

David J Miller

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

7,593
citations

66343

42
h-index

58581

82
g-index

104
all docs

104
docs citations

104
times ranked

6118
citing authors

#	ARTICLE	IF	CITATIONS
1	The Role of DNA Methylation in Genome Defense in Cnidaria and Other Invertebrates. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	10
2	Urbanization comprehensively impairs biological rhythms in coral holobionts. <i>Global Change Biology</i> , 2022, 28, 3349-3364.	9.5	14
3	DMSP Production by Coral-Associated Bacteria. <i>Frontiers in Marine Science</i> , 2022, 9, .	2.5	17
4	Newly Discovered Peptides from the Coral <i>Heliofungia actiniformis</i> Show Structural and Functional Diversity. <i>Journal of Natural Products</i> , 2022, 85, 1789-1798.	3.0	2
5	ampir: an R package for fast genome-wide prediction of antimicrobial peptides. <i>Bioinformatics</i> , 2021, 36, 5262-5263.	4.1	19
6	Conservation and turnover of miRNAs and their highly complementary targets in early branching animals. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20203169.	2.6	9
7	Testing cophylogeny between coral reef invertebrates and their bacterial and archaeal symbionts. <i>Molecular Ecology</i> , 2021, 30, 3768-3782.	3.9	11
8	Biogeography, reproductive biology and phylogenetic divergence within the Fungiidae (mushroom) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	2.7	7
9	Acroporaâ€”The Most-Studied Coral Genus. , 2021, , 173-193.		3
10	Identification and Characterization of a Peptide from the Stony Coral <i>Heliofungia actiniformis</i> . <i>Journal of Natural Products</i> , 2020, 83, 3454-3463.	3.0	4
11	An enhanced target-enrichment bait set for Hexacorallia provides phylogenomic resolution of the staghorn corals (Acroporidae) and close relatives. <i>Molecular Phylogenetics and Evolution</i> , 2020, 153, 106944.	2.7	59
12	Dual RNAâ€sequencing analyses of a coral and its native symbiont during the establishment of symbiosis. <i>Molecular Ecology</i> , 2020, 29, 3921-3937.	3.9	26
13	Comparative transcriptomic analyses of Chromera and Symbiodiniaceae. <i>Environmental Microbiology Reports</i> , 2020, 12, 435-443.	2.4	4
14	Early eukaryotic origins and metazoan elaboration of MAPR family proteins. <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106814.	2.7	17
15	Diverse coral reef invertebrates exhibit patterns of phyllosymbiosis. <i>ISME Journal</i> , 2020, 14, 2211-2222.	9.8	43
16	Genomic signatures in the coral holobiont reveal host adaptations driven by Holocene climate change and reef specific symbionts. <i>Science Advances</i> , 2020, 6, .	10.3	44
17	Molecular techniques and their limitations shape our view of the holobiont. <i>Zoology</i> , 2019, 137, 125695.	1.2	5
18	A genomic view of the reef-building coral <i>Porites lutea</i> and its microbial symbionts. <i>Nature Microbiology</i> , 2019, 4, 2090-2100.	13.3	160

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19	Host-Microbe Coevolution: Applying Evidence from Model Systems to Complex Marine Invertebrate Holobionts. <i>MBio</i> , 2019, 10, .	4.1	88
20	The Whole-Genome Sequence of the Coral <i>Acropora millepora</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 1374-1379.	2.5	64
21	Resolving structure and function of metaorganisms through a holistic framework combining reductionist and integrative approaches. <i>Zoology</i> , 2019, 133, 81-87.	1.2	53
22	Transcriptomic analyses highlight the likely metabolic consequences of colonization of a cnidarian host by native or non-native <i>Symbiodinium</i> species. <i>Biology Open</i> , 2019, 8, .	1.2	19
23	Transcriptomic analysis reveals protein homeostasis breakdown in the coral <i>Acropora millepora</i> during hypo-saline stress. <i>BMC Genomics</i> , 2019, 20, 148.	2.8	33
24	Finding Nemo's Genes: A chromosome-scale reference assembly of the genome of the orange clownfish <i>Amphiprion percula</i> . <i>Molecular Ecology Resources</i> , 2019, 19, 570-585.	4.8	55
25	Expression of the neuropeptides RFamide and LWamide during development of the coral <i>Acropora millepora</i> in relation to settlement and metamorphosis. <i>Developmental Biology</i> , 2019, 446, 56-67.	2.0	19
26	Deciphering the nature of the coral- <i>Chromera</i> association. <i>ISME Journal</i> , 2018, 12, 776-790.	9.8	56
27	Universal target-enrichment baits for anthozoan (Cnidaria) phylogenomics: New approaches to long-standing problems. <i>Molecular Ecology Resources</i> , 2018, 18, 281-295.	4.8	114
28	Comparative genomics reveals the distinct evolutionary trajectories of the robust and complex coral lineages. <i>Genome Biology</i> , 2018, 19, 175.	8.8	57
29	<i>Symbiodinium</i> genomes reveal adaptive evolution of functions related to coral-dinoflagellate symbiosis. <i>Communications Biology</i> , 2018, 1, 95.	4.4	154
30	Setting the pace: host rhythmic behaviour and gene expression patterns in the facultatively symbiotic cnidarian <i>Aiptasia</i> are determined largely by <i>Symbiodinium</i> . <i>Microbiome</i> , 2018, 6, 83.	11.1	45
31	The microbiome of the octocoral <i>Lobophytum pauciflorum</i> : minor differences between sexes and resilience to short-term stress. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	36
32	Back to the Basics: Cnidarians Start to Fire. <i>Trends in Neurosciences</i> , 2017, 40, 92-105.	8.6	102
33	Rapid adaptive responses to climate change in corals. <i>Nature Climate Change</i> , 2017, 7, 627-636.	18.8	327
34	Transcriptomic analysis of the response of <i>Acropora millepora</i> to hypo-osmotic stress provides insights into DMSP biosynthesis by corals. <i>BMC Genomics</i> , 2017, 18, 612.	2.8	22
35	Analyses of Corallimorpharian Transcriptomes Provide New Perspectives on the Evolution of Calcification in the Scleractinia (Corals). <i>Genome Biology and Evolution</i> , 2017, 9, 150-160.	2.5	16
36	Loss and Gain of Group I Introns in the Mitochondrial Gene of the Scleractinia (Cnidaria; Anthozoa). <i>Zoological Studies</i> , 2017, 56, e9.	0.3	3

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37	Never Ending Analysis of a Century Old Evolutionary Debate: “Unringing” the Urmetazoon Bell. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	2.2	15
38	Near-future pH conditions severely impact calcification, metabolism and the nervous system in the pteropod <i>Heliconoides inflatus</i> . <i>Global Change Biology</i> , 2016, 22, 3888-3900.	9.5	68
39	Functional conservation of the apoptotic machinery from coral to man: the diverse and complex Bcl-2 and caspase repertoires of <i>Acropora millepora</i> . <i>BMC Genomics</i> , 2016, 17, 62.	2.8	45
40	Evolutionary analyses of caspase-8 and its paralogs: Deep origins of the apoptotic signaling pathways. <i>BioEssays</i> , 2015, 37, 767-776.	2.5	48
41	The organizer in evolution—gastrulation and organizer gene expression highlight the importance of Brachyury during development of the coral, <i>Acropora millepora</i> . <i>Developmental Biology</i> , 2015, 399, 337-347.	2.0	28
42	Host Coenzyme Q Redox State Is an Early Biomarker of Thermal Stress in the Coral <i>Acropora millepora</i> . <i>PLoS ONE</i> , 2015, 10, e0139290.	2.5	25
43	The “Naked Coral” Hypothesis Revisited—Evidence for and Against Scleractinian Monophyly. <i>PLoS ONE</i> , 2014, 9, e94774.	2.5	50
44	Simultaneous determination of coenzyme Q and plastoquinone redox states in the coral—Symbiodinium symbiosis during thermally induced bleaching. <i>Journal of Experimental Marine Biology and Ecology</i> , 2014, 455, 1-6.	1.5	9
45	The Apoptotic Initiator Caspase-8: Its Functional Ubiquity and Genetic Diversity during Animal Evolution. <i>Molecular Biology and Evolution</i> , 2014, 31, 3282-3301.	8.9	25
46	How do environmental factors influence life cycles and development? An experimental framework for early-diverging metazoans. <i>BioEssays</i> , 2014, 36, 1185-1194.	2.5	38
47	Deltocyathiidae, an early-diverging family of Robust corals (Anthozoa, Scleractinia). <i>Zoologica Scripta</i> , 2013, 42, 201-212.	1.7	15
48	The Complex NOD-Like Receptor Repertoire of the Coral <i>Acropora digitifera</i> Includes Novel Domain Combinations. <i>Molecular Biology and Evolution</i> , 2013, 30, 167-176.	8.9	109
49	The Skeletal Proteome of the Coral <i>Acropora millepora</i> : The Evolution of Calcification by Co-Option and Domain Shuffling. <i>Molecular Biology and Evolution</i> , 2013, 30, 2099-2112.	8.9	155
50	The acute transcriptional response of the coral <i>Acropora millepora</i> to immune challenge: expression of GiMAP/IAN genes links the innate immune responses of corals with those of mammals and plants. <i>BMC Genomics</i> , 2013, 14, 400.	2.8	44
51	Asexual reproduction by marginal budding in the tropical corallimorpharian, <i>Ricordea yuma</i> (Corallimorpharia; Ricordeidae). <i>Galaxea</i> , 2013, 15, 41-42.	0.7	2
52	The first modern solitary Agariciidae (Anthozoa, Scleractinia) revealed by molecular and microstructural analysis. <i>Invertebrate Systematics</i> , 2012, 26, 303.	1.3	30
53	A “Neural” Enzyme in Nonbilaterian Animals and Algae: Preneural Origins for Peptidylglycine γ -Amidating Monooxygenase. <i>Molecular Biology and Evolution</i> , 2012, 29, 3095-3109.	8.9	32
54	Major Cellular and Physiological Impacts of Ocean Acidification on a Reef Building Coral. <i>PLoS ONE</i> , 2012, 7, e34659.	2.5	262

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55	The Neuronal Calcium Sensor Protein Acrocalcin: A Potential Target of Calmodulin Regulation during Development in the Coral <i>Acropora millepora</i> . PLoS ONE, 2012, 7, e51689.	2.5	12
56	Coral Thermal Tolerance: Tuning Gene Expression to Resist Thermal Stress. PLoS ONE, 2012, 7, e50685.	2.5	140
57	Differential Gene Expression at Coral Settlement and Metamorphosis - A Subtractive Hybridization Study. PLoS ONE, 2011, 6, e26411.	2.5	47
58	Coral genomics and transcriptomics "Ushering in a new era in coral biology. Journal of Experimental Marine Biology and Ecology, 2011, 408, 114-119.	1.5	22
59	The ancient evolutionary origins of Scleractinia revealed by azooxanthellate corals. BMC Evolutionary Biology, 2011, 11, 316.	3.2	153
60	Using the <i>Acropora digitifera</i> genome to understand coral responses to environmental change. Nature, 2011, 476, 320-323.	27.8	758
61	Defining the Origins of the NOD-Like Receptor System at the Base of Animal Evolution. Molecular Biology and Evolution, 2011, 28, 1687-1702.	8.9	119
62	Phylogenomics Reveals an Anomalous Distribution of USP Genes in Metazoans. Molecular Biology and Evolution, 2011, 28, 153-161.	8.9	19
63	Patterns of Gene Expression in a Scleractinian Coral Undergoing Natural Bleaching. Marine Biotechnology, 2010, 12, 594-604.	2.4	87
64	New tricks with old genes: the genetic bases of novel cnidarian traits. Trends in Genetics, 2010, 26, 154-158.	6.7	50
65	A Comprehensive Phylogenetic Analysis of the Scleractinia (Cnidaria, Anthozoa) Based on Mitochondrial CO1 Sequence Data. PLoS ONE, 2010, 5, e11490.	2.5	213
66	Monophyletic origin of <i>Caryophyllia</i> (Scleractinia, Caryophylliidae), with descriptions of six new species. Systematics and Biodiversity, 2010, 8, 91-118.	1.2	34
67	Differential expression of three galaxin-related genes during settlement and metamorphosis in the scleractinian coral <i>Acropora millepora</i> . BMC Evolutionary Biology, 2009, 9, 178.	3.2	58
68	Microarray analysis reveals transcriptional plasticity in the reef building coral <i>Acropora millepora</i> . Molecular Ecology, 2009, 18, 3062-3075.	3.9	80
69	Sox genes in the coral <i>Acropora millepora</i> : divergent expression patterns reflect differences in developmental mechanisms within the Anthozoa. BMC Evolutionary Biology, 2008, 8, 311.	3.2	44
70	Microarray analysis identifies candidate genes for key roles in coral development. BMC Genomics, 2008, 9, 540.	2.8	119
71	Cryptic complexity captured: the <i>Nematostella</i> genome reveals its secrets. Trends in Genetics, 2008, 24, 1-4.	6.7	32
72	The evolution of immunity: a low-life perspective. Trends in Immunology, 2007, 28, 449-454.	6.8	89

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73	The innate immune repertoire in Cnidaria - ancestral complexity and stochastic gene loss. <i>Genome Biology</i> , 2007, 8, R59.	9.6	322
74	Components of both major axial patterning systems of the Bilateria are differentially expressed along the primary axis of a "radiate" animal, the anthozoan cnidarian <i>Acropora millepora</i> . <i>Developmental Biology</i> , 2006, 298, 632-643.	2.0	62
75	Axial Patterning and Diversification in the Cnidaria Predate the Hox System. <i>Current Biology</i> , 2006, 16, 920-926.	3.9	116
76	Maintenance of ancestral complexity and non-metazoan genes in two basal cnidarians. <i>Trends in Genetics</i> , 2005, 21, 633-639.	6.7	315
77	Tandem organization of independently duplicated homeobox genes in the basal cnidarian <i>Acropora millepora</i> . <i>Development Genes and Evolution</i> , 2005, 215, 268-273.	0.9	11
78	A simple plan "cnidarians and the origins of developmental mechanisms. <i>Nature Reviews Genetics</i> , 2004, 5, 567-577.	16.3	108
79	snail expression during embryonic development of the coral <i>Acropora</i> : blurring the diploblast/triploblast divide?. <i>Development Genes and Evolution</i> , 2004, 214, 257-260.	0.9	39
80	EST Analysis of the Cnidarian <i>Acropora millepora</i> Reveals Extensive Gene Loss and Rapid Sequence Divergence in the Model Invertebrates. <i>Current Biology</i> , 2003, 13, 2190-2195.	3.9	321
81	Localized expression of a dpp/BMP2/4 ortholog in a coral embryo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8106-8111.	7.1	126
82	The Mitochondrial Genome of <i>Acropora tenuis</i> (Cnidaria; Scleractinia) Contains a Large Group I Intron and a Candidate Control Region. <i>Journal of Molecular Evolution</i> , 2002, 55, 1-13.	1.8	111
83	Coral development: from classical embryology to molecular control. <i>International Journal of Developmental Biology</i> , 2002, 46, 671-8.	0.6	54
84	The Evolutionary History of the Coral Genus <i>Acropora</i> (Scleractinia, Cnidaria) Based on a Mitochondrial and a Nuclear Marker: Reticulation, Incomplete Lineage Sorting, or Morphological Convergence?. <i>Molecular Biology and Evolution</i> , 2001, 18, 1315-1329.	8.9	256
85	Gene structure and larval expression of <i>cnox-2Am</i> from the coral <i>Acropora millepora</i> . <i>Development Genes and Evolution</i> , 2001, 211, 10-19.	0.9	66
86	Conservation of a DPP/BMP signaling pathway in the nonbilateral cnidarian <i>Acropora millepora</i> . <i>Evolution & Development</i> , 2001, 3, 241-250.	2.0	43
87	Patterns of coral-dinoflagellate associations in <i>Acropora</i> : significance of local availability and physiology of <i>Symbiodinium</i> strains and host-symbiont selectivity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2001, 268, 1759-1767.	2.6	259
88	The coral <i>Acropora</i> : What it can contribute to our knowledge of metazoan evolution and the evolution of developmental processes. <i>BioEssays</i> , 2000, 22, 291-296.	2.5	39
89	Evolution of homeobox genes: Q 50 Paired-like genes founded the Paired class. <i>Development Genes and Evolution</i> , 1999, 209, 186-197.	0.9	169
90	Atypically low rate of cytochrome b evolution in the scleractinian coral genus <i>Acropora</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999, 266, 179-183.	2.6	95

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91	Linkage of genes encoding enolase (eno) and CTP synthase (pyrG) in the α -subdivision proteobacterium <i>Nitrosomonas europaea</i> . <i>FEMS Microbiology Letters</i> , 1998, 165, 153-157.	1.8	5
92	Genetic transformation of dinoflagellates (<i>Amphidinium</i> and <i>Symbiodinium</i>): expression of GUS in microalgae using heterologous promoter constructs. <i>Plant Journal</i> , 1998, 13, 427-435.	5.7	120
93	HYPERMETHYLATION AT CPG-MOTIFS IN THE DINOFLAGELLATES <i>AMPHIDIINIUM CARTERAE</i> (DINOPHYCEAE) AND <i>SYMBIODINIUM MICROADRIATICUM</i> (DINOPHYCEAE): EVIDENCE FROM RESTRICTION ANALYSES, 5-AZACYTIDINE AND ETHIONINE TREATMENT. <i>Journal of Phycology</i> , 1998, 34, 152-159.	2.3	16
94	Light-Regulated Transcription of Genes Encoding Peridinin Chlorophyll a Proteins and the Major Intrinsic Light-Harvesting Complex Proteins in the Dinoflagellate <i>Amphidinium carterae</i> Hulburt (<i>Dinophyceae</i>)1. <i>Plant Physiology</i> , 1998, 117, 189-196.	4.8	41
95	Quaternary structure of the hydroxylamine oxidoreductase from <i>Nitrosomonas europaea</i> . <i>Archives of Microbiology</i> , 1995, 163, 300-306.	2.2	9
96	Quaternary structure of the hydroxylamine oxidoreductase from <i>Nitrosomonas europaea</i> . <i>Archives of Microbiology</i> , 1995, 163, 300-306.	2.2	2
97	Homeobox genes and the zootype. <i>Nature</i> , 1993, 365, 215-216.	27.8	72