

Matthew W Hahn

List of Publications by Year in descending order

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Version: 2024-02-01

157
papers

23,521
citations

14614

66
h-index

10424

139
g-index

199
all docs

199
docs citations

199
times ranked

23774
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
2	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
3	The Evolution of Transcriptional Regulation in Eukaryotes. <i>Molecular Biology and Evolution</i> , 2003, 20, 1377-1419.	3.5	1,034
4	Reanalysis suggests that genomic islands of speciation are due to reduced diversity, not reduced gene flow. <i>Molecular Ecology</i> , 2014, 23, 3133-3157.	2.0	937
5	Sex Determination: Why So Many Ways of Doing It?. <i>PLoS Biology</i> , 2014, 12, e1001899.	2.6	916
6	Estimating Gene Gain and Loss Rates in the Presence of Error in Genome Assembly and Annotation Using CAFE 3. <i>Molecular Biology and Evolution</i> , 2013, 30, 1987-1997.	3.5	650
7	Genomic Islands of Speciation in <i>Anopheles gambiae</i> . <i>PLoS Biology</i> , 2005, 3, e285.	2.6	637
8	Population Genomics: Whole-Genome Analysis of Polymorphism and Divergence in <i>Drosophila simulans</i> . <i>PLoS Biology</i> , 2007, 5, e310.	2.6	583
9	Comparative Genomics of Centrality and Essentiality in Three Eukaryotic Protein-Interaction Networks. <i>Molecular Biology and Evolution</i> , 2005, 22, 803-806.	3.5	582
10	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	13.7	573
11	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541
12	Extensive introgression in a malaria vector species complex revealed by phylogenomics. <i>Science</i> , 2015, 347, 1258524.	6.0	527
13	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258522.	6.0	492
14	How reticulated are species?. <i>BioEssays</i> , 2016, 38, 140-149.	1.2	449
15	Convergent evolution of the genomes of marine mammals. <i>Nature Genetics</i> , 2015, 47, 272-275.	9.4	392
16	Phylogenomics Reveals Three Sources of Adaptive Variation during a Rapid Radiation. <i>PLoS Biology</i> , 2016, 14, e1002379.	2.6	364
17	New Methods to Calculate Concordance Factors for Phylogenomic Datasets. <i>Molecular Biology and Evolution</i> , 2020, 37, 2727-2733.	3.5	354
18	Distinguishing Among Evolutionary Models for the Maintenance of Gene Duplicates. <i>Journal of Heredity</i> , 2009, 100, 605-617.	1.0	350

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19	Genomic Variation in Natural Populations of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2012, 192, 533-598.	1.2	325
20	Gene Family Evolution across 12 <i>Drosophila</i> Genomes. <i>PLoS Genetics</i> , 2007, 3, e197.	1.5	320
21	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	13.7	320
22	The Evolution of Mammalian Gene Families. <i>PLoS ONE</i> , 2006, 1, e85.	1.1	285
23	Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17230-17235.	3.3	281
24	Extensive Error in the Number of Genes Inferred from Draft Genome Assemblies. <i>PLoS Computational Biology</i> , 2014, 10, e1003998.	1.5	262
25	Estimating the tempo and mode of gene family evolution from comparative genomic data. <i>Genome Research</i> , 2005, 15, 1153-1160.	2.4	259
26	Detection and Polarization of Introgression in a Five-Taxon Phylogeny. <i>Systematic Biology</i> , 2015, 64, 651-662.	2.7	244
27	The life and death of gene families. <i>BioEssays</i> , 2009, 31, 29-39.	1.2	242
28	CAFE 5 models variation in evolutionary rates among gene families. <i>Bioinformatics</i> , 2021, 36, 5516-5518.	1.8	218
29	Rates and Genomic Consequences of Spontaneous Mutational Events in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2013, 194, 937-954.	1.2	210
30	Disentangling the Effects of Demography and Selection in Human History. <i>Molecular Biology and Evolution</i> , 2004, 22, 63-73.	3.5	200
31	TOWARD A SELECTION THEORY OF MOLECULAR EVOLUTION. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 255-265.	1.1	194
32	Testing the Ortholog Conjecture with Comparative Functional Genomic Data from Mammals. <i>PLoS Computational Biology</i> , 2011, 7, e1002073.	1.5	185
33	The Neutral Theory in Light of Natural Selection. <i>Molecular Biology and Evolution</i> , 2018, 35, 1366-1371.	3.5	180
34	Irrational exuberance for resolved species trees. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 7-17.	1.1	177
35	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , 2020, 18, 1.	1.7	177
36	Adaptive evolution of young gene duplicates in mammals. <i>Genome Research</i> , 2009, 19, 859-867.	2.4	176

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37	Regular rates of popular culture change reflect random copying. <i>Evolution and Human Behavior</i> , 2007, 28, 151-158.	1.4	166
38	Ecological Genomics of <i>Anopheles gambiae</i> Along a Latitudinal Cline: A Population-Resequencing Approach. <i>Genetics</i> , 2012, 190, 1417-1432.	1.2	157
39	Ancient and Recent Positive Selection Transformed Opioid cis-Regulation in Humans. <i>PLoS Biology</i> , 2005, 3, e387.	2.6	155
40	Gene Tree Discordance Causes Apparent Substitution Rate Variation. <i>Systematic Biology</i> , 2016, 65, 711-721.	2.7	153
41	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020, 21, 15.	3.8	150
42	Revisiting classic clines in <i>Drosophila melanogaster</i> in the age of genomics. <i>Trends in Genetics</i> , 2015, 31, 434-444.	2.9	148
43	Accelerated Rate of Gene Gain and Loss in Primates. <i>Genetics</i> , 2007, 177, 1941-1949.	1.2	146
44	Molecular Evolution in Large Genetic Networks: Does Connectivity Equal Constraint?. <i>Journal of Molecular Evolution</i> , 2004, 58, 203-211.	0.8	138
45	Pervasive Multinucleotide Mutational Events in Eukaryotes. <i>Current Biology</i> , 2011, 21, 1051-1054.	1.8	137
46	Bias in phylogenetic tree reconciliation methods: implications for vertebrate genome evolution. <i>Genome Biology</i> , 2007, 8, R141.	13.9	133
47	The g-value paradox. <i>Evolution & Development</i> , 2002, 4, 73-75.	1.1	129
48	Gene copy-number polymorphism in nature. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 3213-3221.	1.2	125
49	Positive Selection on a Human-Specific Transcription Factor Binding Site Regulating IL4 Expression. <i>Current Biology</i> , 2003, 13, 2118-2123.	1.8	124
50	Multinucleotide mutations cause false inferences of lineage-specific positive selection. <i>Nature Ecology and Evolution</i> , 2018, 2, 1280-1288.	3.4	121
51	Genomic islands of speciation or genomic islands and speciation?. <i>Molecular Ecology</i> , 2010, 19, 848-850.	2.0	117
52	Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. <i>Nature Ecology and Evolution</i> , 2018, 2, 669-679.	3.4	117
53	The comparative genomics and complex population history of <i>Papio</i> baboons. <i>Science Advances</i> , 2019, 5, eaau6947.	4.7	115
54	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). <i>Genome Research</i> , 2015, 25, 1921-1933.	2.4	114

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55	Why Concatenation Fails Near the Anomaly Zone. <i>Systematic Biology</i> , 2018, 67, 158-169.	2.7	109
56	Determining the Null Model for Detecting Adaptive Convergence from Genomic Data: A Case Study using Echolocating Mammals. <i>Molecular Biology and Evolution</i> , 2015, 32, 1232-1236.	3.5	102
57	Soft Shoulders Ahead: Spurious Signatures of Soft and Partial Selective Sweeps Result from Linked Hard Sweeps. <i>Genetics</i> , 2015, 200, 267-284.	1.2	98
58	Reticulate evolutionary history and extensive introgression in mosquito species revealed by phylogenetic network analysis. <i>Molecular Ecology</i> , 2016, 25, 2361-2372.	2.0	98
59	Reproductive Longevity Predicts Mutation Rates in Primates. <i>Current Biology</i> , 2018, 28, 3193-3197.e5.	1.8	94
60	Radical remodeling of the Y chromosome in a recent radiation of malaria mosquitoes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2114-23.	3.3	92
61	MORE ACCURATE PHYLOGENIES INFERRED FROM LOW-RECOMBINATION REGIONS IN THE PRESENCE OF INCOMPLETE LINEAGE SORTING. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2376-2384.	1.1	90
62	Gene Copy-Number Polymorphism Caused by Retrotransposition in Humans. <i>PLoS Genetics</i> , 2013, 9, e1003242.	1.5	88
63	Speciation as a sieve for ancestral polymorphism. <i>Molecular Ecology</i> , 2017, 26, 5362-5368.	2.0	88
64	A Complex Suite of Forces Drives Gene Traffic from <i>Drosophila</i> X Chromosomes. <i>Genome Biology and Evolution</i> , 2009, 1, 176-188.	1.1	87
65	The Effects of Selection Against Spurious Transcription Factor Binding Sites. <i>Molecular Biology and Evolution</i> , 2003, 20, 901-906.	3.5	85
66	Sooty mangabey genome sequence provides insight into AIDS resistance in a natural SIV host. <i>Nature</i> , 2018, 553, 77-81.	13.7	81
67	Phylogenomic approaches to detecting and characterizing introgression. <i>Genetics</i> , 2022, 220, .	1.2	79
68	Powerful methods for detecting introgressed regions from population genomic data. <i>Molecular Ecology</i> , 2016, 25, 2387-2397.	2.0	78
69	Positive Selection on MMP3 Regulation Has Shaped Heart Disease Risk. <i>Current Biology</i> , 2004, 14, 1531-1539.	1.8	76
70	Localization of Candidate Regions Maintaining a Common Polymorphic Inversion (2La) in <i>Anopheles gambiae</i> . <i>PLoS Genetics</i> , 2007, 3, e217.	1.5	75
71	Gene-Tree Reconciliation with MUL-Trees to Resolve Polyploidy Events. <i>Systematic Biology</i> , 2017, 66, 1007-1018.	2.7	73
72	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. <i>PLoS Biology</i> , 2020, 18, e3000954.	2.6	73

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73	Coding Sequence Divergence Between Two Closely Related Plant Species: <i>Arabidopsis thaliana</i> and <i>Brassica rapa</i> ssp. <i>pekinensis</i> . <i>Journal of Molecular Evolution</i> , 2002, 54, 746-753.	0.8	69
74	Very Few RNA and DNA Sequence Differences in the Human Transcriptome. <i>PLoS ONE</i> , 2011, 6, e25842.	1.1	69
75	Distinguishing Between Selection and Population Expansion in an Experimental Lineage of Bacteriophage T7. <i>Genetics</i> , 2002, 161, 11-20.	1.2	65
76	Locus- and Population-Specific Selection and Differentiation between Incipient Species of <i>Anopheles gambiae</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 2132-2138.	3.5	60
77	No Excess Gene Movement Is Detected off the Avian or Lepidopteran Z Chromosome. <i>Genome Biology and Evolution</i> , 2011, 3, 1381-1390.	1.1	60
78	Dissecting the basis of novel trait evolution in a radiation with widespread phylogenetic discordance. <i>Molecular Ecology</i> , 2018, 27, 3301-3316.	2.0	59
79	Female-biased gene expression in the malaria mosquito <i>Anopheles gambiae</i> . <i>Current Biology</i> , 2005, 15, R192-R193.	1.8	58
80	Genome-wide analysis of retrogene polymorphisms in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2011, 21, 2087-2095.	2.4	58
81	Gene Tree Discordance Can Generate Patterns of Diminishing Convergence over Time. <i>Molecular Biology and Evolution</i> , 2016, 33, 3299-3307.	3.5	58
82	Genus-Wide Characterization of Bumblebee Genomes Provides Insights into Their Evolution and Variation in Ecological and Behavioral Traits. <i>Molecular Biology and Evolution</i> , 2021, 38, 486-501.	3.5	58
83	Similar Efficacies of Selection Shape Mitochondrial and Nuclear Genes in Both <i>Drosophila melanogaster</i> and <i>Homo sapiens</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2165-2176.	0.8	54
84	Genome-Wide Estimates of Transposable Element Insertion and Deletion Rates in <i>Drosophila Melanogaster</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1329-1340.	1.1	54
85	Retrogenes Reveal the Direction of Sex-Chromosome Evolution in Mosquitoes. <i>Genetics</i> , 2010, 186, 763-766.	1.2	53
86	New Approaches for Inferring Phylogenies in the Presence of Paralogs. <i>Trends in Genetics</i> , 2021, 37, 174-187.	2.9	53
87	AGOUTI: improving genome assembly and annotation using transcriptome data. <i>GigaScience</i> , 2016, 5, 31.	3.3	52
88	A Three-Sample Test for Introgression. <i>Molecular Biology and Evolution</i> , 2019, 36, 2878-2882.	3.5	52
89	Sex Chromosomes Evolved from Independent Ancestral Linkage Groups in Winged Insects. <i>Molecular Biology and Evolution</i> , 2012, 29, 1645-1653.	3.5	51
90	Association mapping desiccation resistance within chromosomal inversions in the African malaria vector <i>Anopheles gambiae</i> . <i>Molecular Ecology</i> , 2019, 28, 1333-1342.	2.0	51

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91	The Evolution of the <i>Anopheles</i> 16 Genomes Project. G3: Genes, Genomes, Genetics, 2013, 3, 1191-1194.	0.8	49
92	Quantifying the risk of hemiplasy in phylogenetic inference. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12787-12792.	3.3	49
93	Paternal age in rhesus macaques is positively associated with germline mutation accumulation but not with measures of offspring sociability. Genome Research, 2020, 30, 826-834.	2.4	48
94	Systems genetic analysis of inversion polymorphisms in the malaria mosquito <i>Anopheles gambiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7005-E7014.	3.3	47
95	The ortholog conjecture revisited: the value of orthologs and paralogs in function prediction. Bioinformatics, 2020, 36, i219-i226.	1.8	47
96	Population Genetic and Phylogenetic Evidence for Positive Selection on Regulatory Mutations at the Factor VII Locus in Humans Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY493422, AY493423, AY493424, AY493425, AY493426, AY493427, AY493428, AY493429, AY493430, AY493431, AY493432, AY493433.. Genetics, 2004, 167, 867-877.	1.2	46
97	Differential gene expression in incipient species of <i>Anopheles gambiae</i> . Molecular Ecology, 2008, 17, 2491-2504.	2.0	46
98	Detecting natural selection on cis-regulatory DNA. Genetica, 2006, 129, 7-18.	0.5	45
99	A multispecies coalescent model for quantitative traits. ELife, 2018, 7, .	2.8	44
100	Minimal Effect of Ectopic Gene Conversion Among Recent Duplicates in Four Mammalian Genomes. Genetics, 2009, 182, 615-622.	1.2	43
101	The Limited Contribution of Reciprocal Gene Loss to Increased Speciation Rates Following Whole-Genome Duplication. American Naturalist, 2015, 185, 70-86.	1.0	40
102	The Timing and Direction of Introgression Under the Multispecies Network Coalescent. Genetics, 2019, 211, 1059-1073.	1.2	38
103	The Mutationathon highlights the importance of reaching standardization in estimates of pedigree-based germline mutation rates. ELife, 2022, 11, .	2.8	38
104	Divergent transcriptional response to thermal stress by <i>Anopheles gambiae</i> larvae carrying alternative arrangements of inversion 2La. Molecular Ecology, 2011, 20, 2567-2580.	2.0	37
105	Parallel Evolution of Copy-Number Variation across Continents in <i>Drosophila melanogaster</i> . Molecular Biology and Evolution, 2016, 33, 1308-1316.	3.5	37
106	Sequencing, Assembling, and Correcting Draft Genomes Using Recombinant Populations. G3: Genes, Genomes, Genetics, 2014, 4, 669-679.	0.8	36
107	Gene Conversion Among Paralogs Results in Moderate False Detection of Positive Selection Using Likelihood Methods. Journal of Molecular Evolution, 2009, 68, 679-687.	0.8	34
108	No evidence for biased co-transmission of speciation islands in <i>Anopheles gambiae</i> . Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 374-384.	1.8	34

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109	Molecular mechanisms of postmating prezygotic reproductive isolation uncovered by transcriptome analysis. <i>Molecular Ecology</i> , 2016, 25, 2592-2608.	2.0	33
110	The perils of intralocus recombination for inferences of molecular convergence. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180244.	1.8	33
111	Genome-wide patterns of regulatory divergence revealed by introgression lines. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 696-706.	1.1	32
112	The Human Mutation Rate Is Increasing, Even As It Slows. <i>Molecular Biology and Evolution</i> , 2014, 31, 253-257.	3.5	31
113	Interlocus gene conversion events introduce deleterious mutations into at least 1% of human genes associated with inherited disease. <i>Genome Research</i> , 2012, 22, 429-435.	2.4	30
114	Nonallelic Gene Conversion in the Genus <i>Drosophila</i> . <i>Genetics</i> , 2010, 185, 95-103.	1.2	29
115	Three new genome assemblies support a rapid radiation in <i>Musa acuminata</i> (wild banana). <i>Genome Biology and Evolution</i> , 2018, 10, 3129-3140.	1.1	29
116	Radiation with reticulation marks the origin of a major malaria vector. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31583-31590.	3.3	29
117	Gene expression divergence between malaria vector sibling species <i>Anopheles gambiae</i> and <i>An. coluzzii</i> from rural and urban Yaoundé, Cameroon. <i>Molecular Ecology</i> , 2014, 23, 2242-2259.	2.0	28
118	Lower Linkage Disequilibrium at CNVs is due to Both Recurrent Mutation and Transposing Duplications. <i>Molecular Biology and Evolution</i> , 2010, 27, 103-111.	3.5	26
119	Species Tree Inference Methods Intended to Deal with Incomplete Lineage Sorting Are Robust to the Presence of Paralogs. <i>Systematic Biology</i> , 2022, 71, 367-381.	2.7	26
120	Accurate Inference and Estimation in Population Genomics. <i>Molecular Biology and Evolution</i> , 2006, 23, 911-918.	3.5	25
121	Very Low Rate of Gene Conversion in the Yeast Genome. <i>Molecular Biology and Evolution</i> , 2012, 29, 3817-3826.	3.5	25
122	Genomic evidence of gene flow during reinforcement in Texas <i>Phlox</i> . <i>Molecular Ecology</i> , 2017, 26, 2317-2330.	2.0	25
123	Determining the probability of hemiplasy in the presence of incomplete lineage sorting and introgression. <i>ELife</i> , 2020, 9, .	2.8	25
124	De novo Mutations in Domestic Cat are Consistent with an Effect of Reproductive Longevity on Both the Rate and Spectrum of Mutations. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	22
125	Inferring the History of Interchromosomal Gene Transposition in <i>Drosophila</i> Using n -Dimensional Parsimony. <i>Genetics</i> , 2012, 190, 813-825.	1.2	21
126	Noncoding Sequences Near Duplicated Genes Evolve Rapidly. <i>Genome Biology and Evolution</i> , 2010, 2, 518-533.	1.1	20

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127	The effects of increasing the number of taxa on inferences of molecular convergence. <i>Genome Biology and Evolution</i> , 2017, 9, eww306.	1.1	20
128	Codon bias and selection on single genomes. <i>Nature</i> , 2005, 433, E5-E6.	13.7	18
129	Evaluating methods to visualize patterns of genetic differentiation on a landscape. <i>Molecular Ecology Resources</i> , 2018, 18, 448-460.	2.2	17
130	Referee: Reference Assembly Quality Scores. <i>Genome Biology and Evolution</i> , 2019, 11, 1483-1486.	1.1	14
131	Does a complex life cycle affect adaptation to environmental change? Genome-informed insights for characterizing selection across complex life cycle. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20212122.	1.2	14
132	Patterns of transposable element variation and clinality in <i>Drosophila</i> . <i>Molecular Ecology</i> , 2019, 28, 1523-1536.	2.0	13
133	All Human-Specific Gene Losses Are Present in the Genome as Pseudogenes. <i>Journal of Computational Biology</i> , 2009, 16, 1419-1427.	0.8	12
134	Origins and Long-Term Patterns of Copy-Number Variation in Rhesus Macaques. <i>Molecular Biology and Evolution</i> , 2021, 38, 1460-1471.	3.5	11
135	Abundant genetic variation in transcript level during early <i>Drosophila</i> development. <i>Evolution & Development</i> , 2008, 10, 683-689.	1.1	10
136	Speciation genes are more likely to have discordant gene trees. <i>Evolution Letters</i> , 2018, 2, 281-296.	1.6	10
137	The Frequency and Topology of Pseudoorthologs. <i>Systematic Biology</i> , 2022, 71, 649-659.	2.7	10
138	The strength of transcription-factor binding modulates co-variation in transcriptional networks. <i>Trends in Genetics</i> , 2010, 26, 51-53.	2.9	9
139	The effects of introgression across thousands of quantitative traits revealed by gene expression in wild tomatoes. <i>PLoS Genetics</i> , 2021, 17, e1009892.	1.5	9
140	Transcriptomic analysis links gene expression to unilateral pollen-pistil reproductive barriers. <i>BMC Plant Biology</i> , 2017, 17, 81.	1.6	8
141	Distinct error rates for reference and nonreference genotypes estimated by pedigree analysis. <i>Genetics</i> , 2021, 217, 1-10.	1.2	8
142	The Potential for a Released Autosomal X-Shredder Becoming a Driving-Y Chromosome and Invasively Suppressing Wild Populations of Malaria Mosquitoes. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 752253.	2.0	8
143	A new class of metrics for learning on real-valued and structured data. <i>Data Mining and Knowledge Discovery</i> , 2019, 33, 995-1016.	2.4	7
144	Using all Gene Families Vastly Expands Data Available for Phylogenomic Inference. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7

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145	DETECTING HIGHLY DIFFERENTIATED COPY-NUMBER VARIANTS FROM POOLED POPULATION SEQUENCING. , 2012, , .		6
146	IDENTIFYING PARENT-DAUGHTER RELATIONSHIPS AMONG DUPLICATED GENES. , 2008, , .		5
147	Spread of selfâ€compatibility constrained by an intrapopulation crossing barrier. <i>New Phytologist</i> , 2021, 231, 878-891.	3.5	4
148	Proteomic Evidence for In-Frame and Out-of-Frame Alternatively Spliced Isoforms in Human and Mouse. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1284-1289.	1.9	3
149	The sequencing and interpretation of the genome obtained from a Serbian individual. <i>PLoS ONE</i> , 2018, 13, e0208901.	1.1	3
150	Inferring the Genetic Basis of Sex Determination from the Genome of a Dioecious Nightshade. <i>Molecular Biology and Evolution</i> , 2021, 38, 2946-2957.	3.5	2
151	Localization of Candidate Regions Maintaining a Common Polymorphic Inversion (2La) in <i>Anopheles gambiae</i> . <i>PLoS Genetics</i> , 2005, preprint, e217.	1.5	1
152	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
153	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
154	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
155	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
156	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
157	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0