

Hadi Quesneville

List of Publications by Year in descending order

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113
papers

26,224
citations

23567

58
h-index

23533

111
g-index

118
all docs

118
docs citations

118
times ranked

28570
citing authors

#	ARTICLE	IF	CITATIONS
1	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
2	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
3	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788.	12.6	1,479
4	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	12.6	1,025
5	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	17.5	1,012
6	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	27.8	1,003
7	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	5.6	913
8	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	3.5	902
9	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. <i>Science</i> , 2007, 317, 1400-1402.	12.6	837
10	The <i>Ectocarpus</i> genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010, 465, 617-621.	27.8	774
11	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. <i>Science</i> , 2010, 330, 1543-1546.	12.6	725
12	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017, 49, 1099-1106.	21.4	693
13	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015, 43, W589-W598.	14.5	682
14	<i>Pezizomyces</i> black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	27.8	641
15	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, 9166-9171.	7.1	640
16	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	12.6	629
17	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	12.6	542
18	Effector diversification within compartments of the <i>Leptosphaeria maculans</i> genome affected by Repeat-Induced Point mutations. <i>Nature Communications</i> , 2011, 2, 202.	12.8	481

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19	Considering Transposable Element Diversification in De Novo Annotation Approaches. PLoS ONE, 2011, 6, e16526.	2.5	477
20	Pan genome of the phytoplankton <i>Emiliania</i> underpins its global distribution. Nature, 2013, 499, 209-213.	27.8	448
21	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . Nature Genetics, 2014, 46, 1034-1038.	21.4	391
22	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. Nature Genetics, 2013, 45, 831-835.	21.4	374
23	Combined Evidence Annotation of Transposable Elements in Genome Sequences. PLoS Computational Biology, 2005, 1, e22.	3.2	347
24	The <i>Rosa</i> genome provides new insights into the domestication of modern roses. Nature Genetics, 2018, 50, 772-777.	21.4	344
25	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . Nature, 2017, 541, 536-540.	27.8	332
26	Genome interplay in the grain transcriptome of hexaploid bread wheat. Science, 2014, 345, 1250091.	12.6	318
27	Oak genome reveals facets of long lifespan. Nature Plants, 2018, 4, 440-452.	9.3	303
28	PASTEC: An Automatic Transposable Element Classification Tool. PLoS ONE, 2014, 9, e91929.	2.5	285
29	Genome-wide studies highlight indirect links between human replication origins and gene regulation. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15837-15842.	7.1	267
30	Two genomes of highly polyphagous lepidopteran pests (<i>Spodoptera frugiperda</i> , Noctuidae) with different host-plant ranges. Scientific Reports, 2017, 7, 11816.	3.3	242
31	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. Nature Genetics, 2013, 45, 1092-1096.	21.4	236
32	Linking the International Wheat Genome Sequencing Consortium bread wheat reference genome sequence to wheat genetic and phenomic data. Genome Biology, 2018, 19, 111.	8.8	232
33	A high-quality genome sequence of <i>Rosa chinensis</i> to elucidate ornamental traits. Nature Plants, 2018, 4, 473-484.	9.3	224
34	Formation of plant metabolic gene clusters within dynamic chromosomal regions. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16116-16121.	7.1	204
35	Discovering and detecting transposable elements in genome sequences. Briefings in Bioinformatics, 2007, 8, 382-392.	6.5	189
36	Recurrent insertion and duplication generate networks of transposable element sequences in the <i>Drosophila melanogaster</i> genome. Genome Biology, 2006, 7, R112.	9.6	188

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37	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, 106-114.	5.5	162
38	Genome expansion of <i>Arabis alpina</i> linked with retrotransposition and reduced symmetric DNA methylation. <i>Nature Plants</i> , 2015, 1, 14023.	9.3	156
39	Extensive synteny conservation of holocentric chromosomes in Lepidoptera despite high rates of local genome rearrangements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7680-7685.	7.1	147
40	Genome-wide evidence for local DNA methylation spreading from small RNA-targeted sequences in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2011, 39, 6919-6931.	14.5	142
41	LTR retrotransposons in rice (<i>Oryza sativa</i> , L.): recent burst amplifications followed by rapid DNA loss. <i>BMC Genomics</i> , 2007, 8, 218.	2.8	134
42	Reconciling the evolutionary origin of bread wheat (<i>Triticum aestivum</i>). <i>New Phytologist</i> , 2017, 213, 1477-1486.	7.3	119
43	Distribution, evolution, and diversity of retrotransposons at the <i>flamenco</i> 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, 19842-19847.	7.1	115
44	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. <i>Molecular Ecology Resources</i> , 2016, 16, 254-265.	4.8	108
45	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.	2.8	105
46	Promoter DNA Hypermethylation and Gene Repression in Undifferentiated <i>Arabidopsis</i> Cells. <i>PLoS ONE</i> , 2008, 3, e3306.	2.5	99
47	Wheat syntenome unveils new evidences of contrasted evolutionary plasticity between paleo- and neoduplicated subgenomes. <i>Plant Journal</i> , 2013, 76, 1030-1044.	5.7	99
48	Endogenous florendoviruses are major components of plant genomes and hallmarks of virus evolution. <i>Nature Communications</i> , 2014, 5, 5269.	12.8	99
49	Understanding Brassicaceae evolution through ancestral genome reconstruction. <i>Genome Biology</i> , 2015, 16, 262.	8.8	93
50	Organization and evolution of transposable elements along the bread wheat chromosome 3B. <i>Genome Biology</i> , 2014, 15, 546.	8.8	88
51	A call for benchmarking transposable element annotation methods. <i>Mobile DNA</i> , 2015, 6, 13.	3.6	83
52	A model of segmental duplication formation in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2007, 17, 1458-1470.	5.5	81
53	Search for multifactorial disease susceptibility genes in founder populations. <i>Annals of Human Genetics</i> , 2000, 64, 255-265.	0.8	75
54	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.	2.5	75

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55	Ancestral repeats have shaped epigenome and genome composition for millions of years in <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2014, 5, 4104.	12.8	74
56	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. <i>Frontiers in Plant Science</i> , 2012, 3, 5.	3.6	73
57	Twenty years of transposable element analysis in the <i>Arabidopsis thaliana</i> genome. <i>Mobile DNA</i> , 2020, 11, 28.	3.6	72
58	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, S50-S59.	1.8	68
59	Improved detection and annotation of transposable elements in sequenced genomes using multiple reference sequence sets. <i>Genomics</i> , 2008, 91, 467-475.	2.9	67
60	Stress response, behavior, and development are shaped by transposable element-induced mutations in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2019, 15, e1007900.	3.5	64
61	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.	2.5	62
62	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.	2.8	58
63	Combined Genomic and Genetic Data Integration of Major Agronomical Traits in Bread Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1843.	3.6	55
64	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.	12.8	53
65	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.	2.8	49
66	Karyotype and Gene Order Evolution from Reconstructed Extinct Ancestors Highlight Contrasts in Genome Plasticity of Modern Rosid Crops. <i>Genome Biology and Evolution</i> , 2015, 7, 735-749.	2.5	46
67	Impact of transposable elements on insect genomes and biology. <i>Current Opinion in Insect Science</i> , 2015, 7, 30-36.	4.4	45
68	GnpIS: 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.	3.0	43
69	RepetDB: a unified resource for transposable element references. <i>Mobile DNA</i> , 2019, 10, 6.	3.6	43
70	Dynamics of Transposable Elements in Metapopulations: A Model of P Element Invasion in <i>Drosophila</i> . <i>Theoretical Population Biology</i> , 1998, 54, 175-193.	1.1	41
71	Recurrent Recruitment of the THAP DNA-Binding Domain and Molecular Domestication of the P-Transposable Element. <i>Molecular Biology and Evolution</i> , 2005, 22, 741-746.	8.9	38
72	The <i>Arabidopsis</i> 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.	6.6	37

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73	Towards an open grapevine information system. Horticulture Research, 2016, 3, 16056.	6.3	34
74	Impact and insights from ancient repetitive elements in plant genomes. Current Opinion in Plant Biology, 2016, 30, 41-46.	7.1	34
75	Evolution of the EKA family of powdery mildew avirulence-effector genes from the ORF 1 of a LINE retrotransposon. BMC Genomics, 2015, 16, 917.	2.8	33
76	S-MART, A Software Toolbox to Aid RNA-seq Data Analysis. PLoS ONE, 2011, 6, e25988.	2.5	32
77	Tedna: a transposable element <i>de novo</i> assembler. Bioinformatics, 2014, 30, 2656-2658.	4.1	30
78	Drosophila P element: Transposition, regulation and evolution. Genetica, 1994, 93, 61-78.	1.1	29
79	Comprehensive repeatome annotation reveals strong potential impact of repetitive elements on tomato ripening. BMC Genomics, 2016, 17, 624.	2.8	29
80	Detection of transposable elements by their compositional bias. BMC Bioinformatics, 2004, 5, 94.	2.6	28
81	P elements and MITE relatives in the whole genome sequence of Anopheles gambiae. BMC Genomics, 2006, 7, 214.	2.8	28
82	Developing data interoperability using standards: A wheat community use case. F1000Research, 2017, 6, 1843.	1.6	20
83	The triangle test statistic (TTS): a test of genetic homogeneity using departure from the triangle constraints in IBD distribution among affected sib-pairs. Annals of Human Genetics, 2000, 64, 433-442.	0.8	19
84	The Ectocarpus Genome and Brown Algal Genomics. Advances in Botanical Research, 2012, 64, 141-184.	1.1	18
85	Recurrent Exon Shuffling Between Distant P-Element Families. Molecular Biology and Evolution, 2003, 20, 190-199.	8.9	17
86	Transposable Element Annotation in Completely Sequenced Eukaryote Genomes. Topics in Current Genetics, 2012, , 17-39.	0.7	16
87	Roadmap for Annotating Transposable Elements in Eukaryote Genomes. Methods in Molecular Biology, 2012, 859, 53-68.	0.9	15
88	Correlation of LNCR rasiRNAs Expression with Heterochromatin Formation during Development of the Holocentric Insect Spodoptera frugiperda. PLoS ONE, 2011, 6, e24746.	2.5	14
89	Studying the organization of genes encoding plant cell wall degrading enzymes in <i>Chrysomela tremula</i> provides insights into a leaf beetle genome. Insect Molecular Biology, 2014, 23, 286-300.	2.0	14
90	Developing data interoperability using standards: A wheat community use case. F1000Research, 2017, 6, 1843.	1.6	14

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91	Genetic Algorithm-based Model of Evolutionary Dynamics of Class II Transposable Elements. <i>Journal of Theoretical Biology</i> , 2001, 213, 21-30.	1.7	13
92	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.	3.6	13
93	Hoppel, a P-like Element Without Introns: a P-Element Ancestral Structure or a Retrotranscription Derivative?. <i>Molecular Biology and Evolution</i> , 2003, 20, 869-879.	8.9	12
94	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.	3.6	11
95	A simulation of P element horizontal transfer in <i>Drosophila</i> . <i>Genetica</i> , 1997, 100, 295-307.	1.1	10
96	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0038.	2.8	8
97	De Novo Annotation of Transposable Elements: Tackling the Fat Genome Issue. <i>Proceedings of the IEEE</i> , 2016, , 1-8.	21.3	8
98	On the Probability of Identity States in Permutable Populations: Reply to Cannings. <i>American Journal of Human Genetics</i> , 1998, 62, 728-729.	6.2	7
99	A Genomic Survey of <i>Mayetiola destructor</i> Mobilome Provides New Insights into the Evolutionary History of Transposable Elements in the Cecidomyiid Midges. <i>PLoS ONE</i> , 2021, 16, e0257996.	2.5	6
100	Building a successful international research community through data sharing: The case of the Wheat Information System (WheatIS). <i>F1000Research</i> , 2020, 9, 536.	1.6	5
101	In search of lost trajectories. <i>Mobile Genetic Elements</i> , 2011, 1, 151-154.	1.8	4
102	Efficient comparison of sets of intervals with NC-lists. <i>Bioinformatics</i> , 2013, 29, 933-939.	4.1	4
103	Progress in single-access information systems for wheat and rice crop improvement. <i>Briefings in Bioinformatics</i> , 2019, 20, 565-571.	6.5	4
104	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.	1.7	3
105	Departure from the triangle constraints in discordant sib pairs: A test for genetic heterogeneity. <i>Genetic Epidemiology</i> , 1999, 17, S685-S689.	1.3	3
106	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, 590-596.	2.8	3
107	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.	2.7	3
108	Traces of transposable elements in genome dark matter co-opted by flowering gene regulation networks. , 0, 2, .		3

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109	International Congress on Transposable elements (ICTE 2016) in Saint Malo: mobile elements under the sun of Brittany. <i>Mobile DNA</i> , 2016, 7, 19.	3.6	1
110	Corrections to <i>De Novo</i> Annotation of Transposable Elements: Tackling the Fat Genome Issue [Jamilloux et al., <i>Proc. IEEE</i> , 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.	21.3	1
111	Mining Plant Genomic and Genetic Data Using the GnpIS Information System. <i>Methods in Molecular Biology</i> , 2017, 1533, 103-117.	0.9	1
112	Detection and modeling of disease susceptibility locus effects: How much can be learned from contrast of populations?. <i>Genetic Epidemiology</i> , 1999, 17, S569-S574.	1.3	0
113	International Congress on Transposable Elements (ICTE) 2012 in Saint Malo and the sea of TE stories. <i>Mobile DNA</i> , 2012, 3, 17.	3.6	0