

# Darin R Rokyta

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2565130/publications.pdf>

Version: 2024-02-01

74  
papers

2,850  
citations

168829

31  
h-index

214428

50  
g-index

76  
all docs

76  
docs citations

76  
times ranked

2545  
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrative view of the toxic potential of <i>Conopsis lineatus</i> (Dipsadidae: Xenodontinae), a medically relevant rear-fanged snake. <i>Toxicon</i> , 2022, 205, 38-52.	0.8	3
2	Dynamic genetic differentiation drives the widespread structural and functional convergent evolution of snake venom proteinaceous toxins. <i>BMC Biology</i> , 2022, 20, 4.	1.7	17
3	Contrasting patterns of venom regeneration in a centipede ( <i>Scolopendra viridis</i> ) and a scorpion ( <i>Centruroides hentzi</i> ). <i>Toxicon</i> , 2022, 210, 132-140.	0.8	2
4	Venom Gene Sequence Diversity and Expression Jointly Shape Diet Adaptation in Pitvipers. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	8
5	De Novo Genome Assembly Highlights the Role of Lineage-Specific Gene Duplications in the Evolution of Venom in Fea's Viper ( <i>Azemiops feae</i> ). <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	5
6	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, .	0.2	0
7	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, .	3.3	43
8	Electric Blue: Molecular Evolution of Three-Finger Toxins in the Long-Glanded Coral Snake Species <i>Calliophis bivirgatus</i> . <i>Toxins</i> , 2021, 13, 124.	1.5	9
9	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, .	3.3	48
10	The Chemosensory Repertoire of the Eastern Diamondback Rattlesnake ( <i>Crotalus adamanteus</i> ) Reveals Complementary Genetics of Olfactory and Vomeronasal-Type Receptors. <i>Journal of Molecular Evolution</i> , 2021, 89, 313-328.	0.8	4
11	ToxCodAn: a new toxin annotator and guide to venom gland transcriptomics. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
12	Identification and Characterization of Novel Proteins from Arizona Bark Scorpion Venom That Inhibit Nav1.8, a Voltage-Gated Sodium Channel Regulator of Pain Signaling. <i>Toxins</i> , 2021, 13, 501.	1.5	4
13	Experimental Manipulation of Corticosterone Does Not Affect Venom Composition or Functional Activity in Free-Ranging Rattlesnakes. <i>Physiological and Biochemical Zoology</i> , 2021, 94, 286-301.	0.6	0
14	Varying Intensities of Introgression Obscure Incipient Venom-Associated Speciation in the Timber Rattlesnake ( <i>Crotalus horridus</i> ). <i>Toxins</i> , 2021, 13, 782.	1.5	5
15	Venom Peptides with Dual Modulatory Activity on the Voltage-Gated Sodium Channel Nav1.1 Provide Novel Leads for Development of Antiepileptic Drugs. <i>ACS Pharmacology and Translational Science</i> , 2020, 3, 119-134.	2.5	14
16	Gradual and Discrete Ontogenetic Shifts in Rattlesnake Venom Composition and Assessment of Hormonal and Ecological Correlates. <i>Toxins</i> , 2020, 12, 659.	1.5	7
17	Size Matters: An Evaluation of the Molecular Basis of Ontogenetic Modifications in the Composition of Bothrops jararacussu Snake Venom. <i>Toxins</i> , 2020, 12, 791.	1.5	18
18	Drift, selection and adaptive variation in small populations of a threatened rattlesnake. <i>Molecular Ecology</i> , 2020, 29, 2612-2625.	2.0	8

#	ARTICLE	IF	CITATIONS
19	Trait differentiation and modular toxin expression in palm-pitvipers. BMC Genomics, 2020, 21, 147.	1.2	18
20	Intraspecific sequence and gene expression variation contribute little to venom diversity in sidewinder rattlesnakes ( <i>Crotalus cerastes</i> ). Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190810.	1.2	16
21	Sex-based venom variation in the eastern bark centipede ( <i>Hemiscolopendra marginata</i> ). Toxicon, 2019, 169, 45-58.	0.8	9
22	Convergent recruitment of adamalysin-like metalloproteases in the venom of the red bark centipede ( <i>Scolopocryptops sexspinosus</i> ). Toxicon, 2019, 168, 1-15.	0.8	8
23	No Cost of Complexity in Bacteriophages Adapting to a Complex Environment. Genetics, 2019, 212, 267-276.	1.2	3
24	Biophysical Spandrels form a Hot-Spot for Kosmotropic Mutations in Bacteriophage Thermal Adaptation. Journal of Molecular Evolution, 2019, 87, 27-36.	0.8	2
25	Tipping the Scales: The Migration of Selection Balance Leans toward Selection in Snake Venoms. Molecular Biology and Evolution, 2019, 36, 271-282.	3.5	16
26	Molecular mechanisms underlying intraspecific variation in snake venom. Journal of Proteomics, 2018, 181, 60-72.	1.2	54
27	A Single Mutation Unlocks Cascading Exaptations in the Origin of a Potent Pitviper Neurotoxin. Molecular Biology and Evolution, 2018, 35, 887-898.	3.5	26
28	Additive Phenotypes Underlie Epistasis of Fitness Effects. Genetics, 2018, 208, 339-348.	1.2	22
29	Venom-gland transcriptomics and venom proteomics of the Hentz striped scorpion ( <i>Centruroides Tj ETQq1</i> ). <i>Overlock</i> 14-29. 1 0.784314 rgBT /Overlock	0.8	46
30	Evidence for divergent patterns of local selection driving venom variation in Mojave Rattlesnakes ( <i>Crotalus scutulatus</i> ). Scientific Reports, 2018, 8, 17622.	1.6	42
31	Comparative venom-gland transcriptomics and venom proteomics of four Sidewinder Rattlesnake ( <i>Crotalus cerastes</i> ) lineages reveal little differential expression despite individual variation. Scientific Reports, 2018, 8, 15534.	1.6	41
32	Three-Finger Toxin Diversification in the Venoms of Cat-Eye Snakes (Colubridae: Boiga). Journal of Molecular Evolution, 2018, 86, 531-545.	0.8	14
33	Local prey community composition and genetic distance predict venom divergence among populations of the northern Pacific rattlesnake ( <i>Crotalus oreganus</i> ). Journal of Evolutionary Biology, 2018, 31, 1513-1528.	0.8	29
34	Phenotypic Variation in Mojave Rattlesnake ( <i>Crotalus scutulatus</i> ) Venom Is Driven by Four Toxin Families. Toxins, 2018, 10, 135.	1.5	32
35	Evaluating the Performance of De Novo Assembly Methods for Venom-Gland Transcriptomics. Toxins, 2018, 10, 249.	1.5	54
36	Female-biased population divergence in the venom of the Hentz striped scorpion ( <i>Centruroides Tj ETQq0</i> ). <i>Overlock</i> 10 Tf 50 62. 0 0 0 rgBT /Overlock	0.8	13

#	ARTICLE	IF	CITATIONS
37	Venom-gland transcriptomics and venom proteomics of the giant Florida blue centipede, <i>Scolopendra viridis</i> . <i>Toxicon</i> , 2018, 152, 121-136.	0.8	19
38	Venom-gland transcriptomics and venom proteomics of the black-back scorpion ( <i>Hadrurus spadix</i> ) reveal detectability challenges and an unexplored realm of animal toxin diversity. <i>Toxicon</i> , 2017, 128, 23-37.	0.8	51
39	Selection To Increase Expression, Not Sequence Diversity, Precedes Gene Family Origin and Expansion in Rattlesnake Venom. <i>Genetics</i> , 2017, 206, 1569-1580.	1.2	37
40	Mutation-Driven Parallel Evolution during Viral Adaptation. <i>Molecular Biology and Evolution</i> , 2017, 34, 3243-3253.	3.5	39
41	Quantity, Not Quality: Rapid Adaptation in a Polygenic Trait Proceeded Exclusively through Expression Differentiation. <i>Molecular Biology and Evolution</i> , 2017, 34, 3099-3110.	3.5	64
42	The genetics of venom ontogeny in the eastern diamondback rattlesnake ( <i>Crotalus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,542 Td (ac	0.9	36
43	Expression Differentiation Is Constrained to Low-Expression Proteins over Ecological Timescales. <i>Genetics</i> , 2016, 202, 273-283.	1.2	19
44	Functional characterizations of venom phenotypes in the eastern diamondback rattlesnake ( <i>Crotalus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	25
45	Synergistic Pleiotropy Overrides the Costs of Complexity in Viral Adaptation. <i>Genetics</i> , 2016, 202, 285-295.	1.2	45
46	Viral recombination blurs taxonomic lines: examination of single-stranded DNA viruses in a wastewater treatment plant. <i>PeerJ</i> , 2016, 4, e2585.	0.9	25
47	Phenotypic integration in the feeding system of the eastern diamondback rattlesnake ( <i>Crotalus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	2.0	38
48	Post-transcriptional Mechanisms Contribute Little to Phenotypic Variation in Snake Venoms. G3: Genes, Genomes, <i>Genetics</i> , 2015, 5, 2375-2382.	0.8	68
49	Establishment of the Adventive Centipede <i>Rhysida longipes longipes</i> (Newport, 1845;) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	0.2	0
50	Early significant ontogenetic changes in snake venoms. <i>Toxicon</i> , 2015, 96, 74-81.	0.8	25
51	Contrasting Modes and Tempos of Venom Expression Evolution in Two Snake Species. <i>Genetics</i> , 2015, 199, 165-176.	1.2	44
52	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.	0.8	73
53	Intergenic incompatibilities reduce fitness in hybrids of extremely closely related bacteriophages. <i>PeerJ</i> , 2015, 3, e1320.	0.9	14
54	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.	1.2	50

#	ARTICLE	IF	CITATIONS
55	Payoffs, Not Tradeoffs, in the Adaptation of a Virus to Ostensibly Conflicting Selective Pressures. <i>PLoS Genetics</i> , 2014, 10, e1004611.	1.5	27
56	Environment Determines Epistatic Patterns for a ssDNA Virus. <i>Genetics</i> , 2014, 196, 267-279.	1.2	25
57	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.	1.2	92
58	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.	1.2	95
59	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.	1.2	114
60	The Adaptive Potential of Hybridization Demonstrated with Bacteriophages. <i>Journal of Molecular Evolution</i> , 2013, 77, 221-230.	0.8	11
61	Report from the First Snake Genomics and Integrative Biology Meeting. <i>Standards in Genomic Sciences</i> , 2012, 7, 150-152.	1.5	4
62	The venom-gland transcriptome of the eastern diamondback rattlesnake ( <i>Crotalus adamanteus</i> ). <i>BMC Genomics</i> , 2012, 13, 312.	1.2	250
63	The Consistency of Beneficial Fitness Effects of Mutations across Diverse Genetic Backgrounds. <i>PLoS ONE</i> , 2012, 7, e43864.	1.1	16
64	A high-throughput venom-gland transcriptome for the Eastern Diamondback Rattlesnake ( <i>Crotalus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 657-671.	0.8	116
65	Epistasis between Beneficial Mutations and the Phenotype-to-Fitness Map for a ssDNA Virus. <i>PLoS Genetics</i> , 2011, 7, e1002075.	1.5	88
66	Genic Incompatibilities in Two Hybrid Bacteriophages. <i>Molecular Biology and Evolution</i> , 2009, 26, 2831-2839.	3.5	24
67	The Genetics of Adaptation for Eight Microvirid Bacteriophages. <i>Journal of Molecular Evolution</i> , 2009, 69, 229-239.	0.8	65
68	Beneficial Fitness Effects Are Not Exponential for Two Viruses. <i>Journal of Molecular Evolution</i> , 2008, 67, 368-376.	0.8	97
69	A General Extreme Value Theory Model for the Adaptation of DNA Sequences Under Strong Selection and Weak Mutation. <i>Genetics</i> , 2008, 180, 1627-1643.	1.2	72
70	Testing the Extreme Value Domain of Attraction for Distributions of Beneficial Fitness Effects. <i>Genetics</i> , 2007, 176, 2441-2449.	1.2	53
71	Properties of adaptive walks on uncorrelated landscapes under strong selection and weak mutation. <i>Journal of Theoretical Biology</i> , 2006, 243, 114-120.	0.8	37
72	Horizontal Gene Transfer and the Evolution of Microvirid Coliphage Genomes. <i>Journal of Bacteriology</i> , 2006, 188, 1134-1142.	1.0	106

#	ARTICLE	IF	CITATIONS
73	An empirical test of the mutational landscape model of adaptation using a single-stranded DNA virus. <i>Nature Genetics</i> , 2005, 37, 441-444.	9.4	172
74	Experimental Genomic Evolution: Extensive Compensation for Loss of DNA Ligase Activity in a Virus. <i>Molecular Biology and Evolution</i> , 2002, 19, 230-238.	3.5	65