JÃ©rÃ´me Gouzy

List of Publications by Year
in descending order

96 papers	17,307 citations	29994 54 h-index	37111 96 g-index
104 all docs	104 docs citations	104 times ranked	19181 citing authors

#	Article	IF	Citations
1	*APOK3*, a pollen killer antidote in *Arabidopsis thaliana*. Genetics, 2022, 221, .	1.2	4
2	LeGOO: An Expertized Knowledge Database for the Model Legume Medicago truncatula. Plant and Cell Physiology, 2020, 61, 203-211.	1.5	19
3	Evolution of Fusarium tricinctum and Fusarium avenaceum mitochondrial genomes is driven by mobility of introns and of a new type of palindromic microsatellite repeats. BMC Genomics, 2020, 21, 358.	1.2	8
4	High-quality genome sequence of white lupin provides insight into soil exploration and seed quality. Nature Communications, 2020, 11, 492.	5.8	90
5	Whole-genome sequencing reveals recent and frequent genetic recombination between clonal lineages of Cryphonectria parasitica in western Europe. Fungal Genetics and Biology, 2019, 130, 122-133.	0.9	16
6	EuGene: An Automated Integrative Gene Finder for Eukaryotes and Prokaryotes. Methods in Molecular Biology, 2019, 1962, 97-120.	0.4	42
7	A High-Quality Grapevine Downy Mildew Genome Assembly Reveals Rapidly Evolving and Lineage-Specific Putative Host Adaptation Genes. Genome Biology and Evolution, 2019, 11, 954-969.	1.1	61
8	Population Genome Sequencing of the Scab Fungal Species *Venturia inaequalis*, *Venturia pirina*, *Venturia aucupariae* and *Venturia asperata*. G3: Genes, Genomes, Genetics, 2019, 9, 2405-2414.	0.8	33
9	Sunflower resistance to multiple downy mildew pathotypes revealed by recognition of conserved effectors of the oomycete *Plasmopara halstedii*. Plant Journal, 2019, 97, 730-748.	2.8	74
10	Computational analysis of the Plasmodiophora brassicae genome: mitochondrial sequence description and metabolic pathway database design. Genomics, 2019, 111, 1629-1640.	1.3	27
11	The Rosa genome provides new insights into the domestication of modern roses. Nature Genetics, 2018, 50, 772-777.	9.4	344
12	Comparison of GWAS models to identify non-additive genetic control of flowering time in sunflower hybrids. Theoretical and Applied Genetics, 2018, 131, 319-332.	1.8	38
13	High conservation of the transcriptional response to acetolactate–synthase–inhibiting herbicides across plant species. Weed Research, 2018, 58, 2-7.	0.8	8
14	Whole-genome landscape of Medicago truncatula symbiotic genes. Nature Plants, 2018, 4, 1017-1025.	4.7	192
15	myGenomeBrowser: building and sharing your own genome browser. Bioinformatics, 2017, 33, 1255-1257.	1.8	15
16	Genetic control of plasticity of oil yield for combined abiotic stresses using a joint approach of crop modelling and genome–wide association. Plant, Cell and Environment, 2017, 40, 2276-2291.	2.8	66
17	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. Nature, 2017, 546, 148-152.	13.7	579
18	Genome–wide association studies with proteomics data reveal genes important for synthesis, transport and packaging of globulins in legume seeds. New Phytologist, 2017, 214, 1597-1613.	3.5	38

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19	Widespread selective sweeps throughout the genome of model plant pathogenic fungi and identification of effector candidates. Molecular Ecology, 2017, 26, 2041-2062.	2.0	71
20	Evolutionary strata on young mating-type chromosomes despite the lack of sexual antagonism. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7067-7072.	3.3	92
21	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. Nature Genetics, 2017, 49, 1099-1106.	9.4	693
22	Improved methods and resources for paramecium genomics: transcription units, gene annotation and gene expression. BMC Genomics, 2017, 18, 483.	1.2	54
23	Extraction of high-molecular-weight genomic DNA for long-read sequencing of single molecules. BioTechniques, 2017, 62, xv.	0.8	6
24	Hybridization and polyploidy enable genomic plasticity without sex in the most devastating plant-parasitic nematodes. PLoS Genetics, 2017, 13, e1006777.	1.5	150
25	Extraction of high-molecular-weight genomic DNA for long-read sequencing of single molecules. BioTechniques, 2016, 61, 203-205.	0.8	162
26	<i>RADIS:</i> analysis of <i>RAD</i>-seq data for interspecific phylogeny. Bioinformatics, 2016, 32, 3027-3028.	1.8	15
27	A Laser Dissection-RNAseq Analysis Highlights the Activation of Cytokinin Pathways by Nod Factors in the <i>Medicago truncatula</i> Root Epidermis. Plant Physiology, 2016, 171, 2256-2276.	2.3	128
28	Draft Genome Sequence of <i>Plasmopara viticola</i> , the Grapevine Downy Mildew Pathogen. Genome Announcements, 2016, 4, .	0.8	29
29	A gene-based map of the Nod factor-independent<i>Aeschynomene evenia</i>sheds new light on the evolution of nodulation and legume genomes. DNA Research, 2016, 23, 365-376.	1.5	22
30	Polymorphic Microsatellite Markers for the Tetrapolar Anther-Smut Fungus Microbotryum saponariae Based on Genome Sequencing. PLoS ONE, 2016, 11, e0165656.	1.1	9
31	A Resource Allocation Trade-Off between Virulence and Proliferation Drives Metabolic Versatility in the Plant Pathogen Ralstonia solanacearum. PLoS Pathogens, 2016, 12, e1005939.	2.1	117
32	Enhanced in planta Fitness through Adaptive Mutations in EfpR, a Dual Regulator of Virulence and Metabolic Functions in the Plant Pathogen Ralstonia solanacearum. PLoS Pathogens, 2016, 12, e1006044.	2.1	37
33	Fullâ€length <i>de novo</i> assembly of RNAâ€seq data in pea (<i><scp>P</scp>isum sativum</i> L.) provides a gene expression atlas and gives insights into root nodulation in this species. Plant Journal, 2015, 84, 1-19.	2.8	173
34	Degeneration of the Nonrecombining Regions in the Mating-Type Chromosomes of the Anther-Smut Fungi. Molecular Biology and Evolution, 2015, 32, 928-943.	3.5	49
35	RNA-Seq analysis of rye-grass transcriptomic response to an herbicide inhibiting acetolactate-synthase identifies transcripts linked to non-target-site-based resistance. Plant Molecular Biology, 2015, 87, 473-487.	2.0	115
36	Chaos of Rearrangements in the Mating-Type Chromosomes of the Anther-Smut Fungus <i>Microbotryum lychnidis-dioicae</i>. Genetics, 2015, 200, 1275-1284.	1.2	78

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37	Adaptive Horizontal Gene Transfers between Multiple Cheese-Associated Fungi. Current Biology, 2015, 25, 2562-2569.	1.8	110
38	ALOMYbase, a resource to investigate non-target-site-based resistance to herbicides inhibiting acetolactate-synthase (ALS) in the major grass weed Alopecurus myosuroides (black-grass). BMC Genomics, 2015, 16, 590.	1.2	66
39	The small RNA diversity from Medicago truncatularoots under biotic interactions evidences the environmental plasticity of the miRNAome. Genome Biology, 2014, 15, 457.	3.8	78
40	Multiple recent horizontal transfers of a large genomic region in cheese making fungi. Nature Communications, 2014, 5, 2876.	5.8	195
41	An integrated analysis of plant and bacterial gene expression in symbiotic root nodules using laserâ€capture microdissection coupled to <scp>RNA</scp> sequencing. Plant Journal, 2014, 77, 817-837.	2.8	447
42	A <i>Medicago truncatula rdr6</i> allele impairs transgene silencing and endogenous phased si<scp>RNA</scp> production but not development. Plant Biotechnology Journal, 2014, 12, 1308-1318.	4.1	5
43	EuGene-PP: a next-generation automated annotation pipeline for prokaryotic genomes. Bioinformatics, 2014, 30, 2659-2661.	1.8	33
44	Multihost Experimental Evolution of the Pathogen Ralstonia solanacearum Unveils Genes Involved in Adaptation to Plants. Molecular Biology and Evolution, 2014, 31, 2913-2928.	3.5	72
45	Next-Generation Annotation of Prokaryotic Genomes with EuGene-P: Application to Sinorhizobium meliloti 2011. DNA Research, 2013, 20, 339-354.	1.5	90
46	Singleâ€nucleotide polymorphism discovery and diversity in the model legume M edicago truncatula. Molecular Ecology Resources, 2013, 13, 84-95.	2.2	20
47	Combined linkage and association mapping of flowering time in Sunflower (Helianthus annuus L.). Theoretical and Applied Genetics, 2013, 126, 1337-1356.	1.8	48
48	Draft Genome Sequence and Annotation of the Entomopathogenic Bacterium Xenorhabdus nematophila Strain F1. Genome Announcements, 2013, 1, .	0.8	10
49	A Regulatory Network-Based Approach Dissects Late Maturation Processes Related to the Acquisition of Desiccation Tolerance and Longevity of Medicago truncatula Seeds. Plant Physiology, 2013, 163, 757-774.	2.3	155
50	Consensus mapping of major resistance genes and independent QTL for quantitative resistance to sunflower downy mildew. Theoretical and Applied Genetics, 2012, 125, 909-920.	1.8	48
51	Transcriptome database resource and gene expression atlas for the rose. BMC Genomics, 2012, 13, 638.	1.2	76
52	Genomic insights into strategies used by Xanthomonas albilineans with its reduced artillery to spread within sugarcane xylem vessels. BMC Genomics, 2012, 13, 658.	1.2	50
53	Specific versus Non-Specific Immune Responses in an Invertebrate Species Evidenced by a Comparative de novo Sequencing Study. PLoS ONE, 2012, 7, e32512.	1.1	49
54	A Gene-Phenotype Network Based on Genetic Variability for Drought Responses Reveals Key Physiological Processes in Controlled and Natural Environments. PLoS ONE, 2012, 7, e45249.	1.1	58

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55	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	13.7	1,166
56	Transcription Reprogramming during Root Nodule Development in Medicago truncatula. PLoS ONE, 2011, 6, e16463.	1.1	102
57	The genome of Theobroma cacao. Nature Genetics, 2011, 43, 101-108.	9.4	656
58	Transcriptomic analysis of the interaction between Helianthus annuus and its obligate parasite Plasmopara halstedii shows single nucleotide polymorphisms in CRN sequences. BMC Genomics, 2011, 12, 498.	1.2	32
59	Partial Chromosome Sequence of <i>Spiroplasma citri</i> Reveals Extensive Viral Invasion and Important Gene Decay. Applied and Environmental Microbiology, 2010, 76, 3420-3426.	1.4	57
60	Genome-Wide<i>Medicago truncatula</i>Small RNA Analysis Revealed Novel MicroRNAs and Isoforms Differentially Regulated in Roots and Nodules. Plant Cell, 2009, 21, 2780-2796.	3.1	270
61	FrameDP: sensitive peptide detection on noisy matured sequences. Bioinformatics, 2009, 25, 670-671.	1.8	95
62	The complete genome sequence of Xanthomonas albilineans provides new insights into the reductive genome evolution of the xylem-limited Xanthomonadaceae. BMC Genomics, 2009, 10, 616.	1.2	142
63	Symbiosis-Related Plant Genes Modulate Molecular Responses in an Arbuscular Mycorrhizal Fungus During Early Root Interactions. Molecular Plant-Microbe Interactions, 2009, 22, 341-351.	1.4	29
64	Genome sequence of the metazoan plant-parasitic nematode Meloidogyne incognita. Nature Biotechnology, 2008, 26, 909-915.	9.4	1,012
65	LeARN: a platform for detecting, clustering and annotating non-coding RNAs. BMC Bioinformatics, 2008, 9, 21.	1.2	12
66	The abundant extrachromosomal DNA content of the Spiroplasma citri GII3-3X genome. BMC Genomics, 2008, 9, 195.	1.2	52
67	Narcisse: a mirror view of conserved syntenies. Nucleic Acids Research, 2008, 36, D485-D490.	6.5	27
68	Interoperability with Moby 1.0--It's better than sharing your toothbrush!. Briefings in Bioinformatics, 2008, 9, 220-231.	3.2	91
69	Systemic Signaling of the Plant Nitrogen Status Triggers Specific Transcriptome Responses Depending on the Nitrogen Source in <i>Medicago truncatula</i> Â Â. Plant Physiology, 2008, 146, 2020-2035.	2.3	136
70	Genome Annotation in Plants and Fungi: EuGene as a Model Platform. Current Bioinformatics, 2008, 3, 87-97.	0.7	102
71	Identification of New Potential Regulators of the Medicago truncatulaâ€"Sinorhizobium meliloti Symbiosis Using a Large-Scale Suppression Subtractive Hybridization Approach. Molecular Plant-Microbe Interactions, 2007, 20, 321-332.	1.4	35
72	Phylogenetic exploration of bacterial genomic rearrangements. Bioinformatics, 2007, 23, 1172-1174.	1.8	7

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73	REMORA: a pilot in the ocean of BioMoby web-services. Bioinformatics, 2006, 22, 900-901.	1.8	43
74	Legume genome evolution viewed through the Medicago truncatula and Lotus japonicus genomes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14959-14964.	3.3	286
75	Transcriptional snapshots provide insights into the molecular basis of arbuscular mycorrhiza in the model legume Medicago truncatula. Functional Plant Biology, 2006, 33, 737.	1.1	29
76	FixJ-regulated genes evolved through promoter duplication in Sinorhizobium meliloti. Microbiology (United Kingdom), 2004, 150, 2335-2345.	0.7	26
77	Expression Profiling in Medicago truncatula Identifies More Than 750 Genes Differentially Expressed during Nodulation, Including Many Potential Regulators of the Symbiotic Program. Plant Physiology, 2004, 136, 3159-3176.	2.3	269
78	Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype. Nature, 2004, 431, 946-957.	13.7	1,801
79	Construction and validation of cDNA-based Mt6k-RIT macro- and microarrays to explore root endosymbioses in the model legume Medicago truncatula. Journal of Biotechnology, 2004, 108, 95-113.	1.9	103
80	FrameD: a flexible program for quality check and gene prediction in prokaryotic genomes and noisy matured eukaryotic sequences. Nucleic Acids Research, 2003, 31, 3738-3741.	6.5	85
81	Comparative Sequence Analysis of the Symbiosis Island of Mesorhizobium loti Strain R7A. Journal of Bacteriology, 2002, 184, 3086-3095.	1.0	305
82	Exploring root symbiotic programs in the model legume Medicago truncatula using EST analysis. Nucleic Acids Research, 2002, 30, 5579-5592.	6.5	193
83	InterPro: An integrated documentation resource for protein families, domains and functional sites. Briefings in Bioinformatics, 2002, 3, 225-235.	3.2	155
84	ProDom: Automated clustering of homologous domains. Briefings in Bioinformatics, 2002, 3, 246-251.	3.2	341
85	Genome sequence of the plant pathogen Ralstonia solanacearum. Nature, 2002, 415, 497-502.	13.7	866
86	The Composite Genome of the Legume Symbiont Sinorhizobium meliloti. Science, 2001, 293, 668-672.	6.0	1,098
87	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. Nucleic Acids Research, 2001, 29, 37-40.	6.5	928
88	The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9889-9894.	3.3	282
89	GÃ©nomique de la lÃ©gumineuse modÃ¨le Medicago truncatula : Ã©tat des lieux et perspectives. Oleagineux Corps Gras Lipides, 2001, 8, 478-484.	0.2	6
90	Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9877-9882.	3.3	304

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91	Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti pSymA megaplasmid. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9883-9888.	3.3	278
92	Sequencing theSinorhizobium melilotiGenome. DNA Sequence, 2000, 11, 207-210.	0.7	3
93	ProDom and ProDom-CG: tools for protein domain analysis and whole genome comparisons. Nucleic Acids Research, 2000, 28, 267-269.	6.5	313
94	Whole genome protein domain analysis using a new method for domain clustering. Computers & Chemistry, 1999, 23, 333-340.	1.2	63
95	The ProDom database of protein domain families. Nucleic Acids Research, 1998, 26, 323-326.	6.5	188
96	Regional assignment of genetic markers using a somatic cell hybrid panel: a WWW interactive program available for the pig genome. Bioinformatics, 1997, 13, 69-73.	1.8	40