

# Scott V Edwards

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8395060/publications.pdf>

Version: 2024-02-01

222  
papers

27,151  
citations

13068

68  
h-index

6979

154  
g-index

263  
all docs

263  
docs citations

263  
times ranked

20736  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome phylogeography of the blue-faced honeyeater ( <i>Entomyzon cyanotis</i> ) and discovery and characterization of a <i>scp</i> chromosome. <i>Molecular Ecology</i> , 2023, 32, 1248-1270.	2.0	4
2	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
3	Evolution of the DAN gene family in vertebrates. <i>Developmental Biology</i> , 2022, 482, 34-43.	0.9	4
4	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
5	Understanding the evolution of viviparity using intraspecific variation in reproductive mode and transitional forms of pregnancy. <i>Biological Reviews</i> , 2022, 97, 1179-1192.	4.7	13
6	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	51
7	Comparative Population Genomics of Cryptic Speciation and Adaptive Divergence in Bicknell's and Gray-Cheeked Thrushes (Aves: <i>Catharus bicknelli</i> and <i>Catharus minimus</i> ). <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	7
8	Olfactory receptor subgenome and expression in a highly olfactory procellariiform seabird. <i>Genetics</i> , 2022, 220, .	1.2	8
9	Genomic Consequences of Long-Term Population Decline in Brown Eared Pheasant. <i>Molecular Biology and Evolution</i> , 2021, 38, 263-273.	3.5	36
10	A bird-like genome from a frog: Mechanisms of genome size reduction in the ornate burrowing frog, <i>Platyplectrum ornatum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26
11	Demographic History, Not Mating System, Explains Signatures of Inbreeding and Inbreeding Depression in a Large Outbred Population. <i>American Naturalist</i> , 2021, 197, 658-676.	1.0	11
12	Phylogeography and Phylogenetics in the Nuclear Age. , 2021, , 65-88.		1
13	Early origin of sweet perception in the songbird radiation. <i>Science</i> , 2021, 373, 226-231.	6.0	34
14	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
15	Museum Genomics. <i>Annual Review of Genetics</i> , 2021, 55, 633-659.	3.2	58
16	Genomics of adaptation and acclimation: from field to lab and back. <i>National Science Review</i> , 2020, 7, 128-128.	4.6	2
17	Prospects for sociogenomics in avian cooperative breeding and parental care. <i>Environmental Epigenetics</i> , 2020, 66, 293-306.	0.9	2
18	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	13.7	251

#	ARTICLE	IF	CITATIONS
19	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409.	13.7	105
20	<i>De Novo</i> Assembly of the Northern Cardinal ( <i>Cardinalis cardinalis</i> ) Genome Reveals Candidate Regulatory Regions for Sexually Dichromatic Red Plumage Coloration. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3541-3548.	0.8	9
21	Genetic diversity, demographic history and neo-sex chromosomes in the Critically Endangered Raso lark. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192613.	1.2	23
22	Evidence for the Pleistocene Arc Hypothesis from genome-wide SNPs in a Neotropical dry forest specialist, the Rufous-fronted Thornbird (Furnariidae: <i>Phacellodomus rufifrons</i> ). <i>Molecular Ecology</i> , 2020, 29, 4457-4472.	2.0	15
23	The evolution of a tropical biodiversity hotspot. <i>Science</i> , 2020, 370, 1343-1348.	6.0	179
24	Phylogenetics is the New Genetics (for Most of Biodiversity). <i>Trends in Ecology and Evolution</i> , 2020, 35, 415-425.	4.2	72
25	Digitization and the Future of Natural History Collections. <i>BioScience</i> , 2020, 70, 243-251.	2.2	161
26	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. <i>Systematic Biology</i> , 2020, 69, 795-812.	2.7	47
27	The Global Museum: natural history collections and the future of evolutionary science and public education. <i>PeerJ</i> , 2020, 8, e8225.	0.9	81
28	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. <i>Methods in Molecular Biology</i> , 2019, 1910, 211-239.	0.4	30
29	Attenuated Fgf Signaling Underlies the Forelimb Heterochrony in the Emu <i>Dromaius novaehollandiae</i> . <i>Current Biology</i> , 2019, 29, 3681-3691.e5.	1.8	24
30	The effect of alignment uncertainty, substitution models and priors in building and dating the mammal tree of life. <i>BMC Evolutionary Biology</i> , 2019, 19, 203.	3.2	11
31	Evolutionary Dynamics of Sex Chromosomes of Paleognathous Birds. <i>Genome Biology and Evolution</i> , 2019, 11, 2376-2390.	1.1	47
32	Avian MHC Evolution in the Era of Genomics: Phase 1.0. <i>Cells</i> , 2019, 8, 1152.	1.8	43
33	A review of evolutionary research on birds of the New Guinean savannas and closely associated habitats of riparian rainforests, mangroves and grasslands. <i>Emu</i> , 2019, 119, 317-330.	0.2	15
34	phenotools: An R package for visualizing and analysing phenomic datasets. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1393-1400.	2.2	5
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019, 364, 74-78.	6.0	189
39	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
40	Embracing heterogeneity: coalescing the Tree of Life and the future of phylogenomics. <i>PeerJ</i> , 2019, 7, e6399.	0.9	111
41	Endless forms of sexual selection. <i>PeerJ</i> , 2019, 7, e7988.	0.9	24
42	Genomics of host-pathogen interactions: challenges and opportunities across ecological and spatiotemporal scales. <i>PeerJ</i> , 2019, 7, e8013.	0.9	23
43	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4325-4333.	3.3	652
44	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
45	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
46	Rapid diversification and hybridization have shaped the dynamic history of the genus <i>Elaenia</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 522-533.	1.2	9
47	Genome-scale DNA sequence data and the evolutionary history of placental mammals. <i>Data in Brief</i> , 2018, 18, 1972-1975.	0.5	18
48	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
49	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
50	Editorial: Evolutionary Feedbacks Between Population Biology and Genome Architecture. <i>Frontiers in Genetics</i> , 2018, 9, 329.	1.1	2
51	Conceptual and empirical advances in Neotropical biodiversity research. <i>PeerJ</i> , 2018, 6, e5644.	0.9	107
52	Conserved Nonexonic Elements: A Novel Class of Marker for Phylogenomics. <i>Systematic Biology</i> , 2017, 66, 1028-1044.	2.7	46
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	Comparative Genomics as a Foundation for Evo-Devo Studies in Birds. <i>Methods in Molecular Biology</i> , 2017, 1650, 11-46.	0.4	15
56	Winter storms drive rapid phenotypic, regulatory, and genomic shifts in the green anole lizard. <i>Science</i> , 2017, 357, 495-498.	6.0	204
57	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
58	Climate change, collections and the classroom: using big data to tackle big problems. <i>Evolution: Education and Outreach</i> , 2017, 10, .	0.3	15
59	Genomic footprints of adaptation in a cooperatively breeding tropical bird across a vegetation gradient. <i>Molecular Ecology</i> , 2017, 26, 4483-4496.	2.0	16
60	Gene flow during glacial habitat shifts facilitates character displacement in a Neotropical flycatcher radiation. <i>BMC Evolutionary Biology</i> , 2017, 17, 210.	3.2	16
61	Phylogenomic subsampling: a brief review. <i>Zoologica Scripta</i> , 2016, 45, 63-74.	0.7	49
62	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
63	Ancient horizontal transfers of retrotransposons between birds and ancestors of human pathogenic nematodes. <i>Nature Communications</i> , 2016, 7, 11396.	5.8	76
64	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
65	Climateâ€“mediated adaptation after mainland colonization of an ancestrally subtropical island lizard, <i>A<sup>nolis carolinensis</sup></i> . <i>Journal of Evolutionary Biology</i> , 2016, 29, 2168-2180.	0.8	34
66	<sup>SNP</sup> s across time and space: population genomic signatures of founder events and epizootics in the House Finch ( <i>Haemorhous mexicanus</i> ). <i>Ecology and Evolution</i> , 2016, 6, 7475-7489.	0.8	40
67	The â€œAtlantis Forest hypothesisâ€“does not explain Atlantic Forest phylogeography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2097-8.	3.3	12
68	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 447-462.	1.2	321
69	Next-generation sequencing and the expanding domain of phylogeography. <i>Folia Zoologica</i> , 2015, 64, 187-206.	0.9	47
70	Estimating phylogenetic trees from genomeâ€“scale data. <i>Annals of the New York Academy of Sciences</i> , 2015, 1360, 36-53.	1.8	165
71	Major Histocompatibility Complex Genes Map to Two Chromosomes in an Evolutionarily Ancient Reptile, the Tuatara ( <i>Sphenodon punctatus</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1439-1451.	0.8	28
72	Inferential reasoning and egg rejection in a cooperatively breeding cuckoo. <i>Animal Cognition</i> , 2015, 18, 75-82.	0.9	7

#	ARTICLE	IF	CITATIONS
73	Adaptive Evolution as a Predictor of Species-Specific Innate Immune Response. <i>Molecular Biology and Evolution</i> , 2015, 32, 1717-1729.	3.5	39
74	Plumage color and pathogen-induced gene expression in a wild bird. <i>Behavioral Ecology</i> , 2015, 26, 1100-1110.	1.0	7
75	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	3.3	72
76	Rhetoric vs. reality: A commentary on "Bird Origins Anew" by A. Feduccia. <i>Auk</i> , 2015, 132, 467-480.	0.7	15
77	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
78	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
79	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
80	Morphological and genomic comparisons of <i>Hawaiian</i> and <i>Japanese</i> <i>Black-footed Albatrosses</i> ( <i>Phoebastria nigripes</i> ) using double digest RADseq: implications for conservation. <i>Evolutionary Applications</i> , 2015, 8, 662-678.	1.5	41
81	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
82	Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". <i>Science</i> , 2015, 350, 171-171.	6.0	18
83	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254-1259.	6.0	300
84	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
85	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	6.0	895
86	Molecular evolution of <i>Dmrt1</i> accompanies change of sex-determining mechanisms in reptilia. <i>Biology Letters</i> , 2014, 10, 20140809.	1.0	20
87	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
88	THE EVOLUTION OF BIPEDALISM IN JERBOAS (RODENTIA: DIPODOIDEA): ORIGIN IN HUMID AND FORESTED ENVIRONMENTS. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 2108-2118.	1.1	14
89	Introgression and Phenotypic Assimilation in <i>Zimmerius</i> Flycatchers (Tyrannidae): Population Genetic and Phylogenetic Inferences from Genome-Wide SNPs. <i>Systematic Biology</i> , 2014, 63, 134-152.	2.7	84
90	Evolution of sweet taste perception in hummingbirds by transformation of the ancestral umami receptor. <i>Science</i> , 2014, 345, 929-933.	6.0	169

#	ARTICLE	IF	CITATIONS
91	A house finch ( <i>Haemorrhous mexicanus</i> ) spleen transcriptome reveals intra- and interspecific patterns of gene expression, alternative splicing and genetic diversity in passerines. <i>BMC Genomics</i> , 2014, 15, 305.	1.2	12
92	Natural History Collections as Emerging Resources for Innovative Education. <i>BioScience</i> , 2014, 64, 725-734.	2.2	76
93	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
94	New Frontiers for Organismal Biology. <i>BioScience</i> , 2013, 63, 464-471.	2.2	30
95	The Maluridae: inferring avian biology and evolutionary history from DNA sequences. <i>Emu</i> , 2013, 113, 195-207.	0.2	16
96	Next-generation QTL mapping: crowdsourcing SNPs, without pedigrees. <i>Molecular Ecology</i> , 2013, 22, 3885-3887.	2.0	13
97	Frequent Coinfection Reduces RNA Virus Population Genetic Diversity. <i>Journal of Heredity</i> , 2013, 104, 704-712.	1.0	18
98	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
99	Sex-Biased Expression of Sex-Differentiating Genes <i>FOXL2</i> and <i>FGF9</i> in American Alligators, <i>Alligator mississippiensis</i> . <i>Sexual Development</i> , 2013, 7, 253-260.	1.1	15
100	Multilocus tests of Pleistocene refugia and ancient divergence in a pair of Atlantic Forest antbirds ( <i>Myrmeciza</i> ). <i>Molecular Ecology</i> , 2013, 22, 3996-4013.	2.0	85
101	Cis-regulatory sequence variation and association with <i>Mycoplasma</i> load in natural populations of the house finch ( <i>Carpodacus mexicanus</i> ). <i>Ecology and Evolution</i> , 2013, 3, 655-666.	0.8	11
102	Museums' Role: Increasing Knowledge. <i>Science</i> , 2013, 339, 1148-1149.	6.0	4
103	Evidence from a House Finch ( <i>Haemorrhous mexicanus</i> ) Spleen Transcriptome for Adaptive Evolution and Biased Gene Conversion in Passerine Birds. <i>Molecular Biology and Evolution</i> , 2013, 30, 1046-1050.	3.5	23
104	Reply to Gatesy and Springer: The multispecies coalescent model can effectively handle recombination and gene tree heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1180.	3.3	26
105	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
106	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
107	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
108	Resolving conflict in eutherian mammal phylogeny using phylogenomics and the multispecies coalescent model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14942-14947.	3.3	407

#	ARTICLE	IF	CITATIONS
109	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
110	Editorial of the Proceedings of the 25th International Ornithological Congress. <i>Journal of Ornithology</i> , 2012, 153, 1-1.	0.5	0
111	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
112	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
113	Molecular and Paleontological Evidence for a Post-Cretaceous Origin of Rodents. <i>PLoS ONE</i> , 2012, 7, e46445.	1.1	42
114	Tangled Trees: The Challenge of Inferring Species Trees from Coalescent and Noncoalescent Genes. <i>Methods in Molecular Biology</i> , 2012, 856, 3-28.	0.4	21
115	A Species Tree for the Australo-Papuan Fairy-wrens and Allies (Aves: Maluridae). <i>Systematic Biology</i> , 2012, 61, 253.	2.7	55
116	Eight anonymous nuclear loci for the squamate antbird ( <i>Myrmeciza squamosa</i> ), cross-amplifiable in other species of typical antbirds (Aves, <i>Thamnophilidae</i> ). <i>Conservation Genetics Resources</i> , 2012, 4, 645-647.	0.4	4
117	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
118	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
119	Genetic Introgression: An Integral but neglected component of speciation in birds. <i>Auk</i> , 2011, 128, 620-632.	0.7	227
120	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
121	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
122	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
123	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
124	The Anolis Lizard Genome: An Amniote Genome without Isochores. <i>Genome Biology and Evolution</i> , 2011, 3, 974-984.	1.1	44
125	Molecular Evolution of the Toll-Like Receptor Multigene Family in Birds. <i>Molecular Biology and Evolution</i> , 2011, 28, 1703-1715.	3.5	150
126	Sex Chromosome Evolution in Amniotes: Applications for Bacterial Artificial Chromosome Libraries. <i>Journal of Biomedicine and Biotechnology</i> , 2011, 2011, 1-6.	3.0	8



#	ARTICLE	IF	CITATIONS
127	A Birds-Eye View of Animal Evolution. <i>BioScience</i> , 2011, 61, 331-333.	2.2	0
128	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
129	The Zebra Finch genome and avian genomics in the wild. <i>Emu</i> , 2010, 110, 233-241.	0.2	18
130	A maximum pseudo-likelihood approach for estimating species trees under the coalescent model. <i>BMC Evolutionary Biology</i> , 2010, 10, 302.	3.2	548
131	Gene duplication and fragmentation in the zebra finch major histocompatibility complex. <i>BMC Biology</i> , 2010, 8, 29.	1.7	121
132	GEOGRAPHIC DIFFERENCES IN SEXUAL REASSORTMENT IN RNA PHAGE. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, no-no.	1.1	15
133	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
134	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	13.7	770
135	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
136	Phylogenetic Analysis in the Anomaly Zone. <i>Systematic Biology</i> , 2009, 58, 452-460.	2.7	103
137	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
138	Genome 10K: A Proposal to Obtain Whole-Genome Sequence for 10,000 Vertebrate Species. <i>Journal of Heredity</i> , 2009, 100, 659-674.	1.0	504
139	Recombination and Nucleotide Diversity in the Sex Chromosomal Pseudoautosomal Region of the Emu, <i>Dromaius novaehollandiae</i> . <i>Journal of Heredity</i> , 2009, 100, 125-136.	1.0	24
140	Estimating Species Phylogenies Using Coalescence Times among Sequences. <i>Systematic Biology</i> , 2009, 58, 468-477.	2.7	410
141	Variability in Sex-Determining Mechanisms Influences Genome Complexity in Reptilia. <i>Cytogenetic and Genome Research</i> , 2009, 127, 242-248.	0.6	10
142	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
143	Genome evolution in Reptilia: in silico chicken mapping of 12,000 BAC-end sequences from two reptiles and a basal bird. <i>BMC Genomics</i> , 2009, 10, S8.	1.2	21
144	MHC class I genes of birds of prey: isolation, polymorphism and diversifying selection. <i>Conservation Genetics</i> , 2009, 10, 1349-1355.	0.8	43

#	ARTICLE	IF	CITATIONS
145	Multilocus phylogeography and phylogenetics using sequence-based markers. <i>Genetica</i> , 2009, 135, 439-455.	0.5	281
146	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
147	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
148	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
149	IS A NEW AND GENERAL THEORY OF MOLECULAR SYSTEMATICS EMERGING?. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 1-19.	1.1	926
150	Coalescent methods for estimating phylogenetic trees. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 320-328.	1.2	353
151	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
152	BIRD SPECIATION: SELECTION AND THE ORIGIN OF SPECIES<sup>1</sup>. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 991-995.	1.1	1
153	ESTIMATING SPECIES TREES USING MULTIPLE-ALLELE DNA SEQUENCE DATA. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 2080-2091.	1.1	189
154	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
155	Prevalence and evolutionary origins of autoimmune susceptibility alleles in natural mouse populations. <i>Genes and Immunity</i> , 2008, 9, 61-68.	2.2	21
156	PERSPECTIVE: A <i>smÅ¶rgÅ¶sbord</i> of markers for avian ecology and evolution. <i>Molecular Ecology</i> , 2008, 17, 945-946.	2.0	5
157	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
158	High-Speed Developments in Avian Genomics. <i>BioScience</i> , 2008, 58, 587-595.	2.2	18
159	Three tiers of genome evolution in reptiles. <i>Integrative and Comparative Biology</i> , 2008, 48, 494-504.	0.9	46
160	Characterization, chromosomal location, and genomic neighborhood of a ratite ortholog of a gene with gonadal expression in mammals. <i>Integrative and Comparative Biology</i> , 2008, 48, 505-511.	0.9	3
161	Comparison of Species Tree Methods for Reconstructing the Phylogeny of Bearded Manakins (Aves:) Tj ETQq1 1 0.784314 rgBT /Over 2.7 830	2.7	830
162	Ecology of Avian Influenza Virus in Birds. <i>Journal of Infectious Diseases</i> , 2008, 197, S29-S33.	1.9	62

#	ARTICLE	IF	CITATIONS
163	Amniote Phylogenomics: Testing Evolutionary Hypotheses with BAC Library Scanning and Targeted Clone Analysis of Large-Scale DNA Sequences from Reptiles. <i>Methods in Molecular Biology</i> , 2008, 422, 91-117.	0.4	8
164	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
165	High-resolution species trees without concatenation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5936-5941.	3.3	530
166	Origin of avian genome size and structure in non-avian dinosaurs. <i>Nature</i> , 2007, 446, 180-184.	13.7	262
167	EVOLUTION INTO AND OUT OF THE ANDES: A BAYESIAN ANALYSIS OF HISTORICAL DIVERSIFICATION IN THAMNOPHILUS ANTSHRIKES. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 346-367.	1.1	169
168	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
169	Evolutionary genetics of <i>Carpodacus mexicanus</i> , a recently colonized host of a bacterial pathogen, <i>Mycoplasma gallisepticum</i> . <i>Genetica</i> , 2007, 129, 217-225.	0.5	18
170	Genomics and ornithology. <i>Journal Fur Ornithologie</i> , 2007, 148, 27-33.	1.2	3
171	Mid-Pleistocene divergence of Cuban and North American ivory-billed woodpeckers. <i>Biology Letters</i> , 2006, 2, 466-469.	1.0	43
172	Patterns of Variation in MHC Class II $\hat{\mu}^2$ 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
173	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
174	A cDNA microarray 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
175	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
176	Exploration of phylogenetic data using a global sequence analysis method. <i>BMC Evolutionary Biology</i> , 2005, 5, 63.	3.2	38
177	Conservation genetics and Pacific fisheries bycatch: Mitochondrial differentiation and population assignment in black-footed albatrosses ( <i>Phoebastria nigripes</i> ). <i>Conservation Genetics</i> , 2005, 6, 289-295.	0.8	25
178	Future of Avian Genetic Resources Collections: <i>Archives of Evolutionary and Environmental History</i> . <i>Auk</i> , 2005, 122, 979-984.	0.7	12
179	Future of Avian Genetic Resources Collections: <i>Archives of Evolutionary and Environmental History</i> . <i>Auk</i> , 2005, 122, 979.	0.7	11
180	SPECIATIONAL HISTORY OF AUSTRALIAN GRASS FINCHES (POEPHILA) INFERRED FROM THIRTY GENE TREES*. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2033.	1.1	4

#	ARTICLE	IF	CITATIONS
181	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
182	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
183	Speciation history of Australian grass finches ( <i>Poephila</i> ) inferred from thirty gene trees. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2033-47.	1.1	205
184	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
185	When did Neanderthals and modern humans diverge?. <i>Evolutionary Anthropology</i> , 2003, 11, 60-63.	1.7	12
186	RECONCILING ACTUAL AND INFERRED POPULATION HISTORIES IN THE HOUSE FINCH ( <i>CARPODACUS</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T 2852-2864.	1.1	75
187	The utility of single nucleotide polymorphisms in inferences of population history. <i>Trends in Ecology and Evolution</i> , 2003, 18, 249-256.	4.2	544
188	RECONCILING ACTUAL AND INFERRED POPULATION HISTORIES IN THE HOUSE FINCH ( <i>CARPODACUS</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T 5	1.1	5
189	A Genomic Schism in Birds Revealed by Phylogenetic Analysis of DNA Strings. <i>Systematic Biology</i> , 2002, 51, 599-613.	2.7	66
190	The Evolution of the Major Histocompatibility Complex in Birds. <i>BioScience</i> , 2002, 52, 423.	2.2	129
191	AnMhcComponent to Kin Recognition and Mate Choice in Birds: Predictions, Progress, and Prospects. <i>American Naturalist</i> , 2002, 160, S225-S237.	1.0	124
192	Evolutionary Dynamics of Intron Size, Genome Size, and Physiological Correlates in Archosaurs. <i>American Naturalist</i> , 2002, 160, 539-552.	1.0	96
193	Out of Gondwana: the origin of passerine birds. <i>Trends in Ecology and Evolution</i> , 2002, 17, 347-349.	4.2	68
194	Estimating Divergence Times from Molecular Data on Phylogenetic and Population Genetic Timescales. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2002, 33, 707-740.	6.7	521
195	A phylogeny of the megapodes ( <i>Aves: Megapodiidae</i> ) based on nuclear and mitochondrial DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2002, 23, 408-421.	1.2	53
196	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
197	Cryptic differentiation and geographic variation in genetic diversity of Hall's Babbler <i>Pomatostomus halli</i> . <i>Journal of Avian Biology</i> , 2001, 32, 102-110.	0.6	17
198	Dynamics and Phylogenetic Implications of MtDNA Control Region Sequences in New World Jays ( <i>Aves:</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T 50	0.8	50

#	ARTICLE	IF	CITATIONS
199	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
200	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
201	MHC Class II Pseudogene and Genomic Signature of a 32-kb Cosmid in the House Finch ( <i>Carpodacus</i> ) Tj ETQq1 1 0,784314 rgBT /Ove	2.4	88
202	PERSPECTIVE: GENE DIVERGENCE, POPULATION DIVERGENCE, AND THE VARIANCE IN COALESCENCE TIME IN PHYLOGEOGRAPHIC STUDIES. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1839.	1.1	604
203	Toward an evolutionary genomics of the avian Mhc. <i>Immunological Reviews</i> , 1999, 167, 119-132.	2.8	52
204	Polymorphism across an exon-intron boundary in an avian Mhc class II B gene. <i>Molecular Biology and Evolution</i> , 1999, 16, 1599-1606.	3.5	27
205	Evolution and ecology of MHC molecules: from genomics to sexual selection. <i>Trends in Ecology and Evolution</i> , 1998, 13, 305-311.	4.2	358
206	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
207	Genomics and polymorphism of Agph-DAB1, an Mhc class II B gene in red-winged blackbirds ( <i>Agelaius</i> ) Tj ETQq1 1 0,784314 rgBT /Ove	3.5	77
208	Re: Congruence and Phylogenetic Reanalysis of Perching Bird Cytochrome b Sequences. <i>Molecular Phylogenetics and Evolution</i> , 1997, 7, 266-271.	1.2	10
209	Relevance of Microevolutionary Processes to Higher Level Molecular Systematics. , 1997, , 251-278.		54
210	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
211	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
212	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
213	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
214	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
215	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
216	Homology and Comparative Methods in the Study of Avian Cooperative Breeding. <i>American Naturalist</i> , 1994, 143, 723-733.	1.0	21

#	ARTICLE	IF	CITATIONS
217	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.	1.1	26
218	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
219	The Phylogenetic Component of Cooperative Breeding in Perching Birds. <i>American Naturalist</i> , 1993, 141, 754-789.	1.0	142
220	Dynamics of mitochondrial DNA evolution in animals: amplification and sequencing with conserved primers.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1989, 86, 6196-6200.	3.3	4,373
221	Mitochondrial DNA Variation and the Phylogeny of African Mole Rats (Rodentia: Bathyergidae). <i>Systematic Zoology</i> , 1987, 36, 280.	1.6	42
222	Bicycling, Birding and #BLM across America in a Summer of Chaos. <i>Biodiversity Information Science and Standards</i> , 0, 4, .	0.0	0