

Scott V Edwards

List of Publications by Year in descending order

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Version: 2024-02-01

222
papers

27,151
citations

13099

68
h-index

6996

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.	3.9	4
2	The Evolution of Comparative Phylogeography: Putting the Geography (and More) into Comparative Population Genomics. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	37
3	Evolution of the DAN gene family in vertebrates. <i>Developmental Biology</i> , 2022, 482, 34-43.	2.0	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, .	7.1	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.	10.4	13
6	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	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, .	2.5	7
8	Olfactory receptor subgenome and expression in a highly olfactory procellariiform seabird. <i>Genetics</i> , 2022, 220, .	2.9	8
9	Genomic Consequences of Long-Term Population Decline in Brown Eared Pheasant. <i>Molecular Biology and Evolution</i> , 2021, 38, 263-273.	8.9	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, .	7.1	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.	2.1	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.	12.6	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.	8.3	38
15	Museum Genomics. <i>Annual Review of Genetics</i> , 2021, 55, 633-659.	7.6	58
16	Genomics of adaptation and acclimation: from field to lab and back. <i>National Science Review</i> , 2020, 7, 128-128.	9.5	2
17	Prospects for sociogenomics in avian cooperative breeding and parental care. <i>Environmental Epigenetics</i> , 2020, 66, 293-306.	1.8	2
18	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251

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19	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409.	27.8	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.	1.8	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.	2.6	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.	3.9	15
23	The evolution of a tropical biodiversity hotspot. <i>Science</i> , 2020, 370, 1343-1348.	12.6	179
24	Phylogenetics is the New Genetics (for Most of Biodiversity). <i>Trends in Ecology and Evolution</i> , 2020, 35, 415-425.	8.7	72
25	Digitization and the Future of Natural History Collections. <i>BioScience</i> , 2020, 70, 243-251.	4.9	161
26	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. <i>Systematic Biology</i> , 2020, 69, 795-812.	5.6	47
27	The Global Museum: natural history collections and the future of evolutionary science and public education. <i>PeerJ</i> , 2020, 8, e8225.	2.0	81
28	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. <i>Methods in Molecular Biology</i> , 2019, 1910, 211-239.	0.9	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.	3.9	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.	2.5	47
32	Avian MHC Evolution in the Era of Genomics: Phase 1.0. <i>Cells</i> , 2019, 8, 1152.	4.1	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.	0.6	15
34	phenotools: An r package for visualizing and analysing phenomic datasets. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1393-1400.	5.2	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.	4.0	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.	5.6	88

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37	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2019, 36, 1086-1100.	8.9	39
38	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019, 364, 74-78.	12.6	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.	4.0	71
40	Embracing heterogeneity: coalescing the Tree of Life and the future of phylogenomics. <i>PeerJ</i> , 2019, 7, e6399.	2.0	111
41	Endless forms of sexual selection. <i>PeerJ</i> , 2019, 7, e7988.	2.0	24
42	Genomics of host-pathogen interactions: challenges and opportunities across ecological and spatiotemporal scales. <i>PeerJ</i> , 2019, 7, e8013.	2.0	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.	7.1	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.	3.9	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, .	3.9	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.	2.7	9
47	Genome-scale DNA sequence data and the evolutionary history of placental mammals. <i>Data in Brief</i> , 2018, 18, 1972-1975.	1.0	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.	2.5	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.	3.9	37
50	Editorial: Evolutionary Feedbacks Between Population Biology and Genome Architecture. <i>Frontiers in Genetics</i> , 2018, 9, 329.	2.3	2
51	Conceptual and empirical advances in Neotropical biodiversity research. <i>PeerJ</i> , 2018, 6, e5644.	2.0	107
52	Conserved Nonexonic Elements: A Novel Class of Marker for Phylogenomics. <i>Systematic Biology</i> , 2017, 66, 1028-1044.	5.6	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.	1.9	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.	7.1	37

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55	Comparative Genomics as a Foundation for Evo-Devo Studies in Birds. <i>Methods in Molecular Biology</i> , 2017, 1650, 11-46.	0.9	15
56	Winter storms drive rapid phenotypic, regulatory, and genomic shifts in the green anole lizard. <i>Science</i> , 2017, 357, 495-498.	12.6	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.	7.1	119
58	Climate change, collections and the classroom: using big data to tackle big problems. <i>Evolution: Education and Outreach</i> , 2017, 10, .	0.8	15
59	Genomic footprints of adaptation in a cooperatively breeding tropical bird across a vegetation gradient. <i>Molecular Ecology</i> , 2017, 26, 4483-4496.	3.9	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.	1.7	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.	8.9	69
63	Ancient horizontal transfers of retrotransposons between birds and ancestors of human pathogenic nematodes. <i>Nature Communications</i> , 2016, 7, 11396.	12.8	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.	7.1	130
65	Climateâ€“mediated adaptation after mainland colonization of an ancestrally subtropical island lizard, <i>A^{nolis} carolinensis</i> . <i>Journal of Evolutionary Biology</i> , 2016, 29, 2168-2180.	1.7	34
66	^{SNP} 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.	1.9	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.	7.1	12
68	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 447-462.	2.7	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.	3.8	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.	1.8	28
72	Inferential reasoning and egg rejection in a cooperatively breeding cuckoo. <i>Animal Cognition</i> , 2015, 18, 75-82.	1.8	7

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73	Adaptive Evolution as a Predictor of Species-Specific Innate Immune Response. <i>Molecular Biology and Evolution</i> , 2015, 32, 1717-1729.	8.9	39
74	Plumage color and pathogen-induced gene expression in a wild bird. <i>Behavioral Ecology</i> , 2015, 26, 1100-1110.	2.2	7
75	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	6.4	72
76	Rhetoric vs. reality: A commentary on "Bird Origins Anew" by A. Feduccia. <i>Auk</i> , 2015, 132, 467-480.	1.4	15
77	Feather Development Genes and Associated Regulatory Innovation Predate the Origin of Dinosauria. <i>Molecular Biology and Evolution</i> , 2015, 32, 23-28.	8.9	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.	2.5	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.	12.6	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.	3.1	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.	3.9	38
82	Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". <i>Science</i> , 2015, 350, 171-171.	12.6	18
83	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254-1259.	12.6	300
84	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	12.6	1,583
85	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895
86	Molecular evolution of <i>Dmrt1</i> accompanies change of sex-determining mechanisms in reptilia. <i>Biology Letters</i> , 2014, 10, 20140809.	2.3	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.	8.9	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.	2.3	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.	5.6	84
90	Evolution of sweet taste perception in hummingbirds by transformation of the ancestral umami receptor. <i>Science</i> , 2014, 345, 929-933.	12.6	169

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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.	2.8	12
92	Natural History Collections as Emerging Resources for Innovative Education. <i>BioScience</i> , 2014, 64, 725-734.	4.9	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.	9.6	276
94	New Frontiers for Organismal Biology. <i>BioScience</i> , 2013, 63, 464-471.	4.9	30
95	The Maluridae: inferring avian biology and evolutionary history from DNA sequences. <i>Emu</i> , 2013, 113, 195-207.	0.6	16
96	Next-generation QTL mapping: crowdsourcing SNPs, without pedigrees. <i>Molecular Ecology</i> , 2013, 22, 3885-3887.	3.9	13
97	Frequent Coinfection Reduces RNA Virus Population Genetic Diversity. <i>Journal of Heredity</i> , 2013, 104, 704-712.	2.4	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.	2.8	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.	2.0	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.	3.9	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.	1.9	11
102	Museums' Role: Increasing Knowledge. <i>Science</i> , 2013, 339, 1148-1149.	12.6	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.	8.9	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.	7.1	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.	2.0	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.	3.5	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.	2.3	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.	7.1	407

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109	The Evolution of Intron Size in Amniotes: A Role for Powered Flight?. <i>Genome Biology and Evolution</i> , 2012, 4, 1033-1043.	2.5	71
110	Editorial of the Proceedings of the 25th International Ornithological Congress. <i>Journal of Ornithology</i> , 2012, 153, 1-1.	1.1	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.	1.9	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.	3.9	52
113	Molecular and Paleontological Evidence for a Post-Cretaceous Origin of Rodents. <i>PLoS ONE</i> , 2012, 7, e46445.	2.5	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.	0.9	21
115	A Species Tree for the Australo-Papuan Fairy-wrens and Allies (Aves: Maluridae). <i>Systematic Biology</i> , 2012, 61, 253.	5.6	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.	0.8	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.	3.9	50
118	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011, 477, 587-591.	27.8	575
119	Genetic Introgression: An Integral but neglected component of speciation in birds. <i>Auk</i> , 2011, 128, 620-632.	1.4	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.	2.5	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.	7.1	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.	7.1	132
124	The Anolis Lizard Genome: An Amniote Genome without Isochores. <i>Genome Biology and Evolution</i> , 2011, 3, 974-984.	2.5	44
125	Molecular Evolution of the Toll-Like Receptor Multigene Family in Birds. <i>Molecular Biology and Evolution</i> , 2011, 28, 1703-1715.	8.9	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

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127	A Birds-Eye View of Animal Evolution. <i>BioScience</i> , 2011, 61, 331-333.	4.9	0
128	Conflict between Genetic and Phenotypic Differentiation: The Evolutionary History of a "Lost and Rediscovered" Shorebird. <i>PLoS ONE</i> , 2011, 6, e26995.	2.5	52
129	The Zebra Finch genome and avian genomics in the wild. <i>Emu</i> , 2010, 110, 233-241.	0.6	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.	3.8	121
132	GEOGRAPHIC DIFFERENCES IN SEXUAL REASSORTMENT IN RNA PHAGE. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, no-no.	2.3	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.	3.9	105
134	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	27.8	770
135	Genome Evolution in Reptilia, the Sister Group of Mammals. <i>Annual Review of Genomics and Human Genetics</i> , 2010, 11, 239-264.	6.2	78
136	Phylogenetic Analysis in the Anomaly Zone. <i>Systematic Biology</i> , 2009, 58, 452-460.	5.6	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.	7.1	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.	2.4	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.	2.4	24
140	Estimating Species Phylogenies Using Coalescence Times among Sequences. <i>Systematic Biology</i> , 2009, 58, 468-477.	5.6	410
141	Variability in Sex-Determining Mechanisms Influences Genome Complexity in Reptilia. <i>Cytogenetic and Genome Research</i> , 2009, 127, 242-248.	1.1	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.	2.9	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.	2.8	21
144	MHC class I genes of birds of prey: isolation, polymorphism and diversifying selection. <i>Conservation Genetics</i> , 2009, 10, 1349-1355.	1.5	43

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145	Multilocus phylogeography and phylogenetics using sequence-based markers. <i>Genetica</i> , 2009, 135, 439-455.	1.1	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.	1.8	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.	3.9	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.	1.2	38
149	IS A NEW AND GENERAL THEORY OF MOLECULAR SYSTEMATICS EMERGING?. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 1-19.	2.3	926
150	Coalescent methods for estimating phylogenetic trees. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 320-328.	2.7	353
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