Sushant Kumar

List of Publications by Year in descending order

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

Version: 2024-02-01

932766 1199166 1,958 12 10 12 citations h-index g-index papers 16 16 16 4547 citing authors docs citations times ranked all docs

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