Alida Palmisano

List of Publications by Year
in descending order

30 papers	619 citations	933447 10 h-index	677142 22 g-index
31 all docs	31 docs citations	31 times ranked	1160 citing authors

#	ARTICLE	IF	CITATIONS
1	TPWshiny: an interactive R/Shiny app to explore cell line transcriptional responses to anti-cancer drugs. Bioinformatics, 2022, 38, 570-572.	4.1	3
2	Molecular genomic features associated with <i>inÂvitro</i> response of the NCIâ€60 cancer cell line panel to natural products. Molecular Oncology, 2021, 15, 381-406.	4.6	14
3	MutSpliceDB: A database of splice sites variants with RNAâ€seq based evidence on effects on splicing. Human Mutation, 2021, 42, 342-345.	2.5	9
4	Association of expression of epigenetic molecular factors with DNA methylation and sensitivity to chemotherapeutic agents in cancer cell lines. Clinical Epigenetics, 2021, 13, 49.	4.1	14
5	Molecular Profiling-Based Assignment of Cancer Therapy (NCI-MPACT): A Randomized Multicenter Phase II Trial. JCO Precision Oncology, 2021, 5, 133-144.	3.0	22
6	Bioinformatics Tools and Resources for Cancer Immunotherapy Study. Methods in Molecular Biology, 2020, 2055, 649-678.	0.9	7
7	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
8	Identification of pharmacodynamic biomarkers and common molecular mechanisms of response to genotoxic agents in cancer cell lines. Cancer Chemotherapy and Pharmacology, 2019, 84, 771-780.	2.3	18
9	Efficiently Encoding Complex Biochemical Models with the Multistate Model Builder (MSMB). Methods in Molecular Biology, 2019, 1945, 119-139.	0.9	1
10	Abstract 2480: MutSpliceDB: A database of splice sites mutations effects. , 2019, , .		0
11	JigCell Model Connector: building large molecular network models from components. Simulation, 2018, 94, 993-1008.	1.8	2
12	D3Oncoprint: Stand-Alone Software to Visualize and Dynamically Explore Annotated Genomic Mutation Files. JCO Clinical Cancer Informatics, 2018, 2, 1-9.	2.1	4
13	The NCI Transcriptional Pharmacodynamics Workbench: A Tool to Examine Dynamic Expression Profiling of Therapeutic Response in the NCI-60 Cell Line Panel. Cancer Research, 2018, 78, 6807-6817.	0.9	50
14	OpenGeneMed: a portable, flexible and customizable informatics hub for the coordination of next-generation sequencing studies in support of precision medicine trials. Briefings in Bioinformatics, 2017, 18, bbw059.	6.5	9
15	Molecular Network Dynamics of Cell Cycle Control: Periodicity of Start and Finish. Methods in Molecular Biology, 2017, 1524, 331-349.	0.9	7
16	Feasibility of molecular profiling based assignment of cancer treatment (MPACT): A randomized NCI precision medicine study.. Journal of Clinical Oncology, 2016, 34, 2539-2539.	1.6	7
17	GeneMed: An Informatics Hub for the Coordination of Next-Generation Sequencing Studies that Support Precision Oncology Clinical Trials. Cancer Informatics, 2015, 14s2, CIN.S17282.	1.9	18
18	JigCell Run Manager (JC-RM): a tool for managing large sets of biochemical model parametrizations. BMC Systems Biology, 2015, 9, 95.	3.0	3

#	ARTICLE	IF	CITATIONS
19	A Stochastic Model Correctly Predicts Changes in Budding Yeast Cell Cycle Dynamics upon Periodic Expression of CLN2. PLoS ONE, 2014, 9, e96726.	2.5	9
20	Multistate Model Builder (MSMB): a flexible editor for compact biochemical models. BMC Systems Biology, 2014, 8, 42.	3.0	10
21	BlenX. , 2013, , 150-152.		0
22	The critical size is set at a single-cell level by growth rate to attain homeostasis and adaptation. Nature Communications, 2012, 3, 1012.	12.8	170
23	Molecular Network Dynamics of Cell Cycle Control: Transitions to Start and Finish. Methods in Molecular Biology, 2011, 761, 277-291.	0.9	11
24	Calibration of dynamic models of biological systems with KInfer. European Biophysics Journal, 2010, 39, 1019-1039.	2.2	20
25	Correlation-Based Network Inference and Modelling in Systems Biology: The NF-kappa B Signalling Network Case Study. , 2010, , .		3
26	Studying Irreversible Transitions in a Model of Cell Cycle Regulation. Electronic Notes in Theoretical Computer Science, 2009, 232, 39-53.	0.9	12
27	Estimating the Parameters of Cyclin-Triggered Gene Expression in Cell Cycle Control Network. , 2009, , .		0
28	Deducing Chemical Reaction Rate Constants and Their Regions of Confidence from Noisy Measurements of Time Series of Concentration. , 2009, , .		7
29	On the Parameter Inference in Chaotic Chemical Systems. , 2009, , .		0
30	The Present and the Future Perspectives of Biological Network Inference. Advances in Bioinformatics and Biomedical Engineering Book Series, 0, , 118-140.	0.4	1