

Table S3 - Proteomic Profile of SOL muscle in Response to FS

# Accession	Symbol	Name	Anova (P)	Fold change	Score	%Coverage	# Peptides	Main Biological Process	Main Cellular Component
P63038	HSPD1	60 kDa heat shock protein, mitochondrial	0.048	0.6	26.1	21.1	11	Detoxification, cytoprotection	Mitochondrion
P35700	PRDX1	Peroxiredoxin-1	0.013	0.7	16.6	37.1	7	Detoxification, cytoprotection	Cytoplasm
Q9QZ57	HSPB3	Heat shock protein beta-3	0.038	0.7	4.3	11.0	2	Detoxification, cytoprotection	Cytoplasm
P07310	CKM	Creatine kinase M-type	0.016	0.5	323.3	81.4	43	Energy metabolism	Cytoplasm
Q8QZS1	HIBCH	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	0.042	0.7	7.4	2.9	1	Energy metabolism, Amino-acid degradation	Mitochondrion
Q5RJV4;Q9D0F9	PGM1/2	Phosphoglucomutase-1/2	0.025	0.6	144.1	44.3	21	Energy metabolism, glycogenolysis	Cytoplasm
P21550	ENO3	Beta-enolase	0.018	0.5	323.3	63.1	33	Energy metabolism, Glycolysis	Cytoplasm
P52480	PKM	Pyruvate kinase PKM	0.019	0.6	323.3	58.6	31	Energy metabolism, Glycolysis	Cytoplasm
O70250	PGAM2	Phosphoglycerate mutase 2	0.044	0.6	54.6	28.1	9	Energy metabolism, Glycolysis	Cytoplasm
P54071	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	0.019	0.5	323.3	58.0	29	Energy metabolism, Krebs cycle	Mitochondrion
Q9D051	PDHB	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	0.018	0.6	190.4	28.1	8	Energy metabolism, Krebs cycle	Mitochondrion
P14152	MDH1	Malate dehydrogenase, cytoplasmic	0.018	0.6	323.3	47.9	17	Energy metabolism, Malate-aspartate NADH Shuttle	Cytoplasm
P08249	MDH2	Malate dehydrogenase, mitochondrial	0.023	0.6	87.0	58.3	17	Energy metabolism, Malate-aspartate NADH Shuttle	Mitochondrion
P56480	ATP5B	ATP synthase subunit beta, mitochondrial	0.019	0.6	323.3	53.5	21	Energy metabolism, Oxidative phosphorylation	Mitochondrion
Q9ERS2	NDUFA13	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	0.028	0.6	26.4	53.5	7	Energy metabolism, Oxidative phosphorylation	Mitochondrion
Q8K2B3	SDHA	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	0.035	0.6	309.4	19.4	15	Energy metabolism, Oxidative phosphorylation	Mitochondrion
Q99LY9	NDUFS5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	0.022	0.6	8.8	14.2	1	Energy metabolism, Oxidative phosphorylation	Mitochondrion
P56391	COX6B1	Cytochrome c oxidase subunit 6B1	0.037	0.7	7.8	41.9	4	Energy metabolism, Oxidative phosphorylation	Mitochondrion
P56392	COX7A1	Cytochrome c oxidase subunit 7A1, mitochondrial	0.020	0.7	4.9	28.8	2	Energy metabolism, Oxidative phosphorylation	Mitochondrion
Q8QZT1	ACAT1	Acetyl-CoA acetyltransferase, mitochondrial	0.048	0.7	97.6	30.9	10	Energy metabolism, β -oxydation	Mitochondrion
Q8CGP2;Q8CGP1; Q64475;P10853; Q9D2U9;Q8CGP0; P70696;Q64524	HIST1H2BP/K/B/F/A;HI ST1H2BE; HIST3H2BA/B	Histone H2B type 1-P/K/B/F/A; Histone H2B type 2-E; Histone H2B type 3-A/B	0.015	1.9	66.0	52.0	7	Gene regulation	Nucleus
Q61838	PZP	Alpha-2-macroglobulin	0.038	1.7	17.9	8.2	11	Miscellaneous	Miscellaneous
P02088	HBB-B1	Hemoglobin subunit beta-1	0.020	2.0	323.3	84.4	15	Miscellaneous	Miscellaneous
P01942	HBA	Hemoglobin subunit alpha	0.040	2.0	108.9	53.3	8	Miscellaneous	Miscellaneous
Q8VHX6	FLNC	Filamin-C	0.048	0.5	323.3	37.6	88	Myofilaments and cytoskeleton	Sarcomere
Q9QXS1	PLEC	Plectin	0.023	0.5	323.3	34.5	149	Myofilaments and cytoskeleton	Sarcomere
A2AAJ9	OBSCN	Obscurin	0.001	0.5	323.3	19.0	91	Myofilaments and cytoskeleton	Sarcomere
P09542	MYL3	Myosin light chain 3	0.019	0.6	195.5	66.2	14	Myofilaments and cytoskeleton	Sarcomere
P97457	MYLPF	Myosin regulatory light chain 2, skeletal muscle isoform	0.028	0.6	224.3	78.7	15	Myofilaments and cytoskeleton	Sarcomere
P05213;P68373; P68369;P05214	TUBA1A/B/C; TUBA3A	Tubulin alpha-1A/B/C chain;Tubulin alpha-3 chain	0.047	1.6	11.8	21.3	8	Myofilaments and cytoskeleton	Sarcomere
E9Q616	AHNAK	Desmoyokin	0.019	1.6	2.1	1.5	2	Myofilaments and cytoskeleton	Sarcomere
P63260;P60710	ACTG1/ACTB	Actin, cytoplasmic 2/1	0.040	1.6	5.9	40.0	20	Myofilaments and cytoskeleton	Sarcomere
O88346	TNNT1	Troponin T, slow skeletal muscle	0.017	1.7	323.3	31.3	12	Myofilaments and cytoskeleton	Sarcomere
P17742	PPIA	Peptidyl-prolyl cis-trans isomerase A	0.023	1.4	12.5	23.2	4	Protein biosynthesis, Maturation	Cytoplasm
P70333;O35737; Q9Z2X1	HNRNPH1/2; HNRNPF	Heterogeneous nuclear ribonucleoprotein H2/H/F	0.019	1.3	12.9	5.8	2	Protein biosynthesis, Transcription	Nucleus
P58252	EEF2	Elongation factor 2	0.027	0.6	25.4	11.1	9	Protein biosynthesis, Translation	Cytoplasm
P99027	RPLP2	60S acidic ribosomal protein P2	0.038	0.7	1.6	10.4	1	Protein biosynthesis, Translation	Ribosome
Q8C1A5	THOP1	Thimet oligopeptidase	0.029	0.8	2.5	1.5	1	Miscellaneous	Cytoplasm
Q9D154	SERPINF1A	Leukocyte elastase inhibitor A	0.039	1.7	2.2	5.5	2	Proteolysis	Cytoplasm
P62880;P62874; Q61011	GNB2/1/3	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2/1/3	0.022	1.5	2.2	5.7	2	Signal transduction, Calcium signaling	Cytoplasm
E9PZQ0	RYR1	Ryanodine receptor 1	0.023	0.6	149.1	7.3	34	Transport, Calcium transport	Endoplasmic reticulum
Q02789	CACNA1S	Voltage-dependent L-type calcium channel subunit alpha-1S	0.033	0.8	4.6	7.9	2	Transport, Calcium transport	Membrane
P63254	CRIP1	Cysteine-rich protein 1	0.025	1.3	4.2	16.9	2	Transport, Zinc transport	Cytoplasm

Q6PIE5	ATP1A2	Sodium/potassium-transporting ATPase subunit alpha-2	0.042	0.6	119.2	30.0	25	Transport, Nutrients transport	Membrane
# Accession: UniProt Ids; Symbol: Official Gene Symbol; Name: Musmusculus Protein name; Score: MaxQuant Score; %Coverage: Protein sequence covered by all identified peptides (%); # Peptides: Number of identified peptides									