

Maria I Pires Pacheco

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

646
citations

840119

11
h-index

839053

18
g-index

23
all docs

23
docs citations

23
times ranked

866
citing authors

#	ARTICLE	IF	CITATIONS
1	Bruceine D Identified as a Drug Candidate against Breast Cancer by a Novel Drug Selection Pipeline and Cell Viability Assay. <i>Pharmaceuticals</i> , 2022, 15, 179.	1.7	3
2	Project-based learning course on metabolic network modelling in computational systems biology. <i>PLoS Computational Biology</i> , 2022, 18, e1009711.	1.5	3
3	The gut microbial metabolite formate exacerbates colorectal cancer progression. <i>Nature Metabolism</i> , 2022, 4, 458-475.	5.1	97
4	Loss of Ambra1 promotes melanoma growth and invasion. <i>Nature Communications</i> , 2021, 12, 2550.	5.8	30
5	Importance of the biomass formulation for cancer metabolic modeling and drug prediction. <i>IScience</i> , 2021, 24, 103110.	1.9	8
6	A dynamic multi-tissue model to study human metabolism. <i>Npj Systems Biology and Applications</i> , 2021, 7, 5.	1.4	10
7	DCcov: Repositioning of drugs and drug combinations for SARS-CoV-2 infected lung through constraint-based modeling. <i>IScience</i> , 2021, 24, 103331.	1.9	16
8	Towards the routine use of <i>in silico</i> screenings for drug discovery using metabolic modelling. <i>Biochemical Society Transactions</i> , 2020, 48, 955-969.	1.6	13
9	The Power of LC-MS Based Multiomics: Exploring Adipogenic Differentiation of Human Mesenchymal Stem/Stromal Cells. <i>Molecules</i> , 2019, 24, 3615.	1.7	23
10	Towards the Integration of Metabolic Network Modelling and Machine Learning for the Routine Analysis of High-Throughput Patient Data. <i>Computational Biology</i> , 2019, , 401-424.	0.1	0
11	Identifying and targeting cancer-specific metabolism with network-based drug target prediction. <i>EBioMedicine</i> , 2019, 43, 98-106.	2.7	53
12	Integrated InÂVitro and In Silico Modeling Delineates the Molecular Effects of a Synbiotic Regimen on Colorectal-Cancer-Derived Cells. <i>Cell Reports</i> , 2019, 27, 1621-1632.e9.	2.9	59
13	Towards the network-based prediction of repurposed drugs using patient-specific metabolic models. <i>EBioMedicine</i> , 2019, 43, 26-27.	2.7	7
14	The FASTCORE Family: For the Fast Reconstruction of Compact Context-Specific Metabolic Networks Models. <i>Methods in Molecular Biology</i> , 2018, 1716, 101-110.	0.4	11
15	Integrated metabolic modelling reveals cell-type specific epigenetic control points of the macrophage metabolic network. <i>BMC Genomics</i> , 2015, 16, 809.	1.2	35
16	The neural stem cell fate determinant TRIM32 regulates complex behavioral traits. <i>Frontiers in Cellular Neuroscience</i> , 2015, 9, 75.	1.8	18
17	Towards improved genome-scale metabolic network reconstructions: unification, transcript specificity and beyond. <i>Briefings in Bioinformatics</i> , 2015, 17, bbv100.	3.2	19
18	Benchmarking Procedures for High-Throughput Context Specific Reconstruction Algorithms. <i>Frontiers in Physiology</i> , 2015, 6, 410.	1.3	26

#	ARTICLE	IF	CITATIONS
19	Fast Reconstruction of Compact Context-Specific Metabolic Network Models. PLoS Computational Biology, 2014, 10, e1003424.	1.5	212
20	Integrated in Vitro and in Silico Modelling Delineates the Molecular Effects of a Symbiotic Regimen on Colorectal Cancer-Derived Cells. SSRN Electronic Journal, 0, , .	0.4	0