

Table S1. MS/MS identification of proteins present in membrane-enriched fraction of *L. infantum* promastigotes^a

Putative protein name	Systematic IDs	Predicted <i>Mr</i> (kDa)	Unique peptides ^b (% seq. coverage)	Number of assigned spectra	TMDs (TMHMM v.2.0)	TMDs (TMPred)	FragAnchor (GPI)	Ref ^c
Transport								
AAT8 amino acid permease	LinJ31.1810 LinJ31.1830 LinJ31.1850 LinJ31.1860	66	3 (5.79)	3	11	10	Potential false positive	34
ABCB1 ATP-binding cassette protein subfamily B, member 1, putative	LinJ25.0540	72	4 (6.40)	4	4	5	Potential false positive	34
ABCB3 ATP-binding cassette protein subfamily B, member 3, putative	LinJ32.3280	77	2 (4.12)	2	5	7		
ABCB4 (MDR1) p-glycoprotein	LinJ34.1060	147	5 (5.44)	5	9	10		
ABCC2 ATP-binding cassette protein subfamily C, member 2, putative	LinJ23.0240	172	8 (6.59)	8	8	12		
ABCC3 (MRPA) ABC-thiol transporter	LinJ23.0290	174	2 (1.27)	2	8	12		33, 34
ABCC7 (PRP1) pentamidine resistance protein 1	LinJ31.1460	194	2 (1.55)	2	8	15		33
ABCG1-(2)-(3) ATP-binding cassette protein subfamily G, member 1, putative	LinJ06.0080 LinJ06.0090 LinJ06.0100	73	2 (4.98)	2	5	7	Probable	
ABCG5 ATP-binding cassette protein subfamily G, member 5, putative	LinJ23.0430	135	2 (1.93)	2	10	11	Potential false positive	33, 34
ABC transporter-like protein	LinJ32.2190	78	2 (2.99)	2	6	7		
ADP/ATP mitochondrial carrier-like protein	LinJ14.1050	40	3 (10.90)	3	1	4		33, 34
ANC1 ADP,ATP carrier protein 1, mitochondrial precursor, putative,ADP/ATP translocase 1, putative	LinJ19.0190 LinJ19.0200	35	17 (48.30)	102	4	5		13, 33, 34
ATP synthase F1 subunit gamma protein, putative	LinJ21.2140	34	7 (26.40)	16	0	0		13, 33, 34
ATP synthase, epsilon chain, putative	LinJ30.3660	20	3 (23.20)	7	0	0		33, 34
ATP synthase, putative	LinJ21.1590	54	4 (9.73)	4	0	2		
ATP synthase, putative	LinJ36.3250	25	4 (25.50)	5	0	0		34
ATPase alpha subunit	LinJ05.0500 LinJ05.0510	63	21 (34.00)	107	0	4		13, 33, 34
ATPase beta subunit, putative	LinJ25.1210 LinJ25.2580	56	18 (39.00)	98	0	1		13, 33, 34
calcium motive p-type ATPase, putative	LinJ35.2080	122	2 (1.62)	2	8	11		33, 34
calcium-translocating P-type ATPase	LinJ04.0010	111	2 (2.35)	2	7	10		33, 34

cation transporter, putative	LinJ19.1420	64	2 (2.94)	2	3	6	Potential false positive	34
cation-transporting ATPase, putative	LinJ07.1210	140	12 (11.80)	12	10	13		33, 34
COP-coated vesicle membrane protein erv25 precursor, putative,ER--golgi transport protein erv25 precursor, putative	LinJ36.2280	30	5 (16.00)	5	2	2		33, 34
COP-coated vesicle membrane protein gp25L precursor, putative,ER--golgi transport protein gp25L, putative	LinJ35.1840	24	3 (16.40)	4	2	2		34
endomembrane protein, putative	LinJ13.1280	67	3 (5.77)	3	9	10		34
FT1 folate/biopterin transporter, putative	LinJ10.0400	76	4 (5.68)	4	11	12		
	LinJ10.0410							34
FT5 folate/biopterin transporter, putative	LinJ10.0420	72	2 (3.34)	2	11	11		
glucose transporter, lmg2	LinJ36.6550	61	2 (7.23)	3	12	11		33, 34
H1A-1(2) P-type H ⁺ -ATPase, putative	LinJ18.1500	107	12 (14.90)	16	8	9		
	LinJ18.1510							34
LPG2 lipophosphoglycan biosynthetic protein (lpg2)	LinJ34.4290	37	2 (6.45)	2	9	9		
mitochondrial carrier protein, putative	LinJ02.0640	34	4 (18.50)	4	0	3		33
mitochondrial phosphate transporter, putative	LinJ35.4500	35	8 (30.30)	19	0	4		33, 34
nuclear pore complex protein (NUP155), putative,nucleoporin, putative	LinJ36.7220	144	3 (2.68)	3	0	7		33
nucleoporin interacting component (NUP93), putative	LinJ36.2640	97	5 (7.89)	5	0	2		33, 34
P-type ATPase, putative	LinJ17.0660	122	3 (4.23)	3	6	11		34
sre-2/carboxylate carrier-like protein	LinJ05.0680	38	2 (5.20)	4	2	5		34
transmembrane/endomembrane-like protein	LinJ34.3450	71	6 (11.00)	6	10	10		34
tricarboxylate carrier, putative	LinJ01.0590	36	3 (11.30)	4	3	5		34
vacuolar ATP synthase catalytic subunit A, putative	LinJ34.3460	68	9 (20.80)	9	0	2		13, 34
vacuolar ATP synthase subunit b, putative	LinJ28.2610	56	7 (20.60)	11	0	0		13, 34
vacuolar ATP synthase subunit c, putative	LinJ18.0560	47	2 (4.85)	2	0	1		13, 34
vacuolar ATPase subunit-like protein	LinJ05.1140	42	4 (10.90)	4	0	0		13
vacuolar proton translocating ATPase subunit A, putative	LinJ23.1910	88	3 (7.61)	4	6	6		33
vacuolar-type Ca ²⁺ -ATPase, putative	LinJ07.0510	95	10 (11.30)	10	8	8		33, 34
vacuolar-type Ca ²⁺ -ATPase, putative	LinJ07.0700	102	13 (16.60)	14	6	8		33, 34
vacuolar-type proton translocating pyrophosphatase 1, putative	LinJ31.1240	83	12 (20.30)	34	14	15		13, 33, 34
vesicle-associated membrane protein, putative	LinJ08.0030	24	2 (11.60)	2	1	1	Potential false positive	33, 34
voltage-dependent anion-selective channel,	LinJ02.0420	30	3 (11.20)	3	0	0		33, 34

putative voltage-dependent anion-selective channel,	LinJ02.0430	32	14 (51.20)	19	0	0		33, 34
putative zinc transporter-like protein	LinJ31.2470	48	2 (3.77)	2	5	7		
<u>Surface</u>								
amastin-like surface protein-like protein	LinJ30.0930	24	2 (10.40)	2	4	4		34
expression-site associated gene (ESAG3), putative	LinJ33.1390	76	2 (5.37)	2	1	2		
extracellular receptor, putative	LinJ19.0640	100	2 (3.05)	2	2	7		
FG-GAP repeat protein, putative, integrin alpha chain protein, putative	LinJ31.0120	85	4 (6.24)	7	1	5		
GP63-1(2), leishmanolysin, metallo-peptidase, Clan MA(M), Family M8	LinJ10.0490	64	9 (15.50)	53	1	4	Highly probable	13, 34
lectin, putative	LinJ10.0500							34
lectin, putative	LinJ13.0560	52	3 (7.37)	3	0	0		
leucine-rich repeat protein, putative	LinJ30.0150	23	2 (12.00)	2	1	2	Weakly probable	
MBAP membrane-bound acid phosphatase precursor	LinJ36.2700	57	3 (6.23)	3	2	3		13
phospholipase A1, putative	LinJ35.3070	50	4 (12.80)	5	1	5		33, 34
prohibitin, putative	LinJ16.1710	30	6 (27.60)	8	0	1		34
prohibitin, putative	LinJ35.0070	32	8 (32.20)	10	1	2		33, 34
RAC-B2 receptor-type adenylate cyclase b	LinJ17.0140	152	13 (12.70)	19	1	7		33
surface antigen protein 2, putative	LinJ12.0663	71	4 (6.17)	5	2	6	Highly probable	13
surface antigen protein 2, putative	LinJ12.0665	49	2 (5.83)	3	2	4	Highly probable	
surface antigen protein 2, putative	LinJ12.0666	44	2 (4.32)	2	2	3	Highly probable	
surface protein amastin, putative	LinJ30.0920	21	2 (14.60)	3	4	4	Potential false positive	34
<u>Cytoskeleton</u>								
alpha tubulin	LinJ13.0330	50	18 (43.70)	53	0	1		13, 33, 34
	LinJ13.1460							
beta tubulin	LinJ08.1280	50	21 (40.60)	106	0	2		13, 33, 34
	LinJ21.2240							
beta tubulin	LinJ08.1290	50	22 (50.10)	85	0	2		13, 33, 34
	LinJ33.0860							
clathrin heavy chain, putative	LinJ36.1700	191	3 (2.13)	3	0	0		13, 33, 34
cytoplasmic dynein 2 heavy chain (DYNC2H2), putative; cytoplasmic dynein 2 heavy chain (DYNC2H1), putative	LinJ27.1650	498	2 (0.52)	2	0	2	Potential false positive	33
cytoplasmic dynein 2 heavy chain (DYNC2H1), putative	LinJ34.3990	478	2 (0.54)	2	0	4	Potential false positive	
dynein heavy chain, putative	LinJ25.1010	536	4 (1.08)	4	0	10		33, 34

dynein heavy chain, putative	LinJ34.3690	529	2 (0.58)	2	0	9	33
i/6 autoantigen-like protein	LinJ22.1310	23	2 (10.60)	7	0	0	33, 34
kinesin, putative	LinJ16.1550	305	4 (1.99)	8	0	0	34
kinesin, putative	LinJ19.0680	126	3 (2.48)	4	0	0	33
kinesin, putative	LinJ23.0720	75	8 (11.30)	9	0	1	33, 34
microtubule-associated protein, putative	LinJ05.0380	165	3 (1.71)	6	0	1	33, 34
stomatin-like protein	LinJ05.1040	40	2 (6.44)	3	0	1	13, 33, 34
tubulin-ty 34ine ligase-like protein	LinJ11.0400	120	2 (1.18)	2	0	3	
Metabolism							
1-acyl-sn-glycerol-3-phosphate acyltransferase-like protein, putative	LinJ32.2070	31	2 (10.80)	2	1	2	33, 34
2-oxoglutarate dehydrogenase E1 component, putative	LinJ36.3630	115	10 (13.90)	11	0	2	13, 34
2-oxoglutarate dehydrogenase subunit, putative	LinJ27.0740	112	9 (12.00)	10	0	0	13, 34
2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide succinyltransferase, putative	LinJ28.2600	42	4 (14.10)	6	0	1	13, 33, 34
3-oxo-5-alpha-steroid 4-dehydrogenase, putative	LinJ25.1850	34	14 (40.50)	24	2	4	33, 34
acyl-CoA dehydrogenase, mitochondrial precursor, putative	LinJ07.0150	56	2 (5.59)	3	0	1	33, 34
acyl-CoA dehydrogenase, putative	LinJ28.2700	69	11 (30.20)	11	0	2	13, 34
adenylosuccinate synthetase, putative	LinJ13.1090	78	4 (9.01)	4	0	0	13, 34
ADS1 alkylidihydroxyacetonephosphate synthase	LinJ30.0120	69	6 (15.60)	10	0	1	34
ALD fructose-1,6-bisphosphate aldolase	LinJ36.1320	41	11 (28.80)	30	0	1	13, 33, 34
aldehyde dehydrogenase, putative	LinJ30.2920	64	12 (29.40)	18	0	2	33, 34
aldehyde dehydrogenase, putative	LinJ36.5410	58	6 (19.50)	9	0	2	34
ATP-dependent phosphofructokinase	LinJ29.2620	54	8 (18.10)	12	0	2	13, 33, 34
C-8 sterol isomerase-like protein	LinJ29.2250	25	4 (21.10)	6	1	3	34
C-14 sterol reductase, putative	LinJ32.2470	49	3 (6.18)	3	6	8	
carnitine palmitoyltransferase-like protein	LinJ22.0190	74	3 (5.47)	4	0	1	
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	LinJ26.2500	25	3 (18.90)	5	4	4	34
cytochrome b5-like, putative	LinJ09.1570	13	2 (20.50)	2	1	1	Weakly probable 34
cytochrome b-domain protein, putative	LinJ02.0020	24	4 (17.00)	4	1	1	Highly probable 34
cytochrome c oxidase subunit iv	LinJ12.0620	37	9 (25.20)	11	0	1	34
cytochrome c oxidase subunit V, putative	LinJ26.1690	22	11 (73.50)	19	0	0	34
cytochrome c oxidase VII, putative	LinJ25.1170	19	4 (32.10)	5	1	1	34
cytochrome c1, heme protein, mitochondrial precursor, putative	LinJ07.0210	30	3 (19.40)	6	0	1	34
cytochrome p450-like protein	LinJ27.0090	67	5 (11.00)	5	1	2	

cytochrome p450-like protein	LinJ30.3610	58	6 (15.40)	10	2	5	34
D-alanyl-glycyl endopeptidase-like protein, cysteine peptidase, Clan CA, family C51, putative	LinJ33.3000	44	2 (4.46)	5	1	2	
DAT dihydroxyacetonephosphate acetyltransferase	LinJ34.1170	134	2 (2.01)	2	0	9	13, 34
dehydrogenase-like protein	LinJ10.0070	45	4 (14.80)	4	2	3	13, 33, 34
delta-1-pyrroline-5-carboxylate dehydrogenase, putative	LinJ03.0190	62	12 (27.50)	19	0	1	
delta-12 fatty acid desaturase	LinJ33.3420	45	3 (8.14)	3	4	6	
diacylglycerol acyltransferase, putative	LinJ27.1460	176	4 (2.98)	4	30	33	13, 33, 34
dihydrolipoamide acetyltransferase precursor, putative	LinJ36.2790	49	8 (28.90)	24	0	3	
dihydrolipoamide acetyltransferase precursor-like protein	LinJ21.0610	40	2 (11.40)	2	0	1	34
dolichyl-P-Man:GDP-Man1GlcNAc2-PP-dolichyl	LinJ34.2190	61	2 (4.55)	2	1	3	33
alpha-1,3-mannosyltransferase, putative							34
electron transfer flavoprotein-ubiquinone oxidoreductase, putative	LinJ07.0660	63	4 (9.39)	4	0	2	34
fatty acid desaturase, putative	LinJ24.2340	49	3 (6.73)	3	4	5	34
fatty acid desaturase, putative, sphingolipid delta 4 desaturase, putative	LinJ26.1670	43	4 (7.63)	4	5	5	Potential false positive
fatty acid elongase, putative, beta-ketoacyl-CoA synthase, beta-ketoacyl-coenzyme A	LinJ26.1680						
fatty acid elongase, putative, beta-ketoacyl-CoA synthase, beta-ketoacyl-coenzyme A	LinJ14.0670	32	4 (14.70)	4	7	6	33, 34
fatty acid elongase, putative, beta-ketoacyl-CoA synthase, beta-ketoacyl-coenzyme A	LinJ14.0680	32	4 (16.50)	7	6	5	33, 34
fatty acid elongase, putative, beta-ketoacyl-CoA synthase, beta-ketoacyl-coenzyme A	LinJ14.0700	33	5 (12.60)	8	5	6	34
fatty acid elongase, putative, beta-ketoacyl-CoA synthase, beta-ketoacyl-coenzyme A	LinJ14.0760	37	3 (13.00)	7	5	6	
fatty acyl CoA syntetase 1, putative	LinJ01.0490	78	3 (4.17)	5	0	1	13, 33, 34
GAT glycerol-3-phosphate acyl transferase	LinJ03.0070	71	2 (3.66)	2	3	4	
GCVL-2 dihydrolipoamide dehydrogenase, putative	LinJ32.3510	51	5 (14.10)	5	0	2	13, 33, 34
glutathione peroxidase-like protein, putative	LinJ26.0780	19	2 (8.05)	3	0	0	13, 34
glutathione-S-transferase/glutaredoxin, putative	LinJ14.1580	35	3 (11.60)	4	2	2	33, 34
glyceraldehyde 3-phosphate dehydrogenase, glycosomal	LinJ30.2990	39	4 (10.80)	13	0	1	33, 34
glycerol-3-phosphate dehydrogenase (FAD-dependent), mitochondrial	LinJ30.3000						33, 34
glycerol-3-phosphate dehydrogenase (FAD-dependent), mitochondrial	LinJ28.0240	67	8 (19.20)	8	1	5	
glycosomal malate dehydrogenase	LinJ19.0710	34	2 (8.39)	2	0	4	13, 34
glycosomal phosphoenolpyruvate carboxykinase, putative	LinJ27.1710	58	12 (30.90)	16	0	2	13, 33, 34
	LinJ27.2500						

hexokinase, putative	LinJ21.0300	52	15 (42.90)	18	0	2	Potential false positive	13, 33, 34
	LinJ21.0310							
lanosterol 14-alpha-demethylase, putative	LinJ11.1100	54	7 (15.20)	8	0	3		34
long chain fatty Acyl CoA synthetase, putative	LinJ03.0220	79	12 (14.90)	17	0	3		13, 33, 34
LPG1G GIPL galf transferase, putative	LinJ32.4140	58	2 (4.10)	2	1	4		
malate dehydrogenase	LinJ34.0150	33	2 (7.26)	2	0	1		13, 34
mannosyltransferase-like protein	LinJ31.1820	94	6 (10.60)	6	0	1		
	LinJ31.1920							
monoglyceride lipase, putative	LinJ31.1150	35	2 (9.00)	2	0	2		34
N-acetyltransferase subunit Nat1, putative	LinJ36.1390	81	2 (3.38)	2	0	0		13, 33, 34
NAD(p)-dependent steroid dehydrogenase-like protein	LinJ06.0350	46	5 (11.80)	6	1	1		
NADH-cytochrome B5 reductase, putative	LinJ13.0960	35	10 (33.10)	15	1	2		34
NADH-dependent fumarate reductase, putative	LinJ35.1190	123	6 (7.76)	7	0	3		13, 34
NADH dehydrogenase, putative	LinJ36.5620	57	2 (3.98)	2	0	3		33, 34
orotidine-5-phosphate decarboxylase/orotate phosphoribosyltransferase, putative, OMPDCase-OPRTase, putative	LinJ16.0560	50	4 (8.53)	4	0	2		34
P27 protein	LinJ28.1070	28	7 (31.20)	10	1	1		13, 34
p450 reductase, putative	LinJ28.1350	72	5 (8.99)	7	1	3		33, 34
PGKC phosphoglycerate kinase C, glycosomal	LinJ20.0110	52	3 (7.38)	3	1	1		33, 34
	LinJ20.0120							
phosphatidylethanolaminen-methyltransferase-like protein	LinJ31.3250	67	2 (2.92)	2	8	9		
proline oxidase, mitochondrial precursor-like protein	LinJ26.1590	64	11 (18.50)	15	0	1		34
protoporphyrinogen oxidase-like protein	LinJ06.1340	25	9 (42.40)	14	1	2	Potential false positive	
putative 3-ketoacyl-coa thiolase-like protein	LinJ31.1660	47	6 (19.10)	9	0	2		13, 34
pyruvate dehydrogenase E1 beta subunit, putative	LinJ25.1790	38	11 (29.70)	22	0	1	Potential false positive	13, 34
pyruvate dehydrogenase E1 component alpha subunit, putative	LinJ18.1360	43	9 (29.90)	39	0	1		13, 34
pyruvate phosphate dikinase, putative	LinJ11.1000	100	2 (3.83)	2	0	2		34
reiske iron-sulfur protein precursor, putative	LinJ35.1540	31	2 (6.14)	2	1	2		13, 34
serine palmitoyltransferase-like protein	LinJ34.3530	54	3 (9.02)	3	0	4		34
short chain dehydrogenase, putative	LinJ35.0330	36	2 (6.21)	2	1	4		33
short chain dehydrogenase-like protein	LinJ36.3570	33	3 (12.40)	3	0	4		33
squalene monooxygenase-like protein	LinJ13.1360	63	7 (15.50)	7	0	4		34
sterol 24-c-methyltransferase, putative	LinJ36.2510	40	3 (11.00)	6	0	1		13, 34

	LinJ36.2520							
sterol C-24 reductase, putative	LinJ33.0730	58	3 (7.26)	4	7	9		34
succinate dehydrogenase flavoprotein, putative	LinJ24.1700	67	13 (32.50)	21	0	2		13, 34
succinate dehydrogenase, putative	LinJ15.1050	22	2 (14.20)	3	0	1		34
succinyl-coA:3-ketoacid-coenzyme A transferase, mitochondrial precursor, putative	LinJ33.2470	53	5 (11.20)	5	0	2		13, 34
trifunctional enzyme alpha subunit, mitochondrial precursor-like protein	LinJ26.1530	79	16 (30.20)	23	0	2		13, 34
<u>Protein folding</u>								
chaperone protein DNAj, putative	LinJ35.3030	51	3 (9.21)	3	0	1		34
DNAJ domain protein, putative	LinJ24.0530	89	6 (10.30)	8	0	4		34
endosomal trafficking protein RME-8, putative	LinJ30.2220	273	2 (0.90)	2	0	10		33
glucose-regulated protein 78, putative	LinJ28.1310	72	16 (25.80)	31	1	2		13, 33, 34
heat shock protein 83-1	LinJ33.0350	79	2 (3.79)	3	0	1		13, 33, 34
	LinJ33.0360							
	LinJ33.0370							
heat shock 70-related protein 1, mitochondrial precursor, putative	LinJ30.2470	69	2 (3.62)	2	0	1		13, 33, 34
	LinJ30.2480							
	LinJ30.2530							
	LinJ30.2540							
heat-shock protein hsp70, putative	LinJ28.2950	68	5 (8.86)	7	0	2		13, 33, 34
	LinJ28.2960							
	LinJ28.3000							
	LinJ28.3060							
HSP70-like protein	LinJ01.0660	117	4 (4.23)	4	0	6	Probable	33, 34
LPG3 lipophosphoglycan biosynthetic protein, putative,heat shock protein 90, putative,glucose regulated protein 94, putative	LinJ29.0790	87	6 (7.91)	8	1	2		13, 33, 34
peptidyl-prolyl cis-trans isomerase, macrophage infectivity potentiator precursor, putative	LinJ19.0920	23	3 (14.90)	3	1	1		34
QSOX quiescin sulfhydryl oxidase, putative	LinJ30.0440	63	3 (8.04)	3	2	2		33, 34
<u>Proteolysis</u>								
aminopeptidase, putative,metallo-peptidase, Clan MG, Family M24	LinJ19.0150	43	2 (8.16)	3	0	0		34
ATP-dependent zinc metallopeptidase, putative,metallo-peptidase, Clan MA(E), Family M41	LinJ18.0620	65	2 (4.52)	2	1	3		34
ATP-dependent zinc metallopeptidase, putative,metallo-peptidase, Clan MA(E), Family	LinJ19.1620	65	4 (12.40)	5	1	2		

M41								
ATP-dependent zinc metallopeptidase, putative,metallo-peptidase, Clan MA(E), Family M41	LinJ32.1570	78	2 (4.47)	2	1	2	Potential false positive	33, 34
CAAX prenyl protease 1, putative,metallo-peptidase, Clan M-, Family M48	LinJ27.0040	49	3 (7.49)	4	3	5		33, 34
calpain-like cysteine peptidase, putative,cysteine peptidase, Clan CA, family C2, putative	LinJ27.0500	687	3 (0.50)	5	0	0		33, 34
cytoskeleton-associated protein CAP5.5, putative,cysteine peptidase, Clan CA, family C2, putative	LinJ31.0450	80	6 (11.70)	6	0	1		13, 33, 34
glutaminy cyclase, putative	LinJ05.0950	102	2 (3.20)	2	1	2		
LAP cytosolic leucyl aminopeptidase,metallo-peptidase, Clan MF, Family M17	LinJ23.1120	60	2 (4.96)	2	0	3		33
mitochondrial processing peptidase alpha subunit, putative,metallo-peptidase, Clan ME, Family M16	LinJ13.0760	58	10 (27.30)	11	0	4		34
mitochondrial processing peptidase alpha subunit, putative,metallo-peptidase, Clan ME, Family M16	LinJ21.0400	51	5 (19.10)	6	0	0		34
mitochondrial processing peptidase, beta subunit, putative,metallo-peptidase, Clan ME, Family M16	LinJ35.1390	55	21 (44.30)	62	0	0		34
proteasome regulatory non-ATPase subunit, putative	LinJ29.0120	99	2 (2.75)	2	0	6		13, 33, 34
serine carboxypeptidase (CBP1), putative,serine peptidase, Clan SC, Family S10	LinJ18.0450	52	3 (5.41)	3	1	2		13, 34
<u>Transcription, Translation</u>								
40S ribosomal protein L14, putative	LinJ22.1370	26	8 (31.80)	24	0	1		34
	LinJ22.1410							
40S ribosomal protein S10, putative	LinJ36.1040	19	4 (26.80)	5	0	1		33, 34
	LinJ36.1050							
40S ribosomal protein S12, putative	LinJ13.0460	16	10 (47.50)	20	0	0		34
40S ribosomal protein S13, putative	LinJ19.0390	17	4 (19.90)	5	0	0		33, 34
	LinJ33.3300							
40S ribosomal protein S14	LinJ28.1050	16	8 (39.60)	14	0	0		33, 34
	LinJ30.3650							
40S ribosomal protein S15A, putative	LinJ11.1180	15	3 (21.50)	5	0	0		33, 34
	LinJ29.1920							
40S ribosomal protein S16, putative	LinJ26.0840	17	10 (61.10)	15	0	0		13, 33, 34
	LinJ26.0850							
40S ribosomal protein S17, putative	LinJ28.2750	16	3 (17.50)	5	0	0		33, 34
	LinJ28.2760							

40S ribosomal protein S18, putative	LinJ36.0990	19	9 (25.30)	17	0	0	13, 33, 34
	LinJ36.1000						
40S ribosomal protein S19 protein, putative	LinJ34.2620	20	9 (43.60)	15	0	0	34
40S ribosomal protein S19-like protein	LinJ29.2970	18	3 (24.20)	3	0	0	34
40S ribosomal protein S2	LinJ19.0050	29	8 (26.90)	13	0	0	33, 34
	LinJ32.0460						
40S ribosomal protein S21, putative	LinJ11.0770	17	3 (20.70)	9	0	1	34
	LinJ11.0780						
40S ribosomal protein S27-1, putative	LinJ36.3940	10	2 (26.70)	3	0	0	33, 34
40S ribosomal protein S3, putative	LinJ15.1010	24	12 (47.00)	32	0	0	13, 33, 34
	LinJ33.0960						
40S ribosomal protein S3A, putative	LinJ35.0400	30	12 (40.90)	18	0	0	33, 34
	LinJ35.0410						
40S ribosomal protein S4, putative	LinJ13.1120	31	25 (67.80)	47	0	0	13, 33, 34
	LinJ13.1130						
40S ribosomal protein S5	LinJ11.0960	21	4 (21.60)	7	0	0	34
40S ribosomal protein S8, putative	LinJ24.2160	25	10 (41.40)	20	0	0	13, 34
	LinJ24.2170						
40S ribosomal protein S9, putative	LinJ07.0760	22	11 (35.30)	15	0	0	33, 34
	LinJ36.1310						
40S ribosomal protein SA, putative	LinJ36.5240	28	10 (36.20)	25	0	0	33, 34
	LinJ36.5350						
60S acidic ribosomal protein P2	LinJ15.1190	11	4 (52.30)	5	0	1	34
	LinJ15.1200						
60S acidic ribosomal protein, putative	LinJ36.4880	25	2 (11.00)	2	0	1	34
60S acidic ribosomal subunit protein, putative	LinJ27.1300	35	3 (5.88)	7	0	2	34
	LinJ27.2480						
60S ribosomal protein L10, putative	LinJ04.0750	25	13 (46.90)	44	0	0	34
	LinJ04.0950						
60S ribosomal protein L13, putative	LinJ29.2570	25	5 (29.50)	9	0	0	33, 34
	LinJ29.2580						
60S ribosomal protein L13a, putative	LinJ15.0220	25	10 (43.70)	35	0	0	34
	LinJ34.0910						
60S ribosomal protein L17, putative	LinJ24.0040	19	6 (27.70)	13	0	0	33, 34
	LinJ32.0440						
60S ribosomal protein L18a, putative	LinJ32.0930	21	7 (34.10)	18	0	0	13, 34
	LinJ35.0600						
60S ribosomal protein L19, putative	LinJ06.0410	28	8 (26.90)	23	0	1	34
	LinJ06.0430						
60S ribosomal protein L2, putative	LinJ32.4050	28	5 (13.10)	8	0	0	34

	LinJ35.1440							
	LinJ35.1450							
60S ribosomal protein L21, putative	LinJ34.3440	18	6 (39.00)	7	0	0		13, 34
60S ribosomal protein L21, putative	LinJ16.0470	18	7 (39.60)	13	0	0		13
60S ribosomal protein L22, putative	LinJ36.3430	15	2 (22.50)	4	0	0		34
	LinJ36.4640							
60S ribosomal protein L23, putative	LinJ35.3840	15	2 (20.10)	3	0	0		33, 34
60S ribosomal protein L23a, putative	LinJ06.0590	16	7 (39.30)	8	0	0		33
60S ribosomal protein L26, putative	LinJ24.2140	16	5 (32.20)	9	0	0		33, 34
	LinJ35.1670							
60S ribosomal protein L27A/L29, putative	LinJ35.3810	16	3 (22.10)	4	0	0		34
	LinJ35.3830							
60S ribosomal protein L28, putative	LinJ11.1110	16	2 (10.90)	4	0	0		34
	LinJ11.1130							
60S ribosomal protein L30	LinJ35.0240	11	3 (26.00)	4	0	0		33, 34
60S ribosomal protein L32	LinJ35.2040	15	4 (33.80)	12	0	0		34
60S ribosomal protein L34, putative	LinJ18.1380	19	5 (22.00)	11	0	0		34
	LinJ36.3930							
60S ribosomal protein L35, putative	LinJ26.2350	15	3 (26.80)	19	0	0		34
	LinJ26.2360							
60S Ribosomal protein L36, putative	LinJ21.0800	12	6 (30.50)	19	0	0		34
	LinJ35.1900							
60S ribosomal protein L5, putative	LinJ35.1870	34	6 (18.00)	20	0	1		34
	LinJ35.1880							
60S ribosomal protein L6, putative	LinJ15.1060	21	13 (52.30)	24	0	1		34
	LinJ33.0770							
60S ribosomal protein L7, putative	LinJ26.0150	31	7 (28.80)	23	0	0		34
	LinJ26.0160							
60S ribosomal protein L7a, putative	LinJ07.0550	39	22 (40.80)	82	2	2		13, 33, 34
	LinJ07.0560							
60S ribosomal protein L9, putative	LinJ21.1290	22	12 (56.30)	20	0	0		33, 34
	LinJ30.3390							
60S ribosomal subunit protein L31, putative	LinJ35.3330	27	4 (18.80)	8	0	0		34
	LinJ35.3340							
ATP-dependent DEAD/H RNA helicase, putative	LinJ07.0130	53	4 (10.70)	4	0	0	Potential false positive	13, 34
ATP-dependent DEAD-box RNA helicase, putative	LinJ35.0370	46	3 (7.90)	3	0	1		13, 34
ATP-dependent RNA helicase, putative	LinJ32.0410	67	17 (31.10)	66	0	2		13, 34
ATP-dependent RNA helicase, putative	LinJ35.3150	101	2 (4.76)	2	0	1		34
cell differentiation protein-like protein	LinJ34.4180	41	2 (6.15)	2	0	1		33, 34

EIF3-interacting protein-like protein elongation factor 1-alpha	LinJ36.0270	63	4 (10.70)	6	0	2	13, 34
	LinJ17.0090	49	12 (31.00)	50	0	0	
	LinJ17.0100						
	LinJ17.0110						
	LinJ17.0170						
	LinJ17.0190						
eukaryotic initiation factor 4a, putative	LinJ17.0200						13, 33, 34
	LinJ01.0790	45	2 (5.71)	2	0	0	
eukaryotic translation initiation factor 3 subunit 7-like protein	LinJ01.0800						13, 34
	LinJ30.3080	61	3 (6.97)	3	0	1	
eukaryotic translation initiation factor 3 subunit 8, putative	LinJ36.7320	82	2 (4.24)	3	0	4	13, 34
eukaryotic translation initiation factor 3 subunit, putative	LinJ36.4070	39	3 (12.40)	3	0	1	13, 34
eukaryotic translation initiation factor, putative histone H2A	LinJ28.2480	46	3 (12.30)	4	0	1	13, 34
	LinJ21.1160	14	4 (31.10)	8	0	1	33, 34
	LinJ21.1170						
histone H2B	LinJ09.1410	12	4 (38.70)	19	0	0	33, 34
	LinJ19.0030						
	LinJ19.0040						
histone H3	LinJ10.0920	15	4 (20.80)	5	0	0	33, 34
	LinJ10.1070						
	LinJ16.0600						
	LinJ16.0610						
histone H4	LinJ06.0010	11	3 (48.00)	3	0	0	13, 33, 34
histone H4	LinJ15.0010	11	8 (48.00)	12	0	0	13, 33, 34
	LinJ21.0020						
	LinJ25.2560						
	LinJ31.3320						
	LinJ35.0020						
	LinJ36.0020						
ILERS isoleucyl-tRNA synthetase, putative	LinJ36.5870	126	2 (1.91)	2	0	2	Probable 34
LIP2 60S acidic ribosomal protein P2, putative	LinJ30.3790	10	4 (66.70)	7	0	1	34
mitochondrial RNA binding protein 1,gBP21, MRP1	LinJ27.0980	27	4 (16.70)	5	0	1	33, 34
mitochondrial RNA binding protein 2,MRP2, gBP25	LinJ09.1180	27	4 (20.20)	8	0	1	34
nascent polypeptide associated complex subunit-like protein, copy 2	LinJ04.0760	29	2 (10.90)	2	0	0	34
	LinJ04.0770						
nucleolar GTP-binding protein, putative	LinJ33.1970	74	3 (5.37)	3	0	1	
nucleolar protein, putative	LinJ10.0210	53	2 (4.86)	2	0	1	33, 34

PABP2 poly(a) binding protein, putative	LinJ35.4200	65	2 (3.25)	3	0	1	33, 34
PABP3 poly(A)-binding protein, putative	LinJ25.0080	61	2 (4.96)	2	0	0	34
polyubiquitin	LinJ09.0950	98	2 (19.50)	2	0	0	13, 33, 34
	LinJ31.1930						
	LinJ31.2070						
PRP8 protein homologue, putative,U5 snRNA-associated splicing factor	LinJ35.4000	278	2 (0.99)	2	0	7	
PUF8 pumilio protein 8, putative	LinJ25.2470	65	2 (4.89)	2	0	0	34
pumilio/PUF RNA binding protein 7, putative	LinJ32.1830	85	2 (3.09)	2	0	2	34
ribonucleoprotein p18, mitochondrial precursor, putative	LinJ15.0320	21	8 (43.30)	27	0	0	34
ribonucleoprotein p18, mitochondrial precursor, putative	LinJ15.0330	21	2 (43.30)	11	0	0	
ribosomal protein L15, putative	LinJ30.3710	24	10 (37.30)	22	0	0	33, 34
	LinJ35.1890						
ribosomal protein L1a, putative	LinJ29.1160	41	10 (26.30)	15	0	4	33, 34
	LinJ29.1170						
	LinJ29.1180						
ribosomal protein L24, putative	LinJ36.1130	15	3 (26.60)	8	0	0	34
	LinJ36.1160						
ribosomal protein L27, putative	LinJ32.2830	15	3 (24.60)	5	0	0	34
	LinJ32.2850						
ribosomal protein L3, putative	LinJ32.3320	48	4 (12.60)	4	0	0	34
	LinJ32.3330						
	LinJ34.2730						
ribosomal protein l35a, putative	LinJ10.0050	16	4 (17.40)	7	0	0	34
	LinJ34.2240						
ribosomal protein s11 homolog	LinJ20.1620	16	5 (36.20)	6	0	0	33, 34
	LinJ21.1790						
ribosomal protein s20, putative	LinJ28.1100	13	4 (20.70)	7	0	0	34
	LinJ28.1120						
ribosomal protein s26, putative	LinJ28.0570	13	3 (25.90)	5	0	0	34
	LinJ30.3240						
ribosomal protein S6, putative,NPH2/RS6-like protein	LinJ15.1530	14	4 (36.50)	4	0	0	33, 34
ribosomal protein S7, putative	LinJ01.0430	24	18 (57.00)	86	0	0	33, 34
	LinJ01.0440						
RNA binding protein, putative	LinJ32.0790	25	16 (61.70)	38	0	0	13, 34
RNA helicase, putative	LinJ21.0670	75	2 (3.01)	2	0	4	34
RNA helicase, putative	LinJ21.1820	59	2 (4.26)	2	0	1	13, 34

RNA-binding protein, putative	LinJ27.2020	50	4 (6.68)	7	0	0		33, 34
RNA-binding protein, putative	LinJ35.2240	30	10 (45.60)	15	0	0		34
RNA-binding protein, putative, UPB1(2)	LinJ25.0500	27	4 (15.90)	10	2	2		34
	LinJ25.0510							
RPL10a 60S ribosomal protein L10a, putative	LinJ18.0630	25	12 (43.50)	18	0	0		33, 34
	LinJ36.3950							
RPL11 60S ribosomal protein L11 (L5, L16)	LinJ04.0460	22	3 (18.60)	5	0	0		34
	LinJ22.0004							
RPL18 60S ribosomal protein L18, putative	LinJ13.0450	22	11 (41.40)	40	0	0		34
	LinJ36.4730							
RPS6 40S ribosomal protein S6, putative	LinJ21.2150	28	13 (40.60)	21	0	1		33, 34
	LinJ35.2000							
rRNA biogenesis protein-like protein	LinJ20.0710	81	2 (2.32)	2	0	0		34
S24E-1 40S ribosomal protein S24e	LinJ36.3010	16	6 (27.70)	8	0	0		13, 34
	LinJ36.3020							
S25 ribosomal protein S25	LinJ25.1220	13	6 (40.80)	9	0	0		33, 34
	LinJ34.0460							
splicing factor ptsr1-like protein	LinJ07.1020	42	4 (14.90)	4	0	0		13, 34
TOP2 mitochondrial DNA topoisomerase II	LinJ15.1310	139	4 (4.21)	4	0	1		33, 34
translation initiation factor, putative	LinJ17.1390	81	6 (10.70)	7	0	0		13, 34
translation initiation factor IF-2, putative	LinJ33.2880	93	2 (3.06)	2	0	1	Potential false positive	34
<u>Others</u>								
Gim5A protein, putative, glycosomal membrane protein	LinJ35.3750	25	6 (28.90)	22	0	3	Potential false positive	13, 33, 34
glycosomal membrane like protein	LinJ24.0140	24	2 (12.30)	2	2	4		34
glycosomal membrane protein, putative	LinJ28.2430	24	7 (35.10)	43	0	2		13, 33, 34
GTP-binding protein, putative	LinJ25.1460	24	4 (19.40)	5	0	0		13, 33, 34
GTP-binding protein, putative	LinJ29.2310	78	12 (23.00)	15	0	0		13, 33, 34
GPI16 gpi transamidase component, putative	LinJ34.2560	80	2 (4.34)	2	2	3		33
mannosyltransferase-II, putative	LinJ18.0960	77	3 (5.26)	3	6	12		
nucleoside phosphatase, putative, guanosine diphosphatase, putative	LinJ10.0150	74	4 (6.50)	4	1	3		
oligosaccharyl transferase-like protein	LinJ35.1140	96	6 (9.27)	7	11	13		33, 34
oligosaccharyl transferase-like protein	LinJ35.1150	87	7 (11.00)	10	9	11		
oligosaccharyl transferase subunit, putative	LinJ35.1170	92	4 (6.45)	6	11	12		33, 34
PAPLE22 reticulon domain protein, 22 kDa	LinJ30.2570	22	6 (32.00)	10	3	3		33, 34
potentially aggravating protein (papple22)								
PDI-2 protein disulfide isomerase	LinJ36.7280	52	3 (9.01)	3	1	1		13, 33, 34

pretranslocation protein, alpha subunit, putative,SEC61-like (pretranslocation process) protein, putative	LinJ11.1050	54	5 (11.30)	5	9	9	33, 34
protein ty 34ine phosphatase, putative	LinJ05.0280	25	5 (23.70)	6	4	6	13, 33
rab1 small GTP-binding protein, putative	LinJ10.1250	25	2 (11.60)	2	0	0	34
rer1 family-like protein	LinJ22.0450	21	2 (9.84)	2	3	3	
SCGR6 phosphoglycan beta 1,3 galactosyltransferase	LinJ02.0140	90	3 (3.79)	3	0	3	
signal recognition particle receptor like protein, putative	LinJ36.3730	65	2 (3.97)	2	0	0	Potential false positive
small nuclear ribonucleoprotein component-like protein	LinJ32.2350	110	2 (2.85)	2	0	2	
SMP-1 small myristoylated protein-1, putative	LinJ20.1350	15	3 (18.30)	3	0	0	13, 33, 34
sodium stibogluconate resistance protein, putative	LinJ31.0950	68	2 (4.51)	2	0	2	33
	LinJ31.3380						
	LinJ31.3390						
	LinJ31.3400						
Tob55, putative	LinJ29.1940	53	2 (4.65)	2	0	4	
vesicle-fusing ATPase, putative,N-ethylmaleimide- sensitive factor, putative	LinJ20.0820	81	5 (8.67)	5	0	1	34
vesicular-fusion ATPase-like protein, putative	LinJ27.0940	108	7 (7.82)	8	0	3	33
Zn-finger domain protein, putative	LinJ29.1770	135	2 (1.89)	2	9	9	34
<u>Hypothetical</u>							
hypothetical protein, conserved	LinJ02.0220	123	5 (5.41)	5	1	5	
hypothetical protein, conserved	LinJ04.0630	23	2 (12.00)	3	1	2	
hypothetical protein, conserved	LinJ05.0340	41	2 (6.47)	2	0	0	
hypothetical protein, conserved	LinJ05.0910	119	2 (1.72)	2	0	3	
hypothetical protein, conserved	LinJ05.1030	16	2 (17.90)	2	1	1	34
hypothetical protein, conserved	LinJ06.1140	32	2 (12.90)	2	2	4	33, 34
hypothetical protein, conserved	LinJ07.0450	27	4 (18.50)	4	0	0	34
hypothetical protein, conserved	LinJ08.1010	42	8 (18.40)	11	0	1	13, 33, 34
hypothetical protein, conserved	LinJ10.1180	19	2 (9.04)	3	4	4	34
hypothetical protein, conserved	LinJ10.1370	37	5 (14.00)	5	0	0	13
hypothetical protein, conserved	LinJ11.0020	41	2 (2.99)	2	2	3	
hypothetical protein, conserved	LinJ11.0850	52	2 (5.08)	2	0	4	34
hypothetical protein, conserved	LinJ11.1030	28	5 (28.00)	10	0	3	33, 34
hypothetical protein, conserved	LinJ12.0550	55	4 (9.65)	7	1	4	34
hypothetical protein, conserved	LinJ12.0810	32	2 (8.87)	2	6	7	33
hypothetical protein, conserved	LinJ13.1230	51	2 (4.91)	2	2	6	Potential false

							positive	
hypothetical protein, conserved	LinJ14.1120	29	2 (11.90)	2	0	2		
hypothetical protein, conserved	LinJ14.1540	112	4 (4.87)	7	0	0		33, 34
hypothetical protein, conserved	LinJ15.0600	36	3 (13.50)	3	1	1		33, 34
hypothetical protein, conserved	LinJ16.0270	56	3 (7.07)	3	1	3		33, 34
hypothetical protein, conserved	LinJ16.0530	37	3 (11.60)	4	0	0		13, 34
hypothetical protein, conserved	LinJ16.1040	105	3 (4.46)	4	1	1		
	LinJ16.1050							
	LinJ16.1070							
hypothetical protein, conserved	LinJ16.1080	113	7 (9.52)	8	1	2		
hypothetical protein, conserved	LinJ16.1280	200	3 (2.26)	3	0	4		
hypothetical protein, conserved	LinJ16.1430	66	7 (15.70)	7	1	5		13
hypothetical protein, conserved	LinJ17.0010	88	10 (17.60)	12	0	1		13, 34
hypothetical protein, conserved	LinJ17.0230	36	6 (24.90)	9	0	1		33, 34
hypothetical protein, unknown function	LinJ17.0240	94	3 (3.69)	5	1	3		34
hypothetical protein, conserved	LinJ17.0530	248	7 (3.86)	7	0	7		34
hypothetical protein, conserved	LinJ17.1120	72	4 (6.74)	4	1	3		
hypothetical protein, conserved	LinJ17.1350	117	2 (1.69)	2	0	4		34
hypothetical protein, conserved	LinJ17.1380	8	4 (77.60)	6	1	1		34
hypothetical protein, conserved	LinJ18.0820	290	7 (3.42)	7	0	8		33, 34
hypothetical protein, conserved	LinJ18.0850	299	4 (1.84)	5	0	9		
hypothetical protein, conserved	LinJ18.0940	139	2 (1.67)	2	0	4		
hypothetical protein, conserved	LinJ18.1280	33	4 (17.20)	7	3	5		33
hypothetical protein, conserved	LinJ18.1600	73	2 (3.06)	2	0	1		34
hypothetical protein, conserved	LinJ18.1680	34	4 (19.00)	5	2	5		33
hypothetical protein, conserved	LinJ19.0080	46	2 (4.96)	3	2	2		33
hypothetical protein, conserved	LinJ19.0160	157	3 (2.68)	4	1	18		
hypothetical protein, conserved	LinJ19.1150	41	3 (7.28)	10	0	1		33, 34
hypothetical protein, conserved	LinJ20.0260	29	6 (21.10)	8	1	2	Potential false positive	34
hypothetical protein, conserved	LinJ20.0430	136	2 (2.64)	2	8	10		
hypothetical protein, conserved	LinJ21.0490	47	2 (4.35)	2	0	1		13, 34
hypothetical protein, conserved	LinJ21.0880	249	6 (3.77)	6	0	8		13, 33, 34
hypothetical protein, conserved	LinJ21.1090	22	2 (10.30)	3	2	3		
hypothetical protein, conserved	LinJ21.1180	36	2 (8.38)	3	3	5		33, 34
hypothetical protein, conserved	LinJ21.1830	47	9 (25.30)	34	1	1		13, 34
hypothetical protein, unknown function	LinJ21.1930	73	2 (3.16)	2	14	14		
hypothetical protein, conserved	LinJ22.0080	171	3 (2.28)	3	0	3		34
hypothetical protein, conserved	LinJ22.0180	61	2 (5.35)	2	0	2		34

hypothetical protein, conserved	LinJ22.0290	128	12 (13.90)	16	2	3	
hypothetical protein, conserved	LinJ23.0090	49	2 (4.77)	2	0	0	33, 34
hypothetical protein, conserved	LinJ23.0810	63	7 (16.20)	8	4	3	34
hypothetical protein, conserved	LinJ23.1680	27	8 (35.60)	12	0	1	34
hypothetical protein, conserved	LinJ23.1800	31	2 (10.30)	2	1	1	34
hypothetical predicted transmembrane protein	LinJ24.0440	153	3 (2.69)	12	2	4	
hypothetical protein, conserved	LinJ24.1650	43	2 (6.57)	2	4	5	
hypothetical protein, conserved	LinJ24.2250	38	5 (13.80)	5	0	2	34
hypothetical protein, conserved	LinJ25.1500	29	3 (10.10)	3	4	5	34
hypothetical protein, conserved	LinJ25.1600	80	2 (2.55)	2	0	4	34
hypothetical protein, conserved	LinJ25.1680	17	6 (47.60)	6	0	1	34
hypothetical protein, conserved	LinJ25.2520	109	4 (3.85)	4	0	1	33, 34
hypothetical protein, conserved	LinJ26.0330	38	3 (10.20)	3	1	1	34
hypothetical protein, conserved	LinJ26.0910	93	2 (2.61)	2	0	3	33
hypothetical protein, conserved	LinJ26.1020	60	12 (33.00)	15	1	4	33, 34
							Potential false positive
hypothetical protein, conserved	LinJ26.1250	93	2 (2.01)	3	0	2	
hypothetical protein, conserved	LinJ26.1790	297	4 (2.13)	4	0	14	34
hypothetical protein, conserved	LinJ26.1850	45	2 (5.74)	2	0	2	34
hypothetical protein, conserved	LinJ26.1960	89	10 (17.10)	13	0	2	33, 34
hypothetical protein, conserved	LinJ26.2000	39	7 (16.00)	11	1	1	34
hypothetical protein, conserved	LinJ27.0070	34	2 (10.20)	2	1	2	
hypothetical protein, conserved	LinJ27.0710	70	2 (4.22)	2	0	5	
hypothetical protein, conserved	LinJ27.1360	93	2 (2.93)	2	0	1	34
hypothetical protein, conserved	LinJ27.1430	11	2 (16.70)	3	0	2	34
hypothetical protein, conserved	LinJ27.1630	38	2 (9.44)	3	0	0	33, 34
hypothetical protein, conserved	LinJ27.2100	34	2 (9.76)	2	1	1	
hypothetical protein, conserved	LinJ28.1020	46	7 (17.80)	12	1	4	33, 34
hypothetical protein, conserved	LinJ28.1680	27	3 (14.20)	3	2	2	
hypothetical protein, conserved	LinJ28.2350	108	3 (4.33)	3	1	4	
hypothetical protein, conserved	LinJ29.0220	30	2 (5.99)	2	2	3	34
hypothetical protein, conserved	LinJ29.0450	41	2 (6.33)	2	1	3	
hypothetical protein, conserved	LinJ29.0940	53	12 (35.00)	21	0	1	34
hypothetical protein, conserved	LinJ29.1000	57	2 (3.98)	2	1	1	34
hypothetical protein, conserved	LinJ29.1390	34	2 (10.10)	2	0	0	34
hypothetical protein, conserved	LinJ29.1730	76	2 (3.09)	2	10	10	34
hypothetical protein, conserved	LinJ29.2230	192	10 (6.09)	10	0	3	34
hypothetical protein, conserved	LinJ29.2300	156	14 (11.70)	14	1	10	13, 34
hypothetical protein, conserved	LinJ29.2520	47	2 (6.75)	2	5	5	

hypothetical protein, conserved	LinJ30.1100	29	5 (18.40)	8	0	1		34
hypothetical protein, conserved	LinJ30.1610	41	2 (5.50)	2	2	3		
hypothetical protein, conserved	LinJ30.2670	40	3 (9.24)	5	2	4		
hypothetical protein, conserved	LinJ30.2860	12	2 (23.10)	3	1	1		34
hypothetical protein, conserved	LinJ30.3010	45	3 (13.50)	3	1	1		33
hypothetical protein, conserved	LinJ30.3190	23	4 (19.30)	8	1	2		33, 34
hypothetical protein, conserved	LinJ30.3740	51	3 (10.20)	3	0	0		33, 34
hypothetical protein, conserved	LinJ31.0040	115	2 (2.09)	2	11	13		
hypothetical protein, conserved	LinJ31.0530	64	6 (16.30)	6	1	6		
hypothetical protein, conserved	LinJ31.1110	24	2 (14.90)	2	2	2	Potential false positive	34
hypothetical protein, conserved	LinJ31.2830	52	3 (5.57)	4	2	2		34
hypothetical protein, conserved	LinJ32.0020	56	2 (5.47)	2	0	0		33, 34
hypothetical protein, conserved	LinJ32.0230	114	2 (3.22)	2	1	2	Potential false positive	34
hypothetical protein, conserved	LinJ32.0280	141	14 (12.20)	21	2	6		13, 34
hypothetical protein, conserved	LinJ32.0380	106	5 (6.04)	5	1	3		33
hypothetical protein, conserved	LinJ32.0980	75	3 (5.97)	4	1	6		34
hypothetical protein, conserved	LinJ32.1000	102	10 (14.10)	12	0	0		34
hypothetical protein, conserved	LinJ32.2330	26	5 (19.30)	5	0	0		13, 34
hypothetical protein, conserved	LinJ32.3040	33	2 (8.59)	2	0	1		34
hypothetical protein, conserved	LinJ32.3070	81	2 (2.75)	2	2	3		
hypothetical protein, conserved,leucine rich repeat protein, putative	LinJ32.3200	96	2 (2.97)	3	0	0		33, 34
hypothetical protein, conserved	LinJ32.3600	67	2 (3.64)	2	1	3		
hypothetical protein, conserved	LinJ32.3980	21	3 (18.60)	3	4	4	Potential false positive	34
hypothetical protein, unknown function	LinJ32.4060	34	2 (8.09)	2	2	2		
hypothetical protein, unknown function	LinJ33.1130	28	4 (22.60)	6	1	1		34
hypothetical protein, conserved	LinJ33.1260	73	3 (5.34)	3	0	1		13, 33
hypothetical protein, conserved	LinJ33.1690	36	3 (15.00)	5	1	3		34
hypothetical protein, conserved	LinJ33.2160	87	2 (3.30)	2	0	3		33
hypothetical protein, conserved	LinJ33.2570	56	3 (11.30)	3	0	0		33, 34
hypothetical protein, conserved	LinJ33.2660	145	3 (2.55)	3	0	6		33, 34
hypothetical protein, conserved	LinJ33.2940	17	5 (24.50)	5	0	1		34
hypothetical protein, conserved	LinJ34.0010	33	11 (37.30)	15	2	3		33, 34
hypothetical protein, unknown function	LinJ34.0410	62	4 (11.90)	5	0	4		34
hypothetical protein, conserved	LinJ34.1470	277	5 (2.64)	5	0	15		33, 34
hypothetical protein, conserved	LinJ34.1590	38	4 (13.40)	7	1	3		13

hypothetical protein, conserved	LinJ34.1890	17	3 (26.30)	3	4	4	Highly probable	33, 34
hypothetical protein, conserved	LinJ34.2410	22	8 (40.90)	18	0	0		34
hypothetical protein, conserved	LinJ34.2880	20	2 (21.30)	3	1	1		34
hypothetical protein, conserved	LinJ34.2900	71	2 (4.09)	2	4	4		
hypothetical protein, conserved	LinJ34.2970	55	2 (5.49)	4	2	3		33, 34
hypothetical protein, conserved	LinJ34.3140	24	3 (13.70)	7	0	0		13, 34
hypothetical protein, conserved	LinJ34.3200	56	2 (5.24)	2	0	5		34
hypothetical protein, conserved	LinJ34.3960	87	3 (3.68)	5	1	10		33
hypothetical protein, conserved	LinJ34.4310	43	3 (7.56)	4	0	3		33, 34
hypothetical protein, conserved	LinJ35.0100	24	5 (25.20)	9	0	1		34
hypothetical protein, conserved	LinJ35.1340	63	11 (30.80)	13	2	2		34
hypothetical protein, conserved	LinJ35.1470	36	6 (20.40)	7	0	4		
hypothetical protein, conserved	LinJ35.1590	66	12 (21.60)	15	1	1		
hypothetical protein, conserved	LinJ35.2190	48	3 (9.32)	3	1	4		13
hypothetical protein, conserved	LinJ35.3160	65	2 (6.15)	2	2	4	Potential false positive	
hypothetical protein, conserved	LinJ35.3740	27	5 (22.10)	5	0	6		
hypothetical protein, conserved	LinJ35.4420	146	2 (1.70)	2	9	13	Potential false positive	33
hypothetical protein, conserved	LinJ35.4700	56	2 (6.92)	3	3	3		33, 34
hypothetical protein, conserved	LinJ35.4780	79	3 (5.25)	4	1	2		33, 34
hypothetical protein, conserved	LinJ35.4920	39	6 (22.10)	6	0	1		33, 34
hypothetical protein, conserved	LinJ35.4940	43	5 (12.60)	5	4	4		33, 34
hypothetical protein, conserved	LinJ35.4990	23	2 (11.20)	2	1	1		33, 34
hypothetical protein, conserved	LinJ36.0170	31	2 (6.32)	2	0	3		
hypothetical protein, conserved	LinJ36.0390	30	5 (20.50)	7	2	3		33
hypothetical protein, conserved	LinJ36.0510	26	3 (20.40)	4	0	1		34
hypothetical protein, conserved	LinJ36.1080	61	2 (6.02)	3	3	5		33
hypothetical protein, conserved	LinJ36.1830	60	2 (7.09)	2	1	3		34
hypothetical protein, conserved	LinJ36.1960	70	3 (6.64)	3	0	1		34
hypothetical protein, unknown function	LinJ36.3400	92	2 (3.05)	2	1	5	Potential false positive	
hypothetical protein, conserved	LinJ36.4480	182	2 (1.34)	3	0	4		33
hypothetical protein, conserved	LinJ36.4680	17	3 (15.00)	4	0	0		33, 34
hypothetical protein, conserved	LinJ36.4740	114	3 (3.89)	3	0	7		33
hypothetical protein, conserved	LinJ36.5330	103	2 (2.18)	2	0	4		34
hypothetical protein, conserved	LinJ36.5360	30	2 (12.20)	2	0	0		33, 34
hypothetical protein, conserved, kinesin-like protein, putative	LinJ36.5380	71	5 (11.80)	7	0	1		13, 33, 34

hypothetical protein, conserved	LinJ36.6150	209	5 (4.45)	5	0	13	³⁴
hypothetical protein, conserved	LinJ36.7070	29	10 (43.80)	24	0	0	^{13, 33, 34}
hypothetical protein, conserved	LinJ36.7250	30	2 (9.12)	2	0	0	

^a Mr, molecular weight; TMDs, transmembrane domains. ^b Peptide identifications were accepted if they reached greater than 95% probability as specified by the Peptide Prophet algorithm. ^c Also identified in other studies.