

## Online Supplementary Table 1

### Mass spectrometry identification of adipocyte lipolytic secretome proteins

Protein name	Protein accession numbers/name	Protein molecular weight (Da)	Unique peptide counts	Unique spectra	Total spectrum counts	Percentage sequence coverage
Plectin 7	Q6S388	513,756.00	0	0	3	0.78%
T-complex protein 1 subunit alpha	TCPA	60,449.90	3	3	3	5.04%
Presequence protease	PREP	117,374.40	2	3	4	2.61%
14-3-3 protein epsilon	1433E, Q8BPH1	29,189.90	3	5	15	21.20%
Beta-enolase	ENOB, Q4FK59	46,998.80	1	1	2	6.45%
Uncharacterized protein	Q3TXS9	31,189.20	1	1	3	11.60%
26S proteasome regulatory subunit 7	PRS7, Q3UIH5, Q8BVQ9	48,679.60	2	2	2	4.62%
Fructose-bisphosphate aldolase A (Muscle-type aldolase)	P00883.2	39,343.40	0	0	17	25.30%
D-3-phosphoglycerate dehydrogenase	SERA	56,585.20	5	5	5	10.10%
Collagen alpha-2(I) chain	CO1A2, Q3TU64, Q3TUE2	129,597.30	2	2	3	2.04%
Serine/threonine-protein phosphatase 2A activator	PTPA	36,710.50	2	2	2	7.43%
Heat shock cognate 71 kDa protein	HSP7C, Q3TH56, Q3UBA6	70,873.60	12	18	34	25.70%
Enoyl-CoA delta isomerase 1	ECI1	32,251.50	1	1	6	13.80%
Aspartate aminotransferase	AATM	47,412.30	9	10	11	22.10%
Uncharacterized protein	Q3TGK7	46,141.30	1	1	2	5.67%
3-hydroxyisobutyryl-CoA hydrolase	HIBCH	43,039.40	2	2	5	11.20%
Rho GDP-dissociation inhibitor 1	GDIR1	23,408.00	2	2	2	13.70%
Chaperonin subunit 2 (Beta)	Q542X7	57,478.80	2	2	4	10.30%
L-lactate dehydrogenase B chain	LDHB	36,572.40	2	2	5	15.00%
40S ribosomal protein S30	Q3THB2, Q642K5, Q91V99, Q920W8, RS30	6,647.90	2	3	3	8.27%
Phosphoglycerate mutase	Q3U7Z6	28,832.80	6	9	23	15.40%
Annexin	Q542G9, Q9CZI7	38,610.90	5	5	5	19.20%
Cytoplasmic dynein 1 light intermediate chain 1	DC1L1	56,615.40	2	2	2	5.16%
Probable ATP-dependent RNA helicase DDX17	DDX17, Q3U741	72,586.30	1	1	2	4.00%
Aminopeptidase B	AMPB, E9PYF1, Q8BMH2	68,004.10	3	3	5	5.23%
Uncharacterized protein	Q3U6X2	51,065.80	0	0	12	9.37%
60 kDa heat shock protein	CH60	60,956.80	11	13	19	20.20%
H2-K region expressed gene 6, isoform CRA	A0A068BEQ2, DHB8	26,587.30	3	3	3	15.40%
Phosphoglycerate kinase 1	PGK1	44,551.10	9	11	51	35.30%

Ubiquitin carboxyl-terminal hydrolase	A0A2I3BQ39, Q8BWQ9, UCHL3	29,702.00	0	0	3	10.90%
EH domain-containing protein 2	EHD2	61,176.40	2	2	2	4.24%
Uncharacterized protein	Q3TCL2, Q3UDY1, Q5U415	35,052.00	3	3	6	9.03%
Peroxiredoxin-6	D3Z0Y2, PRDX6, Q6A0D0, Q6GT24	22,495.10	4	4	5	25.00%
GTP-binding nuclear protein Ran	Q14AA6, Q3ULW0, RAN	24,357.30	3	3	5	13.40%
Acetoacetyl-CoA synthetase	AACS	75,201.20	2	2	2	3.12%
Histone H4	H4	11,367.70	3	4	6	33.00%
Receptor of activated protein C kinase 1	RACK1	35,077.00	3	3	3	7.89%
Adenylate kinase 2	F7BP55	7,393.00	1	1	14	54.20%
Vinculin	VINC	116,719.40	6	7	8	5.72%
Carbonyl reductase [NADPH] 3	CBR3	30,953.50	2	2	2	9.03%
Heat shock protein 1 (Chaperonin 10)	Q4KL76	10,962.80	8	13	24	66.70%
40S ribosomal protein S8	Q5M9L9, RS8	24,264.40	2	2	4	12.00%
Heat shock 70 kDa protein 4	HSP74, Q3U2G2, Q571M2, Q99L75	94,209.50	2	2	2	2.62%
Uncharacterized protein	Q3TDE6	70,395.50	4	4	5	7.50%
Nucleoside diphosphate kinase	E9PZF0, NDKB	30,200.40	1	1	13	17.60%
Uncharacterized protein	Q3UD67	106,880.90	5	5	5	6.92%
Uncharacterized protein	Q3TMD2, Q3TWG9, Q8BV87, SERPH	46,520.90	3	3	5	7.67%
Carbonyl reductase 1, isoform CRA	B2RXY7	30,641.40	5	5	13	18.40%
RBR-type E3 ubiquitin transferase	A0A0A6YXB0	36,220.20	1	1	3	7.55%
60S ribosomal protein L6	Q3UFI4, RL6	33,529.90	4	4	5	12.20%
T-complex protein 1 subunit gamma	Q3U4U6, Q3UJP4	60,603.00	3	3	4	6.24%
Collagen, type VI, alpha 3	E9PWQ3	353,931.50	0	0	2	0.79%
Coronin-1B	COR1B	53,912.20	2	2	2	4.75%
Uncharacterized protein	Q3UAX1	53,558.60	0	0	37	30.00%
Major vault protein	MVP	95,924.10	3	3	3	3.48%
Myosin-11	A0A2R8VHF9, E9QPE7, Q69ZX3	228,274.00	1	1	2	1.44%
Prolyl endopeptidase	PPCE, Q3TCS0, Q8C6A3	82,800.30	2	2	3	3.66%
Ptms protein	Q66JR8	23,158.10	1	1	7	9.00%
14-3-3 protein zeta/delta	A0A2I3BQ03	19,064.80	5	5	6	33.70%
Phosphoserine aminotransferase	Q3ULZ3, Q543K5, Q8BTJ1	40,473.70	4	4	5	11.90%
NADH dehydrogenase [ubiquinone] flavoprotein 3	Q3U422, Q3U4K3	49,891.30	2	2	2	4.70%
Enoyl-CoA hydratase	ECHM	31,475.30	5	5	6	16.90%
Serine (or cysteine) peptidase inhibitor, clade B, member 6a	F8WIV2, Q3U3L3, Q4FJQ6	44,775.60	2	2	2	4.51%

Electron transfer flavoprotein subunit beta	ETFB	27,623.20	3	3	5	14.90%
GTP:AMP phosphotransferase AK3	KAD3	25,426.90	3	3	3	11.50%
Elongation factor 1-alpha	Q3UZQ3	50,066.00	1	1	16	13.40%
Medium-chain specific acyl-CoA dehydrogenase	ACADM, Q91WS8	46,438.30	2	2	3	6.18%
Uncharacterized protein	Q3TK73	31,391.60	0	0	2	8.15%
Glycerol-3-phosphate dehydrogenase [NAD(+)]	GPDA	37,572.70	9	10	20	24.40%
Alpha actinin 1a	A1BN54	102,723.90	0	0	4	4.28%
Proteasome subunit alpha type-5	PSA5, Q3TUI9, Q3TUX3	26,397.30	3	3	5	11.60%
Methylmalonate-semialdehyde dehydrogenase [acylating]	MMSA	57,916.30	5	5	7	11.60%
Plectin	PLEC	534,181.10	0	0	3	0.75%
Proteasome subunit beta type-6	PSB6	25,378.90	3	3	4	12.60%
Fatty acid binding protein 5	Q497I3	15,137.30	0	0	2	15.60%
Non-specific lipid-transfer protein	NLTP	59,126.30	2	2	2	3.84%
Poly(rC)-binding protein 1	PCBP1	37,498.20	1	1	6	11.80%
Splicing factor, proline- and glutamine-rich	SFPQ	75,441.90	2	2	3	4.86%
Dihydropyrimidinase-related protein 2	DPYL2	62,277.90	2	2	3	3.67%
Ribosomal protein S14	O70569, RS14	16,300.90	4	4	6	19.90%
Proteasome subunit beta type	Q6RI64	26,373.00	2	3	3	10.00%
Uncharacterized protein	Q8BRW2	26,751.30	3	3	8	8.91%
RuvB-like helicase	Q3U1C2, Q3UJN2	50,215.30	2	2	2	5.48%
Apoptosis-inducing factor 1	AIFM1	66,766.10	6	6	6	9.80%
Tubulin beta-5 chain	TBB5	49,670.60	0	0	5	10.60%
Haloacid dehalogenase-like hydrolase domain-containing protein 3	HDHD3	28,027.00	2	2	4	11.60%
Glutamate dehydrogenase 1	DHE3	61,338.40	1	1	9	12.70%
Diazepam binding inhibitor	Q548W7	10,000.80	3	7	20	34.50%
Heterogeneous nuclear ribonucleoprotein M	B8JK32, B8JK33	68,163.20	0	0	2	3.39%
Adenosylhomocysteinase	Q3TF14, Q3U4D1, Q3U5U5	47,704.00	3	3	3	8.56%
Uncharacterized protein	Q3TFD9, Q3U6S1, Q5FWJ3	53,689.80	1	2	39	32.80%
T-complex protein 1 subunit delta	Q3TII0, TCPD	58,085.80	2	3	3	4.27%
Alpha-actinin-4	A0A1L1SV25, Q3UDJ7, Q3ULT2	104,999.40	1	1	6	7.08%
Stress-70 protein	GRP75	73,462.10	7	8	9	14.10%
Ribosomal protein S23	Q497E1, Q9CWI9, RS23	15,808.60	1	1	6	23.80%
Glutamyl-prolyl-tRNA synthetase	B9EIU1	169,964.20	4	4	4	3.37%

Fructose-bisphosphate aldolase	A6ZI46, Q9CPQ9	45,344.20	0	0	11	16.90%
6-phosphogluconolactonase	6PGL	27,255.30	4	5	11	17.10%
Gamma actin-like protein	Q9QZ83	43,601.80	0	0	27	20.90%
Uncharacterized protein (Fragment)	Q3UEA1	113,050.30	3	3	5	3.87%
14-3-3 protein beta/alpha	1433B	28,087.20	4	5	14	25.60%
Ubiquitin carboxyl-terminal hydrolase	Q3U4W8, UBP5	93,356.40	2	2	3	3.47%
Spectrin beta chain, non-erythrocytic 1	SPTB2	274,227.90	2	2	2	0.93%
Uncharacterized protein	Q3UBI6, RL7	31,352.50	1	1	5	12.20%
Glutathione S-transferase Mu 1	A2AE89, GSTM1	25,971.90	1	1	3	9.43%
Protein disulfide-isomerase A6	PDIA6, Q3THH1	48,658.10	3	3	3	9.77%
Endoplasmic reticulum chaperone BiP	BIP, Q3TI47, Q3TKF8, Q3TWF2, Q3U9G2	72,464.70	8	8	10	15.70%
3-ketoacyl-CoA thiolase A	H3BKL5, Q3UPU8, THIKA	43,997.20	2	2	2	7.51%
Fatty acid synthase	FAS	272,429.30	22	28	40	10.30%
14-3-3 protein gamma subtype	A8IP69	28,303.10	2	3	10	14.20%
Sepiapterin reductase	G3UXX3, Q91XH5, SPRE	23,357.50	2	2	2	13.20%
Elongation factor 1-delta	F6ZFU0	61,392.10	0	0	2	4.53%
Uncharacterized protein	Q3TNN6, Q99LB4	38,715.70	2	2	2	7.45%
Polyadenylate-binding protein	Q8BN32	70,670.40	0	0	2	3.93%
6-phosphogluconate dehydrogenase, decarboxylating	6PGD, Q3UAG2, Q91V28	53,262.90	3	3	4	8.70%
Short/branched chain specific acyl-CoA dehydrogenase	ACDSB, E9Q5L3, Q7TMY2	51,854.80	3	3	3	9.03%
Laminin receptor (Fragment)	B2CY77, RSSA	32,838.10	3	3	5	12.90%
Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2	37,403.30	6	8	12	21.50%
Cytoplasmic aconitate hydratase	ACOC, Q8VDC3	99,104.40	4	4	5	6.52%
Ribosome-binding protein 1	RRBP1	172,876.90	0	0	4	2.93%
40S ribosomal protein S21	RS21	9,141.60	3	4	4	34.90%
Keratin, type II cytoskeletal 1	P04264.5	66,019.20	2	2	4	5.75%
Heat shock protein 90kDa beta (Grp94)	Q3UAD6, Q3UBU0, Q91V38	92,492.60	1	1	8	7.36%
Thioredoxin-dependent peroxide reductase	PRDX3	28,127.00	1	2	8	8.95%
Non-POU domain-containing octamer-binding protein	NONO, Q3TF40, Q3TFC2, Q3TMM5, Q3TTV7, Q3UM20	54,506.90	2	2	3	5.50%
Uncharacterized protein	Q9CWK0	26,317.30	1	1	4	9.69%
Glutathione S-transferase A4	GSTA4	25,565.20	2	3	5	9.46%
Tubulin beta chain	Q9CVR0	32,258.50	1	2	5	12.40%
Isovaleryl-CoA dehydrogenase	IVD	46,326.50	5	5	6	12.00%

40S ribosomal protein S5	D3YYM6, D3Z1S8, Q91V55, RS5	22,877.00	4	4	4	11.00%
Elongation factor 1-delta	A0A0R4J1E2	72,930.20	0	0	2	3.79%
Hydroxyacyl-coenzyme A dehydrogenase	HCDH	34,464.70	3	3	3	12.10%
Keratin, type I cytoskeletal 10	P13645.4	59,512.40	2	2	4	7.25%
Peroxisomal multifunctional enzyme type 2	DHB4, Q3TT11, Q3UHW2	79,424.70	2	2	2	3.81%
Heat shock protein 1-like protein	B2CSK2, HS71L	70,609.30	1	1	6	6.24%
Malate dehydrogenase	MDHM	35,611.90	9	13	36	37.90%
Uncharacterized protein	Q3U9Q3	49,882.40	0	0	12	9.56%
Branched-chain-amino-acid aminotransferase	A0A1B0GX27, Q3ULU3	43,493.90	3	3	4	7.99%
Caveolae-associated protein 1	CAVN1	43,953.70	3	4	4	8.93%
Eukaryotic translation initiation factor 3 subunit I	EIF3I	36,460.90	2	2	2	4.00%
40S ribosomal protein S11	A0A1B0GRR3, Q9DB79, RS11	19,415.20	3	3	3	16.90%
Uncharacterized protein	Q3UKH3, THIM	41,829.20	4	4	4	12.10%
Dihydrolipoyl dehydrogenase	DLDH, Q3TIE8	54,598.60	6	6	6	11.80%
Keratin, type II cytoskeletal 8	K2C8	54,567.00	2	2	3	6.94%
Acetyl-CoA acetyltransferase	THIC	41,296.80	3	3	4	9.32%
Glyceraldehyde-3-phosphate dehydrogenase	A0A0A0MQF6, G3P	38,653.70	5	6	10	16.20%
Carnitine O-acetyltransferase	CACP, H7BX88	68,646.10	4	5	8	12.30%
D-dopachrome tautomerase	Q3UNI8	13,077.60	1	1	3	23.70%
Uncharacterized protein	A0A1S6GWJ8, HNRPM, Q3THB3, Q3TW40, Q570Z0	75,183.40	0	0	2	2.84%
Proteasome subunit alpha type-2	PSA2, Q3UWT6, Q9CZ58	27,509.70	3	3	5	15.00%
S-formylglutathione hydrolase	ESTD, H3BJL6, H3BK43, H3BKH6, H3BLJ9	28,554.20	2	2	3	11.30%
Rpl23a protein	Q4V9X9, Q91YK6, RL23A	16,941.10	3	3	4	21.90%
Isocitrate dehydrogenase [NAD] subunit	A0A1L1STE6, IDH3A	41,520.50	3	4	5	7.29%
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3	84,923.70	2	2	2	3.24%
Alcohol dehydrogenase [NADP(+)]	AK1A1, Q3UJW9	36,615.20	6	6	8	20.30%
Elongation factor 1-gamma	EF1G	50,061.30	4	5	8	8.47%
Prelamin-A/C	LMNA	74,238.90	9	10	11	16.10%
Uncharacterized protein	Q3TLH6	14,415.30	0	0	2	16.20%
Pyruvate carboxylase	E9QPD7, G5E8R3, PYC	129,701.90	22	27	43	19.60%
Cysteine sulfinic acid decarboxylase	CSAD	55,145.40	2	2	3	4.46%
Cytosolic non-specific dipeptidase	CNDP2	52,768.20	4	5	5	6.95%

Bifunctional epoxide hydrolase 2	HYES, Q3UQ71	62,544.90	2	2	2	3.79%
Glycine--tRNA ligase	GARS	81,879.10	2	2	3	3.98%
L-xylulose reductase	DCXR	25,745.40	2	2	2	11.10%
Alpha-1,4 glucan phosphorylase	Q3TFQ8	96,704.40	2	2	2	1.54%
Aldehyde dehydrogenase	A0A0G2JEU1, Q3TVM2, Q3U6I3, Q3U9J7, Q3UJW1, Q544B1	56,595.60	2	2	2	4.88%
60S ribosomal protein L4	RL4	47,155.30	4	8	11	10.70%
Protein disulfide-isomerase A3	PDIA3	56,680.40	7	9	13	14.10%
MCG126220	A3KML3	27,779.40	2	2	3	12.70%
Aconitate hydratase	ACON	85,465.90	10	11	18	14.50%
Heat shock protein HSP 90- alpha	HS90A, Q3UIF3	84,819.20	1	1	7	7.09%
Transketolase	TKT	67,631.90	15	17	27	27.30%
Nicotinamide phosphoribosyltransferase	NAMPT	55,447.60	2	2	3	4.68%
Fatty acid-binding protein, adipocyte	FABP4	14,649.90	6	8	64	71.20%
Fibulin-2	FBLN2, Q3TGL4, Q99K58	126,457.20	2	2	2	1.88%
Uncharacterized protein	Q3TMC5	57,181.70	3	3	3	6.99%
40S ribosomal protein S20	RS20	13,373.00	2	2	2	19.30%
Triosephosphate isomerase	TPIS	32,191.30	10	14	44	39.80%
Collagen alpha-1(I) chain	CO1A1	138,032.70	2	2	2	2.34%
Proteasome subunit alpha type-3	PSA3, Q9DCD8	28,490.80	2	3	4	8.63%
Myosin-9	MYH9	226,378.00	0	0	3	1.84%
Proteasome subunit alpha type	Q3TS44	29,547.00	0	0	5	11.40%
Proteasome subunit beta type-4	PSB4	29,116.60	3	3	3	11.40%
Trypsin precursor	P00761.1	24,409.30	3	4	38	17.30%
Uncharacterized protein	Q3UHS6, Q80TM2, TLN1	272,130.80	0	0	2	0.91%
Heat shock 70 kDa protein 1B	HS71B, Q3TU85	70,177.80	1	1	6	6.23%
Type VI collagen alpha 3 subunit	O88493	286,885.10	0	0	2	0.98%
Perilipin-4	PLIN4	139,411.70	2	2	2	1.43%
Rpl12 protein	Q6DI58	22,987.40	0	0	4	11.00%
Glutamine amidotransferase-like class 1 domain-containing protein 3A	GAL3A	28,089.80	2	2	2	4.89%
Proteasome subunit alpha type-6	PSA6	27,372.50	4	4	4	16.70%
AHNAK nucleoprotein (desmoyokin)	E9Q616	604,257.10	4	4	9	1.93%
Hexokinase-2	E9Q5B5, HXK2	99,215.80	1	1	2	2.14%
Ribosomal protein S3	Q5YLW3, Q9CZP6	26,602.50	3	3	3	15.60%
Peroxisredoxin-5	PRDX5	21,897.60	3	3	7	17.10%

Keratin, type II cytoskeletal 2 epidermal	P35908.1	65,866.40	3	3	6	7.75%
3-hydroxyisobutyrate dehydrogenase	3HIDH, A0ZNJ2	35,523.90	2	3	3	9.25%
High mobility group protein HMGI-C	HMG2, Q6NSP9	11,818.90	2	2	2	33.30%
Ubiquitin-40S ribosomal protein S27a	RS27A	17,951.60	3	3	4	17.30%
Malate dehydrogenase	MDHC	36,512.10	7	7	14	21.90%
40S ribosomal protein S28	RS28	7,840.90	2	2	3	46.40%
Ahnak protein	A0PJF4	164,567.80	0	0	2	1.79%
Protein disulfide-isomerase A4	A0A0R4J0Z1, PDIA4	72,371.70	8	8	9	12.50%
MCG11348	Q58ET1, Q5EBG5, Q6P1A9, Q80UT7	30,474.80	1	1	7	19.20%
Aflatoxin B1 aldehyde reductase member 2	ARK72	40,612.50	2	2	2	7.36%
60S ribosomal protein L27a	RL27A	16,605.40	2	2	3	8.78%
T-complex protein 1 subunit theta	H3BL49, Q3UKQ2, Q6A0F1, Q8BVY8, Q9WVS5, TCPQ	59,557.10	6	6	7	16.00%
Sorbin and SH3 domain-containing protein 1	SRBS1	143,073.90	0	0	2	2.17%
Transaldolase	A0A1B0GR11, TALDO	42,152.70	6	6	7	18.10%
Uncharacterized protein	Q3UJS0, RL8	28,066.90	4	5	6	14.00%
Acyl-coenzyme A thioesterase 2	ACOT2	49,658.00	1	1	3	4.64%
Twinfilin-1	TWF1	40,080.60	2	2	2	6.00%
Serine hydroxymethyltransferase	GLYM	55,760.20	2	2	3	4.17%
Bifunctional purine biosynthesis protein PURH	PUR9	64,217.60	4	4	4	8.95%
Peroxiredoxin-1	PRDX1	22,177.50	4	4	9	24.60%
Cytochrome c oxidase subunit 5A	COX5A	16,101.90	2	4	5	6.85%
Clathrin heavy chain 1	CLH1, Q5SXR6, Q80U89	191,990.50	3	3	3	2.27%
Proteasome subunit beta type-5	PSB5	28,533.00	2	2	2	10.20%
Fumarylacetoacetase	FAAA	46,176.60	3	3	5	7.40%
Succinate--CoA ligase [ADP/GDP-forming] subunit alpha	SUCA	36,155.20	2	2	3	6.94%
Histidine triad nucleotide-binding protein 1	HINT1	13,777.20	2	2	2	18.30%
Cytosol aminopeptidase	AMPL	56,142.70	2	3	3	5.01%
RAS oncogene family protein	A0A068BFR3, Q78ZJ8	24,489.00	2	2	2	10.10%
ATP synthase subunit alpha	ATPA	59,754.10	5	5	7	12.80%
60S ribosomal protein L26	B1ARA3, Q4FZH2	12,217.10	2	2	2	22.30%
40S ribosomal protein S3a	Q3U5P8, Q3UAC2, Q3UJU5, RS3A	29,943.30	2	2	2	7.95%
Histone H2B type 3-A	H2B3A, H2B3B	13,994.70	0	0	20	17.50%

Plasminogen activator inhibitor 1 RNA-binding protein	A0A0N4SV32, PAIRB, Q3UEI6, Q3UJK2, Q3UMP4, Q3V274	42,914.50	2	2	2	8.56%
40S ribosomal protein S16	RS16	16,445.90	3	3	3	21.90%
Peptidyl-prolyl cis-trans isomerase	Q3TE63, Q3UAJ1, Q5SVY2	17,943.80	8	13	39	46.30%
Myosin light polypeptide 6	A0A1W2P6F6, A0A1W2P6G5, A0A1W2P7Q9, MYL6, Q642K0	15,448.00	2	2	2	17.10%
Citrate synthase	CISY	51,738.10	1	2	12	9.70%
Heterogeneous nuclear ribonucleoprotein H2	HNRH2	49,280.00	0	0	3	7.35%
Succinyl-CoA:3-ketoacid-coenzyme A transferase	Q3UK61, SCOT1	56,018.20	0	0	8	6.35%
Far upstream element-binding protein 1	A0A0G2JFY5, A0A0G2JG00, A0A0G2JGW9, FUBP1, Q0P6B2, Q3TIS5, Q3TUE1, Q3UUU2	54,845.40	2	2	2	4.74%
Enolase 1, alpha non-neuron	Q5FW97	47,141.70	2	2	15	21.40%
Glutathione S-transferase omega-1	GSTO1	27,498.60	3	3	6	15.40%
Moesin	MOES	67,768.80	3	3	5	10.20%
Uncharacterized protein	Q3TH46, Q3U111	77,465.30	0	0	2	3.35%
Superoxide dismutase [Cu-Zn]	SODC	15,941.90	1	1	5	17.50%
Aldose reductase-related protein 2	ALD2	36,121.30	2	2	2	6.01%
Heterogeneous nuclear ribonucleoprotein L	G5E924	66,932.80	2	2	2	4.39%
Alanine aminotransferase 1	ALAT1	55,142.70	2	2	2	3.23%
Glucose-6-phosphate 1-dehydrogenase	Q3TNL1, Q790Y8	59,264.60	3	3	3	5.83%
Succinate dehydrogenase [ubiquinone] flavoprotein subunit	SDHA	72,585.60	5	6	6	8.43%
Elongation factor 2	EF2, Q3TW58, Q3UBL9, Q3UDC8, Q3UMI7, Q6P9L9, Q8BMA8, Q8C153	95,260.00	5	6	15	10.70%
Histone H2B type 1-C/E/G	H2B1C, H2B1F, H2B1H	13,920.70	0	0	20	17.50%
Uncharacterized protein	Q3TK29, Q3TSG8, Q3UPJ8, Q922R9, Q922Z3, TRAP1	80,197.40	1	1	4	3.54%
Cofilin-1	F8WGL3, Q544Y7, Q9CX22	24,577.10	1	1	8	14.50%
Filamin, alpha	B7FAU9, B7FAV1, B9EKP5, FLNA	280,491.70	5	5	6	2.84%
Peroxiredoxin-2	PRDX2	21,779.10	1	3	8	14.60%
60S ribosomal protein L13	RL13	24,306.40	2	2	4	10.90%
Methylcrotonoyl-CoA carboxylase beta chain	MCCB	61,380.00	2	2	3	3.91%
L-lactate dehydrogenase	A0A1B0GSR9, A0A1B0GSX0, LDHA,	34,599.60	4	4	12	21.30%



	Q3TCI7, Q3THB4, Q3TI99, Q3UDU4, Q99K20					
Tubulin alpha chain	Q3TIZ0, Q52L87, TBA1A, TBA1B	50,135.70	2	2	13	16.70%
Beta-actin-like protein 2	ACTBL	42,005.10	1	1	8	14.40%
Ran-specific GTPase-activating protein	H7BX22, RANG	17,888.10	3	3	3	21.60%
Uncharacterized protein	Q3TGJ9, Q6PAC1	80,848.80	5	6	11	8.62%
Galectin-1	LEG1	14,866.10	2	2	5	20.00%
UPF0160 protein MYG1	MYG1	42,722.50	1	1	3	8.95%
Citramalyl-CoA lyase	CLYBL	37,549.10	2	2	2	6.51%
Pyruvate kinase PKM	KPYM	57,845.60	2	2	17	15.60%
Transitional endoplasmic reticulum ATPase	TERA	89,324.80	4	5	8	7.20%
40S ribosomal protein S25	A0A1L1SQA8, RS25	10,309.70	2	2	5	20.40%
V-type proton ATPase catalytic subunit A	VATA	68,327.40	2	2	2	3.89%
Heat shock protein 84b	Q71LX8	83,284.30	5	5	18	17.70%
Protein disulfide-isomerase	PDIA1, Q3TF72, Q3THC3, Q3TIM0, Q3TWE3, Q3U738, Q3UBY9, Q3UDR2	57,090.60	3	3	3	5.70%
Uncharacterized protein	Q3U292	22,083.10	1	1	6	16.70%
Poly(rC)-binding protein 2	A0A2R8VHP9, A0A2R8VI25, B2M1R7, PCBP2, Q3TT81	33,300.00	1	1	5	12.50%
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	54,209.30	1	1	2	4.49%
N-acetylglucosamine kinase	Q3U2G9, Q9D997	39,347.60	2	2	2	3.50%
ATP synthase subunit beta	ATPB	56,301.20	5	5	5	12.90%
MCG132477	Q58EW0, Q642K1	21,644.50	2	2	5	13.80%
Mammalian ependymin-related protein 1	EPDR1	25,485.00	2	2	2	10.30%
Uncharacterized protein	Q3UA53	32,666.60	2	2	6	6.57%
Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex	Q7TND9	53,262.00	2	2	3	4.15%
Eukaryotic translation initiation factor 2 subunit 1	IF2A, Q9CV24	17,139.40	2	2	2	6.98%
Uncharacterized protein	Q3TQP7, THIL	44,802.30	3	3	6	9.91%
Isocitrate dehydrogenase [NADP]	IDHC, Q5HZJ8, Q8C338	46,675.80	1	3	8	9.90%
Actin	ACTG, B2RRX1, Q3UAF6, Q3UAF7	41,811.90	1	2	47	33.90%
Uncharacterized protein	Q8C5C0	64,005.50	2	2	2	4.17%
Uncharacterized protein	Q3TK12, Q8BT90, RS17	16,141.10	2	2	2	14.10%
Uncharacterized protein	A0A1S6GWH5	124,238.30	8	11	13	8.77%

Far upstream element-binding protein 2	FUBP2	76,775.20	5	5	5	8.02%
Pgm2 protein	Q66JR7, Q7TNU0	63,456.40	1	1	3	6.27%
2-iminobutanoate/2-iminopropanoate deaminase	RIDA	14,255.50	2	2	2	15.60%
Talin-2	A0A1L1SQ51, B2RY15, E9PUM4	271,925.00	0	0	2	0.90%
Methanethiol oxidase	SBP1	52,515.00	3	3	5	6.57%
Adenylate kinase 2	KAD2	26,469.90	6	7	20	36.80%

## Mass spectrometry methods

3T3-L1 adipocytes were incubated in KRH buffer (116 mM NaCl, 4 mM KCl, 1mM MgCl<sub>2</sub>, 1.8 mM CaCl<sub>2</sub>, 25 mM Glucose, 10 mM HEPES, pH to 7.4) with bead conjugated BSA. For this, fatty acid free BSA (Sigma) was coupled to NHS-activated Sepharose 4 fast flow (GE Healthcare) by dissolving 250 mg BSA into 5 ml coupling buffer (0.2M NaHCO<sub>3</sub>, 0.5M NaCl pH 8.3), acidifying the resin with 1 mM HCl and incubated 16 hours at 4°C to allow coupling. The BSA-resin was blocked in 0.5M ethanolamine, 0.5M NaCl (pH 8.3) for 4 hours at 4°C. The BSA-resin was then washed 4 times with alternating high pH buffer (0.1M Tris; pH 8.5) and low pH buffer (0.1M sodium acetate, 0.5M NaCl; pH 4.5). The BSA beads were put into 5 ml KRH buffer and protein content determined by BCA protein assay. The adipocytes were incubated in KRH with 70 µM bead conjugated BSA and the cells were treated with forskolin, the media recovered, and the beads removed via microcentrifugation.

A 100 ug aliquot of secreted material was proteolytically digested in-solution with trypsin, cleaned on an Oasis C18 SPE cartridge (Waters, Corporation, Milford, MA), and fractionated offline by high pH C18 reversed-phase (RP) chromatography (33). The samples were concatenated and run on a Thermo Fisher Orbitrap Fusion instrument (Thermo Scientific Inc., Waltham, MA). The data was analyzed using the Sequest algorithm (34) in Proteome Discoverer 2.2.0.388 (Thermo Fisher Scientific, San Jose, CA). Scaffold (version 4.8.4, Proteome Software Inc., Portland, OR) was used to validate MS/MS with the FDR set less than 1.0%