

Casey W Dunn

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

8,060
citations

125106

35
h-index

97045

71
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87
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docs citations

87
times ranked

8140
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of Gene Expression across Species and Specialized Zooids in Siphonophora. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	14
2	Integrating siphonophores into marine food web ecology. <i>Limnology and Oceanography Letters</i> , 2022, 7, 81-95.	1.6	12
3	Statewide Longitudinal Trends in Transmitted HIV-1 Drug Resistance in Rhode Island, USA. <i>Open Forum Infectious Diseases</i> , 2022, 9, ofab587.	0.4	1
4	Beyond HIV outbreaks: protocol, rationale and implementation of a prospective study quantifying the benefit of incorporating viral sequence clustering analysis into routine public health interventions. <i>BMJ Open</i> , 2022, 12, e060184.	0.8	3
5	Characterizing the secret diets of siphonophores (Cnidaria: Hydrozoa) using DNA metabarcoding. <i>PLoS ONE</i> , 2022, 17, e0267761.	1.1	13
6	Revising transcriptome assemblies with phylogenetic information. <i>PLoS ONE</i> , 2021, 16, e0244202.	1.1	11
7	The Evolutionary History of Siphonophore Tentilla: Novelty, Convergence, and Integration. <i>Integrative Organismal Biology</i> , 2021, 3, obab019.	0.9	3
8	The evolution of siphonophore tentilla for specialized prey capture in the open ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
9	A genome-scale phylogeny of the kingdom Fungi. <i>Current Biology</i> , 2021, 31, 1653-1665.e5.	1.8	170
10	Longitudinal typing of molecular HIV clusters in a statewide epidemic. <i>Aids</i> , 2021, 35, 1711-1722.	1.0	4
11	Rooting the Animal Tree of Life. <i>Molecular Biology and Evolution</i> , 2021, 38, 4322-4333.	3.5	93
12	Incorporating Within-Host Diversity in Phylogenetic Analyses for Detecting Clusters of New HIV Diagnoses. <i>Frontiers in Microbiology</i> , 2021, 12, 803190.	1.5	3
13	Treeio: An R Package for Phylogenetic Tree Input and Output with Richly Annotated and Associated Data. <i>Molecular Biology and Evolution</i> , 2020, 37, 599-603.	3.5	348
14	Empirical comparison of analytical approaches for identifying molecular HIV-1 clusters. <i>Scientific Reports</i> , 2020, 10, 18547.	1.6	11
15	Phylogenetics is the New Genetics (for Most of Biodiversity). <i>Trends in Ecology and Evolution</i> , 2020, 35, 415-425.	4.2	72
16	Challenges in evaluating the use of viral sequence data to identify HIV transmission networks for public health. <i>Statistical Communications in Infectious Diseases</i> , 2020, 12, .	0.2	2
17	Morphology and development of the Portuguese man of war, <i>Physalia physalis</i> . <i>Scientific Reports</i> , 2019, 9, 15522.	1.6	30
18	Pairwise comparisons across species are problematic when analyzing functional genomic data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E409-E417.	3.3	77

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19	Description of <i>Tottonophyes enigmatica</i> gen. nov., sp. nov. (Hydrozoa, Siphonophora, Calycophorae), with a reappraisal of the function and homology of nectophoral canals. <i>Zootaxa</i> , 2018, 4415, 452.	0.2	4
20	We are not so special. <i>ELife</i> , 2018, 7, .	2.8	2
21	Improved phylogenetic resolution within Siphonophora (Cnidaria) with implications for trait evolution. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 823-833.	1.2	25
22	Ctenophore trees. <i>Nature Ecology and Evolution</i> , 2017, 1, 1600-1601.	3.4	8
23	Insights into the Biodiversity, Behavior, and Bioluminescence of Deep-Sea Organisms Using Molecular and Maritime Technology. <i>Oceanography</i> , 2017, 30, 38-47.	0.5	19
24	Indoles induce metamorphosis in a broad diversity of jellyfish, but not in a crown jelly (Coronatae). <i>PLoS ONE</i> , 2017, 12, e0188601.	1.1	16
25	Animal Evolution: Are Phyla Real?. <i>Current Biology</i> , 2016, 26, R424-R426.	1.8	23
26	Comparative genomics and the diversity of life. <i>Zoologica Scripta</i> , 2016, 45, 5-13.	0.7	15
27	An Integrated Perspective on Phylogenetic Workflows. <i>Trends in Ecology and Evolution</i> , 2016, 31, 116-126.	4.2	16
28	The histology of <i>Nanomia bijuga</i> (Hydrozoa: Siphonophora). <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2015, 324, 435-449.	0.6	14
29	Comparative muscle development of scyphozoan jellyfish with simple and complex life cycles. <i>EvoDevo</i> , 2015, 6, 11.	1.3	19
30	Par system components are asymmetrically localized in ectodermal epithelia, but not during early development in the sea anemone <i>Nematostella vectensis</i> . <i>EvoDevo</i> , 2015, 6, 20.	1.3	20
31	Phylogenomic Analyses Support Traditional Relationships within Cnidaria. <i>PLoS ONE</i> , 2015, 10, e0139068.	1.1	191
32	Fluorescent proteins function as a prey attractant: experimental evidence from the hydromedusa <i>Olindias formosus</i> and other marine organisms. <i>Biology Open</i> , 2015, 4, 1094-1104.	0.6	53
33	Automation and Evaluation of the SOWH Test with SOWHAT. <i>Systematic Biology</i> , 2015, 64, 1048-1058.	2.7	40
34	Stem cells in <i>Nanomia bijuga</i> (Siphonophora), a colonial animal with localized growth zones. <i>EvoDevo</i> , 2015, 6, 22.	1.3	14
35	A phylogenetic backbone for Bivalvia: an RNA-seq approach. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20142332.	1.2	110
36	Spiralian Phylogeny Informs the Evolution of Microscopic Lineages. <i>Current Biology</i> , 2015, 25, 2000-2006.	1.8	242

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37	Correction to Phylogenomic analyses of deep gastropod relationships reject Orthogastropoda. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20142941.	1.2	3
38	The hidden biology of sponges and ctenophores. Trends in Ecology and Evolution, 2015, 30, 282-291.	4.2	173
39	The evolution of animal genomes. Current Opinion in Genetics and Development, 2015, 35, 25-32.	1.5	48
40	Acorn worms in a nutshell. Nature, 2015, 527, 448-449.	13.7	0
41	Phylogenomic Analyses of Echinodermata Support the Sister Groups of Asterozoa and Echinozoa. PLoS ONE, 2015, 10, e0119627.	1.1	87
42	The Global Invertebrate Genomics Alliance (GIGA): Developing Community Resources to Study Diverse Invertebrate Genomes. Journal of Heredity, 2014, 105, 1-18.	1.0	96
43	Reconsidering the phylogenetic utility of miRNA in animals. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12576-12577.	3.3	6
44	Animal Phylogeny and Its Evolutionary Implications. Annual Review of Ecology, Evolution, and Systematics, 2014, 45, 371-395.	3.8	323
45	Phylogenomic analyses of deep gastropod relationships reject Orthogastropoda. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20141739.	1.2	144
46	Bayesian Genome Assembly and Assessment by Markov Chain Monte Carlo Sampling. PLoS ONE, 2014, 9, e99497.	1.1	7
47	Toward a statistically explicit understanding of <i>de novo</i> sequence assembly. Bioinformatics, 2013, 29, 2959-2963.	1.8	22
48	The Genome of the Ctenophore <i>Mnemiopsis leidyi</i> and Its Implications for Cell Type Evolution. Science, 2013, 342, 1242-1249.	6.0	570
49	Agalma: an automated phylogenomics workflow. BMC Bioinformatics, 2013, 14, 330.	1.2	144
50	Evolution: Out of the Ocean. Current Biology, 2013, 23, R241-R243.	1.8	7
51	Characterization of differential transcript abundance through time during <i>Nematostella vectensis</i> development. BMC Genomics, 2013, 14, 266.	1.2	85
52	Phylogenetic Analysis of Gene Expression. Integrative and Comparative Biology, 2013, 53, 847-856.	0.9	65
53	Re-evaluation of characters in Apolemiidae (Siphonophora), with description of two new species from Monterey Bay, California . Zootaxa, 2013, 3702, 201.	0.2	15
54	Differential Gene Expression in the Siphonophore <i>Nanomia bijuga</i> (Cnidaria) Assessed with Multiple Next-Generation Sequencing Workflows. PLoS ONE, 2011, 6, e22953.	1.1	43

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55	Resolving the evolutionary relationships of molluscs with phylogenomic tools. <i>Nature</i> , 2011, 480, 364-367.	13.7	359
56	Higher-level metazoan relationships: recent progress and remaining questions. <i>Organisms Diversity and Evolution</i> , 2011, 11, 151-172.	0.7	247
57	Siphonophores. <i>Current Biology</i> , 2009, 19, R233-R234.	1.8	22
58	Assessing the root of bilaterian animals with scalable phylogenomic methods. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 4261-4270.	1.2	645
59	Assembling the spiralian tree of life. , 2009, , 52-64.		32
60	Broad phylogenomic sampling improves resolution of the animal tree of life. <i>Nature</i> , 2008, 452, 745-749.	13.7	1,698
61	Phylogenetics of Hydroidolina (Hydrozoa: Cnidaria). <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2008, 88, 1663-1672.	0.4	92
62	Phyutility: a phyloinformatics tool for trees, alignments and molecular data. <i>Bioinformatics</i> , 2008, 24, 715-716.	1.8	562
63	Conservative evolution in duplicated genes of the primate Class I ADH cluster. <i>Gene</i> , 2007, 392, 64-76.	1.0	40
64	A modern look at the Animal Tree of Life* <i>&lt;/strong&gt;. Zootaxa</i> , 2007, 1668, 61-79.	0.2	39
65	The evolution of colony-level development in the Siphonophora (Cnidaria:Hydrozoa). <i>Development Genes and Evolution</i> , 2006, 216, 743-754.	0.4	53
66	Broad taxon and gene sampling indicate that chaetognaths are protostomes. <i>Current Biology</i> , 2006, 16, R575-R576.	1.8	128
67	Molecular evidence for deep evolutionary roots of bilaterality in animal development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11195-11200.	3.3	210
68	Complex colony-level organization of the deep-sea siphonophore <i>Bargmannia elongata</i> (Cnidaria,). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2 Dynamics</i> , 2005, 234, 835-845.	0.8	47
69	Molecular Phylogenetics of the Siphonophora (Cnidaria), with Implications for the Evolution of Functional Specialization. <i>Systematic Biology</i> , 2005, 54, 916-935.	2.7	86
70	Bioluminescent and Red-Fluorescent Lures in a Deep-Sea Siphonophore. <i>Science</i> , 2005, 309, 263-263.	6.0	90
71	A re-examination of siphonophore terminology and morphology, applied to the description of two new prayine species with remarkable bio-optical properties. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2005, 85, 695-707.	0.4	49
72	Adaptive evolution of HoxAÁ11 and HoxAÁ13 at the origin of the uterus in mammals. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, 2201-2207.	1.2	31