

Vincenzo Belcastro

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

32
papers

2,321
citations

18
h-index

37
g-index

37
ext. papers

2,658
ext. citations

7.7
avg, IF

4.3
L-index

#	Paper	IF	Citations
32	Discovery of drug mode of action and drug repositioning from transcriptional responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 14621-6	11.5	608
31	How to infer gene networks from expression profiles. <i>Molecular Systems Biology</i> , 2007 , 3, 78	12.2	437
30	A yeast synthetic network for in vivo assessment of reverse-engineering and modeling approaches. <i>Cell</i> , 2009 , 137, 172-81	56.2	298
29	How to infer gene networks from expression profiles. <i>Molecular Systems Biology</i> , 2007 , 3, 122	12.2	191
28	Identification of microRNA-regulated gene networks by expression analysis of target genes. <i>Genome Research</i> , 2012 , 22, 1163-72	9.7	134
27	Human bronchial epithelial cells exposed in vitro to cigarette smoke at the air-liquid interface resemble bronchial epithelium from human smokers. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2013 , 304, L489-503	5.8	107
26	Transcriptional gene network inference from a massive dataset elucidates transcriptome organization and gene function. <i>Nucleic Acids Research</i> , 2011 , 39, 8677-88	20.1	88
25	Quantitative assessment of biological impact using transcriptomic data and mechanistic network models. <i>Toxicology and Applied Pharmacology</i> , 2013 , 272, 863-78	4.6	57
24	Interrogating the microbiome: experimental and computational considerations in support of study reproducibility. <i>Drug Discovery Today</i> , 2018 , 23, 1644-1657	8.8	45
23	Understanding the limits of animal models as predictors of human biology: lessons learned from the sbv IMPROVER Species Translation Challenge. <i>Bioinformatics</i> , 2015 , 31, 471-83	7.2	44
22	Colocalization of coregulated genes: a steered molecular dynamics study of human chromosome 19. <i>PLoS Computational Biology</i> , 2013 , 9, e1003019	5	40
21	The species translation challenge—a systems biology perspective on human and rat bronchial epithelial cells. <i>Scientific Data</i> , 2014 , 1, 140009	8.2	32
20	Reverse engineering gene network identifies new dysferlin-interacting proteins. <i>Journal of Biological Chemistry</i> , 2011 , 286, 5404-13	5.4	26
19	Application of a multi-layer systems toxicology framework for in vitro assessment of the biological effects of Classic Tobacco e-liquid and its corresponding aerosol using an e-cigarette device with MESH technology. <i>Archives of Toxicology</i> , 2019 , 93, 3229-3247	5.8	24
18	The centrosomal OFD1 protein interacts with the translation machinery and regulates the synthesis of specific targets. <i>Scientific Reports</i> , 2017 , 7, 1224	4.9	22
17	A parallel implementation of the network identification by multiple regression (NIR) algorithm to reverse-engineer regulatory gene networks. <i>PLoS ONE</i> , 2010 , 5, e10179	3.7	22
16	Unravelling druggable signalling networks that control F508del-CFTR proteostasis. <i>ELife</i> , 2015 , 4,	8.9	21

15	Effects of cigarette smoke, cessation and switching to a candidate modified risk tobacco product on the liver in Apoe -/- mice--a systems toxicology analysis. <i>Inhalation Toxicology</i> , 2016 , 28, 226-40	2.7	18
14	Confero: an integrated contrast data and gene set platform for computational analysis and biological interpretation of omics data. <i>BMC Genomics</i> , 2013 , 14, 514	4.5	12
13	Crowd-Sourced Verification of Computational Methods and Data in Systems Toxicology: A Case Study with a Heat-Not-Burn Candidate Modified Risk Tobacco Product. <i>Chemical Research in Toxicology</i> , 2017 , 30, 934-945	4	11
12	Reverse engineering and analysis of genome-wide gene regulatory networks from gene expression profiles using high-performance computing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 668-78	3	11
11	Systematic verification of upstream regulators of a computable cellular proliferation network model on non-diseased lung cells using a dedicated dataset. <i>Bioinformatics and Biology Insights</i> , 2013 , 7, 217-30	5.3	10
10	Supporting evidence-based analysis for modified risk tobacco products through a toxicology data-sharing infrastructure. <i>F1000Research</i> , 2017 , 6, 12	3.6	10
9	Systems toxicology assessment of a representative e-liquid formulation using human primary bronchial epithelial cells. <i>Toxicology Reports</i> , 2020 , 7, 67-80	4.8	10
8	A crowd-sourcing approach for the construction of species-specific cell signaling networks. <i>Bioinformatics</i> , 2015 , 31, 484-91	7.2	9
7	A systems biology approach reveals the dose- and time-dependent effect of primary human airway epithelium tissue culture after exposure to cigarette smoke in vitro. <i>Bioinformatics and Biology Insights</i> , 2015 , 9, 19-35	5.3	9
6	The sbv IMPROVER Systems Toxicology Computational Challenge: Identification of Human and Species-Independent Blood Response Markers as Predictors of Smoking Exposure and Cessation Status. <i>Computational Toxicology</i> , 2018 , 5, 38-51	3.1	9
5	Supporting evidence-based analysis for modified risk tobacco products through a toxicology data-sharing infrastructure. <i>F1000Research</i> , 2017 , 6, 12	3.6	7
4	GladiaTOX: GLObal Assessment of Dose-IndicAtor in TOXicology. <i>Bioinformatics</i> , 2019 , 35, 4190-4192	7.2	5
3	Reverse engineering transcriptional gene networks. <i>Methods in Molecular Biology</i> , 2014 , 1101, 179-96	1.4	3
2	Applying Systems Toxicology Methods to Drug Safety 2021 , 330-341		1
1	Toxicological Assessment Via Gene Network Analysis. <i>Methods in Pharmacology and Toxicology</i> , 2015 , 161-180	1.1	