Michael C Schatz

List of Publications by Citations

199 papers	24,537 citations	67 h-index	156 g-index
234 ext. papers	32,189 ext. citations	15 avg, IF	6.93 L-index

#	Paper	IF	Citations
199	Evolution of genes and genomes on the Drosophila phylogeny. *Nature*, **2007**, 450, 203-18	50.4	1586
198	The contribution of de novo coding mutations to autism spectrum disorder. *Nature*, **2014**, 515, 216-21	50.4	1470
197	De novo gene disruptions in children on the autistic spectrum. *Neuron*, **2012**, 74, 285-99	13.9	1052
196	Phased diploid genome assembly with single-molecule real-time sequencing. *Nature Methods*, **2016**, 13, 1050-1054	21.6	1015
195	Genome sequence of Aedes aegypti, a major arbovirus vector. *Science*, **2007**, 316, 1718-23	33.3	867
194	The draft genome of the transgenic tropical fruit tree papaya (Carica papaya Linnaeus). *Nature*, **2008**, 452, 991-6	50.4	826
193	A whole-genome assembly of the domestic cow, Bos taurus. *Genome Biology*, **2009**, 10, R42	18.3	798
192	Hybrid error correction and de novo assembly of single-molecule sequencing reads. *Nature Biotechnology*, **2012**, 30, 693-700	44.5	758
191	Big Data: Astronomical or Genomical?. *PLoS Biology*, **2015**, 13, e1002195	9.7	687
190	Draft genome sequence of the sexually transmitted pathogen Trichomonas vaginalis. *Science*, **2007**, 315, 207-12	33.3	622
189	Accurate detection of complex structural variations using single-molecule sequencing. *Nature Methods*, **2018**, 15, 461-468	21.6	585
188	GenomeScope: fast reference-free genome profiling from short reads. *Bioinformatics*, **2017**, 33, 2202-2204	7.4	540
187	Draft genome of the filarial nematode parasite Brugia malayi. *Science*, **2007**, 317, 1756-60	33.3	513
186	GAGE: A critical evaluation of genome assemblies and assembly algorithms. *Genome Research*, **2012**, 22, 557-67	9.7	485
185	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. *GigaScience*, **2013**, 2, 10	7.6	461
184	CloudBurst: highly sensitive read mapping with MapReduce. *Bioinformatics*, **2009**, 25, 1363-9	7.2	455
183	Major structural differences and novel potential virulence mechanisms from the genomes of multiple campylobacter species. *PLoS Biology*, **2005**, 3, e15	9.7	440

182	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. *Nature Biotechnology*, **2019**, 37, 1155-1162	44.5	427
181	KBase: The United States Department of Energy Systems Biology Knowledgebase. *Nature Biotechnology*, **2018**, 36, 566-569	44.5	419
180	Quake: quality-aware detection and correction of sequencing errors. *Genome Biology*, **2010**, 11, R116	18.3	404
179	The advantages of SMRT sequencing. *Genome Biology*, **2013**, 14,	18.3	379
178	Assemblathon 1: a competitive assessment of de novo short read assembly methods. *Genome Research*, **2011**, 21, 2224-41	9.7	364
177	Searching for SNPs with cloud computing. *Genome Biology*, **2009**, 10, R134	18.3	333
176	Assembly of large genomes using second-generation sequencing. *Genome Research*, **2010**, 20, 1165-73	9.7	313
175	Multi-platform next-generation sequencing of the domestic turkey (Meleagris gallopavo): genome assembly and analysis. *PLoS Biology*, **2010**, 8, e1000475	9.7	311
174	The pineapple genome and the evolution of CAM photosynthesis. *Nature Genetics*, **2015**, 47, 1435-42	36.3	309
173	Genome sequence and rapid evolution of the rice pathogen Xanthomonas oryzae pv. oryzae PXO99A. *BMC Genomics*, **2008**, 9, 204	4.5	275
172	Oxford Nanopore sequencing, hybrid error correction, and de novo assembly of a eukaryotic genome. *Genome Research*, **2015**, 25, 1750-6	9.7	257
171	Piercing the dark matter: bioinformatics of long-range sequencing and mapping. *Nature Reviews Genetics*, **2018**, 19, 329-346	30.1	250
170	Genome of the long-living sacred lotus (Nelumbo nucifera Gaertn.). *Genome Biology*, **2013**, 14, R41	18.3	241
169	Allele-defined genome of the autopolyploid sugarcane Saccharum spontaneum L. *Nature Genetics*, **2018**, 50, 1565-1573	36.3	229
168	The advantages of SMRT sequencing. *Genome Biology*, **2013**, 14, 405	18.3	222
167	Genome assembly forensics: finding the elusive mis-assembly. *Genome Biology*, **2008**, 9, R55	18.3	200
166	Aluminum tolerance in maize is associated with higher MATE1 gene copy number. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 5241-6	11.5	199
165	Insight into the evolution of the Solanaceae from the parental genomes of Petunia hybrida. *Nature Plants*, **2016**, 2, 16074	11.5	198

164	Cloud computing and the DNA data race. *Nature Biotechnology*, **2010**, 28, 691-3	44.5	193
163	High-throughput sequence alignment using Graphics Processing Units. *BMC Bioinformatics*, **2007**, 8, 474	3.6	187
162	RaGOO: fast and accurate reference-guided scaffolding of draft genomes. *Genome Biology*, **2019**, 20, 224	18.3	173
161	Major Impacts of Widespread Structural Variation on Gene Expression and Crop Improvement in Tomato. *Cell*, **2020**, 182, 145-161.e23	56.2	171
160	Whole genome de novo assemblies of three divergent strains of rice, Oryza sativa, document novel gene space of aus and indica. *Genome Biology*, **2014**, 15, 506	18.3	168
159	Genomic analyses of the microsporidian Nosema ceranae, an emergent pathogen of honey bees. *PLoS Pathogens*, **2009**, 5, e1000466	7.6	167
158	Accurate de novo and transmitted indel detection in exome-capture data using microassembly. *Nature Methods*, **2014**, 11, 1033-6	21.6	157
157	Assemblytics: a web analytics tool for the detection of variants from an assembly. *Bioinformatics*, **2016**, 32, 3021-3	7.2	147
156	Two new complete genome sequences offer insight into host and tissue specificity of plant pathogenic Xanthomonas spp. *Journal of Bacteriology*, **2011**, 193, 5450-64	3.5	146
155	GenomeScope 2.0 and Smudgeplot for reference-free profiling of polyploid genomes. *Nature Communications*, **2020**, 11, 1432	17.4	140
154	Interactive analysis and assessment of single-cell copy-number variations. *Nature Methods*, **2015**, 12, 1058-60	21.6	133
153	Current challenges in de novo plant genome sequencing and assembly. *Genome Biology*, **2012**, 13, 243	18.3	131
152	Rate of meristem maturation determines inflorescence architecture in tomato. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 639-44	11.5	117
151	Complex microbiome underlying secondary and primary metabolism in the tunicate-Prochloron symbiosis. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E1423-32	11.5	117
150	Reducing INDEL calling errors in whole genome and exome sequencing data. *Genome Medicine*, **2014**, 6, 89	14.4	109
149	Extending reference assembly models. *Genome Biology*, **2015**, 16, 13	18.3	107
148	The complete sequence of a human genome.. *Science*, **2022**, 376, 44-53	33.3	107
147	Whole genome de novo assemblies of three divergent strains of rice, Oryza sativa , document novel gene space of aus and indica **2014**, 15, 506		105

146	Genomic survey of the ectoparasitic mite Varroa destructor, a major pest of the honey bee Apis mellifera. *BMC Genomics*, **2010**, 11, 602	4.5	99
145	A robust benchmark for detection of germline large deletions and insertions. *Nature Biotechnology*, **2020**, 38, 1347-1355	44.5	98
144	Design patterns for efficient graph algorithms in MapReduce **2010**,		94
143	Assembly complexity of prokaryotic genomes using short reads. *BMC Bioinformatics*, **2010**, 11, 21	3.6	92
142	Comparative genomics of mutualistic viruses of Glyptapanteles parasitic wasps. *Genome Biology*, **2008**, 9, R183	18.3	89
141	Genomic dark matter: the reliability of short read mapping illustrated by the genome mappability score. *Bioinformatics*, **2012**, 28, 2097-105	7.2	86
140	Metassembler: merging and optimizing de novo genome assemblies. *Genome Biology*, **2015**, 16, 207	18.3	78
139	Illuminating the genetics of complex human diseases. *BMC Proceedings*, **2012**, 6,	2.3	78
138	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. *PLoS Genetics*, **2016**, 12, e1005954	6	77
137	SplitMEM: a graphical algorithm for pan-genome analysis with suffix skips. *Bioinformatics*, **2014**, 30, 3476-83	7.3	76
136	Reference quality assembly of the 3.5-Gb genome of from a single linked-read library. *Horticulture Research*, **2018**, 5, 4	7.7	75
135	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line. *Genome Research*, **2018**, 28, 1126-1135	9.7	74
134	Genome and transcriptome of the regeneration-competent flatworm, Macrostomum lignano. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 12462-7	11.5	70
133	Indel variant analysis of short-read sequencing data with Scalpel. *Nature Protocols*, **2016**, 11, 2529-2548	18.8	67
132	High-coverage sequencing and annotated assemblies of the budgerigar genome. *GigaScience*, **2014**, 3, 11	7.6	67
131	Optimizing Data Intensive GPGPU Computations for DNA Sequence Alignment. *Parallel Computing*, **2009**, 35, 429-440	1	65
130	A multi-task convolutional deep neural network for variant calling in single molecule sequencing. *Nature Communications*, **2019**, 10, 998	17.4	63
129	Hawkeye: an interactive visual analytics tool for genome assemblies. *Genome Biology*, **2007**, 8, R34	18.3	62

128	Error correction and assembly complexity of single molecule sequencing reads. **2014**,		59
127	The complete sequence of a human genome		58
126	Third-generation sequencing and the future of genomics		55
125	Paragraph: a graph-based structural variant genotyper for short-read sequence data. *Genome Biology*, **2019**, 20, 291	18.3	55
124	Targeted nanopore sequencing by real-time mapping of raw electrical signal with UNCALLED. *Nature Biotechnology*, **2021**, 39, 431-441	44.5	53
123	Cultivation and complete genome sequencing of Gloeobacter kilaueensis sp. nov., from a lava cave in K□auea Caldera, Hawai□ *PLoS ONE*, **2013**, 8, e76376	3.7	52
122	Genome assembly and geospatial phylogenomics of the bed bug Cimex lectularius. *Nature Communications*, **2016**, 7, 10164	17.4	46
121	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. *Nature Genetics*, **2017**, 49, 825-833	36.3	41
120	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. *Briefings in Bioinformatics*, **2013**, 14, 213-24	13.4	41
119	Structure and evolution of a proviral locus of Glyptapanteles indiensis bracovirus. *BMC Microbiology* , **2007**, 7, 61	4.5	41
118	The DNA Data Deluge: Fast, efficient genome sequencing machines are spewing out more data than geneticists can analyze. *IEEE Spectrum*, **2013**, 50, 26-33	1.7	40
117	Revealing biological modules via graph summarization. *Journal of Computational Biology*, **2009**, 16, 253-64	1.7	40
116	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world□ leading biomass crop. *GigaScience*, **2019**, 8,	7.6	39
115	Addressing confounding artifacts in reconstruction of gene co-expression networks. *Genome Biology*, **2019**, 20, 94	18.3	37
114	Automated correction of genome sequence errors. *Nucleic Acids Research*, **2004**, 32, 562-9	20.1	37
113	Duplication of a domestication locus neutralized a cryptic variant that caused a breeding barrier in tomato. *Nature Plants*, **2019**, 5, 471-479	11.5	35
112	Complete telomere-to-telomere de novo assembly of the Plasmodium falciparum genome through long-read (>11 kb), single molecule, real-time sequencing. *DNA Research*, **2016**, 23, 339-51	4.5	35
111	A robust benchmark for germline structural variant detection		34

110	Nanopore sequencing meets epigenetics. *Nature Methods*, **2017**, 14, 347-348	21.6	33
109	Hybrid assembly with long and short reads improves discovery of gene family expansions. *BMC Genomics*, **2017**, 18, 541	4.5	33
108	The challenge of small-scale repeats for indel discovery. *Frontiers in Bioengineering and Biotechnology*, **2015**, 3, 8	5.8	33
107	Accurate detection of complex structural variations using single molecule sequencing		33
106	Parrot Genomes and the Evolution of Heightened Longevity and Cognition. *Current Biology*, **2018**, 28, 4001-4008.e7	6.3	33
105	The bracteatus pineapple genome and domestication of clonally propagated crops. *Nature Genetics* , **2019**, 51, 1549-1558	36.3	32
104	The evolution of inflorescence diversity in the nightshades and heterochrony during meristem maturation. *Genome Research*, **2016**, 26, 1676-1686	9.7	32
103	Novel circular RNA circNF1 acts as a molecular sponge, promoting gastric cancer by absorbing miR-16. *Endocrine-Related Cancer*, **2019**, 26, 265-277	5.7	32
102	Applying Rapid Whole-Genome Sequencing To Predict Phenotypic Antimicrobial Susceptibility Testing Results among Carbapenem-Resistant Klebsiella pneumoniae Clinical Isolates. *Antimicrobial Agents and Chemotherapy*, **2019**, 63,	5.9	32
101	Ribbon: Visualizing complex genome alignments and structural variation		29
100	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome		29
99	Biological data sciences in genome research. *Genome Research*, **2015**, 25, 1417-22	9.7	28
98	Hypo-osmotic-like stress underlies general cellular defects of aneuploidy. *Nature*, **2019**, 570, 117-121	50.4	27
97	Antibiotic pressure on the acquisition and loss of antibiotic resistance genes in Klebsiella pneumoniae. *Journal of Antimicrobial Chemotherapy*, **2018**, 73, 1796-1803	5.1	27
96	Benchmarking challenging small variants with linked and long reads		26
95	Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. *Genome Research*, **2020**, 30, 1258-1273	9.7	25
94	Scikit-ribo Enables Accurate Estimation and Robust Modeling of Translation Dynamics at Codon Resolution. *Cell Systems*, **2018**, 6, 180-191.e4	10.6	24
93	Genotyping in the cloud with Crossbow. *Current Protocols in Bioinformatics*, **2012**, Chapter 15, Unit15.3	24.2	23

92	TGF-reduces DNA ds-break repair mechanisms to heighten genetic diversity and adaptability of CD44+/CD24- cancer cells. *ELife*, **2017**, 6,	8.9	22
91	Characterization of Insertion Sites in Rainbow Papaya, the First Commercialized Transgenic Fruit Crop. *Tropical Plant Biology*, **2008**, 1, 293-309	1.6	22
90	A diploid assembly-based benchmark for variants in the major histocompatibility complex. *Nature Communications*, **2020**, 11, 4794	17.4	22
89	Dual functions of Macpiwi1 in transposon silencing and stem cell maintenance in the flatworm Macrostomum lignano. *Rna*, **2015**, 21, 1885-97	5.8	21
88	Teaser: Individualized benchmarking and optimization of read mapping results for NGS data. *Genome Biology*, **2015**, 16, 235	18.3	21
87	Integrated microbial survey analysis of prokaryotic communities for the PhyloChip microarray. *Applied and Environmental Microbiology*, **2010**, 76, 5636-8	4.8	21
86	LRSim: A Linked-Reads Simulator Generating Insights for Better Genome Partitioning. *Computational and Structural Biotechnology Journal*, **2017**, 15, 478-484	6.8	20
85	Complete genomic and epigenetic maps of human centromeres.. *Science*, **2022**, 376, eabl4178	33.3	19
84	Rapid parallel genome indexing with MapReduce **2011**,		18
83	Conservation Genomics of the Declining North American Bumblebee Reveals Inbreeding and Selection on Immune Genes. *Frontiers in Genetics*, **2018**, 9, 316	4.5	17
82	Parliament2: Accurate structural variant calling at scale. *GigaScience*, **2020**, 9,	7.6	17
81	Genomic diversity of SARS-CoV-2 during early introduction into the Baltimore-Washington metropolitan area. *JCI Insight*, **2021**, 6,	9.9	17
80	Ribbon: intuitive visualization for complex genomic variation. *Bioinformatics*, **2021**, 37, 413-415	7.2	17
79	Computational thinking in the era of big data biology. *Genome Biology*, **2012**, 13, 177	18.3	16
78	Phased Diploid Genome Assembly with Single Molecule Real-Time Sequencing		16
77	The genetic and epigenetic landscape of the centromeres. *Science*, **2021**, 374, eabi7489	33.3	15
76	Fast and accurate reference-guided scaffolding of draft genomes		15
75	Genomic Diversity of SARS-CoV-2 During Early Introduction into the United States National Capital Region **2020**,		14

74	Precise detection of de novo single nucleotide variants in human genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 5516-5521	11.5	14
73	Epigenetic patterns in a complete human genome.. *Science*, **2022**, 376, eabj5089	33.3	12
72	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements.. *Science*, **2022**, 376, eabk3112	33.3	12
71	A complete reference genome improves analysis of human genetic variation.. *Science*, **2022**, 376, eabl3533	33.3	12
70	Clairvoyante: a multi-task convolutional deep neural network for variant calling in Single Molecule Sequencing		11
69	Genome-wide patterns of transposon proliferation in an evolutionary young hybrid fish. *Molecular Ecology*, **2019**, 28, 1491-1505	5.7	11
68	The missing graphical user interface for genomics. *Genome Biology*, **2010**, 11, 128	18.3	10
67	16GT: a fast and sensitive variant caller using a 16-genotype probabilistic model. *GigaScience*, **2017**, 6, 1-4	7.6	9
66	Molecular genetic diversity and characterization of conjugation genes in the fish parasite Ichthyophthirius multifiliis. *Molecular Phylogenetics and Evolution*, **2015**, 86, 1-7	4.1	9
65	iGenomics: Comprehensive DNA sequence analysis on your Smartphone. *GigaScience*, **2020**, 9,	7.6	9
64	Jasmine: Population-scale structural variant comparison and analysis		9
63	Epigenetic Patterns in a Complete Human Genome		9
62	A complete reference genome improves analysis of human genetic variation		9
61	Sapling: accelerating suffix array queries with learned data models. *Bioinformatics*, **2021**, 37, 744-749	7.2	9
60	Vargas: heuristic-free alignment for assessing linear and graph read aligners. *Bioinformatics*, **2020**, 36, 3712-3718	7.2	8
59	Automated assembly scaffolding elevates a new tomato system for high-throughput genome editing		8
58	SplitThreader: Exploration and analysis of rearrangements in cancer genomes		8
57	Targeted nanopore sequencing by real-time mapping of raw electrical signal with UNCALLED		8

56	Paragraph: A graph-based structural variant genotyper for short-read sequence data		8
55	Complete genomic and epigenetic maps of human centromeres		8
54	De novo genome assembly of Candida glabrata reveals cell wall protein complement and structure of dispersed tandem repeat arrays. *Molecular Microbiology*, **2020**, 113, 1209-1224	4.1	7
53	From telomere to telomere: the transcriptional and epigenetic state of human repeat elements		7
52	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space.. *Cell Genomics*, **2022**, 2, 100085-100085		6
51	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line		6
50	First near complete haplotype phased genome assembly of River buffalo (Bubalus bubalis)		6
49	Clonal Hematopoiesis Before, During, and After Human Spaceflight. *Cell Reports*, **2020**, 33, 108458	10.6	6
48	An anchored chromosome-scale genome assembly of spinach improves annotation and reveals extensive gene rearrangements in euasterids. *Plant Genome*, **2021**, 14, e20101	4.4	6
47	New whole genome de novo assemblies of three divergent strains of rice (O. sativa) documents novel gene space of aus and indica		5
46	GenomeScope: Fast reference-free genome profiling from short reads		5
45	GenomeScope 2.0 and Smudgeplots: Reference-free profiling of polyploid genomes		5
44	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space (AnVIL)		5
43	Cell wall protein variation, break-induced replication, and subtelomere dynamics in Candida glabrata. *Molecular Microbiology*, **2021**, 116, 260-276	4.1	5
42	Local adaptation and archaic introgression shape global diversity at human structural variant loci. *ELife*, **2021**, 10,	8.9	5
41	Sixty years of genome biology. *Genome Biology*, **2013**, 14, 113	18.3	4
40	Assemblytics: a web analytics tool for the detection of assembly-based variants		4
39	SVCollector: Optimized sample selection for validating and long-read resequencing of structural variants		4

38	NanoBLASTer: Fast alignment and characterization of Oxford Nanopore single molecule sequencing reads **2016**,		4
37	Recovering rearranged cancer chromosomes from karyotype graphs. *BMC Bioinformatics*, **2019**, 20, 641	3.6	4
36	The human origin recognition complex is essential for pre-RC assembly, mitosis, and maintenance of nuclear structure. *ELife*, **2021**, 10,	8.9	4
35	Skyhawk: An Artificial Neural Network-based discriminator for reviewing clinically significant genomic variants		3
34	Comprehensive analysis of structural variants in breast cancer genomes using single molecule sequencing		3
33	16GT: a fast and sensitive variant caller using a 16-genotype probabilistic model		3
32	A plasmid locus associated with Klebsiella clinical infections encodes a microbiome-dependent gut fitness factor. *PLoS Pathogens*, **2021**, 17, e1009537	7.6	3
31	The genetic and epigenetic landscape of the Arabidopsis centromeres		3
30	Automated assembly of high-quality diploid human reference genomes		3
29	Long-read sequencing reveals rapid evolution of immunity- and cancer-related genes in bats		2
28	Accurate detection of de novo and transmitted INDELs within exome-capture data using micro-assembly		2
27	SVCollector: Optimized sample selection for cost-efficient long-read population sequencing		2
26	Addressing confounding artifacts in reconstruction of gene co-expression networks		2
25	On Algorithmic Complexity of Biomolecular Sequence Assembly Problem. *Lecture Notes in Computer Science*, **2014**, 183-195	0.9	2
24	Optimized sample selection for cost-efficient long-read population sequencing. *Genome Research*, **2021**, 31, 910-918	9.7	2
23	Machine learning based prediction of gliomas with germline mutations obtained from whole exome sequences from TCGA and 1000 Genomes Project **2019**,		2
22	Local adaptation and archaic introgression shape global diversity at human structural variant loci		2
21	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in. *ELife*, **2021**, 10,	8.9	2

20	Artificial Intelligence and Cardiovascular Genetics.. *Life*, **2022**, 12,	3	2
19	Benchmarking challenging small variants with linked and long reads. *Cell Genomics*, **2022**, 2, 100128		2
18	In memory of James Taylor: the birth of Galaxy. *Genome Biology*, **2020**, 21, 105	18.3	1
17	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. *IScience*, **2019**, 18, 1-10	6.1	1
16	Answering the demands of digital genomics. *Concurrency Computation Practice and Experience*, **2014**, 26, 917-928	1.4	1
15	LongTron: Automated Analysis of Long Read Spliced Alignment Accuracy		1
14	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in C. elegans		1
13	Sapling: Accelerating Suffix Array Queries with Learned Data Models		1
12	LRSim: a Linked Reads Simulator generating insights for better genome partitioning		1
11	iGenomics: Comprehensive DNA Sequence Analysis on your Smartphone		1
10	A plasmid locus associated with Klebsiella clinical infections encodes a microbiome-dependent gut fitness factor		1
9	Scikit-ribo: Accurate estimation and robust modeling of translation dynamics at codon resolution		1
8	The genomic basis of evolutionary differentiation among honey bees. *Genome Research*, **2021**,	9.7	1
7	Natural Genetic Diversity in Tomato Flavor Genes. *Frontiers in Plant Science*, **2021**, 12, 642828	6.2	1
6	Pan-genomic matching statistics for targeted nanopore sequencing. *IScience*, **2021**, 24, 102696	6.1	1
5	High resolution copy number inference in cancer using short-molecule nanopore sequencing. *Nucleic Acids Research*, **2021**, 49, e124	20.1	1
4	Democratizing long-read genome assembly. *Cell Systems*, **2021**, 12, 945-947	10.6	0
3	A master regulator of regeneration. *Science*, **2019**, 363, 1152-1153	33.3	

2	The DNA60IFX contest. *Genome Biology*, **2013**, 14, 124	18.3
1	Same-Cell Co-Occurrence of RAS Hotspot and BRAF V600E Mutations in Treatment-Naive Colorectal Cancer.. *JCO Precision Oncology*, **2022**, 6, e2100365	3.6