# Single amplified genomes (SAGs) of chemoautotrophs from global deep sea samples (Dark ocean chemoautotrophs project)

**Website**: https://www.bco-dmo.org/dataset/666274
**Data Type**: experimental
**Version**: 1
**Version Date**: 2017-10-27

**Project**
» Ocean's dark energy: Global inventory of chemoautotrophs in the aphotic realm (Dark ocean chemoautotrophs)

| Contributors | Affiliation | Role |
|---|---|---|
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| Copley, Nancy | Woods Hole Oceanographic Institution (WHOI BCO-DMO) | BCO-DMO Data Manager |

**Abstract**
This dataset includes accession numbers archived at IMG/M (Integrated Microbial Genomes and Microbiome Samples) at the US Dept. of Energy's Joint Genome Institute. Additional information includes the ocean depth, latitude and longitude, the assembled genome size and count, and the scaffold count.

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## Coverage

**Spatial Extent**: **N**:65.65 **E**:180 **S**:-64.93 **W**:-44
**Temporal Extent**: 2003-11-26 - 2014-05-06

## Dataset Description

Some of the accessions are not yet available [2017-10-27]. A free login account is required to access some of the pages at IMG, in particular, those located at img.jgi.doe.gov/cgi-bin/**mer**/.

**Publications using this dataset:**
Pachiadaki MG, Sintes E, Bergauer K, Brown JM, Record NR, Swan BK, Mathyer ME, Hallam SJ, Lopez-Garcia P, Takaki Y, Nunoura T, Woyke T, Herndl GJ, Stepanauskas R (2017). Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation. Science 358 (6366): 1046-1051.

Bergauer K, Fernandez-Guerra A, Garcia JA, Sprenger RR, Stepanauskas R, Pachiadaki MG, Jensen ON, Herndl GJ (2017). Organic matter processing by microbial communities throughout the Atlantic water column as revealed by metaproteomics. PNAS doi: 10.1073/pnas.1708779115.

### Methods & Sampling

Samples were collected by collaborators, cryopreserved and shipped frozen to Bigelow Laboratory Single Cell Genomics Facility Center (SCGC). Cells were sorted, identified and sequenced by the SCGC, following SCGC's standard practices: https://scgc.bigelow.org/PDFs/SCGC_Services_Description.pdf

On average, at least 5 million 2x150 bp or longer paired-end reads were generated per SAG using in-house MiSeq and with a NextSeq (Illumina) instruments. The obtained reads are were pre-processed and, de novo assembled, and quality-controlled using algorithms SCGC's standard protocols that are optimized for single cell MDA products . A combination of tetramer homogeneity tests and blast searches against reference databases is were used to detect potential DNA contaminants among the assembled contigs. Benchmark data demonstrating SCGC SAG WGS whole genome sequencing pipeline performance are available here: from the SCGC website: http://data.bigelow.org/~scgc/WGS_benchmark_data/.

Genome annotation was performed through IMG (http://img-stage.jgi-psf.org/cgi-bin/submit/main.cgi).

Further information on Bigelow Laboratory Single Cell Genomics Center (SCGC) Facilities (pdf)

**Relevant References:**

*In preparation:*


1. Pachiadaki M, Record N, Bergauer K, Nunoura T, Lopez-Garcia P, Herndl G, Stepanauskas R (2017) Global biogeography of bacterioplankton in the aphotic realm. Status = in preparation; Acknowledgment of Federal Support = Yes; Peer Reviewed = NA
2. Stepanauskas R, Brown J, Fergusson E. (2017) Improved genomic sequencing and *de novo* assembly of microbial single cells. Status = in preparation; Acknowledgment of Federal Support = Yes; Peer Reviewed = NA
3. Landry Z, Swan BK, Herndl JG, Vergin K, Stepanauskas R, Giovannoni S (2017) SAR202 genomes from the dark ocean predict pathways for the oxidation of recalcitrant dissolved organic matter. Status = in preparation; Acknowledgment of Federal Support = Yes; Peer Reviewed = NA
4. Nunoura T, Takaki Y, Minegishi H, Hirai M, Shuto A, Yoshida Y, Nishizawa M, Makabe A, Yanagawa K, Kuroiwa M, Makita T, Kodama T, Yoshida M, Koba K, Kondo R, Yokokawa T, Sunamura M, Stepanauskas R, Takai K (2017) Niche separation of MGI thaumarchaeotes along the water column on the three Northwest Pacific trenches. Status = in preparation; Acknowledgment of Federal Support = Yes; Peer Reviewed = NA
5. Labonté JM, Tupper B, Brown J, Harris C, Record NR, Stepanauskas R (2017) ViruSCope: A bioinformatics pipeline for viral sequence detection in microbial single cell genomes. Status = in preparation; Acknowledgment of Federal Support = Yes; Peer Reviewed = NA


*In review:*


1. Stepanauskas R, Fergusson EA, Brown J, Poulton NJ, Tupper B, Labonté JM, Becraft ED, Brown JM, Pachiadaki MG, Povilaitis T, Jeremian R, Alzbutas G, Thompson BP, Mascena CJ, Bellows WK, Petronis A, Lubys A. Genomics of individual cells and viruses revamped: enhanced gDNA amplification and direct, high throughput matching of cell's genomic and physical properties (2017) Status = in review; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
2. Bowers RM, Kyrpides NC, Stepanauskas R, Harmon-Smith M, Schulz F, Doud D, Reddy TBK, Jarett J, Rivers A, Eloe-Fadrosh EA, Tringe SG, Ivanova NN, Copeland A, Clum A, Becraft ED, Malmstrom RR, Birren B, Schriml L, Podar M, Bork P, Weinstock GM, Banfield JF, Garrity GM, Hugenholtz P, Parks DH, Tyson GW, Rinke C, Dodsworth JA, Yooseph S, Sutton GG, Yilmaz P, Glöckner FO, Meyer F, Gilbert JA, Nelson WC, Hallam SJ, Jungbluth SP, Ettema T, Tighe S, Konstantinidis KT, Liu WT, Baker BJ, Rattei T, Eisen J, Hedlund BP, McMahon KD, Fierer N, Knight R, Finn RD, Mizrachi I, Eren AM, Woyke T (2017) Genome Standards for Single Amplified Genomes and Genomes From Metagenomes of Bacteria and Archaea. Status = in review; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
3. Kashtan N, Roggensack SE, Thompson SE, Stepanauskas R, Chisholm SW (2017) Fundamental differences in diversity and genomic population structure between Atlantic and Pacific Prochlorococcus. Status = in review; Acknowledgment of Federal Support = Yes; Peer Reviewed = NA
4. Hawley AK, Nobu MK, Wright JJ, Durno WE, Morgan-Lang C, Sage B, Schwientek P, Swan B, Rinke C, Liu WT, Stepanauskas R, Woyke T, Hallam SJ (2017) Co-metabolic innovation along eco-thermodynamic gradients. Status = in review; Acknowledgment of Federal Support = Yes; Peer Reviewed = NA
5. Collingro A, Köstlbacher S, Mussmann M, Stepanauskas R, Hallam SJ, Horn M (2017) Marine Chlamydiae encode flagella. Status = in review; Acknowledgment of Federal Support = Yes; Peer Reviewed = NA
6. Jungbluth SP , del Rio TG, Tringe SG, Stepanauskas R, Rappé MS (2017) Genomic comparisons of a bacterial lineage that inhabits both marine and terrestrial deep subsurface systems. Status = in review;

Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes

7. Luo H, Huang Y, Stepanauskas R, Tang J (2017) Excess of Non-Conservative Amino Acid Changes in Marine Bacterioplankton Lineages with Reduced Genomes. Status = in review; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes

*Published:*

1. Wasmund K, Cooper M, Schreiber L, Lloyd KG, Baker BJ, Petersen DJ, Jørgensen BB, Stepanauskas R, Reinhardt R, Schramm A, Loy A and Adrian L (2016). Single cell genome and group-specific dsrAB sequencing implicate marine members of the class Dehalococcoidia (phylum Chloroflexi) in sulfur cycling. Mbio 7:e00266-16. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
2. Dyksma S, Bischof K, Fuchs BM, Hoffmann K, Meier D, Meyerdierks A, Pjevac P, Probandt D, Richter M, Stepanauskas R, Mußmann M. (2016). Ubiquitous Gammaproteobacteria dominate dark carbon fixation in coastal sediments. The ISME Journal, 10: 1939-1953. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
3. Ngugi DK, Blom J, Stepanauskas R, Stingl U. (2016). Diversification and niche adaptations of Nitrospina-like bacteria in the polyextreme interfaces of Red Sea brines. The ISME Journal, 10: 1383-1399. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
4. Zhang Y, Sun Y, Jiao N, Stepanauskas R, Luo H. (2016). Ecological Genomics of the Uncultivated Marine Roseobacter Lineage CHAB-I-5. Applied and Environmental Microbiology, 82(7): 2100-11
5. Labonte JM, Field EK, Lau M, Chivian D, van Heerden E, Wommack KE, Kieft TL, Onstott TC, Stepanauskas R. (2015). Single cell genomics indicates horizontal gene transfer and viral infections in a deep subsurface Firmicutes population. Frontiers in Microbiology, 6: 349. Status = PUBLISHED; Acknowledgment of Federal Support= Yes; Peer Reviewed = Yes
6. Labonté JM, Swan BK, Poulos B, Luo H, Koren S, Hallam SJ, Sullivan MB, Woyke T, Wommack KE, Stepanauskas R. (2015). Single cell genomics-based analysis of virus-host interactions in marine surface bacterioplankton. The ISME Journal, 9: 2386-2399. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
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9. Stepanauskas R. (2015). Crystal Ball: Re-defining microbial diversity from its single-celled building blocks. Environmental Microbiology Reports , 7: 36-37. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
10. Eiler A, Zaremba-Niedzwiedzka K, Martinez-Garcia M, McMahon KD, Stepanauskas R, Andersson SGE, Bertilsson S. (2014). Productivity and salinity structuring of the microplankton revealed by comparative freshwater metagenomics. Environmental Microbiology, 16: 2682-2698. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
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12. Kashtan N, Roggensack SE, Rodrigue S, Thompson JW, Biller SJ, Coe A, Ding H, Marttinen P, Malmstrom R, Stocker R, Follows MJ, Stepanauskas R, Chisholm SW (2014). Single cell genomics reveals hundreds of coexisting subpopulations in wild Prochlorococcus. Science, 344: 416-420. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
13. Kminek G, Conley C, Allen CC, Bartlett DH, Beaty DW, Benning LG, Bhartia R, Boston PJ, Duchaine C, Farmer JD,Flynn GJ, Glavin DP, Gorby Y, Hallsworth JE, Mogul R, Moser D, Buford Price P, Pukall R, Fernandez-Remolar D, Smith CL, Stedman K, Steele A, Stepanauskas R, Sun H, Vago JL, Voytek MA, Weiss PS, Westall F (2014). Report of the workshop for life detection in samples from Mars. Life Sciences in Space Research, 2: 1. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
14. Luo H, Tolar B, Swan B, Zhang C, Stepanauskas R, Moran MA, Hollibaugh JT (2014). Single-cell genomics shedding light on marine Thaumarchaeota diversification. The ISME Journal, 8: 732-736. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
15. Luo H, Swan BK, Stepanauskas R, Hughes AL, Moran MA (2014). Comparing Effective Population Sizes of Dominant Marine Alphaproteobacteria Lineages. Environmental Microbiology Reports, 6: 167-172.

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20. Thrash JC, Temperton B, Swan BK, Landry Z, Woyke T, DeLong EF, Stepanauskas R, Giovannoni SJ (2014). Single-cell enabled comparative genomics of a deep ocean SAR11 bathytype. The ISME Journal, 8: 1440-1451. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
21. Wasmund K, Schreiber L, Lloyd KG, Petersen DG, Schramm A, Stepanauskas R, Jørgensen BB, Adrian L. (2014). Genome sequencing of a single cell of the widely distributed marine subsurface Dehalococcoidia, phylum Chloroflexi. The ISME Journal, 8: 383-397. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
22. Rinke C, Schwientek P, Sczyrba A, Ivanova NN, Anderson IJ, Cheng JF, Darling A, Malfatti S, Swan BK, Gies EA, Dodsworth JA, Hedlund BP, Tsiamis G, Sievert SM, Liu WT, Eisen JA, Hallam S, Kyrpides N, Stepanauskas R, Rubin E, Hugenholtz P, Woyke T (2013). Insights into the phylogeny and coding potential of microbial dark matter. Nature, 499: 431-437. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes;
23. Swan BK, Tupper B, Sczyrba A, Lauro FM, Martinez-Garcia M, González JM, Luo H, Wright JJ, Landry ZC, Hanson NW, Thompson BP, Poulton NJ, Schwientek P, Acinas SG, Giovannoni SJ, Moran MA, Hallam SJ, Cavicchioli R, Woyke T, Stepanauskas R (2013). Prevalent genome streamlining and latitudinal divergence of planktonic bacteria in the surface ocean. Proceedings of the National Academy of Sciences, 110: 11463-11468. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes
24. Lloyd KG, Schreiber L, Petersen DG, Kjeldsen K, Lever MA, Stepanauskas R, Richter M, Kleindienst S, Lenk S, Schramm A, Jorgensen BB. 2013. Predominant archaea in marine sediments degrade detrital proteins. Nature 496:215-218. Status = PUBLISHED; Acknowledgment of Federal Support = Yes; Peer Reviewed = Yes

**Data Processing Description**

**BCO-DMO Processing Notes:**
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- replaced spaces with underscores

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## Data Files

| File |
|---|
| **taxon_table_SAG.csv** (Comma Separated Values (.csv), 75.04 KB) MD5:37da1229f48e2aaa4d13c242129dbd40<br>Primary data file for dataset ID 666274 |

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## Parameters

| Parameter | Description | Units |
|---|---|---|
| SAG | Single amplified genome identifier | unitless |
| IMG_Genome_ID | Accession number from IMG/M (Integrated Microbial Genomes and Microbiome Samples) | unitless |
| date_collection | sample collection date; formatted as yyyy-mm-dd | unitless |
| site_collection_growth_cond | Collection or isolation site; or growth conditions | unitless |
| depth | Collection depth | meters |
| lat | Latitude; north is positive | decimal degrees |
| lon | Longitude; east is positive | decimal degrees |
| Assembled_Genome_Size | Assembled genome size | base pairs |
| Gene_Count | Gene count | genes |
| Scaffold_Count | Scaffold count | scaffolds |
| Availability | Availability: whether the accession is public or date when release is expected | unitless |
| IMG_accession_link | Link to IMG accession page | unitless |

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## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | MiSeq and NextSeq 500 (Illumina) |
| **Generic Instrument Name** | Automated DNA Sequencer |
| **Dataset-specific Description** | Used to read base pairs |
| **Generic Instrument Description** | A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | high-throughput plate reader (BMG) |
| **Generic Instrument Name** | plate reader |
| **Generic Instrument Description** | Plate readers (also known as microplate readers) are laboratory instruments designed to detect biological, chemical or physical events of samples in microtiter plates. They are widely used in research, drug discovery, bioassay validation, quality control and manufacturing processes in the pharmaceutical and biotechnological industry and academic organizations. Sample reactions can be assayed in 6-1536 well format microtiter plates. The most common microplate format used in academic research laboratories or clinical diagnostic laboratories is 96-well (8 by 12 matrix) with a typical reaction volume between 100 and 200 uL per well. Higher density microplates (384- or 1536-well microplates) are typically used for screening applications, when throughput (number of samples per day processed) and assay cost per sample become critical parameters, with a typical assay volume between 5 and 50 µL per well. Common detection modes for microplate assays are absorbance, fluorescence intensity, luminescence, time-resolved fluorescence, and fluorescence polarization. From: http://en.wikipedia.org/wiki/Plate_reader, 2014-09-0-23. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | Roche LC480 |
| **Generic Instrument Name** | Thermal Cycler |
| **Generic Instrument Description** | A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html) |

| | |
|---|---|
| **Dataset-specific Instrument Name** | Covaris focused ultrasonicator |
| **Generic Instrument Name** | ultrasonic cell disrupter (sonicator) |
| **Generic Instrument Description** | Instrument that applies sound energy to agitate particles in a sample. |

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## Deployments

**Bigelow_Stepanauskas_2012**

| | |
|---|---|
| **Website** | https://www.bco-dmo.org/deployment/666293 |
| **Platform** | lab Bigelow |
| **Start Date** | 2012-09-01 |
| **End Date** | 2016-08-31 |
| **Description** | genomics studies |

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## Project Information

**Ocean's dark energy: Global inventory of chemoautotrophs in the aphotic realm (Dark ocean chemoautotrophs)**

**Coverage**: Global

*From NSF award abstract:*
The dark ocean, defined as the water column below the photic, contains one of the largest microbial biomes on earth, composed of active and metabolically diverse microorganisms. These biota impact local processes and the global carbon cycling, e.g. by conducting a large fraction of marine organic matter remineralization. An increasing body of evidence suggests that chemoautotrophy in the dark ocean may also be significant, with potentially major implications to the dark ocean's microbial ecology and biogeochemistry. However, it remains largely unanswered what energy sources and metabolic pathways are used to support this microbial-driven dark carbon fixation and which microbial taxonomic groups possess chemoautotrophic metabolic pathways in the dark ocean.

The overall goal of this project is to obtain a comprehensive, global inventory of chemoautotrophs in the dark ocean through large-scale microbial single cell genomics, supplemented with metagenomic and metatranscriptomic sequencing. The investigators will address the following general hypotheses:

1. Multiple prokaryote taxonomic groups found in the dark ocean contain chemoautotrophic metabolic pathways.

2. Both known and previously unrecognized chemoautotrophy pathways are present in dark ocean's prokaryotes.

3. Dark ocean chemoautotrophs are broadly distributed around the globe, with biogeographic patterns determined by the isopycnal movement of water masses, water mass age, and the downward flux of organic matter.

4. Diverse chemoautotrophy pathways are expressed in the dark ocean.

During the course of the project, single amplified genomes (SAGs) will be generated from all major intermediate and deep water masses around the globe, representing all major taxonomic groups of bacteria and archaea that are known to be present in the dark ocean. These SAGs will be analyzed for specific chemoautotrophy-indicative genes. Whole genome sequencing will be performed on a subset of SAGs, enabling detailed annotation of chemoautotrophy pathways. Metagenomic and metatranscriptomic fragment recruitment will be used to determine global patterns of chemoautotroph distribution and chemoautotrophy pathway expression. This ambitious project is made possible by the recent development of techniques and facilities for high-throughput genomic DNA recovery from individual cells at Bigelow Laboratory, genomic sequencing support provided by the U.S. Department of Energy Joint Genome Institute, and the establishment of a broad network of collaborations among many leading dark ocean microbiologists.

The project will generate a large quantity of unique reference materials, laying a solid foundation for future studies of dark ocean microorganisms, including 207 microbial genomes, representing all major taxonomic groups of bacteria and archaea from the dark ocean, multiple metagenomes, metatranscriptomes and pyrotag data sets, as well as genomic DNA from ~2,000 individual cells from diverse prokaryote taxonomic groups, water masses and geographic locations. The work will improve our understanding of the global carbon cycle, with direct relevance to climate change studies.

Publications produced as a result of this research:
Swan BK, Tupper B, Sczyrba A, Lauro FM, Martinez-Garcia M, González JM, Luo H, Wright JJ, Landry ZC, Hanson NW, Thompson BP, Poulton NJ, Schwientek P, Acinas SG, Giovannoni SJ, Moran MA, Hallam SJ, Cavicchioli R, Woyke T, Stepanauskas, R. 2013. Prevalent genome streamlining and latitudinal divergence of marine planktonic bacteria in the surface ocean. PNAS, v.TBD, p. TBD, published online June 25, 2013. doi: 10.1073/pnas.1304246110

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## Funding


| Funding Source | Award |
| --- | --- |
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1232982 |


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