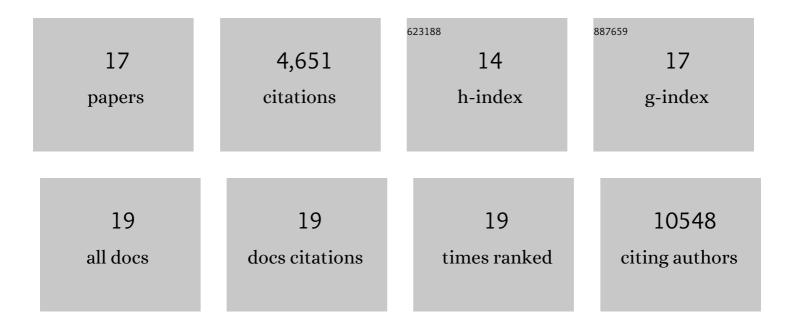
Irma ChacÃ³n

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3290434/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Escalated (Dependent) Oxycodone Self-Administration Is Associated with Cognitive Impairment and Transcriptional Evidence of Neurodegeneration in Human Immunodeficiency Virus (HIV) Transgenic Rats. Viruses, 2022, 14, 669.	1.5	4
2	Hepatoblastomas with carcinoma features represent a biological spectrum of aggressive neoplasms in children and young adults. Journal of Hepatology, 2022, 77, 1026-1037.	1.8	21
3	Inferring clonal composition from multiple tumor biopsies. Npj Systems Biology and Applications, 2020, 6, 27.	1.4	5
4	Concurrent Alterations in EGFR-Mutant Lung Cancers Associated with Resistance to EGFR Kinase Inhibitors and Characterization of MTOR as a Mediator of Resistance. Clinical Cancer Research, 2018, 24, 3108-3118.	3.2	200
5	Effects of Co-occurring Genomic Alterations on Outcomes in Patients with <i>KRAS</i> -Mutant Non–Small Cell Lung Cancer. Clinical Cancer Research, 2018, 24, 334-340.	3.2	323
6	Bronchiolar Adenoma. American Journal of Surgical Pathology, 2018, 42, 1010-1026.	2.1	91
7	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. Nature Medicine, 2017, 23, 703-713.	15.2	2,473
8	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. Cancer Discovery, 2017, 7, 596-609.	7.7	490
9	Reliable Pan-Cancer Microsatellite Instability Assessment by Using Targeted Next-Generation Sequencing Data. JCO Precision Oncology, 2017, 2017, 1-17.	1.5	209
10	Direct ChIP-Seq significance analysis improves target prediction. BMC Genomics, 2015, 16, S4.	1.2	8
11	Engineering of a Histone-Recognition Domain in Dnmt3a Alters the Epigenetic Landscape and Phenotypic Features of Mouse ESCs. Molecular Cell, 2015, 59, 89-103.	4.5	76
12	Interrogation of a Context-Specific Transcription Factor Network Identifies Novel Regulators of Pluripotency. Stem Cells, 2015, 33, 367-377.	1.4	32
13	Cupid: simultaneous reconstruction of microRNA-target and ceRNA networks. Genome Research, 2015, 25, 257-267.	2.4	94
14	Whole Exome Sequencing to Identify a Novel Gene (Caveolin-1) Associated With Human Pulmonary Arterial Hypertension. Circulation: Cardiovascular Genetics, 2012, 5, 336-343.	5.1	333
15	Plasmodium cynomolgi genome sequences provide insight into Plasmodium vivax and the monkey malaria clade. Nature Genetics, 2012, 44, 1051-1055.	9.4	172
16	Exome sequencing identified MYO1E and NEIL1 as candidate genes for human autosomal recessive steroid-resistant nephrotic syndrome. Kidney International, 2011, 80, 389-396.	2.6	69
17	Abstract 4240: Transcription factor networks that regulate pluripotency and lineage differentiation in adult human male germ cell tumors. , 2010, , .		0