

# Fbio C P Navarro

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	STK11/LKB1 Loss of Function Is Associated with Global DNA Hypomethylation and -Adenosyl-Methionine Depletion in Human Lung Adenocarcinoma. <i>Cancer Research</i> , <b>2021</b> , 81, 4194-4204	10.1	1
31	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , <b>2021</b> , 12, 3968	17.4	2
30	FANCY: fast estimation of privacy risk in functional genomics data. <i>Bioinformatics</i> , <b>2021</b> , 36, 5145-5150	7.2	1
29	GENCODE 2021. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D916-D923	20.1	82
28	To mock or not: a comprehensive comparison of mock IP and DNA input for CHIP-seq. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e17	20.1	2
27	Prediction of Immunotherapy Response in Melanoma through Combined Modeling of Neoantigen Burden and Immune-Related Resistance Mechanisms. <i>Clinical Cancer Research</i> , <b>2021</b> , 27, 4265-4276	12.9	4
26	Origins and characterization of variants shared between databases of somatic and germline human mutations. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 227	3.6	3
25	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , <b>2020</b> , 52, 306-319	36.3	122
24	Genomics and data science: an application within an umbrella. <i>Genome Biology</i> , <b>2019</b> , 20, 109	18.3	23
23	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , <b>2019</b> , 10, 1784	17.4	346
22	TeXP: Deconvolving the effects of pervasive and autonomous transcription of transposable elements. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007293	5	15
21	Retroposed copies of RET gene: a somatically acquired event in medullary thyroid carcinoma. <i>BMC Medical Genomics</i> , <b>2019</b> , 12, 104	3.7	3
20	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D766-D773	20.1	1140
19	FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods. <i>Genome Biology</i> , <b>2018</b> , 19, 38	18.3	28
18	Repeat associated mechanisms of genome evolution and function revealed by the and genomes. <i>Genome Research</i> , <b>2018</b> , 28, 448-459	9.7	57
17	Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , <b>2018</b> , 362,	33.3	142
16	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , <b>2018</b> , 362,	33.3	277

15	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , <b>2018</b> , 362,	33.3	434
14	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , <b>2018</b> , 362,	33.3	319
13	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , <b>2018</b> , 50, 1574-1583	36.3	91
12	High IL-1R8 expression in breast tumors promotes tumor growth and contributes to impaired antitumor immunity. <i>Oncotarget</i> , <b>2017</b> , 8, 49470-49483	3.3	17
11	Diverse human extracellular RNAs are widely detected in human plasma. <i>Nature Communications</i> , <b>2016</b> , 7, 11106	17.4	136
10	A Genome-Wide Landscape of Retrocopies in Primate Genomes. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 2265-75	3.9	32
9	ICRmax: an optimized approach to detect tumor-specific interchromosomal rearrangements for clinical application. <i>Genomics</i> , <b>2015</b> , 105, 265-72	4.3	4
8	The PsychENCODE project. <i>Nature Neuroscience</i> , <b>2015</b> , 18, 1707-12	25.5	226
7	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> , <b>2014</b> , 5, 9199-213	3.3	19
6	Gene copy-number polymorphism caused by retrotransposition in humans. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003242	24.2	68
5	RCPedia: a database of retrocopied genes. <i>Bioinformatics</i> , <b>2013</b> , 29, 1235-7	7.2	24
4	SPLOOCE: a new portal for the analysis of human splicing variants. <i>RNA Biology</i> , <b>2012</b> , 9, 1339-43	4.8	7
3	Distinct patterns of somatic alterations in a lymphoblastoid and a tumor genome derived from the same individual. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, 6056-68	20.1	17
2	Multiple laboratory mouse reference genomes define strain specific haplotypes and novel functional loci		7
1	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes		3