

# Stacey D Finley

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/909875/publications.pdf>

Version: 2024-02-01

56  
papers

1,697  
citations

331670

21  
h-index

315739

38  
g-index

77  
all docs

77  
docs citations

77  
times ranked

2132  
citing authors

#	ARTICLE	IF	CITATIONS
1	Elucidating tumor-stromal metabolic crosstalk in colorectal cancer through integration of constraint-based models and LC-MS metabolomics. <i>Metabolic Engineering</i> , 2022, 69, 175-187.	7.0	10
2	Exogenous Lactogenic Signaling Stimulates Beta Cell Replication In Vivo and In Vitro. <i>Biomolecules</i> , 2022, 12, 215.	4.0	4
3	Phosphatases are predicted to govern prolactin-mediated JAK-STAT signaling in pancreatic beta cells. <i>Integrative Biology (United Kingdom)</i> , 2022, 14, 37-48.	1.3	1
4	Multiscale modeling of tumor adaption and invasion following anti-angiogenic therapy. <i>Computational and Systems Oncology</i> , 2022, 2, .	1.5	5
5	Mechanistic characterization of endothelial sprouting mediated by pro-angiogenic signaling. <i>Microcirculation</i> , 2022, 29, e12744.	1.8	2
6	Dynamic Regulation of JAK-STAT Signaling Through the Prolactin Receptor Predicted by Computational Modeling. <i>Cellular and Molecular Bioengineering</i> , 2021, 14, 15-30.	2.1	10
7	Fund Black scientists. <i>Cell</i> , 2021, 184, 561-565.	28.9	107
8	Mechanistic insights into the heterogeneous response to anti-VEGF treatment in tumors. <i>Computational and Systems Oncology</i> , 2021, 1, e1013.	1.5	2
9	Quantitative modeling to understand cell signaling in the tumor microenvironment. <i>Current Opinion in Systems Biology</i> , 2021, 27, 100345.	2.6	9
10	Editorial Overview: Mathematical modeling: It's a matter of scale. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100360.	2.6	0
11	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419.	5.6	6
12	Challenges and opportunities in 2021. <i>Nature Cancer</i> , 2021, 2, 1278-1283.	13.2	1
13	Data-driven analysis of a mechanistic model of CAR T cell signaling predicts effects of cell-to-cell heterogeneity. <i>Journal of Theoretical Biology</i> , 2020, 489, 110125.	1.7	28
14	ERK Activation in CAR T Cells Is Amplified by CD28-Mediated Increase in CD3 $\zeta$ Phosphorylation. <i>iScience</i> , 2020, 23, 101023.	4.1	28
15	ERK and Akt exhibit distinct signaling responses following stimulation by pro-angiogenic factors. <i>Cell Communication and Signaling</i> , 2020, 18, 114.	6.5	37
16	Mathematical Model Predicts Effective Strategies to Inhibit VEGF-eNOS Signaling. <i>Journal of Clinical Medicine</i> , 2020, 9, 1255.	2.4	14
17	Enhancing network activation in natural killer cells: predictions from in silico modeling. <i>Integrative Biology (United Kingdom)</i> , 2020, 12, 109-121.	1.3	13
18	Modeling immune cell behavior across scales in cancer. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1484.	6.6	24

#	ARTICLE	IF	CITATIONS
19	An optimal control approach for enhancing natural killer cells' secretion of cytolytic molecules. <i>APL Bioengineering</i> , 2020, 4, 046107.	6.2	5
20	Multi-scale modeling of macrophage-T cell interactions within the tumor microenvironment. <i>PLoS Computational Biology</i> , 2020, 16, e1008519.	3.2	43
21	Multi-scale modeling of macrophage-T cell interactions within the tumor microenvironment. , 2020, 16, e1008519.		0
22	Multi-scale modeling of macrophage-T cell interactions within the tumor microenvironment. , 2020, 16, e1008519.		0
23	Multi-scale modeling of macrophage-T cell interactions within the tumor microenvironment. , 2020, 16, e1008519.		0
24	Multi-scale modeling of macrophage-T cell interactions within the tumor microenvironment. , 2020, 16, e1008519.		0
25	Integrative Approaches to Cancer Immunotherapy. <i>Trends in Cancer</i> , 2019, 5, 400-410.	7.4	64
26	Exploring the Extracellular Regulation of the Tumor Angiogenic Interaction Network Using a Systems Biology Model. <i>Frontiers in Physiology</i> , 2019, 10, 823.	2.8	10
27	Modeling cell signaling in heterogeneous cancer environments. <i>Current Opinion in Systems Biology</i> , 2019, 17, 15-23.	2.6	1
28	Metabolic reprogramming dynamics in tumor spheroids: Insights from a multicellular, multiscale model. <i>PLoS Computational Biology</i> , 2019, 15, e1007053.	3.2	27
29	The 2019 mathematical oncology roadmap. <i>Physical Biology</i> , 2019, 16, 041005.	1.8	147
30	Understanding the Dynamics of T-Cell Activation in Health and Disease Through the Lens of Computational Modeling. <i>JCO Clinical Cancer Informatics</i> , 2019, 3, 1-8.	2.1	27
31	Deciphering the Extracellular Inhibition of Pro-Angiogenic Signaling Using a Systems Biology Model. <i>FASEB Journal</i> , 2019, 33, .	0.5	0
32	The impact of tumor receptor heterogeneity on the response to anti-angiogenic cancer treatment. <i>Integrative Biology (United Kingdom)</i> , 2018, 10, 253-269.	1.3	14
33	Mechanistic insight into activation of MAPK signaling by pro-angiogenic factors. <i>BMC Systems Biology</i> , 2018, 12, 145.	3.0	50
34	<i>In silico</i> mouse study identifies tumour growth kinetics as biomarkers for the outcome of anti-angiogenic treatment. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180243.	3.4	7
35	Computational Model of Chimeric Antigen Receptors Explains Site-Specific Phosphorylation Kinetics. <i>Biophysical Journal</i> , 2018, 115, 1116-1129.	0.5	35
36	Monitoring Severity of Multiple Organ Dysfunction Syndrome. <i>Pediatric Critical Care Medicine</i> , 2017, 18, S24-S31.	0.5	13

#	ARTICLE	IF	CITATIONS
37	Computational Model Predicts the Effects of Targeting Cellular Metabolism in Pancreatic Cancer. <i>Frontiers in Physiology</i> , 2017, 8, 217.	2.8	47
38	Predictive model identifies strategies to enhance TSP1-mediated apoptosis signaling. <i>Cell Communication and Signaling</i> , 2017, 15, 53.	6.5	19
39	Mechanistic modeling quantifies the influence of tumor growth kinetics on the response to anti-angiogenic treatment. <i>PLoS Computational Biology</i> , 2017, 13, e1005874.	3.2	25
40	Predictive model of thrombospondin-1 and vascular endothelial growth factor in breast tumor tissue. <i>Npj Systems Biology and Applications</i> , 2016, 2, .	3.0	32
41	A multiscale computational model predicts distribution of anti-angiogenic isoform VEGF165b in peripheral arterial disease in human and mouse. <i>Scientific Reports</i> , 2016, 6, 37030.	3.3	17
42	Predictive Model of Lymphocyte-Specific Protein Tyrosine Kinase (LCK) Autoregulation. <i>Cellular and Molecular Bioengineering</i> , 2016, 9, 351-367.	2.1	19
43	A cancer treatment based on synergy between anti-angiogenic and immune cell therapies. <i>Journal of Theoretical Biology</i> , 2016, 394, 197-211.	1.7	22
44	Pharmacokinetics of Anti-VEGF Agent Aflibercept in Cancer Predicted by Data-Driven, Molecular-Detailed Model. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015, 4, 641-649.	2.5	19
45	Computational systems biology approaches to anti-angiogenic cancer therapeutics. <i>Drug Discovery Today</i> , 2015, 20, 187-197.	6.4	62
46	A systems biology view of blood vessel growth and remodelling. <i>Journal of Cellular and Molecular Medicine</i> , 2014, 18, 1491-1508.	3.6	139
47	Compartment Model Predicts VEGF Secretion and Investigates the Effects of VEGF Trap in Tumor-Bearing Mice. <i>Frontiers in Oncology</i> , 2013, 3, 196.	2.8	37
48	Effect of Tumor Microenvironment on Tumor VEGF During Anti-VEGF Treatment: Systems Biology Predictions. <i>Journal of the National Cancer Institute</i> , 2013, 105, 802-811.	6.3	92
49	Predicting the Effects of Anti-angiogenic Agents Targeting Specific VEGF Isoforms. <i>AAPS Journal</i> , 2012, 14, 500-509.	4.4	53
50	Timescale analysis of rule-based biochemical reaction networks. <i>Biotechnology Progress</i> , 2012, 28, 33-44.	2.6	17
51	Inferring relevant control mechanisms for interleukin-12 signaling in naive CD4 <sup>+</sup> T cells. <i>Immunology and Cell Biology</i> , 2011, 89, 100-110.	2.3	24
52	Pharmacokinetics and pharmacodynamics of VEGF-neutralizing antibodies. <i>BMC Systems Biology</i> , 2011, 5, 193.	3.0	58
53	A Two-Compartment Model of VEGF Distribution in the Mouse. <i>PLoS ONE</i> , 2011, 6, e27514.	2.5	38
54	In silico feasibility of novel biodegradation pathways for 1,2,4-trichlorobenzene. <i>BMC Systems Biology</i> , 2010, 4, 7.	3.0	74

#	ARTICLE	IF	CITATIONS
55	Thermodynamic analysis of biodegradation pathways. <i>Biotechnology and Bioengineering</i> , 2009, 103, 532-541.	3.3	45
56	Computational framework for predictive biodegradation. <i>Biotechnology and Bioengineering</i> , 2009, 104, 1086-1097.	3.3	96