

# Steven L Salzberg

## List of Publications by Year in descending order

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334  
papers

284,052  
citations

246  
143  
h-index

162  
323  
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.	19.0	42,357
2	Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. <i>Genome Biology</i> , 2009, 10, R25.	9.6	19,212
3	HISAT: a fast spliced aligner with low memory requirements. <i>Nature Methods</i> , 2015, 12, 357-360.	19.0	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.	17.5	13,805
5	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	12.6	12,623
6	TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. <i>Genome Biology</i> , 2013, 14, R36.	9.6	11,713
7	FLASH: fast length adjustment of short reads to improve genome assemblies. <i>Bioinformatics</i> , 2011, 27, 2957-2963.	4.1	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.	12.0	11,433
9	TopHat: discovering splice junctions with RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 1105-1111.	4.1	11,265
10	StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. <i>Nature Biotechnology</i> , 2015, 33, 290-295.	17.5	8,385
11	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	27.8	8,336
12	Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. <i>Nature Biotechnology</i> , 2019, 37, 907-915.	17.5	6,567
13	Versatile and open software for comparing large genomes. <i>Genome Biology</i> , 2004, 5, R12.	9.6	4,989
14	Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. <i>Nature Protocols</i> , 2016, 11, 1650-1667.	12.0	4,743
15	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	27.8	3,881
16	Kraken: ultrafast metagenomic sequence classification using exact alignments. <i>Genome Biology</i> , 2014, 15, R46.	9.6	3,540
17	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
18	Identifying bacterial genes and endosymbiont DNA with Glimmer. <i>Bioinformatics</i> , 2007, 23, 673-679.	4.1	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.	9.6	2,484
20	Improved microbial gene identification with GLIMMER. <i>Nucleic Acids Research</i> , 1999, 27, 4636-4641.	14.5	2,282
21	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , 2004, 306, 636-640.	12.6	2,121
22	Genomic sequence of a Lyme disease spirochaete, <i>Borrelia burgdorferi</i> . <i>Nature</i> , 1997, 390, 580-586.	27.8	1,985
23	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
24	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	12.6	1,859
25	DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> . <i>Nature</i> , 2000, 406, 477-483.	27.8	1,723
26	Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. <i>Nucleic Acids Research</i> , 2003, 31, 5654-5666.	14.5	1,597
27	The Genome of the African Trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , 2005, 309, 416-422.	12.6	1,496
28	MUMmer4: A fast and versatile genome alignment system. <i>PLoS Computational Biology</i> , 2018, 14, e1005944.	3.2	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.	27.8	1,397
30	Repetitive DNA and next-generation sequencing: computational challenges and solutions. <i>Nature Reviews Genetics</i> , 2012, 13, 36-46.	16.3	1,382
31	TigrScan and GlimmerHMM: two open source ab initio eukaryotic gene-finders. <i>Bioinformatics</i> , 2004, 20, 2878-2879.	4.1	1,323
32	Complete Genome Sequence of a Virulent Isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , 2001, 293, 498-506.	12.6	1,281
33	The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. <i>Science</i> , 2005, 309, 409-415.	12.6	1,273
34	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	27.8	1,272
35	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
36	The MaSuRCA genome assembler. <i>Bioinformatics</i> , 2013, 29, 2669-2677.	4.1	1,127

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37	The genome of woodland strawberry ( <i>Fragaria vesca</i> ). <i>Nature Genetics</i> , 2011, 43, 109-116.	21.4	1,091
38	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	27.8	1,086
39	Complete Genome Sequence of <i>Neisseria meningitidis</i> Serogroup B Strain MC58. <i>Science</i> , 2000, 287, 1809-1815.	12.6	1,083
40	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	12.6	1,025
41	Centrifuge: rapid and sensitive classification of metagenomic sequences. <i>Genome Research</i> , 2016, 26, 1721-1729.	5.5	1,025
42	A whole-genome assembly of the domestic cow, <i>Bos taurus</i> . <i>Genome Biology</i> , 2009, 10, R42.	9.6	1,005
43	Complete Genome Sequence of <i>Treponema pallidum</i> , the Syphilis Spirochete. <i>Science</i> , 1998, 281, 375-388.	12.6	969
44	The draft genome of the transgenic tropical fruit tree papaya ( <i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	27.8	964
45	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	27.8	945
46	Fast algorithms for large-scale genome alignment and comparison. <i>Nucleic Acids Research</i> , 2002, 30, 2478-2483.	14.5	931
47	Bracken: estimating species abundance in metagenomics data. <i>PeerJ Computer Science</i> , 0, 3, e104.	4.5	928
48	Transcriptome assembly from long-read RNA-seq alignments with StringTie2. <i>Genome Biology</i> , 2019, 20, 278.	8.8	897
49	Microbial gene identification using interpolated Markov models. <i>Nucleic Acids Research</i> , 1998, 26, 544-548.	14.5	896
50	Genome Sequence of the Radioresistant Bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999, 286, 1571-1577.	12.6	879
51	Alignment of whole genomes. <i>Nucleic Acids Research</i> , 1999, 27, 2369-2376.	14.5	766
52	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003, 423, 81-86.	27.8	760
53	Comparative genomics of the neglected human malaria parasite <i>Plasmodium vivax</i> . <i>Nature</i> , 2008, 455, 757-763.	27.8	756
54	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	12.6	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.	27.8	724
56	Ballgown bridges the gap between transcriptome assembly and expression analysis. <i>Nature Biotechnology</i> , 2015, 33, 243-246.	17.5	716
57	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	12.6	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.	14.5	696
59	TopHat-Fusion: an algorithm for discovery of novel fusion transcripts. <i>Genome Biology</i> , 2011, 12, R72.	9.6	670
60	Genome sequence and comparative analysis of the model rodent malaria parasite <i>Plasmodium yoelii</i> yoelii. <i>Nature</i> , 2002, 419, 512-519.	27.8	666
61	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	12.6	664
62	Macronuclear Genome Sequence of the Ciliate <i>Tetrahymena thermophila</i> , a Model Eukaryote. <i>PLoS Biology</i> , 2006, 4, e286.	5.6	657
63	On Comparing Classifiers: Pitfalls to Avoid and a Recommended Approach. <i>Data Mining and Knowledge Discovery</i> , 1997, 1, 317-328.	3.7	653
64	Whole-Genome Comparison of <i>Mycobacterium tuberculosis</i> Clinical and Laboratory Strains. <i>Journal of Bacteriology</i> , 2002, 184, 5479-5490.	2.2	645
65	GAGE: A critical evaluation of genome assemblies and assembly algorithms. <i>Genome Research</i> , 2012, 22, 557-567.	5.5	597
66	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	12.6	571
67	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	27.8	563
68	Comparative Genome and Proteome Analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 298, 149-159.	12.6	531
69	Phymm and PhymmBL: metagenomic phylogenetic classification with interpolated Markov models. <i>Nature Methods</i> , 2009, 6, 673-676.	19.0	526
70	GeneSplicer: a new computational method for splice site prediction. <i>Nucleic Acids Research</i> , 2001, 29, 1185-1190.	14.5	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.	7.1	489

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73	Quake: quality-aware detection and correction of sequencing errors. <i>Genome Biology</i> , 2010, 11, R116.	9.6	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.	27.8	469
75	Mugsy: fast multiple alignment of closely related whole genomes. <i>Bioinformatics</i> , 2011, 27, 334-342.	4.1	444
76	Bioinformatics challenges of new sequencing technology. <i>Trends in Genetics</i> , 2008, 24, 142-149.	6.7	438
77	Searching for SNPs with cloud computing. <i>Genome Biology</i> , 2009, 10, R134.	9.6	437
78	Rapid, accurate, computational discovery of Rho-independent transcription terminators illuminates their relationship to DNA uptake. <i>Genome Biology</i> , 2007, 8, R22.	9.6	432
79	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014, 15, R59.	9.6	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.	7.1	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.	27.8	419
83	A weighted nearest neighbor algorithm for learning with symbolic features. <i>Machine Learning</i> , 1993, 10, 57-78.	5.4	415
84	Comparative Genome Sequencing for Discovery of Novel Polymorphisms in <i>Bacillus anthracis</i> . <i>Science</i> , 2002, 296, 2028-2033.	12.6	413
85	What are decision trees?. <i>Nature Biotechnology</i> , 2008, 26, 1011-1013.	17.5	409
86	Assembly of large genomes using second-generation sequencing. <i>Genome Research</i> , 2010, 20, 1165-1173.	5.5	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.	5.5	382
88	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. <i>F1000Research</i> , 2013, 2, 188.	1.6	372
89	A review of methods and databases for metagenomic classification and assembly. <i>Briefings in Bioinformatics</i> , 2019, 20, 1125-1136.	6.5	368
90	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	12.6	357

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91	Minimus: a fast, lightweight genome assembler. BMC Bioinformatics, 2007, 8, 64.	2.6	354
92	Multi-Platform Next-Generation Sequencing of the Domestic Turkey ( <i>Meleagris gallopavo</i> ): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	5.6	348
93	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. Science, 2002, 296, 1661-1671.	12.6	344
94	DAGchainer: a tool for mining segmental genome duplications and synteny. Bioinformatics, 2004, 20, 3643-3646.	4.1	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.	5.6	340
96	A Weighted Nearest Neighbor Algorithm for Learning with Symbolic Features. Machine Learning, 1993, 10, 57-78.	5.4	339
97	The genomes of two key bumblebee species with primitive eusocial organization. Genome Biology, 2015, 16, 76.	8.8	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.	2.8	327
99	The International Nucleotide Sequence Database Collaboration. Nucleic Acids Research, 2012, 40, D33-D37.	14.5	327
100	Liftoff: accurate mapping of gene annotations. Bioinformatics, 2021, 37, 1639-1643.	4.1	322
101	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. Science, 2005, 309, 134-137.	12.6	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.	5.5	294
103	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. F1000Research, 2013, 2, 188.	1.6	293
104	Evidence for symmetric chromosomal inversions around the replication origin in bacteria. Genome Biology, 2000, 1, research0011.1.	9.6	287
105	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. Genetics, 2014, 196, 875-890.	2.9	286
106	Microbial Genes in the Human Genome: Lateral Transfer or Gene Loss?. Science, 2001, 292, 1903-1906.	12.6	284
107	KrakenUniq: confident and fast metagenomics classification using unique k-mer counts. Genome Biology, 2018, 19, 198.	8.8	283
108	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	21.4	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.	5.6	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.	14.5	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.	8.8	263
112	Gene Index analysis of the human genome estimates approximately 120,000 genes. <i>Nature Genetics</i> , 2000, 25, 239-240.	21.4	262
113	How to map billions of short reads onto genomes. <i>Nature Biotechnology</i> , 2009, 27, 455-457.	17.5	257
114	Prediction of operons in microbial genomes. <i>Nucleic Acids Research</i> , 2001, 29, 1216-1221.	14.5	255
115	Pavian: interactive analysis of metagenomics data for microbiome studies and pathogen identification. <i>Bioinformatics</i> , 2020, 36, 1303-1304.	4.1	255
116	In-Depth View of Structure, Activity, and Evolution of Rice Chromosome 10. <i>Science</i> , 2003, 300, 1566-1569.	12.6	245
117	Cloud computing and the DNA data race. <i>Nature Biotechnology</i> , 2010, 28, 691-693.	17.5	242
118	Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 816-820.	27.8	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.	5.7	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.	4.2	231
121	The first near-complete assembly of the hexaploid bread wheat genome, <i>Triticum aestivum</i> . <i>GigaScience</i> , 2017, 6, 1-7.	6.4	224
122	Next-generation genome annotation: we still struggle to get it right. <i>Genome Biology</i> , 2019, 20, 92.	8.8	216
123	A nearest hyperrectangle learning method. <i>Machine Learning</i> , 1991, 6, 251-276.	5.4	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.	2.9	207
125	Finding Genes in DNA with a Hidden Markov Model. <i>Journal of Computational Biology</i> , 1997, 4, 127-141.	1.6	198
126	Comparative genome assembly. <i>Briefings in Bioinformatics</i> , 2004, 5, 237-248.	6.5	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.	4.3	191
128	Pan-genomics in the human genome era. <i>Nature Reviews Genetics</i> , 2020, 21, 243-254.	16.3	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.	2.2	189
130	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 820-823.	27.8	188
131	Interpolated Markov Models for Eukaryotic Gene Finding. <i>Genomics</i> , 1999, 59, 24-31.	2.9	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.	9.6	184
133	Between a chicken and a grape: estimating the number of human genes. <i>Genome Biology</i> , 2010, 11, 206.	9.6	182
134	A probabilistic method for identifying start codons in bacterial genomes. <i>Bioinformatics</i> , 2001, 17, 1123-1130.	4.1	180
135	A Nearest Hyperrectangle Learning Method. <i>Machine Learning</i> , 1991, 6, 251-276.	5.4	177
136	Hierarchical Scaffolding With Bambus. <i>Genome Research</i> , 2003, 14, 149-159.	5.5	172
137	The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. <i>PLoS Computational Biology</i> , 2020, 16, e1007981.	3.2	172
138	Skewed oligomers and origins of replication. <i>Gene</i> , 1998, 217, 57-67.	2.2	171
139	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016, 204, 1613-1626.	2.9	169
140	Sequence of <i>Plasmodium falciparum</i> chromosomes 2, 10, 11 and 14. <i>Nature</i> , 2002, 419, 531-534.	27.8	167
141	Beware of mis-assembled genomes. <i>Bioinformatics</i> , 2005, 21, 4320-4321.	4.1	165
142	A new rhesus macaque assembly and annotation for next-generation sequencing analyses. <i>Biology Direct</i> , 2014, 9, 20.	4.6	165
143	Microbial genome sequencing. <i>Nature</i> , 2000, 406, 799-803.	27.8	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.	3.8	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.	7.1	152
146	Gene prediction with Glimmer for metagenomic sequences augmented by classification and clustering. Nucleic Acids Research, 2012, 40, e9-e9.	14.5	150
147	Full-length messenger RNA sequences greatly improve genome annotation. Genome Biology, 2002, 3, research0029.1.	9.6	147
148	JIGSAW: integration of multiple sources of evidence for gene prediction. Bioinformatics, 2005, 21, 3596-3603.	4.1	147
149	Ultrafast and accurate 16S rRNA microbial community analysis using Kraken 2. Microbiome, 2020, 8, 124.	11.1	146
150	Unexpected cross-species contamination in genome sequencing projects. PeerJ, 2014, 2, e675.	2.0	145
151	Next-generation sequencing in neuropathologic diagnosis of infections of the nervous system. Neurology: Neuroimmunology and NeuroInflammation, 2016, 3, e251.	6.0	142
152	EDGE-pro: Estimated Degree of Gene Expression in Prokaryotic Genomes. Evolutionary Bioinformatics, 2013, 9, EBO.S11250.	1.2	141
153	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	12.8	140
154	GAGE-B: an evaluation of genome assemblers for bacterial organisms. Bioinformatics, 2013, 29, 1718-1725.	4.1	135
155	Optimized Multiplex PCR: Efficiently Closing a Whole-Genome Shotgun Sequencing Project. Genomics, 1999, 62, 500-507.	2.9	131
156	Terminating contamination: large-scale search identifies more than 2,000,000 contaminated entries in GenBank. Genome Biology, 2020, 21, 115.	8.8	130
157	Genome re-annotation: a wiki solution?. Genome Biology, 2007, 8, 102.	8.8	127
158	Open questions: How many genes do we have?. BMC Biology, 2018, 16, 94.	3.8	127
159	Serendipitous discovery of Wolbachia genomes in multiple Drosophila species. Genome Biology, 2005, 6, R23.	9.6	126
160	An optimized protocol for analysis of EST sequences. Nucleic Acids Research, 2000, 28, 3657-3665.	14.5	121
161	DNA uptake signal sequences in naturally transformable bacteria. Research in Microbiology, 1999, 150, 603-616.	2.1	117
162	Next-generation sequencing: insights to advance clinical investigations of the microbiome. Journal of Clinical Investigation, 2022, 132, .	8.2	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.	3.9	115
164	A clustering method for repeat analysis in DNA sequences. <i>Genome Biology</i> , 2001, 2, research0027.1.	9.6	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.	3.5	112
166	Human contamination in bacterial genomes has created thousands of spurious proteins. <i>Genome Research</i> , 2019, 29, 954-960.	5.5	111
167	Computational Gene Prediction Using Multiple Sources of Evidence. <i>Genome Research</i> , 2003, 14, 142-148.	5.5	110
168	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409.	27.8	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.	1.8	103
170	A Decision Tree System for Finding Genes in DNA. <i>Journal of Computational Biology</i> , 1998, 5, 667-680.	1.6	102
171	The Value of Complete Microbial Genome Sequencing (You Get What You Pay For). <i>Journal of Bacteriology</i> , 2002, 184, 6403-6405.	2.2	101
172	PhymmBL expanded: confidence scores, custom databases, parallelization and more. <i>Nature Methods</i> , 2011, 8, 367-367.	19.0	97
173	Detection and correction of false segmental duplications caused by genome mis-assembly. <i>Genome Biology</i> , 2010, 11, R28.	9.6	96
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