Thomas Yu

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/5191609/thomas-yu-publications-by-year.pdf
Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

25 papers	534 citations	9 h-index	23 g-index
27 ext. papers	869 ext. citations	14.8 avg, IF	2.41 L-index

#	Paper	IF	Citations
25	A Scalable Quality Assurance Process for Curating Oncology Electronic Health Records: The Project GENIE Biopharma Collaborative Approach.. *JCO Clinical Cancer Informatics*, **2022**, 6, e2100105	5.2	0
24	A Continuously Benchmarked and Crowdsourced Challenge for Rapid Development and Evaluation of Models to Predict COVID-19 Diagnosis and Hospitalization. *JAMA Network Open*, **2021**, 4, e2124946	10.4	1
23	Crowdsourcing assessment of maternal blood multi-omics for predicting gestational age and preterm birth. *Cell Reports Medicine*, **2021**, 2, 100323	18	5
22	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. *Cell Systems*, **2021**, 12, 827-838.e5	10.6	3
21	Evaluation of Combined Artificial Intelligence and Radiologist Assessment to Interpret Screening Mammograms. *JAMA Network Open*, **2020**, 3, e200265	10.4	105
20	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. *Life Science Alliance*, **2020**, 3,	5.8	11
19	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. *Cell*, **2020**, 183, 818-834.e13	56.2	105
18	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. *Cell Systems*, **2020**, 11, 186-195.e9	10.6	11
17	Linked Entity Attribute Pair (LEAP): A Harmonization Framework for Data Pooling. *JCO Clinical Cancer Informatics*, **2020**, 4, 691-699	5.2	1
16	Piloting a model-to-data approach to enable predictive analytics in health care through patient mortality prediction. *Journal of the American Medical Informatics Association: JAMIA*, **2020**, 27, 1393-1400	8.6	4
15	Reproducible biomedical benchmarking in the cloud: lessons from crowd-sourced data challenges. *Genome Biology*, **2019**, 20, 195	18.3	10
14	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. *Nature Communications*, **2019**, 10, 2674	17.4	119
13	Leveraging crowdsourcing to accelerate global health solutions. *Nature Biotechnology*, **2019**, 37, 848-850	44.5	19
12	Abstract 1690: A tumor deconvolution DREAM Challenge: Inferring immune infiltration from bulk gene expression data **2019**,		2
11	Crowdsourced High-Risk Classifiers for Multiple Myeloma Patients Commonly Identify PHF19 As a Robust Progression Biomarker. *Blood*, **2019**, 134, 4370-4370	2.2	
10	A crowdsourced analysis to identify ab initio molecular signatures predictive of susceptibility to viral infection. *Nature Communications*, **2018**, 9, 4418	17.4	9
9	A high-throughput molecular data resource for cutaneous neurofibromas. *Scientific Data*, **2017**, 4, 170045	8.2	17

8	A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer. *JCO Clinical Cancer Informatics*, **2017**, 1, 1-15	5.2	7
7	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. *Lancet Oncology, The*, **2017**, 18, 132-142	21.7	90
6	Abstract 4725: Multiple Myeloma DREAM Challenge: A crowd-sourced challenge to improve identification of high-risk patients **2017**,		3
5	DreamAI: algorithm for the imputation of proteomics data		3
4	Multiple Myeloma DREAM Challenge Reveals Epigenetic RegulatorPHF19As Marker of Aggressive Disease		2
3	Predicting cellular position in the Drosophila embryo from Single-Cell Transcriptomics data		3
2	Crowdsourcing assessment of maternal blood multi-omics for predicting gestational age and preterm birth		1
1	Evaluation of crowdsourced mortality prediction models as a framework for assessing AI in medicine		2