

Appendix 2. Proteins with differential expression between young and older donors.

Change	Spot No.	W/P*	NCBI**	Protein ID	Function	Expectation***
Metabolism						
Up	1487	68.3/6.6	33357604	Aldehyde dehydrogenase 2	Metabolizes aldehyde substrates using NADP as a cofactor	1.62E-08
Up	3738	54.4/5.7	6137684	Chain H, Human mitochondrial aldehyde dehydrogenase complexed with Nad ⁺ and Mn ²⁺	Metabolizes aldehyde substrates	2.63E-05
Up	2398	40.8/4.9	19913432	ATPase, H ⁺ transporting, lysosomal, V0 subunit D isoform 1	ATP proton pump	6.42E-02
Up	2233	27.3/5.1	14251209	Chloride intracellular channel 1	Chloride channels	2.04E-04
Up	1664	47.4/7.0	4503571	Enolase 1	Multifunction enzyme in glycolysis	9.93E-07
Up	2077	36.9/5.7	54696396	Lactate dehydrogenase B	Anaerobic glycolysis	8.15E-04
Up	3887	80.5/5.9	33519475	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75 kDa precursor	Transfers electrons from NADH to the respiratory chain	1.30E-02
Up	3718	53.6/6.0	55959506	Solute carrier family 25 (mitochondrial carrier phosphate carrier), member	Facilitative transporter	1.29E-03

				24		
No match	1707	47.5/7.0	4503571	Enolase 1	Multifunctional enzyme in glycolysis	4.77E-02
No match	3883	80.5/5.9	33519475	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75 kDa precursor	Transfers electrons from NADH to the respiratory chain	1.70E-05
No match	1835	53.6/6.0	33598954	Solute carrier family 25, member 24 isoform 1	Facilitative transporter	6.70E-04

Antioxidant Proteins

Up	1560	52.5/5.7	4504169	Glutathione synthetase	Catalyze second step of glutathione biosynthesis	2.88E-03
Up	2512	28.1/5.7	11514458	Chain H, Glutathione Transferase P1-1	Antioxidant protection	3.45E-09
Up	2597	27.5/5.7	32189392	Peroxiredoxin 2 isoform a	Antioxidant protection	3.96E-10
Up	3139	12.8/5.2	4506925	SH3 domain binding glutamic acid-rich protein like	Member of thioredoxin-like protein family	5.64E-03
No match	2511	23.6/5.4	2204207	Glutathione S-transferase	Antioxidant protection	2.67E-02
No match	2312	36.8/6.2	4758484	Glutathione-S-transferase omega	Antioxidant protection	1.29E-08

Protein Folding/Degradation

Up	1320	61.2/5.7	306890	Chaperonin (HSP60)	Protein folding and assembly	2.11E-06
Up	3745	74.0/6.0	386785	Heat shock 70 kDa	Protein folding and assembly	1.69E-06
Up	2556	25.5/4.8	558528	Proteasome beta	Degrades	8.54E-14

				6 subunit	unneded or damaged proteins	
Up	2314	28.9/5.8	5453990	Proteasome activator subunit 1 isoform	Binds to proteasomes and stimulate hydrolysis of peptides	5.02E-07
No match	2320	26.5/5.3	5822091	Chain H, Cathepsin D at pH 7.5	Acid protease active in intracellular protein breakdown	5.18E-04
Regulatory Proteins						
Up	4066	44.4/4.9	809190	Chain C, Annexin V, high calcium form	Cellular signal transduction	3.72E-07
Up	963	80.9/5.6	38044288	Gelsolin isoform b	“Calcium-regulated, actin-modulating protein”	2.28E-03
Up	1966	43.3/5.0	14249959	HNRPC	RNA binding protein	1.25E-06
Up	1579	55.4/5.9	5031753	HNRPH1	RNA binding protein	1.17E-03
Up	1321	55.6/5.5	55958544	HNRPK	RNA binding protein	1.30E-03
Up	1106	79.3/6.4	15619018	Protein tyrosine phosphatase, non-receptor type 22(PTPN22)	Regulates Cbl and its associated protein kinases	9.88E-03
Up	2057	34.4/5.7	16933546	Ribosomal protein P0	Protein synthesis	8.63E-04
Up	2671	22.9/5.1	38679884	Sorcini isoform b	Calcium regulation	5.08E-04
Up	1981	43.1/5.4	54696064	TGF-beta receptor-interacting protein -1	Regulates TGF-beta	2.62E-04

Up	2279	36.3/4.6	5803225	Tyrosine 3/tryptophan 5 - monooxygenase activation protein, epsilon polypeptide	14-3-3 family, mediates signal transduction	1.17E-02
No match	3943	44.4/5.0	999937	Annexin V	Cellular signal transduction	2.99E-16
No match	1684	46.0/5.4	6876910	HNRPF	RNA binding protein	4.21E-02
Cytoskeletal Proteins						
Up	1694	47.8/5.6	5031573	ARP3 actin-related protein 3 homolog	Essential for cell shape and motility	1.47E-03
Up	2036	33.1/5.4	5453597	F-actin capping protein alpha-1 subunit	Regulates growth of actin filaments	5.25E-07
No match	3963	49.7/5.2	57471646	Vimentin	Intermediate filament	2.36E-05
No match	3731	53.7/5.1	7576229	Vimentin	Intermediate filament	1.69E-07
Down	1132	74.3/6.4	57014047	Lamin A/C transcript variant 1	Nuclear intermediate filament	1.73E-02
Down	3994	32.9/4.7	27597085	Tropomyosin 1 alpha chain isoform 5	Stabilizes actin filaments	1.19E-02
Down	2014	33.0/4.6	47519616	Tropomyosin 2 (beta) isoform 2	Stabilizes actin filaments	9.37E-04
Other Proteins						
Up	1323	55.7/5.8	50949988	Hypothetical protein	?	9.99E-03
Up	2469	27.9/4.5	40715884	Placental protein 23	Heme-binding protein	8.49E-05
Up	2308	31.2/5.6	4505585	Platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30 kDa	Enzyme that inactivates platelet-activating factor	4.11E-08

No match	2147	31.4/5.3	4557553	Emerin	Interacts with nuclear lamins	2.65E-14
Down	4006	31.3/5.5	7546546	Chain B, Crystal structure of human cathepsin X	Related to inflammatory and immune responses	3.34E-03
Down	923	107.6/5/1	6005942	VCP protein	Structural protein associated with clathrin and Hsv70-Involved in vesicle transport and fusion	3.33E-04

An asterisk denotes that W/P stands for theoretical molecular weight/isoelectric point. The double asterisk means that the numbers in this column are [National Center for Biotechnology Information](#) accession numbers. Three asterisks indicate that the numbers in this column are the probabilities of correct protein identification based on Bayesian statistical analysis of protein sequences in the [NCBI](#) database.