

Vikas Bansal

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5594725/publications.pdf>

Version: 2024-02-01

19
papers

1,337
citations

623574

14
h-index

839398

18
g-index

19
all docs

19
docs citations

19
times ranked

2771
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics of the human and viral m6A RNA methylomes during HIV-1 infection of T cells. <i>Nature Microbiology</i> , 2016, 1, 16011.	5.9	373
2	HapCUT2: robust and accurate haplotype assembly for diverse sequencing technologies. <i>Genome Research</i> , 2017, 27, 801-812.	2.4	285
3	Longshot enables accurate variant calling in diploid genomes from single-molecule long read sequencing. <i>Nature Communications</i> , 2019, 10, 4660.	5.8	156
4	Spectrum of mutations in monogenic diabetes genes identified from high-throughput DNA sequencing of 6888 individuals. <i>BMC Medicine</i> , 2017, 15, 213.	2.3	75
5	Ultralow-input single-tube linked-read library method enables short-read second-generation sequencing systems to routinely generate highly accurate and economical long-range sequencing information. <i>Genome Research</i> , 2020, 30, 898-909.	2.4	68
6	Targeted genotyping of variable number tandem repeats with advNTR. <i>Genome Research</i> , 2018, 28, 1709-1719.	2.4	59
7	Zika virus infection reprograms global transcription of host cells to allow sustained infection. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-10.	3.0	58
8	A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , 2020, 11, 4794.	5.8	56
9	Fast individual ancestry inference from DNA sequence data leveraging allele frequencies for multiple populations. <i>BMC Bioinformatics</i> , 2015, 16, 4.	1.2	52
10	Identification of a missense variant in the WFS1 gene that causes a mild form of Wolfram syndrome and is associated with risk for type 2 diabetes in Ashkenazi Jewish individuals. <i>Diabetologia</i> , 2018, 61, 2180-2188.	2.9	38
11	Sequencing Technologies and Analyses: Where Have We Been and Where Are We Going?. <i>IScience</i> , 2019, 18, 37-41.	1.9	31
12	A computational method for estimating the PCR duplication rate in DNA and RNA-seq experiments. <i>BMC Bioinformatics</i> , 2017, 18, 43.	1.2	23
13	Integrating read-based and population-based phasing for dense and accurate haplotyping of individual genomes. <i>Bioinformatics</i> , 2019, 35, i242-i248.	1.8	23
14	Perfectionism as a mediator of psychological distress: Implications for addressing underlying vulnerabilities to the mental health of medical students. <i>Medical Teacher</i> , 2020, 42, 1301-1307.	1.0	21
15	Sensitive alignment using paralogous sequence variants improves long-read mapping and variant calling in segmental duplications. <i>Nucleic Acids Research</i> , 2020, 48, e114-e114.	6.5	12
16	Robust and accurate estimation of paralog-specific copy number for duplicated genes using whole-genome sequencing. <i>Nature Communications</i> , 2022, 13, .	5.8	4
17	VarCover. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 123-131.	1.2	2
18	InPhaDel: integrative shotgun and proximity-ligation sequencing to phase deletions with single nucleotide polymorphisms. <i>Nucleic Acids Research</i> , 2016, 44, e111-e111.	6.5	1

#	ARTICLE	IF	CITATIONS
19	An accurate algorithm for the detection of DNA fragments from dilution pool sequencing experiments. <i>Bioinformatics</i> , 2018, 34, 155-162.	1.8	0