Christopher E. Mason

List of Publications by Year
in descending order

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242	30,851	15001 68	7234 158
papers	citations	h-index	g-index

314	314	314	50280
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Annotating unknown species of urban microorganisms on a global scale unveils novel functional diversity and local environment association. Environmental Research, 2022, 207, 112183.	3.7	7
2	Landscape and clinical significance of long noncoding <scp>RNAs</scp> involved in multiple myeloma expressed fusion transcripts. American Journal of Hematology, 2022, 97, .	2.0	1
3	Genomic Characterization of Parengyodontium torokii sp. nov., a Biofilm-Forming Fungus Isolated from Mars 2020 Assembly Facility. Journal of Fungi (Basel, Switzerland), 2022, 8, 66.	1.5	4
4	Genes regulated by DNA methylation are involved in distinct phenotypes during melanoma progression and are prognostic factors for patients. Molecular Oncology, 2022, 16, 1913-1930.	2.1	1
5	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. Cell Reports Medicine, 2022, 3, 100522.	3.3	24
6	Betacoronavirus-specific alternate splicing. Genomics, 2022, 114, 110270.	1.3	12
7	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	9.4	90
8	Genomic Characterization of the Titan-like Cell Producing Naganishia tulchinskyi, the First Novel Eukaryote Isolated from the International Space Station. Journal of Fungi (Basel, Switzerland), 2022, 8, 165.	1.5	5
9	Unlocking capacities of genomics for the COVID-19 response and future pandemics. Nature Methods, 2022, 19, 374-380.	9.0	35
10	A collective statement in support of saving pangolins. Science of the Total Environment, 2022, 824, 153666.	3.9	6
11	SETD2 Haploinsufficiency Enhances Germinal Centerâ€“Associated AICDA Somatic Hypermutation to Drive B-cell Lymphomagenesis. Cancer Discovery, 2022, 12, 1782-1803.	7.7	14
12	The Isolation and Characterization of Rare Mycobiome Associated With Spacecraft Assembly Cleanrooms. Frontiers in Microbiology, 2022, 13, 777133.	1.5	7
13	Comparison of Electronegative Filtration to Magnetic Bead-Based Concentration and V2G-qPCR to RT-qPCR for Quantifying Viral SARS-CoV-2 RNA from Wastewater. ACS ES&T Water, 2022, 2, 2004-2013.	2.3	15
14	Deep oncopanel sequencing reveals within block position-dependent quality degradation in FFPE processed samples. Genome Biology, 2022, 23, .	3.8	8
15	Longitudinal Shifts of Solid Tumor and Liquid Biopsy Sequencing Concordance in Metastatic Breast Cancer. JCO Precision Oncology, 2022, , .	1.5	6
16	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. Nature, 2021, 589, 299-305.	13.7	155
17	Single-cell RNA-seq reveals novel mitochondria-related musculoskeletal cell populations during adult axolotl limb regeneration process. Cell Death and Differentiation, 2021, 28, 1110-1125.	5.0	26
18	BCL6 maintains survival and self-renewal of primary human acute myeloid leukemia cells. Blood, 2021, 137, 812-825.	0.6	18

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19	Transcriptional response modules characterize IL-1Î² and IL-6 activity in COVID-19. IScience, 2021, 24, 101896.	1.9	28
20	Characterization of complete lncRNAs transcriptome reveals the functional and clinical impact of lncRNAs in multiple myeloma. Leukemia, 2021, 35, 1438-1450.	3.3	28
21	A diagnostic host response biosignature for COVID-19 from RNA profiling of nasal swabs and blood. Science Advances, 2021, 7, .	4.7	79
22	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. Genome Research, 2021, 31, 635-644.	2.4	39
23	Telomere length dynamics in response to DNA damage in malaria parasites. IScience, 2021, 24, 102082.	1.9	6
24	Efficacy of Daily Intake of Dried Cranberry 500 mg in Women with Overactive Bladder: A Randomized, Double-Blind, Placebo Controlled Study. Journal of Urology, 2021, 205, 507-513.	0.2	2
25	Post-transcriptional regulation of antiviral gene expression by N6-methyladenosine. Cell Reports, 2021, 34, 108798.	2.9	46
26	Methylobacterium ajmalii sp. nov., Isolated From the International Space Station. Frontiers in Microbiology, 2021, 12, 639396.	1.5	46
27	Shotgun transcriptome, spatial omics, and isothermal profiling of SARS-CoV-2 infection reveals unique host responses, viral diversification, and drug interactions. Nature Communications, 2021, 12, 1660.	5.8	132
28	Origin Sample Prediction and Spatial Modeling of Antimicrobial Resistance in Metagenomic Sequencing Data. Frontiers in Genetics, 2021, 12, 642991.	1.1	4
29	Effectiveness of SARS-CoV-2 Decontamination and Containment in a COVID-19 ICU. International Journal of Environmental Research and Public Health, 2021, 18, 2479.	1.2	4
30	The spatial landscape of lung pathology during COVID-19 progression. Nature, 2021, 593, 564-569.	13.7	249
31	74325 Vast sex-specific differences in transcriptional landscapes of pancreatic neuroendocrine tumors. Journal of Clinical and Translational Science, 2021, 5, 103-103.	0.3	0
32	COVID-19 drug practices risk antimicrobial resistance evolution. Lancet Microbe, The, 2021, 2, e135-e136.	3.4	47
33	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	9.4	126
34	Draft Genome Sequences of Various Bacterial Phyla Isolated from the International Space Station. Microbiology Resource Announcements, 2021, 10, .	0.3	7
35	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	3.8	20
36	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. Genome Biology, 2021, 22, 111.	3.8	29

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37	Draft Genome Sequences of Aspergillus and Penicillium Species Isolated from the International Space Station and Crew Resupply Vehicle Capsule. Microbiology Resource Announcements, 2021, 10, .	0.3	5
38	A comprehensive metagenomics framework to characterize organisms relevant for planetary protection. Microbiome, 2021, 9, 82.	4.9	15
39	Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States. Cell, 2021, 184, 2595-2604.e13.	13.5	113
40	Pleckstrin-2 is essential for erythropoiesis in Î²-thalassemic mice, reducing apoptosis and enhancing enucleation. Communications Biology, 2021, 4, 517.	2.0	8
41	Investigation of product-derived lymphoma following infusion of piggyBac-modified CD19 chimeric antigen receptor T cells. Blood, 2021, 138, 1391-1405.	0.6	87
42	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. PLoS Biology, 2021, 19, e3001236.	2.6	200
43	The impact of cross-kingdom molecular forensics on genetic privacy. Microbiome, 2021, 9, 114.	4.9	8
44	RP58 Represses Transcriptional Programs Linked to Nonneuronal Cell Identity and Glioblastoma Subtypes in Developing Neurons. Molecular and Cellular Biology, 2021, 41, e0052620.	1.1	8
45	Diurnal variation in the human skin microbiome affects accuracy of forensic microbiome matching. Microbiome, 2021, 9, 129.	4.9	14
46	Haplotype diversity and sequence heterogeneity of human telomeres. Genome Research, 2021, 31, 1269-1279.	2.4	19
47	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	13.5	164
48	Characterization of Spacesuit Associated Microbial Communities and Their Implications for NASA Missions. Frontiers in Microbiology, 2021, 12, 608478.	1.5	5
49	Sequencing of Circulating Microbial Cell-Free DNA Can Identify Pathogens in Periprosthetic Joint Infections. Journal of Bone and Joint Surgery - Series A, 2021, 103, 1705-1712.	1.4	17
50	Role of miR-2392 in driving SARS-CoV-2 infection. Cell Reports, 2021, 37, 109839.	2.9	52
51	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. Nature Biotechnology, 2021, 39, 1141-1150.	9.4	66
52	Draft Genome Sequences of Heat Shock-Tolerant Microbes Isolated from a Spacecraft Assembly Facility. Microbiology Resource Announcements, 2021, 10, e0065321.	0.3	1
53	Cohesin Core Complex Gene Dosage Contributes to Germinal Center Derived Lymphoma Phenotypes and Outcomes. Frontiers in Immunology, 2021, 12, 688493.	2.2	5
54	Targeted Hybridization Capture of SARS-CoV-2 and Metagenomics Enables Genetic Variant Discovery and Nasal Microbiome Insights. Microbiology Spectrum, 2021, 9, e0019721.	1.2	22

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55	Simulated Microgravity Promotes Horizontal Gene Transfer of Antimicrobial Resistance Genes between Bacterial Genera in the Absence of Antibiotic Selective Pressure. Life, 2021, 11, 960.	1.1	9
56	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. Nature Biotechnology, 2021, 39, 1151-1160.	9.4	39
57	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. Nature Biotechnology, 2021, 39, 1129-1140.	9.4	69
58	Draft Genome Sequences of Fungi Isolated from the International Space Station during the Microbial Tracking-2 Experiment. Microbiology Resource Announcements, 2021, 10, e0075121.	0.3	7
59	DNA methylation landscapes of 1538 breast cancers reveal a replication-linked clock, epigenomic instability and cis-regulation. Nature Communications, 2021, 12, 5406.	5.8	29
60	Genomic Changes Driven by Radiation-Induced DNA Damage and Microgravity in Human Cells. International Journal of Molecular Sciences, 2021, 22, 10507.	1.8	19
61	Epigenetic Forensics for Suspect Identification and Age Prediction. Forensic Genomics, 2021, 1, 83-86.	0.3	1
62	Lessons learned from SARS-CoV-2 measurements in wastewater. Science of the Total Environment, 2021, 798, 149177.	3.9	36
63	Chemotherapy Induces Senescence-Like Resilient Cells Capable of Initiating AML Recurrence. Cancer Discovery, 2021, 11, 1542-1561.	7.7	133
64	Smc3 dosage regulates B cell transit through germinal centers and restricts their malignant transformation. Nature Immunology, 2021, 22, 240-253.	7.0	24
65	Orchestrating and sharing large multimodal data for transparent and reproducible research. Nature Communications, 2021, 12, 5797.	5.8	10
66	Mï»¿etagenomic insights into the microbial communities of inert and oligotrophic outdoor pier surfaces of a coastal city. Microbiome, 2021, 9, 213.	4.9	6
67	The Sequencing Quality Control 2 study: establishing community standards for sequencing in precision medicine. Genome Biology, 2021, 22, 306.	3.8	7
68	DNA methylation-calling tools for Oxford Nanopore sequencing: a survey and human epigenome-wide evaluation. Genome Biology, 2021, 22, 295.	3.8	6
69	DNA methylation-calling tools for Oxford Nanopore sequencing: a survey and human epigenome-wide evaluation. Genome Biology, 2021, 22, 295.	3.8	87
70	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. Scientific Data, 2021, 8, 296.	2.4	15
71	PRMT5 Inhibition Modulates E2F1 and P53 to Restore Cell Cycle Regulation and Drive DNA Damage Response in Ibrutinib-Resistant Mantle Cell Lymphoma. Blood, 2021, 138, 787-787.	0.6	0
72	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170

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73	Viral Dynamics of SARS-CoV-2 Variants in Vaccinated and Unvaccinated Persons. New England Journal of Medicine, 2021, 385, 2489-2491.	13.9	216
74	Comparative Genomics of Novel Agrobacterium G3 Strains Isolated From the International Space Station and Description of Agrobacterium tomkonis sp. nov.. Frontiers in Microbiology, 2021, 12, 765943.	1.5	22
75	A Rapid, Isothermal, and Point-of-Care System for COVID-19 Diagnostics. Journal of Biomolecular Techniques, 2021, 32, 221-227.	0.8	6
76	Loop-Mediated Isothermal Amplification Detection of SARS-CoV-2 and Myriad Other Applications. Journal of Biomolecular Techniques, 2021, 32, 228-275.	0.8	28
77	Systems biology analysis of human genomes points to key pathways conferring spina bifida risk. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	11
78	The SEQC2 epigenomics quality control (EpiQC) study. Genome Biology, 2021, 22, 332.	3.8	20
79	A comprehensive, multidisciplinary, precision medicine approach to discover effective therapy for an undiagnosed, progressive, fibroinflammatory disease. Translational Research, 2020, 215, 31-40.	2.2	0
80	The therapeutic landscape for cells engineered with chimeric antigen receptors. Nature Biotechnology, 2020, 38, 233-244.	9.4	147
81	Altered m6A Modification of Specific Cellular Transcripts Affects Flaviviridae Infection. Molecular Cell, 2020, 77, 542-555.e8.	4.5	129
82	Missing diversity in brain tumor trials. Neuro-Oncology Advances, 2020, 2, vdaa059.	0.4	9
83	Evolution of the Epigenetic Landscape in Childhood B Acute Lymphoblastic Leukemia and Its Role in Drug Resistance. Cancer Research, 2020, 80, 5189-5202.	0.4	9
84	The NASA Twins Study: The Effect of One Year in Space on Long-Chain Fatty Acid Desaturases and Elongases. Lifestyle Genomics, 2020, 13, 107-121.	0.6	13
85	Fundamental Biological Features of Spaceflight: Advancing the Field to Enable Deep-Space Exploration. Cell, 2020, 183, 1162-1184.	13.5	185
86	Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact. Cell, 2020, 183, 1185-1201.e20.	13.5	161
87	Advancing the Integration of Biosciences Data Sharing to Further Enable Space Exploration. Cell Reports, 2020, 33, 108441.	2.9	17
88	Clonal Hematopoiesis Before, During, and After Human Spaceflight. Cell Reports, 2020, 33, 108458.	2.9	30
89	Direct RNA sequencing reveals m6A modifications on adenovirus RNA are necessary for efficient splicing. Nature Communications, 2020, 11, 6016.	5.8	111
90	Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. Cell Reports, 2020, 33, 108448.	2.9	35

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91	Multi-omic, Single-Cell, and Biochemical Profiles of Astronauts Guide Pharmacological Strategies for Returning to Gravity. Cell Reports, 2020, 33, 108429.	2.9	37
92	Telomere Length Dynamics and DNA Damage Responses Associated with Long-Duration Spaceflight. Cell Reports, 2020, 33, 108457.	2.9	48
93	Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers. IScience, 2020, 23, 101844.	1.9	31
94	Improved gastrointestinal health for irritable bowel syndrome with metagenome-guided interventions. Precision Clinical Medicine, 2020, 3, 136-146.	1.3	12
95	Immune complement and coagulation dysfunction in adverse outcomes of SARS-CoV-2 infection. Nature Medicine, 2020, 26, 1609-1615.	15.2	255
96	Draft Genome Sequences of Klebsiella Species Isolated from the International Space Station. Microbiology Resource Announcements, 2020, 9, .	0.3	10
97	End-to-End Protocol for the Detection of SARS-CoV-2 from Built Environments. MSystems, 2020, 5, .	1.7	21
98	Draft Genome Sequences of Enterobacteriales Strains Isolated from the International Space Station. Microbiology Resource Announcements, 2020, 9, .	0.3	7
99	Draft Genome Sequences of Rhodotorula mucilaginosa Strains Isolated from the International Space Station. Microbiology Resource Announcements, 2020, 9, .	0.3	9
100	Obesity and ethnicityÂalter gene expression in skin. Scientific Reports, 2020, 10, 14079.	1.6	8
101	Somatic Mutations Drive Specific, but Reversible, Epigenetic Heterogeneity States in AML. Cancer Discovery, 2020, 10, 1934-1949.	7.7	23
102	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. Nature Biotechnology, 2020, 38, 1021-1024.	9.4	71
103	Temporal Telomere and DNA Damage Responses in the Space Radiation Environment. Cell Reports, 2020, 33, 108435.	2.9	40
104	A New Era for Space Life Science: International Standards for Space Omics Processing. Patterns, 2020, 1, 100148.	3.1	28
105	4565 Sex-Specific Differences in the Genomic Landscape of Pediatric and Adult Glioblastoma. Journal of Clinical and Translational Science, 2020, 4, 112-113.	0.3	0
106	Draft Genome Sequences of Lactobacillales Isolated from the International Space Station. Microbiology Resource Announcements, 2020, 9, .	0.3	3
107	Why Personalized Medicine Is the Frontier of Medicine and Performance for Humans in Space. New Space, 2020, 8, 63-76.	0.4	9
108	Illuminating Genetic Mysteries of the Dead Sea Scrolls. Cell, 2020, 181, 1218-1231.e27.	13.5	10

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109	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. Cancer Cell, 2020, 37, 655-673.e11.	7.7	93
110	Resource: A multiâ€speciesmultiâ€timepoint transcriptome database and webpage for the pineal gland and retina. Journal of Pineal Research, 2020, 69, e12673.	3.4	16
111	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	9.4	233
112	Identification of Radioresponsive Genes in Esophageal Cancer from Longitudinal and Single Cell Exome Sequencing. International Journal of Radiation Oncology Biology Physics, 2020, 108, 1103-1114.	0.4	11
113	A synthesis of bacterial and archaeal phenotypic trait data. Scientific Data, 2020, 7, 170.	2.4	59
114	Draft Genome Sequences of Sphingomonas Species Associated with the International Space Station. Microbiology Resource Announcements, 2020, 9, .	0.3	8
115	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nature Medicine, 2020, 26, 941-951.	15.2	130
116	The case for biotech on Mars. Nature Biotechnology, 2020, 38, 401-407.	9.4	53
117	Long-term spaceflight and the cardiovascular system. Precision Clinical Medicine, 2020, 3, 284-291.	1.3	60
118	Draft Genome Sequences of Tremellomycetes Strains Isolated from the International Space Station. Microbiology Resource Announcements, 2020, 9, .	0.3	9
119	Co-occurrence patterns of bacteria within microbiome of Moscow subway. Computational and Structural Biotechnology Journal, 2020, 18, 314-322.	1.9	25
120	Single-cell sperm transcriptomes and variants from fathers of children with and without autism spectrum disorder. Npj Genomic Medicine, 2020, 5, 14.	1.7	10
121	The Microbiomes of Seven Lichen Genera Reveal Host Specificity, a Reduced Core Community and Potential as Source of Antimicrobials. Frontiers in Microbiology, 2020, 11, 398.	1.5	36
122	Loss of CHD1 Promotes Heterogeneous Mechanisms of Resistance to AR-Targeted Therapy via Chromatin Dysregulation. Cancer Cell, 2020, 37, 584-598.e11.	7.7	96
123	Limits in the detection of m6A changes using MeRIP/m6A-seq. Scientific Reports, 2020, 10, 6590.	1.6	136
124	Forensic Applications of Microbiomics: A Review. Frontiers in Microbiology, 2020, 11, 608101.	1.5	38
125	A Review of the Scientific Rigor, Reproducibility, and Transparency Studies Conducted by the ABRF Research Groups. Journal of Biomolecular Techniques, 2020, 31, 11-26.	0.8	15
126	Draft Genome Sequences of Bacillaceae Strains Isolated from the International Space Station. Microbiology Resource Announcements, 2020, 9, .	0.3	6

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127	Accurate detection of m6A RNA modifications in native RNA sequences. Nature Communications, 2019, 10, 4079.	5.8	322
128	Pre- and peri-implantation Zika virus infection impairs fetal development by targeting trophectoderm cells. Nature Communications, 2019, 10, 4155.	5.8	30
129	QuaPra: Efficient transcript assembly and quantification using quadratic programming with Apriori algorithm. Science China Life Sciences, 2019, 62, 937-946.	2.3	14
130	Rapid antigen diversification through mitotic recombination in the human malaria parasite Plasmodium falciparum. PLoS Biology, 2019, 17, e3000271.	2.6	44
131	Ratio-Based Method To Identify True Biomarkers by Normalizing Circulating ncRNA Sequencing and Quantitative PCR Data. Analytical Chemistry, 2019, 91, 6746-6753.	3.2	18
132	Consent insufficient for data releaseâ€"Response. Science, 2019, 364, 446-446.	6.0	5
133	The Impact of Heterogeneity on Single-Cell Sequencing. Frontiers in Genetics, 2019, 10, 8.	1.1	84
134	Urban metagenomics uncover antibiotic resistance reservoirs in coastal beach and sewage waters. Microbiome, 2019, 7, 35.	4.9	109
135	Best practices for benchmarking germline small-variant calls in human genomes. Nature Biotechnology, 2019, 37, 555-560.	9.4	273
136	Epigenetic Modifications in Acute Myeloid Leukemia: Prognosis, Treatment, and Heterogeneity. Frontiers in Genetics, 2019, 10, 133.	1.1	58
137	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. Science, 2019, 364, .	6.0	576
138	Single-molecule sequencing detection of N6-methyladenine in microbial reference materials. Nature Communications, 2019, 10, 579.	5.8	131
139	Long non-coding RNAs discriminate the stages and gene regulatory states of human humoral immune response. Nature Communications, 2019, 10, 821.	5.8	73
140	Translating current biomedical therapies for long duration, deep space missions. Precision Clinical Medicine, 2019, 2, 259-269.	1.3	24
141	Minerva: an alignment- and reference-free approach to deconvolve Linked-Reads for metagenomics. Genome Research, 2019, 29, 116-124.	2.4	21
142	Sooty mangabey genome sequence provides insight into AIDS resistance in a natural SIV host. Nature, 2018, 553, 77-81.	13.7	81
143	1154. Comparison of Five Testing Modalities for the Assessment of Patient Environment Cleanliness. Open Forum Infectious Diseases, 2018, 5, S347-S347.	0.4	0
144	Multi-drug resistant Enterobacter bugandensis species isolated from the International Space Station and comparative genomic analyses with human pathogenic strains. BMC Microbiology, 2018, 18, 175.	1.3	81

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145	ketu mutant mice uncover an essential meiotic function for the ancient RNA helicase YTHDC2. ELife, 2018, 7, .	2.8	129
146	N6 -methyladenosine modification of hepatitis B virus RNA differentially regulates the viral life cycle. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8829-8834.	3.3	164
147	The Microbe Directory: An annotated, searchable inventory of microbesâ€™ characteristics. Gates Open Research, 2018, 2, 3.	2.0	15
148	Combination Targeted Therapy to Disrupt Aberrant Oncogenic Signaling and Reverse Epigenetic Dysfunction in IDH2- and TET2-Mutant Acute Myeloid Leukemia. Cancer Discovery, 2017, 7, 494-505.	7.7	94
149	PGBD5 promotes site-specific oncogenic mutations in human tumors. Nature Genetics, 2017, 49, 1005-1014.	9.4	69
150	Charting the unknown epitranscriptome. Nature Reviews Molecular Cell Biology, 2017, 18, 339-340.	16.1	49
151	Jak1 Integrates Cytokine Sensing to Regulate Hematopoietic Stem Cell Function and Stress Hematopoiesis. Cell Stem Cell, 2017, 21, 489-501.e7.	5.2	58
152	Communicating the promise, risks, and ethics of large-scale, open space microbiome and metagenome research. Microbiome, 2017, 5, 132.	4.9	26
153	The N6-methyladenosine (m6A)-forming enzyme METTL3 controls myeloid differentiation of normal hematopoietic and leukemia cells. Nature Medicine, 2017, 23, 1369-1376.	15.2	971
154	Genetic and epigenetic heterogeneity and the impact on cancer relapse. Experimental Hematology, 2017, 54, 26-30.	0.2	31
155	Large-scale differences in microbial biodiversity discovery between 16S amplicon and shotgun sequencing. Scientific Reports, 2017, 7, 6589.	1.6	174
156	Chromosome End Repair and Genome Stability in Plasmodium falciparum. MBio, 2017, 8, .	1.8	27
157	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. Nature Biotechnology, 2017, 35, 1127-1128.	9.4	32
158	Genomic approaches to the assessment of human spina bifida risk. Birth Defects Research, 2017, 109, 120-128.	0.8	23
159	Nanopore DNA Sequencing and Genome Assembly on the International Space Station. Scientific Reports, 2017, 7, 18022.	1.6	264
160	International Standards for Genomes, Transcriptomes, and Metagenomes. Journal of Biomolecular Techniques, 2017, 28, 8-18.	0.8	33
161	Precision Metagenomics: Rapid Metagenomic Analyses for Infectious Disease Diagnostics and Public Health Surveillance. Journal of Biomolecular Techniques, 2017, 28, 40-45.	0.8	47
162	rahu is a mutant allele of Dnmt3c, encoding a DNA methyltransferase homolog required for meiosis and transposon repression in the mouse male germline. PLoS Genetics, 2017, 13, e1006964.	1.5	56

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163	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. Genome Biology, 2017, 18, 182.	3.8	260
164	Metagenomic characterization of ambulances across the USA. Microbiome, 2017, 5, 125.	4.9	32
165	Focus on Metagenomics. Journal of Biomolecular Techniques, 2017, 28, 1-1.	0.8	3
166	Assessment of REPLI-g Multiple Displacement Whole Genome Amplification (WGA) Techniques for Metagenomic Applications. Journal of Biomolecular Techniques, 2017, 28, 46-55.	0.8	19
167	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). Journal of Biomolecular Techniques, 2017, 28, 31-39.	0.8	53
168	m6a Regulates Differentiation State and mRNA Translation in Myeloid Leukemia. Blood, 2017, 130, 791-791.	0.6	0
169	Clinical Genomics: Challenges and Opportunities. Critical Reviews in Eukaryotic Gene Expression, 2016, 26, 97-113.	0.4	12
170	Highâ€throughput RNA sequencing reveals structural differences of orthologous brainâ€expressed genes between western lowland gorillas and humans. Journal of Comparative Neurology, 2016, 524, 288-308.	0.9	2
171	Globalizing and crowdsourcing biomedical research. British Medical Bulletin, 2016, 120, 27-33.	2.7	22
172	Complex translocation disrupting TCF4 and altering TCF4 isoform expression segregates as mild autosomal dominant intellectual disability. Orphanet Journal of Rare Diseases, 2016, 11, 62.	1.2	35
173	A benchmark for RNA-seq quantification pipelines. Genome Biology, 2016, 17, 74.	3.8	160
174	Genetic and epigenetic heterogeneity in acute myeloid leukemia. Current Opinion in Genetics and Development, 2016, 36, 100-106.	1.5	130
175	The mitogenome of the bed bug Cimex lectularius (Hemiptera: Cimicidae). Mitochondrial DNA Part B: Resources, 2016, 1, 425-427.	0.2	5
176	Dynamics of the human and viral m6A RNA methylomes during HIV-1 infection of T cells. Nature Microbiology, 2016, 1, 16011.	5.9	373
177	The complete mitochondrial genome of the neotropical helicopter damselflyMegaloprepus caerulatus(Odonata: Zygoptera) assembled from next generation sequencing data. Mitochondrial DNA Part B: Resources, 2016, 1, 497-499.	0.2	19
178	Nanopore sequencing in microgravity. Npj Microgravity, 2016, 2, 16035.	1.9	76
179	DNMT3A mutations promote anthracycline resistance in acute myeloid leukemia via impaired nucleosome remodeling. Nature Medicine, 2016, 22, 1488-1495.	15.2	195
180	Roles for small noncoding RNAs in silencing of retrotransposons in the mammalian brain. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12697-12702.	3.3	77

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181	Extensive sequencing of seven human genomes to characterize benchmark reference materials. Scientific Data, 2016, 3, 160025.	2.4	575
182	Laminin regulates PDGFRÎ²+ cell stemness and muscle development. Nature Communications, 2016, 7, 11415.	5.8	32
183	N6 -Methyladenosine in Flaviviridae Viral RNA Genomes Regulates Infection. Cell Host and Microbe, 2016, 20, 654-665.	5.1	370
184	The Power of Engaging Citizen Scientists for Scientific Progress. Journal of Microbiology and Biology Education, 2016, 17, 7-12.	0.5	49
185	Distinct evolution and dynamics of epigenetic and genetic heterogeneity in acute myeloid leukemia. Nature Medicine, 2016, 22, 792-799.	15.2	322
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