

# Etienne G Danchin

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

93  
papers

9,949  
citations

35  
h-index

99  
g-index

100  
ext. papers

11,977  
ext. citations

8.6  
avg, IF

5.36  
L-index

#	Paper	IF	Citations
93	Dissecting protein domain variability in the core RNA interference machinery of five insect orders. <i>RNA Biology</i> , <b>2021</b> , 18, 1653-1681	4.8	6
92	Targeted transcriptomics reveals signatures of large-scale independent origins and concerted regulation of effector genes in <i>Radopholus similis</i> . <i>PLoS Pathogens</i> , <b>2021</b> , 17, e1010036	7.6	
91	Chromosome-level genome assembly reveals homologous chromosomes and recombination in asexual rotifer. <i>Science Advances</i> , <b>2021</b> , 7, eabg4216	14.3	5
90	Genome Expression Dynamics Reveal the Parasitism Regulatory Landscape of the Root-Knot Nematode and a Promoter Motif Associated with Effector Genes. <i>Genes</i> , <b>2021</b> , 12,	4.2	5
89	Movements of transposable elements contribute to the genomic plasticity and species diversification in an asexually reproducing nematode pest. <i>Evolutionary Applications</i> , <b>2021</b> , 14, 1844-1868	4.8	3
88	Recent Advances in Population Genomics of Plant-Parasitic Nematodes. <i>Phytopathology</i> , <b>2021</b> , 111, 40-48	4.8	4
87	Chromatin Landscape Dynamics in the Early Development of the Plant Parasitic Nematode <i>Meloidogyne incognita</i> . <i>Frontiers in Cell and Developmental Biology</i> , <b>2021</b> , 9, 765690	5.7	
86	Evolutionarily conserved plant genes responsive to root-knot nematodes identified by comparative genomics. <i>Molecular Genetics and Genomics</i> , <b>2020</b> , 295, 1063-1078	3.1	4
85	Genome sequence of the root-knot nematode. <i>Journal of Nematology</i> , <b>2020</b> , 52, 1-5	1.1	14
84	Population genomics supports clonal reproduction and multiple independent gains and losses of parasitic abilities in the most devastating nematode pest. <i>Evolutionary Applications</i> , <b>2020</b> , 13, 442-457	4.8	14
83	Characterization of raffinose metabolism genes uncovers a wild <i>Arachis</i> galactinol synthase conferring tolerance to abiotic stresses. <i>Scientific Reports</i> , <b>2020</b> , 10, 15258	4.9	9
82	Comparative Genomics Reveals Novel Target Genes towards Specific Control of Plant-Parasitic Nematodes. <i>Genes</i> , <b>2020</b> , 11,	4.2	9
81	Genome assembly and annotation of <i>Meloidogyne enterolobii</i> , an emerging parthenogenetic root-knot nematode. <i>Scientific Data</i> , <b>2020</b> , 7, 324	8.2	12
80	Genome structure and content of the rice root-knot nematode ( <i></i> ). <i>Ecology and Evolution</i> , <b>2020</b> , 10, 1100621802113	11.0	13
79	Functional diversification of horizontally acquired glycoside hydrolase family 45 (GH45) proteins in Phytophaga beetles. <i>BMC Evolutionary Biology</i> , <b>2019</b> , 19, 100	3	19
78	Contrasting Effects of Wild Dehydrin Under Abiotic and Biotic Stresses. <i>Frontiers in Plant Science</i> , <b>2019</b> , 10, 497	6.2	12
77	Gene copy number variations as signatures of adaptive evolution in the parthenogenetic, plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Molecular Ecology</i> , <b>2019</b> , 28, 2559-2572	5.7	25

76	Cross-Kingdom Analysis of Diversity, Evolutionary History, and Site Selection within the Eukaryotic Macrophage Migration Inhibitory Factor Superfamily. <i>Genes</i> , <b>2019</b> , 10,	4.2	7
75	A Chemosensory GPCR as a Potential Target to Control the Root-Knot Nematode Parasitism in Plants. <i>Molecules</i> , <b>2019</b> , 24,	4.8	4
74	Signatures of the Evolution of Parthenogenesis and Cryptobiosis in the Genomes of Panagrolaimid Nematodes. <i>IScience</i> , <b>2019</b> , 21, 587-602	6.1	8
73	Teratosphaeria stem canker disease on Eucalypt in Italy. <i>European Journal of Plant Pathology</i> , <b>2019</b> , 153, 503-515	2.1	
72	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> , <b>2018</b> , 19, 321	4.5	6
71	Comparative root transcriptome of wild <i>Arachis</i> reveals NBS-LRR genes related to nematode resistance. <i>BMC Plant Biology</i> , <b>2018</b> , 18, 159	5.3	17
70	Genome-wide analysis of expansin superfamily in wild <i>Arachis</i> discloses a stress-responsive expansin-like B gene. <i>Plant Molecular Biology</i> , <b>2017</b> , 94, 79-96	4.6	27
69	Alienness: Rapid Detection of Candidate Horizontal Gene Transfers across the Tree of Life. <i>Genes</i> , <b>2017</b> , 8,	4.2	23
68	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> , <b>2017</b> , 8,	4.2	14
67	Hybridization and polyploidy enable genomic plasticity without sex in the most devastating plant-parasitic nematodes. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006777	6	87
66	Lateral gene transfer in eukaryotes: tip of the iceberg or of the ice cube?. <i>BMC Biology</i> , <b>2016</b> , 14, 101	7.3	32
65	Prospects of herbivore egg-killing plant defenses for sustainable crop protection. <i>Ecology and Evolution</i> , <b>2016</b> , 6, 6906-6918	2.8	25
64	Horizontal Gene Transfer of Pectinases from Bacteria Preceded the Diversification of Stick and Leaf Insects. <i>Scientific Reports</i> , <b>2016</b> , 6, 26388	4.9	38
63	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> , <b>2016</b> , 17, 124	18.3	95
62	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> , <b>2016</b> , 33, 1571-9	8.3	38
61	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> , <b>2016</b> , 7, 794	6.2	34
60	Signatures of adaptation to plant parasitism in nematode genomes. <i>Parasitology</i> , <b>2015</b> , 142 Suppl 1, S71-84	2.7	50
59	Genomic and transcriptomic analysis of <i>Laccaria bicolor</i> CAZome reveals insights into polysaccharides remodelling during symbiosis establishment. <i>Fungal Genetics and Biology</i> , <b>2014</b> , 72, 168-181	3.9	62

58	Parasitic success without sex [The nematode experience. <i>Journal of Evolutionary Biology</i> , <b>2014</b> , 27, 1323-33		42
57	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> , <b>2014</b> , 6, 2181-94	3.9	35
56	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , <b>2013</b> , 500, 453-7	50.4	274
55	Top 10 plant-parasitic nematodes in molecular plant pathology. <i>Molecular Plant Pathology</i> , <b>2013</b> , 14, 946-61	5.7	836
54	Diversity and evolution of root-knot nematodes, genus <i>Meloidogyne</i> : new insights from the genomic era. <i>Annual Review of Phytopathology</i> , <b>2013</b> , 51, 203-20	10.8	92
53	Identification of novel target genes for safer and more specific control of root-knot nematodes from a pan-genome mining. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003745	7.6	66
52	Single pH buffer refolding screen for protein from inclusion bodies. <i>Protein Expression and Purification</i> , <b>2012</b> , 82, 352-9	2	14
51	A root-knot nematode-secreted protein is injected into giant cells and targeted to the nuclei. <i>New Phytologist</i> , <b>2012</b> , 194, 924-931	9.8	64
50	Contribution of lateral gene transfers to the genome composition and parasitic ability of root-knot nematodes. <i>PLoS ONE</i> , <b>2012</b> , 7, e50875	3.7	46
49	Lateral gene transfers have polished animal genomes: lessons from nematodes. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2012</b> , 2, 27	5.9	25
48	Eukaryote to gut bacteria transfer of a glycoside hydrolase gene essential for starch breakdown in plants. <i>Mobile Genetic Elements</i> , <b>2012</b> , 2, 81-87		12
47	Genomic Perspectives on the Long-Term Absence of Sexual Reproduction in Animals <b>2011</b> , 223-242		8
46	Genomic analysis of the necrotrophic fungal pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002230	6	659
45	Data-mining of the <i>Meloidogyne incognita</i> degradome and comparative analysis of proteases in nematodes. <i>Genomics</i> , <b>2011</b> , 97, 29-36	4.3	21
44	An <i>Arabidopsis</i> (malectin-like) leucine-rich repeat receptor-like kinase contributes to downy mildew disease. <i>Plant, Cell and Environment</i> , <b>2011</b> , 34, 1944-57	8.4	74
43	A <i>Medicago truncatula</i> NADPH oxidase is involved in symbiotic nodule functioning. <i>New Phytologist</i> , <b>2011</b> , 189, 580-92	9.8	115
42	What Nematode genomes tell us about the importance of horizontal gene transfers in the evolutionary history of animals. <i>Mobile Genetic Elements</i> , <b>2011</b> , 1, 269-273		19
41	Horizontal gene transfer in nematodes: a catalyst for plant parasitism?. <i>Molecular Plant-Microbe Interactions</i> , <b>2011</b> , 24, 879-87	3.6	124

40	The plant apoplast is an important recipient compartment for nematode secreted proteins. <i>Journal of Experimental Botany</i> , <b>2011</b> , 62, 1241-53	7	88
39	Identifying discriminative classification-based motifs in biological sequences. <i>Bioinformatics</i> , <b>2011</b> , 27, 1231-8	7.2	55
38	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , <b>2010</b> , 464, 367-73	50.4	1085
37	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> , <b>2010</b> , 107, 17651-6	11.5	244
36	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> , <b>2010</b> , 11, 598	4.5	44
35	The genome of <i>Nectria haematococca</i> : contribution of supernumerary chromosomes to gene expansion. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000618	6	329
34	CASSIOPE: an expert system for conserved regions searches. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 284	3.6	8
33	The genomes of root-knot nematodes. <i>Annual Review of Phytopathology</i> , <b>2009</b> , 47, 333-51	10.8	91
32	The Genome Sequence of <i>Meloidogyne incognita</i> Unveils Mechanisms of Adaptation to Plant-Parasitism in Metazoa <b>2009</b> , 287-302		1
31	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , <b>2008</b> , 452, 88-92	50.4	823
30	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , <b>2008</b> , 26, 909-15	44.5	790
29	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea jecorina</i> ). <i>Nature Biotechnology</i> , <b>2008</b> , 26, 553-60	44.5	920
28	The genome sequence of the model ascomycete fungus <i>Podospora anserina</i> . <i>Genome Biology</i> , <b>2008</b> , 9, R77	18.3	237
27	Evolution of major histocompatibility complex by "en bloc" duplication before mammalian radiation. <i>Immunogenetics</i> , <b>2008</b> , 60, 423-38	3.2	5
26	Biotechnological applications and potential of fungal feruloyl esterases based on prevalence, classification and biochemical diversity. <i>Biotechnology Letters</i> , <b>2008</b> , 30, 387-96	3	119
25	The use of evolutionary biology concepts for genome annotation. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , <b>2007</b> , 308, 26-36	1.8	4
24	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , <b>2007</b> , 25, 221-31	44.5	889
23	Conceptual bases for quantifying the role of the environment on gene evolution: the participation of positive selection and neutral evolution. <i>Biological Reviews</i> , <b>2007</b> , 82, 551-72	13.5	26

22	Computational reconstruction of ancestral genomic regions from evolutionarily conserved gene clusters <b>2007</b> , 139-150		1
21	Where do animal alpha-amylases come from? An interkingdom trip. <i>FEBS Letters</i> , <b>2007</b> , 581, 3927-35	3.8	21
20	Eleven ancestral gene families lost in mammals and vertebrates while otherwise universally conserved in animals. <i>BMC Evolutionary Biology</i> , <b>2006</b> , 6, 5	3	26
19	Dividing the large glycoside hydrolase family 13 into subfamilies: towards improved functional annotations of alpha-amylase-related proteins. <i>Protein Engineering, Design and Selection</i> , <b>2006</b> , 19, 555-62 <sup>1.9</sup>		43 <sup>0</sup>
18	FIGENIX: intelligent automation of genomic annotation: expertise integration in a new software platform. <i>BMC Bioinformatics</i> , <b>2005</b> , 6, 198	3.6	103
17	A rigorous method for multigenic families functional annotation: the peptidyl arginine deiminase (PADs) proteins family example. <i>BMC Genomics</i> , <b>2005</b> , 6, 153	4.5	28
16	High similarity between flanking regions of different microsatellites detected within each of two species of Lepidoptera: Parnassius apollo and Euphydryas aurinia. <i>Molecular Ecology</i> , <b>2004</b> , 13, 1693-700 <sup>5.7</sup>		151
15	The major histocompatibility complex origin. <i>Immunological Reviews</i> , <b>2004</b> , 198, 216-32	11.3	47
14	Towards the reconstruction of the bilaterian ancestral pre-MHC region. <i>Trends in Genetics</i> , <b>2004</b> , 20, 587-91	8.4	36
13	Statistical evidence for a more than 800-million-year-old evolutionarily conserved genomic region in our genome. <i>Journal of Molecular Evolution</i> , <b>2004</b> , 59, 587-97	3.1	16
12	Conservation of the MHC-like region throughout evolution. <i>Immunogenetics</i> , <b>2003</b> , 55, 141-148	3.2	22
11	Evolution of the proto-MHC ancestral region: more evidence for the plesiomorphic organisation of human chromosome 9q34 region. <i>Immunogenetics</i> , <b>2003</b> , 55, 429-36	3.2	21
10	Carbohydrate-Active Enzymes Database: Principles and Classification of Glycosyltransferases <sup>89-118</sup>		3
9	Alienness: Rapid Detection of Candidate Horizontal Gene Transfers across the Tree of Life		2
8	Population genomics supports clonal reproduction and multiple gains and losses of parasitic abilities in the most devastating nematode plant pest		2
7	Peculiar hybrid genomes of devastating plant pests promote plasticity in the absence of sex and meiosis		1
6	Signatures of the evolution of parthenogenesis and cryptobiosis in panagrolaimid nematodes		6
5	Transposable Elements are an evolutionary force shaping genomic plasticity in the parthenogenetic root-knot nematode <i>Meloidogyne incognita</i>		3

- 4 Homologous chromosomes in asexual rotifer *Adineta vaga* suggest automixis 7
- 3 The polyploid genome of the mitotic parthenogenetic root-knot nematode *Meloidogyne enterolobii* 2
- 2 Genome expression dynamics reveals parasitism regulatory landscape of the root-knot nematode *Meloidogyne incognita* and a promoter motif associated with effector genes 1
- 1 Chromatin landscape dynamics in development of the plant parasitic nematode *Meloidogyne incognita* 2