

Caroline Belser

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

2,403
citations

471509

17
h-index

526287

27
g-index

38
all docs

38
docs citations

38
times ranked

3817
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenomic and structural events preclude recombination in <i>Brassica napus</i> . <i>New Phytologist</i> , 2022, 234, 545-559.	7.3	15
2	Oxford Nanopore and Bionano Genomics technologies evaluation for plant structural variation detection. <i>BMC Genomics</i> , 2022, 23, 317.	2.8	4
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	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
5	Evaluating sediment and water sampling methods for the estimation of deep-sea biodiversity using environmental DNA. <i>Scientific Reports</i> , 2021, 11, 7856.	3.3	18
6	Population genomics of apricots unravels domestication history and adaptive events. <i>Nature Communications</i> , 2021, 12, 3956.	12.8	45
7	Sequencing and Chromosome-Scale Assembly of Plant Genomes, <i>Brassica rapa</i> as a Use Case. <i>Biology</i> , 2021, 10, 732.	2.8	15
8	Telomere-to-telomere gapless chromosomes of banana using nanopore sequencing. <i>Communications Biology</i> , 2021, 4, 1047.	4.4	86
9	Diversity and Biogeography of Bathyal and Abyssal Seafloor Bacteria and Archaea Along a Mediterranean–Atlantic Gradient. <i>Frontiers in Microbiology</i> , 2021, 12, 702016.	3.5	2
10	Massive postglacial gene flow between European white oaks uncovered genes underlying species barriers. <i>New Phytologist</i> , 2020, 226, 1183-1197.	7.3	46
11	Genome Size Variation and Comparative Genomics Reveal Intraspecific Diversity in <i>Brassica rapa</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 577536.	3.6	22
12	Long-read assembly of the <i>Brassica napus</i> reference genome Darmor-bzh. <i>GigaScience</i> , 2020, 9, .	6.4	64
13	BiSCoT: improving large eukaryotic genome assemblies with optical maps. <i>PeerJ</i> , 2020, 8, e10150.	2.0	13
14	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, .	0.6	3
15	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	21.4	363
16	The Tara Pacific expedition—A pan-ecosystemic approach of the ‘omics’ complexity of coral reef holobionts across the Pacific Ocean. <i>PLoS Biology</i> , 2019, 17, e3000483.	5.6	48
17	Expanding Tara Oceans Protocols for Underway, Ecosystemic Sampling of the Ocean-Atmosphere Interface During Tara Pacific Expedition (2016–2018). <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	42
18	Chromosome-scale assemblies of plant genomes using nanopore long reads and optical maps. <i>Nature Plants</i> , 2018, 4, 879-887.	9.3	316

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19	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	9.3	303
20	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
21	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	5.3	147
22	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. <i>Molecular Ecology Resources</i> , 2016, 16, 254-265.	4.8	108
23	Genome assembly using Nanopore-guided long and error-free DNA reads. <i>BMC Genomics</i> , 2015, 16, 327.	2.8	177
24	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. <i>BMC Genomics</i> , 2015, 16, 112.	2.8	49
25	Comparison of library preparation methods reveals their impact on interpretation of metatranscriptomic data. <i>BMC Genomics</i> , 2014, 15, 912.	2.8	56
26	The DNA sequence and analysis of human chromosome 14. <i>Nature</i> , 2003, 421, 601-607.	27.8	108
27	A novel association of the SMN protein with two major non-ribosomal nucleolar proteins and its implication in spinal muscular atrophy. <i>Human Molecular Genetics</i> , 2002, 11, 1017-1027.	2.9	45
28	Chromosome-scale assembly of the yellow mealworm genome. <i>Open Research Europe</i> , 0, 1, 94.	2.0	1
29	BAC ends library generation for Illumina sequencing. <i>Protocol Exchange</i> , 0, , .	0.3	0
30	Chromosome-scale assembly of the yellow mealworm genome. <i>Open Research Europe</i> , 0, 1, 94.	2.0	2