

Table S1. ESTs (TCs and singletons) from *Fucus* EST libraries representing genes putatively involved in cellular stress responses, based on homology with genes in the UniProt database (see text for details). The identity of the contig or EST read, number of sequence reads comprising the contig, and its total length in base pairs are shown. The identity of the gene product, an indication of its function, as well as the E-value and UniProt accession of the best hit (Blastx) are also indicated.

a) *Fucus serratus*; heat shock - recovery (FsHS)

TC/EST	Reads	Length (bp)	Description (Blastx vs SP)	function/pathway	Evalue	SP Accession
tc_00430	35	1228	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	1.00E-16	P27396
tc_00428	8	1076	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	3.00E-17	Q84J50
tc_00429	21	992	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	2.00E-09	Q84J50
tc_00435	4	788	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	1.00E-07	Q84J50
tc_00437	35	1259	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	1.00E-16	Q84J50
tc_00439	2	1035	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	5.00E-15	Q84J50
tc_00426	33	1226	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	7.00E-18	Q84Q72
tc_00427	20	1441	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	2.00E-18	Q84Q72
tc_00432	40	1138	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	1.00E-18	Q84Q72
tc_00434	55	1491	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	1.00E-18	Q84Q72
tc_00436	53	1591	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	1.00E-19	Q84Q72
tc_00438	22	1155	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	7.00E-18	Q84Q77
g1raP02H22	1	401	Chaperonin CPN60, mitochondrial (HSP60)	molecular chaperone, GroL family	3.10E-27	P29197
g1repP05K10	1	851	Heat shock 70 kDa protein	molecular chaperone, Hsp70 superfamily	4.00E-134	P41753
tc_00696	5	1078	Heat shock 70 kDa protein, Hsp70	molecular chaperone, Hsp70 superfamily	5.00E-44	P41753
tc_00447	58	2214	Chaperone protein dnaK	molecular chaperone, Hsp70 superfamily	0	Q8DI58
tc_00552	7	1198	Luminal-binding protein 3 (BiP 3)	molecular chaperone, Hsp70 superfamily	1.00E-13	Q03683
gftP07114	1	604	Heat shock protein 90	molecular chaperone, Hsp90 family	4.00E-17	O44001
tc_00597	6	1259	Heat shock-like 85 kDa protein	molecular chaperone, Hsp90 family	7.00E-13	P06660
tc_00870	2	991	Heat shock-like 85 kDa protein	molecular chaperone, Hsp90 family	5.00E-24	P06660
tc_00443	51	2089	Heat shock protein 81-2 (HSP81-2)	molecular chaperone, Hsp90 family	5.00E-163	Q69QQ6
gftP03O21	1	471	Heat shock protein 75 kDa; mitochondrial precursor	molecular chaperone, Hsp90 family	4.00E-21	Q9CQN1
tc_00718	3	1051	Heat shock protein STI	mediates the association of HSC70 and HSP90	4.90E-41	Q43468
tc_00700	4	1028	Eukaryotic translation initiation factor 3	66 kDa tyrosine-rich heat shock protein	6.00E-22	Q8QZY1
g1raP07H01	1	876	Chaperone clpB, Hsp104 family	stress-induced chaperone	8.40E-40	O87444
g1raP05P10	1	618	Chaperone clpB, Hsp104 family	stress-induced chaperone	1.40E-43	Q8YM56
tc_00598	7	1475	ATP-dependent Clp protease ATP-binding subunit	degradation of denatured proteins in the chloroplast	2.00E-142	Q9TM05

g1raP01L10	1	839	ATP-dependent Clp protease, ClpP1	degradation of misfolded proteins	1.50E-55	Q8YXH5
g1raP05C08	1	749	BoIA-like protein 1	Stress-induced protein	4.10E-06	Q5RCE5
g1raP06A15	1	582	Tetratricopeptide repeat protein 1	stress-inducible co-chaperone	4.00E-31	Q91Z38
tc_00452	29	1461	Peptidyl-prolyl cis-trans isomerase (Cyclophilin)	accelerates the folding of proteins	7.00E-28	P34790
tc_00522	8	930	Peptidyl-prolyl cis-trans isomerase (Cyclophilin)	accelerates the folding of proteins	2.00E-51	P21569
tc_00596	5	1143	Peptidyl-prolyl cis-trans isomerase (FKBP)	accelerates the folding of proteins	1.00E-16	O42993
tc_00912	2	430	Peptidyl-prolyl cis-trans isomerase (Cyclophilin)	accelerates the folding of proteins	3.00E-35	P62937
tc_00969	2	1004	Peptidyl-prolyl cis-trans isomerase (FKBP)	accelerates the folding of proteins	2.00E-24	P31106
tc_00733	3	699	Glutaredoxin	cellular redox regulation, response to oxidative stress	1.00E-16	P55143
tc_00544	7	1042	Protein SYM1	cellular response to stress, mitochondria	1.00E-12	Q4P9K6
tc_00517	10	1738	Protein SYM1	cellular response to stress, mitochondria	3.00E-14	Q6BMY0
tc_00720	3	713	Protein SYM1	cellular response to stress, mitochondria	4.00E-23	Q7SCY7
g1raP05B18	1	708	2-cys peroxiredoxin BAS1, chloroplast precursor	cellular redox regulation, response to oxidative stress	5.00E-43	Q96468
gftP02C08	1	316	2-cys peroxiredoxin BAS1, chloroplast precursor	cellular redox regulation, response to oxidative stress	3.00E-33	Q9C5R8
gftP07A08	1	602	Peroxiredoxin Q, chloroplast precursor	cellular redox regulation, response to oxidative stress	8.00E-09	Q9MB35
g1raP07G04	1	803	Glutaredoxin-1	multifunctional, resistance to reactive oxygen species	1.10E-10	P25373
g1raP07H07	1	767	Glutaredoxin	multifunctional, resistance to reactive oxygen species	2.20E-18	P55143
gftP01119	1	353	Superoxide dismutase [Fe]	destroys superoxide radicals	2.00E-23	O15905
g1raP02O23	1	529	Superoxide dismutase [Mn]	destroys superoxide radicals	8.60E-24	Q42684
tc_00464	19	1561	Actin-depolymerizing factor, putative	actin-depolymerizing protein	2.00E-25	Q6EUH7
g1raP02J17	1	295	Polyubiquitin, Ubb	post-translational modification	1.70E-22	P22589
g1raP02P01	1	581	Ubiquitin	post-translational modification	5.30E-23	P22589
g1repP04E06	1	402	Ubiquitin	post-translational modification	1.30E-12	P46574
tc_00787	3	488	Ubiquitin	post-translational modification	2.00E-09	P61862
tc_00632	4	676	ubiquitin/60S ribosomal protein L40 fusion protein	post-translational modification	6.00E-32	-
tc_00590	5	892	ubiquitin/40S ribosomal protein S27a fusion	post-translational modification	4.00E-21	-
g1repP05E17	1	444	Ubiquitin-conjugating enzyme E2	Protein modification; protein ubiquitination	9.50E-64	P46595
tc_01027	2	681	RING-box protein pip1	component of E3 ubiquitin ligase SCF complexes	2.00E-27	O13959
g1raP03D17	1	808	ADP-ribosylation factor 1	ADP-ribosyltransferase	1.60E-86	P36397
tc_00707	3	774	Cell division protease ftsH homologue	ATP-dependent zinc metallopeptidase	6.00E-08	P72991
tc_00484	14	1758	Glyceraldehyde-3-phosphate dehydrogenase, chloroplastic	carbohydrate biosynthesis; Calvin cycle	6.00E-110	O09452
tc_00528	7	719	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	carbohydrate degradation; glycolysis	2.00E-39	P34923

g1raP03A20	1	606	Phosphoglycerate kinase	carbohydrate degradation; glycolysis	5.80E-36	Q7U3V0
g1repP02P15	1	580	Phosphoglycerate kinase	carbohydrate degradation; glycolysis	2.60E-30	Q7U3V0
g1raP05A15	1	645	Phosphoglycerate kinase	carbohydrate degradation; glycolysis	3.80E-52	Q8DGP7
tc_00830	2	877	NADH-ubiquinone oxidoreductase 20 kDa subunit	mitochondrial membrane respiratory chain	4.00E-22	Q42577
tc_00717	3	1018	Zeaxanthin epoxidase	carotenoid biosynthesis, xanthophyll cycle (photoprotection)	8.00E-44	(via Fves)
tc_00913	2	737	Glutamate-1-semialdehyde 2,1-aminomutase	chlorophyll biosynthesis	3.00E-66	Q39566
tc_00472	18	1173	Histone H3	core component of nucleosome, transcription regulation, etc	7.00E-65	P02299
tc_00667	6	1367	Histone H2A	core component of nucleosome, transcription regulation, etc	2.00E-35	P40282
g1raP05G21	1	848	Probable ATP-dependent RNA helicase	post-transcriptional gene expression	4.00E-100	Q9UJV9
gftP04F01	1	638	26S proteasome non-ATPase regulatory subunit 14	degradation of ubiquitinated proteins	1.00E-69	O00487
g1raP01L09	1	849	ADP;ATP carrier protein (ADP/ATP translocase)	ADP/ATP exchange across the mitochondrial inner membrane	2.70E-60	P31692
tc_00470	16	1063	Translationally-controlled tumor protein	involved in calcium binding and microtubule stabilization	7.00E-24	P35681
g1repP01C18	1	531	Isocitrate dehydrogenase [NADP]	oxidoreductase	1.60E-53	O75874
gftP07C08	1	479	Splicing factor 3B subunit 1	pre-mRNA-splicing factor	2.00E-57	O75533
gftP02B10	1	476	Elongation factor 1-alpha (EF-1-alpha)	protein biosynthesis	7.00E-39	P90519
tc_00595	5	1349	14-3-3-like protein	protein-protein interactions, multifunctional chaperone	7.00E-78	Q39757
gftP03C01	1	609	14-3-3-like protein	protein-protein interactions, multifunctional chaperone	6.00E-46	Q39757
g1raP01N13	1	765	Cysteine desulfurase; mitochondrial precursor	removal of sulphur from cysteine to produce alanine	2.60E-27	Q9Y697
g1raP05O11	1	552	40S ribosomal protein S8	ribonucleoprotein	1.10E-64	Q9FIF3
tc_00907	2	692	Lactoylglutathione lyase	secondary metabolite metabolism	3.00E-52	Q6P7Q4
g1repP03G17	1	464	Probable aquaporin	transport of H2O and neutral solutes across cell membranes	5.70E-25	Q651D5

b) *Fucus serratus*; Desiccation – rehydration

Contig/EST	Reads	Length (bp)	Description (Blastx vs SP)	function/pathway	Evalue	Accession
fdfucP05G15	1	469	Luminal-binding protein 3 (BiP 3)	molecular chaperone, Hsp70 family	4.00E-35	P22010
fdfucP04P02	1	400	Chaperone protein dnaK2	molecular chaperone, Hsp70 family	2.00E-46	Q8DI58
tc_00021	7	907	Heat shock protein 81-1	molecular chaperone, Hsp90 family	2.00E-64	A2YWQ1
fdfucP02B16	1	576	T-complex protein 1 subunit delta	molecular chaperone; assists the folding of proteins	2.00E-22	Q9NB32
tc_00149	2	929	ATP-dependent Clp protease ATP-binding subunit	degradation of denatured proteins in the chloroplast	1.00E-100	Q9TM05
tc_00032	6	776	Peptidyl-prolyl cis-trans isomerase (FKBP)	accelerates the folding of proteins	1.00E-15	O42993
tc_00076	3	675	Peptidyl-prolyl cis-trans isomerase (Cyclophilin)	accelerates the folding of proteins	2.00E-11	P34790
tc_00192	2	622	Peptidyl-prolyl cis-trans isomerase (Cyclophilin)	accelerates the folding of proteins	1.00E-15	P52009

fdfucP01M05	1	441	Stress protein DDR48	induced by DNA lesions or heat-shock stress	2.00E-07	P18899
fdfucP03P13	1	591	Serine/threonine-protein kinase Chk1	response to DNA damage, cell cycle arrest	2.00E-18	Q8AYC9
fdfucP07K14	1	402	Protein grpE (HSP-70 cofactor)	response to hyperosmotic and heat shock, thermosensor	6.00E-15	Q59978
fdfucP07O04	1	566	T-complex protein 1 subunit epsilon	assists the folding of proteins	8.00E-55	O04450
fdfucP03J20	1	596	Glutaredoxin-1	cellular redox regulation, response to oxidative stress	6.00E-11	P25373
fdfucP04P11	1	629	Putative peroxiredoxin ycf42	cellular redox regulation, response to oxidative stress	1.00E-70	P51272
fdfucP07L09	1	570	Putative peroxiredoxin ycf42	cellular redox regulation, response to oxidative stress	1.00E-35	P51272
fdfucP02G02	1	612	2-cys peroxiredoxin BAS1, chloroplast precursor	cellular redox regulation, response to oxidative stress	7.00E-25	Q96291
fdfucP02G12	1	600	2-cys peroxiredoxin BAS1, chloroplast precursor	cellular redox regulation, response to oxidative stress	4.00E-20	Q96291
fdfucP06B08	1	626	2-cys peroxiredoxin BAS1, chloroplast precursor	cellular redox regulation, response to oxidative stress	1.00E-20	Q96291
tc_00025	7	1293	Protein SYM1	cellular response to stress, mitochondria	2.00E-14	Q6BMY0
fdfucP05K14	1	566	Protein SYM1	cellular response to stress, mitochondria	5.00E-22	Q7SCY7
fdfucP03N20	1	448	Superoxide dismutase [Fe]	destroys superoxide radicals	3.00E-23	O15905
fdfucP05P05	1	558	Superoxide dismutase [Fe]	destroys superoxide radicals	7.00E-34	O15905
fdfucP05F10	1	533	ubiquitin/60S ribosomal protein L40 fusion protein	post-translational modification	2.00E-21	-
fdfucP07C12	1	533	ubiquitin/40S ribosomal protein S27a fusion	post-translational modification	4.00E-08	-
tc_00222	2	721	Ubiquitin	post-translational modification	3.00E-15	P13117
fdfucP04F08	1	414	Ubiquitin	post-translational modification	1.00E-13	P23398
tc_00070	4	850	Histone H3	core component of nucleosome, transcription regulation, etc	1.00E-54	P02299
tc_00009	11	1007	Translationally-controlled tumor protein homologue	Involved in calcium binding and microtubule stabilization	4.00E-22	P35681
fdfucP05I21	1	512	Adenosylhomocysteinase	Amino-acid biosynthesis; homocysteine biosynthesis	2.00E-49	Q9SP37
fdfucP03L09	1	599	Mg-protoporphyrin IX monomethyl ester cyclase	chlorophyll biosynthesis	4.00E-19	Q1XDK9
tc_00059	4	1052	Glyceraldehyde-3-phosphate dehydrogenase, chloroplastic	carbohydrate biosynthesis; Calvin cycle	4.00E-47	O09452

c) *Fucus vesiculosus*; Desiccation – rehydration

Contig/EST	Reads	Length (bp)	Description (Blastx vs SP)	function/pathway	Value	Accession
g5_P11B21	1	757	Heat shock cognate protein 80	molecular chaperone, Hsp90 family	4.50E-93	P36181
g5_P01N12	1	774	Small heat shock protein (HSP20) family	molecular chaperone, Hsp20 family	8.50E-18	P19243
tc_00462	2	860	Heat shock protein 90	molecular chaperone, Hsp90 family	3.20E-16	O44001
g5_P15E07	1	536	T-complex protein 1 subunit epsilon	Molecular chaperone; assists the folding of proteins	9.60E-34	O04450
g5_P04K06	1	477	T-complex protein 1 subunit delta	molecular chaperone; assists the folding of proteins	2.90E-22	Q9NB32
g5_P10C23	1	787	BolA-like protein 1	stress-induced protein	2.90E-05	Q9Y3E2

g5_P07B06	1	614	ATP-dependent Clp protease ATP-binding subunit	degradation of denatured proteins in the chloroplast	1.10E-37	Q9TM05
g5_P03F16	1	653	ATP-dependent Clp protease proteolytic subunit	degradation of misfolded proteins	1.30E-18	Q8YXH5
tc_00470	2	826	ATP-dependent Clp protease proteolytic subunit	degradation of misfolded proteins	2.30E-28	Q9L4P4
tc_00092	8	1295	Peptidyl-prolyl cis-trans isomerase (FKBP)	accelerates the folding of proteins	3.60E-26	O42993
tc_00174	4	795	Peptidyl-prolyl cis-trans isomerase (Cyclophilin)	accelerates the folding of proteins	1.60E-38	P52009
tc_00373	2	793	Peptidyl-prolyl cis-trans isomerase (rotamase)	accelerates the folding of proteins	1.50E-20	Q9LEK8
tc_00372	2	1086	ATP-dependent hsl protease ATP-binding subunit	Chaperone subunit of a proteasome-like degradation complex	8.30E-10	Q73NE3
g5_P14L09	1	494	Peroxiredoxin-6	cellular redox regulation, response to oxidative stress	2.00E-05	O08709
g5_P10K23	1	846	Glutaredoxin-1	cellular redox regulation, response to oxidative stress	3.50E-07	P25373
tc_00103	8	951	Glutaredoxin	cellular redox regulation, response to oxidative stress	1.60E-27	P55143
tc_00124	6	1027	Putative peroxiredoxin	cellular redox regulation, response to oxidative stress	1.90E-13	P73728
tc_00238	3	791	Superoxide dismutase [Cu-Zn]	destroys superoxide radicals	1.70E-37	P81926
tc_00034	15	606	ubiquitin/40S ribosomal protein S27a fusion	post-translational modification	1.00E-16	-
tc_00055	11	702	ubiquitin/60s ribosomal protein L40 fusion	post-translational modification	2.90E-35	-
g5_P13I09	1	705	Ubiquitin	post-translational modification	1.50E-34	P14624
g5_P11I07	1	909	Ubiquitin	post-translational modification	2.90E-23	P22589
tc_00138	4	618	Ubiquitin	post-translational modification	6.50E-30	P22589
tc_00260	6	1047	Ubiquitin	post-translational modification	2.40E-35	P22589
tc_00365	2	575	Ubiquitin	post-translational modification	6.10E-25	P22589
tc_00409	2	928	Ubiquitin-like protein precursor	post-translational modification	8.00E-08	Q05120
g5_P14N08	1	428	Ubiquitin precursor	post-translational modification	1.90E-10	Q8SWD4
g5_P01E12	1	670	Peroxisomal membrane protein 2	pore-forming, peroxisomal membrane permeability	2.60E-14	Q9NR77
g5_P10M15	1	837	Peroxisomal membrane protein 2	pore-forming, peroxisomal membrane permeability	3.50E-20	Q9NR77
tc_00021	19	1292	Histone H3	core component of nucleosome, transcription regulation, etc	9.70E-40	P22843
tc_00387	2	646	Histone H4	core component of nucleosome, transcription regulation, etc	4.00E-25	Q9U7D0
tc_00128	5	886	Glyceraldehyde-3-phosphate dehydrogenase, chloroplastic	carbohydrate biosynthesis; Calvin cycle	1.70E-12	O09452
tc_00082	8	821	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	carbohydrate degradation; glycolysis	4.10E-34	P49644
tc_00075	8	1183	14-3-3-like protein	protein-protein interactions, multifunctional chaperone	2.30E-45	Q39757
tc_00192	4	753	Cysteine desulfurase, mitochondrial	removal of sulphur from cysteine to produce alanine	1.10E-19	Q9Y697
g5_P10C17	1	865	GrpE protein homologue, mitochondrial	translocation of transit peptide-containing proteins	5.00E-09	Q75C01
tc_00011	24	1710	Translationally-controlled tumor protein	involved in calcium binding and microtubule stabilization	2.90E-21	P35681