

Table S3. Mass Spectrometry parameters for targeted peptide biomarkers. Analytical conditions for each peptide were individually optimized on a Thermo Vantage Triple Quadrupole mass spectrometer, prior to addition to samples and simultaneous analysis of all peptides (light and heavy versions) on the same instrument. ID refers to a laboratory peptide identification number used throughout the manuscript and Supplemental Section. Annotations are from metaproteome identifications or Blastp searches, see Table S4 for representation of each of these targeted peptides within cyanobacterial genomes. Start and stop times refer to scheduled analysis windows on the mass spectrometer.

Peptide ID	Annotation	Peptide Sequence (Cleaved residues), K* or R* isotopically labeled (C13, N15)	z	Parent ion	Product Ions	Collision Energy	Start time	Stop time	S-lens value
27	Iron ABC transporter, substrate binding protein (IdiA) [<i>Prochlorococcus marinus</i> MIT 9515]	(K)SPYNQSLVANQIVNK(G)	2	837.9441	1085.6313	30	16.3	20.3	247
				837.9441	885.5152	20	16.3	20.3	247
				837.9441	786.4468	32	16.3	20.3	247
27	Iron ABC transporter, substrate binding protein (IdiA) [<i>Prochlorococcus marinus</i> MIT 9515]	(K)SPYNQSLVANQIVNK*(G)	2	841.9441	1093.6313	30	16.3	20.3	247
				841.9441	893.5152	20	16.3	20.3	247
				841.9441	794.4468	32	16.3	20.3	247
30	Flavodoxin [<i>Prochlorococcus marinus</i> MIT 9515]	(R)LHNFISSAESPK(D)	2	665.3435	1079.5368	22	11.3	15.3	210
				665.3435	705.3414	26	11.3	15.3	210
				665.3435	608.8015	21	11.3	15.3	210
30	Flavodoxin [<i>Prochlorococcus marinus</i> MIT 9515]	(R)LHNFISSAESPK*(D)	2	669.3435	1087.5368	22	11.3	15.3	210
				669.3435	713.3414	26	11.3	15.3	210
				669.3435	612.8015	21	11.3	15.3	210
31	Flavodoxin [<i>Prochlorococcus marinus</i> MIT 9515]	(K)AGADMVGYVDK(S)	2	563.2659	926.4288	19	11.6	15.6	118
				563.2659	680.3614	19	11.6	15.6	118
				563.2659	581.293	14	11.6	15.6	118
31	Flavodoxin [<i>Prochlorococcus marinus</i> MIT 9515]	(K)AGADMVGYVDK*(S)	2	567.2659	934.4288	19	11.6	15.6	118
				567.2659	688.3614	19	11.6	15.6	118
				567.2659	589.293	14	11.6	15.6	118
32	Flavodoxin [<i>Prochlorococcus marinus</i> MIT 9515]	(M)TVGIYYATTTGK(T)	2	637.835	1074.5466	21	12.6	16.6	139
				637.835	904.4411	18	12.6	16.6	139
				637.835	741.3777	21	12.6	16.6	139
32	Flavodoxin [<i>Prochlorococcus marinus</i> MIT 9515]	(M)TVGIYYATTTGK*(T)	2	641.835	1082.5466	21	12.6	16.6	139
				641.835	912.4411	18	12.6	16.6	139
				641.835	749.3777	21	12.6	16.6	139
34	Nitrogen Regulatory Protein P-II glnB glnK	(K)VNSVIDAIAEAAK(T)	2	650.859	1087.5994	21	23	27	148
				650.859	901.4989	21	23	27	148
				650.859	788.4149	23	23	27	148
34	Nitrogen Regulatory Protein P-II glnB glnK	(K)VNSVIDAIAEAAK*(T)	2	654.859	1095.5994	21	23	27	148
				654.859	909.4989	21	23	27	148
				654.859	796.4149	23	23	27	148
35	Nitrogen Regulatory Protein NtcA	(R)LSHQIAIEAIGSTR(V)	3	485.2634	604.3413	17	14.3	18.3	77
				485.2634	533.3042	15	14.3	18.3	77
				485.2634	420.2201	15	14.3	18.3	77
35	Nitrogen Regulatory Protein NtcA	(R)LSHQIAIEAIGSTR*(V)	3	488.5968	614.3413	17	14.3	18.3	77
				488.5968	543.3042	15	14.3	18.3	77
				488.5968	430.2201	15	14.3	18.3	77
38	Two Component Phosphate Regulator PhoP	(R)SKLEDDPANPELILTAR(G)	3	628.0021	686.4559	22	19.5	23.5	110

38	[Synechococcus WH8109] (45% Identity to Bacillus subtilis PY79 PhoP) Two Component Phosphate Regulator PhoP [Synechococcus WH8109] (45% Identity to Bacillus subtilis PY79 PhoP)	(R)SKLEDDPANPELILTAR*(G)	3	628.0021	573.3719	19	19.5	23.5	110
				628.0021	456.7793	16	19.5	23.5	110
				631.3354	696.4559	22	19.5	23.5	110
				631.3354	583.3719	19	19.5	23.5	110
				631.3354	461.7793	16	19.5	23.5	110
39	Urea ABC transporter, substrate binding protein [Prochlorococcus marinus MIT 9215]	(K)LIDQDGVPPVFGGWTSASR(K)	2	1002.513	1263.648	31	25.5	29.5	184
				1002.513	968.4585	27	25.5	29.5	184
				1002.513	741.3777	28	25.5	29.5	184
39	Urea ABC transporter, substrate binding protein [Prochlorococcus marinus MIT 9215]	(K)LIDQDGVPPVFGGWTSASR*(K)	2	1007.513	1273.648	31	25.5	29.5	184
				1007.513	978.4585	27	25.5	29.5	184
				1007.513	741.3777	28	25.5	29.5	184
41	Urea ABC transporter, substrate binding protein [Prochlorococcus marinus MIT 9215]	(K)VVGEDYLPLGNTEVAPIISK(I)	2	1057.573	1338.7627	31	25	29	241
				1057.573	557.3657	20	25	29	241
				1057.573	776.3825	42	25	29	241
41	Urea ABC transporter, substrate binding protein [Prochlorococcus marinus MIT 9215]	(K)VVGEDYLPLGNTEVAPIISK*(I)	2	1061.573	1346.7627	31	25	29	241
				1061.573	776.3825	20	25	29	241
				1061.573	565.3657	42	25	29	241
42	Urea ABC transporter (Pro and Syn)	(K)IEYIVEDGASDWPTFAEK(S)	2	1035.489	692.3614	26	24.8	28.8	265
				1035.489	406.1973	43	24.8	28.8	265
				1035.489	347.1925	28	24.8	28.8	265
42	Urea ABC transporter (Pro and Syn)	(K)IEYIVEDGASDWPTFAEK*(S)	2	1039.489	700.3614	26	24.8	28.8	265
				1039.489	406.1973	43	24.8	28.8	265
				1039.489	355.1925	28	24.8	28.8	265
25	Nickel-containing superoxide dismutase [Synechococcus sp. WH 8102]	(R)VAAEAVLSMTK(K)	2	560.3075	949.5023	16	15.6	19.6	99
				560.3075	749.4226	20	15.6	19.6	99
				560.3075	579.3171	19	15.6	19.6	99
25	Nickel-containing superoxide dismutase [Synechococcus sp. WH 8102]	(R)VAAEAVLSMTK*(K)	2	564.3075	957.5023	16	15.6	19.6	99
				564.3075	757.4226	20	15.6	19.6	99
				564.3075	587.3171	19	15.6	19.6	99
132	sulfolipid (UDP-sulfoquinovose)	FDYDGDYGTVLNR	2	767.8441	822.4468	36	17.4	21.4	140
				767.8441	659.3835	32	17.4	21.4	140
				767.8441	501.3144	24	17.4	21.4	140
132	sulfolipid (UDP-sulfoquinovose)	FDYDGDYGTVLNR*	2	772.8441	832.4468	36	17.4	21.4	140
				772.8441	669.3835	32	17.4	21.4	140
				772.8441	511.3144	24	17.4	21.4	140
134	sulfolipid (UDP-sulfoquinovose)	NEAVENDLIVDNK	2	736.865	1059.5317	23	9.9	13.9	137
				736.865	475.2511	20	9.9	13.9	137
				736.865	376.1827	22	9.9	13.9	137
134	sulfolipid (UDP-sulfoquinovose)	NEAVENDLIVDNK*	2	740.865	1067.5317	23	9.9	13.9	137
				740.865	483.2511	20	9.9	13.9	137
				740.865	384.1827	22	9.9	13.9	137
171	sulfolipid (UDP-sulfoquinovose)	VASLTGADINYLNPNR	2	850.9519	873.4577	22	20	24	135
				850.9519	596.3515	23	20	24	135

				850.9519	483.2674	23	20	24	135
171	sulfolipid (UDP-sulfoquinovose)	VASLTGADINYLPNPR*	2	855.9519	883.4577	22	20	24	135
				855.9519	606.3515	23	20	24	135
				855.9519	493.2674	23	20	24	135
118	Urease Alpha subunit UreC (<i>Prochlorococcus</i>)	IPEDIAFAESR	2	624.317	908.4472	23	14.7	18.7	112
				624.317	680.3362	23	14.7	18.7	112
				624.317	609.2991	22	14.7	18.7	112
118	Urease Alpha subunit UreC (<i>Prochlorococcus</i>)	IPEDIAFAESR*	2	629.317	918.4472	23	14.7	18.7	112
				629.317	690.3362	23	14.7	18.7	112
				629.317	619.2991	22	14.7	18.7	112
135	Ammonium transporter [<i>Prochlorococcus</i> MIT9312]	EAYPDFASAK	2	549.7587	735.3672	17	8.5	12.5	114
				549.7587	638.3144	21	8.5	12.5	114
				549.7587	523.2875	25	8.5	12.5	114
135	Ammonium transporter [<i>Prochlorococcus</i> MIT9312]	EAYPDFASAK*	2	553.7587	743.3672	17	8.6	12.6	114
				553.7587	646.3144	21	8.6	12.6	114
				553.7587	531.2875	25	8.6	12.6	114
144	Glutamine synthetase, glutamate--ammonia ligase [<i>Prochlorococcus marinus</i> MIT 9215]	FDSLINSADNVMTYK	2	859.4087	1255.5987	22	23.3	27.3	203
				859.4087	1142.5146	23	23.3	27.3	203
				859.4087	1028.4717	26	23.3	27.3	203
144	Glutamine synthetase, glutamate--ammonia ligase [<i>Prochlorococcus marinus</i> MIT 9215]	FDSLINSADNVMTYK*	2	863.4087	1263.5987	22	23.3	27.3	203
				863.4087	1150.5146	23	23.3	27.3	203
				863.4087	1036.4717	26	23.3	27.3	203
145	Glutamine synthetase, glutamate--ammonia ligase [<i>Prochlorococcus marinus</i> MIT 9215]	EGYFPVSPNDTAQDIR	2	904.9261	350.1347	30	17.8	21.8	201
				904.9261	1312.6492	29	17.8	21.8	201
				904.9261	1029.496	28	17.8	21.8	201
145	Glutamine synthetase, glutamate--ammonia ligase [<i>Prochlorococcus marinus</i> MIT 9215]	EGYFPVSPNDTAQDIR*	2	909.9261	350.1347	30	17.8	21.8	201
				909.9261	1322.6492	29	17.8	21.8	201
				909.9261	1039.496	28	17.8	21.8	201
146	Glutamine synthetase, glutamate--ammonia ligase [<i>Synechococcus</i> sp. RS9916]	HAPSFLAFTNPTNSYK	3	632.6477	653.3406	23	20.6	24.6	100
				632.6477	724.3777	19	20.6	24.6	100
				632.6477	810.3992	18	20.6	24.6	100
146	Glutamine synthetase, glutamate--ammonia ligase [<i>Synechococcus</i> sp. RS9916]	HAPSFLAFTNPTNSYK*	3	635.3144	653.3406	23	20.6	24.6	100
				635.3144	724.3777	19	20.6	24.6	100
				635.3144	818.3992	18	20.6	24.6	100

