

Deena M A Gendoo

List of Publications by Year in Descending Order

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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.

13
papers

597
citations

9
h-index

15
g-index

15
ext. papers

854
ext. citations

8.5
avg, IF

3.49
L-index

#	Paper	IF	Citations
13	The anti-tumour activity of DNA methylation inhibitor 5-aza-2-deoxycytidine is enhanced by the common analgesic paracetamol through induction of oxidative stress. <i>Cancer Letters</i> , 2021 , 501, 172-186	9.9	1
12	Bioinformatics and computational approaches for analyzing patient-derived disease models in cancer research. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 375-380	6.8	3
11	Modeling germline mutations in pineoblastoma uncovers lysosome disruption-based therapy. <i>Nature Communications</i> , 2020 , 11, 1825	17.4	7
10	A subgroup of microRNAs defines PTEN-deficient, triple-negative breast cancer patients with poorest prognosis and alterations in RB1, MYC, and Wnt signaling. <i>Breast Cancer Research</i> , 2019 , 21, 18	8.3	20
9	MetaGxData: Clinically Annotated Breast, Ovarian and Pancreatic Cancer Datasets and their Use in Generating a Multi-Cancer Gene Signature. <i>Scientific Reports</i> , 2019 , 9, 8770	4.9	15
8	Whole genomes define concordance of matched primary, xenograft, and organoid models of pancreas cancer. <i>PLoS Computational Biology</i> , 2019 , 15, e1006596	5	29
7	Consensus on Molecular Subtypes of High-Grade Serous Ovarian Carcinoma. <i>Clinical Cancer Research</i> , 2018 , 24, 5037-5047	12.9	43
6	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. <i>Cancer Research</i> , 2017 , 77, 3057-3069	10.1	20
5	Public data and open source tools for multi-assay genomic investigation of disease. <i>Briefings in Bioinformatics</i> , 2016 , 17, 603-15	13.4	38
4	MM2S: personalized diagnosis of medulloblastoma patients and model systems. <i>Source Code for Biology and Medicine</i> , 2016 , 11, 6	1.9	1
3	PharmacGx: an R package for analysis of large pharmacogenomic datasets. <i>Bioinformatics</i> , 2016 , 32, 1244-6	7.2	127
2	Genefu: an R/Bioconductor package for computation of gene expression-based signatures in breast cancer. <i>Bioinformatics</i> , 2016 , 32, 1097-9	7.2	150
1	CD73 is associated with poor prognosis in high-grade serous ovarian cancer. <i>Cancer Research</i> , 2015 , 75, 4494-503	10.1	142