

# Philipp E. Bayer

## List of Publications by Year in descending order

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Version: 2024-02-01

90  
papers

9,988  
citations

109321

35  
h-index

48315

88  
g-index

103  
all docs

103  
docs citations

103  
times ranked

8617  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. <i>Plant Genome</i> , 2022, 15, e20109.	2.8	53
2	The pangenome of banana highlights differences between genera and genomes. <i>Plant Genome</i> , 2022, 15, e20100.	2.8	37
3	<i>Amborella</i> gene presence/absence variation is associated with abiotic stress responses that may contribute to environmental adaptation. <i>New Phytologist</i> , 2022, 233, 1548-1555.	7.3	16
4	Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus cqProt-003. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1443-1455.	3.6	13
5	Genome Analysis of the Broad Host Range Necrotroph <i>Nalanthamala psidii</i> Highlights Genes Associated With Virulence. <i>Frontiers in Plant Science</i> , 2022, 13, 811152.	3.6	1
6	Pangenomes as a Resource to Accelerate Breeding of Under-Utilised Crop Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2671.	4.1	14
7	Expanding Gene-Editing Potential in Crop Improvement with Pangenomes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2276.	4.1	12
8	<i>Brassica napus</i> genes <i>Rlm4</i> and <i>Rlm7</i> , conferring resistance to <i>Leptosphaeria maculans</i> , are alleles of the <i>Rlm9</i> wall-associated kinase-like resistance locus. <i>Plant Biotechnology Journal</i> , 2022, 20, 1229-1231.	8.3	24
9	Machine learning models outperform deep learning models, provide interpretation and facilitate feature selection for soybean trait prediction. <i>BMC Plant Biology</i> , 2022, 22, 180.	3.6	15
10	Pangenomics in crop improvement—from coding structural variations to finding regulatory variants with pangenome graphs. <i>Plant Genome</i> , 2022, 15, e20177.	2.8	33
11	Genetic and Genomic Resources for Soybean Breeding Research. <i>Plants</i> , 2022, 11, 1181.	3.5	5
12	Mining of Cloned Disease Resistance Gene Homologs (CDRHs) in Brassica Species and <i>Arabidopsis thaliana</i> . <i>Biology</i> , 2022, 11, 821.	2.8	4
13	Plant Genotype to Phenotype Prediction Using Machine Learning. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	21
14	Wheat Panache: A pangenome graph database representing presence-absence variation across sixteen bread wheat genomes. <i>Plant Genome</i> , 2022, 15, .	2.8	16
15	Extensive polyploid clonality was a successful strategy for seagrass to expand into a newly submerged environment. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	2.6	27
16	Producing High-Quality Single Nucleotide Polymorphism Data for Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2022, , 153-159.	0.9	2
17	Evaluating Plant Gene Models Using Machine Learning. <i>Plants</i> , 2022, 11, 1619.	3.5	2
18	An SGS Geneloss-Based Method for Constructing a Gene Presence-Absence Table Using Mosdepth. <i>Methods in Molecular Biology</i> , 2022, , 73-80.	0.9	3

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19	In silico integration of disease resistance QTL, genes and markers with the Brassica juncea physical map. <i>Molecular Breeding</i> , 2022, 42, .	2.1	1
20	Machine learning in agriculture: from silos to marketplaces. <i>Plant Biotechnology Journal</i> , 2021, 19, 648-650.	8.3	15
21	Assembly of the non-heading pak choi genome and comparison with the genomes of heading Chinese cabbage and the oilseed yellow sarson. <i>Plant Biotechnology Journal</i> , 2021, 19, 966-976.	8.3	28
22	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021, 8, 50.	5.3	38
23	Candidate Rlm6 resistance genes against <i>Leptosphaeria. maculans</i> identified through a genome-wide association study in <i>Brassica juncea</i> (L.) Czern. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2035-2050.	3.6	5
24	Genotype×Environment mismatch of kelp forests under climate change. <i>Molecular Ecology</i> , 2021, 30, 3730-3746.	3.9	39
25	Resources for image-based high-throughput phenotyping in crops and data sharing challenges. <i>Plant Physiology</i> , 2021, 187, 699-715.	4.8	23
26	The application of pangenomics and machine learning in genomic selection in plants. <i>Plant Genome</i> , 2021, 14, e20112.	2.8	29
27	Current status of structural variation studies in plants. <i>Plant Biotechnology Journal</i> , 2021, 19, 2153-2163.	8.3	65
28	QTL Genetic Mapping Study for Traits Affecting Meal Quality in Winter Oilseed Rape ( <i>Brassica Napus</i> L.). <i>Genes</i> , 2021, 12, 1235.	2.4	11
29	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	8.3	44
30	Fast-forward breeding for a food-secure world. <i>Trends in Genetics</i> , 2021, 37, 1124-1136.	6.7	82
31	Marine heatwaves have minimal influence on the quality of adult Sydney rock oyster flesh. <i>Science of the Total Environment</i> , 2021, 795, 148846.	8.0	9
32	Genome-Wide Identification and Evolution of Receptor-Like Kinases (RLKs) and Receptor like Proteins (RLPs) in <i>Brassica juncea</i> . <i>Biology</i> , 2021, 10, 17.	2.8	20
33	Maize Yield Prediction at an Early Developmental Stage Using Multispectral Images and Genotype Data for Preliminary Hybrid Selection. <i>Remote Sensing</i> , 2021, 13, 3976.	4.0	31
34	High-Throughput Genotyping Technologies in Plant Taxonomy. <i>Methods in Molecular Biology</i> , 2021, 2222, 149-166.	0.9	2
35	Daisychain: Search and Interactive Visualisation of Homologs in Genome Assemblies. <i>Agronomy</i> , 2021, 11, 2587.	3.0	0
36	Characterization of disease resistance genes in the <i>Brassica napus</i> pangenome reveals significant structural variation. <i>Plant Biotechnology Journal</i> , 2020, 18, 969-982.	8.3	83

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37	Pangenomics Comes of Age: From Bacteria to Plant and Animal Applications. <i>Trends in Genetics</i> , 2020, 36, 132-145.	6.7	137
38	Induced Methylation in Plants as a Crop Improvement Tool: Progress and Perspectives. <i>Agronomy</i> , 2020, 10, 1484.	3.0	25
39	Plant pan-genomes are the new reference. <i>Nature Plants</i> , 2020, 6, 914-920.	9.3	302
40	Frontiers in Dissecting and Managing Brassica Diseases: From Reference-Based RGA Candidate Identification to Building Pan-RGAomes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8964.	4.1	14
41	Genome-wide identification and comparative analysis of resistance genes in <i>Brassica juncea</i> . <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	17
42	Resistance Gene Analogs in the Brassicaceae: Identification, Characterization, Distribution, and Evolution. <i>Plant Physiology</i> , 2020, 184, 909-922.	4.8	33
43	Effect of <i>Leptosphaeria maculans</i> Infection on Promoter DNA Methylation of Defence Genes in <i>Brassica napus</i> . <i>Agronomy</i> , 2020, 10, 1072.	3.0	11
44	Trait associations in the pangenome of pigeon pea ( <i>Cajanus cajan</i> ). <i>Plant Biotechnology Journal</i> , 2020, 18, 1946-1954.	8.3	79
45	Climate change and the need for agricultural adaptation. <i>Current Opinion in Plant Biology</i> , 2020, 56, 197-202.	7.1	193
46	Plant pangenomics: approaches, applications and advancements. <i>Current Opinion in Plant Biology</i> , 2020, 54, 18-25.	7.1	88
47	Legume Pangenome Construction Using an Iterative Mapping and Assembly Approach. <i>Methods in Molecular Biology</i> , 2020, 2107, 35-47.	0.9	7
48	Method for Genome-Wide Association Study: A Soybean Example. <i>Methods in Molecular Biology</i> , 2020, 2107, 147-158.	0.9	2
49	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	5.7	113
50	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	21.4	363
51	Genetic Diversity Linked to Haplotype Variation in the World Core Collection of <i>Trifolium subterraneum</i> for Boron Toxicity Tolerance Provides Valuable Markers for Pasture Breeding. <i>Frontiers in Plant Science</i> , 2019, 10, 1043.	3.6	2
52	Variation in abundance of predicted resistance genes in the <i>Brassica oleracea</i> pangenome. <i>Plant Biotechnology Journal</i> , 2019, 17, 789-800.	8.3	92
53	CropSNPdb: a database of SNP array data for Brassica crops and hexaploid bread wheat. <i>Plant Journal</i> , 2019, 98, 142-152.	5.7	21
54	High intraspecific diversity of <i>Restorer</i> and <i>Fertility</i> genes in barley. <i>Plant Journal</i> , 2019, 97, 281-295.	5.7	24

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55	Establishing a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia. <i>Briefings in Bioinformatics</i> , 2019, 20, 384-389.	6.5	11
56	Adapting legume crops to climate change using genomic approaches. <i>Plant, Cell and Environment</i> , 2019, 42, 6-19.	5.7	74
57	INDEL variation in the regulatory region of the major flowering time gene <i>LanFTc1</i> is associated with vernalization response and flowering time in narrow-leaved lupin ( <i>Lupinus angustifolius</i> ) <i>Tj ETQq1 1 05784314 rgt /Over</i>	5.7	114
58	Genome-wide identification and comparative analysis of NBS-LRR resistance genes in <i>Brassica napus</i> . <i>Crop and Pasture Science</i> , 2018, 69, 72.	1.5	70
59	Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution. <i>Journal of Experimental Botany</i> , 2018, 69, 3689-3702.	4.8	27
60	Bias in resistance gene prediction due to repeat masking. <i>Nature Plants</i> , 2018, 4, 762-765.	9.3	58
61	The western Mediterranean region provided the founder population of domesticated narrow-leaved lupin. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2543-2554.	3.6	28
62	Large-Scale Structural Variation Detection in Subterranean Clover Subtypes Using Optical Mapping. <i>Frontiers in Plant Science</i> , 2018, 9, 971.	3.6	10
63	Exploring the genetic and adaptive diversity of a pan-Mediterranean crop wild relative: narrow-leaved lupin. <i>Theoretical and Applied Genetics</i> , 2018, 131, 887-901.	3.6	50
64	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	12.6	768
65	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
66	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1265-1274.	8.3	217
67	The pangenome of hexaploid bread wheat. <i>Plant Journal</i> , 2017, 90, 1007-1013.	5.7	313
68	An advanced reference genome of <i>Trifolium subterraneum</i> L. reveals genes related to agronomic performance. <i>Plant Biotechnology Journal</i> , 2017, 15, 1034-1046.	8.3	38
69	Improvements in Genomic Technologies: Application to Crop Genomics. <i>Trends in Biotechnology</i> , 2017, 35, 547-558.	9.3	72
70	Assembly and comparison of two closely related <i>Brassica napus</i> genomes. <i>Plant Biotechnology Journal</i> , 2017, 15, 1602-1610.	8.3	150
71	runBNC: a software package for BioNano genomic analysis on the command line. <i>Bioinformatics</i> , 2017, 33, 3107-3109.	4.1	10
72	BioNanoAnalyst: a visualisation tool to assess genome assembly quality using BioNano data. <i>BMC Bioinformatics</i> , 2017, 18, 323.	2.6	9

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73	A comprehensive draft genome sequence for lupin ( <i>Lupinus angustifolius</i> ), an emerging health food: insights into plant-microbe interactions and legume evolution. <i>Plant Biotechnology Journal</i> , 2017, 15, 318-330.	8.3	153
74	Climate Clever Clovers: New Paradigm to Reduce the Environmental Footprint of Ruminants by Breeding Low Methanogenic Forages Utilizing Haplotype Variation. <i>Frontiers in Plant Science</i> , 2017, 8, 1463.	3.6	21
75	Genomics of Salinity. , 2016, , 179-194.		0
76	The Genome of a Southern Hemisphere Seagrass Species ( <i>Zostera muelleri</i> ). <i>Plant Physiology</i> , 2016, 172, 272-283.	4.8	88
77	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , 2016, 7, 13390.	12.8	375
78	An efficient approach to BAC based assembly of complex genomes. <i>Plant Methods</i> , 2016, 12, 2.	4.3	22
79	Centromere Locations in <i>Brassica</i> A and C Genomes Revealed Through Half-Tetrad Analysis. <i>Genetics</i> , 2016, 202, 513-523.	2.9	47
80	Genome-Wide Association Study of Genetic Control of Seed Fatty Acid Biosynthesis in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 2062.	3.6	84
81	Skim-Based Genotyping by Sequencing Using a Double Haploid Population to Call SNPs, Infer Gene Conversions, and Improve Genome Assemblies. <i>Methods in Molecular Biology</i> , 2016, 1374, 285-292.	0.9	1
82	High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in <i>Cicer arietinum</i> and <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2015, 128, 1039-1047.	3.6	76
83	Identification and characterization of more than 4 million intervarietal SNPs across the group 7 chromosomes of bread wheat. <i>Plant Biotechnology Journal</i> , 2015, 13, 97-104.	8.3	43
84	Skim-Based Genotyping by Sequencing. <i>Methods in Molecular Biology</i> , 2015, 1245, 257-270.	0.9	39
85	openSNP—A Crowdsourced Web Resource for Personal Genomics. <i>PLoS ONE</i> , 2014, 9, e89204.	2.5	78
86	High-resolution molecular karyotyping uncovers pairing between ancestrally related <i>Brassica</i> chromosomes. <i>New Phytologist</i> , 2014, 202, 964-974.	7.3	31
87	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
88	Acclimation to different depths by the marine angiosperm <i>Posidonia oceanica</i> : transcriptomic and proteomic profiles. <i>Frontiers in Plant Science</i> , 2013, 4, 195.	3.6	38
89	Whole-Genome DNA Methylation Analysis in <i>Brassica rapa</i> subsp. <i>perviridis</i> in Response to <i>Albugo candida</i> Infection. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
90	A pan-genome and chromosome-length reference genome of narrow-leaved lupin ( <i>Lupinus</i> ) <i>Tj ETQqO O O rgBT /Overlock 10 Tf 5 Journal, 0, , .</i>	5.7	9