

# Christopher E. Mason

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3281394/publications.pdf>

Version: 2024-02-01

242  
papers

30,851  
citations

15001

68  
h-index

7234

158  
g-index

314  
all docs

314  
docs citations

314  
times ranked

50280  
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>m</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 N6-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        |
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