

Helene Berges

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

9,644
citations

94433

37
h-index

58581

82
g-index

90
all docs

90
docs citations

90
times ranked

11413
citing authors

#	ARTICLE	IF	CITATIONS
1	A wheat cysteine-rich receptor-like kinase confers broad-spectrum resistance against <i>Septoria tritici</i> blotch. <i>Nature Communications</i> , 2021, 12, 433.	12.8	55
2	A genome sequence resource for the genus <i>Passiflora</i> , the genome of the wild diploid species <i>Passiflora organensis</i> . <i>Plant Genome</i> , 2021, 14, e20117.	2.8	8
3	Influence of CNV on transcript levels of HvCBF genes at Fr-H2 locus revealed by resequencing in resistant barley cv. "Nure" and expression analysis. <i>Plant Science</i> , 2020, 290, 110305.	3.6	5
4	Convergent evolution of the UbiA prenyltransferase family underlies the independent acquisition of furanocoumarins in plants. <i>New Phytologist</i> , 2020, 225, 2166-2182.	7.3	30
5	A Repertory of Rearrangements and the Loss of an Inverted Repeat Region in <i>Passiflora</i> Chloroplast Genomes. <i>Genome Biology and Evolution</i> , 2020, 12, 1841-1857.	2.5	49
6	The wild grape genome sequence provides insights into the transition from dioecy to hermaphroditism during grape domestication. <i>Genome Biology</i> , 2020, 21, 223.	8.8	48
7	Fonio millet genome unlocks African orphan crop diversity for agriculture in a changing climate. <i>Nature Communications</i> , 2020, 11, 4488.	12.8	63
8	High-quality genome sequence of white lupin provides insight into soil exploration and seed quality. <i>Nature Communications</i> , 2020, 11, 492.	12.8	90
9	Identification of passion fruit (<i>Passiflora edulis</i>) chromosomes using BAC-FISH. <i>Chromosome Research</i> , 2019, 27, 299-311.	2.2	10
10	Genetic basis and timing of a major mating system shift in <i>Capsella</i> . <i>New Phytologist</i> , 2019, 224, 505-517.	7.3	23
11	CRISPR/Cas9 technology for DNA isolation coupled to Cas9-assisted targeting for sequencing and assembly of a 30 kb region in plant genome. <i>Nucleic Acids Research</i> , 2019, 47, 8050-8060.	14.5	6
12	Transposable element discovery and characterization of LTR-retrotransposon evolutionary lineages in the tropical fruit species <i>Passiflora edulis</i> . <i>Molecular Biology Reports</i> , 2019, 46, 6117-6133.	2.3	8
13	Gene Duplication in the Sugarcane Genome: A Case Study of Allele Interactions and Evolutionary Patterns in Two Genic Regions. <i>Frontiers in Plant Science</i> , 2019, 10, 553.	3.6	23
14	Development of a Sequence-Based Reference Physical Map of Pea (<i>Pisum sativum</i> L.). <i>Frontiers in Plant Science</i> , 2019, 10, 323.	3.6	13
15	A receptor-like kinase enhances sunflower resistance to <i>Orobanche cumana</i> . <i>Nature Plants</i> , 2019, 5, 1211-1215.	9.3	53
16	Asparagine synthetase genes (<i>AsnS1</i> and <i>AsnS2</i>) in durum wheat: structural analysis and expression under nitrogen stress. <i>Euphytica</i> , 2018, 214, 1.	1.2	21
17	Wheat receptor-kinase-like protein <i>Stb6</i> controls gene-for-gene resistance to fungal pathogen <i>Zymoseptoria tritici</i> . <i>Nature Genetics</i> , 2018, 50, 368-374.	21.4	215
18	Draft genome and reference transcriptomic resources for the urticating pine defoliator <i>Thaumetopoea pityocampa</i> (Lepidoptera: Notodontidae). <i>Molecular Ecology Resources</i> , 2018, 18, 602-619.	4.8	23

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19	Whole-genome landscape of <i>Medicago truncatula</i> symbiotic genes. <i>Nature Plants</i> , 2018, 4, 1017-1025.	9.3	192
20	A gene-rich fraction analysis of the <i>Passiflora edulis</i> genome reveals highly conserved microsyntenic regions with two related Malpighiales species. <i>Scientific Reports</i> , 2018, 8, 13024.	3.3	18
21	FANCM Limits Meiotic Crossovers in Brassica Crops. <i>Frontiers in Plant Science</i> , 2018, 9, 368.	3.6	41
22	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. <i>Nature Communications</i> , 2018, 9, 2638.	12.8	299
23	The Genomic Basis of Color Pattern Polymorphism in the Harlequin Ladybird. <i>Current Biology</i> , 2018, 28, 3296-3302.e7.	3.9	92
24	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
25	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	9.3	303
26	Loss of pollen-specific phospholipase NOT LIKE DAD triggers gynogenesis in maize. <i>EMBO Journal</i> , 2017, 36, 707-717.	7.8	197
27	The Impact of Open Pollination on the Structural Evolutionary Dynamics, Meiotic Behavior, and Fertility of Resynthesized Allotetraploid <i>Brassica napus</i> L. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 705-717.	1.8	28
28	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. <i>Nature</i> , 2017, 546, 148-152.	27.8	579
29	Repeat-length variation in a wheat cellulose synthase-like gene is associated with altered tiller number and stem cell wall composition. <i>Journal of Experimental Botany</i> , 2017, 68, 1519-1529.	4.8	39
30	A bacterial artificial chromosome (<sc>BAC</sc>) genomic approach reveals partial clustering of the furanocoumarin pathway genes in parsnip. <i>Plant Journal</i> , 2017, 89, 1119-1132.	5.7	21
31	Physical Map of the Short Arm of Bread Wheat Chromosome 3D. <i>Plant Genome</i> , 2017, 10, plantgenome2017.03.0021.	2.8	11
32	Map-based cloning of the fertility restoration locus Rfm1 in cultivated barley (<i>Hordeum vulgare</i>). <i>Euphytica</i> , 2017, 213, 1.	1.2	15
33	Patterns of Polymorphism at the Self-Incompatibility Locus in 1,083 <i>Arabidopsis thaliana</i> Genomes. <i>Molecular Biology and Evolution</i> , 2017, 34, 1878-1889.	8.9	48
34	The Chloroplast Genome of <i>Passiflora edulis</i> (Passifloraceae) Assembled from Long Sequence Reads: Structural Organization and Phylogenomic Studies in Malpighiales. <i>Frontiers in Plant Science</i> , 2017, 8, 334.	3.6	79
35	Advancing Eucalyptus Genomics: Cytogenomics Reveals Conservation of Eucalyptus Genomes. <i>Frontiers in Plant Science</i> , 2016, 7, 510.	3.6	18
36	A Metabolic Gene Cluster in the Wheat <i>W1</i> and the Barley <i>Cer-cqu</i> Loci Determines Î²-Diketone Biosynthesis and Glaucousness. <i>Plant Cell</i> , 2016, 28, 1440-1460.	6.6	123

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37	Suppressed recombination and unique candidate genes in the divergent haplotype encoding Fhb1, a major Fusarium head blight resistance locus in wheat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1607-1623.	3.6	103
38	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
39	Comparative Analysis of WRKY Genes Potentially Involved in Salt Stress Responses in <i>Triticum turgidum</i> L. ssp. durum. <i>Frontiers in Plant Science</i> , 2016, 7, 2034.	3.6	26
40	The wheat Sr50 gene reveals rich diversity at a cereal disease resistance locus. <i>Nature Plants</i> , 2015, 1, 15186.	9.3	209
41	The physical map of wheat chromosome 5DS revealed gene duplications and small rearrangements. <i>BMC Genomics</i> , 2015, 16, 453.	2.8	17
42	Sequence-Based Analysis of Structural Organization and Composition of the Cultivated Sunflower (<i>Helianthus annuus</i> L.) Genome. <i>Biology</i> , 2014, 3, 295-319.	2.8	16
43	Dominance hierarchy arising from the evolution of a complex small RNA regulatory network. <i>Science</i> , 2014, 346, 1200-1205.	12.6	61
44	Major haplotype divergence including multiple germin-like protein genes, at the wheat Sr2 adult plant stem rust resistance locus. <i>BMC Plant Biology</i> , 2014, 14, 379.	3.6	36
45	Begin at the beginning: A BAC-end view of the passion fruit (<i>Passiflora</i>) genome. <i>BMC Genomics</i> , 2014, 15, 816.	2.8	34
46	The homoeologous genes encoding chalcone flavanone isomerase in <i>Triticum aestivum</i> L.: Structural characterization and expression in different parts of wheat plant. <i>Gene</i> , 2014, 538, 334-341.	2.2	38
47	<i>FRIZZY PANICLE</i> Drives Supernumerary Spikelets in Bread Wheat. <i>Plant Physiology</i> , 2014, 167, 189-199.	4.8	131
48	Meiotic Gene Evolution: Can You Teach a New Dog New Tricks?. <i>Molecular Biology and Evolution</i> , 2014, 31, 1724-1727.	8.9	71
49	Isolation and molecular characterization of ERF1, an ethylene response factor gene from durum wheat (<i>Triticum turgidum</i> L. subsp. durum), potentially involved in salt-stress responses. <i>Journal of Experimental Botany</i> , 2014, 65, 6359-6371.	4.8	36
50	Building the sugarcane genome for biotechnology and identifying evolutionary trends. <i>BMC Genomics</i> , 2014, 15, 540.	2.8	136
51	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	12.6	542
52	A high density physical map of chromosome 1BL supports evolutionary studies, map-based cloning and sequencing in wheat. <i>Genome Biology</i> , 2013, 14, R64.	8.8	45
53	Exploring the genome of the salt-marsh <i>Spartina maritima</i> (Poaceae, Chloridoideae) through BAC end sequence analysis. <i>Plant Molecular Biology</i> , 2013, 83, 591-606.	3.9	11
54	<i>QRRS1</i> , an <i>R</i> -locus required for <i>Medicago truncatula</i> quantitative resistance to <i>Ralstonia solanacearum</i> . <i>New Phytologist</i> , 2013, 199, 758-772.	7.3	37

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55	The physical map of wheat chromosome 1BS provides insights into its gene space organization and evolution. <i>Genome Biology</i> , 2013, 14, R138.	9.6	40
56	Physical Mapping Integrated with Syntenic Analysis to Characterize the Gene Space of the Long Arm of Wheat Chromosome 1A. <i>PLoS ONE</i> , 2013, 8, e59542.	2.5	26
57	A Physical Map of the Short Arm of Wheat Chromosome 1A. <i>PLoS ONE</i> , 2013, 8, e80272.	2.5	30
58	Contrasted Patterns of Molecular Evolution in Dominant and Recessive Self-Incompatibility Haplotypes in Arabidopsis. <i>PLoS Genetics</i> , 2012, 8, e1002495.	3.5	91
59	Down-regulation of a single auxin efflux transport protein in tomato induces precocious fruit development. <i>Journal of Experimental Botany</i> , 2012, 63, 4901-4917.	4.8	82
60	Deciphering the genomic structure, function and evolution of carotenogenesis related phytoene synthases in grasses. <i>BMC Genomics</i> , 2012, 13, 221.	2.8	59
61	Intraspecific sequence comparisons reveal similar rates of non-collinear gene insertion in the B and D genomes of bread wheat. <i>BMC Plant Biology</i> , 2012, 12, 155.	3.6	18
62	Functional features of a single chromosome arm in wheat (1AL) determined from its structure. <i>Functional and Integrative Genomics</i> , 2012, 12, 173-182.	3.5	24
63	The Medicago genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
64	The Sugarcane Genome Challenge: Strategies for Sequencing a Highly Complex Genome. <i>Tropical Plant Biology</i> , 2011, 4, 145-156.	1.9	91
65	Building up resources and knowledge to unravel transcriptomics dynamics underlying Eucalyptus globulus xylogenesis. <i>BMC Proceedings</i> , 2011, 5, .	1.6	2
66	Deciphering cork formation in <i>Quercus suber</i> . <i>BMC Proceedings</i> , 2011, 5, .	1.6	2
67	Advancing Eucalyptus genomics: identification and sequencing of lignin biosynthesis genes from deep-coverage BAC libraries. <i>BMC Genomics</i> , 2011, 12, 137.	2.8	46
68	Analysis of BAC end sequences in oak, a keystone forest tree species, providing insight into the composition of its genome. <i>BMC Genomics</i> , 2011, 12, 292.	2.8	33
69	A 3,000-Loci Transcription Map of Chromosome 3B Unravels the Structural and Functional Features of Gene Islands in Hexaploid Wheat. <i>Plant Physiology</i> , 2011, 157, 1596-1608.	4.8	49
70	Progress towards a reference genome for sunflower. <i>Botany</i> , 2011, 89, 429-437.	1.0	67
71	Construction and characterization of two BAC libraries representing a deep-coverage of the genome of chicory (<i>Cichorium intybus</i> L., Asteraceae). <i>BMC Research Notes</i> , 2010, 3, 225.	1.4	35
72	Brassica orthologs from BANYULS belong to a small multigene family, which is involved in procyanidin accumulation in the seed. <i>Planta</i> , 2009, 230, 1167-1183.	3.2	37

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73	Fine Mapping and Marker Development for the Crossability Gene SKr on Chromosome 5BS of Hexaploid Wheat (<i>Triticum aestivum</i> L.). <i>Genetics</i> , 2009, 183, 469-481.	2.9	43
74	A Physical Map of the 1-Gigabase Bread Wheat Chromosome 3B. <i>Science</i> , 2008, 322, 101-104.	12.6	356
75	Global Changes in Gene Expression in <i>Sinorhizobium meliloti</i> 1021 under Microoxic and Symbiotic Conditions. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 292-303.	2.6	230
76	Nitrogen regulation in <i>Sinorhizobium meliloti</i> probed with whole genome arrays. <i>FEMS Microbiology Letters</i> , 2004, 241, 33-40.	1.8	16
77	Development of <i>Sinorhizobium meliloti</i> Pilot Macroarrays for Transcriptome Analysis. <i>Applied and Environmental Microbiology</i> , 2003, 69, 1214-1219.	3.1	23
78	A glutamine-amidotransferase-like protein modulates FixT anti-kinase activity in <i>Sinorhizobium meliloti</i> . <i>BMC Microbiology</i> , 2001, 1, 6.	3.3	18
79	Isolation and characterization of a <i>priB</i> mutant of <i>Escherichia coli</i> influencing plasmid copy number of <i>delta rop ColE1</i> -type plasmids. <i>Journal of Bacteriology</i> , 1997, 179, 956-958.	2.2	13
80	A Set of pBR322-Compatible Plasmids Allowing the Testing of Chaperone-Assisted Folding of Proteins Overexpressed in <i>Escherichia coli</i> . <i>Analytical Biochemistry</i> , 1997, 254, 150-152.	2.4	61
81	Combined effects of the signal sequence and the major chaperone proteins on the export of human cytokines in <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 1996, 62, 55-60.	3.1	42