Hans Ellegren

List of Publications by Year in descending order

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322 papers	36,766 citations	3116 95 h-index	5102 172 g-index
328 all docs	328 docs citations	328 times ranked	27692 citing authors

#	Article	IF	Citations
1	Whole-genome resequencing of temporally stratified samples reveals substantial loss of haplotype diversity in the highly inbred Scandinavian wolf population. Genome Research, 2022, 32, 449-458.	2.4	8
2	Potential for increased connectivity between differentiated wolverine populations. Biological Conservation, 2022, 272, 109601.	1.9	7
3	Wholeâ€genome analyses provide no evidence for dog introgression in Fennoscandian wolf populations. Evolutionary Applications, 2021, 14, 721-734.	1.5	19
4	Positive selection plays a major role in shaping signatures of differentiation across the genomic landscape of two independent Ficedula flycatcher species pairs*. Evolution; International Journal of Organic Evolution, 2021, 75, 2179-2196.	1.1	18
5	Genomic inference of contemporary effective population size in a large island population of collared flycatchers (Ficedula albicollis). Molecular Ecology, 2021, 30, 3965-3973.	2.0	17
6	Major population splits coincide with episodes of rapid climate change in a forest-dependent bird. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20211066.	1.2	1
7	Tissue-specific patterns of regulatory changes underlying gene expression differences among Ficedula flycatchers and their naturally occurring F₁ hybrids. Genome Research, 2020, 30, 1727-1739.	2.4	13
8	Recent introgression between Taiga Bean Goose and Tundra Bean Goose results in a largely homogeneous landscape of genetic differentiation. Heredity, 2020, 125, 73-84.	1.2	13
9	How Linked Selection Shapes the Diversity Landscape in Ficedula Flycatchers. Genetics, 2019, 212, 277-285.	1.2	32
10	GC-biased gene conversion conceals the prediction of the nearly neutral theory in avian genomes. Genome Biology, 2019, 20, 5.	3.8	37
11	The evolutionary history of grey wolf Y chromosomes. Molecular Ecology, 2019, 28, 2173-2191.	2.0	14
12	Genotypeâ€free estimation of allele frequencies reduces bias and improves demographic inference from RADSeq data. Molecular Ecology Resources, 2019, 19, 586-596.	2.2	33
13	Footprints of adaptive evolution revealed by whole Z chromosomes haplotypes in flycatchers. Molecular Ecology, 2019, 28, 2290-2304.	2.0	12
14	Abundant recent activity of retrovirusâ€like retrotransposons within and among flycatcher species implies a rich source of structural variation in songbird genomes. Molecular Ecology, 2018, 27, 99-111.	2.0	59
15	Natural selection beyond genes: Identification and analyses of evolutionarily conserved elements in the genome of the collared flycatcher (Ficedula albicollis). Molecular Ecology, 2018, 27, 476-492.	2.0	19
16	Genomic consequences of intensive inbreeding in an isolated wolf population. Nature Ecology and Evolution, 2018, 2, 124-131.	3.4	146
17	Genome sequencing and conservation genomics in the Scandinavian wolverine population. Conservation Biology, 2018, 32, 1301-1312.	2.4	49
18	Sexâ€biased gene expression, sexual antagonism and levels of genetic diversity in the collared flycatcher (Ficedula albicollis) genome. Molecular Ecology, 2018, 27, 3572-3581.	2.0	51

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19	Biased Inference of Selection Due to GC-Biased Gene Conversion and the Rate of Protein Evolution in Flycatchers When Accounting for It. Molecular Biology and Evolution, 2018, 35, 2475-2486.	3.5	32
20	A Genetic Map of Ostrich Z Chromosome and the Role of Inversions in Avian Sex Chromosome Evolution. Genome Biology and Evolution, 2018, 10, 2049-2060.	1.1	24
21	Inferring Individual Inbreeding and Demographic History from Segments of Identity by Descent inFicedulaFlycatcher Genome Sequences. Genetics, 2017, 205, 1319-1334.	1.2	77
22	Association mapping of morphological traits in wild and captive zebra finches: reliable within, but not between populations. Molecular Ecology, 2017, 26, 1285-1305.	2.0	18
23	Covariation in levels of nucleotide diversity in homologous regions of the avian genome long after completion of lineage sorting. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20162756.	1.2	50
24	Wholeâ€genome patterns of linkage disequilibrium across flycatcher populations clarify the causes and consequences of fineâ€scale recombination rate variation in birds. Molecular Ecology, 2017, 26, 4158-4172.	2.0	87
25	Bayesian Inference of Allele-Specific Gene Expression Indicates Abundant Cis-Regulatory Variation in Natural Flycatcher Populations. Genome Biology and Evolution, 2017, 9, 1266-1279.	1.1	22
26	Genomewide patterns of variation in genetic diversity are shared among populations, species and higherâ€order taxa. Molecular Ecology, 2017, 26, 4284-4295.	2.0	75
27	Insights into the genetic architecture of morphological traits in two passerine bird species. Heredity, 2017, 119, 197-205.	1.2	44
28	Parallelism in genomic landscapes of differentiation, conserved genomic features and the role of linked selection. Journal of Evolutionary Biology, 2017, 30, 1516-1518.	0.8	25
29	Making sense of genomic islands of differentiation in light of speciation. Nature Reviews Genetics, 2017, 18, 87-100.	7.7	389
30	Genomic distribution and estimation of nucleotide diversity in natural populations: perspectives from the collared flycatcher (Ficedula albicollis) genome. Molecular Ecology Resources, 2017, 17, 586-597.	2.2	38
31	Wholeâ€genome resequencing of extreme phenotypes in collared flycatchers highlights the difficulty of detecting quantitative trait loci in natural populations. Molecular Ecology Resources, 2016, 16, 727-741.	2.2	66
32	Noninvasive genetic sampling reveals intrasex territoriality in wolverines. Ecology and Evolution, 2016, 6, 1527-1536.	0.8	22
33	<scp>PSMC</scp> analysis of effective population sizes in molecular ecology and its application to blackâ€andâ€white Ficedula flycatchers. Molecular Ecology, 2016, 25, 1058-1072.	2.0	225
34	Genomics advances the study of inbreeding depression in the wild. Evolutionary Applications, 2016, 9, 1205-1218.	1.5	200
35	Direct estimate of the rate of germline mutation in a bird. Genome Research, 2016, 26, 1211-1218.	2.4	190
36	Divergence in gene expression within and between two closely related flycatcher species. Molecular Ecology, 2016, 25, 2015-2028.	2.0	57

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37	Determinants of genetic diversity. Nature Reviews Genetics, 2016, 17, 422-433.	7.7	587
38	Increasing the power of genome wide association studies in natural populations using repeated measures â€“ evaluation and implementation. Methods in Ecology and Evolution, 2016, 7, 792-799.	2.2	55
39	Recombination Rate Variation Modulates Gene Sequence Evolution Mainly via GC-Biased Gene Conversion, Not Hillâ€“Robertson Interference, in an Avian System. Molecular Biology and Evolution, 2016, 33, 216-227.	3.5	59
40	Life History Traits, Protein Evolution, and the Nearly Neutral Theory in Amniotes. Molecular Biology and Evolution, 2016, 33, 1517-1527.	3.5	75
41	High-Resolution Mapping of Crossover and Non-crossover Recombination Events by Whole-Genome Re-sequencing of an Avian Pedigree. PLoS Genetics, 2016, 12, e1006044.	1.5	85
42	GCâ€biased gene conversion links the recombination landscape and demography to genomic base composition. BioEssays, 2015, 37, 1317-1326.	1.2	70
43	Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of Ficedula flycatchers. Genome Research, 2015, 25, 1656-1665.	2.4	385
44	Compensatory immigration counteracts contrasting conservation strategies of wolverines (Gulo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.9	31
45	Evolutionary Consequences of DNA Methylation on the GC Content in Vertebrate Genomes. G3: Genes, Genomes, Genetics, 2015, 5, 441-447.	0.8	54
46	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	0.6	97
47	Resolving Evolutionary Relationships in Closely Related Species with Whole-Genome Sequencing Data. Systematic Biology, 2015, 64, 1000-1017.	2.7	102
48	Evolutionary analysis of the female-specific avian W chromosome. Nature Communications, 2015, 6, 7330.	5.8	121
49	Temporal Dynamics of Avian Populations during Pleistocene Revealed by Whole-Genome Sequences. Current Biology, 2015, 25, 1375-1380.	1.8	243
50	Phylogenomic analyses data of the avian phylogenomics project. GigaScience, 2015, 4, 4.	3.3	72
51	Genome-wide association mapping in a wild avian population identifies a link between genetic and phenotypic variation in a life-history trait. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150156.	1.2	45
52	A prezygotic transmission distorter acting equally in female and male zebra finches Taeniopygia guttata. Molecular Ecology, 2015, 24, 3846-3859.	2.0	11
53	Quantitative Mass Spectrometry Reveals Partial Translational Regulation for Dosage Compensation in Chicken. Molecular Biology and Evolution, 2015, 32, 2716-2725.	3.5	45
54	The Dynamics of Incomplete Lineage Sorting across the Ancient Adaptive Radiation of Neoavian Birds. PLoS Biology, 2015, 13, e1002224.	2.6	223

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55	Evidence for GC-biased gene conversion as a driver of between-lineage differences in avian base composition. Genome Biology, 2014, 15, 549.	3.8	76
56	Genomic identification and characterization of the pseudoautosomal region in highly differentiated avian sex chromosomes. Nature Communications, 2014, 5, 5448.	5.8	44
57	Early Mesozoic Coexistence of Amniotes and Hepadnaviridae. PLoS Genetics, 2014, 10, e1004559.	1.5	61
58	Estimation of linkage disequilibrium and interspecific gene flow in <scp>F</scp>icedula flycatchers by a newly developed 50k singleâ€nucleotide polymorphism array. Molecular Ecology Resources, 2014, 14, 1248-1260.	2.2	58
59	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	6.0	1,583
60	Reconstruction of gross avian genome structure, organization and evolution suggests that the chicken lineage most closely resembles the dinosaur avian ancestor. BMC Genomics, 2014, 15, 1060.	1.2	71
61	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. GigaScience, 2014, 3, 27.	3.3	72
62	K r /K c but not d N /d S correlates positively with body mass in birds, raising implications for inferring lineage-specific selection. Genome Biology, 2014, 15, 542.	3.8	53
63	A highâ€density linkage map enables a secondâ€generation collared flycatcher genome assembly and reveals the patterns of avian recombination rate variation and chromosomal evolution. Molecular Ecology, 2014, 23, 4035-4058.	2.0	220
64	Genome sequencing and population genomics in non-model organisms. Trends in Ecology and Evolution, 2014, 29, 51-63.	4.2	570
65	Patterns of sequencing coverage bias revealed by ultra-deep sequencing of vertebrate mitochondria. BMC Genomics, 2014, 15, 467.	1.2	55
66	Old but Not (So) Degeneratedâ€”Slow Evolution of Largely Homomorphic Sex Chromosomes in Ratites. Molecular Biology and Evolution, 2014, 31, 1444-1453.	3.5	34
67	An extensive candidate gene approach to speciation: diversity, divergence and linkage disequilibrium in candidate pigmentation genes across the European crow hybrid zone. Heredity, 2013, 111, 467-473.	1.2	30
68	Inferring the demographic history of European Ficedula flycatcher populations. BMC Evolutionary Biology, 2013, 13, 2.	3.2	20
69	Genome-wide analysis in chicken reveals that local levels of genetic diversity are mainly governed by the rate of recombination. BMC Genomics, 2013, 14, 86.	1.2	30
70	The Evolutionary Genomics of Birds. Annual Review of Ecology, Evolution, and Systematics, 2013, 44, 239-259.	3.8	96
71	The evolutionary causes and consequences of sex-biased gene expression. Nature Reviews Genetics, 2013, 14, 83-87.	7.7	322
72	Sampling strategies for species trees: The effects on phylogenetic inference of the number of genes, number of individuals, and whether loci are mitochondrial, sex-linked, or autosomal. Molecular Phylogenetics and Evolution, 2013, 67, 358-366.	1.2	50

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73	Demographic Divergence History of Pied Flycatcher and Collared Flycatcher Inferred from Whole-Genome Re-sequencing Data. PLoS Genetics, 2013, 9, e1003942.	1.5	124
74	Lack of Dosage Compensation Accompanies the Arrested Stage of Sex Chromosome Evolution in Ostriches. Molecular Biology and Evolution, 2013, 30, 806-810.	3.5	42
75	Transcriptome Sequencing Reveals the Character of Incomplete Dosage Compensation across Multiple Tissues in Flycatchers. Genome Biology and Evolution, 2013, 5, 1555-1566.	1.1	59
76	Twisted Signatures of GC-Biased Gene Conversion Embedded in an Evolutionary Stable Karyotype. Molecular Biology and Evolution, 2013, 30, 1700-1712.	3.5	41
77	Recombination Drives Vertebrate Genome Contraction. PLoS Genetics, 2012, 8, e1002680.	1.5	69
78	The genomic landscape of species divergence in Ficedula flycatchers. Nature, 2012, 491, 756-760.	13.7	589
79	QTL linkage mapping of wing length in zebra finch using genomeâ€wide single nucleotide polymorphisms markers. Molecular Ecology, 2012, 21, 329-339.	2.0	23
80	QTL LINKAGE MAPPING OF ZEBRA FINCH BEAK COLOR SHOWS AN OLIGOGENIC CONTROL OF A SEXUALLY SELECTED TRAIT. Evolution; International Journal of Organic Evolution, 2012, 66, 18-30.	1.1	50
81	THE GENOMIC SIGNATURE OF SEXUAL SELECTION IN THE GENETIC DIVERSITY OF THE SEX CHROMOSOMES AND AUTOSOMES. Evolution; International Journal of Organic Evolution, 2012, 66, 2138-2149.	1.1	58
82	Heterozygosityâ€“fitness correlations in zebra finches: microsatellite markers can be better than their reputation. Molecular Ecology, 2012, 21, 3237-3249.	2.0	133
83	QTL and quantitative genetic analysis of beak morphology reveals patterns of standing genetic variation in an Estrildid finch. Molecular Ecology, 2012, 21, 3704-3717.	2.0	21
84	Substitution rate variation at human CpG sites correlates with non-CpG divergence, methylation level and GC content. Genome Biology, 2011, 12, R58.	13.9	71
85	Significant Selective Constraint at 4-Fold Degenerate Sites in the Avian Genome and Its Consequence for Detection of Positive Selection. Genome Biology and Evolution, 2011, 3, 1381-1389.	1.1	31
86	A guide to the genomics of ecological speciation in natural animal populations. Ecology Letters, 2011, 14, 9-18.	3.0	57
87	Sex-chromosome evolution: recent progress and the influence of male and female heterogamety. Nature Reviews Genetics, 2011, 12, 157-166.	7.7	204
88	The singing genome. Heredity, 2011, 106, 533-534.	1.2	1
89	Emergence of male-biased genes on the chicken Z-chromosome: Sex-chromosome contrasts between male and female heterogametic systems: Figure 1.. Genome Research, 2011, 21, 2082-2086.	2.4	38
90	Dynamic Evolution of Base Composition: Causes and Consequences in Avian Phylogenomics. Molecular Biology and Evolution, 2011, 28, 2197-2210.	3.5	84

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91	Evolutionary Constraint in Flanking Regions of Avian Genes. Molecular Biology and Evolution, 2011, 28, 2481-2489.	3.5	5
92	Conservation of Neutral Substitution Rate and Substitutional Asymmetries in Mammalian Genes. Genome Biology and Evolution, 2010, 2, 19-28.	1.1	12
93	Obtaining mtDNA genomes from next-generation transcriptome sequencing: A case study on the basal Passerida (Aves: Passeriformes) phylogeny. Molecular Phylogenetics and Evolution, 2010, 57, 466-470.	1.2	36
94	A HIGH-DENSITY SCAN OF THE Z CHROMOSOME IN FICEDULA FLYCATCHERS REVEALS CANDIDATE LOCI FOR DIVERSIFYING SELECTION. Evolution; International Journal of Organic Evolution, 2010, 64, 3461-3475.	1.1	35
95	Ancient DNA reveals traces of Iberian Neolithic and Bronze Age lineages in modern Iberian horses. Molecular Ecology, 2010, 19, 64-78.	2.0	56
96	Comparative genomics based on massive parallel transcriptome sequencing reveals patterns of substitution and selection across 10 bird species. Molecular Ecology, 2010, 19, 266-276.	2.0	105
97	No evidence for Z-chromosome rearrangements between the pied flycatcher and the collared flycatcher as judged by gene-based comparative genetic maps. Molecular Ecology, 2010, 19, 3394-3405.	2.0	13
98	Avian genome evolution: insights from a linkage map of the blue tit (Cyanistes caeruleus). Heredity, 2010, 104, 67-78.	1.2	27
99	Segregation distortion in chicken and the evolutionary consequences of female meiotic drive in birds. Heredity, 2010, 105, 290-298.	1.2	33
100	The genome of a songbird. Nature, 2010, 464, 757-762.	13.7	770
101	Faster-Z Evolution Is Predominantly Due to Genetic Drift. Molecular Biology and Evolution, 2010, 27, 661-670.	3.5	114
102	Copy number variation, chromosome rearrangement, and their association with recombination during avian evolution. Genome Research, 2010, 20, 503-511.	2.4	133
103	The recombination landscape of the zebra finch Taeniopygia guttata genome. Genome Research, 2010, 20, 485-495.	2.4	212
104	Trisomy and triploidy are sources of embryo mortality in the zebra finch. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 2655-2660.	1.2	28
105	Ontogenetic Complexity of Sexual Dimorphism and Sex-Specific Selection. Molecular Biology and Evolution, 2010, 27, 1570-1578.	3.5	99
106	Speciation inFicedulaflycatchers. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 1841-1852.	1.8	89
107	Large-scale noninvasive genetic monitoring of wolverines using scats reveals density dependent adult survival. Biological Conservation, 2010, 143, 113-120.	1.9	51
108	Evolutionary stasis: the stable chromosomes of birds. Trends in Ecology and Evolution, 2010, 25, 283-291.	4.2	245

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109	Molecular evolution of genes in avian genomes. Genome Biology, 2010, 11, R68.	13.9	125
110	Quantification of Adaptive Evolution of Genes Expressed in Avian Brain and the Population Size Effect on the Efficacy of Selection. Molecular Biology and Evolution, 2009, 26, 1073-1079.	3.5	25
111	Nonlinear Dynamics of Nonsynonymous (dN) and Synonymous (dS) Substitution Rates Affects Inference of Selection. Genome Biology and Evolution, 2009, 1, 308-319.	1.1	95
112	Genomic evidence for a large-Z effect. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 361-366.	1.2	55
113	Are sex-biased genes more dispensable?. Biology Letters, 2009, 5, 409-412.	1.0	62
114	The different levels of genetic diversity in sex chromosomes and autosomes. Trends in Genetics, 2009, 25, 278-284.	2.9	123
115	Sex Determination: Two Copies for One Cock. Current Biology, 2009, 19, R909-R910.	1.8	3
116	Identification of conservation units in the European Mergus merganser based on nuclear and mitochondrial DNA markers. Conservation Genetics, 2009, 10, 87-99.	0.8	24
117	Is genetic diversity really higher in large populations?. Journal of Biology, 2009, 8, 41.	2.7	7
118	Population genomics of the inbred Scandinavian wolf. Molecular Ecology, 2009, 18, 1341-1351.	2.0	31
119	All dosage compensation is local: Gene-by-gene regulation of sex-biased expression on the chicken Z chromosome. Heredity, 2009, 102, 312-320.	1.2	125
120	Sex bias in gene expression is not the same as dosage compensation. Heredity, 2009, 103, 434-434.	1.2	19
121	A SELECTION MODEL OF MOLECULAR EVOLUTION INCORPORATING THE EFFECTIVE POPULATION SIZE. Evolution; International Journal of Organic Evolution, 2009, 63, 301-305.	1.1	37
122	SEX-LINKAGE OF SEXUALLY ANTAGONISTIC GENES IS PREDICTED BY FEMALE, BUT NOT MALE, EFFECTS IN BIRDS. Evolution; International Journal of Organic Evolution, 2009, 63, 1464-1472.	1.1	67
123	Genomics of natural bird populations: a geneâ€based set of reference markers evenly spread across the avian genome. Molecular Ecology, 2008, 17, 964-980.	2.0	174
124	Wolf or dog? Genetic identification of predators from saliva collected around bite wounds on prey. Conservation Genetics, 2008, 9, 1275-1279.	0.8	65
125	Adaptive Evolution of Gamete-Recognition Proteins in Birds. Journal of Molecular Evolution, 2008, 67, 488-496.	0.8	18
126	Positive diversifying selection in avian Mx genes. Immunogenetics, 2008, 60, 689-697.	1.2	24

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127	Insertion-deletion polymorphisms (indels) as genetic markers in natural populations. BMC Genetics, 2008, 9, 8.	2.7	116
128	Speciation, introgressive hybridization and nonlinear rate of molecular evolution in flycatchers. Molecular Ecology, 2008, 10, 737-749.	2.0	99
129	Genetic basis of fitness differences in natural populations. Nature, 2008, 452, 169-175.	13.7	304
130	Sequencing goes 454 and takes largeâ€scale genomics into the wild. Molecular Ecology, 2008, 17, 1629-1631.	2.0	111
131	Natural selection in avian protein-coding genes expressed in brain. Molecular Ecology, 2008, 17, 3008-3017.	2.0	51
132	To what extent do microsatellite markers reflect genomeâ€wide genetic diversity in natural populations?. Molecular Ecology, 2008, 17, 3808-3817.	2.0	230
133	Comparative genomics and the study of evolution by natural selection. Molecular Ecology, 2008, 17, 4586-4596.	2.0	133
134	The unique genomic properties of sex-biased genes: Insights from avian microarray data. BMC Genomics, 2008, 9, 148.	1.2	79
135	Sex Chromosomes: Platypus Genome Suggests a Recent Origin for the Human X. Current Biology, 2008, 18, R557-R559.	1.8	17
136	A Gene-Based Genetic Linkage Map of the Collared Flycatcher (Ficedula albicollis) Reveals Extensive Synteny and Gene-Order Conservation During 100 Million Years of Avian Evolution. Genetics, 2008, 179, 1479-1495.	1.2	88
137	The Relationship Between Microsatellite Polymorphism and Recombination Hot Spots in the Human Genome. Molecular Biology and Evolution, 2008, 25, 2579-2587.	3.5	32
138	Genome-wide analysis of microsatellite polymorphism in chicken circumventing the ascertainment bias. Genome Research, 2008, 18, 881-887.	2.4	90
139	The Chicken (Gallus gallus) Z Chromosome Contains at Least Three Nonlinear Evolutionary Strata. Genetics, 2008, 180, 1131-1136.	1.2	88
140	Pleiotropic Constraint Hampers the Resolution of Sexual Antagonism in Vertebrate Gene Expression. American Naturalist, 2008, 171, 35-43.	1.0	143
141	Rapid Evolution of Female-Biased, but Not Male-Biased, Genes Expressed in the Avian Brain. Molecular Biology and Evolution, 2007, 24, 2698-2706.	3.5	72
142	Characteristics, causes and evolutionary consequences of male-biased mutation. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 1-10.	1.2	162
143	Fast-X on the Z: Rapid evolution of sex-linked genes in birds. Genome Research, 2007, 17, 618-624.	2.4	139
144	The Genomic Landscape of Short Insertion and Deletion Polymorphisms in the Chicken (Gallus gallus) Genome: A High Frequency of Deletions in Tandem Duplicates. Genetics, 2007, 176, 1691-1701.	1.2	45

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145	Parallel divergence and degradation of the avian W sex chromosome. Trends in Ecology and Evolution, 2007, 22, 389-391.	4.2	54
146	Molecular evolutionary genomics of birds. Cytogenetic and Genome Research, 2007, 117, 120-130.	0.6	114
147	Paternity and mating system in wolverinesGulo gulo. Wildlife Biology, 2007, 13, 13-30.	0.6	20
148	Faced with inequality: chicken do not have a general dosage compensation of sex-linked genes. BMC Biology, 2007, 5, 40.	1.7	222
149	The evolution of sex-biased genes and sex-biased gene expression. Nature Reviews Genetics, 2007, 8, 689-698.	7.7	796
150	Evolutionary Genomics: A Dinosaur's View of Genome-Size Evolution. Current Biology, 2007, 17, R470-R472.	1.8	6
151	DNA-based monitoring of two newly founded Scandinavian wolverine populations. Conservation Genetics, 2007, 8, 843-852.	0.8	17
152	Bottlenecked but long-lived: high genetic diversity retained in white-tailed eagles upon recovery from population decline. Biology Letters, 2006, 2, 316-319.	1.0	149
153	Levels of linkage disequilibrium in a wild bird population. Biology Letters, 2006, 2, 435-438.	1.0	62
154	NONRANDOM DISTRIBUTION OF GENES WITH SEX-BIASED EXPRESSION IN THE CHICKEN GENOME. Evolution; International Journal of Organic Evolution, 2006, 60, 1945-1951.	1.1	60
155	A test of the multiplex pre-amplification approach in microsatellite genotyping of wolverine faecal DNA. Conservation Genetics, 2006, 7, 289-293.	0.8	16
156	Genetic identification of immigrants to the Scandinavian wolf population. Conservation Genetics, 2006, 7, 225-230.	0.8	19
157	Fast Accumulation of Nonsynonymous Mutations on the Female-Specific W Chromosome in Birds. Journal of Molecular Evolution, 2006, 62, 66-72.	0.8	54
158	Substitution Rate Heterogeneity and the Male Mutation Bias. Journal of Molecular Evolution, 2006, 62, 226-233.	0.8	21
159	Insertion Events of CR1 Retrotransposable Elements Elucidate the Phylogenetic Branching Order in Galliform Birds. Molecular Biology and Evolution, 2006, 24, 338-347.	3.5	76
160	Unequal Contribution of Sexes in the Origin of Dog Breeds. Genetics, 2006, 172, 1121-1128.	1.2	60
161	NONRANDOM DISTRIBUTION OF GENES WITH SEX-BIASED EXPRESSION IN THE CHICKEN GENOME. Evolution; International Journal of Organic Evolution, 2006, 60, 1945.	1.1	12
162	Strong Regional Biases in Nucleotide Substitution in the Chicken Genome. Molecular Biology and Evolution, 2006, 23, 1203-1216.	3.5	91

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163	Genetic Mapping in a Natural Population of Collared Flycatchers (Ficedula albicollis): Conserved Synteny but Gene Order Rearrangements on the Avian Z Chromosome. Genetics, 2006, 174, 377-386.	1.2	93
164	Nonrandom distribution of genes with sex-biased expression in the chicken genome. Evolution; International Journal of Organic Evolution, 2006, 60, 1945-51.	1.1	34
165	SNPs in ecological and conservation studies: a test in the Scandinavian wolf population. Molecular Ecology, 2005, 14, 503-511.	2.0	111
166	Understanding the phylogeographic patterns of European hedgehogs, Erinaceus concolor and E. europaeus using the MHC. Heredity, 2005, 95, 84-90.	1.2	33
167	The dog has its day. Nature, 2005, 438, 745-746.	13.7	14
168	Evolution: Natural Selection in the Evolution of Humans and Chimps. Current Biology, 2005, 15, R919-R922.	1.8	9
169	Genes of domestic mammals augmented by backcrossing with wild ancestors. Trends in Genetics, 2005, 21, 214-218.	2.9	121
170	Microsatellite genotyping of DNA isolated from claws left on tanned carnivore hides. International Journal of Legal Medicine, 2005, 119, 370-373.	1.2	18
171	Cattle domestication in the Near East was followed by hybridization with aurochs bulls in Europe. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 2345-2351.	1.2	151
172	Prehistoric contacts over the Straits of Gibraltar indicated by genetic analysis of Iberian Bronze Age cattle. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 8431-8435.	3.3	109
173	Male-Driven Biased Gene Conversion Governs the Evolution of Base Composition in Human Alu Repeats. Molecular Biology and Evolution, 2005, 22, 1468-1474.	3.5	64
174	Gene Conversion Drives the Evolution of HINTW, an Ampliconic Gene on the Female-Specific Avian W Chromosome. Molecular Biology and Evolution, 2005, 22, 1992-1999.	3.5	65
175	Comparison of the chicken and turkey genomes reveals a higher rate of nucleotide divergence on microchromosomes than macrochromosomes. Genome Research, 2005, 15, 120-125.	2.4	138
176	The avian genome uncovered. Trends in Ecology and Evolution, 2005, 20, 180-186.	4.2	70
177	Chicken W: A genetically uniform chromosome in a highly variable genome. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15967-15969.	3.3	74
178	A temporal analysis shows major histocompatibility complex loci in the Scandinavian wolf population are consistent with neutral evolution. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, 2283-2291.	1.2	47
179	Evolutionary Strata on the Chicken Z Chromosome: Implications for Sex Chromosome Evolution. Genetics, 2004, 167, 367-376.	1.2	192
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