David Zhang

List of Publications by Year
in descending order

15 papers	551 citations	1040056 9 h-index	1125743 13 g-index
23 all docs	23 docs citations	23 times ranked	761 citing authors

#	Article	IF	Citations
1	recount3: summaries and queries for large-scale RNA-seq expression and splicing. Genome Biology, 2021, 22, 323.	8.8	103
2	Mitochondria function associated genes contribute to Parkinsonâ€™s Disease risk and later age at onset. Npj Parkinson's Disease, 2019, 5, 8.	5.3	95
3	ggtranscript: an R package for the visualization and interpretation of transcript isoforms usingggplot2. Bioinformatics, 2022, 38, 3844-3846.	4.1	76
4	Genetic variability in response to amyloid beta deposition influences Alzheimerâ€™s disease risk. Brain Communications, 2019, 1, fcz022.	3.3	67
5	Incomplete annotation has a disproportionate impact on our understanding of Mendelian and complex neurogenetic disorders. Science Advances, 2020, 6, .	10.3	44
6	Neuronal intranuclear inclusion disease is genetically heterogeneous. Annals of Clinical and Translational Neurology, 2020, 7, 1716-1725.	3.7	38
7	Variation at the TRIM11 locus modifies progressive supranuclear palsy phenotype. Annals of Neurology, 2018, 84, 485-496.	5.3	37
8	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. Nature Communications, 2020, 11, 1041.	12.8	22
9	Megadepth: efficient coverage quantification for BigWigs and BAMs. Bioinformatics, 2021, 37, 3014-3016.	4.1	18
10	Duplication of 10q24 locus: broadening the clinical and radiological spectrum. European Journal of Human Genetics, 2019, 27, 525-534.	2.8	13
11	Human-lineage-specific genomic elements are associated with neurodegenerative disease and APOE transcript usage. Nature Communications, 2021, 12, 2076.	12.8	9
12	Mitochondrial-nuclear cross-talk in the human brain is modulated by cell type and perturbed in neurodegenerative disease. Communications Biology, 2021, 4, 1262.	4.4	8
13	Leveraging omic features with F3UTER enables identification of unannotated 3â€™UTRs for synaptic genes. Nature Communications, 2022, 13, 2270.	12.8	4
14	022â€... Functional genomics and transcriptomics further characterise and potentially improve diagnostic yield of hereditary ataxias. Journal of Neurology, Neurosurgery and Psychiatry, 2022, 93, A107.3-A108.	1.9	0
15	Genomic features specific to the human lineage are associated with neurological diseases and intelligence. Journal of Neurology, Neurosurgery and Psychiatry, 2022, 93, A97.1-A97.	1.9	0