Olivier Panaud

List of Publications by Year in descending order

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		136950	144013
58	10,534	32	57
papers	citations	h-index	g-index
63	63	63	12689
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	A unified classification system for eukaryotic transposable elements. Nature Reviews Genetics, 2007, 8, 973-982.	16.3	2,396
2	The banana (Musa acuminata) genome and the evolution of monocotyledonous plants. Nature, 2012, 488, 213-217.	27.8	1,049
3	Reference genome sequence of the model plant Setaria. Nature Biotechnology, 2012, 30, 555-561.	17.5	864
4	Genome analysis of the smallest free-living eukaryote Ostreococcus tauri unveils many unique features. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11647-11652.	7.1	809
5	The genome of Theobroma cacao. Nature Genetics, 2011, 43, 101-108.	21.4	656
6	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . Science, 2009, 324, 268-272.	12.6	591
7	Doubling genome size without polyploidization: Dynamics of retrotransposition-driven genomic expansions in Oryza australiensis, a wild relative of rice. Genome Research, 2006, 16, 1262-1269.	5.5	522
8	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus Oryza. Nature Genetics, 2018, 50, 285-296.	21.4	413
9	The genome sequence of African rice (Oryza glaberrima) and evidence for independent domestication. Nature Genetics, 2014, 46, 982-988.	21.4	342
10	Genome structure and metabolic features in the red seaweed <i>Chondrus crispus</i> shed light on evolution of the Archaeplastida. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5247-5252.	7.1	307
11	Oak genome reveals facets of long lifespan. Nature Plants, 2018, 4, 440-452.	9.3	303
12	The Rice Annotation Project Database (RAP-DB): 2008 update. Nucleic Acids Research, 2007, 36, D1028-D1033.	14.5	295
13	Widespread and frequent horizontal transfers of transposable elements in plants. Genome Research, 2014, 24, 831-838.	5.5	177
14	Comparative Genomic Paleontology across Plant Kingdom Reveals the Dynamics of TE-Driven Genome Evolution. Genome Biology and Evolution, 2013, 5, 954-965.	2.5	148
15	LTR retrotransposons in rice (Oryza sativa, L.): recent burst amplifications followed by rapid DNA loss. BMC Genomics, 2007, 8, 218.	2.8	134
16	Sequencing the extrachromosomal circular mobilome reveals retrotransposon activity in plants. PLoS Genetics, 2017, 13, e1006630.	3 . 5	118
17	Retrotranspositional landscape of Asian rice revealed by 3000 genomes. Nature Communications, 2019, 10, 24.	12.8	102
18	Evolutionary dynamics of an ancient retrotransposon family provides insights into evolution of genome size in the genus <i>Oryza</i> . Plant Journal, 2007, 52, 342-351.	5.7	99

#	Article	IF	CITATIONS
19	Abiotic stress and genome dynamics: specific genes and transposable elements response to iron excess in rice. Rice, 2015, 8, 13.	4.0	87
20	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. BMC Genomics, 2015, 16, 538.	2.8	86
21	Title is missing!. Euphytica, 2001, 120, 143-157.	1.2	83
22	Plant root transcriptome profiling reveals a strain-dependent response during Azospirillum-rice cooperation. Frontiers in Plant Science, 2014, 5, 607.	3.6	74
23	Evidence of multiple horizontal transfers of the long terminal repeat retrotransposon <i>RIRE1</i> within the genus <i>Oryza</i> . Plant Journal, 2008, 53, 950-959.	5.7	70
24	Transpositional landscape of the rice genome revealed by pairedâ€end mapping of highâ€throughput reâ€sequencing data. Plant Journal, 2011, 66, 241-246.	5.7	62
25	Whole genome surveys of rice, maize and sorghum reveal multiple horizontal transfers of the LTR-retrotransposon Route66 in Poaceae. BMC Evolutionary Biology, 2009, 9, 58.	3.2	61
26	Identification of an active LTR retrotransposon in rice. Plant Journal, 2009, 58, 754-765.	5.7	60
27	RetrOryza: a database of the rice LTR-retrotransposons. Nucleic Acids Research, 2007, 35, D66-D70.	14.5	53
28	The impact of transposable elements on the structure, evolution and function of the rice genome. New Phytologist, 2020, 226, 44-49.	7.3	51
29	A Genetic Model for the Female Sterility Barrier Between Asian and African Cultivated Rice Species. Genetics, 2010, 185, 1425-1440.	2.9	46
30	Reply: A unified classification system for eukaryotic transposable elements should reflect their phylogeny. Nature Reviews Genetics, 2009, 10, 276-276.	16.3	41
31	Detection of active transposable elements in Arabidopsis thaliana using Oxford Nanopore Sequencing technology. BMC Genomics, 2017, 18, 537.	2.8	39
32	Horizontal transfers of transposable elements in eukaryotes: The flying genes. Comptes Rendus - Biologies, 2016, 339, 296-299.	0.2	38
33	Horizontal transfer of transposable elements in plants. Communicative and Integrative Biology, 2008, 1, 74-77.	1.4	35
34	A new approach for annotation of transposable elements using small RNA mapping. Nucleic Acids Research, 2015, 43, e84-e84.	14.5	28
35	Use of non-radioactive digoxigenin-labeled DNA probes for RFLP analysis in rice. Plant Molecular Biology Reporter, 1990, 8, 167-171.	1.8	26
36	Assessment of genetic relationships among sexual and asexual forms of Allium cepa using morphological traits and RAPD markers. Heredity, 1997, 78, 403-409.	2.6	26

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37	A protocol for non-radioactive DNA labelling and detection in the RFLP analysis of rice and tomato using single-copy probes. Plant Molecular Biology Reporter, 1993, 11, 54-59.	1.8	24
38	QTL Mapping Combined With Comparative Analyses Identified Candidate Genes for Reduced Shattering in Setaria italica. Frontiers in Plant Science, 2018, 9, 918.	3.6	22
39	Exploration of intra- and inter-population genetic diversity in Hedysarum coronarium L. by AFLP markers. Genetic Resources and Crop Evolution, 2005, 52, 277-284.	1.6	19
40	Horizontal Gene Transfers in Plants. Life, 2021, 11, 857.	2.4	18
41	Evolution of Plant Phenotypes, from Genomes to Traits. G3: Genes, Genomes, Genetics, 2016, 6, 775-778.	1.8	16
42	Amplification dynamics of miniature invertedâ€repeat transposable elements and their impact on rice trait variability. Plant Journal, 2021, 107, 118-135.	5.7	16
43	The molecular bases of cereal domestication and the history of rice. Comptes Rendus - Biologies, 2009, 332, 267-272.	0.2	15
44	Title is missing!. Euphytica, 2002, 128, 301-305.	1.2	11
45	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
46	Diverse and mobile: <scp>eccDNA</scp> â€based identification of carrot lowâ€copyâ€number <scp>LTR</scp> retrotransposons active in callus cultures. Plant Journal, 2022, 110, 1811-1828.	5.7	11
47	Diversity of the Ty-1 copia retrotransposon Tos17 in rice (Oryza sativa L.) and the AA genome of the Oryza genus. Molecular Genetics and Genomics, 2009, 282, 633-652.	2.1	10
48	Use of Next Generation Sequencing (NGS) Technologies for the Genome-Wide Detection of Transposition. Methods in Molecular Biology, 2013, 1057, 265-274.	0.9	9
49	Transposable Element Dynamics in Rice and Its Wild Relatives. , 2013, , 55-69.		9
50	Characterization of the complete plastome of Ophrys aveyronensis, a Euro-Mediterranean orchid with an intriguing disjunct geographic distribution. Mitochondrial DNA Part B: Resources, 2019, 4, 3256-3257.	0.4	8
51	Construction and characterization of a knock-down RNA interference line of <i>OsNRPD1</i> in rice () Tj ETQq1 IB: Biological Sciences, 2020, 375, 20190338.	l 0.784314 4.0	1 rgBT /Ovel 8
52	RDA derived Oryza minuta-specific clones to probe genomic conservation across Oryza and introgression into rice (O. sativa L.). Euphytica, 2010, 176, 269-279.	1.2	6
53	Identification of high-copy number long terminal repeat retrotransposons and their expansion in Phalaenopsis orchids. BMC Genomics, 2020, 21, 807.	2.8	5
54	Paleogenomic Analysis of the Short Arm of Chromosome 3 Reveals the History of the African and Asian Progenitors of Cultivated Rices. Genome Biology and Evolution, 2010, 2, 132-139.	2.5	4

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55	Genome-Wide Analysis of Transposition Using Next Generation Sequencing Technologies. Topics in Current Genetics, 2012, , 59-70.	0.7	3
56	Whole plastid genome-based phylogenomics supports an inner placement of the O. <i>insectifera</i> group rather than a basal position in the rapidly diversifying <i>Ophrys</i> genus (Orchidaceae). Botany Letters, 2021, 168, 452-457.	1.4	2
57	Horizontal Transfers and the New Model of TE-Driven Genome Evolution in Eukaryotes. , 2015, , 77-92.		1
58	The ecology of the genome and the dynamics of the biological dark matter. Journal of Theoretical Biology, 2021, 518, 110641.	1.7	0