

## Saito Lab Marine Bioinorganic Chemistry: Datasets

### Trace Metal Datasets

The CoFeMUG Expedition (Cobalt, Iron, and Microbes from the Upwelling to the Gyre) - R/V Knorr 2007. [BCO-DMO data repository](#).  
[Noble et al, Coastal Plume Limnol. Oceanogr manuscript.](#)

The CORSACS Expedition (Controls on Ross Sea Algal Community Structure) - R/V N.B. Palmer 2005-2006. [BCO-DMO data repository](#).  
[Saito et al., 2010 Biogeosciences Manuscript.](#)

### Experimental Microbial Proteomic Datasets

Diel Cycling of Proteins in *Crocospaera watsonii*

Saito, MA, EM Bertrand, VV Bulygin, DM Moran, S Dutkiewicz, FM Monteiro, MJ Follows, FW Valois, JB Waterbury. 2011. [Iron Conservation by Reduction of Metalloenzyme Inventories in the Marine Diazotroph \*Crocospaera watsonii\*](#). *Proc. Natl. Acad. Sci.* doi:10.1073/pnas.1006943108.

Supplemental Proteomics dataset with spectral counting results and identified tryptic peptides from diel cycle and iron limitation of *Crocospaera watsonii*: [PNAS2011Supplemental](#) (also available on PNAS site as an [open access document](#)).

B12 Limitation of Marine Diatoms

Bertrand EM, Allen AE, Dupont CL, Norden-Krichmar T, Bai J, Saito MA. 2012. [Impact of Cobalamin Starvation on Diatom Molecular Physiology and the Identification of a Novel Cobalamin Acquisition Protein](#). *Proc. Natl. Acad. Sci.*

Spectral Counting results and identified peptides under B12 and iron colimitation: [Supplemental Proteomics Dataset](#)

Phosphorus limitation in *Thalassiosira pseudonana*

ST Dyhrman, BD Jenkins, TA Rynearson, MA Saito, ML Mercier, H Alexander, LP. Whitney, A Drzewianowski, VV Bulygin, EM Bertrand, Z Wu, C Benitez-Nelson, A Heithoff. 2012 [Coordination in the transcriptome and proteome of the diatom \*Thalassiosira pseudonana\* reveals a diverse phosphorus stress response](#). *PLoS One*.

*Supplemental datasets*

Peptides from *Thalassiosira pseudonana* under phosphorus-limited and replete conditions: [Dyhrman\\_PLOSONE2012\\_Table4Peptides](#)

Spectral count and corresponding transcriptome data from phosphorus-limited and replete *Thalassiosira pseudonana*:

[Dyhrman\\_PLOSONE\\_Table5SupplementalSpectralCounts](#)

Phosphorus limitation in *Aureococcus anophagefferens*

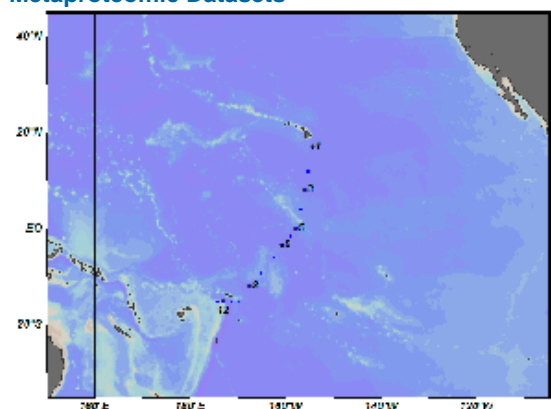
Louie L. Wurch, Erin M. Bertrand, Mak A. Saito, Benjamin A.S. Van Mooy and Sonya T. Dyhrman. 2011. [Proteome changes driven by phosphorus stress and recovery in the brown tide-forming alga, \*Aureococcus anophagefferens\*](#). *PLoS One*.

*Supplemental Proteomics Datasets*

Identified peptides: [Wurch\\_TableS1Peptides](#)

Protein spectral count data and corresponding transcriptome results: [Wurch\\_TableS2SpectralCounts](#)

### Metaproteomic Datasets

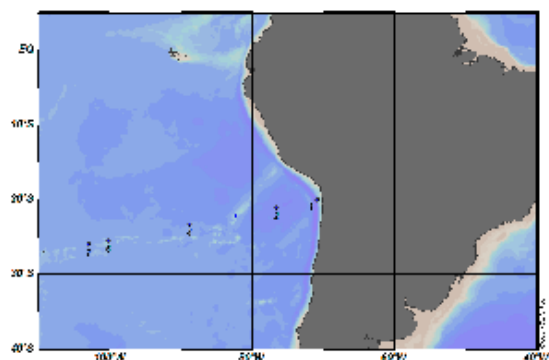


[Enlarge image](#)

METZYME Cruise Track R/V Kilo Moana 2011

METZYME Expedition Hawaii-Samoa Nov-Dec 2011 R/V Kilo Moana  
 Samples analyzed by LC-MS (Thermo LTQ) for initial proteomic discovery work followed by analysis in X!Tandem. Currently identified peptides dataset on station links below (Version July 10, 2013). These samples contain filtered material between 0.2 microns to 3.0 microns in size. Further high resolution and quantitative LC-MS analyses are underway. Funded by the Gordon and Betty Moore Foundation and Chemical Oceanography National Science Foundation.

Station	Station Start Date	Long E	Lat N	Depth (M)
<a href="#">1</a>	10/3/2011	205.60	17.00	50
<a href="#">1</a>	10/3/2011	205.60	17.00	90
<a href="#">1</a>	10/3/2011	205.60	17.00	120
<a href="#">1</a>	10/3/2011	205.60	17.00	200
<a href="#">1</a>	10/3/2011	205.60	17.00	300
<a href="#">1</a>	10/3/2011	205.60	17.00	400
<a href="#">1</a>	10/3/2011	205.60	17.00	600
<a href="#">3</a>	10/8/2011	204.00	8.00	40
<a href="#">3</a>	10/8/2011	204.00	8.00	60



[Enlarge image](#)

BIG RAPA R/V Melville 2010

<a href="#">3</a>	10/8/2011	204.00	8.00	120
<a href="#">3</a>	10/8/2011	204.00	8.00	150
<a href="#">3</a>	10/8/2011	204.00	8.00	200
<a href="#">3</a>	10/8/2011	204.00	8.00	250
<a href="#">3</a>	10/8/2011	204.00	8.00	300
<a href="#">3</a>	10/8/2011	204.00	8.00	500
<a href="#">3</a>	10/8/2011	204.00	8.00	550
<a href="#">3</a>	10/8/2011	204.00	8.00	600
<a href="#">3</a>	10/8/2011	204.00	8.00	800
<a href="#">5</a>	10/13/2011	202.01	0.00	20
<a href="#">5</a>	10/13/2011	202.01	0.00	50
<a href="#">5</a>	10/13/2011	202.01	0.00	80
<a href="#">5</a>	10/13/2011	202.01	0.00	120
<a href="#">5</a>	10/13/2011	202.01	0.00	200
<a href="#">5</a>	10/13/2011	202.01	0.00	300
<a href="#">5</a>	10/13/2011	202.01	0.00	400
<a href="#">5</a>	10/13/2011	202.01	0.00	500
<a href="#">5</a>	10/13/2011	202.01	0.00	600
<a href="#">6</a>	10/17/2011	199.23	-3.50	40
<a href="#">6</a>	10/17/2011	199.23	-3.50	80
<a href="#">6</a>	10/17/2011	199.23	-3.50	200
<a href="#">8</a>	10/19/2011	194.64	-9.25	40
<a href="#">8</a>	10/19/2011	194.64	-9.25	70
<a href="#">8</a>	10/19/2011	194.64	-9.25	200
<a href="#">9</a>	10/20/2011	192.44	-12.00	40
<a href="#">9</a>	10/20/2011	192.44	-12.00	70
<a href="#">9</a>	10/20/2011	192.44	-12.00	380
<a href="#">12</a>	10/23/2011	186.90	-15.00	40
<a href="#">12</a>	10/23/2011	186.90	-15.00	120
<a href="#">12</a>	10/23/2011	186.90	-15.00	300

BIG RAPA Chile-Easter Island Expedition R/V Melville 2010

Samples analyzed by LC-MS (Thermo LTQ) for initial proteomic discovery work followed by analysis in X!Tandem. Currently identified peptides dataset (in preparation). These samples contain filtered material between 0.2 microns to 3.0 microns in size. Further high-resolution and quantitative LC-MS analyses are underway. Funded by the Gordon and Betty Moore Foundation and Center for Microbial Oceanography Research and Education (C-MORE, National Science Foundation).

BIG RAPA MV1015

Nov-Dec 2010

Station	Station Start Date	Long E	Lat N	Depth (M)
1	11/22/2010	289.20	-20.08	25
2	11/25/2010	283.43	-21.18	48
2	11/25/2010	283.43	-21.18	110
2	11/25/2010	283.43	-21.18	800
4	11/29/2010	271.24	-23.46	20
4	11/29/2010	271.24	-23.46	100
4	11/29/2010	271.24	-23.46	200
4	11/29/2010	271.24	-23.46	375
4	11/29/2010	271.24	-23.46	500
4	11/29/2010	271.24	-23.46	650
4	11/29/2010	271.24	-23.46	800
4	11/29/2010	271.24	-23.46	1000
4	11/29/2010	271.24	-23.46	1500
6	12/6/2010	259.86	-25.55	10
6	12/6/2010	259.86	-25.55	20
6	12/6/2010	259.86	-25.55	60
6	12/6/2010	259.86	-25.55	120

6	12/6/2010	259.86	-25.55	250
7	12/7/2010	257.10	-26.05	20
7	12/7/2010	257.10	-26.05	75
7	12/7/2010	257.10	-26.05	175
7	12/7/2010	257.10	-26.05	250
7	12/7/2010	257.10	-26.05	400
7	12/7/2010	257.10	-26.05	500
7	12/7/2010	257.10	-26.05	800
7	12/7/2010	257.10	-26.05	1100
7	12/7/2010	257.10	-26.05	1900

#### Related Files

[Metzyme\\_S1](#)  
[Metzyme\\_S3](#)  
[Metzyme\\_S5](#)  
[Metzyme\\_S6](#)  
[Metzyme\\_S8](#)  
[Metzyme\\_S9](#)  
[Metzyme\\_S12](#)

### Computational Proteomics Tools

#### Redundant Tryptic Peptide Scripts

These scripts provide tools and documentation for detecting redundant tryptic peptides between multiple genomes. These tools are intended to assist proteomics scientists understand the potential for identifying unique and shared tryptic peptides in metaproteomic data.

[Github repository link.](#)

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