

Olivier Jaillon

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

23,258
citations

61984

43
h-index

102487

66
g-index

80
all docs

80
docs citations

80
times ranked

26507
citing authors

#	ARTICLE	IF	CITATIONS
1	Restructuring of plankton genomic biogeography in the surface ocean under climate change. <i>Nature Climate Change</i> , 2022, 12, 393-401.	18.8	21
2	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. <i>Science</i> , 2022, 376, 156-162.	12.6	124
3	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
4	Comparative genomics reveals new functional insights in uncultured MAST species. <i>ISME Journal</i> , 2021, 15, 1767-1781.	9.8	18
5	Eukaryotic virus composition can predict the efficiency of carbon export in the global ocean. <i>IScience</i> , 2021, 24, 102002.	4.1	50
6	Niche adaptation promoted the evolutionary diversification of tiny ocean predators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	12
7	Environmental vulnerability of the global ocean epipelagic plankton community interactome. <i>Science Advances</i> , 2021, 7, .	10.3	54
8	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021, 11, 15714.	3.3	24
9	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
10	Genome Resolved Biogeography of Mamiellales. <i>Genes</i> , 2020, 11, 66.	2.4	21
11	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	28.9	268
12	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	28.9	271
13	Assessing the viral content of uncultured picoeukaryotes in the global ocean by single cell genomics. <i>Molecular Ecology</i> , 2019, 28, 4272-4289.	3.9	25
14	Elucidation of Codon Usage Signatures across the Domains of Life. <i>Molecular Biology and Evolution</i> , 2019, 36, 2328-2339.	8.9	54
15	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
16	Single cell genomics yields a wide diversity of small planktonic protists across major ocean ecosystems. <i>Scientific Reports</i> , 2019, 9, 6025.	3.3	35
17	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	4.9	76
18	Discovering millions of plankton genomic markers from the Atlantic Ocean and the Mediterranean Sea. <i>Molecular Ecology Resources</i> , 2019, 19, 526-535.	4.8	11

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19	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	12.8	101
20	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	12.8	297
21	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	5.3	147
22	Accessing the genomic information of unculturable oceanic picoeukaryotes by combining multiple single cells. <i>Scientific Reports</i> , 2017, 7, 41498.	3.3	47
23	A new sequence data set of <scp>SSU rRNA</scp> gene for Scleractinia and its phylogenetic and ecological applications. <i>Molecular Ecology Resources</i> , 2017, 17, 1054-1071.	4.8	13
24	The rainbow trout genome, an important landmark forÂaquaculture and genomeÂevolution. , 2016, , 21-43.		3
25	Survey of the green picoalga <i>Bathycoccus</i> genomes in the global ocean. <i>Scientific Reports</i> , 2016, 6, 37900.	3.3	54
26	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. <i>ISME Journal</i> , 2016, 10, 1134-1146.	9.8	35
27	Marine protist diversity in <scp>E</scp>uropean coastal waters and sediments as revealed by highâ€throughput sequencing. <i>Environmental Microbiology</i> , 2015, 17, 4035-4049.	3.8	384
28	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	12.6	2,137
29	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	12.6	1,551
30	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
31	The rainbow trout genome provides novel insights into evolution after whole-genome duplication in vertebrates. <i>Nature Communications</i> , 2014, 5, 3657.	12.8	814
32	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. <i>Nature Biotechnology</i> , 2014, 32, 656-662.	17.5	572
33	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , 2013, 500, 453-457.	27.8	352
34	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	9.8	185
35	The banana (<i>Musa acuminata</i>) genome and the evolution of monocotyledonous plants. <i>Nature</i> , 2012, 488, 213-217.	27.8	1,049
36	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	5.6	353

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37	Genome sequence of the stramenopile Blastocystis, a human anaerobic parasite. <i>Genome Biology</i> , 2011, 12, R29.	9.6	159
38	PÃ©rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	27.8	641
39	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. <i>Science</i> , 2010, 330, 1381-1385.	12.6	251
40	â€œChanging by doublingâ€, the impact of Whole Genome Duplications in the evolution of eukaryotes. <i>Comptes Rendus - Biologies</i> , 2009, 332, 241-253.	0.2	48
41	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	17.5	1,012
42	The genome sequence of the model ascomycete fungus <i>Podospora anserina</i> . <i>Genome Biology</i> , 2008, 9, R77.	9.6	301
43	Annotating genomes with massive-scale RNA sequencing. <i>Genome Biology</i> , 2008, 9, R175.	9.6	210
44	Translational control of intron splicing in eukaryotes. <i>Nature</i> , 2008, 451, 359-362.	27.8	200
45	Analysis of sequence variability in the macronuclear DNA of <i>Paramecium tetraurelia</i> : A somatic view of the germline. <i>Genome Research</i> , 2008, 18, 585-596.	5.5	82
46	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 2007, 449, 463-467.	27.8	3,384
47	Gene Loss and Evolutionary Rates Following Whole-Genome Duplication in Teleost Fishes. <i>Molecular Biology and Evolution</i> , 2006, 23, 1808-1816.	8.9	352
48	Global trends of whole-genome duplications revealed by the ciliate <i>Paramecium tetraurelia</i> . <i>Nature</i> , 2006, 444, 171-178.	27.8	744
49	Comparative analysis of BAC and whole genome shotgun sequences from an <i>Anopheles gambiae</i> region related to <i>Plasmodium</i> encapsulation. <i>Insect Biochemistry and Molecular Biology</i> , 2005, 35, 799-814.	2.7	3
50	Whole Genome Sequence Comparisons and "Full-Length" cDNA Sequences: A Combined Approach to Evaluate and Improve <i>Arabidopsis</i> Genome Annotation. <i>Genome Research</i> , 2004, 14, 406-413.	5.5	72
51	Genome duplication in the teleost fish <i>Tetraodon nigroviridis</i> reveals the early vertebrate proto-karyotype. <i>Nature</i> , 2004, 431, 946-957.	27.8	1,801
52	The DNA sequence and analysis of human chromosome 14. <i>Nature</i> , 2003, 421, 601-607.	27.8	108
53	Assessing the <i>Drosophila melanogaster</i> and <i>Anopheles gambiae</i> Genome Annotations Using Genome-Wide Sequence Comparisons. <i>Genome Research</i> , 2003, 13, 1595-1599.	5.5	7
54	An Active Non-LTR Retrotransposon With Tandem Structure in the Compact Genome of the Pufferfish <i>Tetraodon nigroviridis</i> . <i>Genome Research</i> , 2003, 13, 1686-1695.	5.5	44

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55	Genome-wide Analyses Based on Comparative Genomics. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 275-282.	1.1	2
56	Remarkable compartmentalization of transposable elements and pseudogenes in the heterochromatin of the <i>Tetraodon nigroviridis</i> genome. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13636-13641.	7.1	70
57	Exploring root symbiotic programs in the model legume <i>Medicago truncatula</i> using EST analysis. Nucleic Acids Research, 2002, 30, 5579-5592.	14.5	193
58	Four-Hundred Million Years of Conserved Synteny of Human Xp and Xq Genes on Three <i>Tetraodon</i> Chromosomes. Genome Research, 2002, 12, 1316-1322.	5.5	24
59	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . Science, 2002, 298, 129-149.	12.6	1,859
60	Genome-wide Comparisons Between Human and <i>Tetraodon</i> . , 2002, , 11-29.		1
61	Human-Ovine Comparative Sequencing of a 250-kb Imprinted Domain Encompassing the Callipyge (<i>clpg</i>) Locus and Identification of Six Imprinted Transcripts: <i>DLK1</i> , <i>DAT</i> , <i>GTL2</i> , <i>PEG11</i> , <i>antiPEG11</i> , and <i>MEG8</i> . Genome Research, 2001, 11, 850-862.	5.5	183
62	The Complete Genome Sequence of the Lactic Acid Bacterium <i>Lactococcus lactis</i> ssp. <i>lactis</i> IL1403. Genome Research, 2001, 11, 731-753.	5.5	582
63	Estimate of human gene number provided by genome-wide analysis using <i>Tetraodon nigroviridis</i> DNA sequence. Nature Genetics, 2000, 25, 235-238.	21.4	344
64	Karyotype and chromosome location of characteristic tandem repeats in the pufferfish <i>Tetraodon nigroviridis</i> . Cytogenetic and Genome Research, 2000, 88, 50-55.	1.1	54
65	Characterization and Repeat Analysis of the Compact Genome of the Freshwater Pufferfish <i>Tetraodon nigroviridis</i> . Genome Research, 2000, 10, 939-949.	5.5	121
66	The gene encoding the mouse homologue of the human osteoclast-specific 116-kDa V-ATPase subunit bears a deletion in osteosclerotic (<i>oc/oc</i>) mutants. Bone, 2000, 26, 207-213.	2.9	193
67	Le nombre de gènes dans le génome humain : les paris sont ouverts.. Medecine/Sciences, 2000, 16, 988.	0.2	1
68	Amplification and detection of the terminal 3' non-coding region of hepatitis C virus isolates. Research in Virology, 1998, 149, 115-121.	0.7	3