



# Limited carbon cycling due to high-pressure effects on the deep-sea microbiome

---

In the format provided by the  
authors and unedited

## Supplementary information

**Supplementary Table 1. Station details on prokaryotic activity measurements performed in this study.** Information is provided for the on-deck atmospheric pressure samples collected by the sampling rosette with the conductivity-temperature-depth (CTD) system.

Cruise or sampling site	Area	St	Date	Latitude (°)	Longitude (°)	Depth (m)	Temp (°C)	Salinity	DO (μmol kg <sup>-1</sup> )
MODUPLAN	North Atlantic Ocean	8	5-Aug-2014	43.0000 N	9.7165 W	445	11.39	35.67	189
MODUPLAN	North Atlantic Ocean	14	8-Aug-2014	42.9998 N	10.6667 W	1140	10.60	36.12	171
MODUPLAN	North Atlantic Ocean	108	10-Aug-2014	43.0000 N	12.6667 W	1778	4.35	35.05	233
MODUPLAN	North Atlantic Ocean	59	19-Aug-2014	43.9000 N	3.7833 W	1974	3.91	35.03	229
MODUPLAN	North Atlantic Ocean	60	20-Aug-2014	43.8000 N	3.7833 W	990	9.72	35.78	175
MODUPLAN	North Atlantic Ocean	57	21-Aug-2014	44.2917 N	3.7832 W	1975	4.10	35.04	228
Rovinj*	Adriatic Sea	N/A	25-Oct-2014	45.0856 N	13.6394 E	20	19.50	N/D	N/D
RadProf15	North Atlantic Ocean	11	1-Aug-2015	43.0253 N	10.0173 W	2465	3.14	34.96	220
RadProf15	North Atlantic Ocean	111	5-Aug-2015	43.0010 N	14.0328 W	3152	2.79	34.94	213
SO248	Pacific Ocean	16†	26-May-2016	49.9999 N	179.5501 E	999	2.73	34.36	26
SO248*	Pacific Ocean	17	29-May-2016	54.0013 N	179.5813 E	501	3.63	34.08	26
M139*	Atlantic Ocean	A1†	12-Jul-2017	15.8860 N	68.9148 W	2002	4.12	34.98	197
M139	Atlantic Ocean	A3†	22-Jul-2017	23.5538 N	48.0838 W	3998	2.29	34.89	227
M139	Atlantic Ocean	A3†	22-Jul-2017	23.5538 N	48.0838 W	2000	3.68	35.00	223
M139	Atlantic Ocean	A5_6†	31-Jul-2017	10.3388 N	36.9597 W	3999	2.33	34.89	221
M139	Atlantic Ocean	A5_6†	31-Jul-2017	10.3388 N	36.9597 W	3001	2.75	34.93	225
M139	Atlantic Ocean	A5_6†	31-Jul-2017	10.3392 N	36.9617 W	474	8.56	34.90	69
MOBYDICK	Southern Ocean	M2_1†	26-Feb-2018	50.6160 S	72.0010 E	448	2.25	34.38	194
MOBYDICK	Southern Ocean	M3_1†	3-Mar-2018	50.6835 S	68.0622 E	1499	2.00	34.76	190
MOBYDICK	Southern Ocean	M2_2†	6-Mar-2018	50.6252 S	72.0134 E	400	2.16	34.30	211
MOBYDICK*	Southern Ocean	M1	8-Mar-2018	49.8502 S	74.9017 E	2499	1.01	34.72	197
MOBYDICK	Southern Ocean	M2_3	16-Mar-2018	50.6159 S	72.0013 E	175	1.72	33.99	302
MOBYDICK	Southern Ocean	M3_3	18-Mar-2018	50.6877 S	68.0664 E	1498	2.07	34.76	188
RadProf18	North Atlantic Ocean	111	24-Aug-2018	42.9998 N	14.0350 W	3443	2.63	34.93	224
RadCan18	North Atlantic Ocean	C3	27-Aug-2018	43.7668 N	6.1672 W	743	10.23	35.67	182
POSEIDON	Atlantic Ocean	5	7-Mar-2019	36.1575 S	44.3407 W	2565	2.41	34.82	204
POSEIDON	Atlantic Ocean	9	12-Mar-2019	25.4064 S	35.0020 W	3156	2.66	34.91	237
POSEIDON	Atlantic Ocean	13	16-Mar-2019	14.4742 S	30.6714 W	2962	2.69	34.90	229
POSEIDON	Atlantic Ocean	19	23-Mar-2019	5.9091 N	29.7460 W	2375	3.16	34.95	229
POSEIDON	Atlantic Ocean	22	26-Mar-2019	13.5957 N	29.7139 W	3942	2.37	34.89	218
POSEIDON	Atlantic Ocean	27	31-Mar-2019	23.7935 N	23.9188 W	4002	2.40	34.90	219

\*Sample used for instrumental test; †Metaproteomics stations<sup>1</sup>; N/A: not applicable; N/D: not determined; DO-dissolved oxygen measured with an oxygen sensor (Sea-Bird SBE 43 or Aanderaa 4831F).

**Supplementary Table 2. Leucine incorporation rates and incubation conditions under *in situ* and atmospheric pressure conditions.**

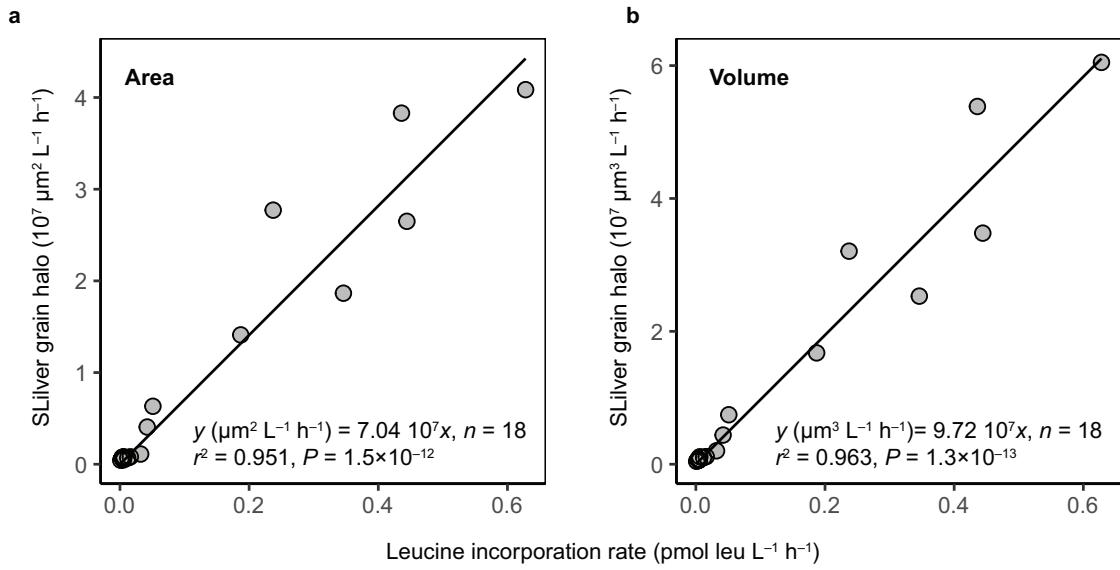
Cruise/ sampling site	St.	Atmospheric pressure condition					<i>In situ</i> condition				
		Depth (m)	Inc. temp. (°C)	Duration (h)	Leu incorp. Mean n	SD or mean – repl.	Depth (m)	Inc. temp. (°C)	Duration (h)	Leu incorp. Mean n	SD or mean – repl.
MODUPLAN	8	445	10	6.2	0.400 1	N/A	500	11.4	6.0	0.289 2	0.035
	14	1140	10	8.0	0.088 2	0.000	1150	10.6	8.0	0.046 2	0.003
	108	1778	4	10.4	0.028 1	N/A	1800	4.4	9.5	0.013 2	0.006
	59	1974	4	8.1	0.077 1	N/A	2000	3.9	8.1	0.009 2	0.004
	60	990	10	8.2	0.074 2	0.032	1000	9.7	8.0	0.053 2	0.002
	57	1975	4	8.1	0.033 2	0.006	2000	4.1	7.7	0.008 2	0.002
RadProf15	11	2465	0–3	12.2	0.047 3	0.017	2500	3.1	11.8	0.011 2	0.004
	111	3152	2.5	12.1	0.014 3	0.010	3200	2.8	12.0	0.007 2	0.000
SO248	16	999	4	8.1	0.088 3	0.003	1000	2.7	7.5	0.058 2	0.018
M139	A3	3998	2.5	12.0	0.011 3	0.000	3983	2.3	12.0	0.003 3	0.000
	A3	2000	2.5	10.2	0.016 3	0.000	1995	3.7	10.0	0.004 3	0.001
	A5_6	3999	2.5	11.0	0.033 3	0.002	4013	2.3	10.6	0.004 2	0.000
	A5_6	3001	2.5	10.7	0.013 3	0.001	3002	2.8	11.0	0.004 2	0.000
	A5_6	474	7	6.0	0.336 3	0.022	453	8.6	6.0	0.205 2	0.018
	M2_1	448	2.2	7.5	1.228 3	0.023	450	2.2	2.8	1.089 2	0.030
MOBYDICK	M3_1	1499	1.9	7.0	0.070 3	0.002	1470	2.0	5.8	0.047 2	0.002
	M2_2	400	1.4	7.3	0.651 3	0.023	400	2.2	7.2	0.484 2	0.048
	M2_3	175	1.4	4.1	1.400 3	0.050	175	1.7	4.2	1.118 2	0.038
	M3_3	1498	1.7	7.2	0.060 3	0.008	1500	2.1	7.6	0.044 2	0.002
RadProf18	111	3443	2.6	8.3	0.007 3	0.000	3501	2.6	8.0	0.003 2	0.000
RadCan18	C3	743	10.2	3.3	0.440 3	0.004	751	10.2	3.3	0.243 2	0.006
POSEIDON	5	2565	2.4	7.6	0.023 2	0.002	2560	2.4	7.0	0.013 2	0.001
	9	3156	2.7	6.9	0.004 2	0.001	3155	2.7	6.8	0.003 2	0.000
	13	2962	2.7	6.8	0.006 2	0.001	2961	2.7	6.6	0.002 2	0.000
	19	2375	3.2	7.5	0.012 2	0.000	2375	3.2	7.2	0.004 2	0.001
	22	3942	2.4	8.2	0.005 2	0.000	3941	2.4	8.3	0.002 2	0.000
	27	4002	2.4	8.6	0.005 2	0.000	4000	2.4	8.4	0.001 2	0.000

Inc. temp.: incubation temperature; Duration: incubation time; Leu incorp.: leucine incorporation rate in pmol leu L<sup>-1</sup> h<sup>-1</sup>; mean – repl.: |mean-replicate| of duplicate bottle incubations; standard deviation (SD) was used when triplicates were available; N/A: not applicable.

**Supplementary Table 3. Oligonucleotide probes applied in MICRO-CARD-FISH analyses.**

Target organisms	Probe	Sequence (5' to 3')	FA (%)
Bacteria	EUB338 <sup>2</sup>	GCTGCCTCCCGTAGGAGT	
	EUB338-II <sup>3</sup>	GCAGGCCACCCGTAGGTGT	55
	EUB338-III <sup>3</sup>	GCTGCCACCCGTAGGTGT	
SAR11 clade	SAR11-152R <sup>4</sup>	ATTAGCACAAAGTTCCYCGTGT	
	SAR11-441R <sup>4</sup>	TACAGTCATTTCTTCCCCGAC	45
	SAR11-542R <sup>4</sup>	TCCGAACTACGCTAGGTC	
SAR202 clade	SAR11-732R <sup>4</sup>	GTCAGTAATGATCCAGAAAGYTG	
	SAR202-312 <sup>5</sup>	TGTCTCAGTCCCCCTCTG	55
	SAR406-97 <sup>6</sup>	CACCCGTTCGCCAGTTA	60
Thaumarchaeota Marine Group I	Cren554 <sup>7</sup>	TTAGGCCAATAATCMTCT	
	Cren537 <sup>8</sup>	TGACCACTTGAGGTGCTG	20
<i>Alteromonas/Colwellia</i>	Alt1413 <sup>9</sup>	TTTGCATCCCCTCAGTAC	55
Bacteroidetes	CF319a <sup>10</sup>	TGGTCCGTGTCTCAGTAC	55
Euryarchaeota Marine Group II	Eury806 <sup>8</sup>	CACAGCGTTTACACCTAG	20
Negative control Bacteria	NON338 <sup>11</sup>	ACTCCTACGGGAGGCAGC	55

FA: Formamide concentration of the hybridization buffer



**Supplementary Fig. 1. Single-cell activity measurements.** Relationship of bulk leucine incorporation rates and silver grain halo around cells expressed as **a**, area and **b**, volume. All the MICRO-CARD-FISH samples under *in situ* and atmospheric pressure conditions at 9 stations (see Methods) were used to obtain the regressions. Plots are shown as mean values of 8 technical replicates which correspond to the number of probes used. A slightly better correlation between bulk leucine incorporation and silver grain halo volume than with halo area was found. Consequently, single-cell leucine uptake was calculated using the regression with halo volume in this study.

## Supplementary references:

- 1 Zhao, Z., Baltar, F. & Herndl, G. J. Linking extracellular enzymes to phylogeny indicates a predominantly particle-associated lifestyle of deep-sea prokaryotes. *Sci. Adv.* **6**, eaaz4354 (2020).
- 2 Amann, R. I. *et al.* Combination of 16S rRNA-targeted oligonucleotide probes with flow cytometry for analyzing mixed microbial populations. *Appl. Environ. Microbiol.* **56**, 1919–1925 (1990).
- 3 Daims, H., Bruhl, A., Amann, R., Schleifer, K. H. & Wagner, M. The domain-specific probe EUB338 is insufficient for the detection of all Bacteria: Development and evaluation of a more comprehensive probe set. *Syst. Appl. Microbiol.* **22**, 434–444 (1999).
- 4 Morris, R. M. *et al.* SAR11 clade dominates ocean surface bacterioplankton communities. *Nature* **420**, 806–810 (2002).
- 5 Morris, R. M., Rappe, M. S., Urbach, E., Connon, S. A. & Giovannoni, S. J. Prevalence of the *Chloroflexi*-related SAR202 bacterioplankton cluster throughout the mesopelagic zone and deep ocean. *Appl. Environ. Microbiol.* **70**, 2836–2842 (2004).
- 6 Fuchs, B. M., Woebken, D., Zubkov, M. V., Burkhill, P. & Amann, R. Molecular identification of picoplankton populations in contrasting waters of the Arabian Sea. *Aquat. Microb. Ecol.* **39**, 145–157 (2005).
- 7 Massana, R., Murray, A. E., Preston, C. M. & DeLong, E. F. Vertical distribution and phylogenetic characterization of marine planktonic *Archaea* in the Santa Barbara Channel. *Appl. Environ. Microbiol.* **63**, 50–56 (1997).
- 8 Teira, E., Reinthaler, T., Pernthaler, A., Pernthaler, J. & Herndl, G. J. Combining catalyzed reporter deposition-fluorescence in situ hybridization and microautoradiography to detect substrate utilization by Bacteria and Archaea in the deep ocean. *Appl. Environ. Microbiol.* **70**, 4411–4414 (2004).
- 9 Eilers, H., Pernthaler, J., Glockner, F. O. & Amann, R. Culturability and in situ abundance of pelagic bacteria from the North Sea. *Appl. Environ. Microbiol.* **66**, 3044–3051 (2000).
- 10 Manz, W., Amann, R., Ludwig, W., Vancanneyt, M. & Schleifer, K. H. Application of a suite of 16S rRNA-specific oligonucleotide probes designed to investigate bacteria of the phylum cytophaga-flavobacter-bacteroides in the natural environment. *Microbiology* **142**, 1097–1106 (1996).
- 11 Wallner, G., Amann, R. & Beisker, W. Optimizing fluorescent in situ hybridization with rRNA-targeted oligonucleotide probes for flow cytometric identification of microorganisms. *Cytometry* **14**, 136–143 (1993).