

Burkhard Steuernagel

List of Publications by Year in descending order

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71
papers

9,047
citations

76322

40
h-index

88628

70
g-index

86
all docs

86
docs citations

86
times ranked

7947
citing authors

#	ARTICLE	IF	CITATIONS
1	Population genomic analysis of <i>Aegilops tauschii</i> identifies targets for bread wheat improvement. <i>Nature Biotechnology</i> , 2022, 40, 422-431.	17.5	102
2	Genome sequences of three <i>Aegilops</i> species of the section Sitopsis reveal phylogenetic relationships and provide resources for wheat improvement. <i>Plant Journal</i> , 2022, 110, 179-192.	5.7	46
3	An Integrated Linkage Map of Three Recombinant Inbred Populations of Pea (<i>Pisum sativum</i> L.). <i>Genes</i> , 2022, 13, 196.	2.4	3
4	<i>Aegilops sharonensis</i> genome-assisted identification of stem rust resistance gene Sr62. <i>Nature Communications</i> , 2022, 13, 1607.	12.8	48
5	Discovery of Resistance Genes in Rye by Targeted Long-Read Sequencing and Association Genetics. <i>Cells</i> , 2022, 11, 1273.	4.1	15
6	MicroRNA-resistant alleles of <i>HOMEODOMAIN-2</i> modify inflorescence branching and increase grain protein content of wheat. <i>Science Advances</i> , 2022, 8, eabn5907.	10.3	19
7	A catalogue of resistance gene homologs and a chromosome-scale reference sequence support resistance gene mapping in winter wheat. <i>Plant Biotechnology Journal</i> , 2022, 20, 1730-1742.	8.3	21
8	The wheat <i>Sr22</i> , <i>Sr33</i> , <i>Sr35</i> and <i>Sr45</i> genes confer resistance against stem rust in barley. <i>Plant Biotechnology Journal</i> , 2021, 19, 273-284.	8.3	14
9	The <i>Aegilops ventricosa</i> 2NvS segment in bread wheat: cytology, genomics and breeding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 529-542.	3.6	48
10	A highly differentiated region of wheat chromosome 7AL encodes a <i>Pm1a</i> immune receptor that recognizes its corresponding <i>AvrPm1a</i> effector from <i>Blumeria graminis</i> . <i>New Phytologist</i> , 2021, 229, 2812-2826.	7.3	72
11	A five-transgene cassette confers broad-spectrum resistance to a fungal rust pathogen in wheat. <i>Nature Biotechnology</i> , 2021, 39, 561-566.	17.5	94
12	A complex resistance locus in <i>Solanum americanum</i> recognizes a conserved <i>Phytophthora</i> effector. <i>Nature Plants</i> , 2021, 7, 198-208.	9.3	62
13	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	21.4	138
14	Wheat <i>Pm4</i> resistance to powdery mildew is controlled by alternative splice variants encoding chimeric proteins. <i>Nature Plants</i> , 2021, 7, 327-341.	9.3	85
15	Identification of specificity-defining amino acids of the wheat immune receptor <i>Pm2</i> and powdery mildew effector <i>AvrPm2</i> . <i>Plant Journal</i> , 2021, 106, 993-1007.	5.7	25
16	Subtelomeric assembly of a multi-gene pathway for antimicrobial defense compounds in cereals. <i>Nature Communications</i> , 2021, 12, 2563.	12.8	51
17	A recombined <i>Sr26</i> and <i>Sr61</i> disease resistance gene stack in wheat encodes unrelated NLR genes. <i>Nature Communications</i> , 2021, 12, 3378.	12.8	39
18	Validation of a novel associative transcriptomics pipeline in <i>Brassica oleracea</i> : identifying candidates for vernalisation response. <i>BMC Genomics</i> , 2021, 22, 539.	2.8	6

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19	High molecular weight glutenin gene diversity in <i>Aegilops tauschii</i> demonstrates unique origin of superior wheat quality. <i>Communications Biology</i> , 2021, 4, 1242.	4.4	14
20	Natural Polymorphisms in <i>Arabidopsis</i> Result in Wide Variation or Loss of the Amylose Component of Starch. <i>Plant Physiology</i> , 2020, 182, 870-881.	4.8	11
21	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	27.8	513
22	Extensive Genetic Variation at the Sr22 Wheat Stem Rust Resistance Gene Locus in the Grasses Revealed Through Evolutionary Genomics and Functional Analyses. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1286-1298.	2.6	6
23	Discovery and characterisation of a new leaf rust resistance gene introgressed in wheat from wild wheat <i>Aegilops peregrina</i> . <i>Scientific Reports</i> , 2020, 10, 7573.	3.3	13
24	The NLR-Annotator Tool Enables Annotation of the Intracellular Immune Receptor Repertoire. <i>Plant Physiology</i> , 2020, 183, 468-482.	4.8	147
25	Stem rust resistance in wheat is suppressed by a subunit of the mediator complex. <i>Nature Communications</i> , 2020, 11, 1123.	12.8	52
26	LYS3 encodes a prolamin-box-binding transcription factor that controls embryo growth in barley and wheat. <i>Journal of Cereal Science</i> , 2020, 93, 102965.	3.7	14
27	Fine mapping of <i>Aegilops peregrina</i> co-segregating leaf and stripe rust resistance genes to distal-most end of 5DS. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1473-1485.	3.6	8
28	The Reference Genome Sequence of <i>Scutellaria baicalensis</i> Provides Insights into the Evolution of Wogonin Biosynthesis. <i>Molecular Plant</i> , 2019, 12, 935-950.	8.3	121
29	Rapid Gene Cloning in Wheat. , 2019, , 65-95.		6
30	The Coiled-Coil NLR <i>Rph1</i> , Confers Leaf Rust Resistance in Barley Cultivar Sudan. <i>Plant Physiology</i> , 2019, 179, 1362-1372.	4.8	53
31	Resistance gene cloning from a wild crop relative by sequence capture and association genetics. <i>Nature Biotechnology</i> , 2019, 37, 139-143.	17.5	280
32	A modified sequence capture approach allowing standard and methylation analyses of the same enriched genomic DNA sample. <i>BMC Genomics</i> , 2018, 19, 250.	2.8	5
33	<i>Rht18</i> Semidwarfism in Wheat Is Due to Increased <i>GA 2-oxidaseA9</i> Expression and Reduced GA Content. <i>Plant Physiology</i> , 2018, 177, 168-180.	4.8	128
34	BED-domain-containing immune receptors confer diverse resistance spectra to yellow rust. <i>Nature Plants</i> , 2018, 4, 662-668.	9.3	194
35	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	12.6	768
36	Chromosome-scale comparative sequence analysis unravels molecular mechanisms of genome dynamics between two wheat cultivars. <i>Genome Biology</i> , 2018, 19, 104.	8.8	54

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37	Rapid Gene Isolation Using MutChromSeq. <i>Methods in Molecular Biology</i> , 2017, 1659, 231-243.	0.9	14
38	Discovery and characterization of two new stem rust resistance genes in <i>Aegilops sharonensis</i> . <i>Theoretical and Applied Genetics</i> , 2017, 130, 1207-1222.	3.6	45
39	A homolog of Blade-On-Petiole 1 and 2 (BOP1/2) controls internode length and homeotic changes of the barley inflorescence. <i>Plant Physiology</i> , 2016, 171, pp.00124.2016.	4.8	41
40	Rapid cloning of disease-resistance genes in plants using mutagenesis and sequence capture. <i>Nature Biotechnology</i> , 2016, 34, 652-655.	17.5	383
41	A pigeonpea gene confers resistance to Asian soybean rust in soybean. <i>Nature Biotechnology</i> , 2016, 34, 661-665.	17.5	87
42	Rapid gene isolation in barley and wheat by mutant chromosome sequencing. <i>Genome Biology</i> , 2016, 17, 221.	8.8	265
43	Chloroplast phylogeny of <i>Triticum/Aegilops</i> species is not incongruent with an ancient homoploid hybrid origin of the ancestor of the bread wheat <i>D</i> genome. <i>New Phytologist</i> , 2015, 208, 9-10.	7.3	28
44	Genome-guided investigation of plant natural product biosynthesis. <i>Plant Journal</i> , 2015, 82, 680-692.	5.7	186
45	The Barley <i>U</i> Gene Encodes a BLADE-ON-PETIOLE-Like Protein That Controls Tillering and Leaf Patterning. <i>Plant Physiology</i> , 2015, 168, 164-174.	4.8	85
46	NLR-parser: rapid annotation of plant NLR complements. <i>Bioinformatics</i> , 2015, 31, 1665-1667.	4.1	103
47	Comprehensive Transcriptome Analysis Unravels the Existence of Crucial Genes Regulating Primary Metabolism during Adventitious Root Formation in <i>Petunia hybrida</i> . <i>PLoS ONE</i> , 2014, 9, e100997.	2.5	38
48	<i>PROTEIN DISULFIDE ISOMERASE LIKE 5-1</i> is a susceptibility factor to plant viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2104-2109.	7.1	85
49	The barley Frost resistance-H2 locus. <i>Functional and Integrative Genomics</i> , 2014, 14, 85-100.	3.5	19
50	High-resolution mapping of the barley Ryd3 locus controlling tolerance to BYDV. <i>Molecular Breeding</i> , 2014, 33, 477-488.	2.1	13
51	A Distorted Circadian Clock Causes Early Flowering and Temperature-Dependent Variation in Spike Development in the <i>Eps-3Am</i> Mutant of Einkorn Wheat. <i>Genetics</i> , 2014, 196, 1253-1261.	2.9	88
52	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788.	12.6	1,479
53	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	12.6	629
54	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms. <i>Plant Physiology</i> , 2014, 164, 412-423.	4.8	77

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55	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	8.8	125
56	Barley whole exome capture: a tool for genomic research in the genus <i>Hordeum</i> and beyond. <i>Plant Journal</i> , 2013, 76, 494-505.	5.7	260
57	Haplotype variability and identification of new functional alleles at the Rdg2a leaf stripe resistance gene locus. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1575-1586.	3.6	9
58	Conserved synteny-based anchoring of the barley genome physical map. <i>Functional and Integrative Genomics</i> , 2013, 13, 339-350.	3.5	10
59	Genomics-based high-resolution mapping of the BaMMV/BaYMV resistance gene rym11 in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 1201-1212.	3.6	28
60	A putative role for amino acid permeases in sink-source communication of barley tissues uncovered by RNA-seq. <i>BMC Plant Biology</i> , 2012, 12, 154.	3.6	46
61	Genome Dynamics Explain the Evolution of Flowering Time CCT Domain Gene Families in the Poaceae. <i>PLoS ONE</i> , 2012, 7, e45307.	2.5	93
62	Induced mutations in circadian clock regulator <i>Mat-a</i> facilitated short-season adaptation and range extension in cultivated barley. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4326-4331.	7.1	163
63	Molecular, phylogenetic and comparative genomic analysis of the cytokinin oxidase/dehydrogenase gene family in the Poaceae. <i>Plant Biotechnology Journal</i> , 2012, 10, 67-82.	8.3	47
64	Frequent Gene Movement and Pseudogene Evolution Is Common to the Large and Complex Genomes of Wheat, Barley, and Their Relatives. <i>Plant Cell</i> , 2011, 23, 1706-1718.	6.6	190
65	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. <i>Plant Cell</i> , 2011, 23, 1249-1263.	6.6	448
66	Sequencing of BAC pools by different next generation sequencing platforms and strategies. <i>BMC Research Notes</i> , 2011, 4, 411.	1.4	13
67	Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21611-21616.	7.1	259
68	Gene Content and Virtual Gene Order of Barley Chromosome 1H. <i>Plant Physiology</i> , 2009, 151, 496-505.	4.8	135
69	De novo 454 sequencing of barcoded BAC pools for comprehensive gene survey and genome analysis in the complex genome of barley. <i>BMC Genomics</i> , 2009, 10, 547.	2.8	69
70	Genes driving potato tuber initiation and growth: identification based on transcriptional changes using the POCI array. <i>Functional and Integrative Genomics</i> , 2008, 8, 329-340.	3.5	114
71	Using Data Warehouse Technology in Crop Plant Bioinformatics. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 145-159.	1.5	4