Vikas Bansal

List of Publications by Year
in descending order

19	1,337	623734 14	839539 18
papers	citations	h-index	g-index

19	19	19	2771
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Dynamics of the human and viral m6A RNA methylomes during HIV-1 infection of T cells. Nature Microbiology, 2016, 1, 16011.	13.3	373
2	HapCUT2: robust and accurate haplotype assembly for diverse sequencing technologies. Genome Research, 2017, 27, 801-812.	5.5	285
3	Longshot enables accurate variant calling in diploid genomes from single-molecule long read sequencing. Nature Communications, 2019, 10, 4660.	12.8	156
4	Spectrum of mutations in monogenic diabetes genes identified from high-throughput DNA sequencing of 6888 individuals. BMC Medicine, 2017, 15, 213.	5.5	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. Genome Research, 2020, 30, 898-909.	5.5	68
6	Targeted genotyping of variable number tandem repeats with adVNTR. Genome Research, 2018, 28, 1709-1719.	5.5	59
7	Zika virus infection reprograms global transcription of host cells to allow sustained infection. Emerging Microbes and Infections, 2017, 6, 1-10.	6.5	58
8	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	12.8	56
9	Fast individual ancestry inference from DNA sequence data leveraging allele frequencies for multiple populations. BMC Bioinformatics, 2015, 16, 4.	2.6	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. Diabetologia, 2018, 61, 2180-2188.	6.3	38
11	Sequencing Technologies and Analyses: Where Have We Been and Where Are We Going?. IScience, 2019, 18, 37-41.	4.1	31
12	A computational method for estimating the PCR duplication rate in DNA and RNA-seq experiments. BMC Bioinformatics, 2017, 18, 43.	2.6	23
13	Integrating read-based and population-based phasing for dense and accurate haplotyping of individual genomes. Bioinformatics, 2019, 35, i242-i248.	4.1	23
14	Perfectionism as a mediator of psychological distress: Implications for addressing underlying vulnerabilities to the mental health of medical students. Medical Teacher, 2020, 42, 1301-1307.	1.8	21
15	Sensitive alignment using paralogous sequence variants improves long-read mapping and variant calling in segmental duplications. Nucleic Acids Research, 2020, 48, e114-e114.	14.5	12
16	Robust and accurate estimation of paralog-specific copy number for duplicated genes using whole-genome sequencing. Nature Communications, 2022, 13, .	12.8	4
17	VarCover. Journal of Molecular Diagnostics, 2020, 22, 123-131.	2.8	2
18	InPhaDel: integrative shotgun and proximity-ligation sequencing to phase deletions with single nucleotide polymorphisms. Nucleic Acids Research, 2016, 44, e111-e111.	14.5	1

#	Article	IF	Citations
19	An accurate algorithm for the detection of DNA fragments from dilution pool sequencing experiments. Bioinformatics, 2018, 34, 155-162.	4.1	0