

Christopher E. Mason

List of Publications by Year in descending order

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242
papers

30,851
citations

12330
69
h-index

6131
159
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. Cell, 2012, 149, 1635-1646.	28.9	3,152
2	RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays. Genome Research, 2008, 18, 1509-1517.	5.5	2,393
3	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
4	methyKit: a comprehensive R package for the analysis of genome-wide DNA methylation profiles. Genome Biology, 2012, 13, R87.	9.6	1,541
5	Single-nucleotide-resolution mapping of m6A and m6Am throughout the transcriptome. Nature Methods, 2015, 12, 767-772.	19.0	1,157
6	Multiple Recurrent De Novo CNVs, Including Duplications of the 7q11.23 Williams Syndrome Region, Are Strongly Associated with Autism. Neuron, 2011, 70, 863-885.	8.1	1,146
7	The N6-methyladenosine (m6A)-forming enzyme METTL3 controls myeloid differentiation of normal hematopoietic and leukemia cells. Nature Medicine, 2017, 23, 1369-1376.	30.7	971
8	Recurrent somatic TET2 mutations in normal elderly individuals with clonal hematopoiesis. Nature Genetics, 2012, 44, 1179-1181.	21.4	692
9	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	30.7	604
10	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. Science, 2019, 364, .	12.6	576
11	Extensive sequencing of seven human genomes to characterize benchmark reference materials. Scientific Data, 2016, 3, 160025.	5.3	575
12	Assembly and diploid architecture of an individual human genome via single-molecule technologies. Nature Methods, 2015, 12, 780-786.	19.0	465
13	The birth of the Epitranscriptome: deciphering the function of RNA modifications. Genome Biology, 2012, 13, 175.	9.6	375
14	Dynamics of the human and viral m6A RNA methylomes during HIV-1 infection of T cells. Nature Microbiology, 2016, 1, 16011.	13.3	373
15	N6 -Methyladenosine in Flaviviridae Viral RNA Genomes Regulates Infection. Cell Host and Microbe, 2016, 20, 654-665.	11.0	370
16	Distinct evolution and dynamics of epigenetic and genetic heterogeneity in acute myeloid leukemia. Nature Medicine, 2016, 22, 792-799.	30.7	322
17	Accurate detection of m6A RNA modifications in native RNA sequences. Nature Communications, 2019, 10, 4079.	12.8	322
18	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. Nature Communications, 2014, 5, 3230.	12.8	316

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19	The Pivotal Regulatory Landscape of RNA Modifications. Annual Review of Genomics and Human Genetics, 2014, 15, 127-150.	6.2	284
20	Best practices for benchmarking germline small-variant calls in human genomes. Nature Biotechnology, 2019, 37, 555-560.	17.5	273
21	Relapse-specific mutations in NT5C2 in childhood acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 290-294.	21.4	264
22	Nanopore DNA Sequencing and Genome Assembly on the International Space Station. Scientific Reports, 2017, 7, 18022.	3.3	264
23	Base-Pair Resolution DNA Methylation Sequencing Reveals Profoundly Divergent Epigenetic Landscapes in Acute Myeloid Leukemia. PLoS Genetics, 2012, 8, e1002781.	3.5	263
24	genomation: a toolkit to summarize, annotate and visualize genomic intervals. Bioinformatics, 2015, 31, 1127-1129.	4.1	263
25	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. Genome Biology, 2017, 18, 182.	8.8	260
26	Immune complement and coagulation dysfunction in adverse outcomes of SARS-CoV-2 infection. Nature Medicine, 2020, 26, 1609-1615.	30.7	255
27	The spatial landscape of lung pathology during COVID-19 progression. Nature, 2021, 593, 564-569.	27.8	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.	9.4	247
29	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. Cell Systems, 2015, 1, 72-87.	6.2	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.	6.4	237
31	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
32	Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study. Nature Biotechnology, 2014, 32, 915-925.	17.5	217
33	Viral Dynamics of SARS-CoV-2 Variants in Vaccinated and Unvaccinated Persons. New England Journal of Medicine, 2021, 385, 2489-2491.	27.0	216
34	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. PLoS Biology, 2021, 19, e3001236.	5.6	200
35	DNMT3A mutations promote anthracycline resistance in acute myeloid leukemia via impaired nucleosome remodeling. Nature Medicine, 2016, 22, 1488-1495.	30.7	195
36	Mutational Cooperativity Linked to Combinatorial Epigenetic Gain of Function in Acute Myeloid Leukemia. Cancer Cell, 2015, 27, 502-515.	16.8	191

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37	Fundamental Biological Features of Spaceflight: Advancing the Field to Enable Deep-Space Exploration. Cell, 2020, 183, 1162-1184.	28.9	185
38	Detecting and correcting systematic variation in large-scale RNA sequencing data. Nature Biotechnology, 2014, 32, 888-895.	17.5	174
39	Large-scale differences in microbial biodiversity discovery between 16S amplicon and shotgun sequencing. Scientific Reports, 2017, 7, 6589.	3.3	174
40	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
41	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.	7.1	164
42	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	28.9	164
43	A Hybrid Mechanism of Action for BCL6 in B Cells Defined by Formation of Functionally Distinct Complexes at Enhancers and Promoters. Cell Reports, 2013, 4, 578-588.	6.4	161
44	Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact. Cell, 2020, 183, 1185-1201.e20.	28.9	161
45	A benchmark for RNA-seq quantification pipelines. Genome Biology, 2016, 17, 74.	8.8	160
46	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. Nature, 2021, 589, 299-305.	27.8	155
47	The therapeutic landscape for cells engineered with chimeric antigen receptors. Nature Biotechnology, 2020, 38, 233-244.	17.5	147
48	Limits in the detection of m6A changes using MeRIP/m6A-seq. Scientific Reports, 2020, 10, 6590.	3.3	136
49	Good laboratory practice for clinical next-generation sequencing informatics pipelines. Nature Biotechnology, 2015, 33, 689-693.	17.5	134
50	Chemotherapy Induces Senescence-Like Resilient Cells Capable of Initiating AML Recurrence. Cancer Discovery, 2021, 11, 1542-1561.	9.4	133
51	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.	12.8	132
52	Single-molecule sequencing detection of N6-methyladenine in microbial reference materials. Nature Communications, 2019, 10, 579.	12.8	131
53	Genetic and epigenetic heterogeneity in acute myeloid leukemia. Current Opinion in Genetics and Development, 2016, 36, 100-106.	3.3	130
54	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nature Medicine, 2020, 26, 941-951.	30.7	130

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55	ketu mutant mice uncover an essential meiotic function for the ancient RNA helicase YTHDC2. ELife, 2018, 7, .	6.0	129
56	Altered m6A Modification of Specific Cellular Transcripts Affects Flaviviridae Infection. Molecular Cell, 2020, 77, 542-555.e8.	9.7	129
57	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	17.5	126
58	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
59	Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States. Cell, 2021, 184, 2595-2604.e13.	28.9	113
60	Direct RNA sequencing reveals m6A modifications on adenovirus RNA are necessary for efficient splicing. Nature Communications, 2020, 11, 6016.	12.8	111
61	Urban metagenomics uncover antibiotic resistance reservoirs in coastal beach and sewage waters. Microbiome, 2019, 7, 35.	11.1	109
62	An optimized algorithm for detecting and annotating regional differential methylation. BMC Bioinformatics, 2013, 14, S10.	2.6	105
63	The impact of read length on quantification of differentially expressed genes and splice junction detection. Genome Biology, 2015, 16, 131.	8.8	98
64	Loss of CHD1 Promotes Heterogeneous Mechanisms of Resistance to AR-Targeted Therapy via Chromatin Dysregulation. Cancer Cell, 2020, 37, 584-598.e11.	16.8	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. Cancer Discovery, 2017, 7, 494-505.	9.4	94
66	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. Cancer Cell, 2020, 37, 655-673.e11.	16.8	93
67	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	17.5	90
68	Enhanced Reduced Representation Bisulfite Sequencing for Assessment of DNA Methylation at Base Pair Resolution. Journal of Visualized Experiments, 2015, , e52246.	0.3	89
69	Investigation of product-derived lymphoma following infusion of <i>piggyBac</i>-modified CD19 chimeric antigen receptor T cells. Blood, 2021, 138, 1391-1405.	1.4	87
70	DNA methylation-calling tools for Oxford Nanopore sequencing: a survey and human epigenome-wide evaluation. Genome Biology, 2021, 22, 295.	8.8	87
71	The Impact of Heterogeneity on Single-Cell Sequencing. Frontiers in Genetics, 2019, 10, 8.	2.3	84
72	Sooty mangabey genome sequence provides insight into AIDS resistance in a natural SIV host. Nature, 2018, 553, 77-81.	27.8	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.	3.3	81
74	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , 2016, 7, 10164.	12.8	79
75	A diagnostic host response biosignature for COVID-19 from RNA profiling of nasal swabs and blood. <i>Science Advances</i> , 2021, 7, .	10.3	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.	7.1	77
77	Nanopore sequencing in microgravity. <i>Npj Microgravity</i> , 2016, 2, 16035.	3.7	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.	12.8	73
79	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. <i>Nature Biotechnology</i> , 2020, 38, 1021-1024.	17.5	71
80	miR-29a maintains mouse hematopoietic stem cell self-renewal by regulating Dnmt3a. <i>Blood</i> , 2015, 125, 2206-2216.	1.4	70
81	PGBD5 promotes site-specific oncogenic mutations in human tumors. <i>Nature Genetics</i> , 2017, 49, 1005-1014.	21.4	69
82	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. <i>Nature Biotechnology</i> , 2021, 39, 1129-1140.	17.5	69
83	Dynamic evolution of clonal epialleles revealed by methclone. <i>Genome Biology</i> , 2014, 15, 472.	8.8	67
84	Genomic DNA transposition induced by human PGBD5. <i>ELife</i> , 2015, 4, .	6.0	67
85	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1141-1150.	17.5	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.	14.5	61
87	Long-term spaceflight and the cardiovascular system. <i>Precision Clinical Medicine</i> , 2020, 3, 284-291.	3.3	60
88	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020, 7, 170.	5.3	59
89	International community consensus standard for reporting derivation of human embryonic stem cell lines. <i>Regenerative Medicine</i> , 2007, 2, 349-362.	1.7	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.	11.1	58

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91	Epigenetic Modifications in Acute Myeloid Leukemia: Prognosis, Treatment, and Heterogeneity. <i>Frontiers in Genetics</i> , 2019, 10, 133.	2.3	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.	3.5	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.	1.5	53
94	The case for biotech on Mars. <i>Nature Biotechnology</i> , 2020, 38, 401-407.	17.5	53
95	Role of miR-2392 in driving SARS-CoV-2 infection. <i>Cell Reports</i> , 2021, 37, 109839.	6.4	52
96	The Power of Engaging Citizen Scientists for Scientific Progress. <i>Journal of Microbiology and Biology Education</i> , 2016, 17, 7-12.	1.0	49
97	Charting the unknown epitranscriptome. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 339-340.	37.0	49
98	Telomere Length Dynamics and DNA Damage Responses Associated with Long-Duration Spaceflight. <i>Cell Reports</i> , 2020, 33, 108457.	6.4	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.	1.5	47
100	COVID-19 drug practices risk antimicrobial resistance evolution. <i>Lancet Microbe</i> , The, 2021, 2, e135-e136.	7.3	47
101	Post-transcriptional regulation of antiviral gene expression by N6-methyladenosine. <i>Cell Reports</i> , 2021, 34, 108798.	6.4	46
102	<i>Methylobacterium ajmalii</i> sp. nov., Isolated From the International Space Station. <i>Frontiers in Microbiology</i> , 2021, 12, 639396.	3.5	46
103	Rapid antigen diversification through mitotic recombination in the human malaria parasite <i>Plasmodium falciparum</i> . <i>PLoS Biology</i> , 2019, 17, e3000271.	5.6	44
104	Temporal Telomere and DNA Damage Responses in the Space Radiation Environment. <i>Cell Reports</i> , 2020, 33, 108435.	6.4	40
105	Novel RNA regulatory mechanisms revealed in the epitranscriptome. <i>RNA Biology</i> , 2013, 10, 342-346.	3.1	39
106	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. <i>Genome Research</i> , 2021, 31, 635-644.	5.5	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.	17.5	39
108	Faster sequencers, larger datasets, new challenges. <i>Genome Biology</i> , 2012, 13, 314.	9.6	38

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109	Forensic Applications of Microbiomics: A Review. <i>Frontiers in Microbiology</i> , 2020, 11, 608101.	3.5	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.	6.4	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.	3.5	36
112	Lessons learned from SARS-CoV-2 measurements in wastewater. <i>Science of the Total Environment</i> , 2021, 798, 149177.	8.0	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.	2.7	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.	2.5	35
115	Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. <i>Cell Reports</i> , 2020, 33, 108448.	6.4	35
116	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	19.0	35
117	Assessment of pharmacogenomic agreement. <i>F1000Research</i> , 2016, 5, 825.	1.6	34
118	International Standards for Genomes, Transcriptomes, and Metagenomes. <i>Journal of Biomolecular Techniques</i> , 2017, 28, 8-18.	1.5	33
119	Laminin regulates PDGFR β cell stemness and muscle development. <i>Nature Communications</i> , 2016, 7, 11415.	12.8	32
120	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. <i>Nature Biotechnology</i> , 2017, 35, 1127-1128.	17.5	32
121	Metagenomic characterization of ambulances across the USA. <i>Microbiome</i> , 2017, 5, 125.	11.1	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.	3.1	31
123	Genetic and epigenetic heterogeneity and the impact on cancer relapse. <i>Experimental Hematology</i> , 2017, 54, 26-30.	0.4	31
124	Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers. <i>IScience</i> , 2020, 23, 101844.	4.1	31
125	Pre- and peri-implantation Zika virus infection impairs fetal development by targeting trophectoderm cells. <i>Nature Communications</i> , 2019, 10, 4155.	12.8	30
126	Clonal Hematopoiesis Before, During, and After Human Spaceflight. <i>Cell Reports</i> , 2020, 33, 108458.	6.4	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.	8.8	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.	12.8	29
129	Characterizing Multi-omic Data in Systems Biology. <i>Advances in Experimental Medicine and Biology</i> , 2014, 799, 15-38.	1.6	28
130	A New Era for Space Life Science: International Standards for Space Omics Processing. <i>Patterns</i> , 2020, 1, 100148.	5.9	28
131	Transcriptional response modules characterize IL-1 β and IL-6 activity in COVID-19. <i>IScience</i> , 2021, 24, 101896.	4.1	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.	7.2	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.	1.5	28
134	Chromosome End Repair and Genome Stability in <i>Plasmodium falciparum</i> . <i>MBio</i> , 2017, 8, .	4.1	27
135	Communicating the promise, risks, and ethics of large-scale, open space microbiome and metagenome research. <i>Microbiome</i> , 2017, 5, 132.	11.1	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.	11.2	26
137	Pervasive sequence patents cover the entire human genome. <i>Genome Medicine</i> , 2013, 5, 27.	8.2	25
138	Co-occurrence patterns of bacteria within microbiome of Moscow subway. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 314-322.	4.1	25
139	Translating current biomedical therapies for long duration, deep space missions. <i>Precision Clinical Medicine</i> , 2019, 2, 259-269.	3.3	24
140	Smc3 dosage regulates B cell transit through germinal centers and restricts their malignant transformation. <i>Nature Immunology</i> , 2021, 22, 240-253.	14.5	24
141	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. <i>Cell Reports Medicine</i> , 2022, 3, 100522.	6.5	24
142	Genomic approaches to the assessment of human spina bifida risk. <i>Birth Defects Research</i> , 2017, 109, 120-128.	1.5	23
143	Somatic Mutations Drive Specific, but Reversible, Epigenetic Heterogeneity States in AML. <i>Cancer Discovery</i> , 2020, 10, 1934-1949.	9.4	23
144	Globalizing and crowdsourcing biomedical research. <i>British Medical Bulletin</i> , 2016, 120, 27-33.	6.9	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.	3.0	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.	3.5	22
147	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. <i>Scientific Data</i> , 2014, 1, 140020.	5.3	21
148	Minerva: an alignment- and reference-free approach to deconvolve Linked-Reads for metagenomics. <i>Genome Research</i> , 2019, 29, 116-124.	5.5	21
149	End-to-End Protocol for the Detection of SARS-CoV-2 from Built Environments. <i>MSystems</i> , 2020, 5, .	3.8	21
150	Modern Methods for Delineating Metagenomic Complexity. <i>Cell Systems</i> , 2015, 1, 6-7.	6.2	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.	8.8	20
152	The SEQC2 epigenomics quality control (EpiQC) study. <i>Genome Biology</i> , 2021, 22, 332.	8.8	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.	0.4	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.	1.5	19
155	Haplotype diversity and sequence heterogeneity of human telomeres. <i>Genome Research</i> , 2021, 31, 1269-1279.	5.5	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.	4.1	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.	6.5	18
158	BCL6 maintains survival and self-renewal of primary human acute myeloid leukemia cells. <i>Blood</i> , 2021, 137, 812-825.	1.4	18
159	Advancing the Integration of Biosciences Data Sharing to Further Enable Space Exploration. <i>Cell Reports</i> , 2020, 33, 108441.	6.4	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.	3.0	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.	7.4	16
162	A comprehensive metagenomics framework to characterize organisms relevant for planetary protection. <i>Microbiome</i> , 2021, 9, 82.	11.1	15

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163	The Microbe Directory: An annotated, searchable inventory of microbes™ characteristics. Gates Open Research, 2018, 2, 3.	1.1	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.	1.5	15
165	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. Scientific Data, 2021, 8, 296.	5.3	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.	4.6	15
167	QuaPra: Efficient transcript assembly and quantification using quadratic programming with Apriori algorithm. Science China Life Sciences, 2019, 62, 937-946.	4.9	14
168	Diurnal variation in the human skin microbiome affects accuracy of forensic microbiome matching. Microbiome, 2021, 9, 129.	11.1	14
169	SETD2 Haploinsufficiency Enhances Germinal Center-Associated AICDA Somatic Hypermutation to Drive B-cell Lymphomagenesis. Cancer Discovery, 2022, 12, 1782-1803.	9.4	14
170	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.	1.7	13
171	Clinical Genomics: Challenges and Opportunities. Critical Reviews in Eukaryotic Gene Expression, 2016, 26, 97-113.	0.9	12
172	Improved gastrointestinal health for irritable bowel syndrome with metagenome-guided interventions. Precision Clinical Medicine, 2020, 3, 136-146.	3.3	12
173	Betacoronavirus-specific alternate splicing. Genomics, 2022, 114, 110270.	2.9	12
174	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.	0.8	11
175	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, .	7.1	11
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