

# Yun-Ching Chen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4953322/publications.pdf>

Version: 2024-02-01

16  
papers

719  
citations

933447

10  
h-index

996975

15  
g-index

16  
all docs

16  
docs citations

16  
times ranked

2090  
citing authors

#	ARTICLE	IF	CITATIONS
1	Ultra-Small Lung Cysts Impair Diffusion Without Obstructing Air Flow in Lymphangioleiomyomatosis. <i>Chest</i> , 2021, 160, 199-208.	0.8	7
2	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1141-1150.	17.5	66
3	Aberrant DNA methylation defines isoform usage in cancer, with functional implications. <i>PLoS Computational Biology</i> , 2019, 15, e1007095.	3.2	16
4	Diverging Clonal Evolution during Sequential Therapy with Chemoimmunotherapy Followed By BTK Inhibitors. <i>Blood</i> , 2019, 134, 850-850.	1.4	1
5	Spatial Genomic Heterogeneity in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2019, 134, 3017-3017.	1.4	0
6	Human retinoic acid-regulated CD161+ regulatory T cells support wound repair in intestinal mucosa. <i>Nature Immunology</i> , 2018, 19, 1403-1414.	14.5	86
7	High density lipoprotein proteome is associated with cardiovascular risk factors and atherosclerosis burden as evaluated by coronary CT angiography. <i>Atherosclerosis</i> , 2018, 278, 278-285.	0.8	39
8	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. <i>Human Mutation</i> , 2017, 38, 1266-1276.	2.5	14
9	Significant associations between driver gene mutations and DNA methylation alterations across many cancer types. <i>PLoS Computational Biology</i> , 2017, 13, e1005840.	3.2	39
10	CpG island methylator phenotype in adenocarcinomas from the digestive tract: Methods, conclusions, and controversies. <i>World Journal of Gastrointestinal Oncology</i> , 2017, 9, 105.	2.0	9
11	Exome Sequencing of Familial Bipolar Disorder. <i>JAMA Psychiatry</i> , 2016, 73, 590.	11.0	97
12	Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. <i>Cancer Discovery</i> , 2016, 6, 166-175.	9.4	282
13	A Probabilistic Model to Predict Clinical Phenotypic Traits from Genome Sequencing. <i>PLoS Computational Biology</i> , 2014, 10, e1003825.	3.2	10
14	A Hybrid Likelihood Model for Sequence-Based Disease Association Studies. <i>PLoS Genetics</i> , 2013, 9, e1003224.	3.5	19
15	Exonic DNA Sequencing of ERBB4 in Bipolar Disorder. <i>PLoS ONE</i> , 2011, 6, e20242.	2.5	13
16	Profile analysis of expressed sequence tags derived from the ovary of tilapia, <i>Oreochromis mossambicus</i> . <i>Aquaculture</i> , 2006, 251, 537-548.	3.5	21