

# Pascal M Hingamp

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

14,844  
citations

101543

36  
h-index

138484

58  
g-index

62  
all docs

62  
docs citations

62  
times ranked

17637  
citing authors

#	ARTICLE	IF	CITATIONS
1	Minimum information about a microarray experiment (MIAME)â€”toward standards for microarray data. <i>Nature Genetics</i> , 2001, 29, 365-371.	21.4	3,750
2	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	12.6	2,137
3	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	12.6	1,551
4	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	27.8	670
5	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	12.6	617
6	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
7	The EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , 2000, 28, 19-23.	14.5	493
8	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
9	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	5.6	353
10	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	12.8	298
11	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	12.8	297
12	Linking Virus Genomes with Host Taxonomy. <i>Viruses</i> , 2016, 8, 66.	3.3	295
13	Metagenomic <scp>16S rDNA I</scp>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.	3.8	291
14	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	28.9	271
15	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	28.9	268
16	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	9.8	185
17	<scp>QDD</scp> version 3.1: a userâ€™friendly computer program for microsatellite selection and primer design revisited: experimental validation of variables determining genotyping success rate. <i>Molecular Ecology Resources</i> , 2014, 14, 1302-1313.	4.8	170
18	mRNA deep sequencing reveals 75 new genes and a complex transcriptional landscape in Mimivirus. <i>Genome Research</i> , 2010, 20, 664-674.	5.5	160

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19	Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015, 348, 1261447.	12.6	158
20	Standards for Microarray Data. <i>Science</i> , 2002, 298, 539-539.	12.6	147
21	The Ocean Gene Atlas: exploring the biogeography of plankton genes online. <i>Nucleic Acids Research</i> , 2018, 46, W289-W295.	14.5	126
22	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. <i>Science</i> , 2022, 376, 156-162.	12.6	124
23	Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean. <i>MSphere</i> , 2017, 2, .	2.9	114
24	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	4.4	107
25	Submission of Microarray Data to Public Repositories. <i>PLoS Biology</i> , 2004, 2, e317.	5.6	102
26	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	12.8	101
27	Taxon Richness of "Megaviridae" Exceeds those of Bacteria and Archaea in the Ocean. <i>Microbes and Environments</i> , 2018, 33, 162-171.	1.6	83
28	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	4.9	76
29	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. <i>Nature Communications</i> , 2016, 7, 11071.	12.8	72
30	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	6.5	70
31	Divergent N-Terminal Sequences Target an Inducible Testis Deubiquitinating Enzyme to Distinct Subcellular Structures. <i>Molecular and Cellular Biology</i> , 2000, 20, 6568-6578.	2.3	68
32	Breast cancer revisited using DNA array-based gene expression profiling. <i>International Journal of Cancer</i> , 2003, 103, 565-571.	5.1	59
33	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , 2021, 6, 1561-1574.	13.3	57
34	A Novel Rat Homolog of the <i>Saccharomyces cerevisiae</i> Ubiquitin-Conjugating Enzymes UBC4 and UBC5 with Distinct Biochemical Features Is Induced during Spermatogenesis. <i>Molecular and Cellular Biology</i> , 1996, 16, 4064-4072.	2.3	52
35	Locality and diel cycling of viral production revealed by a 24 h time course cross-omics analysis in a coastal region of Japan. <i>ISME Journal</i> , 2018, 12, 1287-1295.	9.8	44
36	An open letter to the scientific journals. <i>Bioinformatics</i> , 2002, 18, 1409-1409.	4.1	40

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37	Characterization of a ubiquitinated protein which is externally located in African swine fever virions. <i>Journal of Virology</i> , 1995, 69, 1785-1793.	3.4	39
38	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. <i>ISME Journal</i> , 2016, 10, 1134-1146.	9.8	35
39	EMBL-Align: a new public nucleotide and amino acid multiple sequence alignment database. <i>Bioinformatics</i> , 2002, 18, 763-764.	4.1	34
40	Prognosis of Breast Cancer and Gene Expression Profiling Using DNA Arrays. <i>Annals of the New York Academy of Sciences</i> , 2002, 975, 217-231.	3.8	33
41	DNA microarray data and contextual analysis of correlation graphs. <i>BMC Bioinformatics</i> , 2003, 4, 15.	2.6	33
42	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. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3150-3160.	3.1	30
43	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.	14.5	26
44	Degenerate PCR Primers to Reveal the Diversity of Giant Viruses in Coastal Waters. <i>Viruses</i> , 2018, 10, 496.	3.3	25
45	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021, 11, 15714.	3.3	24
46	Microarray Data Standards: An Open Letter. <i>Environmental Health Perspectives</i> , 2004, 112, A666-7.	6.0	23
47	Mice Lacking the UBC4-testis Gene Have a Delay in Postnatal Testis Development but Normal Spermatogenesis and Fertility. <i>Molecular and Cellular Biology</i> , 2005, 25, 6346-6354.	2.3	22
48	The Ocean barcode atlas: A web service to explore the biodiversity and biogeography of marine organisms. <i>Molecular Ecology Resources</i> , 2021, 21, 1347-1358.	4.8	19
49	Metagenome Annotation Using a Distributed Grid of Undergraduate Students. <i>PLoS Biology</i> , 2008, 6, e296.	5.6	19
50	Diversity and evolution of bacterial bioluminescence genes in the global ocean. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa018.	3.2	14
51	The EMBL Nucleotide Sequence Database: Contributing and Accessing Data. <i>Molecular Biotechnology</i> , 1999, 12, 255-268.	2.4	12
52	A guide to microarray experiments-an open letter to the scientific journals. <i>Lancet, The</i> , 2002, 360, 1019.	13.7	11
53	Deep sequencing of amplified <i>Prasinovirus</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.	2.4	8
54	Divergent N-Terminal Sequences Target an Inducible Testis Deubiquitinating Enzyme to Distinct Subcellular Structures. <i>Molecular and Cellular Biology</i> , 2000, 20, 6568-6578.	2.3	5

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55	MicroArray Facility: a laboratory information management system with extended support for Nylon based technologies. BMC Genomics, 2006, 7, 240.	2.8	4
56	What bioinformatics can tell us about ourselves and our environment?. , 2009, , .		0