

Michael C Schatz

List of Publications by Year in Descending Order

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Version: 2024-04-23

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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, 100085-100085		6
198	Artificial Intelligence and Cardiovascular Genetics.. <i>Life</i> , 2022 , 12,	3	2
197	Same-Cell Co-Occurrence of RAS Hotspot and BRAF V600E Mutations in Treatment-Naive Colorectal Cancer.. <i>JCO Precision Oncology</i> , 2022 , 6, e2100365	3.6	
196	Epigenetic patterns in a complete human genome.. <i>Science</i> , 2022 , 376, eabj5089	33.3	12
195	Complete genomic and epigenetic maps of human centromeres.. <i>Science</i> , 2022 , 376, eabl4178	33.3	19
194	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements.. <i>Science</i> , 2022 , 376, eabk3112	33.3	12
193	A complete reference genome improves analysis of human genetic variation.. <i>Science</i> , 2022 , 376, eabl3533	33.3	12
192	The complete sequence of a human genome.. <i>Science</i> , 2022 , 376, 44-53	33.3	107
191	Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , 2022 , 2, 100128		2
190	The genetic and epigenetic landscape of the centromeres. <i>Science</i> , 2021 , 374, eabi7489	33.3	15
189	Democratizing long-read genome assembly. <i>Cell Systems</i> , 2021 , 12, 945-947	10.6	0
188	Genomic diversity of SARS-CoV-2 during early introduction into the Baltimore-Washington metropolitan area. <i>JCI Insight</i> , 2021 , 6,	9.9	17
187	Optimized sample selection for cost-efficient long-read population sequencing. <i>Genome Research</i> , 2021 , 31, 910-918	9.7	2
186	A plasmid locus associated with Klebsiella clinical infections encodes a microbiome-dependent gut fitness factor. <i>PLoS Pathogens</i> , 2021 , 17, e1009537	7.6	3
185	The genomic basis of evolutionary differentiation among honey bees. <i>Genome Research</i> , 2021 ,	9.7	1
184	Natural Genetic Diversity in Tomato Flavor Genes. <i>Frontiers in Plant Science</i> , 2021 , 12, 642828	6.2	1
183	An anchored chromosome-scale genome assembly of spinach improves annotation and reveals extensive gene rearrangements in euasterids. <i>Plant Genome</i> , 2021 , 14, e20101	4.4	6

182	Pan-genomic matching statistics for targeted nanopore sequencing. <i>IScience</i> , 2021 , 24, 102696	6.1	1
181	Ribbon: intuitive visualization for complex genomic variation. <i>Bioinformatics</i> , 2021 , 37, 413-415	7.2	17
180	Targeted nanopore sequencing by real-time mapping of raw electrical signal with UNCALLED. <i>Nature Biotechnology</i> , 2021 , 39, 431-441	44.5	53
179	Sapling: accelerating suffix array queries with learned data models. <i>Bioinformatics</i> , 2021 , 37, 744-749	7.2	9
178	The human origin recognition complex is essential for pre-RC assembly, mitosis, and maintenance of nuclear structure. <i>ELife</i> , 2021 , 10,	8.9	4
177	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in. <i>ELife</i> , 2021 , 10,	8.9	2
176	Cell wall protein variation, break-induced replication, and subtelomere dynamics in <i>Candida glabrata</i> . <i>Molecular Microbiology</i> , 2021 , 116, 260-276	4.1	5
175	High resolution copy number inference in cancer using short-molecule nanopore sequencing. <i>Nucleic Acids Research</i> , 2021 , 49, e124	20.1	1
174	Local adaptation and archaic introgression shape global diversity at human structural variant loci. <i>ELife</i> , 2021 , 10,	8.9	5
173	In memory of James Taylor: the birth of Galaxy. <i>Genome Biology</i> , 2020 , 21, 105	18.3	1
172	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020 , 38, 1347-1355	44.5	98
171	Major Impacts of Widespread Structural Variation on Gene Expression and Crop Improvement in Tomato. <i>Cell</i> , 2020 , 182, 145-161.e23	56.2	171
170	GenomeScope 2.0 and Smudgeplot for reference-free profiling of polyploid genomes. <i>Nature Communications</i> , 2020 , 11, 1432	17.4	140
169	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	4.1	7
168	Vargas: heuristic-free alignment for assessing linear and graph read aligners. <i>Bioinformatics</i> , 2020 , 36, 3712-3718	7.2	8
167	Parliament2: Accurate structural variant calling at scale. <i>GigaScience</i> , 2020 , 9,	7.6	17
166	Genomic Diversity of SARS-CoV-2 During Early Introduction into the United States National Capital Region 2020 ,		14
165	Clonal Hematopoiesis Before, During, and After Human Spaceflight. <i>Cell Reports</i> , 2020 , 33, 108458	10.6	6

164	iGenomics: Comprehensive DNA sequence analysis on your Smartphone. <i>GigaScience</i> , 2020 , 9,	7.6	9
163	Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. <i>Genome Research</i> , 2020 , 30, 1258-1273	9.7	25
162	A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , 2020 , 11, 4794	17.4	22
161	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019 , 51, 1549-1558	36.3	32
160	Hypo-osmotic-like stress underlies general cellular defects of aneuploidy. <i>Nature</i> , 2019 , 570, 117-121	50.4	27
159	Addressing confounding artifacts in reconstruction of gene co-expression networks. <i>Genome Biology</i> , 2019 , 20, 94	18.3	37
158	Duplication of a domestication locus neutralized a cryptic variant that caused a breeding barrier in tomato. <i>Nature Plants</i> , 2019 , 5, 471-479	11.5	35
157	A master regulator of regeneration. <i>Science</i> , 2019 , 363, 1152-1153	33.3	
156	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019 , 37, 1155-1162	44.5	427
155	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. <i>IScience</i> , 2019 , 18, 1-10	6.1	1
154	RaGOO: fast and accurate reference-guided scaffolding of draft genomes. <i>Genome Biology</i> , 2019 , 20, 224	18.3	173
153	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	5.7	32
152	A multi-task convolutional deep neural network for variant calling in single molecule sequencing. <i>Nature Communications</i> , 2019 , 10, 998	17.4	63
151	Machine learning based prediction of gliomas with germline mutations obtained from whole exome sequences from TCGA and 1000 Genomes Project 2019 ,		2
150	Paragraph: a graph-based structural variant genotyper for short-read sequence data. <i>Genome Biology</i> , 2019 , 20, 291	18.3	55
149	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,	7.6	39
148	Recovering rearranged cancer chromosomes from karyotype graphs. <i>BMC Bioinformatics</i> , 2019 , 20, 641	3.6	4
147	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,	5.9	32

146	Genome-wide patterns of transposon proliferation in an evolutionary young hybrid fish. <i>Molecular Ecology</i> , 2019 , 28, 1491-1505	5.7	11
145	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	5.1	27
144	Scikit-ribo Enables Accurate Estimation and Robust Modeling of Translation Dynamics at Codon Resolution. <i>Cell Systems</i> , 2018 , 6, 180-191.e4	10.6	24
143	Reference quality assembly of the 3.5-Gb genome of from a single linked-read library. <i>Horticulture Research</i> , 2018 , 5, 4	7.7	75
142	Accurate detection of complex structural variations using single-molecule sequencing. <i>Nature Methods</i> , 2018 , 15, 461-468	21.6	585
141	Piercing the dark matter: bioinformatics of long-range sequencing and mapping. <i>Nature Reviews Genetics</i> , 2018 , 19, 329-346	30.1	250
140	Conservation Genomics of the Declining North American Bumblebee Reveals Inbreeding and Selection on Immune Genes. <i>Frontiers in Genetics</i> , 2018 , 9, 316	4.5	17
139	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018 , 36, 566-569	44.5	419
138	Parrot Genomes and the Evolution of Heightened Longevity and Cognition. <i>Current Biology</i> , 2018 , 28, 4001-4008.e7	6.3	33
137	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L. <i>Nature Genetics</i> , 2018 , 50, 1565-1573	36.3	229
136	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	11.5	14
135	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	9.7	74
134	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. <i>Nature Genetics</i> , 2017 , 49, 825-833	36.3	41
133	16GT: a fast and sensitive variant caller using a 16-genotype probabilistic model. <i>GigaScience</i> , 2017 , 6, 1-4	7.6	9
132	GenomeScope: fast reference-free genome profiling from short reads. <i>Bioinformatics</i> , 2017 , 33, 2202-2204	4	540
131	Nanopore sequencing meets epigenetics. <i>Nature Methods</i> , 2017 , 14, 347-348	21.6	33
130	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017 , 18, 541	4.5	33
129	LRSim: A Linked-Reads Simulator Generating Insights for Better Genome Partitioning. <i>Computational and Structural Biotechnology Journal</i> , 2017 , 15, 478-484	6.8	20

128	TGF- β reduces DNA ds-break repair mechanisms to heighten genetic diversity and adaptability of CD44+/CD24- cancer cells. <i>ELife</i> , 2017 , 6,	8.9	22
127	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016 , 13, 1050-1054	21.6	1015
126	Indel variant analysis of short-read sequencing data with Scalpel. <i>Nature Protocols</i> , 2016 , 11, 2529-2548	18.8	67
125	Insight into the evolution of the Solanaceae from the parental genomes of <i>Petunia hybrida</i> . <i>Nature Plants</i> , 2016 , 2, 16074	11.5	198
124	The evolution of inflorescence diversity in the nightshades and heterochrony during meristem maturation. <i>Genome Research</i> , 2016 , 26, 1676-1686	9.7	32
123	Assemblytics: a web analytics tool for the detection of variants from an assembly. <i>Bioinformatics</i> , 2016 , 32, 3021-3	7.2	147
122	Complete telomere-to-telomere de novo assembly of the <i>Plasmodium falciparum</i> genome through long-read (>11 kb), single molecule, real-time sequencing. <i>DNA Research</i> , 2016 , 23, 339-51	4.5	35
121	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , 2016 , 7, 10164	17.4	46
120	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , 2016 , 12, e1005954	6	77
119	NanoBLASter: Fast alignment and characterization of Oxford Nanopore single molecule sequencing reads 2016 ,		4
118	Extending reference assembly models. <i>Genome Biology</i> , 2015 , 16, 13	18.3	107
117	Biological data sciences in genome research. <i>Genome Research</i> , 2015 , 25, 1417-22	9.7	28
116	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, 12462-7	11.5	70
115	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015 , 47, 1435-42	36.3	309
114	Oxford Nanopore sequencing, hybrid error correction, and de novo assembly of a eukaryotic genome. <i>Genome Research</i> , 2015 , 25, 1750-6	9.7	257
113	Dual functions of Macpiw1 in transposon silencing and stem cell maintenance in the flatworm <i>Macrostomum lignano</i> . <i>Rna</i> , 2015 , 21, 1885-97	5.8	21
112	Interactive analysis and assessment of single-cell copy-number variations. <i>Nature Methods</i> , 2015 , 12, 1058-60	21.6	133
111	Metassembler: merging and optimizing de novo genome assemblies. <i>Genome Biology</i> , 2015 , 16, 207	18.3	78

110	The challenge of small-scale repeats for indel discovery. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015 , 3, 8	5.8	33
109	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	4.1	9
108	Teaser: Individualized benchmarking and optimization of read mapping results for NGS data. <i>Genome Biology</i> , 2015 , 16, 235	18.3	21
107	Big Data: Astronomical or Genomical?. <i>PLoS Biology</i> , 2015 , 13, e1002195	9.7	687
106	The contribution of de novo coding mutations to autism spectrum disorder. <i>Nature</i> , 2014 , 515, 216-21	50.4	1470
105	SplitMEM: a graphical algorithm for pan-genome analysis with suffix skips. <i>Bioinformatics</i> , 2014 , 30, 3476-83	7.83	76
104	High-coverage sequencing and annotated assemblies of the budgerigar genome. <i>GigaScience</i> , 2014 , 3, 11	7.6	67
103	Accurate de novo and transmitted indel detection in exome-capture data using microassembly. <i>Nature Methods</i> , 2014 , 11, 1033-6	21.6	157
102	Error correction and assembly complexity of single molecule sequencing reads. 2014 ,		59
101	Answering the demands of digital genomics. <i>Concurrency Computation Practice and Experience</i> , 2014 , 26, 917-928	1.4	1
100	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	18.3	168
99	Reducing INDEL calling errors in whole genome and exome sequencing data. <i>Genome Medicine</i> , 2014 , 6, 89	14.4	109
98	Whole genome de novo assemblies of three divergent strains of rice, <i>Oryza sativa</i> , document novel gene space of aus and indica 2014 , 15, 506		105
97	On Algorithmic Complexity of Biomolecular Sequence Assembly Problem. <i>Lecture Notes in Computer Science</i> , 2014 , 183-195	0.9	2
96	The advantages of SMRT sequencing. <i>Genome Biology</i> , 2013 , 14,	18.3	379
95	The DNA Data Deluge: Fast, efficient genome sequencing machines are spewing out more data than geneticists can analyze. <i>IEEE Spectrum</i> , 2013 , 50, 26-33	1.7	40
94	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. <i>Briefings in Bioinformatics</i> , 2013 , 14, 213-24	13.4	41
93	Genome of the long-living sacred lotus (<i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 2013 , 14, R41	18.3	241

92	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
91	Sixty years of genome biology. <i>Genome Biology</i> , 2013 , 14, 113	18.3	4
90	The DNA60IFX contest. <i>Genome Biology</i> , 2013 , 14, 124	18.3	
89	Aluminum tolerance in maize is associated with higher MATE1 gene copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 5241-6	11.5	199
88	The advantages of SMRT sequencing. <i>Genome Biology</i> , 2013 , 14, 405	18.3	222
87	Cultivation and complete genome sequencing of <i>Gloeobacter kilaueensis</i> sp. nov., from a lava cave in Kīlauea Caldera, Hawaii. <i>PLoS ONE</i> , 2013 , 8, e76376	3.7	52
86	Computational thinking in the era of big data biology. <i>Genome Biology</i> , 2012 , 13, 177	18.3	16
85	Current challenges in de novo plant genome sequencing and assembly. <i>Genome Biology</i> , 2012 , 13, 243	18.3	131
84	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, 639-44	11.5	117
83	De novo gene disruptions in children on the autistic spectrum. <i>Neuron</i> , 2012 , 74, 285-99	13.9	1052
82	Genotyping in the cloud with Crossbow. <i>Current Protocols in Bioinformatics</i> , 2012 , Chapter 15, Unit15.3	24.2	23
81	Illuminating the genetics of complex human diseases. <i>BMC Proceedings</i> , 2012 , 6,	2.3	78
80	GAGE: A critical evaluation of genome assemblies and assembly algorithms. <i>Genome Research</i> , 2012 , 22, 557-67	9.7	485
79	Genomic dark matter: the reliability of short read mapping illustrated by the genome mappability score. <i>Bioinformatics</i> , 2012 , 28, 2097-105	7.2	86
78	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012 , 30, 693-700	44.5	758
77	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, 5450-64	3.5	146
76	Rapid parallel genome indexing with MapReduce 2011 ,		18
75	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364

74	Complex microbiome underlying secondary and primary metabolism in the tunicate-Prochloron symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E1423-32	11.5	117
73	Cloud computing and the DNA data race. <i>Nature Biotechnology</i> , 2010 , 28, 691-3	44.5	193
72	Integrated microbial survey analysis of prokaryotic communities for the PhyloChip microarray. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5636-8	4.8	21
71	Design patterns for efficient graph algorithms in MapReduce 2010 ,		94
70	Multi-platform next-generation sequencing of the domestic turkey (<i>Meleagris gallopavo</i>): genome assembly and analysis. <i>PLoS Biology</i> , 2010 , 8, e1000475	9.7	311
69	Quake: quality-aware detection and correction of sequencing errors. <i>Genome Biology</i> , 2010 , 11, R116	18.3	404
68	The missing graphical user interface for genomics. <i>Genome Biology</i> , 2010 , 11, 128	18.3	10
67	Assembly of large genomes using second-generation sequencing. <i>Genome Research</i> , 2010 , 20, 1165-73	9.7	313
66	Assembly complexity of prokaryotic genomes using short reads. <i>BMC Bioinformatics</i> , 2010 , 11, 21	3.6	92
65	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	4.5	99
64	CloudBurst: highly sensitive read mapping with MapReduce. <i>Bioinformatics</i> , 2009 , 25, 1363-9	7.2	455
63	Optimizing Data Intensive GPGPU Computations for DNA Sequence Alignment. <i>Parallel Computing</i> , 2009 , 35, 429-440	1	65
62	Genomic analyses of the microsporidian <i>Nosema ceranae</i> , an emergent pathogen of honey bees. <i>PLoS Pathogens</i> , 2009 , 5, e1000466	7.6	167
61	Searching for SNPs with cloud computing. <i>Genome Biology</i> , 2009 , 10, R134	18.3	333
60	A whole-genome assembly of the domestic cow, <i>Bos taurus</i> . <i>Genome Biology</i> , 2009 , 10, R42	18.3	798
59	Revealing biological modules via graph summarization. <i>Journal of Computational Biology</i> , 2009 , 16, 253-64	4.7	40
58	The draft genome of the transgenic tropical fruit tree papaya (<i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008 , 452, 991-6	50.4	826
57	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	4.5	275

56	Comparative genomics of mutualistic viruses of <i>Glyptapanteles</i> parasitic wasps. <i>Genome Biology</i> , 2008 , 9, R183	18.3	89
55	Genome assembly forensics: finding the elusive mis-assembly. <i>Genome Biology</i> , 2008 , 9, R55	18.3	200
54	Characterization of Insertion Sites in Rainbow Papaya, the First Commercialized Transgenic Fruit Crop. <i>Tropical Plant Biology</i> , 2008 , 1, 293-309	1.6	22
53	Genome sequence of <i>Aedes aegypti</i> , a major arbovirus vector. <i>Science</i> , 2007 , 316, 1718-23	33.3	867
52	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
51	High-throughput sequence alignment using Graphics Processing Units. <i>BMC Bioinformatics</i> , 2007 , 8, 474	3.6	187
50	Structure and evolution of a proviral locus of <i>Glyptapanteles indiensis</i> bracovirus. <i>BMC Microbiology</i> , 2007 , 7, 61	4.5	41
49	Hawkeye: an interactive visual analytics tool for genome assemblies. <i>Genome Biology</i> , 2007 , 8, R34	18.3	62
48	Draft genome sequence of the sexually transmitted pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007 , 315, 207-12	33.3	622
47	Draft genome of the filarial nematode parasite <i>Brugia malayi</i> . <i>Science</i> , 2007 , 317, 1756-60	33.3	513
46	Major structural differences and novel potential virulence mechanisms from the genomes of multiple campylobacter species. <i>PLoS Biology</i> , 2005 , 3, e15	9.7	440
45	Automated correction of genome sequence errors. <i>Nucleic Acids Research</i> , 2004 , 32, 562-9	20.1	37
44	Long-read sequencing reveals rapid evolution of immunity- and cancer-related genes in bats		2
43	LongTron: Automated Analysis of Long Read Spliced Alignment Accuracy		1
42	Automated assembly scaffolding elevates a new tomato system for high-throughput genome editing		8
41	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in <i>C. elegans</i>		1
40	Sapling: Accelerating Suffix Array Queries with Learned Data Models		1
39	Accurate detection of de novo and transmitted INDELS within exome-capture data using micro-assembly		2

38	New whole genome de novo assemblies of three divergent strains of rice (<i>O. sativa</i>) documents novel gene space of aus and indica	5
37	Assemblytics: a web analytics tool for the detection of assembly-based variants	4
36	Third-generation sequencing and the future of genomics	55
35	Phased Diploid Genome Assembly with Single Molecule Real-Time Sequencing	16
34	GenomeScope: Fast reference-free genome profiling from short reads	5
33	Ribbon: Visualizing complex genome alignments and structural variation	29
32	SplitThreader: Exploration and analysis of rearrangements in cancer genomes	8
31	LRSim: a Linked Reads Simulator generating insights for better genome partitioning	1
30	Accurate detection of complex structural variations using single molecule sequencing	33
29	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line	6
28	Targeted nanopore sequencing by real-time mapping of raw electrical signal with UNCALLED	8
27	iGenomics: Comprehensive DNA Sequence Analysis on your Smartphone	1
26	A plasmid locus associated with <i>Klebsiella</i> clinical infections encodes a microbiome-dependent gut fitness factor	1
25	Benchmarking challenging small variants with linked and long reads	26
24	SVCollector: Optimized sample selection for cost-efficient long-read population sequencing	2
23	Addressing confounding artifacts in reconstruction of gene co-expression networks	2
22	Clairvoyante: a multi-task convolutional deep neural network for variant calling in Single Molecule Sequencing	11
21	Skyhawk: An Artificial Neural Network-based discriminator for reviewing clinically significant genomic variants	3

20	SVCollector: Optimized sample selection for validating and long-read resequencing of structural variants	4
19	Highly-accurate long-read sequencing improves variant detection and assembly of a human genome	29
18	Fast and accurate reference-guided scaffolding of draft genomes	15
17	First near complete haplotype phased genome assembly of River buffalo (<i>Bubalus bubalis</i>)	6
16	Paragraph: A graph-based structural variant genotyper for short-read sequence data	8
15	A robust benchmark for germline structural variant detection	34
14	GenomeScope 2.0 and Smudgeplots: Reference-free profiling of polyploid genomes	5
13	Comprehensive analysis of structural variants in breast cancer genomes using single molecule sequencing	3
12	16GT: a fast and sensitive variant caller using a 16-genotype probabilistic model	3
11	Scikit-ribo: Accurate estimation and robust modeling of translation dynamics at codon resolution	1
10	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space (AnVIL)	5
9	The genetic and epigenetic landscape of the <i>Arabidopsis</i> centromeres	3
8	Jasmine: Population-scale structural variant comparison and analysis	9
7	The complete sequence of a human genome	58
6	Epigenetic Patterns in a Complete Human Genome	9
5	From telomere to telomere: the transcriptional and epigenetic state of human repeat elements	7
4	A complete reference genome improves analysis of human genetic variation	9
3	Complete genomic and epigenetic maps of human centromeres	8

2	Local adaptation and archaic introgression shape global diversity at human structural variant loci	2
1	Automated assembly of high-quality diploid human reference genomes	3