

Shaun D Jackman

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.

48 papers	8,834 citations	27 h-index	52 g-index
52 ext. papers	10,618 ext. citations	9.2 avg, IF	5.14 L-index

#	Paper	IF	Citations
48	ABYSS: a parallel assembler for short read sequence data. <i>Genome Research</i> , 2009 , 19, 1117-23	9.7	2508
47	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011 , 476, 298-303	50.4	1180
46	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013 , 45, 279-84	36.3	717
45	De novo assembly and analysis of RNA-seq data. <i>Nature Methods</i> , 2010 , 7, 909-12	21.6	701
44	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012 , 488, 49-56	50.4	596
43	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
42	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
41	De novo transcriptome assembly with ABYSS. <i>Bioinformatics</i> , 2009 , 25, 2872-7	7.2	326
40	ABYSS 2.0: resource-efficient assembly of large genomes using a Bloom filter. <i>Genome Research</i> , 2017 , 27, 768-777	9.7	305
39	Assembling the 20 Gb white spruce (<i>Picea glauca</i>) genome from whole-genome shotgun sequencing data. <i>Bioinformatics</i> , 2013 , 29, 1492-7	7.2	278
38	Concurrent CIC mutations, IDH mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. <i>Journal of Pathology</i> , 2012 , 226, 7-16	9.4	226
37	Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <i>Genome Biology</i> , 2013 , 14, R27	18.3	212
36	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
35	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020 , 38, 1347-1355	44.5	98
34	Sealer: a scalable gap-closing application for finishing draft genomes. <i>BMC Bioinformatics</i> , 2015 , 16, 230	3.6	79
33	Whole genome duplication and enrichment of metal cation transporters revealed by de novo genome sequencing of extremely halotolerant black yeast <i>Hortaea werneckii</i> . <i>PLoS ONE</i> , 2013 , 8, e71328	3.7	72
32	BioBloom tools: fast, accurate and memory-efficient host species sequence screening using bloom filters. <i>Bioinformatics</i> , 2014 , 30, 3402-4	7.2	58

31	The genome and transcriptome of the pine saprophyte <i>Ophiostoma piceae</i> , and a comparison with the bark beetle-associated pine pathogen <i>Grosmannia clavigera</i> . <i>BMC Genomics</i> , 2013 , 14, 373	4.5	54
30	On the Representation of de Bruijn Graphs. <i>Lecture Notes in Computer Science</i> , 2014 , 35-55	0.9	45
29	ABYSS-Explorer: visualizing genome sequence assemblies. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2009 , 15, 881-8	4	43
28	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
27	ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. <i>BMC Bioinformatics</i> , 2018 , 19, 234	3.6	36
26	Tigmint: correcting assembly errors using linked reads from large molecules. <i>BMC Bioinformatics</i> , 2018 , 19, 393	3.6	35
25	A robust benchmark for germline structural variant detection		34
24	Updated genome assembly and annotation of <i>Paenibacillus</i> larvae, the agent of American foulbrood disease of honey bees. <i>BMC Genomics</i> , 2011 , 12, 450	4.5	31
23	On the representation of de Bruijn graphs. <i>Journal of Computational Biology</i> , 2015 , 22, 336-52	1.7	30
22	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X GenomicsVGMCode Sequencing Data. <i>PLoS ONE</i> , 2016 , 11, e0163059	3.7	27
21	Genome sequence of <i>Mycoplasma capricolum</i> subsp. <i>capripneumoniae</i> strain M1601. <i>Journal of Bacteriology</i> , 2011 , 193, 6098-9	3.5	21
20	Assembling genomes using short-read sequencing technology. <i>Genome Biology</i> , 2010 , 11, 202	18.3	17
19	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
18	The Genome of the North American Brown Bear or Grizzly: <i>Ursus arctos</i> ssp. <i>horribilis</i> . <i>Genes</i> , 2018 , 9,	4.2	13
17	Konnector v2.0: pseudo-long reads from paired-end sequencing data. <i>BMC Medical Genomics</i> , 2015 , 8 Suppl 3, S1	3.7	12
16	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. <i>BMC Genomics</i> , 2013 , 14, 550	4.5	10
15	DIDA: Distributed Indexing Dispatched Alignment. <i>PLoS ONE</i> , 2015 , 10, e0126409	3.7	8
14	Kleat: cleavage site analysis of transcriptomes. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015 , 347-58	1.3	8

13	ORCA: a comprehensive bioinformatics container environment for education and research. <i>Bioinformatics</i> , 2019 , 35, 4448-4450	7.2	6
12	Largest Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce (<i>Picea sitchensis</i>), Indicates Complex Physical Structure		6
11	KLEAT: CLEAVAGE SITE ANALYSIS OF TRANSCRIPTOMES 2014 ,		5
10	Konnector: Connecting paired-end reads using a bloom filter de Bruijn graph 2014 ,		5
9	Spaced Seed Data Structures for De Novo Assembly. <i>International Journal of Genomics</i> , 2015 , 2015, 19652-19655	4.5	4
8	ABYSS 2.0: Resource-Efficient Assembly of Large Genomes using a Bloom Filter		4
7	The Genome of the Steller Sea Lion (). <i>Genes</i> , 2019 , 10,	4.2	3
6	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
5	Complete Chloroplast Genome Sequence of an Engelmann Spruce (, Genotype Se404-851) from Western Canada. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
4	Spaced seed data structures 2014 ,		1
3	Identification of Genes Frequently Mutated In FL and DLBCL with Transcriptome, Genome and Exome Sequencing. <i>Blood</i> , 2010 , 116, 804-804	2.2	1
2	UniqTag: Content-Derived Unique and Stable Identifiers for Gene Annotation. <i>PLoS ONE</i> , 2015 , 10, e0128026	3.7	0
1	Base-Pair Resolution of Somatic and Germline-Derived Genome Rearrangement Breakpoints in Follicular Lymphoma.. <i>Blood</i> , 2009 , 114, 439-439	2.2	