

# Matthew W Hahn

## List of Publications by Year in descending order

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157  
papers

23,521  
citations

14614

66  
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10424

139  
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199  
docs citations

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times ranked

23774  
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#	ARTICLE	IF	CITATIONS
1	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
2	Phylogenomic approaches to detecting and characterizing introgression. <i>Genetics</i> , 2022, 220, .	1.2	79
3	The Mutationathon highlights the importance of reaching standardization in estimates of pedigree-based germline mutation rates. <i>ELife</i> , 2022, 11, .	2.8	38
4	The Frequency and Topology of Pseudoorthologs. <i>Systematic Biology</i> , 2022, 71, 649-659.	2.7	10
5	Using all Gene Families Vastly Expands Data Available for Phylogenomic Inference. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
6	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
7	New Approaches for Inferring Phylogenies in the Presence of Paralogs. <i>Trends in Genetics</i> , 2021, 37, 174-187.	2.9	53
8	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
9	CAFE 5 models variation in evolutionary rates among gene families. <i>Bioinformatics</i> , 2021, 36, 5516-5518.	1.8	218
10	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
11	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
12	Spread of self-incompatibility constrained by an intrapopulation crossing barrier. <i>New Phytologist</i> , 2021, 231, 878-891.	3.5	4
13	Distinct error rates for reference and nonreference genotypes estimated by pedigree analysis. <i>Genetics</i> , 2021, 217, 1-10.	1.2	8
14	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
15	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
16	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
17	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , 2020, 18, 1.	1.7	177
18	The ortholog conjecture revisited: the value of orthologs and paralogs in function prediction. <i>Bioinformatics</i> , 2020, 36, i219-i226.	1.8	47

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19	New Methods to Calculate Concordance Factors for Phylogenomic Datasets. <i>Molecular Biology and Evolution</i> , 2020, 37, 2727-2733.	3.5	354
20	Paternal age in rhesus macaques is positively associated with germline mutation accumulation but not with measures of offspring sociability. <i>Genome Research</i> , 2020, 30, 826-834.	2.4	48
21	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020, 21, 15.	3.8	150
22	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
23	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. <i>PLoS Biology</i> , 2020, 18, e3000954.	2.6	73
24	Determining the probability of hemiplasy in the presence of incomplete lineage sorting and introgression. <i>ELife</i> , 2020, 9, .	2.8	25
25	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
26	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
27	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
28	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
29	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
30	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
31	A Three-Sample Test for Introgression. <i>Molecular Biology and Evolution</i> , 2019, 36, 2878-2882.	3.5	52
32	The comparative genomics and complex population history of <i>Papio</i> baboons. <i>Science Advances</i> , 2019, 5, eaau6947.	4.7	115
33	The Timing and Direction of Introgression Under the Multispecies Network Coalescent. <i>Genetics</i> , 2019, 211, 1059-1073.	1.2	38
34	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
35	Referee: Reference Assembly Quality Scores. <i>Genome Biology and Evolution</i> , 2019, 11, 1483-1486.	1.1	14
36	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

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37	Patterns of transposable element variation and clinality in <i>Drosophila</i> . <i>Molecular Ecology</i> , 2019, 28, 1523-1536.	2.0	13
38	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
39	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
40	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
41	Evaluating methods to visualize patterns of genetic differentiation on a landscape. <i>Molecular Ecology Resources</i> , 2018, 18, 448-460.	2.2	17
42	Sooty mangabey genome sequence provides insight into AIDS resistance in a natural SIV host. <i>Nature</i> , 2018, 553, 77-81.	13.7	81
43	The Neutral Theory in Light of Natural Selection. <i>Molecular Biology and Evolution</i> , 2018, 35, 1366-1371.	3.5	180
44	Why Concatenation Fails Near the Anomaly Zone. <i>Systematic Biology</i> , 2018, 67, 158-169.	2.7	109
45	The sequencing and interpretation of the genome obtained from a Serbian individual. <i>PLoS ONE</i> , 2018, 13, e0208901.	1.1	3
46	Quantifying the risk of hemiplasy in phylogenetic inference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12787-12792.	3.3	49
47	Reproductive Longevity Predicts Mutation Rates in Primates. <i>Current Biology</i> , 2018, 28, 3193-3197.e5.	1.8	94
48	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
49	Speciation genes are more likely to have discordant gene trees. <i>Evolution Letters</i> , 2018, 2, 281-296.	1.6	10
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	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
52	Systems genetic analysis of inversion polymorphisms in the malaria mosquito <i>Anopheles gambiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7005-E7014.	3.3	47
53	A multispecies coalescent model for quantitative traits. <i>ELife</i> , 2018, 7, .	2.8	44
54	Genomic evidence of gene flow during reinforcement in Texas <i>Phlox</i> . <i>Molecular Ecology</i> , 2017, 26, 2317-2330.	2.0	25

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55	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
56	Gene-Tree Reconciliation with MUL-Trees to Resolve Polyploidy Events. <i>Systematic Biology</i> , 2017, 66, 1007-1018.	2.7	73
57	The effects of increasing the number of taxa on inferences of molecular convergence. <i>Genome Biology and Evolution</i> , 2017, 9, evw306.	1.1	20
58	Speciation as a sieve for ancestral polymorphism. <i>Molecular Ecology</i> , 2017, 26, 5362-5368.	2.0	88
59	Transcriptomic analysis links gene expression to unilateral pollen-pistil reproductive barriers. <i>BMC Plant Biology</i> , 2017, 17, 81.	1.6	8
60	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
61	Molecular mechanisms of postmating prezygotic reproductive isolation uncovered by transcriptome analysis. <i>Molecular Ecology</i> , 2016, 25, 2592-2608.	2.0	33
62	Powerful methods for detecting introgressed regions from population genomic data. <i>Molecular Ecology</i> , 2016, 25, 2387-2397.	2.0	78
63	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
64	How reticulated are species?. <i>BioEssays</i> , 2016, 38, 140-149.	1.2	449
65	Irrational exuberance for resolved species trees. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 7-17.	1.1	177
66	Gene Tree Discordance Can Generate Patterns of Diminishing Convergence over Time. <i>Molecular Biology and Evolution</i> , 2016, 33, 3299-3307.	3.5	58
67	AGOUTI: improving genome assembly and annotation using transcriptome data. <i>GigaScience</i> , 2016, 5, 31.	3.3	52
68	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
69	Parallel Evolution of Copy-Number Variation across Continents in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 1308-1316.	3.5	37
70	Gene Tree Discordance Causes Apparent Substitution Rate Variation. <i>Systematic Biology</i> , 2016, 65, 711-721.	2.7	153
71	Phylogenomics Reveals Three Sources of Adaptive Variation during a Rapid Radiation. <i>PLoS Biology</i> , 2016, 14, e1002379.	2.6	364
72	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

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73	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
74	The Limited Contribution of Reciprocal Gene Loss to Increased Speciation Rates Following Whole-Genome Duplication. <i>American Naturalist</i> , 2015, 185, 70-86.	1.0	40
75	Convergent evolution of the genomes of marine mammals. <i>Nature Genetics</i> , 2015, 47, 272-275.	9.4	392
76	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
77	Detection and Polarization of Introgression in a Five-Taxon Phylogeny. <i>Systematic Biology</i> , 2015, 64, 651-662.	2.7	244
78	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
79	The genome of the vervet ( <i>Chlorocebus aethiops sabaeus</i> ). <i>Genome Research</i> , 2015, 25, 1921-1933.	2.4	114
80	Extensive introgression in a malaria vector species complex revealed by phylogenomics. <i>Science</i> , 2015, 347, 1258524.	6.0	527
81	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258522.	6.0	492
82	Extensive Error in the Number of Genes Inferred from Draft Genome Assemblies. <i>PLoS Computational Biology</i> , 2014, 10, e1003998.	1.5	262
83	Sex Determination: Why So Many Ways of Doing It?. <i>PLoS Biology</i> , 2014, 12, e1001899.	2.6	916
84	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
85	The Human Mutation Rate Is Increasing, Even As It Slows. <i>Molecular Biology and Evolution</i> , 2014, 31, 253-257.	3.5	31
86	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
87	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
88	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	13.7	320
89	Sequencing, Assembling, and Correcting Draft Genomes Using Recombinant Populations. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 669-679.	0.8	36
90	Rates and Genomic Consequences of Spontaneous Mutational Events in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2013, 194, 937-954.	1.2	210

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91	Gene Copy-Number Polymorphism Caused by Retrotransposition in Humans. <i>PLoS Genetics</i> , 2013, 9, e1003242.	1.5	88
92	The Evolution of the <i>Anopheles</i> 16 Genomes Project. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1191-1194.	0.8	49
93	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
94	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
95	No evidence for biased co-transmission of speciation islands in <i>Anopheles gambiae</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 374-384.	1.8	34
96	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
97	Inferring the History of Interchromosomal Gene Transposition in <i>Drosophila</i> Using <i>n</i> -Dimensional Parsimony. <i>Genetics</i> , 2012, 190, 813-825.	1.2	21
98	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
99	Very Low Rate of Gene Conversion in the Yeast Genome. <i>Molecular Biology and Evolution</i> , 2012, 29, 3817-3826.	3.5	25
100	DETECTING HIGHLY DIFFERENTIATED COPY-NUMBER VARIANTS FROM POOLED POPULATION SEQUENCING. , 2012, , .		6
101	Genomic Variation in Natural Populations of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2012, 192, 533-598.	1.2	325
102	Sex Chromosomes Evolved from Independent Ancestral Linkage Groups in Winged Insects. <i>Molecular Biology and Evolution</i> , 2012, 29, 1645-1653.	3.5	51
103	Very Few RNA and DNA Sequence Differences in the Human Transcriptome. <i>PLoS ONE</i> , 2011, 6, e25842.	1.1	69
104	Divergent transcriptional response to thermal stress by <i>Anopheles gambiae</i> larvae carrying alternative arrangements of inversion 2La. <i>Molecular Ecology</i> , 2011, 20, 2567-2580.	2.0	37
105	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541
106	Pervasive Multinucleotide Mutational Events in Eukaryotes. <i>Current Biology</i> , 2011, 21, 1051-1054.	1.8	137
107	Genome-wide analysis of retrogene polymorphisms in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2011, 21, 2087-2095.	2.4	58
108	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

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109	Testing the Ortholog Conjecture with Comparative Functional Genomic Data from Mammals. <i>PLoS Computational Biology</i> , 2011, 7, e1002073.	1.5	185
110	The strength of transcription-factor binding modulates co-variation in transcriptional networks. <i>Trends in Genetics</i> , 2010, 26, 51-53.	2.9	9
111	Genomic islands <i>of</i> speciation or genomic islands <i>and</i> speciation?. <i>Molecular Ecology</i> , 2010, 19, 848-850.	2.0	117
112	Retrogenes Reveal the Direction of Sex-Chromosome Evolution in Mosquitoes. <i>Genetics</i> , 2010, 186, 763-766.	1.2	53
113	Gene copy-number polymorphism in nature. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 3213-3221.	1.2	125
114	Nonallelic Gene Conversion in the Genus <i>Drosophila</i> . <i>Genetics</i> , 2010, 185, 95-103.	1.2	29
115	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
116	Noncoding Sequences Near Duplicated Genes Evolve Rapidly. <i>Genome Biology and Evolution</i> , 2010, 2, 518-533.	1.1	20
117	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
118	Adaptive evolution of young gene duplicates in mammals. <i>Genome Research</i> , 2009, 19, 859-867.	2.4	176
119	Minimal Effect of Ectopic Gene Conversion Among Recent Duplicates in Four Mammalian Genomes. <i>Genetics</i> , 2009, 182, 615-622.	1.2	43
120	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
121	Distinguishing Among Evolutionary Models for the Maintenance of Gene Duplicates. <i>Journal of Heredity</i> , 2009, 100, 605-617.	1.0	350
122	The life and death of gene families. <i>BioEssays</i> , 2009, 31, 29-39.	1.2	242
123	Gene Conversion Among Paralogs Results in Moderate False Detection of Positive Selection Using Likelihood Methods. <i>Journal of Molecular Evolution</i> , 2009, 68, 679-687.	0.8	34
124	TOWARD A SELECTION THEORY OF MOLECULAR EVOLUTION. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 255-265.	1.1	194
125	Abundant genetic variation in transcript level during early <i>Drosophila</i> development. <i>Evolution &amp; Development</i> , 2008, 10, 683-689.	1.1	10
126	Differential gene expression in incipient species of <i>Anopheles gambiae</i> . <i>Molecular Ecology</i> , 2008, 17, 2491-2504.	2.0	46



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127	IDENTIFYING PARENT-DAUGHTER RELATIONSHIPS AMONG DUPLICATED GENES. , 2008, , .		5
128	Population Genomics: Whole-Genome Analysis of Polymorphism and Divergence in <i>Drosophila simulans</i> . <i>PLoS Biology</i> , 2007, 5, e310.	2.6	583
129	Gene Family Evolution across 12 <i>Drosophila</i> Genomes. <i>PLoS Genetics</i> , 2007, 3, e197.	1.5	320
130	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
131	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
132	Accelerated Rate of Gene Gain and Loss in Primates. <i>Genetics</i> , 2007, 177, 1941-1949.	1.2	146
133	Bias in phylogenetic tree reconciliation methods: implications for vertebrate genome evolution. <i>Genome Biology</i> , 2007, 8, R141.	13.9	133
134	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
135	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	13.7	573
136	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
137	Regular rates of popular culture change reflect random copying. <i>Evolution and Human Behavior</i> , 2007, 28, 151-158.	1.4	166
138	The Evolution of Mammalian Gene Families. <i>PLoS ONE</i> , 2006, 1, e85.	1.1	285
139	Detecting natural selection on cis-regulatory DNA. <i>Genetica</i> , 2006, 129, 7-18.	0.5	45
140	Accurate Inference and Estimation in Population Genomics. <i>Molecular Biology and Evolution</i> , 2006, 23, 911-918.	3.5	25
141	Codon bias and selection on single genomes. <i>Nature</i> , 2005, 433, E5-E6.	13.7	18
142	Female-biased gene expression in the malaria mosquito <i>Anopheles gambiae</i> . <i>Current Biology</i> , 2005, 15, R192-R193.	1.8	58
143	Genomic Islands of Speciation in <i>Anopheles gambiae</i> . <i>PLoS Biology</i> , 2005, 3, e285.	2.6	637
144	Ancient and Recent Positive Selection Transformed Opioid cis-Regulation in Humans. <i>PLoS Biology</i> , 2005, 3, e387.	2.6	155

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145	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
146	Estimating the tempo and mode of gene family evolution from comparative genomic data. <i>Genome Research</i> , 2005, 15, 1153-1160.	2.4	259
147	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
148	Disentangling the Effects of Demography and Selection in Human History. <i>Molecular Biology and Evolution</i> , 2004, 22, 63-73.	3.5	200
149	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. <i>Genetics</i> , 2004, 167, 867-877.	1.2	46
150	Positive Selection on MMP3 Regulation Has Shaped Heart Disease Risk. <i>Current Biology</i> , 2004, 14, 1531-1539.	1.8	76
151	Molecular Evolution in Large Genetic Networks: Does Connectivity Equal Constraint?. <i>Journal of Molecular Evolution</i> , 2004, 58, 203-211.	0.8	138
152	Positive Selection on a Human-Specific Transcription Factor Binding Site Regulating IL4 Expression. <i>Current Biology</i> , 2003, 13, 2118-2123.	1.8	124
153	The Evolution of Transcriptional Regulation in Eukaryotes. <i>Molecular Biology and Evolution</i> , 2003, 20, 1377-1419.	3.5	1,034
154	The Effects of Selection Against Spurious Transcription Factor Binding Sites. <i>Molecular Biology and Evolution</i> , 2003, 20, 901-906.	3.5	85
155	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
156	The g-value paradox. <i>Evolution &amp; Development</i> , 2002, 4, 73-75.	1.1	129
157	Distinguishing Between Selection and Population Expansion in an Experimental Lineage of Bacteriophage T7. <i>Genetics</i> , 2002, 161, 11-20.	1.2	65