

Webb Miller

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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	Basic local alignment search tool. <i>Journal of Molecular Biology</i> , 1990 , 215, 403-10	6.5	65807
179	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002 , 420, 520-62	50.4	5376
178	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
177	A greedy algorithm for aligning DNA sequences. <i>Journal of Computational Biology</i> , 2000 , 7, 203-14	1.7	3220
176	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005 , 15, 1034-50	9.7	2643
175	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
174	Galaxy: a platform for interactive large-scale genome analysis. <i>Genome Research</i> , 2005 , 15, 1451-5	9.7	1509
173	Complete genome sequence of <i>Salmonella enterica</i> serovar Typhimurium LT2. <i>Nature</i> , 2001 , 413, 852-6	50.4	1500
172	Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , 2007 , 316, 222-34	33.3	1072
171	Aligning multiple genomic sequences with the threaded blockset aligner. <i>Genome Research</i> , 2004 , 14, 708-15	9.7	1006
170	Human-mouse alignments with BLASTZ. <i>Genome Research</i> , 2003 , 13, 103-7	9.7	920
169	PipMaker--a web server for aligning two genomic DNA sequences. <i>Genome Research</i> , 2000 , 10, 577-86	9.7	906
168	A time-efficient, linear-space local similarity algorithm. <i>Advances in Applied Mathematics</i> , 1991 , 12, 337-353		841
167	EvolutionQ 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, 11484-9	11.5	624
166	A computer program for aligning a cDNA sequence with a genomic DNA sequence. <i>Genome Research</i> , 1998 , 8, 967-74	9.7	622
165	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008 , 453, 175-83	50.4	545
164	Comparison of DNA sequences with protein sequences. <i>Genomics</i> , 1997 , 46, 24-36	4.3	505

163	Metagenomics to paleogenomics: large-scale sequencing of mammoth DNA. <i>Science</i> , 2006 , 311, 392-4	33.3	435
162	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011 , 469, 529-33	50.4	431
161	CleaveLand: a pipeline for using degradome data to find cleaved small RNA targets. <i>Bioinformatics</i> , 2009 , 25, 130-1	7.2	429
160	Identification and classification of conserved RNA secondary structures in the human genome. <i>PLoS Computational Biology</i> , 2006 , 2, e33	5	394
159	HbVar: A relational database of human hemoglobin variants and thalassemia mutations at the globin gene server. <i>Human Mutation</i> , 2002 , 19, 225-33	4.7	354
158	Using genomic data to unravel the root of the placental mammal phylogeny. <i>Genome Research</i> , 2007 , 17, 413-21	9.7	350
157	Complete Khoisan and Bantu genomes from southern Africa. <i>Nature</i> , 2010 , 463, 943-7	50.4	342
156	The <i>Chlamydomonas reinhardtii</i> plastid chromosome: islands of genes in a sea of repeats. <i>Plant Cell</i> , 2002 , 14, 2659-79	11.6	332
155	Updates of the HbVar database of human hemoglobin variants and thalassemia mutations. <i>Nucleic Acids Research</i> , 2014 , 42, D1063-9	20.1	289
154	Long human-mouse sequence alignments reveal novel regulatory elements: a reason to sequence the mouse genome. <i>Genome Research</i> , 1997 , 7, 959-66	9.7	268
153	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, D537-41	20.1	250
152	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	11.5	243
151	Sequencing the nuclear genome of the extinct woolly mammoth. <i>Nature</i> , 2008 , 456, 387-90	50.4	242
150	Transcription-associated mutational asymmetry in mammalian evolution. <i>Nature Genetics</i> , 2003 , 33, 514-36.3	36.3	238
149	Covariation in frequencies of substitution, deletion, transposition, and recombination during eutherian evolution. <i>Genome Research</i> , 2003 , 13, 13-26	9.7	234
148	Molecular and genomic data identify the closest living relative of primates. <i>Science</i> , 2007 , 318, 792-4	33.3	233
147	Reconstructing contiguous regions of an ancestral genome. <i>Genome Research</i> , 2006 , 16, 1557-65	9.7	216
146	Locus control regions of mammalian beta-globin gene clusters: combining phylogenetic analyses and experimental results to gain functional insights. <i>Gene</i> , 1997 , 205, 73-94	3.8	207

145	28-way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007 , 17, 1797-808	9.7	204
144	Mulan: multiple-sequence local alignment and visualization for studying function and evolution. <i>Genome Research</i> , 2005 , 15, 184-94	9.7	199
143	Whole-genome shotgun sequencing of mitochondria from ancient hair shafts. <i>Science</i> , 2007 , 317, 1927-30	9.3	191
142	Evolution and functional classification of vertebrate gene deserts. <i>Genome Research</i> , 2005 , 15, 137-45	9.7	179
141	MultiPipMaker and supporting tools: Alignments and analysis of multiple genomic DNA sequences. <i>Nucleic Acids Research</i> , 2003 , 31, 3518-24	20.1	174
140	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, 12348-53	11.5	164
139	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. <i>Genome Research</i> , 2005 , 15, 1051-60	9.7	164
138	Erythroid GATA1 function revealed by genome-wide analysis of transcription factor occupancy, histone modifications, and mRNA expression. <i>Genome Research</i> , 2009 , 19, 2172-84	9.7	163
137	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007 , 17, 760-74	9.7	163
136	HbVar database of human hemoglobin variants and thalassemia mutations: 2007 update. <i>Human Mutation</i> , 2007 , 28, 206	4.7	150
135	Characterization of the human and mouse unconventional myosin XV genes responsible for hereditary deafness DFNB3 and shaker 2. <i>Genomics</i> , 1999 , 61, 243-58	4.3	141
134	Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. <i>Nucleic Acids Research</i> , 2007 , 35, 1-10	20.1	136
133	Comparative genomics. <i>Annual Review of Genomics and Human Genetics</i> , 2004 , 5, 15-56	9.7	136
132	The gene mutated in bare patches and striated mice encodes a novel 3beta-hydroxysteroid dehydrogenase. <i>Nature Genetics</i> , 1999 , 22, 182-7	36.3	135
131	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, 8327-32	11.5	130
130	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, 315-29	9.7	126
129	Systematic documentation and analysis of human genetic variation in hemoglobinopathies using the microattribution approach. <i>Nature Genetics</i> , 2011 , 43, 295-301	36.3	125
128	zPicture: dynamic alignment and visualization tool for analyzing conservation profiles. <i>Genome Research</i> , 2004 , 14, 472-7	9.7	119

127	Approximate matching of regular expressions. <i>Bulletin of Mathematical Biology</i> , 1989 , 51, 5-37	2.1	118
126	Fast-evolving noncoding sequences in the human genome. <i>Genome Biology</i> , 2007 , 8, R118	18.3	116
125	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, 5053-7	11.5	114
124	A framework for collaborative analysis of ENCODE data: making large-scale analyses biologist-friendly. <i>Genome Research</i> , 2007 , 17, 960-4	9.7	105
123	A file comparison program. <i>Software - Practice and Experience</i> , 1985 , 15, 1025-1040	2.5	104
122	Distinguishing regulatory DNA from neutral sites. <i>Genome Research</i> , 2003 , 13, 64-72	9.7	103
121	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. <i>Genome Research</i> , 2011 , 21, 1659-71	9.7	100
120	Reconstructing large regions of an ancestral mammalian genome in silico. <i>Genome Research</i> , 2004 , 14, 2412-23	9.7	98
119	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, 4795-800	11.5	98
118	ESPERR: learning strong and weak signals in genomic sequence alignments to identify functional elements. <i>Genome Research</i> , 2006 , 16, 1596-604	9.7	97
117	Alignment of Escherichia coli K12 DNA sequences to a genomic restriction map. <i>Nucleic Acids Research</i> , 1990 , 18, 313-21	20.1	97
116	Mobile DNA in Old World monkeys: a glimpse through the rhesus macaque genome. <i>Science</i> , 2007 , 316, 238-40	33.3	93
115	Regulatory potential scores from genome-wide three-way alignments of human, mouse, and rat. <i>Genome Research</i> , 2004 , 14, 700-7	9.7	84
114	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). <i>Genome Research</i> , 2009 , 19, 213-20	9.7	83
113	Elephantid Genomes Reveal the Molecular Bases of Woolly Mammoth Adaptations to the Arctic. <i>Cell Reports</i> , 2015 , 12, 217-28	10.6	79
112	Sequence comparison with concave weighting functions. <i>Bulletin of Mathematical Biology</i> , 1988 , 50, 97-120		79
111	Analysis of complete mitochondrial genomes from extinct and extant rhinoceroses reveals lack of phylogenetic resolution. <i>BMC Evolutionary Biology</i> , 2009 , 9, 95	3	77
110	A space-efficient algorithm for local similarities. <i>Bioinformatics</i> , 1990 , 6, 373-81	7.2	73

109	PhenCode: connecting ENCODE data with mutations and phenotype. <i>Human Mutation</i> , 2007 , 28, 554-62	4.7	72
108	Mapping sequenced E.coli genes by computer: software, strategies and examples. <i>Nucleic Acids Research</i> , 1991 , 19, 637-47	20.1	72
107	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. <i>Journal of Biological Chemistry</i> , 1997 , 272, 369-78	5.4	70
106	A combinatorial network of evolutionarily conserved myelin basic protein regulatory sequences confers distinct glial-specific phenotypes. <i>Journal of Neuroscience</i> , 2003 , 23, 10214-23	6.6	69
105	Multispecies comparative analysis of a mammalian-specific genomic domain encoding secretory proteins. <i>Genomics</i> , 2003 , 82, 417-32	4.3	66
104	The infinite sites model of genome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 14254-61	11.5	65
103	Aligning two sequences within a specified diagonal band. <i>Bioinformatics</i> , 1992 , 8, 481-7	7.2	63
102	Genomic structure and functional control of the Dlx3-7 bigene cluster. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 780-5	11.5	62
101	Finding cis-regulatory elements using comparative genomics: some lessons from ENCODE data. <i>Genome Research</i> , 2007 , 17, 775-86	9.7	61
100	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005 , 434, 724-31	50.4	61
99	An O(NP) sequence comparison algorithm. <i>Information Processing Letters</i> , 1990 , 35, 317-323	0.8	61
98	Patterns of insertions and their covariation with substitutions in the rat, mouse, and human genomes. <i>Genome Research</i> , 2004 , 14, 517-27	9.7	60
97	Comparison of sequencing platforms for single nucleotide variant calls in a human sample. <i>PLoS ONE</i> , 2013 , 8, e55089	3.7	59
96	Genomic sequence analysis of the mouse Naip gene array. <i>Genome Research</i> , 2000 , 10, 1095-102	9.7	56
95	Genome-wide identification of conserved regulatory function in diverged sequences. <i>Genome Research</i> , 2011 , 21, 1139-49	9.7	54
94	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. <i>Genome Research</i> , 2002 , 12, 3-15	9.7	54
93	Analysis of the quality and utility of random shotgun sequencing at low redundancies. <i>Genome Research</i> , 1998 , 8, 1074-84	9.7	53
92	Dynamic programming algorithms for biological sequence comparison. <i>Methods in Enzymology</i> , 1992 , 210, 575-601	1.7	53

91	Khoisan hunter-gatherers have been the largest population throughout most of modern-human demographic history. <i>Nature Communications</i> , 2014 , 5, 5692	17.4	49
90	Experimental validation of predicted mammalian erythroid cis-regulatory modules. <i>Genome Research</i> , 2006 , 16, 1480-92	9.7	49
89	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, 126-35	3.9	48
88	DUPCAR: reconstructing contiguous ancestral regions with duplications. <i>Journal of Computational Biology</i> , 2008 , 15, 1007-27	1.7	48
87	Sequences flanking hypersensitive sites of the beta-globin locus control region are required for synergistic enhancement. <i>Molecular and Cellular Biology</i> , 2001 , 21, 2969-80	4.8	47
86	Use of subtractive hybridization for comprehensive surveys of prokaryotic genome differences. <i>FEMS Microbiology Letters</i> , 2002 , 211, 175-82	2.9	46
85	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. <i>Journal of Biological Chemistry</i> , 1996 , 271, 11871-8	5.4	46
84	Polar bears exhibit genome-wide signatures of bioenergetic adaptation to life in the arctic environment. <i>Genome Biology and Evolution</i> , 2014 , 6, 433-50	3.9	44
83	Human-macaque comparisons illuminate variation in neutral substitution rates. <i>Genome Biology</i> , 2008 , 9, R76	18.3	44
82	Comparative analysis of the locus control region of the rabbit beta-like gene cluster: HS3 increases transient expression of an embryonic epsilon-globin gene. <i>Nucleic Acids Research</i> , 1993 , 21, 1265-72	20.1	44
81	Comparative Sequence of Human and Mouse BAC Clones from the mnd2 Region of Chromosome 2p13. <i>Genome Research</i> , 1999 , 9, 53-61	9.7	44
80	GALA, a database for genomic sequence alignments and annotations. <i>Genome Research</i> , 2003 , 13, 732-41	1.7	39
79	The human and mouse MHC class III region: a parade of 21 genes at the centromeric segment. <i>Trends in Immunology</i> , 2000 , 21, 320-8		39
78	Alignments without low-scoring regions. <i>Journal of Computational Biology</i> , 1998 , 5, 197-210	1.7	39
77	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. <i>Journal of Molecular Biology</i> , 1991 , 222, 233-49	6.5	38
76	Comparative sequence analysis of the mouse and human Lgn1/SMA interval. <i>Genomics</i> , 1999 , 60, 137-51	4.3	37
75	Recent developments in linear-space alignment methods: a survey. <i>Journal of Computational Biology</i> , 1994 , 1, 271-91	1.7	37
74	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, 1352-65	20.1	36

73	Calling SNPs without a reference sequence. <i>BMC Bioinformatics</i> , 2010 , 11, 130	3.6	35
72	Phylogenetic Footprinting of Hypersensitive Site 3 of the β Globin Locus Control Region. <i>Blood</i> , 1997 , 89, 3457-3469	2.2	35
71	Electronic access to sequence alignments, experimental results, and human mutations as an aid to studying globin gene regulation. <i>Genomics</i> , 1998 , 47, 429-37	4.3	35
70	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. <i>Genomics</i> , 1997 , 39, 90-4	4.3	34
69	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, 5823-8	11.5	31
68	Databases of human hemoglobin variants and other resources at the globin gene server. <i>Hemoglobin</i> , 2001 , 25, 183-93	0.6	31
67	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, 344-53	4.3	31
66	Software for Roundoff Analysis. <i>ACM Transactions on Mathematical Software</i> , 1975 , 1, 108-128	2.3	31
65	Software tools for analyzing pairwise alignments of long sequences. <i>Nucleic Acids Research</i> , 1991 , 19, 4663-7	20.1	30
64	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	4.5	29
63	Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif. <i>Genome Research</i> , 2008 , 18, 1896-905	9.7	28
62	PipTools: a computational toolkit to annotate and analyze pairwise comparisons of genomic sequences. <i>Genomics</i> , 2002 , 80, 681-90	4.3	28
61	Comparative analysis of the alpha-like globin clusters in mouse, rat, and human chromosomes indicates a mechanism underlying breaks in conserved synteny. <i>Genome Research</i> , 2004 , 14, 623-30	9.7	26
60	Web-based visualization tools for bacterial genome alignments. <i>Nucleic Acids Research</i> , 2000 , 28, 3486-96	10.1	26
59	Approximating the Spanning Star Forest Problem and Its Application to Genomic Sequence Alignment. <i>SIAM Journal on Computing</i> , 2008 , 38, 946-962	1.1	25
58	Positive and negative regulatory elements of the rabbit embryonic epsilon-globin gene revealed by an improved multiple alignment program and functional analysis. <i>DNA Sequence</i> , 1993 , 4, 163-76		25
57	Sequencing and analysis of a South Asian-Indian personal genome. <i>BMC Genomics</i> , 2012 , 13, 440	4.5	23
56	Aligning a DNA sequence with a protein sequence. <i>Journal of Computational Biology</i> , 1997 , 4, 339-49	1.7	23

55	EnteriX 2003: Visualization tools for genome alignments of Enterobacteriaceae. <i>Nucleic Acids Research</i> , 2003 , 31, 3527-32	20.1	22
54	Computational reconstruction of ancestral DNA sequences. <i>Methods in Molecular Biology</i> , 2008 , 422, 171-84	1.4	21
53	Multiple regulatory elements in the 5' flanking sequence of the human epsilon-globin gene. <i>Journal of Biological Chemistry</i> , 1998 , 273, 10202-9	5.4	19
52	Chaining multiple-alignment blocks. <i>Journal of Computational Biology</i> , 1994 , 1, 217-26	1.7	19
51	Galaxy tools to study genome diversity. <i>GigaScience</i> , 2013 , 2, 17	7.6	18
50	Comparative genomic analysis using the UCSC genome browser. <i>Methods in Molecular Biology</i> , 2007 , 395, 17-34	1.4	18
49	Genomic Variants Among Threatened Corals. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 1633-1646	3.2	17
48	Candidate genes required for embryonic development: a comparative analysis of distal mouse chromosome 14 and human chromosome 13q22. <i>Genomics</i> , 2002 , 79, 154-61	4.3	17
47	A negative cis-element regulates the level of enhancement by hypersensitive site 2 of the beta-globin locus control region. <i>Journal of Biological Chemistry</i> , 2001 , 276, 6289-98	5.4	16
46	PipMaker: a World Wide Web server for genomic sequence alignments. <i>Current Protocols in Bioinformatics</i> , 2003 , Chapter 10, Unit 10.2	24.2	15
45	Computer Search for Numerical Instability. <i>Journal of the ACM</i> , 1975 , 22, 512-521	2	14
44	The mouse cornichon gene family. <i>Development Genes and Evolution</i> , 1999 , 209, 120-5	1.8	13
43	Quadratic convergence in interval arithmetic, part II. <i>BIT Numerical Mathematics</i> , 1972 , 12, 291-298	1.7	13
42	A database of experimental results on globin gene expression. <i>Genomics</i> , 1998 , 53, 325-37	4.3	12
41	Quadratic convergence in interval arithmetic, part I. <i>BIT Numerical Mathematics</i> , 1972 , 12, 284-290	1.7	12
40	An effective method for detecting gene conversion events in whole genomes. <i>Journal of Computational Biology</i> , 2010 , 17, 1281-97	1.7	11
39	Optimization methods for selecting founder individuals for captive breeding or reintroduction of endangered species. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2010 , 43-53 ¹⁻³		11
38	Conversion events in gene clusters. <i>BMC Evolutionary Biology</i> , 2011 , 11, 226	3	10

37	Significance of interspecies matches when evolutionary rate varies. <i>Journal of Computational Biology</i> , 2003 , 10, 537-54	1.7	10
36	CAGE: Combinatorial Analysis of Gene-cluster Evolution. <i>Journal of Computational Biology</i> , 2010 , 17, 1227-42	3.7	9
35	Functional and binding studies of HS3.2 of the beta-globin locus control region. <i>Gene</i> , 2002 , 283, 185-97	3.8	9
34	Constrained sequence alignment. <i>Bulletin of Mathematical Biology</i> , 1993 , 55, 503-24	2.1	9
33	Row replacement algorithms for screen editors. <i>ACM Transactions on Programming Languages and Systems</i> , 1989 , 11, 33-56	1.6	9
32	Revealing mammalian evolutionary relationships by comparative analysis of gene clusters. <i>Genome Biology and Evolution</i> , 2012 , 4, 586-601	3.9	8
31	A tool for aligning very similar DNA sequences. <i>Bioinformatics</i> , 1997 , 13, 75-80	7.2	8
30	Reconstructing the Evolutionary History of Complex Human Gene Clusters 2008 , 29-49		8
29	Evaluation of methods for detecting conversion events in gene clusters. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 1, S45	3.6	7
28	MultiPipMaker: comparative alignment server for multiple DNA sequences. <i>Current Protocols in Bioinformatics</i> , 2005 , Chapter 10, Unit10.4	24.2	7
27	On an interval-arithmetic matrix method. <i>BIT Numerical Mathematics</i> , 1972 , 12, 213-219	1.7	7
26	Phylogenomic resources at the UCSC Genome Browser. <i>Methods in Molecular Biology</i> , 2008 , 422, 133-44	1.4	7
25	MultiPipMaker: a comparative alignment server for multiple DNA sequences. <i>Current Protocols in Bioinformatics</i> , 2010 , Chapter 10, Unit10.4	24.2	6
24	Improvements to GALA and dBERGE II: databases featuring genomic sequence alignment, annotation and experimental results. <i>Nucleic Acids Research</i> , 2005 , 33, D466-70	20.1	6
23	On the stability of finite numerical procedures. <i>Numerische Mathematik</i> , 1972 , 19, 425-432	2.2	6
22	Parametric recomputing in alignment graphs. <i>Lecture Notes in Computer Science</i> , 1994 , 87-101	0.9	6
21	Evolutionary history reconstruction for Mammalian complex gene clusters. <i>Journal of Computational Biology</i> , 2009 , 16, 1051-70	1.7	5
20	Comment on "Whole-genome shotgun sequencing of mitochondria from ancient hair shafts". <i>Science</i> , 2008 , 322, 857; author reply 857	33.3	5

19	An algorithm for searching restriction maps. <i>Bioinformatics</i> , 1990 , 6, 247-52	7.2	5
18	Functional Architecture of Deleterious Genetic Variants in the Genome of a Wrangel Island Mammoth. <i>Genome Biology and Evolution</i> , 2020 , 12, 48-58	3.9	4
17	Significance Of inter-species matches when evolutionary rate varies 2002 ,		4
16	Winnowing sequences from a database search. <i>Journal of Computational Biology</i> , 2000 , 7, 293-302	1.7	4
15	Simultaneous history reconstruction for complex gene clusters in multiple species. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2009 , 162-73	1.3	4
14	Genome-wide evidence for a hybrid origin of modern polar bears		3
13	Controlling Size When Aligning Multiple Genomic Sequences with Duplications. <i>Lecture Notes in Computer Science</i> , 2006 , 138-149	0.9	3
12	Winnowing sequences from a database search 1999 ,		2
11	Improved algorithms for searching restriction maps. <i>Bioinformatics</i> , 1991 , 7, 447-56	7.2	2
10	A simple row-replacement method. <i>Software - Practice and Experience</i> , 1988 , 18, 597-611	2.5	2
9	Whole-Genome Analysis of Gene Conversion Events. <i>Lecture Notes in Computer Science</i> , 2009 , 181-192	0.9	2
8	Aligning Two Genomic Sequences That Contain Duplications. <i>Lecture Notes in Computer Science</i> , 2009 , 98-110	0.9	1
7	SIMULTANEOUS HISTORY RECONSTRUCTION FOR COMPLEX GENE CLUSTERS IN MULTIPLE SPECIES 2008 ,		1
6	A Heuristic Algorithm for Reconstructing Ancestral Gene Orders with Duplications. <i>Lecture Notes in Computer Science</i> , 2007 , 122-135	0.9	1
5	Inferring the Recent Duplication History of a Gene Cluster. <i>Lecture Notes in Computer Science</i> , 2009 , 111-125	1.25	1
4	Functional architecture of deleterious genetic variants in the Wrangel Island mammoth genome		1
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	3.4	1
2	Some phenotype association tools in Galaxy: looking for disease SNPs in a full genome. <i>Current Protocols in Bioinformatics</i> , 2012 , Chapter 15, Unit15.2	24.2	

- 1 My adventure using computer science on the Genome project. *ACM SIGBIO Newsletter*, **1999**, 19, 15-16