

# Carsten Marr

## List of Publications by Year in descending order

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Version: 2024-02-01

79  
papers

3,830  
citations

159585

30  
h-index

149698

56  
g-index

108  
all docs

108  
docs citations

108  
times ranked

6633  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>destiny</i> : diffusion maps for large-scale single-cell data in R. <i>Bioinformatics</i> , 2016, 32, 1241-1243.	4.1	518
2	A BaSiC tool for background and shading correction of optical microscopy images. <i>Nature Communications</i> , 2017, 8, 14836.	12.8	213
3	Early myeloid lineage choice is not initiated by random PU.1 to GATA1 protein ratios. <i>Nature</i> , 2016, 535, 299-302.	27.8	180
4	Software tools for single-cell tracking and quantification of cellular and molecular properties. <i>Nature Biotechnology</i> , 2016, 34, 703-706.	17.5	162
5	Prospective identification of hematopoietic lineage choice by deep learning. <i>Nature Methods</i> , 2017, 14, 403-406.	19.0	160
6	Social Transfer of Pathogenic Fungus Promotes Active Immunisation in Ant Colonies. <i>PLoS Biology</i> , 2012, 10, e1001300.	5.6	158
7	Hierarchical Differentiation of Myeloid Progenitors Is Encoded in the Transcription Factor Network. <i>PLoS ONE</i> , 2011, 6, e22649.	2.5	137
8	Network plasticity of pluripotency transcription factors in embryonic stem cells. <i>Nature Cell Biology</i> , 2015, 17, 1235-1246.	10.3	130
9	Intronic microRNAs support their host genes by mediating synergistic and antagonistic regulatory effects. <i>BMC Genomics</i> , 2010, 11, 224.	2.8	126
10	Human-level recognition of blast cells in acute myeloid leukaemia with convolutional neural networks. <i>Nature Machine Intelligence</i> , 2019, 1, 538-544.	16.0	122
11	An automatic method for robust and fast cell detection in bright field images from high-throughput microscopy. <i>BMC Bioinformatics</i> , 2013, 14, 297.	2.6	117
12	Entangled-state preparation via dissipation-assisted adiabatic passages. <i>Physical Review A</i> , 2003, 68, .	2.5	100
13	Dissecting the logical types of network control in gene expression profiles. <i>BMC Systems Biology</i> , 2008, 2, 18.	3.0	88
14	T cells armed with C-X-C chemokine receptor type 6 enhance adoptive cell therapy for pancreatic tumours. <i>Nature Biomedical Engineering</i> , 2021, 5, 1246-1260.	22.5	80
15	Metabolic regulation of pluripotency and germ cell fate through $\alpha$ -ketoglutarate. <i>EMBO Journal</i> , 2019, 38, .	7.8	77
16	Stability and Multiattractor Dynamics of a Toggle Switch Based on a Two-Stage Model of Stochastic Gene Expression. <i>Biophysical Journal</i> , 2012, 102, 19-29.	0.5	76
17	Zebrafish reward mutants reveal novel transcripts mediating the behavioral effects of amphetamine. <i>Genome Biology</i> , 2009, 10, R81.	9.6	71
18	Injury triggers fascia fibroblast collective cell migration to drive scar formation through N-cadherin. <i>Nature Communications</i> , 2020, 11, 5653.	12.8	66

#	ARTICLE	IF	CITATIONS
19	Highly accurate differentiation of bone marrow cell morphologies using deep neural networks on a large image data set. <i>Blood</i> , 2021, 138, 1917-1927.	1.4	62
20	fastER: a user-friendly tool for ultrafast and robust cell segmentation in large-scale microscopy. <i>Bioinformatics</i> , 2017, 33, 2020-2028.	4.1	58
21	CHIP and hips: clonal hematopoiesis is common in patients undergoing hip arthroplasty and is associated with autoimmune disease. <i>Blood</i> , 2021, 138, 1727-1732.	1.4	58
22	Combined tumor-directed recruitment and protection from immune suppression enable CAR T cell efficacy in solid tumors. <i>Science Advances</i> , 2021, 7, .	10.3	56
23	Gene Networks with Transcriptional Bursting Recapitulate Rare Transient Coordinated High Expression States in Cancer. <i>Cell Systems</i> , 2020, 10, 363-378.e12.	6.2	54
24	Domain Model Explains Propagation Dynamics and Stability of Histone H3K27 and H3K36 Methylation Landscapes. <i>Cell Reports</i> , 2020, 30, 1223-1234.e8.	6.4	54
25	miTALOS: Analyzing the tissue-specific regulation of signaling pathways by human and mouse microRNAs. <i>Rna</i> , 2011, 17, 809-819.	3.5	52
26	MitoSegNet: Easy-to-use Deep Learning Segmentation for Analyzing Mitochondrial Morphology. <i>IScience</i> , 2020, 23, 101601.	4.1	44
27	Opposing effects of allogrooming on disease transmission in ant societies. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140108.	4.0	43
28	Topology regulates pattern formation capacity of binary cellular automata on graphs. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2005, 354, 641-662.	2.6	42
29	Single-cell gene expression profiling and cell state dynamics: collecting data, correlating data points and connecting the dots. <i>Current Opinion in Biotechnology</i> , 2016, 39, 207-214.	6.6	36
30	Increasing Neural Stem Cell Division Asymmetry and Quiescence Are Predicted to Contribute to the Age-Related Decline in Neurogenesis. <i>Cell Reports</i> , 2018, 25, 3231-3240.e8.	6.4	35
31	Live cell-lineage tracing and machine learning reveal patterns of organ regeneration. <i>ELife</i> , 2018, 7, .	6.0	35
32	Similar impact of topological and dynamic noise on complex patterns. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2006, 349, 302-305.	2.1	30
33	Outer-totalistic cellular automata on graphs. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2009, 373, 546-549.	2.1	30
34	Analysis of Cell Lineage Trees by Exact Bayesian Inference Identifies Negative Autoregulation of Nanog in Mouse Embryonic Stem Cells. <i>Cell Systems</i> , 2016, 3, 480-490.e13.	6.2	30
35	Topology regulates the distribution pattern of excitations in excitable dynamics on graphs. <i>Physical Review E</i> , 2006, 74, 016112.	2.1	28
36	A sparse deep learning approach for automatic segmentation of human vasculature in multispectral optoacoustic tomography. <i>Photoacoustics</i> , 2020, 20, 100203.	7.8	26

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37	A geometric analysis of fast-slow models for stochastic gene expression. <i>Journal of Mathematical Biology</i> , 2016, 72, 87-122.	1.9	25
38	Lineage marker synchrony in hematopoietic genealogies refutes the PU.1/GATA1 toggle switch paradigm. <i>Nature Communications</i> , 2018, 9, 2697.	12.8	24
39	Multiclass Deep Active Learning for Detecting Red Blood Cell Subtypes in Brightfield Microscopy. <i>Lecture Notes in Computer Science</i> , 2019, , 685-693.	1.3	24
40	Time-dependent propagators for stochastic models of gene expression: an analytical method. <i>Journal of Mathematical Biology</i> , 2018, 77, 261-312.	1.9	23
41	NG2-Glia Transiently Overcome Their Homeostatic Network and Contribute to Wound Closure After Brain Injury. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 662056.	3.7	23
42	Multi-scale modeling of GMP differentiation based on single-cell genealogies. <i>FEBS Journal</i> , 2012, 279, 3488-3500.	4.7	19
43	Combinatorial Histone Acetylation Patterns Are Generated by Motif-Specific Reactions. <i>Cell Systems</i> , 2016, 2, 49-58.	6.2	19
44	Single-Cell Tracing Dissects Regulation of Maintenance and Inheritance of Transcriptional Reinduction Memory. <i>Molecular Cell</i> , 2020, 78, 915-925.e7.	9.7	18
45	N6-methyladenosine (m <sup>6</sup> A) depletion regulates pluripotency exit by activating signaling pathways in embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	18
46	Regularizing capacity of metabolic networks. <i>Physical Review E</i> , 2007, 75, 041917.	2.1	16
47	Tissue-Specific Target Analysis of Disease-Associated MicroRNAs in Human Signaling Pathways. <i>PLoS ONE</i> , 2010, 5, e11154.	2.5	16
48	Patterns of Subnet Usage Reveal Distinct Scales of Regulation in the Transcriptional Regulatory Network of <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2010, 6, e1000836.	3.2	15
49	An adaptive scheduling scheme for calculating Bayes factors with thermodynamic integration using Simpson's rule. <i>Statistics and Computing</i> , 2016, 26, 663-677.	1.5	15
50	cgCorrect: a method to correct for confounding cell-cell variation due to cell growth in single-cell transcriptomics. <i>Physical Biology</i> , 2017, 14, 036001.	1.8	15
51	Tens of images can suffice to train neural networks for malignant leukocyte detection. <i>Scientific Reports</i> , 2021, 11, 7995.	3.3	15
52	SimiRa: A tool to identify coregulation between microRNAs and RNA-binding proteins. <i>RNA Biology</i> , 2015, 12, 998-1009.	3.1	14
53	Attention Based Multiple Instance Learning for Classification of Blood Cell Disorders. <i>Lecture Notes in Computer Science</i> , 2020, , 246-256.	1.3	13
54	Twist1 induces distinct cell states depending on TGFBR1-activation. <i>Oncotarget</i> , 2016, 7, 30396-30407.	1.8	12

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55	A Topological Characterization of Medium-Dependent Essential Metabolic Reactions. <i>Metabolites</i> , 2012, 2, 632-647.	2.9	11
56	Cellular connectomes as arbiters of local circuit models in the cerebral cortex. <i>Nature Communications</i> , 2021, 12, 2785.	12.8	11
57	Cellular Automata on Graphs: Topological Properties of ER Graphs Evolved towards Low-Entropy Dynamics. <i>Entropy</i> , 2012, 14, 993-1010.	2.2	10
58	InstantDL: an easy-to-use deep learning pipeline for image segmentation and classification. <i>BMC Bioinformatics</i> , 2021, 22, 103.	2.6	10
59	MCA: Multiresolution Correlation Analysis, a graphical tool for subpopulation identification in single-cell gene expression data. <i>BMC Bioinformatics</i> , 2014, 15, 240.	2.6	9
60	Image analysis of neural stem cell division patterns in the zebrafish brain. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2018, 93, 314-322.	1.5	9
61	Biologically meaningful update rules increase the critical connectivity of generalized Kauffman networks. <i>Journal of Theoretical Biology</i> , 2010, 266, 436-448.	1.7	8
62	A case study on the use of scale separation-based analytical propagators for parameter inference in models of stochastic gene regulation. <i>Journal of Coupled Systems and Multiscale Dynamics</i> , 2015, 3, 164-173.	0.2	8
63	Automatic identification of relevant genes from low-dimensional embeddings of single-cell RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 4291-4295.	4.1	7
64	Computational modeling of stem and progenitor cell kinetics identifies plausible hematopoietic lineage hierarchies. <i>IScience</i> , 2021, 24, 102120.	4.1	7
65	H4K20 Methylation Is Differently Regulated by Dilution and Demethylation in Proliferating and Cell-Cycle-Arrested <i>Xenopus</i> Embryos. <i>Cell Systems</i> , 2020, 11, 653-662.e8.	6.2	6
66	A single-cell micro-trench platform for automatic monitoring of cell division and apoptosis after chemotherapeutic drug administration. <i>Scientific Reports</i> , 2018, 8, 18042.	3.3	5
67	The value of longitudinal clinical data and paired CT scans in predicting the deterioration of COVID-19 revealed by an artificial intelligence system. <i>IScience</i> , 2022, 25, 104227.	4.1	5
68	Parameter inference with analytical propagators for stochastic models of autoregulated gene expression. <i>International Journal of Nonlinear Sciences and Numerical Simulation</i> , 2022, 23, 565-577.	1.0	4
69	Inference of spatiotemporal effects on cellular state transitions from time-lapse microscopy. <i>BMC Systems Biology</i> , 2015, 9, 61.	3.0	3
70	Centroid Clustering of Cellular Lineage Trees. <i>Lecture Notes in Computer Science</i> , 2014, , 15-29.	1.3	3
71	Reoccurring neural stem cell divisions in the adult zebrafish telencephalon are sufficient for the emergence of aggregated spatiotemporal patterns. <i>PLoS Biology</i> , 2020, 18, e3000708.	5.6	3
72	Structure-based assessment of cancerous mitochondria using deep networks. , 2016, , .		2

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73	Mechanistic models of blood cell fate decisions in the era of single-cell data. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100355.	2.6	2
74	Reply to "Comment on "Regularizing capacity of metabolic networks". <i>Physical Review E</i> , 2008, 78, 1		1
75	Fourier Transform of Percoll Gradients Boosts CNN Classification of Hereditary Hemolytic Anemias. , 2021, , .		1
76	Evaluation of Domain Adaptation Approaches for Robust Classification of Heterogeneous Biological Data Sets. <i>Lecture Notes in Computer Science</i> , 2019, , 673-686.	1.3	1
77	In-Silico Staining from Bright-Field and Fluorescent Images Using Deep Learning. <i>Lecture Notes in Computer Science</i> , 2019, , 184-186.	1.3	1
78	Histopathology-Based Deep-Learning Predicts Atherosclerotic Lesions in Intravascular Imaging. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 779807.	2.4	1
79	MicroRNA as an Integral Part of Cell Communication: Regularized Target Prediction and Network Prediction. <i>Lecture Notes in Bioengineering</i> , 2018, , 85-100.	0.4	0