

# **A Multi-Bioassay Integrated Approach to Assess the Antifouling Potential of the Cyanobacterial Metabolites Portoamides**

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## List of Supplementary Materials

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**Table S1:** Summary of LC-MS/MS protein identification results.

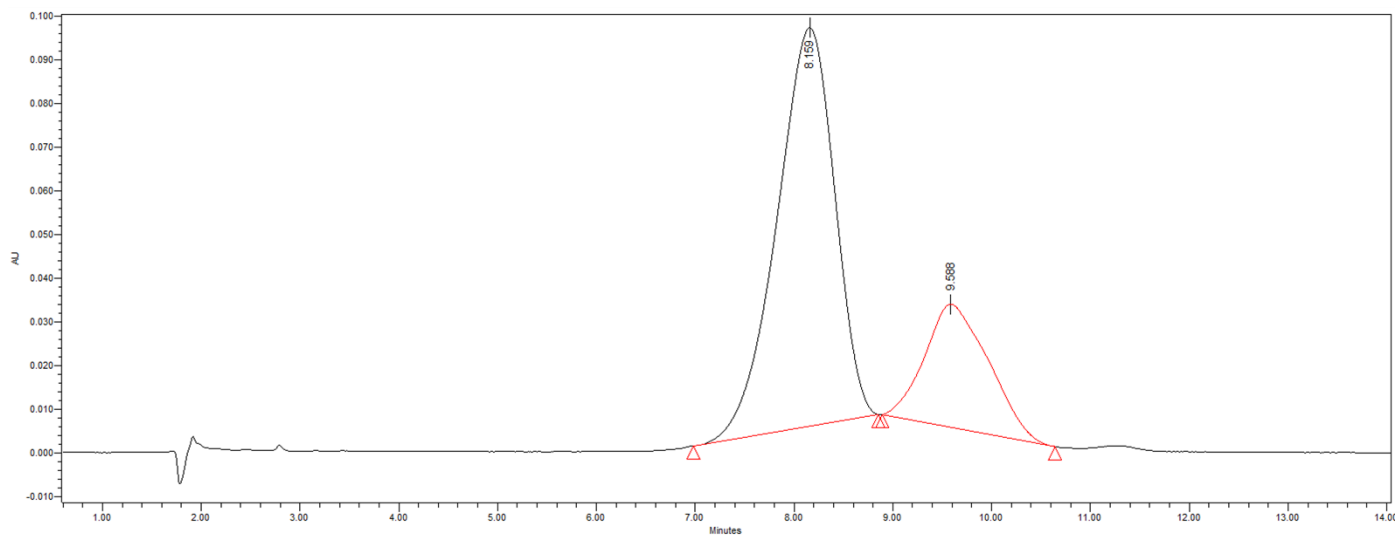
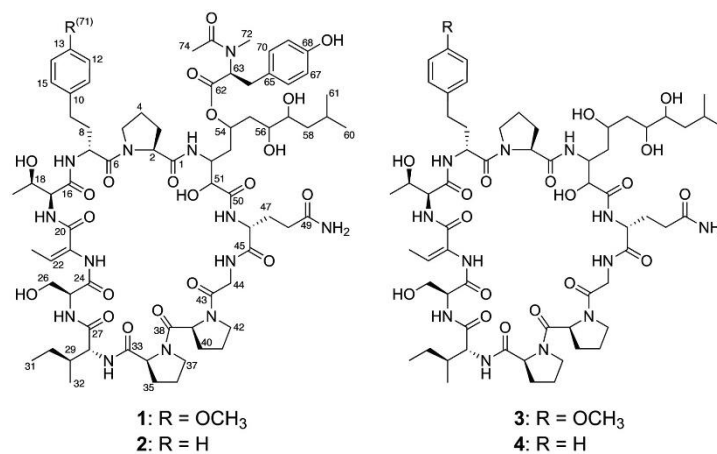
**Figure S1:** Structures and relative proportions of portoamides A and B.

**Table S1.** Summary of LC-MS/MS protein Identification results. The QTOF data from the Impact HD mass spectrometer equipped with a CaptiveSpray source (Bruker Daltonik, Bremen, Germany) were searched using the Peaks Studio 8.5 search algorithm (Bioinformatics Solutions, Waterloo, ON, Canada).

Protein Name	Accession	Significance	Coverage (%)	#Peptides	#Unique Peptides	PTM	Avg. Mass
<b>Energy Metabolism</b>							
ATP synthase subunit d, mitochondrial	XP_009028970.1	14.86	7	1	1	N	20040
ATP synthase subunit beta mitochondrial	XP_021356377.1	57.57	30	13	13	Y	56361
H+ ATPase a subunit mitochondrial	ABJ51956.1	151.76	22	12	12	N	59490 59490
ATP synthase subunit gamma	XP_009064140.1	68.99	11	3	3	N	32306
Isocitrate dehydrogenase	AFI56365.1	32.31	12	5	5	N	50501
Malate dehydrogenase	AAF27650.1	25.87	7	2	2	N	35955
Glutamate dehydrogenase mitochondrial	XP_022314664.1	8.96	2	1	1	N	60325
<b>Structural</b>							
Myosin heavy chain striated muscle	XP_022317649.1	200	25	47	41	Y	228093
Pedal retractor muscle	CAB64663.1	153.53	33	21	19	N	87460
Tubulin beta chain	XP_014664190.1	200	28	9	5	Y	49949
Tubulin alpha-1A chain	XP_021370666.1	50.58	39	13	2	Y	38578
Cilia- and flagella-associated protein	XP_022332848.1	23.01	8	2	2	N	33218
Myosin heavy chain	KFB49247.1	139.38	39	6	5	Y	20888
Tubulin beta chain	NP_001292292.1	37.69	23	6	2	Y	33218
Tubulin beta chain	XP_009029528.1	9.32	30	5	1	N	27930

Myosin heavy chain	XP_021350592.1	65.88	5	8	8	Y	230478
Tektin-4	XP_011416098.1	24.6	6	2	2	N	52138
Radial spoke head protein 4	XP_021370563.1	8.73	4	1	1	N	50579
Radial spoke head protein 9	XP_021363337.1	8.56	4	1	1	N	36000
Tektin-3	XP_011450983.1	49.81	13	7	7	Y	62040
Collagen, type VI, alpha 3	XP_021375365.1	18.34	7	1	1	N	15965
<b>Protein Activity Regulation</b>							
Dolichyl-diphosphooligosaccharide protein glycosyltransferase	XP_021341263.1	27.49	8	4	4	N	68234
Arginine kinase	AKS48144.1	132.06	20	6	6	Y	42147
Dolichyl-diphosphooligosaccharide protein glycosyltransferase 48 kDa subunit	XP_021367901.1	22.72	4	2	2	N	48797
14-3-3 protein	XP_018019106.1	200	26	6	4	Y	29977
Peptidyl-prolyl cis-trans isomerase	XP_011444269.1	26.14	9	2	2	N	29564
heat shock protein 90	CAJ85741.1	82.08	12	8	8	N	83125
Protein disulfide-isomerase A6	XP_011446200.1	8.85	2	1	1	N	47641
<b>Gene Transcription/Translation</b>							
Histone H2A	Q6WV66.3	8.82	37	4	1	N	13360
Histone H2A	XP_021377317.1	8.79	34	4	1	Y	14212
Leucine-rich repeat flightless-interacting protein 2	XP_021363857.1	9.33	3	1	1	N	45577
Histone H4	XP_014590042.1	200	50	6	6	Y	11367
Heterogeneous nuclear ribonucleoprotein 87F	XP_012945445.1	18.28	3	1	1	N	36578

60S ribosomal protein L7a	XP_021369622.1	8.9	5	1	1	N	30513
40S ribosomal protein S4	XP_022290789.1	24.47	7	2	2	N	29583
40S ribosomal protein S3	XP_011438308.1	33.34	9	2	2	N	26632
40S ribosomal protein S13	XP_011441368.1	8.94	8	1	1	N	17356
40S ribosomal protein S25	XP_021370373.1	27.7	18	2	2	N	16837
60S ribosomal protein L11	XP_013068480.1	30.49	13	2	2	N	20256
<b>Transport</b>							
Clathrin heavy chain 1	XP_021354511.1	11.55	1	1	1	N	192108
Annexin B9	XP_022317867.1	8.76	5	1	1	N	35854
ADP, ATP carrier protein	SCN46548.1	77.98	15	4	4	Y	33267
Voltage-dependent anion channel	ADI56517.1	75.71	12	3	3	N	30686
<b>Other processes</b>							
6-phosphogluconate dehydrogenase decarboxylating	XP_022343934.1	8.76	2	1	1	N	53103
Glutathione S-transferase sigma 2	AFQ35984.1	22.18	11	2	2	N	23359



**Figure S1.** Absorption spectra (A) obtained by the analytic method with the absorbance as function of time. The first peak represents portoamide A, while the second peak is portoamide B. The PDA spectrum (B), for each absorbance spectrum, with absorbance in the wavelength of 276.0 nm. Structures as represented by Leão et al. [25].