

Jennifer J Linderman

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

56
papers

1,782
citations

26
h-index

41
g-index

57
ext. papers

2,259
ext. citations

4.7
avg, IF

5
L-index

#	Paper	IF	Citations
56	A virtual host model of Mycobacterium tuberculosis infection identifies early immune events as predictive of infection outcomes.. <i>Journal of Theoretical Biology</i> , 2022 , 111042	2.3	0
55	Neutrophil Dynamics Affect Granuloma Outcomes and Dissemination. <i>Frontiers in Immunology</i> , 2021 , 12, 712457	8.4	1
54	Simulating the Selection of Resistant Cells with Bystander Killing and Antibody Coadministration in Heterogeneous HER2 Positive Tumors. <i>Drug Metabolism and Disposition</i> , 2021 ,	4	2
53	A multi-scale pipeline linking drug transcriptomics with pharmacokinetics predicts in vivo interactions of tuberculosis drugs. <i>Scientific Reports</i> , 2021 , 11, 5643	4.9	2
52	Computational methods for characterizing and learning from heterogeneous cell signaling data. <i>Current Opinion in Systems Biology</i> , 2021 , 26, 98-108	3.2	0
51	Pre-existing Cell States Control Heterogeneity of Both EGFR and CXCR4 Signaling. <i>Cellular and Molecular Bioengineering</i> , 2021 , 14, 49-64	3.9	1
50	: A Calibration Protocol That Utilizes Parameter Density Estimation to Explore Parameter Space and Calibrate Complex Biological Models. <i>Cellular and Molecular Bioengineering</i> , 2021 , 14, 31-47	3.9	3
49	A computational model tracks whole-lung Mycobacterium tuberculosis infection and predicts factors that inhibit dissemination. <i>PLoS Computational Biology</i> , 2020 , 16, e1007280	5	9
48	An Agent-Based Systems Pharmacology Model of the Antibody-Drug Conjugate Kadcyca to Predict Efficacy of Different Dosing Regimens. <i>AAPS Journal</i> , 2020 , 22, 29	3.7	10
47	Both Pharmacokinetic Variability and Granuloma Heterogeneity Impact the Ability of the First-Line Antibiotics to Sterilize Tuberculosis Granulomas. <i>Frontiers in Pharmacology</i> , 2020 , 11, 333	5.6	10
46	Spatial Organization and Recruitment of Non-Specific T Cells May Limit T Cell-Macrophage Interactions Within Granulomas. <i>Frontiers in Immunology</i> , 2020 , 11, 613638	8.4	4
45	Data-Driven Model Validation Across Dimensions. <i>Bulletin of Mathematical Biology</i> , 2019 , 81, 1853-1866	2.1	5
44	Fluoroquinolone Efficacy against Tuberculosis Is Driven by Penetration into Lesions and Activity against Resident Bacterial Populations. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	24
43	A Two-Pulse Cellular Stimulation Test Elucidates Variability and Mechanisms in Signaling Pathways. <i>Biophysical Journal</i> , 2019 , 116, 962-973	2.9	7
42	Short-term cellular memory tunes the signaling responses of the chemokine receptor CXCR4. <i>Science Signaling</i> , 2019 , 12,	8.8	15
41	Global sensitivity analysis of biological multi-scale models. <i>Current Opinion in Biomedical Engineering</i> , 2019 , 11, 109-116	4.4	13
40	Emergence and selection of isoniazid and rifampin resistance in tuberculosis granulomas. <i>PLoS ONE</i> , 2018 , 13, e0196322	3.7	13

39	Dynamic balance of pro- and anti-inflammatory signals controls disease and limits pathology. <i>Immunological Reviews</i> , 2018 , 285, 147-167	11.3	84
38	Improved Tumor Penetration and Single-Cell Targeting of Antibody-Drug Conjugates Increases Anticancer Efficacy and Host Survival. <i>Cancer Research</i> , 2018 , 78, 758-768	10.1	48
37	The Role of Dimensionality in Understanding Granuloma Formation. <i>Computation</i> , 2018 , 6,	2.2	7
36	Integrating Non-human Primate, Human, and Mathematical Studies to Determine the Influence of BCG Timing on H56 Vaccine Outcomes. <i>Frontiers in Microbiology</i> , 2018 , 9, 1734	5.7	6
35	A review of computational and mathematical modeling contributions to our understanding of Mycobacterium tuberculosis within-host infection and treatment. <i>Current Opinion in Systems Biology</i> , 2017 , 3, 170-185	3.2	31
34	Applying optimization algorithms to tuberculosis antibiotic treatment regimens. <i>Cellular and Molecular Bioengineering</i> , 2017 , 10, 523-535	3.9	11
33	Identifying mechanisms driving formation of granuloma-associated fibrosis during Mycobacterium tuberculosis infection. <i>Journal of Theoretical Biology</i> , 2017 , 429, 1-17	2.3	22
32	Deletion of TGF- β Increases Bacterial Clearance by Cytotoxic T Cells in a Tuberculosis Granuloma Model. <i>Frontiers in Immunology</i> , 2017 , 8, 1843	8.4	27
31	Comparing efficacies of moxifloxacin, levofloxacin and gatifloxacin in tuberculosis granulomas using a multi-scale systems pharmacology approach. <i>PLoS Computational Biology</i> , 2017 , 13, e1005650	5	37
30	The CXCL12/CXCR7 signaling axis, isoforms, circadian rhythms, and tumor cellular composition dictate gradients in tissue. <i>PLoS ONE</i> , 2017 , 12, e0187357	3.7	7
29	Multiscale Model of Mycobacterium tuberculosis Infection Maps Metabolite and Gene Perturbations to Granuloma Sterilization Predictions. <i>Infection and Immunity</i> , 2016 , 84, 1650-1669	3.7	28
28	Computational and Empirical Studies Predict Mycobacterium tuberculosis-Specific T Cells as a Biomarker for Infection Outcome. <i>PLoS Computational Biology</i> , 2016 , 12, e1004804	5	30
27	Computational Modeling Predicts Simultaneous Targeting of Fibroblasts and Epithelial Cells Is Necessary for Treatment of Pulmonary Fibrosis. <i>Frontiers in Pharmacology</i> , 2016 , 7, 183	5.6	24
26	A multi-scale approach to designing therapeutics for tuberculosis. <i>Integrative Biology (United Kingdom)</i> , 2015 , 7, 591-609	3.7	19
25	Identifying Mechanisms of Homeostatic Signaling in Fibroblast Differentiation. <i>Bulletin of Mathematical Biology</i> , 2015 , 77, 1556-82	2.1	17
24	A computational tool integrating host immunity with antibiotic dynamics to study tuberculosis treatment. <i>Journal of Theoretical Biology</i> , 2015 , 367, 166-179	2.3	49
23	Strategies for efficient numerical implementation of hybrid multi-scale agent-based models to describe biological systems. <i>Cellular and Molecular Bioengineering</i> , 2015 , 8, 119-136	3.9	65
22	models of infection provide a route to new therapies. <i>Drug Discovery Today: Disease Models</i> , 2015 , 15, 37-41	1.3	12

21	Macrophage polarization drives granuloma outcome during Mycobacterium tuberculosis infection. <i>Infection and Immunity</i> , 2015 , 83, 324-38	3.7	103
20	In silico evaluation and exploration of antibiotic tuberculosis treatment regimens. <i>BMC Systems Biology</i> , 2015 , 9, 79	3.5	30
19	Computational modeling predicts IL-10 control of lesion sterilization by balancing early host immunity-mediated antimicrobial responses with caseation during mycobacterium tuberculosis infection. <i>Journal of Immunology</i> , 2015 , 194, 664-77	5.3	55
18	Cell, isoform, and environment factors shape gradients and modulate chemotaxis. <i>PLoS ONE</i> , 2015 , 10, e0123450	3.7	17
17	Strategic Priming with Multiple Antigens can Yield Memory Cell Phenotypes Optimized for Infection with Mycobacterium tuberculosis: A Computational Study. <i>Frontiers in Microbiology</i> , 2015 , 6, 1477	5.7	12
16	Tuneable resolution as a systems biology approach for multi-scale, multi-compartment computational models. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2014 , 6, 289-309	6.6	41
15	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	8.4	29
14	A Comprehensive Analysis of CXCL12 Isoforms in Breast Cancer. <i>Translational Oncology</i> , 2014 , 7, 429-429	4.9	30
13	CXCR7 controls competition for recruitment of β arrestin 2 in cells expressing both CXCR4 and CXCR7. <i>PLoS ONE</i> , 2014 , 9, e98328	3.7	42
12	Multi-scale modeling predicts a balance of tumor necrosis factor- β and interleukin-10 controls the granuloma environment during Mycobacterium tuberculosis infection. <i>PLoS ONE</i> , 2013 , 8, e68680	3.7	90
11	Differential risk of tuberculosis reactivation among anti-TNF therapies is due to drug binding kinetics and permeability. <i>Journal of Immunology</i> , 2012 , 188, 3169-78	5.3	73
10	NF- κ B Signaling Dynamics Play a Key Role in Infection Control in Tuberculosis. <i>Frontiers in Physiology</i> , 2012 , 3, 170	4.6	67
9	Multiscale computational modeling reveals a critical role for TNF- α receptor 1 dynamics in tuberculosis granuloma formation. <i>Journal of Immunology</i> , 2011 , 186, 3472-83	5.3	134
8	Identification of key processes that control tumor necrosis factor availability in a tuberculosis granuloma. <i>PLoS Computational Biology</i> , 2010 , 6, e1000778	5	44
7	Characterizing the dynamics of CD4+ T cell priming within a lymph node. <i>Journal of Immunology</i> , 2010 , 184, 2873-85	5.3	48
6	Modeling of G-protein-coupled receptor signaling pathways. <i>Journal of Biological Chemistry</i> , 2009 , 284, 5427-31	5.4	36
5	Lipid raft-mediated regulation of G-protein coupled receptor signaling by ligands which influence receptor dimerization: a computational study. <i>PLoS ONE</i> , 2009 , 4, e6604	3.7	68
4	Mathematical and computational approaches can complement experimental studies of host-pathogen interactions. <i>Cellular Microbiology</i> , 2009 , 11, 531-539	3.9	45

3	Nanoscale Adhesion Ligand Organization Regulates Osteoblast Proliferation and Differentiation. <i>Nano Letters</i> , 2004 , 4, 1501-1506	11.5	154
2	Validation of flow cytometric competitive binding protocols and characterization of fluorescently labeled ligands. <i>Cytometry</i> , 2001 , 45, 102-14		20
1	Mathematical Models of Anti-TNF Therapies and their Correlation with Tuberculosis83-104		1