

Nils Stein

List of Publications by Year in descending order

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Version: 2024-02-01

227
papers

28,874
citations

6606

79
h-index

6128

159
g-index

247
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. <i>Theoretical and Applied Genetics</i> , 2022, 135, 571-590.	1.8	7
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.	2.8	46
3	Chromosome-scale assembly of barley cv. "Haruna Nijo"™ as a resource for barley genetics. <i>DNA Research</i> , 2022, 29, .	1.5	6
4	<i>Aegilops sharonensis</i> genome-assisted identification of stem rust resistance gene Sr62. <i>Nature Communications</i> , 2022, 13, 1607.	5.8	48
5	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
6	Mining for New Sources of Resistance to Powdery Mildew in Genetic Resources of Winter Wheat. <i>Frontiers in Plant Science</i> , 2022, 13, 836723.	1.7	8
7	Prospects of telomere-to-telomere assembly in barley: Analysis of sequence gaps in the MorexV3 reference genome. <i>Plant Biotechnology Journal</i> , 2022, 20, 1373-1386.	4.1	24
8	Transposable Element Populations Shed Light on the Evolutionary History of Wheat and the Complex Co-Evolution of Autonomous and Non-Autonomous Retrotransposons. <i>Genetics & Genomics Next</i> , 2022, 3, .	0.8	12
9	The barley leaf rust resistance gene Rph3 encodes a predicted membrane protein and is induced upon infection by avirulent pathotypes of <i>Puccinia hordei</i> . <i>Nature Communications</i> , 2022, 13, 2386.	5.8	12
10	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
11	The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119.	13.7	70
12	<sc>BaRTv2</sc>: a highly resolved barley reference transcriptome for accurate transcript-specific <sc>RNA</sc>-seq quantification. <i>Plant Journal</i> , 2022, 111, 1183-1202.	2.8	17
13	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
14	Six-rowed wild-growing barleys are hybrids of diverse origins. <i>Plant Journal</i> , 2022, 111, 849-858.	2.8	1
15	Why 2022 is a revolutionary year for potato genomics. <i>Molecular Plant</i> , 2022, , .	3.9	0
16	High-resolution mapping of Rym14Hb, a wild relative resistance gene to barley yellow mosaic disease. <i>Theoretical and Applied Genetics</i> , 2021, 134, 823-833.	1.8	10
17	The <i>Aegilops ventricosa</i> 2NvS segment in bread wheat: cytology, genomics and breeding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 529-542.	1.8	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. <i>Plant and Cell Physiology</i> , 2021, 62, 8-27.	1.5	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.	9.4	164
20	Genomic prediction models trained with historical records enable populating the German ex situ genebank bio-digital resource center of barley (<i>Hordeum Åsp.</i>) with information on resistances to soilborne barley mosaic viruses. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2181-2196.	1.8	5
21	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
22	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	3.1	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.	1.7	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.	6.0	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.	1.7	6
26	Improved genome assembly and pan-genome provide key insights into eggplant domestication and breeding. <i>Plant Journal</i> , 2021, 107, 579-596.	2.8	56
27	Chromosome-scale assembly of wild barley accession 'G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	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, .	3.3	48
29	The reinvention of potato. <i>Cell Research</i> , 2021, 31, 1144-1145.	5.7	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.	1.7	7
31	Building pan-genome infrastructures for crop plants and their use in association genetics. <i>DNA Research</i> , 2021, 28, .	1.5	57
32	Assembling the Rye Genome. <i>Compendium of Plant Genomes</i> , 2021, , 101-116.	0.3	0
33	COMPOSITUM 1 contributes to the architectural simplification of barley inflorescence via meristem identity signals. <i>Nature Communications</i> , 2020, 11, 5138.	5.8	37
34	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	13.7	314
35	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
36	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	3.9	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.	1.7	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.	1.7	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.	1.7	26
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	Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding. <i>Nature Genetics</i> , 2019, 51, 1076-1081.	9.4	176
42	Detecting Large Chromosomal Modifications Using Short Read Data From Genotyping-by-Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 1133.	1.7	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.	2.8	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.	1.7	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.	3.1	52
46	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.	9.4	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.	2.8	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.	1.7	27
49	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	9.4	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.	0.4	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, .	1.4	15
53	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	3.8	179
54	Genebank genomics highlights the diversity of a global barley collection. <i>Nature Genetics</i> , 2019, 51, 319-326.	9.4	322

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55	Prospects of pan-genomics in barley. <i>Theoretical and Applied Genetics</i> , 2019, 132, 785-796.	1.8	38
56	TILLING in Barley. <i>Methods in Molecular Biology</i> , 2019, 1900, 73-94.	0.4	14
57	High intraspecific diversity of <i>Restorer</i> of fertility genes in barley. <i>Plant Journal</i> , 2019, 97, 281-295.	2.8	24
58	Origin and evolution of qingke barley in Tibet. <i>Nature Communications</i> , 2018, 9, 5433.	5.8	141
59	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
60	Genomic approaches for studying crop evolution. <i>Genome Biology</i> , 2018, 19, 140.	3.8	54
61	Evolutionarily conserved partial gene duplication in the Triticeae tribe of grasses confers pathogen resistance. <i>Genome Biology</i> , 2018, 19, 116.	3.8	9
62	High-throughput development of SSR marker candidates and their chromosomal assignment in rye (<i>Secale cereale</i> L.). <i>Plant Breeding</i> , 2018, 137, 561-572.	1.0	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. <i>Hereditas</i> , 2018, 155, 10.	0.5	14
64	Molecular Mapping and Cloning of Genes and QTLs. <i>Compendium of Plant Genomes</i> , 2018, , 139-154.	0.3	7
65	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	6.0	768
66	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
67	Barley Genome Sequencing and Assembly – A First Version Reference Sequence. <i>Compendium of Plant Genomes</i> , 2018, , 57-71.	0.3	3
68	The pseudogenes of barley. <i>Plant Journal</i> , 2018, 93, 502-514.	2.8	14
69	Tethered Chromosome Conformation Capture Sequencing in Triticeae: A Valuable Tool for Genome Assembly. <i>Bio-protocol</i> , 2018, 8, e2955.	0.2	6
70	Sequence diversification in recessive alleles of two host factor genes suggests adaptive selection for bymovirus resistance in cultivated barley from East Asia. <i>Theoretical and Applied Genetics</i> , 2017, 130, 331-344.	1.8	21
71	Natural diversity of inflorescence architecture traces cryptic domestication genes in barley (<i>Hordeum vulgare</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 843-853.	0.8	11
72	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

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73	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	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.	2.4	130
75	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	6.0	781
76	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017, 8, 22.	1.3	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.	1.6	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.	2.3	41
79	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1511-1522.	4.1	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.	1.0	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.	9.4	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.	9.4	122
83	The INDETERMINATE DOMAIN Protein BROAD LEAF1 Limits Barley Leaf Width by Restricting Lateral Proliferation. <i>Current Biology</i> , 2016, 26, 903-909.	1.8	37
84	Mitogen-Activated Protein Kinase Kinase 3 Regulates Seed Dormancy in Barley. <i>Current Biology</i> , 2016, 26, 775-781.	1.8	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.	1.0	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.	2.8	32
87	Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.04.0021.	1.6	45
88	The Barley <i>Ucn4</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
89	High-throughput physical map anchoring via BAC-pool sequencing. <i>BMC Plant Biology</i> , 2015, 15, 99.	1.6	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.	2.8	76

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91	Evolution of the Grain Dispersal System in Barley. <i>Cell</i> , 2015, 162, 527-539.	13.5	265
92	Chromosomal genomics facilitates fine mapping of a Russian wheat aphid resistance gene. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1373-1383.	1.8	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.	1.8	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.	1.0	4
95	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	3.8	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.	2.8	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.	2.0	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.	3.3	126
99	BARLEX – the Barley Draft Genome Explorer. <i>Molecular Plant</i> , 2015, 8, 964-966.	3.9	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.	3.9	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.	1.8	20
102	Transposable Element Junctions in Marker Development and Genomic Characterization of Barley. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0036.	1.6	9
103	Genetic anchoring of whole-genome shotgun assemblies. <i>Frontiers in Genetics</i> , 2014, 5, 208.	1.1	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.	0.6	3
105	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
106	Unlocking the secondary gene pool of barley with next-generation sequencing. <i>Plant Biotechnology Journal</i> , 2014, 12, 1122-1131.	4.1	111
107	Biotechnological Approaches to Barley Improvement. <i>Biotechnology in Agriculture and Forestry</i> , 2014, , .	0.2	7
108	<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

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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.	0.6	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.	1.2	102
111	Plant genome sequencing " applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014, 26, 31-37.	3.3	164
112	The barley Frost resistance-H2 locus. <i>Functional and Integrative Genomics</i> , 2014, 14, 85-100.	1.4	19
113	High-resolution mapping of the barley <i>Ryd3</i> locus controlling tolerance to BYDV. <i>Molecular Breeding</i> , 2014, 33, 477-488.	1.0	13
114	Reduced chlorophyll biosynthesis in heterozygous barley magnesium chelatase mutants. <i>Plant Physiology and Biochemistry</i> , 2014, 78, 10-14.	2.8	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.	2.8	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.	1.2	88
117	Mapping-by-sequencing accelerates forward genetics in barley. <i>Genome Biology</i> , 2014, 15, R78.	13.9	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.	1.8	16
119	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788.	6.0	1,479
120	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014, 345, 1250091.	6.0	318
121	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	6.0	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.	2.3	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.	1.1	190
126	Plant Sequence Capture Optimised for Illumina Sequencing. <i>Bio-protocol</i> , 2014, 4, .	0.2	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.	3.8	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.	1.0	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.	2.8	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.	1.8	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.	1.4	10
133	Mapping nonrecombining regions in barley using multicolor FISH. <i>Chromosome Research</i> , 2013, 21, 739-751.	1.0	37
134	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013, 76, 718-727.	2.8	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.	2.8	43
136	Divergence of expression pattern contributed to neofunctionalization of duplicated HDZ transcription factor in barley. <i>New Phytologist</i> , 2013, 197, 939-948.	3.5	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.	1.8	28
138	A versatile fluorescence-based multiplexing assay for CAPS genotyping on capillary electrophoresis systems. <i>Molecular Breeding</i> , 2013, 32, 61-69.	1.0	18
139	Feeding the future. <i>Nature</i> , 2013, 499, 23-24.	13.7	464
140	Reticulate Evolution of the Rye Genome. <i>Plant Cell</i> , 2013, 25, 3685-3698.	3.1	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.	3.3	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.	1.1	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.	3.3	173

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145	Integrating cereal genomics to support innovation in the Triticeae. <i>Functional and Integrative Genomics</i> , 2012, 12, 573-583.	1.4	39
146	Clusters of genes encoding fructan biosynthesizing enzymes in wheat and barley. <i>Plant Molecular Biology</i> , 2012, 80, 299-314.	2.0	29
147	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416
148	Natural variation in a homolog of <i>Antirrhinum CENTRORADIALIS</i> contributed to spring growth habit and environmental adaptation in cultivated barley. <i>Nature Genetics</i> , 2012, 44, 1388-1392.	9.4	477
149	Genome Dynamics Explain the Evolution of Flowering Time CCT Domain Gene Families in the Poaceae. <i>PLoS ONE</i> , 2012, 7, e45307.	1.1	93
150	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.	3.3	163
151	Analysis of the barley bract suppression gene <i>Trd1</i> . <i>Theoretical and Applied Genetics</i> , 2012, 125, 33-45.	1.8	35
152	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.	4.1	47
153	Interspecies sequence comparison of <i>Brachypodium</i> reveals how transposon activity corrodes genome colinearity. <i>Plant Journal</i> , 2012, 71, 550-563.	2.8	26
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