

Tiana M Scott

List of Publications by Year in descending order

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Version: 2024-02-01

11
papers

109
citations

1936888

4
h-index

1473754

9
g-index

11
all docs

11
docs citations

11
times ranked

125
citing authors

#	ARTICLE	IF	CITATIONS
1	BICRA, a SWI/SNF Complex Member, Is Associated with BAF-Disorder Related Phenotypes in Humans and Model Organisms. <i>American Journal of Human Genetics</i> , 2020, 107, 1096-1112.	2.6	32
2	Clinical exome sequencing data reveal high diagnostic yields for congenital diaphragmatic hernia plus (CDH+) and new phenotypic expansions involving CDH. <i>Journal of Medical Genetics</i> , 2022, 59, 270-278.	1.5	27
3	Retrospective analysis of a clinical exome sequencing cohort reveals the mutational spectrum and identifies candidate disease-associated loci for BAFopathies. <i>Genetics in Medicine</i> , 2022, 24, 364-373.	1.1	12
4	<i>BAZ2B</i> haploinsufficiency as a cause of developmental delay, intellectual disability, and autism spectrum disorder. <i>Human Mutation</i> , 2020, 41, 921-925.	1.1	11
5	A signaling pathway-driven bioinformatics pipeline for predicting therapeutics against emerging infectious diseases. <i>F1000Research</i> , 0, 10, 330.	0.8	8
6	Delineation of a novel neurodevelopmental syndrome associated with <i>PAX5</i> haploinsufficiency. <i>Human Mutation</i> , 2022, 43, 461-470.	1.1	5
7	Defining the genotypic and phenotypic spectrum of X-linked MSL3-related disorder. <i>Genetics in Medicine</i> , 2021, 23, 384-395.	1.1	4
8	A signaling pathway-driven bioinformatics pipeline for predicting therapeutics against emerging infectious diseases. <i>F1000Research</i> , 2021, 10, 330.	0.8	4
9	Comparison of Whole Genome Sequencing and Repetitive Element PCR for Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Strain Typing. <i>Journal of Molecular Diagnostics</i> , 2021, , .	1.2	3
10	RERE deficiency contributes to the development of orofacial clefts in humans and mice. <i>Human Molecular Genetics</i> , 2021, 30, 595-602.	1.4	2
11	Preprocessing of Public RNA-Sequencing Datasets to Facilitate Downstream Analyses of Human Diseases. <i>Data</i> , 2021, 6, 75.	1.2	1