

Table S1. Protein identifications (using MS/MS) of spots changing with temperature acclimation in *Mytilus trossulus*

Spot ID	Protein ID	Estimated molecular weight (kDa)	Estimated pI	Predicted molecular weight (kDa)	Predicted pI	GenBank ID	Mascot score	Peptide matches	Sequence coverage(%)	Average volume (relative to 13°C)		Functional category
										7°C	19°C	
2	Hsp70	70	5.73	70	5.30	gil145885532	273	3	16	0.84	3.39	Molecular chaperone
5	mitochondrial Aldehyde dehydrogenase	57	5.59	56	6.70	gil58307245	89	2	9	1.16	0.29	Proteolysis/energy metabolism
8	Ubiquinol cytochrome <i>c</i> reductase	49	5.72	48	5.93	gil223027244	182	4	23	0.54	2.46	Energy metabolism
12	$\beta$ -Tubulin	53	5.12	43	5.76	gil164592164	228	5	17	0.95	1.66	Cytoskeletal
13	$\beta$ -Tubulin	54	5.13	43	5.76	gil164592164	314	8	25	0.94	1.80	Cytoskeletal
14	$\beta$ -Tubulin	50	5.00	43	5.76	gil164592164	304	7	22	0.89	2.35	Cytoskeletal
15	$\alpha$ -Tubulin	67	5.18	58	4.90	gil238782438	486	7	27	1.37	2.48	Cytoskeletal
16	$\alpha$ -Tubulin	66	5.24	58	4.90	gil238782438	404	5	19	0.90	2.86	Cytoskeletal
17	$\beta$ -Tubulin	53	4.95	43	5.76	gil164592164	196	4	17	0.55	1.38	Cytoskeletal
18	Hsp25	57	5.69	22	6.52	gil212814271	115	2	9	1.08	0.45	Molecular chaperone
24	$\beta$ -Tubulin	51	5.59	54	4.92	gil145890511	181	4	12	1.39	5.39	Cytoskeletal
25	Ubiquinol cytochrome <i>c</i> reductase	50	5.4	48	9.00	gil212817136	68	2	4	1.14	2.91	Proteolysis/energy metabolism
27	Heavy metal binding protein	37	5.31	27	5.00	gil58308171	152	2	13	0.68	0.65	Unspecified
28	Hsp25	31	5.26	22	6.52	gil212814271	108	2	9	0.53	0.49	Molecular chaperone
32	Dyp-type peroxidase	35	6.48	42	7.00	gil145886780	95	3	12	0.59	2.56	Energy metabolism
36	Quinoid dihydropteridine reductase	31	6.62	25	6.58	gil212827262	116	3	10	0.88	0.25	Energy metabolism
37	Dyp-type peroxidase	33	6.49	42	7.00	gil145886780	111	3	12	1.06	0.30	Energy metabolism
40	Hsp25	33	6.31	22	6.52	gil212814271	82	2	9	1.08	2.82	Molecular chaperone
43	Hsc71	76	5.33	71	5.29	gil212816159	79	5	16	1.12	0.40	Molecular chaperone
45	Gelsolin	49	6.16	42	5.22	gil149382505	228	3	17	1.69	8.44	Cytoskeletal
52	Hsp70	60	5.98	70	5.30	gil145885532	170	2	10	1.10	0.26	Molecular chaperone
54	Tektin-3	53	5.9	57	7.22	gil212812350	98	2	13	1.04	0.53	Cytoskeletal
55	Ubiquinol cytochrome <i>c</i> reductase	47	5.81	48	5.93	gil223027244	182	4	23	0.60	1.86	Proteolysis/energy metabolism
58	Ubiquinol cytochrome <i>c</i> reductase	49	5.95	48	5.93	gil223027244	89	2	13	1.20	3.46	Proteolysis/energy metabolism
59	$\beta$ -Actin	49	5.88	39	5.80	gil49868	92	2	7	0.57	3.06	Cytoskeletal

60	Radial spoke head 9	38	6.07	31	4.97	gil223025866	78	2	9	0.78	0.38	Unspecified
61	$\beta$ -Actin	50	5.82	39	5.80	gil49868	154	4	15	0.81	0.37	Cytoskeletal
67	$\alpha$ -Tubulin	47	5.41	58	4.90	gil238782438	404	5	19	1.59	0.56	Cytoskeletal
68	Isocitrate dehydrogenase (NADP)	45	6.61	51	7.91	gil223026036	178	4	18	1.41	1.30	Energy metabolism
73	Isocitrate dehydrogenase (NADP)	44	6.49	51	7.91	gil223026036	77	3	13	1.79	1.14	Energy metabolism
76	78kD glucose regulated protein	88	6.48	73	5.00	gil46359618	73	2	3	2.44	0.88	Unspecified
78	$\beta$ -Tubulin	57	4.79	43	5.69	gil58307872	151	5	23	1.10	0.37	Cytoskeletal
79	78kD glucose regulated protein	89	4.85	73	5.00	gil238639954	245	4	24	0.88	2.53	Unspecified

pI, isoelectric point.

Table S2. Protein identifications (using MS/MS) of spots changing with temperature acclimation in *Mytilus galloprovincialis*

Spot ID	Protein ID	Estimated molecular weight (kDa)	Estimated pI	Predicted molecular weight (kDa)	Predicted pI	GenBank ID	Mascot score	Peptide matches	Sequence coverage (%)	Average volume (relative to 13°C)		Functional category
										7°C	19°C	
2	Prohibitin	30	5.43	30	5.30	gi 238643256	211	5	17	0.99	0.25	Molecular chaperone
4	Carbonyl reductase	31	5.18	30	8.50	gi 145883693	59	2	8	0.75	0.28	Energy metabolism
9	NADH dehydrogenase	28	4.75	24	5.74	gi 223028674	43	2	14	0.55	0.25	Energy metabolism
11	Actin	29	5.55	42	5.30	gi 212814343	104	4	19	0.61	0.30	Cytoskeletal
12	Hsp21	34	5.52	21	6.70	gi 238642855	107	3	16	0.48	0.22	Molecular chaperone
26	Succinate dehydrogenase (Ubiquinone)	66	5.89	72	6.70	gi 18426858	80	3	5	0.39	4.08	Energy metabolism
30	$\alpha$ -Tubulin	56	5.08	57	5.00	gi 145887917	233	5	18	0.45	0.64	Cytoskeletal
34	Selenium binding protein-1	55	5.78	54	6.50	gi 58307672	51	2	11	1.09	0.57	Unspecified
37	$\alpha$ -Tubulin	53	4.94	58	4.90	gi 238782438	260	6	25	0.37	0.38	Cytoskeletal
38	$\alpha$ -Tubulin	56	5	57	5.00	gi 145887917	238	5	15	0.33	0.48	Cytoskeletal
39	$\alpha$ -Tubulin	56	4.98	57	5.00	gi 145887917	159	5	15	0.47	0.16	Cytoskeletal
41	$\alpha$ -Tubulin	55	5.16	57	5.00	gi 212817436	204	5	18	0.35	0.37	Cytoskeletal
44	$\alpha$ -Tubulin	55	5.03	53	5.00	gi 58307555	89	2	13	0.30	0.19	Cytoskeletal
45	$\alpha$ -Tubulin	53	4.82	47	5.23	gi 154349830	158	3	12	0.75	0.19	Cytoskeletal
46	$\beta$ -Tubulin	53	4.85	43	5.76	gi 164592164	180	6	17	0.44	0.04	Cytoskeletal
48	$\alpha$ -Tubulin	53	4.88	47	5.23	gi 154349830	202	3	12	0.35	0.22	Cytoskeletal
52	$\beta$ -Tubulin	53	4.73	54	4.92	gi 145890511	95	4	8	0.73	0.29	Cytoskeletal
54	$\beta$ -Tubulin	52	5.03	54	4.90	gi 145890511	124	4	12	0.35	1.25	Cytoskeletal
55	Ubiquinol cytochrome <i>c</i> reductase	52	5.74	53	5.40	gi 145883486	56	2	9	0.19	5.51	Energy metabolism
56	Tropomyosin	51	5.1	33	4.70	gi 14285796	167	6	15	0.40	6.03	Cytoskeletal
58	Intermediate filament	51	5.16	71	5.40	gi 212812257	53	3	16	0.42	6.61	Cytoskeletal
59	ATP synthase $\beta$ -subunit	50	4.84	57	5.38	gi 212812392	490	8	42	0.40	0.61	Energy metabolism
62	Mitochondrial aldehyde dehydrogenase	50	5.56	56	6.70	gi 58307245	74	2	9	0.63	12.55	Energy metabolism
66	$\beta$ -Tubulin	49	4.97	43	5.80	gi 164592164	247	7	17	0.40	7.95	Cytoskeletal
75	Isocitrate dehydrogenase (NADP)	46	6.79	51	7.91	gi 223026036	102	3	13	8.33	4.67	Energy metabolism
77	Actin	45	5.24	42	5.30	gi 145892505	78	5	13	0.95	0.50	Cytoskeletal
78	Ubiquinol cytochrome <i>c</i> reductase	46	5.68	53	5.40	gi 164595882	80	3	9	1.59	13.13	Energy metabolism
87	Actin	43	5.22	42	5.30	gi 212827318	210	4	18	0.73	4.15	Cytoskeletal
88	Actin	43	5.27	42	5.30	gi 212827318	166	4	18	0.66	3.52	Cytoskeletal
89	Actin	43	5.41	42	5.30	gi 212827318	185	4	18	0.20	2.04	Cytoskeletal
93	$\alpha$ -Tubulin	39	5.39	58	4.90	gi 238782438	261	7	29	0.71	5.44	Cytoskeletal
103	$\beta$ -Tubulin	36	5.36	43	5.80	gi 164592164	151	6	22	0.88	2.96	Cytoskeletal
106	Radial spoke head 9	36	5.98	31	4.97	gi 223025866	250	6	29	1.49	0.49	Unspecified
113	Esterase D/formylglutathione	33	6.42	31	6.00	gi 223022457	67	2	12	0.18	0.16	Energy metabolism

hydrolase												
120	β-Tubulin	32	4.9	43	5.80	gil164592164	185	6	20	1.01	0.22	Cytoskeletal
123	Fibrinogen related domain	31	6.79	27	6.10	gil154349256	75	3	7	4.35	3.39	Cytoskeletal
124	Hsp21	31	5.85	21	6.70	gil238642855	226	4	28	1.25	0.14	Molecular chaperone
125	Proteasome α-type-4	32	6.26	30	6.90	gil164594998	65	2	9	2.17	1.22	Protein degradation
126	Cyclophilin 3	30	6.74	27	5.10	gil145882165	186	5	15	4.76	5.57	Cytoskeletal
128	Proteasome α-type-6	30	6.31	27	6.35	gil212811956	111	2	9	1.28	0.41	Protein degradation
132	T complex protein-1	29	6.2	53	5.46	gil212817064	54	2	9	1.19	0.04	Unspecified
133	Mitochondrial aldehyde dehydrogenase	28	6.48	56	6.69	gil58307245	58	2	9	1.35	0.26	Energy metabolism
135	Thioredoxin peroxidase	26	6.63	32	5.50	gil145895058	89	4	12	2.56	0.33	Energy metabolism
141	Prolyl 4-hydroxylase β-subunit precursor	56	4.55	57	4.80	gil212815598	73	2	9	0.84	0.44	Energy metabolism
143	ATP synthase β-subunit	48	4.83	57	5.40	gil212812392	306	7	32	0.85	4.44	Energy metabolism
144	Major Vault Protein	108	5.73	96	5.70	gil223026493	61	3	13	2.78	1.61	Unspecified
145	Pyruvate dehydrogenase	35	5.45	39	5.80	gil58307688	44	2	3	1.02	0.58	Energy metabolism
146	Actin	41	5.01	42	5.30	gil145892505	252	6	21	0.44	0.49	Cytoskeletal

pI, isoelectric point.