Boris Hayete

List of Publications by Year
in descending order

19 papers	**4,517** citations	1162367 **8** h-index	1125271 **13** g-index
20 all docs	**20** docs citations	**20** times ranked	**7071** citing authors

#	Article	IF	Citations
1	A Common Mechanism of Cellular Death Induced by Bactericidal Antibiotics. Cell, 2007, 130, 797-810.	13.5	2,334
2	Large-Scale Mapping and Validation of Escherichia coli Transcriptional Regulation from a Compendium of Expression Profiles. PLoS Biology, 2007, 5, e8.	2.6	1,308
3	Gyrase inhibitors induce an oxidative damage cellular death pathway in Escherichia coli. Molecular Systems Biology, 2007, 3, 91.	3.2	397
4	Many Microbe Microarrays Database: uniformly normalized Affymetrix compendia with structured experimental metadata. Nucleic Acids Research, 2007, 36, D866-D870.	6.5	227
5	Large-scale identification of clinical and genetic predictors of motor progression in patients with newly diagnosed Parkinson's disease: a longitudinal cohort study and validation. Lancet Neurology, The, 2017, 16, 908-916.	4.9	132
6	Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. Leukemia, 2020, 34, 1866-1874.	3.3	36
7	Size matters: network inference tackles the genome scale. Molecular Systems Biology, 2007, 3, 77.	3.2	26
8	Systems biology and in vitro validation identifies family with sequence similarity 129 member A (FAM129A) as an asthma steroid response modulator. Journal of Allergy and Clinical Immunology, 2018, 142, 1479-1488.e12.	1.5	15
9	GOTREES: PREDICTING GO ASSOCIATIONS FROM PROTEIN DOMAIN COMPOSITION USING DECISION TREES. , 2004, , .		15
10	A Bayesian mathematical model of motor and cognitive outcomes in Parkinson's disease. PLoS ONE, 2017, 12, e0178982.	1.1	11
11	Bayesian Network Models of Multiple Myeloma: Drivers of High Risk and Durable Response. Blood, 2016, 128, 4406-4406.	0.6	5
12	Inferring Gene Networks for Strains of Dehalococcoides Highlights Conserved Relationships between Genes Encoding Core Catabolic and Cell-Wall Structural Proteins. PLoS ONE, 2016, 11, e0166234.	1.1	4
13	Preclinical Validation Studies Support Causal Machine Learning Based Identification of Novel Drug Targets for High-Risk Multiple Myeloma. Blood, 2018, 132, 3210-3210.	0.6	3
14	Statistical modeling of CALGB 80405 (Alliance) to identify influential factors in metastatic colorectal cancer (CRC) dependent on primary (1o) tumor side.. Journal of Clinical Oncology, 2017, 35, 3528-3528.	0.8	1
15	Abstract 5299: Machine learning approach to personalized medicine in breast cancer patients: Development of data-driven, personalized, causal modeling through identification and understanding of optimal treatments for predicting better disease outcomes. , 2018, , .		1
16	Abstract 5663: Confirmation of peroxiredoxin II as a driver gene for doxorubicin sensitivity identified from drug-induced expression profiling of the NCI-60 cell lines using Reverse Engineering (REFS) network models. , 2012, , .		0
17	Investigation of Mechanisms of Response in Multiple Myeloma Via Bayesian Causal Inference: An Early Analysis of the Commpass Study Data. Blood, 2015, 126, 1794-1794.	0.6	0
18	Causal modeling of CALGB 80405 (Alliance) to identify network drivers of metastatic colorectal cancer (CRC).. Journal of Clinical Oncology, 2018, 36, 3570-3570.	0.8	0

#	ARTICLE	IF	CITATIONS
19	Crowdsourced High-Risk Classifiers for Multiple Myeloma Patients Commonly Identify PHF19 As a Robust Progression Biomarker. Blood, 2019, 134, 4370-4370.	0.6	0