This is a readme for Metabolomics Workbench data deposition.

Project Title: Metabolite flux from temperature-acclimated diatom strains

Project Summary: The temperature increase occurring in the surface ocean has fundamental implications for physiological rates and processes of marine microbes. Here we asked whether the temperature at which a marine diatom strain is acclimated affects carbon transfer to a co-cultured heterotrophic bacterium. Model systems were established in which the diatom *Thalassiosira pseudonana* was acclimated for three months at temperatures below (14°C), equal to (20°C), and above (28°C) the temperature of optimal growth, and then inoculated with the heterotrophic bacterium *Ruegeria pomeroyi*. This deposition is for results obtained from a drawdown experiment of phytoplankton metabolites using *R. pomeroyi* conducted during this study.

\* mwTab file name: (Automatically assigned)

\* Name of archive file to be uploaded: UGA\_temp\_Oct2023\_drawdown\_zip

\* Data type being submitted: NMR

\* Protocol methods filename(s):

2\_Collection protocol\_UGA\_temp\_Oct2023\_drawdown.docx

3\_Treatment protocol\_UGA\_temp\_Oct2023\_drawdown.docx

4\_Sample preparation protocol\_UGA\_temp\_Oct2023\_drawdown.docx

5\_Analysis protocol\_UGA\_temp\_Oct2023\_drawdown.docx

\* MS/NMR instrument manufacturer: Bruker

\* MS/NMR instrument model: Bruker AVANCE lll

\* Binary data format: .ser

\* Open source text formats: .csv

\* Multi-part study: No

\* Embargo: No

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UGA\_phytoplankton\_Oct2022\_zip contains:

File: 1\_Study design\_UGA\_temp\_Oct2023\_drawdown.xlsx

File: 2\_Collection protocol\_UGA\_temp\_Oct2023\_drawdown.docx

File: 3\_Treatment protocol\_UGA\_temp\_Oct2023\_drawdown.docx

File: 4\_Sample preparation protocol\_UGA\_temp\_Oct2023\_drawdown.docx

File: 5\_Analysis protocol\_UGA\_temp\_Oct2023\_drawdown.docx

File: 6\_Acquisition and processing parameters\_UGA\_temp\_Oct2023\_drawdown.xlsx

Folder: Spectra

Folder: Data\_analysis

Note: We excluded a media-blank sample from ‘MW\_tab\_data.txt’ to create a metadata sheet in the Metabolomics Workbench system because this sample can’t have the required factors. Although that sample is not in the metadata sheet, the data for the sample (‘rawFiles/125’) is still included in the deposited file package.