

Electronic Supplementary Information

Investigating the response of cuproproteins from oyster (*Crassostrea gigas*) after waterborne copper exposure by metallomic and proteomic approaches

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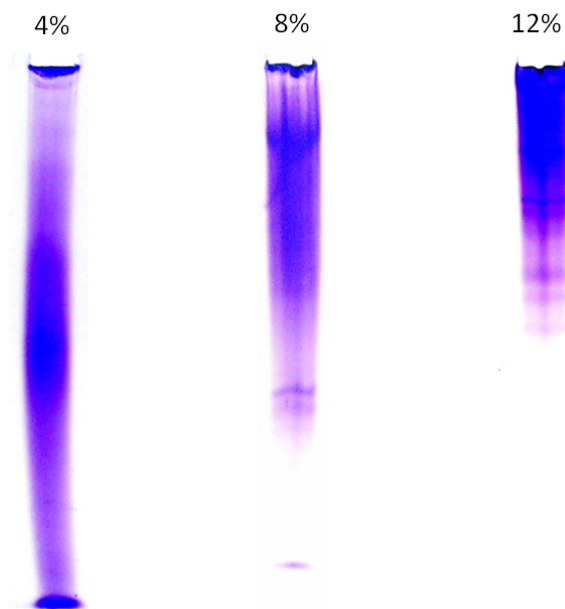


Fig. S1 Three polyacrylamide gels (4%, 8% and 12%) were compared for separating the digestive gland cytosols of oyster.

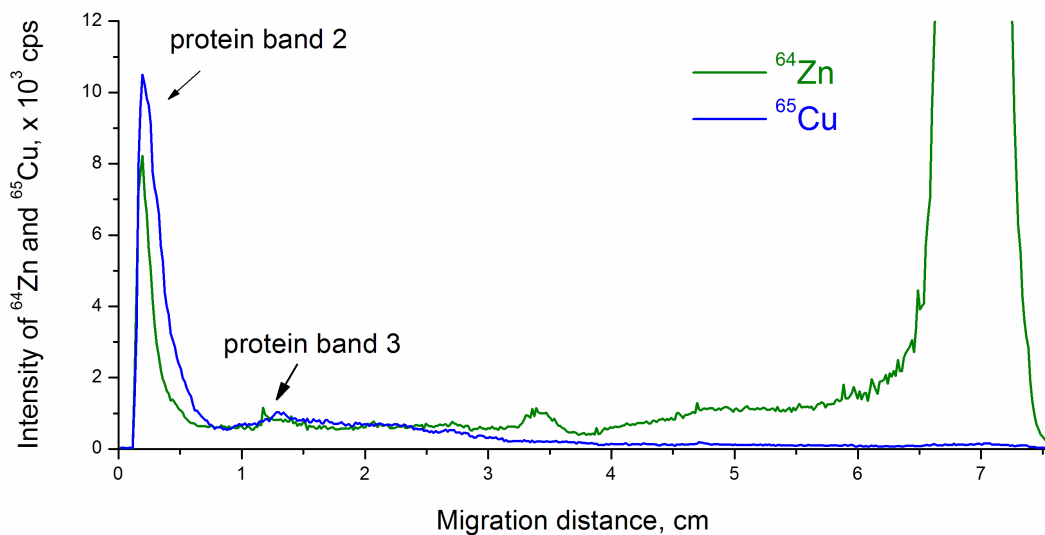


Fig. S2 ⁶⁵Cu and ⁶⁴Zn ND-PAGE-LA-ICP MS electropherograms of digestive gland cytosol from Cu-exposed oysters. The peaks marked with arrows respectively correspond to the protein band 2 and 3 in Fig. 3b and 3c. 8% polyacrylamide gel was used for separation.

Table S1. Proteins identified by ND-PAGE and μ RPC-ESI-MS/MS. ^a

Protein band ^b	No.	NCBI accession no.	Protein ^c	Score	Sequence coverage	Identified peptides
1	1	gi 405972837	Retinal dehydrogenase 1	246	22%	9
	2	gi 405964580	Actin	125	25%	9
	3	gi 405978782	Nucleoside diphosphate kinase B	123	21%	3
	4	gi 405970056	Kyphoscoliosis peptidase	104	15%	2
	5	gi 405956273	Amidase	49	9%	4
	6	gi 40643026	Ferritin	42	14%	2
	7	gi 405960663	Extracellular superoxide dismutase [Cu-Zn]	27	20%	2
2	1	gi 405972837	Retinal dehydrogenase 1	746	38%	25
	2	gi 405964580	Actin	638	42%	13
	3	gi 56603668	alpha-tubulin	162	12%	3
	4	gi 405962873	Filamin-C	130	4%	11
	5	gi 405960663	Extracellular superoxide dismutase [Cu-Zn]	117	13%	2
	6	gi 44885729	Arginine kinase	113	11%	2
	7	gi 53801335	beta-tubulin	100	11%	3
	8	gi 405961263	Phosphoenolpyruvate carboxykinase [GTP]	80	10%	5
	9	gi 405970056	Kyphoscoliosis peptidase	65	15%	2
	10	gi 46359620	Elongation factor 1 alpha	52	5%	2
	11	gi 4838561	Heat shock protein 70	50	4%	2
	12	gi 405975242	Calponin-2	41	3%	2
3	1	gi 405972837	Retinal dehydrogenase 1	959	40%	28
	2	gi 405957058	Glyceraldehyde 3-phosphate dehydrogenase	353	43%	12
	3	gi 405977320	Neural cell adhesion molecule 1	334	14%	10
	4	gi 405966217	Prostaglandin reductase 1	225	9%	3
	5	gi 405978782	Nucleoside diphosphate kinase B	222	28%	4

6	gi 405965686	Cell adhesion molecule 4	219	14%	4
7	gi 405970867	Enolase	192	4%	3
8	gi 405978716	Alpha-actinin, sarcomeric	177	8%	6
9	gi 405950795	Non-neuronal cytoplasmic intermediate filament protein	170	15%	8
10	gi 405956520	Putative aminopeptidase	167	15%	8
11	gi 405973112	Aspartate aminotransferase	159	30%	11
12	gi 405973252	Fructose-bisphosphate aldolase	157	33%	8
13	gi 405976102	Omega-crystallin	147	11%	2
14	gi 405970056	Kyphoscoliosis peptidase	137	10%	2
15	gi 405963822	UPF0663 transmembrane protein C17orf28	107	6%	4
16	gi 405965163	Beta-hexosaminidase subunit beta	104	14%	5
17	gi 405959834	Catalase	98	17%	3
18	gi 405964580	Actin	82	26%	8
19	gi 405971457	Natterin-3	78	42%	6
20	gi 405951523	Ubiquitin	69	34%	4
21	gi 405968187	L-ascorbate oxidase	64	4%	3
22	gi 405975242	Calponin-2	62	3%	2
23	gi 405966618	Carbonic anhydrase 2	60	6%	2
24	gi 4838561	Heat shock protein 70	59	3%	2
25	gi 405967652	Hypothetical protein CGI_10017178	45	4%	2

^a NCBI database; ^b Protein band in **Fig. 3**; ^c Taxonomy is restricted to *Crassostrea gigas*.