

# Shaun D Jackman

## List of Publications by Year in descending order

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Version: 2024-02-01

46  
papers

11,575  
citations

201385

27  
h-index

276539

41  
g-index

52  
all docs

52  
docs citations

52  
times ranked

20685  
citing authors

#	ARTICLE	IF	CITATIONS
1	ABYSS: A parallel assembler for short read sequence data. <i>Genome Research</i> , 2009, 19, 1117-1123.	2.4	3,134
2	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011, 476, 298-303.	13.7	1,428
3	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 279-284.	9.4	990
4	De novo assembly and analysis of RNA-seq data. <i>Nature Methods</i> , 2010, 7, 909-912.	9.0	886
5	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012, 488, 49-56.	13.7	761
6	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582
7	ABYSS 2.0: resource-efficient assembly of large genomes using a Bloom filter. <i>Genome Research</i> , 2017, 27, 768-777.	2.4	526
8	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
9	<i>De novo</i> transcriptome assembly with ABYSS. <i>Bioinformatics</i> , 2009, 25, 2872-2877.	1.8	371
10	Assembling the 20 Gb white spruce (<i>Picea glauca</i>) genome from whole-genome shotgun sequencing data. <i>Bioinformatics</i> , 2013, 29, 1492-1497.	1.8	356
11	Concurrent <i>CIC</i> mutations, <i>IDH</i> mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. <i>Journal of Pathology</i> , 2012, 226, 7-16.	2.1	272
12	Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <i>Genome Biology</i> , 2013, 14, R27.	13.9	260
13	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020, 38, 1347-1355.	9.4	233
14	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.	2.8	200
15	Sealer: a scalable gap-closing application for finishing draft genomes. <i>BMC Bioinformatics</i> , 2015, 16, 230.	1.2	122
16	Tigmint: correcting assembly errors using linked reads from large molecules. <i>BMC Bioinformatics</i> , 2018, 19, 393.	1.2	97
17	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.	1.1	96
18	BioBloom tools: fast, accurate and memory-efficient host species sequence screening using bloom filters. <i>Bioinformatics</i> , 2014, 30, 3402-3404.	1.8	95

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19	ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. BMC Bioinformatics, 2018, 19, 234.	1.2	81
20	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> . BMC Genomics, 2013, 14, 373.	1.2	72
21	On the Representation of de Bruijn Graphs. Lecture Notes in Computer Science, 2014, , 35-55.	1.0	67
22	ABYSS-Explorer: Visualizing Genome Sequence Assemblies. IEEE Transactions on Visualization and Computer Graphics, 2009, 15, 881-888.	2.9	53
23	Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce ( <i>Picea sitchensis</i> ), Indicates a Complex Physical Structure. Genome Biology and Evolution, 2020, 12, 1174-1179.	1.1	49
24	Organellar Genomes of White Spruce ( <i>Picea glauca</i> ): Assembly and Annotation. Genome Biology and Evolution, 2016, 8, 29-41.	1.1	46
25	On the Representation of De Bruijn Graphs. Journal of Computational Biology, 2015, 22, 336-352.	0.8	44
26	Updated genome assembly and annotation of <i>Paenibacillus</i> larvae, the agent of American foulbrood disease of honey bees. BMC Genomics, 2011, 12, 450.	1.2	35
27	The Genome of the North American Brown Bear or Grizzly: <i>Ursus arctos</i> ssp. <i>horribilis</i> . Genes, 2018, 9, 598.	1.0	34
28	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomics™ GemCode Sequencing Data. PLoS ONE, 2016, 11, e0163059.	1.1	31
29	Genome Sequence of <i>Mycoplasma capricolum</i> subsp. <i>capripneumoniae</i> Strain M1601. Journal of Bacteriology, 2011, 193, 6098-6099.	1.0	23
30	Assembling genomes using short-read sequencing technology. Genome Biology, 2010, 11, 202.	13.9	19
31	Konnector v2.0: pseudo-long reads from paired-end sequencing data. BMC Medical Genomics, 2015, 8, S1.	0.7	19
32	KLEAT: CLEAVAGE SITE ANALYSIS OF TRANSCRIPTOMES. , 2014, , .		14
33	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. BMC Genomics, 2013, 14, 550.	1.2	12
34	DIDA: Distributed Indexing Dispatched Alignment. PLoS ONE, 2015, 10, e0126409.	1.1	10
35	ORCA: a comprehensive bioinformatics container environment for education and research. Bioinformatics, 2019, 35, 4448-4450.	1.8	10
36	Konnector: Connecting paired-end reads using a bloom filter de Bruijn graph. , 2014, , .		8

#	ARTICLE	IF	CITATIONS
37	Kleat: cleavage site analysis of transcriptomes. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 347-58.	0.7	8
38	Complete Chloroplast Genome Sequence of a White Spruce ( <i>Picea glauca</i> , Genotype WS77111) from Eastern Canada. Microbiology Resource Announcements, 2019, 8, .	0.3	7
39	Spaced Seed Data Structures for De Novo Assembly. International Journal of Genomics, 2015, 2015, 1-8.	0.8	6
40	Physlr: Next-Generation Physical Maps. Dna, 2022, 2, 116-130.	0.4	5
41	The Genome of the Steller Sea Lion ( <i>Eumetopias jubatus</i> ). Genes, 2019, 10, 486.	1.0	4
42	Complete Chloroplast Genome Sequence of an Engelmann Spruce ( <i>Picea engelmannii</i> , Genotype) Tj ETQq0,0,0 rgBT /Overlock 1	0.3	4
43	Spaced seed data structures. , 2014, , .		1
44	Identification of Genes Frequently Mutated In FL and DLBCL with Transcriptome, Genome and Exome Sequencing. Blood, 2010, 116, 804-804.	0.6	1
45	Base-Pair Resolution of Somatic and Germline-Derived Genome Rearrangement Breakpoints in Follicular Lymphoma.. Blood, 2009, 114, 439-439.	0.6	0
46	UniqTag: Content-Derived Unique and Stable Identifiers for Gene Annotation. PLoS ONE, 2015, 10, e0128026.	1.1	0