

Kazuhiro Sato

List of Publications by Year in descending order

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156
papers

9,710
citations

57752

44
h-index

40976

93
g-index

161
all docs

161
docs citations

161
times ranked

7506
citing authors

#	ARTICLE	IF	CITATIONS
1	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	27.8	1,416
2	Development and implementation of high-throughput SNP genotyping in barley. <i>BMC Genomics</i> , 2009, 10, 582.	2.8	570
3	An Aluminum-Activated Citrate Transporter in Barley. <i>Plant and Cell Physiology</i> , 2007, 48, 1081-1091.	3.1	475
4	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. <i>Plant Cell</i> , 2011, 23, 1249-1263.	6.6	448
5	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
6	Barley grain with adhering hulls is controlled by an ERF family transcription factor gene regulating a lipid biosynthesis pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4062-4067.	7.1	296
7	Evolution of the Grain Dispersal System in Barley. <i>Cell</i> , 2015, 162, 527-539.	28.9	265
8	Comprehensive Sequence Analysis of 24,783 Barley Full-Length cDNAs Derived from 12 Clone Libraries. <i>Plant Physiology</i> , 2011, 156, 20-28.	4.8	201
9	The International Barley Sequencing Consortium. At the Threshold of Efficient Access to the Barley Genome. <i>Plant Physiology</i> , 2009, 149, 142-147.	4.8	195
10	The HvNramp5 Transporter Mediates Uptake of Cadmium and Manganese, But Not Iron. <i>Plant Physiology</i> , 2016, 172, 1899-1910.	4.8	183
11	Direct links between the vernalization response and other key traits of cereal crops. <i>Nature Communications</i> , 2015, 6, 5882.	12.8	177
12	Molecular mapping of the Oregon Wolfe Barleys: a phenotypically polymorphic doubled-haploid population. <i>Theoretical and Applied Genetics</i> , 2001, 103, 415-424.	3.6	161
13	Acquisition of aluminium tolerance by modification of a single gene in barley. <i>Nature Communications</i> , 2012, 3, 713.	12.8	155
14	An Improved Consensus Linkage Map of Barley Based on Flow-Sorted Chromosomes and Single Nucleotide Polymorphism Markers. <i>Plant Genome</i> , 2011, 4, 238-249.	2.8	150
15	An atlas of gene expression from seed to seed through barley development. <i>Functional and Integrative Genomics</i> , 2006, 6, 202-211.	3.5	138
16	QTL analysis of malting quality in barley based on the doubled-haploid progeny of two elite North American varieties representing different germplasm groups. <i>Theoretical and Applied Genetics</i> , 2000, 101, 173-184.	3.6	131
17	QTL analysis of agronomic traits in barley based on the doubled haploid progeny of two elite North American varieties representing different germplasm groups. <i>Theoretical and Applied Genetics</i> , 2001, 103, 625-637.	3.6	124
18	A high-density transcript linkage map of barley derived from a single population. <i>Heredity</i> , 2009, 103, 110-117.	2.6	119

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19	Development and characterization of recombinant chromosome substitution lines (RCSLs) using <i>Hordeum vulgare</i> subsp. <i>spontaneum</i> as a source of donor alleles in a <i>Hordeum vulgare</i> subsp. <i>vulgare</i> background. <i>Genome</i> , 2003, 46, 1010-1023.	2.0	112
20	Differential Al resistance and citrate secretion in barley (<i>Hordeum vulgare</i> L.). <i>Planta</i> , 2003, 217, 794-800.	3.2	109
21	Genome-Edited Triple-Recessive Mutation Alters Seed Dormancy in Wheat. <i>Cell Reports</i> , 2019, 28, 1362-1369.e4.	6.4	102
22	Alanine aminotransferase controls seed dormancy in barley. <i>Nature Communications</i> , 2016, 7, 11625.	12.8	101
23	Development of 5006 Full-Length cDNAs in Barley: A Tool for Accessing Cereal Genomics Resources. <i>DNA Research</i> , 2009, 16, 81-89.	3.4	99
24	Antagonistic regulation of the gibberellic acid response during stem growth in rice. <i>Nature</i> , 2020, 584, 109-114.	27.8	98
25	Molecular mapping of a gene responsible for Al-activated secretion of citrate in barley. <i>Journal of Experimental Botany</i> , 2004, 55, 1335-1341.	4.8	94
26	Genome-wide association mapping of cadmium accumulation in different organs of barley. <i>New Phytologist</i> , 2015, 208, 817-829.	7.3	93
27	A SHORT INTERNODES (SHI) family transcription factor gene regulates awn elongation and pistil morphology in barley. <i>Journal of Experimental Botany</i> , 2012, 63, 5223-5232.	4.8	86
28	Mitogen-Activated Protein Kinase Kinase 3 Regulates Seed Dormancy in Barley. <i>Current Biology</i> , 2016, 26, 775-781.	3.9	85
29	Identification of AFLP and microsatellite markers linked with an aluminium tolerance gene in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2002, 105, 458-464.	3.6	82
30	Efficient construction of high-density linkage map and its application to QTL analysis in barley. <i>Theoretical and Applied Genetics</i> , 2003, 107, 806-813.	3.6	81
31	Genotypic variation in silicon concentration of barley grain. <i>Plant and Soil</i> , 2003, 249, 383-387.	3.7	76
32	Chromosome-scale genome assembly of the transformation-amenable common wheat cultivar 'Felder'. <i>DNA Research</i> , 2021, 28, .	3.4	74
33	Construction of a novel beer proteome map and its use in beer quality control. <i>Food Chemistry</i> , 2010, 118, 566-574.	8.2	70
34	The domestication of cultivated barley. <i>Developments in Plant Genetics and Breeding</i> , 2003, , 9-27.	0.6	64
35	Chromosomal assignment and deletion mapping of barley EST markers. <i>Genes and Genetic Systems</i> , 2005, 80, 357-366.	0.7	64
36	Detection of seed dormancy QTL in multiple mapping populations derived from crosses involving novel barley germplasm. <i>Theoretical and Applied Genetics</i> , 2007, 115, 869-876.	3.6	62

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37	Identification of novel haze-active beer proteins by proteome analysis. <i>Journal of Cereal Science</i> , 2009, 49, 141-147.	3.7	58
38	Origin of wheat B-genome chromosomes inferred from RNA sequencing analysis of leaf transcripts from section Sitopsis species of <i>Aegilops</i> . <i>DNA Research</i> , 2019, 26, 171-182.	3.4	58
39	A wheat homologue of <i>PHYTOCLOCK 1</i> is a candidate gene conferring the early heading phenotype to einkorn wheat. <i>Genes and Genetic Systems</i> , 2012, 87, 357-367.	0.7	55
40	Novel Prediction Method of Beer Foam Stability Using Protein Z, Barley Dimeric α -Amylase Inhibitor-1 (BDAl-1) and Yeast Thioredoxin. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 8664-8671.	5.2	54
41	An application of high-throughput SNP genotyping for barley genome mapping and characterization of recombinant chromosome substitution lines. <i>Theoretical and Applied Genetics</i> , 2009, 119, 613-619.	3.6	53
42	Genetic diversity for quantitatively inherited agronomic and malting quality traits. <i>Developments in Plant Genetics and Breeding</i> , 2003, 7, 201-226.	0.6	51
43	Natural Variation of Barley Vernalization Requirements: Implication of Quantitative Variation of Winter Growth Habit as an Adaptive Trait in East Asia. <i>Plant and Cell Physiology</i> , 2011, 52, 775-784.	3.1	49
44	Methylobacterium Species Promoting Rice and Barley Growth and Interaction Specificity Revealed with Whole-Cell Matrix-Assisted Laser Desorption / Ionization-Time-of-Flight Mass Spectrometry (MALDI-TOF/MS) Analysis. <i>PLoS ONE</i> , 2015, 10, e0129509.	2.5	48
45	The Influence of Barley Malt Protein Modification on Beer Foam Stability and Their Relationship to the Barley Dimeric α -Amylase Inhibitor-I (BDAl-I) as a Possible Foam-Promoting Protein. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 1458-1464.	5.2	47
46	QTL analysis of Fusarium head blight resistance using a high-density linkage map in barley. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1661-1672.	3.6	46
47	Dissection of barley chromosome 3H in common wheat and a comparison of 3H physical and genetic maps. <i>Genes and Genetic Systems</i> , 2009, 84, 25-34.	0.7	45
48	NBRP databases: databases of biological resources in Japan. <i>Nucleic Acids Research</i> , 2010, 38, D26-D32.	14.5	44
49	Breeding for low cadmium barley by introgression of a Sukkula-like transposable element. <i>Nature Food</i> , 2020, 1, 489-499.	14.0	44
50	Dissection of barley chromosome 5H in common wheat. <i>Genes and Genetic Systems</i> , 2007, 82, 123-133.	0.7	43
51	Genome-wide marker development for the wheat D genome based on single nucleotide polymorphisms identified from transcripts in the wild wheat progenitor <i>Aegilops tauschii</i> . <i>Theoretical and Applied Genetics</i> , 2014, 127, 261-271.	3.6	43
52	Detection of QTLs for salt tolerance in Asian barley (<i>Hordeum vulgare</i> L.) by association analysis with SNP markers. <i>Breeding Science</i> , 2014, 64, 378-388.	1.9	41
53	Mitochondrial genome sequences from wild and cultivated barley (<i>Hordeum vulgare</i>). <i>BMC Genomics</i> , 2016, 17, 824.	2.8	41
54	Construction and Characterization of a Bacterial Artificial Chromosome (BAC) Library from the Japanese Malting Barley variety 'Haruna Nijo'. <i>Breeding Science</i> , 2007, 57, 29-38.	1.9	40

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55	QTL Analysis in Recombinant Chromosome Substitution Lines and Doubled Haploid Lines Derived from a Cross between <i>Hordeum vulgare</i> ssp. <i>vulgare</i> and <i>Hordeum vulgare</i> ssp. <i>spontaneum</i> . <i>Molecular Breeding</i> , 2005, 16, 295-311.	2.1	39
56	Proteome analysis of the wort boiling process. <i>Food Research International</i> , 2012, 45, 262-271.	6.2	39
57	<i>Agrobacterium tumefaciens</i> Enhances Biosynthesis of Two Distinct Auxins in the Formation of Crown Galls. <i>Plant and Cell Physiology</i> , 2019, 60, 29-37.	3.1	39
58	Mapping resistance to cereal aphids in barley. <i>Theoretical and Applied Genetics</i> , 1997, 94, 592-596.	3.6	38
59	Analysis of Intraspecies Diversity in Wheat and Barley Genomes Identifies Breakpoints of Ancient Haplotypes and Provides Insight into the Structure of Diploid and Hexaploid Triticeae Gene Pools. <i>Plant Physiology</i> , 2009, 149, 258-270.	4.8	38
60	Purification of barley dimeric Î±-amylase inhibitor-1 (BDAl-1) and avenin-like protein-a (ALP) from beer and their impact on beer foam stability. <i>Food Chemistry</i> , 2015, 172, 257-264.	8.2	38
61	Mapping nonrecombining regions in barley using multicolor FISH. <i>Chromosome Research</i> , 2013, 21, 739-751.	2.2	37
62	Endogenous hormone levels affect the regeneration ability of callus derived from different organs in barley. <i>Plant Physiology and Biochemistry</i> , 2016, 99, 66-72.	5.8	36
63	Isolation and Characterization of a Barley Yellow Stripe-Like Gene, HvYSL5. <i>Plant and Cell Physiology</i> , 2011, 52, 765-774.	3.1	35
64	Beer proteomics analysis for beer quality control and malting barley breeding. <i>Food Research International</i> , 2013, 54, 1013-1020.	6.2	34
65	Genomic regions responsible for amenability to <i>Agrobacterium</i> -mediated transformation in barley. <i>Scientific Reports</i> , 2016, 6, 37505.	3.3	34
66	Single Nucleotide Polymorphism Mapping and Alignment of Recombinant Chromosome Substitution Lines in Barley. <i>Plant and Cell Physiology</i> , 2011, 52, 728-737.	3.1	32
67	Improvement of barley genome annotations by deciphering the Haruna Nijo genome. <i>DNA Research</i> , 2016, 23, dsv033.	3.4	32
68	Exome QTL-seq maps monogenic locus and QTLs in barley. <i>BMC Genomics</i> , 2017, 18, 125.	2.8	32
69	Mapping genes for deep-seeding tolerance in barley. <i>Euphytica</i> , 2001, 122, 37-43.	1.2	31
70	RMo1 Confers Blast Resistance in Barley and Is Located within the Complex of Resistance Genes Containing Mla, a Powdery Mildew Resistance Gene. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1034-1041.	2.6	31
71	Barley EST Markers Enhance Map Saturation and QTL Mapping in Diploid Wheat. <i>Breeding Science</i> , 2007, 57, 39-45.	1.9	30
72	Discovery of High-Confidence Single Nucleotide Polymorphisms from Large-Scale De Novo Analysis of Leaf Transcripts of <i>Aegilops tauschii</i> , A Wild Wheat Progenitor. <i>DNA Research</i> , 2012, 19, 487-497.	3.4	29

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73	History and future perspectives of barley genomics. <i>DNA Research</i> , 2020, 27, .	3.4	29
74	Extended Application of Barley EST Markers for the Analysis of Alien Chromosomes Added to Wheat Genetic Background. <i>Breeding Science</i> , 2005, 55, 335-341.	1.9	29
75	Genomic differentiation of <i>Hordeum chilense</i> from <i>H. vulgare</i> as revealed by repetitive and EST sequences. <i>Genes and Genetic Systems</i> , 2005, 80, 147-159.	0.7	28
76	QTL analysis of resistance to the rice blast pathogen in barley (<i>Hordeum vulgare</i>). <i>Theoretical and Applied Genetics</i> , 2001, 102, 916-920.	3.6	27
77	Mapping multiple disease resistance genes using a barley mapping population evaluated in Peru, Mexico, and the USA. <i>Molecular Breeding</i> , 2006, 18, 355-366.	2.1	27
78	Detection of <i>Fusarium</i> head blight resistance QTLs using five populations of top-cross progeny derived from two-row—two-row crosses in barley. <i>Molecular Breeding</i> , 2008, 22, 517-526.	2.1	27
79	The Relationships between Development and Low Temperature Tolerance in Barley Near Isogenic Lines Differing for Flowering Behavior. <i>Plant and Cell Physiology</i> , 2015, 56, 2312-2324.	3.1	27
80	RNA-seq analysis reveals considerable genetic diversity and provides genetic markers saturating all chromosomes in the diploid wild wheat relative <i>Aegilops umbellulata</i> . <i>BMC Plant Biology</i> , 2018, 18, 271.	3.6	27
81	Retrotransposon Insertion and DNA Methylation Regulate Aluminum Tolerance in European Barley Accessions. <i>Plant Physiology</i> , 2018, 178, 716-727.	4.8	27
82	Genetic analysis of seed dormancy QTL in barley. <i>Breeding Science</i> , 2009, 59, 645-650.	1.9	27
83	Genome-wide identification of novel genetic markers from RNA sequencing assembly of diverse <i>Aegilops tauschii</i> accessions. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1681-1694.	2.1	26
84	Nicotinamide mononucleotide and related metabolites induce disease resistance against fungal phytopathogens in <i>Arabidopsis</i> and barley. <i>Scientific Reports</i> , 2017, 7, 6389.	3.3	26
85	Mapping Genes for Callus Growth and Shoot Regeneration in Barley(<i>Hordeum vulgare</i> L.). <i>Breeding Science</i> , 1996, 46, 137-142.	0.2	25
86	Net blotch resistance in wild species of <i>Hordeum</i> . <i>Euphytica</i> , 1997, 95, 179-185.	1.2	25
87	Ecogeographical diversity – a Vavilovian approach. <i>Developments in Plant Genetics and Breeding</i> , 2003, 7, 53-76.	0.6	25
88	Genetic Variation in Component Traits of Heading Date in <i>Hordeum vulgare</i> subsp. <i>spontaneum</i> Accessions Characterized in Controlled Environments. <i>Crop Science</i> , 2004, 44, 1622-1632.	1.8	25
89	Genotypic variation in Fe concentration of barley grain. <i>Soil Science and Plant Nutrition</i> , 2004, 50, 1115-1117.	1.9	25
90	QTL Analysis of <i>Fusarium</i> Head Blight Severity in Recombinant Inbred Population Derived from a Cross between Two-rowed Barley Varieties. <i>Breeding Science</i> , 2006, 56, 25-30.	1.9	25

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91	In planta Genome Editing in Commercial Wheat Varieties. <i>Frontiers in Plant Science</i> , 2021, 12, 648841.	3.6	25
92	Selection of transformation-efficient barley genotypes based on TFA (transformation amenability) haplotype and higher resolution mapping of the TFA loci. <i>Plant Cell Reports</i> , 2017, 36, 611-620.	5.6	24
93	Indigenous knowledge and traditional conservation of hulless barley (<i>Hordeum vulgare</i>) germplasm resources in the Tibetan communities of Shangri-la, Yunnan, SW China. <i>Genetic Resources and Crop Evolution</i> , 2011, 58, 645-655.	1.6	22
94	A single nucleotide polymorphism in the <i>α</i> - <i>Fra</i> -gene results in fractured starch granules in barley. <i>Theoretical and Applied Genetics</i> , 2018, 131, 353-364.	3.6	22
95	Development of DNA markers associated with beer foam stability for barley breeding. <i>Theoretical and Applied Genetics</i> , 2011, 122, 199-210.	3.6	21
96	Development of Genome-Wide SNP Markers for Barley via Reference- Based RNA-Seq Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 577.	3.6	21
97	Mutation Analysis of Barley Malt Protein Z4 and Protein Z7 on Beer Foam Stability. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 1548-1554.	5.2	20
98	Perspectives on Low Temperature Tolerance and Vernalization Sensitivity in Barley: Prospects for Facultative Growth Habit. <i>Frontiers in Plant Science</i> , 2020, 11, 585927.	3.6	19
99	A high-resolution physical map integrating an anchored chromosome with the BAC physical maps of wheat chromosome 6B. <i>BMC Genomics</i> , 2015, 16, 595.	2.8	18
100	Sequence differences in the seed dormancy gene <i>Qsd1</i> among various wheat genomes. <i>BMC Genomics</i> , 2017, 18, 497.	2.8	16
101	Quantitative Trait Loci and Maternal Effects Affecting the Strong Grain Dormancy of Wild Barley (<i>Hordeum vulgare</i> ssp. <i>spontaneum</i>). <i>Frontiers in Plant Science</i> , 2017, 8, 1840.	3.6	16
102	East Asian origin of the widespread alpine snowbed herb, <i>Primula cuneifolia</i> (Primulaceae), in the northern Pacific region. <i>Journal of Biogeography</i> , 2020, 47, 2181-2193.	3.0	16
103	Mapping of the <i>eibi1</i> gene responsible for the drought hypersensitive cuticle in wild barley (<i>Hordeum</i>) Tj ETQq1 1 0,784314 rgBT /Over E5	1.9	15
104	Malting quality quantitative trait loci on a high-density map of Mikamo golden—Harrington cross in barley (<i>Hordeum vulgare</i> L.). <i>Molecular Breeding</i> , 2012, 30, 103-112.	2.1	15
105	454 sequencing of pooled BAC clones on chromosome 3H of barley. <i>BMC Genomics</i> , 2011, 12, 246.	2.8	14
106	Differences in dry matter production, grain production, and photosynthetic rate in barley cultivars under long-term salinity. <i>Plant Production Science</i> , 2017, 20, 288-299.	2.0	14
107	QTLs maintaining grain fertility under salt stress detected by exome QTL-seq and interval mapping in barley. <i>Breeding Science</i> , 2018, 68, 561-570.	1.9	14
108	Marker-trait associations in two-rowed spring barley accessions from Kazakhstan and the USA. <i>PLoS ONE</i> , 2018, 13, e0205421.	2.5	14

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109	Expression of barley <i>Glutathione S-Transferase13</i> gene reduces accumulation of reactive oxygen species by trichothecenes and paraquat in Arabidopsis plants. <i>Plant Biotechnology</i> , 2018, 35, 71-79.	1.0	14
110	Chromosome-scale assembly of wild barley accession ‘OUH602’. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	14
111	Effects of Leaf Color, Epicuticular Wax Amount and Gramine Content in Barley Hybrids on Cereal Aphid Populations. <i>Applied Entomology and Zoology</i> , 1997, 32, 1-8.	1.2	14
112	Barley diversity ‘ an introduction. <i>Developments in Plant Genetics and Breeding</i> , 2003, 7, 3-8.	0.6	13
113	Diversity in resistance to biotic stresses. <i>Developments in Plant Genetics and Breeding</i> , 2003, , 143-178.	0.6	13
114	Regulation of germination by targeted mutagenesis of grain dormancy genes in barley. <i>Plant Biotechnology Journal</i> , 2022, 20, 37-46.	8.3	13
115	Novel barley (<i>Hordeum vulgare</i> L.) germplasm resistant to acidic soil. <i>Crop and Pasture Science</i> , 2010, 61, 540.	1.5	12
116	Genome-wide polymorphisms from RNA sequencing assembly of leaf transcripts facilitate phylogenetic analysis and molecular marker development in wild einkorn wheat. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1327-1341.	2.1	12
117	Mapping of Quantitative Trait Loci Conferring Resistance to Barley Yellow Mosaic Virus in a Chinese Barley Landrace Mokusekko 3.. <i>Breeding Science</i> , 2001, 51, 171-177.	1.9	11
118	QTLs in barley controlling seedling elongation of deep-sown seeds. <i>Euphytica</i> , 2008, 164, 761-768.	1.2	11
119	Expression and functional analysis of the barley Nud gene using transgenic rice. <i>Breeding Science</i> , 2011, 61, 35-42.	1.9	11
120	RNA Sequencing-Based Bulk Segregant Analysis Facilitates Efficient D-genome Marker Development for a Specific Chromosomal Region of Synthetic Hexaploid Wheat. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3749.	4.1	11
121	Genomic distribution of MITEs in barley determined by MITE-AFLP mapping. <i>Genome</i> , 2006, 49, 1616-1620.	2.0	10
122	Genomic characterization of the <i>Hordeum vulgare</i> DEP1 (<i>HvDEP1</i>) gene and its diversity in a collection of barley accessions. <i>Euphytica</i> , 2014, 198, 29-41.	1.2	10
123	Population Structure and Genetic Diversity of Two-Rowed Barley Accessions from Kazakhstan Based on SNP Genotyping Data. <i>Plants</i> , 2021, 10, 2025.	3.5	10
124	Genetic characterization of wild barley populations (<i>Hordeum vulgare</i> ssp. <i>spontaneum</i>) from Kazakhstan based on genome wide SNP analysis. <i>Breeding Science</i> , 2014, 64, 399-403.	1.9	9
125	Introgression of chromosomal segments conferring early heading date from wheat diploid progenitor, <i>Aegilops tauschii</i> Coss., into Japanese elite wheat cultivars. <i>PLoS ONE</i> , 2020, 15, e0228397.	2.5	9
126	Effect of the Dwarfing Gene From <i>Dee-geo-woo-gen</i> on Culm and Internode Lengths, and its Response to Fertilizer in Rice.. <i>Breeding Science</i> , 1995, 45, 7-14.	0.2	9

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127	A Root-specific O-Methyltransferase Gene Expressed in Salt-tolerant Barley. <i>Bioscience, Biotechnology and Biochemistry</i> , 2003, 67, 966-972.	1.3	8
128	Validation of rice blast resistance genes in barley using a QTL mapping population and near-isolines. <i>Breeding Science</i> , 2009, 59, 341-349.	1.9	8
129	Transcriptome analysis of barley identifies heat shock and HD-Zip I transcription factors up-regulated in response to multiple abiotic stresses. <i>Molecular Breeding</i> , 2014, 34, 761-768.	2.1	8
130	Inheritance of gramine content in barley. <i>Euphytica</i> , 1999, 106, 181-185.	1.2	7
131	NBRP, National Bioresource Project of Japan and plant bioresource management. <i>Breeding Science</i> , 2010, 60, 461-468.	1.9	7
132	Accession difference in leaf photosynthesis, root hydraulic conductance and gene expression of root aquaporins under salt stress in barley seedlings. <i>Plant Production Science</i> , 2021, 24, 73-82.	2.0	7
133	Mapping of QTL for intermedium spike on barley chromosome 4H using EST-based markers. <i>Breeding Science</i> , 2009, 59, 383-390.	1.9	7
134	A crucial role for a node-localized transporter, HvSPDT, in loading phosphorus into barley grains. <i>New Phytologist</i> , 2022, 234, 1249-1261.	7.3	7
135	Genetic diversity analysis of hulless barley from Shangri-la region revealed by SSR and AFLP markers. <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 1543-1552.	1.6	6
136	Detection of QTLs controlling alpha-amylase activity in a diversity panel of 343 barley accessions. <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	6
137	Diploid genome differentiation conferred by RNA sequencing-based survey of genome-wide polymorphisms throughout homoeologous loci in Triticum and Aegilops. <i>BMC Genomics</i> , 2020, 21, 246.	2.8	6
138	Chromosome-scale assembly of barley cv. "Haruna Nijo"™ as a resource for barley genetics. <i>DNA Research</i> , 2022, 29, .	3.4	6
139	Protocol for Genome Editing to Produce Multiple Mutants in Wheat. <i>STAR Protocols</i> , 2020, 1, 100053.	1.2	5
140	Identification of a Locus Conferring Dominant Susceptibility to <i>Pyrenophora tritici-repentis</i> in Barley. <i>Frontiers in Plant Science</i> , 2020, 11, 158.	3.6	5
141	RACE1, a Japanese <i>Blumeria graminis</i> f. sp. <i>hordei</i> isolate, is capable of overcoming partially mlo-mediated penetration resistance in barley in an allele-specific manner. <i>PLoS ONE</i> , 2021, 16, e0256574.	2.5	5
142	RNA-Seq-based DNA marker analysis of the genetics and molecular evolution of Triticeae species. <i>Functional and Integrative Genomics</i> , 2021, 21, 535-542.	3.5	4
143	Germplasm evaluation for crop improvement: Analysis of grain quality and cadmium accumulation in barley. <i>Journal of Cereal Science</i> , 2021, 101, 103297.	3.7	4
144	Barley diversity "an outlook. <i>Developments in Plant Genetics and Breeding</i> , 2003, , 269-278.	0.6	3

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145	Genetic Factors Associated with Heading Responses Revealed by Field Evaluation of 274 Barley Accessions for 20 Seasons. <i>IScience</i> , 2020, 23, 101146.	4.1	3
146	Beer and Wort Proteomics. <i>Methods in Molecular Biology</i> , 2014, 1072, 737-754.	0.9	3
147	Genetic analysis of the resistance of barley to cryptic species of <i>Pyricularia</i> . <i>Journal of General Plant Pathology</i> , 2016, 82, 302-306.	1.0	2
148	Genomics Approaches to Mining Barley Germplasm Collections. <i>Compendium of Plant Genomes</i> , 2018, , 155-169.	0.5	2
149	Genetic Characterization of Genetic Resources of <i>Aegilops tauschii</i> , Wheat D Genome Donor, Newly Collected in North Caucasia. <i>American Journal of Plant Sciences</i> , 2017, 08, 2769-2784.	0.8	2
150	Whole Exome-Sequencing of Pooled Genomic DNA Samples to Detect Quantitative Trait Loci in Esotropia and Exotropia of Strabismus in Japanese. <i>Life</i> , 2022, 12, 41.	2.4	2
151	Detection of splicing variants in the leaf and spike transcripts of wild diploid wheat <i>Aegilops tauschii</i> and transmission of the splicing patterns to synthetic hexaploid wheat. <i>Plant Gene</i> , 2017, 9, 6-12.	2.3	1
152	Editorial: Use of Barley and Wheat Reference Sequences: Downstream Applications in Breeding, Gene Isolation, GWAS, and Evolution. <i>Frontiers in Plant Science</i> , 2020, 11, 1017.	3.6	1
153	Cereal Resources in National BioResource Project of Japan. <i>Interdisciplinary Bio Central</i> , 2010, 2, 13.1-13.8.	0.1	0
154	Development of Recombinant Chromosome Substitution Lines for Aluminum Tolerance in Barley. , 2013, , 339-347.		0
155	Analysis of barley genome diversity and its application to breeding. <i>Ikushugaku Kenkyu</i> , 2013, 15, 167-172.	0.3	0
156	Diallel analysis of husk content in malting barley.. <i>Breeding Science</i> , 1989, 39, 471-480.	0.2	0