

Todd A Castoe

List of Publications by Year in descending order

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Version: 2024-02-01

110
papers

8,017
citations

100601

38
h-index

62345

84
g-index

113
all docs

113
docs citations

113
times ranked

12207
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of an integrated stress and growth response signaling switch that directs vertebrate intestinal regeneration. <i>BMC Genomics</i> , 2022, 23, 6.	1.2	1
2	A chromosome-level genome assembly and annotation of the desert horned lizard, <i>Phrynosoma platyrhinos</i> , provides insight into chromosomal rearrangements among reptiles. <i>GigaScience</i> , 2022, 11, .	3.3	12
3	A genomic can of worms for schistosome host-specificity. <i>Trends in Parasitology</i> , 2022, 38, 496-497.	1.5	1
4	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.	2.4	14
5	The roles of balancing selection and recombination in the evolution of rattlesnake venom. <i>Nature Ecology and Evolution</i> , 2022, 6, 1367-1380.	3.4	13
6	Origins, genomic structure and copy number variation of snake venom myotoxins. <i>Toxicon</i> , 2022, 216, 92-106.	0.8	5
7	<i>PhyloWGA</i> : chromosome-aware phylogenetic interrogation of whole genome alignments. <i>Bioinformatics</i> , 2021, 37, 1923-1925.	1.8	1
8	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.	3.5	28
9	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.	1.3	8
10	Population genomic analyses of schistosome parasites highlight critical challenges facing endgame elimination efforts. <i>Scientific Reports</i> , 2021, 11, 6884.	1.6	8
11	Genome-wide data implicate terminal fusion automixis in king cobra facultative parthenogenesis. <i>Scientific Reports</i> , 2021, 11, 7271.	1.6	10
12	The effects of climate and demographic history in shaping genomic variation across populations of the Desert Horned Lizard (<i>Phrynosoma platyrhinos</i>). <i>Molecular Ecology</i> , 2021, 30, 4481-4496.	2.0	8
13	Population Genomic Analyses Confirm Male-Biased Mutation Rates in Snakes. <i>Journal of Heredity</i> , 2021, 112, 221-227.	1.0	5
14	Probabilistic Species Tree Distances: Implementing the Multispecies Coalescent to Compare Species Trees Within the Same Model-Based Framework Used to Estimate Them. <i>Systematic Biology</i> , 2020, 69, 194-207.	2.7	2
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.	3.5	18
16	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020, 5, 1408-1417.	5.9	772
17	Genome-wide SNPs clarify lineage diversity confused by coloration in coralsnakes of the <i>Micrurus diastema</i> species complex (Serpentes: Elapidae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 147, 106770.	1.2	20
18	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.	1.6	11

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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.	1.3	13
20	Snake Recombination Landscapes Are Concentrated in Functional Regions despite PRDM9. <i>Molecular Biology and Evolution</i> , 2020, 37, 1272-1294.	3.5	45
21	Vertebrate Lineages Exhibit Diverse Patterns of Transposable Element Regulation and Expression across Tissues. <i>Genome Biology and Evolution</i> , 2020, 12, 506-521.	1.1	29
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.	1.2	10
23	Genomic Basis of Convergent Island Phenotypes in Boa Constrictors. <i>Genome Biology and Evolution</i> , 2019, 11, 3123-3143.	1.1	14
24	Supergene validation: A model-based protocol for assessing the accuracy of non-model-based supergene methods. <i>MethodsX</i> , 2019, 6, 2181-2188.	0.7	1
25	Recent Advances in the Inference of Gene Flow from Population Genomic Data. <i>Current Molecular Biology Reports</i> , 2019, 5, 107-115.	0.8	1
26	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.	0.7	25
27	The origins and evolution of chromosomes, dosage compensation, and mechanisms underlying venom regulation in snakes. <i>Genome Research</i> , 2019, 29, 590-601.	2.4	114
28	The transcriptome of the veiled chameleon (<i>Chamaeleo calypttratus</i>): A resource for studying the evolution and development of vertebrates. <i>Developmental Dynamics</i> , 2019, 248, 702-708.	0.8	26
29	Statistical binning leads to profound model violation due to gene tree error incurred by trying to avoid gene tree error. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 164-171.	1.2	20
30	Solenodon genome reveals convergent evolution of venom in eulipotyphlan mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25745-25755.	3.3	42
31	Shifts in Selective Pressures on Snake Phototransduction Genes Associated with Photoreceptor Transmutation and Dim-Light Ancestry. <i>Molecular Biology and Evolution</i> , 2018, 35, 1376-1389.	3.5	26
32	ThetaMater: Bayesian estimation of population size parameter $\hat{\theta}$ from genomic data. <i>Bioinformatics</i> , 2018, 34, 1072-1073.	1.8	8
33	Evidence for divergent patterns of local selection driving venom variation in Mojave Rattlesnakes (<i>Crotalus scutulatus</i>). <i>Scientific Reports</i> , 2018, 8, 17622.	1.6	42
34	Evolution: Plasticity versus Selection, or Plasticity and Selection?. <i>Current Biology</i> , 2018, 28, R1104-R1106.	1.8	16
35	Novel ecological and climatic conditions drive rapid adaptation in invasive Florida Burmese pythons. <i>Molecular Ecology</i> , 2018, 27, 4744-4757.	2.0	30
36	Plasticity and local adaptation explain lizard cold tolerance. <i>Molecular Ecology</i> , 2018, 27, 2173-2175.	2.0	7

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37	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.	1.1	72
38	Squamate reptiles challenge paradigms of genomic repeat element evolution set by birds and mammals. <i>Nature Communications</i> , 2018, 9, 2774.	5.8	101
39	Assessing the Impacts of Positive Selection on Coalescent-Based Species Tree Estimation and Species Delimitation. <i>Systematic Biology</i> , 2018, 67, 1076-1090.	2.7	20
40	Cryptic genetic diversity, population structure, and gene flow in the Mojave rattlesnake (<i>Crotalus</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.2	33
41	<i>GppFst</i> : genomic posterior predictive simulations of <i>FST</i> and <i>dXY</i> for identifying outlier loci from population genomic data. <i>Bioinformatics</i> , 2017, 33, 1414-1415.	1.8	9
42	Hormonally Mediated Increases in Sex-Biased Gene Expression Accompany the Breakdown of Between-Sex Genetic Correlations in a Sexually Dimorphic Lizard. <i>American Naturalist</i> , 2017, 189, 315-332.	1.0	54
43	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.	0.8	34
44	Contrasting gene expression programs correspond with predator-induced phenotypic plasticity within and across generations in <i>Daphnia</i> . <i>Molecular Ecology</i> , 2017, 26, 5003-5015.	2.0	39
45	The Discovery of XY Sex Chromosomes in a Boa and Python. <i>Current Biology</i> , 2017, 27, 2148-2153.e4.	1.8	105
46	Growth and stress response mechanisms underlying post-feeding regenerative organ growth in the Burmese python. <i>BMC Genomics</i> , 2017, 18, 338.	1.2	32
47	Targeted capture of complete coding regions across divergent species. <i>Genome Biology and Evolution</i> , 2017, 9, evx005.	1.1	15
48	Whole Genome Amplification and Reduced-Representation Genome Sequencing of <i>Schistosoma japonicum</i> Miracidia. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005292.	1.3	23
49	Genetic surfing, not allopatric divergence, explains spatial sorting of mitochondrial haplotypes in venomous coralsnakes. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1435-1449.	1.1	33
50	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.	1.2	47
51	A suite of potentially amplifiable microsatellite loci for ten reptiles of conservation concern from Africa and Asia. <i>Conservation Genetics Resources</i> , 2016, 8, 307-311.	0.4	3
52	EpiRADseq: scalable analysis of genomewide patterns of methylation using next-generation sequencing. <i>Methods in Ecology and Evolution</i> , 2016, 7, 60-69.	2.2	74
53	A cryptic palm-pitviper species (Squamata: Viperidae: <i>Bothriechis</i>) from the Costa Rican highlands, with notes on the variation within <i>B. nigroviridis</i> . <i>Zootaxa</i> , 2016, 4138, 271-90.	0.2	13
54	Historical Contingency in a Multigene Family Facilitates Adaptive Evolution of Toxin Resistance. <i>Current Biology</i> , 2016, 26, 1616-1621.	1.8	47

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55	Local adaptation in transgenerational responses to predators. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152271.	1.2	65
56	Contrasting patterns of evolutionary diversification in the olfactory repertoires of reptile and bird genomes. <i>Genome Biology and Evolution</i> , 2016, 8, evw013.	1.1	28
57	Microsatellite landscape evolutionary dynamics across 450 million years of vertebrate genome evolution. <i>Genome</i> , 2016, 59, 295-310.	0.9	40
58	Incipient speciation with biased gene flow between two lineages of the Western Diamondback Rattlesnake (<i>Crotalus atrox</i>). <i>Molecular Phylogenetics and Evolution</i> , 2015, 83, 213-223.	1.2	43
59	Development of 13 microsatellites for Gunnison Sage-grouse (<i>Centrocercus minimus</i>) using next-generation shotgun sequencing and their utility in Greater Sage-grouse (<i>Centrocercus</i>)	1.0	10
60	Rapid changes in gene expression direct rapid shifts in intestinal form and function in the Burmese python after feeding. <i>Physiological Genomics</i> , 2015, 47, 147-157.	1.0	28
61	Comparative venomomics of the Prairie Rattlesnake (<i>Crotalus viridis viridis</i>) from Colorado: Identification of a novel pattern of ontogenetic changes in venom composition and assessment of the immunoreactivity of the commercial antivenom CroFab®. <i>Journal of Proteomics</i> , 2015, 121, 28-43.	1.2	70
62	Expression of Venom Gene Homologs in Diverse Python Tissues Suggests a New Model for the Evolution of Snake Venom. <i>Molecular Biology and Evolution</i> , 2015, 32, 173-183.	3.5	93
63	Genetic consequences of postglacial range expansion in two codistributed rodents (genus)	2.0	46
64	Two Low Coverage Bird Genomes and a Comparison of Reference-Guided versus De Novo Genome Assemblies. <i>PLoS ONE</i> , 2014, 9, e106649.	1.1	30
65	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	6.0	300
66	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014, 3, 27.	3.3	72
67	New insights on facultative parthenogenesis in pythons. <i>Biological Journal of the Linnean Society</i> , 2014, 112, 461-468.	0.7	31
68	Phylogenetic relationships of the enigmatic longtailed rattlesnakes (<i>Crotalus ericsmithi</i> , <i>C. lannomi</i>)	1.2	36
69	Development and characterization of thirteen microsatellite loci in Clark's nutcracker (<i>Nucifraga</i>)	0.4	2
70	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20645-20650.	3.3	260
71	The king cobra genome reveals dynamic gene evolution and adaptation in the snake venom system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20651-20656.	3.3	412
72	Comparative Phylogeographic Analyses Illustrate the Complex Evolutionary History of Threatened Cloud Forests of Northern Mesoamerica. <i>PLoS ONE</i> , 2013, 8, e56283.	1.1	144

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73	Chinese alligator genome illustrates molecular adaptations. <i>Cell Research</i> , 2013, 23, 1254-1255.	5.7	3
74	Germline TRAV5D-4 T-Cell Receptor Sequence Targets a Primary Insulin Peptide of NOD Mice. <i>Diabetes</i> , 2012, 61, 857-865.	0.3	31
75	Transcriptome sequencing of black grouse (<i>Tetrao tetrix</i>) for immune gene discovery and microsatellite development. <i>Open Biology</i> , 2012, 2, 120054.	1.5	26
76	LTR Retrotransposons Contribute to Genomic Gigantism in Plethodontid Salamanders. <i>Genome Biology and Evolution</i> , 2012, 4, 168-183.	1.1	152
77	Report from the First Snake Genomics and Integrative Biology Meeting. <i>Standards in Genomic Sciences</i> , 2012, 7, 150-152.	1.5	4
78	Thousands of microsatellite loci from the venomous coral snake <i>Micrurus fulvius</i> and variability of select loci across populations and related species. <i>Molecular Ecology Resources</i> , 2012, 12, 1105-1113.	2.2	26
79	Rapid Microsatellite Identification from Illumina Paired-End Genomic Sequencing in Two Birds and a Snake. <i>PLoS ONE</i> , 2012, 7, e30953.	1.1	208
80	Cryptic diversity in disjunct populations of Middle American Montane Pitvipers: a systematic reassessment of <i>Cerrophidion godmani</i> . <i>Zoologica Scripta</i> , 2012, 41, 455-470.	0.7	23
81	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011, 477, 587-591.	13.7	575
82	Sequencing the genome of the Burmese python (<i>Python molurus bivittatus</i>) as a model for studying extreme adaptations in snakes. <i>Genome Biology</i> , 2011, 12, 406.	13.9	58
83	Bayesian Analysis of High-Throughput Quantitative Measurement of Protein-DNA Interactions. <i>PLoS ONE</i> , 2011, 6, e26105.	1.1	2
84	Discovery of Highly Divergent Repeat Landscapes in Snake Genomes Using High-Throughput Sequencing. <i>Genome Biology and Evolution</i> , 2011, 3, 641-653.	1.1	87
85	A proposal to sequence the genome of a garter snake (<i>Thamnophis sirtalis</i>). <i>Standards in Genomic Sciences</i> , 2011, 4, 257-270.	1.5	31
86	A multi-organ transcriptome resource for the Burmese Python (<i>Python molurus bivittatus</i>). <i>BMC Research Notes</i> , 2011, 4, 310.	0.6	18
87	Repetitive Elements May Comprise Over Two-Thirds of the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002384.	1.5	907
88	Comparison of Normalization Methods for Construction of Large, Multiplex Amplicon Pools for Next-Generation Sequencing. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3863-3868.	1.4	71
89	Adaptive molecular convergences. <i>Communicative and Integrative Biology</i> , 2010, 3, 67-69.	0.6	13
90	Rapid identification of thousands of copperhead snake (<i>Agkistrodon contortrix</i>) microsatellite loci from modest amounts of 454 shotgun genome sequence. <i>Molecular Ecology Resources</i> , 2010, 10, 341-347.	2.2	179

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91	Identifying DNA Strands Using a Kernel of Classified Sequences. , 2009, , .		0
92	Evidence for an ancient adaptive episode of convergent molecular evolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8986-8991.	3.3	284
93	Comparative phylogeography of pitvipers suggests a consensus of ancient Middle American highland biogeography. Journal of Biogeography, 2009, 36, 88-103.	1.4	157
94	Identification of repeat structure in large genomes using repeat probability clouds. Analytical Biochemistry, 2008, 380, 77-83.	1.1	51
95	Adaptive Evolution and Functional Redesign of Core Metabolic Proteins in Snakes. PLoS ONE, 2008, 3, e2201.	1.1	113
96	An ancient adaptive episode of convergent molecular evolution confounds phylogenetic inference. Nature Precedings, 2008, , .	0.1	1
97	A novel group of type I polyketide synthases (PKS) in animals and the complex phylogenomics of PKSs. Gene, 2007, 392, 47-58.	1.0	59
98	Phylogeographic structure and historical demography of the western diamondback rattlesnake (<i>Crotalus atrox</i>): A perspective on North American desert biogeography. Molecular Phylogenetics and Evolution, 2007, 42, 193-212.	1.2	127
99	Bayesian mixed models and the phylogeny of pitvipers (Viperidae: Serpentes). Molecular Phylogenetics and Evolution, 2006, 39, 91-110.	1.2	189
100	Modeling nucleotide evolution at the mesoscale: The phylogeny of the Neotropical pitvipers of the Porthidium group (Viperidae: Crotalinae). Molecular Phylogenetics and Evolution, 2005, 37, 881-898.	1.2	60
101	Phylogenetic taxonomy of the Cercosaurini (Squamata: Gymnophthalmidae), with new genera for species of <i>Neusticurus</i> and <i>Proctoporus</i> . Zoological Journal of the Linnean Society, 2005, 143, 405-416.	1.0	57
102	Historical perspectives on population genetics and conservation of three marine turtle species. Conservation Genetics, 2005, 6, 235-251.	0.8	38
103	Evidence of Population Genetic Structure within the Florida Worm Lizard, <i>Rhineura floridana</i> (<i>Amphisbaenia</i> : <i>Rhineuridae</i>). Journal of Herpetology, 2005, 39, 118-124.	0.2	15
104	PHYLOGENETIC RELATIONSHIPS OF THE GENUS PROCTOPORUS SENSU STRICTO (SQUAMATA:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2 325-336.	0.2	14
105	Sciurid phylogeny and the paraphyly of Holarctic ground squirrels (<i>Spermophilus</i>). Molecular Phylogenetics and Evolution, 2004, 31, 1015-1030.	1.2	116
106	Data Partitions and Complex Models in Bayesian Analysis: The Phylogeny of Gymnophthalmid Lizards. Systematic Biology, 2004, 53, 448-469.	2.7	201
107	MOLECULAR SYSTEMATICS OF THE MIDDLE AMERICAN JUMPING PITVIPERS (GENUS ATROPOIDES) AND PHYLOGEOGRAPHY OF THE ATROPOIDES NUMMIFER COMPLEX. Herpetologica, 2003, 59, 420-431.	0.2	32
108	USING MORPHOLOGICAL AND MOLECULAR EVIDENCE TO INFER SPECIES BOUNDARIES WITHIN PROCTOPORUS BOLIVIANUS WERNER (SQUAMATA: GYMNOPHTHALMIDAE). Herpetologica, 2003, 59, 432-449.	0.2	29

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109	The Hemipenes of Some Snakes of the Semifossorial Genus <i>Atractus</i> , with Comments on Variation in the Genus. <i>Journal of Herpetology</i> , 2003, 37, 718-721.	0.2	17
110	Higher-level phylogeny of Asian and American coralsnakes, their placement within the Elapidae (Squamata), and the systematic affinities of the enigmatic Asian coralsnake <i>Hemibungarus calligaster</i> (Wiegmann, 1834). <i>Zoological Journal of the Linnean Society</i> , 0, 151, 809-831.	1.0	50