

Pascal M Hingamp

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

14,844
citations

101384

36
h-index

138251

58
g-index

62
all docs

62
docs citations

62
times ranked

17637
citing authors

#	ARTICLE	IF	CITATIONS
1	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. <i>Science</i> , 2022, 376, 156-162.	6.0	124
2	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
3	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	3.0	70
4	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.	2.2	19
5	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	2.0	107
6	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021, 11, 15714.	1.6	24
7	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
8	Diversity and evolution of bacterial bioluminescence genes in the global ocean. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa018.	1.5	14
9	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	13.5	268
10	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	13.5	271
11	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	13.5	541
12	Community-level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	1.9	76
13	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	5.8	298
14	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
15	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.	4.4	44
16	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	5.8	101
17	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	5.8	297
18	Degenerate PCR Primers to Reveal the Diversity of Giant Viruses in Coastal Waters. <i>Viruses</i> , 2018, 10, 496.	1.5	25

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19	The Ocean Gene Atlas: exploring the biogeography of plankton genes online. <i>Nucleic Acids Research</i> , 2018, 46, W289-W295.	6.5	126
20	Taxon Richness of "Megaviridae" Exceeds those of Bacteria and Archaea in the Ocean. <i>Microbes and Environments</i> , 2018, 33, 162-171.	0.7	83
21	Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean. <i>MSphere</i> , 2017, 2, .	1.3	114
22	Linking Virus Genomes with Host Taxonomy. <i>Viruses</i> , 2016, 8, 66.	1.5	295
23	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
24	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	13.7	670
25	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. <i>ISME Journal</i> , 2016, 10, 1134-1146.	4.4	35
26	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. <i>Environmental Microbiology Reports</i> , 2015, 7, 979-989.	1.0	8
27	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	6.0	617
28	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
29	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	6.0	1,551
30	Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015, 348, 1261447.	6.0	158
31	Metagenomic 16S rDNA Illumina 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
32	QDD version 3.1: a user-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.	2.2	170
33	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.	1.4	30
34	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	4.4	185
35	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	2.6	353
36	mRNA deep sequencing reveals 75 new genes and a complex transcriptional landscape in Mimivirus. <i>Genome Research</i> , 2010, 20, 664-674.	2.4	160

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37	What bioinformatics can tell us about ourselves and our environment?. , 2009, , .		0
38	Metagenome Annotation Using a Distributed Grid of Undergraduate Students. PLoS Biology, 2008, 6, e296.	2.6	19
39	MicroArray Facility: a laboratory information management system with extended support for Nylon based technologies. BMC Genomics, 2006, 7, 240.	1.2	4
40	Mice Lacking the UBC4-testis Gene Have a Delay in Postnatal Testis Development but Normal Spermatogenesis and Fertility. Molecular and Cellular Biology, 2005, 25, 6346-6354.	1.1	22
41	Microarray Data Standards: An Open Letter. Environmental Health Perspectives, 2004, 112, A666-7.	2.8	23
42	Submission of Microarray Data to Public Repositories. PLoS Biology, 2004, 2, e317.	2.6	102
43	DNA microarray data and contextual analysis of correlation graphs. BMC Bioinformatics, 2003, 4, 15.	1.2	33
44	Breast cancer revisited using DNA array-based gene expression profiling. International Journal of Cancer, 2003, 103, 565-571.	2.3	59
45	Standards for Microarray Data. Science, 2002, 298, 539b-539.	6.0	147
46	An open letter to the scientific journals. Bioinformatics, 2002, 18, 1409-1409.	1.8	40
47	EMBL-Align: a new public nucleotide and amino acid multiple sequence alignment database. Bioinformatics, 2002, 18, 763-764.	1.8	34
48	A guide to microarray experiments-an open letter to the scientific journals. Lancet, The, 2002, 360, 1019.	6.3	11
49	Prognosis of Breast Cancer and Gene Expression Profiling Using DNA Arrays. Annals of the New York Academy of Sciences, 2002, 975, 217-231.	1.8	33
50	Minimum information about a microarray experiment (MIAME)â€”toward standards for microarray data. Nature Genetics, 2001, 29, 365-371.	9.4	3,750
51	Divergent N-Terminal Sequences Target an Inducible Testis Deubiquitinating Enzyme to Distinct Subcellular Structures. Molecular and Cellular Biology, 2000, 20, 6568-6578.	1.1	68
52	The EMBL Nucleotide Sequence Database. Nucleic Acids Research, 2000, 28, 19-23.	6.5	493
53	Divergent N-Terminal Sequences Target an Inducible Testis Deubiquitinating Enzyme to Distinct Subcellular Structures. Molecular and Cellular Biology, 2000, 20, 6568-6578.	1.1	5
54	The EMBL Nucleotide Sequence Database: Contributing and Accessing Data. Molecular Biotechnology, 1999, 12, 255-268.	1.3	12

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55	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.	1.1	52
56	Characterization of a ubiquitinated protein which is externally located in African swine fever virions. <i>Journal of Virology</i> , 1995, 69, 1785-1793.	1.5	39