

SUPPLEMENTARY TABLE S1A. RESULTS OF SINGLE STEP TANDEM AFFINITY PURIFICATIONS OF BOLA1

<i>GI</i>	<i>Peptides neg.</i>	<i>Peptides pos.</i>	<i>emPAI neg.</i>	<i>emPAI pos.</i>	<i>emPAI pos./neg.</i>	<i>Background peptides</i>	<i>Protein</i>
42516576	0	3	0	3.64	9999	0	Glutaredoxin 5
4826848	0	1	0	0.58	9999	1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5
11024700	0	1	0	0.46	9999	0	Translocase of inner mitochondrial membrane 13
4758788	0	2	0	0.35	9999	3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30 kDa (NADH-coenzyme Q reductase)
32483377	0	1	0	0.23	9999	15	Peroxiredoxin 3 isoform b
153791313	0	1	0	0.19	9999	0	Cytochrome oxidase deficient homolog 2
4503607	0	1	0	0.16	9999	2	Electron transfer flavoprotein, alpha polypeptide isoform a
11321583	0	1	0	0.10	9999	2	Succinate-CoA ligase, ADP-forming, beta subunit precursor
7705638	4	11	2.72	99	36.29	0	bolA-like 1
95113651	3	10	0.50	4.81	9.60	13	Glutaredoxin 3
32189392	1	3	0.25	0.99	3.84	17	Peroxiredoxin 2 isoform a
16596694	1	2	0.46	1.15	2.46	0	Mitochondrial ribosomal protein L53
183227678	1	1	0.33	0.77	2.33	31	Parkinson disease protein 7
171906593	2	3	0.31	0.71	2.31	4	Branched chain ketoacid dehydrogenase kinase isoform b
4507231	1	2	0.29	0.66	2.29	20	Single-stranded DNA binding protein 1
31542947	8	13	1.27	2.72	2.13	181	Chaperonin
46593007	1	2	0.11	0.24	2.11	1	Ubiquinol-cytochrome c reductase core protein I
21735621	3	5	0.43	0.83	1.89	63	Mitochondrial malate dehydrogenase precursor
155722983	5	8	0.40	0.71	1.78	38	TNF receptor-associated protein 1
4885079	2	3	0.42	0.70	1.64	13	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma subunit isoform H (heart) precursor
4757732	4	6	0.37	0.61	1.63	19	Programmed cell death 8 isoform 1
21361114	2	3	0.29	0.46	1.60	27	Solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11
4505773	6	7	1.37	2.16	1.57	77	Prohibitin
4758638	4	5	1.03	1.42	1.38	48	Peroxiredoxin 6
4502491	4	5	0.93	1.27	1.37	39	Complement component 1, q subcomponent binding protein precursor
47132595	4	5	0.66	0.89	1.34	32	Solute carrier family 25 member 3 isoform b precursor
11386135	14	15	5.06	6.40	1.26	33	Branched chain keto acid dehydrogenase E1, alpha polypeptide
70995211	5	5	1.25	1.58	1.26	17	Peroxisomal enoyl-coenzyme A hydratase-like protein
65506442	32	33	10.93	13.25	1.21	288	Propionyl-Coenzyme A carboxylase, alpha polypeptide isoform a precursor
32189394	8	8	0.93	1.09	1.17	118	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, beta subunit precursor
41872631	10	10	0.22	0.25	1.11	160	Fatty acid synthase
119943100	23	21	5.89	5.89	1	209	Propionyl Coenzyme A carboxylase, beta polypeptide
4557353	8	8	3.21	3.21	1	12	Branched chain keto acid dehydrogenase E1 beta polypeptide precursor
24234688	17	17	2.51	2.51	1	137	Heat shock 70 kDa protein 9 precursor
50345984	13	13	2.30	2.30	1	99	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit precursor
94538322	4	4	1.27	1.27	1	4	Hydroxyacyl glutathione hydrolase isoform 1
4505591	3	3	0.77	0.77	1	78	Peroxiredoxin 1
5453607	4	3	0.55	0.55	1	56	Chaperonin containing TCP1, subunit 7 isoform a
34147630	4	4	0.42	0.42	1	40	Tu translation elongation factor, mitochondrial precursor
4758504	2	2	0.42	0.42	1	25	Hydroxysteroid (17-beta) dehydrogenase 10 isoform 1
50592994	1	1	0.38	0.38	1	26	Thioredoxin

(continued)

SUPPLEMENTARY TABLE S1A. (CONTINUED)

<i>GI</i>	<i>Peptides neg.</i>	<i>Peptides pos.</i>	<i>emPAI neg.</i>	<i>emPAI pos.</i>	<i>emPAI pos./neg.</i>	<i>Background peptides</i>	<i>Protein</i>
13376007	1	1	0.25	0.25	1	0	Isochorismatase domain containing 2 isoform 2
13129148	1	1	0.25	0.25	1	0	Apolipoprotein O
8923390	1	1	0.23	0.23	1	3	Coiled-coil-helix-coiled-coil-helix domain containing 3
4557237	2	2	0.22	0.22	1	11	Acetyl-Coenzyme A acetyltransferase 1 precursor
38569421	4	4	0.18	0.18	1	31	ATP citrate lyase isoform 1
4502013	1	1	0.17	0.17	1	1	Adenylate kinase 2 isoform a
5031815	2	2	0.17	0.17	1	3	Lysyl-tRNA synthetase isoform 2
42476028	2	2	0.17	0.17	1	0	ATPase family, AAA domain containing 3A
21361565	1	1	0.15	0.15	1	8	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit B1 precursor

We generated HEK293 T-REx cells that inducibly express the proteins with a C-terminal TAP-tagged BOLA1. Cell lysates were affinity purified and eluates were analyzed using nanospray ionization liquid chromatography tandem mass spectrometry (nLC-MS/MS) to identify interacting proteins. The procedure was carried out without induction (neg.) as well as 24 h after antibiotic induction (pos.) of TAP-tagged protein. The list is limited to proteins in mitochondrial compendium (11). Background peptides denote number of peptides of the protein copurified with TAP-tagged control proteins. Proteins that were not copurified with control proteins and only copurified after antibiotic induction are marked with bold typeface. GI, Protein Genbank Identifier Accession; emPAI, exponentially modified Protein Abundance Index.