

# Francisco MartÃ-nez-JimÃ©nez

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1343003/publications.pdf>

Version: 2024-02-01

12  
papers

1,149  
citations

933447

10  
h-index

1199594

12  
g-index

14  
all docs

14  
docs citations

14  
times ranked

2455  
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of oncogenic and clinically actionable mutations in cancer genomes critically depends on variant calling tools. <i>Bioinformatics</i> , 2022, 38, 3181-3191.	4.1	9
2	In silico saturation mutagenesis of cancer genes. <i>Nature</i> , 2021, 596, 428-432.	27.8	61
3	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021, 53, 1348-1359.	21.4	81
4	Systematic analysis of alterations in the ubiquitin proteolysis system reveals its contribution to driver mutations in cancer. <i>Nature Cancer</i> , 2020, 1, 122-135.	13.2	30
5	Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	203
6	A compendium of mutational cancer driver genes. <i>Nature Reviews Cancer</i> , 2020, 20, 555-572.	28.4	605
7	Rational design of non-resistant targeted cancer therapies. <i>Scientific Reports</i> , 2017, 7, 46632.	3.3	11
8	Should network biology be used for drug discovery?. <i>Expert Opinion on Drug Discovery</i> , 2016, 11, 1135-1137.	5.0	4
9	Release of 50 new, drug-like compounds and their computational target predictions for open source anti-tubercular drug discovery. <i>PLoS ONE</i> , 2015, 10, e0142293.	2.5	38
10	Ligand-Target Prediction by Structural Network Biology Using nAnnoLyze. <i>PLoS Computational Biology</i> , 2015, 11, e1004157.	3.2	16
11	A Novel Family of Soluble Minimal Scaffolds Provides Structural Insight into the Catalytic Domains of Integral Membrane Metallopeptidases. <i>Journal of Biological Chemistry</i> , 2013, 288, 21279-21294.	3.4	35
12	Target Prediction for an Open Access Set of Compounds Active against <i>Mycobacterium tuberculosis</i> . <i>PLoS Computational Biology</i> , 2013, 9, e1003253.	3.2	51