## Tae Hyun Hwang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2581133/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Androgen Receptor Splice Variants Mediate Enzalutamide Resistance in Castration-Resistant Prostate Cancer Cell Lines. Cancer Research, 2013, 73, 483-489.	0.9	570
2	Targeting renal cell carcinoma with a HIF-2 antagonist. Nature, 2016, 539, 112-117.	27.8	521
3	Arid1a Has Context-Dependent Oncogenic and Tumor Suppressor Functions in Liver Cancer. Cancer Cell, 2017, 32, 574-589.e6.	16.8	172
4	TALEN-engineered AR gene rearrangements reveal endocrine uncoupling of androgen receptor in prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17492-17497.	7.1	147
5	Truncation and constitutive activation of the androgen receptor by diverse genomic rearrangements in prostate cancer. Nature Communications, 2016, 7, 13668.	12.8	134
6	Inhibition of Discoidin Domain Receptor 1 Reduces Collagen-mediated Tumorigenicity in Pancreatic Ductal Adenocarcinoma. Molecular Cancer Therapeutics, 2017, 16, 2473-2485.	4.1	86
7	Review of Biological Network Data and Its Applications. Genomics and Informatics, 2013, 11, 200.	0.8	79
8	DNA Methylation Regulates Alternative Polyadenylation via CTCF and the Cohesin Complex. Molecular Cell, 2020, 78, 752-764.e6.	9.7	62
9	mRNA 3′-UTR shortening is a molecular signature of mTORC1 activation. Nature Communications, 2015, 6, 7218.	12.8	55
10	PROTOCADHERIN 7 Acts through SET and PP2A to Potentiate MAPK Signaling by EGFR and KRAS during Lung Tumorigenesis. Cancer Research, 2017, 77, 187-197.	0.9	55
11	Diverse <i>AR</i> Gene Rearrangements Mediate Resistance to Androgen Receptor Inhibitors in Metastatic Prostate Cancer. Clinical Cancer Research, 2020, 26, 1965-1976.	7.0	55
12	Single cell RNA sequencing of AML initiating cells reveals RNA-based evolution during disease progression. Leukemia, 2021, 35, 2799-2812.	7.2	41
13	Transfer learning across ontologies for phenome–genome association prediction. Bioinformatics, 2017, 33, 529-536.	4.1	35
14	An integrative somatic mutation analysis to identify pathways linked with survival outcomes across 19 cancer types. Bioinformatics, 2016, 32, 1643-1651.	4.1	35
15	Comprehensive <i>Ex Vivo</i> Transposon Mutagenesis Identifies Genes That Promote Growth Factor Independence and Leukemogenesis. Cancer Research, 2016, 76, 773-786.	0.9	28
16	Hispanic/Latino Patients with Gastric Adenocarcinoma Have Distinct Molecular Profiles Including a High Rate of Germline <i>CDH1</i> Variants. Cancer Research, 2020, 80, 2114-2124.	0.9	21
17	A novel <i>TP53-KPNA3</i> translocation defines a de novo treatment-resistant clone in osteosarcoma. Journal of Physical Education and Sports Management, 2016, 2, a000992.	1.2	13
18	Radiomics Features of 18F-Fluorodeoxyglucose Positron-Emission Tomography as a Novel Prognostic Signature in Colorectal Cancer. Cancers, 2021, 13, 392.	3.7	10

Tae Hyun Hwang

#	Article	IF	CITATIONS
19	Machine Learning and Artificial Intelligence–driven Spatial Analysis of the Tumor Immune Microenvironment in Pathology Slides. European Urology Focus, 2021, 7, 706-709.	3.1	10
20	Integrated omics-analysis reveals Wnt-mediated NAD+ metabolic reprogramming in cancer stem-like cells. Oncotarget, 2016, 7, 48562-48576.	1.8	8
21	SHEAR: sample heterogeneity estimation and assembly by reference. BMC Genomics, 2014, 15, 84.	2.8	7
22	A spatiotemporal analysis of opioid poisoning mortality in Ohio from 2010 to 2016. Scientific Reports, 2021, 11, 4692.	3.3	5
23	Identifying miRNA Biomarkers and Predicted Targets Associated with Venous Thromboembolism in Colorectal Cancer Patients. Blood, 2019, 134, 3643-3643.	1.4	5
24	Intersection of DNA Privacy and Whole-Genome Sequencing. Clinical Chemistry, 2015, 61, 900-902.	3.2	2
25	Bioinformatics Data Analysis of Next-Generation Sequencing Data from Heterogeneous Tumor Samples. Methods in Molecular Biology, 2017, 1633, 185-192.	0.9	1
26	Statistical Local Binary Patterns (SLBP): Application To Prostate Cancer Gleason Score Prediction From whole Slide Pathology Images. , 2019, , .		1
27	Bayesian semi-nonnegative matrix tri-factorization to identify pathways associated with cancer phenotypes. , 2019, , .		1
28	A 30 gene panel as prognostic for survival outcomes in clinically resectable gastric cancer Journal of Clinical Oncology, 2016, 34, 4039-4039.	1.6	0