

# Christopher E. Mason

## List of Publications by Year in descending order

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242  
papers

30,851  
citations

13068

68  
h-index

6282

158  
g-index

314  
all docs

314  
docs citations

314  
times ranked

45781  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Analysis of mRNA Methylation Reveals Enrichment in 3' UTRs and near Stop Codons. <i>Cell</i> , 2012, 149, 1635-1646.	13.5	3,152
2	RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays. <i>Genome Research</i> , 2008, 18, 1509-1517.	2.4	2,393
3	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	13.7	1,994
4	methylKit: a comprehensive R package for the analysis of genome-wide DNA methylation profiles. <i>Genome Biology</i> , 2012, 13, R87.	13.9	1,541
5	Single-nucleotide-resolution mapping of m6A and m6Am throughout the transcriptome. <i>Nature Methods</i> , 2015, 12, 767-772.	9.0	1,157
6	Multiple Recurrent De Novo CNVs, Including Duplications of the 7q11.23 Williams Syndrome Region, Are Strongly Associated with Autism. <i>Neuron</i> , 2011, 70, 863-885.	3.8	1,146
7	The N6-methyladenosine (m6A)-forming enzyme METTL3 controls myeloid differentiation of normal hematopoietic and leukemia cells. <i>Nature Medicine</i> , 2017, 23, 1369-1376.	15.2	971
8	Recurrent somatic TET2 mutations in normal elderly individuals with clonal hematopoiesis. <i>Nature Genetics</i> , 2012, 44, 1179-1181.	9.4	692
9	Toward understanding and exploiting tumor heterogeneity. <i>Nature Medicine</i> , 2015, 21, 846-853.	15.2	604
10	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. <i>Science</i> , 2019, 364, .	6.0	576
11	Extensive sequencing of seven human genomes to characterize benchmark reference materials. <i>Scientific Data</i> , 2016, 3, 160025.	2.4	575
12	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , 2015, 12, 780-786.	9.0	465
13	The birth of the Epitranscriptome: deciphering the function of RNA modifications. <i>Genome Biology</i> , 2012, 13, 175.	13.9	375
14	Dynamics of the human and viral m6A RNA methylomes during HIV-1 infection of T cells. <i>Nature Microbiology</i> , 2016, 1, 16011.	5.9	373
15	N6 -Methyladenosine in Flaviviridae Viral RNA Genomes Regulates Infection. <i>Cell Host and Microbe</i> , 2016, 20, 654-665.	5.1	370
16	Distinct evolution and dynamics of epigenetic and genetic heterogeneity in acute myeloid leukemia. <i>Nature Medicine</i> , 2016, 22, 792-799.	15.2	322
17	Accurate detection of m6A RNA modifications in native RNA sequences. <i>Nature Communications</i> , 2019, 10, 4079.	5.8	322
18	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. <i>Nature Communications</i> , 2014, 5, 3230.	5.8	316

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19	The Pivotal Regulatory Landscape of RNA Modifications. Annual Review of Genomics and Human Genetics, 2014, 15, 127-150.	2.5	284
20	Best practices for benchmarking germline small-variant calls in human genomes. Nature Biotechnology, 2019, 37, 555-560.	9.4	273
21	Relapse-specific mutations in NT5C2 in childhood acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 290-294.	9.4	264
22	Nanopore DNA Sequencing and Genome Assembly on the International Space Station. Scientific Reports, 2017, 7, 18022.	1.6	264
23	Base-Pair Resolution DNA Methylation Sequencing Reveals Profoundly Divergent Epigenetic Landscapes in Acute Myeloid Leukemia. PLoS Genetics, 2012, 8, e1002781.	1.5	263
24	genomation: a toolkit to summarize, annotate and visualize genomic intervals. Bioinformatics, 2015, 31, 1127-1129.	1.8	263
25	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. Genome Biology, 2017, 18, 182.	3.8	260
26	Immune complement and coagulation dysfunction in adverse outcomes of SARS-CoV-2 infection. Nature Medicine, 2020, 26, 1609-1615.	15.2	255
27	The spatial landscape of lung pathology during COVID-19 progression. Nature, 2021, 593, 564-569.	13.7	249
28	Cell-Cycle Reprogramming for PI3K Inhibition Overrides a Relapse-Specific C481S<i>BTK</i> Mutation Revealed by Longitudinal Functional Genomics in Mantle Cell Lymphoma. Cancer Discovery, 2014, 4, 1022-1035.	7.7	247
29	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. Cell Systems, 2015, 1, 72-87.	2.9	241
30	DNA Hydroxymethylation Profiling Reveals that WT1 Mutations Result in Loss of TET2 Function in Acute Myeloid Leukemia. Cell Reports, 2014, 9, 1841-1855.	2.9	237
31	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	9.4	233
32	Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study. Nature Biotechnology, 2014, 32, 915-925.	9.4	217
33	Viral Dynamics of SARS-CoV-2 Variants in Vaccinated and Unvaccinated Persons. New England Journal of Medicine, 2021, 385, 2489-2491.	13.9	216
34	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. PLoS Biology, 2021, 19, e3001236.	2.6	200
35	DNMT3A mutations promote anthracycline resistance in acute myeloid leukemia via impaired nucleosome remodeling. Nature Medicine, 2016, 22, 1488-1495.	15.2	195
36	Mutational Cooperativity Linked to Combinatorial Epigenetic Gain of Function in Acute Myeloid Leukemia. Cancer Cell, 2015, 27, 502-515.	7.7	191

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37	Fundamental Biological Features of Spaceflight: Advancing the Field to Enable Deep-Space Exploration. <i>Cell</i> , 2020, 183, 1162-1184.	13.5	185
38	Detecting and correcting systematic variation in large-scale RNA sequencing data. <i>Nature Biotechnology</i> , 2014, 32, 888-895.	9.4	174
39	Large-scale differences in microbial biodiversity discovery between 16S amplicon and shotgun sequencing. <i>Scientific Reports</i> , 2017, 7, 6589.	1.6	174
40	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
41	<i>N</i> <sup>6</sup> -methyladenosine modification of hepatitis B virus RNA differentially regulates the viral life cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8829-8834.	3.3	164
42	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	13.5	164
43	A Hybrid Mechanism of Action for BCL6 in B Cells Defined by Formation of Functionally Distinct Complexes at Enhancers and Promoters. <i>Cell Reports</i> , 2013, 4, 578-588.	2.9	161
44	Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact. <i>Cell</i> , 2020, 183, 1185-1201.e20.	13.5	161
45	A benchmark for RNA-seq quantification pipelines. <i>Genome Biology</i> , 2016, 17, 74.	3.8	160
46	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. <i>Nature</i> , 2021, 589, 299-305.	13.7	155
47	The therapeutic landscape for cells engineered with chimeric antigen receptors. <i>Nature Biotechnology</i> , 2020, 38, 233-244.	9.4	147
48	Limits in the detection of m6A changes using MeRIP/m6A-seq. <i>Scientific Reports</i> , 2020, 10, 6590.	1.6	136
49	Good laboratory practice for clinical next-generation sequencing informatics pipelines. <i>Nature Biotechnology</i> , 2015, 33, 689-693.	9.4	134
50	Chemotherapy Induces Senescence-Like Resilient Cells Capable of Initiating AML Recurrence. <i>Cancer Discovery</i> , 2021, 11, 1542-1561.	7.7	133
51	Shotgun transcriptome, spatial omics, and isothermal profiling of SARS-CoV-2 infection reveals unique host responses, viral diversification, and drug interactions. <i>Nature Communications</i> , 2021, 12, 1660.	5.8	132
52	Single-molecule sequencing detection of N <sup>6</sup> -methyladenine in microbial reference materials. <i>Nature Communications</i> , 2019, 10, 579.	5.8	131
53	Genetic and epigenetic heterogeneity in acute myeloid leukemia. <i>Current Opinion in Genetics and Development</i> , 2016, 36, 100-106.	1.5	130
54	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , 2020, 26, 941-951.	15.2	130

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55	ketu mutant mice uncover an essential meiotic function for the ancient RNA helicase YTHDC2. <i>ELife</i> , 2018, 7, .	2.8	129
56	Altered m6A Modification of Specific Cellular Transcripts Affects Flaviviridae Infection. <i>Molecular Cell</i> , 2020, 77, 542-555.e8.	4.5	129
57	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	9.4	126
58	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014, 5, 5125.	5.8	122
59	Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States. <i>Cell</i> , 2021, 184, 2595-2604.e13.	13.5	113
60	Direct RNA sequencing reveals m6A modifications on adenovirus RNA are necessary for efficient splicing. <i>Nature Communications</i> , 2020, 11, 6016.	5.8	111
61	Urban metagenomics uncover antibiotic resistance reservoirs in coastal beach and sewage waters. <i>Microbiome</i> , 2019, 7, 35.	4.9	109
62	An optimized algorithm for detecting and annotating regional differential methylation. <i>BMC Bioinformatics</i> , 2013, 14, S10.	1.2	105
63	The impact of read length on quantification of differentially expressed genes and splice junction detection. <i>Genome Biology</i> , 2015, 16, 131.	3.8	98
64	Loss of CHD1 Promotes Heterogeneous Mechanisms of Resistance to AR-Targeted Therapy via Chromatin Dysregulation. <i>Cancer Cell</i> , 2020, 37, 584-598.e11.	7.7	96
65	Combination Targeted Therapy to Disrupt Aberrant Oncogenic Signaling and Reverse Epigenetic Dysfunction in <i>IDH2</i> - and <i>TET2</i> -Mutant Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2017, 7, 494-505.	7.7	94
66	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. <i>Cancer Cell</i> , 2020, 37, 655-673.e11.	7.7	93
67	Curated variation benchmarks for challenging medically relevant autosomal genes. <i>Nature Biotechnology</i> , 2022, 40, 672-680.	9.4	90
68	Enhanced Reduced Representation Bisulfite Sequencing for Assessment of DNA Methylation at Base Pair Resolution. <i>Journal of Visualized Experiments</i> , 2015, , e52246.	0.2	89
69	Investigation of product-derived lymphoma following infusion of <i>piggyBac</i> -modified CD19 chimeric antigen receptor T cells. <i>Blood</i> , 2021, 138, 1391-1405.	0.6	87
70	DNA methylation-calling tools for Oxford Nanopore sequencing: a survey and human epigenome-wide evaluation. <i>Genome Biology</i> , 2021, 22, 295.	3.8	87
71	The Impact of Heterogeneity on Single-Cell Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 8.	1.1	84
72	Sooty mangabey genome sequence provides insight into AIDS resistance in a natural SIV host. <i>Nature</i> , 2018, 553, 77-81.	13.7	81

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73	Multi-drug resistant <i>Enterobacter bugandensis</i> species isolated from the International Space Station and comparative genomic analyses with human pathogenic strains. <i>BMC Microbiology</i> , 2018, 18, 175.	1.3	81
74	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , 2016, 7, 10164.	5.8	79
75	A diagnostic host response biosignature for COVID-19 from RNA profiling of nasal swabs and blood. <i>Science Advances</i> , 2021, 7, .	4.7	79
76	Roles for small noncoding RNAs in silencing of retrotransposons in the mammalian brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12697-12702.	3.3	77
77	Nanopore sequencing in microgravity. <i>Npj Microgravity</i> , 2016, 2, 16035.	1.9	76
78	Long non-coding RNAs discriminate the stages and gene regulatory states of human humoral immune response. <i>Nature Communications</i> , 2019, 10, 821.	5.8	73
79	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. <i>Nature Biotechnology</i> , 2020, 38, 1021-1024.	9.4	71
80	miR-29a maintains mouse hematopoietic stem cell self-renewal by regulating <i>Dnmt3a</i> . <i>Blood</i> , 2015, 125, 2206-2216.	0.6	70
81	PGBD5 promotes site-specific oncogenic mutations in human tumors. <i>Nature Genetics</i> , 2017, 49, 1005-1014.	9.4	69
82	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. <i>Nature Biotechnology</i> , 2021, 39, 1129-1140.	9.4	69
83	Dynamic evolution of clonal epialleles revealed by methclone. <i>Genome Biology</i> , 2014, 15, 472.	3.8	67
84	Genomic DNA transposition induced by human PGBD5. <i>ELife</i> , 2015, 4, .	2.8	67
85	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1141-1150.	9.4	66
86	Tissue-specific transcriptome sequencing analysis expands the non-human primate reference transcriptome resource (NHPRTR). <i>Nucleic Acids Research</i> , 2015, 43, D737-D742.	6.5	61
87	Long-term spaceflight and the cardiovascular system. <i>Precision Clinical Medicine</i> , 2020, 3, 284-291.	1.3	60
88	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020, 7, 170.	2.4	59
89	International community consensus standard for reporting derivation of human embryonic stem cell lines. <i>Regenerative Medicine</i> , 2007, 2, 349-362.	0.8	58
90	Jak1 Integrates Cytokine Sensing to Regulate Hematopoietic Stem Cell Function and Stress Hematopoiesis. <i>Cell Stem Cell</i> , 2017, 21, 489-501.e7.	5.2	58

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91	Epigenetic Modifications in Acute Myeloid Leukemia: Prognosis, Treatment, and Heterogeneity. <i>Frontiers in Genetics</i> , 2019, 10, 133.	1.1	58
92	rahu is a mutant allele of Dnmt3c, encoding a DNA methyltransferase homolog required for meiosis and transposon repression in the mouse male germline. <i>PLoS Genetics</i> , 2017, 13, e1006964.	1.5	56
93	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). <i>Journal of Biomolecular Techniques</i> , 2017, 28, 31-39.	0.8	53
94	The case for biotech on Mars. <i>Nature Biotechnology</i> , 2020, 38, 401-407.	9.4	53
95	Role of miR-2392 in driving SARS-CoV-2 infection. <i>Cell Reports</i> , 2021, 37, 109839.	2.9	52
96	The Power of Engaging Citizen Scientists for Scientific Progress. <i>Journal of Microbiology and Biology Education</i> , 2016, 17, 7-12.	0.5	49
97	Charting the unknown epitranscriptome. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 339-340.	16.1	49
98	Telomere Length Dynamics and DNA Damage Responses Associated with Long-Duration Spaceflight. <i>Cell Reports</i> , 2020, 33, 108457.	2.9	48
99	Precision Metagenomics: Rapid Metagenomic Analyses for Infectious Disease Diagnostics and Public Health Surveillance. <i>Journal of Biomolecular Techniques</i> , 2017, 28, 40-45.	0.8	47
100	COVID-19 drug practices risk antimicrobial resistance evolution. <i>Lancet Microbe</i> , The, 2021, 2, e135-e136.	3.4	47
101	Post-transcriptional regulation of antiviral gene expression by N6-methyladenosine. <i>Cell Reports</i> , 2021, 34, 108798.	2.9	46
102	<i>Methylobacterium ajmalii</i> sp. nov., Isolated From the International Space Station. <i>Frontiers in Microbiology</i> , 2021, 12, 639396.	1.5	46
103	Rapid antigen diversification through mitotic recombination in the human malaria parasite <i>Plasmodium falciparum</i> . <i>PLoS Biology</i> , 2019, 17, e3000271.	2.6	44
104	Temporal Telomere and DNA Damage Responses in the Space Radiation Environment. <i>Cell Reports</i> , 2020, 33, 108435.	2.9	40
105	Novel RNA regulatory mechanisms revealed in the epitranscriptome. <i>RNA Biology</i> , 2013, 10, 342-346.	1.5	39
106	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. <i>Genome Research</i> , 2021, 31, 635-644.	2.4	39
107	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1151-1160.	9.4	39
108	Faster sequencers, larger datasets, new challenges. <i>Genome Biology</i> , 2012, 13, 314.	13.9	38

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109	Forensic Applications of Microbiomics: A Review. <i>Frontiers in Microbiology</i> , 2020, 11, 608101.	1.5	38
110	Multi-omic, Single-Cell, and Biochemical Profiles of Astronauts Guide Pharmacological Strategies for Returning to Gravity. <i>Cell Reports</i> , 2020, 33, 108429.	2.9	37
111	The Microbiomes of Seven Lichen Genera Reveal Host Specificity, a Reduced Core Community and Potential as Source of Antimicrobials. <i>Frontiers in Microbiology</i> , 2020, 11, 398.	1.5	36
112	Lessons learned from SARS-CoV-2 measurements in wastewater. <i>Science of the Total Environment</i> , 2021, 798, 149177.	3.9	36
113	Complex translocation disrupting TCF4 and altering TCF4 isoform expression segregates as mild autosomal dominant intellectual disability. <i>Orphanet Journal of Rare Diseases</i> , 2016, 11, 62.	1.2	35
114	Genome Sequence and Analysis of <i>Escherichia coli</i> MRE600, a Colicinogenic, Nonmotile Strain that Lacks RNase I and the Type I Methyltransferase, EcoKI. <i>Genome Biology and Evolution</i> , 2016, 8, 742-752.	1.1	35
115	Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. <i>Cell Reports</i> , 2020, 33, 108448.	2.9	35
116	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	9.0	35
117	Assessment of pharmacogenomic agreement. <i>F1000Research</i> , 2016, 5, 825.	0.8	34
118	International Standards for Genomes, Transcriptomes, and Metagenomes. <i>Journal of Biomolecular Techniques</i> , 2017, 28, 8-18.	0.8	33
119	Laminin regulates PDGFR $\beta$ cell stemness and muscle development. <i>Nature Communications</i> , 2016, 7, 11415.	5.8	32
120	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. <i>Nature Biotechnology</i> , 2017, 35, 1127-1128.	9.4	32
121	Metagenomic characterization of ambulances across the USA. <i>Microbiome</i> , 2017, 5, 125.	4.9	32
122	Mining the Archives: A Cross-Platform Analysis of Gene Expression Profiles in Archival Formalin-Fixed Paraffin-Embedded Tissues. <i>Toxicological Sciences</i> , 2015, 148, 460-472.	1.4	31
123	Genetic and epigenetic heterogeneity and the impact on cancer relapse. <i>Experimental Hematology</i> , 2017, 54, 26-30.	0.2	31
124	Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers. <i>IScience</i> , 2020, 23, 101844.	1.9	31
125	Pre- and peri-implantation Zika virus infection impairs fetal development by targeting trophectoderm cells. <i>Nature Communications</i> , 2019, 10, 4155.	5.8	30
126	Clonal Hematopoiesis Before, During, and After Human Spaceflight. <i>Cell Reports</i> , 2020, 33, 108458.	2.9	30



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127	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , 2021, 22, 111.	3.8	29
128	DNA methylation landscapes of 1538 breast cancers reveal a replication-linked clock, epigenomic instability and cis-regulation. <i>Nature Communications</i> , 2021, 12, 5406.	5.8	29
129	Characterizing Multi-omic Data in Systems Biology. <i>Advances in Experimental Medicine and Biology</i> , 2014, 799, 15-38.	0.8	28
130	A New Era for Space Life Science: International Standards for Space Omics Processing. <i>Patterns</i> , 2020, 1, 100148.	3.1	28
131	Transcriptional response modules characterize IL-1 $\beta$ and IL-6 activity in COVID-19. <i>IScience</i> , 2021, 24, 101896.	1.9	28
132	Characterization of complete lncRNAs transcriptome reveals the functional and clinical impact of lncRNAs in multiple myeloma. <i>Leukemia</i> , 2021, 35, 1438-1450.	3.3	28
133	Loop-Mediated Isothermal Amplification Detection of SARS-CoV-2 and Myriad Other Applications. <i>Journal of Biomolecular Techniques</i> , 2021, 32, 228-275.	0.8	28
134	Chromosome End Repair and Genome Stability in <i>Plasmodium falciparum</i> . <i>MBio</i> , 2017, 8, .	1.8	27
135	Communicating the promise, risks, and ethics of large-scale, open space microbiome and metagenome research. <i>Microbiome</i> , 2017, 5, 132.	4.9	26
136	Single-cell RNA-seq reveals novel mitochondria-related musculoskeletal cell populations during adult axolotl limb regeneration process. <i>Cell Death and Differentiation</i> , 2021, 28, 1110-1125.	5.0	26
137	Pervasive sequence patents cover the entire human genome. <i>Genome Medicine</i> , 2013, 5, 27.	3.6	25
138	Co-occurrence patterns of bacteria within microbiome of Moscow subway. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 314-322.	1.9	25
139	Translating current biomedical therapies for long duration, deep space missions. <i>Precision Clinical Medicine</i> , 2019, 2, 259-269.	1.3	24
140	Smc3 dosage regulates B cell transit through germinal centers and restricts their malignant transformation. <i>Nature Immunology</i> , 2021, 22, 240-253.	7.0	24
141	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. <i>Cell Reports Medicine</i> , 2022, 3, 100522.	3.3	24
142	Genomic approaches to the assessment of human spina bifida risk. <i>Birth Defects Research</i> , 2017, 109, 120-128.	0.8	23
143	Somatic Mutations Drive Specific, but Reversible, Epigenetic Heterogeneity States in AML. <i>Cancer Discovery</i> , 2020, 10, 1934-1949.	7.7	23
144	Globalizing and crowdsourcing biomedical research. <i>British Medical Bulletin</i> , 2016, 120, 27-33.	2.7	22

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145	Targeted Hybridization Capture of SARS-CoV-2 and Metagenomics Enables Genetic Variant Discovery and Nasal Microbiome Insights. <i>Microbiology Spectrum</i> , 2021, 9, e0019721.	1.2	22
146	Comparative Genomics of Novel <i>Agrobacterium</i> G3 Strains Isolated From the International Space Station and Description of <i>Agrobacterium tomkonis</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2021, 12, 765943.	1.5	22
147	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. <i>Scientific Data</i> , 2014, 1, 140020.	2.4	21
148	Minerva: an alignment- and reference-free approach to deconvolve Linked-Reads for metagenomics. <i>Genome Research</i> , 2019, 29, 116-124.	2.4	21
149	End-to-End Protocol for the Detection of SARS-CoV-2 from Built Environments. <i>MSystems</i> , 2020, 5, .	1.7	21
150	Modern Methods for Delineating Metagenomic Complexity. <i>Cell Systems</i> , 2015, 1, 6-7.	2.9	20
151	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	3.8	20
152	The SEQC2 epigenomics quality control (EpiQC) study. <i>Genome Biology</i> , 2021, 22, 332.	3.8	20
153	The complete mitochondrial genome of the neotropical helicopter damselfly <i>Megaloprepus caerulatus</i> (Odonata: Zygoptera) assembled from next generation sequencing data. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 497-499.	0.2	19
154	Assessment of REPLI-g Multiple Displacement Whole Genome Amplification (WGA) Techniques for Metagenomic Applications. <i>Journal of Biomolecular Techniques</i> , 2017, 28, 46-55.	0.8	19
155	Haplotype diversity and sequence heterogeneity of human telomeres. <i>Genome Research</i> , 2021, 31, 1269-1279.	2.4	19
156	Genomic Changes Driven by Radiation-Induced DNA Damage and Microgravity in Human Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10507.	1.8	19
157	Ratio-Based Method To Identify True Biomarkers by Normalizing Circulating ncRNA Sequencing and Quantitative PCR Data. <i>Analytical Chemistry</i> , 2019, 91, 6746-6753.	3.2	18
158	BCL6 maintains survival and self-renewal of primary human acute myeloid leukemia cells. <i>Blood</i> , 2021, 137, 812-825.	0.6	18
159	Advancing the Integration of Biosciences Data Sharing to Further Enable Space Exploration. <i>Cell Reports</i> , 2020, 33, 108441.	2.9	17
160	Sequencing of Circulating Microbial Cell-Free DNA Can Identify Pathogens in Periprosthetic Joint Infections. <i>Journal of Bone and Joint Surgery - Series A</i> , 2021, 103, 1705-1712.	1.4	17
161	Resource: A multi-species multi-timepoint transcriptome database and webpage for the pineal gland and retina. <i>Journal of Pineal Research</i> , 2020, 69, e12673.	3.4	16
162	A comprehensive metagenomics framework to characterize organisms relevant for planetary protection. <i>Microbiome</i> , 2021, 9, 82.	4.9	15

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163	The Microbe Directory: An annotated, searchable inventory of microbesâ€™ characteristics. Gates Open Research, 2018, 2, 3.	2.0	15
164	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
165	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. Scientific Data, 2021, 8, 296.	2.4	15
166	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
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