Lachlan J Coin

List of Publications by Year
in descending order

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141 papers	50,412 citations	30551 56 h-index	10955 142 g-index
182 all docs	182 docs citations	182 times ranked	82303 citing authors

#	Article	IF	Citations
1	Positive-unlabeled learning in bioinformatics and computational biology: a brief review. Briefings in Bioinformatics, 2022, 23, .	3.2	26
2	Nanoq: ultra-fast quality control for nanopore reads. Journal of Open Source Software, 2022, 7, 2991.	2.0	18
3	Computational analysis and prediction of PE_PGRS proteins using machine learning. Computational and Structural Biotechnology Journal, 2022, 20, 662-674.	1.9	12
4	Understanding Detrimental Host Response to Infectionâ€"The Promise of Transcriptomics*. Pediatric Critical Care Medicine, 2022, 23, 133-135.	0.2	1
5	Phylodynamic Inference of Bacterial Outbreak Parameters Using Nanopore Sequencing. Molecular Biology and Evolution, 2022, 39, .	3.5	9
6	Long-Read RNA Sequencing Identifies Polyadenylation Elongation and Differential Transcript Usage of Host Transcripts During SARS-CoV-2 In Vitro Infection. Frontiers in Immunology, 2022, 13, 832223.	2.2	9
7	Evolution and spread of a highly drug resistant strain of Mycobacterium tuberculosis in Papua New Guinea. BMC Infectious Diseases, 2022, 22, 437.	1.3	8
8	Real-time resolution of short-read assembly graph using ONT long reads. PLoS Computational Biology, 2021, 17, e1008586.	1.5	4
9	Identification of Reduced Host Transcriptomic Signatures for Tuberculosis Disease and Digital PCR-Based Validation and Quantification. Frontiers in Immunology, 2021, 12, 637164.	2.2	25
10	New technologies for diagnosing active TB: the VANTDET diagnostic accuracy study. Efficacy and Mechanism Evaluation, 2021, 8, 1-160.	0.9	2
11	Genomic epidemiology of tuberculosis in eastern Malaysia: insights for strengthening public health responses. Microbial Genomics, 2021, 7, .	1.0	4
12	Transcriptional and epi-transcriptional dynamics of SARS-CoV-2 during cellular infection. Cell Reports, 2021, 35, 109108.	2.9	25
13	Optimising Treatment Outcomes for Children and Adults Through Rapid Genome Sequencing of Sepsis Pathogens. A Study Protocol for a Prospective, Multi-Centre Trial (DIRECT). Frontiers in Cellular and Infection Microbiology, 2021, 11, 667680.	1.8	10
14	No evidence of SARS-CoV-2 reverse transcription and integration as the origin of chimeric transcripts in patient tissues. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	28
15	Signatures of TSPAN8 variants associated with human metabolic regulation and diseases. IScience, 2021, 24, 102893.	1.9	5
16	Data-driven estimation of COVID-19 community prevalence through wastewater-based epidemiology. Science of the Total Environment, 2021, 789, 147947.	3.9	54
17	Molecular Methods for Pathogenic Bacteria Detection and Recent Advances in Wastewater Analysis. Water (Switzerland), 2021, 13, 3551.	1.2	18
18	Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively associated Î²-carotene and starch content in hexaploid sweetpotato [Ipomoea batatas (L.) Lam.]. Theoretical and Applied Genetics, 2020, 133, 23-36.	1.8	59

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19	Assembly of whole-chromosome pseudomolecules for polyploid plant genomes using outbred mapping populations. Nature Genetics, 2020, 52, 1256-1264.	9.4	13
20	Nanopore sequencing as a scalable, cost-effective platform for analyzing polyclonal vector integration sites following clinical T cell therapy. , 2020, 8, e000299.		5
21	Whole-exome Sequencing for the Identification of Rare Variants in Primary Immunodeficiency Genes in Children With Sepsis: A Prospective, Population-based Cohort Study. Clinical Infectious Diseases, 2020, 71, e614-e623.	2.9	12
22	Evaluating the genome and resistome of extensively drug-resistant Klebsiella pneumoniae using native DNA and RNA Nanopore sequencing. GigaScience, 2020, 9, .	3.3	22
23	Complete Genome Sequences of Clinical Pandoraea fibrosis Isolates. Microbiology Resource Announcements, 2020, 9, .	0.3	1
24	Comparison of long-read methods for sequencing and assembly of a plant genome. GigaScience, 2020, 9, .	3.3	62
25	Rapid diagnosis of Capnocytophaga canimorsus septic shock in an immunocompetent individual using real-time Nanopore sequencing: a case report. BMC Infectious Diseases, 2019, 19, 660.	1.3	16
26	LobSig is a multigene predictor of outcome in invasive lobular carcinoma. Npj Breast Cancer, 2019, 5, 18.	2.3	28
27	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	4.7	86
28	HLA-C variants associated with amino acid substitutions in the peptide binding groove influence susceptibility to Kawasaki disease. Human Immunology, 2019, 80, 731-738.	1.2	5
29	Modelling pathogen load dynamics to elucidate mechanistic determinants of hostâ€“Plasmodium falciparum interactions. Nature Microbiology, 2019, 4, 1592-1602.	5.9	19
30	Identification of regulatory variants associated with genetic susceptibility to meningococcal disease. Scientific Reports, 2019, 9, 6966.	1.6	3
31	The Early Growth Genetics (EGG) and EArly Genetics and Lifecourse Epidemiology (EAGLE) consortia: design, results and future prospects. European Journal of Epidemiology, 2019, 34, 279-300.	2.5	26
32	Cross-Border Movement of Highly Drug-Resistant Mycobacterium tuberculosis from Papua New Guinea to Australia through Torres Strait Protected Zone, 2010â€“2015. Emerging Infectious Diseases, 2019, 25, 406-415.	2.0	19
33	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. Clinical Cancer Research, 2019, 25, 1749-1755.	3.2	18
34	Genotype-free demultiplexing of pooled single-cell RNA-seq. Genome Biology, 2019, 20, 290.	3.8	55
35	Retooling phage display with electrohydrodynamic nanomixing and nanopore sequencing. Lab on A Chip, 2019, 19, 4083-4092.	3.1	8
36	Plasma lipid profiles discriminate bacterial from viral infection in febrile children. Scientific Reports, 2019, 9, 17714.	1.6	15

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37	Octapeptin C4 and polymyxin resistance occur via distinct pathways in an epidemic XDRKlebsiella pneumoniaeST258 isolate. Journal of Antimicrobial Chemotherapy, 2019, 74, 582-593.	1.3	16
38	Chiron: translating nanopore raw signal directly into nucleotide sequence using deep learning. GigaScience, 2018, 7, .	3.3	123
39	Simulating the dynamics of targeted capture sequencing with CapSim. Bioinformatics, 2018, 34, 873-874.	1.8	14
40	Mycobacterium tuberculosis Exploits a Molecular Off Switch of the Immune System for Intracellular Survival. Scientific Reports, 2018, 8, 661.	1.6	33
41	Transcriptomic Studies of Malaria: a Paradigm for Investigation of Systemic Host-Pathogen Interactions. Microbiology and Molecular Biology Reviews, 2018, 82, .	2.9	45
42	Ongoing human chromosome end extension revealed by analysis of BioNano and nanopore data. Scientific Reports, 2018, 8, 16616.	1.6	1
43	Multifactorial chromosomal variants regulate polymyxin resistance in extensively drug-resistant Klebsiella pneumoniae. Microbial Genomics, 2018, 4, .	1.0	39
44	Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement. Nature Communications, 2018, 9, 4580.	5.8	181
45	Triclosan at environmentally relevant concentrations promotes horizontal transfer of multidrug resistance genes within and across bacterial genera. Environment International, 2018, 121, 1217-1226.	4.8	182
46	Life-threatening infections in children in Europe (the EUCLIDS Project): a prospective cohort study. The Lancet Child and Adolescent Health, 2018, 2, 404-414.	2.7	69
47	Integrated pathogen load and dual transcriptome analysis of systemic host-pathogen interactions in severe malaria. Science Translational Medicine, 2018, 10, .	5.8	98
48	Diagnosis of Kawasaki Disease Using a Minimal Whole-Blood Gene Expression Signature. JAMA Pediatrics, 2018, 172, e182293.	3.3	92
49	nplnv: accurate detection and genotyping of inversions using long read sub-alignment. BMC Bioinformatics, 2018, 19, 261.	1.2	29
50	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. Microbial Genomics, 2018, 4, .	1.0	33
51	GtTR: Bayesian estimation of absolute tandem repeat copy number using sequence capture and high throughput sequencing. BMC Bioinformatics, 2018, 19, 267.	1.2	2
52	Non-antibiotic antimicrobial triclosan induces multiple antibiotic resistance through genetic mutation. Environment International, 2018, 118, 257-265.	4.8	131
53	A complete high-quality MinION nanopore assembly of an extensively drug-resistant Mycobacterium tuberculosis Beijing lineage strain identifies novel variation in repetitive PE/PPE gene regions. Microbial Genomics, 2018, 4, .	1.0	35
54	Insights into population structure of East African sweetpotato cultivars from hybrid assembly of chloroplast genomes. Gates Open Research, 2018, 2, 41.	2.0	1

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55	Insights into population structure of East African sweetpotato cultivars from hybrid assembly of chloroplast genomes. Gates Open Research, 2018, 2, 41.	2.0	1
56	Scaffolding and completing genome assemblies in real-time with nanopore sequencing. Nature Communications, 2017, 8, 14515.	5.8	104
57	Diagnosis of Bacterial Infection Using a 2-Transcript Host RNA Signature in Febrile Infants 60 Days or Younger. JAMA - Journal of the American Medical Association, 2017, 317, 1577.	3.8	46
58	Metabolic profiling of polycystic ovary syndrome reveals interactions with abdominal obesity. International Journal of Obesity, 2017, 41, 1331-1340.	1.6	64
59	Real-time demultiplexing Nanopore barcoded sequencing data with npBarcode. Bioinformatics, 2017, 33, 3988-3990.	1.8	6
60	sCNAphase: using haplotype resolved read depth to genotype somatic copy number alterations from low cellularity aneuploid tumors. Nucleic Acids Research, 2017, 45, e34-e34.	6.5	7
61	Childhood tuberculosis is associated with decreased abundance of T cell gene transcripts and impaired T cell function. PLoS ONE, 2017, 12, e0185973.	1.1	15
62	Complete Genome Sequence of Klebsiella quasipneumoniae subsp. similipneumoniae Strain ATCC 700603. Genome Announcements, 2016, 4, .	0.8	44
63	Natural resistance to Meningococcal Disease related to CFH loci: Meta-analysis of genome-wide association studies. Scientific Reports, 2016, 6, 35842.	1.6	33
64	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. American Journal of Human Genetics, 2016, 98, 830-842.	2.6	201
65	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	9.4	273
66	Diagnostic Test Accuracy of a 2-Transcript Host RNA Signature for Discriminating Bacterial vs Viral Infection in Febrile Children. JAMA - Journal of the American Medical Association, 2016, 316, 835.	3.8	263
67	Genetic Variation in the SLC8A1 Calcium Signaling Pathway Is Associated With Susceptibility to Kawasaki Disease and Coronary Artery Abnormalities. Circulation: Cardiovascular Genetics, 2016, 9, 559-568.	5.1	45
68	Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinION™ sequencing. GigaScience, 2016, 5, 32.	3.3	79
69	Realtime analysis and visualization of MinION sequencing data with npReader. Bioinformatics, 2016, 32, 764-766.	1.8	25
70	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
71	cnvOffSeq: detecting intergenic copy number variation using off-target exome sequencing data. Bioinformatics, 2014, 30, i639-i645.	1.8	13
72	Diagnosis of Childhood Tuberculosis and Host RNA Expression in Africa. New England Journal of Medicine, 2014, 370, 1712-1723.	13.9	324

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73	cnvCapSeq: detecting copy number variation in long-range targeted resequencing data. Nucleic Acids Research, 2014, 42, e158-e158.	6.5	14
74	Genetic variability in the regulation of gene expression in ten regions of the human brain. Nature Neuroscience, 2014, 17, 1418-1428.	7.1	620
75	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	2.6	73
76	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. Nature Genetics, 2013, 45, 902-906.	9.4	221
77	The Effect of Genomic Inversions on Estimation of Population Genetic Parameters from SNP Data. Genetics, 2013, 193, 243-253.	1.2	12
78	A new scoring system derived from base excess and platelet count at presentation predicts mortality in paediatric meningococcal sepsis. Critical Care, 2013, 17, R68.	2.5	24
79	YHap: a population model for probabilistic assignment of Y haplogroups from re-sequencing data. BMC Bioinformatics, 2013, 14, 331.	1.2	6
80	Detection of Tuberculosis in HIV-Infected and -Uninfected African Adults Using Whole Blood RNA Expression Signatures: A Case-Control Study. PLoS Medicine, 2013, 10, e1001538.	3.9	314
81	Demographic and motor features associated with the occurrence of neuropsychiatric and sleep complications of Parkinson's disease. Journal of Neurology, Neurosurgery and Psychiatry, 2013, 84, 883-887.	0.9	25
82	A population model for genotyping indels from next-generation sequence data. Nucleic Acids Research, 2013, 41, e46-e46.	6.5	12
83	Rare Genomic Structural Variants in Complex Disease: Lessons from the Replication of Associations with Obesity. PLoS ONE, 2013, 8, e58048.	1.1	33
84	Dysregulation of Complement System and CD4+ T Cell Activation Pathways Implicated in Allergic Response. PLoS ONE, 2013, 8, e74821.	1.1	14
85	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
86	Fine-Scale Estimation of Location of Birth from Genome-Wide Single-Nucleotide Polymorphism Data. Genetics, 2012, 190, 669-677.	1.2	8
87	An exome sequencing pipeline for identifying and genotyping common CNVs associated with disease with application to psoriasis. Bioinformatics, 2012, 28, i370-i374.	1.8	24
88	Common variants at 6q22 and 17q21 are associated with intracranial volume. Nature Genetics, 2012, 44, 539-544.	9.4	126
89	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	9.4	130
90	Gene-Targeted Analysis of Copy Number Variants Identifies 3 Novel Associations With Coronary Heart Disease Traits. Circulation: Cardiovascular Genetics, 2012, 5, 555-560.	5.1	9

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91	Novel association approach for variable number tandem repeats (VNTRs) identifies DOCK5 as a susceptibility gene for severe obesity. Human Molecular Genetics, 2012, 21, 3727-3738.	1.4	37
92	Highly interconnected genes in disease-specific networks are enriched for disease-associated polymorphisms. Genome Biology, 2012, 13, R46.	13.9	60
93	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
94	cnvHiTSeq: integrative models for high-resolution copy number variation detection and genotyping using population sequencing data. Genome Biology, 2012, 13, R120.	13.9	26
95	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
96	MultiPhen: Joint Model of Multiple Phenotypes Can Increase Discovery in GWAS. PLoS ONE, 2012, 7, e34861.	1.1	339
97	Genome-Wide Association Studies of Asthma in Population-Based Cohorts Confirm Known and Suggested Loci and Identify an Additional Association near HLA. PLoS ONE, 2012, 7, e44008.	1.1	111
98	Transforming Growth Factor-Î² Signaling Pathway in Patients With Kawasaki Disease. Circulation: Cardiovascular Genetics, 2011, 4, 16-25.	5.1	127
99	TTC12-ANKK1-DRD2 and CHRNA5-CHRNA3-CHRNB4 Influence Different Pathways Leading to Smoking Behavior from Adolescence to Mid-Adulthood. Biological Psychiatry, 2011, 69, 650-660.	0.7	67
100	Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome de novo assembly. Nature Biotechnology, 2011, 29, 723-730.	9.4	113
101	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	13.7	394
102	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
103	Haplotype and isoform specific expression estimation using multi-mapping RNA-seq reads. Genome Biology, 2011, 12, R13.	13.9	224
104	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. Diabetes, 2011, 60, 2624-2634.	0.3	335
105	A genome-wide meta-analysis of genetic variants associated with allergic rhinitis and grass sensitization and their interaction with birth order. Journal of Allergy and Clinical Immunology, 2011, 128, 996-1005.	1.5	212
106	Investigation of the HIN200 Locus in UK SLE Families Identifies Novel Copy Number Variants. Annals of Human Genetics, 2011, 75, 383-397.	0.3	5
107	Accurate Single-Nucleotide Polymorphism Allele Assignment in Trisomic or Duplicated Regions by Using a Single Baseâ€“Extension Assay with MALDI-TOF Mass Spectrometry. Clinical Chemistry, 2011, 57, 1188-1195.	1.5	10
108	Obesity-susceptibility loci have a limited influence on birth weight: a meta-analysis of up to 28,219 individuals. American Journal of Clinical Nutrition, 2011, 93, 851-860.	2.2	58

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109	famCNV: copy number variant association for quantitative traits in families. Bioinformatics, 2011, 27, 1873-1875.	1.8	10
110	Pathway-driven gene stability selection of two rheumatoid arthritis GWAS identifies and validates new susceptibility genes in receptor mediated signalling pathways. Human Molecular Genetics, 2011, 20, 3494-3506.	1.4	72
111	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7119-7124.	3.3	258
112	A new highly penetrant form of obesity due to deletions on chromosome 16p11.2. Nature, 2010, 463, 671-675.	13.7	476
113	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
114	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. Nature Genetics, 2010, 42, 430-435.	9.4	223
115	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
116	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
117	cnvHap: an integrative population and haplotypeâ€“based multiplatform model of SNPs and CNVs. Nature Methods, 2010, 7, 541-546.	9.0	44
118	Inferring combined CNV/SNP haplotypes from genotype data. Bioinformatics, 2010, 26, 1437-1445.	1.8	31
119	Genome-Wide Association Study Reveals Multiple Loci Associated with Primary Tooth Development during Infancy. PLoS Genetics, 2010, 6, e1000856.	1.5	64
120	invertFREGENE: software for simulating inversions in population genetic data. Bioinformatics, 2010, 26, 838-840.	1.8	12
121	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
122	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
123	Pathway Analysis of GWAS Provides New Insights into Genetic Susceptibility to 3 Inflammatory Diseases. PLoS ONE, 2009, 4, e8068.	1.1	131
124	Genetic Loci Associated With C-Reactive Protein Levels and Risk of Coronary Heart Disease. JAMA - Journal of the American Medical Association, 2009, 302, 37.	3.8	544
125	Genetic Determinants of Height Growth Assessed Longitudinally from Infancy to Adulthood in the Northern Finland Birth Cohort 1966. PLoS Genetics, 2009, 5, e1000409.	1.5	131
126	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. Nature Genetics, 2009, 41, 35-46.	9.4	676

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127	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
128	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
129	Genome-wide association study for early-onset and morbid adult obesity identifies three new risk loci in European populations. Nature Genetics, 2009, 41, 157-159.	9.4	585
130	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
131	Inference of haplotypic phase and missing genotypes in polyploid organisms and variable copy number genomic regions. BMC Bioinformatics, 2008, 9, 513.	1.2	23
132	Disease association tests by inferring ancestral haplotypes using a hidden markov model. Bioinformatics, 2008, 24, 972-978.	1.8	22
133	Small Deletion Variants Have Stable Breakpoints Commonly Associated with Alu Elements. PLoS ONE, 2008, 3, e3104.	1.1	52
134	TreeFam: 2008 Update. Nucleic Acids Research, 2007, 36, D735-D740.	6.5	294
135	Improved techniques for the identification of pseudogenes. Bioinformatics, 2004, 20, i94-i100.	1.8	21
136	A census of human cancer genes. Nature Reviews Cancer, 2004, 4, 177-183.	12.8	2,868
137	Enhanced protein domain discovery using taxonomy. BMC Bioinformatics, 2004, 5, 56.	1.2	18
138	The Pfam protein families database. Nucleic Acids Research, 2004, 32, 138D-141.	6.5	3,084
139	Enhanced protein domain discovery by using language modeling techniques from speech recognition. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4516-4520.	3.3	47
140	Signatures of TSPAN8 Variants Associated with Human Metabolic Regulation and Diseases. SSRN Electronic Journal, 0, , .	0.4	0
141	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing. F1000Research, 0, 9, 1084.	0.8	0