

Twelve years of SAMtools and BCFtools

GigaScience

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Citation Report

#	ARTICLE	IF	CITATIONS
1	HTSlib: C library for reading/writing high-throughput sequencing data. <i>GigaScience</i> , 2021, 10, .	3.3	191
3	Prediction of antimicrobial resistance based on whole-genome sequencing and machine learning. <i>Bioinformatics</i> , 2022, 38, 325-334.	1.8	54
4	The genome of <i>Tripterygium wilfordii</i> and characterization of the celastrol biosynthesis pathway. <i>GigaByte</i> , 0, 2021, 1-32.	0.0	3
19	Patterns in Genotype Composition of Indian Isolates of the <i>Bombyx mori</i> Nucleopolyhedrovirus and <i>Bombyx mori</i> Bidensovirus. <i>Viruses</i> , 2021, 13, 901.	1.5	5
20	Genomic Resources for the North American Water Vole (<i>Microtus richardsoni</i>) and the Montane Vole (<i>Microtus montanus</i>). <i>GigaByte</i> , 0, 2021, 1-13.	0.0	1
21	Comparison of mitochondrial genomes provides insights into intron dynamics and evolution in <i>Botryosphaeria dothidea</i> and <i>B. kuwatsukai</i> . <i>Environmental Microbiology</i> , 2021, 23, 5320-5333.	1.8	4
22	Estimating infectiousness throughout SARS-CoV-2 infection course. <i>Science</i> , 2021, 373, .	6.0	389
26	BiSulfite Bolt: A bisulfite sequencing analysis platform. <i>GigaScience</i> , 2021, 10, .	3.3	31
37	Phenotypic and Genotypic Properties of Fluoroquinolone-Resistant, qnr-Carrying <i>Escherichia coli</i> Isolated from the German Food Chain in 2017. <i>Microorganisms</i> , 2021, 9, 1308.	1.6	7
39	Genes with 5' terminal oligopyrimidine tracts preferentially escape global suppression of translation by the SARS-CoV-2 Nsp1 protein. <i>Rna</i> , 2021, 27, 1025-1045.	1.6	38
40	Gapless indica rice genome reveals synergistic contributions of active transposable elements and segmental duplications to rice genome evolution. <i>Molecular Plant</i> , 2021, 14, 1745-1756.	3.9	50
44	A genome-wide association study suggests correlations of common genetic variants with peritoneal solute transfer rates in patients with kidney failure receiving peritoneal dialysis. <i>Kidney International</i> , 2021, 100, 1101-1111.	2.6	13
45	Cnidarian-bilaterian comparison reveals the ancestral regulatory logic of the β -catenin dependent axial patterning. <i>Nature Communications</i> , 2021, 12, 4032.	5.8	29
46	Fusion transcripts FYN-TRAF3IP2 and KHDRBS1-LCK hijack T cell receptor signaling in peripheral T-cell lymphoma, not otherwise specified. <i>Nature Communications</i> , 2021, 12, 3705.	5.8	21
50	BIGwas: Single-command quality control and association testing for multi-cohort and biobank-scale GWAS/PheWAS data. <i>GigaScience</i> , 2021, 10, .	3.3	13
51	Transcriptome analysis of gene expression changes upon enzymatic dissociation in skeletal myoblasts. <i>Genes To Cells</i> , 2021, 26, 530-540.	0.5	6
53	Transient Mitochondria Dysfunction Confers Fungal Cross-Resistance against Phagocytic Killing and Fluconazole. <i>MBio</i> , 2021, 12, e0112821.	1.8	15
54	Systematic benchmarking of tools for CpG methylation detection from nanopore sequencing. <i>Nature Communications</i> , 2021, 12, 3438.	5.8	71

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55	Gene Expression and Survival of Acute Lymphoblastic Leukemia Cells After Allogeneic Transplant. <i>Anticancer Research</i> , 2021, 41, 2781-2793.	0.5	1
56	Towards scalable genomic data access. <i>Nature Computational Science</i> , 0, , .	3.8	0
57	Vocal Fold Fibroblasts in Reinke's Edema Show Alterations Involved in Extracellular Matrix Production, Cytokine Response and Cell Cycle Control. <i>Biomedicines</i> , 2021, 9, 735.	1.4	5
60	Optimizing experimental design for genome sequencing and assembly with Oxford Nanopore Technologies. <i>GigaByte</i> , 0, 2021, 1-26.	0.0	10
62	Highly contiguous assemblies of 101 drosophilid genomes. <i>ELife</i> , 2021, 10, .	2.8	108
64	Genomic monitoring unveil the early detection of the SARS-CoV-2 B.1.351 (beta) variant (20H/501Y.V2) in Brazil. <i>Journal of Medical Virology</i> , 2021, 93, 6782-6787.	2.5	24
67	Draft Genome Sequences of Nitrogen-Fixing Bradyrhizobia Isolated from Root Nodules of Peanut, <i>Arachis hypogaea</i> , Cultivated in Southern Tunisia. <i>Microbiology Resource Announcements</i> , 2021, 10, e0043421.	0.3	1
68	BC-Monitor: Towards a Routinely Accessible Circulating Tumor DNA-Based Tool for Real-Time Monitoring Breast Cancer Progression and Treatment Effectiveness. <i>Cancers</i> , 2021, 13, 3489.	1.7	3
69	Functional validation of a finding from a mouse genome-wide association study shows that Azi2 influences the acute locomotor simulant response to methamphetamine. <i>Genes, Brain and Behavior</i> , 2021, 20, e12760.	1.1	5
70	Genome Sequences of Two Novel Coronavirus (SARS-CoV-2) Isolates from Dhaka, Bangladesh. <i>Microbiology Resource Announcements</i> , 2021, 10, e0051121.	0.3	3
71	Pleiotropy method reveals genetic overlap between orofacial clefts at multiple novel loci from GWAS of multi-ethnic trios. <i>PLoS Genetics</i> , 2021, 17, e1009584.	1.5	18
72	Founder reconstruction enables scalable and seamless pangenomic analysis. <i>Bioinformatics</i> , 2021, 37, 4611-4619.	1.8	7
76	snpQT: flexible, reproducible, and comprehensive quality control and imputation of genomic data. <i>F1000Research</i> , 2021, 10, 567.	0.8	1
77	poreCov-An Easy to Use, Fast, and Robust Workflow for SARS-CoV-2 Genome Reconstruction via Nanopore Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 711437.	1.1	24
78	NPSV: A simulation-driven approach to genotyping structural variants in whole-genome sequencing data. <i>GigaScience</i> , 2021, 10, .	3.3	4
79	A Panel of rSNPs Demonstrating Allelic Asymmetry in Both ChIP-seq and RNA-seq Data and the Search for Their Phenotypic Outcomes through Analysis of DEGs. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7240.	1.8	6
82	LGAAP: Leishmaniinae Genome Assembly and Annotation Pipeline. <i>Microbiology Resource Announcements</i> , 2021, 10, e0043921.	0.3	8
87	Whole genome sequence data of <i>Bacillus australimaris</i> strain B28A, isolated from Marine Water in India. <i>Data in Brief</i> , 2021, 37, 107240.	0.5	1

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90	A Draft Genome of the Ginger Species <i>Alpinia nigra</i> and New Insights into the Genetic Basis of Flexistyly. <i>Genes</i> , 2021, 12, 1297.	1.0	6
94	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> Strain PE591, a Polyethylene-Degrading Bacterium Isolated from Savanna Soil. <i>Microbiology Resource Announcements</i> , 2021, 10, e0049021.	0.3	4
96	A high-quality draft genome for <i>Melaleuca alternifolia</i> (tea tree): a new platform for evolutionary genomics of myrtaceous terpene-rich species. <i>GigaByte</i> , 0, 2021, 1-15.	0.0	11
97	OVarFlow: a resource optimized GATK4 based Open source Variant calling workFlow. <i>BMC Bioinformatics</i> , 2021, 22, 402.	1.2	16
98	Diversity and Paleodemography of the Addax (<i>Addax nasomaculatus</i>), a Saharan Antelope on the Verge of Extinction. <i>Genes</i> , 2021, 12, 1236.	1.0	8
99	Inhibition of YTHDF2 triggers proteotoxic cell death in MYC-driven breast cancer. <i>Molecular Cell</i> , 2021, 81, 3048-3064.e9.	4.5	86
100	Clinical and Histopathologic Features of a Feline SARS-CoV-2 Infection Model Are Analogous to Acute COVID-19 in Humans. <i>Viruses</i> , 2021, 13, 1550.	1.5	20
101	Mutational bias in spermatogonia impacts the anatomy of regulatory sites in the human genome. <i>Genome Research</i> , 2021, 31, 1994-2007.	2.4	4
102	AQPX-cluster aquaporins and aquaglyceroporins are asymmetrically distributed in trypanosomes. <i>Communications Biology</i> , 2021, 4, 953.	2.0	4
104	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread. <i>PLoS Pathogens</i> , 2021, 17, e1009824.	2.1	19
106	Short- and long-range cis interactions between integrated HPV genomes and cellular chromatin dysregulate host gene expression in early cervical carcinogenesis. <i>PLoS Pathogens</i> , 2021, 17, e1009875.	2.1	18
107	The <i>gigA/gigB</i> Genes Regulate the Growth, Stress Response, and Virulence of <i>Acinetobacter baumannii</i> ATCC 17978 Strain. <i>Frontiers in Microbiology</i> , 2021, 12, 723949.	1.5	3
110	Whole Genome Sequence Analysis of <i>Brucella melitensis</i> Phylogeny and Virulence Factors. <i>Microbiology Research</i> , 2021, 12, 698-710.	0.8	3
113	VENUS, a Novel Selection Approach to Improve the Accuracy of Neoantigens Prediction. <i>Vaccines</i> , 2021, 9, 880.	2.1	8
114	A Study on Burrows-Wheeler Aligner's Performance Optimization for Ancient DNA Mapping. <i>Lecture Notes in Networks and Systems</i> , 2022, , 105-114.	0.5	1
115	Cross reactivity of neutralizing antibodies to the encephalitic California Serogroup orthobunyaviruses varies by virus and genetic relatedness. <i>Scientific Reports</i> , 2021, 11, 16424.	1.6	4
119	Near-Complete Genome Sequence of Ndumu Virus from Garissa, Kenya, 1997. <i>Microbiology Resource Announcements</i> , 2021, 10, e0055121.	0.3	0
121	Whole-genome sequencing reveals forgotten lineages and recurrent hybridizations within the kelp genus <i>Alaria</i> (Phaeophyceae). <i>Journal of Phycology</i> , 2021, 57, 1721-1738.	1.0	10

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123	Global Transcriptome Profile of the Oleaginous Yeast <i>Saitozyma podzolica</i> DSM 27192 Cultivated in Glucose and Xylose. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 758.	1.5	11
125	Alignment-free methods for polyploid genomes: Quick and reliable genetic distance estimation. <i>Molecular Ecology Resources</i> , 2022, 22, 612-622.	2.2	5
126	Mutation of the EPHA2 Tyrosine-Kinase Domain Dysregulates Cell Pattern Formation and Cytoskeletal Gene Expression in the Lens. <i>Cells</i> , 2021, 10, 2606.	1.8	9
127	An inferred functional impact map of genetic variants in rice. <i>Molecular Plant</i> , 2021, 14, 1584-1599.	3.9	48
129	Chromosome-scale genome sequencing, assembly and annotation of six genomes from subfamily Leishmaniinae. <i>Scientific Data</i> , 2021, 8, 234.	2.4	5
130	Nanopore Dwell Time Analysis Permits Sequencing and Conformational Assignment of Pseudouridine in SARS-CoV-2. <i>ACS Central Science</i> , 2021, 7, 1707-1717.	5.3	46
131	DNA methylation is required to maintain both DNA replication timing precision and 3D genome organization integrity. <i>Cell Reports</i> , 2021, 36, 109722.	2.9	39
132	Chromosome-Scale Genome Assembly and Transcriptome Assembly of Kawakawa <i>Euthynnus affinis</i> ; A Tuna-Like Species. <i>Frontiers in Genetics</i> , 2021, 12, 739781.	1.1	3
135	Single-cell multimodal glioma analyses identify epigenetic regulators of cellular plasticity and environmental stress response. <i>Nature Genetics</i> , 2021, 53, 1456-1468.	9.4	111
138	Demographic history and patterns of molecular evolution from whole genome sequencing in the radiation of Galapagos giant tortoises. <i>Molecular Ecology</i> , 2021, 30, 6325-6339.	2.0	7
139	A <i>Wolbachia</i> Transinfection Displays Stable Phenotypic Effects across Divergent <i>Aedes aegypti</i> Mosquito Backgrounds. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0126421.	1.4	20
140	Molecular differences in mitochondrial DNA genomes of dogs with malignant mammary tumours. <i>Veterinary and Comparative Oncology</i> , 2022, 20, 256-264.	0.8	7
141	A whole genome atlas of 81 <i>Psilocybe</i> genomes as a resource for psilocybin production.. <i>F1000Research</i> , 0, 10, 961.	0.8	6
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149	Alphaproteobacteria facilitate <i>Trichodesmium</i> community trimethylamine utilization. <i>Environmental Microbiology</i> , 2021, 23, 6798-6810.	1.8	2

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150	Highly integrated adaptive mechanisms in <i>Spiribacter halalkaliphilus</i> , a bacterium abundant in Chinese soda saline lakes. <i>Environmental Microbiology</i> , 2021, 23, 6463-6482.	1.8	4
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152	Genomic impact of stress-induced transposable element mobility in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2021, 49, 10431-10447.	6.5	60
154	Broad betacoronavirus neutralization by a stem helix-specific human antibody. <i>Science</i> , 2021, 373, 1109-1116.	6.0	262
155	Incursions of divergent genotypes, evolution of virulence and host jumps shape a continental clonal population of the stripe rust pathogen <i>Puccinia striiformis</i> . <i>Molecular Ecology</i> , 2021, 30, 6566-6584.	2.0	19
156	Identification of covalent inhibitors that disrupt <i>M.Âtuberculosis</i> growth by targeting multiple serine hydrolases involved in lipid metabolism. <i>Cell Chemical Biology</i> , 2022, 29, 897-909.e7.	2.5	18
157	RNA editing signatures identify melanoma patients who respond to Pembrolizumab or Nivolumab treatment. <i>Translational Oncology</i> , 2021, 14, 101197.	1.7	2
158	The draft genome of the Asian corn borer yields insights into ecological adaptation of a devastating maize pest. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 138, 103638.	1.2	8
159	SomaMutDB: a database of somatic mutations in normal human tissues. <i>Nucleic Acids Research</i> , 2022, 50, D1100-D1108.	6.5	21
160	Twelve years of SAMtools and BCFtools. <i>GigaScience</i> , 2021, 10, .	3.3	4,546
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170	Genomic prediction for testes weight of the tiger pufferfish, <i>Takifugu rubripes</i> , using medium to low density SNPs. <i>Scientific Reports</i> , 2021, 11, 20372.	1.6	5
171	A chromosome-scale draft genome sequence of horsegram (<i>Macrotyloma uniflorum</i>). <i>GigaByte</i> , 0, 2021, 1-23.	0.0	7
178	Combined nanopore adaptive sequencing and enzyme-based host depletion efficiently enriched microbial sequences and identified missing respiratory pathogens. <i>BMC Genomics</i> , 2021, 22, 732.	1.2	29
180	Strategy and Performance Evaluation of Low-Frequency Variant Calling for SARS-CoV-2 Using Targeted Deep Illumina Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 747458.	1.5	15
182	Comparative genomics suggests local adaptations in the invasive small hive beetle. <i>Ecology and Evolution</i> , 2021, 11, 15780-15791.	0.8	8

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190	Chromosome-Level Genome Assembly of <i>Nephotettix cincticeps</i> (Uhler, 1896) (Hemiptera: Tj ETQq1 1 0.784314 rgBT ₇ /Overlook	1.1	7
191	Identification and Characterization of Swine Influenza Virus H1N1 Variants Generated in Vaccinated and Nonvaccinated, Challenged Pigs. Viruses, 2021, 13, 2087.	1.5	9
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200	Genome Sequencing of SARS-CoV-2 Allows Monitoring of Variants of Concern through Wastewater. Water (Switzerland), 2021, 13, 3018.	1.2	21
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206	A small number of early introductions seeded widespread transmission of SARS-CoV-2 in Québec, Canada. Genome Medicine, 2021, 13, 169.	3.6	19
207	<i>Mycobacterium intracellulare</i> subsp. <i>chimaera</i> from Cardio Surgery Heating-Cooling Units and from Clinical Samples in Israel Are Genetically Unrelated. Pathogens, 2021, 10, 1392.	1.2	3

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209	Whole-Genome Sequencing and Annotation of Selected <i>Lactobacillales</i> Isolated from Commercial Cucumber Fermentation. <i>Microbiology Resource Announcements</i> , 2021, 10, e0062521.	0.3	6
210	Nanopore sequencing of a forensic combined STR and SNP multiplex. <i>Forensic Science International: Genetics</i> , 2022, 56, 102621.	1.6	12
212	High-quality reference genome and annotation aids understanding of berry development for evergreen blueberry (<i>Vaccinium darrowii</i>). <i>Horticulture Research</i> , 2021, 8, 228.	2.9	17
214	Evaluating Selective Pressures Driving Clades Differentiation of the <i>Faecalibacterium prausnitzii</i> Complex. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
215	CRISPRroots: on- and off-target assessment of RNA-seq data in CRISPR-Cas9 edited cells. <i>Nucleic Acids Research</i> , 2022, 50, e20-e20.	6.5	11
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226	Genome-Wide Analysis of H3K27me3 in Porcine Embryonic Muscle Development. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 739321.	1.8	5
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228	VPMBench: a test bench for variant prioritization methods. <i>BMC Bioinformatics</i> , 2021, 22, 543.	1.2	0
229	Assessment of Genetic Diversity of Rice in Registered Cultivars and Farmers' Fields in Burkina Faso. <i>Crops</i> , 2021, 1, 129-140.	0.6	12
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272	Organelle genome assembly uncovers the dynamic genome reorganization and cytoplasmic male sterility associated genes in tomato. <i>Horticulture Research</i> , 2021, 8, 250.	2.9	5
273	Mismatch Repair Deficiency and Somatic Mutations in Human Sinonasal Tumors. <i>Cancers</i> , 2021, 13, 6081.	1.7	9
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276	Association analysis and functional annotation of imputed sequence data within genomic regions influencing resistance to gastro-intestinal parasites detected by an LDLA approach in a nucleus flock of Sarda dairy sheep. <i>Genetics Selection Evolution</i> , 2022, 54, 2.	1.2	11
277	Recombinant inbred lines and next-generation sequencing enable rapid identification of candidate genes involved in morphological and agronomic traits in foxtail millet. <i>Scientific Reports</i> , 2022, 12, 218.	1.6	9
279	Genome-Wide Analysis of Multiple Organellar RNA Editing Factor (MORF) Family in Kiwifruit (Actinidia) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.6	10
281	High-Quality Reference Genome for an Arid-Adapted Mammal, the Banner-Tailed Kangaroo Rat (<i>Dipodomys spectabilis</i>). <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	3
282	A MADS-box gene with similarity to <i>FLC</i> is induced by cold and correlated with epigenetic changes to control budbreak in kiwifruit. <i>New Phytologist</i> , 2022, 233, 2111-2126.	3.5	25
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1919	Genetic Adaptation of Siberian Larch (<i>Larix sibirica</i> Ledeb.) to High Altitudes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4530.	1.8	4
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1943	Isolation and characterization of a novel <i>Tenacibaculum</i> species and a corresponding bacteriophage from a Mediterranean fish hatchery: Description of <i>Tenacibaculum larymnensis</i> sp. nov. and <i>Tenacibaculum</i> phage Larrie. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
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1951	Genomics Insight into cfr-Mediated Linezolid-Resistant LA-MRSA in Italian Pig Holdings. <i>Antibiotics</i> , 2023, 12, 530.	1.5	1
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1962	Structurally Complex Osteosarcoma Genomes Exhibit Limited Heterogeneity within Individual Tumors and across Evolutionary Time. <i>Cancer Research Communications</i> , 2023, 3, 564-575.	0.7	4
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1982	MangoBase: A Genomics Portal and Gene Expression Atlas for <i>Mangifera indica</i> . <i>Plants</i> , 2023, 12, 1273.	1.6	3
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1984	<scp>iGDP</scp>: An integrated genome decontamination pipeline for wild ciliated microeukaryotes. <i>Molecular Ecology Resources</i> , 2023, 23, 1182-1193.	2.2	2
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