

# Miguel Vazquez

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5130473/publications.pdf>

Version: 2024-02-01

23  
papers

2,846  
citations

623734

14  
h-index

642732

23  
g-index

27  
all docs

27  
docs citations

27  
times ranked

6183  
citing authors

#	ARTICLE	IF	CITATIONS
1	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 47-52.	21.4	893
2	GeneCodis: interpreting gene lists through enrichment analysis and integration of diverse biological information. <i>Nucleic Acids Research</i> , 2009, 37, W317-W322.	14.5	391
3	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015, 12, 615-621.	19.0	297
4	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. <i>Nature Genetics</i> , 2013, 45, 1464-1469.	21.4	224
5	CHEMDNER: The drugs and chemical names extraction challenge. <i>Journal of Cheminformatics</i> , 2015, 7, S1.	6.1	179
6	The CHEMDNER corpus of chemicals and drugs and its annotation principles. <i>Journal of Cheminformatics</i> , 2015, 7, S2.	6.1	166
7	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013, 10, 723-729.	19.0	161
8	The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. <i>BMC Bioinformatics</i> , 2011, 12, S3.	2.6	121
9	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, 729.	12.8	73
10	Quantification of miRNA-mRNA Interactions. <i>PLoS ONE</i> , 2012, 7, e30766.	2.5	67
11	Text Mining for Drugs and Chemical Compounds: Methods, Tools and Applications. <i>Molecular Informatics</i> , 2011, 30, 506-519.	2.5	66
12	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
13	How to link ontologies and protein-protein interactions to literature: text-mining approaches and the BioCreative experience. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas017-bas017.	3.0	27
14	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020, 11, 3400.	12.8	23
15	Clmbinator: a web-based tool for drug synergy analysis in small- and large-scale datasets. <i>Bioinformatics</i> , 2017, 33, 2410-2412.	4.1	15
16	Chapter 14: Cancer Genome Analysis. <i>PLoS Computational Biology</i> , 2012, 8, e1002824.	3.2	14
17	A Middle-Out Modeling Strategy to Extend a Colon Cancer Logical Model Improves Drug Synergy Predictions in Epithelial-Derived Cancer Cell Lines. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 502573.	3.5	13
18	The Markyt visualisation, prediction and benchmark platform for chemical and gene entity recognition at BioCreative/CHEMDNER challenge. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw120.	3.0	10

#	ARTICLE	IF	CITATIONS
19	Strategies to Enhance Logic Modeling-Based Cell Line-Specific Drug Synergy Prediction. <i>Frontiers in Physiology</i> , 2020, 11, 862.	2.8	10
20	Immune analysis of lymph nodes in relation to the presence or absence of tumor infiltrating lymphocytes in triple-negative breast cancer. <i>European Journal of Cancer</i> , 2021, 148, 134-145.	2.8	10
21	wKinMut: An integrated tool for the analysis and interpretation of mutations in human protein kinases. <i>BMC Bioinformatics</i> , 2013, 14, 345.	2.6	5
22	Patient Dossier: Healthcare queries over distributed resources. <i>PLoS Computational Biology</i> , 2019, 15, e1007291.	3.2	2
23	Named Entity Recognition and Normalization: A Domain-Specific Language Approach. <i>Advances in Soft Computing</i> , 0, , 147-155.	0.4	2