

# Irma Chacn

## 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.

14  
papers

3,084  
citations

13  
h-index

19  
g-index

19  
ext. papers

3,981  
ext. citations

13.5  
avg, IF

3.8  
L-index

#	Paper	IF	Citations
14	Inferring clonal composition from multiple tumor biopsies. <i>Npj Systems Biology and Applications</i> , <b>2020</b> , 6, 27	5	3
13	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> , <b>2018</b> , 24, 3108-3118	12.9	123
12	Effects of Co-occurring Genomic Alterations on Outcomes in Patients with -Mutant Non-Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , <b>2018</b> , 24, 334-340	12.9	173
11	Bronchiolar Adenoma: Expansion of the Concept of Ciliated Muconodular Papillary Tumors With Proposal for Revised Terminology Based on Morphologic, Immunophenotypic, and Genomic Analysis of 25 Cases. <i>American Journal of Surgical Pathology</i> , <b>2018</b> , 42, 1010-1026	6.7	42
10	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. <i>Nature Medicine</i> , <b>2017</b> , 23, 703-713	50.5	1638
9	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. <i>Cancer Discovery</i> , <b>2017</b> , 7, 596-609	24.4	317
8	Reliable Pan-Cancer Microsatellite Instability Assessment by Using Targeted Next-Generation Sequencing Data. <i>JCO Precision Oncology</i> , <b>2017</b> , 2017,	3.6	128
7	Interrogation of a context-specific transcription factor network identifies novel regulators of pluripotency. <i>Stem Cells</i> , <b>2015</b> , 33, 367-77	5.8	24
6	Cupid: simultaneous reconstruction of microRNA-target and ceRNA networks. <i>Genome Research</i> , <b>2015</b> , 25, 257-67	9.7	78
5	Direct ChIP-Seq significance analysis improves target prediction. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 5, S4	4.5	4
4	Engineering of a Histone-Recognition Domain in Dnmt3a Alters the Epigenetic Landscape and Phenotypic Features of Mouse ESCs. <i>Molecular Cell</i> , <b>2015</b> , 59, 89-103	17.6	56
3	Whole exome sequencing to identify a novel gene (caveolin-1) associated with human pulmonary arterial hypertension. <i>Circulation: Cardiovascular Genetics</i> , <b>2012</b> , 5, 336-43		268
2	Plasmodium cynomolgi genome sequences provide insight into Plasmodium vivax and the monkey malaria clade. <i>Nature Genetics</i> , <b>2012</b> , 44, 1051-5	36.3	133
1	Exome sequencing identified MYO1E and NEIL1 as candidate genes for human autosomal recessive steroid-resistant nephrotic syndrome. <i>Kidney International</i> , <b>2011</b> , 80, 389-96	9.9	63