

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	Peripheral blood immune cell dynamics reflect antitumor immune responses and predict clinical response to immunotherapy. , 2022, 10, e004688.		34
2	Early detection of lung cancer using cfDNA fragmentation.. Journal of Clinical Oncology, 2021, 39, 8519-8519.	1.6	3
3	Abstract 1617: Sex-specific genomic determinants of response to immunotherapy. , 2021, , .		0
4	Abstract 1662: Immunogenomic mechanisms of response and resistance to combined radiation and immunotherapy in lung cancer. , 2021, , .		0
5	Detection and characterization of lung cancer using cell-free DNA fragmentomes. Nature Communications, 2021, 12, 5060.	12.8	161
6	Durvalumab with platinum-pemetrexed for unresectable pleural mesothelioma: survival, genomic and immunologic analyses from the phase 2 PrE0505 trial. Nature Medicine, 2021, 27, 1910-1920.	30.7	62
7	Multimodal genomic features predict outcome of immune checkpoint blockade in non-small-cell lung cancer. Nature Cancer, 2020, 1, 99-111.	13.2	141
8	Integrative Tumor and Immune Cell Multi-omic Analyses Predict Response to Immune Checkpoint Blockade in Melanoma. Cell Reports Medicine, 2020, 1, 100139.	6.5	45
9	Genomic characterization of malignant progression in neoplastic pancreatic cysts. Nature Communications, 2020, 11, 4085.	12.8	77
10	Integrative tumor and immune cell multi-omic analyses to predict melanoma response to immune checkpoint blockade.. Journal of Clinical Oncology, 2020, 38, 10009-10009.	1.6	1
11	Intraductal Papillary Mucinous Neoplasms Arise From Multiple Independent Clones, Each With Distinct Mutations. Gastroenterology, 2019, 157, 1123-1137.e22.	1.3	82
12	Genome-wide cell-free DNA fragmentation in patients with cancer. Nature, 2019, 570, 385-389.	27.8	764
13	Characterization of genetic subclonal evolution in pancreatic cancer mouse models. Nature Communications, 2019, 10, 5435.	12.8	14
14	Dynamics of Tumor and Immune Responses during Immune Checkpoint Blockade in Non-€Small Cell Lung Cancer. Cancer Research, 2019, 79, 1214-1225.	0.9	226
15	Genome-wide cell-free DNA fragmentation profiling for early cancer detection.. Journal of Clinical Oncology, 2019, 37, 3018-3018.	1.6	1
16	Ipilimumab plus nivolumab and DNA-repair defects in AR-V7-expressing metastatic prostate cancer. Oncotarget, 2018, 9, 28561-28571.	1.8	129
17	A machine learning approach for somatic mutation discovery. Science Translational Medicine, 2018, 10, .	12.4	80
18	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. Human Mutation, 2017, 38, 1266-1276.	2.5	14

#	ARTICLE	IF	CITATIONS
19	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
20	High grade serous ovarian carcinomas originate in the fallopian tube. <i>Nature Communications</i> , 2017, 8, 1093.	12.8	515
21	Epigenetic Therapy Ties MYC Depletion to Reversing Immune Evasion and Treating Lung Cancer. <i>Cell</i> , 2017, 171, 1284-1300.e21.	28.9	366
22	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
23	Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. <i>Cancer Discovery</i> , 2016, 6, 166-175.	9.4	282
24	Whole-Genome Sequencing of Salivary Gland Adenoid Cystic Carcinoma. <i>Cancer Prevention Research</i> , 2016, 9, 265-274.	1.5	80
25	A Combination of Molecular Markers and Clinical Features Improve the Classification of Pancreatic Cysts. <i>Gastroenterology</i> , 2015, 149, 1501-1510.	1.3	376
26	The genomic landscape of response to EGFR blockade in colorectal cancer. <i>Nature</i> , 2015, 526, 263-267.	27.8	398
27	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
28	A Probabilistic Model to Predict Clinical Phenotypic Traits from Genome Sequencing. <i>PLoS Computational Biology</i> , 2014, 10, e1003825.	3.2	10
29	MuPIT interactive: webserver for mapping variant positions to annotated, interactive 3D structures. <i>Human Genetics</i> , 2013, 132, 1235-1243.	3.8	68
30	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
31	Biomechanical Factors in Planning of Periacetabular Osteotomy. <i>Frontiers in Bioengineering and Biotechnology</i> , 2013, 1, 20.	4.1	16