

Gordon Saksena

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/780393/publications.pdf>

Version: 2024-02-01

11
papers

12,472
citations

933447

10
h-index

1281871

11
g-index

13
all docs

13
docs citations

13
times ranked

25589
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013, 499, 214-218.	27.8	4,761
2	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	28.9	1,695
3	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	28.9	1,670
4	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013, 45, 1134-1140.	21.4	1,616
5	The genomic complexity of primary human prostate cancer. <i>Nature</i> , 2011, 470, 214-220.	27.8	1,107
6	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	6.2	605
7	Oncotator: Cancer Variant Annotation Tool. <i>Human Mutation</i> , 2015, 36, E2423-E2429.	2.5	448
8	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	27.8	424
9	Sporadic Early-Onset Diffuse Gastric Cancers Have High Frequency of Somatic CDH1 Alterations, but Low Frequency of Somatic RHOA Mutations Compared With Late-Onset Cancers. <i>Gastroenterology</i> , 2017, 153, 536-549.e26.	1.3	90
10	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748.	12.8	27
11	Framework for quality assessment of whole genome cancer sequences. <i>Nature Communications</i> , 2020, 11, 5040.	12.8	5