Nicos Angelopoulos

List of Publications by Year
in descending order

27 papers	1,881 citations	687363 13 h-index	642732 23 g-index
29 all docs	29 docs citations	29 times ranked	4362 citing authors

#	Article	IF	Citations
1	Bayesian networks elucidate complex genomic landscapes in cancer. Communications Biology, 2022, 5, 306.	4.4	5
2	mmsig: a fitting approach to accurately identify somatic mutational signatures in hematological malignancies. Communications Biology, 2021, 4, 424.	4.4	21
3	Molecular Evolution of <i>IDH</i> Wild-Type Glioblastomas Treated With Standard of Care Affects Survival and Design of Precision Medicine Trials: A Report From the EORTC 1542 Study. Journal of Clinical Oncology, 2020, 38, 81-99.	1.6	84
4	Revealing the Impact of Structural Variants in Multiple Myeloma. Blood Cancer Discovery, 2020, 1, 258-273.	5.0	81
5	Targeting of EGFR by a combination of antibodies mediates unconventional EGFR trafficking and degradation. Scientific Reports, 2020, 10, 663.	3.3	23
6	Timing the initiation of multiple myeloma. Nature Communications, 2020, 11, 1917.	12.8	99
7	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. Nature Communications, 2019, 10, 3835.	12.8	183
8	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. Cell, 2018, 173, 611-623.e17.	28.9	398
9	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. New England Journal of Medicine, 2018, 379, 1416-1430.	27.0	442
10	Accessing biological data as Prolog facts. , 2017, , .		1
11	Distributional logic programming for Bayesian knowledge representation. International Journal of Approximate Reasoning, 2017, 80, 52-66.	3.3	5
12	Proteome-wide dataset supporting functional study of tyrosine kinases in breast cancer. Data in Brief, 2016, 7, 740-746.	1.0	3
13	Advances in integrative statistics for logic programming. International Journal of Approximate Reasoning, 2016, 78, 103-115.	3.3	2
14	ATG9A loss confers resistance to trastuzumab via c-Cbl mediated Her2 degradation. Oncotarget, 2016, 7, 27599-27612.	1.8	21
15	LMTK3 Represses Tumor Suppressor-like Genes through Chromatin Remodeling in Breast Cancer. Cell Reports, 2015, 12, 837-849.	6.4	21
16	Characterization of the Tyrosine Kinase-Regulated Proteome in Breast Cancer by Combined use of RNA interference (RNAi) and Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC) Quantitative Proteomics. Molecular and Cellular Proteomics, 2015, 14, 2479-2492.	3.8	17
17	The vaginal microbiome during pregnancy and the postpartum period in a European population. Scientific Reports, 2015, 5, 8988.	3.3	415
18	Proteomic profile of KSR1-regulated signalling in response to genotoxic agents in breast cancer. Breast Cancer Research and Treatment, 2015, 151, 555-568.	2.5	10

#	Article	IF	Citations
19	Selective Chemical Intervention in the Proteome of <i>Caenorhabditis elegans</i>. Journal of Proteome Research, 2010, 9, 6060-6070.	3.7	1
20	Bayesian Model Averaging for Ligand Discovery. Journal of Chemical Information and Modeling, 2009, 49, 1547-1557.	5.4	13
21	Bayesian learning of Bayesian networks with informative priors. Annals of Mathematics and Artificial Intelligence, 2008, 54, 53-98.	1.3	15
22	Probabilistic Space Partitioning in Constraint Logic Programming. Lecture Notes in Computer Science, 2004, , 48-62.	1.3	0
23	Extending the CLP Engine for Reasoning under Uncertainty. Lecture Notes in Computer Science, 2003, , 365-373.	1.3	0
24	clp(pdf(y)): Constraints for Probabilistic Reasoning in Logic Programming. Lecture Notes in Computer Science, 2003, , 784-788.	1.3	1
25	Architecture of a mediator for a bioinformatics database federation. IEEE Transactions on Information Technology in Biomedicine, 2002, 6, 116-122.	3.2	13
26	Probabilistic Finite Domains: A Brief Overview. Lecture Notes in Computer Science, 2002, , 475-475.	1.3	5
27	Advances in Big Data Bio Analytics. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 306, 309-322.	0.8	1