92	Tb927.9.2470	nucleolar protein	C							C	87.6	NC	4	C
93	Tb927.8.1160	vacuolar-type Ca2 -ATPase, putative								M	87.6	NC	3	PM
94	Tb927.7.2700	NADH-cytochrome b5 reductase, putative								P	87.6			
95	Tb927.10.470	choline dehydrogenase, putative								P	81.4			
96	Tb927.8.1180	vacuolar-type Ca2 -ATPase 1								P	87.6	NC	4	PM
97	Tb927.11.13280	mitochondrial RNA binding protein 2								G	87.6			M
98	Tb927.5.1210	short-chain dehydrogenase, putative	S		S	1				ER	93.9	S	2	S
99	Tb927.6.2170	co-chaperone GrpE, putative								M	81.4	M	4	M
100	Tb927.7.6360	histone H2A variant	M		M	1				P	93.9	NC	3	
101	Tb927.10.12500	P-type H -ATPase, putative										NC	5	PM
102	Tb927.5.3810	orotidine-5-phosphate decarboxylase/orotate phosphoribosyltransferase, putative,OMPDCase-OPRTase, putative								G	87.6			
103	Tb927.10.13510	zinc metallopeptidase, putative								M	87.6	NC	3	
104	Tb927.5.520	stomatol-like protein, putative								L	87.6	S	2	
105	Tb927.11.3250	dynein heavy chain, putative								C	93.9	NC	6	C
106	Tb927.10.11310	intraflagellar transport protein IFT55/IFT57, putative	C							C	100	NC	6	C
107	Tb927.8.3060	cytosolic leucyl aminopeptidase, putative,metallo-peptidase, Clan MF, Family M17								P	81.4			
108	Tb927.8.1330	60S ribosomal protein L7a, putative								N	87.6	NC	3	N
	Tb927.8.1340	60S ribosomal protein L7a, putative								N	87.6	NC	3	N
109	Tb927.10.6910	Sterol methyltransferase, putative												
	Tb927.10.6950	sterol 24-c-methyltransferase, putative												
110	Tb927.9.9660	hypothetical protein, conserved										NC	6	
111	Tb927.2.2510	voltage-dependent anion-selective channel										NC	3	
	Tb927.2.2520	voltage-dependent anion-selective channel										NC	3	
112	Tb927.11.6460	hypothetical protein, conserved								P	81.4			PM
113	Tb927.7.6670	hypothetical protein, conserved								G	81.4			

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180	Tb927.10.3260	Long-chain-fatty-acid-CoA ligase 5 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 5) (LACS 5), putative	C			C	93.9	NC	2			C
181	Tb927.3.2180	hypothetical protein, conserved				M	81.4					
182	Tb927.10.560	40S ribosomal proteins S11, putative	NC			N	93.9	NC	3		C	NC
183	Tb927.7.4770	cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative	C			C	81.4	NC	3			C
184	Tb927.11.550	hypothetical protein SCD6.10									M	
185	Tb927.8.890	small GTP-binding protein Rab1, putative										
186	Tb927.7.2570	mRNA processing protein, putative	M		M	G	93.9	M	2		M	M
187	Tb927.10.15180	nucleosome assembly protein, putative	C			C	93.9	NC	6			C
188	Tb927.11.1430	hypothetical protein, conserved	C			C	81.4	NC	3			C
189	Tb927.9.9550	hypothetical protein, conserved	N			N	100	NC	6		N	N
190	Tb927.4.5010	calreticulin, putative			S							
	Tb927.8.7410	calreticulin, putative			S							
191	Tb927.7.3740	hypothetical protein, conserved	N			N	93.9	NC	5			N
192	Tb927.10.9570	paraflagellar rod component, putative	C			C	93.9	NC	3			C
193	Tb927.8.1570	hypothetical protein, conserved						NC	3			
194	Tb927.10.6180	hypothetical protein, conserved	S		S	PM	81.4	S	4			S
195	Tb927.10.1390	hypoxanthine-guanine phosphoribosyltransferase, putative	C			P	93.9	NC	3		C	C
196	Tb927.11.12220	vacuolar transporter chaperone 4						NC	3		PM	
197	Tb927.8.6660	paraflagellar rod component, putative	N			N	93.9	NC	4			N
198	Tb927.8.4780	hypothetical protein, conserved	N			N	100	NC	3			N
199	Tb927.3.3460	hypothetical protein, conserved	M			M	81.4	M	2		M	M
200	Tb927.11.9080	hypothetical protein, conserved	C			C	93.9	NC	6			C
201	Tb927.11.14130	ribosomal protein L18, putative	N			N	81.4	NC	2			N
	Tb927.10.3840	60S ribosomal protein L18a, putative				N	81.4	NC	2			N
202	Tb927.10.4880	hypothetical protein, conserved				G	93.9					
203	Tb927.9.11220	hypothetical protein, conserved				P	81.4	NC	2			
204	Tb927.8.3870	hypothetical protein, conserved	N			N	87.6	NC	4		N	N
205	Tb927.2.5160	chaperone protein DNAJ, putative	C			C	100	NC	6			C
206	Tb927.10.240	peroxin 14, putative	N			N	100	NC	5			N
207	Tb927.10.8230	protein disulfide isomerase,bloodstream- specific protein 2 precursor				ER	93.9					
208	Tb927.6.4210	aldehyde dehydrogenase, putative										
209	Tb927.6.3150	Hydin,flagellar component										
210	Tb927.10.7090	alternative oxidase				P	93.9	NC	2			
211	Tb927.11.1710	mitochondrial RNA binding protein 1.gBP21, MRP1	M			M	100	M	3		M	M
212	Tb927.3.1810	hypothetical protein, conserved										
213	Tb927.9.9450	hypothetical protein, conserved,zinc finger protein family member, putative	N			N	100	NC	2			N
214	Tb927.11.8160	dynein heavy chain, putative	C			C	87.6	NC	7			C
215	Tb927.4.3590	translation elongation factor 1-beta, putative				C	87.6					
216	Tb927.9.2450	electron transport protein SCO1/SCO2, putative	C			C	81.4	NC	5			C
217	Tb927.3.2440	serine/threonine-protein kinase, putative,protein kinase, putative	N			P	81.4	NC	6		N	N
218	Tb927.9.4190	fatty acyl CoA syntetase 1				G	93.9					
219	Tb927.4.4070	mevalonate kinase, putative	C			C	100	NC	3			C
220	Tb927.10.2530	adenylate kinase, putative	C			C	100	NC	2		C	C
221	Tb927.5.500	hypothetical protein, conserved				N	87.6					
222	Tb927.2.3800	mRNA processing protein, putative	M		M	M	93.9	M	2			M
223	Tb927.7.2170	hypothetical protein, conserved	N			N	87.6	NC	2		N	N
224	Tb927.8.1990	peroxidoxin	M		M	M	81.4	M	3		M	M
225	Tb927.10.12840	mitochondrial carrier protein, putative,mitochondrial 2-oxoglutarate/malate carrier protein, putative										
226	Tb927.7.2390	hypothetical protein, conserved	N			N	100	NC	2			N
227	Tb927.4.1330	DNA topoisomerase IB, large subunit	C			C	100	NC	3			C
228	Tb927.11.12230	heat shock protein HslVU, ATPase subunit HslU, putative,ATP-dependent hsl protease ATP-binding subunit hslU, putative				M	87.6					
229	Tb927.8.3690	isocitrate dehydrogenase [NADP], mitochondrial precursor, putative	M		M	M	87.6	M	2		M	M
230	Tb927.11.15040	chaperonin HSP60, mitochondrial precursor, putative,heat shock protein 60				M	87.6					
231	Tb927.6.3050	aldehyde dehydrogenase family, putative	C			C	93.9	NC	4			C
232	Tb927.8.5120	cytochrome c				P	93.9	NC	3			
233	Tb927.6.1500	alkyl-dihydroxyacetone phosphate synthase	C			C	81.4	NC	5			C
234	Tb927.2.5660	adenylate kinase, putative	C			C	93.9	NC	2			C
235	Tb927.10.5770	valosin-containing protein homolog,Transitional endoplasmic reticulum ATPase, putative	C			C	93.9	NC	4			C
236	Tb927.11.5290	mitochondrial carrier protein, putative				PM	93.9					
237	Tb927.9.5690	60S acidic ribosomal protein, putative				P	87.6					
238	Tb927.11.6140	40S ribosomal protein S15A, putative				P	81.4					
239	Tb927.11.600	hypothetical protein, conserved				M	81.4					
240	Tb927.2.5800	sedoheptulose-1,7-bisphosphatase				P	81.4					
241	Tb927.4.2080	hypothetical protein, conserved	N			N	93.9	NC	6			N
242	Tb927.10.8780	hypothetical protein, conserved	C			C	93.9	NC	4			C
243	Tb927.10.15750	hypothetical protein, conserved	N			N	87.6	NC	2			N
244	Tb927.9.4500	heat shock protein, putative,HSP70-like protein	S		S			S	5			S
245	Tb927.9.4680	ATP-dependent DEAD box helicase, putative	NC			C	93.9	NC	7		N	NC
246	Tb927.4.870	dynein heavy chain, putative				G	93.9					
247	Tb927.10.5760	adenylate kinase, putative				M	87.6	NC	3			
248	Tb927.10.13180	hypothetical protein, conserved						NC	4			
249	Tb927.11.14780	phosphomannose isomerase, putative	C			C	93.9	NC	3			C

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250	Tb927.2.2940	hypothetical protein, conserved	N				N	87.6	NC	4			N
251	Tb927.10.10360	microtubule-associated protein, putative	N				N	100	NC	8			N
252	Tb927.4.1360	hypothetical protein, conserved	C				M	93.9	NC	2			C
253	Tb927.11.15150	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative	S	S	1		ER	100	S	4		C	C
254	Tb927.10.8200	hypothetical protein, conserved	N				N	81.4	NC	3			S
255	Tb927.7.4900	5'-3' exonuclease XRNA, putative,exoribonuclease 1, putative	N				G	87.6	NC	3			N
256	Tb927.9.5960	succinate dehydrogenase, putative					S	87.6					
257	Tb927.11.9400	hypothetical protein, conserved	C				C	100	NC	5			C
258	Tb927.7.210	proline dehydrogenase	M				M	87.6	M	2		M	M
259	Tb927.11.8870	mitochondrial DEAD box protein,KREH1	M				G	87.6	M	3		M	M
260	Tb927.11.1980	hypothetical protein, conserved,zinc finger protein family member, putative	M	M	1		P	87.6	NC	3			
261	Tb927.4.4910	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative					G	93.9					
262	Tb927.10.16150	ATP-dependent zinc metallopeptidase, putative,metallo-peptidase, Clan MA(E) Family M41					P	87.6	NC	3			
263	Tb927.11.8050	hypothetical protein, conserved	N				N	100	NC	7		N	N
264	Tb927.10.2950	hypothetical protein, conserved					G	81.4					
265	Tb927.8.1550	paraflagellar rod component, putative	N				N	93.9	NC	3			N
266	Tb927.5.4420	nucleolar RNA helicase II, putative,nucleolar RNA helicase Gu, putative	C				C	93.9	NC	5			C
267	Tb927.10.770	hypothetical protein, conserved	M	M	1		M	81.4				M	M
268	Tb927.11.3360	hypothetical protein, conserved							NC	2			
269	Tb927.6.4980	40S ribosomal protein S14	N				N	87.6	NC	5			N
270	Tb927.10.10280	microtubule-associated protein, putative	N				N	100	NC	8			N
271	Tb927.3.1840	3-oxo-5-alpha-steroid 4-dehydrogenase, putative					P	87.6	NC	4			
272	Tb927.11.4450	hypothetical protein, conserved					P	87.6	NC	3			
273	Tb927.7.3370	hypothetical protein, conserved	N				N	93.9	NC	2		N	N
274	Tb927.8.4400	hypothetical protein, conserved					N	93.9					
275	Tb927.11.10760	kinesin-like protein, putative					P	93.9	NC	2			
276	Tb927.10.9780	ATP-dependent DEAD/H RNA helicase, putative,ATP- dependent RNA helicase, putative	N				N	100	NC	2		N	N
277	Tb927.11.16510	hypothetical protein, conserved					M	87.6					
278	Tb927.11.17000	hypothetical protein, conserved,leucine-rich repeat protein (LRRP), putative					P	87.6	NC	2			
279	Tb927.9.15360	40S ribosomal protein S6, putative					P	100	NC	5			
280	Tb927.10.170	pseudouridine synthase, Cbf5p	C				P	87.6	NC	4		C	C
281	Tb927.3.5570	syntaxin, putative	C				C	87.6	NC	3			C
282	Tb927.10.6630	ATP-dependent DEAD/H RNA helicase HEL64, putative	N				N	81.4	NC	5		N	N
283	Tb927.8.2740	mitochondrial RNA binding protein					P	81.4					
284	Tb927.10.2770	eukaryotic translation initiation factor 5, putative	C				C	100	NC	5			C
285	Tb927.7.3980	immunodominant antigen, putative,tc40 antigen-like	N				N	87.6	NC	5			N
286	Tb927.3.3590	U3 small nucleolar ribonucleoprotein protein MPP10, putative	N				N	87.6	NC	4			N
287	Tb927.11.11540	DNA topoisomerase II, putative	C				C	100	NC	5			C
288	Tb927.7.1290	hypothetical protein, conserved	S	S	1				S	3			S
289	Tb927.11.2790	hypothetical protein, conserved	N				N	93.9	NC	3			N
290	Tb927.8.2000	cyclophilin, putative											
291	Tb927.8.1860	pitriylisin-like metalloprotease,metallo-peptidase, Clan ME, Family M16C										M	
292	Tb927.11.6210	sterol 14-alpha-demethylase	S	S	1				S	4		ER	S
293	Tb927.6.4130	hypothetical protein, conserved	M				M	100				M	M
294	Tb927.9.13990	RNA-binding protein, putative	N				N	87.6	NC	7		S	N
295	Tb927.6.2050	ribosome biogenesis regulatory protein (RRS1), putative							NC	2			
296	Tb927.4.410	CAF 40							NC	3			
297	Tb927.7.280	cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative					PM	87.6					
298	Tb927.10.6050	clathrin heavy chain					P	81.4	NC	2			
299	Tb927.9.14200	hypothetical protein, conserved					G	87.6	M	2			
300	Tb927.3.5020	hypothetical protein, conserved					P	87.6	NC	3			
301	Tb927.8.6390	lysophospholipase, putative,alpha/beta hydrolase, putative					P	81.4	NC	4			
302	Tb927.11.6050	hypothetical protein, conserved					N	87.6	NC	3			
303	Tb927.2.4550	FtsJ cell division protein, putative	N				N	93.9	NC	3		PM	N
304	Tb927.9.15330	hypothetical protein, conserved	N				N	93.9	NC	2			N
305	Tb927.11.5220	chaperone protein DNAJ, putative	S	S	1				S	3		S	S
306	Tb927.11.3500	hypothetical protein, conserved							NC	4			
307	Tb927.6.1470	hypothetical protein, conserved	N				N	93.9	NC	5		N	N
308	Tb927.1.1700	hypothetical protein, conserved	N				N	100	NC	4			N
309	Tb927.2.5130	hypothetical protein, conserved	C				C	87.6	NC	4			C
310	Tb927.8.2630	kinesin, putative	N				N	100	NC	4			N
311	Tb927.11.6300	40S ribosomal protein S5, putative	C				C	87.6				C	C
312	Tb927.9.1750	hypothetical protein, conserved	C				C	81.4	NC	3		C	C
313	Tb927.9.11000	small GTPase, putative,GTP-binding protein, putative					G	93.9	NC	2			
314	Tb927.9.11850	structural maintenance of chromosome 1, putative	N				N	93.9	NC	2			N
315	Tb927.10.4760	hypothetical protein, conserved											
316	Tb927.6.3890	replication factor C, subunit 2, putative										S	
317	Tb927.11.16480	enoyl-CoA hydratase/isomerase family protein, putative	C				C	93.9	NC	5			C
318	Tb927.7.2190	hypothetical protein, conserved											
319	Tb927.7.3430	cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative		S	1				S	2			
320	Tb927.11.3770	hypothetical protein, conserved					P	81.4					
321	Tb927.7.3330	hypothetical protein, conserved	N				N	93.9	NC	6			N

Subcellular (Non-plant)

538	Tb927.6.5090	hypothetical protein, conserved				PM			PM	81.4		NC	5		PM		PM
539	Tb927.11.460	hypothetical protein, conserved,predicted WD40 repeat protein										NC	2				
540	Tb927.11.11250	cytosolic malate dehydrogenase										NC	2				
541	Tb927.6.1550	hypothetical protein, conserved,leucine-rich repeat protein (LRRP), putative							PM	87.6		NC	3				
542	Tb927.7.540	chaperone protein DNAj, putative										NC	2				
543	Tb927.7.5320	hypothetical protein, conserved							C	81.4		NC	3				C
544	Tb927.10.14720	peroxin 13							N	100		NC	3				N
545	Tb927.4.1600	hypothetical protein, conserved							G	81.4							
546	Tb927.9.3370	thioredoxin							C	100		NC	2				C
547	Tb927.10.10800	hypothetical protein, conserved							S	81.4		S	2				S
548	Tb927.7.3810	hypothetical protein, conserved		S	1				ER	81.4					PM		
549	Tb927.10.7700	ABC transporter, putative							G	81.4					M		
550	Tb927.8.8120	hypothetical protein, conserved										NC	4		PM		
551	Tb927.7.2670	hypothetical protein, conserved,zinc finger protein family member, putative		S	1							S	4		PM		
552	Tb927.9.10070	hypothetical protein, conserved							N	81.4		NC	3		S		S
553	Tb927.10.15950	TFIID-like protein, putative							M	87.6							N
554	Tb927.5.1160	hypothetical protein, conserved							C	87.6		NC	8				C
555	Tb927.6.2720	calcium-binding protein, putative							S			S	3				S
556	Tb927.6.2720	calcium-binding protein, putative		S	1							NC	5		S		S
557	Tb927.11.15240	small GTPase, putative,ras-related protein rab-2a, putative							C			NC	2				C
558	Tb927.10.600	hypothetical protein, conserved							C	87.6		M	2		C		C
559	Tb927.9.15060	rRNA processing protein, putative							N	93.9		NC	6		N		N
560	Tb927.9.5040	cAMP-specific phosphodiesterase							C	93.9		NC	5				C
561	Tb927.8.4500	eukaryotic translation initiation factor 4 gamma, putative							P	81.4		NC	3				C
562	Tb927.9.5280	hypothetical protein, conserved							G	93.9		M	2				
563	Tb927.2.4090	hypothetical protein, conserved		S	1							S	3				S
564	Tb927.8.4890	endoplasmic reticulum oxidoreductin, putative,pol-associated gene 1		S	1				L	87.6		S	4		S		S
565	Tb927.10.790	vesicle-associated membrane protein, putative,synaptobrevin, putative							M	81.4							
566	Tb927.11.3240	T-complex protein 1, zeta subunit, putative							M	93.9		NC	2				
567	Tb927.11.10170	hypothetical protein, conserved							G	87.6							
568	Tb927.10.10880	ATP-binding cassette protein, putative,ABC transporter, putative,ATPase, putative							P	93.9		NC	5				
569	Tb927.11.2570	hypothetical protein, conserved															
570	Tb927.8.3150	T-complex protein 1, gamma subunit, putative							C	93.9		NC	2				C
571	Tb927.11.11160	sodium/sulphate symporter, putative										NC	4		PM		
572	Tb927.10.14030	hypothetical protein, conserved		S	1							S	4		S		S
573	Tb927.11.2120	hypothetical protein, conserved							G	81.4		NC	4				
574	Tb927.11.14960	pumilio/PUF RNA binding protein 7, putative							P	81.4							
575	Tb927.6.4970	serine/arginine-rich protein specific kinase SRPK, putative,protein kinase, putative							N	100		NC	3		N		N
576	Tb927.10.14390	hypothetical protein, conserved										NC	2				
577	Tb927.9.9940	PACRGB flagellar component							P	100		NC	2				
578	Tb927.10.4430	pumilio RNA binding protein PUF1							C	100		NC	4				C
579	Tb927.6.5210	variant surface glycoprotein (VSG, pseudogene), putative.variant surface glycoprotein, frameshift							N	81.4							
580	Tb927.8.1240	electron transfer flavoprotein-ubiquinone oxidoreductase, putative															
	Tb927.10.12260	cytosolic nonspecific dipeptidase, putative,peptidase (M20/M25/M40 family), putative							P	81.4		NC	4				