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	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 47-52.	9.4	893
2	GeneCodis: interpreting gene lists through enrichment analysis and integration of diverse biological information. Nucleic Acids Research, 2009, 37, W317-W322.	6.5	391
3	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	9.0	297
4	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. Nature Genetics, 2013, 45, 1464-1469.	9.4	224
5	CHEMDNER: The drugs and chemical names extraction challenge. Journal of Cheminformatics, 2015, 7, S1.	2.8	179
6	The CHEMDNER corpus of chemicals and drugs and its annotation principles. Journal of Cheminformatics, 2015, 7, S2.	2.8	166
7	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	9.0	161
8	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
9	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
10	Quantification of miRNA-mRNA Interactions. PLoS ONE, 2012, 7, e30766.	1.1	67
11	Text Mining for Drugs and Chemical Compounds: Methods, Tools and Applications. Molecular Informatics, 2011, 30, 506-519.	1.4	66
12	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	3.2	53
13	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
14	A user guide for the online exploration and visualization of PCAWG data. Nature Communications, 2020, 11, 3400.	5.8	23
15	CImbinator: a web-based tool for drug synergy analysis in small- and large-scale datasets. Bioinformatics, 2017, 33, 2410-2412.	1.8	15
16	Chapter 14: Cancer Genome Analysis. PLoS Computational Biology, 2012, 8, e1002824.	1.5	14
17	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
18	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

#	Article	IF	Citations
19	Strategies to Enhance Logic Modeling-Based Cell Line-Specific Drug Synergy Prediction. Frontiers in Physiology, 2020, 11, 862.	1.3	10
20	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
21	wKinMut: An integrated tool for the analysis and interpretation of mutations in human protein kinases. BMC Bioinformatics, 2013, 14, 345.	1.2	5
22	Patient Dossier: Healthcare queries over distributed resources. PLoS Computational Biology, 2019, 15, e1007291.	1.5	2
23	Named Entity Recognition and Normalization: A Domain-Specific Language Approach. Advances in Soft Computing, 0, , 147-155.	0.4	2