

# 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	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
2	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
3	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
4	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	6.0	1,551
5	The banana ( <i>Musa acuminata</i> ) genome and the evolution of monocotyledonous plants. <i>Nature</i> , 2012, 488, 213-217.	13.7	1,049
6	Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015, 348, 1262073.	6.0	842
7	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	13.7	670
8	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	13.7	629
9	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	6.0	617
10	Insights into global diatom distribution and diversity in the world's ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1516-25.	3.3	561
11	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	13.5	541
12	Fifty thousand years of Arctic vegetation and megafaunal diet. <i>Nature</i> , 2014, 506, 47-51.	13.7	505
13	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
14	Mapping the Epigenetic Basis of Complex Traits. <i>Science</i> , 2014, 343, 1145-1148.	6.0	403
15	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	2.6	353
16	The <i>Rosa</i> genome provides new insights into the domestication of modern roses. <i>Nature Genetics</i> , 2018, 50, 772-777.	9.4	344
17	Chromosome-scale assemblies of plant genomes using nanopore long reads and optical maps. <i>Nature Plants</i> , 2018, 4, 879-887.	4.7	316
18	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

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19	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	5.8	297
20	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
21	Unravelling the genomic mosaic of a ubiquitous genus of marine cyanobacteria. <i>Genome Biology</i> , 2008, 9, R90.	13.9	288
22	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	13.5	271
23	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	13.5	268
24	Tara Oceans: towards global ocean ecosystems biology. <i>Nature Reviews Microbiology</i> , 2020, 18, 428-445.	13.6	227
25	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813.	5.8	220
26	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	4.4	185
27	Genome assembly using Nanopore-guided long and error-free DNA reads. <i>BMC Genomics</i> , 2015, 16, 327.	1.2	177
28	Delineating ecologically significant taxonomic units from global patterns of marine picocyanobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3365-74.	3.3	159
29	Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015, 348, 1261447.	6.0	158
30	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	2.4	147
31	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
32	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021, 598, 634-640.	13.7	142
33	Transposition favors the generation of large effect mutations that may facilitate rapid adaption. <i>Nature Communications</i> , 2019, 10, 3421.	5.8	134
34	Biosynthetic potential of the global ocean microbiome. <i>Nature</i> , 2022, 607, 111-118.	13.7	128
35	de novo assembly and population genomic survey of natural yeast isolates with the Oxford Nanopore MinION sequencer. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	123
36	Global patterns of pelagic dinoflagellate diversity across protist size classes unveiled by metabarcoding. <i>Environmental Microbiology</i> , 2016, 18, 609-626.	1.8	105

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37	Extreme Diversity of Diplonemid Eukaryotes in the Ocean. <i>Current Biology</i> , 2016, 26, 3060-3065.	1.8	105
38	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
39	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	5.8	101
40	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
41	Organization and evolution of transposable elements along the bread wheat chromosome 3B. <i>Genome Biology</i> , 2014, 15, 546.	3.8	88
42	Telomere-to-telomere gapless chromosomes of banana using nanopore sequencing. <i>Communications Biology</i> , 2021, 4, 1047.	2.0	86
43	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. <i>Nature</i> , 2021, 600, 86-92.	13.7	81
44	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
45	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	1.9	76
46	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. <i>Nature Communications</i> , 2016, 7, 11071.	5.8	72
47	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
48	Long-read assembly of the <i>Brassica napus</i> reference genome Darmor-bzh. <i>GigaScience</i> , 2020, 9, .	3.3	64
49	Global distribution patterns of marine nitrogen-fixers by imaging and molecular methods. <i>Nature Communications</i> , 2021, 12, 4160.	5.8	58
50	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
51	Survey of the green picoalga <i>Bathycoccus</i> genomes in the global ocean. <i>Scientific Reports</i> , 2016, 6, 37900.	1.6	54
52	Environmental vulnerability of the global ocean epipelagic plankton community interactome. <i>Science Advances</i> , 2021, 7, .	4.7	54
53	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
54	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

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55	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
56	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
57	Accessing the genomic information of unculturable oceanic picoeukaryotes by combining multiple single cells. <i>Scientific Reports</i> , 2017, 7, 41498.	1.6	47
58	Population genomics of apricots unravels domestication history and adaptive events. <i>Nature Communications</i> , 2021, 12, 3956.	5.8	45
59	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
60	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
61	Diversity and ecological footprint of Global Ocean RNA viruses. <i>Science</i> , 2022, 376, 1202-1208.	6.0	41
62	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
63	New insights into global biogeography, population structure and natural selection from the genome of the epipelagic copepod <i>Oithona</i> . <i>Molecular Ecology</i> , 2017, 26, 4467-4482.	2.0	37
64	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
65	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
66	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. <i>ISME Journal</i> , 2016, 10, 1134-1146.	4.4	35
67	Hunting down fungal secretomes using liquidâ€”phase IEF prior to high resolution 2â€”DE. <i>Electrophoresis</i> , 2009, 30, 4118-4136.	1.3	31
68	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
69	A robust approach to estimate relative phytoplankton cell abundances from metagenomes. <i>Molecular Ecology Resources</i> , 2023, 23, 16-40.	2.2	29
70	TE-Tracker: systematic identification of transposition events through whole-genome resequencing. <i>BMC Bioinformatics</i> , 2014, 15, 377.	1.2	27
71	Priorities for ocean microbiome research. <i>Nature Microbiology</i> , 2022, 7, 937-947.	5.9	27
72	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

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73	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
74	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021, 11, 15714.	1.6	24
75	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
76	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
77	Genome Resolved Biogeography of Mamiellales. <i>Genes</i> , 2020, 11, 66.	1.0	21
78	Restructuring of plankton genomic biogeography in the surface ocean under climate change. <i>Nature Climate Change</i> , 2022, 12, 393-401.	8.1	21
79	Comparative genomics reveals new functional insights in uncultured MAST species. <i>ISME Journal</i> , 2021, 15, 1767-1781.	4.4	18
80	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
81	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
82	Tempo and drivers of plant diversification in the European mountain system. <i>Nature Communications</i> , 2022, 13, 2750.	5.8	15
83	A new sequence data set of <i>SSU rRNA</i> gene for Scleractinia and its phylogenetic and ecological applications. <i>Molecular Ecology Resources</i> , 2017, 17, 1054-1071.	2.2	13
84	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
85	Chitin distribution in the <i>Oithona</i> digestive and reproductive systems revealed by fluorescence microscopy. <i>PeerJ</i> , 2018, 6, e4685.	0.9	10
86	A framework for in situ molecular characterization of coral holobionts using nanopore sequencing. <i>Scientific Reports</i> , 2020, 10, 15893.	1.6	9
87	Deep sequencing of amplified <i>P</i> and <i>rasinovirus</i> and host green algal genes from an Indian Ocean transect reveals interacting trophic dependencies and new genotypes. <i>Environmental Microbiology Reports</i> , 2015, 7, 979-989.	1.0	8
88	Subtle limits to connectivity revealed by outlier loci within two divergent metapopulations of the deep-sea hydrothermal gastropod <i>Ifrimeria nautilei</i> . <i>Molecular Ecology</i> , 2022, 31, 2796-2813.	2.0	7
89	Into the bloom: Molecular response of pelagic tunicates to fluctuating food availability. <i>Molecular Ecology</i> , 2020, 29, 292-307.	2.0	6
90	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. <i>SSRN Electronic Journal</i> , 2019, .	0.4	4

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91	A thousand plantsâ€™ phylogeny. <i>Nature Plants</i> , 2019, 5, 1106-1107.	4.7	1
92	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