## Victoria Yao

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3928746/publications.pdf Version: 2024-02-01

		858243	1051228	
16	1,440	12	16	
papers	citations	h-index	g-index	
21	21	0.1	2042	
21	21	21	3043	
all docs	docs citations	times ranked	citing authors	

<u> VICTORIA ΥΛΟ</u>

#	Article	IF	CITATIONS
1	Current progress and open challenges for applying deep learning across the biosciences. Nature Communications, 2022, 13, 1728.	5.8	105
2	Mapping the physiological and molecular markers of stress and SSRI antidepressant treatment in S100a10 corticostriatal neurons. Molecular Psychiatry, 2020, 25, 1112-1129.	4.1	18
3	Discriminatory Power of Combinatorial Antigen Recognition in Cancer T Cell Therapies. Cell Systems, 2020, 11, 215-228.e5.	2.9	52
4	RNA Identification of PRIME Cells Predicting Rheumatoid Arthritis Flares. New England Journal of Medicine, 2020, 383, 218-228.	13.9	111
5	Selective Neuronal Vulnerability in Alzheimer's Disease: A Network-Based Analysis. Neuron, 2020, 107, 821-835.e12.	3.8	99
6	Accurate genome-wide predictions of spatio-temporal gene expression during embryonic development. PLoS Genetics, 2019, 15, e1008382.	1.5	9
7	An integrative tissue-network approach to identify and test human disease genes. Nature Biotechnology, 2018, 36, 1091-1099.	9.4	54
8	A loop-counting method for covariate-corrected low-rank biclustering of gene-expression and genome-wide association study data. PLoS Computational Biology, 2018, 14, e1006105.	1.5	3
9	Enabling Precision Medicine through Integrative Network Models. Journal of Molecular Biology, 2018, 430, 2913-2923.	2.0	15
10	Transcriptome analysis of adult Caenorhabditis elegans cells reveals tissue-specific gene and isoform expression. PLoS Genetics, 2018, 14, e1007559.	1.5	151
11	Genome-wide prediction and functional characterization of the genetic basis of autism spectrum disorder. Nature Neuroscience, 2016, 19, 1454-1462.	7.1	359
12	Metabolic network rewiring of propionate flux compensates vitamin B12 deficiency in C. elegans. ELife, 2016, 5, .	2.8	96
13	FNTM: a server for predicting functional networks of tissues in mouse. Nucleic Acids Research, 2015, 43, W182-W187.	6.5	25
14	IMP 2.0: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. Nucleic Acids Research, 2015, 43, W128-W133.	6.5	60
15	A community computational challenge to predict the activity of pairs of compounds. Nature Biotechnology, 2014, 32, 1213-1222.	9.4	264
16	Nucleosome-coupled expression differences in closely-related species. BMC Genomics, 2011, 12, 466.	1.2	7