

Noushin Niknafs

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4718659/publications.pdf>

Version: 2024-02-01

31
papers

5,379
citations

331670

21
h-index

501196

28
g-index

31
all docs

31
docs citations

31
times ranked

11440
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide cell-free DNA fragmentation in patients with cancer. <i>Nature</i> , 2019, 570, 385-389.	27.8	764
2	Evolution of Neoantigen Landscape during Immune Checkpoint Blockade in Non-Small Cell Lung Cancer. <i>Cancer Discovery</i> , 2017, 7, 264-276.	9.4	706
3	Exome sequencing identifies frequent inactivating mutations in BAP1, ARID1A and PBRM1 in intrahepatic cholangiocarcinomas. <i>Nature Genetics</i> , 2013, 45, 1470-1473.	21.4	564
4	High grade serous ovarian carcinomas originate in the fallopian tube. <i>Nature Communications</i> , 2017, 8, 1093.	12.8	515
5	The genomic landscape of response to EGFR blockade in colorectal cancer. <i>Nature</i> , 2015, 526, 263-267.	27.8	398
6	A Combination of Molecular Markers and Clinical Features Improve the Classification of Pancreatic Cysts. <i>Gastroenterology</i> , 2015, 149, 1501-1510.	1.3	376
7	Epigenetic Therapy Ties MYC Depletion to Reversing Immune Evasion and Treating Lung Cancer. <i>Cell</i> , 2017, 171, 1284-1300.e21.	28.9	366
8	Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. <i>Cancer Discovery</i> , 2016, 6, 166-175.	9.4	282
9	Dynamics of Tumor and Immune Responses during Immune Checkpoint Blockade in Non-Small Cell Lung Cancer. <i>Cancer Research</i> , 2019, 79, 1214-1225.	0.9	226
10	Detection and characterization of lung cancer using cell-free DNA fragmentomes. <i>Nature Communications</i> , 2021, 12, 5060.	12.8	161
11	Multimodal genomic features predict outcome of immune checkpoint blockade in non-small-cell lung cancer. <i>Nature Cancer</i> , 2020, 1, 99-111.	13.2	141
12	Ipilimumab plus nivolumab and DNA-repair defects in AR-V7-expressing metastatic prostate cancer. <i>Oncotarget</i> , 2018, 9, 28561-28571.	1.8	129
13	Exome-Scale Discovery of Hotspot Mutation Regions in Human Cancer Using 3D Protein Structure. <i>Cancer Research</i> , 2016, 76, 3719-3731.	0.9	103
14	Intraductal Papillary Mucinous Neoplasms Arise From Multiple Independent Clones, Each With Distinct Mutations. <i>Gastroenterology</i> , 2019, 157, 1123-1137.e22.	1.3	82
15	Whole-Genome Sequencing of Salivary Gland Adenoid Cystic Carcinoma. <i>Cancer Prevention Research</i> , 2016, 9, 265-274.	1.5	80
16	A machine learning approach for somatic mutation discovery. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	80
17	Genomic characterization of malignant progression in neoplastic pancreatic cysts. <i>Nature Communications</i> , 2020, 11, 4085.	12.8	77
18	MuPIT interactive: webserver for mapping variant positions to annotated, interactive 3D structures. <i>Human Genetics</i> , 2013, 132, 1235-1243.	3.8	68

#	ARTICLE	IF	CITATIONS
19	Durvalumab with platinum-pemetrexed for unresectable pleural mesothelioma: survival, genomic and immunologic analyses from the phase 2 PrE0505 trial. <i>Nature Medicine</i> , 2021, 27, 1910-1920.	30.7	62
20	SubClonal Hierarchy Inference from Somatic Mutations: Automatic Reconstruction of Cancer Evolutionary Trees from Multi-region Next Generation Sequencing. <i>PLoS Computational Biology</i> , 2015, 11, e1004416.	3.2	61
21	Integrative Tumor and Immune Cell Multi-omic Analyses Predict Response to Immune Checkpoint Blockade in Melanoma. <i>Cell Reports Medicine</i> , 2020, 1, 100139.	6.5	45
22	Peripheral blood immune cell dynamics reflect antitumor immune responses and predict clinical response to immunotherapy. , 2022, 10, e004688.		34
23	Biomechanical Factors in Planning of Periacetabular Osteotomy. <i>Frontiers in Bioengineering and Biotechnology</i> , 2013, 1, 20.	4.1	16
24	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. <i>Human Mutation</i> , 2017, 38, 1266-1276.	2.5	14
25	Characterization of genetic subclonal evolution in pancreatic cancer mouse models. <i>Nature Communications</i> , 2019, 10, 5435.	12.8	14
26	A Probabilistic Model to Predict Clinical Phenotypic Traits from Genome Sequencing. <i>PLoS Computational Biology</i> , 2014, 10, e1003825.	3.2	10
27	Early detection of lung cancer using cfDNA fragmentation.. <i>Journal of Clinical Oncology</i> , 2021, 39, 8519-8519.	1.6	3
28	Genome-wide cell-free DNA fragmentation profiling for early cancer detection.. <i>Journal of Clinical Oncology</i> , 2019, 37, 3018-3018.	1.6	1
29	Integrative tumor and immune cell multi-omic analyses to predict melanoma response to immune checkpoint blockade.. <i>Journal of Clinical Oncology</i> , 2020, 38, 10009-10009.	1.6	1
30	Abstract 1617: Sex-specific genomic determinants of response to immunotherapy. , 2021, , .		0
31	Abstract 1662: Immunogenomic mechanisms of response and resistance to combined radiation and immunotherapy in lung cancer. , 2021, , .		0