

# Etienne G Danchin

## List of Publications by Year in descending order

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84  
papers

13,285  
citations

94433

37  
h-index

60623

81  
g-index

100  
all docs

100  
docs citations

100  
times ranked

13009  
citing authors

#	ARTICLE	IF	CITATIONS
1	Top 10 plant-parasitic nematodes in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2013, 14, 946-961.	4.2	1,454
2	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	27.8	1,442
3	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i> ) Tj ETQq1 1 0,784314 rgBT /Over	17.5	1,516
4	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231.	17.5	1,047
5	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	17.5	1,012
6	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	27.8	1,003
7	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	3.5	902
8	Dividing the large glycoside hydrolase family 13 into subfamilies: towards improved functional annotations of A-amylase-related proteins. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 555-562.	2.1	530
9	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	3.5	402
10	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , 2013, 500, 453-457.	27.8	352
11	The genome sequence of the model ascomycete fungus <i>Podospora anserina</i> . <i>Genome Biology</i> , 2008, 9, R77.	9.6	301
12	Multiple lateral gene transfers and duplications have promoted plant parasitism ability in nematodes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17651-17656.	7.1	300
13	High similarity between flanking regions of different microsatellites detected within each of two species of Lepidoptera: <i>Parnassius apollo</i> and <i>Euphydryas aurinia</i> . <i>Molecular Ecology</i> , 2004, 13, 1693-1700.	3.9	157
14	The genome of the yellow potato cyst nematode, <i>Globodera rostochiensis</i> , reveals insights into the basis of parasitism and virulence. <i>Genome Biology</i> , 2016, 17, 124.	8.8	156
15	Hybridization and polyploidy enable genomic plasticity without sex in the most devastating plant-parasitic nematodes. <i>PLoS Genetics</i> , 2017, 13, e1006777.	3.5	150
16	Horizontal Gene Transfer in Nematodes: A Catalyst for Plant Parasitism?. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 879-887.	2.6	146
17	A <i>Medicago truncatula</i> NADPH oxidase is involved in symbiotic nodule functioning. <i>New Phytologist</i> , 2011, 189, 580-592.	7.3	145
18	Biotechnological applications and potential of fungal feruloyl esterases based on prevalence, classification and biochemical diversity. <i>Biotechnology Letters</i> , 2008, 30, 387-396.	2.2	136

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19	Diversity and Evolution of Root-Knot Nematodes, Genus <i>Meloidogyne</i> : New Insights from the Genomic Era. Annual Review of Phytopathology, 2013, 51, 203-220.	7.8	135
20	The plant apoplasm is an important recipient compartment for nematode secreted proteins. Journal of Experimental Botany, 2011, 62, 1241-1253.	4.8	113
21	FIGENIX: intelligent automation of genomic annotation: expertise integration in a new software platform. BMC Bioinformatics, 2005, 6, 198.	2.6	109
22	The Genomes of Root-Knot Nematodes. Annual Review of Phytopathology, 2009, 47, 333-351.	7.8	104
23	An <i>Arabidopsis</i> (malectin-like) leucine-rich repeat receptor-like kinase contributes to downy mildew disease. Plant, Cell and Environment, 2011, 34, 1944-1957.	5.7	93
24	Identifying discriminative classification-based motifs in biological sequences. Bioinformatics, 2011, 27, 1231-1238.	4.1	93
25	Identification of Novel Target Genes for Safer and More Specific Control of Root-Knot Nematodes from a Pan-Genome Mining. PLoS Pathogens, 2013, 9, e1003745.	4.7	90
26	A root-knot nematode-secreted protein is injected into giant cells and targeted to the nuclei. New Phytologist, 2012, 194, 924-931.	7.3	85
27	Genomic and transcriptomic analysis of <i>Laccaria bicolor</i> CAZome reveals insights into polysaccharides remodelling during symbiosis establishment. Fungal Genetics and Biology, 2014, 72, 168-181.	2.1	81
28	Horizontal Gene Transfer of Pectinases from Bacteria Preceded the Diversification of Stick and Leaf Insects. Scientific Reports, 2016, 6, 26388.	3.3	78
29	Signatures of adaptation to plant parasitism in nematode genomes. Parasitology, 2015, 142, S71-S84.	1.5	68
30	Contribution of Lateral Gene Transfers to the Genome Composition and Parasitic Ability of Root-Knot Nematodes. PLoS ONE, 2012, 7, e50875.	2.5	57
31	Parasitic success without sex – the nematode experience. Journal of Evolutionary Biology, 2014, 27, 1323-1333.	1.7	56
32	Nod Factor Effects on Root Hair-Specific Transcriptome of <i>Medicago truncatula</i> : Focus on Plasma Membrane Transport Systems and Reactive Oxygen Species Networks. Frontiers in Plant Science, 2016, 7, 794.	3.6	55
33	The major histocompatibility complex origin. Immunological Reviews, 2004, 198, 216-232.	6.0	54
34	Horizontal Gene Transfer from Bacteria Has Enabled the Plant-Parasitic Nematode <i>Globodera pallida</i> to Feed on Host-Derived Sucrose. Molecular Biology and Evolution, 2016, 33, 1571-1579.	8.9	52
35	Genome-wide survey and analysis of microsatellites in nematodes, with a focus on the plant-parasitic species <i>Meloidogyne incognita</i> . BMC Genomics, 2010, 11, 598.	2.8	45
36	Lateral gene transfer in eukaryotes: tip of the iceberg or of the ice cube?. BMC Biology, 2016, 14, 101.	3.8	44

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37	Genome-wide analysis of expansin superfamily in wild <i>Arachis</i> discloses a stress-responsive expansin-like B gene. <i>Plant Molecular Biology</i> , 2017, 94, 79-96.	3.9	43
38	Towards the reconstruction of the bilaterian ancestral pre-MHC region. <i>Trends in Genetics</i> , 2004, 20, 587-591.	6.7	40
39	Alienness: Rapid Detection of Candidate Horizontal Gene Transfers across the Tree of Life. <i>Genes</i> , 2017, 8, 248.	2.4	40
40	The Transcriptome of <i>Nacobbus aberrans</i> Reveals Insights into the Evolution of Sedentary Endoparasitism in Plant-Parasitic Nematodes. <i>Genome Biology and Evolution</i> , 2014, 6, 2181-2194.	2.5	39
41	Gene copy number variations as signatures of adaptive evolution in the parthenogenetic, plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Molecular Ecology</i> , 2019, 28, 2559-2572.	3.9	39
42	Prospects of herbivore egg-killing plant defenses for sustainable crop protection. <i>Ecology and Evolution</i> , 2016, 6, 6906-6918.	1.9	38
43	Characterization of raffinose metabolism genes uncovers a wild <i>Arachis</i> galactinol synthase conferring tolerance to abiotic stresses. <i>Scientific Reports</i> , 2020, 10, 15258.	3.3	37
44	Genome sequence of the root-knot nematode <i>Meloidogyne luci</i> . <i>Journal of Nematology</i> , 2020, 52, 1-5.	0.9	37
45	A rigorous method for multigenic families' functional annotation: the peptidyl arginine deiminase (PADs) proteins family example. <i>BMC Genomics</i> , 2005, 6, 153.	2.8	34
46	Eleven ancestral gene families lost in mammals and vertebrates while otherwise universally conserved in animals. <i>BMC Evolutionary Biology</i> , 2006, 6, 5.	3.2	33
47	Genome assembly and annotation of <i>Meloidogyne enterolobii</i> , an emerging parthenogenetic root-knot nematode. <i>Scientific Data</i> , 2020, 7, 324.	5.3	33
48	Where do animal $\alpha$ -amylases come from? An interkingdom trip. <i>FEBS Letters</i> , 2007, 581, 3927-3935.	2.8	30
49	Functional diversification of horizontally acquired glycoside hydrolase family 45 (GH45) proteins in <i>Phytophaga</i> beetles. <i>BMC Evolutionary Biology</i> , 2019, 19, 100.	3.2	30
50	Chromosome-level genome assembly reveals homologous chromosomes and recombination in asexual rotifer <i>Adineta vaga</i> . <i>Science Advances</i> , 2021, 7, eabg4216.	10.3	30
51	Comparative Genomics Reveals Novel Target Genes towards Specific Control of Plant-Parasitic Nematodes. <i>Genes</i> , 2020, 11, 1347.	2.4	29
52	Conceptual bases for quantifying the role of the environment on gene evolution: the participation of positive selection and neutral evolution. <i>Biological Reviews</i> , 2007, 82, 551-572.	10.4	28
53	Lateral gene transfers have polished animal genomes: lessons from nematodes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 27.	3.9	27
54	Comparative root transcriptome of wild <i>Arachis</i> reveals NBS-LRR genes related to nematode resistance. <i>BMC Plant Biology</i> , 2018, 18, 159.	3.6	27

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55	Signatures of the Evolution of Parthenogenesis and Cryptobiosis in the Genomes of Panagrolaimid Nematodes. <i>IScience</i> , 2019, 21, 587-602.	4.1	27
56	Genome structure and content of the rice root-knot nematode ( <i>Meloidogyne graminicola</i> ). <i>Ecology and Evolution</i> , 2020, 10, 11006-11021.	1.9	27
57	Conservation of the MHC-like region throughout evolution. <i>Immunogenetics</i> , 2003, 55, 141-148.	2.4	25
58	Genome Expression Dynamics Reveal the Parasitism Regulatory Landscape of the Root-Knot Nematode <i>Meloidogyne incognita</i> and a Promoter Motif Associated with Effector Genes. <i>Genes</i> , 2021, 12, 771.	2.4	24
59	Evolution of the proto-MHC ancestral region: more evidence for the plesiomorphic organisation of human chromosome 9q34 region. <i>Immunogenetics</i> , 2003, 55, 429-436.	2.4	23
60	Data-mining of the <i>Meloidogyne incognita</i> degradome and comparative analysis of proteases in nematodes. <i>Genomics</i> , 2011, 97, 29-36.	2.9	23
61	What Nematode genomes tell us about the importance of horizontal gene transfers in the evolutionary history of animals. <i>Mobile Genetic Elements</i> , 2011, 1, 269-292.	1.8	23
62	Population genomics supports clonal reproduction and multiple independent gains and losses of parasitic abilities in the most devastating nematode pest. <i>Evolutionary Applications</i> , 2020, 13, 442-457.	3.1	23
63	Single pH buffer refolding screen for protein from inclusion bodies. <i>Protein Expression and Purification</i> , 2012, 82, 352-359.	1.3	19
64	The Transcriptomes of <i>Xiphinema index</i> and <i>Longidorus elongatus</i> Suggest Independent Acquisition of Some Plant Parasitism Genes by Horizontal Gene Transfer in Early-Branching Nematodes. <i>Genes</i> , 2017, 8, 287.	2.4	19
65	Cross-Kingdom Analysis of Diversity, Evolutionary History, and Site Selection within the Eukaryotic Macrophage Migration Inhibitory Factor Superfamily. <i>Genes</i> , 2019, 10, 740.	2.4	19
66	Genome-wide expert annotation of the epigenetic machinery of the plant-parasitic nematodes <i>Meloidogyne</i> spp., with a focus on the asexually reproducing species. <i>BMC Genomics</i> , 2018, 19, 321.	2.8	18
67	Contrasting Effects of Wild <i>Arachis</i> Dehydrin Under Abiotic and Biotic Stresses. <i>Frontiers in Plant Science</i> , 2019, 10, 497.	3.6	18
68	Statistical Evidence for a More Than 800-Million-Year-Old Evolutionarily Conserved Genomic Region in Our Genome. <i>Journal of Molecular Evolution</i> , 2004, 59, 587-597.	1.8	17
69	Dissecting protein domain variability in the core RNA interference machinery of five insect orders. <i>RNA Biology</i> , 2021, 18, 1653-1681.	3.1	16
70	Evolutionarily conserved plant genes responsive to root-knot nematodes identified by comparative genomics. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1063-1078.	2.1	14
71	Movements of transposable elements contribute to the genomic plasticity and species diversification in an asexually reproducing nematode pest. <i>Evolutionary Applications</i> , 2021, 14, 1844-1866.	3.1	14
72	Eukaryote to gut bacteria transfer of a glycoside hydrolase gene essential for starch breakdown in plants. <i>Mobile Genetic Elements</i> , 2012, 2, 81-87.	1.8	12

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73	Recent Advances in Population Genomics of Plant-Parasitic Nematodes. <i>Phytopathology</i> , 2021, 111, 40-48.	2.2	12
74	A Chemosensory GPCR as a Potential Target to Control the Root-Knot Nematode <i>Meloidogyne incognita</i> Parasitism in Plants. <i>Molecules</i> , 2019, 24, 3798.	3.8	11
75	CASSIOPE: An expert system for conserved regions searches. <i>BMC Bioinformatics</i> , 2009, 10, 284.	2.6	9
76	Genomic Perspectives on the Long-Term Absence of Sexual Reproduction in Animals. , 2011, , 223-242.		9
77	Evolution of major histocompatibility complex by whole genome duplication before mammalian radiation. <i>Immunogenetics</i> , 2008, 60, 423-438.	2.4	5
78	The use of evolutionary biology concepts for genome annotation. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007, 308B, 26-36.	1.3	4
79	Carbohydrate-Active Enzymes Database: Principles and Classification of Glycosyltransferases. , 0, , 89-118.		3
80	The Genome Sequence of <i>Meloidogyne incognita</i> Unveils Mechanisms of Adaptation to Plant-Parasitism in Metazoa. , 2009, , 287-302.		3
81	Targeted transcriptomics reveals signatures of large-scale independent origins and concerted regulation of effector genes in <i>Radopholus similis</i> . <i>PLoS Pathogens</i> , 2021, 17, e1010036.	4.7	2
82	Chromatin Landscape Dynamics in the Early Development of the Plant Parasitic Nematode <i>Meloidogyne incognita</i> . <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 765690.	3.7	2
83	Computational reconstruction of ancestral genomic regions from evolutionarily conserved gene clusters. , 2007, , 139-150.		1
84	Teratosphaeria stem canker disease on Eucalypt in Italy. <i>European Journal of Plant Pathology</i> , 2019, 153, 503-515.	1.7	0