Romain Guyot

List of Publications by Year
in descending order

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60 papers	3,758 citations	218677 26 h-index	144013 57 g-index
63 all docs	63 docs citations	63 times ranked	5055 citing authors

#	Article	IF	Citations
1	Functional Definition of Thyroid Hormone Response Elements Based on a Synthetic STARR-seq Screen. Endocrinology, 2022, 163, .	2.8	3
2	A disease-associated mutation in thyroid hormone receptor Î±1 causes hearing loss and sensory hair cell patterning defects in mice. Science Signaling, 2022, 15, .	3.6	4
3	Two Novel Cases of Resistance to Thyroid Hormone Due to <i>THRA</i> Mutation. Thyroid, 2020, 30, 1217-1221.	4.5	16
4	A Pivotal Genetic Program Controlled by Thyroid Hormone during the Maturation of GABAergic Neurons. IScience, 2020, 23, 100899.	4.1	28
5	High-quality genome sequence of white lupin provides insight into soil exploration and seed quality. Nature Communications, 2020, 11, 492.	12.8	90
6	Retrotransposons in Plant Genomes: Structure, Identification, and Classification through Bioinformatics and Machine Learning. International Journal of Molecular Sciences, 2019, 20, 3837.	4.1	56
7	Evaluation of chloroplast genome annotation tools and application to analysis of the evolution of coffee species. PLoS ONE, 2019, 14, e0216347.	2.5	31
8	Evidence for hormonal control of heart regenerative capacity during endothermy acquisition. Science, 2019, 364, 184-188.	12.6	252
9	An integrated analysis of mRNA and sRNA transcriptional profiles in Coffea arabica L. roots: insights on nitrogen starvation responses. Functional and Integrative Genomics, 2019, 19, 151-169.	3.5	28
10	A systematic review of the application of machine learning in the detection and classification of transposable elements. PeerJ, 2019, 7, e8311.	2.0	22
11	Genome-wide association study reveals candidate genes influencing lipids and diterpenes contents in Coffea arabica L. Scientific Reports, 2018, 8, 465.	3.3	53
12	Transposable Elements in theÂPineapple Genome. Plant Genetics and Genomics: Crops and Models, 2018, , 155-165.	0.3	1
13	CRISPR/Cas9-mediated efficient targeted mutagenesis has the potential to accelerate the domestication of Coffea canephora. Plant Cell, Tissue and Organ Culture, 2018, 134, 383-394.	2.3	64
14	Structure and Distribution of Centromeric Retrotransposons at Diploid and Allotetraploid Coffea Centromeric and Pericentromeric Regions. Frontiers in Plant Science, 2018, 9, 175.	3.6	31
15	Inpactor, Integrated and Parallel Analyzer and Classifier of LTR Retrotransposons and Its Application for Pineapple LTR Retrotransposons Diversity and Dynamics. Biology, 2018, 7, 32.	2.8	21
16	CRISPR/Cas9 Editing of the Mouse <i>Thra</i> Gene Produces Models with Variable Resistance to Thyroid Hormone. Thyroid, 2018, 28, 139-150.	4.5	20
17	Genotyping-by-sequencing provides the first well-resolved phylogeny for coffee (Coffea) and insights into the evolution of caffeine content in its species. Molecular Phylogenetics and Evolution, 2017, 109, 351-361.	2.7	59
18	Distribution of Divo in Coffea genomes, a poorly described family of angiosperm LTR-Retrotransposons. Molecular Genetics and Genomics, 2017, 292, 741-754.	2.1	7

#	Article	IF	Citations
19	Application of Data Mining Algorithms to Classify Biological Data: The Coffea canephora Genome Case. Communications in Computer and Information Science, 2017, , 156-170.	0.5	7
20	Parallel Programming in Biological Sciences, Taking Advantage of Supercomputing in Genomics. Communications in Computer and Information Science, 2017, , 627-643.	0.5	2
21	The pomegranate (<i>Punica granatum</i> L.) genome and the genomics of punicalagin biosynthesis. Plant Journal, 2017, 91, 1108-1128.	5.7	109
22	Identification by the DArTseq method of the genetic origin of the Coffea canephora cultivated in Vietnam and Mexico. BMC Plant Biology, 2016, 16, 242.	3.6	43
23	Pineapple Genome: A Reference for Monocots and CAM Photosynthesis. Trends in Genetics, 2016, 32, 690-696.	6.7	19
24	Partial sequencing reveals the transposable element composition of Coffea genomes and provides evidence for distinct evolutionary stories. Molecular Genetics and Genomics, 2016, 291, 1979-1990.	2.1	16
25	Developmental programmed cell death during asymmetric microsporogenesis in holocentric species ofRhynchospora(Cyperaceae). Journal of Experimental Botany, 2016, 67, 5391-5401.	4.8	13
26	Active transposable elements recover species boundaries and geographic structure in Madagascan coffee species. Molecular Genetics and Genomics, 2016, 291, 155-168.	2.1	6
27	Assessment of genetic and epigenetic changes during cell culture ageing and relations with somaclonal variation in Coffea arabica. Plant Cell, Tissue and Organ Culture, 2015, 122, 517-531.	2.3	63
28	Genome-wide analysis of LTR-retrotransposons in oil palm. BMC Genomics, 2015, 16, 795.	2.8	18
29	Terminal-Repeat Retrotransposons with GAG Domain in Plant Genomes: A New Testimony on the Complex World of Transposable Elements. Genome Biology and Evolution, 2015, 7, 493-504.	2.5	23
30	Origin and domestication of papaya Y^h chromosome. Genome Research, 2015, 25, 524-533.	5.5	87
31	The pineapple genome and the evolution of CAM photosynthesis. Nature Genetics, 2015, 47, 1435-1442.	21.4	472
32	Large distribution and high sequence identity of a Copia-type retrotransposon in angiosperm families. Plant Molecular Biology, 2015, 89, 83-97.	3.9	10
33	Chromosomal distribution and evolution of abundant retrotransposons in plants: gypsy elements in diploid and polyploid Brachiaria forage grasses. Chromosome Research, 2015, 23, 571-582.	2.2	41
34	Coffea Genome Organization and Evolution. , 2015, , 29-37.		11
35	Caffeine-free Species in the Genus Coffea. , 2015, , 39-44.		8
36	Toxicogenomic analysis of the ability of brominated flame retardants TBBPA and BDE-209 to disrupt thyroid hormone signaling in neural cells. Toxicology, 2014, 325, 125-132.	4.2	51

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37	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. Science, 2014, 345, 1181-1184.	12.6	520
38	BAC-end sequences analysis provides first insights into coffee (Coffea canephora P.) genome composition and evolution. Plant Molecular Biology, 2013, 83, 177-189.	3.9	15
39	Genetic structure and diversity of coffee (Coffea) across Africa and the Indian Ocean islands revealed using microsatellites. Annals of Botany, 2013, 111, 229-248.	2.9	30
40	Genome-wide analysis of thyroid hormone receptors shared and specific functions in neural cells. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E766-75.	7.1	105
41	Geographical gradients in the genome size variation of wild coffee trees (Coffea) native to Africa and Indian Ocean islands. Tree Genetics and Genomes, 2012, 8, 1345-1358.	1.6	26
42	Ancestral synteny shared between distantly-related plant species from the asterid (Coffea canephora) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.8	27
43	Microâ€collinearity and genome evolution in the vicinity of an ethylene receptor gene of cultivated diploid and allotetraploid coffee species (<i>Coffea</i>). Plant Journal, 2011, 67, 305-317.	5.7	55
44	Two novel Ty1-copia retrotransposons isolated from coffee trees can effectively reveal evolutionary relationships in the Coffea genus (Rubiaceae). Molecular Genetics and Genomics, 2011, 285, 447-460.	2.1	20
45	Site-Specific Insertion Polymorphism of the MITE Alex-1 in the Genus Coffea Suggests Interspecific Gene Flow. International Journal of Evolutionary Biology, 2011, 2011, 1-9.	1.0	3
46	Patterns of Sequence Divergence and Evolution of the S1 Orthologous Regions between Asian and African Cultivated Rice Species. PLoS ONE, 2011, 6, e17726.	2.5	7
47	In planta gene expression analysis of Xanthomonas oryzae pathovar oryzae, African strain MAI1. BMC Microbiology, 2010, 10, 170.	3.3	26
48	A Genetic Model for the Female Sterility Barrier Between Asian and African Cultivated Rice Species. Genetics, 2010, 185, 1425-1440.	2.9	46
49	Life and death among plant lysophosphatidic acid acyltransferases. Plant Signaling and Behavior, 2010, 5, 913-915.	2.4	2
50	Advances in Coffea Genomics. Advances in Botanical Research, 2010, , 23-63.	1.1	23
51	Microcollinearity in an ethylene receptor coding gene region of the Coffea canephora genome is extensively conserved with Vitis vinifera and other distant dicotyledonous sequenced genomes. BMC Plant Biology, 2009, 9, 22.	3.6	21
52	RetrOryza: a database of the rice LTR-retrotransposons. Nucleic Acids Research, 2007, 35, D66-D70.	14.5	53
53	From Rice to Other Cereals: Comparative Genomics. , 2007, , 429-479.		3
54	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

#	ARTICLE	IF	CITATIONS
55	Updating of transposable element annotations from large wheat genomic sequences reveals diverse activities and gene associations. Molecular Genetics and Genomics, 2005, 274, 119-130.	2.1	82
56	Complex Organization and Evolution of the Tomato Pericentromeric Region at the <i>FER</i> Gene Locus. Plant Physiology, 2005, 138, 1205-1215.	4.8	30
57	A new structural element containing glycine-rich proteins and rhamnogalacturonan I in the protoxylem of seed plants. Journal of Cell Science, 2004, 117, 1179-1190.	2.0	27
58	In silico comparative analysis reveals a mosaic conservation of genes within a novel colinear region in wheat chromosome 1AS and rice chromosome 5S. Functional and Integrative Genomics, 2004, 4, 47-58.	3.5	56
59	Ancestral genome duplication in rice. Genome, 2004, 47, 610-614.	2.0	131
60	CACTA Transposons in Triticeae. A Diverse Family of High-Copy Repetitive Elements. Plant Physiology, 2003, 132, 52-63.	4.8	143