

# Christopher E. Mason

## List of Publications by Citations

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

258  
papers

19,397  
citations

57  
h-index

137  
g-index

314  
ext. papers

26,163  
ext. citations

14.7  
avg, IF

6.68  
L-index

#	Paper	IF	Citations
258	Comprehensive analysis of mRNA methylation reveals enrichment in 3' UTRs and near stop codons. <i>Cell</i> , <b>2012</b> , 149, 1635-46	56.2	2100
257	RNA-seq: an assessment of technical reproducibility and comparison with gene expression arrays. <i>Genome Research</i> , <b>2008</b> , 18, 1509-17	9.7	2051
256	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , <b>2015</b> , 526, 75-81	50.4	1368
255	Multiple recurrent de novo CNVs, including duplications of the 7q11.23 Williams syndrome region, are strongly associated with autism. <i>Neuron</i> , <b>2011</b> , 70, 863-85	13.9	932
254	methylKit: a comprehensive R package for the analysis of genome-wide DNA methylation profiles. <i>Genome Biology</i> , <b>2012</b> , 13, R87	18.3	893
253	Single-nucleotide-resolution mapping of m6A and m6Am throughout the transcriptome. <i>Nature Methods</i> , <b>2015</b> , 12, 767-72	21.6	774
252	The N-methyladenosine (m <sup>6</sup> A)-forming enzyme METTL3 controls myeloid differentiation of normal hematopoietic and leukemia cells. <i>Nature Medicine</i> , <b>2017</b> , 23, 1369-1376	50.5	584
251	Recurrent somatic TET2 mutations in normal elderly individuals with clonal hematopoiesis. <i>Nature Genetics</i> , <b>2012</b> , 44, 1179-81	36.3	552
250	Toward understanding and exploiting tumor heterogeneity. <i>Nature Medicine</i> , <b>2015</b> , 21, 846-53	50.5	441
249	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , <b>2015</b> , 12, 780-6	21.6	383
248	Extensive sequencing of seven human genomes to characterize benchmark reference materials. <i>Scientific Data</i> , <b>2016</b> , 3, 160025	8.2	345
247	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. <i>Science</i> , <b>2019</b> , 364,	33.3	300
246	The birth of the Epitranscriptome: deciphering the function of RNA modifications. <i>Genome Biology</i> , <b>2012</b> , 13, 175	18.3	275
245	Dynamics of the human and viral m(6)A RNA methylomes during HIV-1 infection of T cells. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16011	26.6	262
244	N6-Methyladenosine in Flaviviridae Viral RNA Genomes Regulates Infection. <i>Cell Host and Microbe</i> , <b>2016</b> , 20, 654-665	23.4	244
243	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. <i>Nature Communications</i> , <b>2014</b> , 5, 3230	17.4	225
242	Base-pair resolution DNA methylation sequencing reveals profoundly divergent epigenetic landscapes in acute myeloid leukemia. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002781	6	223

241	Distinct evolution and dynamics of epigenetic and genetic heterogeneity in acute myeloid leukemia. <i>Nature Medicine</i> , <b>2016</b> , 22, 792-9	50.5	217
240	Relapse-specific mutations in NT5C2 in childhood acute lymphoblastic leukemia. <i>Nature Genetics</i> , <b>2013</b> , 45, 290-4	36.3	216
239	Cell-cycle reprogramming for PI3K inhibition overrides a relapse-specific C481S BTK mutation revealed by longitudinal functional genomics in mantle cell lymphoma. <i>Cancer Discovery</i> , <b>2014</b> , 4, 1022-35	34.4	203
238	The pivotal regulatory landscape of RNA modifications. <i>Annual Review of Genomics and Human Genetics</i> , <b>2014</b> , 15, 127-50	9.7	203
237	DNA hydroxymethylation profiling reveals that WT1 mutations result in loss of TET2 function in acute myeloid leukemia. <i>Cell Reports</i> , <b>2014</b> , 9, 1841-1855	10.6	183
236	Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 915-925	44.5	169
235	Accurate detection of mA RNA modifications in native RNA sequences. <i>Nature Communications</i> , <b>2019</b> , 10, 4079	17.4	166
234	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. <i>Cell Systems</i> , <b>2015</b> , 1, 72-87	10.6	164
233	Nanopore DNA Sequencing and Genome Assembly on the International Space Station. <i>Scientific Reports</i> , <b>2017</b> , 7, 18022	4.9	162
232	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. <i>Genome Biology</i> , <b>2017</b> , 18, 182	18.3	152
231	Mutational cooperativity linked to combinatorial epigenetic gain of function in acute myeloid leukemia. <i>Cancer Cell</i> , <b>2015</b> , 27, 502-15	24.3	145
230	Immune complement and coagulation dysfunction in adverse outcomes of SARS-CoV-2 infection. <i>Nature Medicine</i> , <b>2020</b> , 26, 1609-1615	50.5	142
229	DNMT3A mutations promote anthracycline resistance in acute myeloid leukemia via impaired nucleosome remodeling. <i>Nature Medicine</i> , <b>2016</b> , 22, 1488-1495	50.5	140
228	Genomation: a toolkit to summarize, annotate and visualize genomic intervals. <i>Bioinformatics</i> , <b>2015</b> , 31, 1127-9	7.2	137
227	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> , <b>2013</b> , 4, 578-88	10.6	127
226	Best practices for benchmarking germline small-variant calls in human genomes. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 555-560	44.5	125
225	Detecting and correcting systematic variation in large-scale RNA sequencing data. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 888-95	44.5	125
224	A benchmark for RNA-seq quantification pipelines. <i>Genome Biology</i> , <b>2016</b> , 17, 74	18.3	117

223	Good laboratory practice for clinical next-generation sequencing informatics pipelines. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 689-93	44.5	115
222	Large-scale differences in microbial biodiversity discovery between 16S amplicon and shotgun sequencing. <i>Scientific Reports</i> , <b>2017</b> , 7, 6589	4.9	110
221	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1347-1355	44.5	98
220	mutant mice uncover an essential meiotic function for the ancient RNA helicase YTHDC2. <i>ELife</i> , <b>2018</b> , 7,	8.9	93
219	-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> , <b>2018</b> , 115, 8829-8834	11.5	91
218	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , <b>2014</b> , 5, 5125	17.4	89
217	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. <i>PLoS Biology</i> , <b>2021</b> , 19, e3001236	9.7	85
216	Genetic and epigenetic heterogeneity in acute myeloid leukemia. <i>Current Opinion in Genetics and Development</i> , <b>2016</b> , 36, 100-6	4.9	79
215	An optimized algorithm for detecting and annotating regional differential methylation. <i>BMC Bioinformatics</i> , <b>2013</b> , 14 Suppl 5, S10	3.6	78
214	1154. Comparison of Five Testing Modalities for the Assessment of Patient Environment Cleanliness. <i>Open Forum Infectious Diseases</i> , <b>2018</b> , 5, S347-S347	1	78
213	Single-molecule sequencing detection of N6-methyladenine in microbial reference materials. <i>Nature Communications</i> , <b>2019</b> , 10, 579	17.4	77
212	Viral dynamics of SARS-CoV-2 variants in vaccinated and unvaccinated individuals		76
211	The therapeutic landscape for cells engineered with chimeric antigen receptors. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 233-244	44.5	75
210	The spatial landscape of lung pathology during COVID-19 progression. <i>Nature</i> , <b>2021</b> , 593, 564-569	50.4	72
209	Limits in the detection of mA changes using MeRIP/mA-seq. <i>Scientific Reports</i> , <b>2020</b> , 10, 6590	4.9	71
208	Combination Targeted Therapy to Disrupt Aberrant Oncogenic Signaling and Reverse Epigenetic Dysfunction in - and -Mutant Acute Myeloid Leukemia. <i>Cancer Discovery</i> , <b>2017</b> , 7, 494-505	24.4	68
207	The impact of read length on quantification of differentially expressed genes and splice junction detection. <i>Genome Biology</i> , <b>2015</b> , 16, 131	18.3	67
206	Altered mA Modification of Specific Cellular Transcripts Affects Flaviviridae Infection. <i>Molecular Cell</i> , <b>2020</b> , 77, 542-555.e8	17.6	66

205	Enhanced reduced representation bisulfite sequencing for assessment of DNA methylation at base pair resolution. <i>Journal of Visualized Experiments</i> , <b>2015</b> , e52246	1.6	65
204	Viral Dynamics of SARS-CoV-2 Variants in Vaccinated and Unvaccinated Persons.. <i>New England Journal of Medicine</i> , <b>2021</b> , 385, 2489-2491	59.2	63
203	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> , <b>2021</b> , 12, 1660	17.4	60
202	Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact. <i>Cell</i> , <b>2020</b> , 183, 1185-1201.e20	56.2	58
201	Urban metagenomics uncover antibiotic resistance reservoirs in coastal beach and sewage waters. <i>Microbiome</i> , <b>2019</b> , 7, 35	16.6	57
200	Sooty mangabey genome sequence provides insight into AIDS resistance in a natural SIV host. <i>Nature</i> , <b>2018</b> , 553, 77-81	50.4	57
199	miR-29a maintains mouse hematopoietic stem cell self-renewal by regulating Dnmt3a. <i>Blood</i> , <b>2015</b> , 125, 2206-16	2.2	57
198	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. <i>Nature</i> , <b>2021</b> , 589, 299-305	50.4	56
197	Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States. <i>Cell</i> , <b>2021</b> , 184, 2595-2604.e13	56.2	55
196	International community consensus standard for reporting derivation of human embryonic stem cell lines. <i>Regenerative Medicine</i> , <b>2007</b> , 2, 349-62	2.5	54
195	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> , <b>2016</b> , 113, 12697-12702	11.5	52
194	Shotgun Transcriptome and Isothermal Profiling of SARS-CoV-2 Infection Reveals Unique Host Responses, Viral Diversification, and Drug Interactions <b>2020</b> ,		51
193	Direct RNA sequencing reveals mA modifications on adenovirus RNA are necessary for efficient splicing. <i>Nature Communications</i> , <b>2020</b> , 11, 6016	17.4	51
192	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , <b>2020</b> , 26, 941-951	50.5	50
191	Nanopore sequencing in microgravity. <i>Npj Microgravity</i> , <b>2016</b> , 2, 16035	5.3	50
190	Fundamental Biological Features of Spaceflight: Advancing the Field to Enable Deep-Space Exploration. <i>Cell</i> , <b>2020</b> , 183, 1162-1184	56.2	50
189	Long non-coding RNAs discriminate the stages and gene regulatory states of human humoral immune response. <i>Nature Communications</i> , <b>2019</b> , 10, 821	17.4	49
188	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> , <b>2018</b> , 18, 175	4.5	49

187	Dynamic evolution of clonal epialleles revealed by methclone. <i>Genome Biology</i> , <b>2014</b> , 15, 472	18.3	48
186	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. <i>Cancer Cell</i> , <b>2020</b> , 37, 655-673.e11	24.3	47
185	Genomic DNA transposition induced by human PGBD5. <i>ELife</i> , <b>2015</b> , 4,	8.9	47
184	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , <b>2016</b> , 7, 10164	17.4	46
183	Tissue-specific transcriptome sequencing analysis expands the non-human primate reference transcriptome resource (NHPRTR). <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D737-42	20.1	46
182	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1021-1024	44.5	45
181	The Impact of Heterogeneity on Single-Cell Sequencing. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 8	4.5	43
180	Loss of CHD1 Promotes Heterogeneous Mechanisms of Resistance to AR-Targeted Therapy via Chromatin Dysregulation. <i>Cancer Cell</i> , <b>2020</b> , 37, 584-598.e11	24.3	42
179	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , <b>2021</b> , 184, 3376-3393.e17	35.1	42
178	PGBD5 promotes site-specific oncogenic mutations in human tumors. <i>Nature Genetics</i> , <b>2017</b> , 49, 1005-1014	3.3	40
177	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> , <b>2017</b> , 13, e1006964	6	40
176	Epigenetic Modifications in Acute Myeloid Leukemia: Prognosis, Treatment, and Heterogeneity. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 133	4.5	38
175	Jak1 Integrates Cytokine Sensing to Regulate Hematopoietic Stem Cell Function and Stress Hematopoiesis. <i>Cell Stem Cell</i> , <b>2017</b> , 21, 489-501.e7	18	35
174	A robust benchmark for germline structural variant detection		34
173	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). <i>Journal of Biomolecular Techniques</i> , <b>2017</b> , 28, 31-39	1.1	31
172	Novel RNA regulatory mechanisms revealed in the epitranscriptome. <i>RNA Biology</i> , <b>2013</b> , 10, 342-6	4.8	31
171	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 1115-1128	44.5	31
170	Charting the unknown epitranscriptome. <i>Nature Reviews Molecular Cell Biology</i> , <b>2017</b> , 18, 339-340	48.7	30

169	Chemotherapy Induces Senescence-Like Resilient Cells Capable of Initiating AML Recurrence. <i>Cancer Discovery</i> , <b>2021</b> , 11, 1542-1561	24.4	30
168	Laminin regulates PDGFR(+) cell stemness and muscle development. <i>Nature Communications</i> , <b>2016</b> , 7, 11415	17.4	29
167	Faster sequencers, larger datasets, new challenges. <i>Genome Biology</i> , <b>2012</b> , 13, 314	18.3	29
166	Precision Metagenomics: Rapid Metagenomic Analyses for Infectious Disease Diagnostics and Public Health Surveillance. <i>Journal of Biomolecular Techniques</i> , <b>2017</b> , 28, 40-45	1.1	28
165	Genome Sequence and Analysis of Escherichia coli MRE600, a Colicinogenic, Nonmotile Strain that Lacks RNase I and the Type I Methyltransferase, EcoKI. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 742-52	3.9	27
164	Investigation of product-derived lymphoma following infusion of piggyBac-modified CD19 chimeric antigen receptor T cells. <i>Blood</i> , <b>2021</b> , 138, 1391-1405	2.2	26
163	The Power of Engaging Citizen Scientists for Scientific Progress. <i>Journal of Microbiology and Biology Education</i> , <b>2016</b> , 17, 7-12	1.3	25
162	Assessment of pharmacogenomic agreement. <i>F1000Research</i> , <b>2016</b> , 5, 825	3.6	25
161	Mining the Archives: A Cross-Platform Analysis of Gene Expression Profiles in Archival Formalin-Fixed Paraffin-Embedded Tissues. <i>Toxicological Sciences</i> , <b>2015</b> , 148, 460-72	4.4	24
160	Rapid antigen diversification through mitotic recombination in the human malaria parasite Plasmodium falciparum. <i>PLoS Biology</i> , <b>2019</b> , 17, e3000271	9.7	23
159	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 1127-1128	44.5	23
158	Genetic and epigenetic heterogeneity and the impact on cancer relapse. <i>Experimental Hematology</i> , <b>2017</b> , 54, 26-30	3.1	22
157	A diagnostic host response biosignature for COVID-19 from RNA profiling of nasal swabs and blood. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	22
156	The case for biotech on Mars. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 401-407	44.5	21
155	International Standards for Genomes, Transcriptomes, and Metagenomes. <i>Journal of Biomolecular Techniques</i> , <b>2017</b> , 28, 8-18	1.1	21
154	Characterizing multi-omic data in systems biology. <i>Advances in Experimental Medicine and Biology</i> , <b>2014</b> , 799, 15-38	3.6	21
153	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , <b>2020</b> , 7, 170	8.2	20
152	Pervasive sequence patents cover the entire human genome. <i>Genome Medicine</i> , <b>2013</b> , 5, 27	14.4	20

151	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. <i>Genome Research</i> , <b>2021</b> , 31, 635-644	9.7	20
150	Pre- and peri-implantation Zika virus infection impairs fetal development by targeting trophectoderm cells. <i>Nature Communications</i> , <b>2019</b> , 10, 4155	17.4	19
149	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , <b>2021</b> , 27, 1885-1892	50.5	19
148	Complex translocation disrupting TCF4 and altering TCF4 isoform expression segregates as mild autosomal dominant intellectual disability. <i>Orphanet Journal of Rare Diseases</i> , <b>2016</b> , 11, 62	4.2	19
147	Communicating the promise, risks, and ethics of large-scale, open space microbiome and metagenome research. <i>Microbiome</i> , <b>2017</b> , 5, 132	16.6	18
146	Chromosome End Repair and Genome Stability in. <i>MBio</i> , <b>2017</b> , 8,	7.8	18
145	Viral dynamics and duration of PCR positivity of the SARS-CoV-2 Omicron variant		18
144	Temporal Telomere and DNA Damage Responses in the Space Radiation Environment. <i>Cell Reports</i> , <b>2020</b> , 33, 108435	10.6	17
143	The Microbiomes of Seven Lichen Genera Reveal Host Specificity, a Reduced Core Community and Potential as Source of Antimicrobials. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 398	5.7	17
142	Metagenomic characterization of ambulances across the USA. <i>Microbiome</i> , <b>2017</b> , 5, 125	16.6	17
141	COVID-19 drug practices risk antimicrobial resistance evolution. <i>Lancet Microbe</i> , <b>2021</b> , 2, e135-e136		17
140	A New Era for Space Life Science: International Standards for Space Omics Processing. <i>Patterns</i> , <b>2020</b> , 1, 100148	5.1	16
139	Long-term spaceflight and the cardiovascular system. <i>Precision Clinical Medicine</i> , <b>2020</b> , 3, 284-291	6.7	16
138	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. <i>Scientific Data</i> , <b>2014</b> , 1, 140020	8.2	16
137	Global Genetic Cartography of Urban Metagenomes and Anti-Microbial Resistance		16
136	The complete mitochondrial genome of the neotropical helicopter damselfly (Odonata: Zygoptera) assembled from next generation sequencing data. <i>Mitochondrial DNA Part B: Resources</i> , <b>2016</b> , 1, 497-499	0.5	15
135	Globalizing and crowdsourcing biomedical research. <i>British Medical Bulletin</i> , <b>2016</b> , 120, 27-33	5.4	15
134	Genomic approaches to the assessment of human spina bifida risk. <i>Birth Defects Research</i> , <b>2017</b> , 109, 120-128	2.9	14

133	Multi-omic, Single-Cell, and Biochemical Profiles of Astronauts Guide Pharmacological Strategies for Returning to Gravity. <i>Cell Reports</i> , <b>2020</b> , 33, 108429	10.6	14
132	Telomere Length Dynamics and DNA Damage Responses Associated with Long-Duration Spaceflight. <i>Cell Reports</i> , <b>2020</b> , 33, 108457	10.6	14
131	Transcriptional response modules characterize IL-1 $\beta$ and IL-6 activity in COVID-19. <i>IScience</i> , <b>2021</b> , 24, 101896	6.1	14
130	Modern Methods for Delineating Metagenomic Complexity. <i>Cell Systems</i> , <b>2015</b> , 1, 6-7	10.6	13
129	Hidden genomic diversity of SARS-CoV-2: implications for qRT-PCR diagnostics and transmission <b>2020</b> ,		13
128	Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. <i>Cell Reports</i> , <b>2020</b> , 33, 108448	10.6	13
127	Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers. <i>IScience</i> , <b>2020</b> , 23, 101844	6.1	13
126	sp. nov., Isolated From the International Space Station. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 639396	5.7	13
125	Curated variation benchmarks for challenging medically relevant autosomal genes.. <i>Nature Biotechnology</i> , <b>2022</b> ,	44.5	12
124	Post-transcriptional regulation of antiviral gene expression by N6-methyladenosine. <i>Cell Reports</i> , <b>2021</b> , 34, 108798	10.6	12
123	Translating current biomedical therapies for long duration, deep space missions. <i>Precision Clinical Medicine</i> , <b>2019</b> , 2, 259-269	6.7	12
122	Smc3 dosage regulates B cell transit through germinal centers and restricts their malignant transformation. <i>Nature Immunology</i> , <b>2021</b> , 22, 240-253	19.1	12
121	Assessment of REPLI-g Multiple Displacement Whole Genome Amplification (WGA) Techniques for Metagenomic Applications. <i>Journal of Biomolecular Techniques</i> , <b>2017</b> , 28, 46-55	1.1	11
120	End-to-End Protocol for the Detection of SARS-CoV-2 from Built Environments. <i>MSystems</i> , <b>2020</b> , 5,	7.6	11
119	Minerva: an alignment- and reference-free approach to deconvolve Linked-Reads for metagenomics. <i>Genome Research</i> , <b>2019</b> , 29, 116-124	9.7	11
118	Forensic Applications of Microbiomics: A Review. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 608101	5.7	11
117	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 1141-1150	44.5	11
116	Ratio-Based Method To Identify True Biomarkers by Normalizing Circulating ncRNA Sequencing and Quantitative PCR Data. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 6746-6753	7.8	10

115	Nanopore detection of bacterial DNA base modifications		10
114	Accurate detection of m6A RNA modifications in native RNA sequences		10
113	Single-cell RNA-seq reveals novel mitochondria-related musculoskeletal cell populations during adult axolotl limb regeneration process. <i>Cell Death and Differentiation</i> , <b>2021</b> , 28, 1110-1125	12.7	10
112	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 1129-1140	44.5	10
111	The Microbe Directory: An annotated, searchable inventory of microbes' characteristics. <i>Gates Open Research</i> , <b>2018</b> , 2, 3	2.4	9
110	Early introductions and community transmission of SARS-CoV-2 variant B.1.1.7 in the United States <b>2021</b> ,		9
109	Co-occurrence patterns of bacteria within microbiome of Moscow subway. <i>Computational and Structural Biotechnology Journal</i> , <b>2020</b> , 18, 314-322	6.8	8
108	Somatic Mutations Drive Specific, but Reversible, Epigenetic Heterogeneity States in AML. <i>Cancer Discovery</i> , <b>2020</b> , 10, 1934-1949	24.4	8
107	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , <b>2021</b> , 22, 111	18.3	8
106	Towards a Comprehensive Variation Benchmark for Challenging Medically-Relevant Autosomal Genes		8
105	Characterization of complete lncRNAs transcriptome reveals the functional and clinical impact of lncRNAs in multiple myeloma. <i>Leukemia</i> , <b>2021</b> , 35, 1438-1450	10.7	8
104	Resource: A multi-species multi-timepoint transcriptome database and webpage for the pineal gland and retina. <i>Journal of Pineal Research</i> , <b>2020</b> , 69, e12673	10.4	7
103	Clinical Genomics: Challenges and Opportunities. <i>Critical Reviews in Eukaryotic Gene Expression</i> , <b>2016</b> , 26, 97-113	1.3	7
102	Role of miR-2392 in driving SARS-CoV-2 infection. <i>Cell Reports</i> , <b>2021</b> , 37, 109839	10.6	7
101	QuaPra: Efficient transcript assembly and quantification using quadratic programming with Apriori algorithm. <i>Science China Life Sciences</i> , <b>2019</b> , 62, 937-946	8.5	6
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33	A metagenomic DNA sequencing assay that is robust against environmental DNA contamination <b>2021</b> ,		1
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29	Elevation of Gut-Derived p-Cresol During Spaceflight and its Effect on Drug Metabolism and Performance in Astronauts		1
28	The SEQC2 Epigenomics Quality Control (EpiQC) Study: Comprehensive Characterization of Epigenetic Methods, Reproducibility, and Quantification		1
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26	DNA methylation calling tools for Oxford Nanopore sequencing: a survey and human epigenome-wide evaluation		1

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