

Miguel Vazquez

List of Publications by Year in descending order

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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	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
2	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
3	A Middle-Out Modeling Strategy to Extend a Colon Cancer Logical Model Improves Drug Synergy Predictions in Epithelial-Derived Cancer Cell Lines. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 502573.	3.5	13
4	Strategies to Enhance Logic Modeling-Based Cell Line-Specific Drug Synergy Prediction. <i>Frontiers in Physiology</i> , 2020, 11, 862.	2.8	10
5	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020, 11, 3400.	12.8	23
6	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, 729.	12.8	73
7	Patient Dossier: Healthcare queries over distributed resources. <i>PLoS Computational Biology</i> , 2019, 15, e1007291.	3.2	2
8	Climinator: a web-based tool for drug synergy analysis in small- and large-scale datasets. <i>Bioinformatics</i> , 2017, 33, 2410-2412.	4.1	15
9	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
10	CHEMDNER: The drugs and chemical names extraction challenge. <i>Journal of Cheminformatics</i> , 2015, 7, S1.	6.1	179
11	The CHEMDNER corpus of chemicals and drugs and its annotation principles. <i>Journal of Cheminformatics</i> , 2015, 7, S2.	6.1	166
12	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015, 12, 615-621.	19.0	297
13	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013, 10, 723-729.	19.0	161
14	Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy. <i>Nature Genetics</i> , 2013, 45, 1464-1469.	21.4	224
15	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
16	Chapter 14: Cancer Genome Analysis. <i>PLoS Computational Biology</i> , 2012, 8, e1002824.	3.2	14
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Quantification of miRNA-mRNA Interactions. PLoS ONE, 2012, 7, e30766.	2.5	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.	2.6	121
21	Text Mining for Drugs and Chemical Compounds: Methods, Tools and Applications. Molecular Informatics, 2011, 30, 506-519.	2.5	66
22	GeneCodis: interpreting gene lists through enrichment analysis and integration of diverse biological information. Nucleic Acids Research, 2009, 37, W317-W322.	14.5	391
23	Named Entity Recognition and Normalization: A Domain-Specific Language Approach. Advances in Soft Computing, 0, , 147-155.	0.4	2