

Table S2: Phosphorylation changes following 15 minute of arginine deprivation in *L. donovani* promastigotes

Accession number	Description	Phosphorylated tryptic peptide	Repeat 1	Repeat 2
			Log ₂ fold from non-starved	
LinJ.27.1700	protein kinase-like protein	GpSPDVDDKFVDVGDATK	6.67	1.68
LinJ.24.0160	hypothetical protein, conserved	GGEEEGTNFIVDpSDDDEDEAVAAIR	6.6	1.9
LinJ.15.0810	protein kinase, putative	APPVSYNEPGHEQLDpSR	6.55	1.73
LinJ.13.1330	hypothetical protein, conserved	LSYSAATAEpSPSK	5.48	1.55
LinJ.35.2530	hypothetical protein, conserved	AGpSpSIADTPARPWPEDAGLSLK	5.05	2.06
LinJ.35.4450	hypothetical protein, conserved	APIADpSDSpDDDEPVR	4.64	3.31
LinJ.08.0630	hypothetical protein, conserved	ASSpTEGSPVAAGTIPAVAAK	4.28	2.67
LinJ.30.0520	hypothetical protein, conserved	FApSPDKLETVTPTK	4.25	0.95
LinJ.22.1070	hypothetical protein, conserved	pSLDGAAGDAEECADAAASASTGFPR	3.34	1.36
LinJ.09.0840	hypothetical protein, conserved	pSPLATPTAVFSPNSK	2.76	6.74
LinJ.34.3220	DNA topoisomerase IB, large subunit	VVpSDDDDVPLAALR	2.08	1.62
LinJ.27.1100	hypothetical protein, conserved	VpSNGQTIMQLQDELETLHR	2.02	1.12
LinJ.31.0450	cytoskeleton-associated protein CAP5.5, putative,	VPQPEAQpSAKVpSpSETApSVVEEQR	1.84	1.75
LinJ.35.3150	ATP-dependent RNA helicase, putative	GGGpTGNEDDDYEDGGYDAYR	1.77	1.92
LinJ.35.4450	hypothetical protein, conserved	APIADpSDpSDDDEPVRKPVLAKE	1.66	1.29
LinJ.36.5290	hypothetical protein, conserved	VQVMTEDMNEDGpSNDR	1.63	1.48
LinJ.36.2260	DEAD box RNA helicase, putative	FDpYSpSDDDDSDARPAK	1.61	1.29
LinJ.01.0790	eukaryotic initiation factor 4a, putative	FCETFVGGpTR	1.59	1.88
LinJ.36.6110	hypothetical protein, conserved	KCpSAPELPPR	1.57	3.48
LinJ.35.0920	hypothetical protein, conserved	LLNNENADDLLpSpSDDEEPK	1.48	1.91
LinJ.25.1100	hypothetical protein, conserved	FpSIEGNEPEQKPLVPTSHLR	1.39	2.48

LinJ.13.0700	hypothetical protein, conserved	GDNLLHSDQTPCDAAAAAGSSIVANN p TPR	1.37	1.23
LinJ.11.1110	60S ribosomal protein L28, putative	AVAAVRPDLADV p SFRR	1.36	1.19
LinJ.14.1300	hypothetical protein, conserved	AV p SVVDGPHGPHAR	1.34	2.14
LinJ.35.2240	RNA-binding protein, putative	H p SHG p SNDEIQNGGDTDNFR	1.29	3.4
LinJ.31.2440	hypothetical protein, conserved	GNTD p SPDTAELAAAALQALSPQGVLHTDSR	1.26	1.73
LinJ.35.2610	hypothetical protein, conserved	TNTSATVT p SEGNSNSEK	1.24	0.77
LinJ.08.1040	Phosphoribosylpyrophosphate synthetase	MTEVHAMSGTV p SPHTEK	1.22	0.99
LinJ.35.4450	hypothetical protein, conserved	APIAD p SD p SDDDEPVRKPVAK	1.22	1.1
LinJ.35.4060	protein kinase A catalytic subunit isoform 1	SPGDTSNFEKYPD p SPVDR	1.19	1.13
LinJ.31.2700	serine/threonine protein phosphatase pp1(5.9), putative	DAN p SPLSSFAR	1.16	1.68
LinJ.27.1630	hypothetical protein, conserved	NLP p SVDDGLYQK	1.14	1.46
LinJ.04.0060	hypothetical protein, conserved	GNEEEERNE p TPRDCK	1.01	1.18
LinJ.01.0480	hypothetical protein, conserved	AVAESAP p SPTTGK	0.98	0.9
LinJ.33.2570	hypothetical protein, conserved	Q p SATATTAAPGEDVDPMEAK	0.97	0.95
LinJ.33.2570	hypothetical protein, conserved	Q p SATATTAAPGEDVDPMEAK	0.97	0.89
LinJ.36.2490	tyrosine aminotransferase	AGNSTG p SLTEER	0.94	1.25
LinJ.36.2490	tyrosine aminotransferase	AGN p STGSLTEER	0.94	1.1
LinJ.31.0090	hypothetical protein, conserved	p SAEKAPEKPVADKEAEDA EK	0.68	0.78
LinJ.11.0150	hypothetical protein, conserved	IQDVNEDSGLPFDVE p SAHREGD p SPAR	0.55	1.3
LinJ.34.0500	calcium channel protein, putative, ion transporter, putative	LYRQP p SLPATEMGF p SVVGTPQQR	-0.81	-1.94
LinJ.13.1350	MCAK-like kinesin, putative	ERVAEQPRPM p SAQR	-0.85	-3.31
LinJ.20.1130	hypothetical protein, conserved	GYEG p TD p SEDGENHHHSAAGAGKK	-0.85	-0.63
LinJ.35.4450	hypothetical protein, conserved	RP p SPK p SPK	-0.9	-3.01
LinJ.32.0370	hypothetical protein, conserved	SAAAGAG p SAKRPA GLSPGAAAALAADEK	-0.92	-0.93
LinJ.36.1560	hypothetical protein, conserved	AGKQH p SDEEVELSVK	-0.94	-1.71

LinJ.19.1140	hypothetical protein, conserved	GDD p SEDREH p SDVDDDDGHKSGAAGTVADVAAA AEK	-1.03	-1.78
LinJ.19.1140	hypothetical protein, conserved	GDDSEDREH p SDVDDDDGHKSGAAGTVADVAAA AEK	-1.03	-2.24
LinJ.13.0290	flagellar radial spoke protein, putative	ITSSTTIAPQGALEEPEPE QEp TEEDEDEDAEDGAQRK PK	-1.05	-6.65
LinJ.19.1140	hypothetical protein, conserved	QRHT p SPSPYEQV PK	-1.2	-1.94
LinJ.29.1510	RNA binding protein, putative	D p TPLLL PR	-1.29	-1.22
LinJ.29.2540	hypothetical protein, unknown function	RYVPPSEEQDAEAAG Qp SAS R	-1.5	-4.52
LinJ.21.0920	hypothetical protein, conserved	AR p SQLAAVRDDLA QR	-1.52	-2.51
LinJ.32.2950	RNA-binding protein, putative	AR p SGEDDCDDEENTFN FKR	-1.59	-6.7
LinJ.30.0580	hypothetical protein, conserved	TTGRDPNED p SG p SDAEEVTEEELAA RK	-1.61	-4.87
LinJ.25.1920	hypothetical protein, conserved	AKPVVPFDVSDYEDKKV Qp SP K	-1.65	-2.61
LinJ.33.3230	hypothetical protein, conserved	VG p TPVEPHRGALEG p SPVD AR	-1.72	-3.42
LinJ.33.3230	hypothetical protein, conserved	VG p TPVEPHRGALEGAS PVDAR	-1.72	-6.33
LinJ.12.0720	hypothetical protein, conserved	DLLAR p TPDVGDDDD EDLRR	-1.77	-1.63
LinJ.22.0060	hypothetical protein, conserved	ASVENARH p SAQNAVD NAK	-1.78	-1.29
LinJ.16.1550	kinesin, putative	SV p SGTG p SKGT FKR	-1.8	-1.37
LinJ.18.1510	P-type H ⁺ -ATPase, putative	KYELDAAAFEDKPE p SH p SDAEMTPQKP QRR	-1.8	-2.79
LinJ.05.0140	nucleolar RNA helicase II, putative	ISAKA p SDHGNGVAVE K	-1.81	-2.03
LinJ.20.1670	hypothetical protein, conserved	EQR p SPATVVAPED KK	-1.86	-5.88
LinJ.34.0700	hypothetical protein, conserved	AAPELADADGVEPSSGPTSS Rp SPT GR	-1.88	-1.23
LinJ.36.6780	ubiquitin fusion degradation protein, putative	VAAG p TPPLKHLPGSSSPSS GPK	-1.95	-6.75
LinJ.15.0300	hypothetical protein, conserved	AALPEALAVHAHDWD p SSSSGR R	-1.97	-1.95
LinJ.11.0520	nucleobase transporter	YLADSG p SEKKAELLETEHGDV TAR	-1.99	-1.34
LinJ.29.0280	hypothetical protein, conserved	LAAR p SPAK p SP AR	-2	-1.44
LinJ.17.1310	hypothetical protein, unknown function	VFNRDG p SAVA QR	-2.07	-2.77
LinJ.21.1850	hypothetical protein, conserved	MRVEQVLAHQ Mp SPSAS GR	-2.09	-1.63

LinJ.36.6110	hypothetical protein, conserved	KRGG p SINGATALLR	-2.17	-6.7
LinJ.27.1220	hypothetical protein, conserved	HVF p TPEGCKYGDK	-2.27	-6.75
LinJ.29.0120	proteasome regulatory non-ATPase subunit, putative	EGNA p SEEEAAKPEEEKTAPLNHK	-2.36	-1.57
LinJ.34.3220	DNA topoisomerase IB, large subunit	ANKVV p SDDDDVPLAALRV	-2.39	-2.74
LinJ.04.0060	hypothetical protein, conserved	NE p TPRDPCKL p TDVSTDHYAK	-2.4	-6.67
LinJ.21.0920	hypothetical protein, conserved	AL p SAV p SEKNADFNDLRR	-2.65	-1.21
LinJ.05.0100	phosphoprotein phosphatase, putative	ETKGPV p SPR	-2.7	-2.6
LinJ.04.0060	hypothetical protein, conserved	VNIDNVERHPPVPEGVN p TPR	-2.87	-6.67
LinJ.34.1610	hypothetical protein, conserved	DVGDHREApSVL p TAAGR	-2.93	-2.37
LinJ.14.0860	hypothetical protein, conserved	KASAGGDDDEA Qp SPESPKETK	-3.05	-6.73
LinJ.36.6290	hypothetical protein, conserved	EAVEHA p SVQDTAAKEVEATK	-3.13	-3.63
LinJ.24.2180	hypothetical protein, conserved	AHKDYVVPELPEEPMWPLIGH p TP	-3.17	-1.52
LinJ.18.1510	P-type H -ATPase, putative	ALEGLREDTHVLNEST p SPVNAFSPK	-3.28	-1.74
LinJ.31.1230	hypothetical protein, conserved	AER p SPFGGFECPEGYWVCSVEHGGCSK	-4.6	-4.91
LinJ.29.0280	hypothetical protein, conserved	SPAK p SPARAN p SPEPQMSTSASSTPR	-4.72	-6.38
LinJ.13.1350	MCAK-like kinesin, putative	VQAAIQAPALPARIP p TPLRR	-4.76	-4.32
LinJ.07.0620	hypothetical protein, conserved	KAAAAQRGDD p T p SDNEAVNAQAR	-5.09	-3.61
LinJ.25.1120	hypothetical protein, conserved	p SNFG p SRVDLHNLGDLR	-5.67	-2.07
LinJ.25.1120	hypothetical protein, conserved	SNFG p SRVDLHNLGDLR	-5.67	-4.08
LinJ.32.0370	hypothetical protein, conserved	RPAGLSPGAAAALAADEK QAp SCAACH	-5.76	-6.45
LinJ.15.0060	hypothetical protein, conserved	KPL p TPPRLILAPPTALG Qp SPDVKPK	-5.95	-6.25
LinJ.13.0700	hypothetical protein, conserved	R p SRSPVAWTASIGGAAK	-6.51	-3.13
LinJ.13.0620	ubiquitin-like protein	RSDDSLQFEQDASQQPT p SPLLPPQAPVKAPAASAFDR	-6.7	-2.37
LinJ.35.0300	hypothetical protein, conserved	AP p SPDFLGSQLLAEYRGEAASLQLAK	-6.86	-5.37
LinJ.18.0590	RNA binding protein, putative	A p SPQQAAVQSAPGKIEYLR	-6.94	-4.48

LinJ.23.1190	hypothetical protein, unknown function	NEpSDDMERQADEKR	-7.31	-7.1
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Di methylation of tryptic peptides extracted from *L. donovani* promastigotes 15 min after arginine deprivation initiated. Phosphopeptide enrichment, mass spectrometry and data analysis is described in detail in Experimental Procedures