

Axel Himmelbach

List of Publications by Year in descending order

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Version: 2024-02-01

95
papers

12,565
citations

53660

45
h-index

40881

93
g-index

108
all docs

108
docs citations

108
times ranked

10545
citing authors

#	ARTICLE	IF	CITATIONS
1	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
2	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
3	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	6.0	781
4	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	9.4	576
5	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
6	Relay and control of abscisic acid signaling. <i>Current Opinion in Plant Biology</i> , 2003, 6, 470-479.	3.5	401
7	Genebank genomics highlights the diversity of a global barley collection. <i>Nature Genetics</i> , 2019, 51, 319-326.	9.4	322
8	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	13.7	314
9	Homeodomain protein ATHB6 is a target of the protein phosphatase ABI1 and regulates hormone responses in <i>Arabidopsis</i> . <i>EMBO Journal</i> , 2002, 21, 3029-3038.	3.5	309
10	Evolution of the Grain Dispersal System in Barley. <i>Cell</i> , 2015, 162, 527-539.	13.5	265
11	Anchoring and ordering <sc>NGS</sc> contig assemblies by population sequencing (<sc>POPSEQ</sc>). <i>Plant Journal</i> , 2013, 76, 718-727.	2.8	264
12	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.	2.8	260
13	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. <i>Nature Genetics</i> , 2016, 48, 1024-1030.	9.4	259
14	CRISPR-Cas9 Targeted Mutagenesis Leads to Simultaneous Modification of Different Homoeologous Gene Copies in Polyploid Oilseed Rape (<i>Brassica napus</i>). <i>Plant Physiology</i> , 2017, 174, 935-942.	2.3	257
15	A Set of Modular Binary Vectors for Transformation of Cereals. <i>Plant Physiology</i> , 2007, 145, 1192-1200.	2.3	205
16	The Multigene Family Encoding Germin-Like Proteins of Barley. Regulation and Function in Basal Host Resistance. <i>Plant Physiology</i> , 2006, 142, 181-192.	2.3	181
17	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	3.8	179
18	<i>Six-rowed spike4</i> (<i>Vrs4</i>) controls spikelet determinacy and row-type in barley. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13198-13203.	3.3	140

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19	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
20	Mapping-by-sequencing accelerates forward genetics in barley. <i>Genome Biology</i> , 2014, 15, R78.	13.9	131
21	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	2.4	130
22	ABA signal transduction. <i>Current Opinion in Plant Biology</i> , 1998, 1, 412-418.	3.5	129
23	Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. <i>Nature Genetics</i> , 2016, 48, 1089-1093.	9.4	122
24	Fibrillin expression is regulated by abscisic acid response regulators and is involved in abscisic acid-mediated photoprotection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6061-6066.	3.3	115
25	BARLEX – the Barley Draft Genome Explorer. <i>Molecular Plant</i> , 2015, 8, 964-966.	3.9	114
26	Unlocking the secondary gene pool of barley with next-generation sequencing. <i>Plant Biotechnology Journal</i> , 2014, 12, 1122-1131.	4.1	111
27	Mapping-by-Sequencing Identifies <i>HvPHYTOCHROME C</i> as a Candidate Gene for the early maturity 5 Locus Modulating the Circadian Clock and Photoperiodic Flowering in Barley. <i>Genetics</i> , 2014, 198, 383-396.	1.2	102
28	Promoters of the Barley Germin-Like <i>GER4</i> Gene Cluster Enable Strong Transgene Expression in Response to Pathogen Attack. <i>Plant Cell</i> , 2010, 22, 937-952.	3.1	100
29	Nuclear localization of the mutant protein phosphatase <i>abi1</i> is required for insensitivity towards ABA responses in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2008, 54, 806-819.	2.8	91
30	Signalling of abscisic acid to regulate plant growth. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 1998, 353, 1439-1444.	1.8	89
31	A Distorted Circadian Clock Causes Early Flowering and Temperature-Dependent Variation in Spike Development in the <i>Eps-3A</i> Mutant of Einkorn Wheat. <i>Genetics</i> , 2014, 196, 1253-1261.	1.2	88
32	Presence versus absence of <i>CYP734A50</i> underlies the style-length dimorphism in primroses. <i>ELife</i> , 2016, 5, .	2.8	86
33	<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.	3.3	85
34	The Barley <i>Uniculme4</i> Gene Encodes a BLADE-ON-PETIOLE-Like Protein That Controls Tillering and Leaf Patterning. <i>Plant Physiology</i> , 2015, 168, 164-174.	2.3	85
35	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms. <i>Plant Physiology</i> , 2014, 164, 412-423.	2.3	77
36	Expression of the <i>Arabidopsis</i> Mutant <i>abi1</i> Gene Alters Abscisic Acid Sensitivity, Stomatal Development, and Growth Morphology in Gray Poplars. <i>Plant Physiology</i> , 2009, 151, 2110-2119.	2.3	72

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37	The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119.	13.7	70
38	The <i>abi1-1</i> mutation blocks ABA signaling downstream of cADPR action. <i>Plant Journal</i> , 2003, 34, 307-315.	2.8	69
39	Genes on B chromosomes: Old questions revisited with new tools. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 64-70.	0.9	68
40	A Genome Assembly of the Barley "Transformation Reference"™ Cultivar Golden Promise. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1823-1827.	0.8	61
41	Interaction between Cauliflower Mosaic Virus Inclusion Body Protein and Capsid Protein: Implications for Viral Assembly. <i>Virology</i> , 1996, 217, 147-157.	1.1	59
42	Bulbosum to Go: A Toolbox to Utilize <i>Hordeum vulgare</i> /bulbosum Introgressions for Breeding and Beyond. <i>Molecular Plant</i> , 2015, 8, 1507-1519.	3.9	58
43	Nonhost Resistance of Barley to Different Fungal Pathogens Is Associated with Largely Distinct, Quantitative Transcriptional Responses. <i>Plant Physiology</i> , 2010, 152, 2053-2066.	2.3	56
44	Discovery of genes affecting resistance of barley to adapted and non-adapted powdery mildew fungi. <i>Genome Biology</i> , 2014, 15, 518.	3.8	52
45	Leaf Variegation and Impaired Chloroplast Development Caused by a Truncated CCT Domain Gene in <i>Hordeum vulgare</i> Barley. <i>Plant Cell</i> , 2019, 31, 1430-1445.	3.1	52
46	Rye B chromosomes encode a functional Argonaute-like protein with <i>in vitro</i> slicer activities similar to its A chromosome paralog. <i>New Phytologist</i> , 2017, 213, 916-928.	3.5	51
47	Genetic diversity and relationship between domesticated rye and its wild relatives as revealed through genotyping-by-sequencing. <i>Evolutionary Applications</i> , 2019, 12, 66-77.	1.5	50
48	SSR-seq: Genotyping of microsatellites using next-generation sequencing reveals higher level of polymorphism as compared to traditional fragment size scoring. <i>Ecology and Evolution</i> , 2018, 8, 10817-10833.	0.8	48
49	Global range expansion history of pepper (<i>Capsicum</i> spp.) revealed by over 10,000 genebank accessions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	48
50	<i>Aegilops sharonensis</i> genome-assisted identification of stem rust resistance gene Sr62. <i>Nature Communications</i> , 2022, 13, 1607.	5.8	48
51	Sequencing of Single Pollen Nuclei Reveals Meiotic Recombination Events at Megabase Resolution and Circumvents Segregation Distortion Caused by Postmeiotic Processes. <i>Frontiers in Plant Science</i> , 2017, 8, 1620.	1.7	46
52	Genome sequences of three <i>Aegilops</i> species of the section <i>Sitopsis</i> reveal phylogenetic relationships and provide resources for wheat improvement. <i>Plant Journal</i> , 2022, 110, 179-192.	2.8	46
53	Telomere-mediated truncation of barley chromosomes. <i>Chromosoma</i> , 2012, 121, 181-190.	1.0	41
54	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.	2.3	41

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55	Transgene expression systems in the Triticeae cereals. <i>Journal of Plant Physiology</i> , 2011, 168, 30-44.	1.6	39
56	The INDETERMINATE DOMAIN Protein BROAD LEAF1 Limits Barley Leaf Width by Restricting Lateral Proliferation. <i>Current Biology</i> , 2016, 26, 903-909.	1.8	37
57	COMPOSITUM 1 contributes to the architectural simplification of barley inflorescence via meristem identity signals. <i>Nature Communications</i> , 2020, 11, 5138.	5.8	37
58	Regulation of gene expression by chromosome 5A during cold hardening in wheat. <i>Molecular Genetics and Genomics</i> , 2010, 283, 351-363.	1.0	31
59	Supernumerary B chromosomes of <i>Aegilops speltoides</i> undergo precise elimination in roots early in embryo development. <i>Nature Communications</i> , 2020, 11, 2764.	5.8	30
60	Allele Mining in Barley Genetic Resources Reveals Genes of Race-Non-Specific Powdery Mildew Resistance. <i>Frontiers in Plant Science</i> , 2011, 2, 113.	1.7	27
61	High Resolution Genetic and Physical Mapping of a Major Powdery Mildew Resistance Locus in Barley. <i>Frontiers in Plant Science</i> , 2019, 10, 146.	1.7	27
62	Discovery of multi-Megabase polymorphic inversions by chromosome conformation capture sequencing in large genome plant species. <i>Plant Journal</i> , 2018, 96, 1309-1316.	2.8	26
63	In Situ Hi-C for Plants: An Improved Method to Detect Long-Range Chromatin Interactions. <i>Methods in Molecular Biology</i> , 2019, 1933, 441-472.	0.4	26
64	Female self-incompatibility type in heterostylous <i>Primula</i> is determined by the brassinosteroid-inactivating cytochrome P450 CYP734A50. <i>Current Biology</i> , 2022, 32, 671-676.e5.	1.8	25
65	Detecting major introgressions in wheat and their putative origins using coverage analysis. <i>Scientific Reports</i> , 2022, 12, 1908.	1.6	23
66	Mapping resistance to powdery mildew in barley reveals a large-effect nonhost resistance QTL. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1031-1045.	1.8	22
67	Detecting Large Chromosomal Modifications Using Short Read Data From Genotyping-by-Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 1133.	1.7	22
68	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.	4.1	21
69	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1511-1522.	4.1	20
70	The barley Frost resistance-H2 locus. <i>Functional and Integrative Genomics</i> , 2014, 14, 85-100.	1.4	19
71	Fine mapping and identification of a candidate gene for the barley Un8 true loose smut resistance gene. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1343-1357.	1.8	19
72	Transcriptomic basis for reinforcement of elm antiherbivore defence mediated by insect egg deposition. <i>Molecular Ecology</i> , 2018, 27, 4901-4915.	2.0	18

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73	A High-Density, Sequence-Enriched Genetic Map of <i>Hordeum bulbosum</i> and Its Collinearity to <i>H. vulgare</i> . <i>Plant Genome</i> , 2017, 10, plantgenome2017.06.0049.	1.6	17
74	De Novo Genome Assembly of the Japanese Wheat Cultivar Norin 61 Highlights Functional Variation in Flowering Time and Fusarium-Resistant Genes in East Asian Genotypes. <i>Plant and Cell Physiology</i> , 2021, 62, 8-27.	1.5	16
75	Convergent evidence for a role of WIR1 proteins during the interaction of barley with the powdery mildew fungus <i>Blumeria graminis</i> . <i>Journal of Plant Physiology</i> , 2011, 168, 20-29.	1.6	15
76	The contribution of cis- and trans-acting variants to gene regulation in wild and domesticated barley under cold stress and control conditions. <i>Journal of Experimental Botany</i> , 2020, 71, 2573-2584.	2.4	15
77	A reference-guided TILLING by amplicon-sequencing platform supports forward and reverse genetics in barley. <i>Plant Communications</i> , 2022, 3, 100317.	3.6	15
78	Mutations in the gene of the G β subunit of the heterotrimeric G protein are the cause for the brachytic1 semi-dwarf phenotype in barley and applicable for practical breeding. <i>Hereditas</i> , 2018, 155, 10.	0.5	14
79	Chromosome-scale assembly of wild barley accession ‘‘OUH602’’: G3: <i>Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	14
80	Exome association analysis sheds light onto leaf rust (<i>Puccinia triticina</i>) resistance genes currently used in wheat breeding (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2020, 18, 1396-1408.	4.1	13
81	Plant Sequence Capture Optimised for Illumina Sequencing. <i>Bio-protocol</i> , 2014, 4, .	0.2	11
82	Physical geography, isolation by distance and environmental variables shape genomic variation of wild barley (<i>Hordeum vulgare</i> L. ssp. <i>spontaneum</i>) in the Southern Levant. <i>Heredity</i> , 2022, 128, 107-119.	1.2	10
83	Evolutionarily conserved partial gene duplication in the Triticeae tribe of grasses confers pathogen resistance. <i>Genome Biology</i> , 2018, 19, 116.	3.8	9
84	Genome-wide identification of loci modifying spike-branching in tetraploid wheat. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1925-1943.	1.8	9
85	Dissecting the Genetic Basis of Lateral and Central Spikelet Development and Grain Traits in Intermedium-Spike Barley (<i>Hordeum vulgare</i> Convar. <i>Intermedium</i>). <i>Plants</i> , 2020, 9, 1655.	1.6	7
86	The barley mutant multiflorus2.b reveals quantitative genetic variation for new spikelet architecture. <i>Theoretical and Applied Genetics</i> , 2022, 135, 571-590.	1.8	7
87	Tethered Chromosome Conformation Capture Sequencing in Triticeae: A Valuable Tool for Genome Assembly. <i>Bio-protocol</i> , 2018, 8, e2955.	0.2	6
88	Chromosome-scale assembly of barley cv. ‘‘Haruna Nijo’’™ as a resource for barley genetics. <i>DNA Research</i> , 2022, 29, .	1.5	6
89	Recombination Landscape Divergence Between Populations is Marked by Larger Low-Recombining Regions in Domesticated Rye. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	5
90	Initial Description of the Genome of <i>Aeluropus littoralis</i> , a Halophile Grass. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5

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91	DEFECTIVE ENDOSPERM-D1 (Dee-D1) is crucial for endosperm development in hexaploid wheat. Communications Biology, 2020, 3, 791.	2.0	3
92	Rye B chromosomes differently influence the expression of A chromosome-encoded genes depending on the host species. Chromosome Research, 2022, 30, 335-349.	1.0	3
93	Quantification of Recombination Rate and Segregation Distortion by Genotyping and Sequencing of Single Pollen Nuclei. Methods in Molecular Biology, 2020, 2061, 281-300.	0.4	1
94	Six-rowed wild-growing barleys are hybrids of diverse origins. Plant Journal, 2022, 111, 849-858.	2.8	1
95	Targets of modifying plant growth and development by ABA-mediated signaling. , 2000, , 223-232.		0