

# Sushant Kumar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3493907/publications.pdf>

Version: 2024-02-01

12  
papers

1,958  
citations

932766

10  
h-index

1199166

12  
g-index

16  
all docs

16  
docs citations

16  
times ranked

4547  
citing authors

#	ARTICLE	IF	CITATIONS
1	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , 2021, 372, .	6.0	358
2	Whole-genome sequencing of phenotypically distinct inflammatory breast cancers reveals similar genomic alterations to non-inflammatory breast cancers. <i>Genome Medicine</i> , 2021, 13, 70.	3.6	8
3	SVFX: a machine learning framework to quantify the pathogenicity of structural variants. <i>Genome Biology</i> , 2020, 21, 274.	3.8	24
4	Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences. <i>Cell</i> , 2020, 180, 915-927.e16.	13.5	98
5	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	13.7	424
6	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	5.8	636
7	Leveraging protein dynamics to identify cancer mutational hotspots using 3D structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18962-18970.	3.3	26
8	Insights into genetics, human biology and disease gleaned from family based genomic studies. <i>Genetics in Medicine</i> , 2019, 21, 798-812.	1.1	161
9	Reliability of Whole-Exome Sequencing for Assessing Intratumor Genetic Heterogeneity. <i>Cell Reports</i> , 2018, 25, 1446-1457.	2.9	76
10	Identifying Allosteric Hotspots with Dynamics: Application to Inter- and Intra-species Conservation. <i>Structure</i> , 2016, 24, 826-837.	1.6	55
11	Reads meet rotamers: structural biology in the age of deep sequencing. <i>Current Opinion in Structural Biology</i> , 2015, 35, 125-134.	2.6	6
12	Localized structural frustration for evaluating the impact of sequence variants. <i>Nucleic Acids Research</i> , 2013, 44, 10062-10073.	6.5	13