

Webb Miller

List of Publications by Year in descending order

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179
papers

130,148
citations

8159

76
h-index

4323

173
g-index

184
all docs

184
docs citations

184
times ranked

123858
citing authors

#	ARTICLE	IF	CITATIONS
1	Basic local alignment search tool. <i>Journal of Molecular Biology</i> , 1990, 215, 403-410.	2.0	82,180
2	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
3	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
4	A Greedy Algorithm for Aligning DNA Sequences. <i>Journal of Computational Biology</i> , 2000, 7, 203-214.	0.8	4,325
5	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005, 15, 1034-1050.	2.4	3,517
6	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
7	Galaxy: A platform for interactive large-scale genome analysis. <i>Genome Research</i> , 2005, 15, 1451-1455.	2.4	1,795
8	Complete genome sequence of <i>Salmonella enterica</i> serovar Typhimurium LT2. <i>Nature</i> , 2001, 413, 852-856.	13.7	1,712
9	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. <i>Genome Research</i> , 2004, 14, 708-715.	2.4	1,290
10	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
11	Human-Mouse Alignments with BLASTZ. <i>Genome Research</i> , 2003, 13, 103-107.	2.4	1,071
12	PipMaker--A Web Server for Aligning Two Genomic DNA Sequences. <i>Genome Research</i> , 2000, 10, 577-586.	2.4	1,070
13	A time-efficient, linear-space local similarity algorithm. <i>Advances in Applied Mathematics</i> , 1991, 12, 337-357.	0.4	933
14	Evolution's cauldron: Duplication, deletion, and rearrangement in the mouse and human genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11484-11489.	3.3	792
15	A Computer Program for Aligning a cDNA Sequence with a Genomic DNA Sequence. <i>Genome Research</i> , 1998, 8, 967-974.	2.4	683
16	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	13.7	657
17	CleaveLand: a pipeline for using degradome data to find cleaved small RNA targets. <i>Bioinformatics</i> , 2009, 25, 130-131.	1.8	642
18	Comparison of DNA Sequences with Protein Sequences. <i>Genomics</i> , 1997, 46, 24-36.	1.3	557

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19	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541
20	Metagenomics to Paleogenomics: Large-Scale Sequencing of Mammoth DNA. <i>Science</i> , 2006, 311, 392-394.	6.0	519
21	Identification and Classification of Conserved RNA Secondary Structures in the Human Genome. <i>PLoS Computational Biology</i> , 2006, 2, e33.	1.5	439
22	HbVar: A relational database of human hemoglobin variants and thalassemia mutations at the globin gene server. <i>Human Mutation</i> , 2002, 19, 225-233.	1.1	400
23	Complete Khoisan and Bantu genomes from southern Africa. <i>Nature</i> , 2010, 463, 943-947.	13.7	400
24	Using genomic data to unravel the root of the placental mammal phylogeny. <i>Genome Research</i> , 2007, 17, 413-421.	2.4	394
25	The <i>Chlamydomonas reinhardtii</i> Plastid Chromosome. <i>Plant Cell</i> , 2002, 14, 2659-2679.	3.1	390
26	Updates of the HbVar database of human hemoglobin variants and thalassemia mutations. <i>Nucleic Acids Research</i> , 2014, 42, D1063-D1069.	6.5	361
27	Polar and brown bear genomes reveal ancient admixture and demographic footprints of past climate change. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2382-90.	3.3	310
28	Long Human-Mouse Sequence Alignments Reveal Novel Regulatory Elements: A Reason to Sequence the Mouse Genome. <i>Genome Research</i> , 1997, 7, 959-966.	2.4	294
29	Improvements in the HbVar database of human hemoglobin variants and thalassemia mutations for population and sequence variation studies. <i>Nucleic Acids Research</i> , 2004, 32, 537D-541.	6.5	285
30	Sequencing the nuclear genome of the extinct woolly mammoth. <i>Nature</i> , 2008, 456, 387-390.	13.7	283
31	Molecular and Genomic Data Identify the Closest Living Relative of Primates. <i>Science</i> , 2007, 318, 792-794.	6.0	282
32	Transcription-associated mutational asymmetry in mammalian evolution. <i>Nature Genetics</i> , 2003, 33, 514-517.	9.4	271
33	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. <i>Genome Research</i> , 2003, 13, 13-26.	2.4	263
34	Reconstructing contiguous regions of an ancestral genome. <i>Genome Research</i> , 2006, 16, 1557-1565.	2.4	246
35	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007, 17, 1797-1808.	2.4	237
36	Locus control regions of mammalian β -globin gene clusters: combining phylogenetic analyses and experimental results to gain functional insights. <i>Gene</i> , 1997, 205, 73-94.	1.0	226

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37	Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts. <i>Science</i> , 2007, 317, 1927-1930.	6.0	220
38	Mulan: Multiple-sequence local alignment and visualization for studying function and evolution. <i>Genome Research</i> , 2005, 15, 184-194.	2.4	218
39	Evolution and functional classification of vertebrate gene deserts. <i>Genome Research</i> , 2005, 15, 137-145.	2.4	203
40	MultiPipMaker and supporting tools: alignments and analysis of multiple genomic DNA sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3518-3524.	6.5	196
41	Genetic diversity and population structure of the endangered marsupial <i>Sarcophilus harrisii</i> (Tasmanian devil). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12348-12353.	3.3	189
42	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. <i>Genome Research</i> , 2005, 15, 1051-1060.	2.4	185
43	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	2.4	184
44	Erythroid GATA1 function revealed by genome-wide analysis of transcription factor occupancy, histone modifications, and mRNA expression. <i>Genome Research</i> , 2009, 19, 2172-2184.	2.4	184
45	HbVar database of human hemoglobin variants and thalassemia mutations: 2007 update. <i>Human Mutation</i> , 2007, 28, 206-206.	1.1	175
46	Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. <i>Nucleic Acids Research</i> , 2006, 35, 1-10.	6.5	166
47	Fast-evolving noncoding sequences in the human genome. <i>Genome Biology</i> , 2007, 8, R118.	13.9	163
48	COMPARATIVE GENOMICS. <i>Annual Review of Genomics and Human Genetics</i> , 2004, 5, 15-56.	2.5	156
49	Characterization of the Human and Mouse Unconventional Myosin XV Genes Responsible for Hereditary Deafness DFNB3 and Shaker 2. <i>Genomics</i> , 1999, 61, 243-258.	1.3	153
50	Intraspecific phylogenetic analysis of Siberian woolly mammoths using complete mitochondrial genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8327-8332.	3.3	149
51	The gene mutated in bare patches and striated mice encodes a novel 3 β -hydroxysteroid dehydrogenase. <i>Nature Genetics</i> , 1999, 22, 182-187.	9.4	147
52	A file comparison program. <i>Software - Practice and Experience</i> , 1985, 15, 1025-1040.	2.5	146
53	Systematic documentation and analysis of human genetic variation in hemoglobinopathies using the microattribution approach. <i>Nature Genetics</i> , 2011, 43, 295-301.	9.4	142
54	Complete mitochondrial genome of a Pleistocene jawbone unveils the origin of polar bear. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5053-5057.	3.3	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. <i>Genome Research</i> , 1997, 7, 315-329.	2.4	131
56	Approximate matching of regular expressions. <i>Bulletin of Mathematical Biology</i> , 1989, 51, 5-37.	0.9	130
57	zPicture: Dynamic Alignment and Visualization Tool for Analyzing Conservation Profiles. <i>Genome Research</i> , 2004, 14, 472-477.	2.4	128
58	Elephantid Genomes Reveal the Molecular Bases of Woolly Mammoth Adaptations to the Arctic. <i>Cell Reports</i> , 2015, 12, 217-228.	2.9	127
59	Sequence comparison with concave weighting functions. <i>Bulletin of Mathematical Biology</i> , 1988, 50, 97-120.	0.9	124
60	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. <i>Genome Research</i> , 2007, 17, 960-964.	2.4	122
61	Reconstructing large regions of an ancestral mammalian genome in silico. <i>Genome Research</i> , 2004, 14, 2412-2423.	2.4	121
62	Distinguishing Regulatory DNA From Neutral Sites. <i>Genome Research</i> , 2003, 13, 64-72.	2.4	118
63	Mobile DNA in Old World Monkeys: A Glimpse Through the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 238-240.	6.0	116
64	Alignment of <i>Escherichia coli</i> K12 DNA sequences to a genomic restriction map. <i>Nucleic Acids Research</i> , 1990, 18, 313-321.	6.5	111
65	ESPERR: Learning strong and weak signals in genomic sequence alignments to identify functional elements. <i>Genome Research</i> , 2006, 16, 1596-1604.	2.4	111
66	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. <i>Genome Research</i> , 2011, 21, 1659-1671.	2.4	110
67	An initial strategy for the systematic identification of functional elements in the human genome by low-redundancy comparative sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4795-4800.	3.3	107
68	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). <i>Genome Research</i> , 2009, 19, 213-220.	2.4	102
69	A space-efficient algorithm for local similarities. <i>Bioinformatics</i> , 1990, 6, 373-381.	1.8	99
70	Aligning two sequences within a specified diagonal band. <i>Bioinformatics</i> , 1992, 8, 481-487.	1.8	94
71	Regulatory Potential Scores From Genome-Wide Three-Way Alignments of Human, Mouse, and Rat. <i>Genome Research</i> , 2004, 14, 700-707.	2.4	93
72	Analysis of complete mitochondrial genomes from extinct and extant rhinoceroses reveals lack of phylogenetic resolution. <i>BMC Evolutionary Biology</i> , 2009, 9, 95.	3.2	92

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73	An O(NP) sequence comparison algorithm. Information Processing Letters, 1990, 35, 317-323.	0.4	90
74	Mapping sequenced E.coli genes by computer: software, strategies and examples. Nucleic Acids Research, 1991, 19, 637-647.	6.5	85
75	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. Nature, 2005, 434, 724-731.	13.7	85
76	Multispecies comparative analysis of a mammalian-specific genomic domain encoding secretory proteins. Genomics, 2003, 82, 417-432.	1.3	82
77	PhenCode: connecting ENCODE data with mutations and phenotype. Human Mutation, 2007, 28, 554-562.	1.1	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.	3.3	79
79	A Combinatorial Network of Evolutionarily Conserved Myelin Basic Protein Regulatory Sequences Confers Distinct Glial-Specific Phenotypes. Journal of Neuroscience, 2003, 23, 10214-10223.	1.7	77
80	[27] Dynamic programming algorithms for biological sequence comparison. Methods in Enzymology, 1992, 210, 575-601.	0.4	76
81	Conserved E Boxes Function as Part of the Enhancer in Hypersensitive Site 2 of the β^2 -Globin Locus Control Region. Journal of Biological Chemistry, 1997, 272, 369-378.	1.6	74
82	Patterns of Insertions and Their Covariation With Substitutions in the Rat, Mouse, and Human Genomes. Genome Research, 2004, 14, 517-527.	2.4	73
83	Generation and Comparative Analysis of 3.3 Mb of Mouse Genomic Sequence Orthologous to the Region of Human Chromosome 7q11.23 Implicated in Williams Syndrome. Genome Research, 2002, 12, 3-15.	2.4	72
84	Genome-wide identification of conserved regulatory function in diverged sequences. Genome Research, 2011, 21, 1139-1149.	2.4	72
85	Comparison of Sequencing Platforms for Single Nucleotide Variant Calls in a Human Sample. PLoS ONE, 2013, 8, e55089.	1.1	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.	3.3	69
87	Finding cis-regulatory elements using comparative genomics: Some lessons from ENCODE data. Genome Research, 2007, 17, 775-786.	2.4	69
88	Khoisan hunter-gatherers have been the largest population throughout most of modern-human demographic history. Nature Communications, 2014, 5, 5692.	5.8	65
89	Genomic Sequence Analysis of the Mouse Naip Gene Array. Genome Research, 2000, 10, 1095-1102.	2.4	60
90	Analysis of the Quality and Utility of Random Shotgun Sequencing at Low Redundancies. Genome Research, 1998, 8, 1074-1084.	2.4	59

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91	A Genome Sequence Resource for the Aye-Aye (<i>Daubentonia madagascariensis</i>), a Nocturnal Lemur from Madagascar. <i>Genome Biology and Evolution</i> , 2012, 4, 126-135.	1.1	59
92	Experimental validation of predicted mammalian erythroid cis-regulatory modules. <i>Genome Research</i> , 2006, 16, 1480-1492.	2.4	56
93	Comparative Sequence of Human and Mouse BAC Clones from the <i>mnd2</i> Region of Chromosome 2p13. <i>Genome Research</i> , 1999, 9, 53-61.	2.4	55
94	Human-macaque comparisons illuminate variation in neutral substitution rates. <i>Genome Biology</i> , 2008, 9, R76.	13.9	54
95	Role of DNA Sequences Outside the Cores of DNase Hypersensitive Sites (HSs) in Functions of the $\hat{\nu}^2$ -Globin Locus Control Region. <i>Journal of Biological Chemistry</i> , 1996, 271, 11871-11878.	1.6	52
96	Polar Bears Exhibit Genome-Wide Signatures of Bioenergetic Adaptation to Life in the Arctic Environment. <i>Genome Biology and Evolution</i> , 2014, 6, 433-450.	1.1	52
97	Recent Developments in Linear-Space Alignment Methods: A Survey. <i>Journal of Computational Biology</i> , 1994, 1, 271-291.	0.8	51
98	DUPCAR: Reconstructing Contiguous Ancestral Regions with Duplications. <i>Journal of Computational Biology</i> , 2008, 15, 1007-1027.	0.8	51
99	Sequences Flanking Hypersensitive Sites of the $\hat{\nu}^2$ -Globin Locus Control Region Are Required for Synergistic Enhancement. <i>Molecular and Cellular Biology</i> , 2001, 21, 2969-2980.	1.1	49
100	Use of subtractive hybridization for comprehensive surveys of prokaryotic genome differences. <i>FEMS Microbiology Letters</i> , 2002, 211, 175-182.	0.7	49
101	Comparative analysis of the gene-dense <i>ACHE/TFR2</i> region on human chromosome 7q22 with the orthologous region on mouse chromosome 5. <i>Nucleic Acids Research</i> , 2001, 29, 1352-1365.	6.5	48
102	Comparative analysis of the locus control region of the rabbit $\hat{\nu}^2$ -like globin gene cluster: HS3 increases transient expression of an embryonic $\hat{\nu}^{\mu}$ -globin gene. <i>Nucleic Acids Research</i> , 1993, 21, 1265-1272.	6.5	47
103	Alignments Without Low-Scoring Regions. <i>Journal of Computational Biology</i> , 1998, 5, 197-210.	0.8	46
104	GALA, a Database for Genomic Sequence Alignments and Annotations. <i>Genome Research</i> , 2003, 13, 732-741.	2.4	45
105	The human and mouse MHC class III region: a parade of 21 genes at the centromeric segment. <i>Trends in Immunology</i> , 2000, 21, 320-328.	7.5	42
106	Sequence and comparative analysis of the rabbit $\hat{\nu}^{\pm}$ -like globin gene cluster reveals a rapid mode of evolution in a G + C-rich region of mammalian genomes. <i>Journal of Molecular Biology</i> , 1991, 222, 233-249.	2.0	40
107	Comparative Sequence Analysis of the Mouse and Human <i>Lgn1/SMA</i> Interval. <i>Genomics</i> , 1999, 60, 137-151.	1.3	39
108	Software for Roundoff Analysis. <i>ACM Transactions on Mathematical Software</i> , 1975, 1, 108-128.	1.6	38

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109	Genome-wide analysis of signatures of selection in populations of African honey bees (<i>Apis mellifera</i>) using new web-based tools. <i>BMC Genomics</i> , 2015, 16, 518.	1.2	38
110	Calling SNPs without a reference sequence. <i>BMC Bioinformatics</i> , 2010, 11, 130.	1.2	37
111	Software tools for analyzing pairwise alignments of long sequences. <i>Nucleic Acids Research</i> , 1991, 19, 4663-4667.	6.5	36
112	Aye-aye population genomic analyses highlight an important center of endemism in northern Madagascar. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5823-5828.	3.3	36
113	Globin Gene Server: A Prototype E-Mail Database Server Featuring Extensive Multiple Alignments and Data Compilation for Electronic Genetic Analysis. <i>Genomics</i> , 1994, 21, 344-353.	1.3	35
114	Phylogenetic Footprinting of Hypersensitive Site 3 of the $\hat{\gamma}$ -Globin Locus Control Region. <i>Blood</i> , 1997, 89, 3457-3469.	0.6	35
115	PROGRAM DESCRIPTION. <i>Genomics</i> , 1998, 47, 429-437.	1.3	35
116	DATABASES OF HUMAN HEMOGLOBIN VARIANTS AND OTHER RESOURCES AT THE GLOBIN GENE SERVER. <i>Hemoglobin</i> , 2001, 25, 183-193.	0.4	35
117	The Complete Sequences of the Galago and Rabbit $\hat{\gamma}$ -Globin Locus Control Regions: Extended Sequence and Functional Conservation Outside the Cores of DNase Hypersensitive Sites. <i>Genomics</i> , 1997, 39, 90-94.	1.3	34
118	PipTools: A Computational Toolkit to Annotate and Analyze Pairwise Comparisons of Genomic Sequences. <i>Genomics</i> , 2002, 80, 681-690.	1.3	32
119	Approximating the Spanning Star Forest Problem and Its Application to Genomic Sequence Alignment. <i>SIAM Journal on Computing</i> , 2008, 38, 946-962.	0.8	32
120	Aligning a DNA Sequence with a Protein Sequence. <i>Journal of Computational Biology</i> , 1997, 4, 339-349.	0.8	31
121	Genomic Variants Among Threatened <i>Acropora</i> Corals. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1633-1646.	0.8	31
122	Web-based visualization tools for bacterial genome alignments. <i>Nucleic Acids Research</i> , 2000, 28, 3486-3496.	6.5	29
123	Comparative Analysis of the $\hat{\gamma}$ -Like Globin Clusters in Mouse, Rat, and Human Chromosomes Indicates a Mechanism Underlying Breaks in Conserved Synteny. <i>Genome Research</i> , 2004, 14, 623-630.	2.4	29
124	Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif. <i>Genome Research</i> , 2008, 18, 1896-1905.	2.4	29
125	Sequencing and analysis of a South Asian-Indian personal genome. <i>BMC Genomics</i> , 2012, 13, 440.	1.2	29
126	Positive and negative regulatory elements of the rabbit embryonic $\hat{\mu}$ -globin gene revealed by an improved multiple alignment program and functional analysis. <i>DNA Sequence</i> , 1993, 4, 163-176.	0.7	26

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127	Chaining Multiple-Alignment Blocks. <i>Journal of Computational Biology</i> , 1994, 1, 217-226.	0.8	24
128	Multiple Regulatory Elements in the 5' Flanking Sequence of the Human β -Globin Gene. <i>Journal of Biological Chemistry</i> , 1998, 273, 10202-10209.	1.6	23
129	EnteriX 2003: visualization tools for genome alignments of Enterobacteriaceae. <i>Nucleic Acids Research</i> , 2003, 31, 3527-3532.	6.5	23
130	Computational Reconstruction of Ancestral DNA Sequences. <i>Methods in Molecular Biology</i> , 2008, 422, 171-184.	0.4	23
131	Comparative Genomic Analysis Using the UCSC Genome Browser. <i>Methods in Molecular Biology</i> , 2007, 395, 17-33.	0.4	23
132	Constrained sequence alignment. <i>Bulletin of Mathematical Biology</i> , 1993, 55, 503-524.	0.9	19
133	So many genomes, so little time. <i>Nature Biotechnology</i> , 2000, 18, 148-149.	9.4	19
134	Galaxy tools to study genome diversity. <i>GigaScience</i> , 2013, 2, 17.	3.3	19
135	Computer Search for Numerical Instability. <i>Journal of the ACM</i> , 1975, 22, 512-521.	1.8	18
136	A Negative Cis-element Regulates the Level of Enhancement by Hypersensitive Site 2 of the β -Globin Locus Control Region. <i>Journal of Biological Chemistry</i> , 2001, 276, 6289-6298.	1.6	17
137	Candidate Genes Required for Embryonic Development: A Comparative Analysis of Distal Mouse Chromosome 14 and Human Chromosome 13q22. <i>Genomics</i> , 2002, 79, 154-161.	1.3	17
138	Quadratic convergence in interval arithmetic, part I. <i>BIT Numerical Mathematics</i> , 1972, 12, 284-290.	1.0	16
139	PipMaker: A World Wide Web Server for Genomic Sequence Alignments. <i>Current Protocols in Bioinformatics</i> , 2003, 00, Unit 10.2.	25.8	16
140	The mouse cornichon gene family. <i>Development Genes and Evolution</i> , 1999, 209, 120-125.	0.4	15
141	Quadratic convergence in interval arithmetic, part II. <i>BIT Numerical Mathematics</i> , 1972, 12, 291-298.	1.0	14
142	A tool for aligning very similar DNA sequences. <i>Bioinformatics</i> , 1997, 13, 75-80.	1.8	14
143	A Database of Experimental Results on Globin Gene Expression. <i>Genomics</i> , 1998, 53, 325-337.	1.3	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. <i>Journal of Computational Biology</i> , 2003, 10, 537-554.	0.8	12
146	MultiPipMaker: A Comparative Alignment Server for Multiple DNA Sequences. <i>Current Protocols in Bioinformatics</i> , 2010, 30, Unit10.4.	25.8	12
147	Conversion events in gene clusters. <i>BMC Evolutionary Biology</i> , 2011, 11, 226.	3.2	12
148	Row replacement algorithms for screen editors. <i>ACM Transactions on Programming Languages and Systems</i> , 1989, 11, 33-56.	1.7	11
149	MultiPipMaker: Comparative Alignment Server for Multiple DNA Sequences. <i>Current Protocols in Bioinformatics</i> , 2005, 9, Unit10.4.	25.8	11
150	An Effective Method for Detecting Gene Conversion Events in Whole Genomes. <i>Journal of Computational Biology</i> , 2010, 17, 1281-1297.	0.8	11
151	CAGE: Combinatorial Analysis of Gene-Cluster Evolution. <i>Journal of Computational Biology</i> , 2010, 17, 1227-1242.	0.8	10
152	Parametric recomputing in alignment graphs. <i>Lecture Notes in Computer Science</i> , 1994, , 87-101.	1.0	10
153	On an interval-arithmetic matrix method. <i>BIT Numerical Mathematics</i> , 1972, 12, 213-219.	1.0	9
154	Functional and binding studies of HS3.2 of the beta-globin locus control region. <i>Gene</i> , 2002, 283, 185-197.	1.0	9
155	Improvements to GALA and dbERGE II: databases featuring genomic sequence alignment, annotation and experimental results. <i>Nucleic Acids Research</i> , 2004, 33, D466-D470.	6.5	9
156	Revealing Mammalian Evolutionary Relationships by Comparative Analysis of Gene Clusters. <i>Genome Biology and Evolution</i> , 2012, 4, 586-601.	1.1	9
157	Functional Architecture of Deleterious Genetic Variants in the Genome of a Wrangel Island Mammoth. <i>Genome Biology and Evolution</i> , 2020, 12, 48-58.	1.1	9
158	Reconstructing the Evolutionary History of Complex Human Gene Clusters. , 2008, , 29-49.		9
159	On the stability of finite numerical procedures. <i>Numerische Mathematik</i> , 1972, 19, 425-432.	0.9	8
160	An algorithm for searching restriction maps. <i>Bioinformatics</i> , 1990, 6, 247-252.	1.8	8
161	Evolutionary History Reconstruction for Mammalian Complex Gene Clusters. <i>Journal of Computational Biology</i> , 2009, 16, 1051-1070.	0.8	7
162	Evaluation of methods for detecting conversion events in gene clusters. <i>BMC Bioinformatics</i> , 2011, 12, S45.	1.2	7

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163	Phylogenomic Resources at the UCSC Genome Browser. <i>Methods in Molecular Biology</i> , 2008, 422, 133-144.	0.4	7
164	Winnowing Sequences from a Database Search. <i>Journal of Computational Biology</i> , 2000, 7, 293-302.	0.8	6
165	Response to Comment on "Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts". <i>Science</i> , 2008, 322, 857-857.	6.0	6
166	Improved algorithms for searching restriction maps. <i>Bioinformatics</i> , 1991, 7, 447-456.	1.8	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. <i>Lecture Notes in Computer Science</i> , 2006, , 138-149.	1.0	4
171	Simultaneous history reconstruction for complex gene clusters in multiple species. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2009, , 162-73.	0.7	4
172	A simple row-replacement method. <i>Software - Practice and Experience</i> , 1988, 18, 597-611.	2.5	3
173	Some Phenotype Association Tools in Galaxy: Looking for Disease SNPs in a Full Genome. <i>Current Protocols in Bioinformatics</i> , 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. <i>Biochemical and Biophysical Research Communications</i> , 2016, 474, 29-34.	1.0	2
175	Whole-Genome Analysis of Gene Conversion Events. <i>Lecture Notes in Computer Science</i> , 2009, , 181-192.	1.0	2
176	Aligning Two Genomic Sequences That Contain Duplications. <i>Lecture Notes in Computer Science</i> , 2009, , 98-110.	1.0	1
177	Inferring the Recent Duplication History of a Gene Cluster. <i>Lecture Notes in Computer Science</i> , 2009, , 111-125.	1.0	1
178	A Heuristic Algorithm for Reconstructing Ancestral Gene Orders with Duplications. <i>Lecture Notes in Computer Science</i> , 2007, , 122-135.	1.0	1
179	My adventure using computer science on the Genome project. <i>ACM SIGBIO Newsletter</i> , 1999, 19, 15-16.	0.1	0