Brent S Pedersen

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8036286/publications.pdf

Version: 2024-02-01

45 papers	5,964 citations	218677 26 h-index	233421 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. PLoS Computational Biology, 2022, 18, e1009123.	3.2	84
2	Go Get Data (GGD) is a framework that facilitates reproducible access to genomic data. Nature Communications, 2021, 12, 2151.	12.8	9
3	CaBagE: A Cas9-based Background Elimination strategy for targeted, long-read DNA sequencing. PLoS ONE, 2021, 16, e0241253.	2.5	17
4	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.	6.2	57
5	Samplot: a platform for structural variant visual validation and automated filtering. Genome Biology, 2021, 22, 161.	8.8	52
6	Unfazed: parent-of-origin detection for large and small de novo variants. Bioinformatics, 2021, 37, 4860-4861.	4.1	4
7	Balancing efficient analysis and storage of quantitative genomics data with the D4 format and d4tools. Nature Computational Science, 2021, 1, 441-447.	8.0	4
8	Effective variant filtering and expected candidate variant yield in studies of rare human disease. Npj Genomic Medicine, 2021, 6, 60.	3.8	51
9	Somalier: rapid relatedness estimation for cancer and germline studies using efficient genome sketches. Genome Medicine, 2020, 12, 62.	8.2	48
10	Duphold: scalable, depth-based annotation and curation of high-confidence structural variant calls. GigaScience, 2019, 8, .	6.4	45
11	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.	7.1	155
12	A map of constrained coding regions in the human genome. Nature Genetics, 2019, 51, 88-95.	21.4	201
13	Large, three-generation human families reveal post-zygotic mosaicism and variability in germline mutation accumulation. ELife, 2019, 8, .	6.0	116
14	Nanopore sequencing and assembly of a human genome with ultra-long reads. Nature Biotechnology, 2018, 36, 338-345.	17.5	1,443
15	Mosdepth: quick coverage calculation for genomes and exomes. Bioinformatics, 2018, 34, 867-868.	4.1	638
16	GIGGLE: a search engine for large-scale integrated genome analysis. Nature Methods, 2018, 15, 123-126.	19.0	154
17	hts-nim: scripting high-performance genomic analyses. Bioinformatics, 2018, 34, 3387-3389.	4.1	28
18	SV-plaudit: A cloud-based framework for manually curating thousands of structural variants. GigaScience, 2018, 7, .	6.4	30

#	Article	IF	Citations
19	GOATOOLS: A Python library for Gene Ontology analyses. Scientific Reports, 2018, 8, 10872.	3.3	717
20	Whole-genome analysis for effective clinical diagnosis and gene discovery in early infantile epileptic encephalopathy. Npj Genomic Medicine, 2018, 3, 22.	3.8	64
21	Methylene-tetrahydrofolate reductase contributes to allergic airway disease. PLoS ONE, 2018, 13, e0190916.	2.5	4
22	Regulation of MUC5B Expression in Idiopathic Pulmonary Fibrosis. American Journal of Respiratory Cell and Molecular Biology, 2017, 57, 91-99.	2.9	75
23	Whoâ€™s Who? Detecting and Resolving Sample Anomalies in Human DNA Sequencing Studies with Peddy. American Journal of Human Genetics, 2017, 100, 406-413.	6.2	173
24	cyvcf2: fast, flexible variant analysis with Python. Bioinformatics, 2017, 33, 1867-1869.	4.1	66
25	Combating subclonal evolution of resistant cancer phenotypes. Nature Communications, 2017, 8, 1231.	12.8	124
26	The nasal methylome and childhood atopic asthma. Journal of Allergy and Clinical Immunology, 2017, 139, 1478-1488.	2.9	133
27	Indexcov: fast coverage quality control for whole-genome sequencing. GigaScience, 2017, 6, 1-6.	6.4	36
28	bÃ©go/hts: high throughput sequence handling for the Go language. Journal of Open Source Software, 2017, 2, 168.	4.6	4
29	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
30	Vcfanno: fast, flexible annotation of genetic variants. Genome Biology, 2016, 17, 118.	8.8	157
31	Novel Innate Immune Genes Regulating the Macrophage Response to Gram Positive Bacteria. Genetics, 2016, 204, 327-336.	2.9	9
32	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.	3.2	1
33	Unique DNA Methylation Patterns in Offspring of Hypertensive Pregnancy. Clinical and Translational Science, 2015, 8, 740-745.	3.1	20
34	In Utero Cigarette Smoke Affects Allergic Airway Disease But Does Not Alter the Lung Methylome. PLoS ONE, 2015, 10, e0144087.	2.5	9
35	Signatures of accelerated somatic evolution in gene promoters in multiple cancer types. Nucleic Acids Research, 2015, 43, 5307-5317.	14.5	28
36	DNA methylation and childhood asthma in the inner city. Journal of Allergy and Clinical Immunology, 2015, 136, 69-80.	2.9	189

#	Article	IF	Citations
37	Relationship of DNA Methylation and Gene Expression in Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2014, 190, 1263-1272.	5.6	140
38	CruzDB: software for annotation of genomic intervals with UCSC genome-browser database. Bioinformatics, 2013, 29, 3003-3006.	4.1	22
39	Loss of heterozygosity preferentially occurs in early replicating regions in cancer genomes. Nucleic Acids Research, 2013, 41, 7615-7624.	14.5	26
40	Copy neutral loss of heterozygosity is more frequent in older ovarian cancer patients. Genes Chromosomes and Cancer, 2013, 52, 794-801.	2.8	21
41	Comb-p: software for combining, analyzing, grouping and correcting spatially correlated P-values. Bioinformatics, 2012, 28, 2986-2988.	4.1	331
42	MethylCoder: software pipeline for bisulfite-treated sequences. Bioinformatics, 2011, 27, 2435-2436.	4.1	76
43	Gobe: an interactive, web-based tool for comparative genomic visualization. Bioinformatics, 2011, 27, 1015-1016.	4.1	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.	4.0	63