

Todd A Castoe

List of Publications by Year in descending order

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110
papers

8,017
citations

87888
38
h-index

54911
84
g-index

113
all docs

113
docs citations

113
times ranked

10953
citing authors

#	ARTICLE	IF	CITATIONS
1	Repetitive Elements May Comprise Over Two-Thirds of the Human Genome. PLoS Genetics, 2011, 7, e1002384.	3.5	907
2	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. Nature Microbiology, 2020, 5, 1408-1417.	13.3	772
3	The genome of the green anole lizard and a comparative analysis with birds and mammals. Nature, 2011, 477, 587-591.	27.8	575
4	The king cobra genome reveals dynamic gene evolution and adaptation in the snake venom system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20651-20656.	7.1	412
5	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449.	12.6	300
6	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.	7.1	284
7	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20645-20650.	7.1	260
8	Rapid Microsatellite Identification from Illumina Paired-End Genomic Sequencing in Two Birds and a Snake. PLoS ONE, 2012, 7, e30953.	2.5	208
9	Data Partitions and Complex Models in Bayesian Analysis: The Phylogeny of Gymnophthalmid Lizards. Systematic Biology, 2004, 53, 448-469.	5.6	201
10	Bayesian mixed models and the phylogeny of pitvipers (Viperidae: Serpentes). Molecular Phylogenetics and Evolution, 2006, 39, 91-110.	2.7	189
11	Rapid identification of thousands of copperhead snake (<i>Agkistrodon contortrix</i>) microsatellite loci from modest amounts of 454 shotgun genome sequence. Molecular Ecology Resources, 2010, 10, 341-347.	4.8	179
12	Comparative phylogeography of pitvipers suggests a consensus of ancient Middle American highland biogeography. Journal of Biogeography, 2009, 36, 88-103.	3.0	157
13	LTR Retrotransposons Contribute to Genomic Gigantism in Plethodontid Salamanders. Genome Biology and Evolution, 2012, 4, 168-183.	2.5	152
14	Comparative Phylogeographic Analyses Illustrate the Complex Evolutionary History of Threatened Cloud Forests of Northern Mesoamerica. PLoS ONE, 2013, 8, e56283.	2.5	144
15	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.	2.7	127
16	Sciurid phylogeny and the paraphyly of Holarctic ground squirrels (<i>Spermophilus</i>). Molecular Phylogenetics and Evolution, 2004, 31, 1015-1030.	2.7	116
17	The origins and evolution of chromosomes, dosage compensation, and mechanisms underlying venom regulation in snakes. Genome Research, 2019, 29, 590-601.	5.5	114
18	Adaptive Evolution and Functional Redesign of Core Metabolic Proteins in Snakes. PLoS ONE, 2008, 3, e2201.	2.5	113

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19	The Discovery of XY Sex Chromosomes in a Boa and Python. <i>Current Biology</i> , 2017, 27, 2148-2153.e4.	3.9	105
20	Squamate reptiles challenge paradigms of genomic repeat element evolution set by birds and mammals. <i>Nature Communications</i> , 2018, 9, 2774.	12.8	101
21	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.	8.9	93
22	Discovery of Highly Divergent Repeat Landscapes in Snake Genomes Using High-Throughput Sequencing. <i>Genome Biology and Evolution</i> , 2011, 3, 641-653.	2.5	87
23	EpiRADseq: scalable analysis of genomewide patterns of methylation using next-generation sequencing. <i>Methods in Ecology and Evolution</i> , 2016, 7, 60-69.	5.2	74
24	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014, 3, 27.	6.4	72
25	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
26	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.	3.1	71
27	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.	2.4	70
28	Local adaptation in transgenerational responses to predators. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152271.	2.6	65
29	Modeling nucleotide evolution at the mesoscale: The phylogeny of the Neotropical pitvipers of the Porthidium group (Viperidae: Crotalinae). <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 881-898.	2.7	60
30	A novel group of type I polyketide synthases (PKS) in animals and the complex phylogenomics of PKSs. <i>Gene</i> , 2007, 392, 47-58.	2.2	59
31	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.	9.6	58
32	Phylogenetic taxonomy of the Cercosaurini (Squamata: Gymnophthalmidae), with new genera for species of Neusticurus and Proctoporus. <i>Zoological Journal of the Linnean Society</i> , 2005, 143, 405-416.	2.3	57
33	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.	2.1	54
34	Identification of repeat structure in large genomes using repeat probability clouds. <i>Analytical Biochemistry</i> , 2008, 380, 77-83.	2.4	51
35	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.	2.3	50
36	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

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37	Historical Contingency in a Multigene Family Facilitates Adaptive Evolution of Toxin Resistance. <i>Current Biology</i> , 2016, 26, 1616-1621.	3.9	47
38	Genetic consequences of postglacial range expansion in two codistributed rodents (genus) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 To</i>	3.9	46
39	Snake Recombination Landscapes Are Concentrated in Functional Regions despite PRDM9. <i>Molecular Biology and Evolution</i> , 2020, 37, 1272-1294.	8.9	45
40	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.	2.7	43
41	Evidence for divergent patterns of local selection driving venom variation in Mojave Rattlesnakes (<i>Crotalus scutulatus</i>). <i>Scientific Reports</i> , 2018, 8, 17622.	3.3	42
42	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.	7.1	42
43	Microsatellite landscape evolutionary dynamics across 450 million years of vertebrate genome evolution. <i>Genome</i> , 2016, 59, 295-310.	2.0	40
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.	3.9	39
45	Historical perspectives on population genetics and conservation of three marine turtle species. <i>Conservation Genetics</i> , 2005, 6, 235-251.	1.5	38
46	Phylogenetic relationships of the enigmatic longtailed rattlesnakes (<i>Crotalus ericsmithi</i> , <i>C. lannomi</i> ,) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 To</i>	2.7	36
47	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
48	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.	2.3	33
49	Cryptic genetic diversity, population structure, and gene flow in the Mojave rattlesnake (<i>Crotalus</i>) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 702 To</i>	2.7	33
50	MOLECULAR SYSTEMATICS OF THE MIDDLE AMERICAN JUMPING PITVIPERS (GENUS <i>ATROPOIDES</i>) AND PHYLOGEOGRAPHY OF THE <i>ATROPOIDES NUMMIFER</i> COMPLEX. <i>Herpetologica</i> , 2003, 59, 420-431.	0.4	32
51	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
52	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
53	Germline TRAV5D-4 T-Cell Receptor Sequence Targets a Primary Insulin Peptide of NOD Mice. <i>Diabetes</i> , 2012, 61, 857-865.	0.6	31
54	New insights on facultative parthenogenesis in pythons. <i>Biological Journal of the Linnean Society</i> , 2014, 112, 461-468.	1.6	31

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55	Two Low Coverage Bird Genomes and a Comparison of Reference-Guided versus De Novo Genome Assemblies. PLoS ONE, 2014, 9, e106649.	2.5	30
56	Novel ecological and climatic conditions drive rapid adaptation in invasive Florida Burmese pythons. Molecular Ecology, 2018, 27, 4744-4757.	3.9	30
57	USING MORPHOLOGICAL AND MOLECULAR EVIDENCE TO INFER SPECIES BOUNDARIES WITHIN PROCTOPORUS BOLIVIANUS WERNER (SQUAMATA: GYMNOPTHALMIDAE). Herpetologica, 2003, 59, 432-449.	0.4	29
58	Vertebrate Lineages Exhibit Diverse Patterns of Transposable Element Regulation and Expression across Tissues. Genome Biology and Evolution, 2020, 12, 506-521.	2.5	29
59	Rapid changes in gene expression direct rapid shifts in intestinal form and function in the Burmese python after feeding. Physiological Genomics, 2015, 47, 147-157.	2.3	28
60	Contrasting patterns of evolutionary diversification in the olfactory repertoires of reptile and bird genomes. Genome Biology and Evolution, 2016, 8, evw013.	2.5	28
61	Microchromosomes Exhibit Distinct Features of Vertebrate Chromosome Structure and Function with Underappreciated Ramifications for Genome Evolution. Molecular Biology and Evolution, 2021, 38, 904-910.	8.9	28
62	Transcriptome sequencing of black grouse (Tetrao tetrix) for immune gene discovery and microsatellite development. Open Biology, 2012, 2, 120054.	3.6	26
63	Thousands of microsatellite loci from the venomous coralsnake M icrurus fulvius and variability of select loci across populations and related species. Molecular Ecology Resources, 2012, 12, 1105-1113.	4.8	26
64	Shifts in Selective Pressures on Snake Phototransduction Genes Associated with Photoreceptor Transmutation and Dim-Light Ancestry. Molecular Biology and Evolution, 2018, 35, 1376-1389.	8.9	26
65	The transcriptome of the veiled chameleon (Chamaeleo calytratus): A resource for studying the evolution and development of vertebrates. Developmental Dynamics, 2019, 248, 702-708.	1.8	26
66	Allopatric divergence and secondary contact with gene flow: a recurring theme in rattlesnake speciation. Biological Journal of the Linnean Society, 2019, 128, 149-169.	1.6	25
67	Cryptic diversity in disjunct populations of Middle American Montane Pitvipers: a systematic reassessment of <i>Cerrophidion godmani</i>. Zoologica Scripta, 2012, 41, 455-470.	1.7	23
68	Whole Genome Amplification and Reduced-Representation Genome Sequencing of Schistosoma japonicum Miracidia. PLoS Neglected Tropical Diseases, 2017, 11, e0005292.	3.0	23
69	Assessing the Impacts of Positive Selection on Coalescent-Based Species Tree Estimation and Species Delimitation. Systematic Biology, 2018, 67, 1076-1090.	5.6	20
70	Statistical binning leads to profound model violation due to gene tree error incurred by trying to avoid gene tree error. Molecular Phylogenetics and Evolution, 2019, 134, 164-171.	2.7	20
71	Genome-wide SNPs clarify lineage diversity confused by coloration in coralsnakes of the Micrurus diastema species complex (Serpentes: Elapidae). Molecular Phylogenetics and Evolution, 2020, 147, 106770.	2.7	20
72	A multi-organ transcriptome resource for the Burmese Python (Python molurus bivittatus). BMC Research Notes, 2011, 4, 310.	1.4	18

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73	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
74	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.	0.5	17
75	Evolution: Plasticity versus Selection, or Plasticity and Selection?. <i>Current Biology</i> , 2018, 28, R1104-R1106.	3.9	16
76	Evidence of Population Genetic Structure within the Florida Worm Lizard, <i>Rhineura floridana</i> (Amphisbaenia: Rhineuridae). <i>Journal of Herpetology</i> , 2005, 39, 118-124.	0.5	15
77	Targeted capture of complete coding regions across divergent species. <i>Genome Biology and Evolution</i> , 2017, 9, evx005.	2.5	15
78	PHYLOGENETIC RELATIONSHIPS OF THE GENUS PROCTOPORUS SENSU STRICTO (SQUAMATA:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5 325-336.	0.4	14
79	Genomic Basis of Convergent Island Phenotypes in Boa Constrictors. <i>Genome Biology and Evolution</i> , 2019, 11, 3123-3143.	2.5	14
80	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
81	Adaptive molecular convergences. <i>Communicative and Integrative Biology</i> , 2010, 3, 67-69.	1.4	13
82	A cryptic palm-pitviper species (Squamata: Viperidae: Bothriechis) from the Costa Rican highlands, with notes on the variation within <i>B. nigroviridis</i> . <i>Zootaxa</i> , 2016, 4138, 271-90.	0.5	13
83	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
84	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
85	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, .	6.4	12
86	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
87	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>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 5	0.8	11
88	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
89	Genome-wide data implicate terminal fusion automixis in king cobra facultative parthenogenesis. <i>Scientific Reports</i> , 2021, 11, 7271.	3.3	10
90	<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.	4.1	9

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91	ThetaMater: Bayesian estimation of population size parameter $\hat{\theta}$ from genomic data. Bioinformatics, 2018, 34, 1072-1073.	4.1	8
92	Patterns of relatedness and genetic diversity inferred from whole genome sequencing of archival blood fluke miracidia (<i>Schistosoma japonicum</i>). PLoS Neglected Tropical Diseases, 2021, 15, e0009020.	3.0	8
93	Population genomic analyses of schistosome parasites highlight critical challenges facing endgame elimination efforts. Scientific Reports, 2021, 11, 6884.	3.3	8
94	The effects of climate and demographic history in shaping genomic variation across populations of the Desert Horned Lizard (<i>Phrynosoma platyrhinos</i>). Molecular Ecology, 2021, 30, 4481-4496.	3.9	8
95	Plasticity and local adaptation explain lizard cold tolerance. Molecular Ecology, 2018, 27, 2173-2175.	3.9	7
96	Population Genomic Analyses Confirm Male-Biased Mutation Rates in Snakes. Journal of Heredity, 2021, 112, 221-227.	2.4	5
97	Origins, genomic structure and copy number variation of snake venom myotoxins. Toxicon, 2022, 216, 92-106.	1.6	5
98	Report from the First Snake Genomics and Integrative Biology Meeting. Standards in Genomic Sciences, 2012, 7, 150-152.	1.5	4
99	Chinese alligator genome illustrates molecular adaptations. Cell Research, 2013, 23, 1254-1255.	12.0	3
100	A suite of potentially amplifiable microsatellite loci for ten reptiles of conservation concern from Africa and Asia. Conservation Genetics Resources, 2016, 8, 307-311.	0.8	3
101	Bayesian Analysis of High-Throughput Quantitative Measurement of Protein-DNA Interactions. PLoS ONE, 2011, 6, e26105.	2.5	2
102	Development and characterization of thirteen microsatellite loci in Clark's nutcracker (<i>Nucifraga</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 0.8	0.8	2
103	Probabilistic Species Tree Distances: Implementing the Multispecies Coalescent to Compare Species Trees Within the Same Model-Based Framework Used to Estimate Them. Systematic Biology, 2020, 69, 194-207.	5.6	2
104	An ancient adaptive episode of convergent molecular evolution confounds phylogenetic inference. Nature Precedings, 2008, , .	0.1	1
105	Supergene validation: A model-based protocol for assessing the accuracy of non-model-based supergene methods. MethodsX, 2019, 6, 2181-2188.	1.6	1
106	Recent Advances in the Inference of Gene Flow from Population Genomic Data. Current Molecular Biology Reports, 2019, 5, 107-115.	1.6	1
107	<i>PhyloWGA</i> : chromosome-aware phylogenetic interrogation of whole genome alignments. Bioinformatics, 2021, 37, 1923-1925.	4.1	1
108	Identification of an integrated stress and growth response signaling switch that directs vertebrate intestinal regeneration. BMC Genomics, 2022, 23, 6.	2.8	1

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109	A genomic can of worms for schistosome host-specificity. Trends in Parasitology, 2022, 38, 496-497.	3.3	1
110	Identifying DNA Strands Using a Kernel of Classified Sequences. , 2009, , .		0