

Nikos Sidiropoulos

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

14
papers

2,258
citations

11
h-index

15
g-index

15
ext. papers

3,745
ext. citations

27.7
avg, IF

7.04
L-index

#	Paper	IF	Citations
14	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
13	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017 , 547, 311-317	50.4	472
12	Patterns of somatic structural variation in human cancer genomes. <i>Nature</i> , 2020 , 578, 112-121	50.4	232
11	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
10	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020 , 52, 331-341	36.3	168
9	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , 2018 , 34, 996-1011.e8	24.3	89
8	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , 2020 , 52, 294-305	36.3	81
7	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , 2017 , 18, 18	18.3	70
6	The whole-genome panorama of cancer drivers		38
5	The splicing factor RBM25 controls MYC activity in acute myeloid leukemia. <i>Nature Communications</i> , 2019 , 10, 172	17.4	22
4	SinaPlot: An Enhanced Chart for Simple and Truthful Representation of Single Observations Over Multiple Classes. <i>Journal of Computational and Graphical Statistics</i> , 2018 , 27, 673-676	1.4	16
3	Reproducible Analysis of Sequencing-Based RNA Structure Probing Data with User-Friendly Tools. <i>Methods in Enzymology</i> , 2015 , 558, 153-180	1.7	8
2	Somatic structural variant formation is guided by and influences genome architecture		1
1	Somatic structural variant formation is guided by and influences genome architecture.. <i>Genome Research</i> , 2022 ,	9.7	1