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List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

4,119
citations

361413

20
h-index

434195

31
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37
all docs

37
docs citations

37
times ranked

4908
citing authors

#	ARTICLE	IF	CITATIONS
1	The biology and evolution of spider venoms. <i>Biological Reviews</i> , 2022, 97, 163-178.	10.4	42
2	Morphological Analysis Reveals a Compartmentalized Duct in the Venom Apparatus of the Wasp Spider (<i>Argiope bruennichi</i>). <i>Toxins</i> , 2021, 13, 270.	3.4	5
3	A Spider Toxin Exemplifies the Promises and Pitfalls of Cell-Free Protein Production for Venom Biodiscovery. <i>Toxins</i> , 2021, 13, 575.	3.4	3
4	An Economic Dilemma between Molecular Weapon Systems May Explain an Arachno-Atypical Venom in Wasp Spiders (<i>Argiope bruennichi</i>). <i>Biomolecules</i> , 2020, 10, 978.	4.0	13
5	Proteo-Transcriptomic Analysis Identifies Potential Novel Toxins Secreted by the Predatory, Prey-Piercing Ribbon Worm <i>Amphiporus lactifloreus</i> . <i>Marine Drugs</i> , 2020, 18, 407.	4.6	16
6	The complete mitochondrial genome of the hymenopteran hunting robber fly <i>Dasypogon diadema</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1584-1585.	0.4	0
7	Parallel Evolution of Complex Centipede Venoms Revealed by Comparative Proteotranscriptomic Analyses. <i>Molecular Biology and Evolution</i> , 2019, 36, 2748-2763.	8.9	24
8	Toxins from scratch? Diverse, multimodal gene origins in the predatory robber fly <i>Dasypogon diadema</i> indicate a dynamic venom evolution in dipteran insects. <i>GigaScience</i> , 2019, 8, .	6.4	25
9	Proteo-Transcriptomic Characterization of the Venom from the Endoparasitoid Wasp <i>Pimpla turionellae</i> with Aspects on Its Biology and Evolution. <i>Toxins</i> , 2019, 11, 721.	3.4	18
10	A Dipteran's Novel Sucker Punch: Evolution of Arthropod Atypical Venom with a Neurotoxic Component in Robber Flies (<i>Asilidae</i> , <i>Diptera</i>). <i>Toxins</i> , 2018, 10, 29.	3.4	33
11	Studying Smaller and Neglected Organisms in Modern Evolutionary Venomics Implementing RNASeq (Transcriptomics) – A Critical Guide. <i>Toxins</i> , 2018, 10, 292.	3.4	26
12	A dipteran's sucker punch: Diverse venom composition of the robber flies. <i>Toxicon</i> , 2018, 149, 99.	1.6	0
13	Venomics of Remipede Crustaceans Reveals Novel Peptide Diversity and Illuminates the Venom's Biological Role. <i>Toxins</i> , 2017, 9, 234.	3.4	27
14	Response to Comment on "Phylogenomics resolves the timing and pattern of insect evolution". <i>Science</i> , 2015, 349, 487-487.	12.6	17
15	23 RNA in phylogenetic reconstruction. , 2014, , 531-538.		1
16	Quo Vadis Venomics? A Roadmap to Neglected Venomous Invertebrates. <i>Toxins</i> , 2014, 6, 3488-3551.	3.4	90
17	15 Advances in molecular phylogeny of crustaceans in the light of phylogenomic data. , 2014, , 385-398.		0
18	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	12.6	2,096

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19	A Polychaete's Powerful Punch: Venom Gland Transcriptomics of <i>Glycera</i> Reveals a Complex Cocktail of Toxin Homologs. <i>Genome Biology and Evolution</i> , 2014, 6, 2406-2423.	2.5	66
20	The First Venomous Crustacean Revealed by Transcriptomics and Functional Morphology: Remipede Venom Glands Express a Unique Toxin Cocktail Dominated by Enzymes and a Neurotoxin. <i>Molecular Biology and Evolution</i> , 2014, 31, 48-58.	8.9	80
21	Accessing transcriptomic data for ecologically important genes in the goose barnacle (<i>Pollicipes</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	1.1	2
22	A priori assessment of data quality in molecular phylogenetics. <i>Algorithms for Molecular Biology</i> , 2014, 9, .	1.2	23
23	Serotonin-immunoreactive neurons in the ventral nerve cord of Remipedia (Crustacea): support for a sister group relationship of Remipedia and Hexapoda?. <i>BMC Evolutionary Biology</i> , 2013, 13, 119.	3.2	27
24	Selecting informative subsets of sparse supermatrices increases the chance to find correct trees. <i>BMC Bioinformatics</i> , 2013, 14, 348.	2.6	98
25	<i>De novo Ixodes ricinus</i> salivary gland transcriptome analysis using two next-generation sequencing methodologies. <i>FASEB Journal</i> , 2013, 27, 4745-4756.	0.5	88
26	A comprehensive analysis of bilaterian mitochondrial genomes and phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 352-364.	2.7	183
27	Pancrustacean Phylogeny in the Light of New Phylogenomic Data: Support for Remipedia as the Possible Sister Group of Hexapoda. <i>Molecular Biology and Evolution</i> , 2012, 29, 1031-1045.	8.9	223
28	Phylogeography of the burnet moth <i>Zygaena transalpina</i> complex: molecular and morphometric differentiation suggests glacial refugia in Southern France, Western France and micro-refugia within the Alps. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2012, 50, 38-50.	1.4	14
29	Dating the arthropod tree based on large-scale transcriptome data. <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 880-887.	2.7	118
30	Arthropod phylogeny revisited, with a focus on crustacean relationships. <i>Arthropod Structure and Development</i> , 2010, 39, 88-110.	1.4	72
31	Parametric and non-parametric masking of randomness in sequence alignments can be improved and leads to better resolved trees. <i>Frontiers in Zoology</i> , 2010, 7, 10.	2.0	204
32	A Phylogenomic Approach to Resolve the Arthropod Tree of Life. <i>Molecular Biology and Evolution</i> , 2010, 27, 2451-2464.	8.9	308
33	Hemocyanin Suggests a Close Relationship of Remipedia and Hexapoda. <i>Molecular Biology and Evolution</i> , 2009, 26, 2711-2718.	8.9	60
34	Can comprehensive background knowledge be incorporated into substitution models to improve phylogenetic analyses? A case study on major arthropod relationships. <i>BMC Evolutionary Biology</i> , 2009, 9, 119.	3.2	112
35	Cationic composition and acid-base state of the extracellular fluid, and specific buffer value of hemoglobin from the branchiopod crustacean <i>Triops cancriformis</i> . <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2009, 179, 369-381.	1.5	1
36	Aspects of Quality and Project Management in Analyses of Large Scale Sequencing Data. , 0, , .		0