Tomas W Fitzgerald

List of Publications by Year
in descending order

14 papers	3,395 citations	840585 11 h-index	940416 16 g-index
26 all docs	26 docs citations	26 times ranked	8392 citing authors

#	Article	IF	Citations
1	The Medaka Inbred Kiyosu-Karlsruhe (MIKK) panel. Genome Biology, 2022, 23, 59.	3.8	6
2	Genomic variations and epigenomic landscape of the Medaka Inbred Kiyosu-Karlsruhe (MIKK) panel. Genome Biology, 2022, 23, 58.	3.8	5
3	Selective clonal persistence of human retroviruses in vivo: Radial chromatin organization, integration site, and host transcription. Science Advances, 2022, 8, eabm6210.	4.7	15
4	The contribution of common regulatory and protein-coding TYR variants to the genetic architecture of albinism. Nature Communications, 2022, 13, .	5.8	17
5	Genetic variation affects morphological retinal phenotypes extracted from UK Biobank optical coherence tomography images. PLoS Genetics, 2021, 17, e1009497.	1.5	50
6	Integrative analysis of genomic variants reveals new associations of candidate haploinsufficient genes with congenital heart disease. PLoS Genetics, 2021, 17, e1009679.	1.5	17
7	RNA modifications detection by comparative Nanopore direct RNA sequencing. Nature Communications, 2021, 12, 7198.	5.8	163
8	Comparison of Associations with Different Macular Inner Retinal Thickness Parameters in a Large Cohort. Ophthalmology, 2020, 127, 62-71.	2.5	64
9	Histone Lysine Methylases and Demethylases in the Landscape of Human Developmental Disorders. American Journal of Human Genetics, 2018, 102, 175-187.	2.6	204
10	The human leukemia virus HTLV-1 alters the structure and transcription of host chromatin in cis. ELife, 2018, 7, .	2.8	64
11	ChromoTrace: Computational reconstruction of 3D chromosome configurations for super-resolution microscopy. PLoS Computational Biology, 2018, 14, e1006002.	1.5	5
12	Distinct genetic architectures for syndromic and nonsyndromic congenital heart defects identified by exome sequencing. Nature Genetics, 2016, 48, 1060-1065.	9.4	351
13	Genetic diagnosis of developmental disorders in the DDD study: a scalable analysis of genome-wide research data. Lancet, The, 2015, 385, 1305-1314.	6.3	651
14	Origins and functional impact of copy number variation in the human genome. Nature, 2010, 464, 704-712.	13.7	1,721