

Rory J Bowden

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.

88

papers

6,957

citations

43

h-index

83

g-index

96

ext. papers

8,909

ext. citations

12

avg, IF

5.3

L-index

#	Paper	IF	Citations
88	Whole-genome sequencing to delineate Mycobacterium tuberculosis outbreaks: a retrospective observational study. <i>Lancet Infectious Diseases, The</i> , 2013 , 13, 137-46	25.5	615
87	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012 , 13, 601-612	30.1	508
86	Diverse sources of C. difficile infection identified on whole-genome sequencing. <i>New England Journal of Medicine</i> , 2013 , 369, 1195-205	59.2	471
85	Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination. <i>Science</i> , 2010 , 327, 876-9	33.3	465
84	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases, The</i> , 2015 , 15, 1193-1202	25.5	391
83	Multilocus sequence typing of Clostridium difficile. <i>Journal of Clinical Microbiology</i> , 2010 , 48, 770-8	9.7	310
82	Structural Remodeling of the Human Colonic Mesenchyme in Inflammatory Bowel Disease. <i>Cell</i> , 2018 , 175, 372-386.e17	56.2	224
81	A fine-scale chimpanzee genetic map from population sequencing. <i>Science</i> , 2012 , 336, 193-8	33.3	218
80	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. <i>F1000Research</i> , 2015 , 4, 1075	3.6	210
79	Multiple instances of ancient balancing selection shared between humans and chimpanzees. <i>Science</i> , 2013 , 339, 1578-82	33.3	204
78	Evolutionary dynamics of Staphylococcus aureus during progression from carriage to disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 4550-5	11.5	195
77	Microevolutionary analysis of Clostridium difficile genomes to investigate transmission. <i>Genome Biology</i> , 2012 , 13, R118	18.3	151
76	Evolution and diversity in human herpes simplex virus genomes. <i>Journal of Virology</i> , 2014 , 88, 1209-27	6.6	141
75	Within-host evolution of Staphylococcus aureus during asymptomatic carriage. <i>PLoS ONE</i> , 2013 , 8, e61319	3.7	141
74	Whole-genome sequencing shows that patient-to-patient transmission rarely accounts for acquisition of Staphylococcus aureus in an intensive care unit. <i>Clinical Infectious Diseases</i> , 2014 , 58, 609-18	11.6	112
73	Improved workflows for high throughput library preparation using the transposome-based Nextera system. <i>BMC Biotechnology</i> , 2013 , 13, 104	3.5	106
72	Recombination and population structure in Salmonella enterica. <i>PLoS Genetics</i> , 2011 , 7, e1002191	6	105

71	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, 203-10	5.3	91
70	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014 , 5, 3956	17.4	90
69	Sequencing of human genomes with nanopore technology. <i>Nature Communications</i> , 2019 , 10, 1869	17.4	89
68	Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . <i>Genome Biology and Evolution</i> , 2015 , 7, 1313-28	3.9	86
67	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	8	84
66	Pneumococcal genome sequencing tracks a vaccine escape variant formed through a multi-fragment recombination event. <i>Nature Genetics</i> , 2012 , 44, 352-5	36.3	82
65	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	36.3	81
64	Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 2470-84	9.7	78
63	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015 , 13, e1002229	9.7	76
62	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , 2018 , 9, 5034	17.4	71
61	High recombination rate in herpes simplex virus type 1 natural populations suggests significant co-infection. <i>Infection, Genetics and Evolution</i> , 2004 , 4, 115-23	4.5	70
60	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	18	67
59	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	5.6	64
58	Genome-wide association mapping in bacteria?. <i>Trends in Microbiology</i> , 2006 , 14, 353-5	12.4	60
57	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	23.4	60
56	A single-cell atlas of the human substantia nigra reveals cell-specific pathways associated with neurological disorders. <i>Nature Communications</i> , 2020 , 11, 4183	17.4	59
55	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017 , 6,	8.9	55
54	Cellular Synuclein pathology is associated with bioenergetic dysfunction in Parkinson's iPSC-derived dopamine neurons. <i>Human Molecular Genetics</i> , 2019 , 28, 2001-2013	5.6	55

53	Factors influencing meiotic recombination revealed by whole-genome sequencing of single sperm. <i>Science</i> , 2019 , 363,	33.3	54
52	A modified RNA-Seq approach for whole genome sequencing of RNA viruses from faecal and blood samples. <i>PLoS ONE</i> , 2013 , 8, e66129	3.7	52
51	Recombination in human herpesvirus-8 strains from Uganda and evolution of the K15 gene. <i>Journal of General Virology</i> , 2001 , 82, 2393-2404	4.9	50
50	Transcriptomic profiling of purified patient-derived dopamine neurons identifies convergent perturbations and therapeutics for Parkinson's disease. <i>Human Molecular Genetics</i> , 2017 , 26, 552-566	5.6	47
49	Single-cell atlas of colonic CD8 T cells in ulcerative colitis. <i>Nature Medicine</i> , 2020 , 26, 1480-1490	50.5	46
48	Genomic tools for evolution and conservation in the chimpanzee: Pan troglodytes ellioti is a genetically distinct population. <i>PLoS Genetics</i> , 2012 , 8, e1002504	6	45
47	Evidence for the evolutionary steps leading to mecA-mediated β -lactam resistance in staphylococci. <i>PLoS Genetics</i> , 2017 , 13, e1006674	6	44
46	Resistance analysis of genotype 3 hepatitis C virus indicates subtypes inherently resistant to nonstructural protein 5A inhibitors. <i>Hepatology</i> , 2019 , 69, 1861-1872	11.2	43
45	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). <i>Scientific Reports</i> , 2019 , 9, 7081	4.9	41
44	A practical solution for preserving single cells for RNA sequencing. <i>Scientific Reports</i> , 2018 , 8, 2151	4.9	41
43	Evolutionary Origin of the Staphylococcal Cassette Chromosome (SCC). <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	39
42	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	3.7	39
41	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	3.6	39
40	Evolutionary dynamics of reveals complex genomic relationships between isolates with independent emergence of vancomycin resistance. <i>Microbial Genomics</i> , 2016 , 2,	4.4	37
39	Dynamics of acquisition and loss of carriage of Staphylococcus aureus strains in the community: the effect of clonal complex. <i>Journal of Infection</i> , 2014 , 68, 426-39	18.9	36
38	Biofilm Morphotypes and Population Structure among Staphylococcus epidermidis from Commensal and Clinical Samples. <i>PLoS ONE</i> , 2016 , 11, e0151240	3.7	34
37	Evaluation of Viremia Frequencies of a Novel Human Pegivirus by Using Bioinformatic Screening and PCR. <i>Emerging Infectious Diseases</i> , 2016 , 22, 671-8	10.2	34
36	Panton-Valentine leucocidin is the key determinant of pyomyositis in a bacterial GWAS. <i>ELife</i> , 2019 , 8,	8.9	30

35	Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2017 , 9, 830-842	3.9	29
34	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	7.8	26
33	Characterization of Hepatitis C Virus Recombination in Cameroon by Use of Nonspecific Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 3155-64	9.7	25
32	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	5.7	25
31	Patterns of Eurasian HSV-1 molecular diversity and inferences of human migrations. <i>Infection, Genetics and Evolution</i> , 2006 , 6, 63-74	4.5	21
30	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	4.8	18
29	Interferon lambda 4 impacts the genetic diversity of hepatitis C virus. <i>ELife</i> , 2019 , 8,	8.9	17
28	Insights into Platypus Population Structure and History from Whole-Genome Sequencing. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1238-1252	8.3	15
27	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	11.2	15
26	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	15
25	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	4.5	13
24	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	8	13
23	Oxford Nanopore MinION Sequencing Enables Rapid Whole Genome Assembly of in a Resource-Limited Setting. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020 , 102, 408-414	3.2	11
22	High-resolution transcriptional landscape of xeno-free human induced pluripotent stem cell-derived cerebellar organoids. <i>Scientific Reports</i> , 2021 , 11, 12959	4.9	9
21	Targeted metagenomic sequencing enhances the identification of pathogens associated with acute infection		7
20	Prolonged Zika Virus RNA Detection in Semen of Immunosuppressed Patient. <i>Emerging Infectious Diseases</i> , 2019 , 25, 1598-1600	10.2	6
19	Targeted RNA sequencing enhances gene expression profiling of ultra-low input samples. <i>RNA Biology</i> , 2020 , 17, 1741-1753	4.8	5
18	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 , 11, 1119-1135	4.2	5

17	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	5.1	5
16	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	4.9	4
15	Severe infections emerge from the microbiome by adaptive evolution		4
14	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	5.7	4
13	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	7	4
12	Viral genome wide association study identifies novel hepatitis C virus polymorphisms associated with sofosbuvir treatment failure. <i>Nature Communications</i> , 2021 , 12, 6105	17.4	3
11	Negative regulation of ACE2 by interferons in vivo and its genetic control		3
10	A comprehensive genomics solution for HIV surveillance and clinical monitoring in a global health setting		3
9	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	4.9	3
8	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. <i>Nature Communications</i> , 2021 , 12, 5125	17.4	3
7	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV)		2
6	Targeted capture and sequencing of <i>Orientia tsutsugamushi</i> genomes from chiggers and humans. <i>Infection, Genetics and Evolution</i> , 2021 , 91, 104818	4.5	2
5	Dual RNA sequencing reveals dendritic cell reprogramming in response to typhoidal <i>Salmonella</i> invasion.. <i>Communications Biology</i> , 2022 , 5, 111	6.7	0
4	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	4.8	0
3	In vivo negative regulation of SARS-CoV-2 receptor, ACE2, by interferons and its genetic control. <i>Wellcome Open Research</i> , 2020 , 6, 47	4.8	0
2	Targeted single-cell RNA sequencing of transcription factors enhances the identification of cell types and trajectories. <i>Genome Research</i> , 2021 , 31, 1069-1081	9.7	0
1	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	4.8	