FÃ¡bio C P Navarro

List of Publications by Year
in descending order

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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	FANCY: fast estimation of privacy risk in functional genomics data. Bioinformatics, 2021, 36, 5145-5150.	1.8	3
2	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	6.5	633
3	To mock or not: a comprehensive comparison of mock IP and DNA input for ChIP-seq. Nucleic Acids Research, 2021, 49, e17-e17.	6.5	8
4	STK11/LKB1 Loss of Function Is Associated with Global DNA Hypomethylation and S-Adenosyl-Methionine Depletion in Human Lung Adenocarcinoma. Cancer Research, 2021, 81, 4194-4204.	0.4	4
5	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	5.8	48
6	Prediction of Immunotherapy Response in Melanoma through Combined Modeling of Neoantigen Burden and Immune-Related Resistance Mechanisms. Clinical Cancer Research, 2021, 27, 4265-4276.	3.2	23
7	Origins and characterization of variants shared between databases of somatic and germline human mutations. BMC Bioinformatics, 2020, 21, 227.	1.2	14
8	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275
9	TeXP: Deconvolving the effects of pervasive and autonomous transcription of transposable elements. PLoS Computational Biology, 2019, 15, e1007293.	1.5	24
10	Retroposed copies of RET gene: a somatically acquired event in medullary thyroid carcinoma. BMC Medical Genomics, 2019, 12, 104.	0.7	10
11	Genomics and data science: an application within an umbrella. Genome Biology, 2019, 20, 109.	3.8	46
12	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
13	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	6.5	2,350
14	FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods. Genome Biology, 2018, 19, 38.	3.8	46
15	Repeat associated mechanisms of genome evolution and function revealed by the Mus caroli and Mus pahari genomes. Genome Research, 2018, 28, 448-459.	2.4	99
16	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	6.0	220
17	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
18	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805

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19	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	6.0	618
20	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	9.4	169
21	High IL-1R8 expression in breast tumors promotes tumor growth and contributes to impaired antitumor immunity. Oncotarget, 2017, 8, 49470-49483.	0.8	24
22	Diverse human extracellular RNAs are widely detected in human plasma. Nature Communications, 2016, 7, 11106.	5.8	170
23	A Genome-Wide Landscape of Retrocopies in Primate Genomes. Genome Biology and Evolution, 2015, 7, 2265-2275.	1.1	46
24	ICRmax: An optimized approach to detect tumor-specific interchromosomal rearrangements for clinical application. Genomics, 2015, 105, 265-272.	1.3	4
25	The PsychENCODE project. Nature Neuroscience, 2015, 18, 1707-1712.	7.1	371
26	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, 9199-9213.	0.8	31
27	Gene Copy-Number Polymorphism Caused by Retrotransposition in Humans. PLoS Genetics, 2013, 9, e1003242.	1.5	88
28	RCPedia: a database of retrocopied genes. Bioinformatics, 2013, 29, 1235-1237.	1.8	32
29	SPLOOCE. RNA Biology, 2012, 9, 1339-1343.	1.5	7
30	Distinct patterns of somatic alterations in a lymphoblastoid and a tumor genome derived from the same individual. Nucleic Acids Research, 2011, 39, 6056-6068.	6.5	19