

Steven L Salzberg

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	PhyloCSF++: a fast and user-friendly implementation of PhyloCSF with annotation tools. <i>Bioinformatics</i> , 2022, 38, 1440-1442.	4.1	8
2	Genome-wide association identifies candidate genes for drought tolerance in coast redwood and giant sequoia. <i>Plant Journal</i> , 2022, 109, 7-22.	5.7	17
3	The SAMBA tool uses long reads to improve the contiguity of genome assemblies. <i>PLoS Computational Biology</i> , 2022, 18, e1009860.	3.2	22
4	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, .	1.8	28
5	A reference-quality, fully annotated genome from a Puerto Rican individual. <i>Genetics</i> , 2022, 220, .	2.9	7
6	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
7	Next-generation sequencing: insights to advance clinical investigations of the microbiome. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	116
8	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. <i>Nature Communications</i> , 2022, 13, 2047.	12.8	30
9	Effects of transcriptional noise on estimates of gene and transcript expression in RNA sequencing experiments. <i>Genome Research</i> , 2021, 31, 301-308.	5.5	13
10	Liftoff: accurate mapping of gene annotations. <i>Bioinformatics</i> , 2021, 37, 1639-1643.	4.1	322
11	Dissecting the Polygenic Basis of Cold Adaptation Using Genome-Wide Association of Traits and Environmental Data in Douglas-fir. <i>Genes</i> , 2021, 12, 110.	2.4	14
12	Balrog: A universal protein model for prokaryotic gene prediction. <i>PLoS Computational Biology</i> , 2021, 17, e1008727.	3.2	21
13	Guillain-Barré Syndrome Outbreak in Peru 2019 Associated With <i>Campylobacter jejuni</i> Infection. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2021, 8, .	6.0	20
14	Rapid detection of inter-clade recombination in SARS-CoV-2 with Bolotie. <i>Genetics</i> , 2021, 218, .	2.9	58
15	Rapidly fatal infection with <i>Bacillus cereus/thuringiensis</i> : genome assembly of the responsible pathogen and consideration of possibly contributing toxins. <i>Diagnostic Microbiology and Infectious Disease</i> , 2021, 101, 115534.	1.8	1
16	Releasing the Kraken. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	2.1	7
17	Pavian: interactive analysis of metagenomics data for microbiome studies and pathogen identification. <i>Bioinformatics</i> , 2020, 36, 1303-1304.	4.1	255
18	Genomic basis of white pine blister rust quantitative disease resistance and its relationship with qualitative resistance. <i>Plant Journal</i> , 2020, 104, 365-376.	5.7	32

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19	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409.	27.8	105
20	A Reference Genome Sequence for Giant Sequoia. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3907-3919.	1.8	67
21	Ultrafast and accurate 16S rRNA microbial community analysis using Kraken 2. <i>Microbiome</i> , 2020, 8, 124.	11.1	146
22	Chromosome-Scale Assembly of the Bread Wheat Genome Reveals Thousands of Additional Gene Copies. <i>Genetics</i> , 2020, 216, 599-608.	2.9	34
23	Microbial Diagnostics for Cancer: A Step Forward but Not Prime Time Yet. <i>Cancer Cell</i> , 2020, 37, 625-627.	16.8	1
24	Terminating contamination: large-scale search identifies more than 2,000,000 contaminated entries in GenBank. <i>Genome Biology</i> , 2020, 21, 115.	8.8	130
25	High-quality chromosome-scale assembly of the walnut (<i>Juglans regia</i> L.) reference genome. <i>CigaScience</i> , 2020, 9, .	6.4	83
26	Assembly and annotation of an Ashkenazi human reference genome. <i>Genome Biology</i> , 2020, 21, 129.	8.8	42
27	The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. <i>PLoS Computational Biology</i> , 2020, 16, e1007981.	3.2	172
28	Pan-genomics in the human genome era. <i>Nature Reviews Genetics</i> , 2020, 21, 243-254.	16.3	191
29	Genome assembly and characterization of a complex zBED-NLR gene-containing disease resistance locus in Carolina Gold Select rice with Nanopore sequencing. <i>PLoS Genetics</i> , 2020, 16, e1008571.	3.5	112
30	SkewIT: The Skew Index Test for large-scale GC Skew analysis of bacterial genomes. <i>PLoS Computational Biology</i> , 2020, 16, e1008439.	3.2	40
31	The genome of the American groundhog, <i>Marmota monax</i> . <i>F1000Research</i> , 2020, 9, 1137.	1.6	3
32	The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. , 2020, 16, e1007981.		0
33	The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. , 2020, 16, e1007981.		0
34	The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. , 2020, 16, e1007981.		0
35	The genome polishing tool POLCA makes fast and accurate corrections in genome assemblies. , 2020, 16, e1007981.		0
36	The Terabase Search Engine: a large-scale relational database of short-read sequences. <i>Bioinformatics</i> , 2019, 35, 665-670.	4.1	8

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37	Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. <i>Nature Biotechnology</i> , 2019, 37, 907-915.	17.5	6,567
38	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. <i>Chest</i> , 2019, 156, 1068-1079.	0.8	5
39	Human contamination in bacterial genomes has created thousands of spurious proteins. <i>Genome Research</i> , 2019, 29, 954-960.	5.5	111
40	Next-generation genome annotation: we still struggle to get it right. <i>Genome Biology</i> , 2019, 20, 92.	8.8	216
41	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, AB296.	2.9	0
42	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. <i>Nature Communications</i> , 2019, 10, 880.	12.8	71
43	Transcriptome assembly from long-read RNA-seq alignments with StringTie2. <i>Genome Biology</i> , 2019, 20, 278.	8.8	897
44	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. <i>Nature Genetics</i> , 2019, 51, 30-35.	21.4	276
45	Genomic architecture of complex traits in loblolly pine. <i>New Phytologist</i> , 2019, 221, 1789-1801.	7.3	60
46	A review of methods and databases for metagenomic classification and assembly. <i>Briefings in Bioinformatics</i> , 2019, 20, 1125-1136.	6.5	368
47	Cretaceous dinosaur bone contains recent organic material and provides an environment conducive to microbial communities. <i>ELife</i> , 2019, 8, .	6.0	38
48	Genomic characterization of chromosome translocations in patients with T/myeloid mixed-phenotype acute leukemia. <i>Leukemia and Lymphoma</i> , 2018, 59, 1231-1238.	1.3	8
49	KrakenUniq: confident and fast metagenomics classification using unique k-mer counts. <i>Genome Biology</i> , 2018, 19, 198.	8.8	283
50	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
51	Genomic Variation Among and Within Six <i>Juglans</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2153-2165.	1.8	73
52	Removing contaminants from databases of draft genomes. <i>PLoS Computational Biology</i> , 2018, 14, e1006277.	3.2	85
53	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018, 9, 2606.	12.8	79
54	Development and Optimization of Metagenomic Next-Generation Sequencing Methods for Cerebrospinal Fluid Diagnostics. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	65

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55	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	12.8	140
56	Identifying Corneal Infections in Formalin-Fixed Specimens Using Next Generation Sequencing. , 2018, 59, 280.		51
57	Open questions: How many genes do we have?. BMC Biology, 2018, 16, 94.	3.8	127
58	MUMmer4: A fast and versatile genome alignment system. PLoS Computational Biology, 2018, 14, e1005944.	3.2	1,412
59	Short Read Mapping: An Algorithmic Tour. Proceedings of the IEEE, 2017, 105, 436-458.	21.3	63
60	The novel fusion transcript NR5A2â€KLHL29FT is generated by an insertion at the KLHL29 locus. Cancer, 2017, 123, 1507-1515.	4.1	4
61	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. Genome Research, 2017, 27, 787-792.	5.5	382
62	Horizontal gene transfer is not a hallmark of the human genome. Genome Biology, 2017, 18, 85.	8.8	55
63	16GT: a fast and sensitive variant caller using a 16-genotype probabilistic model. GigaScience, 2017, 6, 1-4.	6.4	11
64	First Draft Genome Sequence of the Pathogenic Fungus <i>Lomentospora prolificans</i> (Formerly) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	9.8	11
65	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. G3: Genes, Genomes, Genetics, 2017, 7, 3157-3167.	1.8	103
66	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . Nature, 2017, 551, 498-502.	27.8	563
67	Presence of Human Hepatitis B Virus in a Cohort of People Who Inject Drugs. Annals of Internal Medicine, 2017, 167, 1.	3.9	28
68	The first near-complete assembly of the hexaploid bread wheat genome, <i>Triticum aestivum</i> . GigaScience, 2017, 6, 1-7.	6.4	224
69	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. GigaScience, 2017, 6, 1-4.	6.4	71
70	First Draft Assembly and Annotation of the Genome of a California Endemic Oak <i>Quercus lobata</i> (Fagaceae). G3: Genes, Genomes, Genetics, 2016, 6, 3485-3495.	1.8	95
71	Reminder to deposit DNA sequences. Nature, 2016, 533, 179-179.	27.8	8
72	Reminder to deposit DNA sequences. Science, 2016, 352, 780-780.	12.6	24

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73	Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. Nature Protocols, 2016, 11, 1650-1667.	12.0	4,743
74	Centrifuge: rapid and sensitive classification of metagenomic sequences. Genome Research, 2016, 26, 1721-1729.	5.5	1,025
75	Sequence of the Sugar Pine Megagenome. Genetics, 2016, 204, 1613-1626.	2.9	169
76	The walnut (<i>Juglans regia</i>) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. Plant Journal, 2016, 87, 507-532.	5.7	233
77	Next-generation sequencing in neuropathologic diagnosis of infections of the nervous system. Neurology: Neuroimmunology and NeuroInflammation, 2016, 3, e251.	6.0	142
78	Use and mis-use of supplementary material in science publications. BMC Bioinformatics, 2015, 16, 237.	2.6	36
79	Single molecule real-time sequencing of <i>Xanthomonas oryzae</i> genomes reveals a dynamic structure and complex TAL (transcription activator-like) effector gene relationships. Microbial Genomics, 2015, 1, .	2.0	86
80	Broad CTL response is required to clear latent HIV-1 due to dominance of escape mutations. Nature, 2015, 517, 381-385.	27.8	469
81	StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. Nature Biotechnology, 2015, 33, 290-295.	17.5	8,385
82	HISAT: a fast spliced aligner with low memory requirements. Nature Methods, 2015, 12, 357-360.	19.0	16,262
83	Ballgown bridges the gap between transcriptome assembly and expression analysis. Nature Biotechnology, 2015, 33, 243-246.	17.5	716
84	The genomes of two key bumblebee species with primitive eusocial organization. Genome Biology, 2015, 16, 76.	8.8	330
85	Genomic signatures of evolutionary transitions from solitary to group living. Science, 2015, 348, 1139-1143.	12.6	357
86	Genome-wide annotation of microRNA primary transcript structures reveals novel regulatory mechanisms. Genome Research, 2015, 25, 1401-1409.	5.5	91
87	Re-analysis of metagenomic sequences from acute flaccid myelitis patients reveals alternatives to enterovirus D68 infection. F1000Research, 2015, 4, 180.	1.6	9
88	Re-analysis of metagenomic sequences from acute flaccid myelitis patients reveals alternatives to enterovirus D68 infection. F1000Research, 2015, 4, 180.	1.6	6
89	Arioc: high-throughput read alignment with GPU-accelerated exploration of the seed-and-extend search space. PeerJ, 2015, 3, e808.	2.0	33
90	A new rhesus macaque assembly and annotation for next-generation sequencing analyses. Biology Direct, 2014, 9, 20.	4.6	165

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91	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. <i>Genetics</i> , 2014, 196, 875-890.	2.9	286
92	Kraken: ultrafast metagenomic sequence classification using exact alignments. <i>Genome Biology</i> , 2014, 15, R46.	9.6	3,540
93	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014, 15, R59.	9.6	424
94	DIAMUND : Direct Comparison of Genomes to Detect Mutations. <i>Human Mutation</i> , 2014, 35, 283-288.	2.5	9
95	Genomic Features of a Bumble Bee Symbiont Reflect Its Host Environment. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3793-3803.	3.1	53
96	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
97	Unexpected cross-species contamination in genome sequencing projects. <i>PeerJ</i> , 2014, 2, e675.	2.0	145
98	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
99	The MaSuRCA genome assembler. <i>Bioinformatics</i> , 2013, 29, 2669-2677.	4.1	1,127
100	GAGE-B: an evaluation of genome assemblers for bacterial organisms. <i>Bioinformatics</i> , 2013, 29, 1718-1725.	4.1	135
101	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. <i>Briefings in Bioinformatics</i> , 2013, 14, 213-224.	6.5	54
102	NIH funding: It does support innovators. <i>Nature</i> , 2013, 493, 26-26.	27.8	1
103	Sequestration: inadvertently killing biomedical research to score political points. <i>Genome Biology</i> , 2013, 14, 109.	9.6	2
104	Open access to tree genomes: the path to a better forest. <i>Genome Biology</i> , 2013, 14, 120.	8.8	46
105	Genome-Guided Transcriptome Assembly in the Age of Next-Generation Sequencing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1234-1240.	3.0	16
106	The COMBEX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	5.6	54
107	EDGE-pro: Estimated Degree of Gene Expression in Prokaryotic Genomes. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S11250.	1.2	141
108	Insights into the Loblolly Pine Genome: Characterization of BAC and Fosmid Sequences. <i>PLoS ONE</i> , 2013, 8, e72439.	2.5	46

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109	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. F1000Research, 2013, 2, 188.	1.6	372
110	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. F1000Research, 2013, 2, 188.	1.6	293
111	Gene prediction with Glimmer for metagenomic sequences augmented by classification and clustering. Nucleic Acids Research, 2012, 40, e9-e9.	14.5	150
112	The Perils of Gene Patents. Clinical Pharmacology and Therapeutics, 2012, 91, 969-971.	4.7	7
113	Genome interpretation and assembly—recent progress and next steps. Nature Biotechnology, 2012, 30, 1081-1083.	17.5	10
114	The International Nucleotide Sequence Database Collaboration. Nucleic Acids Research, 2012, 40, D33-D37.	14.5	327
115	Thousands of missed genes found in bacterial genomes and their analysis with COMBREX. Biology Direct, 2012, 7, 37.	4.6	28
116	Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. Nature Protocols, 2012, 7, 562-578.	12.0	11,433
117	Fast gapped-read alignment with Bowtie 2. Nature Methods, 2012, 9, 357-359.	19.0	42,357
118	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. Nature, 2012, 487, 94-98.	27.8	1,086
119	GAGE: A critical evaluation of genome assemblies and assembly algorithms. Genome Research, 2012, 22, 557-567.	5.5	597
120	Repetitive DNA and next-generation sequencing: computational challenges and solutions. Nature Reviews Genetics, 2012, 13, 36-46.	16.3	1,382
121	Mis-Assembled “Segmental Duplications” in Two Versions of the Bos taurus Genome. PLoS ONE, 2012, 7, e42680.	2.5	22
122	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic Xanthomonas spp. Journal of Bacteriology, 2011, 193, 5450-5464.	2.2	189
123	TopHat-Fusion: an algorithm for discovery of novel fusion transcripts. Genome Biology, 2011, 12, R72.	9.6	670
124	Complete Columbian mammoth mitogenome suggests interbreeding with woolly mammoths. Genome Biology, 2011, 12, R51.	9.6	56
125	Closure of the NCBI SRA and implications for the long-term future of genomics data storage. Genome Biology, 2011, 12, 402.	8.8	29
126	Genome Assembly Has a Major Impact on Gene Content: A Comparison of Annotation in Two Bos Taurus Assemblies. PLoS ONE, 2011, 6, e21400.	2.5	65

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127	The genome of woodland strawberry (<i>Fragaria vesca</i>). <i>Nature Genetics</i> , 2011, 43, 109-116.	21.4	1,091
128	PhymmBL expanded: confidence scores, custom databases, parallelization and more. <i>Nature Methods</i> , 2011, 8, 367-367.	19.0	97
129	Improving pan-genome annotation using whole genome multiple alignment. <i>BMC Bioinformatics</i> , 2011, 12, 272.	2.6	38
130	Detection of lineage-specific evolutionary changes among primate species. <i>BMC Bioinformatics</i> , 2011, 12, 274.	2.6	19
131	COMBREX: a project to accelerate the functional annotation of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2011, 39, D11-D14.	14.5	47
132	FLASH: fast length adjustment of short reads to improve genome assemblies. <i>Bioinformatics</i> , 2011, 27, 2957-2963.	4.1	11,573
133	<i>Bacillus anthracis</i> comparative genome analysis in support of the Amerithrax investigation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5027-5032.	7.1	152
134	Mugsy: fast multiple alignment of closely related whole genomes. <i>Bioinformatics</i> , 2011, 27, 334-342.	4.1	444
135	Assembly of large genomes using second-generation sequencing. <i>Genome Research</i> , 2010, 20, 1165-1173.	5.5	390
136	Clustering metagenomic sequences with interpolated Markov models. <i>BMC Bioinformatics</i> , 2010, 11, 544.	2.6	90
137	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.	2.8	74
138	Cloud computing and the DNA data race. <i>Nature Biotechnology</i> , 2010, 28, 691-693.	17.5	242
139	Mind the gaps. <i>Nature Methods</i> , 2010, 7, 105-106.	19.0	10
140	Genome Sequence of the Dioxin-Mineralizing Bacterium <i>Sphingomonas wittichii</i> RW1. <i>Journal of Bacteriology</i> , 2010, 192, 6101-6102.	2.2	93
141	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (<i>Meleagris gallopavo</i>): Genome Assembly and Analysis. <i>PLoS Biology</i> , 2010, 8, e1000475.	5.6	348
142	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
143	Quake: quality-aware detection and correction of sequencing errors. <i>Genome Biology</i> , 2010, 11, R116.	9.6	470
144	Do-it-yourself genetic testing. <i>Genome Biology</i> , 2010, 11, 404.	8.8	16

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145	Detection and correction of false segmental duplications caused by genome mis-assembly. <i>Genome Biology</i> , 2010, 11, R28.	9.6	96
146	Genes and genomes, an imperfect world: comparison of gene annotations of two <i>Bos taurus</i> draft assemblies. <i>Genome Biology</i> , 2010, 11, P13.	9.6	1
147	Between a chicken and a grape: estimating the number of human genes. <i>Genome Biology</i> , 2010, 11, 206.	9.6	182
148	Recent advances in RNA sequence analysis. <i>F1000 Biology Reports</i> , 2010, 2, 64.	4.0	13
149	EFFORTS TO DEREGULATE RAINBOW PAPAYA IN JAPAN: MOLECULAR CHARACTERIZATION OF TRANSGENE AND VECTOR INSERTS. <i>Acta Horticulturae</i> , 2010, , 235-240.	0.2	0
150	2009 Swine-Origin Influenza A (H1N1) Resembles Previous Influenza Isolates. <i>PLoS ONE</i> , 2009, 4, e6402.	2.5	31
151	OperonDB: a comprehensive database of predicted operons in microbial genomes. <i>Nucleic Acids Research</i> , 2009, 37, D479-D482.	14.5	83
152	Insignia: a DNA signature search web server for diagnostic assay development. <i>Nucleic Acids Research</i> , 2009, 37, W229-W234.	14.5	37
153	Open Access: The Sooner the Better. <i>Science</i> , 2009, 325, 266-266.	12.6	0
154	Genome Sequence of the <i>Wolbachia</i> Endosymbiont of <i>Culex quinquefasciatus</i> JHB. <i>Journal of Bacteriology</i> , 2009, 191, 1725-1725.	2.2	44
155	The Complete Genome Sequence of <i>Bacillus anthracis</i> Ames "Ancestor". <i>Journal of Bacteriology</i> , 2009, 191, 445-446.	2.2	88
156	Efficient oligonucleotide probe selection for pan-genomic tiling arrays. <i>BMC Bioinformatics</i> , 2009, 10, 293.	2.6	25
157	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	27.8	945
158	How to map billions of short reads onto genomes. <i>Nature Biotechnology</i> , 2009, 27, 455-457.	17.5	257
159	Phymm and PhymmBL: metagenomic phylogenetic classification with interpolated Markov models. <i>Nature Methods</i> , 2009, 6, 673-676.	19.0	526
160	TopHat: discovering splice junctions with RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 1105-1111.	4.1	11,265
161	Searching for SNPs with cloud computing. <i>Genome Biology</i> , 2009, 10, R134.	9.6	437
162	A whole-genome assembly of the domestic cow, <i>Bos taurus</i> . <i>Genome Biology</i> , 2009, 10, R42.	9.6	1,005

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163	Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. <i>Genome Biology</i> , 2009, 10, R25.	9.6	19,212
164	Genome-Wide Analysis of Repetitive Elements in Papaya. <i>Tropical Plant Biology</i> , 2008, 1, 191-201.	1.9	24
165	Characterization of Insertion Sites in Rainbow Papaya, the First Commercialized Transgenic Fruit Crop. <i>Tropical Plant Biology</i> , 2008, 1, 293-309.	1.9	25
166	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
167	Comparative genomics of the neglected human malaria parasite <i>Plasmodium vivax</i> . <i>Nature</i> , 2008, 455, 757-763.	27.8	756
168	The contents of the syringe. <i>Nature</i> , 2008, 454, 160-161.	27.8	39
169	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>BMC Genomics</i> , 2008, 9, 204.	2.8	327
170	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.	2.8	33
171	Bioinformatics challenges of new sequencing technology. <i>Trends in Genetics</i> , 2008, 24, 142-149.	6.7	438
172	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
173	What are decision trees?. <i>Nature Biotechnology</i> , 2008, 26, 1011-1013.	17.5	409
174	Gene-Boosted Assembly of a Novel Bacterial Genome from Very Short Reads. <i>PLoS Computational Biology</i> , 2008, 4, e1000186.	3.2	46
175	Re-Assembly of the Genome of <i>Francisella tularensis</i> Subsp. <i>holarctica</i> OSU18. <i>PLoS ONE</i> , 2008, 3, e3427.	2.5	9
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177	Comprehensive DNA Signature Discovery and Validation. <i>PLoS Computational Biology</i> , 2007, 3, e98.	3.2	63
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