Noushin Niknafs

List of Publications by Year in Descending Order

28 papers	**3,343** citations	**19** h-index	**31** g-index
31 ext. papers	**4,484** ext. citations	**16.8** avg, IF	**4.23** L-index

#	Paper	IF	Citations
28	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	50.5	14
27	Early detection of lung cancer using cfDNA fragmentation.. *Journal of Clinical Oncology*, **2021**, 39, 8519-8519	2.2	2
26	Detection and characterization of lung cancer using cell-free DNA fragmentomes. *Nature Communications*, **2021**, 12, 5060	17.4	21
25	Integrative tumor and immune cell multi-omic analyses to predict melanoma response to immune checkpoint blockade.. *Journal of Clinical Oncology*, **2020**, 38, 10009-10009	2.2	0
24	Multimodal genomic features predict outcome of immune checkpoint blockade in non-small-cell lung cancer. *Nature Cancer*, **2020**, 1, 99-111	15.4	67
23	Integrative Tumor and Immune Cell Multi-omic Analyses Predict Response to Immune Checkpoint Blockade in Melanoma. *Cell Reports Medicine*, **2020**, 1, 100139	18	17
22	Genomic characterization of malignant progression in neoplastic pancreatic cysts. *Nature Communications*, **2020**, 11, 4085	17.4	27
21	Intraductal Papillary Mucinous Neoplasms Arise From Multiple Independent Clones, Each With Distinct Mutations. *Gastroenterology*, **2019**, 157, 1123-1137.e22	13.3	40
20	Genome-wide cell-free DNA fragmentation in patients with cancer. *Nature*, **2019**, 570, 385-389	50.4	339
19	Genome-wide cell-free DNA fragmentation profiling for early cancer detection.. *Journal of Clinical Oncology*, **2019**, 37, 3018-3018	2.2	
18	Characterization of genetic subclonal evolution in pancreatic cancer mouse models. *Nature Communications*, **2019**, 10, 5435	17.4	11
17	Dynamics of Tumor and Immune Responses during Immune Checkpoint Blockade in Non-Small Cell Lung Cancer. *Cancer Research*, **2019**, 79, 1214-1225	10.1	117
16	Ipilimumab plus nivolumab and DNA-repair defects in AR-V7-expressing metastatic prostate cancer. *Oncotarget*, **2018**, 9, 28561-28571	3.3	92
15	A machine learning approach for somatic mutation discovery. *Science Translational Medicine*, **2018**, 10,	17.5	44
14	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. *Human Mutation*, **2017**, 38, 1266-1276	4.7	9
13	Evolution of Neoantigen Landscape during Immune Checkpoint Blockade in Non-Small Cell Lung Cancer. *Cancer Discovery*, **2017**, 7, 264-276	24.4	491
12	High grade serous ovarian carcinomas originate in the fallopian tube. *Nature Communications*, **2017**, 8, 1093	17.4	325

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11	Epigenetic Therapy Ties MYC Depletion to Reversing Immune Evasion and Treating Lung Cancer. *Cell*, **2017**, 171, 1284-1300.e21	56.2	215
10	Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. *Cancer Discovery*, **2016**, 6, 166-75	24.4	206
9	Whole-Genome Sequencing of Salivary Gland Adenoid Cystic Carcinoma. *Cancer Prevention Research*, **2016**, 9, 265-74	3.2	59
8	Exome-Scale Discovery of Hotspot Mutation Regions in Human Cancer Using 3D Protein Structure. *Cancer Research*, **2016**, 76, 3719-31	10.1	61
7	A combination of molecular markers and clinical features improve the classification of pancreatic cysts. *Gastroenterology*, **2015**, 149, 1501-10	13.3	286
6	The genomic landscape of response to EGFR blockade in colorectal cancer. *Nature*, **2015**, 526, 263-7	50.4	310
5	SubClonal Hierarchy Inference from Somatic Mutations: Automatic Reconstruction of Cancer Evolutionary Trees from Multi-region Next Generation Sequencing. *PLoS Computational Biology*, **2015**, 11, e1004416	5	47
4	A probabilistic model to predict clinical phenotypic traits from genome sequencing. *PLoS Computational Biology*, **2014**, 10, e1003825	5	8
3	MuPIT interactive: webserver for mapping variant positions to annotated, interactive 3D structures. *Human Genetics*, **2013**, 132, 1235-43	6.3	56
2	Exome sequencing identifies frequent inactivating mutations in BAP1, ARID1A and PBRM1 in intrahepatic cholangiocarcinomas. *Nature Genetics*, **2013**, 45, 1470-1473	36.3	464
1	Biomechanical factors in planning of periacetabular osteotomy. *Frontiers in Bioengineering and Biotechnology*, **2013**, 1, 20	5.8	13