

FINAL CRUISE REPORT OF THE TARA OCEANS MISSION

(Including Tara Oceans and Tara Oceans Polar Circle missions)
(2009 – 2013)



Photo 1: ©Francis Latreille - Tara Ocean Foundation

PARTNERS OF THE TARA OCEANS MISSIONS

Tara Oceans (which includes the Tara Oceans and Tara Oceans Polar Circle missions) would not exist without the leadership of the Tara Ocean Foundation and the continuous support of 23 partner institutes. We further thank the commitment of the following sponsors: the French CNRS (in particular Groupement de Recherche GDR3280 and the Research Federation for the Study of Global Ocean Systems Ecology and Evolution FR2022/Tara GOSEE), the French Facility for Global Environment (FFEM), the European Molecular Biology Laboratory and its Advanced Light Microscopy Facility (ALMF), Genoscope/CEA, the Vlaams Instituut voor Biotechnologie (VIB), Stazione Zoologica Anton Dohrn, UNIMIB, Fund for Scientific Research – Flanders, Rega Institute, KU Leuven, the French Ministry of Research and the French Government Investissements d'Avenir programmes OCEANOMICS (ANR-11- BTBR-0008), FRANCE GENOMIQUE (ANR-10- INBS-09-08) and MEMO LIFE (ANR-10- LABX-54), the PSL research university (ANR-11- IDEX-0001-02) and EMBRC- France (ANR-10- INBS-02), ANR (projects POSEIDON/ANR-09-BLAN-0348, PHYTBAC/ANR-2010-1709-01, PROMETHEUS/ANR-09-PCS-GENM-217, TARA-GIRUS/ANR-09-PCS-GENM 218, European Union FP7 (MicroB3/No.287589, IHMS/HEALTH-F4-2010-261376, ERC Advanced Grant Awards to CB (Diatomite: 294823), Gordon and Betty Moore Foundation grant (#3790) to MBS, Spanish Ministry of Science and Innovation grant CGL2011-26848/BOS MicroOcean PANGENOMICS to SGA, TANIT (CONES 2010-0036) from the Agència de Gestió d'Ajuts Universitaris i Reserca funded to SGA, JSPS KAKENHI Grant Number 26430184 to HO, FWO, BIO5, Biosphere 2. Funding for the collection and processing of the Tara Oceans dataset was provided by the NASA Ocean Biology and Biogeochemistry Program under grants NNX11AQ14G, NNX09AU43G, NNX13AE58G and NNX15AC08G (to the University of Maine), the Canada Excellence Research Chair in Remote Sensing of Canada's New Arctic Frontier and the Canada Foundation for Innovation. We also thank Agnès b. and E. Bourgois, the Prince Albert II de Monaco Foundation, the Veolia Foundation, Region Bretagne, Lorient Agglomération, Serge Ferrari, Worldcourier, Illumina, the EDF Foundation, FRB and KAUST for support and commitment. The global sampling effort was made possible by countless scientists and crew who performed sampling aboard the schooner Tara from 2009 to 2013, and we thank MERCATOR- CORIOLIS and ACRI- ST for providing daily satellite data during the expeditions. We are also grateful to the French Ministry of Foreign Affairs for supporting the expedition and to the countries who graciously granted sampling permissions. We declare that all data reported herein are fully and freely available from the date of publication, with no restrictions, and that all of the samples, analyses, publications, and ownership of data are free from legal entanglement or restriction of any sort by the various nations whose waters the Tara Oceans missions sampled in.

Tara Oceans consortium

European Molecular Biology Laboratory (EMBL) | Le Centre National De Recherche Scientifique (CNRS) | L'Université Pierre et Marie Curie - (PARIS 6) (UPMC) | L'Ecole Normale Supérieure (ENS) | Le Commissariat à l'Energie Atomique et aux Energies Alternatives (CEA) | Vlaams Instituut voor Biotechnologie (VIB) | Arizona Board of Regents on behalf of the University of Arizona | UNIVERSITY OF BREMEN (UniHB) | Muséum National d'Histoire Naturelle (MNHN) | Università' Degli Studi di Milano – Bicocca (UNIMIB) | Instituto de Ciencias del Marítimo, CSIC (ICM-CSIC) | Bigelow Laboratory (Bigelow) | University College Dublin (UCD) | Stazione Zoologica di Napoli (SZN) |

Scientific project coordinators and researchers

Patrick WINCKER (Génomique Métabolique, Genoscope, Institut de biologie François Jacob, Commissariat à l'Energie Atomique (CEA), CNRS, Université Evry, Université Paris-Saclay, Evry, France) | **Jean WEISSENBACH** (Génomique Métabolique, Genoscope, Institut de biologie François Jacob, Commissariat à l'Energie Atomique (CEA), CNRS, Université Evry, Université Paris-Saclay, Evry, France) | **Didier VELAYOUDON** (DVIP Consulting, Sèvres, France) | **Shinichi SUNAGAWA** (Structural and Computational Biology, European Molecular Biology Laboratory, Meyerhofstr. 1, 69117 Heidelberg, Germany) | **Matthew B. SULLIVAN** (Department of Microbiology, The Ohio State University, Columbus, OH

TARA OCEANS – FINAL CRUISE REPORT

43214, USA) | **Lars STEMMANN** (Sorbonne Universités, UPMC Université Paris 06, CNRS, Laboratoire d'océanographie de Villefranche (LOV), Observatoire Océanologique, 06230 Villefranche-sur-Mer, France) | **Sabrina SPEICH** (Laboratoire de Physique des Océans, UBO-IUEM, Place Copernic, 29820 Plouzané, France) | **Mike SIERACKI** (National Science Foundation, Arlington, VA 22230, USA) | **Christian SARDET** (Sorbonne Universités, UPMC Université Paris 06, CNRS, Laboratoire d'océanographie de Villefranche (LOV), Observatoire Océanologique, 06230 Villefranche-sur-Mer, France) | **Emmanuel G. REYNAUD** (Earth Institute, University College Dublin, Dublin, Ireland) | **Jeroen RAES** (Department of Microbiology and Immunology, Rega Institute, KU Leuven, Herestraat 49, 3000 Leuven, Belgium) | **Stéphane PESANT** (MARUM, Center for Marine Environmental Sciences, University of Bremen, Bremen, Germany) | **Hiroyuki OGATA** (Institute for Chemical Research, Kyoto University, Gokasho, Uji, Kyoto, 611-001, Japan) | **Fabrice NOT** (CNRS, UMR 7144, Sorbonne Universités, UPMC Université Paris 06, Station Biologique de Roscoff, 29680 Roscoff, France) | **Uros KRZIC** (Cell Biology and Biophysics, European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany) | **Eric KARSENTI** (Ecole Normale Supérieure, PSL Research University, Institut de Biologie de l'Ecole Normale Supérieure (IBENS), CNRS UMR 8197, INSERM U1024, 46 rue d'Ulm, F-75005 Paris, France) | **Lee KARP-BOSS** (School of Marine Sciences, University of Maine, Orono, Maine 04469, USA) | **Stefanie KANDELS** (Structural and Computational Biology, European Molecular Biology Laboratory, Meyerhofstr. 1, 69117 Heidelberg, Germany) | **Olivier JAILLON** (Génomique Métabolique, Genoscope, Institut de biologie François Jacob, Commissariat à l'Energie Atomique (CEA), CNRS, Université Evry, Université Paris-Saclay, Evry, France) | **Daniele IUDICONE** (Stazione Zoologica Anton Dohrn, Villa Comunale, 80121 Naples, Italy) | **Pascal HINGAMP** (Aix Marseille Univ, Université de Toulon, CNRS, IRD, MIO, Marseille, France) | **Nigel GRIMSLEY** (CNRS, UMR 7232, BIOM, Avenue du Fontaulé, 66650 Banyuls-sur-Mer, France) | **Gabriel GORSKY** (Sorbonne Universités, UPMC Université Paris 06, CNRS, Laboratoire d'océanographie de Villefranche (LOV), Observatoire Océanologique, 06230 Villefranche-sur-Mer, France) | **Mick FOLLOWS** (Department of Earth, Atmospheric and Planetary Sciences, Massachusetts Institute of Technology, Cambridge, MA, USA) | **Colomban DE VARGAS** (CNRS, UMR 7144, EPEP & Sorbonne Universités, UPMC Université Paris 06, Station Biologique de Roscoff, 29680 Roscoff, France) | **Chris BOWLER** (Ecole Normale Supérieure, PSL Research University, Institut de Biologie de l'Ecole Normale Supérieure (IBENS), CNRS UMR 8197, INSERM U1024, 46 rue d'Ulm, F-75005 Paris, France) | **Emmanuel BOSS** (School of Marine Sciences, University of Maine, Orono, Maine 04469, USA) | **Peer BORK** (Structural and Computational Biology, European Molecular Biology Laboratory, Meyerhofstr. 1, 69117 Heidelberg, Germany) | **Silvia G. ACINAS** (Department of Marine Biology and Oceanography, Institut de Ciències del Mar (CSIC), Barcelona, Catalonia, Spain) | **Francesca BENZONI** (Università degli Studi di Milano-Bicocca IT / Coral Reefs) | **Gilles REVERDIN** (CNRS/UPMC, FR / Physico-Chemistry) | **Pascal JOANNOT** (MNHN, FR / Archiving/Authorizations) | **Detlev ARENDT** (EMBL / Evo Devo).

Tara Oceans Polar Circle Coordinators and Participants

Silvia G. Acinas (Department of Marine Biology and Oceanography, Institut de Ciències del Mar (CSIC), Barcelona, Catalonia, Spain) | **Marcel Babin** (Département de biologie, Québec Océan and Takuvik Joint International Laboratory (UMI3376), Université Laval (Canada) - CNRS (France), Université Laval, Québec, QC, G1V 0A6, Canada) | **Peer Bork** (Structural and Computational Biology, European Molecular Biology Laboratory, Meyerhofstr. 1, 69117 Heidelberg, Germany) | **Emmanuel Boss** (School of Marine Sciences, University of Maine, Orono, Maine 04469, USA) | **Chris Bowler** (Ecole Normale Supérieure, PSL Research University, Institut de Biologie de l'Ecole Normale Supérieure (IBENS), CNRS UMR 8197, INSERM U1024, 46 rue d'Ulm, F-75005 Paris, France) | **Guy Cochrane** (European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Wellcome Trust Genome Campus, Hinxton, Cambridge, UK) | **Colomban de Vargas** (CNRS, UMR 7144, EPEP & Sorbonne Universités, UPMC Université Paris 06, Station Biologique de Roscoff, 29680 Roscoff, France) | **Mick Follows** (Department of Earth, Atmospheric and Planetary Sciences, Massachusetts Institute of Technology, Cambridge, MA, USA) | **Gabriel Gorsky** (Sorbonne Universités, UPMC Université Paris 06, CNRS, Laboratoire d'océanographie de Villefranche (LOV), Observatoire Océanologique, 06230 Villefranche-sur-Mer, France) | **Lionel Guidi** (Sorbonne Universités, UPMC Université Paris 06, CNRS, Laboratoire d'océanographie de Villefranche (LOV), Observatoire Océanologique, 06230 Villefranche-sur-Mer, France) | **Nigel Grimsley** (CNRS, UMR 7232, BIOM, Avenue du Fontaulé, 66650 Banyuls-sur-Mer, France) | **Pascal Hingamp** (Aix Marseille Univ,

TARA OCEANS – FINAL CRUISE REPORT

Université de Toulon, CNRS, IRD, MIO, Marseille, France) | **Daniele Iudicone** (Stazione Zoologica Anton Dohrn, Villa Comunale, 80121 Naples, Italy) | **Olivier Jaillon** (CEA - Institut de Génomique, Genoscope, 2 rue Gaston Crémieux, Evry France) | **Stefanie Kandels** (Structural and Computational Biology, European Molecular Biology Laboratory, Meyerhofstr. 1, 69117 Heidelberg, Germany) | **Lee Karp-Boss** (School of Marine Sciences, University of Maine, Orono, Maine 04469, USA) | **Eric Karsenti** (Ecole Normale Supérieure, PSL Research University, Institut de Biologie de l'Ecole Normale Supérieure (IBENS), CNRS UMR 8197, INSERM U1024, 46 rue d'Ulm, F-75005 Paris, France) | **Fabrice Not** (CNRS, UMR 7144, Sorbonne Universités, UPMC Université Paris 06, Station Biologique de Roscoff, 29680 Roscoff, France) | **Hiroyuki Ogata** (Institute for Chemical Research, Kyoto University, Gokasho, Uji, Kyoto, 611-001, Japan) | **Nicole Poulton** (Bigelow Laboratory for Ocean Sciences, East Boothbay, ME, 04544, USA) | **Stéphane Pesant** (MARUM, Center for Marine Environmental Sciences, University of Bremen, Bremen, Germany) | **Jeroen Raes** (Department of Microbiology and Immunology, Rega Institute, KU Leuven, Herestraat 49, 3000 Leuven, Belgium) | **Christian Sardet** (Sorbonne Universités, UPMC Université Paris 06, CNRS, Laboratoire d'océanographie de Villefranche (LOV), Observatoire Océanologique, 06230 Villefranche-sur-Mer, France) | **Sabrina Speich** (Laboratoire de Physique des Océans, UBO-IUEM, Place Copernic, 29820 Plouzané, France) | **Lars Stemmann** (Sorbonne Universités, UPMC Université Paris 06, CNRS, Laboratoire d'océanographie de Villefranche (LOV), Observatoire Océanologique, 06230 Villefranche-sur-Mer, France) | **Matthew B. Sullivan** (Department of Microbiology, The Ohio State University, Columbus, OH 43214, USA) | **Shinichi Sunagawa** (Department of Biology, Institute of Microbiology and Swiss Institute of Bioinformatics, ETH Zurich, Vladimir-Prelog-Weg 4, 8093 Zurich, Switzerland) | **Patrick Wincker** (CEA - Institut de Génomique, Genoscope, 2 rue Gaston Crémieux, Evry France).

And

Joannie Ferland (Département de biologie, Québec Océan and Takuvik Joint International Laboratory (UMI 3376), Université Laval (Canada) - CNRS (France), Université Laval, Québec, QC, G1V 0A6, Canada) | **Claudie Marec** (Département de biologie, Québec Océan and Takuvik Joint International Laboratory (UMI 3376), Université Laval (Canada) - CNRS (France), Université Laval, Québec, QC, G1V 0A6, Canada) | **Marc Picheral** (Sorbonne Universités, UPMC Univ Paris 06, UMR 7093 LOV, F-75005, Paris, France) | **Céline Dimier** (CNRS, UMR 7144, EPEP & Sorbonne Universités, UPMC Université Paris 06, Station Biologique de Roscoff, 29680 Roscoff, France) | **Julie Poulain** (Génomique Métabolique, Genoscope, Institut François Jacob, CEA, CNRS, Univ Evry, Université Paris-Saclay) | **Sergey Pisarev** (Shirshov Institute of Oceanology of Russian Academy of Sciences, 36 Nakhimovskiy prosp, 117997, Moscow, Russia) | **Margaux Carmichael** (Sorbonne Université, CNRS, Station Biologique de Roscoff, AD2M ECOMAP, 29680 Roscoff, France).

TABLE OF CONTENTS

PARTNERS OF THE TARA OCEANS MISSIONS -----	2
TARA OCEANS CONSORTIUM -----	2
SCIENTIFIC PROJECT COORDINATORS AND RESEARCHERS -----	2
TARA OCEANS POLAR CIRCLE COORDINATORS AND PARTICIPANTS -----	3
TABLE OF CONTENTS -----	5
ABOUT THE TARA OCEANS MISSIONS -----	7
CRUISE NAME : TARA OCEANS -----	7
RESEARCH UNIT: -----	7
CHIEF SCIENTIST : ERIC KARSENTI -----	7
GENERAL CONTEXT OF THE CRUISES -----	7
WHO IS THE TARA OCEAN FOUNDATION? -----	8
WHY THE TARA OCEANS MISSIONS? -----	8
WHERE DO THE MISSIONS TAKE PLACE ? -----	8
OBJECTIVES OF THE CRUISES -----	9
WHY PLANKTON ? -----	9
ABOUT OUR SAMPLING STRATEGY -----	10
GLOBAL RESULTS OF THE TARA OCEANS MISSION -----	11
THE “-OMICS” DATA -----	11
THE “IMAGING” DATA -----	12
THE “ECOLOGICAL” DATA -----	12
VIRUSES -----	12
PROKARYOTES -----	14
PROTISTS -----	15
METAZOANS -----	16
PLANKTON SYSTEMS ECOLOGY -----	17
PLANKTON SCREENING -----	17
TARA OCEANS’ KNOWLEDGE BASE -----	18

TARA OCEANS – FINAL CRUISE REPORT

BIBLIOGRAPHY ----- **20**

DATA BASE OF THE TARA OCEANS MISSION ----- **20**

LIST OF SCIENTIFIC PUBLICATIONS ----- **20**

ABOUT THE TARA OCEANS MISSIONS

CRUISE NAME : Tara Oceans

Research vessel: Tara (schooner)	
Start date: September 2009	Departure port: Lorient (France)
End date: December 2013	Arrival port: Lorient (France)

RESEARCH UNIT:

A consortium of scientists mainly from France's National Centre for Scientific Research (CNRS), the European Molecular Biology Laboratory (EMBL), France's Alternative Energies and Atomic Energy Commission (CEA), the Ohio state University, University of Sorbonne, Roscoff marine station, the Ecole normale supérieure, Stazione Zoologica Anton Dohrn, Genoscope, Bremen University, Kyoto University and ETH Zurich.

CHIEF SCIENTIST : Eric Karsenti

Research unit:

European Molecular Biology Laboratory

Address:

Phone:

Tel: +33 6 23 06 83 97 (France)

Email:

Karsenti@embl.de



Photo 3: Abaigan Island - Kiribati ©Nicolas De La Brosse - Tara Ocean Foundation

GENERAL CONTEXT OF THE CRUISES

Who is the Tara Ocean Foundation?

The Tara Oceans mission is a one-of-a-kind expedition. The sampling and study research have been conducted aboard the Tara Ocean Foundation schooner called *Tara*.

Tara Ocean Foundation is a non-profit organization working in favour of the environment and research. Tara is a schooner built for extreme conditions. For 12 years, Tara has been constantly on the move: the schooner has travelled 400,000 kilometres across all the world's oceans. We have accomplished 10 missions to study and understand the impacts of climate change and the ecological crisis on the ocean, with concrete results.

Why the Tara Oceans Missions?

There have been four major global cruises to map ocean plankton so far: the Challenger Expedition (1872-1876), Craig Venter's Global Ocean Survey (2003-2008), the Malaspina Expedition (2010), and the Tara Oceans expeditions (Tara Oceans, 2009-2012; Tara Oceans Polar Circle, 2012-2013). Only the latter sought to study viruses to fish larvae, organisms spanning 8 orders of magnitude in size, using the most cutting-edge molecular and imaging techniques available. During two circum-global navigations, we systematically collected eco-morpho-genetic data at 210 sites, 3 depths, covering most biogeographic provinces of the world's ocean.

The objectives of Tara oceans mission, an international, multidisciplinary project, was to get a planetary scale understanding of the ocean ecosystem, particularly in light of climate change and to assess the complexity of ocean life across comprehensive taxonomic and spatial scales.

Where do the missions take place ?

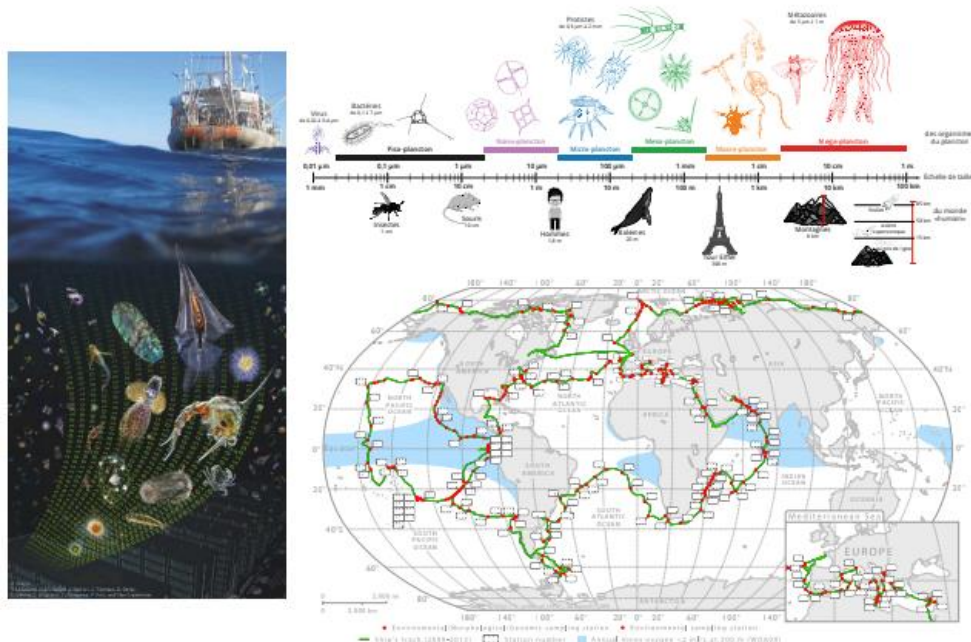


Figure 1. The Tara Oceans expeditions systematically sampled the world's ocean at 210 sites, 3 depths, and across 11 organismal size fractions covering 8 orders of size magnitude from viruses to animals. The 40,000 standardized plankton samples embedded into a rich context of physico-chemical parameters cover unique global spatial, seasonal, and taxonomic scales.

TARA OCEANS – FINAL CRUISE REPORT



Figure 1: The sea route followed by the Tara Oceans mission

OBJECTIVES OF THE CRUISES

The goal of Tara Oceans mission was to improve our understanding of plankton, how it evolves, how it interconnects and moves constantly from one ocean to another. How are micro-organisms distributed in the oceans and what is their biodiversity? We only know a tenth, perhaps a hundredth, of what there is to know. And what about the risks to plankton, the bacteria and the viruses? Are all these kingdoms linked and reliant on each other? In localized areas or everywhere? How many of them are there? What influence does temperature, salinity, acidity and physico-chemical parameters have on these strange creatures, and in which regions?

In 2008, to answer these questions and with the help of the Tara Ocean Foundation, Eric Karsenti, cell biologist and sailor, assembled a team of researchers with complementary skills in ocean biology and ecology, physical oceanography, cell and systems biology, genomics and imaging, around the schooner Tara and a common dream: assessing a planetary ecosystem globally, from viruses to animals, from genes to the entire community, and integrating biological data into a rich context of physico-chemical parameters.

Why Plankton ?

Plankton, with its relative biological simplicity and homogeneity, the small size of all organisms from viruses to fish larvae, the constant re-organization of communities with high-turnover, and the continuous fossil record of some of its components, is arguably the best global ecosystem to achieve this dream of understanding the ecological and evolutionary principles underlying the functioning of a complex adaptive ecological system on our planet. What's more, planktonic ecosystems, at the base of the oceanic food web, have generated our oxygenic atmosphere long before terrestrial plants emerged, are still today performing ~half of the photosynthesis on our planet, and sequester massive amounts of atmospheric CO₂ into the ocean interior. Into this context the Tara Oceans project to systematically sample plankton ecosystems across the world's ocean was born.



Figure 2: Photo 4: Tara's bow - Pete West - Bioquest Production

ABOUT OUR SAMPLING STRATEGY

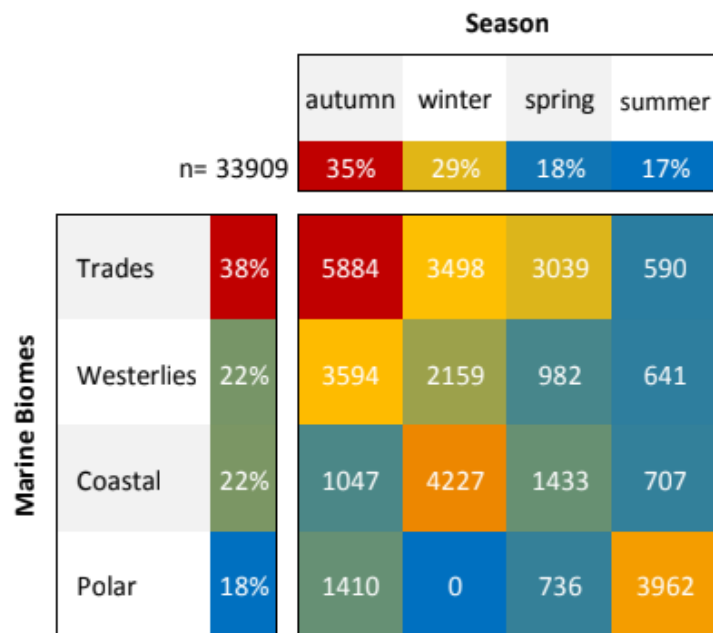
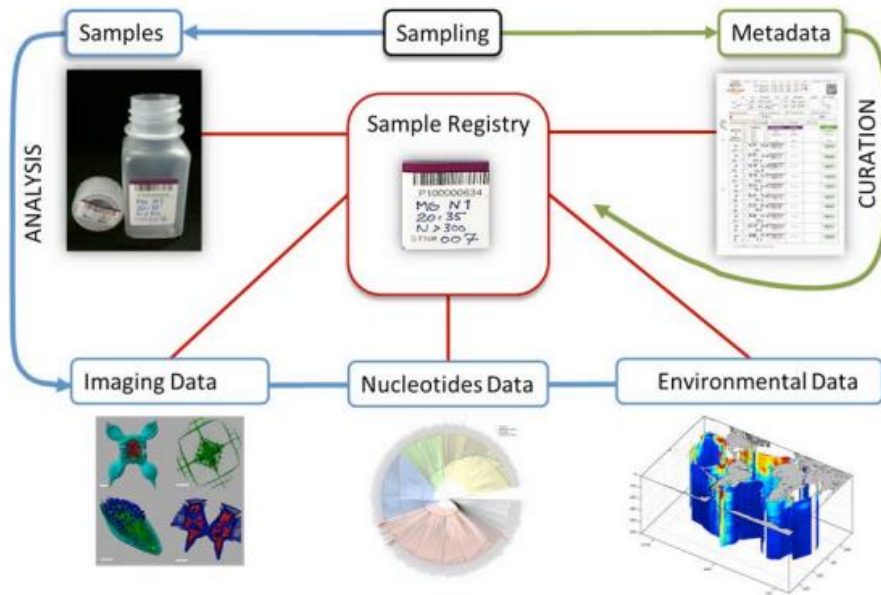


Figure 2. Tara Oceans (TO) strategy for samples, data, and metadata archiving and integration.

Upper part: the origin of the ~40,000 samples is key to connecting biological, chemical, and physical data, and Tara Oceans has set the trend in marine science with the most comprehensive registries of sample provenance and context to date (*Deliverables B, C*). Bottom part: Example of a contextual heatmap based on TO sample registries, indicating how available samples are distributed with respect to their origins and environmental contexts.

GLOBAL RESULTS OF THE TARA OCEANS MISSION

On board the schooner *Tara*, Tara Oceans' team sampled plankton at **210** globally distributed sites at depths down to **1,000m**. We described publicly available resources of molecular, morphological and environmental data, and discuss how an ecosystems biology approach has expanded our understanding of plankton diversity and ecology in the ocean as a planetary, interconnected ecosystem. These efforts illustrated how global-scale concepts and data can help to integrate biological complexity into models and serve as a baseline for assessing ecosystem changes and the future habitability of our planet in the Anthropocene epoch.

Tara Oceans mission came back with a treasure-trove of **~40,000** standardized plankton samples embedded into a rich context of physico-chemical parameters. Thanks to the French 'Investissement d'Avenir' grant OCEANOMICS and France-Genomics, we could generate, organize, and start analyzing data generated from these samples: >250 billion paired DNA reads (or >50 Terabases of raw DNA data) and >6 million images of single plankton (>30 Terabytes of raw data), obtained across 11 organismal size-fractions (>8 500 plankton subcommunities) with a combination of innovative approaches in multi-omics technologies and automated imaging. **This represents today by far the most comprehensive, publicly available, description of a planetary biome, and a critical base line to assess Earth-system changes.**

This report briefly synthesizes the Tara Oceans 'omics', 'imaging' and 'ecological' data, their integration in European permanent and public databases, and their use to provide a new view of plankton ecosystems, within each domain of life (viruses, prokaryotes, protists, and metazoans).

We declare that all data reported herein are only used for fundamental research purposes and are not meant to be used for commercial purposes.

The “-OMICS” data

We used high-throughput DNA/RNA sequencing to assess the genetic complexity of Tara Oceans plankton samples. Multi-marker DNA metabarcoding (metaB) provided a primary vision of the diversity and abundance of prokaryotic and eukaryotic taxa inhabiting the ocean globally. Metagenomics (metaG) and metatranscriptomics (metaT) revealed the gene content and functional potential of viruses, prokaryotes and eukaryotes, generating large databases that can be leveraged to provide insights into population structure, gene evolution and mutation pressure across the three kingdoms of Life.

In addition, metaT provide information about gene expression in natural conditions for both eukaryotes and prokaryotes. These efforts have

led to the creation of large metabarcodes and gene collections, annotated for their taxonomic and functional content, as well as their abundance in the ocean, a unique resource not only for marine biology and ecology, but also for other disciplines.

In total, the current sequencing effort has produced >250 billion DNA paired reads out of >4 300 size-fractionated plankton communities, being by far the largest homogeneous multi-omics data set for any

Table 1. Summary of Tara Oceans 'omics' datasets, generated from size-fractionated plankton samples, and single cells collected across the world oceans (see Fig. 1).

Size Fractions (μm)	Target groups	Omics type	# of plankton communities analysed	Mean # of reads/sample (in million of paired reads)	Total # of reads (in billion of paired reads)
< 0.2	phages	metaG	112	86	9.6
0.2-1.6; 0.1-0.2; 0.45-0.8; 0.2-0.45	giruses (giant DNA viruses)	metaG	73	111	9
0.2-1.6; 0.2-3	giruses and prokaryotes	metaT (random priming)	153	160	33
		metaG	243	117	25
		16S metaB	1142	0.5	0.44
0.8-inf; 3-inf; 0.8-5; (0.8-3); 5-20 (3-20); 20-180; 180-2000	protists and metazoa	16S metaB	968	0.5	0.44
		18S metaB	850	1.9	1.7
		metaG	401	160	83
		metaT (polyA RNA)	441	160	86
Transcriptomes	protists	De novo sequencing	78 cultured organisms	30	2.1
SAGs samples	protists	De novo sequencing	281 single cells	33	11
TOTAL			4 383 communities		252 billion paired reads

TARA OCEANS – FINAL CRUISE REPORT

biome (>50 Terabytes of raw data). Finally, metagenetics catalogs were produced for viruses, prokaryotes, and eukaryotes, using new bioinformatics pipelines adapted to each kingdom of Life, allowing gene-centric analyses to be performed, and paving the way toward genome-based meta-analyses.

The “IMAGING” data

On top of our multi-omics approach to assess ocean genomes and genes, we used a series of innovative, automated imaging tools to identify the concentration, taxonomic composition, and morphological

Table 2. Key features, size, and completion of imaging datasets generated from >9 200 plankton samples collected by the Tara Oceans (TO) and Tara Oceans Polar Circle (TOPC) expeditions.

Imaging dataset (Instrument & plankton samples)	Plankton size range	Voyage	# of plankton samples analysed	Sample imaging & processing	# objects	Classification (predicted P, curated C)	EcoTaxa Release
UVP	100 > 1 mm	TO + TOPC	776	100%	769 497	P + C (100%)	available
ZooScan Regent 680	100 > 0.68 mm	TO	189	100%	126 389	P + C (36%)	available
ZooScan WP2 200	10 > 0.2 mm	TO + TOPC	203	100%	394 956	P + C (95%)	available
ZooScan Multinet	10 > 0.2 mm	TO	285	100%	397 723	P + C (92%)	available
ZooScan Bongo 300	10 > 0.3 mm	TO	92	100%	154 624	P + C (30%)	available
ZooScan Regent 680	10 > 0.68 mm	TOPC	23	100%	14 433	P + C (16%)	available
ZooScan Bongo 300	10 > 300 µm	TOPC	19	100%	42 365	P + C (8%)	available
FlowCAM Bongo 180	180 > 20 µm	TOPC	317	100%	704 053	P + C (15%)	available
IFCB	160 > 5 µm	TOPC	6982	100%	2 307 437	P + C (30%)	available
e-HCFM HS 5-20	20 > 5 µm	TO	76	100%	336 655	P + C (5.5%)	available
e-HCFM H20 20-180	180 > 20 µm	TO + TOPC	128	100%	>10 ⁶	-	2017
e-HCFM H0.2 >0.2	> 0.2 µm	TOPC	14	100%	-	-	2017
HiRes 3D-CLSM	2000 > 1 µm	TO	65	50%	3 551	C (100%)	2017
SEM	200 > 0.1 µm	TO	31	STEFlexp	427	C (100%)	2017
TEM virus	< 0.1 µm	TO + TOPC	43	100%	4300	C (100%)	2017
TOTAL			9 243		> 6 million		

characteristics of plankton and non-living suspended particles across organismal size-fractions.

These included Underwater Video Profiler (UVP), Zooscan, FlowCAM, Imaging FlowCytobot (IFCB), Flow Cytometry, and a brand-new high content screening 3D-microscopy workflow, together encompassing a comprehensive organismal size range, from pico-plankton to large gelatinous zooplankton and marine snow, across different taxonomic and trophic groups, and generating 11 different datasets. More classical imaging techniques were also used to generate smaller datasets at higher resolution, including confocal (3D-CLSM) and electron (SEM and TEM)

microscopy (Table 2). The full strategy was used from surface to 1000 m depth, with a current production of >6 million images of single plankton from >9,200 size-fractionated plankton communities (>30 Terabytes).

In the absence of an international framework to share and annotate environmental images (the equivalent of GenBank for DNA sequences), we developed a web-based application, EcoTaxa (<http://ecotaxa.sb-roscoff.fr/>), which allowed for the first-time online archiving, exploration and collaborative annotation of plankton images by experts worldwide. EcoTaxa also provided tools for computer-assisted image recognition (including deep learning algorithms) to accelerate time consuming taxonomic assignment by experts. The taxonomy implemented in EcoTaxa corresponded to the universal eukaryotic framework developed online with the world community of expert taxonomists in the UniEuk effort, allowing future cross-comparison between imaging and DNA sequencing data.

The “Ecological” data

Viruses

In 2009, the baseline knowledge of ocean virus diversity and ecological genomics was incredibly low. This is because viruses have until very recently been near impossible to study due to the lack of experimental and informatics tools to ‘access’ viruses in nature. Tara Oceans transformed all that. We now know that there are tens of thousands of viral ‘types’ in the oceans, most of which were captured in the Global Ocean Virome dataset and are now incorporated into a novel network-based taxonomy that is currently serving as the best tool to explore the ‘dark matter’ that dominates the virosphere. Novel analytical approaches have also linked many of these viruses to ecologically important marine prokaryotic hosts and advanced our understanding of how viruses metabolically reprogram their hosts during infection by directly modulating key metabolic genes.

TARA OCEANS – FINAL CRUISE REPORT

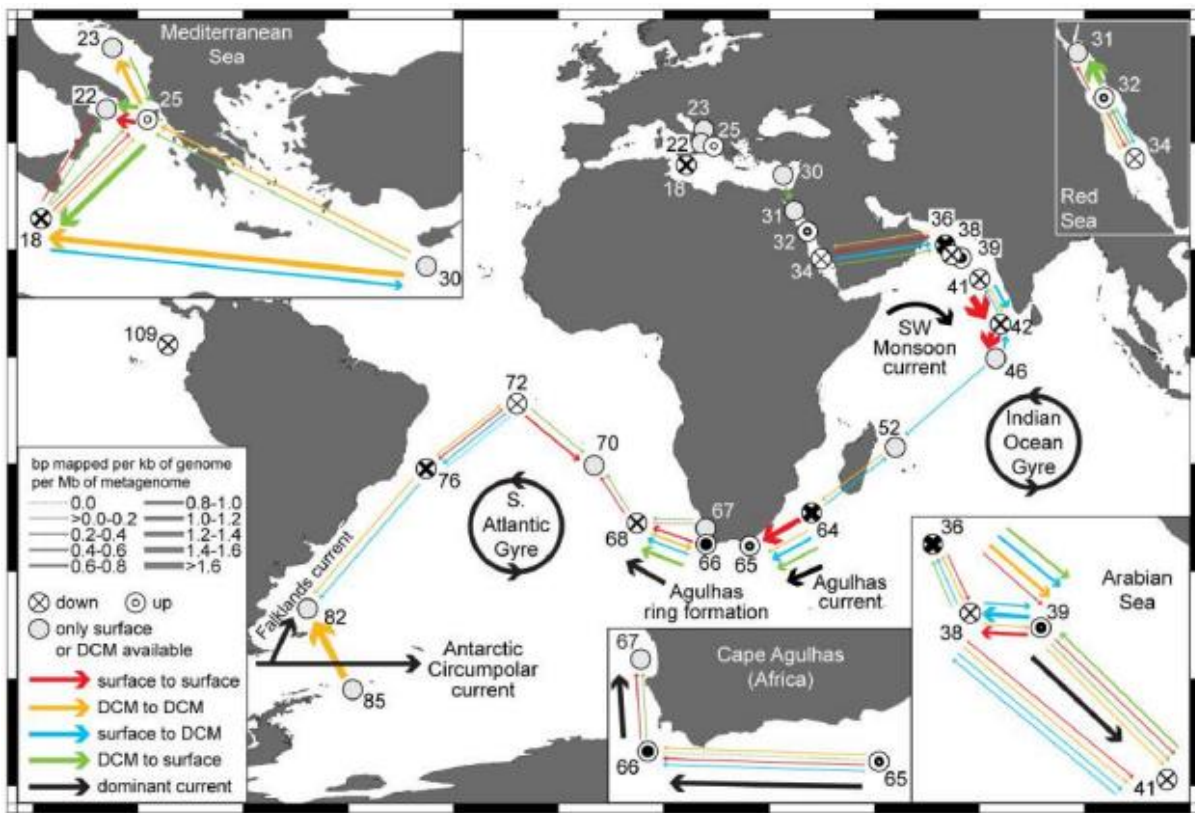
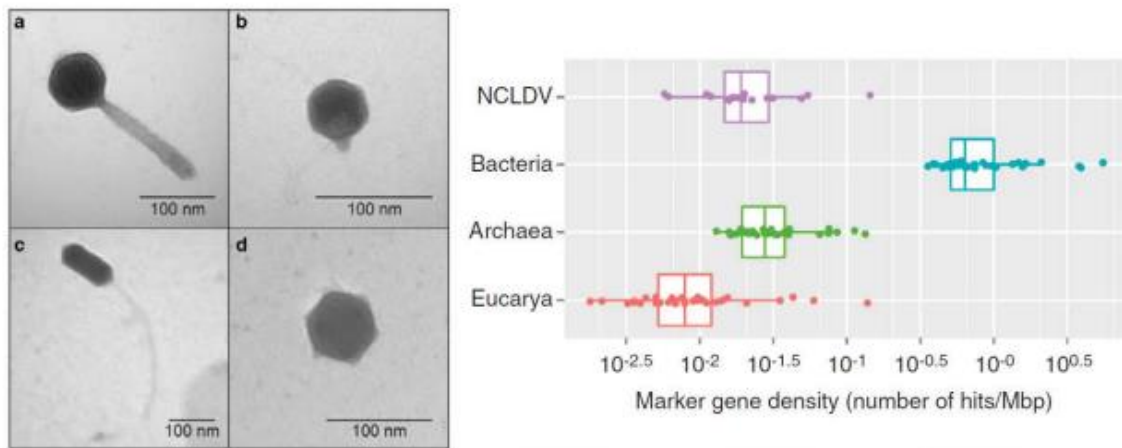


Figure 3. Tara Oceans virus morpho-genetic study. *Upper left:* Morphologies of prokaryote-infecting viruses observed in Tara Oceans samples: (a) myovirus; (b) podovirus; (c) siphovirus; (d) non-tailed virus. The understudied non-tailed viruses emerged as being the most representative in our meta-omics datasets. *Upper right:* taxonomy marker genes suggest that the abundance of giant DNA viruses (NCLDV) infecting eukaryotes exceed the abundance of their host by one order of magnitude, a pattern reminiscent of the 1 to 10 ratio between the abundance of bacteria and phages. *Bottom panel:* (f) Our first global virome analysis indicated that viral communities were passively transported by oceanic currents and locally structured by environmental conditions that affect host community structure.

Prokaryotes

In Tara Oceans, we generated the largest ocean microbial sequencing data set available to date and developed new bioinformatics approaches to explore the frontiers of global ocean microbial diversity. We found a minimum boundary of 35,000 prokaryotic 'species' in the pelagic realm, whose community structure appears to be essentially driven by seawater temperature in surface oceans. Analysis of the >200 metagenomes resulted in the first Ocean Microbial Reference Gene Catalogue comprising >40 million non-redundant genes, which now serves as a treasure for biologists and marine scientists.

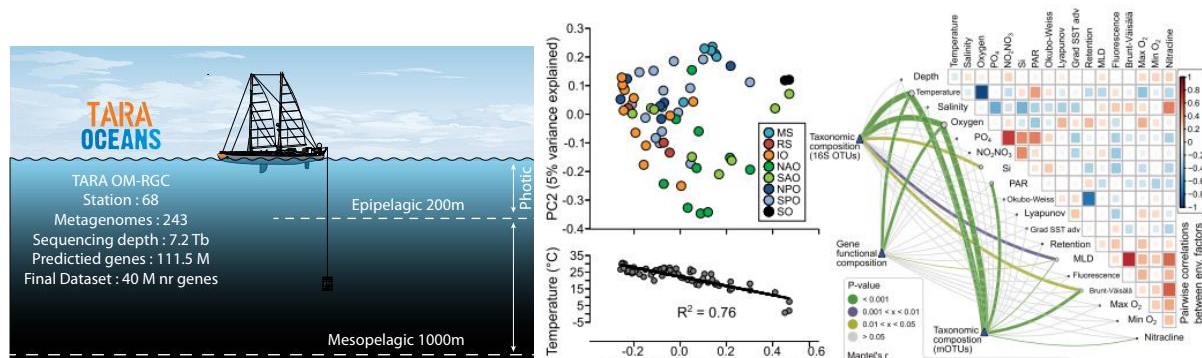


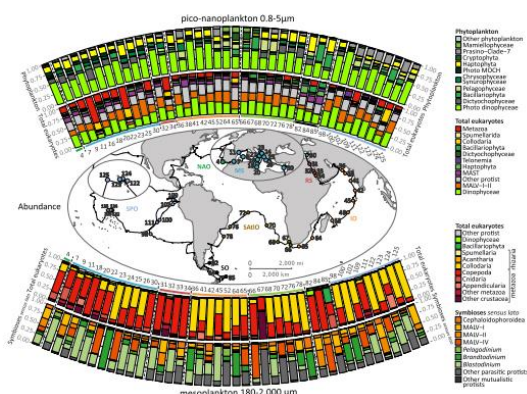
Figure 4. Upper panel: Numerical breakdown of the Ocean Microbial Reference Gene Catalog.

The OM-RGC contains >40 million non-redundant genes from marine viruses, archaea, bacteria and picoeukaryotes sampled from 243 Tara Oceans (TO) metagenomes generated from a 1000 m depth layer of the world oceans. **Lower panel: Use of TO prokaryotic 'omics' data to unveil environmental drivers of surface microbial community composition.** The principal coordinate (PC) analysis shows that plankton communities are not clearly grouped by their geographic origin (top), but rather separated by the local temperatures (bottom: strong correlation between the first PC and temperature). On the right, **correlations** [green lines: geographic distance-corrected Mantel tests] **of plankton taxonomic** [two independent methods: miTags and mOTUs] **and functional** [biochemical KEGG modules] **compositions to key environmental parameters.** The environmental parameters are also compared between themselves, with a colour gradient denoting pairwise Spearman's correlation coefficients. Edge width corresponds to the Mantel's r statistic for the corresponding distance correlations, and edge colour denotes the statistical significance based on 9,999 permutations (Sunagawa et al. 2015).

The OM-RGC improved our understanding of biogeography and microbial functional capabilities across oceanic regions and ecosystems. A notable derivative was the inference of the first world ocean "interactome" uncovering organismal interactions across all domains of life including viruses and showing the predominance of biotic relations in shaping the global plankton network. We further used the power of Tara Oceans' multi-omics and morphological data to unveil the functional and ecological significance of critical nitrogen-fixing cyanobacteria-haptophyte symbioses in the euphotic zone worldwide. A better understanding of the genetic capacity for mixotrophy and the factors controlling the biogeographic distribution of the two most abundant and widespread phototrophs on Earth (Prochlorococcus and Synechococcus) was established.

Protists

In Tara Oceans, we focused >45% of the morpho-genetic sampling effort on protists. We then applied the full power of our multi-omics and automated imaging (see 'Omics' and 'Imaging' sections above) workflow to generate ~170 billion DNA paired-reads and >1.5 million images from ~1,000 plankton communities in 4 organismal size- fractions from pico- to micro-plankton. This is by far the largest consistent morpho-genetic dataset of protist biocomplexity from a single biome, which we leveraged by creating a series of new metaB transcriptomes, and single-cell genomes - reference databases for annotating taxonomically and functionally the deluge of new environmental data. We are also building a universal taxonomic framework for eukaryotes implemented at EBI, in order to unite the complex phen-omics protist data under a single ontology.



Our primary large-scale DNA metabarcoding analysis revealed ~150,000 eukaryotic genera in the euphotic zone, >85% of which are protists, essentially heterotrophic taxa, including many uncharacterized parasites and symbionts, in addition to the better-known components of plankton ecosystems such as diatoms and ciliates. Reconstruction of a global plankton interactome and plankton sub-networks confirmed the central role of parasitic and photosymbiotic protists as keystone taxa increasing the connectivity of plankton food-webs and the flux of carbon to deeper layers of the ocean. Underwater video-profiling

reinforced the abundance of giant photosymbiotic rhizarian protists whose biomass exceeds that of all zooplankton in (sub)tropical oceans.

Tara Oceans enable to make protists emerge today as the richest biotic compartment in the world plankton, their fundamentally symbiotic nature increasing the complexity and connectivity of ecosystems.

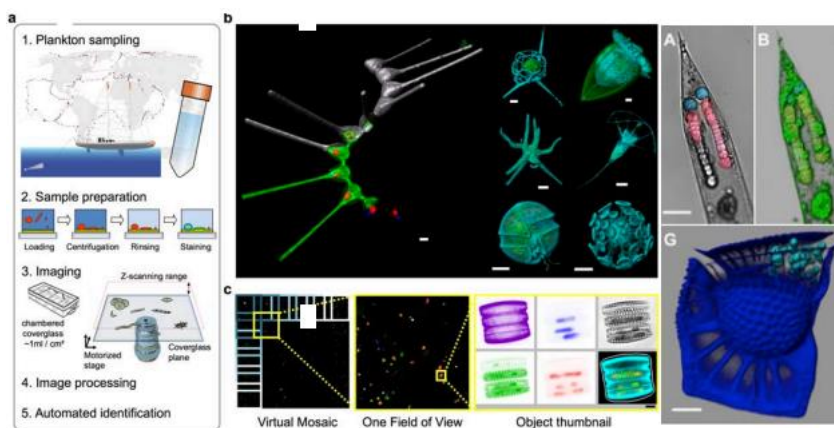


Figure 5. Upper panel: We used **rDNA metabarcoding** to estimate the relative biovolume of **eukaryotic plankton taxa** in the world sunlit ocean (above the map: phytoplankton and total eukaryotes in piconanoplankton; below the map: total eukaryotes and known symbiotic protists for the mesoplankton). The importance of dinophyceae and collodarians in the smallest and largest size-fractions, respectively, came as a surprise. **Lower panel:** For future, sub-cellular exploration of marine protists eco-biocomplexity, we developed eHCFM (environmental High Content Fluorescence Microscopy; Colin *et al.* *eLIFE*, in review). e-HCFM enables automated **quantitative 3D-fluorescence imaging of eukaryotic cell structures** (including symbionts; see for instance cyanobacterial symbionts in a diatom and a dinoflagellate on the right side) **across the full diversity of microbial eukaryotes**, while recognizing and classifying the imaged taxa.

Metazoans

In Tara Oceans, we used five different types of nets to collect a unique collection of ~1 500 standardized zooplankton samples from surface to a few hundred meters depth across the world ocean. Imaging and 'omics' tools were then used to assess the morpho-genetic complexity of zooplankton communities in well-defined oceanographic provinces.

In terms of imaging, all zooplankton samples have now been analyzed and their great majority validated by experts using EcoTaxa (>6 million images on <http://ecotaxa.sb-roscoff.fr/>).

Images were used to assess the mechanisms contributing to the limited dispersal of Indian Ocean plankton populations into the Atlantic. In the Indian Ocean, combined imaging datasets have shown the absence of metazoan plankton in the Oxygen Minimum Zone, and its effect on carbon flux. Based on in situ video profiling (UVP) performed at each

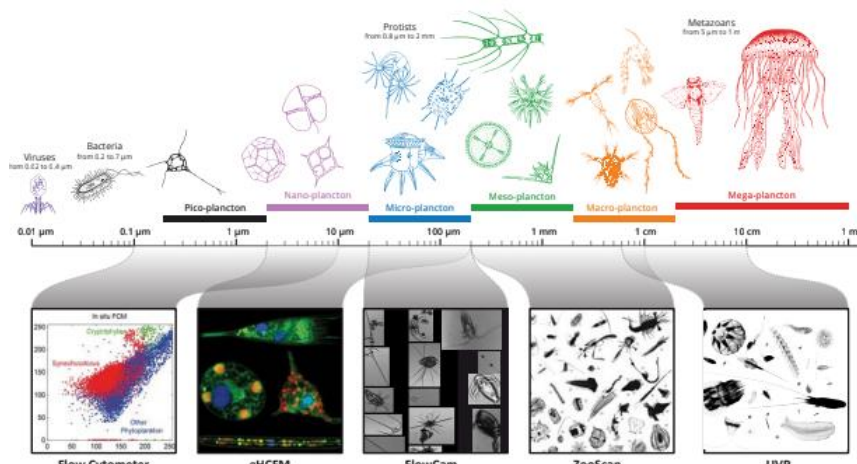


Figure 6. Zooplankton automated imaging strategy. Upper panel. The suite of automated imaging workflows implemented in Tara Oceans, from Flow-Cytometry to Underwater Video Profiler (UVP), are generating millions of single plankton images from <math><1\mu\text{m}</math> to a few cm. Single organisms' images are stored and organized online via the expert-annotation platform EcoTaxa (<http://ecotaxa.sb-roscoff.fr>).

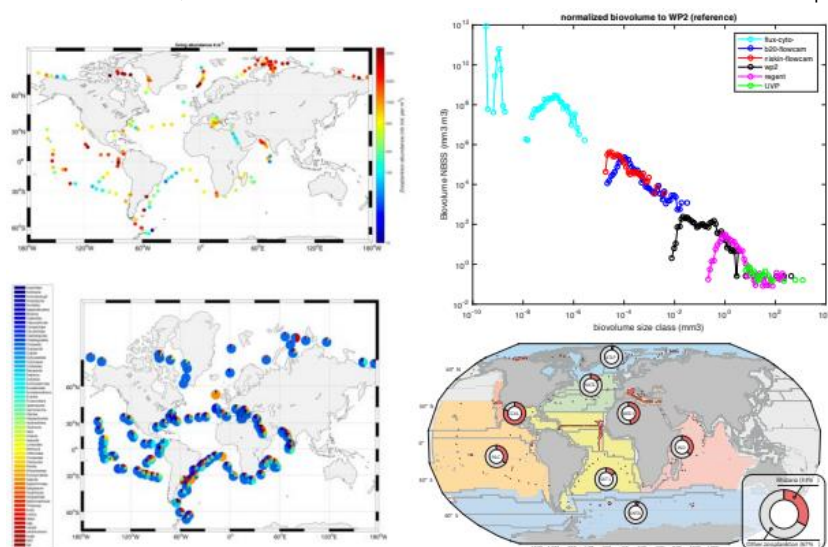


Figure 6. (following) Medium panels. Left: abundance (# of individual/ m^3) of total zooplankton from the WP2-net samples (200 μm -1cm, Zooscan-data) in all Tara Oceans stations. Note the relatively high zooplankton abundance in polar and tropical upwelling ecosystems. Right: Example of a meta-plankton sample based on total plankton abundance data measured by Flow Cytometer, FlowCam (both total water and 20 μm net samples), ZooScan (from 200 μm -WP2 and 680 μm -Regent nets samples), and UVP (*in situ* imaging), at a single station (here TO Polar Circle Station 168). It shows how the suite of imaging methods can be merged to provide a holistic and quantitative morphological view of a plankton community. Lower panels: Left: relative abundance of >60 taxonomic groups of zooplankton as measured by ZooScan on the Regent-net (680 μm -1cm) samples, showing how metazoan diversity behaves along the Tara Oceans stations, with an overall dominance of copepods (in blue). Right: The dominance of copepods was challenged by the non-destructive view of meso/macro plankton provided by the UVP. Global UVP data (~700 profiles down to 500m depth here) show that giant protists (rhizaria) are more abundant than all metazoan plankton together in (sub)tropical biomes.

Tara Oceans station, we demonstrated that the biomass of rhizarian protists, undersampled by nets because of their fragility, may in fact be equivalent to that of all other mesozooplankton in the oligotrophic inter-tropical open oceans. On the 'omics' front, Tara Oceans samples were used to reconstruct the macro-evolutionary history of sea snails (Thecosomata) using a combination of morphological and molecular data.

However, these studies are just scratching the tip of the iceberg of morphogenetic information hidden in the Tara Oceans comprehensive zooplankton collection, and efforts to sequence metabarcodes and genomes of the main players and correlate genetic to imaging information is needed.

Plankton systems ecology

Drafting the first global plankton interactome spanning all domains of life, to our surprise we discovered that biotic interactions predominate over environmental influences in shaping community structure. A further potentially paradigm-shifting finding was the prevalence of symbiosis *sensu lato*, challenging the classical view of food webs of producers and consumers. In Guidi et al (2016) we went further, and applied systems biology inspired network-partitioning methods to identify euphotic plankton sub-communities and gene modules associated with carbon export from the upper photic zone to the ocean interior, demonstrating our capacity to shift focus from genes to ecosystems and extract insightful hypotheses about key ocean biogeochemical processes (Fig. 7).

The Villar et al (2015) study of the impact of the Agulhas choke point on plankton ecosystems demonstrated how we can address basin scale oceanographic questions. The resulting hypothesis about the impact of Agulhas Rings on transported communities from the Indian to the Atlantic Ocean, successfully simulated in the MIT-GCM model, was only possible via the integration of *in situ* metagenomics data with fine grained physico-chemical contextual measurements.

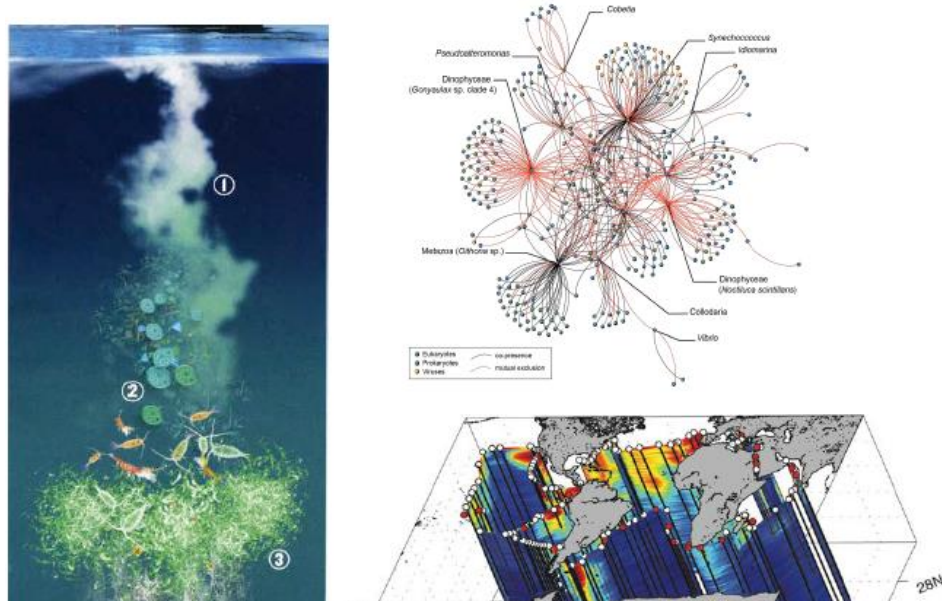


Figure 7. How Tara Oceans global eco-systemic data allow scaling up from genes or biomarkers' communities to global ecosystem behavior. Left panel: Schematic representation of the biological carbon pump in the ocean. Atmospheric CO₂ is transformed into organic carbon by phytoplankton in the sunlit layer, then incorporated into the highly-complex plankton interactome, and partly exported to deep oceanic layers and sediments through dead organisms, fecal pellets, and marine 'snow' (drawing from A. de Chastenet; note that depth, organisms and particle sizes are not to scale). **Right side:** we used systems-biology graph-based methods to integrate eukaryotic, prokaryotic and viral 'omics' data (top), and correlate their respective sub-networks to carbon export fluxes down to 500 m, as estimated at each Tara Oceans station from particle size distribution and abundance measured with the underwater vision profiler (UVP) (bottom). We could also identify keystone taxa or genes in the subnetworks (hubs) that can predict accurately carbon export.

This milestone achievement in deciphering plankton dispersal has been continued with a global analysis of the influence of ocean circulation on plankton biogeography

that shows the dominating role of lagrangian currents in shaping plankton communities on a characteristic timescale of 1.5 years. Finally, in Caputi et al (2017) we described the dynamic plankton response, from genes to communities, to the key micronutrient iron. Specifically, we identified sub-communities that displayed global distribution patterns associated with iron concentrations, responding locally to iron with different evolutionary strategies. Collectively, these initial studies represent unprecedented scale systems biology analyses of a global ecosystem and are today an international reference. Future effort making use of dedicated modeling will further our understanding of interactions, adaptation and evolution of ocean's life in the context of ongoing climate changes.

Plankton screening

TARA OCEANS – FINAL CRUISE REPORT

Building upon the *Tara Oceans* knowledge base on global plankton eco-systems, we initiated an informed **screening of plankton strains for secondary metabolites and lipidomics, with potential applications in biomedicine and pharmaceuticals, bioenergy, green chemistry, and dermo-cosmetics**. To reach this goal, we teamed up with industrial partners (*Soliance-Givaudan* and *GreenSea*) and developed together a strategy described in two articles (*Abida et al., Marine Drugs, 2013; Baratte et al., Médecine et Sciences 2015*), and based on screening a wide phylogenetic range of eukaryotic plankton strains maintained in the *Roscoff Culture Collection* (RCC - <http://roscoff-culture-collection.org> - which maintains >4,000 strains of marine microalgae, bacteria, and viruses). Following RCC strain selection, our workflow consists of: (i) **biomass production** by industrial partners; (ii) **metabolomic screening** (extraction, purification of compounds and their structural determination) by Nice University; (iii) **bioactivity assays** for anti-cancer and antimicrobial activities by, respectively, the KISS facility at Roscoff and the University of Brest; (iv) **lipidomic screening** at the LPCV facility in Grenoble; (v) creation of a **database of plankton chemical and biological activity** information (Fig. 8). All extracts and purified compounds are frozen in microplates and stored in a collection of plankton extracts. The pipeline is now fully operational, and 17 strains (microalgae and marine fungi) have been chemically analysed in a test phase. Four of them produced an interesting array of chemical compounds, including some with promising bioactivity against *Jurkat* and *U2OS* tumoural cells, related to leukemia and osteosarcoma, respectively. Glycerolipids found in planktonic cells comprise fatty acids with an immense chemical diversity of chain lengths and number of double bonds, from 20-22 carbons and 5-6 double bonds (in omega-3 configuration), with high potential for biomedical, feed and food applications, to 8-14 carbons and at most one double bond, having a high potential as a surrogate for fossil fuel and scaffold for green chemistry. The Grenoble and Roscoff teams have developed all the **imaging fluorimetric tools to monitor the screening of phytoplankton and identify wild strains with highest glycerolipid yields**. In addition, the Grenoble partner has built a lipidomic platform, which has become an international leader to analyse microalgal lipids, with results published regularly in *Plant Physiology* (2015, 2016, 2017) and *Plant Cell* (2015) and protected by a series of patents in 2014, 2015, 2016 and to be submitted in 2017. **Samples of the RCC collection screened for secondary metabolites and bioactivity (see above) have been transferred to the Grenoble lipidomic platform for refined qualification and quantification of glycerolipids**. The project is today ready to start a large-scale screening of the *Tara Oceans* samples via high throughput fluorimetry imaging, and of RCC plankton strains using the analytical pipeline developed at the Grenoble lipidomic platform.



Figure 8. The *Tara Oceans* OCEANOMICS public-private workflow for extraction, purification, and structural characterization of bioactive planktonic natural products.

TARA OCEANS' KNOWLEDGE BASE

TARA OCEANS – FINAL CRUISE REPORT

Tara Oceans provided a foundational knowledge base in Global Ecology that allows unprecedented in-depth exploration of our Ocean's ecosystems. Leveraging the most advanced technologies from environmental science, genomics and scientific imaging, it provided data sets that are both deep and rich in their respective domains. In addition, though, it is unique in bringing together these three perspectives into an integrated, richly described and deeply structured data set that already provided, and will provide long into the future, a basis for the world's interpretation of marine life in its context.

Tara Oceans drew its success from: a consistent sampling across the world's ocean, describing 210 contrasting ecosystems in 20 biogeographic provinces (Pesant et al., *Sci. Data*, 2015) a coherent suite of protocols that effectively collected eco morpho-genetic plankton samples and data across the entire size and diversity spectrum of life, from viruses to animals (Pesant et al., *Sci. Data*, 2015); a unique and persistent identification of ~40,000 samples and a systematic record of their provenance and integration with all data derived therefrom; and an extensive set of environmental contextual information obtained from concurrent field measurements, satellite products, climatology and gazetteers.

The regularity and quality of collected samples enabled state-of-the-art imaging and sequencing, and data were progressively released in open access, representing the largest coherent set of environmental, imaging and sequencing data collected in the global ocean and available to the international community. Yet only a fraction of samples has been analyzed, while replicates are preserved in trusted collections and biobanks for the next generation (Deliverables A).



Photo 4: Sailing - Pierre de Parscau - Tara Ocean Foundation

Tara Oceans fostered an ambitious, long-term infrastructure of open access archives for DNA sequences (ENA, <http://www.ebi.ac.uk/ena>), images (EuBI, <http://www.eurobioimaging.eu/>) (Deliverables D), and environmental data (PANGAEA, <http://www.pangaea.de>), ensuring that its knowledge base remains FAIR (Findable, Accessible, Interoperable and Reusable; Wilkinson et al. 2016) to all (Fig. 2). On the genomics side, the systematic validated sequencing methodologies used provide extensive data that are deeply integrated, through the sample identification system, with data from the environmental and imaging approaches. Comprising raw data, data derivatives that have undergone systematic quality-control, and a variety of derived data types such as gene catalogues, taxonomic profiles and functional diversity analyses, the publicly available genomics data set currently amounts to 12 gigabytes of data covering >40 million genes. Image data from Tara Oceans have similar diversity and dimension. Spanning 2D and 3D imaging methods across EM and light platforms, the image data sets reveal morphology, ecological associations, distribution data and many more insights. Web services are in place to use the Tara Oceans samples registries and navigate the infrastructure (<https://ws.pangaea.de/dds-fdp/>). Exploring the Tara Oceans multi-domains dataset required innovative bioinformatics tools, cloud computing, and next generation global ocean modeling. Although a number of bioinformatics and modeling tools are emerging in the framework of Tara Oceans (Deliverables E), there is a pressing need to develop new interfaces enabling scientists to exploit the full potential of the Tara Oceans knowledge base, in particular to further our understanding of interactions and the evolutionary trajectories of ocean life.

BIBLIOGRAPHY

Data Base of the Tara Oceans mission

All Campaign Summary Report, Oceanographic Report, environmental and genetics data were registered on online platforms : PANGAEA, ZENODO and ENA. Raw data was as well fully released together with manuscript.

Sequencing data were deposited at the free, open-access European Nucleotides Archive (<https://www.ebi.ac.uk/ena/>); environmental data are deposited at the free, open-access PANGAEA database (<https://www.pangaea.de/>); and both archives are interlinked via the sample registry available online at BioSamples (<https://www.ebi.ac.uk/biosamples/>).

Raw contextual and environmental data are already released in Zenodo (<https://zenodo.org/record/4068293#.X-HQKeIkhBU>).

The **White Paper** of the Tara Oceans mission can be found by following this link : https://drive.google.com/file/d/1hy93XsX9_EKGPRwel_DclZkzCqXuCgFF/view?usp=sharing

List of scientific publications

121. Macroscale patterns of oceanic zooplankton composition and size structure

Brandao, M.C., Benedetti, F., Martini, S., Soviadan, Y.D., Irisson, J.O., Romagnan, J.B., Elineau, A., Desnos, C., Jalabert, L., Freire, A.S., Picheral, M., Guidi, L., Gorsky, G., Bowler, C., Karp-Boss, L., Henry, N., de Vargas, C., Sullivan, M.B.; Tara Oceans Consortium Coordinators, Stemmann, L., Lombard, F., *Sci Rep* 11(1):15714: 2021.

<https://doi.org/10.1038/s41598-021-94615-5>

120. Environmental vulnerability of the global ocean epipelagic plankton community interactome

Chaffron, S., Delage, E., Budinich, M., Vintache, D., Henry, N., Nef, C., Ardyna, M., Zayed, A.A., Junger, P.C., Galand, P.E., Lovejoy, C., Murray, A.E., Sarmiento, H.; Tara Oceans coordinators, Acinas, S.G., Babin, M., Iudicone, D., Jaillon, O., Karsenti, E., Wincker, P., Karp-Boss, L., Sullivan, M.B., Bowler, C., de Vargas, C., Eveillard, D., *Sci Adv* 7(35):eabg1921: 2021.

<https://doi.org/10.1126/sciadv.abg1921>

119. efam: an expanded, metaproteome-supported HMM profile database of viral protein families

Zayed, A.A., Lucking, D., Mohssen, M., Cronin, D., Bolduc, B., Gregory, A.C., Hargreaves, K.R., Piehowski, P.D., White, R.A., Huang, E.L., Adkins, J.N., Roux, S., Moraru, C., Sullivan, M.B., *Bioinformatics*, btab451: 2021.

<https://doi.org/10.1093/bioinformatics/btab451>

118. Global distribution patterns of marine nitrogen-fixers by imaging and molecular methods

Pierella Karlusich, J.J., Pelletier, E., Lombard, F., Carsique, M., Dvorak, E., Colin, S., Picheral, M., Cornejo-Castillo, F.M., Acinas, S.G., Pepperkok, R., Karsenti, E., de Vargas, C., Wincker, P., Bowler, C., Foster, R.A., *Nat Commun* 12(1):4160: 2021.

<https://doi.org/10.1038/s41467-021-24299-y>

117. Discovery of viral myosin genes with complex evolutionary history within plankton

Kijima, S., Delmont, T.O., Miyazaki, U., Gaia, M., Endo, H., Ogata, H., *Front Microbiol* 12:683294: 2021.

<https://doi.org/10.3389/fmicb.2021.683294>

116. Phylogenomics of *Porites* from the Arabian Peninsula

Terraneo, T. I., F. Benzoni, R. Arrigoni, A. H. Baird, K. G. Mariappan, Z. H. Forsman, M. K. Wooster, J. Bouwmeester, A. Marshall and M. L. Berumen, *Molecular Phylogenetics and Evolution*: 2021.

<https://doi.org/10.1016/j.ympev.2021.107173>

TARA OCEANS – FINAL CRUISE REPORT

115. Carbon Dioxide Concentration Mechanisms in Natural Populations of Marine Diatoms: Insights From Tara Oceans

Pierella Karlusich, *Frontiers in Plant Science*: 2021.
<https://doi.org/10.3389/fpls.2021.657821>

114. Quantitative Assessment of Nucleocytoplasmic Large DNA Virus and Host Interactions Predicted by Co-occurrence Analyses

Meng, L., H. Endo, R. Blanc-Mathieu, S. Chaffron, R. Hernandez-Velazquez, H. Kaneko and H. Ogata, *mSphere*: 2021.
<https://doi.org/10.1128/mSphere.01298-20>

113. Integrative systematics of the scleractinian coral genera *Caulastraea*, *Erythrastrea* and *Oulophyllia*

Arrigoni, R., D. Huang, M. L. Berumen, A. F. Budd, S. Montano, Z. T. Richards, T. I. Terraneo and F. Benzoni, *Zoologica Scripta*: 2021.
<https://doi.org/10.1111/zsc.12481>

112. Complex Response of the Chlorarachniophyte *Bigelowiella natans* to Iron Availability

Kotabova, E., R. Malych, J. J. Pierella Karlusich, E. Kazamia, M. Eichner, J. Mach, E. Lesuisse, C. Bowler, O. Prasil and R. Sutak, *mSystems* 6(1): 2021.
<https://doi.org/10.1128/mSystems.00738-20>

111. The Ocean barcode atlas: A web service to explore the biodiversity and biogeography of marine organisms

Vernette, C., N. Henry, J. Lecubin, C. de Vargas, P. Hingamp and M. Lescot, *Mol Ecol Resour*: 2021.
<https://doi.org/10.1111/1755-0998.13322>

110. Eukaryotic virus composition can predict the efficiency of carbon export in the global ocean

Kaneko, H., R. Blanc-Mathieu, H. Endo, S. Chaffron, T. O. Delmont, M. Gaia, N. Henry, R. Hernandez-Velazquez, C. H. Nguyen, H. Mamitsuka, P. Forterre, O. Jaillon, C. de Vargas, M. B. Sullivan, C. A. Suttle, L. Guidi and H. Ogata, *iScience* 24(1): 102002: 2021.
<https://doi.org/10.1016/j.isci.2020.102002>

109. Exploration of marine phytoplankton: From their historical appreciation to the omics era

Pierella Karlusich, J. J., F. Ibarbalz and C. Bowler, *Journal of Plankton Research* 42: 2020.
<https://doi.org/10.1093/plankt/fbaa049>

108. Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions

Endo, H., R. Blanc-Mathieu, Y. Li, G. Salazar, N. Henry, K. Labadie, C. de Vargas, M. B. Sullivan, C. Bowler, P. Wincker, L. Karp-Boss, S. Sunagawa and H. Ogata, *Nat Ecol Evol* 4(12): 1639-1649: 2020.
<https://doi.org/10.1038/s41559-020-01288-w>

107. Diversity and distribution of marine heterotrophic bacteria from a large culture collection

Sanz-Saez, I., G. Salazar, P. Sanchez, E. Lara, M. Royo-Llonch, E. L. Sa, T. Lucena, M. J. Pujalte, D. Vaque, C. M. Duarte, J. M. Gasol, C. Pedros-Alio, O. Sanchez and S. G. Acinas, *BMC Microbiol* 20(1): 207: 2020.
<https://doi.org/10.1186/s12866-020-01884-7>

106. Investigating population-scale allelic differential expression in wild populations of *Oithona similis* (Cyclopoida, Claus, 1866)

Laso-Jadart, R., K. Sugier, E. Petit, K. Labadie, P. Peterlongo, C. Ambroise, P. Wincker, J. L. Jamet and M. A. Madoui, *Ecol Evol* 10(16): 8894-8905: 2020.
<https://doi.org/10.1002/ece3.6588>

105. *Mesonia oceanica* sp. nov., isolated from oceans during the Tara oceans expedition, with a preference for mesopelagic waters

TARA OCEANS – FINAL CRUISE REPORT

Lucena, T., I. Sanz-Saez, D. R. Arahal, S. G. Acinas, O. Sanchez, C. Pedros-Alio, R. Aznar and M. J. Pujalte, *Int J Syst Evol Microbiol* 70(7): 4329-4338: 2020.
<https://doi.org/0.1099/ijsem.0.004296>

104. Transcriptome reconstruction and functional analysis of eukaryotic marine plankton communities via high-throughput metagenomics and metatranscriptomics

Vorobev, A., M. Dupouy, Q. Carradec, T. O. Delmont, A. Annamale, P. Wincker and E. Pelletier, *Genome Res* 30(4): 647-659: 2020.
<https://doi.org/0.1101/gr.253070.119>

103. Towards a rigorous species delimitation framework for scleractinian corals based on RAD sequencing: the case study of *Leptastrea* from the Indo-Pacific

Arrigoni, R., M. Berumen, K. Mariappan, P. Beck, A. Hulver, S. Montano, M. Pichon, G. Strona, T. I. Terraneo and F. Benzoni, *Coral Reefs* 39: 2020.
<https://doi.org/0.1007/s00338-020-01924-8>

102. Diatoms Are Selective Segregators in Global Ocean Planktonic Communities

Vincent, F. and C. Bowler, *mSystems* 5(1): 2020.
<https://doi.org/0.1128/mSystems.00444-19>

101. Diversity and evolution of bacterial bioluminescence genes in the global ocean

Vannier, T., P. Hingamp, F. Turrel, L. Tanet, M. Lescot and Y. Timsit, *NAR Genom Bioinform* 2(2): lqaa018: 2020.
<https://doi.org/0.1093/nargab/lqaa018>

100. Tara Oceans: towards global ocean ecosystems biology

Sunagawa, S., S. G. Acinas, P. Bork, C. Bowler, C. Tara Oceans, D. Eveillard, G. Gorsky, L. Guidi, D. Iudicone, E. Karsenti, F. Lombard, H. Ogata, S. Pesant, M. B. Sullivan, P. Wincker and C. de Vargas, *Nat Rev Microbiol* 18(8): 428-445: 2020.
<https://doi.org/0.1038/s41579-020-0364-5>

99. Genome Resolved Biogeography of Mamiellales

Leconte, J., L. F. Benites, T. Vannier, P. Wincker, G. Piganeau and O. Jaillon, *Genes (Basel)* 11(1): 2020.
<https://doi.org/0.3390/genes11010066>

98.

,

97. Into the bloom: Molecular response of pelagic tunicates to fluctuating food availability

Sordino, P., S. D'Aniello, E. Pelletier, P. Wincker, V. Nittoli, L. Stemmann, M. G. Mazzocchi, F. Lombard, D. Iudicone and L. Caputi, *Mol Ecol* 29(2): 292-307: 2020.
<https://doi.org/0.1111/mec.15321>

96. Ecological and functional capabilities of an uncultured *Kordia* sp

Royo-Llonch, M., P. Sanchez, J. M. Gonzalez, C. Pedros-Alio and S. G. Acinas, *Syst Appl Microbiol* 43(1): 126045: 2020.
<https://doi.org/0.1016/j.syapm.2019.126045>

95. Observational Needs Supporting Marine Ecosystems Modeling and Forecasting: From the Global Ocean to Regional and Coastal Systems

Capotondi, A., M. Jacox, C. Bowler, M. Kavanaugh, P. Lehodey, D. Barrie, S. Brodie, S. Chaffron, W. Cheng, D. F. Dias, D. Eveillard, L. Guidi, D. Iudicone, N. S. Lovenduski, J. A. Nye, I. Ortiz, D. Pirhalla, M. Pozo Buil, V. Saba, S. Sheridan, S. Siedlecki, A. Subramanian, C. de Vargas, E. Di Lorenzo, S. C. Doney, A. J. Hermann, T. Joyce, M. Merrifield, A. J. Miller, F. Not and S. Pesant, *Frontiers in Marine Science* 6(623): 2019.
<https://doi.org/0.3389/fmars.2019.00623>

94. Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome

Salazar, G., L. Paoli, A. Alberti, J. Huerta-Cepas, H. J. Ruscheweyh, M. Cuenca, C. M. Field, L. P. Coelho, C. Cruaud, S. Engelen, A. C. Gregory, K. Labadie, C. Marec, E. Pelletier, M. Royo-Llonch, S. Roux, P. Sanchez, H. Uehara, A. A. Zayed, G. Zeller, M. Carmichael, C. Dimier, J. Ferland, S. Kandels, M. Picheral, S. Pisarev, J. Poulain, C. Tara Oceans, S. G. Acinas, M. Babin, P. Bork, C. Bowler, C. de Vargas, L. Guidi, P. Hingamp, D. Iudicone, L. Karp-Boss, E. Karsenti, H. Ogata, S. Pesant, S. Speich, M. B. Sullivan, P. Wincker and S. Sunagawa, *Cell* 179(5): 1068-1083 e1021: 2019.
<https://doi.org/0.1016/j.cell.2019.10.014>

93. Global Trends in Marine Plankton Diversity across Kingdoms of Life

Ibarbalz, F. M., N. Henry, M. C. Brandao, S. Martini, G. Busseni, H. Byrne, L. P. Coelho, H. Endo, J. M. Gasol, A. C. Gregory, F. Mahe, J. Rigonato, M. Royo-Llonch, G. Salazar, I. Sanz-Saez, E. Scalco, D. Siviadan, A. A. Zayed, A. Zingone, K. Labadie, J. Ferland, C. Marec, S. Kandels, M. Picheral, C. Dimier, J. Poulain, S. Pisarev, M. Carmichael, S. Pesant, C. Tara Oceans, M. Babin, E. Boss, D. Iudicone, O. Jaillon, S. G. Acinas, H. Ogata, E. Pelletier, L. Stemann, M. B. Sullivan, S. Sunagawa, L. Bopp, C. de Vargas, L. Karp-Boss, P. Wincker, F. Lombard, C. Bowler and L. Zinger, *Cell* 179(5): 1084-1097 e1021: 2019.
<https://doi.org/0.1016/j.cell.2019.10.008>

92. Assessing the viral content of uncultured picoeukaryotes in the global-ocean by single cell genomics

Castillo, Y. M., J. F. Mangot, L. F. Benites, R. Logares, M. Kuronishi, H. Ogata, O. Jaillon, R. Massana, M. Sebastian and D. Vaque, *Mol Ecol* 28(18): 4272-4289: 2019.
<https://doi.org/0.1111/mec.15210>

91. Single cell ecogenomics reveals mating types of individual cells and ssDNA viral infections in the smallest photosynthetic eukaryotes

Benites, L. F., N. Poulton, K. Labadie, M. E. Sieracki, N. Grimsley and G. Piganeau, *Philos Trans R Soc Lond B Biol Sci* 374(1786): 20190089: 2019.
<https://doi.org/0.1098/rstb.2019.0089>

90. Meta-omics reveals genetic flexibility of diatom nitrogen transporters in response to environmental changes

Busseni, G., F. R. J. Vieira, A. Amato, E. Pelletier, J. J. Pierella Karlusich, M. I. Ferrante, P. Wincker, A. Rogato, C. Bowler, R. Sanges, L. Maiorano, M. Chiurazzi, M. R. d'Alcala, L. Caputi and D. Iudicone, *Mol Biol Evol*: 2019.
<https://doi.org/0.1093/molbev/msz157>

89. Phytoplankton in the Tara Ocean

Pierella Karlusich, J. J., F. Ibarbalz and C. Bowler, *Annual Review of Marine Science* 12: 233-265: 2020.
<https://doi.org/0.1146/annurev-marine-010419-010706>

88. The Earth Is Small for Leviathans: Long Distance Dispersal of Giant Viruses across Aquatic Environments

Li, Y., H. Endo, Y. Gotoh, H. Watai, N. Ogawa, R. Blanc-Mathieu, T. Yoshida and H. Ogata, *Microbes Environ* 34(3): 334-339: 2019.
<https://doi.org/0.1264/jsme2.ME19037>

87. Single cell genomics yields a wide diversity of small planktonic protists across major ocean ecosystems

Sieracki, M. E., N. J. Poulton, O. Jaillon, P. Wincker, C. de Vargas, L. Rubinat-Ripoll, R. Stepanauskas, R. Logares and R. Massana, *Sci Rep* 9(1): 6025: 2019.
<https://doi.org/0.1038/s41598-019-42487-1>

86. Marine DNA Viral Macro- and Microdiversity from Pole to Pole

Gregory, A. C., A. A. Zayed, N. Conceicao-Neto, B. Temperton, B. Bolduc, A. Alberti, M. Ardyna, K. Arkhipova, M. Carmichael, C. Cruaud, C. Dimier, G. Dominguez-Huerta, J. Ferland, S. Kandels, Y. Liu, C. Marec, S. Pesant, M. Picheral, S. Pisarev, J. Poulain, J. E. Tremblay, D. Vik, C. Tara Oceans, M. Babin, C.

TARA OCEANS – FINAL CRUISE REPORT

Bowler, A. I. Culley, C. de Vargas, B. E. Dutilh, D. Iudicone, L. Karp-Boss, S. Roux, S. Sunagawa, P. Wincker and M. B. Sullivan, *Cell* 177(5): 1109-1123 e1114: 2019.

<https://doi.org/0.1016/j.cell.2019.03.040>

85. Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems

Caputi, L., Q. Carradec, D. Eveillard, A. Kirilovsky, E. Pelletier, J. J. Pierella Karlusich, F. Vieira, E. Villar, S. Chaffron, S. Malviya, E. Scalco, S. Acinas, A. Alberti, J.-M. Aury, A.-S. Benoiston, A. Bertrand, T. Biard, L. Bittner, M. Boccara and J. Weissenbach, *Global Biogeochemical Cycles* 33: 2019.

<https://doi.org/0.1029/2018GB006022>

84. Mixotrophic protists display contrasted biogeographies in the global ocean

Faure, E., F. Not, A. S. Benoiston, K. Labadie, L. Bittner and S. D. Ayata, *ISME J* 13(4): 1072-1083: 2019.

<https://doi.org/0.1038/s41396-018-0340-5>

83. Discovering millions of plankton genomic markers from the Atlantic Ocean and the Mediterranean Sea

Arif, M., J. Gauthier, K. Sugier, D. Iudicone, O. Jaillon, P. Wincker, P. Peterlongo and M. A. Madoui, *Mol Ecol Resour* 19(2): 526-535: 2019.

<https://doi.org/0.1111/1755-0998.12985>

82. Degenerate PCR Primers to Reveal the Diversity of Giant Viruses in Coastal Waters

Li, Y., P. Hingamp, H. Watai, H. Endo, T. Yoshida and H. Ogata, *Viruses* 10: 496: 2018.

<https://doi.org/0.3390/v10090496>

81. UCYN-A3, a newly characterized open ocean sublineage of the symbiotic N₂-fixing cyanobacterium *Candidatus Atelocyanobacterium thalassa*

Cornejo-Castillo, F. M., M. D. C. Munoz-Marin, K. A. Turk-Kubo, M. Royo-Llonch, H. Farnelid, S. G. Acinas and J. P. Zehr, *Environ Microbiol* 21(1): 111-124: 2019.

<https://doi.org/0.1111/1462-2920.14429>

80. Clade-specific diversification dynamics of marine diatoms since the Jurassic

Lewitus, E., L. Bittner, S. Malviya, C. Bowler and H. Morlon, *Nat Ecol Evol* 2(11): 1715-1723: 2018.

<https://doi.org/0.1038/s41559-018-0691-3>

79. Morphological and genetic divergence between Mediterranean and Caribbean populations of *Madracis pharensis* (Heller 1868) (Scleractinia, Pocilloporidae): Too much for one species?

Benzoni, F., R. Arrigoni, M. Berumen, M. Taviani, P. Bongaerts and P. Frade, *Zootaxa* 4471: 473–492: 2018.

<https://doi.org/0.11646/zootaxa.4471.3.3>

78. Worldwide Occurrence and Activity of the Reef-Building Coral Symbiont *Symbiodinium* in the Open Ocean

Decelle, J., Q. Carradec, X. Pochon, N. Henry, S. Romac, F. Mahe, M. Dunthorn, A. Kourlaiev, C. R. Voolstra, P. Wincker and C. de Vargas, *Curr Biol* 28(22): 3625-3633 e3623: 2018.

<https://doi.org/0.1016/j.cub.2018.09.024>

77. Coral responses to a repeat bleaching event in Mayotte in 2010

Obura, D. O., L. Bigot and F. Benzoni, *PeerJ* 6: e5305: 2018.

<https://doi.org/0.7717/peerj.5305>

76. Ubiquitous abundance distribution of non-dominant plankton across the global ocean

Ser-Giacomi, E., L. Zinger, S. Malviya, C. De Vargas, E. Karsenti, C. Bowler and S. De Monte, *Nat Ecol Evol* 2(8): 1243-1249: 2018.

<https://doi.org/0.1038/s41559-018-0587-2>

75. The Ocean Gene Atlas: exploring the biogeography of plankton genes online

TARA OCEANS – FINAL CRUISE REPORT

Villar, E., T. Vannier, C. Vernet, M. Lescot, M. Cuenca, A. Alexandre, P. Bachelerie, T. Rosnet, E. Pelletier, S. Sunagawa and P. Hingamp, *Nucleic Acids Res* 46(W1): W289-W295: 2018.
<https://doi.org/0.1093/nar/gky376>

74. Endocytosis-mediated siderophore uptake as a strategy for Fe acquisition in diatoms

Kazamia, E., R. Sutak, J. Paz-Yepes, R. G. Dorrell, F. R. J. Vieira, J. Mach, J. Morrissey, S. Leon, F. Lam, E. Pelletier, J. M. Camadro, C. Bowler and E. Lesuisse, *Sci Adv* 4(5): eaar4536: 2018.
<https://doi.org/0.1126/sciadv.aar4536>

73. Uncovering hidden coral diversity: a new cryptic lobophylliid scleractinian from the Indian Ocean

Arrigoni, R., M. Berumen, J. Stolarski, T. I. Terraneo and F. Benzoni, *Cladistics* 35: 2018.
<https://doi.org/0.1111/cla.12346>

72. Taxon Richness of Megaviridae Exceeds those of Bacteria and Archaea in the Ocean

Mihara, T., H. Koyano, P. Hingamp, N. Grimsley, S. Goto and H. Ogata, *Microbes Environ* 33(2): 162-171: 2018.
<https://doi.org/0.1264/jsme2.ME17203>

71. Nanoplanktonic diatoms are globally overlooked but play a role in spring blooms and carbon export

Leblanc, K., B. Queguiner, F. Diaz, V. Cornet, M. Michel-Rodriguez, X. Durrieu de Madron, C. Bowler, S. Malviya, M. Thyssen, G. Gregori, M. Rembauville, O. Grosso, J. Poulain, C. de Vargas, M. Pujo-Pay and P. Conan, *Nat Commun* 9(1): 953: 2018.
<https://doi.org/0.1038/s41467-018-03376-9>

70. Competition between Silicifiers and Non-silicifiers in the Past and Present Ocean and Its Evolutionary Impacts

Hendry, K. R., A. O. Marron, F. Vincent, D. J. Conley, M. Gehlen, F. M. Ibarbalz, B. Quéguiner and C. Bowler, *Frontiers in Marine Science* 5(22): 2018.
<https://doi.org/0.3389/fmars.2018.00022>

69. Light color acclimation is a key process in the global ocean distribution of *Synechococcus cyanobacteria*

Grebert, T., H. Dore, F. Partensky, G. K. Farrant, E. S. Boss, M. Picheral, L. Guidi, S. Pesant, D. J. Scanlan, P. Wincker, S. G. Acinas, D. M. Kehoe and L. Garczarek, *Proc Natl Acad Sci U S A* 115(9): E2010-E2019: 2018.
<https://doi.org/0.1073/pnas.1717069115>

68. Neobodonids are dominant kinetoplastids in the global ocean

Flegontova, O., P. Flegontov, S. Malviya, J. Poulain, C. de Vargas, C. Bowler, J. Lukes and A. Horak, *Environ Microbiol* 20(2): 878-889: 2018.
<https://doi.org/0.1111/1462-2920.14034>

67. The epibiotic life of the cosmopolitan diatom *Fragilariopsis doliolus* on heterotrophic ciliates in the open ocean

Vincent, F. J., S. Colin, S. Romac, E. Scalco, L. Bittner, Y. Garcia, R. M. Lopes, J. R. Dolan, A. Zingone, C. de Vargas and C. Bowler, *ISME J* 12(4): 1094-1108: 2018.
<https://doi.org/0.1038/s41396-017-0029-1>

66. Locality and diel cycling of viral production revealed by a 24 h time course cross-omics analysis in a coastal region of Japan

Yoshida, T., Y. Nishimura, H. Watai, N. Haruki, D. Morimoto, H. Kaneko, T. Honda, K. Yamamoto, P. Hingamp, Y. Sako, S. Goto and H. Ogata, *ISME J* 12(5): 1287-1295: 2018.
<https://doi.org/0.1038/s41396-018-0052-x>

65. Influence of diatom diversity on the ocean biological carbon pump

TARA OCEANS – FINAL CRUISE REPORT

Tréguer, P., C. Bowler, B. Moriceau, S. Dutkiewicz, M. Gehlen, O. Aumont, L. Bittner, R. Dugdale, Z. Finkel, D. Iudicone, O. Jahn, L. Guidi, M. Lasbleiz, K. Leblanc, M. Levy and P. Pondaven, *Nature Geoscience* 11(1): 27-37: 2018.
<https://doi.org/0.1038/s41561-017-0028-x>

64. Pan-Arctic optical characteristics of colored dissolved organic matter: Tracing dissolved organic carbon in changing Arctic waters using satellite ocean color data

Matsuoka, A., E. Boss, M. Babin, L. Karp-Boss, M. Hafez, A. Chekalyuk, C. W. Proctor, P. J. Werdell and A. Bricaud, *Remote Sensing of Environment* 200: 89-101: 2017.
<https://doi.org/10.1016/j.rse.2017.08.009>

63. Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans

Seeleuthner, Y., S. Mondy, V. Lombard, Q. Carradec, E. Pelletier, M. Wessner, J. Leconte, J. F. Mangot, J. Poulain, K. Labadie, R. Logares, S. Sunagawa, V. de Berardinis, M. Salanoubat, C. Dimier, S. Kandels-Lewis, M. Picheral, S. Searson, C. Tara Oceans, S. Pesant, N. Poulton, R. Stepanauskas, P. Bork, C. Bowler, P. Hingamp, M. B. Sullivan, D. Iudicone, R. Massana, J. M. Aury, B. Henrissat, E. Karsenti, O. Jaillon, M. Sieracki, C. de Vargas and P. Wincker, *Nat Commun* 9(1): 310: 2018.
<https://doi.org/0.1038/s41467-017-02235-3>

62. A global ocean atlas of eukaryotic genes

Carradec, Q., E. Pelletier, C. Da Silva, A. Alberti, Y. Seeleuthner, R. Blanc-Mathieu, G. Lima-Mendez, F. Rocha, L. Tirichine, K. Labadie, A. Kirilovsky, A. Bertrand, S. Engelen, M. A. Madoui, R. Meheust, J. Poulain, S. Romac, D. J. Richter, G. Yoshikawa, C. Dimier, S. Kandels-Lewis, M. Picheral, S. Searson, C. Tara Oceans, O. Jaillon, J. M. Aury, E. Karsenti, M. B. Sullivan, S. Sunagawa, P. Bork, F. Not, P. Hingamp, J. Raes, L. Guidi, H. Ogata, C. de Vargas, D. Iudicone, C. Bowler and P. Wincker, *Nat Commun* 9(1): 373: 2018.
<https://doi.org/0.1038/s41467-017-02342-1>

61. Surface ocean metabarcoding confirms limited diversity in planktonic foraminifera but reveals unknown hyper-abundant lineages

Morard, R., M. J. Garet-Delmas, F. Mahe, S. Romac, J. Poulain, M. Kucera and C. de Vargas, *Sci Rep* 8(1): 2539: 2018.
<https://doi.org/0.1038/s41598-018-20833-z>

60. Quantitative 3D-imaging for cell biology and ecology of environmental microbial eukaryotes

Colin, S., L. P. Coelho, S. Sunagawa, C. Bowler, E. Karsenti, P. Bork, R. Pepperkok and C. de Vargas, *Elife* 6: 2017.
<https://doi.org/0.7554/eLife.26066>

59. Biological and physical influences on marine snowfall at the equator

Kiko, R., A. Biastoch, P. Brandt, S. Cravatte, H. Hauss, R. Hummels, I. Kriest, F. Marin, A. M. P. McDonnell, A. Oschlies, M. Picheral, F. U. Schwarzkopf, A. M. Thurnherr and L. Stemmann, *Nature Geoscience* 10(11): 852-858: 2017.
<https://doi.org/0.1038/ngeo3042>

58. Evaluation of single-cell genomics to address evolutionary questions using three SAGs of the choanoflagellate *Monosiga brevicollis*

Lopez-Escardo, D., X. Grau-Bove, A. Guillaumet-Adkins, M. Gut, M. E. Sieracki and I. Ruiz-Trillo, *Sci Rep* 7(1): 11025: 2017.
<https://doi.org/0.1038/s41598-017-11466-9>

57. Exploring Microdiversity in Novel *Kordia* sp. (Bacteroidetes) with Proteorhodopsin from the Tropical Indian Ocean via Single Amplified Genomes

Royo-Llonch, M., I. Ferrera, F. M. Cornejo-Castillo, P. Sanchez, G. Salazar, R. Stepanauskas, J. M. Gonzalez, M. E. Sieracki, S. Speich, L. Stemmann, C. Pedros-Alio and S. G. Acinas, *Front Microbiol* 8: 1317: 2017.
<https://doi.org/0.3389/fmicb.2017.01317>

56. New insights into global biogeography, population structure and natural selection from the genome of the epipelagic copepod *Oithona*

Madoui, M. A., J. Poulain, K. Sugier, M. Wessner, B. Noel, L. Berline, K. Labadie, A. Cornils, L. Blanco-Bercial, L. Stemann, J. L. Jamez and P. Wincker, *Mol Ecol* 26(17): 4467-4482: 2017.
<https://doi.org/0.1111/mec.14214>

55. The evolution of diatoms and their biogeochemical functions

Benoiston, A. S., F. M. Ibarbalz, L. Bittner, L. Guidi, O. Jahn, S. Dutkiewicz and C. Bowler, *Philos Trans R Soc Lond B Biol Sci* 372(1728): 2017.
<https://doi.org/0.1098/rstb.2016.0397>

54. A myovirus encoding both photosystem I and II proteins enhances cyclic electron flow in infected *Prochlorococcus* cells

Fridman, S., J. Flores-Uribe, S. Larom, O. Alalouf, O. Liran, I. Yacoby, F. Salama, B. Bailleul, F. Rappaport, T. Ziv, I. Sharon, F. M. Cornejo-Castillo, A. Philosofo, C. L. Dupont, P. Sanchez, S. G. Acinas, F. L. Rohwer, D. Lindell and O. Beja, *Nat Microbiol* 2(10): 1350-1357: 2017.
<https://doi.org/0.1038/s41564-017-0002-9>

53. Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition

Alberti, A., J. Poulain, S. Engelen, K. Labadie, S. Romac, I. Ferrera, G. Albin, J. M. Aury, C. Belser, A. Bertrand, C. Cruaud, C. Da Silva, C. Dossat, F. Gavory, S. Gas, J. Guy, M. Haquelle, E. Jacoby, O. Jaillon, A. Lemainque, E. Pelletier, G. Samson, M. Wessner, T. Genoscope Technical, S. G. Acinas, M. Royo-Llonch, F. M. Cornejo-Castillo, R. Logares, B. Fernandez-Gomez, C. Bowler, G. Cochrane, C. Amid, P. T. Hoopen, C. De Vargas, N. Grimsley, E. Desgranges, S. Kandels-Lewis, H. Ogata, N. Poulton, M. E. Sieracki, R. Stepanauskas, M. B. Sullivan, J. R. Brum, M. B. Duhaime, B. T. Poulos, B. L. Hurwitz, C. Tara Oceans Consortium, S. Pesant, E. Karsenti and P. Wincker, *Sci Data* 4: 170093: 2017.
<https://doi.org/0.1038/sdata.2017.93>

52. The Arctic Ocean as a dead end for floating plastics in the North Atlantic branch of the Thermohaline Circulation

Cózar, A., E. Martí, C. Duarte, J. Lomas, E. Seville, T. Ballatore, V. Eguíluz, J. González-Gordillo, M. L. Pedrotti, F. Echevarría, R. Troublè and X. Irigoien, *Science Advances* 3: e1600582: 2017.
<https://doi.org/0.1126/sciadv.1600582>

51. Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean

Nishimura, Y., H. Watai, T. Honda, T. Mihara, K. Omae, S. Roux, R. Blanc-Mathieu, K. Yamamoto, P. Hingamp, Y. Sako, M. B. Sullivan, S. Goto, H. Ogata and T. Yoshida, *mSphere* 2(2): 2017.
<https://doi.org/0.1128/mSphere.00359-16>

50. Biogeography and diversity of Collodaria (Radiolaria) in the global ocean

Biard, T., E. Bigeard, S. Audic, J. Poulain, A. Gutierrez-Rodríguez, S. Pesant, L. Stemann and F. Not, *ISME J* 11(6): 1331-1344: 2017.
<https://doi.org/0.1038/ismej.2017.12>

49. A new sequence data set of SSU rRNA gene for Scleractinia and its phylogenetic and ecological applications

Arrigoni, R., B. Vacherie, F. Benzoni, F. Stefani, E. Karsenti, O. Jaillon, F. Not, F. Nunes, C. Payri, P. Wincker and V. Barbe, *Mol Ecol Resour* 17(5): 1054-1071: 2017.
<https://doi.org/0.1111/1755-0998.12640>

48. Survey of the green picoalga *Bathycoccus* genomes in the global ocean

Vannier, T., J. Leconte, Y. Seeleuthner, S. Mondy, E. Pelletier, J. M. Aury, C. de Vargas, M. Sieracki, D. Iudicone, D. Vaultot, P. Wincker and O. Jaillon, *Sci Rep* 6: 37900: 2016.
<https://doi.org/0.1038/srep37900>

47. Extreme Diversity of Diplonemid Eukaryotes in the Ocean

Flegontova, O., P. Flegontov, S. Malviya, S. Audic, P. Wincker, C. de Vargas, C. Bowler, J. Lukes and A. Horak, *Curr Biol* 26(22): 3060-3065: 2016.
<https://doi.org/0.1016/j.cub.2016.09.031>

46. Full-field interferometry for counting and differentiating aquatic biotic nanoparticles: from laboratory to Tara Oceans

Boccaro, M., Y. Fedala, C. V. Bryan, M. Bailly-Bechet, C. Bowler and A. C. Boccaro, *Biomed Opt Express* 7(9): 3736-3746: 2016.
<https://doi.org/0.1364/BOE.7.003736>

45. Species delimitation in the reef coral genera *Echinophyllia* and *Oxypora* (Scleractinia, Lobophylliidae) with a description of two new species

Arrigoni, R., M. L. Berumen, C. A. Chen, T. I. Terraneo, A. H. Baird, C. Payri and F. Benzoni, *Mol Phylogenet Evol* 105: 146-159: 2016.
<https://doi.org/0.1016/j.ympev.2016.08.023>

44. When forms meet genes: Revision of the scleractinian genera *Micromussa* and *Homophyllia* (Lobophylliidae) with a description of two new species and one new genus

Arrigoni, R., F. Benzoni, D. Huang, H. Fukami, C. Chen, M. Berumen, M. Hoogenboom, D. Thomson, B. Hoeksema, A. Budd, Y. Zayasu, T. I. Terraneo, Y. Kitano and A. Baird, *Contributions to zoology Bijdragen tot de dierkunde* 85: 387-422: 2016.
<https://doi.org/0.1163/18759866-08504002>

43. Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses

Roux, S., J. R. Brum, B. E. Dutilh, S. Sunagawa, M. B. Duhaime, A. Loy, B. T. Poulos, N. Solonenko, E. Lara, J. Poulain, S. Pesant, S. Kandels-Lewis, C. Dimier, M. Picheral, S. Searson, C. Cruaud, A. Alberti, C. M. Duarte, J. M. Gasol, D. Vaque, C. Tara Oceans, P. Bork, S. G. Acinas, P. Wincker and M. B. Sullivan, *Nature* 537(7622): 689-693: 2016.
<https://doi.org/0.1038/nature19366>

42. Species delimitation in the coral genus *Goniopora* (Scleractinia, Poritidae) from the Saudi Arabian Red Sea

Terraneo, T. I., F. Benzoni, R. Arrigoni and M. L. Berumen, *Mol Phylogenet Evol* 102: 278-294: 2016.
<https://doi.org/0.1016/j.ympev.2016.06.003>

41. Delineating ecologically significant taxonomic units from global patterns of marine picocyanobacteria

Farrant, G. K., H. Dore, F. M. Cornejo-Castillo, F. Partensky, M. Ratin, M. Ostrowski, F. D. Pitt, P. Wincker, D. J. Scanlan, D. Iudicone, S. G. Acinas and L. Garczarek, *Proc Natl Acad Sci U S A* 113(24): E3365-3374: 2016.
<https://doi.org/0.1073/pnas.1524865113>

40. Biogeochemical characteristics of a long-lived anticyclonic eddy in the eastern South Pacific Ocean

Cornejo-D'Ottone, M., L. Bravo, M. Ramos, O. Pizarro, J. Karstensen, M. Gallegos, M. Correa-Ramirez, N. Silva, L. Farias and L. Karp-Boss, *Biogeosciences* 13: 2971-2979: 2016.
<https://doi.org/0.5194/bg-13-2971-2016>

39. Global genetic capacity for mixotrophy in marine picocyanobacteria

Yelton, A. P., S. G. Acinas, S. Sunagawa, P. Bork, C. Pedros-Alio and S. W. Chisholm, *ISME J* 10(12): 2946-2957: 2016.
<https://doi.org/0.1038/ismej.2016.64>

38. In situ imaging reveals the biomass of giant protists in the global ocean

Biard, T., L. Stemann, M. Picheral, N. Mayot, P. Vandromme, H. Hauss, G. Gorsky, L. Guidi, R. Kiko and F. Not, *Nature* 532(7600): 504-507: 2016.
<https://doi.org/0.1038/nature17652>

37. Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton

Cornejo-Castillo, F. M., A. M. Cabello, G. Salazar, P. Sanchez-Baracaldo, G. Lima-Mendez, P. Hingamp, A. Alberti, S. Sunagawa, P. Bork, C. de Vargas, J. Raes, C. Bowler, P. Wincker, J. P. Zehr, J. M. Gasol, R. Massana and S. G. Acinas, *Nat Commun* 7: 11071: 2016.
<https://doi.org/0.1038/ncomms11071>

36. Insights into global diatom distribution and diversity in the world's ocean

Malviya, S., E. Scalco, S. Audic, F. Vincent, A. Veluchamy, J. Poulain, P. Wincker, D. Iudicone, C. de Vargas, L. Bittner, A. Zingone and C. Bowler, *Proc Natl Acad Sci U S A* 113(11): E1516-1525: 2016.
<https://doi.org/0.1073/pnas.1509523113>

35. Illuminating structural proteins in viral dark matter with metaproteomics

Brum, J. R., J. C. Ignacio-Espinoza, E. H. Kim, G. Trubl, R. M. Jones, S. Roux, N. C. VerBerkmoes, V. I. Rich and M. B. Sullivan, *Proc Natl Acad Sci U S A* 113(9): 2436-2441: 2016.
<https://doi.org/0.1073/pnas.1525139113>

34. Plankton networks driving carbon export in the oligotrophic ocean

Guidi, L., S. Chaffron, L. Bittner, D. Eveillard, A. Larhlimi, S. Roux, Y. Darzi, S. Audic, L. Berline, J. Brum, L. P. Coelho, J. C. I. Espinoza, S. Malviya, S. Sunagawa, C. Dimier, S. Kandels-Lewis, M. Picheral, J. Poulain, S. Searson, c. Tara Oceans, L. Stemmann, F. Not, P. Hingamp, S. Speich, M. Follows, L. Karp-Boss, E. Boss, H. Ogata, S. Pesant, J. Weissenbach, P. Wincker, S. G. Acinas, P. Bork, C. de Vargas, D. Iudicone, M. B. Sullivan, J. Raes, E. Karsenti, C. Bowler and G. Gorsky, *Nature* 532(7600): 465-470: 2016.
<https://doi.org/0.1038/nature16942>

33. The symbiotic life of Symbiodinium in the open ocean within a new species of calcifying ciliate (*Tiarina* sp.)

Mordret, S., S. Romac, N. Henry, S. Colin, M. Carmichael, C. Berney, S. Audic, D. J. Richter, X. Pochon, C. de Vargas and J. Decelle, *ISME J* 10(6): 1424-1436: 2016.
<https://doi.org/0.1038/ismej.2015.211>

32. Deep sequencing of amplified Prasinovirus and host green algal genes from an Indian Ocean transect reveals interacting trophic dependencies and new genotypes

Clerissi, C., Y. Desdèvises, S. Romac, S. Audic, C. de Vargas, S. G. Acinas, R. Casotti, J. Poulain, P. Wincker, P. Hingamp, H. Ogata and N. Grimsley, *Environ Microbiol Rep* 7(6): 979-989: 2015.
<https://doi.org/0.1111/1758-2229.12345>

31. Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages

Lescot, M., P. Hingamp, K. K. Kojima, E. Villar, S. Romac, A. Veluchamy, M. Boccara, O. Jaillon, D. Iudicone, C. Bowler, P. Wincker, J. M. Claverie and H. Ogata, *ISME J* 10(5): 1134-1146: 2016.
<https://doi.org/0.1038/ismej.2015.192>

30. Closing the gaps on the viral photosystem-I psaDCAB gene organization

Roitman, S., J. Flores-Urbe, A. Filosof, B. Knowles, F. Rohwer, J. C. Ignacio-Espinoza, M. B. Sullivan, F. M. Cornejo-Castillo, P. Sanchez, S. G. Acinas, C. L. Dupont and O. Beja, *Environ Microbiol* 17(12): 5100-5108: 2015.
<https://doi.org/0.1111/1462-2920.13036>

29. Global patterns of pelagic dinoflagellate diversity across protist size classes unveiled by metabarcoding

Le Bescot, N., F. Mahe, S. Audic, C. Dimier, M. J. Garet, J. Poulain, P. Wincker, C. de Vargas and R. Siano, *Environ Microbiol* 18(2): 609-626: 2016.
<https://doi.org/0.1111/1462-2920.13039>

TARA OCEANS – FINAL CRUISE REPORT

28. A new look at ocean carbon remineralization for estimating deep-water sequestration

Guidi, L., L. Legendre, G. Reygondeau, J. Uitz, L. Stemann and S. Henson, *Global Biogeochemical Cycles*: n/a-n/a: 2015.

<https://doi.org/0.1002/2014GB005063>

27. Regional ocean-colour chlorophyll algorithms for the Red Sea

Brewin, R. J. W., D. E. Raitsos, G. Dall'Olmo, N. Zarokanellos, T. Jackson, M.-F. Racault, E. S. Boss, S. Sathyendranath, B. H. Jones and I. Hoteit, *Remote Sensing of Environment* 165: 64-85: 2015.

<https://doi.org/10.1016/j.rse.2015.04.024>

26. Open science resources for the discovery and analysis of Tara Oceans data

Pesant, S., F. Not, M. Picheral, S. Kandels-Lewis, N. Le Bescot, G. Gorsky, D. Iudicone, E. Karsenti, S. Speich, R. Trouble, C. Dimier, S. Searson and C. Tara Oceans Consortium, *Sci Data* 2: 150023: 2015.

<https://doi.org/0.1038/sdata.2015.23>

25. Determinants of community structure in the global plankton interactome

Lima-Mendez, G., K. Faust, N. Henry, J. Decelle, S. Colin, F. Carcillo, S. Chaffron, J. C. Ignacio-Espinosa, S. Roux, F. Vincent, L. Bittner, Y. Darzi, J. Wang, S. Audic, L. Berline, G. Bontempi, A. M. Cabello, L. Coppola, F. M. Cornejo-Castillo, F. d'Ovidio, L. De Meester, I. Ferrera, M. J. Garet-Delmas, L. Guidi, E. Lara, S. Pesant, M. Royo-Llonch, G. Salazar, P. Sanchez, M. Sebastian, C. Souffreau, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, c. Tara Oceans, G. Gorsky, F. Not, H. Ogata, S. Speich, L. Stemann, J. Weissenbach, P. Wincker, S. G. Acinas, S. Sunagawa, P. Bork, M. B. Sullivan, E. Karsenti, C. Bowler, C. de Vargas and J. Raes, *Science* 348(6237): 1262073: 2015.

<https://doi.org/0.1126/science.1262073>

24. Eukaryotic plankton diversity in the sunlit ocean

de Vargas, C., S. Audic, N. Henry, J. Decelle, F. Mahe, R. Logares, E. Lara, C. Berney, N. Le Bescot, I. Probert, M. Carmichael, J. Poulain, S. Romac, S. Colin, J. M. Aury, L. Bittner, S. Chaffron, M. Dunthorn, S. Engelen, O. Flegontova, L. Guidi, A. Horak, O. Jaillon, G. Lima-Mendez, J. Lukes, S. Malviya, R. Morard, M. Mulot, E. Scalco, R. Siano, F. Vincent, A. Zingone, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, C. Tara Oceans, S. G. Acinas, P. Bork, C. Bowler, G. Gorsky, N. Grimsley, P. Hingamp, D. Iudicone, F. Not, H. Ogata, S. Pesant, J. Raes, M. E. Sieracki, S. Speich, L. Stemann, S. Sunagawa, J. Weissenbach, P. Wincker and E. Karsenti, *Science* 348(6237): 1261605: 2015.

<https://doi.org/0.1126/science.1261605>

23. Structure and function of the global ocean microbiome

Sunagawa, S., L. P. Coelho, S. Chaffron, J. R. Kultima, K. Labadie, G. Salazar, B. Djahanschiri, G. Zeller, D. R. Mende, A. Alberti, F. M. Cornejo-Castillo, P. I. Costea, C. Cruaud, F. d'Ovidio, S. Engelen, I. Ferrera, J. M. Gasol, L. Guidi, F. Hildebrand, F. Kokoszka, C. Lepoivre, G. Lima-Mendez, J. Poulain, B. T. Poulos, M. Royo-Llonch, H. Sarmiento, S. Vieira-Silva, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, c. Tara Oceans, C. Bowler, C. de Vargas, G. Gorsky, N. Grimsley, P. Hingamp, D. Iudicone, O. Jaillon, F. Not, H. Ogata, S. Pesant, S. Speich, L. Stemann, M. B. Sullivan, J. Weissenbach, P. Wincker, E. Karsenti, J. Raes, S. G. Acinas and P. Bork, *Science* 348(6237): 1261359: 2015.

<https://doi.org/0.1126/science.1261359>

22. Patterns and ecological drivers of ocean viral communities

Brum, J. R., J. C. Ignacio-Espinoza, S. Roux, G. Doucier, S. G. Acinas, A. Alberti, S. Chaffron, C. Cruaud, C. de Vargas, J. M. Gasol, G. Gorsky, A. C. Gregory, L. Guidi, P. Hingamp, D. Iudicone, F. Not, H. Ogata, S. Pesant, B. T. Poulos, S. M. Schwenck, S. Speich, C. Dimier, S. Kandels-Lewis, M. Picheral, S. Searson, C. Tara Oceans, P. Bork, C. Bowler, S. Sunagawa, P. Wincker, E. Karsenti and M. B. Sullivan, *Science* 348(6237): 1261498: 2015.

<https://doi.org/0.1126/science.1261498>

21. Environmental characteristics of Agulhas rings affect interocean plankton transport

Villar, E., G. K. Farrant, M. Follows, L. Garczarek, S. Speich, S. Audic, L. Bittner, B. Blanke, J. R. Brum, C. Brunet, R. Casotti, A. Chase, J. R. Dolan, F. d'Ortenzio, J. P. Gattuso, N. Grima, L. Guidi, C. N. Hill, O. Jahn, J. L.

TARA OCEANS – FINAL CRUISE REPORT

Jamet, H. Le Goff, C. Lepoivre, S. Malviya, E. Pelletier, J. B. Romagnan, S. Roux, S. Santini, E. Scalco, S. M. Schwenck, A. Tanaka, P. Testor, T. Vannier, F. Vincent, A. Zingone, C. Dimier, M. Picheral, S. Searson, S. Kandels-Lewis, C. Tara Oceans, S. G. Acinas, P. Bork, E. Boss, C. de Vargas, G. Gorsky, H. Ogata, S. Pesant, M. B. Sullivan, S. Sunagawa, P. Wincker, E. Karsenti, C. Bowler, F. Not, P. Hingamp and D. Iudicone, *Science* 348(6237): 1261447: 2015.

<https://doi.org/0.1126/science.1261447>

20. Comprehensive model of annual plankton succession based on the whole-plankton time series approach

Romagnan, J. B., L. Legendre, L. Guidi, J. L. Jamet, D. Jamet, L. Mousseau, M. L. Pedrotti, M. Picheral, G. Gorsky, C. Sardet and L. Stemann, *PLoS One* 10(3): e0119219: 2015.

<https://doi.org/0.1371/journal.pone.0119219>

19. Evolutionary history of Chaetognatha inferred from molecular and morphological data: a case study for body plan simplification

Gasmi, S., G. Neve, N. Pech, S. Tekaya, A. Gilles and Y. Perez, *Front Zool* 11(1): 84: 2014.

<https://doi.org/0.1186/s12983-014-0084-7>

18. Taxonomy and phylogenetic relationships of the coral genera Australomussa and Parascolymia (Scleractinia, Lobophylliidae)

Arrigoni, R., R. Z.T, C. Chen, A. Baird and F. Benzoni, *Contributions to Zoology Bijdragen tot de dierkunde* 83: 195-215: 2014.

<https://doi.org/0.1163/18759866-08303004>

17. A phylogeny reconstruction of the Dendrophylliidae (Cnidaria, Scleractinia) based on molecular and micromorphological criteria, and its ecological implications

Arrigoni, R., Y. Kitano, J. Stolarski, B. Hoeksema, H. Fukami, F. Stefani, P. Galli, S. Montano, E. Castoldi and F. Benzoni, *Zoologica Scripta* 43: 661-688: 2014.

<https://doi.org/0.1111/zsc.12072>

16. Validation of a new catalysed reporter deposition-fluorescence in situ hybridization probe for the accurate quantification of marine Bacteroidetes populations

Acinas, S. G., I. Ferrera, H. Sarmiento, C. Diez-Vives, I. Forn, C. Ruiz-Gonzalez, F. M. Cornejo-Castillo, G. Salazar and J. M. Gasol, *Environ Microbiol* 17(10): 3557-3569: 2015.

<https://doi.org/0.1111/1462-2920.12517>

15. An inexpensive, accurate, and precise wet-mount method for enumerating aquatic viruses

Cunningham, B. R., J. R. Brum, S. M. Schwenck, M. B. Sullivan and S. G. John, *Appl Environ Microbiol* 81(9): 2995-3000: 2015.

<https://doi.org/0.1128/AEM.03642-14>

14. Phylogenetic relationships and revision of the genus Blastomussa (Cnidaria: Anthozoa: Scleractinia) with description of a new species

Benzoni, F., R. Arrigoni, Z. Waheed, F. Stefani and B. Hoeksema, *The Raffles bulletin of zoology* 62: 358-378: 2014.

13. Unveiling of the diversity of Prasinoviruses (Phycodnaviridae) in marine samples by using high-throughput sequencing analyses of PCR-amplified DNA polymerase and major capsid protein genes

Clerissi, C., N. Grimsley, H. Ogata, P. Hingamp, J. Poulain and Y. Desdèvises, *Appl Environ Microbiol* 80(10): 3150-3160: 2014.

<https://doi.org/0.1128/AEM.00123-14>

12. Decomposition of in situ particulate absorption spectra

Chase, A., E. Boss, R. Zaneveld, A. Bricaud, H. Claustre, J. Ras, G. Dall'Olmo and T. K. Westberry, *Methods in Oceanography* 7: 110-124: 2013.

<https://doi.org/10.1016/j.mio.2014.02.002>

11. The characteristics of particulate absorption, scattering and attenuation coefficients in the surface ocean; Contribution of the Tara Oceans expedition

Boss, E., M. Picheral, T. Leeuw, A. Chase, E. Karsenti, G. Gorsky, L. Taylor, W. Slade, J. Ras and H. Claustre, *Methods in Oceanography* 7: 52-62: 2013.
<https://doi.org/10.1016/j.mio.2013.11.002>

10. Bioprospecting marine plankton

Abida, H., S. Ruchaud, L. Rios, A. Humeau, I. Probert, C. De Vargas, S. Bach and C. Bowler, *Mar Drugs* 11(11): 4594-4611: 2013.
<https://doi.org/0.3390/md11114594>

9. Underway sampling of marine inherent optical properties on the Tara Oceans expedition as a novel resource for ocean color satellite data product validation

Werdell, P. J., C. W. Proctor, E. Boss, T. Leeuw and M. Ouhssain, *Methods in Oceanography* 7: 40-51: 2013.
<https://doi.org/10.1016/j.mio.2013.09.001>

8. Metagenomic 16S rDNA Illumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities

Logares, R., S. Sunagawa, G. Salazar, F. M. Cornejo-Castillo, I. Ferrera, H. Sarmiento, P. Hingamp, H. Ogata, C. de Vargas, G. Lima-Mendez, J. Raes, J. Poulain, O. Jaillon, P. Wincker, S. Kandels-Lewis, E. Karsenti, P. Bork and S. G. Acinas, *Environ Microbiol* 16(9): 2659-2671: 2014.
<https://doi.org/0.1111/1462-2920.12250>

7. Echinophyllia tarae sp. n. (Cnidaria, Anthozoa, Scleractinia), a new reef coral species from the Gambier Islands, French Polynesia

Benzoni, F., *Zookeys*(318): 59-79: 2013.
<https://doi.org/0.3897/zookeys.318.5351>

6. Prevalent genome streamlining and latitudinal divergence of planktonic bacteria in the surface ocean

Swan, B. K., B. Tupper, A. Sczyrba, F. M. Lauro, M. Martinez-Garcia, J. M. Gonzalez, H. Luo, J. J. Wright, Z. C. Landry, N. W. Hanson, B. P. Thompson, N. J. Poulton, P. Schwientek, S. G. Acinas, S. J. Giovannoni, M. A. Moran, S. J. Hallam, R. Cavicchioli, T. Woyke and R. Stepanauskas, *Proc Natl Acad Sci U S A* 110(28): 11463-11468: 2013.
<https://doi.org/0.1073/pnas.1304246110>

5. Sequencing platform and library preparation choices impact viral metagenomes

Solonenko, S. A., J. C. Ignacio-Espinoza, A. Alberti, C. Cruaud, S. Hallam, K. Konstantinidis, G. Tyson, P. Wincker and M. B. Sullivan, *BMC Genomics* 14: 320: 2013.
<https://doi.org/0.1186/1471-2164-14-320>

4. Global morphological analysis of marine viruses shows minimal regional variation and dominance of non-tailed viruses

Brum, J. R., R. O. Schenck and M. B. Sullivan, *ISME J* 7(9): 1738-1751: 2013.
<https://doi.org/0.1038/ismej.2013.67>

3. Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes

Hingamp, P., N. Grimsley, S. G. Acinas, C. Clerissi, L. Subirana, J. Poulain, I. Ferrera, H. Sarmiento, E. Villar, G. Lima-Mendez, K. Faust, S. Sunagawa, J. M. Claverie, H. Moreau, Y. Desdevises, P. Bork, J. Raes, C. de Vargas, E. Karsenti, S. Kandels-Lewis, O. Jaillon, F. Not, S. Pesant, P. Wincker and H. Ogata, *ISME J* 7(9): 1678-1695: 2013.
<https://doi.org/0.1038/ismej.2013.59>

2. Phylogenetic analysis of Thecosomata Blainville, 1824 (holoplanktonic opisthobranchia) using morphological and molecular data

Corse, E., J. Rampal, C. Cuoc, N. Pech, Y. Perez and A. Gilles, *PLoS One* 8(4): e59439: 2013.

TARA OCEANS – FINAL CRUISE REPORT

<https://doi.org/0.1371/journal.pone.0059439>

1. A holistic approach to marine eco-systems biology

Karsenti, E., S. G. Acinas, P. Bork, C. Bowler, C. De Vargas, J. Raes, M. Sullivan, D. Arendt, F. Benzoni, J. M. Claverie, M. Follows, G. Gorsky, P. Hingamp, D. Iudicone, O. Jaillon, S. Kandels-Lewis, U. Krzic, F. Not, H. Ogata, S. Pesant, E. G. Reynaud, C. Sardet, M. E. Sieracki, S. Speich, D. Velayoudon, J. Weissenbach, P. Wincker and C. Tara Oceans, PLoS Biol 9(10): e1001177.: 2011.

<https://doi.org/0.1371/journal.pbio.1001177>