# Raw LC-MS/MS data with list of identified peptides in xml format from a proteomic analysis performed on protein extracts of M. ferrooxydans

**Website**: https://www.bco-dmo.org/dataset/636621
**Data Type**: experimental, Other Field Results
**Version**: 27 Jan 2016
**Version Date**: 2016-01-27

## Project
» Proteomic profiling of neutrophilic, iron-oxidizing Mariprofundus ferrooxydans, strain PV-1 (Proteomic profiling of Mariprofundus ferrooxydans)

## Program
» Center for Dark Energy Biosphere Investigations (C-DEBI)

| Contributors | Affiliation | Role |
|---|---|---|
| Barco, Roman A. | Bigelow Laboratory for Ocean Sciences | Principal Investigator |
| Edwards, Katrina | University of Southern California (USC) | Co-Principal Investigator |
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## Dataset Description

Raw LC-MS/MS data with list of identified peptides in xml format.

Related publications:
Barco, RA, Edwards, KJ. 2014. Interactions of proteins with biogenic iron oxyhydroxides and a new culturing technique to increase biomass yields of neutrophilic, iron-oxidizing bacteria. Front. Microbiol. 5:259. doi: 10.3389/fmicb.2014.00259

### Methods & Sampling

Proteomic analysis was performed on protein extracts of *M. ferrooxydans* by following two methodologies: osmotic shock and alkaline lysis (extraction with NaOH). A total of 8 liters of *M. ferrooxydans* PV-1 was harvested on 0.22 um filters and treated for osmotic-shock per Neu and Heppel (1965). For the alkaline lysis protocol (crude extract), of a total 8 L of *M. ferrooxydans* PV-1 was harvested on 0.22 um filters and immersed in a total of 80 mL 0.1 N NaOH. Samples were run on SDS-PAGE gels.

### Data Processing Description

Excised bands were trypsin-digested and submitted for LC-MS/MS analysis a Thermo LTQ-Orbitrap XL mass

spectrometer equipped with an Eksigent Nanoliquid Chromatography 1-D plus system. The resulting MS/MS spectra were searched against the proteome of Mariprofundus ferrooxydans PV-1 in the Uniprot database using the Proteome Discoverer SEQUEST Daemon search engine.

Raw files are publicly available through the PRIDE Archive at
http://www.ebi.ac.uk/pride/archive/projects/PXD000937

## Data Files

| File |
| --- |
| **raw_LCMS.csv** (Comma Separated Values (.csv), 246 bytes) <br> MD5:2667b4d139d1de4dd5a8251604d38180 <br><br> Primary data file for dataset ID 636621 |

## Parameters

| Parameter | Description | Units |
| --- | --- | --- |
| taxon | Taxon studied. | dimensionless |
| description | Description of method. | dimensionless |
| PRIDE_project | PRIDE database project ID number. | dimensionless |
| data_URL | Link to PRIDE database. | dimensionless |

## Instruments

| Dataset-specific Instrument Name | Thermo LTQ-Orbitrap XL |
| --- | --- |
| Generic Instrument Name | Mass Spectrometer |
| Dataset-specific Description | Excised bands were trypsin-digested and submitted for LC-MS/MS analysis a Thermo LTQ-Orbitrap XL mass spectrometer equipped with an Eksigent Nanoliquid Chromatography 1-D plus system. |
| 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. |

## Project Information

**Proteomic profiling of neutrophilic, iron-oxidizing Mariprofundus ferrooxydans, strain PV-1 (Proteomic profiling of Mariprofundus ferrooxydans)**

Description from [C-DEBI website](#):
The aim of this proposal is to gain a better understanding of what subsets of proteins are actually being expressed during neutrophilic, microbial iron (Fe)-oxidation. The recently isolated *Mariprofundus ferrooxydans*, strain PV-1, will be used as a marine model organism to investigate proteomic differences under different Fe substrates: aqueous Fe2+ and solid Fe0. Two-dimensional gel electrophoresis (2D-GE) and shotgun proteomic methods (LC-MS/MS) will be employed to obtain results from the cultures grown under different conditions. The research being proposed would constitute the foundation for the development of diagnostic tools for the accordance, distribution, and activity level of Fe-oxidation, a globally important biogeochemical process at and below the ocean floor.

This project was funded by a C-DEBI Graduate Student Fellowship.

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## Program Information

**Center for Dark Energy Biosphere Investigations (C-DEBI)**

**Website**: [http://www.darkenergybiosphere.org](http://www.darkenergybiosphere.org)

**Coverage**: Global

The mission of the Center for Dark Energy Biosphere Investigations (C-DEBI) is to explore life beneath the seafloor and make transformative discoveries that advance science, benefit society, and inspire people of all ages and origins.

C-DEBI provides a framework for a large, multi-disciplinary group of scientists to pursue fundamental questions about life deep in the sub-surface environment of Earth. The fundamental science questions of C-DEBI involve exploration and discovery, uncovering the processes that constrain the sub-surface biosphere below the oceans, and implications to the Earth system. What type of life exists in this deep biosphere, how much, and how is it distributed and dispersed? What are the physical-chemical conditions that promote or limit life? What are the important oxidation-reduction processes and are they unique or important to humankind? How does this biosphere influence global energy and material cycles, particularly the carbon cycle? Finally, can we discern how such life evolved in geological settings beneath the ocean floor, and how this might relate to ideas about the origin of life on our planet?

C-DEBI's scientific goals are pursued with a combination of approaches:
(1) coordinate, integrate, support, and extend the research associated with four major programs—Juan de Fuca Ridge flank (JdF), South Pacific Gyre (SPG), North Pond (NP), and Dorado Outcrop (DO)—and other field sites;
(2) make substantial investments of resources to support field, laboratory, analytical, and modeling studies of the deep subseafloor ecosystems;
(3) facilitate and encourage synthesis and thematic understanding of submarine microbiological processes, through funding of scientific and technical activities, coordination and hosting of meetings and workshops, and support of (mostly junior) researchers and graduate students; and
(4) entrain, educate, inspire, and mentor an interdisciplinary community of researchers and educators, with an emphasis on undergraduate and graduate students and early-career scientists.

Note: Katrina Edwards was a former PI of C-DEBI; James Cowen is a former co-PI.

**Data Management:**
C-DEBI is committed to ensuring all the data generated are publically available and deposited in a data repository for long-term storage as stated in their [Data Management Plan (PDF)](#) and in compliance with the [NSF Ocean Sciences Sample and Data Policy](#). The data types and products resulting from C-DEBI-supported research include a wide variety of geophysical, geological, geochemical, and biological information, in addition to education and outreach materials, technical documents, and samples. All data and information generated by C-DEBI-supported research projects are required to be made publically available either following publication of

research results or within two (2) years of data generation.

To ensure preservation and dissemination of the diverse data-types generated, C-DEBI researchers are working with BCO-DMO Data Managers make data publicly available online. The partnership with BCO-DMO helps ensure that the C-DEBI data are discoverable and available for reuse. Some C-DEBI data is better served by specialized repositories (NCBI's GenBank for sequence data, for example) and, in those cases, BCO-DMO provides dataset documentation (metadata) that includes links to those external repositories.

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## Funding

| Funding Source | Award |
|---|---|
| NSF Division of Ocean Sciences (NSF OCE) | OCE-0939564 |

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