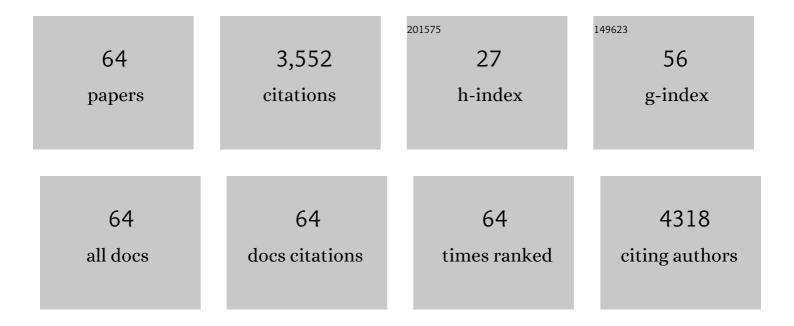
Dee R Denver

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11707350/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Genomic Analyses of Globodera pallida, A Quarantine Agricultural Pathogen in Idaho. Pathogens, 2021, 10, 363.	1.2	1
2	Phylogenetic evidence for the invasion of a commercialized European Phasmarhabditis hermaphrodita lineage into North America and New Zealand. PLoS ONE, 2020, 15, e0237249.	1.1	20
3	Lethality of four species of Phasmarhabditis (Nematoda: Rhabditidae) to the invasive slug, Deroceras reticulatum (Gastropoda: Agriolimacidae) in laboratory infectivity trials. Biological Control, 2020, 150, 104349.	1.4	21

First report of a gastropod parasitic nematode <i>Phasmarhabditis californica</i> (Nematoda:) Tj ETQq0 0 0 rgBT / $_{0.4}^{0}$ / $_{10}^{0}$ Tf 50 62:

•		0.1	10
5	Mitochondrial DNA Variation and Selfish Propagation Following Experimental Bottlenecking in Two Distantly Related Caenorhabditis briggsae Isolates. Genes, 2020, 11, 77.	1.0	5
6	First report of molecular characterization and phylogeny of <i>Trichuris fossor</i> Hall, 1916 (Nematoda: Trichuridae). Journal of Nematology, 2020, 52, 1-6.	0.4	2
7	Title is missing!. , 2020, 15, e0237249.		0
8	Title is missing!. , 2020, 15, e0237249.		0
9	Title is missing!. , 2020, 15, e0237249.		0
10	Title is missing!. , 2020, 15, e0237249.		0
11	Complex Transmission Patterns and Age-Related Dynamics of a Selfish mtDNA Deletion. Integrative and Comparative Biology, 2019, 59, 983-993.	0.9	4
12	Sex and Mitonuclear Adaptation in Experimental <i>Caenorhabditis elegans</i> Populations. Genetics, 2019, 211, 1045-1058.	1.2	18
13	Analysis of nematode-endosymbiont coevolution in the Xiphinema americanum species complex using molecular markers of variableÂevolutionary rates. Nematology, 2019, 21, 533-546.	0.2	4
14	Variable Abundance and Distribution of Wolbachia and Cardinium Endosymbionts in Plant-Parasitic Nematode Field Populations. Frontiers in Microbiology, 2019, 10, 964.	1.5	25
15	Genome Announcement: The Draft Genomes of Two Radopholus similis populations from Costa Rica. Journal of Nematology, 2019, 51, 1-4.	0.4	6
16	Comparative Genomics of Wolbachia–Cardinium Dual Endosymbiosis in a Plant-Parasitic Nematode. Frontiers in Microbiology, 2018, 9, 2482.	1.5	36
17	Comparative Genomic Analysis of 130 Bacteriophages Infecting Bacteria in the Genus Pseudomonas. Frontiers in Microbiology, 2018, 9, 1456.	1.5	20
18	Molecular signatures of host specificity linked to habitat specialization in <i>Exaiptasia</i> sea anemones. Ecology and Evolution, 2018, 8, 5413-5426.	0.8	9

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19	First Report of the Gastropod-Killing Nematode, <i>Phasmarhabditis hermaphrodita</i> , in Oregon, U.S.A Journal of Nematology, 2018, 50, 77-78.	0.4	12
20	Natural Variation in Responses to Acute Heat and Cold Stress in a Sea Anemone Model System for Coral Bleaching. Biological Bulletin, 2017, 233, 168-181.	0.7	10
21	Transcription through the eye of a needle: daily and annual cyclic gene expression variation in Douglas-fir needles. BMC Genomics, 2017, 18, 558.	1.2	35
22	Adaptive Evolution under Extreme Genetic Drift in Oxidatively Stressed Caenorhabditis elegans. Genome Biology and Evolution, 2017, 9, 3008-3022.	1.1	10
23	Introduction to Nematode Genome and Transcriptome Announcements inÂthe Journal of Nematology. Journal of Nematology, 2017, 49, 125-126.	0.4	1
24	The Draft Genome of Globodera ellingtonae. Journal of Nematology, 2017, 49, 127-128.	0.4	17
25	Paths of Heritable Mitochondrial DNA Mutation and Heteroplasmy in Reference and gas-1 Strains of Caenorhabditis elegans. Frontiers in Genetics, 2016, 7, 51.	1.1	16
26	Genomic evidence for plant-parasitic nematodes as the earliest Wolbachia hosts. Scientific Reports, 2016, 6, 34955.	1.6	54
27	Paternal Mitochondrial Transmission in Intra-SpeciesCaenorhabditis briggsaeHybrids: Table 1. Molecular Biology and Evolution, 2016, 33, 3158-3160.	3.5	15
28	The mitochondrial genome of Globodera ellingtonae is composed of two circles with segregated gene content and differential copy numbers. BMC Genomics, 2016, 17, 706.	1.2	27
29	Genome-wide polymorphism and signatures of selection in the symbiotic sea anemone Aiptasia. BMC Genomics, 2016, 17, 160.	1.2	22
30	The genomic basis of parasitism in the Strongyloides clade of nematodes. Nature Genetics, 2016, 48, 299-307.	9.4	226
31	Genome Skimming: A Rapid Approach to Gaining Diverse Biological Insights into Multicellular Pathogens. PLoS Pathogens, 2016, 12, e1005713.	2.1	41
32	Selfish Mitochondrial DNA Proliferates and Diversifies in Small, but not Large, Experimental Populations of <i>Caenorhabditis briggsae</i> . Genome Biology and Evolution, 2015, 7, 2023-2037.	1.1	30
33	Comparative Genomics of a Plant-Parasitic Nematode Endosymbiont Suggest a Role in Nutritional Symbiosis. Genome Biology and Evolution, 2015, 7, 2727-2746.	1.1	42
34	A Broadly Implementable Research Course in Phage Discovery and Genomics for First-Year Undergraduate Students. MBio, 2014, 5, e01051-13.	1.8	424
35	Endogenous ROS levels in C. elegans under exogenous stress support revision of oxidative stress theory of life-history tradeoffs. BMC Evolutionary Biology, 2014, 14, 161.	3.2	23
36	Sea anemones possess dynamic mitogenome structures. Molecular Phylogenetics and Evolution, 2014, 75, 184-193.	1.2	38

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#	Article	IF	CITATIONS
37	Using Mitogenomic and Nuclear Ribosomal Sequence Data to Investigate the Phylogeny of the Xiphinema americanum Species Complex. PLoS ONE, 2014, 9, e90035.	1.1	21
38	Natural variation in Caenorhabditis briggsae mitochondrial form and function suggests a novel model of organelle dynamics. Mitochondrion, 2013, 13, 44-51.	1.6	9
39	Evolution of a Higher Intracellular Oxidizing Environment in Caenorhabditis elegans under Relaxed Selection. PLoS ONE, 2013, 8, e65604.	1.1	7
40	Variation in Base-Substitution Mutation in Experimental and Natural Lineages of Caenorhabditis Nematodes. Genome Biology and Evolution, 2012, 4, 513-522.	1.1	114
41	Selfish Little Circles: Transmission Bias and Evolution of Large Deletion-Bearing Mitochondrial DNA in Caenorhabditis briggsae Nematodes. PLoS ONE, 2012, 7, e41433.	1.1	51
42	In Vivo Quantification Reveals Extensive Natural Variation in Mitochondrial Form and Function in Caenorhabditis briggsae. PLoS ONE, 2012, 7, e43837.	1.1	31
43	FITNESS RECOVERY AND COMPENSATORY EVOLUTION IN NATURAL MUTANT LINES OF C. ELEGANS. Evolution; International Journal of Organic Evolution, 2011, 65, 2335-2344.	1.1	40
44	Natural variation in life history and aging phenotypes is associated with mitochondrial DNA deletion frequency in Caenorhabditis briggsae. BMC Evolutionary Biology, 2011, 11, 11.	3.2	33
45	Expanding the Diversity of Mycobacteriophages: Insights into Genome Architecture and Evolution. PLoS ONE, 2011, 6, e16329.	1.1	133
46	High Rate of Large Deletions in Caenorhabditis briggsae Mitochondrial Genome Mutation Processes. Genome Biology and Evolution, 2010, 2, 29-38.	1.1	48
47	Spontaneous Mutations Decrease Sensitivity of Gene Expression to Random Environmental Variation in Caenorhabditis elegans. PLoS ONE, 2010, 5, e8750.	1.1	3
48	Selective sweeps and parallel mutation in the adaptive recovery from deleterious mutation in <i>Caenorhabditis elegans</i> . Genome Research, 2010, 20, 1663-1671.	2.4	34
49	Evolution of Caenorhabditis Mitochondrial Genome Pseudogenes and Caenorhabditis briggsae Natural Isolates. Molecular Biology and Evolution, 2010, 27, 1087-1096.	3.5	29
50	A genome-wide view of <i>Caenorhabditis elegans</i> base-substitution mutation processes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16310-16314.	3.3	251
51	Molecular evolution in Panagrolaimus nematodes: origins of parthenogenesis, hermaphroditism and the Antarctic species P. davidi. BMC Evolutionary Biology, 2009, 9, 15.	3.2	31
52	TileQC: A system for tile-based quality control of Solexa data. BMC Bioinformatics, 2008, 9, 250.	1.2	30
53	Muller's Ratchet and compensatory mutation in Caenorhabditis briggsae mitochondrial genome evolution. BMC Evolutionary Biology, 2008, 8, 62.	3.2	77
54	Natural selection governs local, but not global, evolutionary gene coexpression networks in Caenorhabditis elegans. BMC Systems Biology, 2008, 2, 96.	3.0	12

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#	Article	IF	CITATIONS
55	Reply to: Mutation rate variation in eukaryotes: evolutionary implications of site-specific mechanisms. Nature Reviews Genetics, 2007, 8, 902-902.	7.7	0
56	Mutation rate variation in multicellular eukaryotes: causes and consequences. Nature Reviews Genetics, 2007, 8, 619-631.	7.7	389
57	The Relative Roles of Three DNA Repair Pathways in Preventing Caenorhabditis elegans Mutation Accumulation. Genetics, 2006, 174, 57-65.	1.2	48
58	The transcriptional consequences of mutation and natural selection in Caenorhabditis elegans. Nature Genetics, 2005, 37, 544-548. Mutation Rates, Spectra and Hotspots in Mismatch Repair Deficient Caenorhabditis elegans.	9.4	242
59	data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY863110, AY863111, AY863112, AY863113, AY863114, AY863115, AY863116, AY863117, AY863118, AY8631 AY863121, AY863122, AY863123, AY863124, AY863125, AY863126, AY863127, AY863128, AY863129, AY8631 AY863131, AY863132, AY863133, AY863134, AY863135, AY863136, AY863137, AY863138, AY863139, AY8631	.30,2	3120, 45
60	Genetics, 2005, 170, 107-113. Mutation Accumulation in Populations of Varying Size: The Distribution of Mutational Effects for Fitness Correlates in Caenorhabditis elegans. Genetics, 2004, 166, 1269-1279.	1.2	100
61	High mutation rate and predominance of insertions in the Caenorhabditis elegans nuclear genome. Nature, 2004, 430, 679-682.	13.7	320
62	Abundance, Distribution, and Mutation Rates of Homopolymeric Nucleotide Runs in the Genome of Caenorhabditis elegans. Journal of Molecular Evolution, 2004, 58, 584-595.	0.8	63
63	Phylogenetics in Caenorhabditis elegans: An Analysis of Divergence and Outcrossing. Molecular Biology and Evolution, 2003, 20, 393-400.	3.5	78
64	An Evolutionary Analysis of the Helix-Hairpin-Helix Superfamily of DNA Repair Glycosylases. Molecular Biology and Evolution, 2003, 20, 1603-1611.	3.5	89