

Tomas W Fitzgerald

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3530701/publications.pdf>

Version: 2024-02-01

14
papers

3,395
citations

840119

11
h-index

940134

16
g-index

26
all docs

26
docs citations

26
times ranked

8392
citing authors

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