

Steven L Salzberg

List of Publications by Year in descending order

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334
papers

284,052
citations

263

141
h-index

169

321
g-index

419
all docs

419
docs citations

419
times ranked

216930
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast gapped-read alignment with Bowtie 2. <i>Nature Methods</i> , 2012, 9, 357-359.	9.0	42,357
2	Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. <i>Genome Biology</i> , 2009, 10, R25.	13.9	19,212
3	HISAT: a fast spliced aligner with low memory requirements. <i>Nature Methods</i> , 2015, 12, 357-360.	9.0	16,262
4	Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. <i>Nature Biotechnology</i> , 2010, 28, 511-515.	9.4	13,805
5	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623
6	TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. <i>Genome Biology</i> , 2013, 14, R36.	13.9	11,713
7	FLASH: fast length adjustment of short reads to improve genome assemblies. <i>Bioinformatics</i> , 2011, 27, 2957-2963.	1.8	11,573
8	Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. <i>Nature Protocols</i> , 2012, 7, 562-578.	5.5	11,433
9	TopHat: discovering splice junctions with RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 1105-1111.	1.8	11,265
10	StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. <i>Nature Biotechnology</i> , 2015, 33, 290-295.	9.4	8,385
11	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	13.7	8,336
12	Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. <i>Nature Biotechnology</i> , 2019, 37, 907-915.	9.4	6,567
13	Versatile and open software for comparing large genomes. <i>Genome Biology</i> , 2004, 5, R12.	13.9	4,989
14	Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. <i>Nature Protocols</i> , 2016, 11, 1650-1667.	5.5	4,743
15	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
16	Kraken: ultrafast metagenomic sequence classification using exact alignments. <i>Genome Biology</i> , 2014, 15, R46.	13.9	3,540
17	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	6.0	3,227
18	Identifying bacterial genes and endosymbiont DNA with Glimmer. <i>Bioinformatics</i> , 2007, 23, 673-679.	1.8	2,684

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19	Automated eukaryotic gene structure annotation using EvidenceModeler and the Program to Assemble Spliced Alignments. <i>Genome Biology</i> , 2008, 9, R7.	13.9	2,484
20	Improved microbial gene identification with GLIMMER. <i>Nucleic Acids Research</i> , 1999, 27, 4636-4641.	6.5	2,282
21	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , 2004, 306, 636-640.	6.0	2,121
22	Genomic sequence of a Lyme disease spirochaete, <i>Borrelia burgdorferi</i> . <i>Nature</i> , 1997, 390, 580-586.	13.7	1,985
23	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
24	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	6.0	1,859
25	DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> . <i>Nature</i> , 2000, 406, 477-483.	13.7	1,723
26	Improving the <i>Arabidopsis</i> genome annotation using maximal transcript alignment assemblies. <i>Nucleic Acids Research</i> , 2003, 31, 5654-5666.	6.5	1,597
27	The Genome of the African Trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , 2005, 309, 416-422.	6.0	1,496
28	MUMmer4: A fast and versatile genome alignment system. <i>PLoS Computational Biology</i> , 2018, 14, e1005944.	1.5	1,412
29	Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of <i>Thermotoga maritima</i> . <i>Nature</i> , 1999, 399, 323-329.	13.7	1,397
30	Repetitive DNA and next-generation sequencing: computational challenges and solutions. <i>Nature Reviews Genetics</i> , 2012, 13, 36-46.	7.7	1,382
31	TigrScan and GlimmerHMM: two open source ab initio eukaryotic gene-finders. <i>Bioinformatics</i> , 2004, 20, 2878-2879.	1.8	1,323
32	Complete Genome Sequence of a Virulent Isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , 2001, 293, 498-506.	6.0	1,281
33	The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. <i>Science</i> , 2005, 309, 409-415.	6.0	1,273
34	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	13.7	1,272
35	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	6.0	1,222
36	The MaSuRCA genome assembler. <i>Bioinformatics</i> , 2013, 29, 2669-2677.	1.8	1,127

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37	The genome of woodland strawberry (<i>Fragaria vesca</i>). <i>Nature Genetics</i> , 2011, 43, 109-116.	9.4	1,091
38	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	13.7	1,086
39	Complete Genome Sequence of <i>Neisseria meningitidis</i> Serogroup B Strain MC58. <i>Science</i> , 2000, 287, 1809-1815.	6.0	1,083
40	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	6.0	1,025
41	Centrifuge: rapid and sensitive classification of metagenomic sequences. <i>Genome Research</i> , 2016, 26, 1721-1729.	2.4	1,025
42	A whole-genome assembly of the domestic cow, <i>Bos taurus</i> . <i>Genome Biology</i> , 2009, 10, R42.	13.9	1,005
43	Complete Genome Sequence of <i>Treponema pallidum</i> , the Syphilis Spirochete. , 1998, 281, 375-388.		969
44	The draft genome of the transgenic tropical fruit tree papaya (<i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	13.7	964
45	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	13.7	945
46	Fast algorithms for large-scale genome alignment and comparison. <i>Nucleic Acids Research</i> , 2002, 30, 2478-2483.	6.5	931
47	Bracken: estimating species abundance in metagenomics data. <i>PeerJ Computer Science</i> , 0, 3, e104.	2.7	928
48	Transcriptome assembly from long-read RNA-seq alignments with StringTie2. <i>Genome Biology</i> , 2019, 20, 278.	3.8	897
49	Microbial gene identification using interpolated Markov models. <i>Nucleic Acids Research</i> , 1998, 26, 544-548.	6.5	896
50	Genome Sequence of the Radioresistant Bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999, 286, 1571-1577.	6.0	879
51	Alignment of whole genomes. <i>Nucleic Acids Research</i> , 1999, 27, 2369-2376.	6.5	766
52	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003, 423, 81-86.	13.7	760
53	Comparative genomics of the neglected human malaria parasite <i>Plasmodium vivax</i> . <i>Nature</i> , 2008, 455, 757-763.	13.7	756
54	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	6.0	731

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55	Sequence and analysis of chromosome 2 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 1999, 402, 761-768.	13.7	724
56	Ballgown bridges the gap between transcriptome assembly and expression analysis. <i>Nature Biotechnology</i> , 2015, 33, 243-246.	9.4	716
57	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	6.0	713
58	Genome sequences of <i>Chlamydia trachomatis</i> MoPn and <i>Chlamydia pneumoniae</i> AR39. <i>Nucleic Acids Research</i> , 2000, 28, 1397-1406.	6.5	696
59	TopHat-Fusion: an algorithm for discovery of novel fusion transcripts. <i>Genome Biology</i> , 2011, 12, R72.	13.9	670
60	Genome sequence and comparative analysis of the model rodent malaria parasite <i>Plasmodium yoelii yoelii</i> . <i>Nature</i> , 2002, 419, 512-519.	13.7	666
61	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	6.0	664
62	Macronuclear Genome Sequence of the Ciliate <i>Tetrahymena thermophila</i> , a Model Eukaryote. <i>PLoS Biology</i> , 2006, 4, e286.	2.6	657
63	On Comparing Classifiers: Pitfalls to Avoid and a Recommended Approach. , 1997, 1, 317-328.		653
64	Whole-Genome Comparison of <i>Mycobacterium tuberculosis</i> Clinical and Laboratory Strains. <i>Journal of Bacteriology</i> , 2002, 184, 5479-5490.	1.0	645
65	GAGE: A critical evaluation of genome assemblies and assembly algorithms. <i>Genome Research</i> , 2012, 22, 557-567.	2.4	597
66	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	6.0	571
67	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	13.7	563
68	Comparative Genome and Proteome Analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 298, 149-159.	6.0	531
69	Phymm and PhymmBL: metagenomic phylogenetic classification with interpolated Markov models. <i>Nature Methods</i> , 2009, 6, 673-676.	9.0	526
70	GeneSplicer: a new computational method for splice site prediction. <i>Nucleic Acids Research</i> , 2001, 29, 1185-1190.	6.5	514
71	Using MUMmer to Identify Similar Regions in Large Sequence Sets. <i>Current Protocols in Bioinformatics</i> , 2003, 00, Unit 10.3.	25.8	505
72	Complete genome sequence of <i>Caulobacter crescentus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 4136-4141.	3.3	489

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73	Quake: quality-aware detection and correction of sequencing errors. <i>Genome Biology</i> , 2010, 11, R116.	13.9	470
74	Broad CTL response is required to clear latent HIV-1 due to dominance of escape mutations. <i>Nature</i> , 2015, 517, 381-385.	13.7	469
75	Mugsy: fast multiple alignment of closely related whole genomes. <i>Bioinformatics</i> , 2011, 27, 334-342.	1.8	444
76	Bioinformatics challenges of new sequencing technology. <i>Trends in Genetics</i> , 2008, 24, 142-149.	2.9	438
77	Searching for SNPs with cloud computing. <i>Genome Biology</i> , 2009, 10, R134.	13.9	437
78	Rapid, accurate, computational discovery of Rho-independent transcription terminators illuminates their relationship to DNA uptake. <i>Genome Biology</i> , 2007, 8, R22.	13.9	432
79	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014, 15, R59.	13.9	424
80	The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13148-13153.	3.3	422
81	Chromosome 2 Sequence of the Human Malaria Parasite <i>Plasmodium falciparum</i> . , 1998, 282, 1126-1132.		419
82	Large-scale sequencing of human influenza reveals the dynamic nature of viral genome evolution. <i>Nature</i> , 2005, 437, 1162-1166.	13.7	419
83	A weighted nearest neighbor algorithm for learning with symbolic features. <i>Machine Learning</i> , 1993, 10, 57-78.	3.4	415
84	Comparative Genome Sequencing for Discovery of Novel Polymorphisms in <i>Bacillus anthracis</i> . <i>Science</i> , 2002, 296, 2028-2033.	6.0	413
85	What are decision trees?. <i>Nature Biotechnology</i> , 2008, 26, 1011-1013.	9.4	409
86	Assembly of large genomes using second-generation sequencing. <i>Genome Research</i> , 2010, 20, 1165-1173.	2.4	390
87	Hybrid assembly of the large and highly repetitive genome of <i>Aegilops tauschii</i> , a progenitor of bread wheat, with the MaSuRCA mega-reads algorithm. <i>Genome Research</i> , 2017, 27, 787-792.	2.4	382
88	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. <i>F1000Research</i> , 2013, 2, 188.	0.8	372
89	A review of methods and databases for metagenomic classification and assembly. <i>Briefings in Bioinformatics</i> , 2019, 20, 1125-1136.	3.2	368
90	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	6.0	357

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91	Minimus: a fast, lightweight genome assembler. BMC Bioinformatics, 2007, 8, 64.	1.2	354
92	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (<i>Meleagris gallopavo</i>): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	2.6	348
93	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. Science, 2002, 296, 1661-1671.	6.0	344
94	DAGchainer: a tool for mining segmental genome duplications and synteny. Bioinformatics, 2004, 20, 3643-3646.	1.8	340
95	Whole-Genome Analysis of Human Influenza A Virus Reveals Multiple Persistent Lineages and Reassortment among Recent H3N2 Viruses. PLoS Biology, 2005, 3, e300.	2.6	340
96	A Weighted Nearest Neighbor Algorithm for Learning with Symbolic Features. Machine Learning, 1993, 10, 57-78.	3.4	339
97	The genomes of two key bumblebee species with primitive eusocial organization. Genome Biology, 2015, 16, 76.	3.8	330
98	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. BMC Genomics, 2008, 9, 204.	1.2	327
99	The International Nucleotide Sequence Database Collaboration. Nucleic Acids Research, 2012, 40, D33-D37.	6.5	327
100	Liftoff: accurate mapping of gene annotations. Bioinformatics, 2021, 37, 1639-1643.	1.8	322
101	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. Science, 2005, 309, 134-137.	6.0	309
102	Understanding the Adaptation of <i>Halobacterium</i> Species NRC-1 to Its Extreme Environment through Computational Analysis of Its Genome Sequence. Genome Research, 2001, 11, 1641-1650.	2.4	294
103	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. F1000Research, 2013, 2, 188.	0.8	293
104	Evidence for symmetric chromosomal inversions around the replication origin in bacteria. Genome Biology, 2000, 1, research0011.1.	13.9	287
105	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. Genetics, 2014, 196, 875-890.	1.2	286
106	Microbial Genes in the Human Genome: Lateral Transfer or Gene Loss?. Science, 2001, 292, 1903-1906.	6.0	284
107	KrakenUniq: confident and fast metagenomics classification using unique k-mer counts. Genome Biology, 2018, 19, 198.	3.8	283
108	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	9.4	276

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109	Genomic Insights into Methanotrophy: The Complete Genome Sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004, 2, e303.	2.6	275
110	Genome sequence of <i>Chlamydomonas reinhardtii</i> (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae. <i>Nucleic Acids Research</i> , 2003, 31, 2134-2147.	6.5	266
111	CHESS: a new human gene catalog curated from thousands of large-scale RNA sequencing experiments reveals extensive transcriptional noise. <i>Genome Biology</i> , 2018, 19, 208.	3.8	263
112	Gene Index analysis of the human genome estimates approximately 120,000 genes. <i>Nature Genetics</i> , 2000, 25, 239-240.	9.4	262
113	How to map billions of short reads onto genomes. <i>Nature Biotechnology</i> , 2009, 27, 455-457.	9.4	257
114	Prediction of operons in microbial genomes. <i>Nucleic Acids Research</i> , 2001, 29, 1216-1221.	6.5	255
115	Pavian: interactive analysis of metagenomics data for microbiome studies and pathogen identification. <i>Bioinformatics</i> , 2020, 36, 1303-1304.	1.8	255
116	In-Depth View of Structure, Activity, and Evolution of Rice Chromosome 10. <i>Science</i> , 2003, 300, 1566-1569.	6.0	245
117	Cloud computing and the DNA data race. <i>Nature Biotechnology</i> , 2010, 28, 691-693.	9.4	242
118	Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 816-820.	13.7	234
119	The walnut (<i>Juglans regia</i>) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. <i>Plant Journal</i> , 2016, 87, 507-532.	2.8	233
120	Prediction of transcription terminators in bacterial genomes 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 2000, 301, 27-33.	2.0	231
121	The first near-complete assembly of the hexaploid bread wheat genome, <i>Triticum aestivum</i> . <i>GigaScience</i> , 2017, 6, 1-7.	3.3	224
122	Next-generation genome annotation: we still struggle to get it right. <i>Genome Biology</i> , 2019, 20, 92.	3.8	216
123	A nearest hyperrectangle learning method. <i>Machine Learning</i> , 1991, 6, 251-276.	3.4	215
124	Unique Features of the Loblolly Pine (<i>Pinus taeda</i> L.) Megagenome Revealed Through Sequence Annotation. <i>Genetics</i> , 2014, 196, 891-909.	1.2	207
125	Finding Genes in DNA with a Hidden Markov Model. <i>Journal of Computational Biology</i> , 1997, 4, 127-141.	0.8	198
126	Comparative genome assembly. <i>Briefings in Bioinformatics</i> , 2004, 5, 237-248.	3.2	193

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127	Genome Analysis Linking Recent European and African Influenza (H5N1) Viruses. <i>Emerging Infectious Diseases</i> , 2007, 13, 713-718.	2.0	191
128	Pan-genomics in the human genome era. <i>Nature Reviews Genetics</i> , 2020, 21, 243-254.	7.7	191
129	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic <i>Xanthomonas</i> spp. <i>Journal of Bacteriology</i> , 2011, 193, 5450-5464.	1.0	189
130	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 820-823.	13.7	188
131	Interpolated Markov Models for Eukaryotic Gene Finding. <i>Genomics</i> , 1999, 59, 24-31.	1.3	184
132	Computational identification of developmental enhancers: conservation and function of transcription factor binding-site clusters in <i>Drosophila melanogaster</i> and <i>Drosophila pseudoobscura</i> . <i>Genome Biology</i> , 2004, 5, R61.	13.9	184
133	Between a chicken and a grape: estimating the number of human genes. <i>Genome Biology</i> , 2010, 11, 206.	13.9	182
134	A probabilistic method for identifying start codons in bacterial genomes. <i>Bioinformatics</i> , 2001, 17, 1123-1130.	1.8	180
135	A Nearest Hyperrectangle Learning Method. <i>Machine Learning</i> , 1991, 6, 251-276.	3.4	177
136	Hierarchical Scaffolding With Bambus. <i>Genome Research</i> , 2003, 14, 149-159.	2.4	172
137	The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. <i>PLoS Computational Biology</i> , 2020, 16, e1007981.	1.5	172
138	Skewed oligomers and origins of replication. <i>Gene</i> , 1998, 217, 57-67.	1.0	171
139	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016, 204, 1613-1626.	1.2	169
140	Sequence of <i>Plasmodium falciparum</i> chromosomes 2, 10, 11 and 14. <i>Nature</i> , 2002, 419, 531-534.	13.7	167
141	Beware of mis-assembled genomes. <i>Bioinformatics</i> , 2005, 21, 4320-4321.	1.8	165
142	A new rhesus macaque assembly and annotation for next-generation sequencing analyses. <i>Biology Direct</i> , 2014, 9, 20.	1.9	165
143	Microbial genome sequencing. <i>Nature</i> , 2000, 406, 799-803.	13.7	164
144	The sequence of rice chromosomes 11 and 12, rich in disease resistance genes and recent gene duplications. <i>BMC Biology</i> , 2005, 3, 20.	1.7	158

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145	<i>Bacillus anthracis</i> comparative genome analysis in support of the Amerithrax investigation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5027-5032.	3.3	152
146	Gene prediction with Glimmer for metagenomic sequences augmented by classification and clustering. Nucleic Acids Research, 2012, 40, e9-e9.	6.5	150
147	Full-length messenger RNA sequences greatly improve genome annotation. Genome Biology, 2002, 3, research0029.1.	13.9	147
148	JIGSAW: integration of multiple sources of evidence for gene prediction. Bioinformatics, 2005, 21, 3596-3603.	1.8	147
149	Ultrafast and accurate 16S rRNA microbial community analysis using Kraken 2. Microbiome, 2020, 8, 124.	4.9	146
150	Unexpected cross-species contamination in genome sequencing projects. PeerJ, 2014, 2, e675.	0.9	145
151	Next-generation sequencing in neuropathologic diagnosis of infections of the nervous system. Neurology: Neuroimmunology and NeuroInflammation, 2016, 3, e251.	3.1	142
152	EDGE-pro: Estimated Degree of Gene Expression in Prokaryotic Genomes. Evolutionary Bioinformatics, 2013, 9, EBO.S11250.	0.6	141
153	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	5.8	140
154	GAGE-B: an evaluation of genome assemblers for bacterial organisms. Bioinformatics, 2013, 29, 1718-1725.	1.8	135
155	Optimized Multiplex PCR: Efficiently Closing a Whole-Genome Shotgun Sequencing Project. Genomics, 1999, 62, 500-507.	1.3	131
156	Terminating contamination: large-scale search identifies more than 2,000,000 contaminated entries in GenBank. Genome Biology, 2020, 21, 115.	3.8	130
157	Genome re-annotation: a wiki solution?. Genome Biology, 2007, 8, 102.	3.8	127
158	Open questions: How many genes do we have?. BMC Biology, 2018, 16, 94.	1.7	127
159	Serendipitous discovery of Wolbachia genomes in multiple Drosophila species. Genome Biology, 2005, 6, R23.	13.9	126
160	An optimized protocol for analysis of EST sequences. Nucleic Acids Research, 2000, 28, 3657-3665.	6.5	121
161	DNA uptake signal sequences in naturally transformable bacteria. Research in Microbiology, 1999, 150, 603-616.	1.0	117
162	Next-generation sequencing: insights to advance clinical investigations of the microbiome. Journal of Clinical Investigation, 2022, 132, .	3.9	116

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163	The age of the <i>Arabidopsis thaliana</i> genome duplication. <i>Plant Molecular Biology</i> , 2003, 51, 859-866.	2.0	115
164	A clustering method for repeat analysis in DNA sequences. <i>Genome Biology</i> , 2001, 2, research0027.1.	13.9	114
165	Genome assembly and characterization of a complex zfBED-NLR gene-containing disease resistance locus in Carolina Gold Select rice with Nanopore sequencing. <i>PLoS Genetics</i> , 2020, 16, e1008571.	1.5	112
166	Human contamination in bacterial genomes has created thousands of spurious proteins. <i>Genome Research</i> , 2019, 29, 954-960.	2.4	111
167	Computational Gene Prediction Using Multiple Sources of Evidence. <i>Genome Research</i> , 2003, 14, 142-148.	2.4	110
168	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409.	13.7	105
169	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3157-3167.	0.8	103
170	A Decision Tree System for Finding Genes in DNA. <i>Journal of Computational Biology</i> , 1998, 5, 667-680.	0.8	102
171	The Value of Complete Microbial Genome Sequencing (You Get What You Pay For). <i>Journal of Bacteriology</i> , 2002, 184, 6403-6405.	1.0	101
172	PhymmBL expanded: confidence scores, custom databases, parallelization and more. <i>Nature Methods</i> , 2011, 8, 367-367.	9.0	97
173	Detection and correction of false segmental duplications caused by genome mis-assembly. <i>Genome Biology</i> , 2010, 11, R28.	13.9	96
174	First Draft Assembly and Annotation of the Genome of a California Endemic Oak <i>Quercus lobata</i> (Fagaceae). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3485-3495.	0.8	95
175	Genome Sequence of the Dioxin-Mineralizing Bacterium <i>Sphingomonas wittichii</i> RW1. <i>Journal of Bacteriology</i> , 2010, 192, 6101-6102.	1.0	93
176	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 183-191.	0.5	92
177	Genome-wide annotation of microRNA primary transcript structures reveals novel regulatory mechanisms. <i>Genome Research</i> , 2015, 25, 1401-1409.	2.4	91
178	Clustering metagenomic sequences with interpolated Markov models. <i>BMC Bioinformatics</i> , 2010, 11, 544.	1.2	90
179	Acquisition and Evolution of Plant Pathogenesis-Associated Gene Clusters and Candidate Determinants of Tissue-Specificity in <i>Xanthomonas</i> . <i>PLoS ONE</i> , 2008, 3, e3828.	1.1	89
180	The Complete Genome Sequence of <i>Bacillus anthracis</i> Ames Ancestor. <i>Journal of Bacteriology</i> , 2009, 191, 445-446.	1.0	88

#	ARTICLE	IF	CITATIONS
181	Single molecule real-time sequencing of <i>Xanthomonas oryzae</i> genomes reveals a dynamic structure and complex TAL (transcription activator-like) effector gene relationships. <i>Microbial Genomics</i> , 2015, 1, .	1.0	86
182	Removing contaminants from databases of draft genomes. <i>PLoS Computational Biology</i> , 2018, 14, e1006277.	1.5	85
183	OperonDB: a comprehensive database of predicted operons in microbial genomes. <i>Nucleic Acids Research</i> , 2009, 37, D479-D482.	6.5	83
184	High-quality chromosome-scale assembly of the walnut (<i>Juglans regia</i> L.) reference genome. <i>GigaScience</i> , 2020, 9, .	3.3	83
185	Predicting protein secondary structure with a nearest-neighbor algorithm. <i>Journal of Molecular Biology</i> , 1992, 227, 371-374.	2.0	82
186	A computational survey of candidate exonic splicing enhancer motifs in the model plant <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2007, 8, 159.	1.2	81
187	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018, 9, 2606.	5.8	79
188	A method for identifying splice sites and translational start sites in eukaryotic mRNA. <i>Bioinformatics</i> , 1997, 13, 365-376.	1.8	78
189	Probing the pan-genome of <i>Listeria monocytogenes</i> : new insights into intraspecific niche expansion and genomic diversification. <i>BMC Genomics</i> , 2010, 11, 500.	1.2	74
190	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. <i>Genome Research</i> , 2005, 15, 1284-1291.	2.4	73
191	Genomic Variation Among and Within Six <i>Juglans</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2153-2165.	0.8	73
192	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. <i>GigaScience</i> , 2017, 6, 1-4.	3.3	71
193	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. <i>Nature Communications</i> , 2019, 10, 880.	5.8	71
194	A Reference Genome Sequence for Giant Sequoia. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3907-3919.	0.8	67
195	Sequence and analysis of the <i>Arabidopsis</i> genome. <i>Current Opinion in Plant Biology</i> , 2001, 4, 105-110.	3.5	66
196	Hawkeye: an interactive visual analytics tool for genome assemblies. <i>Genome Biology</i> , 2007, 8, R34.	13.9	66
197	Genome Assembly Has a Major Impact on Gene Content: A Comparison of Annotation in Two <i>Bos Taurus</i> Assemblies. <i>PLoS ONE</i> , 2011, 6, e21400.	1.1	65
198	Development and Optimization of Metagenomic Next-Generation Sequencing Methods for Cerebrospinal Fluid Diagnostics. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	65

#	ARTICLE	IF	CITATIONS
199	Locating Protein Coding Regions in Human DNA Using a Decision Tree Algorithm. <i>Journal of Computational Biology</i> , 1995, 2, 473-485.	0.8	64
200	Comprehensive DNA Signature Discovery and Validation. <i>PLoS Computational Biology</i> , 2007, 3, e98.	1.5	63
201	Short Read Mapping: An Algorithmic Tour. <i>Proceedings of the IEEE</i> , 2017, 105, 436-458.	16.4	63
202	Computational Discovery of Internal Micro-Exons. <i>Genome Research</i> , 2003, 13, 1216-1221.	2.4	62
203	Title is missing!. <i>Machine Learning</i> , 1994, 16, 235-240.	3.4	61
204	JIGSAW, GeneZilla, and GlimmerHMM: puzzling out the features of human genes in the ENCODE regions. <i>Genome Biology</i> , 2006, 7, S9.	13.9	61
205	Decision trees for automated identification of cosmic-ray hits in Hubble Space Telescope images. <i>Publications of the Astronomical Society of the Pacific</i> , 1995, 107, 279.	1.0	60
206	Genome sequence assembly: algorithms and issues. <i>Computer</i> , 2002, 35, 47-54.	1.2	60
207	GlimmerM, Exonomy and Unveil: three ab initio eukaryotic genefinders. <i>Nucleic Acids Research</i> , 2003, 31, 3601-3604.	6.5	60
208	Genomic architecture of complex traits in loblolly pine. <i>New Phytologist</i> , 2019, 221, 1789-1801.	3.5	60
209	The sequence and analysis of <i>Trypanosoma brucei</i> chromosome II. <i>Nucleic Acids Research</i> , 2003, 31, 4856-4863.	6.5	59
210	Rapid detection of inter-clade recombination in SARS-CoV-2 with Bolotie. <i>Genetics</i> , 2021, 218, .	1.2	58
211	Complete Columbian mammoth mitogenome suggests interbreeding with woolly mammoths. <i>Genome Biology</i> , 2011, 12, R51.	13.9	56
212	Insight into the genome of <i>Aspergillus fumigatus</i> : analysis of a 922kb region encompassing the nitrate assimilation gene cluster. <i>Fungal Genetics and Biology</i> , 2004, 41, 443-453.	0.9	55
213	Horizontal gene transfer is not a hallmark of the human genome. <i>Genome Biology</i> , 2017, 18, 85.	3.8	55
214	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. <i>Briefings in Bioinformatics</i> , 2013, 14, 213-224.	3.2	54
215	The COMBREX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	2.6	54
216	Genomic Features of a Bumble Bee Symbiont Reflect Its Host Environment. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3793-3803.	1.4	53

#	ARTICLE	IF	CITATIONS
217	Identifying Corneal Infections in Formalin-Fixed Specimens Using Next Generation Sequencing. , 2018, 59, 280.		51
218	Physiogenomic resources for rat models of heart, lung and blood disorders. Nature Genetics, 2006, 38, 234-239.	9.4	48
219	COMBREX: a project to accelerate the functional annotation of prokaryotic genomes. Nucleic Acids Research, 2011, 39, D11-D14.	6.5	47
220	Rice Bioinformatics. Analysis of Rice Sequence Data and Leveraging the Data to Other Plant Species. Plant Physiology, 2001, 125, 1166-1174.	2.3	46
221	Gene-Boosted Assembly of a Novel Bacterial Genome from Very Short Reads. PLoS Computational Biology, 2008, 4, e1000186.	1.5	46
222	Open access to tree genomes: the path to a better forest. Genome Biology, 2013, 14, 120.	3.8	46
223	Insights into the Loblolly Pine Genome: Characterization of BAC and Fosmid Sequences. PLoS ONE, 2013, 8, e72439.	1.1	46
224	Genome Sequence of the <i>Wolbachia</i> Endosymbiont of <i>Culex quinquefasciatus</i> JHB. Journal of Bacteriology, 2009, 191, 1725-1725.	1.0	44
225	Automated correction of genome sequence errors. Nucleic Acids Research, 2004, 32, 562-569.	6.5	42
226	Assembly and annotation of an Ashkenazi human reference genome. Genome Biology, 2020, 21, 129.	3.8	42
227	Computational gene finding in plants. Plant Molecular Biology, 2002, 48, 39-48.	2.0	41
228	SkewIT: The Skew Index Test for large-scale GC Skew analysis of bacterial genomes. PLoS Computational Biology, 2020, 16, e1008439.	1.5	40
229	The contents of the syringe. Nature, 2008, 454, 160-161.	13.7	39
230	Learning with Nested Generalized Exemplars. Kluwer International Series in Engineering and Computer Science, 1990, , .	0.2	38
231	Efficient implementation of a generalized pair hidden Markov model for comparative gene finding. Bioinformatics, 2005, 21, 1782-1788.	1.8	38
232	Improving pan-genome annotation using whole genome multiple alignment. BMC Bioinformatics, 2011, 12, 272.	1.2	38
233	Cretaceous dinosaur bone contains recent organic material and provides an environment conducive to microbial communities. ELife, 2019, 8, .	2.8	38
234	Uncensored exchange of scientific results. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1464-1464.	3.3	37

#	ARTICLE	IF	CITATIONS
235	Insignia: a DNA signature search web server for diagnostic assay development. <i>Nucleic Acids Research</i> , 2009, 37, W229-W234.	6.5	37
236	Use and mis-use of supplementary material in science publications. <i>BMC Bioinformatics</i> , 2015, 16, 237.	1.2	36
237	A probabilistic framework for memory-based reasoning. <i>Artificial Intelligence</i> , 1998, 104, 287-311.	3.9	35
238	Efficient decoding algorithms for generalized hidden Markov model gene finders. <i>BMC Bioinformatics</i> , 2005, 6, 16.	1.2	34
239	Chromosome-Scale Assembly of the Bread Wheat Genome Reveals Thousands of Additional Gene Copies. <i>Genetics</i> , 2020, 216, 599-608.	1.2	34
240	Managing information for concurrent engineering: Challenges and barriers. <i>Research in Engineering Design - Theory, Applications, and Concurrent Engineering</i> , 1990, 2, 35-52.	1.2	33
241	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>BMC Genomics</i> , 2008, 9, 534.	1.2	33
242	Arioc: high-throughput read alignment with GPU-accelerated exploration of the seed-and-extend search space. <i>PeerJ</i> , 2015, 3, e808.	0.9	33
243	Genomic basis of white pine blister rust quantitative disease resistance and its relationship with qualitative resistance. <i>Plant Journal</i> , 2020, 104, 365-376.	2.8	32
244	Statement on the consideration of biodefence and biosecurity. <i>Nature</i> , 2003, 421, 771-771.	18.7	31
245	2009 Swine-Origin Influenza A (H1N1) Resembles Previous Influenza Isolates. <i>PLoS ONE</i> , 2009, 4, e6402.	1.1	31
246	The Genome Assembly Archive: A New Public Resource. <i>PLoS Biology</i> , 2004, 2, e285.	2.6	30
247	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. <i>Nature Communications</i> , 2022, 13, 2047.	5.8	30
248	Closure of the NCBI SRA and implications for the long-term future of genomics data storage. <i>Genome Biology</i> , 2011, 12, 402.	3.8	29
249	Thousands of missed genes found in bacterial genomes and their analysis with COMBREX. <i>Biology Direct</i> , 2012, 7, 37.	1.9	28
250	Presence of Human Hepatitis E Virus-1 in a Cohort of People Who Inject Drugs. <i>Annals of Internal Medicine</i> , 2017, 167, 1.	2.0	28
251	Assembled and annotated 26.5 Gbp coast redwood genome: a resource for estimating evolutionary adaptive potential and investigating hexaploid origin. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	28
252	Towards a Better Understanding of Memory-Based Reasoning Systems. , 1994, , 242-250.		27

#	ARTICLE	IF	CITATIONS
253	Characterization of Insertion Sites in Rainbow Papaya, the First Commercialized Transgenic Fruit Crop. <i>Tropical Plant Biology</i> , 2008, 1, 293-309.	1.0	25
254	Efficient oligonucleotide probe selection for pan-genomic tiling arrays. <i>BMC Bioinformatics</i> , 2009, 10, 293.	1.2	25
255	Genome-Wide Analysis of Repetitive Elements in Papaya. <i>Tropical Plant Biology</i> , 2008, 1, 191-201.	1.0	24
256	Reminder to deposit DNA sequences. <i>Science</i> , 2016, 352, 780-780.	6.0	24
257	An empirical analysis of training protocols for probabilistic gene finders. <i>BMC Bioinformatics</i> , 2004, 5, 206.	1.2	23
258	Mis-Assembled "Segmental Duplications" in Two Versions of the <i>Bos taurus</i> Genome. <i>PLoS ONE</i> , 2012, 7, e42680.	1.1	22
259	The SAMBA tool uses long reads to improve the contiguity of genome assemblies. <i>PLoS Computational Biology</i> , 2022, 18, e1009860.	1.5	22
260	Balrog: A universal protein model for prokaryotic gene prediction. <i>PLoS Computational Biology</i> , 2021, 17, e1008727.	1.5	21
261	Best-case results for nearest-neighbor learning. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 1995, 17, 599-608.	9.7	20
262	A Teaching Strategy for Memory-Based Control. , 1997, 11, 343-370.		20
263	Guillain-Barré Syndrome Outbreak in Peru 2019 Associated With <i>Campylobacter jejuni</i> Infection. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2021, 8, .	3.1	20
264	Detection of lineage-specific evolutionary changes among primate species. <i>BMC Bioinformatics</i> , 2011, 12, 274.	1.2	19
265	Finding genes in <i>Plasmodium falciparum</i> . <i>Nature</i> , 2000, 404, 34-34.	13.7	18
266	Distance metrics for instance-based learning. <i>Lecture Notes in Computer Science</i> , 1991, , 399-408.	1.0	18
267	Finding genes in <i>Plasmodium falciparum</i> . <i>Nature</i> , 2000, 404, 34-35.	13.7	17
268	Learning to Catch: Applying Nearest Neighbor Algorithms to Dynamic Control Tasks. <i>Lecture Notes in Statistics</i> , 1994, , 321-328.	0.1	17
269	Genome-wide association identifies candidate genes for drought tolerance in coast redwood and giant sequoia. <i>Plant Journal</i> , 2022, 109, 7-22.	2.8	17
270	Do-it-yourself genetic testing. <i>Genome Biology</i> , 2010, 11, 404.	3.8	16

#	ARTICLE	IF	CITATIONS
271	Genome-Guided Transcriptome Assembly in the Age of Next-Generation Sequencing. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1234-1240.	1.9	16
272	Contamination in the Draft of the Human Genome Masquerades As Lateral Gene Transfer. DNA Sequence, 2002, 13, 75-76.	0.7	15
273	Yeast rises again. Nature, 2003, 423, 233-234.	13.7	14
274	Dissecting the Polygenic Basis of Cold Adaptation Using Genome-Wide Association of Traits and Environmental Data in Douglas-fir. Genes, 2021, 12, 110.	1.0	14
275	Effects of transcriptional noise on estimates of gene and transcript expression in RNA sequencing experiments. Genome Research, 2021, 31, 301-308.	2.4	13
276	Recent advances in RNA sequence analysis. F1000 Biology Reports, 2010, 2, 64.	4.0	13
277	Chapter 18 Committees of decision trees. Advances in Psychology, 1996, 113, 305-317.	0.1	12
278	Computational gene finding in plants. Plant Molecular Biology, 2002, 48, 39-48.	2.0	12
279	New names for old strains? Wolbachia wSim is actually wRi. Genome Biology, 2005, 6, 401.	13.9	11
280	A Unified Model Explaining the Offsets of Overlapping and Near-Overlapping Prokaryotic Genes. Molecular Biology and Evolution, 2007, 24, 2091-2098.	3.5	11
281	16GT: a fast and sensitive variant caller using a 16-genotype probabilistic model. GigaScience, 2017, 6, 1-4.	3.3	11
282	First Draft Genome Sequence of the Pathogenic Fungus <i>Lomentospora prolificans</i> (Formerly) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.8	11
283	Gene discovery in DNA sequences. IEEE Intelligent Systems, 1999, 14, 44-48.	0.2	10
284	A phylogenetic generalized hidden Markov model for predicting alternatively spliced exons. Algorithms for Molecular Biology, 2006, 1, 14.	0.3	10
285	Mind the gaps. Nature Methods, 2010, 7, 105-106.	9.0	10
286	Genome interpretation and assembly—recent progress and next steps. Nature Biotechnology, 2012, 30, 1081-1083.	9.4	10
287	DIAMUND : Direct Comparison of Genomes to Detect Mutations. Human Mutation, 2014, 35, 283-288.	1.1	9
288	Re-analysis of metagenomic sequences from acute flaccid myelitis patients reveals alternatives to enterovirus D68 infection. F1000Research, 2015, 4, 180.	0.8	9

#	ARTICLE	IF	CITATIONS
289	Re-Assembly of the Genome of <i>Francisella tularensis</i> Subsp. <i>holarctica</i> OSU18. <i>PLoS ONE</i> , 2008, 3, e3427.	1.1	9
290	A Teaching Strategy for Memory-Based Control. , 1997, , 343-370.		9
291	Reminder to deposit DNA sequences. <i>Nature</i> , 2016, 533, 179-179.	13.7	8
292	Genomic characterization of chromosome translocations in patients with T/myeloid mixed-phenotype acute leukemia. <i>Leukemia and Lymphoma</i> , 2018, 59, 1231-1238.	0.6	8
293	The Terabase Search Engine: a large-scale relational database of short-read sequences. <i>Bioinformatics</i> , 2019, 35, 665-670.	1.8	8
294	PhyloCSF++: a fast and user-friendly implementation of PhyloCSF with annotation tools. <i>Bioinformatics</i> , 2022, 38, 1440-1442.	1.8	8
295	The Perils of Gene Patents. <i>Clinical Pharmacology and Therapeutics</i> , 2012, 91, 969-971.	2.3	7
296	A reference-quality, fully annotated genome from a Puerto Rican individual. <i>Genetics</i> , 2022, 220, .	1.2	7
297	Releasing the Kraken. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	7
298	Unrestricted free access works and must continue. <i>Nature</i> , 2003, 422, 801-801.	13.7	6
299	A Method to Improve the Performance of Translation Start Site Detection and Its Application for Gene Finding. <i>Lecture Notes in Computer Science</i> , 2002, , 210-219.	1.0	6
300	Re-analysis of metagenomic sequences from acute flaccid myelitis patients reveals alternatives to enterovirus D68 infection. <i>F1000Research</i> , 2015, 4, 180.	0.8	6
301	Using GlimmerM to Find Genes in Eukaryotic Genomes. <i>Current Protocols in Bioinformatics</i> , 2003, 00, Unit 4.4.	25.8	5
302	Shared data are key to beating threat from flu. <i>Nature</i> , 2006, 440, 605-605.	13.7	5
303	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. <i>Chest</i> , 2019, 156, 1068-1079.	0.4	5
304	Decision trees and Markov chains for gene finding. <i>New Comprehensive Biochemistry</i> , 1998, , 187-203.	0.1	4
305	The novel fusion transcript NR5A2â€KLHL29FT is generated by an insertion at the KLHL29 locus. <i>Cancer</i> , 2017, 123, 1507-1515.	2.0	4
306	An introduction to biological sequence analysis. <i>New Comprehensive Biochemistry</i> , 1998, 32, 29-42.	0.1	3

#	ARTICLE	IF	CITATIONS
307	Finding Repeats in Genome Sequences. , 0, , 197-233.		3
308	Nested hyper-rectangles for exemplar-based learning. Lecture Notes in Computer Science, 1989, , 184-201.	1.0	3
309	The genome of the American groundhog, <i>Marmota monax</i> . F1000Research, 2020, 9, 1137.	0.8	3
310	Testing orthogonal shapes. Computational Geometry: Theory and Applications, 1995, 5, 33-49.	0.3	2
311	Learning nested concept classes with limited storage. Journal of Experimental and Theoretical Artificial Intelligence, 1996, 8, 129-147.	1.8	2
312	Testing simple polygons. Computational Geometry: Theory and Applications, 1997, 8, 97-114.	0.3	2
313	A preliminary comparison of the mouse and human genomes. International Congress Series, 2002, 1246, 169-181.	0.2	2
314	It is time to end the patenting of software. Bioinformatics, 2006, 22, 1416-1417.	1.8	2
315	Sequestration: inadvertently killing biomedical research to score political points. Genome Biology, 2013, 14, 109.	13.9	2
316	Identification of microbial agents in tissue specimens of ocular and periocular sarcoidosis using a metagenomics approach. F1000Research, 0, 10, 820.	0.8	2
317	Genes and genomes, an imperfect world: comparison of gene annotations of two <i>Bos taurus</i> draft assemblies. Genome Biology, 2010, 11, P13.	13.9	1
318	NIH funding: It does support innovators. Nature, 2013, 493, 26-26.	13.7	1
319	Microbial Diagnostics for Cancer: A Step Forward but Not Prime Time Yet. Cancer Cell, 2020, 37, 625-627.	7.7	1
320	Rapidly fatal infection with <i>Bacillus cereus/thuringiensis</i> : genome assembly of the responsible pathogen and consideration of possibly contributing toxins. Diagnostic Microbiology and Infectious Disease, 2021, 101, 115534.	0.8	1
321	Genomics of <i>Theileria Parva</i> . World Class Parasites, 2002, , 85-92.	0.3	1
322	Gemina: A Web-Based Epidemiology and Genomic Metadata System Designed to Identify Infectious Agents. , 2007, , 228-229.		1
323	Computational gene finding in plants. , 2002, , 39-48.		1
324	A tutorial introduction to computation for biologists. New Comprehensive Biochemistry, 1998, , 11-27.	0.1	0

#	ARTICLE	IF	CITATIONS
325	Bioinformatics Methods for Microbial Detection and Forensic Diagnostic Design. , 2005, , 313-353.		0
326	Foreword by Steven Salzberg. , 0, , xi-xii.		0
327	Open Access: The Sooner the Better. Science, 2009, 325, 266-266.	6.0	0
328	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Journal of Allergy and Clinical Immunology, 2019, 143, AB296.	1.5	0
329	EFFORTS TO DEREGULATE RAINBOW PAPAYA IN JAPAN: MOLECULAR CHARACTERIZATION OF TRANSGENE AND VECTOR INSERTS. Acta Horticulturae, 2010, , 235-240.	0.1	0
330	Using Protein Domains to Improve the Accuracy of Ab Initio Gene Finding. Lecture Notes in Computer Science, 2007, , 208-215.	1.0	0
331	The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. , 2020, 16, e1007981.		0
332	The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. , 2020, 16, e1007981.		0
333	The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. , 2020, 16, e1007981.		0
334	The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. , 2020, 16, e1007981.		0