

# Karine Labadie

## List of Publications by Year in descending order

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Version: 2024-02-01

89  
papers

18,479  
citations

61945

43  
h-index

42364

92  
g-index

123  
all docs

123  
docs citations

123  
times ranked

22977  
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	The banana ( <i>Musa acuminata</i> ) genome and the evolution of monocotyledonous plants. <i>Nature</i> , 2012, 488, 213-217.	13.7	1,049
5	Genome evolution across 1,011 <i>Saccharomyces cerevisiae</i> isolates. <i>Nature</i> , 2018, 556, 339-344.	13.7	952
6	The rainbow trout genome provides novel insights into evolution after whole-genome duplication in vertebrates. <i>Nature Communications</i> , 2014, 5, 3657.	5.8	814
7	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. <i>Nature Biotechnology</i> , 2014, 32, 656-662.	9.4	572
8	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184.	6.0	520
9	Thirty-thousand-year-old distant relative of giant icosahedral DNA viruses with a pandoravirus morphology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4274-4279.	3.3	468
10	Chikungunya disease in nonhuman primates involves long-term viral persistence in macrophages. <i>Journal of Clinical Investigation</i> , 2010, 120, 894-906.	3.9	447
11	Mapping the Epigenetic Basis of Complex Traits. <i>Science</i> , 2014, 343, 1145-1148.	6.0	403
12	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	9.4	363
13	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , 2013, 500, 453-457.	13.7	352
14	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
15	Genome structure and metabolic features in the red seaweed <i>Chondrus crispus</i> shed light on evolution of the Archaeplastida. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5247-5252.	3.3	307
16	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	4.7	303
17	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	5.8	297
18	In-depth study of <i>Mollivirus sibericum</i> , a new 30,000-y-old giant virus infecting <i>Acanthamoeba</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5327-35.	3.3	284

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19	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	13.5	271
20	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	13.5	268
21	Two genomes of highly polyphagous lepidopteran pests ( <i>Spodoptera frugiperda</i> , Noctuidae) with different host-plant ranges. <i>Scientific Reports</i> , 2017, 7, 11816.	1.6	242
22	Host-range determinants on the PB2 protein of influenza A viruses control the interaction between the viral polymerase and nucleoprotein in human cells. <i>Virology</i> , 2007, 362, 271-282.	1.1	168
23	The <i>Paramecium</i> Germline Genome Provides a Niche for Intragenic Parasitic DNA: Evolutionary Dynamics of Internal Eliminated Sequences. <i>PLoS Genetics</i> , 2012, 8, e1002984.	1.5	154
24	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	2.4	147
25	Features of the <i>Arabidopsis</i> recombination landscape resulting from the combined loss of sequence variation and DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16240-16245.	3.3	145
26	Rapid protein evolution, organellar reductions, and invasive intronic elements in the marine aerobic parasite dinoflagellate <i>Amoebophrya</i> spp. <i>BMC Biology</i> , 2021, 19, 1.	1.7	135
27	Paradoxical Effect of Chloroquine Treatment in Enhancing Chikungunya Virus Infection. <i>Viruses</i> , 2018, 10, 268.	1.5	126
28	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. <i>Science</i> , 2022, 376, 156-162.	6.0	124
29	Diversity and evolution of the emerging Pandoraviridae family. <i>Nature Communications</i> , 2018, 9, 2285.	5.8	122
30	<i>Spodoptera frugiperda</i> (Lepidoptera: Noctuidae) host-plant variants: two host strains or two distinct species?. <i>Genetica</i> , 2015, 143, 305-316.	0.5	117
31	Adaptive introgression as a driver of local adaptation to climate in European white oaks. <i>New Phytologist</i> , 2020, 226, 1171-1182.	3.5	117
32	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. <i>Molecular Ecology Resources</i> , 2016, 16, 254-265.	2.2	108
33	Genome-defence small RNAs exapted for epigenetic mating-type inheritance. <i>Nature</i> , 2014, 509, 447-452.	13.7	105
34	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	5.8	101
35	Identification of Novel Target Genes for Safer and More Specific Control of Root-Knot Nematodes from a Pan-Genome Mining. <i>PLoS Pathogens</i> , 2013, 9, e1003745.	2.1	90
36	Telomere-to-telomere gapless chromosomes of banana using nanopore sequencing. <i>Communications Biology</i> , 2021, 4, 1047.	2.0	86

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37	The Rise and Fall of African Rice Cultivation Revealed by Analysis of 246 New Genomes. <i>Current Biology</i> , 2018, 28, 2274-2282.e6.	1.8	84
38	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
39	Genetic Architecture of a Rice Nested Association Mapping Population. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1913-1926.	0.8	71
40	The cacao Criollo genome v2.0: an improved version of the genome for genetic and functional genomic studies. <i>BMC Genomics</i> , 2017, 18, 730.	1.2	71
41	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	3.0	70
42	Coprolites as a source of information on the genome and diet of the cave hyena. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 2825-2830.	1.2	65
43	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
44	Mixotrophic protists display contrasted biogeographies in the global ocean. <i>ISME Journal</i> , 2019, 13, 1072-1083.	4.4	55
45	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. <i>Scientific Reports</i> , 2015, 5, 11571.	1.6	50
46	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
47	Different waves of effector genes with contrasted genomic location are expressed by <i>Leptosphaeria maculans</i> during cotyledon and stem colonization of oilseed rape. <i>Molecular Plant Pathology</i> , 2017, 18, 1113-1126.	2.0	46
48	Massive postglacial gene flow between European white oaks uncovered genes underlying species barriers. <i>New Phytologist</i> , 2020, 226, 1183-1197.	3.5	46
49	Diversity and ecological footprint of Global Ocean RNA viruses. <i>Science</i> , 2022, 376, 1202-1208.	6.0	41
50	Complete DNA Sequence of <i>Kuraishia capsulata</i> Illustrates Novel Genomic Features among Budding Yeasts (Saccharomycotina). <i>Genome Biology and Evolution</i> , 2013, 5, 2524-2539.	1.1	39
51	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
52	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
53	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
54	Implication of the suberin pathway in adaptation to waterlogging and hypertrophied lenticels formation in pedunculate oak ( <i>Quercus robur</i> L.). <i>Tree Physiology</i> , 2016, 36, tpw056.	1.4	36

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55	Chromosome reciprocal translocations have accompanied subspecies evolution in bananas. <i>Plant Journal</i> , 2020, 104, 1698-1711.	2.8	35
56	Silencing viruses by RNA interference. <i>Microbes and Infection</i> , 2005, 7, 767-775.	1.0	32
57	Complete Cure of Persistent Virus Infections by Antiviral siRNAs. <i>Molecular Therapy</i> , 2006, 13, 142-150.	3.7	30
58	Massive colonization of protein-coding exons by selfish genetic elements in <i>Paramecium</i> germline genomes. <i>PLoS Biology</i> , 2021, 19, e3001309.	2.6	30
59	Chromosome-level genome assembly reveals homologous chromosomes and recombination in asexual rotifer <i>Adineta vaga</i> . <i>Science Advances</i> , 2021, 7, eabg4216.	4.7	30
60	Poliovirus mutants excreted by a chronically infected hypogammaglobulinemic patient establish persistent infections in human intestinal cells. <i>Virology</i> , 2004, 318, 66-78.	1.1	29
61	Characterization of <i>Mollivirus kamchatka</i> , the First Modern Representative of the Proposed <i>Molliviridae</i> Family of Giant Viruses. <i>Journal of Virology</i> , 2020, 94, .	1.5	29
62	TE-Tracker: systematic identification of transposition events through whole-genome resequencing. <i>BMC Bioinformatics</i> , 2014, 15, 377.	1.2	27
63	Chromosomal scale assembly of parasitic wasp genome reveals symbiotic virus colonization. <i>Communications Biology</i> , 2021, 4, 104.	2.0	27
64	Global repositioning of transcription start sites in a plant-fermenting bacterium. <i>Nature Communications</i> , 2016, 7, 13783.	5.8	25
65	Genome-wide evolutionary response of European oaks during the Anthropocene. <i>Evolution Letters</i> , 2022, 6, 4-20.	1.6	24
66	Evolution of the Banana Genome ( <i>Musa acuminata</i> ) Is Impacted by Large Chromosomal Translocations. <i>Molecular Biology and Evolution</i> , 2017, 34, 2140-2152.	3.5	23
67	Novel metabolic features in <i>Acinetobacter baylyi</i> ADP1 revealed by a multiomics approach. <i>Metabolomics</i> , 2014, 10, 1223-1238.	1.4	22
68	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
69	The Transcriptomes of <i>Xiphinema index</i> and <i>Longidorus elongatus</i> Suggest Independent Acquisition of Some Plant Parasitism Genes by Horizontal Gene Transfer in Early-Branching Nematodes. <i>Genes</i> , 2017, 8, 287.	1.0	19
70	Comparative Time-Scale Gene Expression Analysis Highlights the Infection Processes of Two <i>Amoebophrya</i> Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 2251.	1.5	19
71	Evolution of a Biomass-Fermenting Bacterium To Resist Lignin Phenolics. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	18
72	Colonization kinetics and implantation follow-up of the sewage microbiome in an urban wastewater treatment plant. <i>Scientific Reports</i> , 2020, 10, 11634.	1.6	17

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73	A Chromosome-Level Genome Assembly of the European Beech ( <i>Fagus sylvatica</i> ) Reveals Anomalies for Organelle DNA Integration, Repeat Content and Distribution of SNPs. <i>Frontiers in Genetics</i> , 2021, 12, 691058.	1.1	17
74	Continuous Culture Adaptation of <i>Methylobacterium extorquens</i> AM1 and TK 0001 to Very High Methanol Concentrations. <i>Frontiers in Microbiology</i> , 2019, 10, 1313.	1.5	16
75	Two large reciprocal translocations characterized in the disease resistance-rich burmannica genetic group of <i>Musa acuminata</i> . <i>Annals of Botany</i> , 2019, 124, 319-329.	1.4	15
76	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
77	Diversity and Evolution of Pigment Types in Marine <i>Synechococcus</i> Cyanobacteria. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	15
78	Complete Genome Sequence of the Facultative Methylophilic <i>Methylobacterium extorquens</i> TK 0001 Isolated from Soil in Poland. <i>Genome Announcements</i> , 2018, 6, .	0.8	14
79	Development of a Sequence-Based Reference Physical Map of Pea ( <i>Pisum sativum</i> L.). <i>Frontiers in Plant Science</i> , 2019, 10, 323.	1.7	13
80	Single cell ecogenomics reveals mating types of individual cells and ssDNA viral infections in the smallest photosynthetic eukaryotes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190089.	1.8	11
81	Reduced Apoptosis in Human Intestinal Cells Cured of Persistent Poliovirus Infection. <i>Journal of Virology</i> , 2007, 81, 3033-3036.	1.5	9
82	Investigating population-scale allelic differential expression in wild populations of <i>Oithona similis</i> (Cyclopoida, Claus, 1866). <i>Ecology and Evolution</i> , 2020, 10, 8894-8905.	0.8	9
83	Ion channel profiling of the <i>Lymnaea stagnalis</i> ganglia via transcriptome analysis. <i>BMC Genomics</i> , 2021, 22, 18.	1.2	8
84	Impact of biotic and abiotic factors on the expression of fungal effector-encoding genes in axenic growth conditions. <i>Fungal Genetics and Biology</i> , 2017, 99, 1-12.	0.9	7
85	Sequence diversity and evolution of a group of iflaviruses associated with ticks. <i>Archives of Virology</i> , 2021, 166, 1843-1852.	0.9	6
86	Transcriptome of the synganglion in the tick <i>Ixodes ricinus</i> and evolution of the cys-loop ligand-gated ion channel family in ticks. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
87	Draft Genome Sequence of <i>Tubulinosema ratisbonensis</i> , a Microsporidian Species Infecting the Model Organism <i>Drosophila melanogaster</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
88	Construction and characterization of a BAC library for functional genomics in <i>Xenopus tropicalis</i> . <i>Developmental Biology</i> , 2017, 426, 255-260.	0.9	2
89	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