

Supplementary information

Table 1. Proteins identified in this work using snapshot imprinting

| Accession | Description | Senescent cells, fmol | Control cells, fmol |
|--|--|--------------------------|------------------------|
| A0A173GMX0;A4UCT3 | Actin alpha cardiac muscle 1 | 206±89 | 485±98 |
| P62736 | Actin aortic smooth muscle | 2104±297 | 4019±169 |
| P60709;P63261;Q1KLZ0;Q53G76;Q53GK6;B4D VQ0;B4E335;B4E3A4; Q53G99 | Actin cytoplasmic | 1661±291 | 10618±499 |
| P53999;Q59G24;Q6IBA2;B7Z1Z0;Q6E433 | Activated RNA polymerase II transcriptional coactivator p15 | 735±56 | 6912±486 |
| P13798;A0A024R2U9;C9JIF9;H7C393;C9JLK2;F 8WEH5;H7C1U0 | Acylamino-acid-releasing enzyme | 44.4±30.6 | 2198±264 |
| P05141;P12236;Q59EI9; A0A0S2Z3H3 | ADP/ATP translocase 2 | 2070±681 | 3553±136 |
| Q9Y2Y0 | ADP-ribosylation factor-like protein 2-binding protein | 87±1.6 | 80±21 |
| A0A1P7ZIN0;A8MQ02;E9PFY5;F8W9I4;G1UI2 2;J3KN01;P55196;Q5TIG5 | L-afadin | 168.2±53 | 959±75 |
| P00330 | Alcohol dehydrogenase 1 | 133±2.6 | 67.3±32.3 |
| A0A024R4F1;A4UCS8;E2DRY6; K7EM90;P06733 | Alpha-enolase | 654±486 | 2046±199 |
| L8EAQ2 | Alternative protein RIMS3 | 91±108 | 1323±175 |
| A0A024R5Z7;B4DNH8;H0YKL9;H0YKS4;H0Y | Annexin | 57±16.7 | 909±44 |

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| KV8;H0YKX9;H0YKZ7 | | | |
| P25705;V9HW26;B4DGW3;K7EK77;K7ERX7;K7EJP1;K7EQH4;K7ENJ4 | ATP synthase subunit alpha mitochondrial | 203±248 | 1979±111 |
| P06576;Q0QEN7;V9HW31;H0YH81;F8W0P7 | ATP synthase subunit beta mitochondrial | 170±20 | 5867±448 |
| P56385 | ATP synthase subunit e mitochondrial | 1057±94 | 7302±785 |
| P48047 | ATP synthase subunit O mitochondrial | 23±32 | 806±179 |
| A0A024R5H0;O75531 | Barrier to autointegration factor 1 isoform CRA a | 219±170 | 5600±862 |
| P38398;A0A024R1V8;A0A024R1W0;A0A024R1Y0;A0A024R1Y1;G8I0D8... | Breast cancer type 1 susceptibility protein | 747±35 | 994±137 |
| A8MX76;B7Z467;D6W573 | Calpain-14 | 364±7.1 | 410±7 |
| B4DHR1;B4E2Y9;K7EJB9;P27797;Q53G71;V9HW88 | Calreticulin | 0.0 | 728±101 |
| P0DMU7;P0DMU8;P0DMU9;P0DMV0;P0DMV1;P0DMV2 | Cancer/testis antigen family 45-member A6 | 290±81 | 840±23 |
| Q8N299;Q96Q07 | cDNA FLJ33611 fis clone BRAMY2016002 | 129±12 | 128±91 |
| B4DMC6;B4DPU3;B4DRE8;P13639 | cDNA FLJ60696_ highly similar to Elongation factor 2 | 2688±285 | 2814±133 |
| Q9NX34 | cDNA FLJ20465 fis clone KAT06236 | 173±60 | 3211±562 |
| B2R6V2;B7Z5H7;O00311;Q6JSD6 | Cell division cycle 7-related protein kinase | 5721±234 | 0.00 |
| P49454 | Centromere protein F | 225±11 | 177±18 |
| A8K4M4;H0YKH6;Q5SZE1;Q5SZE2;Q5SZE3;Q5SZE4;Q96G23 | Ceramide synthase | 1273±95 | 2813±131 |
| A0A140T8X2;A0A182DWE8;Q6ZTR5 | Cilia- and flagella-associated protein 47 | 20.5±2.3 | 59±1.8 |
| A8TX70;E9PAL5 | Collagen alpha-5(VI) chain | 47±1.6 | 35±1 |

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| P19876 | C-X-C motif chemokine 3 | 33±2 | 35±2 |
| Q9NZV1 | Cysteine-rich motor neuron 1 protein | 25±0.7 | 5.6±3.2 |
| F8VUJ9 | Dynamin-1-like protein | 177±169 | 930±166 |
| Q15075 | Early endosome antigen 1 | 88.5±3.9 | 106±26 |
| A0A087WVQ9;A8K9C4;B4DNE0;P68104;Q53G85;Q53G89;Q53GE9;Q53HM9 | Elongation factor 1-alpha | 1870±549 | 12420±686 |
| P57679 | Ellis-van Creveld syndrome protein | 321±42 | 685±17 |
| P14625;Q5CAQ5;V9HWP2;B4DHT9;B4DU71;Q59FC6 | Endoplasmic reticulum resident protein 29 | 81±31 | 1008±51.5 |
| F8VY02;P30040;V9HW71 | Endoplasmic reticulum resident protein 29 | 2.4±3.4 | 882±86 |
| B2R6J2;B7Z437;B7Z5V2;E7EQR4;J7M2B1;P15311;Q6NUR7 | Ezrin | 81±115 | 1059±139 |
| Q92915 | Fibroblast growth factor 14 | 40±0.6 | 23±16 |
| H3BMQ8;H3BPS8;H3BQN4;H3BR04;H3BUH7;J3KPS3;P04075;V9HWN7 | Fructose-bisphosphate aldolase A | 231±29 | 1257±103 |
| P11021;V9HWP4;B4DEF7 | 78 kDa glucose-regulated protein | 320±246 | 8973±1091 |
| P04406;V9HVZ4;E7EUT5;Q2TSD0;Q0QET;A4UCT1;B4DRV9;Q5ZEY3 | Glyceraldehyde-3-phosphate dehydrogenase | 144±193 | 13580±1359 |
| Q14789;E7EU81 | Golgin subfamily B member 1 | 73±2 | 56±25 |
| Q9UBI6 | Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 | 382±279 | 1364±66 |
| P61604;B8ZZL8;Q9UNM1;S4R3N1;A0A024R3X7;B8ZZ54 | 10 kDa heat shock protein_mitochondrial | 810.4±182.5 | 24979±608 |
| P10809;A0A024R3X4;B3GQS7;B7Z597;B7Z5E7; | 60 kDa heat shock protein_mitochondrial | 845±1106 | 21306±1747 |

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| E7ESH4 | | | |
| A0A024RD80;B4DGL0;B4DMA2;P08238; A0A140VJY2 | Heat shock protein 90kDa alpha (Cytosolic)_ class B member 1 isoform CRA_a | 62±14 | 644±39 |
| A0A024R228;B3KU16;B4DFF1;B4DUQ1;P6197 8 | Heterogeneous nuclear ribonucleoprotein K_ isoform CRA_d | 48±3 | 767±99 |
| A0A087X0X3;M0R2I7;P52272;Q59ES8 | Heterogeneous nuclear ribonucleoprotein M | 7990±1630 | 9485±327 |
| A0A024R017;P04908;Q08AJ9;Q7L7L0;Q93077; A0A024RAS2;A0A0U1RR32 | Histone H2A | 235.5±23.8 | 7038±854 |
| A0A024QZZ7;A0A024RCJ9;A0A024RCL8;A8K 9J7;B2R4S9 | Histone H2B | 694±145 | 4949±401 |
| P33778;A0A024RCJ2;P06899;P23527;Q16778;Q 8N257;Q96A08;L0R4T3 | Histone H2B type 1-B | 1855±389 | 13236±1072 |
| Q16695;B2R4P9;B4E380;K7EK07;P68431;P8424 3;Q71DI3 | Histone H3.1t | 10222±30 | 27054±2103 |
| P62805;B2R4R0;Q0VAS5;Q6B823 | Histone H4 | 4911±428 | 18839±1452 |
| C9JPEAK5;E7EQW5;E7ERX5;E7EUI6; E9PLR6;P05556;Q5T3E6 | Integrin beta-1 | 562±4 | 5751±1057 |
| P33176;A8K048;C1PHA2; M1VE89 | Kinesin-1 heavy chain | 119±10 | 70.5±49 |
| P00338;V9HWP9;B4DJI1;F5GXH2;F5GXY2;F5 GYU2;F5H5J4;F5H6W8 | L-lactate dehydrogenase A chain | 913±585 | 6347±553 |
| Q13751;A0A0S2Z3R6 | Laminin subunit beta-3 | 101±0.5 | 95±4 |
| P48449;B2R694;C9J315 | Lanosterol synthase | 336±40.5 | 1177±124 |
| E9PIC3 | Large neutral amino acids transporter small subunit 2 | 94.9±3.3 | 53.6±4.1 |
| I3VM53;I3VM54;Q9Y2K7 | Lysine-specific demethylase 2A | 77±12 | 57±21 |

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| A0A024R4K3;P40926;Q0QF37;Q6FHZ0;Q75MT9;B3KTM1;G3XAL0 | Malate dehydrogenase | 298±88 | 3926±613 |
| A0A023VT86;A0A061CLB2;A0A075M4J2;A0A090KNI9;A0A090KQC9 | MHC class II antigen | 240±21 | 234±12 |
| P35749;A0A024QZJ4;A0A024QZJ6;A0A024R1N1;A0A0U4BW16 | Myosin-11 | 862±509 | 3710±330 |
| A0A024R592;B4DJ30;B4DSM6;F5H6X6;Q14697 | Neutral alpha-glucosidase AB | 66.7±35.8 | 2035±261 |
| A0A0A0MTJ9;A0A0R4J2G3;Q6PIU2 | Neutral cholesterol ester hydrolase 1 | 486±616 | 6692±1521 |
| Q96J73 | NNP3 | 265±1.3 | 255±22.7 |
| P06748;A0A0S2Z491;A0A0S2Z4G7;Q9BTI9 | Nucleophosmin | 9.9±2.7 | 2669±460 |
| A0A087WYL6; A0A087WZG6;A0A087X1S9; Q587I4; Q8TEW8 | Partitioning defective 3 homolog B | 6748±735 | 27±16 |
| A8K486;B2RE56;B4DM82;P62937;Q71V99;V9HWF5 | Peptidyl-prolyl cis-trans isomerase | 250±46 | 2526±282 |
| P23284;V9HWC6 | Peptidyl-prolyl cis-trans isomerase B | 483±20 | 3179±277 |
| A0A075B759;A0A075B767;A0A0B4J2A2;P0DN26;P0DN37;Q9Y536 | Peptidyl-prolyl cis-trans isomerase A-like 4E | 53.5±3 | 43.4±1.5 |
| A0A024RDS2;A0A024RDT5;B1ALD9;C0IMJ3;Q15063;B7Z6G1 | Periostin_ osteoblast specific factor_ isoform CRA_c | 483±54.5 | 2301±86.6 |
| A0A0A0MSI0;B2R4P2;Q06830;A0A0A0MRQ5;B4DF70;P32119;V9HW12 | Peroxiredoxin-1 | 293±33 | 1185±116 |
| Q86YQ7 | Phospholipase D2 | 164±85 | 1396±124 |
| A8K964;B4DTD4;B4E392;Q9H307 | Pinin | 3.8±5.3 | 6634±996 |
| P07737;I3L3D5;K7EJ44 | Profilin-1 | 72±39 | 2504±80 |

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| B2RDG0;H0YL69;H0YLC2;H0YLS6; H0YMA1 | Proteasome subunit alpha type | 3802±492 | 2315±82 |
| P49721;A0A140VJS6;B7Z478;Q59FJ0 | Proteasome subunit beta type-2 | 2176±235 | 12851±1254 |
| H0YJM8;P28074 | Proteasome subunit beta type-5 | 853±542 | 996±79 |
| Q9P219;G3V3S0 | Protein Daple | 2186±149 | 15027±1381 |
| B3KQT9;P30101;V9HVV3;B3KQT2;B4DDM1;B 4DJ98;H7BZJ3 | Protein disulfide-isomerase | 130±7.5 | 3369±333 |
| A0A024R7F1;A0A0S2Z4A0;A0A0S2Z4D8;A0A0 S2Z4W7 | Protein kinase C substrate 80K-H_ isoform CRA_a | 158±21 | 1026±160 |
| Q9H397 | PRO2852 | 23±5.6 | 854±85 |
| Q6P158;A0A087WZ11;B4DKW2 | Putative ATP-dependent RNA helicase DHX57 | 11675±660 | 2150±238 |
| P0C7P4;P47985 | Putative cytochrome b-c1 complex subunit Rieske-like protein 1 | 1655±1229 | 1681±174 |
| A8K6R4;C9JNL8;Q3MIT2 | Putative tRNA pseudouridine synthase Pus10 | 1.6±2.3 | 1089±118 |
| Q2TAK8;A0A0D9SGJ8;D6W5Y8;J3KNX4;K7EP 97;K7ES53 | PWWP domain-containing protein MUM1 | 1020±167 | 2139±129 |
| Q9UL26 | Ras-related protein Rab-22A | 80±5.9 | 69±9.4 |
| D3DS95;P30050;Q59FI9 | 60S ribosomal protein L12 | 12.1±17.1 | 1144±233 |
| A0A024RAE1;Q9UKD2 | Ribosome assembly factor mrt4 | 397±52 | 2070±125 |
| H7C2F9;Q15032;Q53SQ1;B4DLH6;C9JIX1;Q9B VG5 | R3H domain-containing protein 1 | 170±23 | 110±8.5 |
| H7BZW9;H7C3M8;H7C5G9; Q14BN4 | Sarcolemmal membrane-associated protein | 195±20 | 171±7.3 |
| D6RDG7;D6RFI0;Q9H9B4;S4R2X2;D6RAE9;H0 Y9J5 | Sideroflexin-1 | 76.2±51 | 1112±44 |

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| A0A0G2JLD8;A4D1U3;B7Z268;C9K0U8;E7EUY5;Q04837;Q567R6 | Single-stranded DNA-binding protein mitochondrial | 96±73 | 1242±238 |
| A4D1U3;Q04837;Q567R6;A0A0G2JLD8;B7Z268;C9K0U8;E7EUY5 | Single-stranded DNA binding protein 1 | 2854±747 | 5942±289 |
| Q9UKG4;V9GYC7; V9GZ66 | Solute carrier family 13 member 4 | 148±24 | 115±5.6 |
| Q59G27 | Stathmin | 132±132 | 2456±114 |
| B7Z1V7;B7Z4V2;P38646;Q8N1C8;V9HW84;D6RJI2;B7Z4T3;D6RA73;Q2F839 | Stress-70 protein_ mitochondrial | 1821±269 | 3604±145 |
| H3BR38;I3L2E7 | Target of rapamycin complex subunit LST8 | 2128±896 | 1176±118 |
| H3BR71;Q15572 | TATA box-binding protein-associated factor RNA polymerase I subunit C | 79±12 | 52±7.4 |
| A0A075B702 | T-cell receptor alpha joining 41 | 360±32 | 1623±184 |
| A0A140VJI4;B4DEH1;Q3SX58;Q6P184;Q86TM7;Q9P2X0 | Testicular tissue protein Li 58 | 446±114 | 1069±116 |
| A0A140VJP9;E9PSB6;Q8N9H8 | Testicular tissue protein Li 125 | 205±160 | 1.6±2.2 |
| A0A024RDC1;Q96KC9 | Testis development protein NYD-SP26 isoform CRA_a | 44.8±13.8 | 41.3±3.6 |
| A0A1W2PS94;B2RU27;D3DSV6;Q9BXT5 | Testis-expressed protein 15 | 186±29 | 181±22 |
| Q96AN5 | Transmembrane protein 143 | 13.7±1 | 51±2 |
| P68363;A0A1W2PQM2;B3KPS3;F5H5D3;Q53GA7 | Tubulin alpha-1B chain | 2764±190 | 5961±451 |
| B7ZAF0;P07437;Q5JP53;Q5SU16;B2R6L0;B7ZAK1;Q13885;Q5ST81 | Tubulin beta chain | 108±118 | 2514±353 |
| A0A024R991;Q8N8Y2 | V-type proton ATPase subunit | 694±710 | 2545±41 |
| B2RB72;B3KMC8;O75554 | WW domain binding protein | 1365±541 | 4185±445 |

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| O60765 | Zinc finger protein 354A | 204±28 | 210±17 |
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Table 2. Proteins identified in this work using the shaving approach

| Accession | Description | Senescent cells, fmol | Control cells, fmol |
|---|---|-----------------------|---------------------|
| P62736 | Actin aortic smooth muscle | 12.2 ± 6.7 | 31.4 ± 17 |
| P60709;P60712;P63258;P63261;P62739;P63267;P68032;P68133;P68138;Q3ZC07;Q5E9B5;A5A3E0;Q6S8J3;P0CG38;P0CG39;Q9BYX7 | Actin cytoplasmic | 32.5 ± 20.1 | 92.5 ± 52.9 |
| P53999 | Activated RNA polymerase II transcriptional coactivator | 3.5 ± 2.8 | 6.5 ± 1.3 |
| P05141;P32007;Q8SQH5 | ADP/ATP translocase | 2.4 ± 1.8 | 4.9 ± 1.2 |
| P18085;P61204;P84077;P84080;P84081;P84085;Q3SZF2;Q5E9I6 | ADP-ribosylation factor | 4.7 ± 3.8 | 8.4 ± 0.5 |
| P00330 | Alcohol dehydrogenase | 101 ± 26.1 | 392.6 ± 121.1 |
| P01009 | Alpha-1-antitrypsin | 8.2 ± 6.9 | 20.6 ± 4.2 |
| P06733;Q9XSJ4;P09104;P13929;Q3ZC09 | Alpha-enolase | 9.3 ± 7.1 | 12.6 ± 1.5 |
| P04083 | Annexin A1 | 4.7 ± 3.8 | 6.7 ± 1.3 |

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| P07355;P04272;A6NMY6 | Annexin A2 | 50.3 ± 15 | 145.9 ± 37.1 |
| P08758;P81287 | Annexin A5 | 6.9 ± 3.8 | 3 ± 1.4 |
| P25705;P19483 | ATP synthase subunit alpha_mitochondrial | 7.1 ± 5.6 | 1.1 ± 0.6 |
| P06576;P00829 | ATP synthase subunit beta_mitochondrial | 7.1 ± 5.8 | 0 ± 0 |
| P48047 | ATP synthase subunit O_mitochondrial | 2 ± 1.6 | 0 ± 0 |
| P35613;Q865R3 | Basigin | 6.1 ± 1.7 | 7 ± 3.2 |
| P80723;P80724 | Brain acid soluble protein 1 | 3.6 ± 0.5 | 5.1 ± 1.8 |
| Q6IMN6 | Caprin-2 | 5.4 ± 3.9 | 6.2 ± 1.6 |
| P16070 | CD44 antigen | 5.5 ± 2.9 | 10.8 ± 5.9 |
| O76074;Q28156 | cGMP-specific 3'_5'-cyclic phosphodiesterase | 3.3 ± 2.7 | 5.1 ± 1.1 |
| P23528;Q5E9F7;Q148F1;Q9Y281 | Cofilin-1 | 7 ± 5.5 | 28.3 ± 5.8 |
| Q3SZX9;Q9H0I3 | Coiled-coil domain-containing protein 113 | 8.2 ± 4.7 | 4.4 ± 0.9 |
| P00403 | Cytochrome c oxidase subunit 2 | 2.6 ± 2.2 | 3.9 ± 0.6 |

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| P68104;Q5VTE0;Q05639;Q32PH8 | Elongation factor 1-alpha | 21.7 ± 16 | 30.2 ± 9.9 |
| P60842;Q14240;Q3SZ54;Q3SZ65 | Eukaryotic initiation factor 4A-I | 2.7 ± 1.9 | 1 ± 0.8 |
| P21333;O75369;Q14315 | Filamin-A | 4.2 ± 0.7 | 6.7 ± 2 |
| P04406;P10096 | Glyceraldehyde-3-phosphate dehydrogenase | 20.7 ± 11.3 | 30.9 ± 5.9 |
| P04899;A8MTJ3;P04695;P04696;P04896;P08239; P08754;P09471;P0C7Q4;P11488;P19087;P38405; P63092;P63096;P63097;Q03113;Q14344;Q5JWF2 | Guanine nucleotide-binding protein G(i) subunit alpha-2 | 5.2 ± 1.1 | 5.7 ± 3.5 |
| Q9UBI6;Q28024 | Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 | 3.3 ± 1.2 | 6 ± 2.8 |
| P11142;P19120;P34933;P0CB32;P0DMV8;P0DM V9;P17066;P34931;P48741;Q27965;Q27975 | Heat shock cognate 71 kDa protein | 3.7 ± 2.5 | 4.3 ± 1.4 |
| P07900;Q76LV2 | Heat shock protein HSP 90-alpha | 2.1 ± 1.5 | 3.6 ± 0.4 |
| P08238;Q76LV1;Q58FF7;Q14568;Q58FF6;Q58F F8;Q12931;Q2TBI4;Q58FG0 | Heat shock protein HSP 90-beta | 7.8 ± 4.6 | 12.8 ± 0.6 |
| P61603;P61604 | 10 kDa heat shock protein_ mitochondrial | 6.8 ± 5.5 | 7.1 ± 2.8 |
| P10809;P31081 | 60 kDa heat shock protein_ mitochondrial | 5.1 ± 4.1 | 1.4 ± 0.8 |
| P04908;P0C0S8;P0C0S9;P20671;Q16777;Q3ZBX 9;Q6F113;Q7L7L0;Q93077;Q96KK5;Q99878;Q9 BTM1;P0C0S4;P0C0S5;P16104;Q32LA7;Q71UI9 | Histone H2A type 2-C | 17.2 ± 14 | 0.1 ± 0.1 |

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| ;Q8IUE6;Q96QV6 | | | |
| O60814;P06899;P23527;P33778;P58876;P62807;P62808;Q16778;Q2M2T1;Q32L48;Q5QNW6;Q93079;Q99877;Q99879;P57053;Q96A08;Q99880;Q8N257 | Histone H2B type 1-B | 19 ± 15.2 | 1.7 ± 1.1 |
| Q16695;A5PK61;P68431;P68432;P84227;P84243;Q5E9F8;Q71DI3;Q6NXT2;Q3SZB8 | Histone H3.1t | 19.2 ± 8.9 | 18.8 ± 4.8 |
| P62803;P62805 | Histone H4 | 10.3 ± 8.4 | 1 ± 0.8 |
| P01889;P01893;P03989;P04222;P04439;P05534;P10319;P13746;P13747;P16188;P17693;P18463;P18464;P18465;P30443;P30447;P30455;P30460;P30461;P30462;P30464;P30466;P30475;P30479;P30480;P30481;P30483;P30484;P30485;P30487;P30488;P30490;P30491;P30492;P30493;P30495;P30498;P30501;P30504;P30505;P30508;P30510;P30685;Q04826;Q07000;Q29718;Q29836;Q29865;Q29940;Q29960;Q29963;Q95365;Q9TNN7 | HLA class I histocompatibility antigen_ B-7 alpha chain | 5.2 ± 2.4 | 1.9 ± 0.6 |
| F1MMS9;P26006 | Integrin alpha-3 | 5.6 ± 0.7 | 6.5 ± 1.8 |
| P05556 | Integrin beta-1 | 3.4 ± 0.5 | 6.9 ± 0.9 |
| P18564;Q8SQB8 | Integrin beta-6 | 6.2 ± 1.2 | 8.7 ± 0.8 |

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| P00338;P19858;Q5E9B1 | L-lactate dehydrogenase A chain | 10 ± 7 | 19.1 ± 3.5 |
| Q9UPN3 | Microtubule-actin cross-linking factor 1_ isoforms 1/2/3/5 | 19 ± 3.5 | 36.6 ± 3.8 |
| P35579 | Myosin-9 | 2.9 ± 2.2 | 8.2 ± 3.5 |
| P14649;P60660;P60661 | Myosin light chain 6B | 6.3 ± 3.6 | 11.5 ± 3.6 |
| A4IF97;O14950;P19105;Q5E9E2 | Myosin regulatory light chain 12B | 2.8 ± 1.9 | 4.9 ± 1.6 |
| Q09666 | Neuroblast differentiation-associated protein AHNAK | 4.2 ± 3.4 | 34.7 ± 10.9 |
| P21589 | 5'-Nucleotidase | 1.7 ± 1.4 | 2.5 ± 0.7 |
| P62937;P62935 | Peptidyl-prolyl cis-trans isomerase A | 3.2 ± 2.6 | 6.4 ± 1.9 |
| Q06830;Q5E947;P32119 | Peroxiredoxin-1 | 10.4 ± 8 | 21.1 ± 4.8 |
| P12234;Q00325 | Phosphate carrier protein_ mitochondrial | 5.2 ± 4.2 | 0 |
| Q5VZY2 | Phospholipid phosphatase 4 | 4 ± 3.3 | 3.7 ± 1.7 |
| P0CG47;P0CG48;P0CG53;P0CH28;P62979;P62987;P62992;P63048 | Polyubiquitin-B | 14.9 ± 11.9 | 20.4 ± 5.5 |
| Q5H9U9 | Probable ATP-dependent RNA helicase DDX60-like | 8.7 ± 6.7 | 8.5 ± 3.5 |

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| P07737;P02584 | Profilin-1 | 7.1 ± 5.3 | 15.4 ± 2.7 |
| Q9Y2J8 | Protein-arginine deiminase type-2 | 3.2 ± 2.6 | 0.3 ± 0.3 |
| P06703 | Protein S100-A6 | 30.7 ± 24.4 | 37.1 ± 12.1 |
| P31949 | Protein S100-A11 | 16.7 ± 13.2 | 27.5 ± 3.5 |
| P63103;P63104;P27348;P31946;P68250;Q3SZI4 | 14-3-3 protein zeta/delta | 6.8 ± 3 | 9.8 ± 1 |
| Q5E9U1 | P2X purinoceptor 4 | 3.3 ± 2.7 | 0 |
| O60361;P15531;P22392;P52174;P52175;Q3T0Q4 | Putative nucleoside diphosphate kinase | 3.2 ± 2.6 | 4.5 ± 1.1 |
| P14618;P30613 | Pyruvate kinase PKM | 14.5 ± 8.9 | 18.9 ± 1.3 |
| Q8NFH8 | RalBP1-associated Eps domain-containing protein 2 | 1.8 ± 1.5 | 2.1 ± 0.4 |
| P46940 | Ras GTPase-activating-like protein IQGAP1 | 2.2 ± 1.8 | 5.6 ± 2.7 |
| P23396;Q3T169 | 40S ribosomal protein S3 | 2.2 ± 1.8 | 0.6 ± 0.2 |
| P62263 | 40S ribosomal protein S14 | 3.2 ± 2.6 | 4.8 ± 0.6 |
| P62851;Q56JX5 | 40S ribosomal protein S25 | 3.8 ± 3.1 | 5.1 ± 1.3 |

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|---------------|--|-------------|--------------|
| P36578;Q58DW0 | 60S ribosomal protein L4 | 2.9 ± 2.4 | 3.9 ± 0.9 |
| P18124;Q58DT1 | 60S ribosomal protein L7 | 3.8 ± 2.9 | 5.2 ± 1.6 |
| P62913;Q3T087 | 60S ribosomal protein L11 | 3 ± 2.4 | 4.1 ± 0.9 |
| P30050;P61284 | 60S ribosomal protein L12 | 2.3 ± 1.9 | 2.3 ± 0.9 |
| P35268 | 60S ribosomal protein L22 | 2.3 ± 1.5 | 3.3 ± 0.6 |
| P02769 | Serum albumin | 3.6 ± 3 | 8.6 ± 5.1 |
| Q04837 | Single-stranded DNA-binding protein_ mitochondrial | 2.7 ± 2.1 | 0.3 ± 0.3 |
| Q14524 | Sodium channel protein type 5 subunit alpha | 14.9 ± 10 | 25.6 ± 8.8 |
| P38646;Q3ZCH0 | Stress-70 protein_ mitochondrial | 2.6 ± 2.1 | 0 |
| A6NHR9 | Structural maintenance of chromosomes flexible hinge domain-containing protein 1 | 10.7 ± 8.6 | 15.8 ± 1.1 |
| Q9Y6N5 | Sulfide:quinone oxidoreductase_ mitochondrial | 1.8 ± 1.4 | 0.4 ± 0.5 |
| Q99536 | Synaptic vesicle membrane protein VAT-1 homolog | 3 ± 2.5 | 3.5 ± 0.3 |
| Q9Y4F4 | TOG array regulator of axonemal microtubules protein 1 | 105.6 ± 3.6 | 381.5 ± 12.8 |

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|---|---|-------------|-------------|
| Q32PH0;Q96Q05 | Trafficking protein particle complex subunit 9 | 86.3 ± 29.5 | 77.2 ± 23.1 |
| Q2KJJ5 | Transducin beta-like protein 3 | 13.6 ± 2.6 | 80.8 ± 6.4 |
| Q9H2D6 | TRIO and F-actin-binding protein | 74.5 ± 59 | 18.7 ± 0.8 |
| O15016 | Tripartite motif-containing protein 66 | 4.9 ± 2.1 | 39.3 ± 3.4 |
| P68363;P81947;Q2HJ86;Q3ZCJ7;Q71U36;Q9BQE3;Q13748;Q32KN8;P68366;P81948;Q6PEY2;Q2HJB8;Q9NY65;A6NHL2 | Tubulin alpha-1B chain | 18.2 ± 6.9 | 16.9 ± 5.1 |
| P07437;Q2KJD0;Q13885;Q6B856;Q9BVA1;Q13509;Q2T9S0;Q2HJ81;A6NNZ2;Q9BUF5;Q9H4B7 | Tubulin beta chain | 9.7 ± 7.4 | 8.9 ± 3.2 |
| P68371;Q3MHM5;P04350;Q3ZBU7;Q3ZCM7 | Tubulin beta-4B chain | 2.2 ± 1.7 | 1.9 ± 0.9 |
| P08670;P48616;P17661;O62654 | Vimentin | 3.2 ± 2.6 | 0.6 ± 0.4 |
| P18206 | Vinculin | 2.1 ± 1.7 | 3.2 ± 0.5 |
| P21796;P45879 | Voltage-dependent anion-selective channel protein 1 | 4 ± 3.1 | 0.2 ± 0.2 |
| P45880;P68002 | Voltage-dependent anion-selective channel protein 2 | 5 ± 3.8 | 0.5 ± 0.5 |
| Q5SXM1 | Zinc finger protein 678 | 3.3 ± 2.6 | 4.1 ± 2.4 |

