Daniel Cameron

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2850666/publications.pdf

Version: 2024-02-01

20 papers 1,071 citations

758635 12 h-index 752256 20 g-index

29 all docs

29 docs citations

times ranked

29

2358 citing authors

#	Article	IF	CITATIONS
1	GRIDSS: sensitive and specific genomic rearrangement detection using positional de Bruijn graph assembly. Genome Research, 2017, 27, 2050-2060.	2.4	255
2	Comprehensive evaluation and characterisation of short read general-purpose structural variant calling software. Nature Communications, 2019, 10, 3240.	5.8	184
3	Barcoding reveals complex clonal behavior in patient-derived xenografts of metastatic triple negative breast cancer. Nature Communications, 2019, 10, 766.	5.8	99
4	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, $2021, 1, 100029$.	3.0	94
5	GRIDSS2: comprehensive characterisation of somatic structural variation using single breakend variants and structural variant phasing. Genome Biology, 2021, 22, 202.	3.8	73
6	Evolution of late-stage metastatic melanoma is dominated by aneuploidy and whole genome doubling. Nature Communications, 2021, 12, 1434.	5.8	46
7	TERT structural rearrangements in metastatic pheochromocytomas. Endocrine-Related Cancer, 2018, 25, 1-9.	1.6	45
8	Optical mapping reveals a higher level of genomic architecture of chained fusions in cancer. Genome Research, 2018, 28, 726-738.	2.4	41
9	Unscrambling cancer genomes via integrated analysis of structural variation and copy number. Cell Genomics, 2022, 2, 100112.	3.0	34
10	Relationship between CD4 T cell turnover, cellular differentiation and HIV persistence during ART. PLoS Pathogens, 2021, 17, e1009214.	2.1	25
11	Knowledge-Based Autonomous Dynamic Colour Calibration. Lecture Notes in Computer Science, 2004, , 226-237.	1.0	24
12	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification. Cell Genomics, 2021, 1, 100027.	3.0	18
13	VIRUSBreakend: Viral Integration Recognition Using Single Breakends. Bioinformatics, 2021, 37, 3115-3119.	1.8	15
14	A multi-platform reference for somatic structural variation detection. Cell Genomics, 2022, 2, 100139.	3.0	10
15	Detection of clinically relevant early genomic lesions in Bâ€cell malignancies from circulating tumour <scp>DNA</scp> using a single hybridisationâ€based next generation sequencing assay. British Journal of Haematology, 2018, 183, 146-149.	1.2	8
16	Digital PCR of Genomic Rearrangements for Monitoring Circulating Tumour DNA. Advances in Experimental Medicine and Biology, 2016, 924, 139-146.	0.8	6
17	StructuralVariantAnnotation: a R/Bioconductor foundation for a caller-agnostic structural variant software ecosystem. Bioinformatics, 2022, 38, 2046-2048.	1.8	4
18	AnÂinternationalÂvirtualÂhackathon toÂbuildÂtools for theÂanalysis ofÂstructuralÂvariants withinÂspeciesÂranging fromÂcoronaviruses toÂvertebrates. F1000Research, 2021, 10, 246.	0.8	3

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19	AnÂinternationalÂvirtualÂhackathon toÂbuildÂtools for theÂanalysis ofÂstructuralÂvariants withinÂspeciesÂranging fromÂcoronaviruses toÂvertebrates. F1000Research, 2021, 10, 246.	0.8	2
20	Bioinformatics Analysis of Sequence Data. , 2016, , 317-333.		0