Jennifer J Linderman

List of Publications by Year
in descending order

55 papers	2,563 citations	172207 29 h-index	214527 47 g-index
57 all docs	57 docs citations	57 times ranked	3176 citing authors

#	Article	IF	Citations
1	Dynamic balance of pro–and anti–inflammatory signals controls disease and limits pathology. Immunological Reviews, 2018, 285, 147-167.	2.8	175
2	Nanoscale Adhesion Ligand Organization Regulates Osteoblast Proliferation and Differentiation. Nano Letters, 2004, 4, 1501-1506.	4.5	164
3	Multiscale Computational Modeling Reveals a Critical Role for TNF-α Receptor 1 Dynamics in Tuberculosis Granuloma Formation. Journal of Immunology, 2011, 186, 3472-3483.	0.4	158
4	Macrophage Polarization Drives Granuloma Outcome during Mycobacterium tuberculosis Infection. Infection and Immunity, 2015, 83, 324-338.	1.0	149
5	NF-κB Signaling Dynamics Play a Key Role in Infection Control in Tuberculosis. Frontiers in Physiology, 2012, 3, 170.	1.3	112
6	Multi-Scale Modeling Predicts a Balance of Tumor Necrosis Factor-α and Interleukin-10 Controls the Granuloma Environment during Mycobacterium tuberculosis Infection. PLoS ONE, 2013, 8, e68680.	1.1	109
7	Strategies for Efficient Numerical Implementation of Hybrid Multi-scale Agent-Based Models to Describe Biological Systems. Cellular and Molecular Bioengineering, 2015, 8, 119-136.	1.0	87
8	Differential Risk of Tuberculosis Reactivation among Anti-TNF Therapies Is Due to Drug Binding Kinetics and Permeability. Journal of Immunology, 2012, 188, 3169-3178.	0.4	86
9	Lipid Raft-Mediated Regulation of G-Protein Coupled Receptor Signaling by Ligands which Influence Receptor Dimerization: A Computational Study. PLoS ONE, 2009, 4, e6604.	1.1	79
10	Improved Tumor Penetration and Single-Cell Targeting of Antibody–Drug Conjugates Increases Anticancer Efficacy and Host Survival. Cancer Research, 2018, 78, 758-768.	0.4	77
11	A computational tool integrating host immunity with antibiotic dynamics to study tuberculosis treatment. Journal of Theoretical Biology, 2015, 367, 166-179.	0.8	68
12	Computational Modeling Predicts IL-10 Control of Lesion Sterilization by Balancing Early Host Immunity–Mediated Antimicrobial Responses with Caseation during <i>Mycobacterium tuberculosis</i> Infection. Journal of Immunology, 2015, 194, 664-677.	0.4	63
13	A review of computational and mathematical modeling contributions to our understanding of Mycobacterium tuberculosis within-host infection and treatment. Current Opinion in Systems Biology, 2017, 3, 170-185.	1.3	61
14	Identification of Key Processes that Control Tumor Necrosis Factor Availability in a Tuberculosis Granuloma. PLoS Computational Biology, 2010, 6, e1000778.	1.5	57
15	Comparing efficacies of moxifloxacin, levofloxacin and gatifloxacin in tuberculosis granulomas using a multi-scale systems pharmacology approach. PLoS Computational Biology, 2017, 13, e1005650.	1.5	57
16	Characterizing the Dynamics of CD4+ T Cell Priming within a Lymph Node. Journal of Immunology, 2010, 184, 2873-2885.	0.4	54
17	Tuneable resolution as a systems biology approach for multi–scale, multi–compartment computational models. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2014, 6, 289-309.	6.6	53
18	Identifying mechanisms driving formation of granuloma-associated fibrosis during Mycobacterium tuberculosis infection. Journal of Theoretical Biology, 2017, 429, 1-17.	0.8	49

#	Article	IF	Citations
19	Mathematical and computational approaches can complement experimental studies of host-pathogen interactions. Cellular Microbiology, 2009, 11, 531-539.	1.1	48
20	Multiscale Model of Mycobacterium tuberculosis Infection Maps Metabolite and Gene Perturbations to Granuloma Sterilization Predictions. Infection and Immunity, 2016, 84, 1650-1669.	1.0	48
21	CXCR7 Controls Competition for Recruitment of Î²-Arrestin 2 in Cells Expressing Both CXCR4 and CXCR7. PLoS ONE, 2014, 9, e98328.	1.1	45
22	Modeling of G-protein-coupled Receptor Signaling Pathways. Journal of Biological Chemistry, 2009, 284, 5427-5431.	1.6	44
23	Fluoroquinolone Efficacy against Tuberculosis Is Driven by Penetration into Lesions and Activity against Resident Bacterial Populations. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	42
24	In silico evaluation and exploration of antibiotic tuberculosis treatment regimens. BMC Systems Biology, 2015, 9, 79.	3.0	41
25	Harnessing the Heterogeneity of T Cell Differentiation Fate to Fine-Tune Generation of Effector and Memory T Cells. Frontiers in Immunology, 2014, 5, 57.	2.2	39
26	Deletion of TGF-Î²1 Increases Bacterial Clearance by Cytotoxic T Cells in a Tuberculosis Granuloma Model. Frontiers in Immunology, 2017, 8, 1843.	2.2	39
27	Computational and Empirical Studies Predict Mycobacterium tuberculosis-Specific T Cells as a Biomarker for Infection Outcome. PLoS Computational Biology, 2016, 12, e1004804.	1.5	38
28	Computational Modeling Predicts Simultaneous Targeting of Fibroblasts and Epithelial Cells Is Necessary for Treatment of Pulmonary Fibrosis. Frontiers in Pharmacology, 2016, 7, 183.	1.6	35
29	Global sensitivity analysis of biological multiscale models. Current Opinion in Biomedical Engineering, 2019, 11, 109-116.	1.8	35
30	A Comprehensive Analysis of CXCL12 Isoforms in Breast Cancer1,2. Translational Oncology, 2014, 7, 429-438.	1.7	33
31	Applying Optimization Algorithms to Tuberculosis Antibiotic Treatment Regimens. Cellular and Molecular Bioengineering, 2017, 10, 523-535.	1.0	26
32	Short-term cellular memory tunes the signaling responses of the chemokine receptor CXCR4. Science Signaling, 2019, 12, .	1.6	26
33	Both Pharmacokinetic Variability and Granuloma Heterogeneity Impact the Ability of the First-Line Antibiotics to Sterilize Tuberculosis Granulomas. Frontiers in Pharmacology, 2020, 11, 333.	1.6	26
34	Cell, Isoform, and Environment Factors Shape Gradients and Modulate Chemotaxis. PLoS ONE, 2015, 10, e0123450.	1.1	25
35	A multi-scale approach to designing therapeutics for tuberculosis. Integrative Biology (United) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.6	24
36	Validation of flow cytometric competitive binding protocols and characterization of fluorescently labeled ligands. Cytometry, 2001, 45, 102-114.	1.8	23

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37	Neutrophil Dynamics Affect Mycobacterium tuberculosis Granuloma Outcomes and Dissemination. Frontiers in Immunology, 2021, 12, 712457.	2.2	22
38	A computational model tracks whole-lung Mycobacterium tuberculosis infection and predicts factors that inhibit dissemination. PLoS Computational Biology, 2020, 16, e1007280.	1.5	21
39	Emergence and selection of isoniazid and rifampin resistance in tuberculosis granulomas. PLoS ONE, 2018, 13, e0196322.	1.1	20
40	An Agent-Based Systems Pharmacology Model of the Antibody-Drug Conjugate Kadcyla to Predict Efficacy of Different Dosing Regimens. AAPS Journal, 2020, 22, 29.	2.2	19
41	CaliPro: A Calibration Protocol That Utilizes Parameter Density Estimation to Explore Parameter Space and Calibrate Complex Biological Models. Cellular and Molecular Bioengineering, 2021, 14, 31-47.	1.0	19
42	Identifying Mechanisms of Homeostatic Signaling in Fibroblast Differentiation. Bulletin of Mathematical Biology, 2015, 77, 1556-1582.	0.9	18
43	A virtual host model of Mycobacterium tuberculosis infection identifies early immune events as predictive of infection outcomes. Journal of Theoretical Biology, 2022, 539, 111042.	0.8	17
44	Strategic Priming with Multiple Antigens can Yield Memory Cell Phenotypes Optimized for Infection with Mycobacterium tuberculosis: A Computational Study. Frontiers in Microbiology, 2016, 6, 1477.	1.5	16
45	Spatial Organization and Recruitment of Non-Specific T Cells May Limit T Cell-Macrophage Interactions Within Mycobacterium tuberculosis Granulomas. Frontiers in Immunology, 2020, 11, 613638.	2.2	16
46	A multi-scale pipeline linking drug transcriptomics with pharmacokinetics predicts in vivo interactions of tuberculosis drugs. Scientific Reports, 2021, 11, 5643.	1.6	15
47	In silico models of M. tuberculosis infection provide a route to new therapies. Drug Discovery Today: Disease Models, 2015, 15, 37-41.	1.2	12
48	Integrating Non-human Primate, Human, and Mathematical Studies to Determine the Influence of BCG Timing on H56 Vaccine Outcomes. Frontiers in Microbiology, 2018, 9, 1734.	1.5	12
49	The Role of Dimensionality in Understanding Granuloma Formation. Computation, 2018, 6, 58.	1.0	11
50	A Two-Pulse Cellular Stimulation Test Elucidates Variability and Mechanisms in Signaling Pathways. Biophysical Journal, 2019, 116, 962-973.	0.2	11
51	The CXCL12/CXCR7 signaling axis, isoforms, circadian rhythms, and tumor cellular composition dictate gradients in tissue. PLoS ONE, 2017, 12, e0187357.	1.1	10
52	Data-Driven Model Validation Across Dimensions. Bulletin of Mathematical Biology, 2019, 81, 1853-1866.	0.9	7
53	Simulating the Selection of Resistant Cells with Bystander Killing and Antibody Coadministration in Heterogeneous Human Epidermal Growth Factor Receptor 2â€"Positive Tumors. Drug Metabolism and Disposition, 2022, 50, 8-16.	1.7	7
54	Pre-existing Cell States Control Heterogeneity of Both EGFR and CXCR4 Signaling. Cellular and Molecular Bioengineering, 2021, 14, 49-64.	1.0	6

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55	Computational methods for characterizing and learning from heterogeneous cell signaling data. Current Opinion in Systems Biology, 2021, 26, 98-108.	1.3	6