

Etienne G Danchin

List of Publications by Year in descending order

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84
papers

13,285
citations

94269

37
h-index

60497

81
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100
all docs

100
docs citations

100
times ranked

13009
citing authors

#	ARTICLE	IF	CITATIONS
1	Dissecting protein domain variability in the core RNA interference machinery of five insect orders. <i>RNA Biology</i> , 2021, 18, 1653-1681.	1.5	16
2	Recent Advances in Population Genomics of Plant-Parasitic Nematodes. <i>Phytopathology</i> , 2021, 111, 40-48.	1.1	12
3	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.	1.0	24
4	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.	1.5	14
5	Chromosome-level genome assembly reveals homologous chromosomes and recombination in asexual rotifer <i>Adineta vaga</i> . <i>Science Advances</i> , 2021, 7, eabg4216.	4.7	30
6	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.	2.1	2
7	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.	1.8	2
8	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.	1.5	23
9	Characterization of raffinose metabolism genes uncovers a wild <i>Arachis galactinol synthase</i> conferring tolerance to abiotic stresses. <i>Scientific Reports</i> , 2020, 10, 15258.	1.6	37
10	Comparative Genomics Reveals Novel Target Genes towards Specific Control of Plant-Parasitic Nematodes. <i>Genes</i> , 2020, 11, 1347.	1.0	29
11	Genome assembly and annotation of <i>Meloidogyne enterolobii</i> , an emerging parthenogenetic root-knot nematode. <i>Scientific Data</i> , 2020, 7, 324.	2.4	33
12	Genome structure and content of the rice root-knot nematode (<i>Meloidogyne graminicola</i>). <i>Ecology and Evolution</i> , 2020, 10, 11006-11021.	0.8	27
13	Evolutionarily conserved plant genes responsive to root-knot nematodes identified by comparative genomics. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1063-1078.	1.0	14
14	Genome sequence of the root-knot nematode <i>Meloidogyne luci</i> . <i>Journal of Nematology</i> , 2020, 52, 1-5.	0.4	37
15	Cross-Kingdom Analysis of Diversity, Evolutionary History, and Site Selection within the Eukaryotic Macrophage Migration Inhibitory Factor Superfamily. <i>Genes</i> , 2019, 10, 740.	1.0	19
16	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.	1.7	11
17	Functional diversification of horizontally acquired glycoside hydrolase family 45 (GH45) proteins in Phytophaga beetles. <i>BMC Evolutionary Biology</i> , 2019, 19, 100.	3.2	30
18	Contrasting Effects of Wild <i>Arachis</i> Dehydrin Under Abiotic and Biotic Stresses. <i>Frontiers in Plant Science</i> , 2019, 10, 497.	1.7	18

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19	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.	2.0	39
20	Signatures of the Evolution of Parthenogenesis and Cryptobiosis in the Genomes of Panagrolaimid Nematodes. <i>IScience</i> , 2019, 21, 587-602.	1.9	27
21	Teratosphaeria stem canker disease on Eucalypt in Italy. <i>European Journal of Plant Pathology</i> , 2019, 153, 503-515.	0.8	0
22	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.	1.2	18
23	Comparative root transcriptome of wild <i>Arachis</i> reveals NBS-LRR genes related to nematode resistance. <i>BMC Plant Biology</i> , 2018, 18, 159.	1.6	27
24	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.	2.0	43
25	Alienness: Rapid Detection of Candidate Horizontal Gene Transfers across the Tree of Life. <i>Genes</i> , 2017, 8, 248.	1.0	40
26	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.	1.0	19
27	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
28	Nod Factor Effects on Root Hair-Specific Transcriptome of <i>Medicago truncatula</i> : Focus on Plasma Membrane Transport Systems and Reactive Oxygen Species Networks. <i>Frontiers in Plant Science</i> , 2016, 7, 794.	1.7	55
29	Lateral gene transfer in eukaryotes: tip of the iceberg or of the ice cube?. <i>BMC Biology</i> , 2016, 14, 101.	1.7	44
30	Prospects of herbivore egg-killing plant defenses for sustainable crop protection. <i>Ecology and Evolution</i> , 2016, 6, 6906-6918.	0.8	38
31	Horizontal Gene Transfer of Pectinases from Bacteria Preceded the Diversification of Stick and Leaf Insects. <i>Scientific Reports</i> , 2016, 6, 26388.	1.6	78
32	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.	3.8	156
33	Horizontal Gene Transfer from Bacteria Has Enabled the Plant-Parasitic Nematode <i>Globodera pallida</i> to Feed on Host-Derived Sucrose. <i>Molecular Biology and Evolution</i> , 2016, 33, 1571-1579.	3.5	52
34	Signatures of adaptation to plant parasitism in nematode genomes. <i>Parasitology</i> , 2015, 142, S71-S84.	0.7	68
35	Parasitic success without sex – the nematode experience. <i>Journal of Evolutionary Biology</i> , 2014, 27, 1323-1333.	0.8	56
36	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.	1.1	39

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37	Genomic and transcriptomic analysis of <i>Laccaria bicolor</i> CAZome reveals insights into polysaccharides remodelling during symbiosis establishment. <i>Fungal Genetics and Biology</i> , 2014, 72, 168-181.	0.9	81
38	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , 2013, 500, 453-457.	13.7	352
39	Top 10 plant-parasitic nematodes in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2013, 14, 946-961.	2.0	1,454
40	Diversity and Evolution of Root-Knot Nematodes, Genus <i>Meloidogyne</i> : New Insights from the Genomic Era. <i>Annual Review of Phytopathology</i> , 2013, 51, 203-220.	3.5	135
41	Identification of Novel Target Genes for Safer and More Specific Control of Root-Knot Nematodes from a Pan-Genome Mining. <i>PLoS Pathogens</i> , 2013, 9, e1003745.	2.1	90
42	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
43	Single pH buffer refolding screen for protein from inclusion bodies. <i>Protein Expression and Purification</i> , 2012, 82, 352-359.	0.6	19
44	A root-knot nematode-secreted protein is injected into giant cells and targeted to the nuclei. <i>New Phytologist</i> , 2012, 194, 924-931.	3.5	85
45	Contribution of Lateral Gene Transfers to the Genome Composition and Parasitic Ability of Root-Knot Nematodes. <i>PLoS ONE</i> , 2012, 7, e50875.	1.1	57
46	Lateral gene transfers have polished animal genomes: lessons from nematodes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 27.	1.8	27
47	Genomic Perspectives on the Long-Term Absence of Sexual Reproduction in Animals. , 2011, , 223-242.		9
48	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	1.5	902
49	Data-mining of the <i>Meloidogyne incognita</i> degradome and comparative analysis of proteases in nematodes. <i>Genomics</i> , 2011, 97, 29-36.	1.3	23
50	An <i>Arabidopsis</i> (malectin-like) leucine-rich repeat receptor-like kinase contributes to downy mildew disease. <i>Plant, Cell and Environment</i> , 2011, 34, 1944-1957.	2.8	93
51	A <i>Medicago truncatula</i> NADPH oxidase is involved in symbiotic nodule functioning. <i>New Phytologist</i> , 2011, 189, 580-592.	3.5	145
52	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
53	Horizontal Gene Transfer in Nematodes: A Catalyst for Plant Parasitism?. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 879-887.	1.4	146
54	The plant apoplasm is an important recipient compartment for nematode secreted proteins. <i>Journal of Experimental Botany</i> , 2011, 62, 1241-1253.	2.4	113

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55	Identifying discriminative classification-based motifs in biological sequences. <i>Bioinformatics</i> , 2011, 27, 1231-1238.	1.8	93
56	Genome-wide survey and analysis of microsatellites in nematodes, with a focus on the plant-parasitic species <i>Meloidogyne incognita</i> . <i>BMC Genomics</i> , 2010, 11, 598.	1.2	45
57	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	13.7	1,442
58	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.	3.3	300
59	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	1.5	402
60	CASSIOPE: An expert system for conserved regions searches. <i>BMC Bioinformatics</i> , 2009, 10, 284.	1.2	9
61	The Genomes of Root-Knot Nematodes. <i>Annual Review of Phytopathology</i> , 2009, 47, 333-351.	3.5	104
62	The Genome Sequence of <i>Meloidogyne incognita</i> Unveils Mechanisms of Adaptation to Plant-Parasitism in Metazoa. , 2009, , 287-302.		3
63	Evolution of major histocompatibility complex by α -globin duplication before mammalian radiation. <i>Immunogenetics</i> , 2008, 60, 423-438.	1.2	5
64	Biotechnological applications and potential of fungal feruloyl esterases based on prevalence, classification and biochemical diversity. <i>Biotechnology Letters</i> , 2008, 30, 387-396.	1.1	136
65	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	13.7	1,003
66	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	9.4	1,012
67	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i>) Tj ETQq1 1 0.784314 r gBT /Ov 9.4 1,516	9.4	1,516
68	The genome sequence of the model ascomycete fungus <i>Podospira anserina</i> . <i>Genome Biology</i> , 2008, 9, R77.	13.9	301
69	Computational reconstruction of ancestral genomic regions from evolutionarily conserved gene clusters. , 2007, , 139-150.		1
70	Where do animal α -amylases come from? An interkingdom trip. <i>FEBS Letters</i> , 2007, 581, 3927-3935.	1.3	30
71	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.	0.6	4
72	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231.	9.4	1,047

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73	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.	4.7	28
74	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
75	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.	1.0	530
76	FIGENIX: intelligent automation of genomic annotation: expertise integration in a new software platform. <i>BMC Bioinformatics</i> , 2005, 6, 198.	1.2	109
77	A rigorous method for multigenic families' functional annotation: the peptidyl arginine deiminase (PADs) proteins family example. <i>BMC Genomics</i> , 2005, 6, 153.	1.2	34
78	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.	2.0	157
79	The major histocompatibility complex origin. <i>Immunological Reviews</i> , 2004, 198, 216-232.	2.8	54
80	Towards the reconstruction of the bilaterian ancestral pre-MHC region. <i>Trends in Genetics</i> , 2004, 20, 587-591.	2.9	40
81	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.	0.8	17
82	Conservation of the MHC-like region throughout evolution. <i>Immunogenetics</i> , 2003, 55, 141-148.	1.2	25
83	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.	1.2	23
84	Carbohydrate-Active Enzymes Database: Principles and Classification of Glycosyltransferases. , 0, , 89-118.		3