

Lachlan J Coin

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.

156
papers

38,495
citations

52
h-index

182
g-index

182
ext. papers

45,923
ext. citations

13.6
avg, IF

6.1
L-index

#	Paper	IF	Citations
156	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
155	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049
154	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2004 , 32, D138-41	20.1	2720
153	A census of human cancer genes. <i>Nature Reviews Cancer</i> , 2004 , 4, 177-83	31.3	2424
152	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010 , 42, 937-48	36.3	2267
151	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010 , 42, 105-16	36.3	1673
150	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010 , 467, 832-8	50.4	1514
149	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , 2009 , 41, 25-34	36.3	1368
148	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009 , 41, 666-76	36.3	970
147	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010 , 42, 949-60	36.3	724
146	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. <i>Nature Genetics</i> , 2009 , 41, 35-46	36.3	588
145	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009 , 41, 77-81	36.3	584
144	Genome-wide association study for early-onset and morbid adult obesity identifies three new risk loci in European populations. <i>Nature Genetics</i> , 2009 , 41, 157-9	36.3	521
143	Genetic variability in the regulation of gene expression in ten regions of the human brain. <i>Nature Neuroscience</i> , 2014 , 17, 1418-1428	25.5	483
142	Genetic Loci associated with C-reactive protein levels and risk of coronary heart disease. <i>JAMA - Journal of the American Medical Association</i> , 2009 , 302, 37-48	27.4	459
141	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011 , 43, 1131-8	36.3	415
140	A new highly penetrant form of obesity due to deletions on chromosome 16p11.2. <i>Nature</i> , 2010 , 463, 671-5	50.4	403

139	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. <i>PLoS Genetics</i> , 2009 , 5, e1000508	6	393
138	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. <i>PLoS Genetics</i> , 2012 , 8, e1002607	6	326
137	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. <i>Nature</i> , 2011 , 478, 97-102	50.4	322
136	Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. <i>Diabetes</i> , 2011 , 60, 2624-34	0.9	285
135	MultiPhen: joint model of multiple phenotypes can increase discovery in GWAS. <i>PLoS ONE</i> , 2012 , 7, e34867	5.7	240
134	TreeFam: 2008 Update. <i>Nucleic Acids Research</i> , 2008 , 36, D735-40	20.1	234
133	Diagnosis of childhood tuberculosis and host RNA expression in Africa. <i>New England Journal of Medicine</i> , 2014 , 370, 1712-1723	59.2	229
132	Detection of tuberculosis in HIV-infected and -uninfected African adults using whole blood RNA expression signatures: a case-control study. <i>PLoS Medicine</i> , 2013 , 10, e1001538	11.6	224
131	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 7119-24	11.5	218
130	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016 , 48, 593-9	36.3	204
129	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. <i>Nature Genetics</i> , 2013 , 45, 902-906	36.3	191
128	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. <i>Nature Genetics</i> , 2010 , 42, 430-5	36.3	184
127	Haplotype and isoform specific expression estimation using multi-mapping RNA-seq reads. <i>Genome Biology</i> , 2011 , 12, R13	18.3	179
126	A genome-wide meta-analysis of genetic variants associated with allergic rhinitis and grass sensitization and their interaction with birth order. <i>Journal of Allergy and Clinical Immunology</i> , 2011 , 128, 996-1005	11.5	170
125	Diagnostic Test Accuracy of a 2-Transcript Host RNA Signature for Discriminating Bacterial vs Viral Infection in Febrile Children. <i>JAMA - Journal of the American Medical Association</i> , 2016 , 316, 835-45	27.4	166
124	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. <i>American Journal of Human Genetics</i> , 2016 , 98, 830-842	11	153
123	A genome-wide association search for type 2 diabetes genes in African Americans. <i>PLoS ONE</i> , 2012 , 7, e29202	3.7	138
122	Genetic determinants of height growth assessed longitudinally from infancy to adulthood in the northern Finland birth cohort 1966. <i>PLoS Genetics</i> , 2009 , 5, e1000409	6	113

121	Pathway analysis of GWAS provides new insights into genetic susceptibility to 3 inflammatory diseases. <i>PLoS ONE</i> , 2009 , 4, e8068	3.7	110
120	Common variants at 6q22 and 17q21 are associated with intracranial volume. <i>Nature Genetics</i> , 2012 , 44, 539-44	36.3	104
119	Triclosan at environmentally relevant concentrations promotes horizontal transfer of multidrug resistance genes within and across bacterial genera. <i>Environment International</i> , 2018 , 121, 1217-1226	12.9	104
118	Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome de novo assembly. <i>Nature Biotechnology</i> , 2011 , 29, 723-30	44.5	99
117	Transforming growth factor-beta signaling pathway in patients with Kawasaki disease. <i>Circulation: Cardiovascular Genetics</i> , 2011 , 4, 16-25		96
116	Common variants at 12q15 and 12q24 are associated with infant head circumference. <i>Nature Genetics</i> , 2012 , 44, 532-538	36.3	94
115	Genome-wide association studies of asthma in population-based cohorts confirm known and suggested loci and identify an additional association near HLA. <i>PLoS ONE</i> , 2012 , 7, e44008	3.7	89
114	Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement. <i>Nature Communications</i> , 2018 , 9, 4580	17.4	86
113	Non-antibiotic antimicrobial triclosan induces multiple antibiotic resistance through genetic mutation. <i>Environment International</i> , 2018 , 118, 257-265	12.9	81
112	Chiron: translating nanopore raw signal directly into nucleotide sequence using deep learning. <i>GigaScience</i> , 2018 , 7,	7.6	80
111	Scaffolding and completing genome assemblies in real-time with nanopore sequencing. <i>Nature Communications</i> , 2017 , 8, 14515	17.4	72
110	Pathway-driven gene stability selection of two rheumatoid arthritis GWAS identifies and validates new susceptibility genes in receptor mediated signalling pathways. <i>Human Molecular Genetics</i> , 2011 , 20, 3494-506	5.6	62
109	Direct RNA sequencing and early evolution of SARS-CoV-2		61
108	Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinION(TM) sequencing. <i>GigaScience</i> , 2016 , 5, 32	7.6	58
107	TTC12-ANKK1-DRD2 and CHRNA5-CHRNA3-CHRNA4 influence different pathways leading to smoking behavior from adolescence to mid-adulthood. <i>Biological Psychiatry</i> , 2011 , 69, 650-60	7.9	56
106	Integrated pathogen load and dual transcriptome analysis of systemic host-pathogen interactions in severe malaria. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	54
105	Diagnosis of Kawasaki Disease Using a Minimal Whole-Blood Gene Expression Signature. <i>JAMA Pediatrics</i> , 2018 , 172, e182293	8.3	52
104	Effects of long-term averaging of quantitative blood pressure traits on the detection of genetic associations. <i>American Journal of Human Genetics</i> , 2014 , 95, 49-65	11	52

103	Highly interconnected genes in disease-specific networks are enriched for disease-associated polymorphisms. <i>Genome Biology</i> , 2012 , 13, R46	18.3	50
102	Genome-wide association study reveals multiple loci associated with primary tooth development during infancy. <i>PLoS Genetics</i> , 2010 , 6, e1000856	6	50
101	Obesity-susceptibility loci have a limited influence on birth weight: a meta-analysis of up to 28,219 individuals. <i>American Journal of Clinical Nutrition</i> , 2011 , 93, 851-60	7	50
100	Small deletion variants have stable breakpoints commonly associated with alu elements. <i>PLoS ONE</i> , 2008 , 3, e3104	3.7	49
99	Metabolic profiling of polycystic ovary syndrome reveals interactions with abdominal obesity. <i>International Journal of Obesity</i> , 2017 , 41, 1331-1340	5.5	43
98	Enhanced protein domain discovery by using language modeling techniques from speech recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 4516-20	11.5	42
97	Life-threatening infections in children in Europe (the EUCLIDS Project): a prospective cohort study. <i>The Lancet Child and Adolescent Health</i> , 2018 , 2, 404-414	14.5	40
96	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. <i>Science Advances</i> , 2019 , 5, eaaw3095	14.3	39
95	cnvHap: an integrative population and haplotype-based multiplatform model of SNPs and CNVs. <i>Nature Methods</i> , 2010 , 7, 541-6	21.6	37
94	Genetic Variation in the SLC8A1 Calcium Signaling Pathway Is Associated With Susceptibility to Kawasaki Disease and Coronary Artery Abnormalities. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 559-568		33
93	Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively associated β-carotene and starch content in hexaploid sweetpotato [<i>Ipomoea batatas</i> (L.) Lam.]. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 23-36	6	33
92	Inferring combined CNV/SNP haplotypes from genotype data. <i>Bioinformatics</i> , 2010 , 26, 1437-45	7.2	29
91	Novel association approach for variable number tandem repeats (VNTRs) identifies DOCK5 as a susceptibility gene for severe obesity. <i>Human Molecular Genetics</i> , 2012 , 21, 3727-38	5.6	29
90	Multifactorial chromosomal variants regulate polymyxin resistance in extensively drug-resistant <i>Klebsiella pneumoniae</i> . <i>Microbial Genomics</i> , 2018 , 4,	4.4	28
89	Rare genomic structural variants in complex disease: lessons from the replication of associations with obesity. <i>PLoS ONE</i> , 2013 , 8, e58048	3.7	27
88	A complete high-quality MinION nanopore assembly of an extensively drug-resistant <i>Mycobacterium tuberculosis</i> Beijing lineage strain identifies novel variation in repetitive PE/PPE gene regions. <i>Microbial Genomics</i> , 2018 , 4,	4.4	26
87	Natural resistance to Meningococcal Disease related to CFH loci: Meta-analysis of genome-wide association studies. <i>Scientific Reports</i> , 2016 , 6, 35842	4.9	26
86	Diagnosis of Bacterial Infection Using a 2-Transcript Host RNA Signature in Febrile Infants 60 Days or Younger. <i>JAMA - Journal of the American Medical Association</i> , 2017 , 317, 1577-1578	27.4	25

85	Mycobacterium tuberculosis Exploits a Molecular Off Switch of the Immune System for Intracellular Survival. <i>Scientific Reports</i> , 2018 , 8, 661	4.9	25
84	cnvHiTSeq: integrative models for high-resolution copy number variation detection and genotyping using population sequencing data. <i>Genome Biology</i> , 2012 , 13, R120	18.3	24
83	Transcriptomic Studies of Malaria: a Paradigm for Investigation of Systemic Host-Pathogen Interactions. <i>Microbiology and Molecular Biology Reviews</i> , 2018 , 82,	13.2	22
82	Realtime analysis and visualization of MinION sequencing data with npReader. <i>Bioinformatics</i> , 2016 , 32, 764-6	7.2	22
81	nplnv: accurate detection and genotyping of inversions using long read sub-alignment. <i>BMC Bioinformatics</i> , 2018 , 19, 261	3.6	22
80	Comparison of long-read methods for sequencing and assembly of a plant genome. <i>GigaScience</i> , 2020 , 9,	7.6	22
79	An exome sequencing pipeline for identifying and genotyping common CNVs associated with disease with application to psoriasis. <i>Bioinformatics</i> , 2012 , 28, i370-i374	7.2	21
78	Disease association tests by inferring ancestral haplotypes using a hidden markov model. <i>Bioinformatics</i> , 2008 , 24, 972-8	7.2	21
77	Demographic and motor features associated with the occurrence of neuropsychiatric and sleep complications of Parkinson's disease. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2013 , 84, 883-7	5.5	20
76	Multi-clonal evolution of multi-drug-resistant/extensively drug-resistant Mycobacterium tuberculosis in a high-prevalence setting of Papua New Guinea for over three decades. <i>Microbial Genomics</i> , 2018 , 4,	4.4	19
75	LobSig is a multigene predictor of outcome in invasive lobular carcinoma. <i>Npj Breast Cancer</i> , 2019 , 5, 18	7.8	19
74	A new scoring system derived from base excess and platelet count at presentation predicts mortality in paediatric meningococcal sepsis. <i>Critical Care</i> , 2013 , 17, R68	10.8	19
73	Improved techniques for the identification of pseudogenes. <i>Bioinformatics</i> , 2004 , 20 Suppl 1, i94-100	7.2	19
72	Complete Genome Sequence of <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> Strain ATCC 700603. <i>Genome Announcements</i> , 2016 , 4,		19
71	Genotype-free demultiplexing of pooled single-cell RNA-seq. <i>Genome Biology</i> , 2019 , 20, 290	18.3	19
70	The Early Growth Genetics (EGG) and EARly Genetics and Lifecourse Epidemiology (EAGLE) consortia: design, results and future prospects. <i>European Journal of Epidemiology</i> , 2019 , 34, 279-300	12.1	18
69	Inference of haplotypic phase and missing genotypes in polyploid organisms and variable copy number genomic regions. <i>BMC Bioinformatics</i> , 2008 , 9, 513	3.6	18
68	Data-driven estimation of COVID-19 community prevalence through wastewater-based epidemiology. <i>Science of the Total Environment</i> , 2021 , 789, 147947	10.2	17

67	Enhanced protein domain discovery using taxonomy. <i>BMC Bioinformatics</i> , 2004 , 5, 56	3.6	14
66	Evaluating the genome and resistome of extensively drug-resistant <i>Klebsiella pneumoniae</i> using native DNA and RNA Nanopore sequencing. <i>GigaScience</i> , 2020 , 9,	7.6	13
65	Modelling pathogen load dynamics to elucidate mechanistic determinants of host- <i>Plasmodium falciparum</i> interactions. <i>Nature Microbiology</i> , 2019 , 4, 1592-1602	26.6	12
64	A population model for genotyping indels from next-generation sequence data. <i>Nucleic Acids Research</i> , 2013 , 41, e46	20.1	12
63	Dysregulation of complement system and CD4+ T cell activation pathways implicated in allergic response. <i>PLoS ONE</i> , 2013 , 8, e74821	3.7	12
62	Octapeptin C4 and polymyxin resistance occur via distinct pathways in an epidemic XDR <i>Klebsiella pneumoniae</i> ST258 isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 582-593	5.1	11
61	No evidence of SARS-CoV-2 reverse transcription and integration as the origin of chimeric transcripts in patient tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	11
60	Cross-Border Movement of Highly Drug-Resistant <i>Mycobacterium tuberculosis</i> from Papua New Guinea to Australia through Torres Strait Protected Zone, 2010-2015. <i>Emerging Infectious Diseases</i> , 2019 , 25, 406-415	10.2	9
59	The effect of genomic inversions on estimation of population genetic parameters from SNP data. <i>Genetics</i> , 2013 , 193, 243-53	4	9
58	cnvOffSeq: detecting intergenic copy number variation using off-target exome sequencing data. <i>Bioinformatics</i> , 2014 , 30, i639-45	7.2	9
57	invertFREGENE: software for simulating inversions in population genetic data. <i>Bioinformatics</i> , 2010 , 26, 838-40	7.2	9
56	famCNV: copy number variant association for quantitative traits in families. <i>Bioinformatics</i> , 2011 , 27, 1873-5	7.2	9
55	Childhood tuberculosis is associated with decreased abundance of T cell gene transcripts and impaired T cell function. <i>PLoS ONE</i> , 2017 , 12, e0185973	3.7	9
54	Transcriptional and epi-transcriptional dynamics of SARS-CoV-2 during cellular infection. <i>Cell Reports</i> , 2021 , 35, 109108	10.6	9
53	Phase I Trial of Inducible Caspase 9 T Cells in Adult Stem Cell Transplant Demonstrates Massive Clonotypic Proliferative Potential and Long-term Persistence of Transgenic T Cells. <i>Clinical Cancer Research</i> , 2019 , 25, 1749-1755	12.9	8
52	Rapid diagnosis of <i>Capnocytophaga canimorsus</i> septic shock in an immunocompetent individual using real-time Nanopore sequencing: a case report. <i>BMC Infectious Diseases</i> , 2019 , 19, 660	4	8
51	cnvCapSeq: detecting copy number variation in long-range targeted resequencing data. <i>Nucleic Acids Research</i> , 2014 , 42, e158	20.1	8
50	Accurate single-nucleotide polymorphism allele assignment in trisomic or duplicated regions by using a single base-extension assay with MALDI-TOF mass spectrometry. <i>Clinical Chemistry</i> , 2011 , 57, 1188-95	5.5	8

49	Scaffolding and Completing Genome Assemblies in Real-time with Nanopore Sequencing		8
48	Fine-scale estimation of location of birth from genome-wide single-nucleotide polymorphism data. <i>Genetics</i> , 2012 , 190, 669-77	4	7
47	Gene-targeted analysis of copy number variants identifies 3 novel associations with coronary heart disease traits. <i>Circulation: Cardiovascular Genetics</i> , 2012 , 5, 555-60		7
46	Assembly of whole-chromosome pseudomolecules for polyploid plant genomes using outbred mapping populations. <i>Nature Genetics</i> , 2020 , 52, 1256-1264	36.3	7
45	Positive-unlabeled learning in bioinformatics and computational biology: a brief review. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	6
44	Simulating the dynamics of targeted capture sequencing with CapSim. <i>Bioinformatics</i> , 2018 , 34, 873-874	7.2	5
43	Investigation of the HIN200 locus in UK SLE families identifies novel copy number variants. <i>Annals of Human Genetics</i> , 2011 , 75, 383-97	2.2	5
42	Genotype-free demultiplexing of pooled single-cell RNA-seq		5
41	Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinION™ sequencing		5
40	Identification of reduced host transcriptomic signatures for tuberculosis and digital PCR-based validation and quantification		5
39	Plasma lipid profiles discriminate bacterial from viral infection in febrile children. <i>Scientific Reports</i> , 2019 , 9, 17714	4.9	5
38	HLA-C variants associated with amino acid substitutions in the peptide binding groove influence susceptibility to Kawasaki disease. <i>Human Immunology</i> , 2019 , 80, 731-738	2.3	4
37	Whole-exome Sequencing for the Identification of Rare Variants in Primary Immunodeficiency Genes in Children With Sepsis: A Prospective, Population-based Cohort Study. <i>Clinical Infectious Diseases</i> , 2020 , 71, e614-e623	11.6	4
36	sCNPhase: using haplotype resolved read depth to genotype somatic copy number alterations from low cellularity aneuploid tumors. <i>Nucleic Acids Research</i> , 2017 , 45, e34	20.1	4
35	Real-time demultiplexing Nanopore barcoded sequencing data with npBarcode. <i>Bioinformatics</i> , 2017 , 33, 3988-3990	7.2	4
34	Chiron: Translating nanopore raw signal directly into nucleotide sequence using deep learning		4
33	Identification of Reduced Host Transcriptomic Signatures for Tuberculosis Disease and Digital PCR-Based Validation and Quantification. <i>Frontiers in Immunology</i> , 2021 , 12, 637164	8.4	4
32	Identification of regulatory variants associated with genetic susceptibility to meningococcal disease. <i>Scientific Reports</i> , 2019 , 9, 6966	4.9	3

31	YHap: a population model for probabilistic assignment of Y haplogroups from re-sequencing data. <i>BMC Bioinformatics</i> , 2013 , 14, 331	3.6	3
30	Comparison of long read methods for sequencing and assembly of a plant genome		3
29	GtTR: Bayesian estimation of absolute tandem repeat copy number using sequence capture and high throughput sequencing. <i>BMC Bioinformatics</i> , 2018 , 19, 267	3.6	2
28	Correction for Schumann et al., Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 9316-9316	11.5	2
27	Computational analysis and prediction of PE_PGRS proteins using machine learning.. <i>Computational and Structural Biotechnology Journal</i> , 2022 , 20, 662-674	6.8	2
26	A complete high quality nanopore-only assembly of an XDR Mycobacterium tuberculosis Beijing lineage strain identifies novel variation in repetitive PE/PPE gene regions		2
25	Real-time resolution of short-read assembly graph using ONT long reads. <i>PLoS Computational Biology</i> , 2021 , 17, e1008586	5	2
24	Complete Genome Sequences of Clinical <i>Pandora</i> fibrosis Isolates. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
23	Understanding Detrimental Host Response to Infection-The Promise of Transcriptomics.. <i>Pediatric Critical Care Medicine</i> , 2022 , 23, 133-135	3	1
22	Insights into population structure of East African sweetpotato cultivars from hybrid assembly of chloroplast genomes. <i>Gates Open Research</i> , 2018 , 2, 41	2.4	1
21	Nanoq: ultra-fast quality control for nanopore reads. <i>Journal of Open Source Software</i> , 2022 , 7, 2991	5.2	1
20	GtTR: Bayesian estimation of absolute tandem repeat copy number using sequence capture and high throughput sequencing		1
19	Insights into population structure of East African sweetpotato cultivars from hybrid assembly of chloroplast genomes. <i>Gates Open Research</i> , 2018 , 2, 41	2.4	1
18	Assembly of whole-chromosome pseudomolecules for polyploid plant genomes using outcrossed mapping populations		1
17	npInv: accurate detection and genotyping of inversions mediated by non-allelic homologous recombination using long read sub-alignment		1
16	Octapeptin C4 Induces Less Resistance and Novel Mutations in an Epidemic Carbapenemase-producing <i>Klebsiella pneumoniae</i> ST258 Clinical Isolate Compared to Polymyxins		1
15	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing		1
14	Real-time demultiplexing Nanopore barcoded sequencing data with npBarcode		1

13	Simulating the Dynamics of Targeted Capture Sequencing with CapSim		1
12	Multi-clonal evolution of MDR/XDRM. tuberculosis in a high prevalence setting in Papua New Guinea over three decades		1
11	Genomic epidemiology of tuberculosis in eastern Malaysia: insights for strengthening public health responses. <i>Microbial Genomics</i> , 2021 , 7,	4.4	1
10	Optimising Treatment Outcomes for Children and Adults Through Rapid Genome Sequencing of Sepsis Pathogens. A Study Protocol for a Prospective, Multi-Centre Trial (DIRECT). <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 667680	5.9	1
9	Retooling phage display with electrohydrodynamic nanomixing and nanopore sequencing. <i>Lab on a Chip</i> , 2019 , 19, 4083-4092	7.2	1
8	Ongoing human chromosome end extension revealed by analysis of BioNano and nanopore data. <i>Scientific Reports</i> , 2018 , 8, 16616	4.9	1
7	Molecular Methods for Pathogenic Bacteria Detection and Recent Advances in Wastewater Analysis. <i>Water (Switzerland)</i> , 2021 , 13, 3551	3	1
6	Long-read RNA sequencing identifies polyadenylation elongation and differential transcript usage of host transcripts during SARS-CoV-2 in vitro infection		1
5	New technologies for diagnosing active TB: the VANTDET diagnostic accuracy study. <i>Efficacy and Mechanism Evaluation</i> , 2021 , 8, 1-160	1.7	0
4	Signatures of TSPAN8 variants associated with human metabolic regulation and diseases. <i>iScience</i> , 2021 , 24, 102893	6.1	0
3	Long-Read RNA Sequencing Identifies Polyadenylation Elongation and Differential Transcript Usage of Host Transcripts During SARS-CoV-2 Infection.. <i>Frontiers in Immunology</i> , 2022 , 13, 832223	8.4	0
2	Evolution and spread of a highly drug resistant strain of Mycobacterium tuberculosis in Papua New Guinea.. <i>BMC Infectious Diseases</i> , 2022 , 22, 437	4	0
1	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing. <i>F1000Research</i> , 9, 1084	3.6	