

Diel proteomes of cultured *Trichodesmium erythraeum* sp. IMS101 from laboratory experiments conducted in November of 2018

Website: <https://www.bco-dmo.org/dataset/783873>

Data Type: experimental

Version: 1

Version Date: 2019-12-10

Project

» [New technology for high resolution analysis of proteins and other organic materials produced by marine microorganisms](#) (MM Proteins and Organics Tech)

» [Marine Microbial Investigator Award: Investigator Mak Saito](#) (MM Saito)

Contributors	Affiliation	Role
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Abstract

Diel proteomes of cultured *Trichodesmium erythraeum* sp. IMS101 from laboratory experiments conducted in November of 2018.

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Coverage

Dataset Description

Diel proteomes of cultured *Trichodesmium erythraeum* sp. IMS101 from laboratory experiments conducted in November of 2018.

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE [1] partner repository with the dataset identifier PXD016332 and 10.6019/PXD016332 but are not yet public.

Project Name: *Trichodesmium erythraeum* sp. IMS101 Diel proteomes

Project accession: PXD016332

Project DOI: 10.6019/PXD016332

The format of these data in the BCO-DMO data system is tabular. For a version formatted as a matrix, see the "Data Files" section.

Acquisition Description

A batch culture (1.5L) of *Trichodesmium erythraeum* sp. IMS101 was grown in a 27°C incubator with a 14:10 light cycle that ramps up and down mimicking dawn and dusk. Sampling occurred every 1-3 hours with concentrated sampling at dawn and dusk. 70mL of the culture was sterically subsampled and collected on 0.2mm Supor filters, then frozen at -80°C. 10mL was collected and filtered on combusted GFF filters for CHN analysis.

Proteins were extracted in sodium dodecyl sulfate and digested in gel similar to Saito et al., 2014 (Science).

Peptides were analyzed by LC-MS/MS on a Thermo Orbitrap Fusion using LC x LC/MS chromatography with high and low pH reversed phase chromatography.

Processing Description

Peptide to spectrum matching was performed in SEQUEST implemented in Proteome Discoverer 2.2 using the *Trichodesmium erythraeum* sp. IMS101 genome. Statistical validation was performed at the 1% protein and peptide FD levels calculated in Scaffold (Proteome Software).

BCO-DMO Data Manager Processing Notes:

* originally submitted file "dielproteindata.csv" in matrix format added to "Data Files" section.

* a tabular version of dielproteindata.csv was created and imported into the BCO-DMO data system. Data was unpivoted to transform from the matrix into a table with columns for

hours_post_dawn,cnratio,relative_protein_abundance.

* added a conventional header with dataset name, PI name, version date

* modified parameter names to conform with BCO-DMO naming conventions (spaces, +, and - changed to underscores). Units in parentheses removed and added to Parameter Description metadata section.

* blank values in this dataset are displayed as "nd" for "no data." nd is the default missing data identifier in the BCO-DMO system

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Data Files

File	Version
<p>dielproteindata.csv (Comma Separated Values (.csv), 398.85 KB) MD5:5d6ee8ebc660a58d8816f1823db02066</p> <p><i>Diel proteomes Tricho IMS101 data.</i></p> <p><i>This file contains relative protein abundance, normalized spectral counts formatted as a matrix. This is the format originally submitted to BCO-DMO which was unpivoted into a tabular version in the BCO-DMO data system.</i></p> <p><i>row 1: hourspostdawn, hours after incubator light is on</i> <i>row 2: cnratio, POC:PON ratio of culture</i> <i>column 1 (rows 3-2392): protein name</i> <i>columns 2-14 (rows 3-2392): Relative protein abundance, normalized spectral counts</i></p>	original

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Related Publications

ProteomeXchange dataset. (n.d.). doi:10.6019/pxd016332 <https://doi.org/10.6019/PXD016332>
[\[details\]](#)

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Parameters

Parameter	Description	Units
protein_name	Protein name	unitless
hours_post_dawn	Hours post dawn. Hours after incubator light is on	hours
cnratio	POC:PON ratio of culture. Ratio of particulate organic carbon to particulate organic nitrogen	dimensionless
relative_protein_abundance	Relative protein abundance. Normalized spectral counts.	unitless

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Instruments

Dataset-specific Instrument Name	Thermo Orbitrap Fusion mass spectrometer
Generic Instrument Name	Mass Spectrometer
Generic Instrument Description	General term for instruments used to measure the mass-to-charge ratio of ions; generally used to find the composition of a sample by generating a mass spectrum representing the masses of sample components.

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Project Information

New technology for high resolution analysis of proteins and other organic materials produced by marine microorganisms (MM Proteins and Organics Tech)

Website: <https://www.moore.org/grant-detail?grantId=GBMF3934>

In support of acquiring a high resolution mass spectrometer that incorporates the latest

technologies for analyzing proteins and other organic materials.

Marine Microbial Investigator Award: Investigator Mak Saito (MM Saito)

In support of obtaining deeper knowledge of major biogeochemically relevant proteins to inform a mechanistic understanding of global marine biogeochemical cycles.

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Funding

Funding Source	Award
Gordon and Betty Moore Foundation (GBMF)	GBMF3934
Gordon and Betty Moore Foundation: Marine Microbiology Initiative (MMI)	GBMF3782

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