

# Rory J Bowden

## List of Publications by Year in descending order

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83  
papers

10,051  
citations

47006

47  
h-index

56724

83  
g-index

96  
all docs

96  
docs citations

96  
times ranked

15961  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome sequencing to delineate Mycobacterium tuberculosis outbreaks: a retrospective observational study. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 137-146.	9.1	786
2	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012, 13, 601-612.	16.3	684
3	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
4	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
5	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
6	Structural Remodeling of the Human Colonic Mesenchyme in Inflammatory Bowel Disease. <i>Cell</i> , 2018, 175, 372-386.e17.	28.9	454
7	Multilocus Sequence Typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2010, 48, 770-778.	3.9	399
8	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. <i>Science</i> , 2012, 336, 193-198.	12.6	273
9	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. <i>F1000Research</i> , 2015, 4, 1075.	1.6	270
10	Multiple Instances of Ancient Balancing Selection Shared Between Humans and Chimpanzees. <i>Science</i> , 2013, 339, 1578-1582.	12.6	253
11	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
12	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012, 13, R118.	9.6	199
13	Within-Host Evolution of <i>Staphylococcus aureus</i> during Asymptomatic Carriage. <i>PLoS ONE</i> , 2013, 8, e61319.	2.5	194
14	Evolution and Diversity in Human Herpes Simplex Virus Genomes. <i>Journal of Virology</i> , 2014, 88, 1209-1227.	3.4	187
15	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
16	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
17	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
18	Improved workflows for high throughput library preparation using the transposome-based nextera system. <i>BMC Biotechnology</i> , 2013, 13, 104.	3.3	141

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19	Sequencing of human genomes with nanopore technology. <i>Nature Communications</i> , 2019, 10, 1869.	12.8	140
20	Recombination and Population Structure in <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2011, 7, e1002191.	3.5	135
21	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
22	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
23	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
24	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014, 5, 3956.	12.8	128
25	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
26	Single-cell atlas of colonic CD8+ T cells in ulcerative colitis. <i>Nature Medicine</i> , 2020, 26, 1480-1490.	30.7	126
27	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
28	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015, 13, e1002229.	5.6	120
29	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , 2018, 9, 5034.	12.8	115
30	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
31	Cellular $\alpha$ -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
32	Factors influencing meiotic recombination revealed by whole-genome sequencing of single sperm. <i>Science</i> , 2019, 363, .	12.6	98
33	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017, 6, .	6.0	93
34	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
35	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
36	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

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37	Genome-wide association mapping in bacteria?. Trends in Microbiology, 2006, 14, 353-355.	7.7	81
38	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). Scientific Reports, 2019, 9, 7081.	3.3	75
39	Resistance analysis of genotype 3 hepatitis C virus indicates subtypes inherently resistant to nonstructural protein 5A inhibitors. Hepatology, 2019, 69, 1861-1872.	7.3	68
40	ve-SEQ: Robust, unbiased enrichment for streamlined detection and whole-genome sequencing of HCV and other highly diverse pathogens. F1000Research, 2015, 4, 1062.	1.6	66
41	A practical solution for preserving single cells for RNA sequencing. Scientific Reports, 2018, 8, 2151.	3.3	65
42	Evolutionary Origin of the Staphylococcal Cassette Chromosome <i>mecA</i> (SCC <i>mecA</i> ). Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	64
43	Evidence for the evolutionary steps leading to <i>mecA</i> -mediated $\beta$ -lactam resistance in staphylococci. PLoS Genetics, 2017, 13, e1006674.	3.5	63
44	A Modified RNA-Seq Approach for Whole Genome Sequencing of RNA Viruses from Faecal and Blood Samples. PLoS ONE, 2013, 8, e66129.	2.5	62
45	Transcriptomic profiling of purified patient-derived dopamine neurons identifies convergent perturbations and therapeutics for Parkinson's disease. Human Molecular Genetics, 2017, 26, ddw412.	2.9	62
46	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. Lancet HIV, 2020, 7, e173-e183.	4.7	59
47	Recombination in human herpesvirus-8 strains from Uganda and evolution of the K15 gene. Journal of General Virology, 2001, 82, 2393-2404.	2.9	58
48	Panton's Valentine leucocidin is the key determinant of Staphylococcus aureus pyomyositis in a bacterial GWAS. ELife, 2019, 8, .	6.0	56
49	Genomic Tools for Evolution and Conservation in the Chimpanzee: Pan troglodytes ellioti Is a Genetically Distinct Population. PLoS Genetics, 2012, 8, e1002504.	3.5	53
50	Long-read whole genome sequencing and comparative analysis of six strains of the human pathogen Orientia tsutsugamushi. PLoS Neglected Tropical Diseases, 2018, 12, e0006566.	3.0	50
51	Evolutionary dynamics of Enterococcus faecium reveals complex genomic relationships between isolates with independent emergence of vancomycin resistance. Microbial Genomics, 2016, 2, .	2.0	50
52	Biofilm Morphotypes and Population Structure among Staphylococcus epidermidis from Commensal and Clinical Samples. PLoS ONE, 2016, 11, e0151240.	2.5	49
53	MicroRNA Expression in Abdominal and Gluteal Adipose Tissue Is Associated with mRNA Expression Levels and Partly Genetically Driven. PLoS ONE, 2011, 6, e27338.	2.5	46
54	Evaluation of Viremia Frequencies of a Novel Human Pegivirus by Using Bioinformatic Screening and PCR. Emerging Infectious Diseases, 2016, 22, 671-678.	4.3	46

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55	Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 830-842.	2.5	46
56	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
57	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
58	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
59	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
60	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
61	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
62	Interferon lambda 4 impacts the genetic diversity of hepatitis C virus. <i>ELife</i> , 2019, 8, .	6.0	28
63	Insights into Platypus Population Structure and History from Whole-Genome Sequencing. <i>Molecular Biology and Evolution</i> , 2018, 35, 1238-1252.	8.9	27
64	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
65	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
66	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
67	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
68	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
69	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
70	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
71	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
72	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

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73	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
74	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
75	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
76	Dual RNA sequencing reveals dendritic cell reprogramming in response to typhoidal <i>Salmonella</i> invasion. <i>Communications Biology</i> , 2022, 5, 111.	4.4	11
77	Targeted RNA sequencing enhances gene expression profiling of ultra-low input samples. <i>RNA Biology</i> , 2020, 17, 1741-1753.	3.1	10
78	Prolonged Zika Virus RNA Detection in Semen of Immunosuppressed Patient. <i>Emerging Infectious Diseases</i> , 2019, 25, 1598-1600.	4.3	8
79	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
80	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
81	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
82	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
83	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