



Supplementary Materials

Salivary glands after prolonged aluminum exposure: proteomic approach underlying biochemical and morphological impairments in rats

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Table S1. Identified proteins with significant different status of regulation in the parotid glands of rats exposed to aluminum (Exposed group vs. Control group)

Accession ID ^a	Protein Name	PLGS	Fold
		Score	Change
P47942	Dihydropyrimidinase-related protein 2	67.84	15.64
P54708	Potassium-transporting ATPase alpha chain 2	32.04	14.15
Q64541	Sodium/potassium-transporting ATPase subunit alpha-4	32.04	14.15
Q05511	Serine protease hepsin	126.6	5.47
P07335	Creatine kinase B-type	161.62	5.16
Q68FR8	Tubulin alpha-3 chain	1011.09	5.16
P50398	Rab GDP dissociation inhibitor alpha	56.32	5.05
Q6P9V9	Tubulin alpha-1B chain	1190.77	4.85
Q9Z2L0	Voltage-dependent anion-selective channel protein 1	68.45	4.57
Q29RW1	Myosin-4	20.35	4.01
P00564	Creatine kinase M-type	69.39	3.9
P48675	Desmin	38.96	3.9
P11980	Pyruvate kinase PKM	183.96	3.42
P35704	Peroxiredoxin-2	130.15	3.35
P50399	Rab GDP dissociation inhibitor beta	65.89	3.32
P09117	Fructose-bisphosphate aldolase C	199.56	3.22
O35412	Signal-induced proliferation-associated 1-like protein 1	294.34	3.19
P07632	Superoxide dismutase [Cu-Zn]	148.7	3.16
P00507	Aspartate aminotransferase, mitochondrial	95.88	3.13

P10888	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	117.42	3.1
P11442	Clathrin heavy chain 1	46.33	2.8
P05065	Fructose-bisphosphate aldolase A	71.84	2.77
O88989	Malate dehydrogenase, cytoplasmic	171.18	2.69
P00406	Cytochrome c oxidase subunit 2	529.24	2.59
P0DP30	Calmodulin-2	166.25	2.56
P16617	Phosphoglycerate kinase 1	76.33	2.56
P0DP29	Calmodulin-1	166.25	2.53
P0DP31	Calmodulin-3	166.25	2.51
P11240	Cytochrome c oxidase subunit 5A, mitochondrial	277.53	2.51
P35213	14-3-3 protein beta/alpha	125.06	2.48
P68511	14-3-3 protein eta	125.06	2.48
P68255	14-3-3 protein theta	125.06	2.48
P61983	14-3-3 protein gamma	125.06	2.46
O70417	Prolactin-inducible protein homolog	2677.87	2.46
P48500	Triosephosphate isomerase	355.39	2.44
P21704	Deoxyribonuclease-1	3766.11	2.41
P62260	14-3-3 protein epsilon	206.65	2.29
P63102	14-3-3 protein zeta/delta	419.94	2.23
P45592	Cofilin-1	380.9	2.16
P11030	Acyl-CoA-binding protein	720.64	2.16
P04636	Malate dehydrogenase, mitochondrial	364.74	2.05
P06686	Sodium/potassium-transporting ATPase subunit alpha-2	57.33	2.03
P06687	Sodium/potassium-transporting ATPase subunit alpha-3	57.33	2.01
Q9ER34	Aconitate hydratase, mitochondrial	66.53	1.95
P17764	Acetyl-CoA acetyltransferase, mitochondrial	117.63	1.86
Q9ESV6	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific	86.11	1.82
P06685	Sodium/potassium-transporting ATPase subunit alpha-1	68.7	1.72

O88767	Protein/nucleic acid deglycase DJ-1	251.68	1.68
P15429	Beta-enolase	33.13	1.65
Q05962	ADP/ATP translocase 1	57.97	1.63
P63029	Translationally-controlled tumor protein	700.39	1.63
P50137	Transketolase	74.27	1.6
P19944	60S acidic ribosomal protein P1	599.01	1.57
Q06647	ATP synthase subunit O, mitochondrial	76.99	1.57
P04797	Glyceraldehyde-3-phosphate dehydrogenase	1694.24	1.54
Q5XI73	Rho GDP-dissociation inhibitor 1	105.87	1.54
P04642	L-lactate dehydrogenase A chain	110.59	1.52
Q6AY56	Tubulin alpha-8 chain	775.22	1.52
Q63471	BPI fold-containing family A member 2	3098.57	1.51
P56574	Isocitrate dehydrogenase [NADP], mitochondrial	123.58	1.48
Q6RY07	Acidic mammalian chitinase	10981.75	1.46
Q9WTT6	Guanine deaminase	108.74	1.43
P15999	ATP synthase subunit alpha, mitochondrial	460.83	1.4
P38983	40S ribosomal protein AS	409.09	1.38
P04764	Alpha-enolase	511.54	1.36
P63018	Heat shock cognate 71 kDa protein	775.94	1.35
P62083	40S ribosomal protein S7	477.82	1.32
P06761	Endoplasmic reticulum chaperone BiP	1280.33	1.32
Q6P9T8	Tubulin beta-4B chain	878.95	1.31
Q5XIF6	Endoplasmin	397.33	1.3
P62630	Elongation factor 1-alpha 1	2887.93	1.28
Q66HD0	Tubulin alpha-4A chain	993.58	1.26
P04906	Glutathione S-transferase P	242.17	1.25
Q63716	Peroxisredoxin-1	264.94	1.25
P85108	Tubulin beta-2A chain	818.22	1.25

Q4QRB4	Tubulin beta-3 chain	451.9	1.25
P18418	Calreticulin	120.36	1.22
P68370	Tubulin alpha-1A chain	1194.16	1.22
Q3KRE8	Tubulin beta-2B chain	814.85	1.22
P69897	Tubulin beta-5 chain	915.07	1.22
P63039	60 kDa heat shock protein, mitochondrial	74.89	1.21
P12020	Cysteine-rich secretory protein 1	7698.82	1.21
P0DMW0	Heat shock 70 kDa protein 1A	336.58	1.21
Q64057	Alpha-aminoadipic semialdehyde dehydrogenase	207.59	1.2
P62632	Elongation factor 1-alpha 2	1272.4	1.2
P0DMW1	Heat shock 70 kDa protein 1B	336.58	1.2
P55063	Heat shock 70 kDa protein 1-like	336.58	1.2
P04785	Protein disulfide-isomerase	341.37	1.19
P10719	ATP synthase subunit beta, mitochondrial	915.78	1.17
Q6AYZ1	Tubulin alpha-1C chain	1062.01	1.15
P10111	Peptidyl-prolyl cis-trans isomerase A	2191.43	1.11
Q6P6Q2	Keratin, type II cytoskeletal 5	133.48	-0.51
P00689	Pancreatic alpha-amylase	1733.1	-0.52
P32551	Cytochrome b-c1 complex subunit 2, mitochondrial	39.23	-0.54
Q6LED0	Histone H3.1	774.82	-0.6
P84245	Histone H3.3	774.82	-0.6
P02466	Collagen alpha-2(I) chain	138.73	-0.62
P0C0S7	Histone H2A.Z	3302.7	-0.66
Q6IE52	Murinoglobulin-2	97.41	-0.66
P02091	Hemoglobin subunit beta-1	16061.07	-0.7
P11517	Hemoglobin subunit beta-2	3174.66	-0.7
Q63279	Keratin, type I cytoskeletal 19	191.73	-0.71
Q64119	Myosin light polypeptide 6	303.88	-0.71

P02262	Histone H2A type 1	10690.25	-0.72
P0C169	Histone H2A type 1-C	10690.25	-0.72
P0C170	Histone H2A type 1-E	10690.25	-0.72
Q4FZT6	Histone H2A type 3	10690.25	-0.72
A9UMV8	Histone H2A.J	10690.25	-0.72
P68035	Actin, alpha cardiac muscle 1	7131.74	-0.73
P68136	Actin, alpha skeletal muscle	7057.67	-0.73
P62738	Actin, aortic smooth muscle	6437.13	-0.73
P63269	Actin, gamma-enteric smooth muscle	6437.13	-0.73
Q64598	Histone H2A type 1-F	10690.25	-0.73
P0CC09	Histone H2A type 2-A	10690.25	-0.73
Q00728	Histone H2A type 4	10690.25	-0.73
P60711	Actin, cytoplasmic 1	14760.75	-0.74
P63259	Actin, cytoplasmic 2	14760.75	-0.74
P02770	Serum albumin	10533.53	-0.74
Q00729	Histone H2B type 1-A	2677.81	-0.75
Q5BJY9	Keratin, type I cytoskeletal 18	1256.79	-0.76
P0CG51	Polyubiquitin-B	517.5	-0.78
Q10758	Keratin, type II cytoskeletal 8	2152.34	-0.79
Q63429	Polyubiquitin-C	517.5	-0.79
P12346	Serotransferrin	580.1	-0.79
P62982	Ubiquitin-40S ribosomal protein S27a	517.5	-0.79
P62986	Ubiquitin-60S ribosomal protein L40	517.5	-0.79
P20760	Ig gamma-2A chain C region	1255.75	-0.82
P01946	Hemoglobin subunit alpha-1/2	25408.2	-0.84
Q00715	Histone H2B type 1	14623.03	-0.89
P62804	Histone H4	12183.1	-0.89
Q641X9	39S ribosomal protein L9, mitochondrial	122.25	-

Q9JKL8	Activity-dependent neuroprotector homeobox protein	40.46	-
O89046	Coronin-1B	66.86	-
Q9JM01	Cyclin-dependent kinase-like 3	47.42	-
O35964	Endophilin-A2	82.8	-
Q499U2	Engulfment and cell motility protein 3	47.63	-
P31977	Ezrin	31.89	-
Q00960	Glutamate receptor ionotropic, NMDA 2B	28.32	-
D3ZIZ1	GRAM domain-containing 2A	66.87	-
D4A3K5	Histone H1.1	38.92	-
P15865	Histone H1.4	177.24	-
P06349	Histone H1t	177.24	-
P20762	Ig gamma-2C chain C region	63.41	-
P01836	Ig kappa chain C region, A allele	653.96	-
P20767	Ig lambda-2 chain C region	93.45	-
F1LZ52	Kelch-like protein 3	55.87	-
Q6IMF3	Keratin, type II cytoskeletal 1	79.27	-
Q6IG01	Keratin, type II cytoskeletal 1b	79.27	-
Q4FZU2	Keratin, type II cytoskeletal 6A	79.27	-
Q6IG04	Keratin, type II cytoskeletal 72	79.27	-
Q6AYL9	Kinetochore protein Nuf2	48.53	-
P30349	Leukotriene A-4 hydrolase	70.99	-
P30919	N(4)-(Beta-N-acetylglucosaminy)-L-asparaginase	65.27	-
O35260	Nucleus accumbens-associated protein 1	30.54	-
P24368	Peptidyl-prolyl cis-trans isomerase B	108.87	-
P21807	Peripherin	61.32	-
Q63945	Protein SET	206.16	-
P81128	Rho GTPase-activating protein 35	56.27	-
Q62868	Rho-associated protein kinase 2	46.84	-

Q9Z220	Testis-specific gene 10 protein	29.82	-
B5DEL3	Tetratricopeptide repeat protein 17	39.23	-
P63312	Thymosin beta-10	498.09	-
Q9EQS0	Transaldolase	128.06	-
Q5U2W5	Transducin beta-like protein 3	49.32	-
Q64350	Translation initiation factor eIF-2B subunit epsilon	58.14	-
D3ZFH6	UBX domain-containing protein 440S ribosomal protein S3a	56.11	-

^aAccession ID according to Uniprot.org database. Positive and negative values of fold change, indicate up and downregulated proteins, respectively. Results of the comparison between aluminum group and control group. Signs of - indicate absence expression in the exposed group.

Table S2. Identified proteins with significant different status of regulation in the submandibular glands of rats exposed to aluminum (Exposed group vs. Control group)

Accession ID ^a	Protein Name	<i>PLGS</i>	Fold
		Score	Change
P36375	Glandular kallikrein-10	374.62	1.43
P07647	Submandibular glandular kallikrein-9	321.87	1.42
P60711	Actin, cytoplasmic 1	153.3	1.14
P63259	Actin, cytoplasmic 2	153.3	1.14
P02091	Hemoglobin subunit beta-1	571.39	-0.55
P11517	Hemoglobin subunit beta-2	447.55	-0.59
P01946	Hemoglobin subunit alpha-1/2	1091.38	-0.6
Q64598	Histone H2A type 1-F	421.36	-0.69
P0C170	Histone H2A type 1-E	421.36	-0.7
Q4FZT6	Histone H2A type 3	421.36	-0.7
Q00728	Histone H2A type 4	421.36	-0.7
P62804	Histone H4	384.08	-0.75
O70417	Prolactin-inducible protein homolog	781.02	-0.88
P62246	40S ribosomal protein S15a	75.79	+

P04644	40S ribosomal protein S17	533.72	+
P62083	40S ribosomal protein S7	130.26	+
P38983	40S ribosomal protein SA	232.16	+
P63039	60 kDa heat shock protein, mitochondrial	51.94	+
P19944	60S acidic ribosomal protein P1	741.43	+
P23358	60S ribosomal protein L12	105.16	+
P17764	Acetyl-CoA acetyltransferase, mitochondrial	130.35	+
Q9ER34	Aconitate hydratase, mitochondrial	46.82	+
P11030	Acyl-CoA-binding protein	279.62	+
P15429	Beta-enolase	89.14	+
P18418	Calreticulin	69.26	+
P18886	Carnitine O-palmitoyltransferase 2, mitochondrial	39.64	+
P02454	Collagen alpha-1(I) chain	38.15	+
P25809	Creatine kinase U-type, mitochondrial	235.38	+
P07153	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	32.19	+
Q5XIL8	Dynein intermediate chain 1, axonemal	50.59	+
P13803	Electron transfer flavoprotein subunit alpha, mitochondrial	58.82	+
Q68FU3	Electron transfer flavoprotein subunit beta	115.73	+
P05197	Elongation factor 2	92.56	+
Q66HD0	Endoplasmin	49.99	+
P07323	Gamma-enolase	52.23	+
P09606	Glutamine synthetase	30.17	+
P04797	Glyceraldehyde-3-phosphate dehydrogenase	377.03	+
P63018	Heat shock cognate 71 kDa protein	62.79	+
P14659	Heat shock-related 70 kDa protein 2	37.44	+
Q6LED0	Histone H3.1	183.65	+
P84245	Histone H3.3	183.65	+
P5674	Isocitrate dehydrogenase [NADP], mitochondrial	109.56	+

Q6IG12	Keratin, type II cytoskeletal 7	202.32	+
O88989	Malate dehydrogenase, cytoplasmic	119.16	+
Q9R063	Peroxiredoxin-5, mitochondrial	118.02	+
P62963	Profilin-1	278.67	+
P11598	Protein disulfide-isomerase A3	58.71	+
Q62902	Protein ERGIC-53	139.98	+
P11980	Pyruvate kinase PKM	45.9	+
Q4QR99	Queuine tRNA-ribosyltransferase catalytic subunit 1	59.01	+
P50398	Rab GDP dissociation inhibitor alpha	32.99	+
P50399	Rab GDP dissociation inhibitor beta	42.49	+
Q6NYB7	Ras-related protein Rab-1A	174.7	+
Q5XI73	Rho GDP-dissociation inhibitor 1	210.91	+
P13432	SMR1 protein	299.2	+
Q66X93	Staphylococcal nuclease domain-containing protein 1	60.78	+
P68370	Tubulin alpha-1A chain	122.88	+
Q6P9V9	Tubulin alpha-1B chain	122.88	+
Q6AYZ1	Tubulin alpha-1C chain	122.88	+
Q68FR8	Tubulin alpha-3 chain	83.38	+
Q5XIF6	Tubulin alpha-4A chain	54.94	+
F1LNJ2	U5 small nuclear ribonucleoprotein 200 kDa helicase	20.79	+
Q6IG05	Keratin, type II cytoskeletal 75	36.89	-

^aAccession ID according to Uniprot.org database. Positive and negative values of fold change, indicate up and downregulated proteins, respectively. Results of the comparison between aluminum group and control group. Signs of + and - indicate exclusive or absence expression in the exposed group, respectively.



Table S3. Description of all analysis values of the study.

Analyze	Description of unit	Mean (Control)	Mean (AlCl ₃)	SD (Control)	SD (AlCl ₃)	SEM (Control)	SEM (AlCl ₃)	Power (1-β err prob)
ACAP - Parotid gland	% of control	100	57.79	23.79	15.16	8.993	5.73	98.85%
LPO - Parotid gland	% of control	100	140.4	15.87	22.07	5.612	9.011	98.76%
ACAP - Submandibular gland	% of control	100	36.9	21.64	21.01	8.179	7.941	100%
LPO - Submandibular gland	% of control	100	194.1	31.79	41.4	15.89	23.9	99.91%
Parenchyma - Parotid gland	μm ²	64563	58262	4525	2460	2613	1100	93.32%
Stroma - Parotid gland	μm ²	21980	28803	1098	1469	634.2	734.7	100%
Acini - Parotid gland	μm ²	62676	55020	5304	853.3	3062	426.7	98.08%
Ducts - Parotid gland	μm ²	2325	2159	1060	625.5	611.8	279.7	5.367%
Parenchyma - Submandibular gland	μm ²	69726	54543	3830	3830	1713	1564	100%
Stroma - Submandibular gland	μm ²	4941	24263	2457	3607	1099	1473	100%
Acini - Submandibular gland	μm ²	66660	50606	4158	4682	2079	1911	100%
Ducts - Submandibular gland	μm ²	3002	4022	571.9	625.1	285.9	255.2	92.68%

Table S3: Oxidative biochemistry assays (ACAP: Antioxidant Capacity Against Peroxyl Radicals and LPO: Lipid Peroxidation) and Morphometric analysis (Parenchyma, stroma, acini and ducts areas) values of the experimental study. Results are expressed as mean, SD: Standard deviation, SEM: Standard error of mean and Test Power (1-β error probability).