

Shaun D Jackman

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/6833806/shaun-d-jackman-publications-by-year.pdf>
Version: 2024-04-11

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
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	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
47	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020 , 38, 1347-1355	44.5	98
46	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
45	ORCA: a comprehensive bioinformatics container environment for education and research. <i>Bioinformatics</i> , 2019 , 35, 4448-4450	7.2	6
44	The Genome of the Steller Sea Lion (). <i>Genes</i> , 2019 , 10,	4.2	3
43	Complete Chloroplast Genome Sequence of an Engelmann Spruce (, Genotype Se404-851) from Western Canada. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
42	ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. <i>BMC Bioinformatics</i> , 2018 , 19, 234	3.6	36
41	Tigmint: correcting assembly errors using linked reads from large molecules. <i>BMC Bioinformatics</i> , 2018 , 19, 393	3.6	35
40	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
39	ABYSS 2.0: resource-efficient assembly of large genomes using a Bloom filter. <i>Genome Research</i> , 2017 , 27, 768-777	9.7	305
38	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X GenomicsVGMCode Sequencing Data. <i>PLoS ONE</i> , 2016 , 11, e0163059	3.7	27
37	On the representation of de Bruijn graphs. <i>Journal of Computational Biology</i> , 2015 , 22, 336-52	1.7	30
36	Sealer: a scalable gap-closing application for finishing draft genomes. <i>BMC Bioinformatics</i> , 2015 , 16, 230	3.6	79
35	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
34	Konnector v2.0: pseudo-long reads from paired-end sequencing data. <i>BMC Medical Genomics</i> , 2015 , 8 Suppl 3, S1	3.7	12
33	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
32	DIDA: Distributed Indexing Dispatched Alignment. <i>PLoS ONE</i> , 2015 , 10, e0126409	3.7	8

31	Spaced Seed Data Structures for De Novo Assembly. <i>International Journal of Genomics</i> , 2015 , 2015, 1965-1971	2.1	4
30	Kleat: cleavage site analysis of transcriptomes. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015 , 347-58	1.3	8
29	UniqTag: Content-Derived Unique and Stable Identifiers for Gene Annotation. <i>PLoS ONE</i> , 2015 , 10, e0123026	3.7	26
28	KLEAT: CLEAVAGE SITE ANALYSIS OF TRANSCRIPTOMES 2014 ,		5
27	Konnector: Connecting paired-end reads using a bloom filter de Bruijn graph 2014 ,		5
26	Spaced seed data structures 2014 ,		1
25	BioBloom tools: fast, accurate and memory-efficient host species sequence screening using bloom filters. <i>Bioinformatics</i> , 2014 , 30, 3402-4	7.2	58
24	On the Representation of de Bruijn Graphs. <i>Lecture Notes in Computer Science</i> , 2014 , 35-55	0.9	45
23	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
22	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
21	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
20	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. <i>BMC Genomics</i> , 2013 , 14, 550	4.5	10
19	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013 , 45, 279-84	36.3	717
18	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
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	3.7	72
16	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
15	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012 , 488, 49-56	50.4	596
14	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011 , 476, 298-303	50.4	1180

13	Updated genome assembly and annotation of <i>Paenibacillus larvae</i> , the agent of American foulbrood disease of honey bees. <i>BMC Genomics</i> , 2011 , 12, 450	4.5	31
12	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
11	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
10	De novo assembly and analysis of RNA-seq data. <i>Nature Methods</i> , 2010 , 7, 909-12	21.6	701
9	Assembling genomes using short-read sequencing technology. <i>Genome Biology</i> , 2010 , 11, 202	18.3	17
8	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
7	ABYSS: a parallel assembler for short read sequence data. <i>Genome Research</i> , 2009 , 19, 1117-23	9.7	2508
6	De novo transcriptome assembly with ABYSS. <i>Bioinformatics</i> , 2009 , 25, 2872-7	7.2	326
5	ABYSS-Explorer: visualizing genome sequence assemblies. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2009 , 15, 881-8	4	43
4	Base-Pair Resolution of Somatic and Germline-Derived Genome Rearrangement Breakpoints in Follicular Lymphoma.. <i>Blood</i> , 2009 , 114, 439-439	2.2	
3	ABYSS 2.0: Resource-Efficient Assembly of Large Genomes using a Bloom Filter		4
2	Largest Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce (<i>Picea sitchensis</i>), Indicates Complex Physical Structure		6
1	A robust benchmark for germline structural variant detection		34