

Appendix 1. Proteins with similar expression between young and older donors.

Spot No.	W/P*	NCBI**	Protein ID	Expectation***
3166	14.7/5.3	56554351	A Chain, X-ray crystal structure of R111h human galectin-1	4.60496E-08
897	107.3/5.7	38202257	Alpha glucosidase II	1.32636E-06
3937/3943	44.4/5.0	999937	Annexin V	0.00260409
3873/3977	56.9/5.4	32189394	ATP synthase beta subunit	2.74834E-07
2604	26.3/5.2	5453559	ATP synthase, H ⁺ transporting mitochondrial FO complex, subunit d isoform a	0.00146817
1600	54.6/8.4	50345982	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit isoform b	1.077E-10
4006	31.3/5.5	7546546	B Chain, Crystal structure of human cathepsin X	0.000144605
3919	34.6/6.5	999893	B Chain, Triosephosphate isomerase	0.0151839
3869	42.1/5.3	4501885	Beta actin	0.000300383
3853	55.7/4.7	338695	Beta-tubulin	0.00460906
3937	44.4/5.0	809190	C Chain, Annexin V	4.65753E-06
2250	34.3/5.3	24158607	C Chain, Cathepsin B complexed with dipeptidyl nitrile inhibitor	4.28311E-06
2390	32.0/5.0	18314496	Calpain, small subunit 1	2.49582E-11

1760	48.5/4.5	54697146	Calumenin	8.56074E-10
2329	54.0/6.1	4503143	Cathepsin D preprotein	0.0661959
3756	61.2/5.7	41399285	Chaperonin (HSP60)	1.28525E-05
2569	22.4/5.9	16936542	Crystallin, beta A2	6.13435E-08
2538	26.5/5.2	999911	D Chain, Cathepsin B	0.0437362
3907	44.9/7.9	704416	Elongation factor Tu	2.27836E-09
2382	29.0/6.8	5803013	Endoplasmic reticulum protein 29 isoform 1 precursor	2.18273E-05
1459	57.2/5.9	2245365	ER-60	4.16353E-09
3919	30.3/6.4	9954651	ETHE1 protein	6.85393E-10
2071	39.0/4.9	25453472	Eukaryotic translation elongation factor 1 delta isoform 2	2.78643E-05
2032	40.9/5.4	5453597	F-actin capping protein alpha-1 subunit	2.52537E-08
3819	63.5/4.9	33469985	FK506 binding protein 9	3.45082E-06
3974	42.0/5.6	11321585	Guanine nucleotide-binding protein, beta-1 subunit	0.000479411
2298	26.5/6.3	5822091	H Chain, Cathepsin D at pH 7.5	0.000233777
1100	96.2/5.1	16507237	Heat shock 70 kDa protein 5	2.66392E-10
1134	71.1/5.4	5729877	Heat shock 70k Da protein 8 isoform 1	0.000005459

3984	66.5/5.6	24234686	Heat shock 70 kDa protein 8 isoform 2	0.000846241
1135	74.1/6.0	21040386	Heat shock 70 kDa protein 9B precursor	6.60347E-15
4011	120.7/4.7	15010550	Heat shock protein gp96 precursor	6.61451E-06
4003	43.3/5.0	14249959	HNRPC protein	3.31812E-09
1836	37.3/5.8	6841440	HSPC108	0.000137081
2394	26.2/5.3	6624942	Hypothetical protein	4.23526E-09
2395	49.5/5.3	6808437	Hypothetical protein	0.00109799
2411	21.7/5.2	10835147	Interleukin 1 receptor isoform 3	0.0309126
1971	48.9/6.5	5031777	Isocitrate dehydrogenase 3 alpha precursor	9.06634E-06
1110	68.7/6.4	386856	Lamin A protein	0.00331921
3901	65.2/6.4	5031875	Lamin A/C isoform 2	3.86223E-07
3898	74.3/6.7	57014043	Lamin A/C isoform variant 1	0.00134689
3744	67.8/5.3	27436951	Lamin B2	0.000190173
3817	99.6/5.3	19913410	Major vault protein	0.000399908
3081	17.1/4.5	48735275	MYL6 protein	1.43401E-14
2859	19.8/4.7	2605594	Myosin regulatory light chain MRCL2	4.32889E-07
2003	40.5/4.5	16307090	NPM1 protein	4.55811E-09
2516	30.8/7.1	32483377	Peroxiredoxin 3 isoform b	1.32216E-12
2388	35.9/6.7	4505753	Phosphoglycerate	0.000938808

			mutase 1 (brain)	
2396	35.8/5.9	49456297	PRDX4, peroxiredoxin 4	6.00556E-09
2317	29.8/5.6	4505773	Prohibitin	6.81955E-07
1334	61.0/5.5	23274221	Prolyl 4- hydroxylase, alpha II subunit, isoform 2 precursor	0.0198584
4055	57.5/4.8	20070125	Prolyl 4- hydroxylase, beta subunit	1.59117E-10
2062	43.8/5.3	387010	Pyruvate dehydrogenase E1-beta subunit precursor	2.34908E-05
3846	35.6/4.7	57997573	Tropomyosin 3	1.32161E-06
2248	38.4/4.7	54696136	Tropomyosin 4	6.59982E-18
2349	27.9/4.7	21735625	Tyrosine 3/tryptophan 5 - monooxygenase activation protein, zeta polypeptide	1.13936E-07
4047	53.7/5.1	57471646	Vimentin	4.2353E-07
1749	53.8/5.0	340219	Vimentin	1.61553E-09

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