Supplementary Table S4. *S*-Guanylated Proteins in Intact Mitochondria Treated *In Vitro* with 8-Nitro-cGMP as Identified by Means of 2D-PAGE and LC-MS/MS

Spot no.	Acc no.[a]	Protein name	Sequence coverage (%)	No. of matched peptides	Mascot score	Mw[b]	pI[c]
1	Q66HD0	Endoplasmin	52	34	1328	92713	4.72
3	P06761	78 kDa glucose-regulated protein	64	30	2094	72302	5.07
	P31000	Vimentin	34	11	152	53700	5.06
4	P48721	Stress-70 protein, mitochondrial	54	30	2293	73812	5.97
	P48679	Prelamin-A/C	23	15	167	74279	6.54
	P48037	Annexin A6	5	3	53	75706	5.39
5	P48721	Stress-70 protein, mitochondrial	64	33	2917	73812	5.97
6	P63039	60 kDa heat shock protein, mitochondrial	63	26	3169	60917	5.91
7	P31000	Vimentin	80	33	2716	53700	5.06
	P68370	Tubulin alpha-1A chain	40	14	701	50104	4.94
8	P69897	Tubulin beta-5 chain	46	16	1186	49639	4.78
	P85108	Tubulin beta-2A chain	46	16	1059	49875	4.78
	Q6P9T8	Tubulin beta-4B chain	40	15	998	49769	4.79
	Q4QRB4	Tubulin beta-3 chain	28	10	672	50386	4.82
	P10719	ATP synthase subunit beta, mitochondrial	12	5	97	56318	5.19
9	P10719	ATP synthase subunit beta, mitochondrial	59	21	2118	56318	5.19
10	P11598	Protein disulfide-isomerase A3	20	10	190	56588	5.88
11	P11598	Protein disulfide-isomerase A3	35	18	506	56588	5.88
12	P63259	Actin, cytoplasmic 2	69	18	2208	41766	5.31
	P62738	Actin, aortic smooth muscle	33	12	643	41982	5.23

13	P63259	Actin, cytoplasmic 2	25	9	234	41766	5.31
14	Q4FZT0	Stomatin-like protein 2	73	16	639	38390	8.74
16	P48679	Prelamin-A/C	31	20	777	74279	6.54
	O35763	Moesin	15	7	62	67697	6.16
17	P48679	Prelamin-A/C	52	31	1233	74279	6.54
18	P48679	Prelamin-A/C	61	35	1780	74279	6.54
19	P48679	Prelamin-A/C	46	29	1281	74279	6.54
	Q9QZR6	Septin-9	8	5	39	63752	8.65
20	P48679	Prelamin-A/C	41	26	611	74279	6.54
	Q9QZR6	Septin-9	26	15	184	63752	8.65
21	O35567	Bifunctional purine biosynthesis protein	9	3	33	64168	6.69
22	P11980	Pyruvate kinase isozymes M1/M2	10	5	89	57781	6.63
23	P11980	Pyruvate kinase isozymes M1/M2	41	18	446	57781	6.63
	P04762	Catalase	20	9	104	59719	7.07
24	P10860	Glutamate dehydrogenase 1, mitochondrial	59	25	1438	61377	8.05
	P15999	ATP synthase subunit alpha, mitochondrial	42	20	512	59717	9.22
25	Q99MZ8	LIM and SH3 domain protein 1	14	4	81	29951	6.61
26	Q07936	Annexin A2	64	19	925	38654	7.55
	P04797	Glyceraldehyde-3-phosphate dehydrogenase	34	8	198	35805	8.14
27	P04797	Glyceraldehyde-3-phosphate dehydrogenase	52	12	667	35805	8.14
	Q07936	Annexin A2	55	17	489	38654	7.55
	P36202	PDZ and LIM domain protein 4	5	2	38	35499	8.54
	P24329	Thiosulfate sulfurtransferase	16	5	32	33386	7.71

28	P04797	Glyceraldehyde-3-phosphate dehydrogenase	82	19	1361	35805	8.14
	P36202	PDZ and LIM domain protein 4	11	3	76	35499	8.54
	P04636	Malate dehydrogenase, mitochondrial	24	7	51	35661	8.93
30	P81155	Voltage-dependent anion-selective channel protein 2	3	1	60	31726	7.44
32	P13803	Electron transfer flavoprotein subunit alpha, mitochondrial	55	14	605	34929	8.62
	P81155	Voltage-dependent anion-selective channel protein 2	47	11	449	31726	7.44
33	Q9Z2L0	Voltage-dependent anion-selective channel protein 1	13	3	72	30737	8.62
34	Q9Z2L0	Voltage-dependent anion-selective channel protein 1	43	10	419	30737	8.62

[a] Swiss-Prot accession number.

[b] Calculated molecular weight.

[c] Calculated pI.

Proteins colored in red in this Table are commonly identified in immunoaffinity capture/LC-MS/MS (Supplementary Table S2).