Sai Zhang

List of Publications by Year
in descending order

		759233	794594
21 papers	811 citations	12 h-index	19 g-index
27 all docs	27 docs citations	27 times ranked	1225 citing authors

#	Article	IF	Citations
1	A review of Mendelian randomization in amyotrophic lateral sclerosis. Brain, 2022, 145, 832-842.	7.6	29
2	Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis. Neuron, 2022, 110, 992-1008.e11.	8.1	51
3	Unbiased metabolome screen leads to personalized medicine strategy for amyotrophic lateral sclerosis. Brain Communications, 2022, 4, fcac069.	3.3	10
4	Multiomic analysis reveals cell-type-specific molecular determinants of COVID-19 severity. Cell Systems, 2022, 13, 598-614.e6.	6.2	10
5	DeepRibSt: a multi-feature convolutional neural network for predicting ribosome stalling. Multimedia Tools and Applications, 2021, 80, 17239-17255.	3.9	1
6	Characterizing RNA Pseudouridylation by Convolutional Neural Networks. Genomics, Proteomics and Bioinformatics, 2021, 19, 815-833.	6.9	5
7	Precision medicine in women with epilepsy: The challenge, systematic review, and future direction. Epilepsy and Behavior, 2021, 118, 107928.	1.7	13
8	Physical exercise is a risk factor for amyotrophic lateral sclerosis: Convergent evidence from Mendelian randomisation, transcriptomics and risk genotypes. EBioMedicine, 2021, 68, 103397.	6.1	65
9	Advances in the genetic classification of amyotrophic lateral sclerosis. Current Opinion in Neurology, 2021, 34, 756-764.	3.6	12
10	Membrane lipid raft homeostasis is directly linked to neurodegeneration. Essays in Biochemistry, 2021, 65, 999-1011.	4.7	15
11	Rare Variant Burden Analysis within Enhancers Identifies CAV1 as an ALS Risk Gene. Cell Reports, 2020, 33, 108456.	6.4	24
12	Gene-Environment Interaction in the Era of Precision Medicine. Cell, 2019, 177, 38-44.	28.9	73
13	DeepHINT: understanding HIV-1 integration via deep learning with attention. Bioinformatics, 2019, 35, 1660-1667.	4.1	41
14	Decoding the Genomics of Abdominal Aortic Aneurysm. Cell, 2018, 174, 1361-1372.e10.	28.9	68
15	A deep boosting based approach for capturing the sequence binding preferences of RNA-binding proteins from high-throughput CLIP-seq data. Nucleic Acids Research, 2017, 45, e129-e129.	14.5	19
16	Analysis of Ribosome Stalling and Translation Elongation Dynamics by Deep Learning. Cell Systems, 2017, 5, 212-220.e6.	6.2	58
17	TITER: predicting translation initiation sites by deep learning. Bioinformatics, 2017, 33, i234-i242.	4.1	83
18	Elastic restricted Boltzmann machines for cancer data analysis. Quantitative Biology, 2017, 5, 159-172.	0.5	4

#	Article	IF	Citations
19	A deep learning framework for modeling structural features of RNA-binding protein targets. Nucleic Acids Research, 2016, 44, e32-e32.	14.5	213
20	ROSE: A Deep Learning Based Framework for Predicting Ribosome Stalling. SSRN Electronic Journal, 0, , .	0.4	2
21	Genome-Wide Identification of the Genetic Basis of Amyotrophic Lateral Sclerosis. SSRN Electronic Journal, 0, , .	0.4	1