

Table 1. Significantly down-regulated proteins affected by heat stress in rat small intestine

Unused ^a	%Cov (95) ^b	Accession ^c	Gene Symbol	Name	Peptides (95%)	Fold Ratio ^d	P-Value ^e
17.00	10.53	D3ZW20	Acs15	Acyl-CoA synthetase long-chain family member 5	8	0.65	0.046
17.20	25.14	Q01129	Dcn	Decorin	17	0.61	0.049
43.21	14.67	P07756	CPS1	Carbamoyl-phosphate synthase	25	0.56	0.001
23.64	16.51	Q64428	Hadha	Trifunctional enzyme subunit alpha	13	0.53	0.025
25.51	32.51	Q6P3V8	Eif4a1	Eukaryotic translation initiation factor 4A1	17	0.53	0.021
45.11	41.34	P62630	Eef1a1	Elongation factor 1-alpha 1	32	0.52	0.002
25.23	7.60	G3V7Q7	Iqgap1	IQ motif containing GTPase activating protein 1	13	0.51	0.012
11.91	7.03	P06399	Fga	Fibrinogen alpha chain	6	0.51	0.047
13.11	20.93	P15650	Acadl	Acyl-CoA dehydrogenase, long chain	9	0.50	0.042
33.89	12.3	G3V6P7	Myh9	Myosin, heavy chain 9	32	0.50	0.049
15.52	9.37	G3V6Y6	Pygb	Phosphorylase, glycogen; brain	8	0.49	0.041
22.14	7.11	Q5SGE0	Lrrprc	Leucine-rich PPR motif-containing protein	15	0.48	0.016
93.86	21.29	E9PTI3	Myh11	Myosin, heavy chain 11	73	0.47	0.006
22.63	8.66	F1M779	Cltc	Clathrin, heavy chain (Hc)	13	0.45	0.022
38.94	4.15	P38650	Dync1h1	Cytoplasmic dynein 1 heavy chain 1	21	0.42	0.000
20.66	8.94	F1LQS6	Xdh	Xanthine dehydrogenase	13	0.41	0.022
14.66	15.16	Q60587	Hadhb	Trifunctional enzyme subunit beta	7	0.40	0.014
13.56	22.7	P21913	Sdhb	Succinate dehydrogenase	7	0.39	0.031
47.60	28.09	P05197	Eef2	Eukaryotic translation elongation factor 2	29	0.37	0.005
14.55	11.16	G3V936	Cs	Citrate synthase	7	0.37	0.015
5.45	2.78	G3V6T1	Copa	Coatomer protein complex, subunit alpha	4	0.36	0.024
31.71	23.97	G3V826	Tkt	Transketolase	19	0.35	0.010
18.05	3.87	P12785	FASN	Fas cell surface death receptor	9	0.34	0.006
22.77	32.55	Q09073	Ant2	ADP/ATP translocase 2	17	0.32	0.009
20.20	9.21	Q5BJZ3	Nnt	Nicotinamide nucleotide transhydrogenase	10	0.32	0.004
14.13	13.68	B5DFH4	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	7	0.25	0.002

^a The Unused ProtScore is a measurement of all the peptide evidence for a protein that is not better explained by a higher ranking protein.

^b The percentage of matching amino acids from identified peptides having confidence greater than or equal to 95% divided by the total number of amino acids in the sequence.

^c Accession numbers are from the Uniprot database.

^d Fold Ratio are proteins with ratios of heat stressed/control label less than 0.71.

^e P- value reported by ProteinPilot software can be a useful metric in determining which changes are statistically “real”.