

Vagheesh M Narasimhan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1749841/publications.pdf>

Version: 2024-02-01

13
papers

3,802
citations

759233

12
h-index

1125743

13
g-index

16
all docs

16
docs citations

16
times ranked

9923
citing authors

#	ARTICLE	IF	CITATIONS
1	miqoGraph: fitting admixture graphs using mixed-integer quadratic optimization. <i>Bioinformatics</i> , 2021, 37, 2488-2490.	4.1	7
2	An Ancient Harappan Genome Lacks Ancestry from Steppe Pastoralists or Iranian Farmers. <i>Cell</i> , 2019, 179, 729-735.e10.	28.9	62
3	The formation of human populations in South and Central Asia. <i>Science</i> , 2019, 365, .	12.6	383
4	Estimating the human mutation rate from autozygous segments reveals population differences in human mutational processes. <i>Nature Communications</i> , 2017, 8, 303.	12.8	81
5	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. <i>Nature Communications</i> , 2017, 8, 15927.	12.8	64
6	BCFtools/RoH: a hidden Markov model approach for detecting autozygosity from next-generation sequencing data. <i>Bioinformatics</i> , 2016, 32, 1749-1751.	4.1	506
7	Extensive Proliferation of a Subset of Differentiated, yet Plastic, Medial Vascular Smooth Muscle Cells Contributes to Neointimal Formation in Mouse Injury and Atherosclerosis Models. <i>Circulation Research</i> , 2016, 119, 1313-1323.	4.5	317
8	Human Knockout Carriers: Dead, Diseased, Healthy, or Improved?. <i>Trends in Molecular Medicine</i> , 2016, 22, 341-351.	6.7	31
9	Health and population effects of rare gene knockouts in adult humans with related parents. <i>Science</i> , 2016, 352, 474-477.	12.6	272
10	Transcriptional profiling defines dynamics of parasite tissue sequestration during malaria infection. <i>Genome Medicine</i> , 2015, 7, 19.	8.2	77
11	Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. <i>Science</i> , 2015, 348, 242-245.	12.6	326
12	Inferring Developmental Stage Composition from Gene Expression in Human Malaria. <i>PLoS Computational Biology</i> , 2013, 9, e1003392.	3.2	45
13	Metagenomic microbial community profiling using unique clade-specific marker genes. <i>Nature Methods</i> , 2012, 9, 811-814.	19.0	1,591