

# JÃ©rÃ©me Gouzy

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/332711/publications.pdf>

Version: 2024-02-01

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	Genome duplication in the teleost fish <i>Tetraodon nigroviridis</i> reveals the early vertebrate proto-karyotype. <i>Nature</i> , 2004, 431, 946-957.	13.7	1,801
2	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	13.7	1,166
3	The Composite Genome of the Legume Symbiont <i>Sinorhizobium meliloti</i> . <i>Science</i> , 2001, 293, 668-672.	6.0	1,098
4	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	9.4	1,012
5	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. <i>Nucleic Acids Research</i> , 2001, 29, 37-40.	6.5	928
6	Genome sequence of the plant pathogen <i>Ralstonia solanacearum</i> . <i>Nature</i> , 2002, 415, 497-502.	13.7	866
7	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017, 49, 1099-1106.	9.4	693
8	The genome of <i>Theobroma cacao</i> . <i>Nature Genetics</i> , 2011, 43, 101-108.	9.4	656
9	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. <i>Nature</i> , 2017, 546, 148-152.	13.7	579
10	An integrated analysis of plant and bacterial gene expression in symbiotic root nodules using laser-capture microdissection coupled to RNA sequencing. <i>Plant Journal</i> , 2014, 77, 817-837.	2.8	447
11	The <i>Rosa</i> genome provides new insights into the domestication of modern roses. <i>Nature Genetics</i> , 2018, 50, 772-777.	9.4	344
12	ProDom: Automated clustering of homologous domains. <i>Briefings in Bioinformatics</i> , 2002, 3, 246-251.	3.2	341
13	ProDom and ProDom-CG: tools for protein domain analysis and whole genome comparisons. <i>Nucleic Acids Research</i> , 2000, 28, 267-269.	6.5	313
14	Comparative Sequence Analysis of the Symbiosis Island of <i>Mesorhizobium loti</i> Strain R7A. <i>Journal of Bacteriology</i> , 2002, 184, 3086-3095.	1.0	305
15	Analysis of the chromosome sequence of the legume symbiont <i>Sinorhizobium meliloti</i> strain 1021. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 9877-9882.	3.3	304
16	Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14959-14964.	3.3	286
17	The complete sequence of the 1,683-kb pSymB megaplasmid from the N <sub>2</sub> -fixing endosymbiont <i>Sinorhizobium meliloti</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 9889-9894.	3.3	282
18	Nucleotide sequence and predicted functions of the entire <i>Sinorhizobium meliloti</i> pSymA megaplasmid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 9883-9888.	3.3	278

#	ARTICLE	IF	CITATIONS
19	Genome-Wide <i>Medicago truncatula</i> Small RNA Analysis Revealed Novel MicroRNAs and Isoforms Differentially Regulated in Roots and Nodules. <i>Plant Cell</i> , 2009, 21, 2780-2796.	3.1	270
20	Expression Profiling in <i>Medicago truncatula</i> Identifies More Than 750 Genes Differentially Expressed during Nodulation, Including Many Potential Regulators of the Symbiotic Program. <i>Plant Physiology</i> , 2004, 136, 3159-3176.	2.3	269
21	Multiple recent horizontal transfers of a large genomic region in cheese making fungi. <i>Nature Communications</i> , 2014, 5, 2876.	5.8	195
22	Exploring root symbiotic programs in the model legume <i>Medicago truncatula</i> using EST analysis. <i>Nucleic Acids Research</i> , 2002, 30, 5579-5592.	6.5	193
23	Whole-genome landscape of <i>Medicago truncatula</i> symbiotic genes. <i>Nature Plants</i> , 2018, 4, 1017-1025.	4.7	192
24	The ProDom database of protein domain families. <i>Nucleic Acids Research</i> , 1998, 26, 323-326.	6.5	188
25	Full-length <i>de novo</i> assembly of RNA-seq data in pea ( <i>Pisum sativum</i> L.) provides a gene expression atlas and gives insights into root nodulation in this species. <i>Plant Journal</i> , 2015, 84, 1-19.	2.8	173
26	Extraction of high-molecular-weight genomic DNA for long-read sequencing of single molecules. <i>BioTechniques</i> , 2016, 61, 203-205.	0.8	162
27	InterPro: An integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002, 3, 225-235.	3.2	155
28	A Regulatory Network-Based Approach Dissects Late Maturation Processes Related to the Acquisition of Desiccation Tolerance and Longevity of <i>Medicago truncatula</i> Seeds. <i>Plant Physiology</i> , 2013, 163, 757-774.	2.3	155
29	Hybridization and polyploidy enable genomic plasticity without sex in the most devastating plant-parasitic nematodes. <i>PLoS Genetics</i> , 2017, 13, e1006777.	1.5	150
30	The complete genome sequence of <i>Xanthomonas albilineans</i> provides new insights into the reductive genome evolution of the xylem-limited Xanthomonadaceae. <i>BMC Genomics</i> , 2009, 10, 616.	1.2	142
31	Systemic Signaling of the Plant Nitrogen Status Triggers Specific Transcriptome Responses Depending on the Nitrogen Source in <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2008, 146, 2020-2035.	2.3	136
32	A Laser Dissection-RNAseq Analysis Highlights the Activation of Cytokinin Pathways by Nod Factors in the <i>Medicago truncatula</i> Root Epidermis. <i>Plant Physiology</i> , 2016, 171, 2256-2276.	2.3	128
33	A Resource Allocation Trade-Off between Virulence and Proliferation Drives Metabolic Versatility in the Plant Pathogen <i>Ralstonia solanacearum</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005939.	2.1	117
34	RNA-Seq analysis of rye-grass transcriptomic response to an herbicide inhibiting acetolactate-synthase identifies transcripts linked to non-target-site-based resistance. <i>Plant Molecular Biology</i> , 2015, 87, 473-487.	2.0	115
35	Adaptive Horizontal Gene Transfers between Multiple Cheese-Associated Fungi. <i>Current Biology</i> , 2015, 25, 2562-2569.	1.8	110
36	Construction and validation of cDNA-based Mt6k-RIT macro- and microarrays to explore root endosymbioses in the model legume <i>Medicago truncatula</i> . <i>Journal of Biotechnology</i> , 2004, 108, 95-113.	1.9	103

#	ARTICLE	IF	CITATIONS
37	Genome Annotation in Plants and Fungi: EuGene as a Model Platform. <i>Current Bioinformatics</i> , 2008, 3, 87-97.	0.7	102
38	Transcription Reprogramming during Root Nodule Development in <i>Medicago truncatula</i> . <i>PLoS ONE</i> , 2011, 6, e16463.	1.1	102
39	FrameDP: sensitive peptide detection on noisy matured sequences. <i>Bioinformatics</i> , 2009, 25, 670-671.	1.8	95
40	Evolutionary strata on young mating-type chromosomes despite the lack of sexual antagonism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7067-7072.	3.3	92
41	Interoperability with Moby 1.0–It's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , 2008, 9, 220-231.	3.2	91
42	Next-Generation Annotation of Prokaryotic Genomes with EuGene-P: Application to <i>Sinorhizobium melliloti</i> 2011. <i>DNA Research</i> , 2013, 20, 339-354.	1.5	90
43	High-quality genome sequence of white lupin provides insight into soil exploration and seed quality. <i>Nature Communications</i> , 2020, 11, 492.	5.8	90
44	FrameD: a flexible program for quality check and gene prediction in prokaryotic genomes and noisy matured eukaryotic sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3738-3741.	6.5	85
45	The small RNA diversity from <i>Medicago truncatula</i> roots under biotic interactions evidences the environmental plasticity of the miRNAome. <i>Genome Biology</i> , 2014, 15, 457.	3.8	78
46	Chaos of Rearrangements in the Mating-Type Chromosomes of the Anther-Smut Fungus <i>Microbotryum lychnidis-dioicae</i> . <i>Genetics</i> , 2015, 200, 1275-1284.	1.2	78
47	Transcriptome database resource and gene expression atlas for the rose. <i>BMC Genomics</i> , 2012, 13, 638.	1.2	76
48	Sunflower resistance to multiple downy mildew pathotypes revealed by recognition of conserved effectors of the oomycete <i>Plasmopara halstedii</i> . <i>Plant Journal</i> , 2019, 97, 730-748.	2.8	74
49	Multihost Experimental Evolution of the Pathogen <i>Ralstonia solanacearum</i> Unveils Genes Involved in Adaptation to Plants. <i>Molecular Biology and Evolution</i> , 2014, 31, 2913-2928.	3.5	72
50	Widespread selective sweeps throughout the genome of model plant pathogenic fungi and identification of effector candidates. <i>Molecular Ecology</i> , 2017, 26, 2041-2062.	2.0	71
51	ALOMYbase, a resource to investigate non-target-site-based resistance to herbicides inhibiting acetolactate-synthase (ALS) in the major grass weed <i>Alopecurus myosuroides</i> (black-grass). <i>BMC Genomics</i> , 2015, 16, 590.	1.2	66
52	Genetic control of plasticity of oil yield for combined abiotic stresses using a joint approach of crop modelling and genome-wide association. <i>Plant, Cell and Environment</i> , 2017, 40, 2276-2291.	2.8	66
53	Whole genome protein domain analysis using a new method for domain clustering. <i>Computers &amp; Chemistry</i> , 1999, 23, 333-340.	1.2	63
54	A High-Quality Grapevine Downy Mildew Genome Assembly Reveals Rapidly Evolving and Lineage-Specific Putative Host Adaptation Genes. <i>Genome Biology and Evolution</i> , 2019, 11, 954-969.	1.1	61

#	ARTICLE	IF	CITATIONS
55	A Gene-Phenotype Network Based on Genetic Variability for Drought Responses Reveals Key Physiological Processes in Controlled and Natural Environments. <i>PLoS ONE</i> , 2012, 7, e45249.	1.1	58
56	Partial Chromosome Sequence of <i>Spiroplasma citri</i> Reveals Extensive Viral Invasion and Important Gene Decay. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3420-3426.	1.4	57
57	Improved methods and resources for paramecium genomics: transcription units, gene annotation and gene expression. <i>BMC Genomics</i> , 2017, 18, 483.	1.2	54
58	The abundant extrachromosomal DNA content of the <i>Spiroplasma citri</i> GII3-3X genome. <i>BMC Genomics</i> , 2008, 9, 195.	1.2	52
59	Genomic insights into strategies used by <i>Xanthomonas albilineans</i> with its reduced artillery to spread within sugarcane xylem vessels. <i>BMC Genomics</i> , 2012, 13, 658.	1.2	50
60	Specific versus Non-Specific Immune Responses in an Invertebrate Species Evidenced by a Comparative de novo Sequencing Study. <i>PLoS ONE</i> , 2012, 7, e32512.	1.1	49
61	Degeneration of the Nonrecombining Regions in the Mating-Type Chromosomes of the Anther-Smut Fungi. <i>Molecular Biology and Evolution</i> , 2015, 32, 928-943.	3.5	49
62	Consensus mapping of major resistance genes and independent QTL for quantitative resistance to sunflower downy mildew. <i>Theoretical and Applied Genetics</i> , 2012, 125, 909-920.	1.8	48
63	Combined linkage and association mapping of flowering time in Sunflower ( <i>Helianthus annuus</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 1337-1356.	1.8	48
64	REMORA: a pilot in the ocean of BioMoby web-services. <i>Bioinformatics</i> , 2006, 22, 900-901.	1.8	43
65	EuGene: An Automated Integrative Gene Finder for Eukaryotes and Prokaryotes. <i>Methods in Molecular Biology</i> , 2019, 1962, 97-120.	0.4	42
66	Regional assignment of genetic markers using a somatic cell hybrid panel: a WWW interactive program available for the pig genome. <i>Bioinformatics</i> , 1997, 13, 69-73.	1.8	40
67	Genome-wide association studies with proteomics data reveal genes important for synthesis, transport and packaging of globulins in legume seeds. <i>New Phytologist</i> , 2017, 214, 1597-1613.	3.5	38
68	Comparison of GWAS models to identify non-additive genetic control of flowering time in sunflower hybrids. <i>Theoretical and Applied Genetics</i> , 2018, 131, 319-332.	1.8	38
69	Enhanced in planta Fitness through Adaptive Mutations in EfpR, a Dual Regulator of Virulence and Metabolic Functions in the Plant Pathogen <i>Ralstonia solanacearum</i> . <i>PLoS Pathogens</i> , 2016, 12, e1006044.	2.1	37
70	Identification of New Potential Regulators of the <i>Medicago truncatula</i> – <i>Sinorhizobium meliloti</i> Symbiosis Using a Large-Scale Suppression Subtractive Hybridization Approach. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 321-332.	1.4	35
71	EuGene-PP: a next-generation automated annotation pipeline for prokaryotic genomes. <i>Bioinformatics</i> , 2014, 30, 2659-2661.	1.8	33
72	Population Genome Sequencing of the Scab Fungal Species <i>Venturia inaequalis</i> , <i>Venturia pirina</i> , <i>Venturia aucupariae</i> and <i>Venturia asperata</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2405-2414.	0.8	33

#	ARTICLE	IF	CITATIONS
73	Transcriptomic analysis of the interaction between <i>Helianthus annuus</i> and its obligate parasite <i>Plasmopara halstedii</i> shows single nucleotide polymorphisms in CRN sequences. <i>BMC Genomics</i> , 2011, 12, 498.	1.2	32
74	Symbiosis-Related Plant Genes Modulate Molecular Responses in an Arbuscular Mycorrhizal Fungus During Early Root Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 341-351.	1.4	29
75	Draft Genome Sequence of <i>Plasmopara viticola</i> , the Grapevine Downy Mildew Pathogen. <i>Genome Announcements</i> , 2016, 4, .	0.8	29
76	Transcriptional snapshots provide insights into the molecular basis of arbuscular mycorrhiza in the model legume <i>Medicago truncatula</i> . <i>Functional Plant Biology</i> , 2006, 33, 737.	1.1	29
77	Narcisse: a mirror view of conserved syntenies. <i>Nucleic Acids Research</i> , 2008, 36, D485-D490.	6.5	27
78	Computational analysis of the <i>Plasmodiophora brassicae</i> genome: mitochondrial sequence description and metabolic pathway database design. <i>Genomics</i> , 2019, 111, 1629-1640.	1.3	27
79	FixJ-regulated genes evolved through promoter duplication in <i>Sinorhizobium meliloti</i> . <i>Microbiology (United Kingdom)</i> , 2004, 150, 2335-2345.	0.7	26
80	A gene-based map of the Nod factor-independent <i>Aeschynomene evenia</i> sheds new light on the evolution of nodulation and legume genomes. <i>DNA Research</i> , 2016, 23, 365-376.	1.5	22
81	Single nucleotide polymorphism discovery and diversity in the model legume <i>Medicago truncatula</i> . <i>Molecular Ecology Resources</i> , 2013, 13, 84-95.	2.2	20
82	LeGOO: An Expertized Knowledge Database for the Model Legume <i>Medicago truncatula</i> . <i>Plant and Cell Physiology</i> , 2020, 61, 203-211.	1.5	19
83	Whole-genome sequencing reveals recent and frequent genetic recombination between clonal lineages of <i>Cryphonectria parasitica</i> in western Europe. <i>Fungal Genetics and Biology</i> , 2019, 130, 122-133.	0.9	16
84	<i>RADIS</i> analysis of <i>RAD</i> -seq data for interspecific phylogeny. <i>Bioinformatics</i> , 2016, 32, 3027-3028.	1.8	15
85	myGenomeBrowser: building and sharing your own genome browser. <i>Bioinformatics</i> , 2017, 33, 1255-1257.	1.8	15
86	LeARN: a platform for detecting, clustering and annotating non-coding RNAs. <i>BMC Bioinformatics</i> , 2008, 9, 21.	1.2	12
87	Draft Genome Sequence and Annotation of the Entomopathogenic Bacterium <i>Xenorhabdus nematophila</i> Strain F1. <i>Genome Announcements</i> , 2013, 1, .	0.8	10
88	Polymorphic Microsatellite Markers for the Tetrapolar Anther-Smut Fungus <i>Microbotryum saponariae</i> Based on Genome Sequencing. <i>PLoS ONE</i> , 2016, 11, e0165656.	1.1	9
89	High conservation of the transcriptional response to acetolactate synthase-inhibiting herbicides across plant species. <i>Weed Research</i> , 2018, 58, 2-7.	0.8	8
90	Evolution of <i>Fusarium tricinctum</i> and <i>Fusarium avenaceum</i> mitochondrial genomes is driven by mobility of introns and of a new type of palindromic microsatellite repeats. <i>BMC Genomics</i> , 2020, 21, 358.	1.2	8

#	ARTICLE	IF	CITATIONS
91	Phylogenetic exploration of bacterial genomic rearrangements. <i>Bioinformatics</i> , 2007, 23, 1172-1174.	1.8	7
92	Génomique de la légumineuse modèle <i>Medicago truncatula</i> : État des lieux et perspectives. <i>Oleagineux Corps Gras Lipides</i> , 2001, 8, 478-484.	0.2	6
93	Extraction of high-molecular-weight genomic DNA for long-read sequencing of single molecules. <i>BioTechniques</i> , 2017, 62, xv.	0.8	6
94	A <i>Medicago truncatula</i> <i>rdr6</i> allele impairs transgene silencing and endogenous phased siRNA production but not development. <i>Plant Biotechnology Journal</i> , 2014, 12, 1308-1318.	4.1	5
95	<i>APOK3</i> , a pollen killer antidote in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2022, 221, .	1.2	4
96	Sequencing the <i>Sinorhizobium meliloti</i> Genome. <i>DNA Sequence</i> , 2000, 11, 207-210.	0.7	3