

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	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 2007, 449, 463-467.	27.8	3,384
2	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	12.6	2,137
3	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	12.6	1,859
4	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
5	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	12.6	1,551
6	The banana (<i>Musa acuminata</i>) genome and the evolution of monocotyledonous plants. <i>Nature</i> , 2012, 488, 213-217.	27.8	1,049
7	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	17.5	1,012
8	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
9	Global trends of whole-genome duplications revealed by the ciliate <i>Paramecium tetraurelia</i> . <i>Nature</i> , 2006, 444, 171-178.	27.8	744
10	<i>PË©rigord</i> black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	27.8	641
11	The Complete Genome Sequence of the Lactic Acid Bacterium <i>Lactococcus lactis</i> ssp. <i>lactis</i> IL1403. <i>Genome Research</i> , 2001, 11, 731-753.	5.5	582
12	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
13	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
14	Marine protist diversity in European coastal waters and sediments as revealed by high-throughput sequencing. <i>Environmental Microbiology</i> , 2015, 17, 4035-4049.	3.8	384
15	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	5.6	353
16	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
17	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , 2013, 500, 453-457.	27.8	352
18	Estimate of human gene number provided by genome-wide analysis using <i>Tetraodon nigroviridis</i> DNA sequence. <i>Nature Genetics</i> , 2000, 25, 235-238.	21.4	344

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19	The genome sequence of the model ascomycete fungus <i>Podospora anserina</i> . <i>Genome Biology</i> , 2008, 9, R77.	9.6	301
20	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	12.8	297
21	Metagenomic <sc>16S rDNA l</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.	3.8	291
22	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	28.9	271
23	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	28.9	268
24	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. <i>Science</i> , 2010, 330, 1381-1385.	12.6	251
25	Annotating genomes with massive-scale RNA sequencing. <i>Genome Biology</i> , 2008, 9, R175.	9.6	210
26	Translational control of intron splicing in eukaryotes. <i>Nature</i> , 2008, 451, 359-362.	27.8	200
27	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. <i>Bone</i> , 2000, 26, 207-213.	2.9	193
28	Exploring root symbiotic programs in the model legume <i>Medicago truncatula</i> using EST analysis. <i>Nucleic Acids Research</i> , 2002, 30, 5579-5592.	14.5	193
29	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	9.8	185
30	Humanâ€“Ovine Comparative Sequencing of a 250-kb Imprinted Domain Encompassing the <i>Callipyge</i> (<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> . <i>Genome Research</i> , 2001, 11, 850-862.	5.5	183
31	Genome sequence of the stramenopile <i>Blastocystis</i> , a human anaerobic parasite. <i>Genome Biology</i> , 2011, 12, R29.	9.6	159
32	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	5.3	147
33	Cryptic and abundant marine viruses at the evolutionary origins of Earthâ€™s RNA virome. <i>Science</i> , 2022, 376, 156-162.	12.6	124
34	Characterization and Repeat Analysis of the Compact Genome of the Freshwater Pufferfish <i>Tetraodon nigroviridis</i> . <i>Genome Research</i> , 2000, 10, 939-949.	5.5	121
35	The DNA sequence and analysis of human chromosome 14. <i>Nature</i> , 2003, 421, 601-607.	27.8	108
36	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	12.8	101

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37	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
38	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	4.9	76
39	Whole Genome Sequence Comparisons and "Full-Length" cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation. <i>Genome Research</i> , 2004, 14, 406-413.	5.5	72
40	Remarkable compartmentalization of transposable elements and pseudogenes in the heterochromatin of the <i>Tetraodon nigroviridis</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13636-13641.	7.1	70
41	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
42	Karyotype and chromosome location of characteristic tandem repeats in the pufferfish <i>Tetraodon nigroviridis</i> . <i>Cytogenetic and Genome Research</i> , 2000, 88, 50-55.	1.1	54
43	Survey of the green picoalga <i>Bathycoccus</i> genomes in the global ocean. <i>Scientific Reports</i> , 2016, 6, 37900.	3.3	54
44	Elucidation of Codon Usage Signatures across the Domains of Life. <i>Molecular Biology and Evolution</i> , 2019, 36, 2328-2339.	8.9	54
45	Environmental vulnerability of the global ocean epipelagic plankton community interactome. <i>Science Advances</i> , 2021, 7, .	10.3	54
46	Eukaryotic virus composition can predict the efficiency of carbon export in the global ocean. <i>IScience</i> , 2021, 24, 102002.	4.1	50
47	“Changing by doubling”, the impact of Whole Genome Duplications in the evolution of eukaryotes. <i>Comptes Rendus - Biologies</i> , 2009, 332, 241-253.	0.2	48
48	Accessing the genomic information of unculturable oceanic picoeukaryotes by combining multiple single cells. <i>Scientific Reports</i> , 2017, 7, 41498.	3.3	47
49	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
50	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. <i>ISME Journal</i> , 2016, 10, 1134-1146.	9.8	35
51	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
52	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
53	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
54	Four-Hundred Million Years of Conserved Synteny of Human Xp and Xq Genes on Three <i>Tetraodon</i> Chromosomes. <i>Genome Research</i> , 2002, 12, 1316-1322.	5.5	24

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55	Macroscale patterns of oceanic zooplankton composition and size structure. Scientific Reports, 2021, 11, 15714.	3.3	24
56	Genome Resolved Biogeography of Mamiellales. Genes, 2020, 11, 66.	2.4	21
57	Restructuring of plankton genomic biogeography in the surface ocean under climate change. Nature Climate Change, 2022, 12, 393-401.	18.8	21
58	Comparative genomics reveals new functional insights in uncultured MAST species. ISME Journal, 2021, 15, 1767-1781.	9.8	18
59	A new sequence data set of <scp>SSU rRNA</scp> gene for Scleractinia and its phylogenetic and ecological applications. Molecular Ecology Resources, 2017, 17, 1054-1071.	4.8	13
60	Niche adaptation promoted the evolutionary diversification of tiny ocean predators. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	12
61	Discovering millions of plankton genomic markers from the Atlantic Ocean and the Mediterranean Sea. Molecular Ecology Resources, 2019, 19, 526-535.	4.8	11
62	Assessing the Drosophila melanogaster and Anopheles gambiae Genome Annotations Using Genome-Wide Sequence Comparisons. Genome Research, 2003, 13, 1595-1599.	5.5	7
63	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
64	Comparative analysis of BAC and whole genome shotgun sequences from an Anopheles gambiae region related to Plasmodium encapsulation. Insect Biochemistry and Molecular Biology, 2005, 35, 799-814.	2.7	3
65	The rainbow trout genome, an important landmark forÂaquaculture and genomeÂevolution. , 2016, , 21-43.		3
66	Genome-wide Analyses Based on Comparative Genomics. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 275-282.	1.1	2
67	Le nombre de gÃ©nes dans le gÃ©nome humain : les paris sont ouverts.. Medecine/Sciences, 2000, 16, 988.	0.2	1
68	Genome-wide Comparisons Between Human and Tetraodon. , 2002, , 11-29.		1