

# Michael C Schatz

## List of Publications by Year in descending order

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160  
papers

37,803  
citations

9234

74  
h-index

6979

154  
g-index

234  
all docs

234  
docs citations

234  
times ranked

44676  
citing authors

#	ARTICLE	IF	CITATIONS
1	The contribution of de novo coding mutations to autism spectrum disorder. <i>Nature</i> , 2014, 515, 216-221.	13.7	2,188
2	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
3	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016, 13, 1050-1054.	9.0	1,658
4	De Novo Gene Disruptions in Children on the Autistic Spectrum. <i>Neuron</i> , 2012, 74, 285-299.	3.8	1,311
5	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	6.0	1,222
6	GenomeScope: fast reference-free genome profiling from short reads. <i>Bioinformatics</i> , 2017, 33, 2202-2204.	1.8	1,183
7	Accurate detection of complex structural variations using single-molecule sequencing. <i>Nature Methods</i> , 2018, 15, 461-468.	9.0	1,175
8	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	6.0	1,025
9	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019, 37, 1155-1162.	9.4	1,010
10	A whole-genome assembly of the domestic cow, <i>Bos taurus</i> . <i>Genome Biology</i> , 2009, 10, R42.	13.9	1,005
11	Big Data: Astronomical or Genomical?. <i>PLoS Biology</i> , 2015, 13, e1002195.	2.6	995
12	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
13	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.	9.4	955
14	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012, 30, 693-700.	9.4	946
15	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	6.0	731
16	GenomeScope 2.0 and Smudgeplot for reference-free profiling of polyploid genomes. <i>Nature Communications</i> , 2020, 11, 1432.	5.8	660
17	GAGE: A critical evaluation of genome assemblies and assembly algorithms. <i>Genome Research</i> , 2012, 22, 557-567.	2.4	597
18	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582

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19	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	6.0	571
20	CloudBurst: highly sensitive read mapping with MapReduce. <i>Bioinformatics</i> , 2009, 25, 1363-1369.	1.8	551
21	The advantages of SMRT sequencing. <i>Genome Biology</i> , 2013, 14, .	3.8	487
22	Major Structural Differences and Novel Potential Virulence Mechanisms from the Genomes of Multiple <i>Campylobacter</i> Species. <i>PLoS Biology</i> , 2005, 3, e15.	2.6	483
23	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
24	Quake: quality-aware detection and correction of sequencing errors. <i>Genome Biology</i> , 2010, 11, R116.	13.9	470
25	RaGOO: fast and accurate reference-guided scaffolding of draft genomes. <i>Genome Biology</i> , 2019, 20, 224.	3.8	469
26	Major Impacts of Widespread Structural Variation on Gene Expression and Crop Improvement in Tomato. <i>Cell</i> , 2020, 182, 145-161.e23.	13.5	464
27	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	9.4	463
28	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
29	Searching for SNPs with cloud computing. <i>Genome Biology</i> , 2009, 10, R134.	13.9	437
30	Piercing the dark matter: bioinformatics of long-range sequencing and mapping. <i>Nature Reviews Genetics</i> , 2018, 19, 329-346.	7.7	395
31	Assembly of large genomes using second-generation sequencing. <i>Genome Research</i> , 2010, 20, 1165-1173.	2.4	390
32	Multi-Platform Next-Generation Sequencing of the Domestic Turkey ( <i>Meleagris gallopavo</i> ): Genome Assembly and Analysis. <i>PLoS Biology</i> , 2010, 8, e1000475.	2.6	348
33	Oxford Nanopore sequencing, hybrid error correction, and de novo assembly of a eukaryotic genome. <i>Genome Research</i> , 2015, 25, 1750-1756.	2.4	331
34	Genome of the long-living sacred lotus ( <i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 2013, 14, R41.	13.9	329
35	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.	1.2	327
36	The advantages of SMRT sequencing. <i>Genome Biology</i> , 2013, 14, 405.	3.8	324

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37	Insight into the evolution of the Solanaceae from the parental genomes of <i>Petunia hybrida</i> . <i>Nature Plants</i> , 2016, 2, 16074.	4.7	311
38	Assemblytics: a web analytics tool for the detection of variants from an assembly. <i>Bioinformatics</i> , 2016, 32, 3021-3023.	1.8	295
39	Aluminum tolerance in maize is associated with higher <i>MATE1</i> gene copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5241-5246.	3.3	265
40	Genome assembly forensics: finding the elusive mis-assembly. <i>Genome Biology</i> , 2008, 9, R55.	13.9	248
41	Cloud computing and the DNA data race. <i>Nature Biotechnology</i> , 2010, 28, 691-693.	9.4	242
42	High-throughput sequence alignment using Graphics Processing Units. <i>BMC Bioinformatics</i> , 2007, 8, 474.	1.2	237
43	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020, 38, 1347-1355.	9.4	233
44	Whole genome de novo assemblies of three divergent strains of rice, <i>Oryza sativa</i> , document novel gene space of aus and indica. <i>Genome Biology</i> , 2014, 15, 506.	3.8	228
45	Interactive analysis and assessment of single-cell copy-number variations. <i>Nature Methods</i> , 2015, 12, 1058-1060.	9.0	220
46	Complete genomic and epigenetic maps of human centromeres. <i>Science</i> , 2022, 376, eabl4178.	6.0	204
47	Genomic Analyses of the Microsporidian <i>Nosema ceranae</i> , an Emergent Pathogen of Honey Bees. <i>PLoS Pathogens</i> , 2009, 5, e1000466.	2.1	194
48	Accurate de novo and transmitted indel detection in exome-capture data using microassembly. <i>Nature Methods</i> , 2014, 11, 1033-1036.	9.0	194
49	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
50	The genetic and epigenetic landscape of the <i>Arabidopsis</i> centromeres. <i>Science</i> , 2021, 374, eabi7489.	6.0	188
51	Rate of meristem maturation determines inflorescence architecture in tomato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 639-644.	3.3	171
52	Targeted nanopore sequencing by real-time mapping of raw electrical signal with UNCALLED. <i>Nature Biotechnology</i> , 2021, 39, 431-441.	9.4	160
53	Current challenges in de novo plant genome sequencing and assembly. <i>Genome Biology</i> , 2012, 13, 243.	13.9	157
54	Complex microbiome underlying secondary and primary metabolism in the tunicate- <i>Prochloron</i> symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E1423-32.	3.3	146

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55	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. <i>Science</i> , 2022, 376, eabk3112.	6.0	146
56	Reducing INDEL calling errors in whole genome and exome sequencing data. <i>Genome Medicine</i> , 2014, 6, 89.	3.6	144
57	A complete reference genome improves analysis of human genetic variation. <i>Science</i> , 2022, 376, eabl3533.	6.0	144
58	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line. <i>Genome Research</i> , 2018, 28, 1126-1135.	2.4	142
59	Extending reference assembly models. <i>Genome Biology</i> , 2015, 16, 13.	3.8	139
60	Metassembler: merging and optimizing de novo genome assemblies. <i>Genome Biology</i> , 2015, 16, 207.	3.8	127
61	Design patterns for efficient graph algorithms in MapReduce. , 2010, , .		123
62	Whole genome de novo assemblies of three divergent strains of rice, <i>Oryza sativa</i> , document novel gene space of aus and indica. <i>Genome Biology</i> , 2014, 15, 506.	13.9	123
63	Assembly complexity of prokaryotic genomes using short reads. <i>BMC Bioinformatics</i> , 2010, 11, 21.	1.2	120
64	Genomic survey of the ectoparasitic mite <i>Varroa destructor</i> , a major pest of the honey bee <i>Apis mellifera</i> . <i>BMC Genomics</i> , 2010, 11, 602.	1.2	118
65	Epigenetic patterns in a complete human genome. <i>Science</i> , 2022, 376, eabj5089.	6.0	118
66	Genomic dark matter: the reliability of short read mapping illustrated by the genome mappability score. <i>Bioinformatics</i> , 2012, 28, 2097-2105.	1.8	116
67	Reference quality assembly of the 3.5-Gb genome of <i>Capsicum annuum</i> from a single linked-read library. <i>Horticulture Research</i> , 2018, 5, 4.	2.9	113
68	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. <i>GigaScience</i> , 2019, 8, .	3.3	106
69	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , 2016, 12, e1005954.	1.5	105
70	Paragraph: a graph-based structural variant genotyper for short-read sequence data. <i>Genome Biology</i> , 2019, 20, 291.	3.8	104
71	SplitMEM: a graphical algorithm for pan-genome analysis with suffix skips. <i>Bioinformatics</i> , 2014, 30, 3476-3483.	1.8	102
72	A multi-task convolutional deep neural network for variant calling in single molecule sequencing. <i>Nature Communications</i> , 2019, 10, 998.	5.8	102

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73	Comparative genomics of mutualistic viruses of <i>Glyptapanteles</i> parasitic wasps. <i>Genome Biology</i> , 2008, 9, R183.	13.9	101
74	Indel variant analysis of short-read sequencing data with Scalpel. <i>Nature Protocols</i> , 2016, 11, 2529-2548.	5.5	99
75	Genome and transcriptome of the regeneration-competent flatworm, <i>Macrostomum lignano</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12462-12467.	3.3	90
76	Cultivation and Complete Genome Sequencing of <i>Gloeobacter kilaueensis</i> sp. nov., from a Lava Cave in K��lauea Caldera, Hawai'i. <i>PLoS ONE</i> , 2013, 8, e76376.	1.1	85
77	Optimizing data intensive GPGPU computations for DNA sequence alignment. <i>Parallel Computing</i> , 2009, 35, 429-440.	1.3	83
78	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , 2016, 7, 10164.	5.8	79
79	Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , 2022, 2, 100128.	3.0	77
80	High-coverage sequencing and annotated assemblies of the budgerigar genome. <i>GigaScience</i> , 2014, 3, 11.	3.3	75
81	Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. <i>Genome Research</i> , 2020, 30, 1258-1273.	2.4	72
82	Addressing confounding artifacts in reconstruction of gene co-expression networks. <i>Genome Biology</i> , 2019, 20, 94.	3.8	68
83	The DNA data deluge. <i>IEEE Spectrum</i> , 2013, 50, 28-33.	0.5	67
84	Hawkeye: an interactive visual analytics tool for genome assemblies. <i>Genome Biology</i> , 2007, 8, R34.	13.9	66
85	Hypo-osmotic-like stress underlies general cellular defects of aneuploidy. <i>Nature</i> , 2019, 570, 117-121.	13.7	66
86	Duplication of a domestication locus neutralized a cryptic variant that caused a breeding barrier in tomato. <i>Nature Plants</i> , 2019, 5, 471-479.	4.7	66
87	Applying Rapid Whole-Genome Sequencing To Predict Phenotypic Antimicrobial Susceptibility Testing Results among Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Clinical Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	62
88	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019, 51, 1549-1558.	9.4	60
89	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. <i>Cell Genomics</i> , 2022, 2, 100085.	3.0	59
90	A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , 2020, 11, 4794.	5.8	56

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91	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. <i>Nature Genetics</i> , 2017, 49, 825-833.	9.4	55
92	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. <i>Briefings in Bioinformatics</i> , 2013, 14, 213-224.	3.2	54
93	Nanopore sequencing meets epigenetics. <i>Nature Methods</i> , 2017, 14, 347-348.	9.0	53
94	Parrot Genomes and the Evolution of Heightened Longevity and Cognition. <i>Current Biology</i> , 2018, 28, 4001-4008.e7.	1.8	52
95	The evolution of inflorescence diversity in the nightshades and heterochrony during meristem maturation. <i>Genome Research</i> , 2016, 26, 1676-1686.	2.4	51
96	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	1.2	51
97	Parliament2: Accurate structural variant calling at scale. <i>GigaScience</i> , 2020, 9, .	3.3	51
98	Ribbon: intuitive visualization for complex genomic variation. <i>Bioinformatics</i> , 2021, 37, 413-415.	1.8	48
99	Revealing Biological Modules via Graph Summarization. <i>Journal of Computational Biology</i> , 2009, 16, 253-264.	0.8	47
100	Complete telomere-to-telomere <i>de novo</i> assembly of the <i>Plasmodium falciparum</i> genome through long-read (>11â€‰kb), single molecule, real-time sequencing. <i>DNA Research</i> , 2016, 23, 339-351.	1.5	47
101	Structure and evolution of a proviral locus of <i>Glyptapanteles indiensis</i> bracovirus. <i>BMC Microbiology</i> , 2007, 7, 61.	1.3	45
102	Novel circular RNA circNF1 acts as a molecular sponge, promoting gastric cancer by absorbing miR-16. <i>Endocrine-Related Cancer</i> , 2019, 26, 265-277.	1.6	45
103	Antibiotic pressure on the acquisition and loss of antibiotic resistance genes in <i>Klebsiella pneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1796-1803.	1.3	44
104	Automated correction of genome sequence errors. <i>Nucleic Acids Research</i> , 2004, 32, 562-569.	6.5	42
105	LRSim: A Linked-Reads Simulator Generating Insights for Better Genome Partitioning. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 478-484.	1.9	42
106	The Challenge of Small-Scale Repeats for Indel Discovery. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 8.	2.0	41
107	Scikit-ribo Enables Accurate Estimation and Robust Modeling of Translation Dynamics at Codon Resolution. <i>Cell Systems</i> , 2018, 6, 180-191.e4.	2.9	41
108	Biological data sciences in genome research. <i>Genome Research</i> , 2015, 25, 1417-1422.	2.4	40

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109	TGF- $\beta$ 2 reduces DNA ds-break repair mechanisms to heighten genetic diversity and adaptability of CD44+/CD24 <sup>low</sup> cancer cells. <i>ELife</i> , 2017, 6, .	2.8	37
110	Local adaptation and archaic introgression shape global diversity at human structural variant loci. <i>ELife</i> , 2021, 10, .	2.8	33
111	Conservation Genomics of the Declining North American Bumblebee <i>Bombus terricola</i> Reveals Inbreeding and Selection on Immune Genes. <i>Frontiers in Genetics</i> , 2018, 9, 316.	1.1	31
112	Genomic diversity of SARS-CoV-2 during early introduction into the Baltimore-Washington metropolitan area. <i>JCI Insight</i> , 2021, 6, .	2.3	31
113	Genotyping in the Cloud with Crossbow. <i>Current Protocols in Bioinformatics</i> , 2012, 39, Unit15.3.	25.8	30
114	Clonal Hematopoiesis Before, During, and After Human Spaceflight. <i>Cell Reports</i> , 2020, 33, 108458.	2.9	30
115	The rise of a digital immune system. <i>GigaScience</i> , 2012, 1, 4.	3.3	29
116	Dual functions of Macpiw1 in transposon silencing and stem cell maintenance in the flatworm <i>Macrostomum lignano</i> . <i>Rna</i> , 2015, 21, 1885-1897.	1.6	26
117	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
118	Rapid parallel genome indexing with MapReduce. , 2011, , .		25
119	Teaser: Individualized benchmarking and optimization of read mapping results for NGS data. <i>Genome Biology</i> , 2015, 16, 235.	3.8	25
120	De novo genome assembly of <i>Candida glabrata</i> reveals cell wall protein complement and structure of dispersed tandem repeat arrays. <i>Molecular Microbiology</i> , 2020, 113, 1209-1224.	1.2	25
121	Integrated Microbial Survey Analysis of Prokaryotic Communities for the PhyloChip Microarray. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5636-5638.	1.4	24
122	A plasmid locus associated with <i>Klebsiella</i> clinical infections encodes a microbiome-dependent gut fitness factor. <i>PLoS Pathogens</i> , 2021, 17, e1009537.	2.1	20
123	iGenomics: Comprehensive DNA sequence analysis on your Smartphone. <i>GigaScience</i> , 2020, 9, .	3.3	19
124	Computational thinking in the era of big data biology. <i>Genome Biology</i> , 2012, 13, 177.	13.9	18
125	Precise detection of de novo single nucleotide variants in human genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5516-5521.	3.3	18
126	Genome-wide patterns of transposon proliferation in an evolutionary young hybrid fish. <i>Molecular Ecology</i> , 2019, 28, 1491-1505.	2.0	18



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127	Vargas: heuristic-free alignment for assessing linear and graph read aligners. <i>Bioinformatics</i> , 2020, 36, 3712-3718.	1.8	17
128	The genomic basis of evolutionary differentiation among honey bees. <i>Genome Research</i> , 2021, 31, 1203-1215.	2.4	17
129	Cell wall protein variation, break-induced replication, and subtelomere dynamics in <i>Candida glabrata</i> . <i>Molecular Microbiology</i> , 2021, 116, 260-276.	1.2	16
130	Natural Genetic Diversity in Tomato Flavor Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 642828.	1.7	16
131	Pan-genomic matching statistics for targeted nanopore sequencing. <i>IScience</i> , 2021, 24, 102696.	1.9	15
132	Molecular genetic diversity and characterization of conjugation genes in the fish parasite <i>Ichthyophthirius multifiliis</i> . <i>Molecular Phylogenetics and Evolution</i> , 2015, 86, 1-7.	1.2	14
133	The human origin recognition complex is essential for pre-RC assembly, mitosis, and maintenance of nuclear structure. <i>ELife</i> , 2021, 10, .	2.8	14
134	High resolution copy number inference in cancer using short-molecule nanopore sequencing. <i>Nucleic Acids Research</i> , 2021, 49, e124-e124.	6.5	14
135	Complete Sequence of a 641-kb Insertion of Mitochondrial DNA in the <i>Arabidopsis thaliana</i> Nuclear Genome. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	14
136	Sapling: accelerating suffix array queries with learned data models. <i>Bioinformatics</i> , 2021, 37, 744-749.	1.8	13
137	An anchored chromosome-scale genome assembly of spinach improves annotation and reveals extensive gene rearrangements in euasterids. <i>Plant Genome</i> , 2021, 14, e20101.	1.6	13
138	Artificial Intelligence and Cardiovascular Genetics. <i>Life</i> , 2022, 12, 279.	1.1	13
139	The missing graphical user interface for genomics. <i>Genome Biology</i> , 2010, 11, 128.	13.9	11
140	16GT: a fast and sensitive variant caller using a 16-genotype probabilistic model. <i>GigaScience</i> , 2017, 6, 1-4.	3.3	11
141	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in <i>C. elegans</i> . <i>ELife</i> , 2021, 10, .	2.8	7
142	Sixty years of genome biology. <i>Genome Biology</i> , 2013, 14, 113.	13.9	6
143	NanoBLASter: Fast alignment and characterization of Oxford Nanopore single molecule sequencing reads. , 2016, , .		6
144	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. <i>IScience</i> , 2019, 18, 1-10.	1.9	6

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145	Recovering rearranged cancer chromosomes from karyotype graphs. BMC Bioinformatics, 2019, 20, 641.	1.2	4
146	Optimized sample selection for cost-efficient long-read population sequencing. Genome Research, 2021, 31, 910-918.	2.4	4
147	The DNA60IFX contest. Genome Biology, 2013, 14, 124.	3.8	3
148	Graph genomes article collection. Genome Biology, 2019, 20, 25.	3.8	3
149	Answering the demands of digital genomics. Concurrency Computation Practice and Experience, 2014, 26, 917-928.	1.4	2
150	Machine learning based prediction of gliomas with germline mutations obtained from whole exome sequences from TCGA and 1000 Genomes Project. , 2019, , .		2
151	On Algorithmic Complexity of Biomolecular Sequence Assembly Problem. Lecture Notes in Computer Science, 2014, , 183-195.	1.0	2
152	Skyhawk: an artificial neural network-based discriminator for reviewing clinically significant genomic variants. International Journal of Computational Biology and Drug Design, 2020, 13, 431.	0.3	2
153	In memory of James Taylor: the birth of Galaxy. Genome Biology, 2020, 21, 105.	3.8	1
154	Democratizing long-read genome assembly. Cell Systems, 2021, 12, 945-947.	2.9	1
155	Same-Cell Co-Occurrence of RAS Hotspot and BRAF V600E Mutations in Treatment-Naive Colorectal Cancer. JCO Precision Oncology, 2022, 6, e2100365.	1.5	1
156	Illuminating the genetics of complex human diseases. BMC Proceedings, 2012, 6, .	1.8	0
157	Large-scale Sequencing and Assembly of Cereal Genomes Using Blacklight. , 2014, , .		0
158	Bioinformatics of DNA. Proceedings of the IEEE, 2017, 105, 419-421.	16.4	0
159	A master regulator of regeneration. Science, 2019, 363, 1152-1153.	6.0	0
160	Abstract 850: Comprehensive genome and transcriptome structural analysis of a breast cancer cell line using single molecule sequencing. , 2016, , .		0