

# Thomas Yu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5191609/publications.pdf>

Version: 2024-02-01

22  
papers

1,155  
citations

840585

11  
h-index

887953

17  
g-index

27  
all docs

27  
docs citations

27  
times ranked

2330  
citing authors

#	ARTICLE	IF	CITATIONS
1	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. <i>Cell</i> , 2020, 183, 818-834.e13.	13.5	287
2	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.	5.8	240
3	Evaluation of Combined Artificial Intelligence and Radiologist Assessment to Interpret Screening Mammograms. <i>JAMA Network Open</i> , 2020, 3, e200265.	2.8	236
4	Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. <i>Lancet Oncology</i> , The, 2017, 18, 132-142.	5.1	124
5	Crowdsourcing assessment of maternal blood multi-omics for predicting gestational age and preterm birth. <i>Cell Reports Medicine</i> , 2021, 2, 100323.	3.3	47
6	Leveraging crowdsourcing to accelerate global health solutions. <i>Nature Biotechnology</i> , 2019, 37, 848-850.	9.4	36
7	A high-throughput molecular data resource for cutaneous neurofibromas. <i>Scientific Data</i> , 2017, 4, 170045.	2.4	22
8	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. <i>Life Science Alliance</i> , 2020, 3, e202000867.	1.3	20
9	Reproducible biomedical benchmarking in the cloud: lessons from crowd-sourced data challenges. <i>Genome Biology</i> , 2019, 20, 195.	3.8	19
10	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. <i>Cell Systems</i> , 2020, 11, 186-195.e9.	2.9	19
11	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. <i>Cell Systems</i> , 2021, 12, 827-838.e5.	2.9	15
12	A crowdsourced analysis to identify ab initio molecular signatures predictive of susceptibility to viral infection. <i>Nature Communications</i> , 2018, 9, 4418.	5.8	14
13	A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer. <i>JCO Clinical Cancer Informatics</i> , 2017, 1, 1-15.	1.0	12
14	A Continuously Benchmarked and Crowdsourced Challenge for Rapid Development and Evaluation of Models to Predict COVID-19 Diagnosis and Hospitalization. <i>JAMA Network Open</i> , 2021, 4, e2124946.	2.8	8
15	Piloting a model-to-data approach to enable predictive analytics in health care through patient mortality prediction. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2020, 27, 1393-1400.	2.2	6
16	A Scalable Quality Assurance Process for Curating Oncology Electronic Health Records: The Project GENIE Biopharma Collaborative Approach. <i>JCO Clinical Cancer Informatics</i> , 2022, 6, e2100105.	1.0	5
17	Abstract 4725: Multiple Myeloma DREAM Challenge: A crowd-sourced challenge to improve identification of high-risk patients. , 2017, , .		4
18	Semantic workflows for benchmark challenges: Enhancing comparability, reusability and reproducibility. , 2018, , .		3

#	ARTICLE	IF	CITATIONS
19	Linked Entity Attribute Pair (LEAP): A Harmonization Framework for Data Pooling. JCO Clinical Cancer Informatics, 2020, 4, 691-699.	1.0	2
20	Abstract 1690: A tumor deconvolution DREAM Challenge: Inferring immune infiltration from bulk gene expression data. , 2019, , .		2
21	Abstract 772: The molecular landscape of dermal neurofibromatosis. , 2016, , .		0
22	Crowdsourced High-Risk Classifiers for Multiple Myeloma Patients Commonly Identify PHF19 As a Robust Progression Biomarker. Blood, 2019, 134, 4370-4370.	0.6	0