Yun-Ching Chen

List of Publications by Year in descending order

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