Webb Miller

List of Publications by Year in Descending Order

180 papers	105,803 citations	72 h-index	183 g-index
183 ext. papers	117,468 ext. citations	11 avg, IF	7.42 L-index

#	Paper	IF	Citations
180	Functional Architecture of Deleterious Genetic Variants in the Genome of a Wrangel Island Mammoth. *Genome Biology and Evolution*, **2020**, 12, 48-58	3.9	4
179	Genomic Variants Among Threatened Corals. *G3: Genes, Genomes, Genetics*, **2019**, 9, 1633-1646	3.2	17
178	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	3.4	1
177	Elephantid Genomes Reveal the Molecular Bases of Woolly Mammoth Adaptations to the Arctic. *Cell Reports*, **2015**, 12, 217-28	10.6	79
176	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	4.5	29
175	Updates of the HbVar database of human hemoglobin variants and thalassemia mutations. *Nucleic Acids Research*, **2014**, 42, D1063-9	20.1	289
174	Khoisan hunter-gatherers have been the largest population throughout most of modern-human demographic history. *Nature Communications*, **2014**, 5, 5692	17.4	49
173	Polar bears exhibit genome-wide signatures of bioenergetic adaptation to life in the arctic environment. *Genome Biology and Evolution*, **2014**, 6, 433-50	3.9	44
172	Galaxy tools to study genome diversity. *GigaScience*, **2013**, 2, 17	7.6	18
171	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, 5823-8	11.5	31
170	Comparison of sequencing platforms for single nucleotide variant calls in a human sample. *PLoS ONE*, **2013**, 8, e55089	3.7	59
169	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	11.5	243
168	Sequencing and analysis of a South Asian-Indian personal genome. *BMC Genomics*, **2012**, 13, 440	4.5	23
167	Some phenotype association tools in Galaxy: looking for disease SNPs in a full genome. *Current Protocols in Bioinformatics*, **2012**, Chapter 15, Unit15.2	24.2	
166	Revealing mammalian evolutionary relationships by comparative analysis of gene clusters. *Genome Biology and Evolution*, **2012**, 4, 586-601	3.9	8
165	A genome sequence resource for the aye-aye (Daubentonia madagascariensis), a nocturnal lemur from Madagascar. *Genome Biology and Evolution*, **2012**, 4, 126-35	3.9	48
164	Systematic documentation and analysis of human genetic variation in hemoglobinopathies using the microattribution approach. *Nature Genetics*, **2011**, 43, 295-301	36.3	125

163	Comparative and demographic analysis of orang-utan genomes. *Nature*, **2011**, 469, 529-33	50.4	431
162	Evaluation of methods for detecting conversion events in gene clusters. *BMC Bioinformatics*, **2011**, 12 Suppl 1, S45	3.6	7
161	Conversion events in gene clusters. *BMC Evolutionary Biology*, **2011**, 11, 226	3	10
160	Genome-wide identification of conserved regulatory function in diverged sequences. *Genome Research*, **2011**, 21, 1139-49	9.7	54
159	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, 12348-53	11.5	164
158	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. *Genome Research*, **2011**, 21, 1659-71	9.7	100
157	Complete Khoisan and Bantu genomes from southern Africa. *Nature*, **2010**, 463, 943-7	50.4	342
156	CAGE: Combinatorial Analysis of Gene-cluster Evolution. *Journal of Computational Biology*, **2010**, 17, 1227-42	1.7	9
155	MultiPipMaker: a comparative alignment server for multiple DNA sequences. *Current Protocols in Bioinformatics*, **2010**, Chapter 10, Unit10.4	24.2	6
154	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, 5053-7	11.5	114
153	An effective method for detecting gene conversion events in whole genomes. *Journal of Computational Biology*, **2010**, 17, 1281-97	1.7	11
152	Optimization methods for selecting founder individuals for captive breeding or reintroduction of endangered species. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2010**, 43-53	1.3	11
151	Calling SNPs without a reference sequence. *BMC Bioinformatics*, **2010**, 11, 130	3.6	35
150	Evolutionary history reconstruction for Mammalian complex gene clusters. *Journal of Computational Biology*, **2009**, 16, 1051-70	1.7	5
149	Erythroid GATA1 function revealed by genome-wide analysis of transcription factor occupancy, histone modifications, and mRNA expression. *Genome Research*, **2009**, 19, 2172-84	9.7	163
148	CleaveLand: a pipeline for using degradome data to find cleaved small RNA targets. *Bioinformatics*, **2009**, 25, 130-1	7.2	429
147	Analysis of complete mitochondrial genomes from extinct and extant rhinoceroses reveals lack of phylogenetic resolution. *BMC Evolutionary Biology*, **2009**, 9, 95	3	77
146	Aligning Two Genomic Sequences That Contain Duplications. *Lecture Notes in Computer Science*, **2009**, 98-110	0.9	1

145	The mitochondrial genome sequence of the Tasmanian tiger (Thylacinus cynocephalus). *Genome Research*, **2009**, 19, 213-20	9.7	83
144	Simultaneous history reconstruction for complex gene clusters in multiple species. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2009**, 162-73	1.3	4
143	Inferring the Recent Duplication History of a Gene Cluster. *Lecture Notes in Computer Science*, **2009**, 111-125	1.3	1
142	Whole-Genome Analysis of Gene Conversion Events. *Lecture Notes in Computer Science*, **2009**, 181-192	0.9	2
141	Genome analysis of the platypus reveals unique signatures of evolution. *Nature*, **2008**, 453, 175-83	50.4	545
140	Sequencing the nuclear genome of the extinct woolly mammoth. *Nature*, **2008**, 456, 387-90	50.4	242
139	Human-macaque comparisons illuminate variation in neutral substitution rates. *Genome Biology*, **2008**, 9, R76	18.3	44
138	Computational reconstruction of ancestral DNA sequences. *Methods in Molecular Biology*, **2008**, 422, 171-84	1.4	21
137	Approximating the Spanning Star Forest Problem and Its Application to Genomic Sequence Alignment. *SIAM Journal on Computing*, **2008**, 38, 946-962	1.1	25
136	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, 8327-32	11.5	130
135	The infinite sites model of genome evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 14254-61	11.5	65
134	Comment on "Whole-genome shotgun sequencing of mitochondria from ancient hair shafts". *Science*, **2008**, 322, 857; author reply 857	33.3	5
133	Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif. *Genome Research*, **2008**, 18, 1896-905	9.7	28
132	DUPCAR: reconstructing contiguous ancestral regions with duplications. *Journal of Computational Biology*, **2008**, 15, 1007-27	1.7	48
131	SIMULTANEOUS HISTORY RECONSTRUCTION FOR COMPLEX GENE CLUSTERS IN MULTIPLE SPECIES **2008**,		1
130	Phylogenomic resources at the UCSC Genome Browser. *Methods in Molecular Biology*, **2008**, 422, 133-44	1.4	7
129	Reconstructing the Evolutionary History of Complex Human Gene Clusters **2008**, 29-49		8
128	Evolutionary and biomedical insights from the rhesus macaque genome. *Science*, **2007**, 316, 222-34	33.3	1072

127	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. *Genome Research*, **2007**, 17, 760-74	9.7	163
126	Finding cis-regulatory elements using comparative genomics: some lessons from ENCODE data. *Genome Research*, **2007**, 17, 775-86	9.7	61
125	PhenCode: connecting ENCODE data with mutations and phenotype. *Human Mutation*, **2007**, 28, 554-62	4.7	72
124	HbVar database of human hemoglobin variants and thalassemia mutations: 2007 update. *Human Mutation*, **2007**, 28, 206	4.7	150
123	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
122	28-way vertebrate alignment and conservation track in the UCSC Genome Browser. *Genome Research*, **2007**, 17, 1797-808	9.7	204
121	Mobile DNA in Old World monkeys: a glimpse through the rhesus macaque genome. *Science*, **2007**, 316, 238-40	33.3	93
120	A framework for collaborative analysis of ENCODE data: making large-scale analyses biologist-friendly. *Genome Research*, **2007**, 17, 960-4	9.7	105
119	Using genomic data to unravel the root of the placental mammal phylogeny. *Genome Research*, **2007**, 17, 413-21	9.7	350
118	Molecular and genomic data identify the closest living relative of primates. *Science*, **2007**, 318, 792-4	33.3	233
117	Fast-evolving noncoding sequences in the human genome. *Genome Biology*, **2007**, 8, R118	18.3	116
116	Whole-genome shotgun sequencing of mitochondria from ancient hair shafts. *Science*, **2007**, 317, 1927-30	33.3	191
115	Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. *Nucleic Acids Research*, **2007**, 35, 1-10	20.1	136
114	A Heuristic Algorithm for Reconstructing Ancestral Gene Orders with Duplications. *Lecture Notes in Computer Science*, **2007**, 122-135	0.9	1
113	Comparative genomic analysis using the UCSC genome browser. *Methods in Molecular Biology*, **2007**, 395, 17-34	1.4	18
112	Experimental validation of predicted mammalian erythroid cis-regulatory modules. *Genome Research*, **2006**, 16, 1480-92	9.7	49
111	ESPERR: learning strong and weak signals in genomic sequence alignments to identify functional elements. *Genome Research*, **2006**, 16, 1596-604	9.7	97
110	Identification and classification of conserved RNA secondary structures in the human genome. *PLoS Computational Biology*, **2006**, 2, e33	5	394

109	Reconstructing contiguous regions of an ancestral genome. *Genome Research*, **2006**, 16, 1557-65	9.7	216
108	Metagenomics to paleogenomics: large-scale sequencing of mammoth DNA. *Science*, **2006**, 311, 392-4	33.3	435
107	Controlling Size When Aligning Multiple Genomic Sequences with Duplications. *Lecture Notes in Computer Science*, **2006**, 138-149	0.9	3
106	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. *Genome Research*, **2005**, 15, 1034-50	9.7	2643
105	Improvements to GALA and dbERGE II: databases featuring genomic sequence alignment, annotation and experimental results. *Nucleic Acids Research*, **2005**, 33, D466-70	20.1	6
104	MultiPipMaker: comparative alignment server for multiple DNA sequences. *Current Protocols in Bioinformatics*, **2005**, Chapter 10, Unit10.4	24.2	7
103	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. *Nature*, **2005**, 434, 724-31	50.4	61
102	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. *Genome Research*, **2005**, 15, 1051-60	9.7	164
101	Mulan: multiple-sequence local alignment and visualization for studying function and evolution. *Genome Research*, **2005**, 15, 184-94	9.7	199
100	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, 4795-800	11.5	98
99	Evolution and functional classification of vertebrate gene deserts. *Genome Research*, **2005**, 15, 137-45	9.7	179
98	Galaxy: a platform for interactive large-scale genome analysis. *Genome Research*, **2005**, 15, 1451-5	9.7	1509
97	Regulatory potential scores from genome-wide three-way alignments of human, mouse, and rat. *Genome Research*, **2004**, 14, 700-7	9.7	84
96	Improvements in the HbVar database of human hemoglobin variants and thalassemia mutations for population and sequence variation studies. *Nucleic Acids Research*, **2004**, 32, D537-41	20.1	250
95	Patterns of insertions and their covariation with substitutions in the rat, mouse, and human genomes. *Genome Research*, **2004**, 14, 517-27	9.7	60
94	Reconstructing large regions of an ancestral mammalian genome in silico. *Genome Research*, **2004**, 14, 2412-23	9.7	98
93	zPicture: dynamic alignment and visualization tool for analyzing conservation profiles. *Genome Research*, **2004**, 14, 472-7	9.7	119
92	Comparative analysis of the alpha-like globin clusters in mouse, rat, and human chromosomes indicates a mechanism underlying breaks in conserved synteny. *Genome Research*, **2004**, 14, 623-30	9.7	26

91	Aligning multiple genomic sequences with the threaded blockset aligner. *Genome Research*, **2004**, 14, 708-15	9.7	1006
90	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature*, **2004**, 428, 493-521	50.4	1689
89	Comparative genomics. *Annual Review of Genomics and Human Genetics*, **2004**, 5, 15-56	9.7	136
88	Human-mouse alignments with BLASTZ. *Genome Research*, **2003**, 13, 103-7	9.7	920
87	A combinatorial network of evolutionarily conserved myelin basic protein regulatory sequences confers distinct glial-specific phenotypes. *Journal of Neuroscience*, **2003**, 23, 10214-23	6.6	69
86	Transcription-associated mutational asymmetry in mammalian evolution. *Nature Genetics*, **2003**, 33, 514-7	6.3	238
85	Multispecies comparative analysis of a mammalian-specific genomic domain encoding secretory proteins. *Genomics*, **2003**, 82, 417-32	4.3	66
84	Covariation in frequencies of substitution, deletion, transposition, and recombination during eutherian evolution. *Genome Research*, **2003**, 13, 13-26	9.7	234
83	PipMaker: a World Wide Web server for genomic sequence alignments. *Current Protocols in Bioinformatics*, **2003**, Chapter 10, Unit 10.2	24.2	15
82	EnteriX 2003: Visualization tools for genome alignments of Enterobacteriaceae. *Nucleic Acids Research*, **2003**, 31, 3527-32	20.1	22
81	MultiPipMaker and supporting tools: Alignments and analysis of multiple genomic DNA sequences. *Nucleic Acids Research*, **2003**, 31, 3518-24	20.1	174
80	GALA, a database for genomic sequence alignments and annotations. *Genome Research*, **2003**, 13, 732-41	9.7	39
79	Distinguishing regulatory DNA from neutral sites. *Genome Research*, **2003**, 13, 64-72	9.7	103
78	Evolution@ 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, 11484-9	11.5	624
77	Significance of interspecies matches when evolutionary rate varies. *Journal of Computational Biology*, **2003**, 10, 537-54	1.7	10
76	HbVar: A relational database of human hemoglobin variants and thalassemia mutations at the globin gene server. *Human Mutation*, **2002**, 19, 225-33	4.7	354
75	Initial sequencing and comparative analysis of the mouse genome. *Nature*, **2002**, 420, 520-62	50.4	5376
74	Use of subtractive hybridization for comprehensive surveys of prokaryotic genome differences. *FEMS Microbiology Letters*, **2002**, 211, 175-82	2.9	46

73	The Chlamydomonas reinhardtii plastid chromosome: islands of genes in a sea of repeats. *Plant Cell* , **2002**, 14, 2659-79	11.6	332
72	Significance Of inter-species matches when evolutionary rate varies **2002**,		4
71	Generation and comparative analysis of approximately 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	9.7	54
70	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, 780-5	11.5	62
69	Candidate genes required for embryonic development: a comparative analysis of distal mouse chromosome 14 and human chromosome 13q22. *Genomics*, **2002**, 79, 154-61	4.3	17
68	PipTools: a computational toolkit to annotate and analyze pairwise comparisons of genomic sequences. *Genomics*, **2002**, 80, 681-90	4.3	28
67	Functional and binding studies of HS3.2 of the beta-globin locus control region. *Gene*, **2002**, 283, 185-97	3.8	9
66	Complete genome sequence of Salmonella enterica serovar Typhimurium LT2. *Nature*, **2001**, 413, 852-6	50.4	1500
65	A negative cis-element regulates the level of enhancement by hypersensitive site 2 of the beta-globin locus control region. *Journal of Biological Chemistry*, **2001**, 276, 6289-98	5.4	16
64	Databases of human hemoglobin variants and other resources at the globin gene server. *Hemoglobin*, **2001**, 25, 183-93	0.6	31
63	Sequences flanking hypersensitive sites of the beta-globin locus control region are required for synergistic enhancement. *Molecular and Cellular Biology*, **2001**, 21, 2969-80	4.8	47
62	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, 1352-65	20.1	36
61	The human and mouse MHC class III region: a parade of 21 genes at the centromeric segment. *Trends in Immunology*, **2000**, 21, 320-8		39
60	Winnowing sequences from a database search. *Journal of Computational Biology*, **2000**, 7, 293-302	1.7	4
59	Genomic sequence analysis of the mouse Naip gene array. *Genome Research*, **2000**, 10, 1095-102	9.7	56
58	PipMaker--a web server for aligning two genomic DNA sequences. *Genome Research*, **2000**, 10, 577-86	9.7	906
57	Web-based visualization tools for bacterial genome alignments. *Nucleic Acids Research*, **2000**, 28, 3486-96	20.1	26
56	A greedy algorithm for aligning DNA sequences. *Journal of Computational Biology*, **2000**, 7, 203-14	1.7	3220

55	Winnowing sequences from a database search **1999**,		2
54	The gene mutated in bare patches and striated mice encodes a novel 3beta-hydroxysteroid dehydrogenase. *Nature Genetics*, **1999**, 22, 182-7	36.3	135
53	The mouse cornichon gene family. *Development Genes and Evolution*, **1999**, 209, 120-5	1.8	13
52	Comparative sequence analysis of the mouse and human Lgn1/SMA interval. *Genomics*, **1999**, 60, 137-51	4.3	37
51	Characterization of the human and mouse unconventional myosin XV genes responsible for hereditary deafness DFNB3 and shaker 2. *Genomics*, **1999**, 61, 243-58	4.3	141
50	Comparative Sequence of Human and Mouse BAC Clones from the mnd2 Region of Chromosome 2p13. *Genome Research*, **1999**, 9, 53-61	9.7	44
49	My adventure using computer science on the Genome project. *ACM SIGBIO Newsletter*, **1999**, 19, 15-16		
48	Electronic access to sequence alignments, experimental results, and human mutations as an aid to studying globin gene regulation. *Genomics*, **1998**, 47, 429-37	4.3	35
47	A database of experimental results on globin gene expression. *Genomics*, **1998**, 53, 325-37	4.3	12
46	Alignments without low-scoring regions. *Journal of Computational Biology*, **1998**, 5, 197-210	1.7	39
45	Multiple regulatory elements in the 5C-flanking sequence of the human epsilon-globin gene. *Journal of Biological Chemistry*, **1998**, 273, 10202-9	5.4	19
44	A computer program for aligning a cDNA sequence with a genomic DNA sequence. *Genome Research*, **1998**, 8, 967-74	9.7	622
43	Analysis of the quality and utility of random shotgun sequencing at low redundancies. *Genome Research*, **1998**, 8, 1074-84	9.7	53
42	A tool for aligning very similar DNA sequences. *Bioinformatics*, **1997**, 13, 75-80	7.2	8
41	Conserved E boxes function as part of the enhancer in hypersensitive site 2 of the beta-globin locus control region. Role of basic helix-loop-helix proteins. *Journal of Biological Chemistry*, **1997**, 272, 369-78	5.4	70
40	Long human-mouse sequence alignments reveal novel regulatory elements: a reason to sequence the mouse genome. *Genome Research*, **1997**, 7, 959-66	9.7	268
39	Large-scale comparative sequence analysis of the human and murine Bruton⠀ tyrosine kinase loci reveals conserved regulatory domains. *Genome Research*, **1997**, 7, 315-29	9.7	126
38	The complete sequences of the galago and rabbit beta-globin locus control regions: extended sequence and functional conservation outside the cores of DNase hypersensitive sites. *Genomics*, **1997**, 39, 90-4	4.3	34

37	Comparison of DNA sequences with protein sequences. *Genomics*, **1997**, 46, 24-36	4.3	505
36	Aligning a DNA sequence with a protein sequence. *Journal of Computational Biology*, **1997**, 4, 339-49	1.7	23
35	Locus control regions of mammalian beta-globin gene clusters: combining phylogenetic analyses and experimental results to gain functional insights. *Gene*, **1997**, 205, 73-94	3.8	207
34	Phylogenetic Footprinting of Hypersensitive Site 3 of the ε-Globin Locus Control Region. *Blood*, **1997**, 89, 3457-3469	2.2	35
33	Role of DNA sequences outside the cores of DNase hypersensitive sites (HSs) in functions of the beta-globin locus control region. Domain opening and synergism between HS2 and HS3. *Journal of Biological Chemistry*, **1996**, 271, 11871-8	5.4	46
32	Globin gene server: a prototype E-mail database server featuring extensive multiple alignments and data compilation for electronic genetic analysis. *Genomics*, **1994**, 21, 344-53	4.3	31
31	Chaining multiple-alignment blocks. *Journal of Computational Biology*, **1994**, 1, 217-26	1.7	19
30	Recent developments in linear-space alignment methods: a survey. *Journal of Computational Biology*, **1994**, 1, 271-91	1.7	37
29	Parametric recomputing in alignment graphs. *Lecture Notes in Computer Science*, **1994**, 87-101	0.9	6
28	Positive and negative regulatory elements of the rabbit embryonic epsilon-globin gene revealed by an improved multiple alignment program and functional analysis. *DNA Sequence*, **1993**, 4, 163-76		25
27	Comparative analysis of the locus control region of the rabbit beta-like gene cluster: HS3 increases transient expression of an embryonic epsilon-globin gene. *Nucleic Acids Research*, **1993**, 21, 1265-72	20.1	44
26	Constrained sequence alignment. *Bulletin of Mathematical Biology*, **1993**, 55, 503-24	2.1	9
25	Aligning two sequences within a specified diagonal band. *Bioinformatics*, **1992**, 8, 481-7	7.2	63
24	Dynamic programming algorithms for biological sequence comparison. *Methods in Enzymology*, **1992**, 210, 575-601	1.7	53
23	A time-efficient, linear-space local similarity algorithm. *Advances in Applied Mathematics*, **1991**, 12, 337-357	1.3	841
22	Improved algorithms for searching restriction maps. *Bioinformatics*, **1991**, 7, 447-56	7.2	2
21	Mapping sequenced E.coli genes by computer: software, strategies and examples. *Nucleic Acids Research*, **1991**, 19, 637-47	20.1	72
20	Software tools for analyzing pairwise alignments of long sequences. *Nucleic Acids Research*, **1991**, 19, 4663-7	20.1	30

19	Sequence and comparative analysis of the rabbit alpha-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, 233-49	6.5	38
18	An O(NP) sequence comparison algorithm. *Information Processing Letters*, **1990**, 35, 317-323	0.8	61
17	An algorithm for searching restriction maps. *Bioinformatics*, **1990**, 6, 247-52	7.2	5
16	A space-efficient algorithm for local similarities. *Bioinformatics*, **1990**, 6, 373-81	7.2	73
15	Alignment of Escherichia coli K12 DNA sequences to a genomic restriction map. *Nucleic Acids Research*, **1990**, 18, 313-21	20.1	97
14	Basic local alignment search tool. *Journal of Molecular Biology*, **1990**, 215, 403-10	6.5	65807
13	Row replacement algorithms for screen editors. *ACM Transactions on Programming Languages and Systems*, **1989**, 11, 33-56	1.6	9
12	Approximate matching of regular expressions. *Bulletin of Mathematical Biology*, **1989**, 51, 5-37	2.1	118
11	Sequence comparison with concave weighting functions. *Bulletin of Mathematical Biology*, **1988**, 50, 97-120	2.1	79
10	A simple row-replacement method. *Software - Practice and Experience*, **1988**, 18, 597-611	2.5	2
9	A file comparison program. *Software - Practice and Experience*, **1985**, 15, 1025-1040	2.5	104
8	Software for Roundoff Analysis. *ACM Transactions on Mathematical Software*, **1975**, 1, 108-128	2.3	31
7	Computer Search for Numerical Instability. *Journal of the ACM*, **1975**, 22, 512-521	2	14
6	On the stability of finite numerical procedures. *Numerische Mathematik*, **1972**, 19, 425-432	2.2	6
5	Quadratic convergence in interval arithmetic, part I. *BIT Numerical Mathematics*, **1972**, 12, 284-290	1.7	12
4	Quadratic convergence in interval arithmetic, part II. *BIT Numerical Mathematics*, **1972**, 12, 291-298	1.7	13
3	On an interval-arithmetic matrix method. *BIT Numerical Mathematics*, **1972**, 12, 213-219	1.7	7
2	Genome-wide evidence for a hybrid origin of modern polar bears		3