

Georgios D Koutsovoulos

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

2,356
citations

279798

23
h-index

395702

33
g-index

46
all docs

46
docs citations

46
times ranked

3653
citing authors

#	ARTICLE	IF	CITATIONS
1	Blobology: exploring raw genome data for contaminants, symbionts and parasites using taxon-annotated GC-coverage plots. <i>Frontiers in Genetics</i> , 2013, 4, 237.	2.3	258
2	No evidence for extensive horizontal gene transfer in the genome of the tardigrade <i>Hypsibius dujardini</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5053-5058.	7.1	214
3	The evolution of parasitism in Nematoda. <i>Parasitology</i> , 2015, 142, S26-S39.	1.5	199
4	Comparative genomics of the tardigrades <i>Hypsibius dujardini</i> and <i>Ramazzottius varieornatus</i> . <i>PLoS Biology</i> , 2017, 15, e2002266.	5.6	170
5	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
6	Formin Is Associated with Left-Right Asymmetry in the Pond Snail and the Frog. <i>Current Biology</i> , 2016, 26, 654-660.	3.9	135
7	The genome of the heartworm, <i>Dirofilaria immitis</i> , reveals drug and vaccine targets. <i>FASEB Journal</i> , 2012, 26, 4650-4661.	0.5	124
8	Ancient and Novel Small RNA Pathways Compensate for the Loss of piRNAs in Multiple Independent Nematode Lineages. <i>PLoS Biology</i> , 2015, 13, e1002061.	5.6	118
9	Silencing of Germline-Expressed Genes by DNA Elimination in Somatic Cells. <i>Developmental Cell</i> , 2012, 23, 1072-1080.	7.0	101
10	The complex hybrid origins of the root knot nematodes revealed through comparative genomics. <i>PeerJ</i> , 2014, 2, e356.	2.0	99
11	The ash dieback invasion of Europe was founded by two genetically divergent individuals. <i>Nature Ecology and Evolution</i> , 2018, 2, 1000-1008.	7.8	82
12	Secretion of an Argonaute protein by a parasitic nematode and the evolution of its siRNA guides. <i>Nucleic Acids Research</i> , 2019, 47, 3594-3606.	14.5	75
13	A single chromosome assembly of <i>Bacteroides fragilis</i> strain BE1 from Illumina and MinION nanopore sequencing data. <i>GigaScience</i> , 2015, 4, 60.	6.4	64
14	Toward 959 nematode genomes. <i>Worm</i> , 2012, 1, 42-50.	1.0	51
15	Phylogenomics and Analysis of Shared Genes Suggest a Single Transition to Mutualism in <i>Wolbachia</i> of Nematodes. <i>Genome Biology and Evolution</i> , 2013, 5, 1668-1674.	2.5	49
16	Palaeosymbiosis Revealed by Genomic Fossils of <i>Wolbachia</i> in a Strongyloidean Nematode. <i>PLoS Genetics</i> , 2014, 10, e1004397.	3.5	49
17	The genome of <i>Romanomermis culicivorax</i> : revealing fundamental changes in the core developmental genetic toolkit in Nematoda. <i>BMC Genomics</i> , 2013, 14, 923.	2.8	43
18	Chromosome-Wide Evolution and Sex Determination in the Three-Sexed Nematode <i>Auanema rhodensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1211-1230.	1.8	39

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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.	3.9	39
20	Genome sequence of the root-knot nematode <i>Meloidogyne luci</i> . <i>Journal of Nematology</i> , 2020, 52, 1-5.	0.9	37
21	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
22	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
23	Reinforcement learning produces dominant strategies for the Iterated Prisoner's Dilemma. <i>PLoS ONE</i> , 2017, 12, e0188046.	2.5	26
24	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
25	Sex- and Gamete-Specific Patterns of X Chromosome Segregation in a Trioecious Nematode. <i>Current Biology</i> , 2018, 28, 93-99.e3.	3.9	22
26	High genetic diversity in the <i>Dirofilaria repens</i> species complex revealed by mitochondrial genomes of feline microfilaria samples from Narathiwat, Thailand. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 389-399.	3.0	22
27	Toward Universal Forward Genetics: Using a Draft Genome Sequence of the Nematode <i>Oscheius tipulae</i> To Identify Mutations Affecting Vulva Development. <i>Genetics</i> , 2017, 206, 1747-1761.	2.9	18
28	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
29	iPhy: an integrated phylogenetic workbench for supermatrix analyses. <i>BMC Bioinformatics</i> , 2011, 12, 30.	2.6	10
30	The Evolution of Tyrosine-Recombinase Elements in Nematoda. <i>PLoS ONE</i> , 2014, 9, e106630.	2.5	6
31	An Open Framework for the Reproducible Study of the Iterated Prisoner's Dilemma. <i>Journal of Open Research Software</i> , 2016, 4, 35.	5.9	6
32	A draft genome for a species of <i>Halicephalobus</i> (Panagrolaimidae). <i>Journal of Nematology</i> , 2019, 51, 1-4.	0.9	4
33	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
34	Phylogenomics of Nematoda. , 0, , 62-83.		1
35	Impact of host and plant phylogenies on parasitoid host range. <i>Biological Control</i> , 2021, 163, 104729.	3.0	1