Miguel Vazquez

List of Publications by Year
in descending order

23 papers	2,846 citations	623188 14 h-index	642321 23 g-index
27 all docs	27 docs citations	27 times ranked	6183 citing authors

#	Article	IF	Citations
1	Immune analysis of lymph nodes in relation to the presence or absence of tumor infiltrating lymphocytes in triple-negative breast cancer. European Journal of Cancer, 2021, 148, 134-145.	1.3	10
2	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	3.2	53
3	A Middle-Out Modeling Strategy to Extend a Colon Cancer Logical Model Improves Drug Synergy Predictions in Epithelial-Derived Cancer Cell Lines. Frontiers in Molecular Biosciences, 2020, 7, 502573.	1.6	13
4	Strategies to Enhance Logic Modeling-Based Cell Line-Specific Drug Synergy Prediction. Frontiers in Physiology, 2020, 11, 862.	1.3	10
5	A user guide for the online exploration and visualization of PCAWG data. Nature Communications, 2020, 11, 3400.	5.8	23
6	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
7	Patient Dossier: Healthcare queries over distributed resources. PLoS Computational Biology, 2019, 15, e1007291.	1.5	2
8	CImbinator: a web-based tool for drug synergy analysis in small- and large-scale datasets. Bioinformatics, 2017, 33, 2410-2412.	1.8	15
9	The Markyt visualisation, prediction and benchmark platform for chemical and gene entity recognition at BioCreative/CHEMDNER challenge. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw120.	1.4	10
10	CHEMDNER: The drugs and chemical names extraction challenge. Journal of Cheminformatics, 2015, 7, S1.	2.8	179
11	The CHEMDNER corpus of chemicals and drugs and its annotation principles. Journal of Cheminformatics, 2015, 7, S2.	2.8	166
12	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	9.0	297
13	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	9.0	161
14	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. Nature Genetics, 2013, 45, 1464-1469.	9.4	224
15	wKinMut: An integrated tool for the analysis and interpretation of mutations in human protein kinases. BMC Bioinformatics, 2013, 14, 345.	1.2	5
16	Chapter 14: Cancer Genome Analysis. PLoS Computational Biology, 2012, 8, e1002824.	1.5	14
17	How to link ontologies and protein-protein interactions to literature: text-mining approaches and the BioCreative experience. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas017-bas017.	1.4	27
18	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 47-52.	9.4	893

#	Article	IF	Citations
19	Quantification of miRNA-mRNA Interactions. PLoS ONE, 2012, 7, e30766.	1.1	67
20	The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. BMC Bioinformatics, 2011, 12, S3.	1.2	121
21	Text Mining for Drugs and Chemical Compounds: Methods, Tools and Applications. Molecular Informatics, 2011, 30, 506-519.	1.4	66
22	GeneCodis: interpreting gene lists through enrichment analysis and integration of diverse biological information. Nucleic Acids Research, 2009, 37, W317-W322.	6.5	391
23	Named Entity Recognition and Normalization: A Domain-Specific Language Approach. Advances in Soft Computing, 0, , 147-155.	0.4	2