

Accession Number	GeneDB Annotation	Annotation Category	Mass (kDa)	log(e)	# of unique identified peptides	Sequence Coverage (%)	NLS (a)	Signal Peptide (b)	TMH domains (b)	Coiled Coils (c)	Pfam Matches (d)	Bioinformatic Notes	GFP localized?
Tb927.1.2380	alpha tubulin	Annotated	49.7	-250.2	47	74.5							
Tb927.5.3400	Calcium-transporting ATPase (Calcium pump)	Annotated	110.2	-244.6	51	47.5							
Tb927.2.4230	NUP-1 protein	Annotated	406.6	-222.9	47	14.4							Yes
Tb927.1.2330	beta tubulin	Annotated	49.6	-215.6	43	74.8							
Tb927.3.1380	ATPase beta subunit	Annotated	55.7	-180.4	33	72.6							
Tb11.02.5500	glucose-regulated protein 78	Annotated	71.3	-171.3	35	61.7							
Tb927.4.4380	vacuolar-type proton translocating pyrophosphatase 1	Annotated	85.8	-162.3	26	31.4							
Tb10.70.5670	TEF1, elongation factor 1-alpha	Annotated	49.0	-161.1	36	66.5							
Tb927.7.7420	ATP synthase alpha chain, mitochondrial precursor	Annotated	63.4	-146.7	35	62.1							
Tb11.01.3110	heat shock protein 70	Annotated	75.3	-143.4	38	62.6							
Tb10.70.2650	elongation factor 2	Annotated	94.2	-132.1	34	49.8							
Tb927.5.1810	lysosomal/endosomal membrane protein p67	Annotated	72.6	-128	21	38.0							
Tb11.02.4150	Glycosomal Pyruvate Phosphate Dikinase	Annotated	100.3	-125.4	37	55.4							
Tb927.6.4280	Glycerolaldehyde-3-phosphate dehydrogenase	Annotated	43.8	-110.6	24	71.1							
Tb927.6.3740	heat shock 70 kDa protein, mitochondrial precursor	Annotated	71.4	-97.8	20	40.6							
Tb09.160.3820	nop5 protein	Annotated	54.9	-96.8	21	53.2							
Tb11.02.1480	mitochondrial processing peptidase alpha subunit, Clan ME, Family M16	Annotated	57.0	-94.3	19	39.9							
Tb10.70.0430	chaperonin Hsp60, mitochondrial precursor	Annotated	59.4	-91.6	16	34.3							
Tb927.5.1210	short-chain dehydrogenase	Annotated	33.8	-89.7	21	69.1							
Tb10.61.1820	mitochondrial carrier protein	Annotated	34.0	-87.9	21	56.0							
Tb927.2.4210	glycosomal phosphoenolpyruvate carboxykinase	Annotated	58.5	-87.4	18	39.6							
Tb927.2.1080	RHS5-c	Annotated	76.5	-86.5	21	31.4							
Tb927.8.3750	Nucleolar Protein, SIK1	Annotated	54.3	-83.3	25	59.8							
H25N7.12	RHS4	Annotated	97.7	-80.5	25	35.5							
Tb11.01.4750	elongation factor 1 gamma	Annotated	60.4	-76.5	20	48.4							
Tb10.70.5800	HK2, hexokinase	Annotated	51.1	-76.1	16	45.0							
Tb10.61.0980	glycosomal malate dehydrogenase	Annotated	33.6	-75.7	15	54.1							
Tb927.4.3590	translation elongation factor 1-beta	Annotated	28.3	-75.2	16	64.3							
Tb927.8.1870	tGLP1, golgi/lysosome glycoprotein 1	Annotated	67.5	-75.2	10	20.2							
Tb11.02.0070	metallo-peptidase, Clan MF, Family M17	Annotated	60.5	-74.7	17	34.8							
Tb10.70.1370	fructose-bisphosphate aldolase, glycosomal	Annotated	41.0	-73.3	15	42.2							
Tb927.3.5370	Conserved hypothetical	Unannotated	34.2	-71.7	10	34.1	***					(e,f)	
Tb927.7.6670	Conserved hypothetical	Unannotated	332.6	-71.5	27	14.7	**	Yes	3	***		(f), large beta sheet presence, however it is very large protein	
Tb09.160.4250	tryparedoxin peroxidase	Annotated	22.4	-69.8	16	81.9							
Tb09.211.3560	glk1, glycerol kinase, glycosomal	Annotated	56.3	-68.7	16	31.0							
Tb927.8.3530	glycerol-3-phosphate dehydrogenase	Annotated	37.7	-66.4	18	52.5							
Tb927.5.1060	mitochondrial processing peptidase, beta subunit	Annotated	54.0	-65.6	17	42.9							
Tb10.389.1180	P-type H+-ATPase	Annotated	100.1	-65.5	23	30.9							
Tb927.4.590	Conserved hypothetical	Unannotated	87.9	-64.9	21	38.7		Yes	1		DUF1620	(e,h), GFP labeling shows a speckled cytosolic pattern	Inconclusive
Tb09.160.2840	ACS4, fatty acyl CoA synthetase 4	Annotated	77.8	-62.8	17	32.3							
Tb927.8.2460	Conserved hypothetical	Unannotated	30.8	-62.7	14	51.4		Yes	4				
Tb11.02.5280	glycerol-3-phosphate dehydrogenase	Annotated	66.9	-62.4	15	32.1							
Tb927.7.6850	TbTS, trans-sialidase	Annotated	84.4	-61.3	15	28.2							
Tb927.3.3580	LPG3, lipophosphoglycan biosynthetic protein	Annotated	87.7	-60.2	13	21.7							
Tb927.3.4300	PFR1, 73 kDa paraflagellar rod protein	Annotated	68.6	-59.7	15	34.8							
Tb927.7.2930	histone H2A	Annotated	14.2	-59.5	10	46.2							
Tb10.v4.0045	prohibitin	Annotated	32.1	-57.5	14	62.7							
Tb10.70.4200	fatty acyl CoA synthetase	Annotated	78.9	-56.5	17	30.5							
Tb10.6k15.0690	Conserved hypothetical	Unannotated	152.8	-55.7	24	27.6						(e,f,g), possible cysteine protease	
Tb10.100.0070	ATP synthase F1 subunit gamma protein	Annotated	34.3	-53.9	13	54.0							
Tb927.4.2850	Conserved hypothetical	Unannotated	72.5	-51.4	15	40.9	**					(e)	
Tb09.211.1750	mitochondrial carrier protein	Annotated	34.2	-51.3	12	42.9							
Tb927.3.3270	TbPFK, ATP-dependent phosphofructokinase	Annotated	53.4	-50.6	16	36.9							
Tb09.160.4710	Conserved hypothetical	Unannotated	170.2	-50.1	13	15.1				***		(f)	
Tb927.4.470	snoRNP protein, GAR1	Annotated	21.7	-50	19	65.9							
Tb10.389.0690	mitochondrial carrier protein	Annotated	33.1	-48.3	11	39.1							
Tb927.5.2930	Conserved hypothetical	Unannotated	43.2	-48.3	11	32.4						(e,f,g)	
Tb11.01.3370	PEX11, glycosomal membrane protein	Annotated	24.0	-47	11	42.6							

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Tb10.70.3290	ATP-dependent DEAD-box RNA helicase, DHH1	Annotated	46.4	-46.7	16	54.4							
Tb05.5K5.70	nucleolar RNA helicase II, Gu	Annotated	68.7	-46.5	12	26.8							
Tb927.5.4020	Hypothetical protein	Unannotated	29.3	-46.2	7	30.8							
Tb09.160.3270	eukaryotic initiation factor 4a	Annotated	45.3	-45.9	12	48.5		Yes		***			
Tb10.70.5110	mMDH, mitochondrial malate dehydrogenase	Annotated	33.1	-45.7	8	43.3							
Tb09.211.4700	RISP, reiske iron-sulfur protein, mitochondrial precursor	Annotated	33.6	-45.5	10	38.7							
Tb11.02.4120	Conserved hypothetical	Unannotated	27.5	-45.2	9	42.7		Yes				(e,f,g)	
Tb09.160.4310	Glutamate dehydrogenase	Annotated	112.0	-44.3	19	26.1							
Tb927.2.2510	Conserved hypothetical	Unannotated	29.1	-44.3	13	50.7						(e,f)	
Tb927.7.4180	long chain fatty acyl elongase	Annotated	33.8	-44.2	9	38.3							
Tb927.5.930	FRDg, NADH-dependent fumarate reductase	Annotated	123.6	-44	12	12.2							
Tb927.7.5940	Conserved hypothetical	Unannotated	67.1	-43.7	11	21.8			14	***	Major Facilitator Superfamily		
Tb927.2.4710	RNA-binding protein, RRM1	Annotated	49.9	-43.3	8	26.0							
Tb11.01.4740	Conserved hypothetical	Unannotated	61.1	-42.9	12	342.0		Yes				(e)	
Tb11.02.5660	Conserved hypothetical	Unannotated	46.2	-42.9	8	24.3			1	***		(e,h)	
Tb09.211.1240	Conserved hypothetical	Unannotated	38.2	-42.7	10	44.4						(e), probable ribosome-binding factor A	
Tb09.160.5480	adenosine transporter	Annotated	50.6	-42.4	12	37.6							
Tb09.211.0540	FBPase, fructose-1,6-bisphosphate, cytosolic	Annotated	38.5	-42	8	26.0							
Tb11.02.4080	lanosterol 14-alpha-demethylase	Annotated	54.3	-42	14	38.6							
Tb10.05.0230	zinc metalloproteinase	Annotated	62.7	-41	7	20.7							
Tb10.6k15.2510	Conserved hypothetical	Unannotated	28.8	-40.8	11	50.9						(e,h)	
Tb927.5.440	Conserved hypothetical	Unannotated	84.5	-40.5	12	22.0		Yes	1			(h). Probable sialidase	
Tb927.3.3330	heat shock protein 20	Annotated	15.8	-39.1	9	65.2							
Tb927.6.4990	ATP synthase, epsilon chain	Annotated	20.1	-39	7	41.7							
Tb927.7.900	Conserved hypothetical	Unannotated	64.7	-39.0	13	36.9		Yes	1			(e), nicalin-like	
Tb927.3.1790	pyruvate dehydrogenase E1 beta subunit	Annotated	37.5	-38.4	8	26.1							
Tb927.7.6360	histone H2A	Annotated	18.6	-37.1	13	67.5							
Tb09.211.2740	Gim5B protein	Annotated	25.9	-36.1	10	51.0							
Tb927.5.1710	ribonucleoprotein p18, mitochondrial precursor	Annotated	21.2	-35.6	6	37.7							
Tb10.70.1100	translation elongation factor 1-beta	Annotated	21.9	-35.5	9	54.2							
Tb927.7.210	proline oxidase	Annotated	63.8	-35.1	10	24.6							
Tb927.8.760	Nopp44/46	Annotated	35.0	-35.1	7	20.7							
Tb927.5.4190	histone H4	Annotated	11.1	-34.8	9	90.0							
Tb09.211.4511	kinetoplastid membrane protein KMP-11	Annotated	11.0	-34.6	6	53.2							
Tb10.v4.0052	microtubule-associated protein 2, MAP2	Annotated	560.8	-34.1	11	3.1							
Tb10.406.0350	histone H2B	Annotated	12.5	-33.7	10	52.6							
Tb10.6k15.1500	Conserved hypothetical	Unannotated	45.3	-33.6	7	25.7						(e,f,g)	
Tb927.6.4210	aldehyde dehydrogenase	Annotated	64.5	-33.5	11	24.2							
Tb10.61.2130	ATP-dependent DEAD/H RNA helicase, DBP1	Annotated	71.3	-33.1	13	27.5							
Tb927.3.5050	60S ribosomal protein L4 (L1)	Annotated	41.8	-31.9	11	41.7							
Tb927.7.2240	Conserved hypothetical	Unannotated	59.6	-31.4	11	41.7							
Tb927.2.100	RHS1	Annotated	94.8	-31.2	16	17.6							
Tb927.5.900	oligosaccharyl transferase subunit	Annotated	92.1	-31.2	11	17.6							
Tb11.01.0480	Conserved hypothetical	Unannotated	63.5	-31.0	7	19.8			9		EF hand, SNARE associated Golgi protein	Vacuole membrane protein 1 (mouse)-like	
Tb927.2.470	retrotransposon hot spot protein RHS4-c .	Annotated	98.2	-30.6	21	10.8							
Tb10.6k15.0410	60S ribosomal protein L18	Annotated	21.8	-30.4	5	26.4							
Tb11.46.0001	60S acidic ribosomal subunit protein	Annotated	34.6	-30.4	10	29.3							
Tb10.61.0150	inosine-5'-monophosphate dehydrogenase	Annotated	48.4	-30	6	16.5							
Tb927.1.2530	Histone H3	Annotated	14.7	-30	7	48.1							
Tb11.0400	Hypothetical protein	Unannotated	27.6	-29.9	11	52.6			1				
Tb11.02.1085	40s ribosomal protein S4	Annotated	30.6	-29.6	8	29.3							
Tb09.211.1800	Conserved hypothetical	Unannotated	53.6	-29.2	7	12.3	**				LiSH	(e,f), Nucleolar -- Confirmed by mAb	
Tb927.4.1330	type IB DNA topoisomerase large subunit .	Annotated	79.2	-29	10	24.1							
Tb927.6.4320	Conserved hypothetical	Unannotated	44.3	-28.9	7	23.5			1		Eukaryotic translation initiation factor 3 subunit 7	(e)	
Tb11.02.3210	triose-phosphate isomerase	Annotated	26.8	-28.8	9	38.8							
Tb10.6k15.1350	pteridine transporter	Annotated	69.9	-28.6	9	15.4							
Tb927.8.1570	Conserved hypothetical	Unannotated	28.8	-28.6	9	42.6					UPF0172	Probable COX4	
Tb927.8.1610	major surface protease gp63	Annotated	62.9	-28.5	8	16.8							
Tb10.v4.0247	s-adenosyl-L-methionine-c-24-delta-sterol-methyl transferase a	Annotated	40.1	-28.3	6	25.0							

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Tb927.1.420	RHS5	Annotated	76.2	-28	19	13.7							
Tb927.3.5620	Conserved hypothetical	Unannotated	112.5	-27.9	13	14.9				***	SPT16, Rtt106	(e,f), Probable transcription factor (FACT complex)	
Tb927.2.1210	RHS4	Annotated	95.1	-27.5	16	14.0							
Tb10.26.0560	60S ribosomal protein L6	Annotated	21.1	-27.4	5	30.7							
Tb927.6.1500	DHAP, alkyl-dihydroxyacetone phosphate synthase	Annotated	69.0	-27.3	8	16.8							
Tb927.3.1840	3-oxo-5-alpha-steroid 4-dehydrogenase	Annotated	33.3	-27.1	8	26.5							
Tb927.8.650	cation-transporting ATPase	Annotated	140.3	-27.1	10	13.2							
Tb927.3.5350	Conserved hypothetical	Unannotated	11.5	-26.9	5	29.5			1			(e)	
Tb09.211.2530	Conserved hypothetical	Unannotated	41.5	-26.8	5	15.7			1			(e)	
Tb10.70.3750	Conserved hypothetical	Unannotated	31.5	-26.6	6	29.2			7			(e,f)	
Tb927.1.860	Conserved hypothetical	Unannotated	29.5	-26.6	8	44.4		Yes	1				
Tb10.26.1080	heat shock protein 83	Annotated	80.7	-26.5	8	17.8							
Tb927.8.5010	PFR2, 69 kDa paraflagellar rod protein	Annotated	69.5	-26.4	7	14.6							
Tb927.7.710	heat shock, 70 Kda	Annotated	70.1	-26.1	13	31.6							
Tb927.3.3890	Conserved hypothetical	Unannotated	36.6	-26.0	5	23.7							
Tb927.4.2530	Conserved hypothetical	Unannotated	16.8	-26.0	7	62.0			3			(e)	
Tb927.5.1780	Conserved hypothetical	Unannotated	48.1	-25.6	5	15.6						(e)	
Tb927.8.7410	calreticulin	Annotated	44.9	-25.6	8	27.5							
Tb927.7.6260	Conserved hypothetical	Unannotated	36.4	-25.4	5	20.1				***	Tetratricopeptide repeat	(e), Tetratricopeptide repeat protein	
Tb927.5.3510	SMC3	Annotated	136.2	-24.3	14	17.7							
Tb927.5.520	stomatol-like protein	Annotated	55.9	-24.3	8	25.2							
Tb09.160.3670	ribosomal protein S6	Annotated	13.5	-23.8	3	49.2							
Tb10.61.0540	Conserved hypothetical	Unannotated	36.3	-23.8	5	25.7	**			***		(e,f,g)	
Tb09.244.2630	40S ribosomal protein S6	Annotated	28.4	-23.5	7	32.4							
Tb927.2.2440	RPN6, proteasome regulatory non-ATPase subunit 6	Annotated	57.2	-23.4	6	24.5							
Tb927.5.2080	inosine-5'-monophosphate dehydrogenase	Annotated	52.2	-23.4	6	19.3							
Tb11.01.4940	AAA ATPase	Annotated	141.0	-23.2	13	16.9							
Tb927.8.1420	acyl-CoA dehydrogenase, mitochondrial precursor	Annotated	55.9	-23.2	5	11.7							
Tb927.5.2530	Conserved hypothetical	Unannotated	114.8	-23.1	13	18.4					DUF699, DUF1726	(g,h)	
Tb927.4.1790	ribosomal protein L3	Annotated	54.3	-22.5	5	18.3							
Tb927.7.2190	Conserved hypothetical	Unannotated	29.2	-22.5	6	23.6		Yes	1			(e), SSR Alpha	
Tb927.7.2370	40S ribosomal protein S15	Annotated	20.0	-22.5	4	30.8							
Tb11.02.2880	DNAJ	Annotated	84.6	-22.4	7	14.6							
Tb927.6.1520	aquaporin 3	Annotated	35.0	-22.2	6	28.9							
Tb927.6.4500	Conserved hypothetical	Unannotated	22.6	-22.2	8	43.3		Yes	1			(e,f)	
Tb927.4.1300	Conserved hypothetical	Unannotated	41.9	-22.1	7	29.4						(e,f,g,h)	
Tb11.0290	RPS14, 40s ribosomal protein S14	Annotated	15.5	-21.9	6	43.0							
Tb09.160.1160	Nop86	Annotated	85.8	-21.8	8	12.1							
Tb09.160.2770	ACS1, fatty acyl CoA syntetase 1	Annotated	78.9	-21.8	9	17.9							
Tb927.1.4100	cytochrome C oxidase subunit IV	Annotated	40.5	-21.7	7	22.3							
Tb927.8.5460	flagellar calcium-binding protein TB-44A	Annotated	45.6	-21.7	5	19.4							
Tb927.4.4620	cytochrome c oxidase VIII (COX VIII)	Annotated	18.7	-21	6	35.0							
Tb10.26.0790	PSSA-2 procyclic form surface glycoprotein	Annotated	46.0	-20.9	4	17.4							
Tb927.8.1740	Conserved hypothetical	Unannotated	62.1	-20.9	9	22.1						(e)	
Tb09.244.2760	cytosolic coat protein	Annotated	24.5	-20.7	7	43.3							
Tb927.6.2550	RNA-binding protein, possible PAB1	Annotated	79.7	-20.7	12	16.2							
Tb927.8.4810	prohibitin	Annotated	31.4	-20.6	10	44.0							
Tb10.389.1500	short-chain dehydrogenase	Annotated	36.0	-20.5	10	48.6							
Tb10.70.3360	40S ribosomal protein S3a	Annotated	29.4	-20.5	7	28.1							
Tb927.3.960	protein transport protein Sec61 gamma subunit	Annotated	7.6	-20.4	4	43.4							
Tb10.6k15.3080	dihydrolipoamide acetyltransferase precursor	Annotated	48.0	-20.3	7	23.5							
Tb927.4.395	cytoskeleton-associated protein CAP5.5	Annotated	94.5	-20.3	8	16.2							
Tb10.70.7770	Conserved hypothetical	Unannotated	37.0	-20.2	6	20.3						(e)	
Tb10.70.3510	60S ribosomal protein L18a	Annotated	20.8	-20.1	6	47.4			1				
Tb10.70.2320	Conserved hypothetical	Unannotated	25.9	-20.0	5	29.0							
Tb10.6k15.3160	mammalian Fibrillar, yNOP1	Annotated	31.6	-19.9	9	43.0							
Tb11.02.0250	heat shock protein, mitochondrial precursor	Annotated	84.1	-19.6	6	15.8			Yes				
Tb11.01.3560	vacuolar ATP synthase subunit B	Annotated	55.5	-19.5	6	18.1							
Tb927.7.4170	fatty acid elongase	Annotated	30.4	-19.4	4	27.6							
Tb10.6k15.1800	Conserved hypothetical	Unannotated	60.5	-19.2	3	10.2			3		ABC1 family		

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Tb10.70.3010	Conserved hypothetical	Unannotated	14.7	-19.2	8	49.1		Yes	1				
Tb10.389.0890	pyruvate dehydrogenase E1 component alpha subunit	Annotated	42.4	-19	6	19.5							
Tb927.3.3490	TDP1 high mobility group protein	Annotated	30.8	-19	3	15.1							
Tb927.4.2070	Antigenic protein, paralogous to NUP-1	Annotated	511.0	-18.9	10	3.7							
Tb927.8.2000	PPLase cyclophilin type peptidyl-prolyl cis-trans isomerase	Annotated	32.8	-18.9	7	27.2							
Tb10.70.6660	hypoxanthine-guanine phosphoribosyltransferase	Annotated	26.3	-18.7	2	14.1							
Tb927.2.340	RHS4-a	Annotated	97.7	-18.3	20	6.1							
Tb09.211.0560	RNA-binding protein, DRDB3	Annotated	36.9	-18.1	9	32.4							
Tb11.02.0750	TCP-1-zeta t-complex protein 1, zeta subunit	Annotated	59.5	-17.9	3	9.9							
Tb11.50.0007	dynein light chain	Annotated	10.4	-17.9	3	35.5							
Tb927.7.990	chaperone protein DNAJ	Annotated	86.5	-17.7	6	10.7							
Tb927.8.2630	kinesin	Annotated	85.1	-17.7	7	13.4							
Tb10.6k15.3610	delta-6 fatty acid desaturase	Annotated	47.9	-17.6	6	21.6							
Tb11.02.4620	Conserved hypothetical	Unannotated	88.9	-17.6	7	10.8	*				BOP1NT, WD domain, G-beta repeat	(g), BOP1-like WD-40, Erb1p homolog (e,f)	
Tb10.70.1570	Conserved hypothetical	Unannotated	107.2	-17.5	10	19.1				***			
Tb11.01.7800	nucleoside diphosphate kinase .	Annotated	16.8	-17.5	5	54.9							
Tb927.2.5160	DNAJ	Annotated	44.7	-17.5	3	12.8							
Tb927.5.1930	Conserved hypothetical	Unannotated	24.1	-17.4	4	28.3		Yes					(e)
Tb927.5.3190	Conserved hypothetical	Unannotated	23.1	-17.4	5	41.3	**						
Tb927.3.4100	Conserved hypothetical	Unannotated	63.2	-17.3	7	19.3		Yes	13		Major Facilitator Superfamily	(e)	
Tb09.211.1550	chaperone protein DNAJ	Annotated	56.6	-17.1	9	19.7							
Tb10.70.0820	universal minicircle sequence binding protein (UMSBP)	Annotated	21.8	-16.9	4	18.7							
Tb10.6k15.3350	40S ribosomal protein S24E	Annotated	15.6	-16.8	2	20.4							
Tb927.3.4920	Conserved hypothetical	Unannotated	42.7	-16.8	3	11.1					LETM1-like protein	(h), mitochondrial	
Tb11.01.3610	membrane-bound acid phosphatase	Annotated	53.3	-16.7	4	18.5							
H25N7.01	RHS2	Annotated	93.6	-16.6	11	11.7							
Tb11.02.2960	mitochondrial carrier protein	Annotated	29.8	-16.5	5	24.4							
Tb10.61.1920	fibrillarin	Annotated	31.6	-16.3	10	32.5							
Tb927.1.2230	calpain-like protein fragment	Annotated	13.5	-16.2	4	30.8							
Tb927.3.1410	COX VII cytochrome c oxidase VII	Annotated	19.2	-16.2	4	23.0							
Tb09.160.4450	RPS3 40S ribosomal protein S3	Annotated	30.3	-16	3	18.4							
Tb09.211.0120	nascent polypeptide associated complex subunit	Annotated	20.1	-16	3	33.5							
Tb927.4.2000	RuvB-like DNA helicase	Annotated	52.5	-16	8	26.3							
Tb10.70.2450	Conserved hypothetical	Unannotated	27.1	-15.9	5	33.0			3		DUF850	(e)	
Tb927.7.4760	Conserved hypothetical	Unannotated	58.7	-15.9	5	15.2			2				
Tb11.02.3310	Conserved hypothetical	Unannotated	13.5	-15.7	4	52.1			1				(e)
Tb927.4.4210	ATP-dependent zinc metallopeptidase	Annotated	96.1	-15.7	6	8.4							
Tb11.01.3860	Conserved hypothetical	Unannotated	18.3	-15.6	5	37.1		Yes					
Tb927.7.5840	Conserved hypothetical	Unannotated	26.1	-15.6	4	23.1			5		***		
Tb11.01.3180	guanine nucleotide-binding protein beta subunit	Annotated	34.6	-15.4	3	12.5							
Tb927.4.1080	V-type ATPase, A subunit	Annotated	67.7	-15.3	5	13.6							
Tb09.160.1070	Conserved hypothetical	Unannotated	41.4	-15.2	5	14.7		Yes			Methyltransferase domain	(f), paralogous to NUP-1	Inconclusive
Tb927.7.3330	Conserved hypothetical	Unannotated	502.3	-15.2	7	2.5				***			
Tb927.7.3120	Sm-D1 small nuclear ribonucleoprotein SmD1	Annotated	11.7	-15.1	3	41.5							
Tb11.02.1680	mannose-specific lectin	Annotated	62.2	-15	5	14.1							
Tb927.3.2230	succinyl-CoA synthetase alpha subunit	Annotated	31.4	-14.8	3	24.2							
Tb927.8.1890	cytochrome c1, heme protein, mitochondrial precursor	Annotated	30.0	-14.8	7	41.8							
Tb09.160.1560	Conserved hypothetical	Unannotated	287.0	-14.6	7	4.9			2		HEAT repeat (expect=0.48)	(h), BAP28	
Tb11.02.1320	Conserved hypothetical	Unannotated	39.0	-14.6	4	13.5							
Tb10.6k15.2020	TH12A glucose transporter	Annotated	56.8	-14.5	3	12.4							
Tb927.7.2700	B5R NADH-cytochrome b5 reductase	Annotated	31.8	-14.5	5	24.0							