Hadi Quesneville

List of Publications by Year
in descending order

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113

papers

26,224

citations

23567

58

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23533

111

g-index

118

all docs

118

docs citations

118

times ranked

28570

citing authors

#	Article	IF	Citations
1	Population-scale long-read sequencing uncovers transposable elements associated with gene expression variation and adaptive signatures in Drosophila. Nature Communications, 2022, 13, 1948.	12.8	53
2	TE Hub: A community-oriented space for sharing and connecting tools, data, resources, and methods for transposable element annotation. Mobile DNA, 2021, 12, 16.	3.6	13
3	A Genomic Survey of Mayetiola destructor Mobilome Provides New Insights into the Evolutionary History of Transposable Elements in the Cecidomyiid Midges. PLoS ONE, 2021, 16, e0257996.	2.5	6
4	Twenty years of transposable element analysis in the Arabidopsis thaliana genome. Mobile DNA, 2020, 11, 28.	3.6	72
5	Building a successful international research community through data sharing: The case of the Wheat Information System (WheatIS). F1000Research, 2020, 9, 536.	1.6	5
6	RepetDB: a unified resource for transposable element references. Mobile DNA, 2019, 10, 6.	3.6	43
7	Stress response, behavior, and development are shaped by transposable element-induced mutations in Drosophila. PLoS Genetics, 2019, 15, e1007900.	3.5	64
8	Progress in single-access information systems for wheat and rice crop improvement. Briefings in Bioinformatics, 2019, 20, 565-571.	6.5	4
9	The Rosa genome provides new insights into the domestication of modern roses. Nature Genetics, 2018, 50, 772-777.	21.4	344
10	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
11	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
12	A high-quality genome sequence of Rosa chinensis to elucidate ornamental traits. Nature Plants, 2018, 4, 473-484.	9.3	224
13	Oak genome reveals facets of long lifespan. Nature Plants, 2018, 4, 440-452.	9.3	303
14	Evolutionary genomics of the cold-adapted diatom Fragilariopsis cylindrus. Nature, 2017, 541, 536-540.	27.8	332
15	Corrections to â€œ<italic>De Novo</italic> Annotation of Transposable Elements: Tackling the Fat Genome Issueâ€•[Jamilloux <italic>et al., Proc. IEEE</italic>, vol. 105, no. 3, pp. 474â€“481, Mar. 2017, DOI: 10.1109/JPROC.2016.2590833]. Proceedings of the IEEE, 2017, 105, 978-978.	21.3	1
16	Two genomes of highly polyphagous lepidopteran pests (Spodoptera frugiperda, Noctuidae) with different host-plant ranges. Scientific Reports, 2017, 7, 11816.	3.3	242
17	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. Nature Genetics, 2017, 49, 1099-1106.	21.4	693
18	Reconciling the evolutionary origin of bread wheat (<i>Triticum aestivum</i>). New Phytologist, 2017, 213, 1477-1486.	7.3	119

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19	Combined Genomic and Genetic Data Integration of Major Agronomical Traits in Bread Wheat (Triticum aestivum L.). Frontiers in Plant Science, 2017, 8, 1843.	3.6	55
20	Developing data interoperability using standards: A wheat community use case. F1000Research, 2017, 6, 1843.	1.6	14
21	Developing data interoperability using standards: A wheat community use case. F1000Research, 2017, 6, 1843.	1.6	20
22	Mining Plant Genomic and Genetic Data Using the GnpIS Information System. Methods in Molecular Biology, 2017, 1533, 103-117.	0.9	1
23	Comprehensive repeatome annotation reveals strong potential impact of repetitive elements on tomato ripening. BMC Genomics, 2016, 17, 624.	2.8	29
24	transPLANT Resources for Triticeae Genomic Data. Plant Genome, 2016, 9, plantgenome2015.06.0038.	2.8	8
25	De Novo Annotation of Transposable Elements: Tackling the Fat Genome Issue. Proceedings of the IEEE, 2016, , 1-8.	21.3	8
26	Towards an open grapevine information system. Horticulture Research, 2016, 3, 16056.	6.3	34
27	The Arabidopsis hnRNP-Q Protein LIF2 and the PRC1 Subunit LHP1 Function in Concert to Regulate the Transcription of Stress-Responsive Genes. Plant Cell, 2016, 28, 2197-2211.	6.6	37
28	International Congress on Transposable elements (ICTE 2016) in Saint Malo: mobile elements under the sun of Brittany. Mobile DNA, 2016, 7, 19.	3.6	1
29	Impact and insights from ancient repetitive elements in plant genomes. Current Opinion in Plant Biology, 2016, 30, 41-46.	7.1	34
30	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. Molecular Ecology Resources, 2016, 16, 254-265.	4.8	108
31	Genome expansion of Arabis alpina linked with retrotransposition and reduced symmetric DNA methylation. Nature Plants, 2015, 1, 14023.	9.3	156
32	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
33	Karyotype and Gene Order Evolution from Reconstructed Extinct Ancestors Highlight Contrasts in Genome Plasticity of Modern Rosid Crops. Genome Biology and Evolution, 2015, 7, 735-749.	2.5	46
34	Understanding Brassicaceae evolution through ancestral genome reconstruction. Genome Biology, 2015, 16, 262.	8.8	93
35	The BioMart community portal: an innovative alternative to large, centralized data repositories. Nucleic Acids Research, 2015, 43, W589-W598.	14.5	682
36	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. BMC Genomics, 2015, 16, 112.	2.8	49

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37	Whole genome comparative analysis of transposable elements provides new insight into mechanisms of their inactivation in fungal genomes. BMC Genomics, 2015, 16, 141.	2.8	105
38	Impact of transposable elements on insect genomes and biology. Current Opinion in Insect Science, 2015, 7, 30-36.	4.4	45
39	Sex and parasites: genomic and transcriptomic analysis of Microbotryum lychnidis-dioicae, the biotrophic and plant-castrating anther smut fungus. BMC Genomics, 2015, 16, 461.	2.8	58
40	A call for benchmarking transposable element annotation methods. Mobile DNA, 2015, 6, 13.	3.6	83
41	PASTEC: An Automatic Transposable Element Classification Tool. PLoS ONE, 2014, 9, e91929.	2.5	285
42	Shared Subgenome Dominance Following Polyploidization Explains Grass Genome Evolutionary Plasticity from a Seven Protochromosome Ancestor with 16K Protogenes. Genome Biology and Evolution, 2014, 6, 12-33.	2.5	75
43	Deep Investigation of Arabidopsis thaliana Junk DNA Reveals a Continuum between Repetitive Elements and Genomic Dark Matter. PLoS ONE, 2014, 9, e94101.	2.5	62
44	Studying the organization of genes encoding plant cell wall degrading enzymes in <i><scp>C</scp></i><i>hrysomela tremula</i> provides insights into a leaf beetle genome. Insect Molecular Biology, 2014, 23, 286-300.	2.0	14
45	Organization and evolution of transposable elements along the bread wheat chromosome 3B. Genome Biology, 2014, 15, 546.	8.8	88
46	Ancestral repeats have shaped epigenome and genome composition for millions of years in Arabidopsis thaliana. Nature Communications, 2014, 5, 4104.	12.8	74
47	Endogenous florendoviruses are major components of plant genomes and hallmarks of virus evolution. Nature Communications, 2014, 5, 5269.	12.8	99
48	Tedna: a transposable element <i>de novo </i> assembler. Bioinformatics, 2014, 30, 2656-2658.	4.1	30
49	The genome of the stress-tolerant wild tomato species Solanum pennellii. Nature Genetics, 2014, 46, 1034-1038.	21.4	391
50	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. Science, 2014, 345, 1251788.	12.6	1,479
51	Structural and functional partitioning of bread wheat chromosome 3B. Science, 2014, 345, 1249721.	12.6	542
52	Genome interplay in the grain transcriptome of hexaploid bread wheat. Science, 2014, 345, 1250091.	12.6	318
53	Ancient hybridizations among the ancestral genomes of bread wheat. Science, 2014, 345, 1250092.	12.6	629
54	Pan genome of the phytoplankton Emiliania underpins its global distribution. Nature, 2013, 499, 209-213.	27.8	448

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55	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. Nature Genetics, 2013, 45, 1092-1096.	21.4	236
56	Distribution, evolution, and diversity of retrotransposons at the <i>flamenco</i> locus reflect the regulatory properties of piRNA clusters. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19842-19847.	7.1	115
57	The Capsella rubella genome and the genomic consequences of rapid mating system evolution. Nature Genetics, 2013, 45, 831-835.	21.4	374
58	Wheat syntenome unveils new evidences of contrasted evolutionary plasticity between paleoâ€•and neoduplicated subgenomes. Plant Journal, 2013, 76, 1030-1044.	5.7	99
59	Efficient comparison of sets of intervals with NC-lists. Bioinformatics, 2013, 29, 933-939.	4.1	4
60	GnpIS: an information system to integrate genetic and genomic data from plants and fungi. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat058.	3.0	43
61	Roadmap for Annotating Transposable Elements in Eukaryote Genomes. Methods in Molecular Biology, 2012, 859, 53-68.	0.9	15
62	The Ectocarpus Genome and Brown Algal Genomics. Advances in Botanical Research, 2012, 64, 141-184.	1.1	18
63	Transposable Element Annotation in Completely Sequenced Eukaryote Genomes. Topics in Current Genetics, 2012, , 17-39.	0.7	16
64	International Congress on Transposable Elements (ICTE) 2012 in Saint Malo and the sea of TE stories. Mobile DNA, 2012, 3, 17.	3.6	0
65	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. Frontiers in Plant Science, 2012, 3, 5.	3.6	73
66	Genomic Analysis of the Necrotrophic Fungal Pathogens Sclerotinia sclerotiorum and Botrytis cinerea. PLoS Genetics, 2011, 7, e1002230.	3.5	902
67	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9166-9171.	7.1	640
68	Considering Transposable Element Diversification in De Novo Annotation Approaches. PLoS ONE, 2011, 6, e16526.	2.5	477
69	Correlation of LNCR rasiRNAs Expression with Heterochromatin Formation during Development of the Holocentric Insect Spodoptera frugiperda. PLoS ONE, 2011, 6, e24746.	2.5	14
70	S-MART, A Software Toolbox to Aid RNA-seq Data Analysis. PLoS ONE, 2011, 6, e25988.	2.5	32
71	In search of lost trajectories. Mobile Genetic Elements, 2011, 1, 151-154.	1.8	4
72	Effector diversification within compartments of the Leptosphaeria maculans genome affected by Repeat-Induced Point mutations. Nature Communications, 2011, 2, 202.	12.8	481

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73	Genome-wide evidence for local DNA methylation spreading from small RNA-targeted sequences in Arabidopsis. Nucleic Acids Research, 2011, 39, 6919-6931.	14.5	142
74	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
75	PÃ©rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. Nature, 2010, 464, 1033-1038.	27.8	641
76	The Ectocarpus genome and the independent evolution of multicellularity in brown algae. Nature, 2010, 465, 617-621.	27.8	774
77	Extensive synteny conservation of holocentric chromosomes in Lepidoptera despite high rates of local genome rearrangements. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7680-7685.	7.1	147
78	Genome Sequence of the Pea Aphid Acyrthosiphon pisum. PLoS Biology, 2010, 8, e1000313.	5.6	913
79	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. Science, 2010, 330, 1543-1546.	12.6	725
80	The genome of Laccaria bicolor provides insights into mycorrhizal symbiosis. Nature, 2008, 452, 88-92.	27.8	1,003
81	Genome sequence of the metazoan plant-parasitic nematode Meloidogyne incognita. Nature Biotechnology, 2008, 26, 909-915.	17.5	1,012
82	Improved detection and annotation of transposable elements in sequenced genomes using multiple reference sequence sets. Genomics, 2008, 91, 467-475.	2.9	67
83	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
84	Promoter DNA Hypermethylation and Gene Repression in Undifferentiated Arabidopsis Cells. PLoS ONE, 2008, 3, e3306.	2.5	99
85	A model of segmental duplication formation in <i>Drosophila melanogaster</i>. Genome Research, 2007, 17, 1458-1470.	5.5	81
86	Discovering and detecting transposable elements in genome sequences. Briefings in Bioinformatics, 2007, 8, 382-392.	6.5	189
87	Spip and Squiq, two novel rice non-autonomous LTR retro-element families related to RIRE3 and RIRE8. Plant Science, 2007, 172, 8-19.	3.6	11
88	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. Science, 2007, 317, 1400-1402.	12.6	837
89	Genome Sequence of Aedes aegypti, a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	12.6	1,025
90	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886

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91	LTR retrotransposons in rice (Oryza sativa, L.): recent burst amplifications followed by rapid DNA loss. BMC Genomics, 2007, 8, 218.	2.8	134
92	Variation in crossing-over rates across chromosome 4 of <i>Arabidopsis thaliana</i> reveals the presence of meiotic recombination â€œhot spotsâ€ Genome Research, 2006, 16, 106-114.	5.5	162
93	Recurrent insertion and duplication generate networks of transposable element sequences in the Drosophila melanogaster genome. Genome Biology, 2006, 7, R112.	9.6	188
94	P elements and MITE relatives in the whole genome sequence of Anopheles gambiae. BMC Genomics, 2006, 7, 214.	2.8	28
95	Combined Evidence Annotation of Transposable Elements in Genome Sequences. PLoS Computational Biology, 2005, 1, e22.	3.2	347
96	Recurrent Recruitment of the THAP DNA-Binding Domain and Molecular Domestication of the P-Transposable Element. Molecular Biology and Evolution, 2005, 22, 741-746.	8.9	38
97	Comparative analysis of BAC and whole genome shotgun sequences from an Anopheles gambiae region related to Plasmodium encapsulation. Insect Biochemistry and Molecular Biology, 2005, 35, 799-814.	2.7	3
98	Detection of transposable elements by their compositional bias. BMC Bioinformatics, 2004, 5, 94.	2.6	28
99	Detection of New Transposable Element Families in Drosophila melanogaster and Anopheles gambiae Genomes. Journal of Molecular Evolution, 2003, 57, S50-S59.	1.8	68
100	Indication of linkage and genetic heterogeneity for asthma and atopy on chromosomes 8p and 12q in 107 French EGEA families. European Journal of Human Genetics, 2003, 11, 590-596.	2.8	3
101	Recurrent Exon Shuffling Between Distant P-Element Families. Molecular Biology and Evolution, 2003, 20, 190-199.	8.9	17
102	Hoppel, a P-like Element Without Introns: a P-Element Ancestral Structure or a Retrotranscription Derivative?. Molecular Biology and Evolution, 2003, 20, 869-879.	8.9	12
103	Genetic Algorithm-based Model of Evolutionary Dynamics of Class II Transposable Elements. Journal of Theoretical Biology, 2001, 213, 21-30.	1.7	13
104	Search for multifactorial disease susceptibility genes in founder populations. Annals of Human Genetics, 2000, 64, 255-265.	0.8	75
105	The triangle test statistic (TTS): a test of genetic homogeneity using departure from the triangle constraints in IBD distribution among affected sibâ€pairs. Annals of Human Genetics, 2000, 64, 433-442.	0.8	19
106	Detection and modeling of disease susceptibility locus effects: How much can be learned from contrast of populations?. Genetic Epidemiology, 1999, 17, S569-S574.	1.3	0
107	Departure from the triangle constraints in discordant sib pairs: A test for genetic heterogeneity. Genetic Epidemiology, 1999, 17, S685-S689.	1.3	3
108	On the Probability of Identity States in Permutable Populations: Reply to Cannings. American Journal of Human Genetics, 1998, 62, 728-729.	6.2	7

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109	Dynamics of Transposable Elements in Metapopulations: A Model of P Element Invasion in Drosophila. Theoretical Population Biology, 1998, 54, 175-193.	1.1	41
110	A simulation of P element horizontal transfer in Drosophila. Genetica, 1997, 100, 295-307.	1.1	10
111	DrosophilaP element: Transposition, regulation and evolution. Genetica, 1994, 93, 61-78.	1.1	29
112	Can transposable element copy number distribution parameters be estimated from natural populations of Drosophila melanogaster?. Journal of Evolutionary Biology, 1994, 7, 13-28.	1.7	3
113	Traces of transposable elements in genome dark matter co-opted by flowering gene regulation networks. , 0, 2, .		3