

Scott V Edwards

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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,	11.5	15
227	Understanding the evolution of viviparity using intraspecific variation in reproductive mode and transitional forms of pregnancy.. <i>Biological Reviews</i> , 2022 ,	13.5	2
226	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	6
225	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,	3.9	1
224	Evolution of the DAN gene family in vertebrates.. <i>Developmental Biology</i> , 2021 , 482, 34-43	3.1	0
223	A bird-like genome from a frog: Mechanisms of genome size reduction in the ornate burrowing frog.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	7
222	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	3.7	2
221	Genomic Consequences of Long-Term Population Decline in Brown Eared Pheasant. <i>Molecular Biology and Evolution</i> , 2021 , 38, 263-273	8.3	10
220	Early origin of sweet perception in the songbird radiation. <i>Science</i> , 2021 , 373, 226-231	33.3	7
219	The evolution of comparative phylogeography: putting the geography (and more) into comparative population genomics. <i>Genome Biology and Evolution</i> , 2021 ,	3.9	3
218	What Have We Learned from the First 500 Avian Genomes?. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2021 , 52,	13.5	7
217	Museum Genomics. <i>Annual Review of Genetics</i> , 2021 , 55, 633-659	14.5	9
216	Olfactory receptor subgenome and expression in a highly olfactory procellariiform seabird. <i>Genetics</i> , 2021 ,	4	1
215	The evolution of a tropical biodiversity hotspot. <i>Science</i> , 2020 , 370, 1343-1348	33.3	42
214	Phylogenetics is the New Genetics (for Most of Biodiversity). <i>Trends in Ecology and Evolution</i> , 2020 , 35, 415-425	10.9	27
213	Digitization and the Future of Natural History Collections. <i>BioScience</i> , 2020 , 70, 243-251	5.7	68
212	The Global Museum: natural history collections and the future of evolutionary science and public education. <i>PeerJ</i> , 2020 , 8, e8225	3.1	39

211	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. <i>Systematic Biology</i> , 2020 , 69, 795-812	8.4	19
210	Genomics of adaptation and acclimation: from field to lab and back. <i>National Science Review</i> , 2020 , 7, 128	10.8	0
209	Prospects for sociogenomics in avian cooperative breeding and parental care. <i>Environmental Epigenetics</i> , 2020 , 66, 293-306	2.4	1
208	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020 , 587, 252-257	50.4	89
207	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020 , 584, 403-409	50.4	49
206	Assembly of the Northern Cardinal () Genome Reveals Candidate Regulatory Regions for Sexually Dichromatic Red Plumage Coloration. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 3541-3548	3.2	2
205	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	4.4	12
204	Evidence for the Pleistocene Arc Hypothesis from genome-wide SNPs in a Neotropical dry forest specialist, the Rufous-fronted Thornbird (Furnariidae: Phacellodomus rufifrons). <i>Molecular Ecology</i> , 2020 , 29, 4457-4472	5.7	5
203	Evolutionary Dynamics of Sex Chromosomes of Paleognathous Birds. <i>Genome Biology and Evolution</i> , 2019 , 11, 2376-2390	3.9	25
202	Avian MHC Evolution in the Era of Genomics: Phase 1.0. <i>Cells</i> , 2019 , 8,	7.9	21
201	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	1.1	10
200	phenotools: An r package for visualizing and analysing phenomic datasets. <i>Methods in Ecology and Evolution</i> , 2019 , 10, 1393-1400	7.7	2
199	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	5.8	23
198	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	8.4	43
197	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2019 , 36, 1086-1100	8.3	17
196	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019 , 364, 74-78	33.3	103
195	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. <i>Methods in Molecular Biology</i> , 2019 , 1910, 211-239	1.4	15
194	Attenuated Fgf Signaling Underlies the Forelimb Heterochrony in the Emu <i>Dromaius novaehollandiae</i> . <i>Current Biology</i> , 2019 , 29, 3681-3691.e5	6.3	12

193	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	5
192	Embracing heterogeneity: coalescing the Tree of Life and the future of phylogenomics. <i>PeerJ</i> , 2019 , 7, e6399	3.1	63
191	Endless forms of sexual selection. <i>PeerJ</i> , 2019 , 7, e7988	3.1	13
190	Genomics of host-pathogen interactions: challenges and opportunities across ecological and spatiotemporal scales. <i>PeerJ</i> , 2019 , 7, e8013	3.1	14
189	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	11.5	334
188	Physiological and regulatory underpinnings of geographic variation in reptilian cold tolerance across a latitudinal cline. <i>Molecular Ecology</i> , 2018 , 27, 2243-2255	5.7	24
187	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	3.9	48
186	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	5.7	17
185	Conceptual and empirical advances in Neotropical biodiversity research. <i>PeerJ</i> , 2018 , 6, e5644	3.1	70
184	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> , 2018 , 374,	5.8	45
183	Core Genome Multilocus Sequence Typing: a Standardized Approach for Molecular Typing of <i>Mycoplasma gallisepticum</i> . <i>Journal of Clinical Microbiology</i> , 2018 , 56,	9.7	21
182	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	4.1	5
181	Genome-scale DNA sequence data and the evolutionary history of placental mammals. <i>Data in Brief</i> , 2018 , 18, 1972-1975	1.2	7
180	Conserved Nonexonic Elements: A Novel Class of Marker for Phylogenomics. <i>Systematic Biology</i> , 2017 , 66, 1028-1044	8.4	33
179	Outlier analyses to test for local adaptation to breeding grounds in a migratory arctic seabird. <i>Ecology and Evolution</i> , 2017 , 7, 2370-2381	2.8	20
178	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	11.5	31
177	Gene flow during glacial habitat shifts facilitates character displacement in a Neotropical flycatcher radiation. <i>BMC Evolutionary Biology</i> , 2017 , 17, 210	3	14
176	Comparative Genomics as a Foundation for Evo-Devo Studies in Birds. <i>Methods in Molecular Biology</i> , 2017 , 1650, 11-46	1.4	9

175	Winter storms drive rapid phenotypic, regulatory, and genomic shifts in the green anole lizard. <i>Science</i> , 2017 , 357, 495-498	33.3	130
174	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	11.5	78
173	Climate change, collections and the classroom: using big data to tackle big problems. <i>Evolution: Education and Outreach</i> , 2017 , 10,	1.6	12
172	Genomic footprints of adaptation in a cooperatively breeding tropical bird across a vegetation gradient. <i>Molecular Ecology</i> , 2017 , 26, 4483-4496	5.7	7
171	Population Genomics Reveals Low Genetic Diversity and Adaptation to Hypoxia in Snub-Nosed Monkeys. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2670-81	8.3	33
170	Ancient horizontal transfers of retrotransposons between birds and ancestors of human pathogenic nematodes. <i>Nature Communications</i> , 2016 , 7, 11396	17.4	55
169	Reticulation, divergence, and the phylogeography-phylogenetics continuum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 8025-32	11.5	91
168	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	2.3	24
167	SNPs across time and space: population genomic signatures of founder events and epizootics in the House Finch (<i>Turdus chrysolaus</i>). <i>Ecology and Evolution</i> , 2016 , 6, 7475-7489	2.8	29
166	The "Atlantis Forest hypothesis" 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	11.5	11
165	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2016 , 94, 447-62	4.1	230
164	Phylogenomic subsampling: a brief review. <i>Zoologica Scripta</i> , 2016 , 45, 63-74	2.5	33
163	Inferential reasoning and egg rejection in a cooperatively breeding cuckoo. <i>Animal Cognition</i> , 2015 , 18, 75-82	3.1	6
162	Adaptive Evolution as a Predictor of Species-Specific Innate Immune Response. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1717-29	8.3	19
161	Plumage color and pathogen-induced gene expression in a wild bird. <i>Behavioral Ecology</i> , 2015 , 26, 1100-1110	1.5	5
160	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015 , 4, 4	7.6	54
159	Rhetoric vs. reality: A commentary on Bird Origins Anew by A. Feduccia. <i>Rhetoric vs. Realidad: Un comentario sobre Bird Origins Anew</i> por A. Feduccia, <i>Auk</i> 130:112-113 Rhetoric vs. reality. <i>Auk</i> , 2015 , 132, 467-480	2.1	13
158	Feather development genes and associated regulatory innovation predate the origin of Dinosauria. <i>Molecular Biology and Evolution</i> , 2015 , 32, 23-8	8.3	42

157	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, 2038-50	3.9	32
156	Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". <i>Science</i> , 2015 , 349, 1460	33.3	37
155	Morphological and genomic comparisons of Hawaiian and Japanese Black-footed Albatrosses (<i>Phoebastria nigripes</i>) using double digest RADseq: implications for conservation. <i>Evolutionary Applications</i> , 2015 , 8, 662-78	4.8	29
154	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	6.3	33
153	Comment on "Statistical binning enables an accurate coalescent-based estimation of the avian tree". <i>Science</i> , 2015 , 350, 171	33.3	16
152	Next-generation sequencing and the expanding domain of phylogeography. <i>Folia Zoologica</i> , 2015 , 64, 187-206	1.3	32
151	Estimating phylogenetic trees from genome-scale data. <i>Annals of the New York Academy of Sciences</i> , 2015 , 1360, 36-53	6.5	122
150	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, 1439-51	3.2	7
149	The evolution of bipedalism in jerboas (rodentia: Dipodoidea): origin in humid and forested environments. <i>Evolution; International Journal of Organic Evolution</i> , 2014 , 68, 2108-18	3.8	12
148	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, 134-52	8.4	67
147	Sensory biology. Evolution of sweet taste perception in hummingbirds by transformation of the ancestral umami receptor. <i>Science</i> , 2014 , 345, 929-33	33.3	117
146	A house finch (<i>Haemorhous 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	4.5	10
145	Natural History Collections as Emerging Resources for Innovative Education. <i>BioScience</i> , 2014 , 64, 725-734	3.7	59
144	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014 , 346, 1254449	33.3	231
143	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
142	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20	33.3	628
141	Molecular evolution of <i>Dmrt1</i> accompanies change of sex-determining mechanisms in reptilia. <i>Biology Letters</i> , 2014 , 10, 20140809	3.6	16
140	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, 2836-46	8.3	42

139	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	18.3	227
138	New Frontiers for Organismal Biology. <i>BioScience</i> , 2013 , 63, 464-471	5.7	18
137	The Maluridae: inferring avian biology and evolutionary history from DNA sequences. <i>Emu</i> , 2013 , 113, 195-207	1.1	14
136	Next-generation QTL mapping: crowdsourcing SNPs, without pedigrees. <i>Molecular Ecology</i> , 2013 , 22, 3885-87	5.7	11
135	Frequent coinfection reduces RNA virus population genetic diversity. <i>Journal of Heredity</i> , 2013 , 104, 704-12	2.4	13
134	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	4.5	31
133	Sex-biased expression of sex-differentiating genes FOXL2 and FGF9 in American alligators, alligator <i>Mississippiensis</i> . <i>Sexual Development</i> , 2013 , 7, 253-60	1.6	12
132	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	5.7	51
131	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, 655-66	2.8	10
130	Museums' role: increasing knowledge. <i>Science</i> , 2013 , 339, 1148-9	33.3	3
129	Evidence from a house finch (<i>Haemorhous mexicanus</i>) spleen transcriptome for adaptive evolution and biased gene conversion in passerine birds. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1046-50	8.3	22
128	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	11.5	23
127	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	3.1	31
126	Innate immunity and the evolution of resistance to an emerging infectious disease in a wild bird. <i>Molecular Ecology</i> , 2012 , 21, 2628-39	5.7	41
125	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, 2274-84	2.8	30
124	High gene flow on a continental scale in the polyandrous Kentish plover <i>Charadrius alexandrinus</i> . <i>Molecular Ecology</i> , 2012 , 21, 5864-79	5.7	39
123	Molecular and paleontological evidence for a post-Cretaceous origin of rodents. <i>PLoS ONE</i> , 2012 , 7, e46445	3.7	33
122	Tangled trees: the challenge of inferring species trees from coalescent and noncoalescent genes. <i>Methods in Molecular Biology</i> , 2012 , 856, 3-28	1.4	17

121	A species tree for the Australo-Papuan Fairy-wrens and allies (Aves: Maluridae). <i>Systematic Biology</i> , 2012 , 61, 253-71	8.4	48
120	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
119	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	6	95
118	Triploid plover female provides support for a role of the W chromosome in avian sex determination. <i>Biology Letters</i> , 2012 , 8, 787-9	3.6	13
117	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, 14942-7	11.5	328
116	The evolution of intron size in amniotes: a role for powered flight?. <i>Genome Biology and Evolution</i> , 2012 , 4, 1033-43	3.9	54
115	Genetic Introgression: An Integral but Neglected Component of Speciation in Birds. <i>Auk</i> , 2011 , 128, 620-632	6.32	182
114	A proposal to sequence the genome of a garter snake (<i>Thamnophis sirtalis</i>). <i>Standards in Genomic Sciences</i> , 2011 , 4, 257-70		24
113	Reptiles and mammals have differentially retained long conserved noncoding sequences from the amniote ancestor. <i>Genome Biology and Evolution</i> , 2011 , 3, 102-13	3.9	27
112	Phylogenomic Approach to the Evolutionary Dynamics of Gene Duplication in Birds 2011 , 253-268		2
111	Major Events in Avian Genome Evolution 2011 , 325-337		8
110	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011 , 477, 587-91	50.4	478
109	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, 7466-71	11.5	78
108	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, 7866-71	11.5	94
107	The Anolis lizard genome: an amniote genome without isochores. <i>Genome Biology and Evolution</i> , 2011 , 3, 974-84	3.9	37
106	Molecular evolution of the toll-like receptor multigene family in birds. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1703-15	8.3	121
105	Sex chromosome evolution in amniotes: applications for bacterial artificial chromosome libraries. <i>Journal of Biomedicine and Biotechnology</i> , 2011 , 2011, 132975		6
104	A Birds-Eye View of Animal Evolution. <i>BioScience</i> , 2011 , 61, 331-333	5.7	

103	Conflict between genetic and phenotypic differentiation: the evolutionary history of a 'lost and rediscovered' shorebird. <i>PLoS ONE</i> , 2011 , 6, e26995	3.7	35
102	Geographic differences in sexual reassortment in RNA phage. <i>Evolution; International Journal of Organic Evolution</i> , 2010 , 64, 3010-23	3.8	12
101	Comparative genomics based on massive parallel transcriptome sequencing reveals patterns of substitution and selection across 10 bird species. <i>Molecular Ecology</i> , 2010 , 19 Suppl 1, 266-76	5.7	97
100	The genome of a songbird. <i>Nature</i> , 2010 , 464, 757-62	50.4	655
99	Genome evolution in Reptilia, the sister group of mammals. <i>Annual Review of Genomics and Human Genetics</i> , 2010 , 11, 239-64	9.7	67
98	The Zebra Finch genome and avian genomics in the wild. <i>Emu</i> , 2010 , 110, 233-241	1.1	15
97	A maximum pseudo-likelihood approach for estimating species trees under the coalescent model. <i>BMC Evolutionary Biology</i> , 2010 , 10, 302	3	413
96	Gene duplication and fragmentation in the zebra finch major histocompatibility complex. <i>BMC Biology</i> , 2010 , 8, 29	7.3	106
95	Phylogenetic analysis in the anomaly zone. <i>Systematic Biology</i> , 2009 , 58, 452-60	8.4	88
94	Natural selection and phylogenetic analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 8799-800	11.5	43
93	Genome 10K: a proposal to obtain whole-genome sequence for 10,000 vertebrate species. <i>Journal of Heredity</i> , 2009 , 100, 659-74	2.4	418
92	Recombination and nucleotide diversity in the sex chromosomal pseudoautosomal region of the emu, <i>Dromaius novaehollandiae</i> . <i>Journal of Heredity</i> , 2009 , 100, 125-36	2.4	22
91	Estimating species phylogenies using coalescence times among sequences. <i>Systematic Biology</i> , 2009 , 58, 468-77	8.4	342
90	Variability in sex-determining mechanisms influences genome complexity in reptilia. <i>Cytogenetic and Genome Research</i> , 2009 , 127, 242-8	1.9	9
89	Nucleotide variation, linkage disequilibrium and founder-facilitated speciation in wild populations of the zebra finch (<i>Taeniopygia guttata</i>). <i>Genetics</i> , 2009 , 181, 645-60	4	82
88	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 Suppl 2, S8	4.5	18
87	MHC class I genes of birds of prey: isolation, polymorphism and diversifying selection. <i>Conservation Genetics</i> , 2009 , 10, 1349-1355	2.6	40
86	Multilocus phylogeography and phylogenetics using sequence-based markers. <i>Genetica</i> , 2009 , 135, 439-55; 247		

85	Structure and evolution of a new avian MHC class II B gene in a sub-Antarctic seabird, the thin-billed prion (Procellariiformes: Pachyptila belcheri). <i>Journal of Molecular Evolution</i> , 2009 , 68, 279-91	3.1	28
84	Looking forwards or looking backwards in avian phylogeography? A comment on Zink and Barrowclough 2008. <i>Molecular Ecology</i> , 2009 , 18, 2930-3; discussion 2934-6	5.7	173
83	Inferring the phylogeography and evolutionary history of the splendid fairy-wren Malurus splendens from mitochondrial DNA and spectrophotometry. <i>Journal of Avian Biology</i> , 2009 , 40, 7-17	1.9	35
82	Is a new and general theory of molecular systematics emerging?. <i>Evolution; International Journal of Organic Evolution</i> , 2009 , 63, 1-19	3.8	743
81	Coalescent methods for estimating phylogenetic trees. <i>Molecular Phylogenetics and Evolution</i> , 2009 , 53, 320-8	4.1	279
80	Prevalence and evolutionary origins of autoimmune susceptibility alleles in natural mouse populations. <i>Genes and Immunity</i> , 2008 , 9, 61-8	4.4	20
79	Extensive polymorphism and geographical variation at a positively selected MHC class II B gene of the lesser kestrel (Falco naumanni). <i>Molecular Ecology</i> , 2008 , 17, 2652-65	5.7	104
78	High-Speed Developments in Avian Genomics. <i>BioScience</i> , 2008 , 58, 587-595	5.7	17
77	Three tiers of genome evolution in reptiles. <i>Integrative and Comparative Biology</i> , 2008 , 48, 494-504	2.8	42
76	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, 505-11	2.8	3
75	Comparison of species tree methods for reconstructing the phylogeny of bearded manakins (Aves: Pipridae, Manacus) from multilocus sequence data. <i>Systematic Biology</i> , 2008 , 57, 719-31	8.4	70
74	Ecology of avian influenza virus in birds. <i>Journal of Infectious Diseases</i> , 2008 , 197 Suppl 1, S29-33	7	41
73	Developing markers for multilocus phylogenetics in non-model organisms: A test case with turtles. <i>Molecular Phylogenetics and Evolution</i> , 2008 , 49, 514-25	4.1	56
72	BIRD SPECIATION: SELECTION AND THE ORIGIN OF SPECIES1. <i>Evolution; International Journal of Organic Evolution</i> , 2008 , 62, 991-995	3.8	1
71	Estimating species trees using multiple-allele DNA sequence data. <i>Evolution; International Journal of Organic Evolution</i> , 2008 , 62, 2080-91	3.8	177
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9	Bayesian detection of convergent rate changes of conserved noncoding elements on phylogenetic trees		2
8	Integrating natural history-derived phenomics with comparative genomics to study the genetic architecture of convergent evolution		1
7	Evolution of the DAN gene family in vertebrates		2
6	Convergent regulatory evolution and the origin of flightlessness in palaeognathous birds		9
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4	Whole-genome analyses resolve the phylogeny of flightless birds (Palaeognathae) in the presence of an empirical anomaly zone		5
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2	Neo-sex chromosomes, genetic diversity and demographic history in the Critically Endangered Raso lark		2
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