

Ren L Warren

List of Publications by Citations

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Version: 2024-04-28

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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.

54
papers

4,660
citations

23
h-index

66
g-index

66
ext. papers

5,864
ext. citations

6.8
avg, IF

5.26
L-index

#	Paper	IF	Citations
54	Fusobacterium nucleatum infection is prevalent in human colorectal carcinoma. <i>Genome Research</i> , 2012 , 22, 299-306	9.7	1120
53	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , 2009 , 461, 809-13	50.4	879
52	Neo-antigens predicted by tumor genome meta-analysis correlate with increased patient survival. <i>Genome Research</i> , 2014 , 24, 743-50	9.7	440
51	Assembling millions of short DNA sequences using SSAKE. <i>Bioinformatics</i> , 2007 , 23, 500-1	7.2	357
50	ABYSS 2.0: resource-efficient assembly of large genomes using a Bloom filter. <i>Genome Research</i> , 2017 , 27, 768-777	9.7	305
49	Profiling the T-cell receptor beta-chain repertoire by massively parallel sequencing. <i>Genome Research</i> , 2009 , 19, 1817-24	9.7	280
48	Co-occurrence of anaerobic bacteria in colorectal carcinomas. <i>Microbiome</i> , 2013 , 1, 16	16.6	195
47	Improved white spruce (<i>Picea glauca</i>) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. <i>Plant Journal</i> , 2015 , 83, 189-212	6.9	136
46	LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. <i>GigaScience</i> , 2015 , 4, 35	7.6	124
45	Derivation of HLA types from shotgun sequence datasets. <i>Genome Medicine</i> , 2012 , 4, 95	14.4	118
44	Sealer: a scalable gap-closing application for finishing draft genomes. <i>BMC Bioinformatics</i> , 2015 , 16, 230	3.6	79
43	ARCS: scaffolding genome drafts with linked reads. <i>Bioinformatics</i> , 2018 , 34, 725-731	7.2	74
42	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. <i>Nature Communications</i> , 2017 , 8, 1433	17.4	56
41	Mating factor linkage and genome evolution in basidiomycetous pathogens of cereals. <i>Fungal Genetics and Biology</i> , 2006 , 43, 655-66	3.9	52
40	Activation of an endogenous retrovirus-associated long non-coding RNA in human adenocarcinoma. <i>Genome Medicine</i> , 2015 , 7, 22	14.4	40
39	Organellar Genomes of White Spruce (<i>Picea glauca</i>): Assembly and Annotation. <i>Genome Biology and Evolution</i> , 2015 , 8, 29-41	3.9	40
38	ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. <i>BMC Bioinformatics</i> , 2018 , 19, 234	3.6	36

37	Profiling model T-cell metagenomes with short reads. <i>Bioinformatics</i> , 2009 , 25, 458-64	7.2	35
36	Tigmint: correcting assembly errors using linked reads from large molecules. <i>BMC Bioinformatics</i> , 2018 , 19, 393	3.6	35
35	Targeted assembly of short sequence reads. <i>PLoS ONE</i> , 2011 , 6, e19816	3.7	31
34	ntEdit: scalable genome sequence polishing. <i>Bioinformatics</i> , 2019 , 35, 4430-4432	7.2	29
33	The Genome of the Beluga Whale (<i>Delphinapterus leucas</i>). <i>Genes</i> , 2017 , 8,	4.2	28
32	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X GenomicsUGemCode Sequencing Data. <i>PLoS ONE</i> , 2016 , 11, e0163059	3.7	27
31	RAILS and Cobbler: Scaffolding and automated finishing of draft genomes using long DNA sequences. <i>Journal of Open Source Software</i> , 2016 , 1, 116	5.2	16
30	The Genome of the Northern Sea Otter (<i>Enhydra lutris kenyoni</i>). <i>Genes</i> , 2017 , 8,	4.2	15
29	HLA predictions from the bronchoalveolar lavage fluid and blood samples of eight COVID-19 patients at the pandemic onset. <i>Bioinformatics</i> , 2021 , 36, 5271-5273	7.2	15
28	Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce (<i>Picea sitchensis</i>), Indicates a Complex Physical Structure. <i>Genome Biology and Evolution</i> , 2020 , 12, 1174-1179	3.9	13
27	Konnector v2.0: pseudo-long reads from paired-end sequencing data. <i>BMC Medical Genomics</i> , 2015 , 8 Suppl 3, S1	3.7	12
26	Retrospective in silico HLA predictions from COVID-19 patients reveal alleles associated with disease prognosis 2020 ,		12
25	Kollector: transcript-informed, targeted de novo assembly of gene loci. <i>Bioinformatics</i> , 2017 , 33, 1782-1788		8
24	ARCS: Assembly Roundup by Chromium Scaffolding		6
23	Largest Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce (<i>Picea sitchensis</i>), Indicates Complex Physical Structure		6
22	RNA-Bloom enables reference-free and reference-guided sequence assembly for single-cell transcriptomes. <i>Genome Research</i> , 2020 , 30, 1191-1200	9.7	6
21	ntJoin: Fast and lightweight assembly-guided scaffolding using minimizer graphs. <i>Bioinformatics</i> , 2020 , 36, 3885-3887	7.2	6
20	Konnector: Connecting paired-end reads using a bloom filter de Bruijn graph 2014 ,		5

19	ABYSS 2.0: Resource-Efficient Assembly of Large Genomes using a Bloom Filter		4
18	ntHits: de novo repeat identification of genomics data using a streaming approach		3
17	Complete Chloroplast Genome Sequence of a White Spruce (<i>Picea glauca</i> , Genotype WS77111) from Eastern Canada. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
16	ChopStitch: exon annotation and splice graph construction using transcriptome assembly and whole genome sequencing data. <i>Bioinformatics</i> , 2018 , 34, 1697-1704	7.2	2
15	Complete Chloroplast Genome Sequence of an Engelmann Spruce (, Genotype Se404-851) from Western Canada. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
14	Complete Genome Sequence of SJ42, a Nonoutbreak Strain from an Immunocompromised Patient with Pulmonary Disease. <i>Genome Announcements</i> , 2017 , 5,		2
13	HLA alleles measured from COVID-19 patient transcriptomes reveal associations with disease prognosis in a New York cohort. <i>PeerJ</i> , 2021 , 9, e12368	3.1	2
12	Establishment of an eHAP1 human haploid cell line hybrid reference genome assembled from short and long reads. <i>Genomics</i> , 2020 , 112, 2379-2384	4.3	1
11	LINKS: Scaffolding genome assemblies with kilobase-long nanopore reads 2015 ,		1
10	Visualizing genome synteny with xmatchview. <i>Journal of Open Source Software</i> , 2018 , 3, 497	5.2	1
9	Visualizing genome synteny with xmatchview		1
8	ntEdit: scalable genome assembly polishing		1
7	Complete Chloroplast Genome Sequence of a Black Spruce (<i>Picea mariana</i>) from Eastern Canada. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
6	LongStitch: high-quality genome assembly correction and scaffolding using long reads. <i>BMC Bioinformatics</i> , 2021 , 22, 534	3.6	0
5	GapPredict - A Language Model for Resolving Gaps in Draft Genome Assemblies. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 2802-2808	3	0
4	ntEdit+Sealer: Efficient Targeted Error Resolution and Automated Finishing of Long-Read Genome Assemblies.. <i>Current Protocols</i> , 2022 , 2, e442		0
3	RNA-Scoop: interactive visualization of transcripts in single-cell transcriptomes. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab105	3.7	
2	Interactive SARS-CoV-2 mutation timemaps. <i>F1000Research</i> , 2021 , 10, 68	3.6	

1 Interactive SARS-CoV-2 mutation timemaps. *F1000Research*, **2021**, 10, 68

3.6