Stacey D Finley

List of Publications by Year
in descending order

56	1,697	331670	315739
papers	citations	21 h-index	38 g-index

77	77	77	2132
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The 2019 mathematical oncology roadmap. Physical Biology, 2019, 16, 041005.	1.8	147
2	A systems biology view of blood vessel growth and remodelling. Journal of Cellular and Molecular Medicine, 2014, 18, 1491-1508.	3.6	139
3	Fund Black scientists. Cell, 2021, 184, 561-565.	28.9	107
4	Computational framework for predictive biodegradation. Biotechnology and Bioengineering, 2009, 104, 1086-1097.	3.3	96
5	Effect of Tumor Microenvironment on Tumor VEGF During Anti-VEGF Treatment: Systems Biology Predictions. Journal of the National Cancer Institute, 2013, 105, 802-811.	6.3	92
6	In silico feasibility of novel biodegradation pathways for 1,2,4-trichlorobenzene. BMC Systems Biology, 2010, 4, 7.	3.0	74
7	Integrative Approaches to Cancer Immunotherapy. Trends in Cancer, 2019, 5, 400-410.	7.4	64
8	Computational systems biology approaches to anti-angiogenic cancer therapeutics. Drug Discovery Today, 2015, 20, 187-197.	6.4	62
9	Pharmacokinetics and pharmacodynamics of VEGF-neutralizing antibodies. BMC Systems Biology, 2011, 5, 193.	3.0	58
10	Predicting the Effects of Anti-angiogenic Agents Targeting Specific VEGF Isoforms. AAPS Journal, 2012, 14, 500-509.	4.4	53
11	Mechanistic insight into activation of MAPK signaling by pro-angiogenic factors. BMC Systems Biology, 2018, 12, 145.	3.0	50
12	Computational Model Predicts the Effects of Targeting Cellular Metabolism in Pancreatic Cancer. Frontiers in Physiology, 2017, 8, 217.	2.8	47
13	Thermodynamic analysis of biodegradation pathways. Biotechnology and Bioengineering, 2009, 103, 532-541.	3.3	45
14	Multi-scale modeling of macrophageâ€”T cell interactions within the tumor microenvironment. PLoS Computational Biology, 2020, 16, e1008519.	3.2	43
15	A Two-Compartment Model of VEGF Distribution in the Mouse. PLoS ONE, 2011, 6, e27514.	2.5	38
16	Compartment Model Predicts VEGF Secretion and Investigates the Effects of VEGF Trap in Tumor-Bearing Mice. Frontiers in Oncology, 2013, 3, 196.	2.8	37
17	ERK and Akt exhibit distinct signaling responses following stimulation by pro-angiogenic factors. Cell Communication and Signaling, 2020, 18, 114.	6.5	37
18	Computational Model of Chimeric Antigen Receptors Explains Site-Specific Phosphorylation Kinetics. Biophysical Journal, 2018, 115, 1116-1129.	0.5	35

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19	Predictive model of thrombospondin-1 and vascular endothelial growth factor in breast tumor tissue. Npj Systems Biology and Applications, 2016, 2, .	3.0	32
20	Data-driven analysis of a mechanistic model of CAR T cell signaling predicts effects of cell-to-cell heterogeneity. Journal of Theoretical Biology, 2020, 489, 110125.	1.7	28
21	ERK Activation in CAR T Cells Is Amplified by CD28-Mediated Increase in CD3Î¶ Phosphorylation. IScience, 2020, 23, 101023.	4.1	28
22	Metabolic reprogramming dynamics in tumor spheroids: Insights from a multicellular, multiscale model. PLoS Computational Biology, 2019, 15, e1007053.	3.2	27
23	Understanding the Dynamics of T-Cell Activation in Health and Disease Through the Lens of Computational Modeling. JCO Clinical Cancer Informatics, 2019, 3, 1-8.	2.1	27
24	Mechanistic modeling quantifies the influence of tumor growth kinetics on the response to anti-angiogenic treatment. PLoS Computational Biology, 2017, 13, e1005874.	3.2	25
25	Inferring relevant control mechanisms for interleukinâ€12 signaling in naÃ¯ve CD4⁺T cells. Immunology and Cell Biology, 2011, 89, 100-110.	2.3	24
26	Modeling immune cell behavior across scales in cancer. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2020, 12, e1484.	6.6	24
27	A cancer treatment based on synergy between anti-angiogenic and immune cell therapies. Journal of Theoretical Biology, 2016, 394, 197-211.	1.7	22
28	Pharmacokinetics of Antiâ€VEGF Agent Aflibercept in Cancer Predicted by Dataâ€Driven, Molecularâ€Detailed Model. CPT: Pharmacometrics and Systems Pharmacology, 2015, 4, 641-649.	2.5	19
29	Predictive Model of Lymphocyte-Specific Protein Tyrosine Kinase (LCK) Autoregulation. Cellular and Molecular Bioengineering, 2016, 9, 351-367.	2.1	19
30	Predictive model identifies strategies to enhance TSP1-mediated apoptosis signaling. Cell Communication and Signaling, 2017, 15, 53.	6.5	19
31	Timescale analysis of ruleâ€based biochemical reaction networks. Biotechnology Progress, 2012, 28, 33-44.	2.6	17
32	A multiscale computational model predicts distribution of anti-angiogenic isoform VEGF165b in peripheral arterial disease in human and mouse. Scientific Reports, 2016, 6, 37030.	3.3	17
33	The impact of tumor receptor heterogeneity on the response to anti-angiogenic cancer treatment. Integrative Biology (United Kingdom), 2018, 10, 253-269.	1.3	14
34	Mathematical Model Predicts Effective Strategies to Inhibit VEGF-eNOS Signaling. Journal of Clinical Medicine, 2020, 9, 1255.	2.4	14
35	Monitoring Severity of Multiple Organ Dysfunction Syndrome. Pediatric Critical Care Medicine, 2017, 18, S24-S31.	0.5	13
36	Enhancing network activation in natural killer cells: predictions from in silico modeling. Integrative Biology (United Kingdom), 2020, 12, 109-121.	1.3	13

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37	Exploring the Extracellular Regulation of the Tumor Angiogenic Interaction Network Using a Systems Biology Model. Frontiers in Physiology, 2019, 10, 823.	2.8	10
38	Dynamic Regulation of JAK-STAT Signaling Through the Prolactin Receptor Predicted by Computational Modeling. Cellular and Molecular Bioengineering, 2021, 14, 15-30.	2.1	10
39	Elucidating tumor-stromal metabolic crosstalk in colorectal cancer through integration of constraint-based models and LC-MS metabolomics. Metabolic Engineering, 2022, 69, 175-187.	7.0	10
40	Quantitative modeling to understand cell signaling in the tumor microenvironment. Current Opinion in Systems Biology, 2021, 27, 100345.	2.6	9
41	In silico mouse study identifies tumour growth kinetics as biomarkers for the outcome of anti-angiogenic treatment. Journal of the Royal Society Interface, 2018, 15, 20180243.	3.4	7
42	A field guide to cultivating computational biology. PLoS Biology, 2021, 19, e3001419.	5.6	6
43	An optimal control approach for enhancing natural killer cells' secretion of cytolytic molecules. APL Bioengineering, 2020, 4, 046107.	6.2	5
44	Multiscale modeling of tumor adaption and invasion following antiâ€angiogenic therapy. Computational and Systems Oncology, 2022, 2, .	1.5	5
45	Exogenous Lactogenic Signaling Stimulates Beta Cell Replication In Vivo and In Vitro. Biomolecules, 2022, 12, 215.	4.0	4
46	Mechanistic insights into the heterogeneous response to antiâ€VEGF treatment in tumors. Computational and Systems Oncology, 2021, 1, e1013.	1.5	2
47	Mechanistic characterization of endothelial sprouting mediated by proâ€angiogenic signaling. Microcirculation, 2022, 29, e12744.	1.8	2
48	Modeling cell signaling in heterogeneous cancer environments. Current Opinion in Systems Biology, 2019, 17, 15-23.	2.6	1
49	Phosphatases are predicted to govern prolactin-mediated JAKâ€“STAT signaling in pancreatic beta cells. Integrative Biology (United Kingdom), 2022, 14, 37-48.	1.3	1
50	Challenges and opportunities in 2021. Nature Cancer, 2021, 2, 1278-1283.	13.2	1
51	Editorial Overview: Mathematical modeling: It's a matter of scale. Current Opinion in Systems Biology, 2021, 28, 100360.	2.6	0
52	Deciphering the Extracellular Inhibition of Proâ€angiogenic Signaling Using a Systems Biology Model. FASEB Journal, 2019, 33, .	0.5	0
53	Multi-scale modeling of macrophageâ€”T cell interactions within the tumor microenvironment. , 2020, 16, e1008519.		0
54	Multi-scale modeling of macrophageâ€”T cell interactions within the tumor microenvironment. , 2020, 16, e1008519.		0

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55	Multi-scale modeling of macrophageâ€"T cell interactions within the tumor microenvironment. , 2020, 16, e1008519.		0
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