Philipp E. Bayer

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

86 papers	5,290 citations	28 h-index	72 g-index
103 ext. papers	8,333 ext. citations	7.8 avg, IF	5.51 L-index

#	Paper	IF	Citations
86	Plant genetics. Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. *Science*, **2014**, 345, 950-3	33.3	1348
85	Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science*, **2018**, 361,	33.3	1296
84	The transcriptional landscape of polyploid wheat. *Science*, **2018**, 361,	33.3	368
83	The pangenome of an agronomically important crop plant Brassica oleracea. *Nature Communications*, **2016**, 7, 13390	17.4	240
82	The pangenome of hexaploid bread wheat. *Plant Journal*, **2017**, 90, 1007-1013	6.9	206
81	A reference genome for pea provides insight into legume genome evolution. *Nature Genetics*, **2019**, 51, 1411-1422	36.3	157
80	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid Brassica napus. *Plant Biotechnology Journal*, **2018**, 16, 1265-1274	11.6	130
79	Plant pan-genomes are the new reference. *Nature Plants*, **2020**, 6, 914-920	11.5	129
78	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	11.6	123
77	Assembly and comparison of two closely related Brassica napus genomes. *Plant Biotechnology Journal*, **2017**, 15, 1602-1610	11.6	103
76	Climate change and the need for agricultural adaptation. *Current Opinion in Plant Biology*, **2020**, 56, 197-202	7.7	64
75	Variation in abundance of predicted resistance genes in the Brassica oleracea pangenome. *Plant Biotechnology Journal*, **2019**, 17, 789-800	11.6	60
74	Pangenomics Comes of Age: From Bacteria to Plant and Animal Applications. *Trends in Genetics*, **2020**, 36, 132-145	8.5	57
73	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, 1039-47	6	52
72	Improvements in Genomic Technologies: Application to Crop Genomics. *Trends in Biotechnology*, **2017**, 35, 547-558	15.1	50
71	openSNP--a crowdsourced web resource for personal genomics. *PLoS ONE*, **2014**, 9, e89204	3.7	49
70	Adapting legume crops to climate change using genomic approaches. *Plant, Cell and Environment*, **2019**, 42, 6-19	8.4	43

69	Plant pangenomics: approaches, applications and advancements. *Current Opinion in Plant Biology*, **2020**, 54, 18-25	9.9	41
68	The Genome of a Southern Hemisphere Seagrass Species (Zostera muelleri). *Plant Physiology*, **2016**, 172, 272-83	6.6	41
67	Characterization of disease resistance genes in the Brassica napus pangenome reveals significant structural variation. *Plant Biotechnology Journal*, **2020**, 18, 969-982	11.6	41
66	Genome-Wide Association Study of Genetic Control of Seed Fatty Acid Biosynthesis in. *Frontiers in Plant Science*, **2016**, 7, 2062	6.2	38
65	Genome-wide identification and comparative analysis of NBS-LRR resistance genes in Brassica napus. *Crop and Pasture Science*, **2018**, 69, 72	2.2	37
64	Trait associations in the pangenome of pigeon pea (Cajanus cajan). *Plant Biotechnology Journal*, **2020**, 18, 1946-1954	11.6	36
63	INDEL variation in the regulatory region of the major flowering time gene LanFTc1 is associated with vernalization response and flowering time in narrow-leafed lupin (Lupinus angustifolius L.). *Plant, Cell and Environment*, **2019**, 42, 174-187	8.4	35
62	Exploring the genetic and adaptive diversity of a pan-Mediterranean crop wild relative: narrow-leafed lupin. *Theoretical and Applied Genetics*, **2018**, 131, 887-901	6	34
61	Identification and characterization of more than 4 million intervarietal SNPs across the group 7 chromosomes of bread wheat. *Plant Biotechnology Journal*, **2015**, 13, 97-104	11.6	32
60	Construction and comparison of three reference-quality genome assemblies for soybean. *Plant Journal*, **2019**, 100, 1066-1082	6.9	32
59	Bias in resistance gene prediction due to repeat masking. *Nature Plants*, **2018**, 4, 762-765	11.5	30
58	Acclimation to different depths by the marine angiosperm Posidonia oceanica: transcriptomic and proteomic profiles. *Frontiers in Plant Science*, **2013**, 4, 195	6.2	27
57	High-resolution molecular karyotyping uncovers pairing between ancestrally related Brassica chromosomes. *New Phytologist*, **2014**, 202, 964-974	9.8	25
56	Centromere Locations in Brassica A and C Genomes Revealed Through Half-Tetrad Analysis. *Genetics*, **2016**, 202, 513-23	4	23
55	Skim-based genotyping by sequencing. *Methods in Molecular Biology*, **2015**, 1245, 257-70	1.4	20
54	The western Mediterranean region provided the founder population of domesticated narrow-leafed lupin. *Theoretical and Applied Genetics*, **2018**, 131, 2543-2554	6	20
53	An advanced reference genome of Trifolium subterraneum L. reveals genes related to agronomic performance. *Plant Biotechnology Journal*, **2017**, 15, 1034-1046	11.6	17
52	High intraspecific diversity of Restorer-of-fertility-like genes in barley. *Plant Journal*, **2019**, 97, 281-295	6.9	17

51	CropSNPdb: a database of SNP array data for Brassica crops and hexaploid bread wheat. *Plant Journal*, **2019**, 98, 142-152	6.9	16
50	Resistance Gene Analogs in the Brassicaceae: Identification, Characterization, Distribution, and Evolution. *Plant Physiology*, **2020**, 184, 909-922	6.6	15
49	Fast-forward breeding for a food-secure world. *Trends in Genetics*, **2021**, 37, 1124-1136	8.5	15
48	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. *Scientific Data*, **2021**, 8, 50	8.2	13
47	Induced Methylation in Plants as a Crop Improvement Tool: Progress and Perspectives. *Agronomy*, **2020**, 10, 1484	3.6	11
46	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. *Plant Genome*, **2021**, e20109	4.4	11
45	An efficient approach to BAC based assembly of complex genomes. *Plant Methods*, **2016**, 12, 2	5.8	10
44	Genome-wide identification and comparative analysis of resistance genes in Brassica juncea. *Molecular Breeding*, **2020**, 40, 1	3.4	10
43	The pangenome of banana highlights differences between genera and genomes. *Plant Genome*, **2021**, e20100	4.4	10
42	Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution. *Journal of Experimental Botany*, **2018**, 69, 3689-3702	7	9
41	Genome-Wide Identification and Evolution of Receptor-Like Kinases (RLKs) and Receptor like Proteins (RLPs) in. *Biology*, **2020**, 10,	4.9	9
40	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	11.6	9
39	Maize Yield Prediction at an Early Developmental Stage Using Multispectral Images and Genotype Data for Preliminary Hybrid Selection. *Remote Sensing*, **2021**, 13, 3976	5	8
38	Establishing a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia. *Briefings in Bioinformatics*, **2019**, 20, 384-389	13.4	8
37	Machine learning in agriculture: from silos to marketplaces. *Plant Biotechnology Journal*, **2021**, 19, 648-650	11.6	8
36	runBNG: a software package for BioNano genomic analysis on the command line. *Bioinformatics*, **2017**, 33, 3107-3109	7.2	7
35	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	6.2	7
34	Genotype-Environment mismatch of kelp forests under climate change. *Molecular Ecology*, **2021**, 30, 3730-3746	5.7	7

33	Current status of structural variation studies in plants. *Plant Biotechnology Journal*, **2021**, 19, 2153-2163	11.6	7
32	Modelling of gene loss propensity in the pangenomes of three Brassica species suggests different mechanisms between polyploids and diploids. *Plant Biotechnology Journal*, **2021**, 19, 2488-2500	11.6	7
31	BioNanoAnalyst: a visualisation tool to assess genome assembly quality using BioNano data. *BMC Bioinformatics*, **2017**, 18, 323	3.6	6
30	Frontiers in Dissecting and Managing Diseases: From Reference-Based RGA Candidate Identification to Building Pan-RGAomes. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	6
29	Large-Scale Structural Variation Detection in Subterranean Clover Subtypes Using Optical Mapping. *Frontiers in Plant Science*, **2018**, 9, 971	6.2	6
28	Effect of Leptosphaeria maculans Infection on Promoter DNA Methylation of Defence Genes in Brassica napus. *Agronomy*, **2020**, 10, 1072	3.6	4
27	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	6	4
26	The application of pangenomics and machine learning in genomic selection in plants. *Plant Genome*, **2021**, 14, e20112	4.4	4
25	Genomic rearrangements have consequences for introgression breeding as revealed by genome assemblies of wild and cultivated lentil species		4
24	QTL Genetic Mapping Study for Traits Affecting Meal Quality in Winter Oilseed Rape (L.). *Genes*, **2021**, 12,	4.2	4
23	Resources for image-based high-throughput phenotyping in crops and data sharing challenges. *Plant Physiology*, **2021**, 187, 699-715	6.6	3
22	Amborella gene presence/absence variation is associated with abiotic stress responses that may contribute to environmental adaptation. *New Phytologist*, **2021**,	9.8	3
21	Legume Pangenome Construction Using an Iterative Mapping and Assembly Approach. *Methods in Molecular Biology*, **2020**, 2107, 35-47	1.4	3
20	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**,	11.6	2
19	Pangenomics in crop improvement-from coding structural variations to finding regulatory variants with pangenome graphs.. *Plant Genome*, **2021**, e20177	4.4	2
18	Genetic Diversity Linked to Haplotype Variation in the World Core Collection of for Boron Toxicity Tolerance Provides Valuable Markers for Pasture Breeding. *Frontiers in Plant Science*, **2019**, 10, 1043	6.2	1
17	Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus cqProt-003.. *Theoretical and Applied Genetics*, **2022**, 135, 1443	6	1
16	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, 285-92	1.4	1

15	Marine heatwaves have minimal influence on the quality of adult Sydney rock oyster flesh. *Science of the Total Environment*, **2021**, 795, 148846	10.2	1
14	Wheat Panache - a pangenome graph database representing presence/absence variation across 16 bread wheat genomes		1
13	Expanding Gene-Editing Potential in Crop Improvement with Pangenomes.. *International Journal of Molecular Sciences*, **2022**, 23,	6.3	1
12	Brassica napus genes Rlm4 and Rlm7, conferring resistance to Leptosphaeria maculans, are alleles of the Rlm9 wall-associated kinase-like resistance locus		1
11	Producing High-Quality Single Nucleotide Polymorphism Data for Genome-Wide Association Studies. *Methods in Molecular Biology*, **2022**, 153-159	1.4	1
10	Genome-Wide Association Studies in Plants1-7		0
9	Method for Genome-Wide Association Study: A Soybean Example. *Methods in Molecular Biology*, **2020**, 2107, 147-158	1.4	0
8	High-Throughput Genotyping Technologies in Plant Taxonomy. *Methods in Molecular Biology*, **2021**, 2222, 149-166	1.4	0
7	Machine learning models outperform deep learning models, provide interpretation and facilitate feature selection for soybean trait prediction.. *BMC Plant Biology*, **2022**, 22, 180	5.3	0
6	Mining of Cloned Disease Resistance Gene Homologs (CDRHs) in Brassica Species and Arabidopsis thaliana. *Biology*, **2022**, 11, 821	4.9	0
5	An SGSGeneloss-Based Method for Constructing a Gene Presence/Absence Table Using Mosdepth. *Methods in Molecular Biology*, **2022**, 73-80	1.4	0
4	Genomics of Salinity **2016**, 179-194		
3	Genome Analysis of the Broad Host Range Necrotroph Highlights Genes Associated With Virulence.. *Frontiers in Plant Science*, **2022**, 13, 811152	6.2	
2	Daisychain: Search and Interactive Visualisation of Homologs in Genome Assemblies. *Agronomy*, **2021**, 11, 2587	3.6	
1	Searching for Homologous Genes Using Daisychain. *Methods in Molecular Biology*, **2022**, 95-101	1.4	