Webb Miller

List of Publications by Year
in descending order

180 papers	130,148 citations	8181 76 h-index	4228 174 g-index
184 all docs	184 docs citations	184 times ranked	123858 citing authors

#	Article	IF	Citations
1	Basic local alignment search tool. Journal of Molecular Biology, 1990, 215, 403-410.	4.2	82,180
2	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
3	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
4	A Greedy Algorithm for Aligning DNA Sequences. Journal of Computational Biology, 2000, 7, 203-214.	1.6	4,325
5	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. Genome Research, 2005, 15, 1034-1050.	5.5	3,517
6	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
7	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	5.5	1,795
8	Complete genome sequence of Salmonella enterica serovar Typhimurium LT2. Nature, 2001, 413, 852-856.	27.8	1,712
9	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. Genome Research, 2004, 14, 708-715.	5.5	1,290
10	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
11	Human–Mouse Alignments with BLASTZ. Genome Research, 2003, 13, 103-107.	5.5	1,071
12	PipMaker—A Web Server for Aligning Two Genomic DNA Sequences. Genome Research, 2000, 10, 577-586.	5.5	1,070
13	A time-efficient, linear-space local similarity algorithm. Advances in Applied Mathematics, 1991, 12, 337-357.	0.7	933
14	Evolution's cauldron: Duplication, deletion, and rearrangement in the mouse and human genomes. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 11484-11489.	7.1	792
15	A Computer Program for Aligning a cDNA Sequence with a Genomic DNA Sequence. Genome Research, 1998, 8, 967-974.	5.5	683
16	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	27.8	657
17	CleaveLand: a pipeline for using degradome data to find cleaved small RNA targets. Bioinformatics, 2009, 25, 130-131.	4.1	642
18	Comparison of DNA Sequences with Protein Sequences. Genomics, 1997, 46, 24-36.	2.9	557

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19	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
20	Metagenomics to Paleogenomics: Large-Scale Sequencing of Mammoth DNA. Science, 2006, 311, 392-394.	12.6	519
21	Identification and Classification of Conserved RNA Secondary Structures in the Human Genome. PLoS Computational Biology, 2006, 2, e33.	3.2	439
22	HbVar: A relational database of human hemoglobin variants and thalassemia mutations at the globin gene server. Human Mutation, 2002, 19, 225-233.	2.5	400
23	Complete Khoisan and Bantu genomes from southern Africa. Nature, 2010, 463, 943-947.	27.8	400
24	Using genomic data to unravel the root of the placental mammal phylogeny. Genome Research, 2007, 17, 413-421.	5.5	394
25	TheChlamydomonas reinhardtiiPlastid Chromosome. Plant Cell, 2002, 14, 2659-2679.	6.6	390
26	Updates of the HbVar database of human hemoglobin variants and thalassemia mutations. Nucleic Acids Research, 2014, 42, D1063-D1069.	14.5	361
27	Polar and brown bear genomes reveal ancient admixture and demographic footprints of past climate change. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2382-90.	7.1	310
28	Long Human–Mouse Sequence Alignments Reveal Novel Regulatory Elements: A Reason to Sequence the Mouse‰Genome. Genome Research, 1997, 7, 959-966.	5.5	294
29	Improvements in the HbVar database of human hemoglobin variants and thalassemia mutations for population and sequence variation studies. Nucleic Acids Research, 2004, 32, 537D-541.	14.5	285
30	Sequencing the nuclear genome of the extinct woolly mammoth. Nature, 2008, 456, 387-390.	27.8	283
31	Molecular and Genomic Data Identify the Closest Living Relative of Primates. Science, 2007, 318, 792-794.	12.6	282
32	Transcription-associated mutational asymmetry in mammalian evolution. Nature Genetics, 2003, 33, 514-517.	21.4	271
33	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. Genome Research, 2003, 13, 13-26.	5.5	263
34	Reconstructing contiguous regions of an ancestral genome. Genome Research, 2006, 16, 1557-1565.	5.5	246
35	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
36	Locus control regions of mammalian β-globin gene clusters: combining phylogenetic analyses and experimental results to gain functional insights. Gene, 1997, 205, 73-94.	2.2	226

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37	Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts. Science, 2007, 317, 1927-1930.	12.6	220
38	Mulan: Multiple-sequence local alignment and visualization for studying function and evolution. Genome Research, 2005, 15, 184-194.	5.5	218
39	Evolution and functional classification of vertebrate gene deserts. Genome Research, 2005, 15, 137-145.	5.5	203
40	MultiPipMaker and supporting tools: alignments and analysis of multiple genomic DNA sequences. Nucleic Acids Research, 2003, 31, 3518-3524.	14.5	196
41	Genetic diversity and population structure of the endangered marsupial *Sarcophilus harrisii* (Tasmanian devil). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12348-12353.	7.1	189
42	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. Genome Research, 2005, 15, 1051-1060.	5.5	185
43	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	5.5	184
44	Erythroid GATA1 function revealed by genome-wide analysis of transcription factor occupancy, histone modifications, and mRNA expression. Genome Research, 2009, 19, 2172-2184.	5.5	184
45	HbVar database of human hemoglobin variants and thalassemia mutations: 2007 update. Human Mutation, 2007, 28, 206-206.	2.5	175
46	Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. Nucleic Acids Research, 2006, 35, 1-10.	14.5	166
47	Fast-evolving noncoding sequences in the human genome. Genome Biology, 2007, 8, R118.	9.6	163
48	COMPARATIVE GENOMICS. Annual Review of Genomics and Human Genetics, 2004, 5, 15-56.	6.2	156
49	Characterization of the Human and Mouse Unconventional Myosin XV Genes Responsible for Hereditary Deafness DFNB3 and Shaker 2. Genomics, 1999, 61, 243-258.	2.9	153
50	Intraspecific phylogenetic analysis of Siberian woolly mammoths using complete mitochondrial genomes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8327-8332.	7.1	149
51	The gene mutated in bare patches and striated mice encodes a novel 3β-hydroxysteroid dehydrogenase. Nature Genetics, 1999, 22, 182-187.	21.4	147
52	A file comparison program. Software - Practice and Experience, 1985, 15, 1025-1040.	3.6	146
53	Systematic documentation and analysis of human genetic variation in hemoglobinopathies using the microattribution approach. Nature Genetics, 2011, 43, 295-301.	21.4	142
54	Complete mitochondrial genome of a Pleistocene jawbone unveils the origin of polar bear. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5053-5057.	7.1	132

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55	Large-Scale Comparative Sequence Analysis of the Human and Murine Bruton's Tyrosine Kinase Loci Reveals Conserved Regulatory Domains. Genome Research, 1997, 7, 315-329.	5.5	131
56	Approximate matching of regular expressions. Bulletin of Mathematical Biology, 1989, 51, 5-37.	1.9	130
57	zPicture: Dynamic Alignment and Visualization Tool for Analyzing Conservation Profiles. Genome Research, 2004, 14, 472-477.	5.5	128
58	Elephantid Genomes Reveal the Molecular Bases of Woolly Mammoth Adaptations to the Arctic. Cell Reports, 2015, 12, 217-228.	6.4	127
59	Sequence comparison with concave weighting functions. Bulletin of Mathematical Biology, 1988, 50, 97-120.	1.9	124
60	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. Genome Research, 2007, 17, 960-964.	5.5	122
61	Reconstructing large regions of an ancestral mammalian genome in silico. Genome Research, 2004, 14, 2412-2423.	5.5	121
62	Distinguishing Regulatory DNA From Neutral Sites. Genome Research, 2003, 13, 64-72.	5.5	118
63	Mobile DNA in Old World Monkeys: A Glimpse Through the Rhesus Macaque Genome. Science, 2007, 316, 238-240.	12.6	116
64	Alignment of Escherichia coli K12 DNA sequences to a genomic restriction map. Nucleic Acids Research, 1990, 18, 313-321.	14.5	111
65	ESPERR: Learning strong and weak signals in genomic sequence alignments to identify functional elements. Genome Research, 2006, 16, 1596-1604.	5.5	111
66	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671.	5.5	110
67	An initial strategy for the systematic identification of functional elements in the human genome by low-redundancy comparative sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4795-4800.	7.1	107
68	The mitochondrial genome sequence of the Tasmanian tiger (*Thylacinus cynocephalus*). Genome Research, 2009, 19, 213-220.	5.5	102
69	A space-efficient algorithm for local similarities. Bioinformatics, 1990, 6, 373-381.	4.1	99
70	Aligning two sequences within a specified diagonal band. Bioinformatics, 1992, 8, 481-487.	4.1	94
71	Regulatory Potential Scores From Genome-Wide Three-Way Alignments of Human, Mouse, and Rat. Genome Research, 2004, 14, 700-707.	5.5	93
72	Analysis of complete mitochondrial genomes from extinct and extant rhinoceroses reveals lack of phylogenetic resolution. BMC Evolutionary Biology, 2009, 9, 95.	3.2	92

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73	An O(NP) sequence comparison algorithm. Information Processing Letters, 1990, 35, 317-323.	0.6	90
74	Mapping sequencedE.coligenes by computer: software, strategies and examples. Nucleic Acids Research, 1991, 19, 637-647.	14.5	85
75	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. Nature, 2005, 434, 724-731.	27.8	85
76	Multispecies comparative analysis of a mammalian-specific genomic domain encoding secretory proteins. Genomics, 2003, 82, 417-432.	2.9	82
77	PhenCode: connecting ENCODE data with mutations and phenotype. Human Mutation, 2007, 28, 554-562.	2.5	79
78	The infinite sites model of genome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14254-14261.	7.1	79
79	A Combinatorial Network of Evolutionarily Conserved<i>Myelin Basic Protein</i>Regulatory Sequences Confers Distinct Glial-Specific Phenotypes. Journal of Neuroscience, 2003, 23, 10214-10223.	3.6	77
80	[27] Dynamic programming algorithms for biological sequence comparison. Methods in Enzymology, 1992, 210, 575-601.	1.0	76
81	Conserved E Boxes Function as Part of the Enhancer in Hypersensitive Site 2 of the Î²-Globin Locus Control Region. Journal of Biological Chemistry, 1997, 272, 369-378.	3.4	74
82	Patterns of Insertions and Their Covariation With Substitutions in the Rat, Mouse, and Human Genomes. Genome Research, 2004, 14, 517-527.	5.5	73
83	Generation and Comparative Analysis of â¼3.3 Mb of Mouse Genomic Sequence Orthologous to the Region of Human Chromosome 7q11.23 Implicated in Williams Syndrome. Genome Research, 2002, 12, 3-15.	5.5	72
84	Genome-wide identification of conserved regulatory function in diverged sequences. Genome Research, 2011, 21, 1139-1149.	5.5	72
85	Comparison of Sequencing Platforms for Single Nucleotide Variant Calls in a Human Sample. PLoS ONE, 2013, 8, e55089.	2.5	70
86	Genomic structure and functional control of the Dlx3-7 bigene cluster. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 780-785.	7.1	69
87	Finding cis-regulatory elements using comparative genomics: Some lessons from ENCODE data. Genome Research, 2007, 17, 775-786.	5.5	69
88	Khoisan hunter-gatherers have been the largest population throughout most of modern-human demographic history. Nature Communications, 2014, 5, 5692.	12.8	65
89	Genomic Sequence Analysis of the Mouse Naip Gene Array. Genome Research, 2000, 10, 1095-1102.	5.5	60
90	Analysis of the Quality and Utility of Random Shotgun Sequencing at Low Redundancies. Genome Research, 1998, 8, 1074-1084.	5.5	59

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91	A Genome Sequence Resource for the Aye-Aye (Daubentonia madagascariensis), a Nocturnal Lemur from Madagascar. Genome Biology and Evolution, 2012, 4, 126-135.	2.5	59
92	Experimental validation of predicted mammalian erythroid cis-regulatory modules. Genome Research, 2006, 16, 1480-1492.	5.5	56
93	Comparative Sequence of Human and Mouse BAC Clones from the mnd2 Region of Chromosome 2p13. Genome Research, 1999, 9, 53-61.	5.5	55
94	Human-macaque comparisons illuminate variation in neutral substitution rates. Genome Biology, 2008, 9, R76.	9.6	54
95	Role of DNA Sequences Outside the Cores of DNase Hypersensitive Sites (HSs) in Functions of the β-Globin Locus Control Region. Journal of Biological Chemistry, 1996, 271, 11871-11878.	3.4	52
96	Polar Bears Exhibit Genome-Wide Signatures of Bioenergetic Adaptation to Life in the Arctic Environment. Genome Biology and Evolution, 2014, 6, 433-450.	2.5	52
97	Recent Developments in Linear-Space Alignment Methods: A Survey. Journal of Computational Biology, 1994, 1, 271-291.	1.6	51
98	DUPCAR: Reconstructing Contiguous Ancestral Regions with Duplications. Journal of Computational Biology, 2008, 15, 1007-1027.	1.6	51
99	Sequences Flanking Hypersensitive Sites of the β-Globin Locus Control Region Are Required for Synergistic Enhancement. Molecular and Cellular Biology, 2001, 21, 2969-2980.	2.3	49
100	Use of subtractive hybridization for comprehensive surveys of prokaryotic genome differences. FEMS Microbiology Letters, 2002, 211, 175-182.	1.8	49
101	Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5. Nucleic Acids Research, 2001, 29, 1352-1365.	14.5	48
102	Comparative analysis of the locus control region of the rabbit β-like globin gene cluster: HS3 increases transient expression of an embryonic ε-globin gene. Nucleic Acids Research, 1993, 21, 1265-1272.	14.5	47
103	Alignments Without Low-Scoring Regions. Journal of Computational Biology, 1998, 5, 197-210.	1.6	46
104	GALA, a Database for Genomic Sequence Alignments and Annotations. Genome Research, 2003, 13, 732-741.	5.5	45
105	The human and mouse MHC class III region: a parade of 21 genes at the centromeric segment. Trends in Immunology, 2000, 21, 320-328.	7.5	42
106	Sequence and comparative analysis of the rabbit α-like globin gene cluster reveals a rapid mode of evolution in a G + C-rich region of mammalian genomes. Journal of Molecular Biology, 1991, 222, 233-249.	4.2	40
107	Comparative Sequence Analysis of the Mouse and Human Lgn1/SMA Interval. Genomics, 1999, 60, 137-151.	2.9	39
108	Software for Roundoff Analysis. ACM Transactions on Mathematical Software, 1975, 1, 108-128.	2.9	38

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109	Genome-wide analysis of signatures of selection in populations of African honey bees (Apis mellifera) using new web-based tools. BMC Genomics, 2015, 16, 518.	2.8	38
110	Calling SNPs without a reference sequence. BMC Bioinformatics, 2010, 11, 130.	2.6	37
111	Software tools for analyzing pairwise alignments of long sequences. Nucleic Acids Research, 1991, 19, 4663-4667.	14.5	36
112	Aye-aye population genomic analyses highlight an important center of endemism in northern Madagascar. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5823-5828.	7.1	36
113	Globin Gene Server: A Prototype E-Mail Database Server Featuring Extensive Multiple Alignments and Data Compilation for Electronic Genetic Analysis. Genomics, 1994, 21, 344-353.	2.9	35
114	Phylogenetic Footprinting of Hypersensitive Site 3 of the Î²-Globin Locus Control Region. Blood, 1997, 89, 3457-3469.	1.4	35
115	PROGRAM DESCRIPTION. Genomics, 1998, 47, 429-437.	2.9	35
116	DATABASES OF HUMAN HEMOGLOBIN VARIANTS AND OTHER RESOURCES AT THE GLOBIN GENE SERVER. Hemoglobin, 2001, 25, 183-193.	0.8	35
117	The Complete Sequences of the Galago and Rabbit Î²-Globin Locus Control Regions: Extended Sequence and Functional Conservation Outside the Cores of DNase Hypersensitive Sites. Genomics, 1997, 39, 90-94.	2.9	34
118	PipTools: A Computational Toolkit to Annotate and Analyze Pairwise Comparisons of Genomic Sequences. Genomics, 2002, 80, 681-690.	2.9	32
119	Approximating the Spanning Star Forest Problem and Its Application to Genomic Sequence Alignment. SIAM Journal on Computing, 2008, 38, 946-962.	1.0	32
120	Aligning a DNA Sequence with a Protein Sequence. Journal of Computational Biology, 1997, 4, 339-349.	1.6	31
121	Genomic Variants Among Threatened<i>Acropora</i>Corals. G3: Genes, Genomes, Genetics, 2019, 9, 1633-1646.	1.8	31
122	Web-based visualization tools for bacterial genome alignments. Nucleic Acids Research, 2000, 28, 3486-3496.	14.5	29
123	Comparative Analysis of the Â-Like Globin Clusters in Mouse, Rat, and Human Chromosomes Indicates a Mechanism Underlying Breaks in Conserved Synteny. Genome Research, 2004, 14, 623-630.	5.5	29
124	Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif. Genome Research, 2008, 18, 1896-1905.	5.5	29
125	Sequencing and analysis of a South Asian-Indian personal genome. BMC Genomics, 2012, 13, 440.	2.8	29
126	Positive and negative regulatory elements of the rabbit embryonic Ïµ-globin gene revealed by an improved multiple alignment program and functional analysis. DNA Sequence, 1993, 4, 163-176.	0.7	26

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127	Chaining Multiple-Alignment Blocks. Journal of Computational Biology, 1994, 1, 217-226.	1.6	24
128	Multiple Regulatory Elements in the 5â€²-Flanking Sequence of the Human Îµ-Globin Gene. Journal of Biological Chemistry, 1998, 273, 10202-10209.	3.4	23
129	EnteriX 2003: visualization tools for genome alignments of Enterobacteriaceae. Nucleic Acids Research, 2003, 31, 3527-3532.	14.5	23
130	Computational Reconstruction of Ancestral DNA Sequences. Methods in Molecular Biology, 2008, 422, 171-184.	0.9	23
131	Comparative Genomic Analysis Using the UCSC Genome Browser. Methods in Molecular Biology, 2007, 395, 17-33.	0.9	23
132	Constrained sequence alignment. Bulletin of Mathematical Biology, 1993, 55, 503-524.	1.9	19
133	So many genomes, so little time. Nature Biotechnology, 2000, 18, 148-149.	17.5	19
134	Galaxy tools to study genome diversity. GigaScience, 2013, 2, 17.	6.4	19
135	Computer Search for Numerical Instability. Journal of the ACM, 1975, 22, 512-521.	2.2	18
136	A Negative Cis-element Regulates the Level of Enhancement by Hypersensitive Site 2 of the Î²-Globin Locus Control Region. Journal of Biological Chemistry, 2001, 276, 6289-6298.	3.4	17
137	Candidate Genes Required for Embryonic Development: A Comparative Analysis of Distal Mouse Chromosome 14 and Human Chromosome 13q22. Genomics, 2002, 79, 154-161.	2.9	17
138	Quadratic convergence in interval arithmetic, part I. BIT Numerical Mathematics, 1972, 12, 284-290.	2.0	16
139	PipMaker: A World Wide Web Server for Genomic Sequence Alignments. Current Protocols in Bioinformatics, 2003, 00, Unit 10.2.	25.8	16
140	The mouse cornichon gene family. Development Genes and Evolution, 1999, 209, 120-125.	0.9	15
141	Quadratic convergence in interval arithmetic, part II. BIT Numerical Mathematics, 1972, 12, 291-298.	2.0	14
142	A tool for aligning very similar DNA sequences. Bioinformatics, 1997, 13, 75-80.	4.1	14
143	A Database of Experimental Results on Globin Gene Expression. Genomics, 1998, 53, 325-337.	2.9	14
144	OPTIMIZATION METHODS FOR SELECTING FOUNDER INDIVIDUALS FOR CAPTIVE BREEDING OR REINTRODUCTION OF ENDANGERED SPECIES. , 2009, , 43-53.		13

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145	Significance of Interspecies Matches when Evolutionary Rate Varies. Journal of Computational Biology, 2003, 10, 537-554.	1.6	12
146	MultiPipMaker: A Comparative Alignment Server for Multiple DNA Sequences. Current Protocols in Bioinformatics, 2010, 30, Unit10.4.	25.8	12
147	Conversion events in gene clusters. BMC Evolutionary Biology, 2011, 11, 226.	3.2	12
148	Row replacement algorithms for screen editors. ACM Transactions on Programming Languages and Systems, 1989, 11, 33-56.	2.1	11
149	MultiPipMaker: Comparative Alignment Server for Multiple DNA Sequences. Current Protocols in Bioinformatics, 2005, 9, Unit10.4.	25.8	11
150	An Effective Method for Detecting Gene Conversion Events in Whole Genomes. Journal of Computational Biology, 2010, 17, 1281-1297.	1.6	11
151	CAGE: Combinatorial Analysis of Gene-Cluster Evolution. Journal of Computational Biology, 2010, 17, 1227-1242.	1.6	10
152	Parametric recomputing in alignment graphs. Lecture Notes in Computer Science, 1994, , 87-101.	1.3	10
153	On an interval-arithmetic matrix method. BIT Numerical Mathematics, 1972, 12, 213-219.	2.0	9
154	Functional and binding studies of HS3.2 of the beta-globin locus control region. Gene, 2002, 283, 185-197.	2.2	9
155	Improvements to GALA and dbERGE II: databases featuring genomic sequence alignment, annotation and experimental results. Nucleic Acids Research, 2004, 33, D466-D470.	14.5	9
156	Revealing Mammalian Evolutionary Relationships by Comparative Analysis of Gene Clusters. Genome Biology and Evolution, 2012, 4, 586-601.	2.5	9
157	Functional Architecture of Deleterious Genetic Variants in the Genome of a Wrangel Island Mammoth. Genome Biology and Evolution, 2020, 12, 48-58.	2.5	9
158	Reconstructing the Evolutionary History of Complex Human Gene Clusters. , 2008, , 29-49.		9
159	On the stability of finite numerical procedures. Numerische Mathematik, 1972, 19, 425-432.	1.9	8
160	An algorithm for searching restriction maps. Bioinformatics, 1990, 6, 247-252.	4.1	8
161	Evolutionary History Reconstruction for Mammalian Complex Gene Clusters. Journal of Computational Biology, 2009, 16, 1051-1070.	1.6	7
162	Evaluation of methods for detecting conversion events in gene clusters. BMC Bioinformatics, 2011, 12, S45.	2.6	7

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163	Phylogenomic Resources at the UCSC Genome Browser. Methods in Molecular Biology, 2008, 422, 133-144.	0.9	7
164	Winnowing Sequences from a Database Search. Journal of Computational Biology, 2000, 7, 293-302.	1.6	6
165	Response to Comment on "Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts". Science, 2008, 322, 857-857.	12.6	6
166	Improved algorithms for searching restriction maps. Bioinformatics, 1991, 7, 447-456.	4.1	5
167	Significance Of inter-species matches when evolutionary rate varies. , 2002, , .		5
168	SIMULTANEOUS HISTORY RECONSTRUCTION FOR COMPLEX GENE CLUSTERS IN MULTIPLE SPECIES. , 2008, , .		5
169	Winnowing sequences from a database search. , 1999, , .		4
170	Controlling Size When Aligning Multiple Genomic Sequences with Duplications. Lecture Notes in Computer Science, 2006, , 138-149.	1.3	4
171	Simultaneous history reconstruction for complex gene clusters in multiple species. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 162-73.	0.7	4
172	A simple row-replacement method. Software - Practice and Experience, 1988, 18, 597-611.	3.6	3
173	Some Phenotype Association Tools in Galaxy: Looking for Disease SNPs in a Full Genome. Current Protocols in Bioinformatics, 2012, 39, Unit15.2.	25.8	2
174	Sex determination by SRY PCR and sequencing of Tasmanian devil facial tumour cell lines reveals non-allograft transmission. Biochemical and Biophysical Research Communications, 2016, 474, 29-34.	2.1	2
175	Whole-Genome Analysis of Gene Conversion Events. Lecture Notes in Computer Science, 2009, , 181-192.	1.3	2
176	Aligning Two Genomic Sequences That Contain Duplications. Lecture Notes in Computer Science, 2009, , 98-110.	1.3	1
177	Inferring the Recent Duplication History of a Gene Cluster. Lecture Notes in Computer Science, 2009, , 111-125.	1.3	1
178	Use of subtractive hybridization for comprehensive surveys of prokaryotic genome differences. FEMS Microbiology Letters, 2002, 211, 175-182.	1.8	1
179	A Heuristic Algorithm for Reconstructing Ancestral Gene Orders with Duplications. Lecture Notes in Computer Science, 2007, , 122-135.	1.3	1
180	My adventure using computer science on the Genome project. ACM SIGBIO Newsletter, 1999, 19, 15-16.	0.1	0