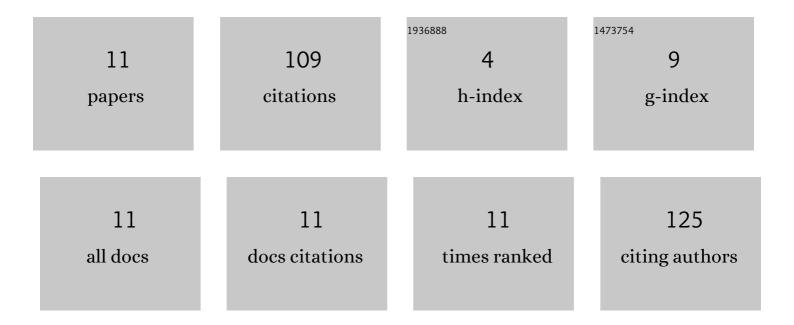
## Tiana M Scott

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5367715/publications.pdf Version: 2024-02-01



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