

Adriana Alberti

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

15,644
citations

81900

39
h-index

106344

65
g-index

79
all docs

79
docs citations

79
times ranked

22611
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, .	12.6	2,424
2	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	12.6	2,137
3	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
4	The banana (<i>Musa acuminata</i>) genome and the evolution of monocotyledonous plants. <i>Nature</i> , 2012, 488, 213-217.	27.8	1,049
5	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
6	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	27.8	629
7	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	12.6	617
8	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	17.5	581
9	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	12.6	542
10	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
11	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184.	12.6	520
12	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	12.8	297
13	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	28.9	268
14	Two genomes of highly polyphagous lepidopteran pests (<i>Spodoptera frugiperda</i> , Noctuidae) with different host-plant ranges. <i>Scientific Reports</i> , 2017, 7, 11816.	3.3	242
15	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813.	12.8	220
16	Genome assembly using Nanopore-guided long and error-free DNA reads. <i>BMC Genomics</i> , 2015, 16, 327.	2.8	177
17	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	5.3	147
18	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.	3.8	135

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19	Improvement of the banana <i>Musa acuminata</i> reference sequence using NGS data and semi-automated bioinformatics methods. BMC Genomics, 2016, 17, 243.	2.8	129
20	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. Science, 2022, 376, 156-162.	12.6	124
21	The Spatiotemporal Program of DNA Replication Is Associated with Specific Combinations of Chromatin Marks in Human Cells. PLoS Genetics, 2014, 10, e1004282.	3.5	123
22	Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (<i>Capra hircus</i>) using WGS data. Frontiers in Genetics, 2015, 6, 107.	2.3	108
23	Genome-defence small RNAs exapted for epigenetic mating-type inheritance. Nature, 2014, 509, 447-452.	27.8	105
24	Deep transcriptome sequencing provides new insights into the structural and functional organization of the wheat genome. Genome Biology, 2015, 16, 29.	8.8	101
25	Sequencing platform and library preparation choices impact viral metagenomes. BMC Genomics, 2013, 14, 320.	2.8	90
26	Functional Diversity of Carbohydrate-Active Enzymes Enabling a Bacterium to Ferment Plant Biomass. PLoS Genetics, 2014, 10, e1004773.	3.5	90
27	Organization and evolution of transposable elements along the bread wheat chromosome 3B. Genome Biology, 2014, 15, 546.	8.8	88
28	The autophagosomal protein LGG-2 acts synergistically with LGG-1 in dauer formation and longevity in <i>C. elegans</i> . Autophagy, 2010, 6, 622-633.	9.1	82
29	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. Nature, 2021, 600, 86-92.	27.8	81
30	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. Global Biogeochemical Cycles, 2019, 33, 391-419.	4.9	76
31	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. Nature Communications, 2016, 7, 11071.	12.8	72
32	The Treasure Vault Can be Opened: Large-Scale Genome Skimming Works Well Using Herbarium and Silica Gel Dried Material. Plants, 2020, 9, 432.	3.5	59
33	Comparison of library preparation methods reveals their impact on interpretation of metatranscriptomic data. BMC Genomics, 2014, 15, 912.	2.8	56
34	Understanding the evolution of holoparasitic plants: the complete plastid genome of the holoparasite <i>Cytinus hypocistis</i> (Cytinaceae). Annals of Botany, 2016, 118, 885-896.	2.9	55
35	Soil Contamination Detected Using Bacterial and Plant Mutagenicity Tests and Chemical Analyses. Environmental Research, 2002, 88, 64-69.	7.5	54
36	Enterococcal Leucine-Rich Repeat-Containing Protein Involved in Virulence and Host Inflammatory Response. Infection and Immunity, 2007, 75, 4463-4471.	2.2	50

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37	Induction of autophagy in ESCRT mutants is an adaptive response for cell survival in <i>C. elegans</i> . <i>Journal of Cell Science</i> , 2012, 125, 685-694.	2.0	50
38	Phylogenomics using low-depth whole genome sequencing: A case study with the olive tribe. <i>Molecular Ecology Resources</i> , 2019, 19, 877-892.	4.8	48
39	Role of β 1- and β 2-adrenoceptor polymorphisms in heart failure: a case-control study. <i>European Heart Journal</i> , 2004, 25, 1534-1541.	2.2	46
40	Large-Scale Screening of a Targeted <i>Enterococcus faecalis</i> Mutant Library Identifies Envelope Fitness Factors. <i>PLoS ONE</i> , 2011, 6, e29023.	2.5	46
41	Diversity and ecological footprint of Global Ocean RNA viruses. <i>Science</i> , 2022, 376, 1202-1208.	12.6	41
42	The Arabidopsis hnRNP-Q Protein LIF2 and the PRC1 Subunit LHP1 Function in Concert to Regulate the Transcription of Stress-Responsive Genes. <i>Plant Cell</i> , 2016, 28, 2197-2211.	6.6	37
43	Phylogenomic fingerprinting of tempo and functions of horizontal gene transfer within ochrophytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	37
44	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. <i>Molecular Ecology Resources</i> , 2019, 19, 1497-1515.	4.8	31
45	The ESCRT-III protein CeVPS-32 is enriched in domains distinct from CeVPS-27 and CeVPS-23 at the endosomal membrane of epithelial cells. <i>Biology of the Cell</i> , 2009, 101, 599-615.	2.0	30
46	Whole Genome Profiling provides a robust framework for physical mapping and sequencing in the highly complex and repetitive wheat genome. <i>BMC Genomics</i> , 2012, 13, 47.	2.8	29
47	TE-Tracker: systematic identification of transposition events through whole-genome resequencing. <i>BMC Bioinformatics</i> , 2014, 15, 377.	2.6	27
48	Continued Adaptation of C4 Photosynthesis After an Initial Burst of Changes in the Andropogoneae Grasses. <i>Systematic Biology</i> , 2020, 69, 445-461.	5.6	27
49	Long-read and chromosome-scale assembly of the hexaploid wheat genome achieves high resolution for research and breeding. <i>GigaScience</i> , 2022, 11, .	6.4	26
50	Global repositioning of transcription start sites in a plant-fermenting bacterium. <i>Nature Communications</i> , 2016, 7, 13783.	12.8	25
51	Differential expression pattern of the four mitochondrial adenine nucleotide transporter <i>ant</i> genes and their roles during the development of <i>Caenorhabditis elegans</i> . <i>Developmental Dynamics</i> , 2008, 237, 1668-1681.	1.8	20
52	Comparative Time-Scale Gene Expression Analysis Highlights the Infection Processes of Two <i>Amoebophrya</i> Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 2251.	3.5	19
53	A de novo approach to disentangle partner identity and function in holobiont systems. <i>Microbiome</i> , 2018, 6, 105.	11.1	19
54	VarGoats project: a dataset of 1159 whole-genome sequences to dissect <i>Capra hircus</i> global diversity. <i>Genetics Selection Evolution</i> , 2021, 53, 86.	3.0	16

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55	Genomic and Transcriptomic Analysis of Growth-Supporting Dehalogenation of Chlorinated Methanes in <i>Methylobacterium</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1600.	3.5	15
56	Tempo and drivers of plant diversification in the European mountain system. <i>Nature Communications</i> , 2022, 13, 2750.	12.8	15
57	Phylogenetic signatures of ecological divergence and leapfrog adaptive radiation in <i>Espeletia</i> . <i>American Journal of Botany</i> , 2021, 108, 113-128.	1.7	13
58	Terrestrial and marine influence on atmospheric bacterial diversity over the north Atlantic and Pacific Oceans. <i>Communications Earth & Environment</i> , 2022, 3, .	6.8	13
59	Analysis of the genomic basis of functional diversity in dinoflagellates using a transcriptome-based sequence similarity network. <i>Molecular Ecology</i> , 2018, 27, 2365-2380.	3.9	12
60	MIG1-dependent and MIG1-independent regulation of GAL gene expression in <i>Saccharomyces cerevisiae</i> : role of Imp2p. <i>Yeast</i> , 2003, 20, 1085-1096.	1.7	9
61	LYS2 gene and its mutation in <i>Kluyveromyces lactis</i> . <i>Yeast</i> , 2003, 20, 1171-1175.	1.7	4
62	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. <i>SSRN Electronic Journal</i> , 2019, , .	0.4	4
63	Evolutionary origins and species delineation of the two Pyrenean endemics <i>Campanula jaubertiana</i> and <i>C. andorrana</i> (Campanulaceae): evidence for transverse alpine speciation. <i>Alpine Botany</i> , 2022, 132, 51-64.	2.4	4
64	Deciphering Metatranscriptomic Data. <i>Methods in Molecular Biology</i> , 2015, 1269, 279-291.	0.9	3
65	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.	2.8	1
66	BAC ends library generation for Illumina sequencing. <i>Protocol Exchange</i> , 0, , .	0.3	0