Vincenzo Belcastro

List of Publications by Year
in descending order

33 papers	2,902 citations	430874 18 h-index	454955 30 g-index
37 all docs	37 docs citations	37 times ranked	6607 citing authors

#	Article	IF	Citations
1	Discovery of drug mode of action and drug repositioning from transcriptional responses. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14621-14626.	7.1	813
2	How to infer gene networks from expression profiles. Molecular Systems Biology, 2007, 3, 78.	7.2	563
3	A Yeast Synthetic Network for In Vivo Assessment of Reverse-Engineering and Modeling Approaches. Cell, 2009, 137, 172-181.	28.9	348
4	How to infer gene networks from expression profiles. Molecular Systems Biology, 2007, 3, 122.	7.2	208
5	Identification of microRNA-regulated gene networks by expression analysis of target genes. Genome Research, 2012, 22, 1163-1172.	5.5	165
6	Human bronchial epithelial cells exposed in vitro to cigarette smoke at the air-liquid interface resemble bronchial epithelium from human smokers. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2013, 304, L489-L503.	2.9	133
7	Transcriptional gene network inference from a massive dataset elucidates transcriptome organization and gene function. Nucleic Acids Research, 2011, 39, 8677-8688.	14.5	102
8	Interrogating the microbiome: experimental and computational considerations in support of study reproducibility. Drug Discovery Today, 2018, 23, 1644-1657.	6.4	63
9	Quantitative assessment of biological impact using transcriptomic data and mechanistic network models. Toxicology and Applied Pharmacology, 2013, 272, 863-878.	2.8	61
10	Understanding the limits of animal models as predictors of human biology: lessons learned from the sbv IMPROVER Species Translation Challenge. Bioinformatics, 2015, 31, 471-483.	4.1	57
11	Colocalization of Coregulated Genes: A Steered Molecular Dynamics Study of Human Chromosome 19. PLoS Computational Biology, 2013, 9, e1003019.	3.2	47
12	The species translation challenge—A systems biology perspective on human and rat bronchial epithelial cells. Scientific Data, 2014, 1, 140009.	5.3	46
13	The centrosomal OFD1 protein interacts with the translation machinery and regulates the synthesis of specific targets. Scientific Reports, 2017, 7, 1224.	3.3	36
14	Reverse Engineering Gene Network Identifies New Dysferlin-interacting Proteins. Journal of Biological Chemistry, 2011, 286, 5404-5413.	3.4	31
15	A Parallel Implementation of the Network Identification by Multiple Regression (NIR) Algorithm to Reverse-Engineer Regulatory Gene Networks. PLoS ONE, 2010, 5, e10179.	2.5	29
16	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. Archives of Toxicology, 2019, 93, 3229-3247.	4.2	26
17	Effects of cigarette smoke, cessation and switching to a candidate modified risk tobacco product on the liver in $Apoe^{-/-}$ mice – a systems toxicology analysis. Inhalation Toxicology, 2016, 28, 226-240.	1.6	22
18	Unravelling druggable signalling networks that control F508del-CFTR proteostasis. ELife, 2015, 4, .	6.0	22

#	Article	IF	Citations
19	Systems toxicology assessment of a representative e-liquid formulation using human primary bronchial epithelial cells. Toxicology Reports, 2020, 7, 67-80.	3.3	16
20	Confero: an integrated contrast data and gene set platform for computational analysis and biological interpretation of omics data. BMC Genomics, 2013, 14, 514.	2.8	15
21	Crowd-Sourced Verification of Computational Methods and Data in Systems Toxicology: A Case Study with a Heat-Not-Burn Candidate Modified Risk Tobacco Product. Chemical Research in Toxicology, 2017, 30, 934-945.	3.3	15
22	Reverse Engineering and Analysis of Genome-Wide Gene Regulatory Networks from Gene Expression Profiles Using High-Performance Computing. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 668-678.	3.0	13
23	The sbv IMPROVER Systems Toxicology computational challenge: Identification of human and species-independent blood response markers as predictors of smoking exposure and cessation status. Computational Toxicology, 2018, 5, 38-51.	3.3	13
24	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. Bioinformatics and Biology Insights, 2015, 9, BBI.S19908.	2.0	11
25	Systematic Verification of Upstream Regulators of a Computable Cellular Proliferation Network Model on Non-Diseased Lung Cells Using a Dedicated Dataset. Bioinformatics and Biology Insights, 2013, 7, BBI.S12167.	2.0	10
26	A crowd-sourcing approach for the construction of species-specific cell signaling networks. Bioinformatics, 2015, 31, 484-491.	4.1	10
27	Supporting evidence-based analysis for modified risk tobacco products through a toxicology data-sharing infrastructure. F1000Research, 2017, 6, 12.	1.6	10
28	Supporting evidence-based analysis for modified risk tobacco products through a toxicology data-sharing infrastructure. F1000Research, 2017, 6, 12.	1.6	7
29	GladiaTOX: GLobal Assessment of Dose-IndicAtor in TOXicology. Bioinformatics, 2019, 35, 4190-4192.	4.1	6
30	Reverse Engineering Transcriptional Gene Networks. Methods in Molecular Biology, 2014, 1101, 179-196.	0.9	3
31	Applying Systems Toxicology Methods to Drug Safety. , 2021, , 330-341.		1
32	Parallel Computing Algorithms for Reverse-Engineering and Analysis of Genome-Wide Gene Regulatory Networks from Gene Expression Profiles. , 2010, , .		0
33	Toxicological Assessment Via Gene Network Analysis. Methods in Pharmacology and Toxicology, 2015, , 161-180.	0.2	0