# SUPPLEMENTARY MATERIAL

This document contains:

**Table S1 –** Proteins identified in this work by mass spectrometry.

**Table S1 –** Proteins identified in this work. For each protein, the accession number, theoretical p*I* and molecular weight are indicated. The protein identification was obtained by mass spectrometry.

| Spot (nr.) | Protein function | Accession Number | MW (KDa)/ p*I* | Mascot score | No. of matched peptides | Sequence coverage (%) |
|---|---|---|---|---|---|---|
| **Structural components and cellular cytoskeleton** | | | | | | |
| 3 | actin, cytoplasmic 1; beta-actin (**ACTB**) | P60709 | 42.1/5.29 | 243 | 5 | 18 |
| 7 | | | 42.1/5.29 | 244 | 6 | 21 |
| 35 | | | 42.1/5.29 | 144 | 4 | 13 |
| 64 | | | 42.1/5.29 | 158 | 3 | 12 |
| 81 | | | 42.1/5.29 | 116 | 4 | 13 |
| 160 | | | 42.1/5.29 | 356 | 15 | 42 |
| 171 | | | 42.1/5.29 | 97 | 5 | 18 |
| 1 | keratin, type II cytoskeletal 1 (**KRT1**) | P04264 | 66.1/8.15 | 154 | 12 | 24 |
| 59 | | | 66.1/8.15 | 96 | 8 | 17 |
| 75 | | | 66.1/8.15 | 58 | 5 | 9 |
| 158 | | | 66.1/8.15 | 91 | 8 | 15 |
| 148 | keratin, type I cytoskeletal 10 (**KRT10**) | P13645 | 59.0/5.13 | 85 | 7 | 10 |
| 178 | | | 59.0/5.13 | 95 | 8 | 18 |
| 33 | vimentin (**VIM**) | P08670 | 53.7/5.06 | 128 | 7 | 23 |
| 39 | | | 53.7/5.06 | 277 | 17 | 29 |
| 41 | | | 53.7/5.06 | 249 | 16 | 44 |
| 55 | | | 53.7/5.06 | 497 | 21 | 41 |
| 56 | | | 53.7/5.06 | 258 | 13 | 34 |
| 58 | | | 53.7/5.06 | 403 | 24 | 49 |
| 67 | | | 53.7/5.06 | 294 | 16 | 39 |
| 74 | | | 53.7/5.06 | 227 | 15 | 37 |
| 78 | | | 53.7/5.06 | 406 | 22 | 34 |
| 79 | | | 53.7/5.06 | 204 | 9 | 21 |
| 87 | | | 53.7/5.06 | 82 | 3 | 7 |
| 106 | | | 53.7/5.06 | 173 | 13 | 29 |
| 113 | | | 53.7/5.06 | 248 | 12 | 27 |
| 124 | | | 53.7/5.06 | 160 | 10 | 30 |
| 128 | | | 53.7/5.06 | 103 | 6 | 16 |
| 131 | | | 53.7/5.06 | 400 | 18 | 39 |

| Spot (nr.) | Protein function | Accession Number | MW (KDa)/ p*I* | Mascot score | No. of matched peptides | Sequence coverage (%) |
|---|---|---|---|---|---|---|
| 202 | | | 53.7/5.06 | 164 | 9 | 27 |
| 484 | | | 53.7/5.06 | 318 | 20 | 45 |
| 603 | | | 53.7/5.06 | 713 | 33 | 63 |
| 98 | | | 53.7/5.06 | 157 | 15 | 46 |
| 121 | | | 53.7/5.06 | 192 | 11 | 29 |
| 146 | | | 53.7/5.06 | 157 | 9 | 24 |
| 198 | | | 53.7/5.06 | 883 | 29 | 59 |
| 236 | | | 53.7/5.06 | 101 | 6 | 16 |
| 353 | | | 35.1/4.7 | 225 | 9 | 37 |
| 795 | | | 53.7/5.06 | 414 | 24 | 57 |
| 849 | | | 53.7/5.06 | 279 | 20 | 48 |
| 879 | | | 53.7/5.06 | 288 | 16 | 35 |
| 20 | macrophage-capping protein (**CAPG**) | P40121 | 38.8/5.88 | 158 | 6 | 23 |
| 53 | fascin homolog 1, actin bundling protein (*Strongylocentrotus purpuratus*) (**FSCN1**) | Q16658 | 55.1/6.84 | 121 | 7 | 17 |
| 77 | capping protein (actin filament) muscle Z-line, alpha 1 (**CAPZA1**) | P52907 | 33.1/5.45 | 115 | 6 | 24 |
| 102 | tubulin beta chain (**TUBB**) | P07437 | 40.6/4.78 | 161 | 9 | 19 |
| 183 | actin, gamma 1 (**ACTG1**) | P63261 | 26.1/5.65 | 136 | 3 | 16 |
| 208 | twinfilin, actin binding protein (**TWF1**) | Q12792 | 39.8/6.37 | 149 | 4 | 20 |
| **Folding of proteins and stress response proteins** | | | | | | |
| 60 | protein disulfide-isomerase (P55) (**P4HB**) | P07237 | 57.4/4.76 | 89 | 6 | 11 |
| 85 | 78 kDa glucose-regulated protein (**HSPA5**) | P11021 | 72.4/5.07 | 266 | 7 | 14 |
| 529 | | | 72.4/5.07 | 243 | 10 | 18 |
| 242 | heat shock 70 kDa protein 9 (mortalin) (**HSPA9**) | P38646 | 73.9/5.87 | 166 | 7 | 13 |
| 581 | | | 73.9/5.87 | 111 | 7 | 15 |
| 144 | heat shock protein beta-1 (HSP 27) (**HSPB1**) | P04792 | 22.8/5.98 | 113 | 3 | 20 |
| 176 | peptidyl-prolyl cis-trans isomerase B (cyclophilin B) (**PPIB**) | P23284 | 23.7/9.42 | 93 | 6 | 30 |
| 207 | heat shock cognate 71 kDa protein (**HSPA8**) | P11142 | 71.1/5.37 | 227 | 9 | 18 |
| 254 | endoplasmic reticulum protein ERp29 (**ERP29**) | P30040 | 29.0/6.77 | 126 | 4 | 19 |
| **Apoptosis** | | | | | | |
| 168 | annexin A1 (**ANXA1**) | P04083 | 38.9/6.57 | 351 | 14 | 49 |
| 698 | | | 38.9/6.57 | 307 | 17 | 50 |
| 364 | annexin A2 (**ANXA2**) | P07355 | 38.8/7.57 | 114 | 6 | 21 |
| 620 | | | 38.8/7.57 | 143 | 8 | 25 |
| 494 | annexin A5 (**ANXA5**) | P08758 | 36.0/4.94 | 121 | 6 | 20 |
| 45 | voltage-dependent anion-selective channel protein 1 (**VDAC1**) | P21796 | 30.9/8.62 | 144 | 3 | 12 |
| **Vesicle trafficking** | | | | | | |
| 610 | septin 11 (**SEPT11**) | Q9NVA2 | 49.7/6.36 | 105 | 6 | 15 |

| Spot (nr.) | Protein function | Accession Number | MW (KDa)/ p*I* | Mascot score | No. of matched peptides | Sequence coverage (%) |
|---|---|---|---|---|---|---|
| **Cell cycle regulation and aging** | | | | | | |
| 15 | eukaryotic translation initiation factor 3, subunit F (**eIF3f**) | O00303 | 37.7/5.24 | 99 | 5 | 19 |
| 34 | eukaryotic translation initiation factor 4A3 (**eIF4A3**) | P38919 | 47.1/6.3 | 154 | 12 | 24 |
| 94 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (**PSMD11**) | O00231 | 47.7/6.08 | 95 | 7 | 20 |
| 194 | poly (rC) binding protein 1 (**PCBP1**) | Q15365 | 38.0/6.66 | 110 | 6 | 23 |
| **Translation pathway** | | | | | | |
| 138 | prohibitin (**PHB**) | P35232 | 29.8/5.57 | 101 | 5 | 21 |
| 156 | ribosomal protein SA pseudogene 58 (**RPSAP58**) | | 18.7/9.64 | 126 | 2 | 17 |
| 239 | polymerase I and transcript release factor (**PTRF**) | Q6N2I2 | 43.5/5.51 | 82 | 5 | 12 |
| **Energy metabolism** | | | | | | |
| 91 | UDP-glucose 6-dehydrogenase (**UGDH**) | O60701 | 55.7/6.73 | 114 | 7 | 16 |
| 99 | citrate synthase, mitochondrial (**CS**) | O75390 | 51.9/8.45 | 90 | 5 | 10 |
| 109 | isocitrate dehydrogenase 1 (NADP+), soluble (**IDH1**) | O75874 | 35.9/6.53 | 85 | 5 | 12 |
| 157 | fructose-biphosphate aldolase A (**ALDOA**) | P04075 | 39.8/8.30 | 163 | 6 | 19 |
| 166 | glyceraldehyde-3-phosphate dehydrogenase (**GAPDH**) | P04406 | 36.2/5.29 | 356 | 6 | 23 |
| 180 | aldo-keto reductase family 1, member A1 (aldehyde reductase) (**AKR1A1**) | P14550 | 36.9/6.32 | 117 | 6 | 18 |
| 193 | glucose-6-phosphate dehydrogenase (**G6PD**) | P11413 | 59.8/6.39 | 121 | 7 | 15 |
| 250 | chain A, structure of human glutamate dehydrogenase-Apo form (**1L1F_A**) | P00367 | 56.3/6.71 | 187 | 12 | 30 |
| 540 | ATP synthase, H$^+$ transporting, mitochondrial F1 complex, beta polypeptide (**ATP5B**) | P06576 | 56.5/5.26 | 135 | 9 | 27 |
| 993 | prolyl 4-hydroxylase, alpha polypeptide II (**P4HA2**) | Q05DA4 | 57.7/5.45 | 137 | 8 | 16 |
| **Lipid metabolism** | | | | | | |
| 97 | enoyl-CoA hydratase, short chain, 1, mitochondrial (**ECHS1**) | P30084 | 31.8/8.34 | 114 | 6 | 23 |
| 139 | acetyl-CoA acetyltransferase (**ACAT2**) | Q9BWD1 | 41.8/6.47 | 107 | 3 | 11 |
| **Muscle development** | | | | | | |
| 111 | lamin A/C (**LMNA**) | P02545 | 57.7/6.40 | 133 | 4 | 11 |
| 126 | | | 65.1/6.40 | 176 | 12 | 25 |
| 257 | | | 74.4/6.57 | 97 | 8 | 14 |
| 451 | | | 74.3/6.40 | 107 | 7 | 11 |
| **Neuronal differentiation** | | | | | | |
| 151 | dihydropyrimidinase-like 2 (**DPYSL2**) | Q16555 | 68.6/5.85 | 84 | 5 | 10 |
| 483 | | | 662.7/5.85 | 85 | 6 | 13 |