

Webb Miller

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	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
2	Genomic Variants Among Threatened <i>Acropora</i> Corals. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1633-1646.	0.8	31
3	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
4	Elephantid Genomes Reveal the Molecular Bases of Woolly Mammoth Adaptations to the Arctic. <i>Cell Reports</i> , 2015, 12, 217-228.	2.9	127
5	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
6	Khoisan hunter-gatherers have been the largest population throughout most of modern-human demographic history. <i>Nature Communications</i> , 2014, 5, 5692.	5.8	65
7	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
8	Updates of the HbVar database of human hemoglobin variants and thalassemia mutations. <i>Nucleic Acids Research</i> , 2014, 42, D1063-D1069.	6.5	361
9	Galaxy tools to study genome diversity. <i>GigaScience</i> , 2013, 2, 17.	3.3	19
10	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
11	Comparison of Sequencing Platforms for Single Nucleotide Variant Calls in a Human Sample. <i>PLoS ONE</i> , 2013, 8, e55089.	1.1	70
12	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
13	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
14	Sequencing and analysis of a South Asian-Indian personal genome. <i>BMC Genomics</i> , 2012, 13, 440.	1.2	29
15	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
16	Revealing Mammalian Evolutionary Relationships by Comparative Analysis of Gene Clusters. <i>Genome Biology and Evolution</i> , 2012, 4, 586-601.	1.1	9
17	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
18	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541

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19	Evaluation of methods for detecting conversion events in gene clusters. BMC Bioinformatics, 2011, 12, S45.	1.2	7
20	Conversion events in gene clusters. BMC Evolutionary Biology, 2011, 11, 226.	3.2	12
21	Genome-wide identification of conserved regulatory function in diverged sequences. Genome Research, 2011, 21, 1139-1149.	2.4	72
22	Genetic diversity and population structure of the endangered marsupial <i>Sarcophilus harrisii</i> (Tasmanian devil). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12348-12353.	3.3	189
23	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671.	2.4	110
24	Calling SNPs without a reference sequence. BMC Bioinformatics, 2010, 11, 130.	1.2	37
25	Complete Khoisan and Bantu genomes from southern Africa. Nature, 2010, 463, 943-947.	13.7	400
26	CAGE: Combinatorial Analysis of Gene-Cluster Evolution. Journal of Computational Biology, 2010, 17, 1227-1242.	0.8	10
27	MultiPipMaker: A Comparative Alignment Server for Multiple DNA Sequences. Current Protocols in Bioinformatics, 2010, 30, Unit10.4.	25.8	12
28	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.	3.3	132
29	An Effective Method for Detecting Gene Conversion Events in Whole Genomes. Journal of Computational Biology, 2010, 17, 1281-1297.	0.8	11
30	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). Genome Research, 2009, 19, 213-220.	2.4	102
31	Evolutionary History Reconstruction for Mammalian Complex Gene Clusters. Journal of Computational Biology, 2009, 16, 1051-1070.	0.8	7
32	Erythroid GATA1 function revealed by genome-wide analysis of transcription factor occupancy, histone modifications, and mRNA expression. Genome Research, 2009, 19, 2172-2184.	2.4	184
33	CleaveLand: a pipeline for using degradome data to find cleaved small RNA targets. Bioinformatics, 2009, 25, 130-131.	1.8	642
34	Analysis of complete mitochondrial genomes from extinct and extant rhinoceroses reveals lack of phylogenetic resolution. BMC Evolutionary Biology, 2009, 9, 95.	3.2	92
35	Aligning Two Genomic Sequences That Contain Duplications. Lecture Notes in Computer Science, 2009, , 98-110.	1.0	1
36	OPTIMIZATION METHODS FOR SELECTING FOUNDER INDIVIDUALS FOR CAPTIVE BREEDING OR REINTRODUCTION OF ENDANGERED SPECIES. , 2009, , 43-53.		13

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37	Inferring the Recent Duplication History of a Gene Cluster. Lecture Notes in Computer Science, 2009, , 111-125.	1.0	1
38	Whole-Genome Analysis of Gene Conversion Events. Lecture Notes in Computer Science, 2009, , 181-192.	1.0	2
39	Simultaneous history reconstruction for complex gene clusters in multiple species. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 162-73.	0.7	4
40	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
41	Sequencing the nuclear genome of the extinct woolly mammoth. Nature, 2008, 456, 387-390.	13.7	283
42	Human-macaque comparisons illuminate variation in neutral substitution rates. Genome Biology, 2008, 9, R76.	13.9	54
43	Computational Reconstruction of Ancestral DNA Sequences. Methods in Molecular Biology, 2008, 422, 171-184.	0.4	23
44	Approximating the Spanning Star Forest Problem and Its Application to Genomic Sequence Alignment. SIAM Journal on Computing, 2008, 38, 946-962.	0.8	32
45	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.	3.3	149
46	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
47	Response to Comment on "Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts". Science, 2008, 322, 857-857.	6.0	6
48	Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif. Genome Research, 2008, 18, 1896-1905.	2.4	29
49	DUPCAR: Reconstructing Contiguous Ancestral Regions with Duplications. Journal of Computational Biology, 2008, 15, 1007-1027.	0.8	51
50	SIMULTANEOUS HISTORY RECONSTRUCTION FOR COMPLEX GENE CLUSTERS IN MULTIPLE SPECIES. , 2008, , .		5
51	Phylogenomic Resources at the UCSC Genome Browser. Methods in Molecular Biology, 2008, 422, 133-144.	0.4	7
52	Reconstructing the Evolutionary History of Complex Human Gene Clusters. , 2008, , 29-49.		9
53	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	2.4	237
54	Mobile DNA in Old World Monkeys: A Glimpse Through the Rhesus Macaque Genome. Science, 2007, 316, 238-240.	6.0	116

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55	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
56	Using genomic data to unravel the root of the placental mammal phylogeny. <i>Genome Research</i> , 2007, 17, 413-421.	2.4	394
57	Molecular and Genomic Data Identify the Closest Living Relative of Primates. <i>Science</i> , 2007, 318, 792-794.	6.0	282
58	Fast-evolving noncoding sequences in the human genome. <i>Genome Biology</i> , 2007, 8, R118.	13.9	163
59	Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts. <i>Science</i> , 2007, 317, 1927-1930.	6.0	220
60	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
61	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
62	Finding cis-regulatory elements using comparative genomics: Some lessons from ENCODE data. <i>Genome Research</i> , 2007, 17, 775-786.	2.4	69
63	PhenCode: connecting ENCODE data with mutations and phenotype. <i>Human Mutation</i> , 2007, 28, 554-562.	1.1	79
64	HbVar database of human hemoglobin variants and thalassemia mutations: 2007 update. <i>Human Mutation</i> , 2007, 28, 206-206.	1.1	175
65	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
66	Comparative Genomic Analysis Using the UCSC Genome Browser. <i>Methods in Molecular Biology</i> , 2007, 395, 17-33.	0.4	23
67	A Heuristic Algorithm for Reconstructing Ancestral Gene Orders with Duplications. <i>Lecture Notes in Computer Science</i> , 2007, , 122-135.	1.0	1
68	Reconstructing contiguous regions of an ancestral genome. <i>Genome Research</i> , 2006, 16, 1557-1565.	2.4	246
69	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
70	Metagenomics to Paleogenomics: Large-Scale Sequencing of Mammoth DNA. <i>Science</i> , 2006, 311, 392-394.	6.0	519
71	Experimental validation of predicted mammalian erythroid cis-regulatory modules. <i>Genome Research</i> , 2006, 16, 1480-1492.	2.4	56
72	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

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73	Identification and Classification of Conserved RNA Secondary Structures in the Human Genome. PLoS Computational Biology, 2006, 2, e33.	1.5	439
74	Controlling Size When Aligning Multiple Genomic Sequences with Duplications. Lecture Notes in Computer Science, 2006, , 138-149.	1.0	4
75	MultiPipMaker: Comparative Alignment Server for Multiple DNA Sequences. Current Protocols in Bioinformatics, 2005, 9, Unit10.4.	25.8	11
76	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. Nature, 2005, 434, 724-731.	13.7	85
77	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. Genome Research, 2005, 15, 1051-1060.	2.4	185
78	Mulan: Multiple-sequence local alignment and visualization for studying function and evolution. Genome Research, 2005, 15, 184-194.	2.4	218
79	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.	3.3	107
80	Evolution and functional classification of vertebrate gene deserts. Genome Research, 2005, 15, 137-145.	2.4	203
81	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	2.4	1,795
82	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. Genome Research, 2005, 15, 1034-1050.	2.4	3,517
83	Regulatory Potential Scores From Genome-Wide Three-Way Alignments of Human, Mouse, and Rat. Genome Research, 2004, 14, 700-707.	2.4	93
84	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.	6.5	285
85	Patterns of Insertions and Their Covariation With Substitutions in the Rat, Mouse, and Human Genomes. Genome Research, 2004, 14, 517-527.	2.4	73
86	Reconstructing large regions of an ancestral mammalian genome in silico. Genome Research, 2004, 14, 2412-2423.	2.4	121
87	zPicture: Dynamic Alignment and Visualization Tool for Analyzing Conservation Profiles. Genome Research, 2004, 14, 472-477.	2.4	128
88	Comparative Analysis of the \hat{A} -Like Globin Clusters in Mouse, Rat, and Human Chromosomes Indicates a Mechanism Underlying Breaks in Conserved Synteny. Genome Research, 2004, 14, 623-630.	2.4	29
89	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. Genome Research, 2004, 14, 708-715.	2.4	1,290
90	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943

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91	COMPARATIVE GENOMICS. Annual Review of Genomics and Human Genetics, 2004, 5, 15-56.	2.5	156
92	Improvements to GALA and dbERGE II: databases featuring genomic sequence alignment, annotation and experimental results. Nucleic Acids Research, 2004, 33, D466-D470.	6.5	9
93	Transcription-associated mutational asymmetry in mammalian evolution. Nature Genetics, 2003, 33, 514-517.	9.4	271
94	Multispecies comparative analysis of a mammalian-specific genomic domain encoding secretory proteins. Genomics, 2003, 82, 417-432.	1.3	82
95	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. Genome Research, 2003, 13, 13-26.	2.4	263
96	PipMaker: A World Wide Web Server for Genomic Sequence Alignments. Current Protocols in Bioinformatics, 2003, 00, Unit 10.2.	25.8	16
97	EnteriX 2003: visualization tools for genome alignments of Enterobacteriaceae. Nucleic Acids Research, 2003, 31, 3527-3532.	6.5	23
98	MultiPipMaker and supporting tools: alignments and analysis of multiple genomic DNA sequences. Nucleic Acids Research, 2003, 31, 3518-3524.	6.5	196
99	GALA, a Database for Genomic Sequence Alignments and Annotations. Genome Research, 2003, 13, 732-741.	2.4	45
100	Distinguishing Regulatory DNA From Neutral Sites. Genome Research, 2003, 13, 64-72.	2.4	118
101	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.	3.3	792
102	Significance of Interspecies Matches when Evolutionary Rate Varies. Journal of Computational Biology, 2003, 10, 537-554.	0.8	12
103	Human-Mouse Alignments with BLASTZ. Genome Research, 2003, 13, 103-107.	2.4	1,071
104	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
105	The Chlamydomonas reinhardtii Plastid Chromosome. Plant Cell, 2002, 14, 2659-2679.	3.1	390
106	Significance Of inter-species matches when evolutionary rate varies. , 2002, , .		5
107	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
108	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

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109	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
110	PipTools: A Computational Toolkit to Annotate and Analyze Pairwise Comparisons of Genomic Sequences. <i>Genomics</i> , 2002, 80, 681-690.	1.3	32
111	Functional and binding studies of HS3.2 of the beta-globin locus control region. <i>Gene</i> , 2002, 283, 185-197.	1.0	9
112	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
113	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
114	Use of subtractive hybridization for comprehensive surveys of prokaryotic genome differences. <i>FEMS Microbiology Letters</i> , 2002, 211, 175-182.	0.7	49
115	Complete genome sequence of <i>Salmonella enterica</i> serovar Typhimurium LT2. <i>Nature</i> , 2001, 413, 852-856.	13.7	1,712
116	A Negative Cis-element Regulates the Level of Enhancement by Hypersensitive Site 2 of the $\hat{\gamma}^2$ -Globin Locus Control Region. <i>Journal of Biological Chemistry</i> , 2001, 276, 6289-6298.	1.6	17
117	DATABASES OF HUMAN HEMOGLOBIN VARIANTS AND OTHER RESOURCES AT THE GLOBIN GENE SERVER. <i>Hemoglobin</i> , 2001, 25, 183-193.	0.4	35
118	Sequences Flanking Hypersensitive Sites of the $\hat{\gamma}^2$ -Globin Locus Control Region Are Required for Synergistic Enhancement. <i>Molecular and Cellular Biology</i> , 2001, 21, 2969-2980.	1.1	49
119	Comparative analysis of the gene-dense ACHE/TFR2 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
120	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
121	So many genomes, so little time. <i>Nature Biotechnology</i> , 2000, 18, 148-149.	9.4	19
122	Winnowing Sequences from a Database Search. <i>Journal of Computational Biology</i> , 2000, 7, 293-302.	0.8	6
123	Genomic Sequence Analysis of the Mouse Naip Gene Array. <i>Genome Research</i> , 2000, 10, 1095-1102.	2.4	60
124	PipMaker--A Web Server for Aligning Two Genomic DNA Sequences. <i>Genome Research</i> , 2000, 10, 577-586.	2.4	1,070
125	Web-based visualization tools for bacterial genome alignments. <i>Nucleic Acids Research</i> , 2000, 28, 3486-3496.	6.5	29
126	A Greedy Algorithm for Aligning DNA Sequences. <i>Journal of Computational Biology</i> , 2000, 7, 203-214.	0.8	4,325

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127	Winnowing sequences from a database search. , 1999, , .		4
128	The gene mutated in bare patches and striated mice encodes a novel 3 β -hydroxysteroid dehydrogenase. Nature Genetics, 1999, 22, 182-187.	9.4	147
129	The mouse cornichon gene family. Development Genes and Evolution, 1999, 209, 120-125.	0.4	15
130	Comparative Sequence Analysis of the Mouse and Human Lgn1/SMA Interval. Genomics, 1999, 60, 137-151.	1.3	39
131	Characterization of the Human and Mouse Unconventional Myosin XV Genes Responsible for Hereditary Deafness DFNB3 and Shaker 2. Genomics, 1999, 61, 243-258.	1.3	153
132	My adventure using computer science on the Genome project. ACM SIGBIO Newsletter, 1999, 19, 15-16.	0.1	0
133	Comparative Sequence of Human and Mouse BAC Clones from the mnd2 Region of Chromosome 2p13. Genome Research, 1999, 9, 53-61.	2.4	55
134	PROGRAM DESCRIPTION. Genomics, 1998, 47, 429-437.	1.3	35
135	A Database of Experimental Results on Globin Gene Expression. Genomics, 1998, 53, 325-337.	1.3	14
136	Alignments Without Low-Scoring Regions. Journal of Computational Biology, 1998, 5, 197-210.	0.8	46
137	Multiple Regulatory Elements in the 5 β -Flanking Sequence of the Human β -Globin Gene. Journal of Biological Chemistry, 1998, 273, 10202-10209.	1.6	23
138	A Computer Program for Aligning a cDNA Sequence with a Genomic DNA Sequence. Genome Research, 1998, 8, 967-974.	2.4	683
139	Analysis of the Quality and Utility of Random Shotgun Sequencing at Low Redundancies. Genome Research, 1998, 8, 1074-1084.	2.4	59
140	A tool for aligning very similar DNA sequences. Bioinformatics, 1997, 13, 75-80.	1.8	14
141	Conserved E Boxes Function as Part of the Enhancer in Hypersensitive Site 2 of the β -Globin Locus Control Region. Journal of Biological Chemistry, 1997, 272, 369-378.	1.6	74
142	Long Human-Mouse Sequence Alignments Reveal Novel Regulatory Elements: A Reason to Sequence the Mouse Genome. Genome Research, 1997, 7, 959-966.	2.4	294
143	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.	2.4	131
144	The Complete Sequences of the Galago and Rabbit β -Globin Locus Control Regions: Extended Sequence and Functional Conservation Outside the Cores of DNase Hypersensitive Sites. Genomics, 1997, 39, 90-94.	1.3	34

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145	Comparison of DNA Sequences with Protein Sequences. <i>Genomics</i> , 1997, 46, 24-36.	1.3	557
146	Aligning a DNA Sequence with a Protein Sequence. <i>Journal of Computational Biology</i> , 1997, 4, 339-349.	0.8	31
147	Locus control regions of mammalian $\hat{\nu}$ -globin gene clusters: combining phylogenetic analyses and experimental results to gain functional insights. <i>Gene</i> , 1997, 205, 73-94.	1.0	226
148	Phylogenetic Footprinting of Hypersensitive Site 3 of the $\hat{\nu}$ -Globin Locus Control Region. <i>Blood</i> , 1997, 89, 3457-3469.	0.6	35
149	Role of DNA Sequences Outside the Cores of DNase Hypersensitive Sites (HSs) in Functions of the $\hat{\nu}$ -Globin Locus Control Region. <i>Journal of Biological Chemistry</i> , 1996, 271, 11871-11878.	1.6	52
150	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
151	Chaining Multiple-Alignment Blocks. <i>Journal of Computational Biology</i> , 1994, 1, 217-226.	0.8	24
152	Recent Developments in Linear-Space Alignment Methods: A Survey. <i>Journal of Computational Biology</i> , 1994, 1, 271-291.	0.8	51
153	Parametric recomputing in alignment graphs. <i>Lecture Notes in Computer Science</i> , 1994, , 87-101.	1.0	10
154	Constrained sequence alignment. <i>Bulletin of Mathematical Biology</i> , 1993, 55, 503-524.	0.9	19
155	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
156	Comparative analysis of the locus control region of the rabbit $\hat{\nu}$ -like globin gene cluster: HS3 increases transient expression of an embryonic $\hat{\mu}$ -globin gene. <i>Nucleic Acids Research</i> , 1993, 21, 1265-1272.	6.5	47
157	Aligning two sequences within a specified diagonal band. <i>Bioinformatics</i> , 1992, 8, 481-487.	1.8	94
158	[27] Dynamic programming algorithms for biological sequence comparison. <i>Methods in Enzymology</i> , 1992, 210, 575-601.	0.4	76
159	Sequence and comparative analysis of the rabbit $\hat{\nu}$ -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
160	A time-efficient, linear-space local similarity algorithm. <i>Advances in Applied Mathematics</i> , 1991, 12, 337-357.	0.4	933
161	Improved algorithms for searching restriction maps. <i>Bioinformatics</i> , 1991, 7, 447-456.	1.8	5
162	Mapping sequenced <i>E. coli</i> genes by computer: software, strategies and examples. <i>Nucleic Acids Research</i> , 1991, 19, 637-647.	6.5	85

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163	Software tools for analyzing pairwise alignments of long sequences. Nucleic Acids Research, 1991, 19, 4663-4667.	6.5	36
164	An O(NP) sequence comparison algorithm. Information Processing Letters, 1990, 35, 317-323.	0.4	90
165	An algorithm for searching restriction maps. Bioinformatics, 1990, 6, 247-252.	1.8	8
166	A space-efficient algorithm for local similarities. Bioinformatics, 1990, 6, 373-381.	1.8	99
167	Alignment of Escherichia coli K12 DNA sequences to a genomic restriction map. Nucleic Acids Research, 1990, 18, 313-321.	6.5	111
168	Basic local alignment search tool. Journal of Molecular Biology, 1990, 215, 403-410.	2.0	82,180
169	Row replacement algorithms for screen editors. ACM Transactions on Programming Languages and Systems, 1989, 11, 33-56.	1.7	11
170	Approximate matching of regular expressions. Bulletin of Mathematical Biology, 1989, 51, 5-37.	0.9	130
171	Sequence comparison with concave weighting functions. Bulletin of Mathematical Biology, 1988, 50, 97-120.	0.9	124
172	A simple row-replacement method. Software - Practice and Experience, 1988, 18, 597-611.	2.5	3
173	A file comparison program. Software - Practice and Experience, 1985, 15, 1025-1040.	2.5	146
174	Software for Roundoff Analysis. ACM Transactions on Mathematical Software, 1975, 1, 108-128.	1.6	38
175	Computer Search for Numerical Instability. Journal of the ACM, 1975, 22, 512-521.	1.8	18
176	On the stability of finite numerical procedures. Numerische Mathematik, 1972, 19, 425-432.	0.9	8
177	Quadratic convergence in interval arithmetic, part I. BIT Numerical Mathematics, 1972, 12, 284-290.	1.0	16
178	Quadratic convergence in interval arithmetic, part II. BIT Numerical Mathematics, 1972, 12, 291-298.	1.0	14
179	On an interval-arithmetic matrix method. BIT Numerical Mathematics, 1972, 12, 213-219.	1.0	9