

# Alexander Donath

## List of Publications by Year in descending order

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Version: 2024-02-01

52  
papers

10,629  
citations

159585

30  
h-index

175258

52  
g-index

59  
all docs

59  
docs citations

59  
times ranked

9836  
citing authors

#	ARTICLE	IF	CITATIONS
1	MITOS: Improved de novo metazoan mitochondrial genome annotation. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 313-319.	2.7	3,919
2	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	12.6	2,096
3	Evolutionary History of the Hymenoptera. <i>Current Biology</i> , 2017, 27, 1013-1018.	3.9	611
4	The evolution and genomic basis of beetle diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24729-24737.	7.1	372
5	Improved annotation of protein-coding genes boundaries in metazoan mitochondrial genomes. <i>Nucleic Acids Research</i> , 2019, 47, 10543-10552.	14.5	324
6	The expansion of the metazoan microRNA repertoire. <i>BMC Genomics</i> , 2006, 7, 25.	2.8	304
7	Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22657-22663.	7.1	291
8	Phylogenomics and the evolution of hemipteroid insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12775-12780.	7.1	275
9	Improved systematic tRNA gene annotation allows new insights into the evolution of mitochondrial tRNA structures and into the mechanisms of mitochondrial genome rearrangements. <i>Nucleic Acids Research</i> , 2012, 40, 2833-2845.	14.5	218
10	A comprehensive analysis of bilaterian mitochondrial genomes and phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 352-364.	2.7	183
11	Evolutionary history of Polyneoptera and its implications for our understanding of early winged insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3024-3029.	7.1	150
12	The evolutionary history of holometabolous insects inferred from transcriptome-based phylogeny and comprehensive morphological data. <i>BMC Evolutionary Biology</i> , 2014, 14, 52.	3.2	147
13	Orthograph: a versatile tool for mapping coding nucleotide sequences to clusters of orthologous genes. <i>BMC Bioinformatics</i> , 2017, 18, 111.	2.6	146
14	An integrative phylogenomic approach illuminates the evolutionary history of cockroaches and termites (Blattodea). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182076.	2.6	143
15	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. <i>Current Biology</i> , 2012, 22, 1309-1313.	3.9	140
16	Re-assessing the diversity of negative strand RNA viruses in insects. <i>PLoS Pathogens</i> , 2019, 15, e1008224.	4.7	101
17	Phylogenetic Origin and Diversification of RNAi Pathway Genes in Insects. <i>Genome Biology and Evolution</i> , 2016, 8, evw281.	2.5	92
18	Transcriptome and target DNA enrichment sequence data provide new insights into the phylogeny of vespid wasps (Hymenoptera: Aculeata: Vespidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 213-226.	2.7	87

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19	Transcriptome sequence-based phylogeny of chalcidoid wasps (Hymenoptera: Chalcidoidea) reveals a history of rapid radiations, convergence, and evolutionary success. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 286-296.	2.7	83
20	Phylogenomic analysis sheds light on the evolutionary pathways towards acoustic communication in Orthoptera. <i>Nature Communications</i> , 2020, 11, 4939.	12.8	82
21	Old World and New World Phasmatodea: Phylogenomics Resolve the Evolutionary History of Stick and Leaf Insects. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	2.2	80
22	Evolution of 7SK RNA and Its Protein Partners in Metazoa. <i>Molecular Biology and Evolution</i> , 2009, 26, 2821-2830.	8.9	76
23	BaitFisher: A Software Package for Multispecies Target DNA Enrichment Probe Design. <i>Molecular Biology and Evolution</i> , 2016, 33, 1875-1886.	8.9	71
24	Mitogenomics at the base of Metazoa. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 339-351.	2.7	70
25	New data, same story: phylogenomics does not support Syrphoidea (Diptera: Syrphidae, Pipunculidae). <i>Systematic Entomology</i> , 2018, 43, 447-459.	3.9	53
26	Polymorphic adaptations in metazoans to establish and maintain photosymbioses. <i>Biological Reviews</i> , 2018, 93, 2006-2020.	10.4	51
27	An integrative phylogenomic approach to elucidate the evolutionary history and divergence times of Neuropterida (Insecta: Holometabola). <i>BMC Evolutionary Biology</i> , 2020, 20, 64.	3.2	48
28	Convergently Evolved Toxic Secondary Metabolites in Plants Drive the Parallel Molecular Evolution of Insect Resistance. <i>American Naturalist</i> , 2017, 190, S29-S43.	2.1	42
29	The molecular evolutionary dynamics of oxidative phosphorylation (OXPHOS) genes in Hymenoptera. <i>BMC Evolutionary Biology</i> , 2017, 17, 269.	3.2	40
30	Phylogenomics of the superfamily Dytiscoidea (Coleoptera: Adephaga) with an evaluation of phylogenetic conflict and systematic error. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 270-285.	2.7	36
31	Viromics of extant insect orders unveil the evolution of the flavi-like superfamily. <i>Virus Evolution</i> , 2021, 7, veab030.	4.9	35
32	Evolutionary history and divergence times of Odonata (dragonflies and damselflies) revealed through transcriptomics. <i>IScience</i> , 2021, 24, 103324.	4.1	25
33	Transcriptomic data from panarthropods shed new light on the evolution of insulator binding proteins in insects. <i>BMC Genomics</i> , 2016, 17, 861.	2.8	23
34	Beyond Drosophila: resolving the rapid radiation of schizophoran flies with phylotranscriptomics. <i>BMC Biology</i> , 2021, 19, 23.	3.8	22
35	Response to Comment on "Phylogenomics resolves the timing and pattern of insect evolution". <i>Science</i> , 2015, 349, 487-487.	12.6	17
36	No signal of deleterious mutation accumulation in conserved gene sequences of extant asexual hexapods. <i>Scientific Reports</i> , 2019, 9, 5338.	3.3	17

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37	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. <i>Genome Biology and Evolution</i> , 2020, 12, 1099-1188.	2.5	17
38	ABCB transporters in a leaf beetle respond to sequestered plant toxins. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201311.	2.6	16
39	Phylogenomics changes our understanding about earwig evolution. <i>Systematic Entomology</i> , 2020, 45, 516-526.	3.9	15
40	Identification of scavenger receptors and thrombospondin-type A1 repeat proteins potentially relevant for plastid recognition in <i>Sacoglossa</i> . <i>Ecology and Evolution</i> , 2020, 10, 12348-12363.	1.9	13
41	Four myriapod relatives “but who are sisters? No end to debates on relationships among the four major myriapod subgroups. <i>BMC Evolutionary Biology</i> , 2020, 20, 144.	3.2	13
42	Split-inducing indels in phylogenomic analysis. <i>Algorithms for Molecular Biology</i> , 2018, 13, 12.	1.2	11
43	Robust reference gene design and validation for expression studies in the large milkweed bug, <i>Oncopeltus fasciatus</i> , upon cardiac glycoside stress. <i>Gene</i> , 2019, 710, 66-75.	2.2	10
44	Cladobranchia (Gastropoda, Nudibranchia) as a Promising Model to Understand the Molecular Evolution of Photosymbiosis in Animals. <i>Frontiers in Marine Science</i> , 2022, 8, .	2.5	10
45	Analysis of RNA-Seq, DNA Target Enrichment, and Sanger Nucleotide Sequence Data Resolves Deep Splits in the Phylogeny of Cuckoo Wasps (Hymenoptera: Chrysididae). <i>Insect Systematics and Diversity</i> , 2021, 5, .	1.7	8
46	25 Molecular morphology: Higher order characters derivable from sequence information. , 2014, , 549-562.		5
47	Transcriptomics provides a robust framework for the relationships of the major clades of cladobranch sea slugs (Mollusca, Gastropoda, Heterobranchia), but fails to resolve the position of the enigmatic genus <i>Embletonia</i> . <i>Bmc Ecology and Evolution</i> , 2021, 21, 226.	1.6	5
48	The complete mitochondrial genome of the “solar-powered” sea slug <i>Plakobranthus cf. ocellatus</i> (Heterobranchia: Panpulmonata: Sacoglossa). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 130-131.	0.4	4
49	The complete mitochondrial genome of the photosymbiotic sea slug <i>Berghia stephanieae</i> (ValdÃ©s, 2005) (Gastropoda, Nudibranchia). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2281-2284.	0.4	4
50	Midgut transcriptome assessment of the cockroach-hunting wasp <i>Ampulex compressa</i> (Apoidea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.5	2
51	Deletion analysis of the 3â€² long terminal repeat sequence of plant retrotransposon Tto1 identifies 125 base pairs redundancy as sufficient for first strand transfer. <i>Virology</i> , 2011, 412, 75-82.	2.4	1
52	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. <i>Current Biology</i> , 2013, 23, 1388.	3.9	1