

Brent S Pedersen

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

5,964
citations

218381

26
h-index

233125

45
g-index

68
all docs

68
docs citations

68
times ranked

12869
citing authors

#	ARTICLE	IF	CITATIONS
1	A spectrum of free software tools for processing the VCF variant call format: vcflib, bio-vcf, cyvcf2, hts-nim and slivar. <i>PLoS Computational Biology</i> , 2022, 18, e1009123.	1.5	84
2	Go Get Data (GGD) is a framework that facilitates reproducible access to genomic data. <i>Nature Communications</i> , 2021, 12, 2151.	5.8	9
3	CaBagE: A Cas9-based Background Elimination strategy for targeted, long-read DNA sequencing. <i>PLoS ONE</i> , 2021, 16, e0241253.	1.1	17
4	De novo structural mutation rates and gamete-of-origin biases revealed through genome sequencing of 2,396 families. <i>American Journal of Human Genetics</i> , 2021, 108, 597-607.	2.6	57
5	Samplot: a platform for structural variant visual validation and automated filtering. <i>Genome Biology</i> , 2021, 22, 161.	3.8	52
6	Unfazed: parent-of-origin detection for large and small <i>de novo</i> variants. <i>Bioinformatics</i> , 2021, 37, 4860-4861.	1.8	4
7	Balancing efficient analysis and storage of quantitative genomics data with the D4 format and d4tools. <i>Nature Computational Science</i> , 2021, 1, 441-447.	3.8	4
8	Effective variant filtering and expected candidate variant yield in studies of rare human disease. <i>Npj Genomic Medicine</i> , 2021, 6, 60.	1.7	51
9	Somalier: rapid relatedness estimation for cancer and germline studies using efficient genome sketches. <i>Genome Medicine</i> , 2020, 12, 62.	3.6	48
10	Duphold: scalable, depth-based annotation and curation of high-confidence structural variant calls. <i>GigaScience</i> , 2019, 8, .	3.3	45
11	Overlooked roles of DNA damage and maternal age in generating human germline mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9491-9500.	3.3	155
12	A map of constrained coding regions in the human genome. <i>Nature Genetics</i> , 2019, 51, 88-95.	9.4	201
13	Large, three-generation human families reveal post-zygotic mosaicism and variability in germline mutation accumulation. <i>ELife</i> , 2019, 8, .	2.8	116
14	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018, 36, 338-345.	9.4	1,443
15	Mosdepth: quick coverage calculation for genomes and exomes. <i>Bioinformatics</i> , 2018, 34, 867-868.	1.8	638
16	GIGGLE: a search engine for large-scale integrated genome analysis. <i>Nature Methods</i> , 2018, 15, 123-126.	9.0	154
17	hts-nim: scripting high-performance genomic analyses. <i>Bioinformatics</i> , 2018, 34, 3387-3389.	1.8	28
18	SV-plaudit: A cloud-based framework for manually curating thousands of structural variants. <i>GigaScience</i> , 2018, 7, .	3.3	30

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19	GOATOOLS: A Python library for Gene Ontology analyses. <i>Scientific Reports</i> , 2018, 8, 10872.	1.6	717
20	Whole-genome analysis for effective clinical diagnosis and gene discovery in early infantile epileptic encephalopathy. <i>Npj Genomic Medicine</i> , 2018, 3, 22.	1.7	64
21	Methylene-tetrahydrofolate reductase contributes to allergic airway disease. <i>PLoS ONE</i> , 2018, 13, e0190916.	1.1	4
22	Regulation of <i>MUC5B</i> Expression in Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017, 57, 91-99.	1.4	75
23	Who's Who? Detecting and Resolving Sample Anomalies in Human DNA Sequencing Studies with Peddy. <i>American Journal of Human Genetics</i> , 2017, 100, 406-413.	2.6	173
24	cyvcf2: fast, flexible variant analysis with Python. <i>Bioinformatics</i> , 2017, 33, 1867-1869.	1.8	66
25	Combating subclonal evolution of resistant cancer phenotypes. <i>Nature Communications</i> , 2017, 8, 1231.	5.8	124
26	The nasal methylome and childhood atopic asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1478-1488.	1.5	133
27	Indexcov: fast coverage quality control for whole-genome sequencing. <i>GigaScience</i> , 2017, 6, 1-6.	3.3	36
28	bolts: high throughput sequence handling for the Go language. <i>Journal of Open Source Software</i> , 2017, 2, 168.	2.0	4
29	Genome-wide imputation study identifies novel HLA locus for pulmonary fibrosis and potential role for auto-immunity in fibrotic idiopathic interstitial pneumonia. <i>BMC Genetics</i> , 2016, 17, 74.	2.7	84
30	Vcfanno: fast, flexible annotation of genetic variants. <i>Genome Biology</i> , 2016, 17, 118.	3.8	157
31	Novel Innate Immune Genes Regulating the Macrophage Response to Gram Positive Bacteria. <i>Genetics</i> , 2016, 204, 327-336.	1.2	9
32	DNA Methylation Changes in Nasal Epithelia Are Associated with Allergic Asthma in the Inner City. <i>Annals of the American Thoracic Society</i> , 2016, 13 Suppl 1, S99-S100.	1.5	1
33	Unique DNA Methylation Patterns in Offspring of Hypertensive Pregnancy. <i>Clinical and Translational Science</i> , 2015, 8, 740-745.	1.5	20
34	In Utero Cigarette Smoke Affects Allergic Airway Disease But Does Not Alter the Lung Methylome. <i>PLoS ONE</i> , 2015, 10, e0144087.	1.1	9
35	Signatures of accelerated somatic evolution in gene promoters in multiple cancer types. <i>Nucleic Acids Research</i> , 2015, 43, 5307-5317.	6.5	28
36	DNA methylation and childhood asthma in the inner city. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 69-80.	1.5	189

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37	Relationship of DNA Methylation and Gene Expression in Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2014, 190, 1263-1272.	2.5	140
38	CruzDB: software for annotation of genomic intervals with UCSC genome-browser database. Bioinformatics, 2013, 29, 3003-3006.	1.8	22
39	Loss of heterozygosity preferentially occurs in early replicating regions in cancer genomes. Nucleic Acids Research, 2013, 41, 7615-7624.	6.5	26
40	Copy neutral loss of heterozygosity is more frequent in older ovarian cancer patients. Genes Chromosomes and Cancer, 2013, 52, 794-801.	1.5	21
41	Comb-p: software for combining, analyzing, grouping and correcting spatially correlated <i>P</i> -values. Bioinformatics, 2012, 28, 2986-2988.	1.8	331
42	MethylCoder: software pipeline for bisulfite-treated sequences. Bioinformatics, 2011, 27, 2435-2436.	1.8	76
43	Gobe: an interactive, web-based tool for comparative genomic visualization. Bioinformatics, 2011, 27, 1015-1016.	1.8	7
44	SOURCES, SINKS, AND THE ZONE OF INFLUENCE OF REFUGES FOR MANAGING INSECT RESISTANCE TO Bt CROPS. , 2004, 14, 1615-1623.		70
45	Single vs. multiple introduction in biological control: the roles of parasitoid efficiency, antagonism and niche overlap. Journal of Applied Ecology, 2004, 41, 973-984.	1.9	63