

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	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
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	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
4	Tempo and drivers of plant diversification in the European mountain system. <i>Nature Communications</i> , 2022, 13, 2750.	12.8	15
5	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
6	Diversity and ecological footprint of Global Ocean RNA viruses. <i>Science</i> , 2022, 376, 1202-1208.	12.6	41
7	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
8	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
9	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
10	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
11	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. <i>Nature</i> , 2021, 600, 86-92.	27.8	81
12	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
13	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
14	The Treasure Vault Can be Opened: Large-Scale Genome Skimming Works Well Using Herbarium and Silica Gel Dried Material. <i>Plants</i> , 2020, 9, 432.	3.5	59
15	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
16	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	28.9	268
17	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
18	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	4.9	76

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19	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
20	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. <i>SSRN Electronic Journal</i> , 2019, , .	0.4	4
21	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813.	12.8	220
22	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
23	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	12.8	297
24	Comparative Time-Scale Gene Expression Analysis Highlights the Infection Processes of Two Amoebophrya Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 2251.	3.5	19
25	A de novo approach to disentangle partner identity and function in holobiont systems. <i>Microbiome</i> , 2018, 6, 105.	11.1	19
26	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
27	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	17.5	581
28	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
29	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	5.3	147
30	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
31	Global repositioning of transcription start sites in a plant-fermenting bacterium. <i>Nature Communications</i> , 2016, 7, 13783.	12.8	25
32	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
33	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	27.8	629
34	Understanding the evolution of holoparasitic plants: the complete plastid genome of the holoparasite <i>Cytinus hypocistis</i> (Cytinaceae). <i>Annals of Botany</i> , 2016, 118, 885-896.	2.9	55
35	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. <i>Nature Communications</i> , 2016, 7, 11071.	12.8	72
36	Improvement of the banana <i>Musa acuminata</i> reference sequence using NGS data and semi-automated bioinformatics methods. <i>BMC Genomics</i> , 2016, 17, 243.	2.8	129

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37	Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (<i>Capra hircus</i>) using WGS data. <i>Frontiers in Genetics</i> , 2015, 6, 107.	2.3	108
38	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	12.6	617
39	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	12.6	2,137
40	Deep transcriptome sequencing provides new insights into the structural and functional organization of the wheat genome. <i>Genome Biology</i> , 2015, 16, 29.	8.8	101
41	Genome assembly using Nanopore-guided long and error-free DNA reads. <i>BMC Genomics</i> , 2015, 16, 327.	2.8	177
42	Deciphering Metatranscriptomic Data. <i>Methods in Molecular Biology</i> , 2015, 1269, 279-291.	0.9	3
43	The Spatiotemporal Program of DNA Replication Is Associated with Specific Combinations of Chromatin Marks in Human Cells. <i>PLoS Genetics</i> , 2014, 10, e1004282.	3.5	123
44	Functional Diversity of Carbohydrate-Active Enzymes Enabling a Bacterium to Ferment Plant Biomass. <i>PLoS Genetics</i> , 2014, 10, e1004773.	3.5	90
45	Comparison of library preparation methods reveals their impact on interpretation of metatranscriptomic data. <i>BMC Genomics</i> , 2014, 15, 912.	2.8	56
46	TE-Tracker: systematic identification of transposition events through whole-genome resequencing. <i>BMC Bioinformatics</i> , 2014, 15, 377.	2.6	27
47	Organization and evolution of transposable elements along the bread wheat chromosome 3B. <i>Genome Biology</i> , 2014, 15, 546.	8.8	88
48	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
49	Genome-defence small RNAs exapted for epigenetic mating-type inheritance. <i>Nature</i> , 2014, 509, 447-452.	27.8	105
50	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184.	12.6	520
51	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	12.6	542
52	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
53	Sequencing platform and library preparation choices impact viral metagenomes. <i>BMC Genomics</i> , 2013, 14, 320.	2.8	90
54	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

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55	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
56	The banana (<i>Musa acuminata</i>) genome and the evolution of monocotyledonous plants. <i>Nature</i> , 2012, 488, 213-217.	27.8	1,049
57	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
58	The autophagosomal protein LGG-2 acts synergistically with LGG-1 in dauer formation and longevity in <i>C. elegans</i> . <i>Autophagy</i> , 2010, 6, 622-633.	9.1	82
59	The ESCRT-III protein CeVPS-2 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
60	Differential expression pattern of the four mitochondrial adenine nucleotide transporter genes and their roles during the development of <i>Caenorhabditis elegans</i> . <i>Developmental Dynamics</i> , 2008, 237, 1668-1681.	1.8	20
61	Enterococcal Leucine-Rich Repeat-Containing Protein Involved in Virulence and Host Inflammatory Response. <i>Infection and Immunity</i> , 2007, 75, 4463-4471.	2.2	50
62	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
63	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
64	LYS2 gene and its mutation in <i>Kluyveromyces lactis</i> . <i>Yeast</i> , 2003, 20, 1171-1175.	1.7	4
65	Soil Contamination Detected Using Bacterial and Plant Mutagenicity Tests and Chemical Analyses. <i>Environmental Research</i> , 2002, 88, 64-69.	7.5	54
66	BAC ends library generation for Illumina sequencing. <i>Protocol Exchange</i> , 0, , .	0.3	0