

# Patrick Wincker

## List of Publications by Year in descending order

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Version: 2024-02-01

92  
papers

21,753  
citations

43973

48  
h-index

40881

93  
g-index

122  
all docs

122  
docs citations

122  
times ranked

23044  
citing authors

#	ARTICLE	IF	CITATIONS
1	A robust approach to estimate relative phytoplankton cell abundances from metagenomes. <i>Molecular Ecology Resources</i> , 2023, 23, 16-40.	2.2	29
2	Heterotrophic bacterial diazotrophs are more abundant than their cyanobacterial counterparts in metagenomes covering most of the sunlit ocean. <i>ISME Journal</i> , 2022, 16, 927-936.	4.4	41
3	Subtle limits to connectivity revealed by outlier loci within two divergent metapopulations of the deep-sea hydrothermal gastropod <i>Uremeria nautili</i> . <i>Molecular Ecology</i> , 2022, 31, 2796-2813.	2.0	7
4	Restructuring of plankton genomic biogeography in the surface ocean under climate change. <i>Nature Climate Change</i> , 2022, 12, 393-401.	8.1	21
5	The Ocean Gene Atlas v2.0: online exploration of the biogeography and phylogeny of plankton genes. <i>Nucleic Acids Research</i> , 2022, 50, W516-W526.	6.5	26
6	Long-read and chromosome-scale assembly of the hexaploid wheat genome achieves high resolution for research and breeding. <i>GigaScience</i> , 2022, 11, .	3.3	26
7	Tempo and drivers of plant diversification in the European mountain system. <i>Nature Communications</i> , 2022, 13, 2750.	5.8	15
8	Biosynthetic potential of the global ocean microbiome. <i>Nature</i> , 2022, 607, 111-118.	13.7	128
9	Diversity and ecological footprint of Global Ocean RNA viruses. <i>Science</i> , 2022, 376, 1202-1208.	6.0	41
10	Priorities for ocean microbiome research. <i>Nature Microbiology</i> , 2022, 7, 937-947.	5.9	27
11	Cyanorak v2.1: a scalable information system dedicated to the visualization and expert curation of marine and brackish picocyanobacteria genomes. <i>Nucleic Acids Research</i> , 2021, 49, D667-D676.	6.5	38
12	Comparative genomics reveals new functional insights in uncultured MAST species. <i>ISME Journal</i> , 2021, 15, 1767-1781.	4.4	18
13	Evaluating sediment and water sampling methods for the estimation of deep-sea biodiversity using environmental DNA. <i>Scientific Reports</i> , 2021, 11, 7856.	1.6	18
14	Microbial community structure in hadal sediments: high similarity along trench axes and strong changes along redox gradients. <i>ISME Journal</i> , 2021, 15, 3455-3467.	4.4	29
15	Population genomics of apricots unravels domestication history and adaptive events. <i>Nature Communications</i> , 2021, 12, 3956.	5.8	45
16	Global distribution patterns of marine nitrogen-fixers by imaging and molecular methods. <i>Nature Communications</i> , 2021, 12, 4160.	5.8	58
17	Male Differentiation in the Marine Copepod <i>Oithona nana</i> Reveals the Development of a New Nervous Ganglion and Lin12-Notch-Repeat Protein-Associated Proteolysis. <i>Biology</i> , 2021, 10, 657.	1.3	1
18	Sequencing and Chromosome-Scale Assembly of Plant Genomes, <i>Brassica rapa</i> as a Use Case. <i>Biology</i> , 2021, 10, 732.	1.3	15

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19	Environmental vulnerability of the global ocean epipelagic plankton community interactome. <i>Science Advances</i> , 2021, 7, .	4.7	54
20	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021, 11, 15714.	1.6	24
21	Telomere-to-telomere gapless chromosomes of banana using nanopore sequencing. <i>Communications Biology</i> , 2021, 4, 1047.	2.0	86
22	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. <i>Nature</i> , 2021, 600, 86-92.	13.7	81
23	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021, 598, 634-640.	13.7	142
24	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , 2021, 6, 1561-1574.	5.9	57
25	Into the bloom: Molecular response of pelagic tunicates to fluctuating food availability. <i>Molecular Ecology</i> , 2020, 29, 292-307.	2.0	6
26	A framework for in situ molecular characterization of coral holobionts using nanopore sequencing. <i>Scientific Reports</i> , 2020, 10, 15893.	1.6	9
27	Evolutionary Mechanisms of Long-Term Genome Diversification Associated With Niche Partitioning in Marine Picocyanobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 567431.	1.5	37
28	Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions. <i>Nature Ecology and Evolution</i> , 2020, 4, 1639-1649.	3.4	78
29	An Assessment of Environmental Metabarcoding Protocols Aiming at Favoring Contemporary Biodiversity in Inventories of Deep-Sea Communities. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	36
30	Tara Oceans: towards global ocean ecosystems biology. <i>Nature Reviews Microbiology</i> , 2020, 18, 428-445.	13.6	227
31	Genome Resolved Biogeography of Mamiellales. <i>Genes</i> , 2020, 11, 66.	1.0	21
32	Transcriptome reconstruction and functional analysis of eukaryotic marine plankton communities via high-throughput metagenomics and metatranscriptomics. <i>Genome Research</i> , 2020, 30, 647-659.	2.4	50
33	Long-read assembly of the <i>Brassica napus</i> reference genome Darmor-bzh. <i>GigaScience</i> , 2020, 9, .	3.3	64
34	Meta-Omics Reveals Genetic Flexibility of Diatom Nitrogen Transporters in Response to Environmental Changes. <i>Molecular Biology and Evolution</i> , 2019, 36, 2522-2535.	3.5	23
35	Transposition favors the generation of large effect mutations that may facilitate rapid adaption. <i>Nature Communications</i> , 2019, 10, 3421.	5.8	134
36	A thousand plantsâ€™ phylogeny. <i>Nature Plants</i> , 2019, 5, 1106-1107.	4.7	1

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37	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	13.5	268
38	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	13.5	271
39	The Tara Pacific expeditionâ€”A pan-ecosystemic approach of the â€œ-omicsâ€-complexity of coral reef holobionts across the Pacific Ocean. <i>PLoS Biology</i> , 2019, 17, e3000483.	2.6	48
40	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	13.5	541
41	Communityâ€Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	1.9	76
42	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. <i>SSRN Electronic Journal</i> , 2019, , .	0.4	4
43	Expanding Tara Oceans Protocols for Underway, Ecosystemic Sampling of the Ocean-Atmosphere Interface During Tara Pacific Expedition (2016â€2018). <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	42
44	Discovering millions of plankton genomic markers from the Atlantic Ocean and the Mediterranean Sea. <i>Molecular Ecology Resources</i> , 2019, 19, 526-535.	2.2	11
45	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813.	5.8	220
46	Light color acclimation is a key process in the global ocean distribution of <i>Synechococcus cyanobacteria</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2010-E2019.	3.3	91
47	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	5.8	101
48	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	5.8	297
49	The Rosa genome provides new insights into the domestication of modern roses. <i>Nature Genetics</i> , 2018, 50, 772-777.	9.4	344
50	An improved primer set and amplification protocol with increased specificity and sensitivity targeting the <i>Symbiodinium</i> ITS2 region. <i>PeerJ</i> , 2018, 6, e4816.	0.9	102
51	Worldwide Occurrence and Activity of the Reef-Building Coral Symbiont <i>Symbiodinium</i> in the Open Ocean. <i>Current Biology</i> , 2018, 28, 3625-3633.e3.	1.8	52
52	Chromosome-scale assemblies of plant genomes using nanopore long reads and optical maps. <i>Nature Plants</i> , 2018, 4, 879-887.	4.7	316
53	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
54	De novo assembly and annotation of three <i>Leptosphaeria</i> genomes using Oxford Nanopore MinION sequencing. <i>Scientific Data</i> , 2018, 5, 180235.	2.4	53

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55	Chitin distribution in the <i>Oithona</i> digestive and reproductive systems revealed by fluorescence microscopy. PeerJ, 2018, 6, e4685.	0.9	10
56	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. Scientific Data, 2017, 4, 170093.	2.4	147
57	Accessing the genomic information of unculturable oceanic picoeukaryotes by combining multiple single cells. Scientific Reports, 2017, 7, 41498.	1.6	47
58	New insights into global biogeography, population structure and natural selection from the genome of the epipelagic copepod <i>Oithona</i> . Molecular Ecology, 2017, 26, 4467-4482.	2.0	37
59	A new sequence data set of <i>SSU rRNA</i> gene for Scleractinia and its phylogenetic and ecological applications. Molecular Ecology Resources, 2017, 17, 1054-1071.	2.2	13
60	de novo assembly and population genomic survey of natural yeast isolates with the Oxford Nanopore MinION sequencer. GigaScience, 2017, 6, 1-13.	3.3	123
61	Global patterns of pelagic dinoflagellate diversity across protist size classes unveiled by metabarcoding. Environmental Microbiology, 2016, 18, 609-626.	1.8	105
62	Survey of the green picoalga <i>Bathycoccus</i> genomes in the global ocean. Scientific Reports, 2016, 6, 37900.	1.6	54
63	Insights into global diatom distribution and diversity in the world's ocean. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1516-25.	3.3	561
64	Extreme Diversity of Diplonemid Eukaryotes in the Ocean. Current Biology, 2016, 26, 3060-3065.	1.8	105
65	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. Nature, 2016, 537, 689-693.	13.7	629
66	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. Nature Communications, 2016, 7, 11071.	5.8	72
67	Delineating ecologically significant taxonomic units from global patterns of marine picocyanobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3365-74.	3.3	159
68	Plankton networks driving carbon export in the oligotrophic ocean. Nature, 2016, 532, 465-470.	13.7	670
69	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. ISME Journal, 2016, 10, 1134-1146.	4.4	35
70	Deep sequencing of amplified <i>P</i> and <i>rasinivirus</i> and host green algal genes from an Indian Ocean transect reveals interacting trophic dependencies and new genotypes. Environmental Microbiology Reports, 2015, 7, 979-989.	1.0	8
71	Determinants of community structure in the global plankton interactome. Science, 2015, 348, 1262073.	6.0	842
72	Patterns and ecological drivers of ocean viral communities. Science, 2015, 348, 1261498.	6.0	617

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73	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
74	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	6.0	1,551
75	Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015, 348, 1261447.	6.0	158
76	Genome assembly using Nanopore-guided long and error-free DNA reads. <i>BMC Genomics</i> , 2015, 16, 327.	1.2	177
77	Life-cycle modification in open oceans accounts for genome variability in a cosmopolitan phytoplankton. <i>ISME Journal</i> , 2015, 9, 1365-1377.	4.4	70
78	TE-Tracker: systematic identification of transposition events through whole-genome resequencing. <i>BMC Bioinformatics</i> , 2014, 15, 377.	1.2	27
79	Organization and evolution of transposable elements along the bread wheat chromosome 3B. <i>Genome Biology</i> , 2014, 15, 546.	3.8	88
80	Metagenomic <sc>16S rDNA I</sc>llumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. <i>Environmental Microbiology</i> , 2014, 16, 2659-2671.	1.8	291
81	Mapping the Epigenetic Basis of Complex Traits. <i>Science</i> , 2014, 343, 1145-1148.	6.0	403
82	Fifty thousand years of Arctic vegetation and megafaunal diet. <i>Nature</i> , 2014, 506, 47-51.	13.7	505
83	Development of a targeted metagenomic approach to study a genomic region involved in light harvesting in marine <i>Synechococcus</i>. <i>FEMS Microbiology Ecology</i> , 2014, 88, 231-249.	1.3	21
84	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
85	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	4.4	185
86	Gene functionalities and genome structure in <i>Bathycoccus prasinos</i> reflect cellular specializations at the base of the green lineage. <i>Genome Biology</i> , 2012, 13, R74.	13.9	143
87	The banana ( <i>Musa acuminata</i> ) genome and the evolution of monocotyledonous plants. <i>Nature</i> , 2012, 488, 213-217.	13.7	1,049
88	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	2.6	353
89	Effector diversification within compartments of the <i>Leptosphaeria maculans</i> genome affected by Repeat-Induced Point mutations. <i>Nature Communications</i> , 2011, 2, 202.	5.8	481
90	Hunting down fungal secretomes using liquidâ€phase IEF prior to high resolution 2â€DE. <i>Electrophoresis</i> , 2009, 30, 4118-4136.	1.3	31

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91	Unravelling the genomic mosaic of a ubiquitous genus of marine cyanobacteria. <i>Genome Biology</i> , 2008, 9, R90.	13.9	288
92	Unique features revealed by the genome sequence of <i>Acinetobacter</i> sp. ADP1, a versatile and naturally transformation competent bacterium. <i>Nucleic Acids Research</i> , 2004, 32, 5766-5779.	6.5	308