

Markus W Covert

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

9,687
citations

101496

36
h-index

118793

62
g-index

67
all docs

67
docs citations

67
times ranked

10967
citing authors

#	ARTICLE	IF	CITATIONS
1	Building Structural Models of a Whole Mycoplasma Cell. <i>Journal of Molecular Biology</i> , 2022, 434, 167351.	2.0	40
2	Vivarium: an interface and engine for integrative multiscale modeling in computational biology. <i>Bioinformatics</i> , 2022, 38, 1972-1979.	1.8	12
3	A multiplexed epitope barcoding strategy that enables dynamic cellular phenotypic screens. <i>Cell Systems</i> , 2022, 13, 376-387.e8.	2.9	6
4	Microbial metabolites in the marine carbon cycle. <i>Nature Microbiology</i> , 2022, 7, 508-523.	5.9	71
5	The Enemy of My Enemy: New Insights Regarding Bacteriophage-Mammalian Cell Interactions. <i>Trends in Microbiology</i> , 2021, 29, 528-541.	3.5	32
6	BUILDING WHOLE-CELL COMPUTATIONAL MODELS TO PREDICT CELLULAR PHENOTYPES AND ACCELERATE DISCOVERY. , 2021, , .		0
7	A forecast for large-scale, predictive biology: Lessons from meteorology. <i>Cell Systems</i> , 2021, 12, 488-496.	2.9	5
8	The E. coli Whole-Cell Modeling Project. <i>EcoSal Plus</i> , 2021, 9, eESP00012020.	2.1	12
9	A Protocol to Engineer Bacteriophages for Live-Cell Imaging of Bacterial Prophage Induction Inside Mammalian Cells. <i>STAR Protocols</i> , 2020, 1, 100084.	0.5	2
10	Simultaneous cross-evaluation of heterogeneous <i>E. coli</i> datasets via mechanistic simulation. <i>Science</i> , 2020, 369, .	6.0	105
11	Engineered Fluorescent <i>E. coli</i> Lysogens Allow Live-Cell Imaging of Functional Prophage Induction Triggered inside Macrophages. <i>Cell Systems</i> , 2020, 10, 254-264.e9.	2.9	14
12	Stress-mediated exit to quiescence restricted by increasing persistence in CDK4/6 activation. <i>ELife</i> , 2020, 9, .	2.8	49
13	Multiscale models of infection. <i>Current Opinion in Biomedical Engineering</i> , 2019, 11, 102-108.	1.8	6
14	Deep learning for cellular image analysis. <i>Nature Methods</i> , 2019, 16, 1233-1246.	9.0	754
15	Techniques for Studying Decoding of Single Cell Dynamics. <i>Frontiers in Immunology</i> , 2019, 10, 755.	2.2	29
16	Simultaneous Cross-Evaluation of Heterogeneous <i>E. coli</i> Datasets via Mechanistic Simulation. <i>Biophysical Journal</i> , 2019, 116, 451a.	0.2	1
17	NF- κ B signaling dynamics is controlled by a dose-sensing autoregulatory loop. <i>Science Signaling</i> , 2019, 12, .	1.6	52
18	Escalating Threat Levels of Bacterial Infection Can Be Discriminated by Distinct MAPK and NF- κ B Signaling Dynamics in Single Host Cells. <i>Cell Systems</i> , 2019, 8, 183-196.e4.	2.9	23

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19	Combinatorial processing of bacterial and host-derived innate immune stimuli at the single-cell level. <i>Molecular Biology of the Cell</i> , 2019, 30, 282-292.	0.9	11
20	An energetic reformulation of kinetic rate laws enables scalable parameter estimation for biochemical networks. <i>Journal of Theoretical Biology</i> , 2019, 461, 145-156.	0.8	26
21	Live-cell measurements of kinase activity in single cells using translocation reporters. <i>Nature Protocols</i> , 2018, 13, 155-169.	5.5	90
22	Measuring Signaling and RNA-Seq in the Same Cell Links Gene Expression to Dynamic Patterns of NF- κ B Activation. <i>Cell Systems</i> , 2017, 4, 458-469.e5.	2.9	141
23	Combining Comprehensive Analysis of Off-Site Lambda Phage Integration with a CRISPR-Based Means of Characterizing Downstream Physiology. <i>MBio</i> , 2017, 8, .	1.8	3
24	Deep Learning Automates the Quantitative Analysis of Individual Cells in Live-Cell Imaging Experiments. <i>PLoS Computational Biology</i> , 2016, 12, e1005177.	1.5	429
25	High-resolution imaging and computational analysis of haematopoietic cell dynamics in vivo. <i>Nature Communications</i> , 2016, 7, 12169.	5.8	27
26	Single-cell variation leads to population invariance in NF- κ B signaling dynamics. <i>Molecular Biology of the Cell</i> , 2015, 26, 583-590.	0.9	44
27	Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models. <i>PLoS Computational Biology</i> , 2015, 11, e1004096.	1.5	35
28	Why Build Whole-Cell Models?. <i>Trends in Cell Biology</i> , 2015, 25, 719-722.	3.6	62
29	NetworkPainter: dynamic intracellular pathway animation in Cytobank. <i>BMC Bioinformatics</i> , 2015, 16, 172.	1.2	3
30	WholeCellSimDB: a hybrid relational/HDF database for whole-cell model predictions. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau095-bau095.	1.4	39
31	The future of whole-cell modeling. <i>Current Opinion in Biotechnology</i> , 2014, 28, 111-115.	3.3	73
32	Incorporation of flexible objectives and time-linked simulation with flux balance analysis. <i>Journal of Theoretical Biology</i> , 2014, 345, 12-21.	0.8	17
33	Nonlytic viral spread enhanced by autophagy components. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13081-13086.	3.3	204
34	High-Sensitivity Measurements of Multiple Kinase Activities in Live Single Cells. <i>Cell</i> , 2014, 157, 1724-1734.	13.5	483
35	Accelerated discovery via a whole-cell model. <i>Nature Methods</i> , 2013, 10, 1192-1195.	9.0	59
36	WholeCellViz: data visualization for whole-cell models. <i>BMC Bioinformatics</i> , 2013, 14, 253.	1.2	23

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37	Towards a whole-cell modeling approach for synthetic biology. <i>Chaos</i> , 2013, 23, 025112.	1.0	62
38	Single-Cell and Population NF- κ B Dynamic Responses Depend on Lipopolysaccharide Preparation. <i>PLoS ONE</i> , 2013, 8, e53222.	1.1	18
39	Determining Host Metabolic Limitations on Viral Replication via Integrated Modeling and Experimental Perturbation. <i>PLoS Computational Biology</i> , 2012, 8, e1002746.	1.5	51
40	WholeCellKB: model organism databases for comprehensive whole-cell models. <i>Nucleic Acids Research</i> , 2012, 41, D787-D792.	6.5	42
41	Neuron-to-neuron transmission of α -synuclein fibrils through axonal transport. <i>Annals of Neurology</i> , 2012, 72, 517-524.	2.8	305
42	Competing pathways control host resistance to virus via tRNA modification and programmed ribosomal frameshifting. <i>Molecular Systems Biology</i> , 2012, 8, 567.	3.2	42
43	A Whole-Cell Computational Model Predicts Phenotype from Genotype. <i>Cell</i> , 2012, 150, 389-401.	13.5	1,177
44	The virus as metabolic engineer. <i>Biotechnology Journal</i> , 2010, 5, 686-694.	1.8	63
45	Computational modeling of mammalian signaling networks. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 194-209.	6.6	61
46	Single-cell NF- κ B dynamics reveal digital activation and analogue information processing. <i>Nature</i> , 2010, 466, 267-271.	13.7	736
47	A Forward-Genetic Screen and Dynamic Analysis of Lambda Phage Host-Dependencies Reveals an Extensive Interaction Network and a New Anti-Viral Strategy. <i>PLoS Genetics</i> , 2010, 6, e1001017.	1.5	78
48	High-throughput, single-cell NF- κ B dynamics. <i>Current Opinion in Genetics and Development</i> , 2010, 20, 677-683.	1.5	27
49	A dynamic network of transcription in LPS-treated human subjects. <i>BMC Systems Biology</i> , 2009, 3, 78.	3.0	36
50	Genome-scale metabolic networks. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2009, 1, 285-297.	6.6	115
51	A Noisy Paracrine Signal Determines the Cellular NF- κ B Response to Lipopolysaccharide. <i>Science Signaling</i> , 2009, 2, ra65.	1.6	124
52	Integrating metabolic, transcriptional regulatory and signal transduction models in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2008, 24, 2044-2050.	1.8	285
53	Integrated Regulatory and Metabolic Models. , 2006, , 191-204.		0
54	Achieving Stability of Lipopolysaccharide-Induced NF- κ B Activation. <i>Science</i> , 2005, 309, 1854-1857.	6.0	557

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55	Integrating high-throughput and computational data elucidates bacterial networks. <i>Nature</i> , 2004, 429, 92-96.	13.7	796
56	Reconstruction of microbial transcriptional regulatory networks. <i>Current Opinion in Biotechnology</i> , 2004, 15, 70-77.	3.3	149
57	Constraints-based models: Regulation of Gene Expression Reduces the Steady-state Solution Space. <i>Journal of Theoretical Biology</i> , 2003, 221, 309-325.	0.8	157
58	Identifying constraints that govern cell behavior: a key to converting conceptual to computational models in biology?. <i>Biotechnology and Bioengineering</i> , 2003, 84, 763-772.	1.7	76
59	Reconciling Gene Expression Data With Known Genome-Scale Regulatory Network Structures. <i>Genome Research</i> , 2003, 13, 2423-2434.	2.4	96
60	Transcriptional Regulation in Constraints-based Metabolic Models of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 28058-28064.	1.6	301
61	Genome-Scale Metabolic Model of <i>Helicobacter pylori</i> 26695. <i>Journal of Bacteriology</i> , 2002, 184, 4582-4593.	1.0	317
62	Metabolic modelling of microbes: the flux-balance approach. <i>Environmental Microbiology</i> , 2002, 4, 133-140.	1.8	335
63	Regulation of Gene Expression in Flux Balance Models of Metabolism. <i>Journal of Theoretical Biology</i> , 2001, 213, 73-88.	0.8	399
64	Metabolic modeling of microbial strains in silico. <i>Trends in Biochemical Sciences</i> , 2001, 26, 179-186.	3.7	291