

Mark J Margres

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

1,572
citations

331670

21
h-index

330143

37
g-index

40
all docs

40
docs citations

40
times ranked

1541
citing authors

#	ARTICLE	IF	CITATIONS
1	Using Morphological, Genetic, and Venom Analyses to Present Current and Historic Evidence of <i>Crotalus horridus</i> x <i>adamanteus</i> Hybridization on Jekyll Island, Georgia. <i>Southeastern Naturalist</i> , 2022, 21, .	0.4	0
2	Genomic Adaptations to Salinity Resist Gene Flow in the Evolution of Floridian Watersnakes. <i>Molecular Biology and Evolution</i> , 2021, 38, 745-760.	8.9	11
3	The Tiger Rattlesnake genome reveals a complex genotype underlying a simple venom phenotype. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	43
4	Phylogenetically diverse diets favor more complex venoms in North American pitvipers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	48
5	Contemporary and historical selection in Tasmanian devils (<i>Sarcophilus harrisii</i>) support novel, polygenic response to transmissible cancer. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210577.	2.6	9
6	Spatial variation in gene expression of Tasmanian devil facial tumors despite minimal host transcriptomic response to infection. <i>BMC Genomics</i> , 2021, 22, 698.	2.8	6
7	Varying Intensities of Introgression Obscure Incipient Venom-Associated Speciation in the Timber Rattlesnake (<i>Crotalus horridus</i>). <i>Toxins</i> , 2021, 13, 782.	3.4	5
8	Gradual and Discrete Ontogenetic Shifts in Rattlesnake Venom Composition and Assessment of Hormonal and Ecological Correlates. <i>Toxins</i> , 2020, 12, 659.	3.4	7
9	Comparative landscape genetics reveals differential effects of environment on host and pathogen genetic structure in Tasmanian devils (<i>Sarcophilus harrisii</i>) and their transmissible tumour. <i>Molecular Ecology</i> , 2020, 29, 3217-3233.	3.9	9
10	A transmissible cancer shifts from emergence to endemism in Tasmanian devils. <i>Science</i> , 2020, 370, .	12.6	24
11	Spontaneous Tumor Regression in Tasmanian Devils Associated with <i>RASL11A</i> Activation. <i>Genetics</i> , 2020, 215, 1143-1152.	2.9	22
12	Trait differentiation and modular toxin expression in palm-pitvipers. <i>BMC Genomics</i> , 2020, 21, 147.	2.8	18
13	Hybridizing salamanders experience accelerated diversification. <i>Scientific Reports</i> , 2020, 10, 6566.	3.3	16
14	Disease swamps molecular signatures of geneticâ€environmental associations to abiotic factors in Tasmanian devil (<i>Sarcophilus harrisii</i>) populations. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 1392-1408.	2.3	18
15	Contemporary Demographic Reconstruction Methods Are Robust to Genome Assembly Quality: A Case Study in Tasmanian Devils. <i>Molecular Biology and Evolution</i> , 2019, 36, 2906-2921.	8.9	84
16	Intraspecific sequence and gene expression variation contribute little to venom diversity in sidewinder rattlesnakes (<i>Crotalus cerastes</i>). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190810.	2.6	16
17	Transcriptomics of Tasmanian Devil (<i>Sarcophilus Harrisii</i>) Ear Tissue Reveals Homogeneous Gene Expression Patterns across a Heterogeneous Landscape. <i>Genes</i> , 2019, 10, 801.	2.4	6
18	Tipping the Scales: The Migrationâ€Selection Balance Leans toward Selection in Snake Venoms. <i>Molecular Biology and Evolution</i> , 2019, 36, 271-282.	8.9	16

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19	The genomic basis of tumor regression in Tasmanian devils (<i>Sarcophilus harrisii</i>). <i>Genome Biology and Evolution</i> , 2018, 10, 3012-3025.	2.5	30
20	Large-effect loci affect survival in Tasmanian devils (<i>Sarcophilus harrisii</i>) infected with a transmissible cancer. <i>Molecular Ecology</i> , 2018, 27, 4189-4199.	3.9	45
21	Local prey community composition and genetic distance predict venom divergence among populations of the northern Pacific rattlesnake (<i>Crotalus oreganus</i>). <i>Journal of Evolutionary Biology</i> , 2018, 31, 1513-1528.	1.7	29
22	Evaluating the Performance of De Novo Assembly Methods for Venom-Gland Transcriptomics. <i>Toxins</i> , 2018, 10, 249.	3.4	54
23	The devil is in the details: Genomics of transmissible cancers in Tasmanian devils. <i>PLoS Pathogens</i> , 2018, 14, e1007098.	4.7	18
24	Selection To Increase Expression, Not Sequence Diversity, Precedes Gene Family Origin and Expansion in Rattlesnake Venom. <i>Genetics</i> , 2017, 206, 1569-1580.	2.9	37
25	Quantity, Not Quality: Rapid Adaptation in a Polygenic Trait Proceeded Exclusively through Expression Differentiation. <i>Molecular Biology and Evolution</i> , 2017, 34, 3099-3110.	8.9	64
26	The genetics of venom ontogeny in the eastern diamondback rattlesnake (<i>Crotalus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 Td (ad	2.0	36
27	Expression Differentiation Is Constrained to Low-Expression Proteins over Ecological Timescales. <i>Genetics</i> , 2016, 202, 273-283.	2.9	19
28	Functional characterizations of venom phenotypes in the eastern diamondback rattlesnake (<i>Crotalus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 Td (ad Toxicon, 2016, 119, 28-38.	1.6	25
29	Phenotypic integration in the feeding system of the eastern diamondback rattlesnake (<i>Crotalus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 462 Td (ad	3.9	38
30	Post-transcriptional Mechanisms Contribute Little to Phenotypic Variation in Snake Venoms. G3: Genes, Genomes, <i>Genetics</i> , 2015, 5, 2375-2382.	1.8	68
31	Early significant ontogenetic changes in snake venoms. <i>Toxicon</i> , 2015, 96, 74-81.	1.6	25
32	Contrasting Modes and Tempos of Venom Expression Evolution in Two Snake Species. <i>Genetics</i> , 2015, 199, 165-176.	2.9	44
33	The transcriptomic and proteomic basis for the evolution of a novel venom phenotype within the Timber Rattlesnake (<i>Crotalus horridus</i>). <i>Toxicon</i> , 2015, 98, 34-48.	1.6	73
34	RNA-seq and high-definition mass spectrometry reveal the complex and divergent venoms of two rear-fanged colubrid snakes. <i>BMC Genomics</i> , 2014, 15, 1061.	2.8	50
35	Linking the transcriptome and proteome to characterize the venom of the eastern diamondback rattlesnake (<i>Crotalus adamanteus</i>). <i>Journal of Proteomics</i> , 2014, 96, 145-158.	2.4	92
36	The genesis of an exceptionally lethal venom in the timber rattlesnake (<i>Crotalus horridus</i>) revealed through comparative venom-gland transcriptomics. <i>BMC Genomics</i> , 2013, 14, 394.	2.8	95

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37	The venom-gland transcriptome of the eastern coral snake (<i>Micrurus fulvius</i>) reveals high venom complexity in the intragenomic evolution of venoms. <i>BMC Genomics</i> , 2013, 14, 531.	2.8	114
38	The venom-gland transcriptome of the eastern diamondback rattlesnake (<i>Crotalus adamanteus</i>). <i>BMC Genomics</i> , 2012, 13, 312.	2.8	250