Electronic Supplementary Material (ESI) for Environmental Science: Nano.

Supplementary Table 3: Expected false discovery rates for the proteins modulated upon exposure to silver nanoparticles

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NOTATION FOR THE METHODS:
SGoF: The SGoF method (Carvajal-Rodriguez et al 2011)
B-H: The Benjamini & Hochberg method (Yekutieli et al. 1999)
SGoF+: The SGoF plus method (Carvajal-Rodriguez et al. 2011)
SFisher: The composite probability method applied sequentially as a step-down adjustment (Diz et al 2010)

			Acute exposure						Chronic exposure		
Uniprot accession number	**Protein name**	P-value acute	B-H	SGoF+(0.238	SFisher	q-value	P-value chronic	B-H	SGoF+(0.178	SFisher	q-value
P61982	14-3-3 gamma protein	0.65718	0.782357	1	1	0.125177	0.0424871	0.0672264	0.0302619	4.07727e-07	0.00537811
P47738	aldehyde dehydrogenase, mitochondrial	0.0571746	0.183252	0.0378524	0.00597412	0.0293203	0.177057	0.201202	1	0.668387	0.0160961
P45376	Aldo-keto reductase family 1 member B1	0.0443199	0.165011	0.000292862	7.4573e-05	0.0264017	0.486804	0.507087	1	0.99004	0.040567
O35639	Annexin A3	0.303726	0.451973	1	0.999965	0.0723157	0.0081995	0.0450815	4.76072e-40	4.57071e-42	0.00360652
P14824	Annexin A6	0.605481	0.733279	1	1	0.117325	0.000888004	0.0322262	1.27193e-62	1.02847e-62	0.00257809
Q9DCX2	ATP synthase subunit d	0.227338	0.373911	1	0.998271	0.0598257	0.0242657	0.0571969	6.83994e-16	8.36223e-22	0.00457575
Q64152	Transcription factor btf3	0.884557	0.937031	1	1	0.149925	0.0206625	0.0571969	2.19469e-19	7.35254e-25	0.00457575
Q64152	Transcription factor btf3	0.671289	0.783302	1	1	0.125328	0.0109626	0.0507526	6.88786e-34	9.41644e-37	0.00406021
Q923D2	Flavin reductase	0.723998	0.809363	1	1	0.129498	0.0357415	0.0633372	5.67824e-05	7.16538e-11	0.00506697
Q9CXW3	Calcyclin binding protein	0.0184793	0.165011	5.96869e-14	5.39758e-13	0.0264017	0.24798	0.276763	1	0.814023	0.0221411
P10605	Cathepsin B	0.309841	0.455649	1	0.999979	0.0729038	0.0389416	0.0657798	0.00131595	4.02953e-09	0.00526238
P18242	Cathepsin D	0.665508	0.792617	1	1	0.512683	0.0351032	0.0649558	2.61359e-07	2.36239e-13	0.0199864
O70370	Cathepsin S	0.275692	0.421631	1	0.999832	0.0674609	0.0199665	0.0571969	1.2039e-21	9.12768e-27	0.00457575
Q9WUU7	Cathepsin Z	0.364381	0.523535	1	0.999993	0.0837657	0.00860237	0.0450815	5.56612e-39	3.75393e-41	0.00360652
P47753	F-actin-capping protein subunit alpha-1	0.213329	0.365289	1	0.994266	0.0584463	0.0204196	0.0571969	3.9955e-20	1.71961e-25	0.00457575
Q9QYB1	Chloride intracellular channel protein 4	0.170953	0.315056	1	0.943076	0.0504089	0.00180467	0.0322262	5.62472e-57	7.74413e-57	0.00257809
P18760	Cofilin 1	0.0879143	0.209666	1	0.194784	0.0335465	0.0456263	0.0684225	0.193143	1.25227e-05	0.0054738
Q9CQ02	COMM domain-containing protein 4	0.00480948	0.165011	1.61379e-18	8.57137e-18	0.0264017	0.0988205	0.132823	1	0.00907059	0.0106259
O88456	Calpain small subunit 1	0.0225012	0.165011	3.35563e-12	1.88495e-11	0.0264017	0.126218	0.160745	1	0.0553218	0.0128596

Q9QXK7	Cleavage and polyadenylation specificity factor subunit 3	0.294975	0.44424	1	0.99994	0.0710784	0.00937696	0.0450815	7.10677e-35	1.27532e-37	0.00360652
O88544	COP9 signalosome complex subunit 4	0.0324337	0.165011	3.93824e-08	5.24467e-08	0.0264017	0.0459799	0.0684225	0.279997	2.83195e-05	0.0054738
Q8BV13	COP9 signalosome complex subunit 7b	0.0905757	0.209666	1	0.343956	0.0335465	0.0487249	0.0700347	0.52742	0.000138053	0.00560277
Q3U1J4	DNA damage-binding protein 1	0.0429718	0.165011	1.20468e-05	5.40002e-06	0.0264017	0.270268	0.298969	1	0.857672	0.0239176
P50171	Estradiol 17-beta-dehydrogenase 8	0.0199061	0.165011	9.03947e-13	5.9327e-12	0.0264017	0.0258338	0.0571969	1.42547e-11	7.65041e-18	0.00457575
Q64442	sorbitol dehydrogenase	0.0284841	0.165011	4.55912e-09	8.4817e-09	0.0264017	0.147376	0.177135	1	0.254934	0.0141708
Q9QYJ0	DnaJ homolog subfamily A member 2	0.874027	0.93379	1	1	0.149406	0.0209365	0.0571969	1.168e-18	3.11234e-24	0.00457575
Q91WN1	DnaJ homolog subfamily C member 9	0.0894301	0.209666	1	0.238956	0.0335465	0.0388023	0.0657798	0.000631807	1.52685e-09	0.00526238
O88487	Cytoplasmic dynein 1 intermediate chain 2	0.0441955	0.165011	0.000138258	3.95989e-05	0.0264017	0.0549155	0.078005	0.861658	0.000613343	0.0062404
P57759	Endoplasmic reticulum resident protein 29	0.0488432	0.171611	0.0169964	0.00307692	0.111002	0.17426	0.202266	1	0.679312	0.0583344
Q99LC5	Electron transfer flavoprotein subunit alpha	0.100706	0.22479	1	0.532714	0.0359663	0.0251248	0.0571969	5.85807e-14	4.39897e-20	0.00457575
Q921I9	Exosome complex component RRP41	0.0269784	0.165011	1.48068e-09	3.26119e-09	0.0264017	0.295524	0.32404	1	0.892994	0.0259232
P23591	GDP-L-fucose synthase	0.0553905	0.182206	0.0230512	0.00377574	0.0291529	0.00658044	0.0450815	1.70583e-44	6.62823e-46	0.00360652
P09528	Ferritin heavy chain	0.0807394	0.209666	0.640008	0.095558	0.0335465	0.00677371	0.0450815	2.34519e-43	6.40021e-45	0.00360652
Q9D964	Glycine amidinotransferase, mitochondrial	0.0634353	0.198235	0.0601995	0.00924493	0.0317177	0.0172325	0.0571969	2.06915e-27	2.04241e-31	0.00457575
O09172	Glutamate--cysteine ligase regulatory subunit	0.393359	0.558748	1	0.999996	0.0893997	0.00602116	0.0450815	5.06419e-48	6.32081e-49	0.00360652
P47791	Glutathione reductase, mitochondrial	0.184847	0.330085	1	0.983255	0.0528135	0.0198726	0.0571969	1.99207e-22	2.08297e-27	0.00457575
Q3SXD3	HD domain-containing protein 2	0.0401323	0.165011	2.0249e-06	1.31377e-06	0.0264017	0.0219132	0.0571969	3.00974e-17	5.30646e-23	0.00457575
P62748	Hippocalcin-like protein 1	0.725189	0.809363	1	1	0.129498	0.0136212	0.0560243	5.06306e-31	2.27545e-34	0.00448194
O35345	Importin subunit alpha-7	0.266127	0.416069	1	0.999573	0.0665711	0.0409741	0.0672264	0.00264617	1.0554e-08	0.00537811
O55023	Inositol monophosphatase 1	0.52024	0.663572	1	1	0.106171	0.000143093	0.00894333	4.19481e-64	6.76401e-65	0.000715466
Q9D8C4	Interferon-induced 35 kDa protein homolog	0.412996	0.573606	1	0.999998	0.091777	0.0185074	0.0571969	1.08114e-25	4.75945e-30	0.00457575
Q9DBP5	UMP-CMP kinase	0.94492	0.95254	1	0.997825	0.152406	0.0255901	0.0571969	3.78348e-12	2.12596e-18	0.00457575

Q99KR3	Endoribonuclease LACTB2	0.0432925	0.165011	6.32475e-05	2.06345e-05	0.0264017	0.556919	0.575329	1	0.995265	0.0460264
P70202	Latexin	0.0905757	0.209666	1	0.404038	0.0335465	0.0348023	0.0633372	5.19958e-07	3.73241e-13	0.00506697
P31938	Dual specificity mitogen-activated protein kinase kinase 1	0.208544	0.362056	1	0.991789	0.0579289	0.0468095	0.0688375	0.391314	6.31421e-05	0.005507
Q6ZQI3	malectin	0.0789024	0.209666	0.500848	0.072701	0.0335465	0.0255714	0.0571969	9.73091e-13	5.88567e-19	0.00457575
Q9CQ65	S-methyl-5'-thioadenosine phosphorylase	0.0344495	0.165011	3.00492e-07	2.76553e-07	0.0264017	0.0315171	0.0625339	6.31122e-08	4.09866e-14	0.00500271
Q9D6J6	NADH dehydrogenase [ubiquinone] flavoprotein 2	0.0342189	0.165011	1.10486e-07	1.2237e-07	0.0264017	0.0677121	0.0940445	1	0.002182	0.00752356
Q9JHW2	Omega-amidase NIT2	0.49871	0.656197	1	1	0.104992	0.0218057	0.0571969	6.02306e-18	1.30314e-23	0.00457575
Q6P3D0	U8 snoRNA-decapping enzyme	0.010907	0.165011	1.7772e-16	1.9735e-15	0.0264017	0.340245	0.366644	1	0.94048	0.0293315
Q9D2G2	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	0.266284	0.416069	1	0.999727	0.0665711	0.0353693	0.0633372	9.60512e-06	8.90032e-12	0.00506697
Q8BMF4	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	0.10661	0.230205	1	0.595285	0.0368328	0.013894	0.0560243	4.26077e-30	1.30112e-33	0.00448194
Q7TQI3	Ubiquitin thioesterase OTUB1	0.514427	0.662921	1	1	0.106067	0.0359755	0.0633372	0.000131204	2.00752e-10	0.00506697
Q61205	Platelet-activating factor acetylhydrolase IB subunit gamma	0.420669	0.577842	1	0.999999	0.0924547	0.00580775	0.0450815	1.79615e-50	5.63537e-51	0.00360652
Q8BH04	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	0.0453442	0.165011	0.000601077	0.000138574	0.0264017	0.12731	0.160745	1	0.0738649	0.0128596
P67778	prohibitin	0.510564	0.662921	1	1	0.106067	0.0120308	0.053709	6.43999e-33	6.25568e-36	0.00429672
Q99K51	Plastin-3	0.0263188	0.165011	4.66187e-10	1.22671e-09	0.0264017	0.00935133	0.0450815	7.07038e-36	1.71785e-38	0.00360652
Q99K51	Plastin-3	0.0947597	0.215363	1	0.46815	0.0344581	0.00907525	0.0450815	6.26078e-38	2.976e-40	0.00360652
Q3UM45	Protein phosphatase 1 regulatory subunit 7	0.0462291	0.165011	0.00119523	0.000252367	0.0264017	0.193046	0.217394	1	0.746257	0.0173915
P62137	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	0.0170791	0.165011	1.46266e-14	1.52863e-13	0.0264017	0.968944	0.968944	1	0.968944	0.0775155
P26516	proteasome non-ATPase regulatory subunit 7	0.915627	0.94265	1	0.999985	0.150824	0.0186932	0.0571969	4.95228e-24	1.0156e-28	0.00457575

Q9CZ13	Cytochrome b-c1 complex subunit 1	0.217157	0.366819	1	0.996069	0.0586911	0.028214	0.0578156	6.7275e-09	3.82992e-15	0.00462525
P46061	Ran GTPase-activating protein 1	0.540349	0.675436	1	1	0.10807	0.0151516	0.0571969	3.46456e-29	7.32476e-33	0.00457575
Q80UW8	DNA-directed RNA polymerases I, II, and III subunit RPABC1	0.0142749	0.165011	3.47205e-15	3.9328e-14	0.0264017	0.410719	0.435084	1	0.9747	0.0348067
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit	0.407416	0.572214	1	0.999997	0.0915543	0.0185367	0.0571969	7.43774e-25	2.2022e-29	0.00457575
Q9DB05	Alpha-soluble NSF attachment protein	0.0704642	0.204092	0.199986	0.028333	0.0326547	0.00619305	0.0450815	7.93484e-47	6.55433e-48	0.00360652
Q91ZR2	Sorting nexin-18	0.342066	0.497189	1	0.999988	0.0795502	0.0079476	0.0450815	3.91468e-41	5.4316e-43	0.00360652
Q60854	Serpin B6	0.610088	0.733279	1	1	0.117325	0.0232576	0.0571969	1.45748e-16	2.14822e-22	0.00457575
Q60854	Serpin B6	0.537893	0.675436	1	1	0.10807	0.0443506	0.0684225	0.0822905	2.33724e-06	0.0054738
Q60854	Serpin B6	0.758542	0.831735	1	1	0.133078	0.0420986	0.0672264	0.0173719	1.66202e-07	0.00537811
Q64105	Sepiapterin reductase	0.898035	0.94265	1	0.999999	0.150824	0.00170673	0.0322262	9.57212e-60	1.21476e-59	0.00257809
P54227	Stathmin	0.0192238	0.165011	2.35972e-13	1.81634e-12	0.0264017	0.159472	0.189848	1	0.312793	0.0151878
Q8CAY6	Acetyl-CoA acetyltransferase, cytosolic	0.0235062	0.165011	1.20725e-11	5.6077e-11	0.0264017	0.941864	0.94946	1	0.996065	0.0759568
Q9QZ06	Toll-interacting protein	0.676773	0.783302	1	1	0.125328	0.02015	0.0571969	7.04685e-21	3.97822e-26	0.00457575
Q9ER38	Torsin-3A	0.0259051	0.165011	1.42286e-10	4.53173e-10	0.0264017	0.0175901	0.0571969	1.52067e-26	9.93581e-31	0.00457575
Q9CYZ2	Tumor protein D54	0.494095	0.656197	1	1	0.104992	0.00401175	0.0450815	1.25041e-55	1.89669e-55	0.00360652
P17751/c	triose phosphate isomerase	0.913239	0.94265	1	0.999997	0.150824	0.0413474	0.0672264	0.00513564	2.67665e-08	0.00537811
Q9CQU0	Thioredoxin domain-containing protein 12	0.17139	0.315056	1	0.967804	0.0504089	0.00596117	0.0450815	3.0876e-49	6.03226e-50	0.00360652
Q8CDN6	Thioredoxin-like protein 1	0.0676076	0.204092	0.0927278	0.0137555	0.0326547	0.0253467	0.0571969	2.42531e-13	1.61576e-19	0.00457575
Q91ZJ5	UTP--glucose-1-phosphate uridylyltransferase	0.119161	0.244182	1	0.80918	0.0390691	0.029601	0.0596795	2.09409e-08	1.27282e-14	0.00477436
Q9QZ88	Vacuolar protein sorting-associated protein 29	0.548122	0.678369	1	1	0.108539	2.78108e-05	0.00347636	1.28812e-65	1.35924e-67	0.000278108
Q9ERF3	WD repeat-containing protein 61	0.0425867	0.165011	5.01662e-06	2.70641e-06	0.0264017	0.331236	0.360039	1	0.920659	0.0288031