

Fãbio C P Navarro

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5096216/publications.pdf>

Version: 2024-02-01

30
papers

7,368
citations

331259

21
h-index

433756

31
g-index

34
all docs

34
docs citations

34
times ranked

16021
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773. | 6.5 | 2,350 |
| 2 | Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018, 362, . | 6.0 | 805 |
| 3 | Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784. | 5.8 | 636 |
| 4 | GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923. | 6.5 | 633 |
| 5 | Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, . | 6.0 | 618 |
| 6 | Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018, 362, . | 6.0 | 516 |
| 7 | The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712. | 7.1 | 371 |
| 8 | Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319. | 9.4 | 275 |
| 9 | Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , 2018, 362, . | 6.0 | 220 |
| 10 | Diverse human extracellular RNAs are widely detected in human plasma. <i>Nature Communications</i> , 2016, 7, 11106. | 5.8 | 170 |
| 11 | Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , 2018, 50, 1574-1583. | 9.4 | 169 |
| 12 | Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes. <i>Genome Research</i> , 2018, 28, 448-459. | 2.4 | 99 |
| 13 | Gene Copy-Number Polymorphism Caused by Retrotransposition in Humans. <i>PLoS Genetics</i> , 2013, 9, e1003242. | 1.5 | 88 |
| 14 | Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , 2021, 12, 3968. | 5.8 | 48 |
| 15 | A Genome-Wide Landscape of Retrocopies in Primate Genomes. <i>Genome Biology and Evolution</i> , 2015, 7, 2265-2275. | 1.1 | 46 |
| 16 | FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods. <i>Genome Biology</i> , 2018, 19, 38. | 3.8 | 46 |
| 17 | Genomics and data science: an application within an umbrella. <i>Genome Biology</i> , 2019, 20, 109. | 3.8 | 46 |
| 18 | RCPedia: a database of retrocopied genes. <i>Bioinformatics</i> , 2013, 29, 1235-1237. | 1.8 | 32 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Mutational analysis of genes coding for cell surface proteins in colorectal cancer cell lines reveal novel altered pathways, druggable mutations and mutated epitopes for targeted therapy. <i>Oncotarget</i> , 2014, 5, 9199-9213. | 0.8 | 31 |
| 20 | High IL-1R8 expression in breast tumors promotes tumor growth and contributes to impaired antitumor immunity. <i>Oncotarget</i> , 2017, 8, 49470-49483. | 0.8 | 24 |
| 21 | TeXP: Deconvolving the effects of pervasive and autonomous transcription of transposable elements. <i>PLoS Computational Biology</i> , 2019, 15, e1007293. | 1.5 | 24 |
| 22 | Prediction of Immunotherapy Response in Melanoma through Combined Modeling of Neoantigen Burden and Immune-Related Resistance Mechanisms. <i>Clinical Cancer Research</i> , 2021, 27, 4265-4276. | 3.2 | 23 |
| 23 | Distinct patterns of somatic alterations in a lymphoblastoid and a tumor genome derived from the same individual. <i>Nucleic Acids Research</i> , 2011, 39, 6056-6068. | 6.5 | 19 |
| 24 | Origins and characterization of variants shared between databases of somatic and germline human mutations. <i>BMC Bioinformatics</i> , 2020, 21, 227. | 1.2 | 14 |
| 25 | Retroposed copies of RET gene: a somatically acquired event in medullary thyroid carcinoma. <i>BMC Medical Genomics</i> , 2019, 12, 104. | 0.7 | 10 |
| 26 | To mock or not: a comprehensive comparison of mock IP and DNA input for ChIP-seq. <i>Nucleic Acids Research</i> , 2021, 49, e17-e17. | 6.5 | 8 |
| 27 | SPLOOCE. <i>RNA Biology</i> , 2012, 9, 1339-1343. | 1.5 | 7 |
| 28 | ICRmax: An optimized approach to detect tumor-specific interchromosomal rearrangements for clinical application. <i>Genomics</i> , 2015, 105, 265-272. | 1.3 | 4 |
| 29 | STK11/LKB1 Loss of Function Is Associated with Global DNA Hypomethylation and S-Adenosyl-Methionine Depletion in Human Lung Adenocarcinoma. <i>Cancer Research</i> , 2021, 81, 4194-4204. | 0.4 | 4 |
| 30 | FANCY: fast estimation of privacy risk in functional genomics data. <i>Bioinformatics</i> , 2021, 36, 5145-5150. | 1.8 | 3 |