Scott V Edwards

List of Publications by Citations

228 papers	21,199 citations	63 h-index	143 g-index
263 ext. papers	24,575 ext. citations	7.8 avg, IF	7.02 L-index

#	Paper	IF	Citations
228	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, 6196-200	11.5	3800
227	Whole-genome analyses resolve early branches in the tree of life of modern birds. *Science*, **2014**, 346, 1320-31	33.3	1182
226	Is a new and general theory of molecular systematics emerging?. *Evolution; International Journal of Organic Evolution*, **2009**, 63, 1-19	3.8	743
225	The genome of a songbird. *Nature*, **2010**, 464, 757-62	50.4	655
224	Comparative genomics reveals insights into avian genome evolution and adaptation. *Science*, **2014**, 346, 1311-20	33.3	628
223	PERSPECTIVE: GENE DIVERGENCE, POPULATION DIVERGENCE, AND THE VARIANCE INCOALESCENCE TIME IN PHYLOGEOGRAPHIC STUDIES. *Evolution; International Journal of Organic Evolution*, **2000**, 54, 1839	3.8	579
222	High-resolution species trees without concatenation. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 5936-41	11.5	485
221	The genome of the green anole lizard and a comparative analysis with birds and mammals. *Nature*, **2011**, 477, 587-91	50.4	478
220	The utility of single nucleotide polymorphisms in inferences of population history. *Trends in Ecology and Evolution*, **2003**, 18, 249-256	10.9	455
219	Estimating Divergence Times from Molecular Data on Phylogenetic and Population Genetic Timescales. *Annual Review of Ecology, Evolution, and Systematics*, **2002**, 33, 707-740		453
218	Genome 10K: a proposal to obtain whole-genome sequence for 10,000 vertebrate species. *Journal of Heredity*, **2009**, 100, 659-74	2.4	418
217	A maximum pseudo-likelihood approach for estimating species trees under the coalescent model. *BMC Evolutionary Biology*, **2010**, 10, 302	3	413
216	Estimating species phylogenies using coalescence times among sequences. *Systematic Biology*, **2009**, 58, 468-77	8.4	342
215	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	11.5	334
214	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, 14942-7	11.5	328
213	Evolution and ecology of MHC molecules: from genomics to sexual selection. *Trends in Ecology and Evolution*, **1998**, 13, 305-11	10.9	304
212	Coalescent methods for estimating phylogenetic trees. *Molecular Phylogenetics and Evolution*, **2009**, 53, 320-8	4.1	279

211	Multilocus phylogeography and phylogenetics using sequence-based markers. *Genetica*, **2009**, 135, 439-55	1.5	247
210	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. *Science*, **2014**, 346, 1254449	33.3	231
209	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. *Molecular Phylogenetics and Evolution*, **2016**, 94, 447-62	4.1	230
208	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. *Genome Biology*, **2013**, 14, R28	18.3	227
207	Origin of avian genome size and structure in non-avian dinosaurs. *Nature*, **2007**, 446, 180-4	50.4	222
206	SPECIATIONAL HISTORY OF AUSTRALIAN GRASS FINCHES (POEPHILA) INFERRED FROM THIRTY GENE TREES*. *Evolution; International Journal of Organic Evolution*, **2005**, 59, 2033-2047	3.8	207
205	Speciational history of Australian grass finches (Poephila) inferred from thirty gene trees. *Evolution; International Journal of Organic Evolution*, **2005**, 59, 2033-47	3.8	200
204	Speciation in birds: genes, geography, and sexual selection. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102 Suppl 1, 6550-7	11.5	194
203	Genetic Introgression: An Integral but Neglected Component of Speciation in Birds. *Auk*, **2011**, 128, 620-632	2.1	182
202	Estimating species trees using multiple-allele DNA sequence data. *Evolution; International Journal of Organic Evolution*, **2008**, 62, 2080-91	3.8	177
201	Looking forwards or looking backwards in avian phylogeography? A comment on Zink and Barrowclough 2008. *Molecular Ecology*, **2009**, 18, 2930-3; discussion 2934-6	5.7	173
200	Divergence across Australia's Carpentarian barrier: statistical phylogeography of the red-backed fairy wren (Malurus melanocephalus). *Evolution; International Journal of Organic Evolution*, **2008**, 62, 3117-34	3.8	145
199	Evolution into and out of the Andes: a Bayesian analysis of historical diversification in Thamnophilus antshrikes. *Evolution; International Journal of Organic Evolution*, **2007**, 61, 346-67	3.8	141
198	Winter storms drive rapid phenotypic, regulatory, and genomic shifts in the green anole lizard. *Science*, **2017**, 357, 495-498	33.3	130
197	The phylogenetic component of cooperative breeding in perching birds. *American Naturalist*, **1993**, 141, 754-89	3.7	124
196	Estimating phylogenetic trees from genome-scale data. *Annals of the New York Academy of Sciences* , **2015**, 1360, 36-53	6.5	122
195	Molecular evolution of the toll-like receptor multigene family in birds. *Molecular Biology and Evolution*, **2011**, 28, 1703-15	8.3	121
194	The Evolution of the Major Histocompatibility Complex in Birds. *BioScience*, **2002**, 52, 423	5.7	121

193	Sensory biology. Evolution of sweet taste perception in hummingbirds by transformation of the ancestral umami receptor. *Science*, **2014**, 345, 929-33	33.3	117
192	Phylogenomics of nonavian reptiles and the structure of the ancestral amniote genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 2767-72	11.5	117
191	An MHC component to kin recognition and mate choice in birds: predictions, progress, and prospects. *American Naturalist*, **2002**, 160 Suppl 6, S225-37	3.7	113
190	Gene duplication and fragmentation in the zebra finch major histocompatibility complex. *BMC Biology*, **2010**, 8, 29	7.3	106
189	Extensive polymorphism and geographical variation at a positively selected MHC class II B gene of the lesser kestrel (Falco naumanni). *Molecular Ecology*, **2008**, 17, 2652-65	5.7	104
188	Convergent regulatory evolution and loss of flight in paleognathous birds. *Science*, **2019**, 364, 74-78	33.3	103
187	Comparative genomics based on massive parallel transcriptome sequencing reveals patterns of substitution and selection across 10 bird species. *Molecular Ecology*, **2010**, 19 Suppl 1, 266-76	5.7	97
186	Ultrafast evolution and loss of CRISPRs following a host shift in a novel wildlife pathogen, Mycoplasma gallisepticum. *PLoS Genetics*, **2012**, 8, e1002511	6	95
185	Rapid evolution of disease resistance is accompanied by functional changes in gene expression in a wild bird. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 7866-71	11.5	94
184	Reticulation, divergence, and the phylogeography-phylogenetics continuum. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 8025-32	11.5	91
183	Dense sampling of bird diversity increases power of comparative genomics. *Nature*, **2020**, 587, 252-257	50.4	89
182	Phylogenetic analysis in the anomaly zone. *Systematic Biology*, **2009**, 58, 452-60	8.4	88
181	Evolutionary dynamics of intron size, genome size, and physiological correlates in archosaurs. *American Naturalist*, **2002**, 160, 539-52	3.7	83
180	Nucleotide variation, linkage disequilibrium and founder-facilitated speciation in wild populations of the zebra finch (Taeniopygia guttata). *Genetics*, **2009**, 181, 645-60	4	82
179	Characterization, polymorphism, and evolution of MHC class II B genes in birds of prey. *Journal of Molecular Evolution*, **2007**, 65, 541-54	3.1	80
178	Genomic evidence reveals a radiation of placental mammals uninterrupted by the KPg boundary. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E7282-E7290	11.5	78
177	Temporal increase in organic mercury in an endangered pelagic seabird assessed by century-old museum specimens. *Proceedings of the National Academy of Sciences of the United States of America* , **2011**, 108, 7466-71	11.5	78
176	Contrasting histories of avian and mammalian Mhc genes revealed by class II B sequences from songbirds. *Proceedings of the National Academy of Sciences of the United States of America*, **1995**, 92, 12200-4	11.5	74

175	Genomics and polymorphism of Agph-DAB1, an Mhc class II B gene in red-winged blackbirds (Agelaius phoeniceus). *Molecular Biology and Evolution*, **1998**, 15, 236-50	8.3	72
174	Reconciling actual and inferred population histories in the house finch (Carpodacus mexicanus) by AFLP analysis. *Evolution; International Journal of Organic Evolution*, **2003**, 57, 2852-64	3.8	71
173	Comparison of species tree methods for reconstructing the phylogeny of bearded manakins (Aves: Pipridae, Manacus) from multilocus sequence data. *Systematic Biology*, **2008**, 57, 719-31	8.4	70
172	Conceptual and empirical advances in Neotropical biodiversity research. *PeerJ*, **2018**, 6, e5644	3.1	70
171	Digitization and the Future of Natural History Collections. *BioScience*, **2020**, 70, 243-251	5.7	68
170	Introgression and phenotypic assimilation in Zimmerius flycatchers (Tyrannidae): population genetic and phylogenetic inferences from genome-wide SNPs. *Systematic Biology*, **2014**, 63, 134-52	8.4	67
169	Genome evolution in Reptilia, the sister group of mammals. *Annual Review of Genomics and Human Genetics*, **2010**, 11, 239-64	9.7	67
168	Dynamics of Mhc evolution in birds and crocodilians: amplification of class II genes with degenerate primers. *Molecular Ecology*, **1995**, 4, 719-29	5.7	67
167	MITOCHONDRIAL GENE GENEALOGY AND GENE FLOW AMONG ISLAND AND MAINLAND POPULATIONS OF A SEDENTARY SONGBIRD, THE GREY-CROWNED BABBLER (POMATOSTOMUS TEMPORALIS). *Evolution; International Journal of Organic Evolution*, **1993**, 47, 1118-1137	3.8	64
166	Embracing heterogeneity: coalescing the Tree of Life and the future of phylogenomics. *PeerJ*, **2019**, 7, e6399	3.1	63
165	Phylogenetics of modern birds in the era of genomics. *Proceedings of the Royal Society B: Biological Sciences*, **2005**, 272, 979-92	4.4	61
164	MHC class II pseudogene and genomic signature of a 32-kb cosmid in the house finch (Carpodacus mexicanus). *Genome Research*, **2000**, 10, 613-23	9.7	60
163	Natural History Collections as Emerging Resources for Innovative Education. *BioScience*, **2014**, 64, 725-734	5.7	59
162	A genomic schism in birds revealed by phylogenetic analysis of DNA strings. *Systematic Biology*, **2002**, 51, 599-613	8.4	57
161	Developing markers for multilocus phylogenetics in non-model organisms: A test case with turtles. *Molecular Phylogenetics and Evolution*, **2008**, 49, 514-25	4.1	56
160	Ancient horizontal transfers of retrotransposons between birds and ancestors of human pathogenic nematodes. *Nature Communications*, **2016**, 7, 11396	17.4	55
159	Phylogenomic analyses data of the avian phylogenomics project. *GigaScience*, **2015**, 4, 4	7.6	54
158	The evolution of intron size in amniotes: a role for powered flight?. *Genome Biology and Evolution*, **2012**, 4, 1033-43	3.9	54

157	Out of Gondwana: the origin of passerine birds. *Trends in Ecology and Evolution*, **2002**, 17, 347-349	10.9	53
156	Ancestral polymorphism of Mhc class II genes in mice: implications for balancing selection and the mammalian molecular clock. *Genetics*, **1997**, 146, 655-68	4	53
155	Multilocus tests of Pleistocene refugia and ancient divergence in a pair of Atlantic Forest antbirds (Myrmeciza). *Molecular Ecology*, **2013**, 22, 3996-4013	5.7	51
154	Toward an evolutionary genomics of the avian Mhc. *Immunological Reviews*, **1999**, 167, 119-32	11.3	49
153	The tuatara genome reveals ancient features of amniote evolution. *Nature*, **2020**, 584, 403-409	50.4	49
152	Molecular Adaptations for Sensing and Securing Prey and Insight into Amniote Genome Diversity from the Garter Snake Genome. *Genome Biology and Evolution*, **2018**, 10, 2110-2129	3.9	48
151	A species tree for the Australo-Papuan Fairy-wrens and allies (Aves: Maluridae). *Systematic Biology*, **2012**, 61, 253-71	8.4	48
150	COMPARATIVE METHODS AT THE SPECIES LEVEL: GEOGRAPHIC VARIATION IN MORPHOLOGY AND GROUP SIZE IN GREY-CROWNED BABBLERS (POMATOSTOMUS TEMPORALIS). *Evolution; International Journal of Organic Evolution*, **1995**, 49, 1134-1146	3.8	48
149	A phylogeny of the megapodes (Aves: Megapodiidae) based on nuclear and mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution*, **2002**, 23, 408-21	4.1	47
148	Dynamics and phylogenetic implications of MtDNA control region sequences in New World Jays (Aves: Corvidae). *Journal of Molecular Evolution*, **2000**, 51, 97-109	3.1	47
147	Relevance of Microevolutionary Processes to Higher Level Molecular Systematics **1997**, 251-278		47
146	Museum specimens of terrestrial vertebrates are sensitive indicators of environmental change in the Anthropocene. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2018**, 374,	5.8	45
145	Songbird genomics: analysis of 45 kb upstream of a polymorphic Mhc class II gene in red-winged blackbirds (Agelaius phoeniceus). *Genomics*, **2001**, 75, 26-34	4.3	44
144	Whole-Genome Analyses Resolve the Phylogeny of Flightless Birds (Palaeognathae) in the Presence of an Empirical Anomaly Zone. *Systematic Biology*, **2019**, 68, 937-955	8.4	43
143	Natural selection and phylogenetic analysis. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 8799-800	11.5	43
142	Feather development genes and associated regulatory innovation predate the origin of Dinosauria. *Molecular Biology and Evolution*, **2015**, 32, 23-8	8.3	42
141	The evolution of a tropical biodiversity hotspot. *Science*, **2020**, 370, 1343-1348	33.3	42
140	Parallel evolution of tetrodotoxin resistance in three voltage-gated sodium channel genes in the garter snake Thamnophis sirtalis. *Molecular Biology and Evolution*, **2014**, 31, 2836-46	8.3	42

139	Three tiers of genome evolution in reptiles. *Integrative and Comparative Biology*, **2008**, 48, 494-504	2.8	42
138	Innate immunity and the evolution of resistance to an emerging infectious disease in a wild bird. *Molecular Ecology*, **2012**, 21, 2628-39	5.7	41
137	Ecology of avian influenza virus in birds. *Journal of Infectious Diseases*, **2008**, 197 Suppl 1, S29-33	7	41
136	Can weighting improve bushy trees? Models of cytochrome b evolution and the molecular systematics of pipits and wagtails (Aves: Motacillidae). *Systematic Biology*, **1998**, 47, 589-603	8.4	41
135	MHC class I genes of birds of prey: isolation, polymorphism and diversifying selection. *Conservation Genetics*, **2009**, 10, 1349-1355	2.6	40
134	A 39-kb sequence around a blackbird Mhc class II gene: ghost of selection past and songbird genome architecture. *Molecular Biology and Evolution*, **2000**, 17, 1384-95	8.3	40
133	High gene flow on a continental scale in the polyandrous Kentish plover Charadrius alexandrinus. *Molecular Ecology*, **2012**, 21, 5864-79	5.7	39
132	The Global Museum: natural history collections and the future of evolutionary science and public education. *PeerJ*, **2020**, 8, e8225	3.1	39
131	Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". *Science*, **2015**, 349, 1460	33.3	37
130	The Anolis lizard genome: an amniote genome without isochores. *Genome Biology and Evolution*, **2011**, 3, 974-84	3.9	37
129	Inferring the phylogeography and evolutionary history of the splendid fairy-wren Malurus splendens from mitochondrial DNA and spectrophotometry. *Journal of Avian Biology*, **2009**, 40, 7-17	1.9	35
128	Mid-Pleistocene divergence of Cuban and North American ivory-billed woodpeckers. *Biology Letters* , **2006**, 2, 466-9	3.6	35
127	Conflict between genetic and phenotypic differentiation: the evolutionary history of a 'lost and rediscovered' shorebird. *PLoS ONE*, **2011**, 6, e26995	3.7	35
126	Patterns of variation in MHC class II beta loci of the little greenbul (Andropadus virens) with comments on MHC evolution in birds. *Journal of Heredity*, **2006**, 97, 133-42	2.4	34
125	Conserved Nonexonic Elements: A Novel Class of Marker for Phylogenomics. *Systematic Biology*, **2017**, 66, 1028-1044	8.4	33
124	Multiple phylogenetically distinct events shaped the evolution of limb skeletal morphologies associated with bipedalism in the jerboas. *Current Biology*, **2015**, 25, 2785-2794	6.3	33
123	Population Genomics Reveals Low Genetic Diversity and Adaptation to Hypoxia in Snub-Nosed Monkeys. *Molecular Biology and Evolution*, **2016**, 33, 2670-81	8.3	33
122	Molecular and paleontological evidence for a post-Cretaceous origin of rodents. *PLoS ONE*, **2012**, 7, e46445	3.7	33

121	Hitchhiking and recombination in birds: evidence from Mhc-linked and unlinked loci in Red-winged Blackbirds (Agelaius phoeniceus). *Genetical Research*, **2004**, 84, 175-92	1.1	33
120	Comparative Methods at the Species Level: Geographic Variation in Morphology and Group Size in Grey-Crowned Babblers (Pomatostomus temporalis). *Evolution; International Journal of Organic Evolution*, **1995**, 49, 1134	3.8	33
119	Phylogenomic subsampling: a brief review. *Zoologica Scripta*, **2016**, 45, 63-74	2.5	33
118	Physical Mapping and Refinement of the Painted Turtle Genome (Chrysemys picta) Inform Amniote Genome Evolution and Challenge Turtle-Bird Chromosomal Conservation. *Genome Biology and Evolution*, **2015**, 7, 2038-50	3.9	32
117	Next-generation sequencing and the expanding domain of phylogeography. *Folia Zoologica*, **2015**, 64, 187-206	1.3	32
116	Mitochondrial DNA Variation and the Phylogeny of African Mole Rats (Rodentia: Bathyergidae). *Systematic Zoology*, **1987**, 36, 280		32
115	Reply to Gatesy and Springer: Claims of homology errors and zombie lineages do not compromise the dating of placental diversification. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E9433-E9434	11.5	31
114	Sequence and gene content of a large fragment of a lizard sex chromosome and evaluation of candidate sex differentiating gene R-spondin 1. *BMC Genomics*, **2013**, 14, 899	4.5	31
113	Major histocompatibility complex class I evolution in songbirds: universal primers, rapid evolution and base compositional shifts in exon 3. *PeerJ*, **2013**, 1, e86	3.1	31
112	Out of Florida: mtDNA reveals patterns of migration and Pleistocene range expansion of the Green Anole lizard (Anolis carolinensis). *Ecology and Evolution*, **2012**, 2, 2274-84	2.8	30
111	Tuatara (Sphenodon) genomics: BAC library construction, sequence survey, and application to the DMRT gene family. *Journal of Heredity*, **2006**, 97, 541-8	2.4	30
110	Morphological and genomic comparisons of Hawaiian and Japanese Black-footed Albatrosses (Phoebastria nigripes) using double digest RADseq: implications for conservation. *Evolutionary Applications*, **2015**, 8, 662-78	4.8	29
109	SNPs across time and space: population genomic signatures of founder events and epizootics in the House Finch (). *Ecology and Evolution*, **2016**, 6, 7475-7489	2.8	29
108	Structure and evolution of a new avian MHC class II B gene in a sub-Antarctic seabird, the thin-billed prion (Procellariiformes: Pachyptila belcheri). *Journal of Molecular Evolution*, **2009**, 68, 279-91	3.1	28
107	A cDNA macroarray approach to parasite-induced gene expression changes in a songbird host: genetic response of house finches to experimental infection by Mycoplasma gallisepticum. *Molecular Ecology*, **2006**, 15, 1263-73	5.7	28
106	Multiple origins of XY female mice (genus Akodon): phylogenetic and chromosomal evidence. *Proceedings of the Royal Society B: Biological Sciences*, **2000**, 267, 1825-31	4.4	28
105	Phylogenetics is the New Genetics (for Most of Biodiversity). *Trends in Ecology and Evolution*, **2020**, 35, 415-425	10.9	27
104	Reptiles and mammals have differentially retained long conserved noncoding sequences from the amniote ancestor. *Genome Biology and Evolution*, **2011**, 3, 102-13	3.9	27

103	Exploration of phylogenetic data using a global sequence analysis method. *BMC Evolutionary Biology*, **2005**, 5, 63	3	27
102	Polymorphism across an exon-intron boundary in an avian Mhc class II B gene. *Molecular Biology and Evolution*, **1999**, 16, 1599-606	8.3	27
101	Molecular, functional and evolutionary characterization of the gene encoding HMG-CoA reductase in the fission yeast, Schizosaccharomyces pombe. *Yeast*, **1996**, 12, 1107-1124	3.4	26
100	Evolutionary Dynamics of Sex Chromosomes of Paleognathous Birds. *Genome Biology and Evolution* , **2019**, 11, 2376-2390	3.9	25
99	Mitochondrial Gene Genealogy and Gene Flow among Island and Mainland Populations of a Sedentary Songbird, the Grey-Crowned Babbler (Pomatostomus temporalis). *Evolution; International Journal of Organic Evolution*, **1993**, 47, 1118	3.8	25
98	Physiological and regulatory underpinnings of geographic variation in reptilian cold tolerance across a latitudinal cline. *Molecular Ecology*, **2018**, 27, 2243-2255	5.7	24
97	Climate-mediated adaptation after mainland colonization of an ancestrally subtropical island lizard, Anolis carolinensis. *Journal of Evolutionary Biology*, **2016**, 29, 2168-2180	2.3	24
96	A proposal to sequence the genome of a garter snake (Thamnophis sirtalis). *Standards in Genomic Sciences*, **2011**, 4, 257-70		24
95	Integrating natural history collections and comparative genomics to study the genetic architecture of convergent evolution. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2019**, 374, 20180248	5.8	23
94	Reply to Gatesy and Springer: the multispecies coalescent model can effectively handle recombination and gene tree heterogeneity. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, E1180	11.5	23
93	Conservation genetics and Pacific fisheries bycatch: Mitochondrial differentiation and population assignment in black-footed albatrosses (Phoebastria nigripes). *Conservation Genetics*, **2005**, 6, 289-295	2.6	23
92	Evidence from a house finch (Haemorhous mexicanus) spleen transcriptome for adaptive evolution and biased gene conversion in passerine birds. *Molecular Biology and Evolution*, **2013**, 30, 1046-50	8.3	22
91	Recombination and nucleotide diversity in the sex chromosomal pseudoautosomal region of the emu, Dromaius novaehollandiae. *Journal of Heredity*, **2009**, 100, 125-36	2.4	22
90	Avian MHC Evolution in the Era of Genomics: Phase 1.0. *Cells*, **2019**, 8,	7.9	21
89	Core Genome Multilocus Sequence Typing: a Standardized Approach for Molecular Typing of Mycoplasma gallisepticum. *Journal of Clinical Microbiology*, **2018**, 56,	9.7	21
88	Outlier analyses to test for local adaptation to breeding grounds in a migratory arctic seabird. *Ecology and Evolution*, **2017**, 7, 2370-2381	2.8	20
87	Prevalence and evolutionary origins of autoimmune susceptibility alleles in natural mouse populations. *Genes and Immunity*, **2008**, 9, 61-8	4.4	20
86	Adaptive Evolution as a Predictor of Species-Specific Innate Immune Response. *Molecular Biology and Evolution*, **2015**, 32, 1717-29	8.3	19

85	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. *Systematic Biology*, **2020**, 69, 795-812	8.4	19
84	New Frontiers for Organismal Biology. *BioScience*, **2013**, 63, 464-471	5.7	18
83	Genome evolution in Reptilia: in silico chicken mapping of 12,000 BAC-end sequences from two reptiles and a basal bird. *BMC Genomics*, **2009**, 10 Suppl 2, S8	4.5	18
82	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. *Molecular Biology and Evolution*, **2019**, 36, 1086-1100	8.3	17
81	Ecology can inform genetics: Disassortative mating contributes to MHC polymorphism in Leach's storm-petrels (Oceanodroma leucorhoa). *Molecular Ecology*, **2018**, 27, 3371	5.7	17
80	Tangled trees: the challenge of inferring species trees from coalescent and noncoalescent genes. *Methods in Molecular Biology*, **2012**, 856, 3-28	1.4	17
79	High-Speed Developments in Avian Genomics. *BioScience*, **2008**, 58, 587-595	5.7	17
78	Homology and Comparative Methods in the Study of Avian Cooperative Breeding. *American Naturalist*, **1994**, 143, 723-733	3.7	17
77	Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". *Science*, **2015**, 350, 171	33.3	16
76	Molecular evolution of Dmrt1 accompanies change of sex-determining mechanisms in reptilia. *Biology Letters*, **2014**, 10, 20140809	3.6	16
75	Cryptic differentiation and geographic variation in genetic diversity of Hall's Babbler Pomatostomus halli. *Journal of Avian Biology*, **2001**, 32, 102-110	1.9	16
74	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. *Methods in Molecular Biology*, **2019**, 1910, 211-239	1.4	15
73	The Zebra Finch genome and avian genomics in the wild. *Emu*, **2010**, 110, 233-241	1.1	15
72	The Earth BioGenome Project 2020: Starting the clock.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	15
71	Gene flow during glacial habitat shifts facilitates character displacement in a Neotropical flycatcher radiation. *BMC Evolutionary Biology*, **2017**, 17, 210	3	14
70	The Maluridae: inferring avian biology and evolutionary history from DNA sequences. *Emu*, **2013**, 113, 195-207	1.1	14
69	Evolutionary genetics of Carpodacus mexicanus, a recently colonized host of a bacterial pathogen, Mycoplasma gallisepticum. *Genetica*, **2007**, 129, 217-25	1.5	14
68	Genomics of host-pathogen interactions: challenges and opportunities across ecological and spatiotemporal scales. *PeerJ*, **2019**, 7, e8013	3.1	14

67	Rhetoric vs. reality: A commentary on Bird Origins Anew by A. FeduccíaRetórica vs. Realidad: Un comentario sobre Bird Origins Anew por A. Feduccia, Auk 130:112Rhetoric vs. reality. *Auk*, **2015**, 132, 467-480	2.1	13
66	Frequent coinfection reduces RNA virus population genetic diversity. *Journal of Heredity*, **2013**, 104, 704-12	2.4	13
65	Triploid plover female provides support for a role of the W chromosome in avian sex determination. *Biology Letters*, **2012**, 8, 787-9	3.6	13
64	Endless forms of sexual selection. *PeerJ*, **2019**, 7, e7988	3.1	13
63	Attenuated Fgf Signaling Underlies the Forelimb Heterochrony in the Emu Dromaius novaehollandiae. *Current Biology*, **2019**, 29, 3681-3691.e5	6.3	12
62	The evolution of bipedalism in jerboas (rodentia: Dipodoidea): origin in humid and forested environments. *Evolution; International Journal of Organic Evolution*, **2014**, 68, 2108-18	3.8	12
61	Climate change, collections and the classroom: using big data to tackle big problems. *Evolution: Education and Outreach*, **2017**, 10,	1.6	12
60	Sex-biased expression of sex-differentiating genes FOXL2 and FGF9 in American alligators, alligator Mississippiensis. *Sexual Development*, **2013**, 7, 253-60	1.6	12
59	Geographic differences in sexual reassortment in RNA phage. *Evolution; International Journal of Organic Evolution*, **2010**, 64, 3010-23	3.8	12
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