

David Edwards

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1244512/david-edwards-publications-by-year.pdf>

Version: 2024-04-18

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.

274
papers

17,475
citations

57
h-index

127
g-index

300
ext. papers

22,991
ext. citations

8.1
avg, IF

6.6
L-index

#	Paper	IF	Citations
274	Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus cqProt-003.. <i>Theoretical and Applied Genetics</i> , 2022 , 135, 1443	6	1
273	Genome Analysis of the Broad Host Range Necrotroph Highlights Genes Associated With Virulence.. <i>Frontiers in Plant Science</i> , 2022 , 13, 811152	6.2	
272	Expanding Gene-Editing Potential in Crop Improvement with Pangenomes.. <i>International Journal of Molecular Sciences</i> , 2022 , 23,	6.3	1
271	Brassica napus genes Rlm4 and Rlm7, conferring resistance to <i>Leptosphaeria maculans</i> , are alleles of the Rlm9 wall-associated kinase-like resistance locus.. <i>Plant Biotechnology Journal</i> , 2022 ,	11.6	2
270	Machine learning models outperform deep learning models, provide interpretation and facilitate feature selection for soybean trait prediction.. <i>BMC Plant Biology</i> , 2022 , 22, 180	5.3	0
269	Advancing designer crops for climate resilience through an integrated genomics approach.. <i>Current Opinion in Plant Biology</i> , 2022 , 67, 102220	9.9	0
268	Mining of Cloned Disease Resistance Gene Homologs (CDRHs) in Brassica Species and <i>Arabidopsis thaliana</i> . <i>Biology</i> , 2022 , 11, 821	4.9	0
267	Producing High-Quality Single Nucleotide Polymorphism Data for Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2022 , 153-159	1.4	1
266	An SGSGeneloss-Based Method for Constructing a Gene Presence/Absence Table Using Mosdepth. <i>Methods in Molecular Biology</i> , 2022 , 73-80	1.4	0
265	Searching for Homologous Genes Using Daisychain. <i>Methods in Molecular Biology</i> , 2022 , 95-101	1.4	
264	Quantitative Trait Locus Mapping of Resistance to Turnip Yellow Virus in and Introgression of These Resistances by Resynthesis Into Allotetraploid Plants for Deployment in .. <i>Frontiers in Plant Science</i> , 2021 , 12, 781385	6.2	2
263	Toward haplotype studies in polyploid plants to assist breeding. <i>Molecular Plant</i> , 2021 , 14, 1969-1972	14.4	0
262	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021 , 599, 622-627	50.4	15
261	Genomic prediction of preliminary yield trials in chickpea: Effect of functional annotation of SNPs and environment. <i>Plant Genome</i> , 2021 , e20166	4.4	0
260	Maize Yield Prediction at an Early Developmental Stage Using Multispectral Images and Genotype Data for Preliminary Hybrid Selection. <i>Remote Sensing</i> , 2021 , 13, 3976	5	8
259	High-Throughput Genotyping Technologies in Plant Taxonomy. <i>Methods in Molecular Biology</i> , 2021 , 2222, 149-166	1.4	0
258	Candidate Rlm6 resistance genes against <i>Leptosphaeria. maculans</i> identified through a genome-wide association study in <i>Brassica juncea</i> (L.) Czern. <i>Theoretical and Applied Genetics</i> , 2021 , 134, 2035-2050	6	4

257	Crop breeding for a changing climate: integrating phenomics and genomics with bioinformatics. <i>Theoretical and Applied Genetics</i> , 2021 , 134, 1677-1690	6	10
256	Studying the Genetic Diversity of Yam Bean Using a New Draft Genome Assembly. <i>Agronomy</i> , 2021 , 11, 953	3.6	1
255	Genome structural evolution in Brassica crops. <i>Nature Plants</i> , 2021 , 7, 757-765	11.5	3
254	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. <i>Plant Genome</i> , 2021 , e20109	4.4	11
253	Genotype-Environment mismatch of kelp forests under climate change. <i>Molecular Ecology</i> , 2021 , 30, 3730-3746	5.7	7
252	Resources for image-based high-throughput phenotyping in crops and data sharing challenges. <i>Plant Physiology</i> , 2021 , 187, 699-715	6.6	3
251	Status and advances in mining for blackleg (<i>Leptosphaeria maculans</i>) quantitative resistance (QR) in oilseed rape (<i>Brassica napus</i>). <i>Theoretical and Applied Genetics</i> , 2021 , 134, 3123-3145	6	1
250	Sorghum Pan-Genome Explores the Functional Utility for Genomic-Assisted Breeding to Accelerate the Genetic Gain. <i>Frontiers in Plant Science</i> , 2021 , 12, 666342	6.2	7
249	De Novo SNP Discovery and Genotyping of Iranian Pimpinella Species Using ddRAD Sequencing. <i>Agronomy</i> , 2021 , 11, 1342	3.6	1
248	The pangenome of banana highlights differences between genera and genomes. <i>Plant Genome</i> , 2021 , e20100	4.4	10
247	The application of pangenomics and machine learning in genomic selection in plants. <i>Plant Genome</i> , 2021 , 14, e20112	4.4	4
246	The Chicken Pan-Genome Reveals Gene Content Variation and a Promoter Region Deletion in IGF2BP1 Affecting Body Size. <i>Molecular Biology and Evolution</i> , 2021 , 38, 5066-5081	8.3	10
245	Machine learning in agriculture: from silos to marketplaces. <i>Plant Biotechnology Journal</i> , 2021 , 19, 648-650.6	10.6	8
244	Assembly of the non-heading pak choi genome and comparison with the genomes of heading Chinese cabbage and the oilseed yellow sarson. <i>Plant Biotechnology Journal</i> , 2021 , 19, 966-976	11.6	9
243	Comparison and evolutionary analysis of Brassica nucleotide binding site leucine rich repeat (NLR) genes and importance for disease resistance breeding. <i>Plant Genome</i> , 2021 , 14, e20060	4.4	2
242	Molecular characterization of disease resistance in Brassica juncea □The current status and the way forward. <i>Plant Pathology</i> , 2021 , 70, 13-34	2.8	10
241	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021 , 8, 50	8.2	13
240	Genomics Armed With Diversity Leads the Way in Improvement in a Changing Global Environment. <i>Frontiers in Genetics</i> , 2021 , 12, 600789	4.5	8

239	Current status of structural variation studies in plants. <i>Plant Biotechnology Journal</i> , 2021 , 19, 2153-2163	11.6	7
238	Draft Genome Assembly and Transcriptome Dataset for European Turnip (<i>L. ssp.</i>), ECD4 Carrying Clubroot Resistance. <i>Frontiers in Genetics</i> , 2021 , 12, 651298	4.5	2
237	Amborella gene presence/absence variation is associated with abiotic stress responses that may contribute to environmental adaptation. <i>New Phytologist</i> , 2021 ,	9.8	3
236	QTL Genetic Mapping Study for Traits Affecting Meal Quality in Winter Oilseed Rape (<i>L.</i>). <i>Genes</i> , 2021 , 12,	4.2	4
235	Genome-Wide Identification, Expression and Functional Analysis Reveal the Involvement of FCS-Like Zinc Finger Gene Family in Submergence Response in Rice. <i>Rice</i> , 2021 , 14, 76	5.8	2
234	Modelling of gene loss propensity in the pangenomes of three Brassica species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021 , 19, 2488-2500	11.6	7
233	Detection of Epistasis for Seed and Some Phytochemical Traits in Coriander under Different Irrigation Regimes. <i>Agronomy</i> , 2021 , 11, 1891	3.6	0
232	Rapid delivery systems for future food security. <i>Nature Biotechnology</i> , 2021 , 39, 1179-1181	44.5	4
231	Fast-forward breeding for a food-secure world. <i>Trends in Genetics</i> , 2021 , 37, 1124-1136	8.5	15
230	Marine heatwaves have minimal influence on the quality of adult Sydney rock oyster flesh. <i>Science of the Total Environment</i> , 2021 , 795, 148846	10.2	1
229	Mapping of partial resistance to <i>Phytophthora sojae</i> in soybean PIs using whole-genome sequencing reveals a major QTL.. <i>Plant Genome</i> , 2021 , e20184	4.4	1
228	Pangenomics in crop improvement-from coding structural variations to finding regulatory variants with pangenome graphs.. <i>Plant Genome</i> , 2021 , e20177	4.4	2
227	Daisychain: Search and Interactive Visualisation of Homologs in Genome Assemblies. <i>Agronomy</i> , 2021 , 11, 2587	3.6	
226	Rice 3D chromatin structure correlates with sequence variation and meiotic recombination rate. <i>Communications Biology</i> , 2020 , 3, 235	6.7	9
225	Virulence/avirulence patterns among <i>Leptosphaeria maculans</i> isolates determines expression of resistance, senescence and yellowing in cotyledons of <i>Brassica napus</i> . <i>European Journal of Plant Pathology</i> , 2020 , 156, 1077-1089	2.1	0
224	Trait associations in the pangenome of pigeon pea (<i>Cajanus cajan</i>). <i>Plant Biotechnology Journal</i> , 2020 , 18, 1946-1954	11.6	36
223	Climate change and the need for agricultural adaptation. <i>Current Opinion in Plant Biology</i> , 2020 , 56, 197-202	9.9	64
222	Plant pangenomics: approaches, applications and advancements. <i>Current Opinion in Plant Biology</i> , 2020 , 54, 18-25	9.9	41

221	Genome-Wide Identification and Evolution of Receptor-Like Kinases (RLKs) and Receptor like Proteins (RLPs) in. <i>Biology</i> , 2020 , 10,	4.9	9
220	Building a successful international research community through data sharing: The case of the Wheat Information System (WheatIS). <i>F1000Research</i> , 2020 , 9, 536	3.6	1
219	Method for Genome-Wide Association Study: A Soybean Example. <i>Methods in Molecular Biology</i> , 2020 , 2107, 147-158	1.4	0
218	Recent Findings Unravel Genes and Genetic Factors Underlying Resistance in and Its Relatives. <i>International Journal of Molecular Sciences</i> , 2020 , 22,	6.3	2
217	The importance of plant pan-genomes in breeding. 2020 , 27-32		4
216	Identification and QTL mapping of resistance to Turnip yellows virus (TuYV) in oilseed rape, <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2020 , 133, 383-393	6	11
215	The improved assembly of 7DL chromosome provides insight into the structure and evolution of bread wheat. <i>Plant Biotechnology Journal</i> , 2020 , 18, 732-742	11.6	3
214	Characterization of disease resistance genes in the <i>Brassica napus</i> pangenome reveals significant structural variation. <i>Plant Biotechnology Journal</i> , 2020 , 18, 969-982	11.6	41
213	Pangenomics Comes of Age: From Bacteria to Plant and Animal Applications. <i>Trends in Genetics</i> , 2020 , 36, 132-145	8.5	57
212	Super-Pangenome by Integrating the Wild Side of a Species for Accelerated Crop Improvement. <i>Trends in Plant Science</i> , 2020 , 25, 148-158	13.1	87
211	Genetic and signalling pathways of dry fruit size: targets for genome editing-based crop improvement. <i>Plant Biotechnology Journal</i> , 2020 , 18, 1124-1140	11.6	21
210	A High-Performance Spectral-Spatial Residual Network for Hyperspectral Image Classification with Small Training Data. <i>Remote Sensing</i> , 2020 , 12, 3137	5	6
209	Induced Methylation in Plants as a Crop Improvement Tool: Progress and Perspectives. <i>Agronomy</i> , 2020 , 10, 1484	3.6	11
208	Plant pan-genomes are the new reference. <i>Nature Plants</i> , 2020 , 6, 914-920	11.5	129
207	Frontiers in Dissecting and Managing Diseases: From Reference-Based RGA Candidate Identification to Building Pan-RGAomes. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	6
206	Genome-wide identification and comparative analysis of resistance genes in <i>Brassica juncea</i> . <i>Molecular Breeding</i> , 2020 , 40, 1	3.4	10
205	Resistance Gene Analogs in the Brassicaceae: Identification, Characterization, Distribution, and Evolution. <i>Plant Physiology</i> , 2020 , 184, 909-922	6.6	15
204	Understanding Host-Pathogen Interactions in in the Omics Era. <i>Plants</i> , 2020 , 9,	4.5	12

203	Effect of <i>Leptosphaeria maculans</i> Infection on Promoter DNA Methylation of Defence Genes in <i>Brassica napus</i> . <i>Agronomy</i> , 2020 , 10, 1072	3.6	4
202	Linkage mapping and QTL analysis of flowering time using ddRAD sequencing with genotype error correction in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2020 , 20, 546	5.3	3
201	Legume Pangenome Construction Using an Iterative Mapping and Assembly Approach. <i>Methods in Molecular Biology</i> , 2020 , 2107, 35-47	1.4	3
200	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019 , 51, 1411-1422	36.3	157
199	Using Genomics to Adapt Crops to Climate Change 2019 , 91-109		2
198	Prediction of pathogenicity genes involved in adaptation to a lupin host in the fungal pathogens <i>Botrytis cinerea</i> and <i>Sclerotinia sclerotiorum</i> via comparative genomics. <i>BMC Genomics</i> , 2019 , 20, 385	4.5	5
197	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019 , 51, 857-864	36.3	116
196	Wild Origins of Macadamia Domestication Identified Through Intraspecific Chloroplast Genome Sequencing. <i>Frontiers in Plant Science</i> , 2019 , 10, 334	6.2	31
195	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019 , 100, 1066-1082	6.9	32
194	Variation in abundance of predicted resistance genes in the <i>Brassica oleracea</i> pangenome. <i>Plant Biotechnology Journal</i> , 2019 , 17, 789-800	11.6	60
193	Insight into the evolution and functional characteristics of the pan-genome assembly from sesame landraces and modern cultivars. <i>Plant Biotechnology Journal</i> , 2019 , 17, 881-892	11.6	43
192	CropSNPdb: a database of SNP array data for <i>Brassica</i> crops and hexaploid bread wheat. <i>Plant Journal</i> , 2019 , 98, 142-152	6.9	16
191	A differential k-mer analysis pipeline for comparing RNA-Seq transcriptome and meta-transcriptome datasets without a reference. <i>Functional and Integrative Genomics</i> , 2019 , 19, 363-371	3.8	1
190	High intraspecific diversity of Restorer-of-fertility-like genes in barley. <i>Plant Journal</i> , 2019 , 97, 281-295	6.9	17
189	Establishing a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia. <i>Briefings in Bioinformatics</i> , 2019 , 20, 384-389	13.4	8
188	Integrated physical map of bread wheat chromosome arm 7DS to facilitate gene cloning and comparative studies. <i>New Biotechnology</i> , 2019 , 48, 12-19	6.4	6
187	Adapting legume crops to climate change using genomic approaches. <i>Plant, Cell and Environment</i> , 2019 , 42, 6-19	8.4	43
186	INDEL variation in the regulatory region of the major flowering time gene <i>LanFTc1</i> is associated with vernalization response and flowering time in narrow-leaved lupin (<i>Lupinus angustifolius</i> L.). <i>Plant, Cell and Environment</i> , 2019 , 42, 174-187	8.4	35

185	Progress in single-access information systems for wheat and rice crop improvement. <i>Briefings in Bioinformatics</i> , 2019 , 20, 565-571	13.4	4
184	Genome-wide identification and comparative analysis of NBS-LRR resistance genes in <i>Brassica napus</i> . <i>Crop and Pasture Science</i> , 2018 , 69, 72	2.2	37
183	Revolution in Genotyping Platforms for Crop Improvement. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018 , 164, 37-52	1.7	8
182	Speed breeding is a powerful tool to accelerate crop research and breeding. <i>Nature Plants</i> , 2018 , 4, 23-29	11.5	448
181	Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution. <i>Journal of Experimental Botany</i> , 2018 , 69, 3689-3702	7	9
180	Differential Regulation of Genes Involved in Root Morphogenesis and Cell Wall Modification is Associated with Salinity Tolerance in Chickpea. <i>Scientific Reports</i> , 2018 , 8, 4855	4.9	36
179	Investigating Drought Tolerance in Chickpea Using Genome-Wide Association Mapping and Genomic Selection Based on Whole-Genome Resequencing Data. <i>Frontiers in Plant Science</i> , 2018 , 9, 190	6.2	69
178	Advances in Integrating Genomics and Bioinformatics in the Plant Breeding Pipeline. <i>Agriculture (Switzerland)</i> , 2018 , 8, 75	3	43
177	Single-Cell Genomic Analysis in Plants. <i>Genes</i> , 2018 , 9,	4.2	21
176	Exploring the genetic and adaptive diversity of a pan-Mediterranean crop wild relative: narrow-leaved lupin. <i>Theoretical and Applied Genetics</i> , 2018 , 131, 887-901	6	34
175	Towards a more predictable plant breeding pipeline with CRISPR/Cas-induced allelic series to optimize quantitative and qualitative traits. <i>Current Opinion in Plant Biology</i> , 2018 , 45, 218-225	9.9	29
174	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018 , 361,	33.3	1296
173	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2018 , 16, 1265-1274	11.6	130
172	Bias in resistance gene prediction due to repeat masking. <i>Nature Plants</i> , 2018 , 4, 762-765	11.5	30
171	Bottlenecks for genome-edited crops on the road from lab to farm. <i>Genome Biology</i> , 2018 , 19, 178	18.3	34
170	The western Mediterranean region provided the founder population of domesticated narrow-leaved lupin. <i>Theoretical and Applied Genetics</i> , 2018 , 131, 2543-2554	6	20
169	Large-Scale Structural Variation Detection in Subterranean Clover Subtypes Using Optical Mapping. <i>Frontiers in Plant Science</i> , 2018 , 9, 971	6.2	6
168	The pangenome of hexaploid bread wheat. <i>Plant Journal</i> , 2017 , 90, 1007-1013	6.9	206

167	An advanced reference genome of <i>Trifolium subterraneum</i> L. reveals genes related to agronomic performance. <i>Plant Biotechnology Journal</i> , 2017 , 15, 1034-1046	11.6	17
166	Improvements in Genomic Technologies: Application to Crop Genomics. <i>Trends in Biotechnology</i> , 2017 , 35, 547-558	15.1	50
165	Assembly and comparison of two closely related <i>Brassica napus</i> genomes. <i>Plant Biotechnology Journal</i> , 2017 , 15, 1602-1610	11.6	103
164	RNA-Seq and metabolic flux analysis of <i>Tetraselmis</i> sp. M8 during nitrogen starvation reveals a two-stage lipid accumulation mechanism. <i>Bioresource Technology</i> , 2017 , 244, 1281-1293	11	22
163	runBNG: a software package for BioNano genomic analysis on the command line. <i>Bioinformatics</i> , 2017 , 33, 3107-3109	7.2	7
162	Genome editors take on crops. <i>Science</i> , 2017 , 355, 1122-1123	33.3	47
161	Copy number variation and disease resistance in plants. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 2479-2490	33	33
160	SNP Discovery Using a Pangenome: Has the Single Reference Approach Become Obsolete?. <i>Biology</i> , 2017 , 6,	4.9	47
159	Databases for Wheat Genomics and Crop Improvement. <i>Methods in Molecular Biology</i> , 2017 , 1679, 277-291	4	4
158	Towards CRISPR/Cas crops - bringing together genomics and genome editing. <i>New Phytologist</i> , 2017 , 216, 682-698	9.8	165
157	BioNanoAnalyst: a visualisation tool to assess genome assembly quality using BioNano data. <i>BMC Bioinformatics</i> , 2017 , 18, 323	3.6	6
156	Genotyping-by-sequencing approaches to characterize crop genomes: choosing the right tool for the right application. <i>Plant Biotechnology Journal</i> , 2017 , 15, 149-161	11.6	159
155	A comprehensive draft genome sequence for lupin (<i>Lupinus angustifolius</i>), an emerging health food: insights into plant-microbe interactions and legume evolution. <i>Plant Biotechnology Journal</i> , 2017 , 15, 318-330	11.6	123
154	Sequencing the Chickpea Genome. <i>Compendium of Plant Genomes</i> , 2017 , 117-123	0.8	
153	Genome Analysis Identified Novel Candidate Genes for Ascochyta Blight Resistance in Chickpea Using Whole Genome Re-sequencing Data. <i>Frontiers in Plant Science</i> , 2017 , 8, 359	6.2	29
152	Climate Clever Clovers: New Paradigm to Reduce the Environmental Footprint of Ruminants by Breeding Low Methanogenic Forages Utilizing Haplotype Variation. <i>Frontiers in Plant Science</i> , 2017 , 8, 1463	6.2	7
151	Assessing and Exploiting Functional Diversity in Germplasm Pools to Enhance Abiotic Stress Adaptation and Yield in Cereals and Food Legumes. <i>Frontiers in Plant Science</i> , 2017 , 8, 1461	6.2	46
150	The Genome of a Southern Hemisphere Seagrass Species (<i>Zostera muelleri</i>). <i>Plant Physiology</i> , 2016 , 172, 272-83	6.6	41

149	The emergence of molecular profiling and omics techniques in seagrass biology; furthering our understanding of seagrasses. <i>Functional and Integrative Genomics</i> , 2016 , 16, 465-80	3.8	24
148	The pangenome of an agronomically important crop plant Brassica oleracea. <i>Nature Communications</i> , 2016 , 7, 13390	17.4	240
147	An efficient approach to BAC based assembly of complex genomes. <i>Plant Methods</i> , 2016 , 12, 2	5.8	10
146	Analytical and Decision Support Tools for Genomics-Assisted Breeding. <i>Trends in Plant Science</i> , 2016 , 21, 354-363	13.1	46
145	Towards plant pangenomics. <i>Plant Biotechnology Journal</i> , 2016 , 14, 1099-105	11.6	130
144	Genome-Wide Association Study of Genetic Control of Seed Fatty Acid Biosynthesis in. <i>Frontiers in Plant Science</i> , 2016 , 7, 2062	6.2	38
143	Genome-wide Association Study Identifies New Loci for Resistance to in Canola. <i>Frontiers in Plant Science</i> , 2016 , 7, 1513	6.2	41
142	A high-density SNP genotyping array for Brassica napus and its ancestral diploid species based on optimised selection of single-locus markers in the allotetraploid genome. <i>Theoretical and Applied Genetics</i> , 2016 , 129, 1887-99	6	138
141	SNP analysis of Macadamia integrifolia chloroplast genomes to determine the genetic structure of wild populations. <i>Acta Horticulturae</i> , 2016 , 175-180	0.3	1
140	Chloroplast genomics: Expanding resources for an evolutionary conserved miniature molecule with enigmatic applications. <i>Current Plant Biology</i> , 2016 , 7-8, 34-38	3.3	5
139	Development and Validation of Thinopyrum elongatum Expressed Molecular Markers Specific for the Long Arm of Chromosome 7E. <i>Crop Science</i> , 2016 , 56, 354-364	2.4	14
138	The Impact of Genomics Technology on Adapting Plants to Climate Change 2016 , 173-178		7
137	BioNano genome mapping of individual chromosomes supports physical mapping and sequence assembly in complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016 , 14, 1523-31	11.6	82
136	Plant Genomics and Climate Change 2016 ,		2
135	The application of genomics and bioinformatics to accelerate crop improvement in a changing climate. <i>Current Opinion in Plant Biology</i> , 2016 , 30, 78-81	9.9	40
134	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016 , 14, 1095-8	11.6	138
133	Advances in genomics for adapting crops to climate change. <i>Current Plant Biology</i> , 2016 , 6, 2-10	3.3	50
132	Gene loss in the fungal canola pathogen Leptosphaeria maculans. <i>Functional and Integrative Genomics</i> , 2015 , 15, 189-96	3.8	30

131	Chromosomal genomics facilitates fine mapping of a Russian wheat aphid resistance gene. <i>Theoretical and Applied Genetics</i> , 2015 , 128, 1373-83	6	4
130	High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in <i>Cicer arietinum</i> and <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2015 , 128, 1039-47	6	52
129	Mapping QTLs of resistance to head splitting in cabbage (<i>Brassica oleracea</i> L.var. capitata L.). <i>Molecular Breeding</i> , 2015 , 35, 1	3.4	9
128	A bi-filtering method for processing single nucleotide polymorphism array data improves the quality of genetic map and accuracy of quantitative trait locus mapping in doubled haploid populations of polyploid <i>Brassica napus</i> . <i>BMC Genomics</i> , 2015 , 16, 409	4.5	14
127	Unfolding the secrets of coral-algal symbiosis. <i>ISME Journal</i> , 2015 , 9, 844-56	11.9	64
126	Identification and characterization of more than 4 million intervarietal SNPs across the group 7 chromosomes of bread wheat. <i>Plant Biotechnology Journal</i> , 2015 , 13, 97-104	11.6	32
125	Prioritization of candidate genes in "QTL-hotspot" region for drought tolerance in chickpea (<i>Cicer arietinum</i> L.). <i>Scientific Reports</i> , 2015 , 5, 15296	4.9	96
124	CicArVarDB: SNP and InDel database for advancing genetics research and breeding applications in chickpea. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015,	5	16
123	Population Diversity of <i>Leptosphaeria maculans</i> in Australia. <i>International Journal of Biology</i> , 2015 , 7,	1.1	3
122	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , 2015 , 6, 563	6.2	161
121	Scanning the effects of ethyl methanesulfonate on the whole genome of <i>Lotus japonicus</i> using second-generation sequencing analysis. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 559-67	3.2	10
120	Genome-wide survey of the seagrass <i>Zostera muelleri</i> suggests modification of the ethylene signalling network. <i>Journal of Experimental Botany</i> , 2015 , 66, 1489-98	7	31
119	High-throughput genotyping for species identification and diversity assessment in germplasm collections. <i>Molecular Ecology Resources</i> , 2015 , 15, 1091-101	8.4	36
118	Transcriptomic Changes in Coral Holobionts Provide Insights into Physiological Challenges of Future Climate and Ocean Change. <i>PLoS ONE</i> , 2015 , 10, e0139223	3.7	47
117	Skim-based genotyping by sequencing. <i>Methods in Molecular Biology</i> , 2015 , 1245, 257-70	1.4	20
116	Bioinformatics: identification of markers from next-generation sequence data. <i>Methods in Molecular Biology</i> , 2015 , 1245, 29-47	1.4	7
115	Molecular marker databases. <i>Methods in Molecular Biology</i> , 2015 , 1245, 49-62	1.4	1
114	Computational Identification and Comparative Analysis of miRNAs in Wheat Group 7 Chromosomes. <i>Plant Molecular Biology Reporter</i> , 2014 , 32, 487-500	1.7	8

113	New technologies for ultrahigh-throughput genotyping in plant taxonomy. <i>Methods in Molecular Biology</i> , 2014 , 1115, 151-75	1.4	2
112	A high-throughput SNP array in the amphidiploid species <i>Brassica napus</i> shows diversity in resistance genes. <i>Functional and Integrative Genomics</i> , 2014 , 14, 643-55	3.8	36
111	SNP markers-based map construction and genome-wide linkage analysis in <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2014 , 12, 851-60	11.6	55
110	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014 , 345, 1251788	33.3	1129
109	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014 , 345, 1250092	33.3	419
108	A chromosomal genomics approach to assess and validate the desi and kabuli draft chickpea genome assemblies. <i>Plant Biotechnology Journal</i> , 2014 , 12, 778-86	11.6	48
107	Plant genetics. Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014 , 345, 950-3	33.3	1348
106	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014 , 5, 3930	17.4	676
105	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid <i>Brassica oleracea</i> . <i>Genome Biology</i> , 2014 , 15, R77	18.3	306
104	A complex recombination pattern in the genome of allotetraploid <i>Brassica napus</i> as revealed by a high-density genetic map. <i>PLoS ONE</i> , 2014 , 9, e109910	3.7	36
103	Structural variations in plant genomes. <i>Briefings in Functional Genomics</i> , 2014 , 13, 296-307	4.9	128
102	The genome sequence of the Antarctic bullhead notothen reveals evolutionary adaptations to a cold environment. <i>Genome Biology</i> , 2014 , 15, 468	18.3	56
101	Early transcriptional changes in the reef-building coral <i>Acropora aspera</i> in response to thermal and nutrient stress. <i>BMC Genomics</i> , 2014 , 15, 1052	4.5	54
100	Next Generation Sequencing and Germplasm Resources 2014 , 369-390		
99	Comparative analysis of Stowaway-like miniature inverted repeat transposable elements in wheat group 7 chromosomes: Abundance, composition, and evolution. <i>Journal of Systematics and Evolution</i> , 2014 , 52, 743-749	2.9	0
98	Genome-wide delineation of natural variation for pod shatter resistance in <i>Brassica napus</i> . <i>PLoS ONE</i> , 2014 , 9, e101673	3.7	133
97	A consensus map of rapeseed (<i>Brassica napus</i> L.) based on diversity array technology markers: applications in genetic dissection of qualitative and quantitative traits. <i>BMC Genomics</i> , 2013 , 14, 277	4.5	49
96	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013 , 31, 240-6	44.5	781

95	Vegetables containing phytochemicals with potential anti-obesity properties: A review. <i>Food Research International</i> , 2013 , 52, 323-333	7	112
94	Dispersion and domestication shaped the genome of bread wheat. <i>Plant Biotechnology Journal</i> , 2013 , 11, 564-71	11.6	55
93	Accessing complex crop genomes with next-generation sequencing. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 1-11	6	210
92	Genetic and physical mapping of flowering time loci in canola (<i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2013 , 126, 119-32	6	80
91	Predicting polymorphic EST-SSRs in silico. <i>Molecular Ecology Resources</i> , 2013 , 13, 538-45	8.4	17
90	Sequence Based DNA Markers and Genotyping for Cereal Genomics and Breeding 2013 , 57-76		3
89	Identifying genetic diversity of avirulence genes in <i>Leptosphaeria maculans</i> using whole genome sequencing. <i>Functional and Integrative Genomics</i> , 2013 , 13, 295-308	3.8	14
88	Functional genomics to study stress responses in crop legumes: progress and prospects. <i>Functional Plant Biology</i> , 2013 , 40, 1221-1233	2.7	37
87	Next generation characterisation of cereal genomes for marker discovery. <i>Biology</i> , 2013 , 2, 1357-77	4.9	11
86	Genetic, Biochemical, and Morphological Diversity of the Legume Biofuel Tree <i>Pongamia pinnata</i> . <i>Journal of Plant Genome Sciences</i> , 2013 , 1, 54-67		13
85	Bioinformatics Tools to Assist Breeding for Climate Change 2013 , 391-414		2
84	Identification of systemic responses in soybean nodulation by xylem sap feeding and complete transcriptome sequencing reveal a novel component of the autoregulation pathway. <i>Plant Biotechnology Journal</i> , 2012 , 10, 680-9	11.6	22
83	Identification and characterization of candidate Rlm4 blackleg resistance genes in <i>Brassica napus</i> using next-generation sequencing. <i>Plant Biotechnology Journal</i> , 2012 , 10, 709-15	11.6	32
82	Bread matters: a national initiative to profile the genetic diversity of Australian wheat. <i>Plant Biotechnology Journal</i> , 2012 , 10, 703-8	11.6	39
81	Single nucleotide polymorphism discovery from wheat next-generation sequence data. <i>Plant Biotechnology Journal</i> , 2012 , 10, 743-9	11.6	80
80	Second-generation sequencing for gene discovery in the Brassicaceae. <i>Plant Biotechnology Journal</i> , 2012 , 10, 750-9	11.6	13
79	Genomic advances will herald new insights into the Brassica: <i>Leptosphaeria maculans</i> pathosystem. <i>Plant Biology</i> , 2012 , 14 Suppl 1, 1-10	3.7	25
78	Sequencing wheat chromosome arm 7BS delimits the 7BS/4AL translocation and reveals homoeologous gene conservation. <i>Theoretical and Applied Genetics</i> , 2012 , 124, 423-32	6	79

77	Coverage-based consensus calling (CbCC) of short sequence reads and comparison of CbCC results to identify SNPs in chickpea (<i>Cicer arietinum</i> ; Fabaceae), a crop species without a reference genome. <i>American Journal of Botany</i> , 2012 , 99, 186-92	2.7	29
76	Transient Nod factor-dependent gene expression in the nodulation-competent zone of soybean (<i>Glycine max</i> [L.] Merr.) roots. <i>Plant Biotechnology Journal</i> , 2012 , 10, 995-1010	11.6	65
75	Bioinformatics tools and databases for analysis of next-generation sequence data. <i>Briefings in Functional Genomics</i> , 2012 , 11, 12-24	4.9	59
74	WheatGenome.info: an integrated database and portal for wheat genome information. <i>Plant and Cell Physiology</i> , 2012 , 53, e2	4.9	39
73	Genomic Databases for Crop Improvement. <i>Agronomy</i> , 2012 , 2, 62-73	3.6	35
72	Discovery of Single Nucleotide Polymorphisms in Complex Genomes Using SGSautoSNP. <i>Biology</i> , 2012 , 1, 370-82	4.9	53
71	Molecular mapping of qualitative and quantitative loci for resistance to <i>Leptosphaeria maculans</i> causing blackleg disease in canola (<i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2012 , 125, 405-18 ⁶		75
70	Next-generation sequencing applications for wheat crop improvement. <i>American Journal of Botany</i> , 2012 , 99, 365-71	2.7	80
69	Development of chromosome-arm-specific microsatellite markers in <i>Triticum aestivum</i> (Poaceae) using NGS technology. <i>American Journal of Botany</i> , 2012 , 99, e369-71	2.7	21
68	Capturing the biofuel wellhead and powerhouse: the chloroplast and mitochondrial genomes of the leguminous feedstock tree <i>Pongamia pinnata</i> . <i>PLoS ONE</i> , 2012 , 7, e51687	3.7	52
67	SNP discovery and applications in <i>Brassica napus</i> . <i>Journal of Plant Biotechnology</i> , 2012 , 39, 49-61	0.6	31
66	Rapid divergence of repetitive DNAs in <i>Brassica</i> relatives. <i>Genomics</i> , 2011 , 97, 173-85	4.3	38
65	Sequencing and assembly of low copy and genic regions of isolated <i>Triticum aestivum</i> chromosome arm 7DS. <i>Plant Biotechnology Journal</i> , 2011 , 9, 768-75	11.6	91
64	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011 , 43, 1035-9	36.3	1490
63	Plant genome sequencing: applications for crop improvement. <i>Plant Biotechnology Journal</i> , 2010 , 8, 2-9	11.6	218
62	CMap3D: a 3D visualization tool for comparative genetic maps. <i>Bioinformatics</i> , 2010 , 26, 273-4	7.2	17
61	Targeted identification of genomic regions using TAGdb. <i>Plant Methods</i> , 2010 , 6, 19	5.8	29
60	Sequence and structure of <i>Brassica rapa</i> chromosome A3. <i>Genome Biology</i> , 2010 , 11, R94	18.3	53

59	Future tools for association mapping in crop plants. <i>Genome</i> , 2010 , 53, 1017-23	2.4	42
58	Molecular Genetic Markers: Discovery, Applications, Data Storage and Visualisation. <i>Current Bioinformatics</i> , 2009 , 4, 16-27	4.7	95
57	De novo sequencing of plant genomes using second-generation technologies. <i>Briefings in Bioinformatics</i> , 2009 , 10, 609-18	13.4	90
56	AutoSNPdb: an annotated single nucleotide polymorphism database for crop plants. <i>Nucleic Acids Research</i> , 2009 , 37, D951-3	20.1	73
55	Genetic map construction and QTL mapping of resistance to blackleg (<i>Leptosphaeria maculans</i>) disease in Australian canola (<i>Brassica napus</i> L.) cultivars. <i>Theoretical and Applied Genetics</i> , 2009 , 120, 71-83	6	60
54	Discovering genetic polymorphisms in next-generation sequencing data. <i>Plant Biotechnology Journal</i> , 2009 , 7, 312-7	11.6	107
53	Single nucleotide polymorphism discovery in barley using autoSNPdb. <i>Plant Biotechnology Journal</i> , 2009 , 7, 326-33	11.6	48
52	New technologies for ultra-high throughput genotyping in plants. <i>Methods in Molecular Biology</i> , 2009 , 513, 19-39	1.4	89
51	Genetic maps and the use of synteny. <i>Methods in Molecular Biology</i> , 2009 , 513, 41-55	1.4	29
50	Mining for SNPs and SSRs using SNPServer, dbSNP and SSR taxonomy tree. <i>Methods in Molecular Biology</i> , 2009 , 537, 303-21	1.4	19
49	Genome sequencing approaches and successes. <i>Methods in Molecular Biology</i> , 2009 , 513, 345-58	1.4	22
48	Genome sequence data: management, storage, and visualization. <i>BioTechniques</i> , 2009 , 46, 333-4, 336	2.5	65
47	Molecular Marker Discovery and Genetic Map Visualisation 2009 , 165-189		6
46	DNA Sequence Databases 2009 , 1-11		3
45	Modification of nitrogen remobilization, grain fill and leaf senescence in maize (<i>Zea mays</i>) by transposon insertional mutagenesis in a protease gene. <i>New Phytologist</i> , 2007 , 173, 481-494	9.8	37
44	Characterization of simple sequence repeat markers derived in silico from <i>Brassica rapa</i> bacterial artificial chromosome sequences and their application in <i>Brassica napus</i> . <i>Molecular Ecology Notes</i> , 2007 , 7, 273-277		20
43	Sixteen new simple sequence repeat markers from <i>Brassica juncea</i> expressed sequences and their cross-species amplification. <i>Molecular Ecology Notes</i> , 2007 , 7, 697-700		27
42	Identification and characterization of simple sequence repeat markers from <i>Brassica napus</i> expressed sequences. <i>Molecular Ecology Notes</i> , 2007 , 7, 886-889		26

41	A comparative map viewer integrating genetic maps for Brassica and Arabidopsis. <i>BMC Plant Biology</i> , 2007 , 7, 40	5.3	20
40	Automated discovery of single nucleotide polymorphism and simple sequence repeat molecular genetic markers. <i>Methods in Molecular Biology</i> , 2007 , 406, 473-94	1.4	9
39	The reference genetic linkage map for the multinational Brassica rapa genome sequencing project. <i>Theoretical and Applied Genetics</i> , 2007 , 115, 777-92	6	144
38	BASC: an integrated bioinformatics system for Brassica research. <i>Nucleic Acids Research</i> , 2007 , 35, D870-30.1	30.1	17
37	What Are SNPs? 2007 , 41-52		27
36	Single Nucleotide Polymorphism Discovery 2007 , 53-76		27
35	Single Nucleotide Polymorphism Genotyping in Plants 2007 , 77-94		27
34	SNP Applications in Plants 2007 , 95-102		39
33	Genomic distribution of simple sequence repeats in Brassica rapa. <i>Molecules and Cells</i> , 2007 , 23, 349-56	3.5	50
32	SSRPrimer and SSR Taxonomy Tree: Biome SSR discovery. <i>Nucleic Acids Research</i> , 2006 , 34, W656-9	20.1	53
31	Transcriptome analysis of Neotyphodium and Epichloa grass endophytes. <i>Fungal Genetics and Biology</i> , 2006 , 43, 465-75	3.9	29
30	Identification and characterization of simple sequence repeat (SSR) markers from Fragaria and banana expressed sequences. <i>Molecular Ecology Notes</i> , 2006 , 6, 319-322		29
29	Identification and characterization of simple sequence repeat (SSR) markers derived in silico from Brassica oleracea genome shotgun sequences. <i>Molecular Ecology Notes</i> , 2006 , 6, 1191-1194		27
28	Comparison of transcription of multiple genes at three developmental stages of the plant pathogen Sclerotinia sclerotiorum. <i>FEMS Microbiology Letters</i> , 2006 , 258, 150-60	2.9	37
27	The auxin-induced K(+) channel gene Zmk1 in maize functions in coleoptile growth and is required for embryo development. <i>Plant Molecular Biology</i> , 2006 , 61, 757-68	4.6	22
26	INTEGRATING AND INTERROGATING DIVERSE BRASSICA DATA WITHIN AN ENSEMBL STRUCTURED DATABASE. <i>Acta Horticulturae</i> , 2006 , 77-82	0.3	5
25	ANALYSIS OF THE BRASSICA [A] AND [C] GENOMES AND COMPARISON WITH THE GENOME OF ARABIDOPSIS THALIANA. <i>Acta Horticulturae</i> , 2006 , 99-104	0.3	3
24	A Survey of the Brassica rapa genome by BAC-end sequence analysis and comparison with Arabidopsis thaliana. <i>Molecules and Cells</i> , 2006 , 22, 300-7	3.5	31

23	SNPServer: a real-time SNP discovery tool. <i>Nucleic Acids Research</i> , 2005 , 33, W493-5	20.1	46
22	Brassica ASTRA: an integrated database for Brassica genomic research. <i>Nucleic Acids Research</i> , 2005 , 33, D656-9	20.1	21
21	Simple sequence repeat marker loci discovery using SSR primer. <i>Bioinformatics</i> , 2004 , 20, 1475-6	7.2	86
20	A transcriptomics resource for wheat functional genomics. <i>Plant Biotechnology Journal</i> , 2004 , 2, 495-506	11.6	53
19	Plant bioinformatics: from genome to phenome. <i>Trends in Biotechnology</i> , 2004 , 22, 232-7	15.1	85
18	New computational tools for brassica genome research. <i>Comparative and Functional Genomics</i> , 2004 , 5, 276-80		20
17	Redundancy based detection of sequence polymorphisms in expressed sequence tag data using autoSNP. <i>Bioinformatics</i> , 2003 , 19, 421-2	7.2	142
16	Mining for single nucleotide polymorphisms and insertions/deletions in maize expressed sequence tag data. <i>Plant Physiology</i> , 2003 , 132, 84-91	6.6	230
15	A high-throughput SNUPE assay for genotyping SNPs in the flanking regions of Zea mays sequence tagged simple sequence repeats. <i>Molecular Breeding</i> , 2003 , 11, 111-120	3.4	34
14	New approaches to brain injury in preterm infants. <i>Developmental Neuroscience</i> , 2002 , 24, 352-4	2.2	4
13	Characterization of the flanking regions of Zea mays microsatellites reveals a large number of useful sequence polymorphisms. <i>Theoretical and Applied Genetics</i> , 2002 , 105, 532-543	6	46
12	Identification of Transposon-Tagged Maize Genes Displaying Homology to Arrayed cDNA Clones with the Use of Mutator Insertion Display. <i>Journal of Genome Science and Technology</i> , 2002 , 1, 48-55		3
11	Identification of transposon-tagged genes by the random sequencing of Mutator-tagged DNA fragments from Zea mays. <i>Plant Journal</i> , 2000 , 23, 557-66	6.9	55
10	Multiple genes encoding the conserved CCAAT-box transcription factor complex are expressed in Arabidopsis. <i>Plant Physiology</i> , 1998 , 117, 1015-22	6.6	136
9	Construction and characterisation of a yeast artificial chromosome library containing three haploid maize genome equivalents. <i>Plant Molecular Biology</i> , 1992 , 19, 299-308	4.6	63
8	Gene Discovery and Microarray-Based Transcriptome Analysis of the Grass-Endophyte Association	103-121	1
7	Genome-Wide Association Studies in Plants	1-7	0
6	Speed breeding: a powerful tool to accelerate crop research and breeding		7

5	Sorghum pan-genome explores the functional utility to accelerate the genetic gain	1
4	Genomic rearrangements have consequences for introgression breeding as revealed by genome assemblies of wild and cultivated lentil species	4
3	Bioinformatics and Plant Genomics for Staple Crops Improvement93-106	6
2	Wheat Panache - a pangenome graph database representing presence/absence variation across 16 bread wheat genomes	1
1	Graph pangenomes find missing heritability. <i>Nature Genetics</i> ,	36.3 1