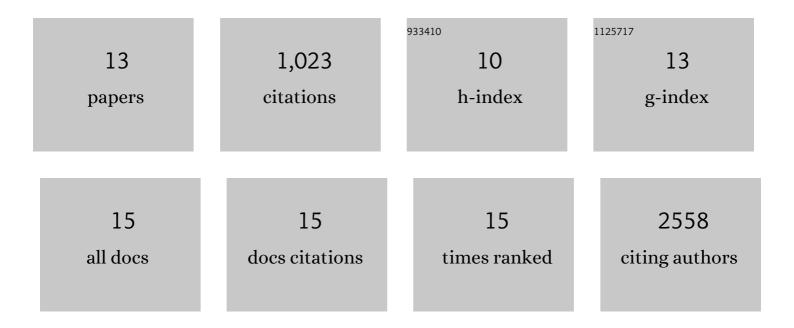
Deena M A Gendoo

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1864606/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Genefu: an R/Bioconductor package for computation of gene expression-based signatures in breast cancer. Bioinformatics, 2016, 32, 1097-1099.	4.1	255
2	PharmacoGx: an R package for analysis of large pharmacogenomic datasets. Bioinformatics, 2016, 32, 1244-1246.	4.1	249
3	CD73 Is Associated with Poor Prognosis in High-Grade Serous Ovarian Cancer. Cancer Research, 2015, 75, 4494-4503.	0.9	186
4	Consensus on Molecular Subtypes of High-Grade Serous Ovarian Carcinoma. Clinical Cancer Research, 2018, 24, 5037-5047.	7.0	93
5	Whole genomes define concordance of matched primary, xenograft, and organoid models of pancreas cancer. PLoS Computational Biology, 2019, 15, e1006596.	3.2	51
6	Public data and open source tools for multi-assay genomic investigation of disease. Briefings in Bioinformatics, 2016, 17, 603-615.	6.5	46
7	A subgroup of microRNAs defines PTEN-deficient, triple-negative breast cancer patients with poorest prognosis and alterations in RB1, MYC, and Wnt signaling. Breast Cancer Research, 2019, 21, 18.	5.0	37
8	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. Cancer Research, 2017, 77, 3057-3069.	0.9	33
9	MetaGxData: Clinically Annotated Breast, Ovarian and Pancreatic Cancer Datasets and their Use in Generating a Multi-Cancer Gene Signature. Scientific Reports, 2019, 9, 8770.	3.3	29
10	Modeling germline mutations in pineoblastoma uncovers lysosome disruption-based therapy. Nature Communications, 2020, 11, 1825.	12.8	21
11	The anti-tumour activity of DNA methylation inhibitor 5-aza-2′-deoxycytidine is enhanced by the common analgesic paracetamol through induction of oxidative stress. Cancer Letters, 2021, 501, 172-186.	7.2	10
12	MM2S: personalized diagnosis of medulloblastoma patients and model systems. Source Code for Biology and Medicine, 2016, 11, 6.	1.7	6
13	Bioinformatics and computational approaches for analyzing patient-derived disease models in cancer research. Computational and Structural Biotechnology Journal, 2020, 18, 375-380.	4.1	6