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List of Publications by Year in descending order

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279798 330143 1,973 38 23 37 citations h-index g-index papers 45 45 45 2787 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Meta-QTL analysis of the genetic control of ear emergence in elite European winter wheat germplasm. Theoretical and Applied Genetics, 2009, 119, 383-395.	3.6	225
2	Phenotyping pipeline reveals major seedling root growth QTL in hexaploid wheat. Journal of Experimental Botany, 2015, 66, 2283-2292.	4.8	196
3	Meta-QTL analysis of the genetic control of crop height in elite European winter wheat germplasm. Molecular Breeding, 2012, 29, 159-171.	2.1	127
4	Delimitation of the <i>Earliness per se D1 </i> (<i>Eps-D1 </i>) flowering gene to a subtelomeric chromosomal deletion in bread wheat (<i>Triticum aestivum </i>). Journal of Experimental Botany, 2016, 67, 287-299.	4.8	100
5	Induction of aneuploidy by increasing chromosomal instability during dedifferentiation of hepatocellular carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1309-1314.	7.1	91
6	Establishing the A. E. Watkins landrace cultivar collection as a resource for systematic gene discovery in bread wheat. Theoretical and Applied Genetics, 2014, 127, 1831-1842.	3.6	89
7	Genetic Dissection of Grain Size and Grain Number Trade-Offs in CIMMYT Wheat Germplasm. PLoS ONE, 2015, 10, e0118847.	2.5	88
8	Analysis of the recombination landscape of hexaploid bread wheat reveals genes controlling recombination and gene conversion frequency. Genome Biology, 2019, 20, 69.	8.8	79
9	A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat. ELife, 2020, 9, .	6.0	78
10	Validation of a 1DL earliness per se (eps) flowering QTL in bread wheat (Triticum aestivum). Molecular Breeding, 2014, 34, 1023-1033.	2.1	76
11	Wheat Landrace Genome Diversity. Genetics, 2017, 205, 1657-1676.	2.9	76
12	Quantitative High-Resolution CpG Island Mapping with Pyrosequencingâ, Reveals Disease-Specific Methylation Patterns of the CDKN2B Gene in Myelodysplastic Syndrome and Myeloid Leukemia. Clinical Chemistry, 2007, 53, 17-23.	3.2	69
13	A haplotype-led approach to increase the precision of wheat breeding. Communications Biology, 2020, 3, 712.	4.4	68
14	Highâ€density genotyping of the A.E. Watkins Collection of hexaploid landraces identifies a large molecular diversity compared to elite bread wheat. Plant Biotechnology Journal, 2018, 16, 165-175.	8.3	67
15	Distinct Methylation Patterns of Benign and Malignant Liver Tumors Revealed by Quantitative Methylation Profiling. Clinical Cancer Research, 2005, 11, 3654-3660.	7.0	60
16	Molecular genetic basis of pod corn (<i>Tunicate</i> maize). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7115-7120.	7.1	48
17	Epigenetic defects of hepatocellular carcinoma are already found in non-neoplastic liver cells from patients with hereditary haemochromatosis. Human Molecular Genetics, 2007, 16, 1335-1342.	2.9	45
18	The identification of new candidate genes <scp><i>Triticum aestivum</i></scp> <i>FLOWERING LOCUS T3â€B1</i> (<i>TaFT3â€B1</i>) and <i>TARGET OF EAT1</i> (<i>TaTOE1â€B1</i>) controlling the shortâ€day photoperiod response in bread wheat. Plant, Cell and Environment, 2017, 40, 2678-2690.	5.7	45

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19	Assessment of Differentiation and Progression of Hepatic Tumors Using Array-Based Comparative Genomic Hybridization. Clinical Gastroenterology and Hepatology, 2006, 4, 1283-1291.	4.4	42
20	The role of gene flow and chromosomal instability in shaping the bread wheat genome. Nature Plants, 2021, 7, 172-183.	9.3	36
21	Application of a library of near isogenic lines to understand context dependent expression of QTL for grain yield and adaptive traits in bread wheat. BMC Plant Biology, 2016, 16, 161.	3.6	35
22	Functional QTL mapping and genomic prediction of canopy height in wheat measured using a robotic field phenotyping platform. Journal of Experimental Botany, 2020, 71, 1885-1898.	4.8	30
23	The Population Genetic Structure of Clonal Organisms Generated by Exponentially Bounded and Fat-Tailed Dispersal. Genetics, 2007, 177, 435-448.	2.9	27
24	Longâ€distance dispersal and its influence on adaptation to host resistance in a heterogeneous landscape. Plant Pathology, 2013, 62, 9-20.	2.4	27
25	Using the UK reference population AvalonÂ×ÂCadenza as a platform to compare breeding strategies in elite Western European bread wheat. Molecular Breeding, 2015, 35, 70.	2.1	24
26	Identification of a major QTL and associated molecular marker for high arabinoxylan fibre in white wheat flour. PLoS ONE, 2020, 15, e0227826.	2.5	20
27	CerealsDBâ€"new tools for the analysis of the wheat genome: update 2020. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	16
28	Natural Selection Towards Wild-Type in Composite Cross Populations of Winter Wheat. Frontiers in Plant Science, 2019, 10, 1757.	3.6	15
29	Communicating BRCA1 and BRCA2 Genetic Test Results. Journal of Clinical Oncology, 2006, 24, 2969-2970.	1.6	12
30	Genetic variation in wheat grain quality is associated with differences in the galactolipid content of flour and the gas bubble properties of dough liquor. Food Chemistry: X, 2020, 6, 100093.	4.3	12
31	Interactions between two QTLs for time to anthesis on spike development and fertility in wheat. Scientific Reports, 2021, 11, 2451.	3.3	10
32	Analysis of Array-CGH Data Using the R and Bioconductor Software Suite. Comparative and Functional Genomics, 2009, 2009, 1-8.	2.0	8
33	Resolving a QTL complex for height, heading, and grain yield on chromosome 3A in bread wheat. Journal of Experimental Botany, 2021, 72, 2965-2978.	4.8	8
34	Diversity of Pod Shape in Pisum. Diversity, 2021, 13, 203.	1.7	7
35	Trend, population structure, and trait mapping from 15 years of national varietal trials of UK winter wheat. G3: Genes, Genomes, Genetics, 2022, 12 , .	1.8	5
36	Opinion Exploiting genomics to improve the benefits of wheat: Prospects and limitations. Journal of Cereal Science, 2022, 105, 103444.	3.7	4

#	Article	IF	CITATIONS
37	An Integrated Linkage Map of Three Recombinant Inbred Populations of Pea (Pisum sativum L.). Genes, 2022, 13, 196.	2.4	3
38	Drug-Response Signature Predicts Outcome in Adult Acute Myeloid Leukemia and Associates Poor Response with Molecular Characteristics of Hematopoietic Stem Cells Blood, 2004, 104, 2024-2024.	1.4	0