

Todd A Castoe

List of Publications by Year in descending order

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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	Repetitive Elements May Comprise Over Two-Thirds of the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002384.	1.5	907
2	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
3	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
4	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
5	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	6.0	300
6	Evidence for an ancient adaptive episode of convergent molecular evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8986-8991.	3.3	284
7	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
8	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
9	Data Partitions and Complex Models in Bayesian Analysis: The Phylogeny of Gymnophthalmid Lizards. <i>Systematic Biology</i> , 2004, 53, 448-469.	2.7	201
10	Bayesian mixed models and the phylogeny of pitvipers (Viperidae: Serpentes). <i>Molecular Phylogenetics and Evolution</i> , 2006, 39, 91-110.	1.2	189
11	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
12	Comparative phylogeography of pitvipers suggests a consensus of ancient Middle American highland biogeography. <i>Journal of Biogeography</i> , 2009, 36, 88-103.	1.4	157
13	LTR Retrotransposons Contribute to Genomic Gigantism in Plethodontid Salamanders. <i>Genome Biology and Evolution</i> , 2012, 4, 168-183.	1.1	152
14	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
15	Phylogeographic structure and historical demography of the western diamondback rattlesnake (<i>Crotalus atrox</i>): A perspective on North American desert biogeography. <i>Molecular Phylogenetics and Evolution</i> , 2007, 42, 193-212.	1.2	127
16	Sciurid phylogeny and the paraphyly of Holarctic ground squirrels (<i>Spermophilus</i>). <i>Molecular Phylogenetics and Evolution</i> , 2004, 31, 1015-1030.	1.2	116
17	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
18	Adaptive Evolution and Functional Redesign of Core Metabolic Proteins in Snakes. <i>PLoS ONE</i> , 2008, 3, e2201.	1.1	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.	1.8	105
20	Squamate reptiles challenge paradigms of genomic repeat element evolution set by birds and mammals. <i>Nature Communications</i> , 2018, 9, 2774.	5.8	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.	3.5	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.	1.1	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.	2.2	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.	3.3	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.	1.1	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.	1.4	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.	1.2	70
28	Local adaptation in transgenerational responses to predators. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152271.	1.2	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.	1.2	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.	1.0	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.	13.9	58
32	Phylogenetic taxonomy of the Cercosaurini (Squamata: Gymnophthalmidae), with new genera for species of <i>Neusticurus</i> and <i>Proctoporus</i> . <i>Zoological Journal of the Linnean Society</i> , 2005, 143, 405-416.	1.0	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.	1.0	54
34	Identification of repeat structure in large genomes using repeat probability clouds. <i>Analytical Biochemistry</i> , 2008, 380, 77-83.	1.1	51
35	Higher-level phylogeny of Asian and American coral snakes, their placement within the Elapidae (Squamata), and the systematic affinities of the enigmatic Asian coral snake <i>Hemibungarus calligaster</i> (Wiegmann, 1834). <i>Zoological Journal of the Linnean Society</i> , 0, 151, 809-831.	1.0	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.	1.2	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.	1.8	47
38	Genetic consequences of postglacial range expansion in two codistributed rodents (genus <i>Tij ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 To</i>)	2.0	46
39	Snake Recombination Landscapes Are Concentrated in Functional Regions despite PRDM9. <i>Molecular Biology and Evolution</i> , 2020, 37, 1272-1294.	3.5	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.	1.2	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.	1.6	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.	3.3	42
43	Microsatellite landscape evolutionary dynamics across 450 million years of vertebrate genome evolution. <i>Genome</i> , 2016, 59, 295-310.	0.9	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.	2.0	39
45	Historical perspectives on population genetics and conservation of three marine turtle species. <i>Conservation Genetics</i> , 2005, 6, 235-251.	0.8	38
46	Phylogenetic relationships of the enigmatic longtailed rattlesnakes (<i>Crotalus ericsmithi</i> , <i>C. lannomi</i>) Tij ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 To	1.2	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.	0.8	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.	1.1	33
49	Cryptic genetic diversity, population structure, and gene flow in the Mojave rattlesnake (<i>Crotalus</i>) Tij ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 702 To	1.2	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.	0.2	32
51	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
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.	0.3	31
54	New insights on facultative parthenogenesis in pythons. <i>Biological Journal of the Linnean Society</i> , 2014, 112, 461-468.	0.7	31

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55	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
56	Novel ecological and climatic conditions drive rapid adaptation in invasive Florida Burmese pythons. <i>Molecular Ecology</i> , 2018, 27, 4744-4757.	2.0	30
57	USING MORPHOLOGICAL AND MOLECULAR EVIDENCE TO INFER SPECIES BOUNDARIES WITHIN PROCTOPORUS BOLIVIANUS WERNER (SQUAMATA: GYMNOPHTHALMIDAE). <i>Herpetologica</i> , 2003, 59, 432-449.	0.2	29
58	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
59	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
60	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
61	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
62	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
63	Thousands of microsatellite loci from the venomous coralsnake <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
64	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
65	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
66	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
67	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
68	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
69	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
70	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
71	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
72	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

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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.	3.5	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.	0.2	17
75	Evolution: Plasticity versus Selection, or Plasticity and Selection?. <i>Current Biology</i> , 2018, 28, R1104-R1106.	1.8	16
76	Evidence of Population Genetic Structure within the Florida Worm Lizard, <i>Rhineura floridana</i> (<i>Amphisbaenia</i> : <i>Rhineuridae</i>). <i>Journal of Herpetology</i> , 2005, 39, 118-124.	0.2	15
77	Targeted capture of complete coding regions across divergent species. <i>Genome Biology and Evolution</i> , 2017, 9, evx005.	1.1	15
78	PHYLOGENETIC RELATIONSHIPS OF THE GENUS <i>PROCTOPORUS</i> SENSU STRICTO (SQUAMATA: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5 325-336.	0.2	14
79	Genomic Basis of Convergent Island Phenotypes in Boa Constrictors. <i>Genome Biology and Evolution</i> , 2019, 11, 3123-3143.	1.1	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.	2.4	14
81	Adaptive molecular convergences. <i>Communicative and Integrative Biology</i> , 2010, 3, 67-69.	0.6	13
82	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
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.	1.3	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.	3.4	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, .	3.3	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.	1.6	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.	1.2	10
89	Genome-wide data implicate terminal fusion automixis in king cobra facultative parthenogenesis. <i>Scientific Reports</i> , 2021, 11, 7271.	1.6	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.	1.8	9

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91	ThetaMater: Bayesian estimation of population size parameter $\hat{\theta}$ from genomic data. <i>Bioinformatics</i> , 2018, 34, 1072-1073.	1.8	8
92	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
93	Population genomic analyses of schistosome parasites highlight critical challenges facing endgame elimination efforts. <i>Scientific Reports</i> , 2021, 11, 6884.	1.6	8
94	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
95	Plasticity and local adaptation explain lizard cold tolerance. <i>Molecular Ecology</i> , 2018, 27, 2173-2175.	2.0	7
96	Population Genomic Analyses Confirm Male-Biased Mutation Rates in Snakes. <i>Journal of Heredity</i> , 2021, 112, 221-227.	1.0	5
97	Origins, genomic structure and copy number variation of snake venom myotoxins. <i>Toxicon</i> , 2022, 216, 92-106.	0.8	5
98	Report from the First Snake Genomics and Integrative Biology Meeting. <i>Standards in Genomic Sciences</i> , 2012, 7, 150-152.	1.5	4
99	Chinese alligator genome illustrates molecular adaptations. <i>Cell Research</i> , 2013, 23, 1254-1255.	5.7	3
100	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
101	Bayesian Analysis of High-Throughput Quantitative Measurement of Protein-DNA Interactions. <i>PLoS ONE</i> , 2011, 6, e26105.	1.1	2
102	Development and characterization of thirteen microsatellite loci in Clark's nutcracker (<i>Nucifraga</i>)	0.4	2
103	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
104	An ancient adaptive episode of convergent molecular evolution confounds phylogenetic inference. <i>Nature Precedings</i> , 2008, , .	0.1	1
105	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
106	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
107	PhyloWGA: chromosome-aware phylogenetic interrogation of whole genome alignments. <i>Bioinformatics</i> , 2021, 37, 1923-1925.	1.8	1
108	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

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109	A genomic can of worms for schistosome host-specificity. Trends in Parasitology, 2022, 38, 496-497.	1.5	1
110	Identifying DNA Strands Using a Kernel of Classified Sequences. , 2009, , .		0