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List of Publications by Year in Descending Order

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

115 papers	19,124 citations	56 h-index	118 g-index
118 ext. papers	23,902 ext. citations	12.8 avg, IF	6.13 L-index

#	Paper	IF	Citations
115	Population-scale long-read sequencing uncovers transposable elements associated with gene expression variation and adaptive signatures in <i>Drosophila</i> .. <i>Nature Communications</i> , 2022 , 13, 1948	17.4	3
114	A Genomic Survey of Mayetiola destructor Mobilome Provides New Insights into the Evolutionary History of Transposable Elements in the Cecidomyiid Midges. <i>PLoS ONE</i> , 2021 , 16, e0257996	3.7	1
113	TE Hub: A community-oriented space for sharing and connecting tools, data, resources, and methods for transposable element annotation. <i>Mobile DNA</i> , 2021 , 12, 16	4.4	2
112	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
111	Twenty years of transposable element analysis in the genome. <i>Mobile DNA</i> , 2020 , 11, 28	4.4	22
110	RepetDB: a unified resource for transposable element references. <i>Mobile DNA</i> , 2019 , 10, 6	4.4	23
109	Stress response, behavior, and development are shaped by transposable element-induced mutations in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2019 , 15, e1007900	6	41
108	Progress in single-access information systems for wheat and rice crop improvement. <i>Briefings in Bioinformatics</i> , 2019 , 20, 565-571	13.4	4
107	The Rosa genome provides new insights into the domestication of modern roses. <i>Nature Genetics</i> , 2018 , 50, 772-777	36.3	194
106	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018 , 361,	33.3	1296
105	Linking the International Wheat Genome Sequencing Consortium bread wheat reference genome sequence to wheat genetic and phenomic data. <i>Genome Biology</i> , 2018 , 19, 111	18.3	119
104	A high-quality genome sequence of <i>Rosa chinensis</i> to elucidate ornamental traits. <i>Nature Plants</i> , 2018 , 4, 473-484	11.5	134
103	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018 , 4, 440-452	11.5	158
102	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017 , 541, 536-540	50.4	226
101	Corrections to De Novo Annotation of Transposable Elements: Tackling the Fat Genome Issue [Jamilloux et al., Proc. IEEE, vol. 105, no. 3, pp. 474-481, Mar. 2017, DOI: 10.1109/JPROC.2016.2590833]. <i>Proceedings of the IEEE</i> , 2017 , 105, 978-978	14.3	1
100	Two genomes of highly polyphagous lepidopteran pests (<i>Spodoptera frugiperda</i> , Noctuidae) with different host-plant ranges. <i>Scientific Reports</i> , 2017 , 7, 11816	4.9	146
99	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017 , 49, 1099-1106	36.3	421

98	Reconciling the evolutionary origin of bread wheat (<i>Triticum aestivum</i>). <i>New Phytologist</i> , 2017 , 213, 1477-1486	7.2	72
97	Combined Genomic and Genetic Data Integration of Major Agronomical Traits in Bread Wheat (L.). <i>Frontiers in Plant Science</i> , 2017 , 8, 1843	6.2	24
96	Developing data interoperability using standards: A wheat community use case. <i>F1000Research</i> , 2017 , 6, 1843	3.6	12
95	Developing data interoperability using standards: A wheat community use case. <i>F1000Research</i> , 2017 , 6, 1843	3.6	14
94	Mining Plant Genomic and Genetic Data Using the GnpIS Information System. <i>Methods in Molecular Biology</i> , 2017 , 1533, 103-117	1.4	
93	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. <i>Molecular Ecology Resources</i> , 2016 , 16, 254-65	8.4	76
92	International Congress on Transposable elements (ICTE 2016) in Saint Malo: mobile elements under the sun of Brittany. <i>Mobile DNA</i> , 2016 , 7, 19	4.4	1
91	Impact and insights from ancient repetitive elements in plant genomes. <i>Current Opinion in Plant Biology</i> , 2016 , 30, 41-6	9.9	22
90	Comprehensive repeatome annotation reveals strong potential impact of repetitive elements on tomato ripening. <i>BMC Genomics</i> , 2016 , 17, 624	4.5	22
89	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016 , 9, plantgenome2015.06.0038	4.4	5
88	. <i>Proceedings of the IEEE</i> , 2016 , 1-8	14.3	6
87	Towards an open grapevine information system. <i>Horticulture Research</i> , 2016 , 3, 16056	7.7	26
86	The Arabidopsis hnRNP-Q Protein LIF2 and the PRC1 Subunit LHP1 Function in Concert to Regulate the Transcription of Stress-Responsive Genes. <i>Plant Cell</i> , 2016 , 28, 2197-2211	11.6	28
85	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. <i>BMC Genomics</i> , 2015 , 16, 112	4.5	37
84	Whole genome comparative analysis of transposable elements provides new insight into mechanisms of their inactivation in fungal genomes. <i>BMC Genomics</i> , 2015 , 16, 141	4.5	67
83	Impact of transposable elements on insect genomes and biology. <i>Current Opinion in Insect Science</i> , 2015 , 7, 30-36	5.1	31
82	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus. <i>BMC Genomics</i> , 2015 , 16, 461	4.5	44
81	A call for benchmarking transposable element annotation methods. <i>Mobile DNA</i> , 2015 , 6, 13	4.4	60

80	Genome expansion of <i>Arabidopsis thaliana</i> linked with retrotransposition and reduced symmetric DNA methylation. <i>Nature Plants</i> , 2015 , 1, 14023	11.5	121
79	Evolution of the EKA family of powdery mildew avirulence-effector genes from the ORF 1 of a LINE retrotransposon. <i>BMC Genomics</i> , 2015 , 16, 917	4.5	21
78	Karyotype and gene order evolution from reconstructed extinct ancestors highlight contrasts in genome plasticity of modern rosoid crops. <i>Genome Biology and Evolution</i> , 2015 , 7, 735-49	3.9	33
77	Understanding Brassicaceae evolution through ancestral genome reconstruction. <i>Genome Biology</i> , 2015 , 16, 262	18.3	61
76	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015 , 43, W589-98	20.1	468
75	Endogenous florendoviruses are major components of plant genomes and hallmarks of virus evolution. <i>Nature Communications</i> , 2014 , 5, 5269	17.4	69
74	Tedna: a transposable element de novo assembler. <i>Bioinformatics</i> , 2014 , 30, 2656-8	7.2	27
73	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014 , 46, 1034-8	36.3	269
72	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014 , 345, 1251788	33.3	1129
71	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014 , 345, 1249721	33.3	397
70	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014 , 345, 1250091	33.3	225
69	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014 , 345, 1250092	33.3	419
68	PASTEC: an automatic transposable element classification tool. <i>PLoS ONE</i> , 2014 , 9, e91929	3.7	159
67	Shared subgenome dominance following polyploidization explains grass genome evolutionary plasticity from a seven protochromosome ancestor with 16K protogenes. <i>Genome Biology and Evolution</i> , 2014 , 6, 12-33	3.9	56
66	Deep investigation of <i>Arabidopsis thaliana</i> junk DNA reveals a continuum between repetitive elements and genomic dark matter. <i>PLoS ONE</i> , 2014 , 9, e94101	3.7	44
65	Studying the organization of genes encoding plant cell wall degrading enzymes in <i>Chrysomela tremula</i> provides insights into a leaf beetle genome. <i>Insect Molecular Biology</i> , 2014 , 23, 286-300	3.4	12
64	Organization and evolution of transposable elements along the bread wheat chromosome 3B. <i>Genome Biology</i> , 2014 , 15, 546	18.3	69
63	Ancestral repeats have shaped epigenome and genome composition for millions of years in <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2014 , 5, 4104	17.4	59

62	Pan genome of the phytoplankton <i>Emiliania</i> underpins its global distribution. <i>Nature</i> , 2013 , 499, 209-13	50.4	356
61	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. <i>Nature Genetics</i> , 2013 , 45, 1092-6	36.3	169
60	Distribution, evolution, and diversity of retrotransposons at the flamenco locus reflect the regulatory properties of piRNA clusters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 19842-7	11.5	72
59	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013 , 45, 831-5	36.3	274
58	Wheat syntenome unveils new evidences of contrasted evolutionary plasticity between paleo- and neoduplicated subgenomes. <i>Plant Journal</i> , 2013 , 76, 1030-44	6.9	61
57	Efficient comparison of sets of intervals with NC-lists. <i>Bioinformatics</i> , 2013 , 29, 933-9	7.2	2
56	GnPLS: an information system to integrate genetic and genomic data from plants and fungi. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat058	5	36
55	Roadmap for annotating transposable elements in eukaryote genomes. <i>Methods in Molecular Biology</i> , 2012 , 859, 53-68	1.4	12
54	The Ectocarpus Genome and Brown Algal Genomics: The Ectocarpus Genome Consortium. <i>Advances in Botanical Research</i> , 2012 , 64, 141-184	2.2	10
53	Transposable Element Annotation in Completely Sequenced Eukaryote Genomes. <i>Topics in Current Genetics</i> , 2012 , 17-39		9
52	International Congress on Transposable Elements (ICTE) 2012 in Saint Malo and the sea of TE stories. <i>Mobile DNA</i> , 2012 , 3, 17	4.4	
51	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. <i>Frontiers in Plant Science</i> , 2012 , 3, 5	6.2	54
50	Genomic analysis of the necrotrophic fungal pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011 , 7, e1002230	6	659
49	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 9166-71	11.5	479
48	Considering transposable element diversification in de novo annotation approaches. <i>PLoS ONE</i> , 2011 , 6, e16526	3.7	333
47	Correlation of LNCR rasiRNAs expression with heterochromatin formation during development of the holocentric insect <i>Spodoptera frugiperda</i> . <i>PLoS ONE</i> , 2011 , 6, e24746	3.7	11
46	S-MART, a software toolbox to aid RNA-Seq data analysis. <i>PLoS ONE</i> , 2011 , 6, e25988	3.7	29
45	In search of lost trajectories: Recovering the diversification of transposable elements. <i>Mobile Genetic Elements</i> , 2011 , 1, 151-154		4

44	Effector diversification within compartments of the <i>Leptosphaeria maculans</i> genome affected by Repeat-Induced Point mutations. <i>Nature Communications</i> , 2011 , 2, 202	17.4	354
43	Genome-wide evidence for local DNA methylation spreading from small RNA-targeted sequences in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2011 , 39, 6919-31	20.1	114
42	Formation of plant metabolic gene clusters within dynamic chromosomal regions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 16116-21	11.5	166
41	Pigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010 , 464, 1033-8	50.4	545
40	The <i>Ectocarpus</i> genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010 , 465, 617-21	50.4	645
39	Extensive synteny conservation of holocentric chromosomes in <i>Lepidoptera</i> despite high rates of local genome rearrangements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 7680-5	11.5	121
38	Genome sequence of the pea aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010 , 8, e1000313	9.7	732
37	Genome expansion and gene loss in powdery mildew fungi reveal tradeoffs in extreme parasitism. <i>Science</i> , 2010 , 330, 1543-6	33.3	577
36	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008 , 452, 88-92	50.4	823
35	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008 , 26, 909-15	44.5	790
34	Improved detection and annotation of transposable elements in sequenced genomes using multiple reference sequence sets. <i>Genomics</i> , 2008 , 91, 467-75	4.3	57
33	Genome-wide studies highlight indirect links between human replication origins and gene regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 15837-42	11.5	226
32	Promoter DNA hypermethylation and gene repression in undifferentiated <i>Arabidopsis</i> cells. <i>PLoS ONE</i> , 2008 , 3, e3306	3.7	92
31	Genome sequence of <i>Aedes aegypti</i> , a major arbovirus vector. <i>Science</i> , 2007 , 316, 1718-23	33.3	867
30	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
29	LTR retrotransposons in rice (<i>Oryza sativa</i> , L.): recent burst amplifications followed by rapid DNA loss. <i>BMC Genomics</i> , 2007 , 8, 218	4.5	112
28	A model of segmental duplication formation in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2007 , 17, 1458-70	9.7	57
27	Discovering and detecting transposable elements in genome sequences. <i>Briefings in Bioinformatics</i> , 2007 , 8, 382-92	13.4	139

26	Spip and Squiq, two novel rice non-autonomous LTR retro-element families related to RIRE3 and RIRE8. <i>Plant Science</i> , 2007 , 172, 8-19	5.3	10
25	The <i>Fusarium graminearum</i> genome reveals a link between localized polymorphism and pathogen specialization. <i>Science</i> , 2007 , 317, 1400-2	33.3	668
24	P elements and MITE relatives in the whole genome sequence of <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2006 , 7, 214	4.5	26
23	Recurrent insertion and duplication generate networks of transposable element sequences in the <i>Drosophila melanogaster</i> genome. <i>Genome Biology</i> , 2006 , 7, R112	18.3	134
22	Variation in crossing-over rates across chromosome 4 of <i>Arabidopsis thaliana</i> reveals the presence of meiotic recombination "hot spots". <i>Genome Research</i> , 2006 , 16, 106-14	9.7	139
21	Comparative analysis of BAC and whole genome shotgun sequences from an <i>Anopheles gambiae</i> region related to <i>Plasmodium</i> encapsulation. <i>Insect Biochemistry and Molecular Biology</i> , 2005 , 35, 799-814	14.5	3
20	Combined evidence annotation of transposable elements in genome sequences. <i>PLoS Computational Biology</i> , 2005 , 1, 166-75	5	257
19	Recurrent recruitment of the THAP DNA-binding domain and molecular domestication of the P-transposable element. <i>Molecular Biology and Evolution</i> , 2005 , 22, 741-6	8.3	34
18	Detection of transposable elements by their compositional bias. <i>BMC Bioinformatics</i> , 2004 , 5, 94	3.6	21
17	Hoppel, a P-like element without introns: a P-element ancestral structure or a retrotranscription derivative?. <i>Molecular Biology and Evolution</i> , 2003 , 20, 869-79	8.3	12
16	Detection of new transposable element families in <i>Drosophila melanogaster</i> and <i>Anopheles gambiae</i> genomes. <i>Journal of Molecular Evolution</i> , 2003 , 57 Suppl 1, S50-9	3.1	54
15	Indication of linkage and genetic heterogeneity for asthma and atopy on chromosomes 8p and 12q in 107 French EGEA families. <i>European Journal of Human Genetics</i> , 2003 , 11, 590-6	5.3	3
14	Recurrent exon shuffling between distant P-element families. <i>Molecular Biology and Evolution</i> , 2003 , 20, 190-9	8.3	17
13	Genetic algorithm-based model of evolutionary dynamics of class II transposable elements. <i>Journal of Theoretical Biology</i> , 2001 , 213, 21-30	2.3	11
12	Search for multifactorial disease susceptibility genes in founder populations. <i>Annals of Human Genetics</i> , 2000 , 64, 255-65	2.2	71
11	The triangle test statistic (TTS): a test of genetic homogeneity using departure from the triangle constraints in IBD distribution among affected sib-pairs. <i>Annals of Human Genetics</i> , 2000 , 64, 433-42	2.2	19
10	Detection and modeling of disease susceptibility locus effects: how much can be learned from contrast of populations?. <i>Genetic Epidemiology</i> , 1999 , 17 Suppl 1, S569-74	2.6	
9	Departure from the triangle constraints in discordant sib pairs: a test for genetic heterogeneity. <i>Genetic Epidemiology</i> , 1999 , 17 Suppl 1, S685-9	2.6	2

8	On the probability of identity states in permutable populations: reply to Cannings. <i>American Journal of Human Genetics</i> , 1998 , 62, 726-7	11	7
7	Dynamics of transposable elements in metapopulations: a model of P element invasion in <i>Drosophila</i> . <i>Theoretical Population Biology</i> , 1998 , 54, 175-93	1.2	38
6	A simulation of P element horizontal transfer in <i>Drosophila</i> . <i>Genetica</i> , 1997 , 100, 295-307	1.5	10
5	<i>Drosophila</i> P element: transposition, regulation and evolution. <i>Genetica</i> , 1994 , 93, 61-78	1.5	23
4	Can transposable element copy number distribution parameters be estimated from natural populations of <i>Drosophila melanogaster</i> ?. <i>Journal of Evolutionary Biology</i> , 1994 , 7, 13-28	2.3	2
3	Population-scale long-read sequencing uncovers transposable elements contributing to gene expression variation and associated with adaptive signatures in <i>Drosophila melanogaster</i>		2
2	Stress response, behavior, and development are shaped by transposable element-induced mutations in <i>Drosophila</i>		3
1	Traces of transposable elements in genome dark matter co-opted by flowering gene regulation networks		6