

Chang Gong

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

651
citations

687363

13
h-index

996975

15
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all docs

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docs citations

15
times ranked

731
citing authors

#	ARTICLE	IF	CITATIONS
1	A Spatial Quantitative Systems Pharmacology Platform spQSP-IO for Simulations of Tumor-Immune Interactions and Effects of Checkpoint Inhibitor Immunotherapy. <i>Cancers</i> , 2021, 13, 3751.	3.7	18
2	Integrating single cell sequencing with a spatial quantitative systems pharmacology model spQSP for personalized prediction of triple-negative breast cancer immunotherapy response. <i>Immunoinformatics</i> , 2021, 1-2, 100002.	2.2	18
3	Digital Pathology Analysis Quantifies Spatial Heterogeneity of CD3, CD4, CD8, CD20, and FoxP3 Immune Markers in Triple-Negative Breast Cancer. <i>Frontiers in Physiology</i> , 2020, 11, 583333.	2.8	42
4	A QSP Model for Predicting Clinical Responses to Monotherapy, Combination and Sequential Therapy Following CTLA-4, PD-1, and PD-L1 Checkpoint Blockade. <i>Scientific Reports</i> , 2019, 9, 11286.	3.3	69
5	A Computational Model of Neoadjuvant PD-1 Inhibition in Non-Small Cell Lung Cancer. <i>AAPS Journal</i> , 2019, 21, 79.	4.4	53
6	Multiscale Agent-Based and Hybrid Modeling of the Tumor Immune Microenvironment. <i>Processes</i> , 2019, 7, 37.	2.8	115
7	Quantitative Characterization of CD8+ T Cell Clustering and Spatial Heterogeneity in Solid Tumors. <i>Frontiers in Oncology</i> , 2018, 8, 649.	2.8	30
8	A computational multiscale agent-based model for simulating spatio-temporal tumour immune response to PD1 and PDL1 inhibition. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20170320.	3.4	118
9	Abstract 4531: Systems pharmacology to predict cellular biomarkers and optimize mono- and combination-therapy regimens: Focusing on immune checkpoint targets PD-1, PD-L1 and CTLA-4. <i>Cancer Research</i> , 2017, 77, 4531-4531.	0.9	2
10	Strategic Priming with Multiple Antigens can Yield Memory Cell Phenotypes Optimized for Infection with <i>Mycobacterium tuberculosis</i> : A Computational Study. <i>Frontiers in Microbiology</i> , 2016, 6, 1477.	3.5	16
11	Computational and Empirical Studies Predict <i>Mycobacterium tuberculosis</i> -Specific T Cells as a Biomarker for Infection Outcome. <i>PLoS Computational Biology</i> , 2016, 12, e1004804.	3.2	38
12	A multi-scale approach to designing therapeutics for tuberculosis. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 1324.	1.3	24
13	A population model capturing dynamics of tuberculosis granulomas predicts host infection outcomes. <i>Mathematical Biosciences and Engineering</i> , 2015, 12, 625-642.	1.9	15
14	Harnessing the Heterogeneity of T Cell Differentiation Fate to Fine-Tune Generation of Effector and Memory T Cells. <i>Frontiers in Immunology</i> , 2014, 5, 57.	4.8	39
15	Predicting lymph node output efficiency using systems biology. <i>Journal of Theoretical Biology</i> , 2013, 335, 169-184.	1.7	54