Fbio C P Navarro

List of Publications by Citations

32 papers	3,661 citations	18 h-index	34 g-index
34 ext. papers	5,864 ext. citations	15.6 avg, IF	4.08 L-index

#	Paper	IF	Citations
32	GENCODE reference annotation for the human and mouse genomes. *Nucleic Acids Research*, **2019**, 47, D766-D773	20.1	1140
31	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. *Science*, **2018**, 362,	33.3	434
30	Multi-platform discovery of haplotype-resolved structural variation in human genomes. *Nature Communications*, **2019**, 10, 1784	17.4	346
29	Comprehensive functional genomic resource and integrative model for the human brain. *Science*, **2018**, 362,	33.3	319
28	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362,	33.3	277
27	The PsychENCODE project. *Nature Neuroscience*, **2015**, 18, 1707-12	25.5	226
26	Transcriptome and epigenome landscape of human cortical development modeled in organoids. *Science*, **2018**, 362,	33.3	142
25	Diverse human extracellular RNAs are widely detected in human plasma. *Nature Communications*, **2016**, 7, 11106	17.4	136
24	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
23	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. *Nature Genetics*, **2018**, 50, 1574-1583	36.3	91
22	GENCODE 2021. *Nucleic Acids Research*, **2021**, 49, D916-D923	20.1	82
21	Gene copy-number polymorphism caused by retrotransposition in humans. *PLoS Genetics*, **2013**, 9, e1003242	6	68
20	Repeat associated mechanisms of genome evolution and function revealed by the and genomes. *Genome Research*, **2018**, 28, 448-459	9.7	57
19	A Genome-Wide Landscape of Retrocopies in Primate Genomes. *Genome Biology and Evolution*, **2015**, 7, 2265-75	3.9	32
18	FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods. *Genome Biology*, **2018**, 19, 38	18.3	28
17	RCPedia: a database of retrocopied genes. *Bioinformatics*, **2013**, 29, 1235-7	7.2	24
16	Genomics and data science: an application within an umbrella. *Genome Biology*, **2019**, 20, 109	18.3	23

List of Publications

15	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. *Oncotarget*, **2014**, 5, 9199-213	3.3	19
14	High IL-1R8 expression in breast tumors promotes tumor growth and contributes to impaired antitumor immunity. *Oncotarget*, **2017**, 8, 49470-49483	3.3	17
13	Distinct patterns of somatic alterations in a lymphoblastoid and a tumor genome derived from the same individual. *Nucleic Acids Research*, **2011**, 39, 6056-68	20.1	17
12	TeXP: Deconvolving the effects of pervasive and autonomous transcription of transposable elements. *PLoS Computational Biology*, **2019**, 15, e1007293	5	15
11	SPLOOCE: a new portal for the analysis of human splicing variants. *RNA Biology*, **2012**, 9, 1339-43	4.8	7
10	Multiple laboratory mouse reference genomes define strain specific haplotypes and novel functional loci		7
9	ICRmax: an optimized approach to detect tumor-specific interchromosomal rearrangements for clinical application. *Genomics*, **2015**, 105, 265-72	4.3	4
8	Prediction of Immunotherapy Response in Melanoma through Combined Modeling of Neoantigen Burden and Immune-Related Resistance Mechanisms. *Clinical Cancer Research*, **2021**, 27, 4265-4276	12.9	4
7	Origins and characterization of variants shared between databases of somatic and germline human mutations. *BMC Bioinformatics*, **2020**, 21, 227	3.6	3
6	Retroposed copies of RET gene: a somatically acquired event in medullary thyroid carcinoma. *BMC Medical Genomics*, **2019**, 12, 104	3.7	3
5	Repeat associated mechanisms of genome evolution and function revealed by the Mus caroli and Mus pahari genomes		3
4	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. *Nature Communications*, **2021**, 12, 3968	17.4	2
3	To mock or not: a comprehensive comparison of mock IP and DNA input for ChIP-seq. *Nucleic Acids Research*, **2021**, 49, e17	20.1	2
2	STK11/LKB1 Loss of Function Is Associated with Global DNA Hypomethylation and -Adenosyl-Methionine Depletion in Human Lung Adenocarcinoma. *Cancer Research*, **2021**, 81, 4194-4204	10.1	1
1	FANCY: fast estimation of privacy risk in functional genomics data. *Bioinformatics*, **2021**, 36, 5145-5150	7.2	1