

Blair W Perry

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,517
citations

623699

14
h-index

526264

27
g-index

27
all docs

27
docs citations

27
times ranked

3106
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020, 5, 1408-1417.	13.3	772
2	The origins and evolution of chromosomes, dosage compensation, and mechanisms underlying venom regulation in snakes. <i>Genome Research</i> , 2019, 29, 590-601.	5.5	114
3	Squamate reptiles challenge paradigms of genomic repeat element evolution set by birds and mammals. <i>Nature Communications</i> , 2018, 9, 2774.	12.8	101
4	Molecular Adaptations for Sensing and Securing Prey and Insight into Amniote Genome Diversity from the Garter Snake Genome. <i>Genome Biology and Evolution</i> , 2018, 10, 2110-2129.	2.5	72
5	Phylogeographic and population genetic analyses reveal multiple species of Boa and independent origins of insular dwarfism. <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 104-116.	2.7	47
6	Snake Recombination Landscapes Are Concentrated in Functional Regions despite PRDM9. <i>Molecular Biology and Evolution</i> , 2020, 37, 1272-1294.	8.9	45
7	Insight into the roles of selection in speciation from genomic patterns of divergence and introgression in secondary contact in venomous rattlesnakes. <i>Ecology and Evolution</i> , 2017, 7, 3951-3966.	1.9	34
8	Cryptic genetic diversity, population structure, and gene flow in the Mojave rattlesnake (<i>Crotalus</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.7	33
9	Growth and stress response mechanisms underlying post-feeding regenerative organ growth in the Burmese python. <i>BMC Genomics</i> , 2017, 18, 338.	2.8	32
10	Novel ecological and climatic conditions drive rapid adaptation in invasive Florida Burmese pythons. <i>Molecular Ecology</i> , 2018, 27, 4744-4757.	3.9	30
11	Vertebrate Lineages Exhibit Diverse Patterns of Transposable Element Regulation and Expression across Tissues. <i>Genome Biology and Evolution</i> , 2020, 12, 506-521.	2.5	29
12	Microchromosomes Exhibit Distinct Features of Vertebrate Chromosome Structure and Function with Underappreciated Ramifications for Genome Evolution. <i>Molecular Biology and Evolution</i> , 2021, 38, 904-910.	8.9	28
13	Allopatric divergence and secondary contact with gene flow: a recurring theme in rattlesnake speciation. <i>Biological Journal of the Linnean Society</i> , 2019, 128, 149-169.	1.6	25
14	No safety in the trees: Local and species-level adaptation of an arboreal squirrel to the venom of sympatric rattlesnakes. <i>Toxicon</i> , 2016, 118, 149-155.	1.6	19
15	Viral CpG Deficiency Provides No Evidence That Dogs Were Intermediate Hosts for SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2020, 37, 2706-2710.	8.9	18
16	Evolution: Plasticity versus Selection, or Plasticity and Selection?. <i>Current Biology</i> , 2018, 28, R1104-R1106.	3.9	16
17	Genomic Basis of Convergent Island Phenotypes in Boa Constrictors. <i>Genome Biology and Evolution</i> , 2019, 11, 3123-3143.	2.5	14
18	Snake venom gene expression is coordinated by novel regulatory architecture and the integration of multiple co-opted vertebrate pathways. <i>Genome Research</i> , 2022, 32, 1058-1073.	5.5	14

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19	Discovery and characterization of New Delhi metallo-β-lactamase-1 inhibitor peptides that potentiate meropenem-dependent killing of carbapenemase-producing Enterobacteriaceae. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2843-2851.	3.0	13
20	The roles of balancing selection and recombination in the evolution of rattlesnake venom. <i>Nature Ecology and Evolution</i> , 2022, 6, 1367-1380.	7.8	13
21	Physiological demands and signaling associated with snake venom production and storage illustrated by transcriptional analyses of venom glands. <i>Scientific Reports</i> , 2020, 10, 18083.	3.3	11
22	Multi-species comparisons of snakes identify coordinated signalling networks underlying post-feeding intestinal regeneration. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190910.	2.6	10
23	Patterns of relatedness and genetic diversity inferred from whole genome sequencing of archival blood fluke miracidia (<i>Schistosoma japonicum</i>). <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009020.	3.0	8
24	Population genomic analyses of schistosome parasites highlight critical challenges facing endgame elimination efforts. <i>Scientific Reports</i> , 2021, 11, 6884.	3.3	8
25	Population Genomic Analyses Confirm Male-Biased Mutation Rates in Snakes. <i>Journal of Heredity</i> , 2021, 112, 221-227.	2.4	5
26	Origins, genomic structure and copy number variation of snake venom myotoxins. <i>Toxicon</i> , 2022, 216, 92-106.	1.6	5
27	Identification of an integrated stress and growth response signaling switch that directs vertebrate intestinal regeneration. <i>BMC Genomics</i> , 2022, 23, 6.	2.8	1