

Nils Stein

List of Publications by Year in descending order

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227
papers

28,874
citations

6613

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6131

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all docs

247
docs citations

247
times ranked

16661
citing authors

#	ARTICLE	IF	CITATIONS
1	The barley mutant multiflorus2.b reveals quantitative genetic variation for new spikelet architecture. Theoretical and Applied Genetics, 2022, 135, 571-590.	3.6	7
2	Genome sequences of three <i>Aegilops</i> species of the section Sitopsis reveal phylogenetic relationships and provide resources for wheat improvement. Plant Journal, 2022, 110, 179-192.	5.7	46
3	Chromosome-scale assembly of barley cv. "Haruna Nijo"™ as a resource for barley genetics. DNA Research, 2022, 29, .	3.4	6
4	Aegilops sharonensis genome-assisted identification of stem rust resistance gene Sr62. Nature Communications, 2022, 13, 1607.	12.8	48
5	A reference-guided TILLING by amplicon-sequencing platform supports forward and reverse genetics in barley. Plant Communications, 2022, 3, 100317.	7.7	15
6	Mining for New Sources of Resistance to Powdery Mildew in Genetic Resources of Winter Wheat. Frontiers in Plant Science, 2022, 13, 836723.	3.6	8
7	Prospects of telomere-to-telomere assembly in barley: Analysis of sequence gaps in the MorexV3 reference genome. Plant Biotechnology Journal, 2022, 20, 1373-1386.	8.3	24
8	Transposable Element Populations Shed Light on the Evolutionary History of Wheat and the Complex Co-evolution of Autonomous and Non-autonomous Retrotransposons. Genetics & Genomics Next, 2022, 3, .	1.5	12
9	The barley leaf rust resistance gene Rph3 encodes a predicted membrane protein and is induced upon infection by avirulent pathotypes of Puccinia hordei. Nature Communications, 2022, 13, 2386.	12.8	12
10	A catalogue of resistance gene homologs and a chromosome-scale reference sequence support resistance gene mapping in winter wheat. Plant Biotechnology Journal, 2022, 20, 1730-1742.	8.3	21
11	The mosaic oat genome gives insights into a uniquely healthy cereal crop. Nature, 2022, 606, 113-119.	27.8	70
12	<scp>BaRTv2</scp>: a highly resolved barley reference transcriptome for accurate transcript-specific <scp>RNA</scp>-seq quantification. Plant Journal, 2022, 111, 1183-1202.	5.7	17
13	Recombination Landscape Divergence Between Populations is Marked by Larger Low-Recombining Regions in Domesticated Rye. Molecular Biology and Evolution, 2022, 39, .	8.9	5
14	Six-rowed wild-growing barleys are hybrids of diverse origins. Plant Journal, 2022, 111, 849-858.	5.7	1
15	Why 2022 is a revolutionary year for potato genomics. Molecular Plant, 2022, , .	8.3	0
16	High-resolution mapping of Rym14Hb, a wild relative resistance gene to barley yellow mosaic disease. Theoretical and Applied Genetics, 2021, 134, 823-833.	3.6	10
17	The Aegilops ventricosa 2NvS segment in bread wheat: cytology, genomics and breeding. Theoretical and Applied Genetics, 2021, 134, 529-542.	3.6	48
18	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. Plant and Cell Physiology, 2021, 62, 8-27.	3.1	16

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19	A high-quality genome assembly highlights rye genomic characteristics and agronomically important genes. <i>Nature Genetics</i> , 2021, 53, 574-584.	21.4	164
20	Genomic prediction models trained with historical records enable populating the German ex situ genebank bio-digital resource center of barley (<i>Hordeum</i> Åsp.) with information on resistances to soilborne barley mosaic viruses. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2181-2196.	3.6	5
21	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	21.4	138
22	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	6.6	180
23	ATP-Dependent Clp Protease Subunit C1, HvClpC1, Is a Strong Candidate Gene for Barley Variegation Mutant luteostrians as Revealed by Genetic Mapping and Genomic Re-sequencing. <i>Frontiers in Plant Science</i> , 2021, 12, 664085.	3.6	2
24	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. <i>Science</i> , 2021, 372, 984-989.	12.6	132
25	The Arabidopsis AAC Proteins CIL and CIA2 Are Sub-functionalized Paralogs Involved in Chloroplast Development. <i>Frontiers in Plant Science</i> , 2021, 12, 681375.	3.6	6
26	Improved genome assembly and pan-genome provide key insights into eggplant domestication and breeding. <i>Plant Journal</i> , 2021, 107, 579-596.	5.7	56
27	Chromosome-scale assembly of wild barley accession â€œOUH602â€œ G3: <i>Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	14
28	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, .	7.1	48
29	The reinvention of potato. <i>Cell Research</i> , 2021, 31, 1144-1145.	12.0	2
30	Mutation of the ALBOSTRIANS Ohnologous Gene HvCMF3 Impairs Chloroplast Development and Thylakoid Architecture in Barley. <i>Frontiers in Plant Science</i> , 2021, 12, 732608.	3.6	7
31	Building pan-genome infrastructures for crop plants and their use in association genetics. <i>DNA Research</i> , 2021, 28, .	3.4	57
32	Assembling the Rye Genome. <i>Compendium of Plant Genomes</i> , 2021, , 101-116.	0.5	0
33	COMPOSITUM 1 contributes to the architectural simplification of barley inflorescence via meristem identity signals. <i>Nature Communications</i> , 2020, 11, 5138.	12.8	37
34	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
35	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	27.8	513
36	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	8.3	50

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37	BRIDGE – A Visual Analytics Web Tool for Barley Genebank Genomics. <i>Frontiers in Plant Science</i> , 2020, 11, 701.	3.6	31
38	High Resolution Mapping of a <i>Hordeum bulbosum</i> -Derived Powdery Mildew Resistance Locus in Barley Using Distinct Homologous Introgression Lines. <i>Frontiers in Plant Science</i> , 2020, 11, 225.	3.6	13
39	Suitability of Single-Nucleotide Polymorphism Arrays Versus Genotyping-By-Sequencing for Genebank Genomics in Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 42.	3.6	26
40	A Genome Assembly of the Barley –Transformation Reference–™ Cultivar Golden Promise. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1823-1827.	1.8	61
41	Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding. <i>Nature Genetics</i> , 2019, 51, 1076-1081.	21.4	176
42	Detecting Large Chromosomal Modifications Using Short Read Data From Genotyping-by-Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 1133.	3.6	22
43	Exome sequences and multi–environment field trials elucidate the genetic basis of adaptation in barley. <i>Plant Journal</i> , 2019, 99, 1172-1191.	5.7	50
44	A Comparison of Mainstream Genotyping Platforms for the Evaluation and Use of Barley Genetic Resources. <i>Frontiers in Plant Science</i> , 2019, 10, 544.	3.6	66
45	Leaf Variegation and Impaired Chloroplast Development Caused by a Truncated CCT Domain Gene in <i>Hordeum bulbosum</i> Barley. <i>Plant Cell</i> , 2019, 31, 1430-1445.	6.6	52
46	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.	21.4	230
47	The highly divergent <i>Jekyll</i> genes, required for sexual reproduction, are lineage specific for the related grass tribes Triticeae and Bromeae. <i>Plant Journal</i> , 2019, 98, 961-974.	5.7	7
48	High Resolution Genetic and Physical Mapping of a Major Powdery Mildew Resistance Locus in Barley. <i>Frontiers in Plant Science</i> , 2019, 10, 146.	3.6	27
49	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	21.4	576
50	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.	0.9	26
51	Progress in Sequencing of Triticeae Genomes and Future Uses. , 2019, , 19-47.		2
52	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	15
53	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	8.8	179
54	Genebank genomics highlights the diversity of a global barley collection. <i>Nature Genetics</i> , 2019, 51, 319-326.	21.4	322

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55	Prospects of pan-genomics in barley. Theoretical and Applied Genetics, 2019, 132, 785-796.	3.6	38
56	TILLING in Barley. Methods in Molecular Biology, 2019, 1900, 73-94.	0.9	14
57	High intraspecific diversity of <i>Restorer</i> and <i>fertility</i> genes in barley. Plant Journal, 2019, 97, 281-295.	5.7	24
58	Origin and evolution of qingke barley in Tibet. Nature Communications, 2018, 9, 5433.	12.8	141
59	Discovery of multi-megabase polymorphic inversions by chromosome conformation capture sequencing in large genome plant species. Plant Journal, 2018, 96, 1309-1316.	5.7	26
60	Genomic approaches for studying crop evolution. Genome Biology, 2018, 19, 140.	8.8	54
61	Evolutionarily conserved partial gene duplication in the Triticeae tribe of grasses confers pathogen resistance. Genome Biology, 2018, 19, 116.	8.8	9
62	High-throughput development of <i>SSR</i> marker candidates and their chromosomal assignment in rye (<i>Secale cereale</i> L.). Plant Breeding, 2018, 137, 561-572.	1.9	14
63	Mutations in the gene of the $G\beta$ subunit of the heterotrimeric G protein are the cause for the brachytic1 semi-dwarf phenotype in barley and applicable for practical breeding. Hereditas, 2018, 155, 10.	1.4	14
64	Molecular Mapping and Cloning of Genes and QTLs. Compendium of Plant Genomes, 2018, , 139-154.	0.5	7
65	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768
66	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
67	Barley Genome Sequencing and Assembly – A First Version Reference Sequence. Compendium of Plant Genomes, 2018, , 57-71.	0.5	3
68	The pseudogenes of barley. Plant Journal, 2018, 93, 502-514.	5.7	14
69	Tethered Chromosome Conformation Capture Sequencing in Triticeae: A Valuable Tool for Genome Assembly. Bio-protocol, 2018, 8, e2955.	0.4	6
70	Sequence diversification in recessive alleles of two host factor genes suggests adaptive selection for bymovirus resistance in cultivated barley from East Asia. Theoretical and Applied Genetics, 2017, 130, 331-344.	3.6	21
71	Natural diversity of inflorescence architecture traces cryptic domestication genes in barley (<i>Hordeum vulgare</i> L.). Genetic Resources and Crop Evolution, 2017, 64, 843-853.	1.6	11
72	CRISPR-Cas9 Targeted Mutagenesis Leads to Simultaneous Modification of Different Homoeologous Gene Copies in Polyploid Oilseed Rape (<i>Brassica napus</i>). Plant Physiology, 2017, 174, 935-942.	4.8	257

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73	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	27.8	1,365
74	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	5.3	130
75	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	12.6	781
76	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017, 8, 22.	3.6	49
77	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.	2.8	17
78	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
79	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1511-1522.	8.3	20
80	Collinearity of homoeologous group 3 chromosomes in the genus <i>Hordeum</i> and <i>Secale cereale</i> as revealed by 3H-derived FISH analysis. <i>Chromosome Research</i> , 2016, 24, 231-242.	2.2	17
81	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. <i>Nature Genetics</i> , 2016, 48, 1024-1030.	21.4	259
82	Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. <i>Nature Genetics</i> , 2016, 48, 1089-1093.	21.4	122
83	The INDETERMINATE DOMAIN Protein BROAD LEAF1 Limits Barley Leaf Width by Restricting Lateral Proliferation. <i>Current Biology</i> , 2016, 26, 903-909.	3.9	37
84	Mitogen-Activated Protein Kinase Kinase 3 Regulates Seed Dormancy in Barley. <i>Current Biology</i> , 2016, 26, 775-781.	3.9	85
85	Comparative study of the structure of chromosome 1 _R derived from <i>Secale montanum</i> and <i>Secale cereale</i> . <i>Plant Breeding</i> , 2015, 134, 675-683.	1.9	3
86	Cytogenetic mapping with centromeric bacterial artificial chromosomes contigs shows that this recombination-poor region comprises more than half of barley chromosome 3 _H . <i>Plant Journal</i> , 2015, 84, 385-394.	5.7	32
87	Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.04.0021.	2.8	45
88	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.	4.8	85
89	High-throughput physical map anchoring via BAC-pool sequencing. <i>BMC Plant Biology</i> , 2015, 15, 99.	3.6	8
90	Dissecting spatiotemporal biomass accumulation in barley under different water regimes using high-throughput image analysis. <i>Plant, Cell and Environment</i> , 2015, 38, 1980-1996.	5.7	76

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91	Evolution of the Grain Dispersal System in Barley. <i>Cell</i> , 2015, 162, 527-539.	28.9	265
92	Chromosomal genomics facilitates fine mapping of a Russian wheat aphid resistance gene. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1373-1383.	3.6	7
93	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.	3.6	19
94	Behavior of a modified Dissociation element in barley: a tool for genetic studies and for breeding transgenic barley. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	4
95	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	8.8	256
96	Sequencing of 15,622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	5.7	36
97	Genetic linkage facilitates cloning of Ert-m regulating plant architecture in barley and identified a strong candidate of Ant1 involved in anthocyanin biosynthesis. <i>Plant Molecular Biology</i> , 2015, 88, 609-626.	3.9	14
98	Point mutation impairs centromeric CENH3 loading and induces haploid plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11211-11216.	7.1	126
99	BARLEX – the Barley Draft Genome Explorer. <i>Molecular Plant</i> , 2015, 8, 964-966.	8.3	114
100	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.	8.3	58
101	High-resolution genetic mapping and physical map construction for the fertility restorer Rfm1 locus in barley. <i>Theoretical and Applied Genetics</i> , 2015, 128, 283-290.	3.6	20
102	Transposable Element Junctions in Marker Development and Genomic Characterization of Barley. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0036.	2.8	9
103	Genetic anchoring of whole-genome shotgun assemblies. <i>Frontiers in Genetics</i> , 2014, 5, 208.	2.3	48
104	FISH Mapping for Physical Map Improvement in the Large Genome of Barley: A Case Study on Chromosome 2H. <i>Cytogenetic and Genome Research</i> , 2014, 143, 275-279.	1.1	3
105	Discovery of genes affecting resistance of barley to adapted and non-adapted powdery mildew fungi. <i>Genome Biology</i> , 2014, 15, 518.	8.8	52
106	Unlocking the secondary gene pool of barley with next-generation sequencing. <i>Plant Biotechnology Journal</i> , 2014, 12, 1122-1131.	8.3	111
107	Biotechnological Approaches to Barley Improvement. <i>Biotechnology in Agriculture and Forestry</i> , 2014, , .	0.2	7
108	PROTEIN DISULFIDE ISOMERASE LIKE 5-1 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

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109	Kmasker - A Tool for in silico Prediction of Single-Copy FISH Probes for the Large-Genome Species <i>Hordeum vulgare</i> . <i>Cytogenetic and Genome Research</i> , 2014, 142, 66-78.	1.1	23
110	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.	2.9	102
111	Plant genome sequencing – applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014, 26, 31-37.	6.6	164
112	The barley Frost resistance-H2 locus. <i>Functional and Integrative Genomics</i> , 2014, 14, 85-100.	3.5	19
113	High-resolution mapping of the barley Ryd3 locus controlling tolerance to BYDV. <i>Molecular Breeding</i> , 2014, 33, 477-488.	2.1	13
114	Reduced chlorophyll biosynthesis in heterozygous barley magnesium chelatase mutants. <i>Plant Physiology and Biochemistry</i> , 2014, 78, 10-14.	5.8	17
115	Whole-genome profiling and shotgun sequencing delivers an anchored, gene-decorated, physical map assembly of bread wheat chromosome 6A. <i>Plant Journal</i> , 2014, 79, 334-347.	5.7	45
116	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
117	Mapping-by-sequencing accelerates forward genetics in barley. <i>Genome Biology</i> , 2014, 15, R78.	9.6	131
118	Analysis of bymovirus resistance genes on proximal barley chromosome 4HL provides the basis for precision breeding for BaMMV/BaYMV resistance. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1625-1634.	3.6	16
119	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
120	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014, 345, 1250091.	12.6	318
121	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	12.6	629
122	The complete genome of <i>Blastobotrys (Arxula) adenivorans</i> LS3 - a yeast of biotechnological interest. <i>Biotechnology for Biofuels</i> , 2014, 7, 66.	6.2	57
123	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
124	Advances in Sequencing the Barley Genome. , 2014, , 391-403.		3
125	Sequencing of Chloroplast Genomes from Wheat, Barley, Rye and Their Relatives Provides a Detailed Insight into the Evolution of the Triticeae Tribe. <i>PLoS ONE</i> , 2014, 9, e85761.	2.5	190
126	Plant Sequence Capture Optimised for Illumina Sequencing. <i>Bio-protocol</i> , 2014, 4, .	0.4	11

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127	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	8.8	125
128	Gene-based high-density mapping of the gene <i>rym7</i> conferring resistance to Barley mild mosaic virus (BaMMV). <i>Molecular Breeding</i> , 2013, 32, 27-37.	2.1	20
129	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
130	Haplotype variability and identification of new functional alleles at the <i>Rdg2a</i> leaf stripe resistance gene locus. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1575-1586.	3.6	9
131	Nitrogen-metabolism related genes in barley - haplotype diversity, linkage mapping and associations with malting and kernel quality parameters. <i>BMC Genetics</i> , 2013, 14, 77.	2.7	5
132	Conserved synteny-based anchoring of the barley genome physical map. <i>Functional and Integrative Genomics</i> , 2013, 13, 339-350.	3.5	10
133	Mapping nonrecombining regions in barley using multicolor FISH. <i>Chromosome Research</i> , 2013, 21, 739-751.	2.2	37
134	Anchoring and ordering <i>NGS</i> contig assemblies by population sequencing (<i>POPSEQ</i>). <i>Plant Journal</i> , 2013, 76, 718-727.	5.7	264
135	Comparative analysis of genome composition in Triticeae reveals strong variation in transposable element dynamics and nucleotide diversity. <i>Plant Journal</i> , 2013, 73, 347-356.	5.7	43
136	Divergence of expression pattern contributed to neofunctionalization of duplicated <i>HD-Zip</i> transcription factor in barley. <i>New Phytologist</i> , 2013, 197, 939-948.	7.3	67
137	Genomics-based high-resolution mapping of the BaMMV/BaYMV resistance gene <i>rym11</i> in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 1201-1212.	3.6	28
138	A versatile fluorescence-based multiplexing assay for CAPS genotyping on capillary electrophoresis systems. <i>Molecular Breeding</i> , 2013, 32, 61-69.	2.1	18
139	Feeding the future. <i>Nature</i> , 2013, 499, 23-24.	27.8	464
140	Reticulate Evolution of the Rye Genome. <i>Plant Cell</i> , 2013, 25, 3685-3698.	6.6	194
141	<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.	7.1	140
142	Application of Genotyping-by-Sequencing on Semiconductor Sequencing Platforms: A Comparison of Genetic and Reference-Based Marker Ordering in Barley. <i>PLoS ONE</i> , 2013, 8, e76925.	2.5	186
143	Advances in BAC-Based Physical Mapping and Map Integration Strategies in Plants. <i>Journal of Biomedicine and Biotechnology</i> , 2012, 2012, 1-11.	3.0	37
144	Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13343-13346.	7.1	173

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145	Integrating cereal genomics to support innovation in the Triticeae. Functional and Integrative Genomics, 2012, 12, 573-583.	3.5	39
146	Clusters of genes encoding fructan biosynthesizing enzymes in wheat and barley. Plant Molecular Biology, 2012, 80, 299-314.	3.9	29
147	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	27.8	1,416
148	Natural variation in a homolog of Antirrhinum CENTRORADIALIS contributed to spring growth habit and environmental adaptation in cultivated barley. Nature Genetics, 2012, 44, 1388-1392.	21.4	477
149	Genome Dynamics Explain the Evolution of Flowering Time CCT Domain Gene Families in the Poaceae. PLoS ONE, 2012, 7, e45307.	2.5	93
150	Induced mutations in circadian clock regulator <i>Mat-a</i> facilitated short-season adaptation and range extension in cultivated barley. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4326-4331.	7.1	163
151	Analysis of the barley bract suppression gene Trd1. Theoretical and Applied Genetics, 2012, 125, 33-45.	3.6	35
152	Molecular, phylogenetic and comparative genomic analysis of the <i>cytokinin oxidase/dehydrogenase</i> gene family in the Poaceae. Plant Biotechnology Journal, 2012, 10, 67-82.	8.3	47
153	Inter-species sequence comparison of <i>Brachypodium</i> reveals how transposon activity corrodes genome colinearity. Plant Journal, 2012, 71, 550-563.	5.7	26
154	High resolution mapping of Dense spike-ar (<i>dsp.ar</i>) to the genetic centromere of barley chromosome 7H. Theoretical and Applied Genetics, 2012, 124, 373-384.	3.6	39
155	Genetic Dissection of Barley Morphology and Development. Plant Physiology, 2011, 155, 617-627.	4.8	188
156	Frequent Gene Movement and Pseudogene Evolution Is Common to the Large and Complex Genomes of Wheat, Barley, and Their Relatives. Plant Cell, 2011, 23, 1706-1718.	6.6	190
157	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. Plant Cell, 2011, 23, 1249-1263.	6.6	448
158	Highly parallel gene-to-BAC addressing using microarrays. BioTechniques, 2011, 50, 165-174.	1.8	8
159	Large-Scale Data Integration Reveals Colocalization of Gene Functional Groups with Meta-QTL for Multiple Disease Resistance in Barley. Molecular Plant-Microbe Interactions, 2011, 24, 1492-1501.	2.6	60
160	Patterns of polymorphism and linkage disequilibrium in cultivated barley. Theoretical and Applied Genetics, 2011, 122, 523-531.	3.6	41
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