

# Ren L Warren

## List of Publications by Year in Descending Order

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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	ntEdit+Sealer: Efficient Targeted Error Resolution and Automated Finishing of Long-Read Genome Assemblies.. <i>Current Protocols</i> , <b>2022</b> , 2, e442		0
53	RNA-Scoop: interactive visualization of transcripts in single-cell transcriptomes. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqab105	3.7	
52	HLA alleles measured from COVID-19 patient transcriptomes reveal associations with disease prognosis in a New York cohort. <i>PeerJ</i> , <b>2021</b> , 9, e12368	3.1	2
51	LongStitch: high-quality genome assembly correction and scaffolding using long reads. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 534	3.6	0
50	Interactive SARS-CoV-2 mutation timemaps. <i>F1000Research</i> , <b>2021</b> , 10, 68	3.6	
49	HLA predictions from the bronchoalveolar lavage fluid and blood samples of eight COVID-19 patients at the pandemic onset. <i>Bioinformatics</i> , <b>2021</b> , 36, 5271-5273	7.2	15
48	GapPredict - A Language Model for Resolving Gaps in Draft Genome Assemblies. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 2802-2808	3	0
47	Interactive SARS-CoV-2 mutation timemaps. <i>F1000Research</i> , <b>2021</b> , 10, 68	3.6	
46	Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce ( <i>Picea sitchensis</i> ), Indicates a Complex Physical Structure. <i>Genome Biology and Evolution</i> , <b>2020</b> , 12, 1174-1179	3.9	13
45	Establishment of an eHAP1 human haploid cell line hybrid reference genome assembled from short and long reads. <i>Genomics</i> , <b>2020</b> , 112, 2379-2384	4.3	1
44	Retrospective in silico HLA predictions from COVID-19 patients reveal alleles associated with disease prognosis <b>2020</b> ,		12
43	Complete Chloroplast Genome Sequence of a Black Spruce ( <i>Picea mariana</i> ) from Eastern Canada. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	1
42	RNA-Bloom enables reference-free and reference-guided sequence assembly for single-cell transcriptomes. <i>Genome Research</i> , <b>2020</b> , 30, 1191-1200	9.7	6
41	ntJoin: Fast and lightweight assembly-guided scaffolding using minimizer graphs. <i>Bioinformatics</i> , <b>2020</b> , 36, 3885-3887	7.2	6
40	Complete Chloroplast Genome Sequence of a White Spruce ( <i>Picea glauca</i> , Genotype WS77111) from Eastern Canada. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	2
39	ntEdit: scalable genome sequence polishing. <i>Bioinformatics</i> , <b>2019</b> , 35, 4430-4432	7.2	29
38	Complete Chloroplast Genome Sequence of an Engelmann Spruce (, Genotype Se404-851) from Western Canada. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	2

37	ChopStitch: exon annotation and splice graph construction using transcriptome assembly and whole genome sequencing data. <i>Bioinformatics</i> , <b>2018</b> , 34, 1697-1704	7.2	2
36	ARCS: scaffolding genome drafts with linked reads. <i>Bioinformatics</i> , <b>2018</b> , 34, 725-731	7.2	74
35	ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 234	3.6	36
34	Visualizing genome synteny with xmatchview. <i>Journal of Open Source Software</i> , <b>2018</b> , 3, 497	5.2	1
33	Tigmint: correcting assembly errors using linked reads from large molecules. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 393	3.6	35
32	Kollector: transcript-informed, targeted de novo assembly of gene loci. <i>Bioinformatics</i> , <b>2017</b> , 33, 1782-1788		8
31	ABYSS 2.0: resource-efficient assembly of large genomes using a Bloom filter. <i>Genome Research</i> , <b>2017</b> , 27, 768-777	9.7	305
30	Complete Genome Sequence of SJ42, a Nonoutbreak Strain from an Immunocompromised Patient with Pulmonary Disease. <i>Genome Announcements</i> , <b>2017</b> , 5,		2
29	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. <i>Nature Communications</i> , <b>2017</b> , 8, 1433	17.4	56
28	The Genome of the Beluga Whale ( <i>Delphinapterus leucas</i> ). <i>Genes</i> , <b>2017</b> , 8,	4.2	28
27	The Genome of the Northern Sea Otter ( <i>Enhydra lutris kenyoni</i> ). <i>Genes</i> , <b>2017</b> , 8,	4.2	15
26	RAILS and Cobbler: Scaffolding and automated finishing of draft genomes using long DNA sequences. <i>Journal of Open Source Software</i> , <b>2016</b> , 1, 116	5.2	16
25	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X GenomicsUGemCode Sequencing Data. <i>PLoS ONE</i> , <b>2016</b> , 11, e0163059	3.7	27
24	Activation of an endogenous retrovirus-associated long non-coding RNA in human adenocarcinoma. <i>Genome Medicine</i> , <b>2015</b> , 7, 22	14.4	40
23	LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. <i>GigaScience</i> , <b>2015</b> , 4, 35	7.6	124
22	Sealer: a scalable gap-closing application for finishing draft genomes. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 230	3.6	79
21	Organellar Genomes of White Spruce ( <i>Picea glauca</i> ): Assembly and Annotation. <i>Genome Biology and Evolution</i> , <b>2015</b> , 8, 29-41	3.9	40
20	Konnector v2.0: pseudo-long reads from paired-end sequencing data. <i>BMC Medical Genomics</i> , <b>2015</b> , 8 Suppl 3, S1	3.7	12

19	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> , <b>2015</b> , 83, 189-212	6.9	136
18	LINKS: Scaffolding genome assemblies with kilobase-long nanopore reads <b>2015</b> ,		1
17	Konnector: Connecting paired-end reads using a bloom filter de Bruijn graph <b>2014</b> ,		5
16	Neo-antigens predicted by tumor genome meta-analysis correlate with increased patient survival. <i>Genome Research</i> , <b>2014</b> , 24, 743-50	9.7	440
15	Co-occurrence of anaerobic bacteria in colorectal carcinomas. <i>Microbiome</i> , <b>2013</b> , 1, 16	16.6	195
14	<i>Fusobacterium nucleatum</i> infection is prevalent in human colorectal carcinoma. <i>Genome Research</i> , <b>2012</b> , 22, 299-306	9.7	1120
13	Derivation of HLA types from shotgun sequence datasets. <i>Genome Medicine</i> , <b>2012</b> , 4, 95	14.4	118
12	Targeted assembly of short sequence reads. <i>PLoS ONE</i> , <b>2011</b> , 6, e19816	3.7	31
11	Profiling model T-cell metagenomes with short reads. <i>Bioinformatics</i> , <b>2009</b> , 25, 458-64	7.2	35
10	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , <b>2009</b> , 461, 809-13	50.4	879
9	Profiling the T-cell receptor beta-chain repertoire by massively parallel sequencing. <i>Genome Research</i> , <b>2009</b> , 19, 1817-24	9.7	280
8	Assembling millions of short DNA sequences using SSAKE. <i>Bioinformatics</i> , <b>2007</b> , 23, 500-1	7.2	357
7	Mating factor linkage and genome evolution in basidiomycetous pathogens of cereals. <i>Fungal Genetics and Biology</i> , <b>2006</b> , 43, 655-66	3.9	52
6	Visualizing genome synteny with xmatchview		1
5	ntEdit: scalable genome assembly polishing		1
4	ABYSS 2.0: Resource-Efficient Assembly of Large Genomes using a Bloom Filter		4
3	ARCS: Assembly Roundup by Chromium Scaffolding		6
2	ntHits: de novo repeat identification of genomics data using a streaming approach		3

- 1 Largest Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce (*Picea sitchensis*), Indicates Complex Physical Structure