

Warren Francis

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8843639/publications.pdf>

Version: 2024-02-01

29
papers

1,514
citations

567281

15
h-index

477307

29
g-index

42
all docs

42
docs citations

42
times ranked

2120
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomic data for <i>Halichondria panicea</i> from Illumina and nanopore sequencing and preliminary genome assemblies for the sponge and two microbial symbionts. <i>BMC Research Notes</i> , 2022, 15, 135.	1.4	5
2	A Winâ€“Loss Interaction on FeO Between Methanogens and Acetogens From a Climate Lake. <i>Frontiers in Microbiology</i> , 2021, 12, 638282.	3.5	7
3	A chromosome-scale genome assembly and karyotype of the ctenophore <i>Hormiphora californensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	18
4	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , 2021, 374, 717-723.	12.6	111
5	Biochemical characterization of diverse deep-sea anthozoan bioluminescence systems. <i>Marine Biology</i> , 2020, 167, 1.	1.5	24
6	Tracing animal genomic evolution with the chromosomal-level assembly of the freshwater sponge <i>Ephydatia muelleri</i> . <i>Nature Communications</i> , 2020, 11, 3676.	12.8	72
7	Conserved novel ORFs in the mitochondrial genome of the ctenophore <i>Beroë forskalii</i> . <i>PeerJ</i> , 2020, 8, e8356.	2.0	16
8	Very few sites can reshape the inferred phylogenetic tree. <i>PeerJ</i> , 2020, 8, e8865.	2.0	20
9	The Role of Homology and Orthology in the Phylogenomic Analysis of Metazoan Gene Content. <i>Molecular Biology and Evolution</i> , 2019, 36, 643-649.	8.9	44
10	Combing Transcriptomes for Secrets of Deep-Sea Survival: Environmental Diversity Drives Patterns of Protein Evolution. <i>Integrative and Comparative Biology</i> , 2019, 59, 786-798.	2.0	4
11	A hybrid <i>de novo</i> assembly of the sea pansy (<i>Renilla muelleri</i>) genome. <i>GigaScience</i> , 2019, 8, .	6.4	27
12	Predicted microbial secretomes and their target substrates in marine sediment. <i>Nature Microbiology</i> , 2018, 3, 32-37.	13.3	85
13	Correction: Animal origins and the Tonian Earth system. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 327-330.	2.6	2
14	Integrating embryonic development and evolutionary history to characterize tentacle-specific cell types in a ctenophore. <i>Molecular Biology and Evolution</i> , 2018, 35, 2940-2956.	8.9	29
15	Fungi in Deep Subsurface Environments. <i>Advances in Applied Microbiology</i> , 2018, 102, 83-116.	2.4	22
16	The last common ancestor of animals lacked the HIF pathway and respired in low-oxygen environments. <i>ELife</i> , 2018, 7, .	6.0	88
17	Comparative genomics and the nature of placozoan species. <i>PLoS Biology</i> , 2018, 16, e2005359.	5.6	73
18	Animal origins and the Tonian Earth system. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 289-298.	2.6	12

#	ARTICLE	IF	CITATIONS
19	Similar Ratios of Introns to Intergenic Sequence across Animal Genomes. <i>Genome Biology and Evolution</i> , 2017, 9, 1582-1598.	2.5	48
20	Transcriptomic Resilience of the <i>Montipora digitata</i> Holobiont to Low pH. <i>Frontiers in Marine Science</i> , 2017, 4, .	2.5	16
21	Symplectin evolved from multiple duplications in bioluminescent squid. <i>PeerJ</i> , 2017, 5, e3633.	2.0	7
22	Bioluminescence spectra from three deep-sea polychaete worms. <i>Marine Biology</i> , 2016, 163, 1.	1.5	13
23	Non-excitable fluorescent protein orthologs found in ctenophores. <i>BMC Evolutionary Biology</i> , 2016, 16, 167.	3.2	7
24	Mitochondrial genomes of the freshwater sponges <i>Spongilla lacustris</i> and <i>Ephydatia cf. muelleri</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 250-251.	0.4	5
25	Occurrence of Isopenicillin-N-Synthase Homologs in Bioluminescent Ctenophores and Implications for Coelenterazine Biosynthesis. <i>PLoS ONE</i> , 2015, 10, e0128742.	2.5	21
26	Characterization of an anthraquinone fluor from the bioluminescent, pelagic polychaete <i>Tomopteris</i> . <i>Luminescence</i> , 2014, 29, 1135-1140.	2.9	19
27	The Genome of the Ctenophore <i>Mnemiopsis leidyi</i> and Its Implications for Cell Type Evolution. <i>Science</i> , 2013, 342, 1242592.	12.6	570
28	A comparison across non-model animals suggests an optimal sequencing depth for de novo transcriptome assembly. <i>BMC Genomics</i> , 2013, 14, 167.	2.8	80
29	The Dark Ocean Is Full of Lights. <i>Frontiers for Young Minds</i> , 0, 8, .	0.8	1