

# Irma ChacÃ³n

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3290434/publications.pdf>

Version: 2024-02-01

17  
papers

4,651  
citations

623734

14  
h-index

888059

17  
g-index

19  
all docs

19  
docs citations

19  
times ranked

10548  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. <i>Nature Medicine</i> , 2017, 23, 703-713.	30.7	2,473
2	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. <i>Cancer Discovery</i> , 2017, 7, 596-609.	9.4	490
3	Whole Exome Sequencing to Identify a Novel Gene (Caveolin-1) Associated With Human Pulmonary Arterial Hypertension. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 336-343.	5.1	333
4	Effects of Co-occurring Genomic Alterations on Outcomes in Patients with KRAS-Mutant Non-Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 334-340.	7.0	323
5	Reliable Pan-Cancer Microsatellite Instability Assessment by Using Targeted Next-Generation Sequencing Data. <i>JCO Precision Oncology</i> , 2017, 2017, 1-17.	3.0	209
6	Concurrent Alterations in EGFR-Mutant Lung Cancers Associated with Resistance to EGFR Kinase Inhibitors and Characterization of MTOR as a Mediator of Resistance. <i>Clinical Cancer Research</i> , 2018, 24, 3108-3118.	7.0	200
7	Plasmodium cynomolgi genome sequences provide insight into Plasmodium vivax and the monkey malaria clade. <i>Nature Genetics</i> , 2012, 44, 1051-1055.	21.4	172
8	Cupid: simultaneous reconstruction of microRNA-target and ceRNA networks. <i>Genome Research</i> , 2015, 25, 257-267.	5.5	94
9	Bronchiolar Adenoma. <i>American Journal of Surgical Pathology</i> , 2018, 42, 1010-1026.	3.7	91
10	Engineering of a Histone-Recognition Domain in Dnmt3a Alters the Epigenetic Landscape and Phenotypic Features of Mouse ESCs. <i>Molecular Cell</i> , 2015, 59, 89-103.	9.7	76
11	Exome sequencing identified MYO1E and NEIL1 as candidate genes for human autosomal recessive steroid-resistant nephrotic syndrome. <i>Kidney International</i> , 2011, 80, 389-396.	5.2	69
12	Interrogation of a Context-Specific Transcription Factor Network Identifies Novel Regulators of Pluripotency. <i>Stem Cells</i> , 2015, 33, 367-377.	3.2	32
13	Hepatoblastomas with carcinoma features represent a biological spectrum of aggressive neoplasms in children and young adults. <i>Journal of Hepatology</i> , 2022, 77, 1026-1037.	3.7	21
14	Direct ChIP-Seq significance analysis improves target prediction. <i>BMC Genomics</i> , 2015, 16, S4.	2.8	8
15	Inferring clonal composition from multiple tumor biopsies. <i>Npj Systems Biology and Applications</i> , 2020, 6, 27.	3.0	5
16	Escalated (Dependent) Oxycodone Self-Administration Is Associated with Cognitive Impairment and Transcriptional Evidence of Neurodegeneration in Human Immunodeficiency Virus (HIV) Transgenic Rats. <i>Viruses</i> , 2022, 14, 669.	3.3	4
17	Abstract 4240: Transcription factor networks that regulate pluripotency and lineage differentiation in adult human male germ cell tumors. , 2010, , .		0