

Jochen C. Reif

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5622306/jochen-c-reif-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

176
papers

7,458
citations

50
h-index

78
g-index

186
ext. papers

9,404
ext. citations

5.9
avg, IF

5.97
L-index

#	Paper	IF	Citations
176	Wheat genetic diversity trends during domestication and breeding. <i>Theoretical and Applied Genetics</i> , 2005 , 110, 859-64	6	271
175	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017 , 35, 969-976	44.5	197
174	Novel throughput phenotyping platforms in plant genetic studies. <i>Trends in Plant Science</i> , 2007 , 12, 433-437	63.1	186
173	Accuracy of genomic selection in European maize elite breeding populations. <i>Theoretical and Applied Genetics</i> , 2012 , 124, 769-76	6	183
172	BreedVision--a multi-sensor platform for non-destructive field-based phenotyping in plant breeding. <i>Sensors</i> , 2013 , 13, 2830-47	3.8	179
171	Hybrid breeding in autogamous cereals. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 1087-96	6	172
170	Hybrid breeding in wheat: technologies to improve hybrid wheat seed production. <i>Journal of Experimental Botany</i> , 2013 , 64, 5411-28	7	157
169	Molecular footprints of domestication and improvement in soybean revealed by whole genome re-sequencing. <i>BMC Genomics</i> , 2013 , 14, 579	4.5	155
168	Linkage disequilibrium in European elite maize germplasm investigated with SSRs. <i>Theoretical and Applied Genetics</i> , 2005 , 111, 723-30	6	152
167	Genebank genomics highlights the diversity of a global barley collection. <i>Nature Genetics</i> , 2019 , 51, 319-326	30.6	151
166	Modelling the genetic architecture of flowering time control in barley through nested association mapping. <i>BMC Genomics</i> , 2015 , 16, 290	4.5	131
165	Modeling Epistasis in Genomic Selection. <i>Genetics</i> , 2015 , 201, 759-68	4	128
164	Genome-based establishment of a high-yielding heterotic pattern for hybrid wheat breeding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 15624-9	11.5	123
163	Population structure, genetic diversity and linkage disequilibrium in elite winter wheat assessed with SNP and SSR markers. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 1477-86	6	121
162	Bridging the gap between marker-assisted and genomic selection of heading time and plant height in hybrid wheat. <i>Heredity</i> , 2014 , 112, 638-45	3.6	116
161	Hybrid wheat: quantitative genetic parameters and consequences for the design of breeding programs. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 2791-801	6	105
160	Yield stability of hybrids versus lines in wheat, barley, and triticale. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 309-16	6	100

159	Genomic selection in a commercial winter wheat population. <i>Theoretical and Applied Genetics</i> , 2016 , 129, 641-51	6	99
158	Association mapping for quality traits in soft winter wheat. <i>Theoretical and Applied Genetics</i> , 2011 , 122, 961-70	6	98
157	Use of SSRs for establishing heterotic groups in subtropical maize. <i>Theoretical and Applied Genetics</i> , 2003 , 107, 947-57	6	97
156	Genomic Prediction of Hybrid Wheat Performance. <i>Crop Science</i> , 2013 , 53, 802-810	2.4	96
155	Detection of segregation distortion loci in triticale (x Triticosecale Wittmack) based on a high-density DArT marker consensus genetic linkage map. <i>BMC Genomics</i> , 2011 , 12, 380	4.5	96
154	Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding. <i>Nature Genetics</i> , 2019 , 51, 1076-1081	36.3	92
153	Mapping QTLs with main and epistatic effects underlying grain yield and heading time in soft winter wheat. <i>Theoretical and Applied Genetics</i> , 2011 , 123, 283-92	6	91
152	A quantitative genetic framework highlights the role of epistatic effects for grain-yield heterosis in bread wheat. <i>Nature Genetics</i> , 2017 , 49, 1741-1746	36.3	89
151	Genomic selection in sugar beet breeding populations. <i>BMC Genetics</i> , 2013 , 14, 85	2.6	86
150	Precision phenotyping of biomass accumulation in triticale reveals temporal genetic patterns of regulation. <i>Scientific Reports</i> , 2013 , 3, 2442	4.9	84
149	Trends in genetic diversity among European maize cultivars and their parental components during the past 50 years. <i>Theoretical and Applied Genetics</i> , 2005 , 111, 838-45	6	83
148	Genomic selection in hybrid breeding. <i>Plant Breeding</i> , 2015 , 134, 1-10	2.4	78
147	Impact of interpopulation divergence on additive and dominance variance in hybrid populations. <i>Genetics</i> , 2007 , 176, 1931-4	4	78
146	Genetic structure and diversity of European flint maize populations determined with SSR analyses of individuals and bulks. <i>Theoretical and Applied Genetics</i> , 2005 , 111, 906-13	6	78
145	Redesigning the exploitation of wheat genetic resources. <i>Trends in Plant Science</i> , 2014 , 19, 631-6	13.1	77
144	Mapping QTLs for root system architecture of maize (<i>Zea mays</i> L.) in the field at different developmental stages. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 1313-24	6	77
143	Genetic Diversity in CIMMYT Nontemperate Maize Germplasm: Landraces, Open Pollinated Varieties, and Inbred Lines. <i>Crop Science</i> , 2008 , 48, 617-624	2.4	76
142	Comparison of biometrical models for joint linkage association mapping. <i>Heredity</i> , 2012 , 108, 332-40	3.6	72

141	Genetic Diversity among CIMMYT Maize Inbred Lines Investigated with SSR Markers: II. Subtropical, Tropical Midaltitude, and Highland Maize Inbred Lines and their Relationships with Elite U.S. and European Maize. <i>Crop Science</i> , 2005 , 45, 2573-2582	2.4	69
140	Development of Heterotic Groups in Triticale. <i>Crop Science</i> , 2010 , 50, 584-590	2.4	64
139	Multiple-trait- and selection indices-genomic predictions for grain yield and protein content in rye for feeding purposes. <i>Theoretical and Applied Genetics</i> , 2016 , 129, 273-87	6	61
138	Genomic prediction of sunflower hybrid performance. <i>Plant Breeding</i> , 2013 , 132, 107-114	2.4	61
137	Association mapping for Fusarium head blight resistance in European soft winter wheat. <i>Molecular Breeding</i> , 2011 , 28, 647-655	3.4	61
136	Extent and genome-wide distribution of linkage disequilibrium in commercial maize germplasm. <i>Theoretical and Applied Genetics</i> , 2011 , 123, 11-20	6	61
135	Grouping of accessions of Mexican races of maize revisited with SSR markers. <i>Theoretical and Applied Genetics</i> , 2006 , 113, 177-85	6	61
134	Genetic variation of growth dynamics in maize (<i>Zea mays</i> L.) revealed through automated non-invasive phenotyping. <i>Plant Journal</i> , 2017 , 89, 366-380	6.9	59
133	Potential and limits of whole genome prediction of resistance to Fusarium head blight and Septoria tritici blotch in a vast Central European elite winter wheat population. <i>Theoretical and Applied Genetics</i> , 2015 , 128, 2471-81	6	57
132	The accuracy of prediction of genomic selection in elite hybrid rye populations surpasses the accuracy of marker-assisted selection and is equally augmented by multiple field evaluation locations and test years. <i>BMC Genomics</i> , 2014 , 15, 556	4.5	57
131	Potential and limits to unravel the genetic architecture and predict the variation of Fusarium head blight resistance in European winter wheat (<i>Triticum aestivum</i> L.). <i>Heredity</i> , 2015 , 114, 318-26	3.6	55
130	Dissecting the genetic architecture of frost tolerance in Central European winter wheat. <i>Journal of Experimental Botany</i> , 2013 , 64, 4453-60	7	53
129	Unlocking the genetic diversity of maize landraces with doubled haploids opens new avenues for breeding. <i>PLoS ONE</i> , 2013 , 8, e57234	3.7	53
128	Genome-wide association mapping of agronomic traits in sugar beet. <i>Theoretical and Applied Genetics</i> , 2011 , 123, 1121-31	6	51
127	Relatedness severely impacts accuracy of marker-assisted selection for disease resistance in hybrid wheat. <i>Heredity</i> , 2014 , 112, 552-61	3.6	50
126	Quantifying novel sequence variation and selective advantage in synthetic hexaploid wheats and their backcross-derived lines using SSR markers. <i>Molecular Breeding</i> , 2005 , 15, 1-10	3.4	49
125	Genetic architecture of resistance to Septoria tritici blotch in European wheat. <i>BMC Genomics</i> , 2013 , 14, 858	4.5	48
124	Mapping dynamic QTL for plant height in triticale. <i>BMC Genetics</i> , 2014 , 15, 59	2.6	47

123	Genetic architecture of complex agronomic traits examined in two testcross populations of rye (<i>Secale cereale</i> L.). <i>BMC Genomics</i> , 2012 , 13, 706	4.5	47
122	Comparison of Linkage Disequilibrium in Elite European Maize Inbred Lines using AFLP and SSR Markers. <i>Molecular Breeding</i> , 2006 , 17, 217-226	3.4	47
121	Targeted association mapping demonstrating the complex molecular genetics of fatty acid formation in soybean. <i>BMC Genomics</i> , 2015 , 16, 841	4.5	44
120	Impact of selective genotyping in the training population on accuracy and bias of genomic selection. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 707-13	6	44
119	Association mapping in an elite maize breeding population. <i>Theoretical and Applied Genetics</i> , 2011 , 123, 847-58	6	44
118	Dissecting the genetic architecture of agronomic traits in multiple segregating populations in rapeseed (<i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2012 , 124, 153-61	6	43
117	Genome-wide association mapping reveals epistasis and genetic interaction networks in sugar beet. <i>Theoretical and Applied Genetics</i> , 2011 , 123, 109-18	6	43
116	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. <i>New Phytologist</i> , 2020 , 227, 260-273	9.8	42
115	Hybrid Breeding in Barley. <i>Crop Science</i> , 2013 , 53, 819-824	2.4	42
114	Advantages and limitations of multiple-trait genomic prediction for Fusarium head blight severity in hybrid wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2018 , 131, 685-701	6	42
113	Improved efficiency of doubled haploid generation in hexaploid triticale by in vitro chromosome doubling. <i>BMC Plant Biology</i> , 2012 , 12, 109	5.3	39
112	Predicting Hybrid Performances for Quality Traits through Genomic-Assisted Approaches in Central European Wheat. <i>PLoS ONE</i> , 2016 , 11, e0158635	3.7	37
111	Multiple-line cross QTL mapping for biomass yield and plant height in triticale (<i>Triticosecale Wittmack</i>). <i>Theoretical and Applied Genetics</i> , 2014 , 127, 251-60	6	36
110	Detection of QTL for flowering time in multiple families of elite maize. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 1539-51	6	35
109	Relevance of Specific versus General Combining Ability in Winter Wheat. <i>Crop Science</i> , 2012 , 52, 2494-2500	3.0	35
108	Broadening the genetic base of European maize heterotic pools with US Cornbelt germplasm using field and molecular marker data. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 301-10	6	34
107	Molecular marker assisted broadening of the Central European heterotic groups in rye with Eastern European germplasm. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 291-9	6	34
106	Combining frost tolerance, high grain yield and good pasta quality in durum wheat. <i>Plant Breeding</i> , 2013 , 132, 353-358	2.4	32

105	Effect of inter- and intragenic epistasis on the heritability of oil content in rapeseed (<i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2013 , 126, 435-41	6	32
104	Optimum design of family structure and allocation of resources in association mapping with lines from multiple crosses. <i>Heredity</i> , 2013 , 110, 71-9	3.6	32
103	Multiple-Line Cross Quantitative Trait Locus Mapping in European Elite Maize. <i>Crop Science</i> , 2011 , 51, 2505-2516	2.4	32
102	Hybrid Breeding in Durum Wheat: Heterosis and Combining Ability. <i>Crop Science</i> , 2010 , 50, 2224-2230	2.4	31
101	Trends in genetic variance components during 30 years of hybrid maize breeding at the University of Hohenheim. <i>Plant Breeding</i> , 2008 , 127, 446-451	2.4	31
100	Haplotype-Based Genome-Wide Prediction Models Exploit Local Epistatic Interactions Among Markers. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 1687-1699	3.2	30
99	Hybrid maize breeding with doubled haploids: I. One-stage versus two-stage selection for testcross performance. <i>Theoretical and Applied Genetics</i> , 2006 , 112, 903-12	6	30
98	A new test for family-based association mapping with inbred lines from plant breeding programs. <i>Theoretical and Applied Genetics</i> , 2006 , 113, 1121-30	6	30
97	Higher grain yield and higher grain protein deviation underline the potential of hybrid wheat for a sustainable agriculture. <i>Plant Breeding</i> , 2018 , 137, 326-337	2.4	29
96	Comparison of biometrical approaches for QTL detection in multiple segregating families. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 987-98	6	29
95	Potential of marker selection to increase prediction accuracy of genomic selection in soybean (L.). <i>Molecular Breeding</i> , 2016 , 36, 113	3.4	28
94	Long-term perspective of hybrid versus line breeding in wheat based on quantitative genetic theory. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 1635-41	6	28
93	The roles of pleiotropy and close linkage as revealed by association mapping of yield and correlated traits of wheat (<i>Triticum aestivum</i> L.). <i>Journal of Experimental Botany</i> , 2017 , 68, 4089-4101	7	28
92	Validating the prediction accuracies of marker-assisted and genomic selection of Fusarium head blight resistance in wheat using an independent sample. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 471-482	6	28
91	Best linear unbiased prediction of triticale hybrid performance. <i>Euphytica</i> , 2013 , 191, 223-230	2.1	28
90	Genome-wide association mapping of QTL underlying seed oil and protein contents of a diverse panel of soybean accessions. <i>Plant Science</i> , 2018 , 266, 95-101	5.3	27
89	Exploitation of yield stability in barley. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 1949-62	6	27
88	Potential for simultaneous improvement of grain and biomass yield in Central European winter triticale germplasm. <i>Field Crops Research</i> , 2011 , 121, 153-157	5.5	27

87	Chilling tolerance of Central European maize lines and their factorial crosses. <i>Annals of Botany</i> , 2007 , 100, 1315-21	4.1	27
86	Prospects and limits of marker imputation in quantitative genetic studies in European elite wheat (<i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2015 , 16, 168	4.5	26
85	Genetic architecture and temporal patterns of biomass accumulation in spring barley revealed by image analysis. <i>BMC Plant Biology</i> , 2017 , 17, 137	5.3	26
84	Genome-wide evaluation of genetic diversity and linkage disequilibrium in winter and spring triticale (x <i>Triticosecale</i> Wittmack). <i>BMC Genomics</i> , 2012 , 13, 235	4.5	26
83	Genome-wide mapping and prediction suggests presence of local epistasis in a vast elite winter wheat populations adapted to Central Europe. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 635-647	6	25
82	Identification of Quantitative Trait Loci Underlying Plant Height and Seed Weight in Soybean. <i>Plant Genome</i> , 2013 , 6, plantgenome2013.03.0006	4.4	24
81	Unraveling epistasis with triple testcross progenies of near-isogenic lines. <i>Genetics</i> , 2009 , 181, 247-57	4	24
80	Hybrid maize breeding with doubled haploids: II. Optimum type and number of testers in two-stage selection for general combining ability. <i>Theoretical and Applied Genetics</i> , 2007 , 114, 393-402	6	24
79	Hybrid maize breeding with doubled haploids: III. Efficiency of early testing prior to doubled haploid production in two-stage selection for testcross performance. <i>Theoretical and Applied Genetics</i> , 2007 , 115, 519-27	6	24
78	Genomic Prediction of Barley Hybrid Performance. <i>Plant Genome</i> , 2016 , 9, plantgenome2016.02.0016	4.4	23
77	Hybrid rye performance under natural drought stress in Europe. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 475-82	6	23
76	Genome-metabolite associations revealed low heritability, high genetic complexity, and causal relations for leaf metabolites in winter wheat (<i>Triticum aestivum</i>). <i>Journal of Experimental Botany</i> , 2017 , 68, 415-428	7	23
75	Exploiting the Rht portfolio for hybrid wheat breeding. <i>Theoretical and Applied Genetics</i> , 2018 , 131, 1433-1442	2.2	
74	Genetic architecture is more complex for resistance to <i>Septoria tritici</i> blotch than to <i>Fusarium</i> head blight in Central European winter wheat. <i>BMC Genomics</i> , 2015 , 16, 430	4.5	22
73	Seed Quality Traits Can Be Predicted with High Accuracy in <i>Brassica napus</i> Using Genomic Data. <i>PLoS ONE</i> , 2016 , 11, e0166624	3.7	22
72	Genetic basis of agronomically important traits in sugar beet (<i>Beta vulgaris</i> L.) investigated with joint linkage association mapping. <i>Theoretical and Applied Genetics</i> , 2010 , 121, 1489-99	6	21
71	Use of genotyping-by-sequencing to determine the genetic structure in the medicinal plant chamomile, and to identify flowering time and alpha-bisabolol associated SNP-loci by genome-wide association mapping. <i>BMC Genomics</i> , 2017 , 18, 599	4.5	20
70	High accuracy of predicting hybrid performance of <i>Fusarium</i> head blight resistance by mid-parent values in wheat. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 461-470	6	20

69	Association between line per se and testcross performance for eight agronomic and quality traits in winter rye. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 33-41	6	19
68	Potential causes of linkage disequilibrium in a European maize breeding program investigated with computer simulations. <i>Theoretical and Applied Genetics</i> , 2007 , 115, 529-36	6	19
67	Hybrid maize breeding with doubled haploids. IV. Number versus size of crosses and importance of parental selection in two-stage selection for testcross performance. <i>Theoretical and Applied Genetics</i> , 2008 , 117, 251-60	6	19
66	Manipulation and prediction of spike morphology traits for the improvement of grain yield in wheat. <i>Scientific Reports</i> , 2018 , 8, 14435	4.9	19
65	Negative dominance and dominance-by-dominance epistatic effects reduce grain-yield heterosis in wide crosses in wheat. <i>Science Advances</i> , 2020 , 6, eaay4897	14.3	18
64	Genome-Based Identification of Heterotic Patterns in Rice. <i>Rice</i> , 2017 , 10, 22	5.8	18
63	Dissecting the genetics underlying the relationship between protein content and grain yield in a large hybrid wheat population. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 489-500	6	18
62	Reciprocal recurrent genomic selection: an attractive tool to leverage hybrid wheat breeding. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 687-698	6	18
61	Genetic dynamics underlying phenotypic development of biomass yield in triticale. <i>BMC Genomics</i> , 2014 , 15, 458	4.5	17
60	Genome-wide association mapping and genome-wide prediction of anther extrusion in CIMMYT spring wheat. <i>Euphytica</i> , 2017 , 213, 1	2.1	16
59	Genetic dissection of agronomic and quality traits based on association mapping and genomic selection approaches in durum wheat grown in Southern Spain. <i>PLoS ONE</i> , 2019 , 14, e0211718	3.7	16
58	Suitability of Single-Nucleotide Polymorphism Arrays Versus Genotyping-By-Sequencing for Genebank Genomics in Wheat. <i>Frontiers in Plant Science</i> , 2020 , 11, 42	6.2	16
57	First insights into the genotype-phenotype map of phenotypic stability in rye. <i>Journal of Experimental Botany</i> , 2015 , 66, 3275-84	7	16
56	Association of single nucleotide polymorphic sites in candidate genes with aggressiveness and deoxynivalenol production in <i>Fusarium graminearum</i> causing wheat head blight. <i>BMC Genetics</i> , 2012 , 13, 14	2.6	16
55	Genome-wide association analyses of plant growth traits during the stem elongation phase in wheat. <i>Plant Biotechnology Journal</i> , 2018 , 16, 2042-2052	11.6	14
54	Identification of QTL hot spots for malting quality in two elite breeding lines with distinct tolerance to abiotic stress. <i>BMC Plant Biology</i> , 2018 , 18, 106	5.3	14
53	Choice of shrinkage parameter and prediction of genomic breeding values in elite maize breeding populations. <i>Plant Breeding</i> , 2013 , 132, 99-106	2.4	14
52	Dissecting the Genetic Basis of Resistance to Soybean Cyst Nematode Combining Linkage and Association Mapping. <i>Plant Genome</i> , 2016 , 9, plantgenome2015.04.0020	4.4	13

51	Unlocking historical phenotypic data from an ex situ collection to enhance the informed utilization of genetic resources of barley (<i>Hordeum</i> sp.). <i>Theoretical and Applied Genetics</i> , 2018 , 131, 2009-2019	6	13
50	Multiple-line cross QTL mapping for grain yield and thousand kernel weight in triticale. <i>Plant Breeding</i> , 2016 , 135, 567-573	2.4	12
49	Hybrid Performance of an Immortalized F Rapeseed Population Is Driven by Additive, Dominance, and Epistatic Effects. <i>Frontiers in Plant Science</i> , 2017 , 8, 815	6.2	12
48	Detecting SNPs underlying domestication-related traits in soybean. <i>BMC Plant Biology</i> , 2014 , 14, 251	5.3	12
47	Impact of Genetic Divergence on the Ratio of Variance Due to Specific vs. General Combining Ability in Winter Triticale. <i>Crop Science</i> , 2009 , 49, 2119-2122	2.4	12
46	Identification of loci controlling adaptation in Chinese soya bean landraces via a combination of conventional and bioclimatic GWAS. <i>Plant Biotechnology Journal</i> , 2020 , 18, 389-401	11.6	12
45	Leveraging the Use of Historical Data Gathered During Seed Regeneration of an Genebank Collection of Wheat. <i>Frontiers in Plant Science</i> , 2018 , 9, 609	6.2	11
44	Hybrid Breeding in Wheat 2015 , 225-232		11
43	Optimum allocation of test resources and comparison of breeding strategies for hybrid wheat. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 2117-26	6	10
42	Development of Insertion and Deletion Markers based on Biparental Resequencing for Fine Mapping Seed Weight in Soybean. <i>Plant Genome</i> , 2014 , 7, plantgenome2014.04.0014	4.4	10
41	Genomics and breeding innovations for enhancing genetic gain for climate resilience and nutrition traits. <i>Theoretical and Applied Genetics</i> , 2021 , 134, 1829-1843	6	10
40	Comparing the Potential of Marker-Assisted Selection and Genomic Prediction for Improving Rust Resistance in Hybrid Wheat. <i>Frontiers in Plant Science</i> , 2020 , 11, 594113	6.2	9
39	Unlocking big data doubled the accuracy in predicting the grain yield in hybrid wheat. <i>Science Advances</i> , 2021 , 7,	14.3	9
38	Efficient strategies to assess yield stability in winter wheat. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 1587-1599	6	8
37	Historical phenotypic data from seven decades of seed regeneration in a wheat ex situ collection. <i>Scientific Data</i> , 2019 , 6, 137	8.2	8
36	Genetic Mapping Reveals Large-Effect QTL for Anther Extrusion in CIMMYT Spring Wheat. <i>Agronomy</i> , 2019 , 9, 407	3.6	8
35	Biparental resequencing coupled with SNP genotyping of a segregating population offers insights into the landscape of recombination and fixed genomic regions in elite soybean. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 553-60	3.2	8
34	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	11.6	8

33	Selecting Closely-Linked SNPs Based on Local Epistatic Effects for Haplotype Construction Improves Power of Association Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 4115-4126	3.2	8
32	Yield performance and stability of CMS-based triticale hybrids. <i>Theoretical and Applied Genetics</i> , 2015 , 128, 291-301	6	7
31	Unbalanced historical phenotypic data from seed regeneration of a barley ex situ collection. <i>Scientific Data</i> , 2018 , 5, 180278	8.2	7
30	Haplotype-based genome-wide association increases the predictability of leaf rust (<i>Puccinia triticina</i>) resistance in wheat. <i>Journal of Experimental Botany</i> , 2020 , 71, 6958-6968	7	7
29	Non-Invasive Phenotyping Reveals Genomic Regions Involved in Pre-Anthesis Drought Tolerance and Recovery in Spring Barley. <i>Frontiers in Plant Science</i> , 2019 , 10, 1307	6.2	6
28	Genomic Selection in Hybrid Breeding 2017 , 149-183		6
27	Stability of Adult-plant Resistance to <i>Septoria tritici</i> blotch in 24 European Winter Wheat Varieties Across Nine Field Environments. <i>Journal of Phytopathology</i> , 2011 , 159, no-no	1.8	6
26	Efficient Algorithms for Calculating Epistatic Genomic Relationship Matrices. <i>Genetics</i> , 2020 , 216, 651-669		6
25	The potential of hybrid breeding to enhance leaf rust and stripe rust resistance in wheat. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 2171-2181	6	6
24	Deep genotyping of the gene GmSNAP facilitates pyramiding resistance to cyst nematode in soybean. <i>Crop Journal</i> , 2019 , 7, 677-684	4.6	5
23	Visual Scorings of Drought Stress Intensity as Covariates for Improved Variety Trial Analysis. <i>Journal of Agronomy and Crop Science</i> , 2013 , 199, 321-330	3.9	5
22	Genome-wide prediction in a hybrid maize population adapted to Northwest China. <i>Crop Journal</i> , 2020 , 8, 830-842	4.6	5
21	Genome-Wide Prediction of the Performance of Three-Way Hybrids in Barley. <i>Plant Genome</i> , 2017 , 10, plantgenome2016.05.0046	4.4	4
20	Genotypic correlations and QTL correspondence between line per se and testcross performance in sugar beet (<i>Beta vulgaris</i> L.) for the three agronomic traits beet yield, potassium content, and sodium content. <i>Molecular Breeding</i> , 2014 , 34, 205-215	3.4	4
19	Exploitation of Elite Maize (<i>Zea mays</i> L.) Germplasm across Maturity Zones. <i>Crop Science</i> , 2012 , 52, 1534-1542	4.42	4
18	Identification of novel genetic factors underlying the host-pathogen interaction between barley (<i>Hordeum vulgare</i> L.) and powdery mildew (<i>Blumeria graminis</i> f. sp. hordei). <i>PLoS ONE</i> , 2020 , 15, e0235563	3.7	3
17	Multiple-line cross quantitative trait locus mapping in sugar beet (<i>Beta vulgaris</i> L.). <i>Molecular Breeding</i> , 2013 , 31, 279-287	3.4	3
16	Hybrid maize breeding with doubled haploids: Comparison between selection criteria. <i>Acta Agronomica Hungarica: an International Multidisciplinary Journal in Agricultural Science</i> , 2006 , 54, 343-350		3

15	Genetic Dissection of Hybrid Performance and Heterosis for Yield-Related Traits in Maize.. <i>Frontiers in Plant Science</i> , 2021 , 12, 774478	6.2	2
14	Genome-wide prediction for hybrids between parents with distinguished difference on exotic introgressions in Brassica napus. <i>Crop Journal</i> , 2020 ,	4.6	2
13	QTL mapping of qSCN3-1 for resistance to soybean cyst nematode in soybean line Zhongpin 03-5373. <i>Crop Journal</i> , 2021 , 9, 351-359	4.6	2
12	Using Genome-Wide Predictions to Assess the Phenotypic Variation of a Barley (sp.) Gene Bank Collection for Important Agronomic Traits and Passport Information. <i>Frontiers in Plant Science</i> , 2020 , 11, 604781	6.2	2
11	Characterization of heterosis and genomic prediction-based establishment of heterotic patterns for developing better hybrids in pigeonpea. <i>Plant Genome</i> , 2021 , 14, e20125	4.4	2
10	Extracting genotype information of Arabidopsis thaliana recombinant inbred lines from transcript profiles established with high-density oligonucleotide arrays. <i>Plant Cell Reports</i> , 2017 , 36, 1871-1881	5.1	1
9	Integration of genomic selection with doubled-haploid evaluation in hybrid breeding: from GS 1.0 to GS 4.0 and beyond.. <i>Molecular Plant</i> , 2022 ,	14.4	1
8	GiPS: Genomics-informed parent selection uncovers the breeding value of wheat genetic resources		1
7	Association mapping of wheat Fusarium head blight resistance-related regions using a candidate-gene approach and their verification in a biparental population. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 341-351	6	1
6	Proof of concept to unmask the breeding value of genetic resources of barley (<i>Hordeum vulgare</i>) with a hybrid strategy. <i>Plant Breeding</i> , 2020 , 139, 536-549	2.4	1
5	Genomic prediction models trained with historical records enable populating the German ex situ genebank bio-digital resource center of barley (<i>Hordeum sp.</i>) with information on resistances to soilborne barley mosaic viruses. <i>Theoretical and Applied Genetics</i> , 2021 , 134, 2181-2196	6	1
4	Optimizing the setup of multienvironmental hybrid wheat yield trials for boosting the selection capability. <i>Plant Genome</i> , 2021 , 14, e20150	4.4	1
3	Hybrid wheat: quantitative genetic parameters and heterosis for quality and rheological traits as well as baking volume.. <i>Theoretical and Applied Genetics</i> , 2022 , 1	6	0
2	Assessing the Suitability of Elite Lines for Hybrid Seed Production and as Testers in Wide Crosses With Wheat Genetic Resources. <i>Frontiers in Plant Science</i> , 2021 , 12, 689825	6.2	0
1	Reciprocal Recurrent Genomic Selection Is Impacted by Genotype-by-Environment Interactions. <i>Frontiers in Plant Science</i> , 2021 , 12, 703419	6.2	0