

Table S5. Proteins detected in *Leishmania mexicana* subjected to clemastine fumarate treatment or untreated, revealing marked changes due to significant temperature variation $\geq 4^{\circ}\text{C}$.

Accession	Gene ID <i>L. mexicana</i>	Description	Tm_{50} ($^{\circ}\text{C}$)		ΔTm ($^{\circ}\text{C}$)
			Clem	DMSO	
E9AU29	LmxM.36.5940	A distinct subfamily of CDD/CDA-like deaminases protein	64.32	37.96	26.36
E9AYZ0	LmxM.27.0880	Putative 2-oxoglutarate dehydrogenase subunit (OGDC) (or α -ketoglutarate dehydrogenase)	69.97	47.08	22.89
E9AZC6	LmxM.27.2200	Thioredoxin domain-containing protein	68.79	55.13	13.66
E9AL45	LmxM.07.0340	Putative ATP-dependent DEAD/H RNA helicase	59.21	46.69	12.52
E8NHP1	LmxM.15.0440a	tb-292 membrane associated protein-like protein	50.00	37.78	12.22
E9AYR5	LmxM.27.0130	Zinc finger protein 2	61.25	50.19	11.06
E9B5Z7	LmxM.34.1180	Putative NADH-dependent fumarate reductase (FRD)	48.3	38.38	9.92
E9B2E4	LmxM.31.0230	Dynein light chain, flagellar outer arm, putative	64.4	55.78	8.62
E9AKM1	LmxM.05.1140	V-type proton ATPase subunit	50.21	41.6	8.61
E9ALJ4	LmxM.08_29.2300	Ubiquitin carboxyl-terminal hydrolase	46.16	37.72	8.44
E9AU79	LmxM.36.6430	Protein transport protein SEC23	45.06	37.27	7.79
E9B686	LmxM.34.2080	Putative calcium motive P-type ATPase	51.75	44.2	7.55
E9B2L9	LmxM.31.0950	Staphylococcal nuclease homologue/Tudor domain containing protein, putative	45.37	37.99	7.38
E9AV49	LmxM.21.0810	methionine--tRNA ligase	44.68	37.35	7.33
E9B1Q4	LmxM.30.1070	Biotin/lipoate protein ligase-like protein	44.45	37.79	6.66
E9B2L2	LmxM.31.0880	60S ribosomal protein L18a	44.96	38.39	6.57
E9AVS1	LmxM.22.0890	Uncharacterized protein	44.51	37.97	6.54
E9B384	LmxM.31.3010	AMPK1_CBM domain-containing protein	49.7	43.3	6.40
E9AKF1	LmxM.05.0450	SKP1 component POZ domain-containing protein	44.39	38.01	6.38
E9ALK7	LmxM.08_29.2160	Rab GDP dissociation inhibitor	50.01	43.65	6.36
E9ATB8	LmxM.36.3390	60S ribosomal protein L29	44.83	38.48	6.35
E9ANG7	LmxM.11.0210	Inorganic diphosphatase	44.76	38.43	6.33
E9AV01	LmxM.21.0340	Mitochondrial processing peptidase alpha subunit, putative	44.71	38.42	6.29
E9ANC1	LmxM.10.1110	LsmAD domain-containing protein	54.74	48.53	6.21
E9AWM1	LmxM.24.0320	fumarate hydratase (FH)	47.76	41.72	6.04
E9B396	LmxM.31.3130	Putative ribosomal protein L3	49.72	43.71	6.01
E9AKM7	LmxM.05.1210	Protein phosphatase type 1 regulator-like protein	48.66	42.65	6.01
E9AZ73	LmxM.27.1710	Putative eukaryotic translation release factor	55.44	49.53	5.91
E9AYL4	LmxM.26.2330	Putative 60S ribosomal protein L35	50.62	45.00	5.62
E9ANP4	LmxM.11.1000	Pyruvate, phosphate dikinase (PPDK)	49.94	44.37	5.57
E9B5X5	LmxM.34.0950	PSP1 C-terminal domain-containing protein	42.88	37.35	5.53
E9ALB7	LmxM.07.1000	RNA binding protein-like protein	61.68	56.51	5.17
E9AQU2	LmxM.16.1310	Putative cytochrome c	59.16	54.2	4.96
E9AKT6	LmxM.06.0570	Putative 60S ribosomal protein L23a	48.64	44.28	4.36
E9AKP0	LmxM.06.0120	Peptidyl-prolyl cis-trans isomerase	52.11	47.76	4.35
E9ASX8	LmxM.36.2030	Chaperonin HSP60, mitochondrial	55.99	51.68	4.31
E9AW54	LmxM.23.0510	Uncharacterized protein	54.42	50.18	4.24
E9AVW5	LmxM.22.1330	Uncharacterized protein	50.07	45.95	4.12
E9AK27	LmxM.04.0460	Adenylosuccinate lyase	42.27	38.19	4.08
E9AKR5	LmxM.06.0370	Putative glutamine synthetase	41.58	37.5	4.08
E9B1G2	LmxM.30.0140	Ubiquitin carboxyl-terminal hydrolase	49.84	45.83	4.01