Brent S Pedersen

List of Publications by Year
in descending order

45	5,964	218381	233125
papers	citations	26 h-index	45 g-index

68	68	68	12869
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Nanopore sequencing and assembly of a human genome with ultra-long reads. Nature Biotechnology, 2018, 36, 338-345.	9.4	1,443
2	GOATOOLS: A Python library for Gene Ontology analyses. Scientific Reports, 2018, 8, 10872.	1.6	717
3	Mosdepth: quick coverage calculation for genomes and exomes. Bioinformatics, 2018, 34, 867-868.	1.8	638
4	Comb-p: software for combining, analyzing, grouping and correcting spatially correlated P-values. Bioinformatics, 2012, 28, 2986-2988.	1.8	331
5	A map of constrained coding regions in the human genome. Nature Genetics, 2019, 51, 88-95.	9.4	201
6	DNA methylation and childhood asthma in the inner city. Journal of Allergy and Clinical Immunology, 2015, 136, 69-80.	1.5	189
7	Whoâ€™s Who? Detecting and Resolving Sample Anomalies in Human DNA Sequencing Studies with Peddy. American Journal of Human Genetics, 2017, 100, 406-413.	2.6	173
8	Vcfanno: fast, flexible annotation of genetic variants. Genome Biology, 2016, 17, 118.	3.8	157
9	Overlooked roles of DNA damage and maternal age in generating human germline mutations. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9491-9500.	3.3	155
10	GIGGLE: a search engine for large-scale integrated genome analysis. Nature Methods, 2018, 15, 123-126.	9.0	154
11	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
12	The nasal methylome and childhood atopic asthma. Journal of Allergy and Clinical Immunology, 2017, 139, 1478-1488.	1.5	133
13	Combating subclonal evolution of resistant cancer phenotypes. Nature Communications, 2017, 8, 1231.	5.8	124
14	Large, three-generation human families reveal post-zygotic mosaicism and variability in germline mutation accumulation. ELife, 2019, 8, .	2.8	116
15	Genome-wide imputation study identifies novel HLA locus for pulmonary fibrosis and potential role for auto-immunity in fibrotic idiopathic interstitial pneumonia. BMC Genetics, 2016, 17, 74.	2.7	84
16	A spectrum of free software tools for processing the VCF variant call format: vcflib, bio-vcf, cyvcf2, hts-nim and slivar. PLoS Computational Biology, 2022, 18, e1009123.	1.5	84
17	MethylCoder: software pipeline for bisulfite-treated sequences. Bioinformatics, 2011, 27, 2435-2436.	1.8	76
18	Regulation of MUC5B Expression in Idiopathic Pulmonary Fibrosis. American Journal of Respiratory Cell and Molecular Biology, 2017, 57, 91-99.	1.4	75

#	Article	IF	Citations
19	SOURCES, SINKS, AND THE ZONE OF INFLUENCE OF REFUGES FOR MANAGING INSECT RESISTANCE TO Bt CROPS. , 2004, 14, 1615-1623.		70
20	cyvcf2: fast, flexible variant analysis with Python. Bioinformatics, 2017, 33, 1867-1869.	1.8	66
21	Whole-genome analysis for effective clinical diagnosis and gene discovery in early infantile epileptic encephalopathy. Npj Genomic Medicine, 2018, 3, 22.	1.7	64
22	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
23	De novo structural mutation rates and gamete-of-origin biases revealed through genome sequencing of 2,396 families. American Journal of Human Genetics, 2021, 108, 597-607.	2.6	57
24	Samplot: a platform for structural variant visual validation and automated filtering. Genome Biology, 2021, 22, 161.	3.8	52
25	Effective variant filtering and expected candidate variant yield in studies of rare human disease. Npj Genomic Medicine, 2021, 6, 60.	1.7	51
26	Somalier: rapid relatedness estimation for cancer and germline studies using efficient genome sketches. Genome Medicine, 2020, 12, 62.	3.6	48
27	Duphold: scalable, depth-based annotation and curation of high-confidence structural variant calls. GigaScience, 2019, 8, .	3.3	45
28	Indexcov: fast coverage quality control for whole-genome sequencing. GigaScience, 2017, 6, 1-6.	3.3	36
29	SV-plaudit: A cloud-based framework for manually curating thousands of structural variants. GigaScience, 2018, 7, .	3.3	30
30	Signatures of accelerated somatic evolution in gene promoters in multiple cancer types. Nucleic Acids Research, 2015, 43, 5307-5317.	6.5	28
31	hts-nim: scripting high-performance genomic analyses. Bioinformatics, 2018, 34, 3387-3389.	1.8	28
32	Loss of heterozygosity preferentially occurs in early replicating regions in cancer genomes. Nucleic Acids Research, 2013, 41, 7615-7624.	6.5	26
33	CruzDB: software for annotation of genomic intervals with UCSC genome-browser database. Bioinformatics, 2013, 29, 3003-3006.	1.8	22
34	Copy neutral loss of heterozygosity is more frequent in older ovarian cancer patients. Genes Chromosomes and Cancer, 2013, 52, 794-801.	1.5	21
35	Unique DNA Methylation Patterns in Offspring of Hypertensive Pregnancy. Clinical and Translational Science, 2015, 8, 740-745.	1.5	20
36	CaBagE: A Cas9-based Background Elimination strategy for targeted, long-read DNA sequencing. PLoS ONE, 2021, 16, e0241253.	1.1	17

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37	In Utero Cigarette Smoke Affects Allergic Airway Disease But Does Not Alter the Lung Methylome. PLoS ONE, 2015, 10, e0144087.	1.1	9
38	Novel Innate Immune Genes Regulating the Macrophage Response to Gram Positive Bacteria. Genetics, 2016, 204, 327-336.	1.2	9
39	Go Get Data (GGD) is a framework that facilitates reproducible access to genomic data. Nature Communications, 2021, 12, 2151.	5.8	9
40	Gobe: an interactive, web-based tool for comparative genomic visualization. Bioinformatics, 2011, 27, 1015-1016.	1.8	7
41	Unfazed: parent-of-origin detection for large and small de novo variants. Bioinformatics, 2021, 37, 4860-4861.	1.8	4
42	Balancing efficient analysis and storage of quantitative genomics data with the D4 format and d4tools. Nature Computational Science, 2021, 1, 441-447.	3.8	4
43	Methylene-tetrahydrofolate reductase contributes to allergic airway disease. PLoS ONE, 2018, 13, e0190916.	1.1	4
44	bÃogo/hts: high throughput sequence handling for the Go language. Journal of Open Source Software, 2017, 2, 168.	2.0	4
45	DNA Methylation Changes in Nasal Epithelia Are Associated with Allergic Asthma in the Inner City. Annals of the American Thoracic Society, 2016, 13 Suppl 1, S99-S100.	1.5	1