

Mark J Margres

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5340771/publications.pdf>

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	The venom-gland transcriptome of the eastern diamondback rattlesnake (<i>Crotalus adamanteus</i>). BMC Genomics, 2012, 13, 312.	2.8	250
2	The venom-gland transcriptome of the eastern coral snake (<i>Micrurus fulvius</i>) reveals high venom complexity in the intragenomic evolution of venoms. BMC Genomics, 2013, 14, 531.	2.8	114
3	The genesis of an exceptionally lethal venom in the timber rattlesnake (<i>Crotalus horridus</i>) revealed through comparative venom-gland transcriptomics. BMC Genomics, 2013, 14, 394.	2.8	95
4	Linking the transcriptome and proteome to characterize the venom of the eastern diamondback rattlesnake (<i>Crotalus adamanteus</i>). Journal of Proteomics, 2014, 96, 145-158.	2.4	92
5	Contemporary Demographic Reconstruction Methods Are Robust to Genome Assembly Quality: A Case Study in Tasmanian Devils. Molecular Biology and Evolution, 2019, 36, 2906-2921.	8.9	84
6	The transcriptomic and proteomic basis for the evolution of a novel venom phenotype within the Timber Rattlesnake (<i>Crotalus horridus</i>). Toxicon, 2015, 98, 34-48.	1.6	73
7	Post-transcriptional Mechanisms Contribute Little to Phenotypic Variation in Snake Venoms. G3: Genes, Genomes, Genetics, 2015, 5, 2375-2382.	1.8	68
8	Quantity, Not Quality: Rapid Adaptation in a Polygenic Trait Proceeded Exclusively through Expression Differentiation. Molecular Biology and Evolution, 2017, 34, 3099-3110.	8.9	64
9	Evaluating the Performance of De Novo Assembly Methods for Venom-Gland Transcriptomics. Toxins, 2018, 10, 249.	3.4	54
10	RNA-seq and high-definition mass spectrometry reveal the complex and divergent venoms of two rear-fanged colubrid snakes. BMC Genomics, 2014, 15, 1061.	2.8	50
11	Phylogenetically diverse diets favor more complex venoms in North American pitvipers. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	48
12	Large-effect loci affect survival in Tasmanian devils (<i>Sarcophilus harrisii</i>) infected with a transmissible cancer. Molecular Ecology, 2018, 27, 4189-4199.	3.9	45
13	Contrasting Modes and Tempos of Venom Expression Evolution in Two Snake Species. Genetics, 2015, 199, 165-176.	2.9	44
14	The Tiger Rattlesnake genome reveals a complex genotype underlying a simple venom phenotype. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	43
15	Phenotypic integration in the feeding system of the eastern diamondback rattlesnake (<i>Crotalus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	3.9	38
16	Selection To Increase Expression, Not Sequence Diversity, Precedes Gene Family Origin and Expansion in Rattlesnake Venom. Genetics, 2017, 206, 1569-1580.	2.9	37
17	The genetics of venom ontogeny in the eastern diamondback rattlesnake (<i>Crotalus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	2.0	36
18	The genomic basis of tumor regression in Tasmanian devils (<i>Sarcophilus harrisii</i>). Genome Biology and Evolution, 2018, 10, 3012-3025.	2.5	30

#	ARTICLE	IF	CITATIONS
19	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
20	Early significant ontogenetic changes in snake venoms. <i>Toxicon</i> , 2015, 96, 74-81.	1.6	25
21	Functional characterizations of venom phenotypes in the eastern diamondback rattlesnake (<i>Crotalus</i>) Tj ETQq1 1 0.784314 rgBT /Ov <i>Toxicon</i> , 2016, 119, 28-38.	1.6	25
22	A transmissible cancer shifts from emergence to endemism in Tasmanian devils. <i>Science</i> , 2020, 370, .	12.6	24
23	Spontaneous Tumor Regression in Tasmanian Devils Associated with <i>RASL11A</i> Activation. <i>Genetics</i> , 2020, 215, 1143-1152.	2.9	22
24	Expression Differentiation Is Constrained to Low-Expression Proteins over Ecological Timescales. <i>Genetics</i> , 2016, 202, 273-283.	2.9	19
25	The devil is in the details: Genomics of transmissible cancers in Tasmanian devils. <i>PLoS Pathogens</i> , 2018, 14, e1007098.	4.7	18
26	Trait differentiation and modular toxin expression in palm-pitvipers. <i>BMC Genomics</i> , 2020, 21, 147.	2.8	18
27	Disease swamps molecular signatures of genetic-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
28	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
29	Tipping the Scales: The Migration-Selection Balance Leans toward Selection in Snake Venoms. <i>Molecular Biology and Evolution</i> , 2019, 36, 271-282.	8.9	16
30	Hybridizing salamanders experience accelerated diversification. <i>Scientific Reports</i> , 2020, 10, 6566.	3.3	16
31	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
32	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
33	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
34	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
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	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