Dataset name: **Proteomics**

|  |  |
| --- | --- |
| Parameter: | * **List of identified proteins** |

PROJECT TITLE: **MOBYDICK**

Oceanographic cruise: **MOBYDICK**

Start date: **18/02/2018**

End date: **27/03/2018**

Project manager: **Bernard Quéguiner** [bernard.queguiner@mio.osupytheas.fr](mailto:bernard.queguiner@mio.osupytheas.fr)

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**Observatoire Océanologique de Banyuls sur mer**

**66650 Banyuls sur mer, France**

Geographic information: **Indian sector of the Southern Ocean**

Latitude: **49.5°S – 52.5°S**

Longitude: **67,0°E – 74.5°E**

Parameter supervisor: **Pavla Debeljak**

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# OPERATIONS

## Sampling device(s)

Water samples were collected from the Niskin bottles at every station (CTD\_Omics\_P casts, surface: 15 m, 150 m, and 350 m depths).

## List of stations sampled

M2\_1 (CTD-3), M4\_1 (CTD-16), M3 (CTD-20), M2\_2 (CTD-34), M1 (CTD-31), M4\_2 (CTD-48), M2\_3 (CTD-55), and M3\_3 (CTD-62).

|  |  |  |  |
| --- | --- | --- | --- |
| Station | Cast | Depth | Samples |
| M2\_1 | CTD-3 | 10m | 3 |
|  |  | 150m | 3 |
|  |  | 350m | 3 |
| M4\_1 | CTD-16 | 10m | 3 |
|  |  | 150m | 3 |
|  |  | 350m | 3 |
| M3 | CTD-20 | 15m | 3 |
| M2\_2 | CTD-34 | 10m | 3 |
|  |  | 150m | 3 |
|  |  | 350m | 3 |
| M1 | CTD-31 | 10m | 3 |
| M4\_2 | CTD-48 | 10m | 3 |
|  |  | 150m | 3 |
|  |  | 350m | 3 |
| M2\_3 | CTD-55 | 10m | 3 |
| M3\_3 | CTD-62 | 10m | 3 |

# INSTRUMENTS

Instrument Type: **Peristaltic pump**

Manufacturer: **Cole Parmer**

Model: **Masterflex L/S Easy-Load II**

Instrument Features / Calibration: **N/A**

Instrument Type: **Mass spectrometer (LC–MS)**

Manufacturer: **ThermoFisher Scientific**

Model: **Orbitrap Exclusive**

Instrument Features / Calibration: **N/A**

# DESCRIPTION of PARAMETERS

## Measurement details

20 L of seawater were collected from 10 or 15 m depth and 50 L of seawater for 150 and 350 m depths. Surface Seawater was prefiltered through a 0.8 µm polycarbonate filter (142 mm), and then onto a 0.2 µm Supor plus membrane (142 mm). The Supor filters were flash frozen in liquid nitrogen and stored in Falcon tubes at –80°C.

## Analytical procedure

Proteins will be extracted from filters (Kleiner *et al.*, 2018) and measured on a LC–MS Orbitrap Exclusive. Obtained protein data will be analysed using the sequenced DNA from contrasting stations (metagenomes)**.**

## Units

N/A

## Sensor precision

N/A

## Post-cruise data analysis/treatment required

N/A

## Estimated Date of Delivery

End of 2018.

# BIBLIOGRAPHY

Kleiner M., Dong X., Hinzke T., Wippler J., Thorson E., Mayer B., Strous M., 2018. Metaproteomics method to determine carbon sources and assimilation pathways of species in microbial communities. *Proceedings of the National Academy of Sciences of the United States of America*, **115**(24), E5576-E5584.   
<http://www.pnas.org/content/115/24/E557>