

Rory J Bowden

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

10,051
citations

47006

47
h-index

56724

83
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96
all docs

96
docs citations

96
times ranked

15961
citing authors

#	ARTICLE	IF	CITATIONS
1	Dual RNA sequencing reveals dendritic cell reprogramming in response to typhoidal Salmonella invasion. <i>Communications Biology</i> , 2022, 5, 111.	4.4	11
2	Short and long-read genome sequencing methodologies for somatic variant detection; genomic analysis of a patient with diffuse large B-cell lymphoma. <i>Scientific Reports</i> , 2021, 11, 6408.	3.3	14
3	Targeted single-cell RNA sequencing of transcription factors enhances the identification of cell types and trajectories. <i>Genome Research</i> , 2021, 31, 1069-1081.	5.5	18
4	High-resolution transcriptional landscape of xeno-free human induced pluripotent stem cell-derived cerebellar organoids. <i>Scientific Reports</i> , 2021, 11, 12959.	3.3	32
5	Targeted capture and sequencing of <i>Orientia tsutsugamushi</i> genomes from chiggers and humans. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104818.	2.3	6
6	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. <i>Nature Communications</i> , 2021, 12, 5125.	12.8	16
7	Viral genome wide association study identifies novel hepatitis C virus polymorphisms associated with sofosbuvir treatment failure. <i>Nature Communications</i> , 2021, 12, 6105.	12.8	11
8	Analysis of Differentiation Protocols Defines a Common Pancreatic Progenitor Molecular Signature and Guides Refinement of Endocrine Differentiation. <i>Stem Cell Reports</i> , 2020, 14, 138-153.	4.8	31
9	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	39
10	Technical Validation of a Hepatitis C Virus Whole Genome Sequencing Assay for Detection of Genotype and Antiviral Resistance in the Clinical Pathway. <i>Frontiers in Microbiology</i> , 2020, 11, 576572.	3.5	13
11	Simultaneous Viral Whole-Genome Sequencing and Differential Expression Profiling in Respiratory Syncytial Virus Infection of Infants. <i>Journal of Infectious Diseases</i> , 2020, 222, S666-S671.	4.0	11
12	Single-cell atlas of colonic CD8+ T cells in ulcerative colitis. <i>Nature Medicine</i> , 2020, 26, 1480-1490.	30.7	126
13	Performance of a high-throughput next-generation sequencing method for analysis of HIV drug resistance and viral load. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3510-3516.	3.0	13
14	A single-cell atlas of the human substantia nigra reveals cell-specific pathways associated with neurological disorders. <i>Nature Communications</i> , 2020, 11, 4183.	12.8	178
15	Epstein-Barr virus reactivation in sepsis due to community-acquired pneumonia is associated with increased morbidity and an immunosuppressed host transcriptomic endotype. <i>Scientific Reports</i> , 2020, 10, 9838.	3.3	13
16	Targeted RNA sequencing enhances gene expression profiling of ultra-low input samples. <i>RNA Biology</i> , 2020, 17, 1741-1753.	3.1	10
17	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV</i> , 2020, 7, e173-e183.	4.7	59
18	Case Report: Application of hepatitis B virus (HBV) deep sequencing to distinguish between acute and chronic infection. <i>Wellcome Open Research</i> , 2020, 5, 240.	1.8	2

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19	Oxford Nanopore MinION Sequencing Enables Rapid Whole Genome Assembly of <i>Rickettsia typhi</i> in a Resource-Limited Setting. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 102, 408-414.	1.4	22
20	Case Report: Application of hepatitis B virus (HBV) deep sequencing to distinguish between acute and chronic infection. <i>Wellcome Open Research</i> , 2020, 5, 240.	1.8	3
21	Prolonged Zika Virus RNA Detection in Semen of Immunosuppressed Patient. <i>Emerging Infectious Diseases</i> , 2019, 25, 1598-1600.	4.3	8
22	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). <i>Scientific Reports</i> , 2019, 9, 7081.	3.3	75
23	Sequencing of human genomes with nanopore technology. <i>Nature Communications</i> , 2019, 10, 1869.	12.8	140
24	Factors influencing meiotic recombination revealed by whole-genome sequencing of single sperm. <i>Science</i> , 2019, 363, .	12.6	98
25	Cellular α -synuclein pathology is associated with bioenergetic dysfunction in Parkinson's iPSC-derived dopamine neurons. <i>Human Molecular Genetics</i> , 2019, 28, 2001-2013.	2.9	102
26	Single-Cell Sequencing of iPSC-Dopamine Neurons Reconstructs Disease Progression and Identifies HDAC4 as a Regulator of Parkinson Cell Phenotypes. <i>Cell Stem Cell</i> , 2019, 24, 93-106.e6.	11.1	123
27	Resistance analysis of genotype 3 hepatitis C virus indicates subtypes inherently resistant to nonstructural protein 5A inhibitors. <i>Hepatology</i> , 2019, 69, 1861-1872.	7.3	68
28	Interferon lambda 4 impacts the genetic diversity of hepatitis C virus. <i>ELife</i> , 2019, 8, .	6.0	28
29	Panton's Valentine leucocidin is the key determinant of <i>Staphylococcus aureus</i> pyomyositis in a bacterial GWAS. <i>ELife</i> , 2019, 8, .	6.0	56
30	Lineage-specific plasmid acquisition and the evolution of specialized pathogens in <i>Bacillus thuringiensis</i> and the <i>Bacillus cereus</i> group. <i>Molecular Ecology</i> , 2018, 27, 1524-1540.	3.9	43
31	A practical solution for preserving single cells for RNA sequencing. <i>Scientific Reports</i> , 2018, 8, 2151.	3.3	65
32	Insights into Platypus Population Structure and History from Whole-Genome Sequencing. <i>Molecular Biology and Evolution</i> , 2018, 35, 1238-1252.	8.9	27
33	Impact of Interferon Lambda 4 Genotype on Interferon-Stimulated Gene Expression During Direct-Acting Antiviral Therapy for Hepatitis C. <i>Hepatology</i> , 2018, 68, 859-871.	7.3	18
34	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , 2018, 9, 5034.	12.8	115
35	Structural Remodeling of the Human Colonic Mesenchyme in Inflammatory Bowel Disease. <i>Cell</i> , 2018, 175, 372-386.e17.	28.9	454
36	Reproducibility of Molecular Phenotypes after Long-Term Differentiation to Human iPSC-Derived Neurons: A Multi-Site Omics Study. <i>Stem Cell Reports</i> , 2018, 11, 897-911.	4.8	135

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37	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , 2018, 23, 855-864.e7.	11.0	82
38	Long-read whole genome sequencing and comparative analysis of six strains of the human pathogen <i>Orientia tsutsugamushi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006566.	3.0	50
39	Characterization of hepatitis C virus resistance to grazoprevir reveals complex patterns of mutations following on-treatment breakthrough that are not observed at relapse. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 1119-1135.	2.7	6
40	Transcriptomic profiling of purified patient-derived dopamine neurons identifies convergent perturbations and therapeutics for Parkinson's disease. <i>Human Molecular Genetics</i> , 2017, 26, ddw412.	2.9	62
41	The nature and nurture of cell heterogeneity: accounting for macrophage gene-environment interactions with single-cell RNA-Seq. <i>BMC Genomics</i> , 2017, 18, 53.	2.8	24
42	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. <i>Nature Genetics</i> , 2017, 49, 666-673.	21.4	129
43	Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 830-842.	2.5	46
44	Evolutionary Origin of the Staphylococcal Cassette Chromosome <i>mecA</i> (SCC <i>mecA</i>). <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	64
45	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017, 6, .	6.0	93
46	Evidence for the evolutionary steps leading to <i>mecA</i> -mediated β -lactam resistance in staphylococci. <i>PLoS Genetics</i> , 2017, 13, e1006674.	3.5	63
47	Evaluation of Viremia Frequencies of a Novel Human Pegivirus by Using Bioinformatic Screening and PCR. <i>Emerging Infectious Diseases</i> , 2016, 22, 671-678.	4.3	46
48	Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2470-2484.	3.9	112
49	Assessing similarity to primary tissue and cortical layer identity in induced pluripotent stem cell-derived cortical neurons through single-cell transcriptomics. <i>Human Molecular Genetics</i> , 2016, 25, 989-1000.	2.9	86
50	Evolutionary dynamics of <i>Enterococcus faecium</i> reveals complex genomic relationships between isolates with independent emergence of vancomycin resistance. <i>Microbial Genomics</i> , 2016, 2, .	2.0	50
51	Biofilm Morphotypes and Population Structure among <i>Staphylococcus epidermidis</i> from Commensal and Clinical Samples. <i>PLoS ONE</i> , 2016, 11, e0151240.	2.5	49
52	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. <i>F1000Research</i> , 2015, 4, 1075.	1.6	270
53	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015, 13, e1002229.	5.6	120
54	Characterization of Hepatitis C Virus Recombination in Cameroon by Use of Nonspecific Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3155-3164.	3.9	28

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55	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1193-1202.	9.1	553
56	Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1313-1328.	2.5	130
57	ve-SEQ: Robust, unbiased enrichment for streamlined detection and whole-genome sequencing of HCV and other highly diverse pathogens. <i>F1000Research</i> , 2015, 4, 1062.	1.6	66
58	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014, 5, 3956.	12.8	128
59	Whole-Genome Sequencing Shows That Patient-to-Patient Transmission Rarely Accounts for Acquisition of <i>Staphylococcus aureus</i> in an Intensive Care Unit. <i>Clinical Infectious Diseases</i> , 2014, 58, 609-618.	5.8	142
60	Dynamics of acquisition and loss of carriage of <i>Staphylococcus aureus</i> strains in the community: The effect of clonal complex. <i>Journal of Infection</i> , 2014, 68, 426-439.	3.3	42
61	Evolution and Diversity in Human Herpes Simplex Virus Genomes. <i>Journal of Virology</i> , 2014, 88, 1209-1227.	3.4	187
62	Diverse Sources of <i>C. difficile</i> Infection Identified on Whole-Genome Sequencing. <i>New England Journal of Medicine</i> , 2013, 369, 1195-1205.	27.0	595
63	Whole-genome sequencing to delineate <i>Mycobacterium tuberculosis</i> outbreaks: a retrospective observational study. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 137-146.	9.1	786
64	Multiple Instances of Ancient Balancing Selection Shared Between Humans and Chimpanzees. <i>Science</i> , 2013, 339, 1578-1582.	12.6	253
65	Improved workflows for high throughput library preparation using the transposome-based nextera system. <i>BMC Biotechnology</i> , 2013, 13, 104.	3.3	141
66	Within-Host Evolution of <i>Staphylococcus aureus</i> during Asymptomatic Carriage. <i>PLoS ONE</i> , 2013, 8, e61319.	2.5	194
67	A Modified RNA-Seq Approach for Whole Genome Sequencing of RNA Viruses from Faecal and Blood Samples. <i>PLoS ONE</i> , 2013, 8, e66129.	2.5	62
68	Genomic Tools for Evolution and Conservation in the Chimpanzee: <i>Pan troglodytes ellioti</i> Is a Genetically Distinct Population. <i>PLoS Genetics</i> , 2012, 8, e1002504.	3.5	53
69	People of the British Isles: preliminary analysis of genotypes and surnames in a UK-control population. <i>European Journal of Human Genetics</i> , 2012, 20, 203-210.	2.8	126
70	Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4550-4555.	7.1	244
71	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. <i>Science</i> , 2012, 336, 193-198.	12.6	273
72	Pneumococcal genome sequencing tracks a vaccine escape variant formed through a multi-fragment recombination event. <i>Nature Genetics</i> , 2012, 44, 352-355.	21.4	144

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73	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012, 13, 601-612.	16.3	684
74	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012, 13, R118.	9.6	199
75	MicroRNA Expression in Abdominal and Gluteal Adipose Tissue Is Associated with mRNA Expression Levels and Partly Genetically Driven. <i>PLoS ONE</i> , 2011, 6, e27338.	2.5	46
76	Recombination and Population Structure in <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2011, 7, e1002191.	3.5	135
77	Drive Against Hotspot Motifs in Primates Implicates the <i>PRDM9</i> Gene in Meiotic Recombination. <i>Science</i> , 2010, 327, 876-879.	12.6	607
78	Multilocus Sequence Typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2010, 48, 770-778.	3.9	399
79	Genome-wide association mapping in bacteria?. <i>Trends in Microbiology</i> , 2006, 14, 353-355.	7.7	81
80	Patterns of Eurasian HSV-1 molecular diversity and inferences of human migrations. <i>Infection, Genetics and Evolution</i> , 2006, 6, 63-74.	2.3	24
81	High recombination rate in herpes simplex virus type 1 natural populations suggests significant co-infection. <i>Infection, Genetics and Evolution</i> , 2004, 4, 115-123.	2.3	81
82	Recombination in human herpesvirus-8 strains from Uganda and evolution of the K15 gene. <i>Journal of General Virology</i> , 2001, 82, 2393-2404.	2.9	58
83	In vivo negative regulation of SARS-CoV-2 receptor, ACE2, by interferons and its genetic control. <i>Wellcome Open Research</i> , 0, 6, 47.	1.8	2