Philipp E. Bayer

List of Publications by Year
in descending order

		109321	48315
90 papers	**9,988** citations	**35** h-index	**88** g-index
103 all docs	**103** docs citations	**103** times ranked	**8617** 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	Early allopolyploid evolution in the post-Neolithic *Brassica napus* oilseed genome. Science, 2014, 345, 950-953.	12.6	2,089
3	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768
4	The pangenome of an agronomically important crop plant Brassica oleracea. Nature Communications, 2016, 7, 13390.	12.8	375
5	A reference genome for pea provides insight into legume genome evolution. Nature Genetics, 2019, 51, 1411-1422.	21.4	363
6	The pangenome of hexaploid bread wheat. Plant Journal, 2017, 90, 1007-1013.	5.7	313
7	Plant pan-genomes are the new reference. Nature Plants, 2020, 6, 914-920.	9.3	302
8	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid *Brassica napus*. Plant Biotechnology Journal, 2018, 16, 1265-1274.	8.3	217
9	Climate change and the need for agricultural adaptation. Current Opinion in Plant Biology, 2020, 56, 197-202.	7.1	193
10	A comprehensive draft genome sequence for lupin (*Lupinus angustifolius*), an emerging health food: insights into plant–microbe interactions and legume evolution. Plant Biotechnology Journal, 2017, 15, 318-330.	8.3	153
11	Assembly and comparison of two closely related *Brassica napus* genomes. Plant Biotechnology Journal, 2017, 15, 1602-1610.	8.3	150
12	Pangenomics Comes of Age: From Bacteria to Plant and Animal Applications. Trends in Genetics, 2020, 36, 132-145.	6.7	137
13	Construction and comparison of three reference-quality genome assemblies for soybean. Plant Journal, 2019, 100, 1066-1082.	5.7	113
14	Variation in abundance of predicted resistance genes in the *Brassica oleracea* pangenome. Plant Biotechnology Journal, 2019, 17, 789-800.	8.3	92
15	The Genome of a Southern Hemisphere Seagrass Species (*Zostera muelleri*). Plant Physiology, 2016, 172, 272-283.	4.8	88
16	Plant pangenomics: approaches, applications and advancements. Current Opinion in Plant Biology, 2020, 54, 18-25.	7.1	88
17	Genome-Wide Association Study of Genetic Control of Seed Fatty Acid Biosynthesis in Brassica napus. Frontiers in Plant Science, 2016, 7, 2062.	3.6	84
18	Characterization of disease resistance genes in the *Brassica napus* pangenome reveals significant structural variation. Plant Biotechnology Journal, 2020, 18, 969-982.	8.3	83

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19	Fast-forward breeding for a food-secure world. Trends in Genetics, 2021, 37, 1124-1136.	6.7	82
20	Trait associations in the pangenome of pigeon pea (<i>Cajanus cajan</i>). Plant Biotechnology Journal, 2020, 18, 1946-1954.	8.3	79
21	openSNPâ€"A Crowdsourced Web Resource for Personal Genomics. PLoS ONE, 2014, 9, e89204.	2.5	78
22	High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in Cicer arietinum and Brassica napus. Theoretical and Applied Genetics, 2015, 128, 1039-1047.	3.6	76
23	Adapting legume crops to climate change using genomic approaches. Plant, Cell and Environment, 2019, 42, 6-19.	5.7	74
24	Improvements in Genomic Technologies: Application to Crop Genomics. Trends in Biotechnology, 2017, 35, 547-558.	9.3	72
25	Genome-wide identification and comparative analysis of NBS-LRR resistance genes in Brassica napus. Crop and Pasture Science, 2018, 69, 72.	1.5	70
26	Current status of structural variation studies in plants. Plant Biotechnology Journal, 2021, 19, 2153-2163.	8.3	65
27	Bias in resistance gene prediction due to repeat masking. Nature Plants, 2018, 4, 762-765.	9.3	58
28	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. Plant Genome, 2022, 15, e20109.	2.8	53
29	INDEL variation in the regulatory region of the major flowering time gene <i>LanFTc1</i> is associated with vernalization response and flowering time in narrowâ€leafed lupin (<i>Lupinus angustifolius</i>) Tj ETQq1 1 0.784314 rgBT /Overl	5.7	51
30	Exploring the genetic and adaptive diversity of a pan-Mediterranean crop wild relative: narrow-leafed lupin. Theoretical and Applied Genetics, 2018, 131, 887-901.	3.6	50
31	Centromere Locations in <i>Brassica</i> A and C Genomes Revealed Through Half-Tetrad Analysis. Genetics, 2016, 202, 513-523.	2.9	47
32	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. Plant Biotechnology Journal, 2021, 19, 2488-2500.	8.3	44
33	Identification and characterization of more than 4 million intervarietal <scp>SNP</scp>s across the group 7 chromosomes of bread wheat. Plant Biotechnology Journal, 2015, 13, 97-104.	8.3	43
34	Genotypeâ€"Environment mismatch of kelp forests under climate change. Molecular Ecology, 2021, 30, 3730-3746.	3.9	39
35	Skim-Based Genotyping by Sequencing. Methods in Molecular Biology, 2015, 1245, 257-270.	0.9	39
36	Acclimation to different depths by the marine angiosperm Posidonia oceanica: transcriptomic and proteomic profiles. Frontiers in Plant Science, 2013, 4, 195.	3.6	38

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37	An advanced reference genome of *Trifolium subterraneum* L. reveals genes related to agronomic performance. Plant Biotechnology Journal, 2017, 15, 1034-1046.	8.3	38
38	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. Scientific Data, 2021, 8, 50.	5.3	38
39	The pangenome of banana highlights differences between genera and genomes. Plant Genome, 2022, 15, e20100.	2.8	37
40	Resistance Gene Analogs in the Brassicaceae: Identification, Characterization, Distribution, and Evolution. Plant Physiology, 2020, 184, 909-922.	4.8	33
41	Pangenomics in crop improvement—from coding structural variations to finding regulatory variants with pangenome graphs. Plant Genome, 2022, 15, e20177.	2.8	33
42	High‐resolution molecular karyotyping uncovers pairing between ancestrally related Brassica chromosomes. New Phytologist, 2014, 202, 964-974.	7.3	31
43	Maize Yield Prediction at an Early Developmental Stage Using Multispectral Images and Genotype Data for Preliminary Hybrid Selection. Remote Sensing, 2021, 13, 3976.	4.0	31
44	The application of pangenomics and machine learning in genomic selection in plants. Plant Genome, 2021, 14, e20112.	2.8	29
45	The western Mediterranean region provided the founder population of domesticated narrow-leafed lupin. Theoretical and Applied Genetics, 2018, 131, 2543-2554.	3.6	28
46	Assembly of the non‐heading pak choi genome and comparison with the genomes of heading Chinese cabbage and the oilseed yellow sarson. Plant Biotechnology Journal, 2021, 19, 966-976.	8.3	28
47	Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution. Journal of Experimental Botany, 2018, 69, 3689-3702.	4.8	27
48	Extensive polyploid clonality was a successful strategy for seagrass to expand into a newly submerged environment. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, .	2.6	27
49	Induced Methylation in Plants as a Crop Improvement Tool: Progress and Perspectives. Agronomy, 2020, 10, 1484.	3.0	25
50	High intraspecific diversity of *Restorer‐of‐fertility‐like* genes in barley. Plant Journal, 2019, 97, 281-295.	5.7	24
51	*Brassica napus* genes *Rlm4* and *Rlm7*, conferring resistance to *Leptosphaeria maculans*, are alleles of the *Rlm9* wall‐associated kinase‐like resistance locus. Plant Biotechnology Journal, 2022, 20, 1229-1231.	8.3	24
52	Resources for image-based high-throughput phenotyping in crops and data sharing challenges. Plant Physiology, 2021, 187, 699-715.	4.8	23
53	An efficient approach to BAC based assembly of complex genomes. Plant Methods, 2016, 12, 2.	4.3	22
54	Climate Clever Clovers: New Paradigm to Reduce the Environmental Footprint of Ruminants by Breeding Low Methanogenic Forages Utilizing Haplotype Variation. Frontiers in Plant Science, 2017, 8, 1463.	3.6	21

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55	CropSNPdb: a database of SNP array data for Brassica crops and hexaploid bread wheat. Plant Journal, 2019, 98, 142-152.	5.7	21
56	Plant Genotype to Phenotype Prediction Using Machine Learning. Frontiers in Genetics, 2022, 13, .	2.3	21
57	Genome-Wide Identification and Evolution of Receptor-Like Kinases (RLKs) and Receptor like Proteins (RLPs) in Brassica juncea. Biology, 2021, 10, 17.	2.8	20
58	Genome-wide identification and comparative analysis of resistance genes in Brassica juncea. Molecular Breeding, 2020, 40, 1.	2.1	17
59	<i>Amborella</i> gene presence/absence variation is associated with abiotic stress responses that may contribute to environmental adaptation. New Phytologist, 2022, 233, 1548-1555.	7.3	16
60	Wheat Panache: A pangenome graph database representing presenceâ€"absence variation across sixteen bread wheat genomes. Plant Genome, 2022, 15, .	2.8	16
61	Machine learning in agriculture: from silos to marketplaces. Plant Biotechnology Journal, 2021, 19, 648-650.	8.3	15
62	Machine learning models outperform deep learning models, provide interpretation and facilitate feature selection for soybean trait prediction. BMC Plant Biology, 2022, 22, 180.	3.6	15
63	Frontiers in Dissecting and Managing Brassica Diseases: From Reference-Based RGA Candidate Identification to Building Pan-RGAomes. International Journal of Molecular Sciences, 2020, 21, 8964.	4.1	14
64	Pangenomes as a Resource to Accelerate Breeding of Under-Utilised Crop Species. International Journal of Molecular Sciences, 2022, 23, 2671.	4.1	14
65	Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus cqProt-003. Theoretical and Applied Genetics, 2022, 135, 1443-1455.	3.6	13
66	Expanding Gene-Editing Potential in Crop Improvement with Pangenomes. International Journal of Molecular Sciences, 2022, 23, 2276.	4.1	12
67	Establishing a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia. Briefings in Bioinformatics, 2019, 20, 384-389.	6.5	11
68	Effect of Leptosphaeria maculans Infection on Promoter DNA Methylation of Defence Genes in Brassica napus. Agronomy, 2020, 10, 1072.	3.0	11
69	QTL Genetic Mapping Study for Traits Affecting Meal Quality in Winter Oilseed Rape (Brassica Napus L.). Genes, 2021, 12, 1235.	2.4	11
70	runBNG: a software package for BioNano genomic analysis on the command line. Bioinformatics, 2017, 33, 3107-3109.	4.1	10
71	Large-Scale Structural Variation Detection in Subterranean Clover Subtypes Using Optical Mapping. Frontiers in Plant Science, 2018, 9, 971.	3.6	10
72	BioNanoAnalyst: a visualisation tool to assess genome assembly quality using BioNano data. BMC Bioinformatics, 2017, 18, 323.	2.6	9

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73	Marine heatwaves have minimal influence on the quality of adult Sydney rock oyster flesh. Science of the Total Environment, 2021, 795, 148846.	8.0	9
74	A pan‐genome and chromosome‐length reference genome of narrow‐leafed lupin (<i>Lupinus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Journal, 0, , .	5.7	9
75	Legume Pangenome Construction Using an Iterative Mapping and Assembly Approach. Methods in Molecular Biology, 2020, 2107, 35-47.	0.9	7
76	Candidate Rlm6 resistance genes against Leptosphaeria. maculans identified through a genome-wide association study in Brassica juncea (L.) Czern. Theoretical and Applied Genetics, 2021, 134, 2035-2050.	3.6	5
77	Genetic and Genomic Resources for Soybean Breeding Research. Plants, 2022, 11, 1181.	3.5	5
78	Mining of Cloned Disease Resistance Gene Homologs (CDRHs) in Brassica Species and Arabidopsis thaliana. Biology, 2022, 11, 821.	2.8	4
79	Whole-Genome DNA Methylation Analysis in Brassica rapa subsp. perviridis in Response to Albugo candida Infection. Frontiers in Plant Science, 0, 13, .	3.6	4
80	An SGSGeneloss-Based Method for Constructing a Gene Presence–Absence Table Using Mosdepth. Methods in Molecular Biology, 2022, , 73-80.	0.9	3
81	Genetic Diversity Linked to Haplotype Variation in the World Core Collection of Trifolium subterraneum for Boron Toxicity Tolerance Provides Valuable Markers for Pasture Breeding. Frontiers in Plant Science, 2019, 10, 1043.	3.6	2
82	Method for Genome-Wide Association Study: A Soybean Example. Methods in Molecular Biology, 2020, 2107, 147-158.	0.9	2
83	High-Throughput Genotyping Technologies in Plant Taxonomy. Methods in Molecular Biology, 2021, 2222, 149-166.	0.9	2
84	Producing High-Quality Single Nucleotide Polymorphism Data for Genome-Wide Association Studies. Methods in Molecular Biology, 2022, , 153-159.	0.9	2
85	Evaluating Plant Gene Models Using Machine Learning. Plants, 2022, 11, 1619.	3.5	2
86	Skim-Based Genotyping by Sequencing Using a Double Haploid Population to Call SNPs, Infer Gene Conversions, and Improve Genome Assemblies. Methods in Molecular Biology, 2016, 1374, 285-292.	0.9	1
87	Genome Analysis of the Broad Host Range Necrotroph Nalanthamala psidii Highlights Genes Associated With Virulence. Frontiers in Plant Science, 2022, 13, 811152.	3.6	1
88	In silico integration of disease resistance QTL, genes and markers with the Brassica juncea physical map. Molecular Breeding, 2022, 42, .	2.1	1
89	Genomics of Salinity. , 2016, , 179-194.		0
90	Daisychain: Search and Interactive Visualisation of Homologs in Genome Assemblies. Agronomy, 2021, 11, 2587.	3.0	0