Helene Berges

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5025177/publications.pdf

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	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
2	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	27.8	1,166
3	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. Nature, 2017, 546, 148-152.	27.8	579
4	Structural and functional partitioning of bread wheat chromosome 3B. Science, 2014, 345, 1249721.	12.6	542
5	A Physical Map of the 1-Gigabase Bread Wheat Chromosome 3B. Science, 2008, 322, 101-104.	12.6	356
6	Oak genome reveals facets of long lifespan. Nature Plants, 2018, 4, 440-452.	9.3	303
7	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. Nature Communications, 2018, 9, 2638.	12.8	299
8	Global Changes in Gene Expression in Sinorhizobium meliloti 1021 under Microoxic and Symbiotic Conditions. Molecular Plant-Microbe Interactions, 2004, 17, 292-303.	2.6	230
9	Wheat receptor-kinase-like protein Stb6 controls gene-for-gene resistance to fungal pathogen Zymoseptoria tritici. Nature Genetics, 2018, 50, 368-374.	21.4	215
10	The wheat Sr50 gene reveals rich diversity at a cereal disease resistance locus. Nature Plants, 2015, 1, 15186.	9.3	209
11	Loss of pollenâ€specific phospholipase NOT LIKE DAD triggers gynogenesis in maize. EMBO Journal, 2017, 36, 707-717.	7.8	197
12	Whole-genome landscape of Medicago truncatula symbiotic genes. Nature Plants, 2018, 4, 1017-1025.	9.3	192
13	Building the sugarcane genome for biotechnology and identifying evolutionary trends. BMC Genomics, 2014, 15, 540.	2.8	136
14	<i>FRIZZY PANICLE</i> Drives Supernumerary Spikelets in Bread Wheat. Plant Physiology, 2014, 167, 189-199.	4.8	131
15	A Metabolic Gene Cluster in the Wheat <i>W1</i> and the Barley <i>Cer-cqu</i> Loci Determines Î²-Diketone Biosynthesis and Glaucousness. Plant Cell, 2016, 28, 1440-1460.	6.6	123
16	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. Molecular Ecology Resources, 2016, 16, 254-265.	4.8	108
17	Suppressed recombination and unique candidate genes in the divergent haplotype encoding Fhb1, a major Fusarium head blight resistance locus in wheat. Theoretical and Applied Genetics, 2016, 129, 1607-1623.	3.6	103
18	The Genomic Basis of Color Pattern Polymorphism in the Harlequin Ladybird. Current Biology, 2018, 28, 3296-3302.e7.	3.9	92

#	ARTICLE	IF	CITATIONS
19	The Sugarcane Genome Challenge: Strategies for Sequencing a Highly Complex Genome. Tropical Plant Biology, 2011, 4, 145-156.	1.9	91
20	Contrasted Patterns of Molecular Evolution in Dominant and Recessive Self-Incompatibility Haplotypes in Arabidopsis. PLoS Genetics, 2012, 8, e1002495.	3.5	91
21	High-quality genome sequence of white lupin provides insight into soil exploration and seed quality. Nature Communications, 2020, 11, 492.	12.8	90
22	Down-regulation of a single auxin efflux transport protein in tomato induces precocious fruit development. Journal of Experimental Botany, 2012, 63, 4901-4917.	4.8	82
23	The Chloroplast Genome of Passiflora edulis (Passifloraceae) Assembled from Long Sequence Reads: Structural Organization and Phylogenomic Studies in Malpighiales. Frontiers in Plant Science, 2017, 8, 334.	3.6	79
24	Meiotic Gene Evolution: Can You Teach a New Dog New Tricks?. Molecular Biology and Evolution, 2014, 31, 1724-1727.	8.9	71
25	Progress towards a reference genome for sunflower. Botany, 2011, 89, 429-437.	1.0	67
26	Fonio millet genome unlocks African orphan crop diversity for agriculture in a changing climate. Nature Communications, 2020, 11, 4488.	12.8	63
27	A Set of pBR322-Compatible Plasmids Allowing the Testing of Chaperone-Assisted Folding of Proteins Overexpressed inEscherichia coli. Analytical Biochemistry, 1997, 254, 150-152.	2.4	61
28	Dominance hierarchy arising from the evolution of a complex small RNA regulatory network. Science, 2014, 346, 1200-1205.	12.6	61
29	Deciphering the genomic structure, function and evolution of carotenogenesis related phytoene synthases in grasses. BMC Genomics, 2012, 13, 221.	2.8	59
30	A wheat cysteine-rich receptor-like kinase confers broad-spectrum resistance against Septoria tritici blotch. Nature Communications, 2021, 12, 433.	12.8	55
31	A receptor-like kinase enhances sunflower resistance to Orobanche cumana. Nature Plants, 2019, 5, 1211-1215.	9.3	53
32	A 3,000-Loci Transcription Map of Chromosome 3B Unravels the Structural and Functional Features of Gene Islands in Hexaploid Wheat Â. Plant Physiology, 2011, 157, 1596-1608.	4.8	49
33	A Repertory of Rearrangements and the Loss of an Inverted Repeat Region in Passiflora Chloroplast Genomes. Genome Biology and Evolution, 2020, 12, 1841-1857.	2.5	49
34	Patterns of Polymorphism at the Self-Incompatibility Locus in 1,083 Arabidopsis thaliana Genomes. Molecular Biology and Evolution, 2017, 34, 1878-1889.	8.9	48
35	The wild grape genome sequence provides insights into the transition from dioecy to hermaphroditism during grape domestication. Genome Biology, 2020, 21, 223.	8.8	48
36	Advancing Eucalyptus genomics: identification and sequencing of lignin biosynthesis genes from deep-coverage BAC libraries. BMC Genomics, 2011, 12, 137.	2.8	46

#	ARTICLE	IF	CITATIONS
37	A high density physical map of chromosome 1BL supports evolutionary studies, map-based cloning and sequencing in wheat. Genome Biology, 2013, 14, R64.	8.8	45
38	Fine Mapping and Marker Development for the Crossability Gene SKr on Chromosome 5BS of Hexaploid Wheat (Triticum aestivum L.). Genetics, 2009, 183, 469-481.	2.9	43
39	Combined effects of the signal sequence and the major chaperone proteins on the export of human cytokines in Escherichia coli. Applied and Environmental Microbiology, 1996, 62, 55-60.	3.1	42
40	FANCM Limits Meiotic Crossovers in Brassica Crops. Frontiers in Plant Science, 2018, 9, 368.	3.6	41
41	The physical map of wheat chromosome 1BS provides insights into its gene space organization and evolution. Genome Biology, 2013, 14, R138.	9.6	40
42	Repeat-length variation in a wheat cellulose synthase-like gene is associated with altered tiller number and stem cell wall composition. Journal of Experimental Botany, 2017, 68, 1519-1529.	4.8	39
43	The homoeologous genes encoding chalconeâ€“flavanone isomerase in Triticum aestivum L.: Structural characterization and expression in different parts of wheat plant. Gene, 2014, 538, 334-341.	2.2	38
44	Brassica orthologs from BANYULS belong to a small multigene family, which is involved in procyanidin accumulation in the seed. Planta, 2009, 230, 1167-1183.	3.2	37
45	<i>Mt<scp>QRRS</scp>1</i>, an <i>R</i>â€locus required for <i>Medicago truncatula</i> quantitative resistance to <i>Ralstonia solanacearum</i>. New Phytologist, 2013, 199, 758-772.	7.3	37
46	Major haplotype divergence including multiple germin-like protein genes, at the wheat Sr2 adult plant stem rust resistance locus. BMC Plant Biology, 2014, 14, 379.	3.6	36
47	Isolation and molecular characterization of ERF1, an ethylene response factor gene from durum wheat (Triticum turgidum L. subsp. durum), potentially involved in salt-stress responses. Journal of Experimental Botany, 2014, 65, 6359-6371.	4.8	36
48	Construction and characterization of two BAC libraries representing a deep-coverage of the genome of chicory (Cichorium intybus L., Asteraceae). BMC Research Notes, 2010, 3, 225.	1.4	35
49	Begin at the beginning: A BAC-end view of the passion fruit (Passiflora) genome. BMC Genomics, 2014, 15, 816.	2.8	34
50	Analysis of BAC end sequences in oak, a keystone forest tree species, providing insight into the composition of its genome. BMC Genomics, 2011, 12, 292.	2.8	33
51	A Physical Map of the Short Arm of Wheat Chromosome 1A. PLoS ONE, 2013, 8, e80272.	2.5	30
52	Convergent evolution of the UbiA prenyltransferase family underlies the independent acquisition of furanocoumarins in plants. New Phytologist, 2020, 225, 2166-2182.	7.3	30
53	The Impact of Open Pollination on the Structural Evolutionary Dynamics, Meiotic Behavior, and Fertility of Resynthesized Allotetraploid<i>Brassica napus</i>L.. G3: Genes, Genomes, Genetics, 2017, 7, 705-717.	1.8	28
54	Physical Mapping Integrated with Syntenic Analysis to Characterize the Gene Space of the Long Arm of Wheat Chromosome 1A. PLoS ONE, 2013, 8, e59542.	2.5	26

#	ARTICLE	IF	CITATIONS
55	Comparative Analysis of WRKY Genes Potentially Involved in Salt Stress Responses in Triticum turgidum L. ssp. durum. Frontiers in Plant Science, 2016, 7, 2034.	3.6	26
56	Functional features of a single chromosome arm in wheat (1AL) determined from its structure. Functional and Integrative Genomics, 2012, 12, 173-182.	3.5	24
57	Development of Sinorhizobium meliloti Pilot Macroarrays for Transcriptome Analysis. Applied and Environmental Microbiology, 2003, 69, 1214-1219.	3.1	23
58	Draft genome and reference transcriptomic resources for the urticating pine defoliator <i>Thaumetopoea pityocampa</i> (Lepidoptera: Notodontidae). Molecular Ecology Resources, 2018, 18, 602-619.	4.8	23
59	Genetic basis and timing of a major mating system shift in <i>Capsella</i>. New Phytologist, 2019, 224, 505-517.	7.3	23
60	Gene Duplication in the Sugarcane Genome: A Case Study of Allele Interactions and Evolutionary Patterns in Two Genic Regions. Frontiers in Plant Science, 2019, 10, 553.	3.6	23
61	A bacterial artificial chromosome (<scp>BAC</scp>) genomic approach reveals partial clustering of the furanocoumarin pathway genes in parsnip. Plant Journal, 2017, 89, 1119-1132.	5.7	21
62	Asparagine synthetase genes (AsnS1 and AsnS2) in durum wheat: structural analysis and expression under nitrogen stress. Euphytica, 2018, 214, 1.	1.2	21
63	A glutamine-amidotransferase-like protein modulates FixT anti-kinase activity in Sinorhizobium meliloti. BMC Microbiology, 2001, 1, 6.	3.3	18
64	Intraspecific sequence comparisons reveal similar rates of non-collinear gene insertion in the B and D genomes of bread wheat. BMC Plant Biology, 2012, 12, 155.	3.6	18
65	Advancing Eucalyptus Genomics: Cytogenomics Reveals Conservation of Eucalyptus Genomes. Frontiers in Plant Science, 2016, 7, 510.	3.6	18
66	A gene-rich fraction analysis of the Passiflora edulis genome reveals highly conserved microsyntenic regions with two related Malpighiales species. Scientific Reports, 2018, 8, 13024.	3.3	18
67	The physical map of wheat chromosome 5DS revealed gene duplications and small rearrangements. BMC Genomics, 2015, 16, 453.	2.8	17
68	Nitrogen regulation inSinorhizobium melilotiprobed with whole genome arrays. FEMS Microbiology Letters, 2004, 241, 33-40.	1.8	16
69	Sequence-Based Analysis of Structural Organization and Composition of the Cultivated Sunflower (Helianthus annuus L.) Genome. Biology, 2014, 3, 295-319.	2.8	16
70	Map-based cloning of the fertility restoration locus Rfm1 in cultivated barley (Hordeum vulgare). Euphytica, 2017, 213, 1.	1.2	15
71	Isolation and characterization of a priB mutant of Escherichia coli influencing plasmid copy number of delta rop ColE1-type plasmids. Journal of Bacteriology, 1997, 179, 956-958.	2.2	13
72	Development of a Sequence-Based Reference Physical Map of Pea (Pisum sativum L.). Frontiers in Plant Science, 2019, 10, 323.	3.6	13

#	ARTICLE	IF	CITATIONS
73	Exploring the genome of the salt-marsh Spartina maritima (Poaceae, Chloridoideae) through BAC end sequence analysis. Plant Molecular Biology, 2013, 83, 591-606.	3.9	11
74	Physical Map of the Short Arm of Bread Wheat Chromosome 3D. Plant Genome, 2017, 10, plantgenome2017.03.0021.	2.8	11
75	Identification of passion fruit (Passiflora edulis) chromosomes using BAC-FISH. Chromosome Research, 2019, 27, 299-311.	2.2	10
76	Transposable element discovery and characterization of LTR-retrotransposon evolutionary lineages in the tropical fruit species Passiflora edulis. Molecular Biology Reports, 2019, 46, 6117-6133.	2.3	8
77	A genome sequence resource for the genus <i>Passiflora</i>, the genome of the wild diploid species <i>Passiflora organensis</i>. Plant Genome, 2021, 14, e20117.	2.8	8
78	Î¼LAS technology for DNA isolation coupled to Cas9-assisted targeting for sequencing and assembly of a 30 kb region in plant genome. Nucleic Acids Research, 2019, 47, 8050-8060.	14.5	6
79	Influence of CNV on transcript levels of HvCBF genes at Fr-H2 locus revealed by resequencing in resistant barley cv. â€˜Nureâ€™ and expression analysis. Plant Science, 2020, 290, 110305.	3.6	5
80	Building up resources and knowledge to unravel transcriptomics dynamics underlying Eucalyptus globulusxylogenesis. BMC Proceedings, 2011, 5, .	1.6	2
81	Deciphering cork formation in Quercus suber. BMC Proceedings, 2011, 5, .	1.6	2