

Supporting information

Title: Utilizing quantitative proteomics to identify species-specific protein therapeutic targets for treatment of leishmaniasis

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Table S1: The protein list of high confidence data.

Accession	Protein name	q-value
A0A3P3Z5D7	1_-2-Dihydroxy-3-keto-5-methylthiopentene_dioxygenase	0
E9BI74	10 kDa heat shock protein, putative	0
A0A640KIV5	10 kDa heat shock protein, putative	0
Q25317	100 kDa heat shock protein (Hsp100)	0
A0A6J8F523	14-3-3_protein_2_putative/GeneDB:LmjF.11.0350	0
A0A3P3ZC87	2-hydroxy-3-oxopropionate_reductase	0
E9BUR6	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	0
A0A3S5H5X9	3-hydroxyacyl-ACP dehydratase, putative	0
A4HVI6	40S ribosomal protein S12	0
E9AZR2	40S ribosomal protein S14	0
A0A640KLV1	40S ribosomal protein S19 protein, putative	0
A0A3S7X558	40S ribosomal protein S2	0
E9AGQ8	40S ribosomal protein S2	0
S24E-1	40S ribosomal protein S24	0
A4HAF8	40S ribosomal protein S25	0
A0A1E1J068	40S ribosomal protein S26	0
A0A640KDX9	40S ribosomal protein S3, putative	0
A0A640KPK0	40S ribosomal protein S33, putative	0
E9BRS2	40S ribosomal protein S3a	0
A4HV06	40S ribosomal protein S5	0
A0A3S7WWY7	40S ribosomal protein S6	0
A0A640KWJ5	40S ribosomal protein SA	0
A0A3P3ZHJ4	4E-interacting_protein	0
A4HSR7	5'-3'_exoribonuclease_A_-_putative	0
Q66VD6	60S acidic ribosomal protein P0 (Fragment)	0
A4HFR6	60S acidic ribosomal protein P0	0
A0A640KDZ6	60S acidic ribosomal protein P2, putative	0
A0A088RTU9	60S ribosomal protein L17, putative	0
A0A088RM49	60S ribosomal protein L21, putative	0
E9AEK1	60S ribosomal protein L30	0
A0A640KII0	60S ribosomal protein L7, putative	0
E9AL63	60S ribosomal protein L7a	0
A0A640KMK9	60S ribosomal protein L9, putative	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A4HWD9	60S_acidic_ribosomal_protein_-_putative	0
A0A6J8FAU2	60S_acidic_ribosomal_protein_P2/GeneDB:LmjF.15.12 03/GeneDB:LmjF.15.1207	0
A0A3P3YXI5	60S_ribosomal_protein_L10	0
RPL10a	60S_ribosomal_protein_L10a_-_putative	0
E9AHW0	60S_ribosomal_protein_L12_-_putative	0
A0A504XPH7	60S_ribosomal_protein_L13a_putative/GeneDB:LmjF.15.0200/GeneDB:LmjF.34.0860	0
A0A3S7WVI6	ABC transport system ATP-binding protein, putative	0
E9BD89	ACB domain-containing protein	0
A0A640KJH1	ACB domain-containing protein	0
A0A088RXI0	Acetyl-CoA carboxylase	0
A0A6J8FBI1	Acetyl-coenzyme A synthetase	0
A4H4X2	Acetylmithine deacetylase	0
A0A3P3Z3G8	Aconitate hydratase	0
C6KJC6	Actin	0
D3K115	Adenosylhomocysteinase	0
Q4Q124	Adenosylhomocysteinase	0
A0A088S2U2	Adenosylhomocysteinase	0
ASL	Adenylosuccinate lyase	0
ARL-3A	ADP-ribosylation factor family protein	0
A4HVW1	AhpC/TSA_family/Thioredoxin-like_-_putative	0
A0A3Q8ICG8	Alanine--tRNA ligase	0
E9AVY6	Alanine--tRNA ligase	0
E9BBA2	Alba domain-containing protein	0
E9AP69	Alba domain-containing protein	0
A0A088S825	Alba domain-containing protein	0
A0A640KCX7	Alba domain-containing protein	0
A4IA34	Alba_-_putative	0
A0A088RR95	Aldose 1-epimerase-like protein	0
A0A3P3Z0Z0	Alpha_tubulin	0
A0A6J8FMZ7	Amastin-like_surface_protein_putative/GeneDB:LmjF.34.0960/GeneDB:LmjF.34.1080	0
A0A504X048	Amidohydrolase family protein	0
E9BMF8	Amino acid permease, putative	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A504X1P4	Amino_acid_transporter_aATP11_putative/GeneDB:LmjF.31.0330/GeneDB:LmjF.31.0340/GeneDB:LmjF.31.0350	0
A0A088S8W7	Aminoacylase, putative	0
A0A640KUD8	Aminoacylase, putative	0
E9BSB0	Aminopeptidase P, putative	0
E9BPK8	Aminopeptidase, putative	0
A0A6J8F609	Aminopeptidase_putative/GeneDB:LmjF.11.0620/GeneDB:LmjF.11.0630	0
A0A3P3ZEJ5	AMMECR1	0
Q4Q4X1	AMPK1_CBM domain-containing protein	0
A4HHC0	ANK_REP_REGION domain-containing protein	0
A0A640KL91	Arginine--tRNA ligase	0
E9BJ55	Arginyl-tRNA synthetase	0
A0A088RW67	Arginyl-tRNA synthetase	0
A0A504XR61	Aspartate carbamoyltransferase	0
A0A1E1IXE4	Aspartate carbamoyltransferase	0
A0A640KCH7	Aspartate carbamoyltransferase	0
A0A504XWI4	Aspartate--ammonia ligase	0
A0A088RMY9	ATG8/AUT7/APG8/PAZ2, putative (Fragment)	0
A0A640KQ71	ATP binding protein-like protein	0
E9AXJ6	ATP synthase subunit beta	0
A4ICB6	ATP_synthase_delta_(OSCP)_subunit_-_putative	0
A0A1E1J4H7	ATP-binding cassette protein subfamily F, member 3, putative	0
pfk	ATP-dependent 6-phosphofructokinase	0
A0A088RKP9	ATP-dependent DEAD/H RNA helicase, putative	0
A0A3Q8IEU7	ATP-dependent DEAD-box RNA helicase, putative	0
E9BSI5	ATP-dependent RNA helicase, putative	0
A0A504XCK1	Axonemal dynein light chain family protein	0
A0A640KHW1	Beta propeller protein, putative	0
Q1PCI3	Beta tubulin (Fragment)	0
A0A3S7X6J0	Beta tubulin	0
Q27359	Beta-tubulin (Fragment)	0
A4H4P8	Bifunctional dihydrofolate reductase-thymidylate synthase	0
A0A6J8FIW1	Biotin/lipoate_protein_ligase-like_protein/GeneDB:LmjF.31.1070	0
E9ATX7	Branchpoint-bridging protein	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A3S7X0S6	BRO1-like domain/ALIX V-shaped domain binding to HIV, putative	0
A0A504XCG6	BT1 family protein	0
A0A504XC61	C3H1-type domain-containing protein	0
A0A088RU13	C3H1-type domain-containing protein	0
A0A504X9Z4	Calcium-transporting ATPase	0
CALA2	Calmodulin	0
E9AFL3	Calmodulin-like protein	0
A4HTS8	Calmodulin-like_protein_containing_EF_hand_domain	0
A0A504X8T1	Calpain cysteine protease family protein	0
A0A504XGG4	Calpain cysteine protease family protein	0
A0A3Q8IHF4	Calpain-like cysteine peptidase, putative	0
A0A3Q8ID62	Calpain-like cysteine peptidase, putative	0
A0A088SCJ7	Calpain-like cysteine peptidase, putative	0
A0A088RWU9	Calpain-like cysteine peptidase, putative	0
A0A640KJF2	Calpain-like cysteine peptidase, putative	0
A0A3S7WSA3	Carboxypeptidase Taq (M32) metallopeptidase family protein	0
A0A3Q8IU74	Carboxypeptidase Taq (M32) metallopeptidase family protein	0
A0A3Q8IBW2	Carboxypeptidase, putative	0
A0A1E1IRP2	Carboxypeptidase, putative,metallo-peptidase,Clan MA(E), family 32	0
Q9GQN7	Cathepsin B cysteine protease	0
A4H9G1	C-CAP/cofactor C-like domain-containing protein	0
E9BJ47	CCT-beta	0
Q4Q5I2	CCT-epsilon	0
A0A1E1J6I2	CCT-eta	0
A0A3P3ZJW6	CCT-theta	0
A4ICD2	CCT-theta	0
E9AUC7	CCT-theta	0
A0A3P3YYK6	Centrin	0
A0A1E1IWK2	Centrin, putative,Ca2-binding EF-hand protein	0
A0A088S3L3	Chaperone protein DNAj, putative	0
A0A640KQY3	Chaperonin containing t-complex protein, putative	0
A0A3Q8IVZ2	Chaperonin GroL	0
A0A3Q8IJA5	Chaperonin HSP60, mitochondrial	0
A0A504XXF5	Citrate synthase	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A4I3Z5	Coatomer subunit gamma	0
E9BKJ8	Cofilin-like protein	0
A0A088RVR1	Cofilin-like protein	0
A4HAY7	Contig, possible fusion of chromosomes 20 and 34	0
A0A3P3ZER2	Cop-coated vesicle membrane protein p24 precursor	0
A0A504XY59	Cornifin (SPRR) family protein	0
A0A504X0S6	Cornifin (SPRR) family protein	0
A0A504XQ11	CS domain family protein	0
E9BNZ2	CS domain-containing protein	0
A0A504WUV1	CS domain-containing protein	0
A4IBY7	CS_domain_containing_protein_-_putative	0
A0A640KSW6	Cystathionine beta-lyase-like protein	0
E9ALZ5	Cysteine peptidase C (CPC)	0
A0A4D5YID9	Cysteine protease (Fragment)	0
A0A4D5YJB0	Cysteine protease (Fragment)	0
Q9TWN9	Cysteine protease group C (Fragment)	0
A0A504XLA4	Cytochrome b5-like Heme/Steroid binding domain family protein	0
A3RGM1	Cytochrome P450-like protein	0
A0A3P3YYF9	Cytokine-induced_anti-apoptosis_inhibitor_1	0
A0A3S7X470	Cytoskeleton-associated protein CAP5.5, putative	0
A0A504X5X1	DEAD/DEAH box helicase family protein	0
A4HRV7	DEAD/DEAH_box_helicase/Type_III_restriction_enzyme_-_res_subunit_-_putative	0
Q4QHL1	Dehydrogenase-like protein	0
A0A3Q8IK74	Developmentally regulated GTP-binding protein 1, putative	0
A0A640KUM4	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex	0
E9BF46	Dihydrolipoamide acetyltransferaselike protein	0
GCVL-2	Dihydrolipoyl dehydrogenase	0
A0A504XW31	Dipeptidyl peptidase 3	0
Q9U6N3	DNA polymerase	0
A0A504XJQ5	Domain found in IF2B/IF5 family protein	0
A4HTN6	Dpy-30_motif_containing_protein_-_putative	0
A0A504X1D9	Dullard-like phosphatase domain protein	0
A0A504XPH1	Dynamin central region family protein	0
A0A640KBF2	Dynein heavy chain, putative	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A4IDJ0	Dynein light chain	0
A0A088S0R4	Dynein light chain roadblock	0
A0A640KDZ7	Dynein light chain roadblock	0
A0A640KIC6	Ecotin, putative	0
A0A1E1ISJ7	Elongation factor 1-alpha	0
eEF1B	Elongation factor 1-beta	0
A0A640KZX5	Elongation factor 2	0
A0A1E1J726	Elongation factor G, mitochondrial	0
A0A3S7WQT0	Elongation factor Tu GTP binding domain family protein	0
A0A3Q8I8H5	Elongation factor-1 gamma	0
A0A6J8FBD6	Elongation_factor_1-alpha/GeneDB:LmjF.17.0080/Gen eDB:LmjF.17.0081/GeneDB:LmjF.17.0082/GeneDB:LmjF.17.0083/Ge neDB:LmjF.17.0084/GeneDB:LmjF.17.0085/GeneDB:LmjF.17.0086	0
A4I1M5	Enoyl-CoA_reductase_-_putative	0
E9BCL9	Eukaryotic translation initiation factor 1A, putative	0
A0A640KHX9	Eukaryotic translation initiation factor 1A, putative	0
A0A504XBY2	Eukaryotic translation initiation factor 2 alpha subunit family protein	0
A0A504XM84	Eukaryotic translation initiation factor 3 subunit 8 N-terminus family protein	0
A0A3Q8IGX0	Eukaryotic translation initiation factor 3 subunit E	0
A0A1E1J905	Eukaryotic translation initiation factor 3 subunit L	0
E9AXF0	Eukaryotic translation initiation factor 5A	0
A4HLY5	Eukaryotic translation initiation factor 5B	0
A4HWL7	Eukaryotic_translation_initiation_factor_4_gamma_type_2_-_putative	0
A0A640KDS6	Exoribonuclease 2, putative	0
A0A640KLN7	FACT complex subunit	0
A0A3P3ZGN8	FAD:protein FMN transferase	0
A4IB12	FAD:protein FMN transferase	0
E9BH33	Fatty acyl-CoA reductase	0
A4HD14	Fer2_3 domain-containing protein	0
E9BE05	Fibrillarin, putative	0
A4HVG6	Flagellar_radial_spoke_protein_-_putative	0
A0A640KBP8	Folate/biopterin transporter, putative	0
A0A504XA96	Fructose-bisphosphatase	0
A0A3P3ZI57	Fructose-bisphosphate aldolase	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A504X5D8	Fructose-bisphosphate aldolase	0
A4HHJ6	Fumarate hydratase	0
fh	Fumarate hydratase	0
E9ACH4	FYVE-type domain-containing protein	0
E9AJR2	FYVE-type domain-containing protein	0
A0A5B8YY65	Glucose-6-phosphate isomerase (Fragment)	0
A0A3P3ZB81	Glutamate dehydrogenase	0
E9AD58	Glutaredoxin-like protein	0
A0A1E1J280	Glyceraldehyde-3-phosphate dehydrogenase	0
A0A6J8FJH8	Glycerol-3-phosphate dehydrogenase	0
GCVH	Glycine cleavage system H protein	0
A4I3V1	Glycoprotein_96-92_-_putative	0
gGAPDH	Glycosomal glyceraldehyde 3-phosphate dehydrogenase (Fragment)	0
E9AFJ4	Glycosomal membrane protein	0
A0A6L0WUF2	GRIP_domain_containing_protein_-_putative	0
A0A504X9C5	GrpE family protein	0
A0A3P3ZCE0	GrpE protein homolog	0
E9ALY9	Guanine deaminase	0
A0A504XRT1	Guanine nucleotide-binding protein subunit beta-like protein	0
A0A504XPX7	Guanine nucleotide-binding protein subunit beta-like protein	0
A0A504XFL7	Guanine nucleotide-binding protein subunit beta-like protein	0
A0A6J8FCB7	Guanine nucleotide-binding protein subunit beta-like protein	0
A0A1E1J3L2	Guanine nucleotide-binding protein subunit beta-like protein	0
E9AZ28	Guanine nucleotide-binding protein subunit beta-like protein	0
Q9GUB0	Guanine nucleotide-binding protein subunit beta-like protein	0
E9BMP8	H(+)-exporting diphosphatase	0
A0A640KTSS	H(+)-transporting two-sector ATPase	0
HSP70	Heat shock 70 kDa protein (Fragment)	0
A0A3Q8IEX7	Heat shock 70-related protein 1, mitochondrial, putative	0
HSP70	Heat shock protein 70 (Fragment)	0
C5MKJ9	Heat shock protein 70 (Fragment)	0
M4T8X9	Heat shock protein 70 (Fragment)	0
E9BID4	Heat shock protein 70-related protein	0
E9AYA3	Heat shock protein 70-related protein	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A1W5T9L2	Heat shock protein 83	0
A0A640K WG2	Heat shock protein 83	0
A0A088RU16	Heat shock protein DNAJ, putative	0
A0A640KSJ7	Heat shock protein, putative	0
A0A3P3ZAP6	Heat_shock_70-related_protein_1	0
A4I3J9	Heat_shock_70-related_protein_1_-_mitochondrial_precursor_-_putative	0
A0A6J8FGP5	Heat_shock_70-related_protein_1_mitochondrial_pre cursor_putative/GeneDB:LmjF.30.2460/GeneDB:LmjF.30.2470/Gen eDB:LmjF.30.2480/GeneDB:LmjF.30.2490/GeneDB:LmjF.30.2550	0
A0A3P3Z3I6	Heat_shock_protein_110	0
A0A6J8FKP5	Heat_shock_protein_83-17/GeneDB:LmjF.33.0365	0
E9AGY8	Heat_shock_protein_DNAJ_-_putative	0
A4I341	Heat_shock_protein_DNAJ_-_putative	0
A0A3S7X5C8	HECT-domain (Ubiquitin-transferase), putative	0
E9ALZ2	High mobility group protein homolog tdp-1,putative	0
A0A3Q8IHR2	Histidine--tRNA ligase	0
G3G3W8	Histone H2A	0
A0A088RLY0	Histone H2A	0
A0A381MG06	Histone H2B	0
A4H7X1	Histone H4	0
Q4JHM4	Histone H4	0
Q4QFI3	Histone H4	0
E9ASB9	Histone H4	0
A0A6J8FPL9	Holliday-junction_resolvase-like_of_SPT6/SH2_doma in_containing_protein_putative/Pfam:PF14639/Pfam:PF14633	0
A0A3P3ZJE3	HslVU_complex_proteolytic_subunit	0
A0A504XPS1	Hsp70 family protein	0
A0A504Y543	Hsp70 family protein	0
A0A504XC31	Hsp70 family protein	0
HSP83	HSP83 protein	0
A0A504Y5J2	Hsp90 family protein	0
A0A504Y1Y6	Hydroxymethylglutaryl-coenzyme A synthase N terminal family protein	0
A0A1E1IXW5	Hypothetical predicted multi-pass transmembrane protein	0
A0A3P3YZF9	Hypothetical_protein	0
A0A3P3Z4X3	Hypothetical_protein	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A3P3Z8E4	Hypothetical_protein	0
A4HRQ0	Hypothetical_protein_-_conserved	0
A4HS97	Hypothetical_protein_-_conserved	0
A0A6L0XKU2	Hypothetical_protein_-_conserved	0
A0A6L0XD14	Hypothetical_protein_-_conserved	0
A4I2D7	Hypothetical_protein_-_conserved	0
A4I2S2	Hypothetical_protein_-_conserved	0
A4I4H4	Hypothetical_protein_-_conserved	0
A4I8V4	Hypothetical_protein_-_conserved	0
A4IAR5	Hypothetical_protein_-_conserved	0
A0A3S7X729	Hypothetical_protein_conserved	0
A0A3S7WPX1	Hypothetical_protein_conserved	0
A0A3S7WYM0	Hypothetical_protein_conserved	0
A0A504XVG4	Hypothetical_protein_conserved	0
A0A3S7X7R9	Hypothetical_protein_conserved	0
A0A504XRH6	Hypothetical_protein_conserved	0
A0A3S5H5H8	Hypothetical_protein_conserved	0
A0A3Q8IH91	Hypothetical_protein_conserved	0
A0A504XV02	Hypothetical_protein_conserved	0
A0A504YBN6	Hypothetical_protein_conserved	0
A0A504XY93	Hypothetical_protein_conserved	0
A0A6J8F5B6	Hypothetical_protein_conserved	0
A0A6J8FB09	Hypothetical_protein_conserved	0
A0A6J8FEJ1	Hypothetical_protein_conserved	0
A0A6J8FEY8	Hypothetical_protein_conserved	0
A0A6J8FPS1	Hypothetical_protein_conserved	0
A0A6J8FED1	I/6_autoantigen-like_protein/GeneDB:LmjF.22.1460	0
A0A1E1J646	IgE-dependent histamine-releasing factor,putative	0
E9AWZ6	IgE-dependent histamine-releasing factor,putative	0
A0A075IY05	Isocitrate dehydrogenase (NADP(+)) (Fragment)	0
A4I994	Isocitrate dehydrogenase [NADP]	0
ICD	Isocitrate dehydrogenase [NADP]	0
E9BUU4	Isoleucyl-tRNA synthetase	0
A0A1E1J9X4	Isoleucyl-tRNA synthetase	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
idi1	Isopentenyl-pyrophosphate isomerase	0
A0A1E1IZK6	Isovaleryl-coA dehydrogenase, putative	0
A0A504XIF1	Kinesin motor domain family protein	0
A0A504Y557	Kinesin motor domain family protein	0
A0A6J8FAZ3	Kinesin_K39_putative/GeneDB:LmjF.14.1100/GeneDB:LmjF.14.1110/GeneDB:LmjF.14.1120	0
A0A504X8P0	Kinesin-like protein	0
A0A504XYS6	Kinesin-like protein	0
A0A088RWH6	Kinesin-like protein	0
A0A504XA70	Kinetoplastid membrane protein 11 family protein	0
KMP-11	Kinetoplastid membrane protein 11	0
O77413	Kinetoplastid membrane protein-11	0
A0A3Q8IDD1	Leucine-rich repeat protein, putative	0
A0A1E1J8Z7	Leucyl-tRNA synthetase	0
E9APD4	Leucyl-tRNA synthetase	0
A0A640KLW3	Lipophosphoglycan biosynthetic protein, putative	0
E9BAG4	LsmAD domain-containing protein	0
Q4QHA3	LsmAD domain-containing protein	0
A0A504X419	Malate dehydrogenase	0
A0A3S7WVE3	Malate dehydrogenase	0
cMDH	Malate dehydrogenase	0
A4I9I3	Malate dehydrogenase	0
A0A5B8YYF2	Mannose phosphate isomerase (Fragment)	0
A0A3P3ZG54	Metallo-peptidase	0
A0A640KCB4	Metallo-peptidase, clan MF, Family M17	0
A0A1E1IYD9	Methenyltetrahydrofolate cyclohydrolase	0
A4I2C8	Methyltransferase_domain_containing_protein_-_putative	0
A0A3S5H742	Mitochondrial carrier protein, putative	0
A0A640KVE8	Mitochondrial phosphate transporter, putative	0
E9APB1	Mitochondrial processing peptidase alpha subunit,putative (Metallo-peptidase, clan me, family m16)	0
A0A640KJ87	Mitochondrial RNA binding protein 1	0
A4ZZ67	Mitochondrial tryparedoxin peroxidase	0
E9BQ78	Mitogen activated protein kinase, putative	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A504XA36	MORN repeat family protein	0
A0A451EJM4	Multifunctional fusion protein	0
A5JV95	N(1),N(8)-bis(glutathionyl)spermidine reductase	0
E9AP13	NADH:flavin oxidoreductase/NADH oxidase,putative	0
E9BCE5	NAD-specific glutamate dehydrogenase	0
E9AQA0	NAD-specific glutamate dehydrogenase	0
NAC	Nascent polypeptide associated complex homologue, alpha chain	0
A4HS73	Nascent polypeptide associated complex subunit-like protein, copy 1	0
A0A640K7Z8	Nascent polypeptide associated complex subunit-like protein, copy 1	0
A0A3S5H6R4	N-inal_conserved_domain_of_Nudc./CS_domain_containing_protein_putative/Pfam:PF14050/Pfam:PF04969	0
A0A504X8T9	NOT2 / NOT3 / NOT5 family protein	0
A0A6J8FHZ9	Nuclear_segregation_protein_putative/GeneDB:LmjF. 32.0020	0
A0A6J8FAJ3	Nuclear_transport_factor_2_(NTF2)_domain_containing_protein_putative/Pfam:PF02136	0
A0A3S5H6F4	Nucleolar protein 56, putative	0
A0A1E1IQR1	Nucleolar protein, putative	0
A0A1E1J450	Nucleoside diphosphate kinase	0
Q9U1E1	Nucleoside diphosphate kinase	0
M1LHN7	Nucleoside hydrolase-like protein (Fragment)	0
A4I6V2	Nucleosome assembly protein-like protein	0
A4HY66	Nucleosome_assembly_protein_-_putative	0
A0A640KI23	Orotate phosphoribosyltransferase	0
A0A1E1J1N8	p22 protein, putative	0
E9B894	Paraflagellar rod component par4, putative	0
A0A504XQ10	Paraflagellar rod family protein	0
A0A640KM90	Paraflagellar rod protein 1D, putative	0
A4H8S1	Paraflagellar rod protein 2C	0
A4I8S7	Paraflagellar_rod_component_-_putative	0
A0A6J8FUN4	Paraflagellar_rod_component_putative/GeneDB:LmjF. 36.4230	0
A0A3S7WWF6	PCI domain family protein	0
A0A3S7X6U2	Peptidase M20/M25/M40 family protein	0
A0A3S7X4P6	Peptidase m20/m25/m40 family-like protein	0
A0A504X3M7	Peptidyl-prolyl cis-trans isomerase	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
E9B400	Peptidyl-prolyl cis-trans isomerase	0
A0A640K8J5	Peptidyl-prolyl cis-trans isomerase	0
A0A640KJ12	Peptidyl-prolyl cis-trans isomerase	0
A4HYI1	Peptidylprolyl isomerase	0
A0A3S7WV15	Phenylalanyl-tRNA synthetase beta subunit	0
Q4QDB1	Phenylalanyl-tRNA synthetase beta subunit	0
A0A504XFJ1	Phosphoenolpyruvate carboxykinase (ATP)	0
E9AZ83	Phosphoenolpyruvate carboxykinase (ATP)	0
A0A504Y6H2	Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I family protein	0
A0A5B8YY82	Phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating) (Fragment)	0
A0A5B8YY94	Phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating) (Fragment)	0
PGKC	Phosphoglycerate kinase, glycosomal	0
A0A3Q8IWN1	Phosphoglycerate mutase (2,3-diphosphoglycerate-independent)	0
pgam	Phosphoglycerate mutase (2,3-diphosphoglycerate-independent)	0
PMM	Phosphomannomutase	0
pmm	Phosphomannomutase	0
A0A5B8Z0A1	Phosphopyruvate hydratase (Fragment)	0
B3VA17	Phosphopyruvate hydratase	0
A0A1E11RW0	Phosphopyruvate hydratase	0
A0A640KBT1	Phosphopyruvate hydratase	0
A0A1E11VQ5	Phosphotransferase	0
A0A3S7WWK3	Plectin, putative	0
A0A640KVJ7	Poly(A) binding protein, putative	0
A0A1E11XL9	Poly(A)-binding protein, putative	0
PABP2	Polyadenylate-binding protein	0
A0A504XKP2	Polyadenylate-binding protein	0
E9AXF3	PPM-type phosphatase domain-containing protein	0
PCNA	Proliferating cell nuclear antigen	0
A0A640KE42	Proliferating cell nuclear antigen	0
A7XAB0	Prolyl oligopeptidase	0
A0A3Q8IJI4	Prolyl oligopeptidase	0
A0A640KG82	Proteasome alpha 5 subunit, putative	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A088RVV0	Proteasome alpha 7 subunit, putative	0
A0A640KWC7	Proteasome regulatory ATPase subunit	0
E9AZ51	Proteasome regulatory non-ATP-ase subunit 3,putative	0
A0A088RH76	Proteasome regulatory non-ATPase subunit 6, putative	0
A0A640KV33	Proteasome regulatory non-ATP-ase subunit 8, putative	0
A0A640KLP7	Proteasome regulatory non-ATPase subunit, putative	0
91E11	Proteasome subunit alpha type	0
Q4QH56	Proteasome subunit alpha type	0
Q4QC13	Proteasome subunit alpha type	0
E9AST1	Proteasome subunit alpha type	0
A0A088RSS0	Proteasome subunit alpha type	0
A0A088S266	Proteasome subunit alpha type	0
A0A3Q8IY4	Proteasome subunit beta	0
A0A6J8FFT5	Proteasome_alpha_7_subunit_putative/GeneDB:LmjF.2 7.0190	0
A4HYC9	Proteasome_regulatory_non-ATP-ase_subunit_9_-_putative	0
E9BV84	Protein disulfide-isomerase	0
A0A504XLV8	Protein kinase domain family protein	0
E9BHI2	Protein phosphatase, putative	0
A0A3P3Z097	Protein_transport_protein_SEC31	0
A0A3P3YZJ7	Pteridine_transporter_(Truncated)	0
A0A504XNP1	P-type H(+)-exporting transporter	0
A4I7Z0	Pumilio/PUF_RNA_binding_protein_7_-_putative	0
A4I011	Putative 40S ribosomal protein L14	0
Q4Q1Y3	Putative 40S ribosomal protein S18	0
E9AJS6	Putative 60S acidic ribosomal protein P2	0
E9B1E6	Putative 60S acidic ribosomal protein P2	0
A4H9H2	Putative 60S ribosomal protein L10a	0
E9ARK0	Putative 60S ribosomal protein L10a	0
A4HST1	Putative 60S ribosomal protein L19	0
E9AKR8	Putative 60S ribosomal protein L19	0
E9AV89	Putative 60S ribosomal protein L9	0
A4HGV3	Putative acyl-CoA dehydrogenase	0
Q4QC71	Putative adenylate kinase	0
Q4QDK5	Putative aminopeptidase	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
E9ALI8	Putative aspartyl aminopeptidase	0
E9AT88	Putative ATP synthase	0
E8NHQ7	Putative ATPase alpha subunit	0
ABCA10	Putative ATP-binding cassette protein subfamily A,member 10	0
E9APT0	Putative calpain-like cysteine peptidase (Putative cysteine peptidase, clan ca, family c2)	0
A4H7N9	Putative calpain-like cysteine peptidase	0
A4HYX1	Putative calpain-like cysteine peptidase	0
E9AD27	Putative calpain-like cysteine peptidase	0
E9AUR8	Putative calpain-like cysteine peptidase	0
E9AP43	Putative carboxypeptidase (Metallo-peptidase, clan ma(E), family 32)	0
Q4Q922	Putative cytochrome c oxidase subunit V	0
Q4Q1J6	Putative developmentally regulated GTP-binding protein 1	0
A4H7F5	Putative dynein heavy chain	0
E9API9	Putative dynein heavy chain	0
Q5UBY5	Putative elongation factor 1 beta	0
A0A1E1J6Y7	Putative elongation factor 2	0
Q4QDW8	Putative elongation factor Tu	0
Q4QHA6	Putative eukaryotic translation initiation factor 4 gamma	0
E9AX71	Putative fatty-acid desaturase	0
Q4QJ42	Putative glutamine synthetase	0
Q4Q843	Putative glycoprotein 96-92	0
E9B125	Putative heat shock 70-related protein 1, mitochondrial	0
A4H7X9	Putative heat shock protein HslVU, ATPase subunit HslU	0
E9AEE2	Putative inosine-adenosine-guanosine-nucleoside hydrolase	0
A4H8S4	Putative kinesin	0
A4HX43	Putative kinesin	0
Q4QEL9	Putative kinesin	0
E9AM02	Putative lipophosphoglycan biosynthetic protein	0
A4HMG0	Putative mitochondrial processing peptidase, beta subunit	0
E9B1G7	Putative nucleolar protein	0
E9AQD3	Putative nucleolar RNA binding protein	0
E9B0M6	Putative p22 protein	0
Q4QHP3	Putative paraflagellar rod component	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
E9B705	Putative peptidyl-prolyl cis-trans isomerase (Cyclophilin-40)	0
A4HPM0	Putative polyubiquitin	0
Q4QJ82	Putative prefoldin subunit	0
E9ACB2	Putative proteasome regulatory non-ATPase subunit 6	0
Q4QIG6	Putative Qc-SNARE protein	0
Q4QJK0	Putative ras-like small GTPases	0
E9AEX6	Putative reiske iron-sulfur protein	0
Q4QFF2	Putative ribonucleoprotein p18, mitochondrial	0
A4I2X5	Putative ribonucleoside-diphosphate reductase small chain	0
E9B578	Putative ribosomal protein L3	0
E9AZP7	Putative RNA binding protein rbp16	0
A4HG34	Putative serine peptidase	0
A4I7A1	Putative serine/threonine-protein kinase	0
E9B602	Putative short chain dehydrogenase	0
E9AHE8	Putative small GTP-binding protein Rab1	0
A0A504XFE0	Putative snoRNA binding domain family protein	0
A4HV28	Putative S-phase kinase-associated protein	0
A4HMX3	Putative ubiquitin-activating enzyme e1	0
A0A504XVC4	Pyridoxal phosphate homeostasis protein	0
E9BDW7	Pyruvate dehydrogenase E1 component alpha subunit, putative	0
A4HEH1	Pyruvate dehydrogenase E1 component subunit beta	0
A0A3P3ZGC0	Pyruvate kinase	0
A0A6L0Y0Y0	Pyruvate kinase	0
A0A3Q8I917	Pyruvate, phosphate dikinase	0
A0A1E1IR88	Pyruvate, phosphate dikinase	0
Q4QGX9	Pyruvate, phosphate dikinase	0
E9ANP4	Pyruvate, phosphate dikinase	0
A0A640KVG1	Rab-GAP TBC domain-containing protein	0
A0A504Y5I1	Radial spokehead-like family protein	0
A0A504X172	RanBP2-type domain-containing protein	0
A0A504XGW3	Ras family protein	0
RPA1	Replication protein A subunit	0
PAPLE22	Reticulon-like protein	0
A0A1E1J0Y4	Ribosomal protein L1a, putative	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A640KLM9	Ribosomal protein L1a, putative	0
A0A1E1IUI9	Ribosomal protein L3, putative	0
A0A504Y2G2	Ribosomal protein S10	0
A0A504XGS2	Ribosomal protein S3	0
A0A640KYQ2	Rieske iron-sulfur protein, putative	0
A0A3Q8IA61	RNA binding protein, putative	0
A0A1E1IWF3	RNA helicase, putative	0
A0A3Q8IF50	RNA recognition motif family protein	0
A0A504XSH7	RNA recognition motif family protein	0
A0A504X9G8	RNA recognition motif family protein	0
A0A6J8F647	RNA_binding_protein-like_protein/GeneDB:LmjF.07.1 000	0
A0A3P3Z845	RNA_recognition_motif_(a.k.a._RRM)	0
E9AG41	RNA_recognition_motif_(A.k.a._RRM_-_RBD_-_or_RNP_domain)_-_putative	0
A0A6J8FBM0	RNA_recognition_motif_(A.k.a._RRM_RBD_or_RNP_domain)/RNA_recognition_motif_(A.k.a._RRM_RBD_or_RNP_domain)_putative/Pfam:PF00076/Pfam:PF14259/Pfam:PF13893	0
A4I5Z0	RNA-binding_protein_42_(RNA-binding_motif_protein_42)_-_putative	0
A0A504WZF6	RRM domain-containing protein	0
A0A088SGN9	RRM_8 domain-containing protein	0
A0A3Q8IEM3	RuvB-like helicase	0
Q4Q2T4	RuvB-like helicase	0
A0A504X261	S-adenosylmethionine synthase	0
A0A1E1J1G3	Serine/threonine-protein kinase, putative,protein kinase, putative	0
Q4QJJ3	Serine/threonine-protein phosphatase	0
A0A3P3ZCB0	Serine/threonine-protein_kinase	0
A0A3S5H6H8	Seryl-tRNA synthetase	0
SGT	Small glutamine-rich tetratricopeptide repeat protein	0
A0A6J8F3S0	Splicing_factor_ptsr1-like_protein/GeneDB:LmjF.07.0870	0
A0A3S7WYJ9	STOP axonemal protein, putative	0
E9B9K2	Stress-induced protein sti1	0
A0A640KEQ1	Stress-induced protein sti1	0
A0A3Q8IJP8	Stress-inducible protein STI1-like	0
Q4QAG8	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	0
E9BU19	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
E9AT73	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial	0
A0A640KWV1	Succinyl-CoA:3-ketoacid-coenzyme A transferase	0
A0A640K939	Sucrose hydrolase-like protein	0
A0A3P3Z1T1	Tb-292_membrane_associated_protein-like_protein	0
A0A3P3Z674	T-complex protein 1 subunit delta	0
A0A504XGI8	T-complex protein 1, zeta subunit	0
A0A504XEG0	Tctex-1 family protein	0
A4I3H2	Tctex-1_family_-_putative	0
A0A504XG10	ThiF family protein	0
A0A504XYA2	Thioredoxin-like family protein	0
A0A1E1J5N6	Threonyl-tRNA synthetase	0
A0A504XU95	TPR repeat family protein	0
E9B1C1	TPR_REGION domain-containing protein	0
A4IAF1	TPR_repeat_-_putative	0
E9AQN5	Transaldolase	0
A0A088S247	Transitional endoplasmic reticulum ATPase, putative	0
A0A6L0XTS2	Transitional_endoplasmic_reticulum_ATPase_-_putative	0
A0A504X7J1	Transketolase	0
A0A088SB09	Transketolase	0
A0A640KN03	Transketolase	0
A0A504XII7	Transketolase, pyrimidine binding domain family protein	0
A0A3Q8IVV7	Translation elongation factor 1-beta, putative	0
E9BGY7	Translation factor sui1, putative	0
A0A3Q8ICH6	Translation initiation factor eIF3 subunit, putative	0
A0A640KF58	Transmembrane protein, putative	0
B5APK4	Triosephosphate isomerase	0
tim	Triosephosphate isomerase	0
A0A3P3ZAF3	Trypanothione_synthetase	0
TXN1	Tryparedoxin	0
Q5UDS8	Tryparedoxin peroxidase 2	0
I3W8N6	Tubulin alpha chain (Fragment)	0
Q25314	Tubulin beta chain (Fragment)	0
A0A3P3YYZ4	Tubulin beta chain	0
A4HZJ3	Tubulin beta chain	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A381MTJ3	Tubulin beta chain	0
Q4QI42	Tubulin beta chain	0
A4I8B9	Tubulin-specific chaperone A	0
A0A640KBV9	Tyrosyl-tRNA synthetase, putative	0
A0A504Y1T2	UBA/TS-N domain family protein	0
A4I763	Ubiquinol-cytochrome-c reductase-like protein	0
E9AWN2	Ubiquitin carboxyl-terminal hydrolase	0
E9BG91	Ubiquitin-activating enzyme e1, putative	0
A0A640KG80	Ubiquitin-activating enzyme E1, putative	0
Q4QFZ6	Ubiquitin-conjugating enzyme-like protein	0
A0A088RKN0	Ubiquitin-conjugating enzyme-like protein	0
A0A640KUE7	Ubiquitin-like domain-containing protein	0
A0A504WWC4	Ubiquitin-related modifier 1 homolog	0
A4IAL6	Uncharacterized protein (Fragment)	0
A4H7K8	Uncharacterized protein	0
A4HEG4	Uncharacterized protein	0
A4HLA5	Uncharacterized protein	0
E9B7H5	Uncharacterized protein	0
E9BA34	Uncharacterized protein	0
E9BAU1	Uncharacterized protein	0
E9BDB8	Uncharacterized protein	0
E9BEA7	Uncharacterized protein	0
E9BFA4	Uncharacterized protein	0
E9BGD5	Uncharacterized protein	0
E9BI92	Uncharacterized protein	0
E9BJ94	Uncharacterized protein	0
E9BKQ8	Uncharacterized protein	0
E9BNK3	Uncharacterized protein	0
E9BNL2	Uncharacterized protein	0
E9BNL3	Uncharacterized protein	0
E9BNP6	Uncharacterized protein	0
E9BQ38	Uncharacterized protein	0
E9BUW8	Uncharacterized protein	0
E9BV86	Uncharacterized protein	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A504Y4G7	Uncharacterized protein	0
A0A504XU23	Uncharacterized protein	0
A0A504XL80	Uncharacterized protein	0
A0A504XJI4	Uncharacterized protein	0
A0A504Y0I8	Uncharacterized protein	0
A0A504XTF0	Uncharacterized protein	0
A0A504X206	Uncharacterized protein	0
A0A504X0A7	Uncharacterized protein	0
A0A504X399	Uncharacterized protein	0
A0A504XYA8	Uncharacterized protein	0
A0A504XWS4	Uncharacterized protein	0
A0A504XJG9	Uncharacterized protein	0
A0A504XME5	Uncharacterized protein	0
A0A504X8W9	Uncharacterized protein	0
A0A504Y1F2	Uncharacterized protein	0
A0A504XYE2	Uncharacterized protein	0
A0A504Y7Y0	Uncharacterized protein	0
A0A504XB46	Uncharacterized protein	0
A0A3Q8I8X0	Uncharacterized protein	0
A0A3Q8ILK3	Uncharacterized protein	0
A0A3S7WXH9	Uncharacterized protein	0
A0A3S7WZ94	Uncharacterized protein	0
A0A3S7X7L7	Uncharacterized protein	0
A0A1E1J9A6	Uncharacterized protein	0
A0A1E1IR23	Uncharacterized protein	0
A0A1E1ITH9	Uncharacterized protein	0
A0A1E1ITV1	Uncharacterized protein	0
A0A1E1J2B8	Uncharacterized protein	0
A4HRG9	Uncharacterized protein	0
Q4QH88	Uncharacterized protein	0
Q4QGD8	Uncharacterized protein	0
Q4QG66	Uncharacterized protein	0
Q4QDS8	Uncharacterized protein	0
Q4QBS4	Uncharacterized protein	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
Q4QBG8	Uncharacterized protein	0
Q4Q976	Uncharacterized protein	0
E9AD64	Uncharacterized protein	0
E9ADV2	Uncharacterized protein	0
Q4Q6X5	Uncharacterized protein	0
Q4Q6U6	Uncharacterized protein	0
Q4Q6S0	Uncharacterized protein	0
Q4Q3I9	Uncharacterized protein	0
E9AFR7	Uncharacterized protein	0
E9AFW8	Uncharacterized protein	0
Q4Q205	Uncharacterized protein	0
Q4Q156	Uncharacterized protein	0
E9AJG4	Uncharacterized protein	0
E9ARU9	Uncharacterized protein	0
E9AUG4	Uncharacterized protein	0
E9AV78	Uncharacterized protein	0
E9AYY9	Uncharacterized protein	0
E9B0L2	Uncharacterized protein	0
E9B1E2	Uncharacterized protein	0
E9B522	Uncharacterized protein	0
A0A088RJ39	Uncharacterized protein	0
A0A088RP57	Uncharacterized protein	0
A0A088RTL3	Uncharacterized protein	0
A0A088RWE1	Uncharacterized protein	0
A0A088RZ05	Uncharacterized protein	0
A0A088S269	Uncharacterized protein	0
A0A088S2W4	Uncharacterized protein	0
A0A640KEL2	Uncharacterized protein	0
A0A640KE76	Uncharacterized protein	0
A0A640KFD7	Uncharacterized protein	0
A0A640KIU0	Uncharacterized protein	0
A0A640KL78	Uncharacterized protein	0
A0A640KN04	Uncharacterized protein	0
A0A640KNU0	Uncharacterized protein	0

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A640KVV2	Uncharacterized protein	0
Q4Q6V9	UV excision repair protein RAD23	0
A0A088RX52	V-type ATPase, C subunit, putative	0
E9ARJ3	V-type proton ATPase subunit C	0
A0A504WVM9	WD domain, G-beta repeat family protein	0
Q4Q5T1	WD_REPEATS_REGION domain-containing protein	0
E8NHK1	WGS CADB00000000 data, contig 48 (Fragment)	0
AAH	Adenine aminohydrolase	0.002
Q4QDJ7	GN3L_Grn1 domain-containing protein	0.002
A0A3S5H6T1	Inositol-3-phosphate synthase	0.002
A0A640K9Z4	Mitochondrial DNA polymerase beta-PAK, putative	0.002
Q6Y9Q8	Phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating) (Fragment)	0.002
E9ASE9	Proteasome subunit beta	0.002
A4HMT8	QA-SNARE protein putative	0.002
A0A088RTI0	RRM domain-containing protein	0.002
Q4QH99	TPH domain-containing protein	0.002
A0A3Q8IK28	Uncharacterized protein	0.002
A0A3Q8IHX6	Uncharacterized protein	0.002
A0A3Q8IA11	Uncharacterized protein	0.002
Q9NJ10	3FI8BORFP (Fragment)	0.004
A0A3Q8IFI6	60S ribosomal protein L13, putative	0.004
A0A3S7WWN3	Adenylate kinase, putative	0.004
A0A504X3J8	Alkyldihydroxyacetonephosphate_synthase/GeneDB:Lm jF.30.0120	0.004
Q25281	Alpha-tubulin DNA, partial cds (Fragment)	0.004
Q4QJH7	ANK_REP_REGION domain-containing protein	0.004
A4I4I8	Carnitine/choline_acetyltransferase_-_putative	0.004
A0A088S0F0	Cell cycle sequence binding phosphoprotein (RBP33), putative	0.004
A4HB65	Contig, possible fusion of chromosomes 20 and 34	0.004
A0A640KG11	Cyclophilin	0.004
A0A3Q8ING8	DNA polymerase delta subunit 2, putative	0.004
A0A504XY66	Elongation of fatty acids protein	0.004
A0A504XM61	Emp24/gp25L/p24 family/GOLD protein	0.004
E9B178	Eukaryotic translation initiation factor 3 subunit 7-like protein	0.004

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A4HV24	Eukaryotic_release_factor_3_-_putative	0.004
A0A3Q8IUP6	Flagellar attachment zone protein, putative	0.004
E9AWM1	Fumarate hydratase	0.004
A0A3P3ZF14	Glucosamine-6-phosphate isomerase	0.004
A0A6J8F833	Glycogen_synthase_kinase_3_putative/GeneDB:LmjF.1 8.0270	0.004
A0A3P3Z113	GPN-loop GTPase	0.004
A0A088RK67	Guanine nucleotide-binding protein subunit beta-like protein	0.004
A0A088RWE9	Importin subunit alpha	0.004
E9AVW9	Intraflagellar transport protein-like protein	0.004
A0A6L0WVD9	NADH:flavin_oxidoreductase/NADH_oxidase_-_putative	0.004
A0A504XQ49	NMDA receptor-regulated protein 1 family protein	0.004
A0A3S7X218	Plastid-encoded RNA polymerase subunit alpha	0.004
A0A3S7WPD8	Proteasome subunit beta	0.004
A0A504XNZ6	Protein transport protein SEC23	0.004
A0A3Q8IBR6	Protein YIPF	0.004
A0A3P3Z0X4	Protein_kinase_A_regulatory_subunit	0.004
A0A3S5H745	Pumilio protein 2, putative	0.004
E9AQ49	Putative ecotin	0.004
E9AD91	Putative intraflagellar transport protein IFT88	0.004
A0A1E1INL4	Putative nascent polypeptide associated complex subunit-like protein, copy 1	0.004
Q4Q3Z4	Putative phosphoribosyl transferase	0.004
E9B2J9	Putative RNA binding protein	0.004
A0A1E1INT0	Putative unspecified product	0.004
FeSODA	Superoxide dismutase	0.004
A4I289	Trifunctional enzyme alpha subunit, mitochondrial-like protein	0.004
A0A3S5H810	Uncharacterized protein	0.004
A4I9N8	Uncharacterized protein	0.004
E9AJY0	Uncharacterized protein	0.004
E9AM96	Uncharacterized protein	0.004
A0A640KR93	Uncharacterized protein	0.004
A0A640KV22	Uncharacterized protein	0.004
E9AXJ1	Aldehyde dehydrogenase, mitochondrial	0.005
ALDH2	Aldehyde dehydrogenase, mitochondrial	0.005
A0A088RW10	Aminopeptidase	0.005

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A1E1J787	Carboxypeptidase, putative,metallo-peptidase,Clan MA(E), Family M32	0.005
A0A088RVG4	Coatomer subunit gamma	0.005
A0A3S7X5G0	COP9 signalosome, subunit CSN8 family protein	0.005
A0A504XFK1	Cytidyltransferase-like domain protein	0.005
A0A3S7WPS2	Cytokine-induced anti-apoptosis inhibitor 1, Fe-S biogenesis, putative	0.005
A0A3Q8IEP9	Divalent cation transporter, putative	0.005
E9AN61	Glycerol-3-phosphate dehydrogenase [NAD(+)]	0.005
A0A088SLT7	GTPase activating protein, putative	0.005
A0A504XJ52	Guanine nucleotide-binding protein subunit beta-like protein	0.005
A0A3P3YZC2	Hypothetical_protein	0.005
A0A6J8F9F3	Hypothetical_protein	0.005
A4HXD7	Hypothetical_protein_-_conserved	0.005
E9AHB4	Hypothetical_protein_-_conserved	0.005
A4I4F8	Hypothetical_protein_-_conserved	0.005
A0A504XNG2	Hypothetical_protein_conserved	0.005
A0A504XE44	Hypothetical_protein_conserved	0.005
A0A504XJ57	Hypothetical_protein_conserved	0.005
A0A3S7X4Y5	Hypothetical_protein_conserved	0.005
A0A504WXA4	Insulinase (Peptidase M16) family protein	0.005
A0A1E1IZB1	Intraflagellar transport protein IFT88, putative	0.005
A0A5B8YYQ6	Isocitrate dehydrogenase (NADP(+)) (Fragment)	0.005
A0A5B8YZ17	Isocitrate dehydrogenase (NADP(+)) (Fragment)	0.005
A0A3S7X0C7	Kinetoplast-associated protein-like protein	0.005
A0A640KP67	Mannose-6-phosphate isomerase	0.005
E9AKE1	N(1),N(8)-bis(glutathionyl)spermidine reductase	0.005
A4I949	Nucleolar GTP-binding protein 1	0.005
A0A1E1J645	Phosphoinositide-binding protein, putative	0.005
A0A3P3Z1N9	Possible_lysinе_decarboxylase	0.005
A1Y2D3	Prostaglandin f2-alpha synthase (Fragment)	0.005
A0A640KPI3	Protein phosphatase 2A catalytic subunit, putative	0.005
A0A640KVP0	Puf1, putative	0.005
E9B669	Putative 60S Ribosomal protein L36	0.005
A0A1E1IYC2	Putative adenine phosphoribosyltransferase	0.005
E9B3K9	Putative autophagocytosis protein	0.005

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
Q4Q7K6	Putative p22 protein	0.005
A0A1E1J315	Putative prostaglandin f2-alpha synthase/D-arabinose dehydrogenase	0.005
Q4QCN3	Putative SNAP protein	0.005
E9ALA2	Putative ubiquitin-conjugating enzyme e2 (Putative ubiquitin-protein ligase) (Putative ubiquitin carrier protein)	0.005
A0A3P3ZHC3	Ribosomal_protein_L32	0.005
A0A640KI19	RRM domain-containing protein	0.005
A0A3P3YYV3	Small_ubiquitin_protein	0.005
Q25308	Squalene synthase	0.005
A0A504XQJ1	T-complex protein 1 subunit gamma	0.005
A0A3S7XAC9	TPR repeat family protein	0.005
TXN2	TXN2 protein	0.005
A4HJE4	Uncharacterized protein (Fragment)	0.005
E9B9E8	Uncharacterized protein	0.005
E9BFA8	Uncharacterized protein	0.005
A0A504XMU4	Uncharacterized protein	0.005
A0A3S7X8X6	Uncharacterized protein	0.005
Q4QFQ3	Uncharacterized protein	0.005
Q4Q154	Uncharacterized protein	0.005
E9AKK0	Uncharacterized protein	0.005
E9AU72	Uncharacterized protein	0.005
A0A640K9C1	Uncharacterized protein	0.005
A0A640KQN3	Uncharacterized protein	0.005
E9AUL9	Vesicle-fusing ATPase	0.005
A0A088RTY6	Vesicular-fusion ATPase-like protein, putative	0.005
E9BD99	VID27 domain-containing protein	0.005
A0A504XYH5	WD_REPEATS_REGION domain-containing protein	0.005
A0A640KU28	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	0.006
A0A088S233	Clathrin heavy chain	0.006
A0A504XE41	Coatomer subunit epsilon	0.006
E9BDQ8	DNA-directed RNA polymerases II, putative	0.006
A0A3Q8IAL4	DNAj-like protein	0.006
A0A1E1IXH9	Dynein light chain, putative	0.006
A0A504XEC6	EF-hand domain pair family protein	0.006

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A504XEU7	Frag1/DRAM/Sfk1 family protein	0.006
A0A504XJ16	Hypothetical_protein_conserved	0.006
A0A6J8FCN9	Hypothetical_protein_conserved	0.006
A0A504XDT4	Intraflagellar transport complex B protein 46 C terminal family protein	0.006
A4I5D9	IQ_calmodulin-binding_motif_containing_protein_-_putative	0.006
A0A504Y4I6	Isochorismatase family protein	0.006
A0A504XUX5	Leucine Rich repeat family protein	0.006
E9BAF3	Nucleoside phosphorylase-like protein	0.006
A4HZT9	Proteasome_regulatory_ATPase_subunit_5_-_putative	0.006
E9ANA1	Putative small GTP-binding protein Rab11	0.006
A0A6J8FPG9	Roadblock/LC7_domain_containing_protein_putative/ Pfam:PF03259	0.006
A0A088S004	Transcription elongation factor-like protein	0.006
A0A504WXU1	Uncharacterized protein	0.006
A0A640KSS9	Uncharacterized protein	0.006
E9BUP8	Vacuolar protein sorting-associated protein 28 homolog	0.006
A0A504X5L7	Ankyrin repeats (3 copies) family protein	0.007
A0A088RZ02	Meiosis-specific nuclear structural protein 1	0.007
A0A3S7WVD1	SNARE protein, putative	0.007
A0A504X2E2	Transcriptional repressor TCF25 family protein	0.007
A0A504WWB2	Ubiquitin carboxyl-terminal hydrolase family protein	0.007
A0A640KIM8	Uncharacterized protein	0.007
A4I3X4	Vacuolar proton pump subunit B	0.007
E9BPG6	WD_REPEATS_REGION domain-containing protein	0.007
A0A504Y8P2	2-oxoisovalerate dehydrogenase subunit alpha	0.008
A0A504YBK0	Acid_Phosphatase_putative/Pfam:PF12689	0.008
E9AZM9	ANK_REP_REGION domain-containing protein	0.008
E9AJY3	Calcium-transporting ATPase	0.008
A0A6J8FT87	CG1104_protein-like_protein/GeneDB:LmjF.36.6800	0.008
A4HYX7	Coatomer subunit beta	0.008
A0A504XS31	Elongation factor Tu GTP binding domain family protein	0.008
A0A3S7X869	Exosome subunit rrp6p-like, putative	0.008
A0A504XJK8	FAD linked oxidase, C-terminal domain family protein	0.008
A0A504XM90	Hypothetical_protein_conserved	0.008
A0A6J8F7H5	Hypothetical_protein_conserved	0.008

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A640KGF0	LsmAD domain-containing protein	0.008
E9AF09	Putative 60S ribosomal protein L5	0.008
E9B1D4	Putative ATP synthase, epsilon chain	0.008
A4HUM8	Putative rab1 small GTP-binding protein	0.008
A0A3S7WZF9	Ribosome production factor 2 homolog	0.008
E9AY57	RRM domain-containing protein	0.008
A0A504XZQ9	Transmembrane amino acid transporter family protein	0.008
A0A3S5H570	Uncharacterized protein	0.008
A0A640KH80	Uncharacterized protein	0.008
A0A640KIX9	Uncharacterized protein	0.008
A0A1E1J828	Vacuolar protein sorting-associated protein 28 homolog	0.008
E9AK29	60S ribosomal protein L11 (L5, L16)	0.009
E9AGI9	Arginine N-methyltransferase-like protein	0.009
E9B0H1	Aspartyl-tRNA synthetase	0.009
A0A640KPZ2	CSN8_PSD8_EIF3K domain-containing protein	0.009
A4I2U7	DNA-directed RNA polymerase II-like protein	0.009
A4I9P6	DNA-directed_RNA_polymerase_III_subunit_-_putative	0.009
A0A640KV90	EF-hand domain-containing protein	0.009
A0A088RNK6	Eukaryotic translation initiation factor 5, putative	0.009
A0A640KB19	Glycosyltransferase family-like protein	0.009
A0A088RLU0	Guanine nucleotide-binding protein subunit beta-like protein	0.009
A0A640KJ19	HpcH_HpaI domain-containing protein	0.009
A0A3P3Z768	Hypothetical_protein	0.009
A0A3Q8IK43	Hypothetical_protein	0.009
A0A504WT12	Hypothetical_protein_conserved	0.009
A0A6J8FEL4	Hypothetical_protein_conserved	0.009
A0A6J8FM46	Hypothetical_protein_conserved	0.009
A0A504X7J7	IQ calmodulin-binding motif family protein	0.009
A4I9B3	MRB1-associated_protein	0.009
A0A504XSF9	Phosphoribosyl transferase domain family protein	0.009
E9B9B7	Proteasome regulatory non-ATP-ase subunit, putative	0.009
A0A3P3ZE43	Protein_transport_protein_SEC13	0.009
Q4Q9Y0	Putative cytochrome c oxidase VII	0.009
P84066	Putative D-tyrosyl-tRNA(Tyr) deacylase 2	0.009

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
E9AEM7	Putative proteophosphoglycan ppg3	0.009
E9ARF9	Putative RNA-binding protein	0.009
E9B9F7	Ribose-phosphate pyrophosphokinase, putative	0.009
A4HXS8	Tubulin_cofactor_C_domain-containing_protein_RP2_-_putative	0.009
E9BEZ1	Uncharacterized protein	0.009
E9BP55	Uncharacterized protein	0.009
E9AS94	Uncharacterized protein	0.009
E9B2V2	Uncharacterized protein	0.009
A0A640KEY4	Uncharacterized protein	0.009
A0A640KQJ3	Uncharacterized protein	0.009
A0A1E1J1A3	Vesicle-fusing ATPase	0.009
A0A1E1J477	AMPK1_CBM domain-containing protein	0.01
A4I7L0	Prostaglandin_f_synthase_-_putative	0.01
A0A088RN80	Uncharacterized protein	0.01
E9AS52	Guanine nucleotide-binding protein subunit beta-like protein	0.011
A4HM86	Proteophosphoglycan ppg4	0.011
O96636	Ribosomal protein L17	0.011
A0A504XDF3	Uncharacterized protein	0.011
A0A1E1J7U6	Uncharacterized protein	0.011
E9AXA5	Uncharacterized protein	0.011
PRO-1	Probable transport protein	0.012
A4H4F0	Uncharacterized protein	0.012
E9AF64	WD_REPEATS_REGION domain-containing protein	0.012
A0A504WWF0	Coatomer subunit delta	0.014
E9BTN0	Poly-zinc finger protein 2, putative	0.014
A0A0R6YBV7	Putative xylulokinase (Fragment)	0.014
E9BJC2	GMP_PDE_delta domain-containing protein	0.016
A0A3S7WXL7	Hypothetical_protein_conserved	0.016
A0A6J8FLI6	Hypothetical_protein_conserved	0.016
A0A6J8FM29	Hypothetical_protein_conserved	0.016
A0A1E1IVZ9	Putative cell division protein kinase 2,cdc2-related kinase	0.016
A0A1E1INF5	Putative unspecified product	0.016
A0A3Q8IG34	Uncharacterized protein	0.016
Q4Q9Y7	Uncharacterized protein	0.016

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
Q4QCU9	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	0.017
A0A640K8D1	26s protease regulatory subunit, putative	0.017
A0A451EJU1	Amidohydrolase family protein	0.017
A0A504Y9I9	dUTPase family protein	0.017
A0A504XT81	Endonuclease/Exonuclease/phosphatase family protein	0.017
A0A3Q8IJA9	Eukaryotic translation initiation factor 4 gamma, putative	0.017
A0A1E1J267	Formyltetrahydrofolate synthetase	0.017
A4HET7	Glutathione peroxidase	0.017
A4I812	Hypothetical_protein_-_conserved	0.017
A0A504X2N2	Methyltransferase	0.017
Q4QH21	Putative 3-methylcrotonoyl-CoA carboxylase beta subunit	0.017
Q95Z92	Putative cAMP-specific phosphodiesterase	0.017
E9BA61	Uncharacterized protein	0.017
A0A504XKN2	Uncharacterized protein	0.017
A0A1E1IND5	Uncharacterized protein	0.017
A0A1E1J6Q6	Uncharacterized protein	0.017
Q4QDX5	Uncharacterized protein	0.017
E9AND2	Uncharacterized protein	0.017
E9AQ01	Uncharacterized protein	0.017
E9B005	Uncharacterized protein	0.017
A0A504Y422	Papain cysteine protease family protein	0.018
A0A088RJ71	AAA family ATPase, putative	0.019
A0A640KKB1	Methylmalonyl-CoA mutase	0.019
E9AZA5	Uncharacterized protein	0.019
A0A640KGU7	40S ribosomal protein S15a	0.02
E9AW96	Actin interacting protein-like protein	0.02
A0A6L0X2H1	ATP pyrophosphate-lyase	0.02
E9AH36	ATP-dependent_DEAD/H_RNA_helicase_-_putative	0.02
A0A504XYX1	DEAD/DEAH box helicase family protein	0.02
A0A3S7WXU8	Dynein heavy chain, putative	0.02
A4HWW6	Eukaryotic translation initiation factor 2A	0.02
EIF6	Eukaryotic translation initiation factor 6	0.02
E9ARV1	Glutamate--cysteine ligase	0.02
A4HH81	Guanine nucleotide-binding protein subunit beta-like protein	0.02

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A4I096	Hypothetical_protein_-_conserved	0.02
A4I1E1	Hypothetical_protein_-_conserved	0.02
A4I5H9	Kinesin_-_putative	0.02
E9B5Y1	Non-specific serine/threonine protein kinase	0.02
A0A504WYD7	Paraflagellar rod family protein	0.02
A4HXP1	Protein-serine/threonine phosphatase	0.02
E9B304	Putative ATP-dependent RNA helicase	0.02
A0A504XKP3	Putative nuclear pore complex protein family protein	0.02
A4I6L8	Putative sodium stibogluconate resistance protein	0.02
E9ADS7	Putative U3 small nucleolar ribonucleoprotein protein MPP10	0.02
E9BN99	Uncharacterized protein	0.02
A0A504Y8N8	Uncharacterized protein	0.02
A0A3Q8IIV0	Uncharacterized protein	0.02
A0A3Q8IFH1	Uncharacterized protein	0.02
A0A1E1J6G7	Uncharacterized protein	0.02
Q4QIZ2	Uncharacterized protein	0.02
E9ADP1	Uncharacterized protein	0.02
E9AWR5	Uncharacterized protein	0.02
E9AZ92	Uncharacterized protein	0.02
E9ASK5	Uncharacterized protein	0.02
A0A640K9Z2	Uncharacterized protein	0.02
A0A640KDN0	Uncharacterized protein	0.02
A0A504XJG5	VHS domain family protein	0.02
A4I9G2	Coatomer subunit beta'	0.024
A0A381MVV1	D-isomer specific 2-hydroxyacid dehydrogenase-like protein	0.024
A0A504XAH6	Hypothetical_protein_conserved	0.024
A4HZ53	La_RNA_binding_protein_-_putative	0.024
A0A3Q8I9I8	OTU-like cysteine protease, putative	0.024
A0A3Q8I1Y1	Proteasome complex subunit Rpn13 ubiquitin receptor family protein	0.024
A0A504XGZ0	Uncharacterized protein	0.024
E9AEK7	Uncharacterized protein	0.024
A0A640KQW0	Chaperonin alpha subunit, putative	0.025
A4HG65	Glycerol-3-phosphate dehydrogenase	0.025
E9AJT7	Putative 26S protease regulatory subunit	0.025

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A504Y3F6	Pyr_redox_2 domain-containing protein	0.025
A4IBY0	Snf7_-putative	0.025
E9B7J0	Uncharacterized protein	0.025
E9AMQ3	Uncharacterized protein	0.025
E9ANW4	Uncharacterized protein	0.025
A0A504XU13	DnaJ domain family protein	0.027
A0A3S7X408	Intergrin alpha chain protein, putative	0.027
A0A1E1J1L9	Rac serine-threonine kinase, putative,protein kinase, putative	0.027
A4H3K7	Uncharacterized protein	0.027
E9ALF6	Uncharacterized protein	0.027
E9B3Z9	Uncharacterized protein	0.027
A0A640K952	Uncharacterized protein	0.027
A0A3Q8IBN2	ATP-dependent RNA helicase, putative	0.028
A0A1E1IYQ0	DNA ligase k alpha, putative	0.028
A0A6J8F4U2	Exocyst_complex_component_Sec3_putative/Pfam:PF09 763	0.028
A4I4K9	Hypothetical_protein_-_conserved	0.028
A4I607	Hypothetical_protein_-_conserved	0.028
A0A3P3Z1S5	Metalloprotease	0.028
A0A640KQ09	Microtubule-associated protein, putative	0.028
A0A3S7X9F4	NLI interacting factor-like phosphatase family protein	0.028
E9B1F3	Peptidyl-prolyl cis-trans isomerase	0.028
A4H3B9	Phosphoglycan beta 1,3 galactosyltransferase	0.028
E9AVW8	Putative farnesyl pyrophosphate synthase	0.028
E9AXH4	Tubulin gamma chain	0.028
A4H491	Uncharacterized protein	0.028
E9B193	3-hydroxy-3-methylglutaryl coenzyme A reductase	0.029
A0A3S5H5D7	Adenylate kinase family protein	0.029
A0A640KDY5	Endoplasmic reticulum oxidoreductin, putative	0.029
A0A3P3ZBN9	Hypothetical_protein	0.029
A4HWT9	Hypothetical_protein_-_conserved	0.029
A4I319	Hypothetical_protein_-_conserved	0.029
A4ICG1	Hypothetical_protein_-_conserved	0.029
A0A6J8FS73	Hypothetical_protein_conserved	0.029
A4ICN4	Intraflagellar transport protein 122 homolog	0.029

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A3S7WT79	Mitochondrial pyruvate carrier	0.029
A0A504Y8T0	Peptidase M3 family protein	0.029
A0A640KLI2	SUI1 domain-containing protein	0.029
A0A3Q8IUB2	Uncharacterized protein	0.029
A0A640KQE8	Uncharacterized protein	0.029
A0A1E1J4R1	Pumilio protein, putative	0.03
A0A1E1INY2	Putative unspecified product	0.03
A0A504WY56	Elongation factor Tu GTP binding domain family protein	0.031
A0A504XUY4	Leishmanolysin	0.031
A0A504Y1G1	Uncharacterized protein	0.031
A0A088RZI2	ABC transporter, putative	0.032
A0A3S7X7M2	ATP-binding cassette protein subfamily B, member 2, putative	0.032
A0A640KP84	C-1-tetrahydrofolate synthase, cytoplasmic, putative	0.032
A0A504Y9W9	Calcineurin-like phosphoesterase family protein	0.032
E9AS44	CAP-Gly domain-containing protein	0.032
A4IA07	Dynamamin_family/50S_ribosome-binding_GTPase_-_putative	0.032
A0A640KFR4	Flagellar protofilament ribbon protein-like protein	0.032
A0A504WX94	Major Facilitator Superfamily protein	0.032
A0A504X152	Protein kinase domain family protein	0.032
A0A3S7WVY1	Pseudouridine synthase TruD, putative	0.032
A0A220QLW6	Putative coat protein	0.032
A4HDG7	Putative pre-mRNA splicing factor	0.032
A0A1E1J105	Uncharacterized protein	0.032
E9B3E0	Uncharacterized protein	0.032
A0A640KFS8	Uncharacterized protein	0.032
A0A6L0XFE2	4-coumarate:coa_ligase-like_protein	0.033
A0A504XYI0	6-phosphofructo-2-kinase family protein	0.033
A0A640KSA8	GTPase protein, putative	0.033
A0A504XKZ4	Helicase associated domain (HA2) family protein	0.033
A0A3P3Z3B7	Hypothetical_protein	0.033
A4I9A8	Hypothetical_protein_-_conserved	0.033
A4H7I2	PX domain-containing protein	0.033
A0A1E1J7B6	Uncharacterized protein	0.033
E9B370	Uncharacterized protein	0.033

Table S1 (cont.): The protein list of high confidence data.

Accession	Protein name	q-value
A0A088RIN8	Uncharacterized protein	0.033
A0A640KKM2	Uncharacterized protein	0.033
A0A504XC32	Valyl-tRNA synthetase	0.033
A4HZU2	Guide_RNA_associated_protein_-_GAP2_-_putative	0.034
A0A3P3Z2K2	Hypothetical_protein	0.034
A4HX35	OTU-like_cysteine_protease_-_putative	0.034
A0A640KHI8	Proteasome regulatory ATPase subunit 1, putative	0.034
A0A640KEB3	Stomatin-like protein	0.034
A0A504Y7Y6	Uncharacterized protein	0.034
Q4QEU7	Uncharacterized protein	0.034
A4I4Y2	40S ribosomal protein S19-like protein	0.036
A4ICN5	40S_ribosomal_protein_S10_-_putative	0.036
A0A640KR98	AAA domain-containing protein	0.036
A4I4V7	Hypothetical_protein_-_conserved	0.036
Q4QBD7	Putative cytochrome c oxidase subunit 10	0.036
A0A640KAC0	RNA helicase, putative	0.036
A0A3S5H7S6	Uncharacterized protein	0.036
E9AF83	Uncharacterized protein	0.036
A4I5E0	WW_domain_containing_protein_-_putative	0.036
A4HM95	Uncharacterized protein	0.038
Q4Q1T2	Uncharacterized protein	0.038
A0A3P3Z716	Galactose_oxidase	0.039
A0A1E1IS56	Cyclic nucleotide-binding domain-containing protein	0.04
A0A3P3Z230	Phosphodiesterase	0.04
A0A504X5J2	Surface_antigen-like_protein/GeneDB:LmjF.09.0580	0.04
E9AMD4	Cyclopropane-fatty-acyl-phospholipid synthase	0.041
A0A504X704	Hypothetical_protein_conserved	0.041
A4I6S7	Uncharacterized protein	0.041
E9B9N8	Uncharacterized protein	0.042
A0A088RKY6	Uncharacterized protein	0.042

Table S2: Accession number of proteins from the Venn-diagram comparing proteins identified from three leishmania species.

<i>L. donovani</i>	<i>L. martiniquensis</i>	<i>L. orientalis</i>	<i>L. donovani and L. martiniquensis</i>	<i>L. donovani and L. orientalis</i>	<i>L. martiniquensis and L. orientalis</i>
Q66VD6	A4HVW1	A0A5B8Z0A1	Q4QHP3	E9B578	A0A3P3ZI57
A0A3S5H5D7	A0A640KHX9	A0A1E1ISJ7	E9ARJ3	A4HY66	A0A3P3ZAP6
A0A504X3J8	E9B0M6	A0A1E1J0Y4		A4I1M5	A0A3P3ZG54
E9BMF8	A0A1E1IUI9	A0A640KYQ2		E9ATX7	A0A088S266
A0A504X1P4	A0A640KE76	A0A640KG80		E9AFL3	E9ANP4
Q4Q4X1		A0A640KDZ6		A0A1E1IXW5	A0A640KEQ1
A0A504XR61		A0A088RW67			
A0A504XGG4		A4HD14			
A0A3Q8IHF4		A0A088RR95			
Q4Q5I2		A0A640KVG1			
A0A504XY66		A0A1E1IVQ5			
A0A504X5D8		E9B1E2			
E9ACH4		A0A4D5YJB0			
E9AGY8		A0A640KIC6			
A4I4H4		A4HB65			
A0A504YBN6		A0A3P3YYV3			
A0A6J8FEJ1		TXN2			
A0A6J8FLI6		A0A640KGF0			
A0A640KLW3		A0A640KH80			
A4HS73		PRO-1			
A0A6J8FHZ9					
A1Y2D3					
E9B9B7					
Q4QC13					
E9B1E6					
Q4QJ42					
A4I2X5					
A0A504XFE0					
A0A6L0Y0Y0					
A4I5Z0					
A0A504WZF6					
A0A3Q8IVV7					
A0A3Q8ICH6					
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