

Scott V Edwards

List of Publications by Year in descending order

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Version: 2024-02-01

222
papers

27,151
citations

13068

68
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6979

154
g-index

263
all docs

263
docs citations

263
times ranked

20736
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics of mitochondrial DNA evolution in animals: amplification and sequencing with conserved primers.. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 6196-6200.	3.3	4,373
2	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	6.0	1,583
3	IS A NEW AND GENERAL THEORY OF MOLECULAR SYSTEMATICS EMERGING?. Evolution; International Journal of Organic Evolution, 2009, 63, 1-19.	1.1	926
4	Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320.	6.0	895
5	The genome of a songbird. Nature, 2010, 464, 757-762.	13.7	770
6	Earth BioGenome Project: Sequencing life for the future of life. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4325-4333.	3.3	652
7	PERSPECTIVE: GENE DIVERGENCE, POPULATION DIVERGENCE, AND THE VARIANCE IN COALESCENCE TIME IN PHYLOGEOGRAPHIC STUDIES. Evolution; International Journal of Organic Evolution, 2000, 54, 1839.	1.1	604
8	The genome of the green anole lizard and a comparative analysis with birds and mammals. Nature, 2011, 477, 587-591.	13.7	575
9	A maximum pseudo-likelihood approach for estimating species trees under the coalescent model. BMC Evolutionary Biology, 2010, 10, 302.	3.2	548
10	The utility of single nucleotide polymorphisms in inferences of population history. Trends in Ecology and Evolution, 2003, 18, 249-256.	4.2	544
11	High-resolution species trees without concatenation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5936-5941.	3.3	530
12	Estimating Divergence Times from Molecular Data on Phylogenetic and Population Genetic Timescales. Annual Review of Ecology, Evolution, and Systematics, 2002, 33, 707-740.	6.7	521
13	Genome 10K: A Proposal to Obtain Whole-Genome Sequence for 10,000 Vertebrate Species. Journal of Heredity, 2009, 100, 659-674.	1.0	504
14	Estimating Species Phylogenies Using Coalescence Times among Sequences. Systematic Biology, 2009, 58, 468-477.	2.7	410
15	Resolving conflict in eutherian mammal phylogeny using phylogenomics and the multispecies coalescent model. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14942-14947.	3.3	407
16	Evolution and ecology of MHC molecules: from genomics to sexual selection. Trends in Ecology and Evolution, 1998, 13, 305-311.	4.2	358
17	Coalescent methods for estimating phylogenetic trees. Molecular Phylogenetics and Evolution, 2009, 53, 320-328.	1.2	353
18	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. Molecular Phylogenetics and Evolution, 2016, 94, 447-462.	1.2	321

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19	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	6.0	300
20	Multilocus phylogeography and phylogenetics using sequence-based markers. <i>Genetica</i> , 2009, 135, 439-455.	0.5	281
21	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <i>Genome Biology</i> , 2013, 14, R28.	13.9	276
22	Origin of avian genome size and structure in non-avian dinosaurs. <i>Nature</i> , 2007, 446, 180-184.	13.7	262
23	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	13.7	251
24	Speciation in birds: Genes, geography, and sexual selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6550-6557.	3.3	228
25	SPECIATIONAL HISTORY OF AUSTRALIAN GRASS FINCHES (POEPHILA) INFERRED FROM THIRTY GENE TREES. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2033-2047.	1.1	227
26	Genetic Introgression: An Integral but neglected component of speciation in birds. <i>Auk</i> , 2011, 128, 620-632.	0.7	227
27	Speciational history of Australian grass finches (Poephila) inferred from thirty gene trees. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2033-47.	1.1	205
28	Winter storms drive rapid phenotypic, regulatory, and genomic shifts in the green anole lizard. <i>Science</i> , 2017, 357, 495-498.	6.0	204
29	Looking forwards or looking backwards in avian phylogeography? A comment on Zink and Barrowclough 2008. <i>Molecular Ecology</i> , 2009, 18, 2930-2933.	2.0	200
30	ESTIMATING SPECIES TREES USING MULTIPLE-ALLELE DNA SEQUENCE DATA. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 2080-2091.	1.1	189
31	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019, 364, 74-78.	6.0	189
32	The evolution of a tropical biodiversity hotspot. <i>Science</i> , 2020, 370, 1343-1348.	6.0	179
33	EVOLUTION INTO AND OUT OF THE ANDES: A BAYESIAN ANALYSIS OF HISTORICAL DIVERSIFICATION IN <i>THAMNOPHILUSANTSHRIKES</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 346-367.	1.1	169
34	Evolution of sweet taste perception in hummingbirds by transformation of the ancestral umami receptor. <i>Science</i> , 2014, 345, 929-933.	6.0	169
35	Estimating phylogenetic trees from genome-scale data. <i>Annals of the New York Academy of Sciences</i> , 2015, 1360, 36-53.	1.8	165
36	DIVERGENCE ACROSS AUSTRALIA'S CARPENTARIAN BARRIER: STATISTICAL PHYLOGEOGRAPHY OF THE RED-BACKED FAIRY WREN (<i>MALURUS MELANOCEPHALUS</i>). <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 3117-3134.	1.1	161

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37	Digitization and the Future of Natural History Collections. <i>BioScience</i> , 2020, 70, 243-251.	2.2	161
38	Molecular Evolution of the Toll-Like Receptor Multigene Family in Birds. <i>Molecular Biology and Evolution</i> , 2011, 28, 1703-1715.	3.5	150
39	Ultrafast Evolution and Loss of CRISPRs Following a Host Shift in a Novel Wildlife Pathogen, <i>Mycoplasma gallisepticum</i> . <i>PLoS Genetics</i> , 2012, 8, e1002511.	1.5	145
40	The Phylogenetic Component of Cooperative Breeding in Perching Birds. <i>American Naturalist</i> , 1993, 141, 754-789.	1.0	142
41	Rapid evolution of disease resistance is accompanied by functional changes in gene expression in a wild bird. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7866-7871.	3.3	132
42	Reticulation, divergence, and the phylogeographyâ€“phylogenetics continuum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8025-8032.	3.3	130
43	The Evolution of the Major Histocompatibility Complex in Birds. <i>BioScience</i> , 2002, 52, 423.	2.2	129
44	Phylogenomics of nonavian reptiles and the structure of the ancestral amniote genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2767-2772.	3.3	126
45	AnMhcComponent to Kin Recognition and Mate Choice in Birds: Predictions, Progress, and Prospects. <i>American Naturalist</i> , 2002, 160, S225-S237.	1.0	124
46	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	124
47	Gene duplication and fragmentation in the zebra finch major histocompatibility complex. <i>BMC Biology</i> , 2010, 8, 29.	1.7	121
48	Genomic evidence reveals a radiation of placental mammals uninterrupted by the KPg boundary. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7282-E7290.	3.3	119
49	Embracing heterogeneity: coalescing the Tree of Life and the future of phylogenomics. <i>PeerJ</i> , 2019, 7, e6399.	0.9	111
50	Extensive polymorphism and geographical variation at a positively selected MHC class II B gene of the lesser kestrel (<i>Falco naumanni</i>). <i>Molecular Ecology</i> , 2008, 17, 2652-2665.	2.0	110
51	Conceptual and empirical advances in Neotropical biodiversity research. <i>PeerJ</i> , 2018, 6, e5644.	0.9	107
52	Comparative genomics based on massive parallel transcriptome sequencing reveals patterns of substitution and selection across 10 bird species. <i>Molecular Ecology</i> , 2010, 19, 266-276.	2.0	105
53	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409.	13.7	105
54	Phylogenetic Analysis in the Anomaly Zone. <i>Systematic Biology</i> , 2009, 58, 452-460.	2.7	103

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55	Evolutionary Dynamics of Intron Size, Genome Size, and Physiological Correlates in Archosaurs. <i>American Naturalist</i> , 2002, 160, 539-552.	1.0	96
56	Temporal increase in organic mercury in an endangered pelagic seabird assessed by century-old museum specimens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7466-7471.	3.3	96
57	Nucleotide Variation, Linkage Disequilibrium and Founder-Facilitated Speciation in Wild Populations of the Zebra Finch (<i>Taeniopygia guttata</i>). <i>Genetics</i> , 2009, 181, 645-660.	1.2	91
58	Whole-Genome Analyses Resolve the Phylogeny of Flightless Birds (Palaeognathae) in the Presence of an Empirical Anomaly Zone. <i>Systematic Biology</i> , 2019, 68, 937-955.	2.7	88
59	Multilocus tests of Pleistocene refugia and ancient divergence in a pair of Atlantic forest antbirds (<i>Myciophobus</i>). <i>Molecular Ecology</i> , 2013, 22, 3996-4013.	2.0	85
60	Characterization, Polymorphism, and Evolution of MHC Class II B Genes in Birds of Prey. <i>Journal of Molecular Evolution</i> , 2007, 65, 541-554.	0.8	84
61	Introgression and Phenotypic Assimilation in Zimmerius Flycatchers (Tyrannidae): Population Genetic and Phylogenetic Inferences from Genome-Wide SNPs. <i>Systematic Biology</i> , 2014, 63, 134-152.	2.7	84
62	Phylogenetics of modern birds in the era of genomics. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 979-992.	1.2	83
63	The Global Museum: natural history collections and the future of evolutionary science and public education. <i>PeerJ</i> , 2020, 8, e8225.	0.9	81
64	Contrasting histories of avian and mammalian Mhc genes revealed by class II B sequences from songbirds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 12200-12204.	3.3	80
65	Comparison of Species Tree Methods for Reconstructing the Phylogeny of Bearded Manakins (Aves: Tyrannidae). <i>Systematic Biology</i> , 2014, 63, 134-152.	2.7	80
66	Genome Evolution in Reptilia, the Sister Group of Mammals. <i>Annual Review of Genomics and Human Genetics</i> , 2010, 11, 239-264.	2.5	78
67	Genomics and polymorphism of Agph-DAB1, an Mhc class II B gene in red-winged blackbirds (<i>Agelaius</i>). <i>Systematic Biology</i> , 2014, 63, 134-152.	3.5	77
68	Natural History Collections as Emerging Resources for Innovative Education. <i>BioScience</i> , 2014, 64, 725-734.	2.2	76
69	Ancient horizontal transfers of retrotransposons between birds and ancestors of human pathogenic nematodes. <i>Nature Communications</i> , 2016, 7, 11396.	5.8	76
70	RECONCILING ACTUAL AND INFERRED POPULATION HISTORIES IN THE HOUSE FINCH (CARPODACUS). <i>Systematic Biology</i> , 2014, 63, 134-152.	1.1	75
71	MITOCHONDRIAL GENE GENEALOGY AND GENE FLOW AMONG ISLAND AND MAINLAND POPULATIONS OF A SEDENTARY SONGBIRD, THE GREY-CROWNED BABBLER (<i>Pomatostomus temporalis</i>). <i>Evolution; International Journal of Organic Evolution</i> , 1993, 47, 1118-1137.	1.1	74
72	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	3.3	72

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73	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
74	Phylogenetics is the New Genetics (for Most of Biodiversity). <i>Trends in Ecology and Evolution</i> , 2020, 35, 415-425.	4.2	72
75	The Evolution of Intron Size in Amniotes: A Role for Powered Flight?. <i>Genome Biology and Evolution</i> , 2012, 4, 1033-1043.	1.1	71
76	Museum specimens of terrestrial vertebrates are sensitive indicators of environmental change in the Anthropocene. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20170387.	1.8	71
77	Population Genomics Reveals Low Genetic Diversity and Adaptation to Hypoxia in Snub-Nosed Monkeys. <i>Molecular Biology and Evolution</i> , 2016, 33, 2670-2681.	3.5	69
78	MHC Class II Pseudogene and Genomic Signature of a 32-kb Cosmid in the House Finch (<i>Carpodacus</i>) Tj ETQq0 0 0,rgBT /Overlock 10 TF	2.4	68
79	Out of Gondwana: the origin of passerine birds. <i>Trends in Ecology and Evolution</i> , 2002, 17, 347-349.	4.2	68
80	Dynamics of <i>Mhc</i> evolution in birds and crocodylians: amplification of class II genes with degenerate primers. <i>Molecular Ecology</i> , 1995, 4, 719-730.	2.0	67
81	A Genomic Schism in Birds Revealed by Phylogenetic Analysis of DNA Strings. <i>Systematic Biology</i> , 2002, 51, 599-613.	2.7	66
82	Ecology of Avian Influenza Virus in Birds. <i>Journal of Infectious Diseases</i> , 2008, 197, S29-S33.	1.9	62
83	Ancestral Polymorphism of <i>Mhc</i> Class II Genes in Mice: Implications for Balancing Selection and the Mammalian Molecular Clock. <i>Genetics</i> , 1997, 146, 655-668.	1.2	61
84	Parallel Evolution of Tetrodotoxin Resistance in Three Voltage-Gated Sodium Channel Genes in the Garter Snake <i>Thamnophis sirtalis</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 2836-2846.	3.5	60
85	Natural selection and phylogenetic analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8799-8800.	3.3	59
86	Museum Genomics. <i>Annual Review of Genetics</i> , 2021, 55, 633-659.	3.2	58
87	Developing markers for multilocus phylogenetics in non-model organisms: A test case with turtles. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 514-525.	1.2	57
88	Feather Development Genes and Associated Regulatory Innovation Predate the Origin of Dinosauria. <i>Molecular Biology and Evolution</i> , 2015, 32, 23-28.	3.5	57
89	A Species Tree for the Australo-Papuan Fairy-wrens and Allies (Aves: Maluridae). <i>Systematic Biology</i> , 2012, 61, 253.	2.7	55
90	Relevance of Microevolutionary Processes to Higher Level Molecular Systematics. , 1997, , 251-278.		54

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91	A phylogeny of the megapodes (Aves: Megapodiidae) based on nuclear and mitochondrial DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2002, 23, 408-421.	1.2	53
92	Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". <i>Science</i> , 2015, 349, 1460-1460.	6.0	53
93	Toward an evolutionary genomics of the avian Mhc. <i>Immunological Reviews</i> , 1999, 167, 119-132.	2.8	52
94	High gene flow on a continental scale in the polyandrous Kentish plover <i>Charadrius alexandrinus</i> . <i>Molecular Ecology</i> , 2012, 21, 5864-5879.	2.0	52
95	Conflict between Genetic and Phenotypic Differentiation: The Evolutionary History of a "Lost and Rediscovered" Shorebird. <i>PLoS ONE</i> , 2011, 6, e26995.	1.1	52
96	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	51
97	Dynamics and Phylogenetic Implications of MtDNA Control Region Sequences in New World Jays (Aves: <i>Turdus</i>). <i>Journal of Molecular Evolution</i> , 2017, 85, 1078-1091.	1.0	50
98	Innate immunity and the evolution of resistance to an emerging infectious disease in a wild bird. <i>Molecular Ecology</i> , 2012, 21, 2628-2639.	2.0	50
99	Phylogenomic subsampling: a brief review. <i>Zoologica Scripta</i> , 2016, 45, 63-74.	0.7	49
100	COMPARATIVE METHODS AT THE SPECIES LEVEL: GEOGRAPHIC VARIATION IN MORPHOLOGY AND GROUP SIZE IN GREY-CROWNED BABBLERS (<i>Pomatostomus temporalis</i>). <i>Evolution; International Journal of Organic Evolution</i> , 1995, 49, 1134-1146.	1.1	48
101	Can Weighting Improve Bushy Trees? Models of Cytochrome b Evolution and the Molecular Systematics of Pipits and Wagtails (Aves: Motacillidae). <i>Systematic Biology</i> , 1998, 47, 589-603.	2.7	48
102	Next-generation sequencing and the expanding domain of phylogeography. <i>Folia Zoologica</i> , 2015, 64, 187-206.	0.9	47
103	Evolutionary Dynamics of Sex Chromosomes of Paleognathous Birds. <i>Genome Biology and Evolution</i> , 2019, 11, 2376-2390.	1.1	47
104	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. <i>Systematic Biology</i> , 2020, 69, 795-812.	2.7	47
105	Songbird Genomics: Analysis of 45 kb Upstream of a Polymorphic Mhc Class II Gene in Red-Winged Blackbirds (<i>Agelaius phoeniceus</i>). <i>Genomics</i> , 2001, 75, 26-34.	1.3	46
106	Three tiers of genome evolution in reptiles. <i>Integrative and Comparative Biology</i> , 2008, 48, 494-504.	0.9	46
107	Physical Mapping and Refinement of the Painted Turtle Genome (<i>Chrysemys picta</i>) Inform Amniote Genome Evolution and Challenge Turtle-Bird Chromosomal Conservation. <i>Genome Biology and Evolution</i> , 2015, 7, 2038-2050.	1.1	46
108	Conserved Nonexonic Elements: A Novel Class of Marker for Phylogenomics. <i>Systematic Biology</i> , 2017, 66, 1028-1044.	2.7	46

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109	Physiological and regulatory underpinnings of geographic variation in reptilian cold tolerance across a latitudinal cline. <i>Molecular Ecology</i> , 2018, 27, 2243-2255.	2.0	46
110	The Anolis Lizard Genome: An Amniote Genome without Isochores. <i>Genome Biology and Evolution</i> , 2011, 3, 974-984.	1.1	44
111	A 39-kb Sequence Around a Blackbird Mhc Class II Gene: Ghost of Selection Past and Songbird Genome Architecture. <i>Molecular Biology and Evolution</i> , 2000, 17, 1384-1395.	3.5	43
112	Mid-Pleistocene divergence of Cuban and North American ivory-billed woodpeckers. <i>Biology Letters</i> , 2006, 2, 466-469.	1.0	43
113	MHC class I genes of birds of prey: isolation, polymorphism and diversifying selection. <i>Conservation Genetics</i> , 2009, 10, 1349-1355.	0.8	43
114	Avian MHC Evolution in the Era of Genomics: Phase 1.0. <i>Cells</i> , 2019, 8, 1152.	1.8	43
115	Mitochondrial DNA Variation and the Phylogeny of African Mole Rats (Rodentia: Bathyergidae). <i>Systematic Zoology</i> , 1987, 36, 280.	1.6	42
116	Molecular and Paleontological Evidence for a Post-Cretaceous Origin of Rodents. <i>PLoS ONE</i> , 2012, 7, e46445.	1.1	42
117	Sequence and gene content of a large fragment of a lizard sex chromosome and evaluation of candidate sex differentiating gene R-spondin 1. <i>BMC Genomics</i> , 2013, 14, 899.	1.2	41
118	Morphological and genomic comparisons of Hawaiian and Japanese black-footed albatrosses (<i>Phoebastria nigripes</i>) using double digest RAD-seq: implications for conservation. <i>Evolutionary Applications</i> , 2015, 8, 662-678.	1.5	41
119	Out of Florida: mtDNA reveals patterns of migration and Pleistocene range expansion of the Green Anole lizard (<i>Anolis carolinensis</i>). <i>Ecology and Evolution</i> , 2012, 2, 2274-2284.	0.8	40
120	SNPs across time and space: population genomic signatures of founder events and epizootics in the House Finch (<i>Haemorrhous mexicanus</i>). <i>Ecology and Evolution</i> , 2016, 6, 7475-7489.	0.8	40
121	Adaptive Evolution as a Predictor of Species-Specific Innate Immune Response. <i>Molecular Biology and Evolution</i> , 2015, 32, 1717-1729.	3.5	39
122	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2019, 36, 1086-1100.	3.5	39
123	Exploration of phylogenetic data using a global sequence analysis method. <i>BMC Evolutionary Biology</i> , 2005, 5, 63.	3.2	38
124	Inferring the phylogeography and evolutionary history of the splendid fairywren (<i>Malurus splendens</i>) from mitochondrial DNA and spectrophotometry. <i>Journal of Avian Biology</i> , 2009, 40, 7-17.	0.6	38
125	Multiple Phylogenetically Distinct Events Shaped the Evolution of Limb Skeletal Morphologies Associated with Bipedalism in the Jerboas. <i>Current Biology</i> , 2015, 25, 2785-2794.	1.8	38
126	What Have We Learned from the First 500 Avian Genomes?. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2021, 52, 611-639.	3.8	38

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127	Tuatara (<i>Sphenodon</i>) Genomics: BAC Library Construction, Sequence Survey, and Application to the DMRT Gene Family. <i>Journal of Heredity</i> , 2006, 97, 541-548.	1.0	37
128	Reply to Gatesy and Springer: Claims of homology errors and zombie lineages do not compromise the dating of placental diversification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9433-E9434.	3.3	37
129	Ecology can inform genetics: Disassortative mating contributes to MHC polymorphism in Leach's storm-petrels (<i>Oceanodroma leucorhoa</i>). <i>Molecular Ecology</i> , 2018, 27, 3371-3385.	2.0	37
130	The Evolution of Comparative Phylogeography: Putting the Geography (and More) into Comparative Population Genomics. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	37
131	Major histocompatibility complex class I evolution in songbirds: universal primers, rapid evolution and base compositional shifts in exon 3. <i>PeerJ</i> , 2013, 1, e86.	0.9	37
132	A cDNA macroarray approach to parasite-induced gene expression changes in a songbird host: genetic response of house finches to experimental infection by <i>Mycoplasma gallisepticum</i> . <i>Molecular Ecology</i> , 2005, 15, 1263-1273.	2.0	36
133	Core Genome Multilocus Sequence Typing: a Standardized Approach for Molecular Typing of <i>Mycoplasma gallisepticum</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	36
134	Genomic Consequences of Long-Term Population Decline in Brown Eared Pheasant. <i>Molecular Biology and Evolution</i> , 2021, 38, 263-273.	3.5	36
135	Comparative Methods at the Species Level: Geographic Variation in Morphology and Group Size in Grey-Crowned Babblers (<i>Pomatostomus temporalis</i>). <i>Evolution; International Journal of Organic Evolution</i> , 1995, 49, 1134.	1.1	34
136	Hitchhiking and recombination in birds: evidence from Mhc-linked and unlinked loci in Red-winged Blackbirds (<i>Agelaius phoeniceus</i>). <i>Genetical Research</i> , 2004, 84, 175-192.	0.3	34
137	Patterns of Variation in MHC Class II Loci of the Little Greenbul (<i>Andropadus virens</i>) with Comments on MHC Evolution in Birds. <i>Journal of Heredity</i> , 2006, 97, 133-142.	1.0	34
138	Climate-mediated adaptation after mainland colonization of an ancestrally subtropical island lizard, <i>Anolis carolinensis</i> . <i>Journal of Evolutionary Biology</i> , 2016, 29, 2168-2180.	0.8	34
139	Early origin of sweet perception in the songbird radiation. <i>Science</i> , 2021, 373, 226-231.	6.0	34
140	Triploid plover female provides support for a role of the W chromosome in avian sex determination. <i>Biology Letters</i> , 2012, 8, 787-789.	1.0	32
141	Integrating natural history collections and comparative genomics to study the genetic architecture of convergent evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180248.	1.8	32
142	Molecular, functional and evolutionary characterization of the gene encoding HMG-CoA reductase in the fission yeast, <i>Schizosaccharomyces pombe</i> . <i>Yeast</i> , 1996, 12, 1107-1124.	0.8	31
143	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
144	New Frontiers for Organismal Biology. <i>BioScience</i> , 2013, 63, 464-471.	2.2	30

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145	Outlier analyses to test for local adaptation to breeding grounds in a migratory arctic seabird. <i>Ecology and Evolution</i> , 2017, 7, 2370-2381.	0.8	30
146	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. <i>Methods in Molecular Biology</i> , 2019, 1910, 211-239.	0.4	30
147	Multiple origins of XY female mice (genus <i>Akodon</i>): phylogenetic and chromosomal evidence. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 1825-1831.	1.2	29
148	Structure and Evolution of a New Avian MHC Class II B Gene in a Sub-Antarctic Seabird, the Thin-Billed Prion (Procellariiformes: <i>Pachyptila belcheri</i>). <i>Journal of Molecular Evolution</i> , 2009, 68, 279-291.	0.8	28
149	Reptiles and Mammals Have Differentially Retained Long Conserved Noncoding Sequences from the Amniote Ancestor. <i>Genome Biology and Evolution</i> , 2011, 3, 102-113.	1.1	28
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