Vikas Bansal

List of Publications by Year
in descending order

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	Robust and accurate estimation of paralog-specific copy number for duplicated genes using whole-genome sequencing. Nature Communications, 2022, 13, .	5.8	4
2	VarCover. Journal of Molecular Diagnostics, 2020, 22, 123-131.	1.2	2
3	Sensitive alignment using paralogous sequence variants improves long-read mapping and variant calling in segmental duplications. Nucleic Acids Research, 2020, 48, e114-e114.	6.5	12
4	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	5.8	56
5	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.	1.0	21
6	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.	2.4	68
7	Sequencing Technologies and Analyses: Where Have We Been and Where Are We Going?. IScience, 2019, 18, 37-41.	1.9	31
8	Longshot enables accurate variant calling in diploid genomes from single-molecule long read sequencing. Nature Communications, 2019, 10, 4660.	5.8	156
9	Integrating read-based and population-based phasing for dense and accurate haplotyping of individual genomes. Bioinformatics, 2019, 35, i242-i248.	1.8	23
10	An accurate algorithm for the detection of DNA fragments from dilution pool sequencing experiments. Bioinformatics, 2018, 34, 155-162.	1.8	0
11	Targeted genotyping of variable number tandem repeats with adVNTR. Genome Research, 2018, 28, 1709-1719.	2.4	59
12	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.	2.9	38
13	Zika virus infection reprograms global transcription of host cells to allow sustained infection. Emerging Microbes and Infections, 2017, 6, 1-10.	3.0	58
14	A computational method for estimating the PCR duplication rate in DNA and RNA-seq experiments. BMC Bioinformatics, 2017, 18, 43.	1.2	23
15	HapCUT2: robust and accurate haplotype assembly for diverse sequencing technologies. Genome Research, 2017, 27, 801-812.	2.4	285
16	Spectrum of mutations in monogenic diabetes genes identified from high-throughput DNA sequencing of 6888 individuals. BMC Medicine, 2017, 15, 213.	2.3	75
17	InPhaDel: integrative shotgun and proximity-ligation sequencing to phase deletions with single nucleotide polymorphisms. Nucleic Acids Research, 2016, 44, e111-e111.	6.5	1
18	Dynamics of the human and viral m6A RNA methylomes during HIV-1 infection of T cells. Nature Microbiology, 2016, 1, 16011.	5.9	373

#	Article	IF	Citations
19	Fast individual ancestry inference from DNA sequence data leveraging allele frequencies for multiple populations. BMC Bioinformatics, 2015, 16, 4.	1.2	52