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	<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
2	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
3	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
4	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
5	Calibration of dynamic models of biological systems with KInfer. European Biophysics Journal, 2010, 39, 1019-1039.	2.2	20
6	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
7	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
8	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
9	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
10	Studying Irreversible Transitions in a Model of Cell Cycle Regulation. Electronic Notes in Theoretical Computer Science, 2009, 232, 39-53.	0.9	12
11	Molecular Network Dynamics of Cell Cycle Control: Transitions to Start and Finish. Methods in Molecular Biology, 2011, 761, 277-291.	0.9	11
12	Multistate Model Builder (MSMB): a flexible editor for compact biochemical models. BMC Systems Biology, 2014, 8, 42.	3.0	10
13	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
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	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
16	Deducing Chemical Reaction Rate Constants and Their Regions of Confidence from Noisy Measurements of Time Series of Concentration. , 2009, , .		7
17	Molecular Network Dynamics of Cell Cycle Control: Periodicity of Start and Finish. Methods in Molecular Biology, 2017, 1524, 331-349.	0.9	7
18	Bioinformatics Tools and Resources for Cancer Immunotherapy Study. Methods in Molecular Biology, 2020, 2055, 649-678.	0.9	7

#	ARTICLE	IF	CITATIONS
19	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
20	D3Oncoprint: Stand-Alone Software to Visualize and Dynamically Explore Annotated Genomic Mutation Files. JCO Clinical Cancer Informatics, 2018, 2, 1-9.	2.1	4
21	Correlation-Based Network Inference and Modelling in Systems Biology: The NF-kappa B Signalling Network Case Study. , 2010, , .		3
22	JigCell Run Manager (JC-RM): a tool for managing large sets of biochemical model parametrizations. BMC Systems Biology, 2015, 9, 95.	3.0	3
23	TPWshiny: an interactive R/Shiny app to explore cell line transcriptional responses to anti-cancer drugs. Bioinformatics, 2022, 38, 570-572.	4.1	3
24	JigCell Model Connector: building large molecular network models from components. Simulation, 2018, 94, 993-1008.	1.8	2
25	Efficiently Encoding Complex Biochemical Models with the Multistate Model Builder (MSMB). Methods in Molecular Biology, 2019, 1945, 119-139.	0.9	1
26	The Present and the Future Perspectives of Biological Network Inference. Advances in Bioinformatics and Biomedical Engineering Book Series, 0, , 118-140.	0.4	1
27	Estimating the Parameters of Cyclin-Triggered Gene Expression in Cell Cycle Control Network. , 2009, , .		0
28	On the Parameter Inference in Chaotic Chemical Systems. , 2009, , .		0
29	BlenX. , 2013, , 150-152.		0
30	Abstract 2480: MutSpliceDB: A database of splice sites mutations effects. , 2019, , .		0