

Marc R Birtwistle

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

3,398
citations

257101

24
h-index

161609

54
g-index

74
all docs

74
docs citations

74
times ranked

6486
citing authors

#	ARTICLE	IF	CITATIONS
1	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , 2018, 6, 13-24.	2.9	327
2	Raf Family Kinases: Old Dogs Have Learned New Tricks. <i>Genes and Cancer</i> , 2011, 2, 232-260.	0.6	322
3	Cell fate decisions are specified by the dynamic ERK interactome. <i>Nature Cell Biology</i> , 2009, 11, 1458-1464.	4.6	264
4	Critical Role of Histone Turnover in Neuronal Transcription and Plasticity. <i>Neuron</i> , 2015, 87, 77-94.	3.8	257
5	Ligand-Specific c-Fos Expression Emerges from the Spatiotemporal Control of ErbB Network Dynamics. <i>Cell</i> , 2010, 141, 884-896.	13.5	217
6	The Mammalian MAPK/ERK Pathway Exhibits Properties of a Negative Feedback Amplifier. <i>Science Signaling</i> , 2010, 3, ra90.	1.6	216
7	Ligand-dependent responses of the ErbB signaling network: experimental and modeling analyses. <i>Molecular Systems Biology</i> , 2007, 3, 144.	3.2	203
8	Evaluating Strategies to Normalise Biological Replicates of Western Blot Data. <i>PLoS ONE</i> , 2014, 9, e87293.	1.1	174
9	Bistability in the Rac1, PAK, and RhoA Signaling Network Drives Actin Cytoskeleton Dynamics and Cell Motility Switches. <i>Cell Systems</i> , 2016, 2, 38-48.	2.9	159
10	A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. <i>Cell Systems</i> , 2019, 9, 35-48.e5.	2.9	95
11	Emergence of bimodal cell population responses from the interplay between analog single-cell signaling and protein expression noise. <i>BMC Systems Biology</i> , 2012, 6, 109.	3.0	89
12	Novel Somatic Mutations to PI3K Pathway Genes in Metastatic Melanoma. <i>PLoS ONE</i> , 2012, 7, e43369.	1.1	87
13	NF- κ B and HIF display synergistic behaviour during hypoxic inflammation. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 1319-1329.	2.4	72
14	Four-dimensional dynamics of MAPK information-processing systems. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2009, 1, 28-44.	6.6	67
15	Drug response consistency in CCLE and CGP. <i>Nature</i> , 2016, 540, E9-E10.	13.7	64
16	ERK2 drives tumour cell migration in 3D microenvironments by suppressing expression of Rab17 and Liprin- β 2. <i>Journal of Cell Science</i> , 2012, 125, 1465-77.	1.2	56
17	A Comparison of mRNA Sequencing with Random Primed and 3'-Directed Libraries. <i>Scientific Reports</i> , 2017, 7, 14626.	1.6	52
18	Cell size assays for mass cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2017, 91, 14-24.	1.1	48

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19	A mechanistic pan-cancer pathway model informed by multi-omics data interprets stochastic cell fate responses to drugs and mitogens. <i>PLoS Computational Biology</i> , 2018, 14, e1005985.	1.5	45
20	Endocytosis and signalling: A meeting with mathematics. <i>Molecular Oncology</i> , 2009, 3, 308-320.	2.1	30
21	Extracellular Signal-Regulated Kinase Regulates RhoA Activation and Tumor Cell Plasticity by Inhibiting Guanine Exchange Factor H1 Activity. <i>Molecular and Cellular Biology</i> , 2013, 33, 4526-4537.	1.1	30
22	Mitochondrial origins of fractional control in regulated cell death. <i>Nature Communications</i> , 2019, 10, 1313.	5.8	30
23	Anti-invasive efficacy and survival benefit of the YAP-TEAD inhibitor verteporfin in preclinical glioblastoma models. <i>Neuro-Oncology</i> , 2022, 24, 694-707.	0.6	29
24	Transcriptomic profiling of human cardiac cells predicts protein kinase inhibitor-associated cardiotoxicity. <i>Nature Communications</i> , 2020, 11, 4809.	5.8	28
25	Mechanistic Systems Modeling to Improve Understanding and Prediction of Cardiotoxicity Caused by Targeted Cancer Therapeutics. <i>Frontiers in Physiology</i> , 2017, 8, 651.	1.3	26
26	Nonlinear signalling networks and cell-to-cell variability transform external signals into broadly distributed or bimodal responses. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140383.	1.5	24
27	A Comparison of Methods for RNA-Seq Differential Expression Analysis and a New Empirical Bayes Approach. <i>Biosensors</i> , 2013, 3, 238-258.	2.3	22
28	Wilmâ€™s tumor 1 promotes memory flexibility. <i>Nature Communications</i> , 2019, 10, 3756.	5.8	20
29	Linear Approaches to Intramolecular Förster Resonance Energy Transfer Probe Measurements for Quantitative Modeling. <i>PLoS ONE</i> , 2011, 6, e27823.	1.1	18
30	Biology using engineering tools. <i>Cell Cycle</i> , 2011, 10, 2069-2076.	1.3	18
31	Integrating Transcriptomic Data with Mechanistic Systems Pharmacology Models for Virtual Drug Combination Trials. <i>ACS Chemical Neuroscience</i> , 2018, 9, 118-129.	1.7	17
32	Predicting <i>In Vivo</i> Efficacy from <i>In Vitro</i> Data: Quantitative Systems Pharmacology Modeling for an Epigenetic Modifier Drug in Cancer. <i>Clinical and Translational Science</i> , 2020, 13, 419-429.	1.5	16
33	Mammalian protein expression noise: scaling principles and the implications for knockdown experiments. <i>Molecular BioSystems</i> , 2012, 8, 3068.	2.9	15
34	Transcriptomes and shRNA Suppressors in a TP53 Allele-Specific Model of Early-Onset Colon Cancer in African Americans. <i>Molecular Cancer Research</i> , 2014, 12, 1029-1041.	1.5	15
35	Dimerization-based control of cooperativity. <i>Molecular BioSystems</i> , 2014, 10, 1824-1832.	2.9	15
36	Fluorescence Multiplexing with Spectral Imaging and Combinatorics. <i>ACS Combinatorial Science</i> , 2018, 20, 653-659.	3.8	15

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37	Silence on the relevant literature and errors in implementation. <i>Nature Biotechnology</i> , 2015, 33, 336-339.	9.4	14
38	Validating Antibodies for Quantitative Western Blot Measurements with Microwestern Array. <i>Scientific Reports</i> , 2018, 8, 11329.	1.6	14
39	A library of induced pluripotent stem cells from clinically well-characterized, diverse healthy human individuals. <i>Stem Cell Reports</i> , 2021, 16, 3036-3049.	2.3	14
40	A Temporal Logic Inference Approach for Model Discrimination. <i>IEEE Life Sciences Letters</i> , 2016, 2, 19-22.	1.2	13
41	A scalable, open-source implementation of a large-scale mechanistic model for single cell proliferation and death signaling. <i>Nature Communications</i> , 2022, 13, .	5.8	12
42	Network pharmacodynamic models for customized cancer therapy. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2015, 7, 243-251.	6.6	11
43	Analysis of copy number loss of the ErbB4 receptor tyrosine kinase in glioblastoma. <i>PLoS ONE</i> , 2018, 13, e0190664.	1.1	10
44	Analytical reduction of combinatorial complexity arising from multiple protein modification sites. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20141215.	1.5	9
45	Mitogen-Inducible Gene-6 Mediates Feedback Inhibition from Mutated BRAF towards the Epidermal Growth Factor Receptor and Thereby Limits Malignant Transformation. <i>PLoS ONE</i> , 2015, 10, e0129859.	1.1	8
46	A Mechanistic Beta-Binomial Probability Model for mRNA Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0157828.	1.1	8
47	Systems Pharmacology: An Overview. <i>AAPS Advances in the Pharmaceutical Sciences Series</i> , 2016, , 53-80.	0.2	7
48	Bayesian multivariate Poisson abundance models for T-cell receptor data. <i>Journal of Theoretical Biology</i> , 2013, 326, 1-10.	0.8	6
49	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. <i>Bioinformatics</i> , 2021, 37, 3702-3706.	1.8	6
50	In silico model-based inference: an emerging approach for inverse problems in engineering better medicines. <i>Current Opinion in Chemical Engineering</i> , 2015, 10, 14-24.	3.8	5
51	Protein structure-based gene expression signatures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	5
52	Leveraging modeling and simulation to optimize the therapeutic window for epigenetic modifier drugs. , 2022, 235, 108162.		5
53	Current Proteomic Methods to Investigate the Dynamics of Histone Turnover in the Central Nervous System. <i>Methods in Enzymology</i> , 2016, 574, 331-354.	0.4	4
54	Highly Multiplexed, Quantitative Tissue Imaging at Cellular Resolution. <i>Current Pathobiology Reports</i> , 2019, 7, 109-118.	1.6	2

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55	Protocol for Creating Antibodies with Complex Fluorescence Spectra. <i>Bioconjugate Chemistry</i> , 2021, 32, 1156-1166.	1.8	2
56	Proteomic cellular signatures of kinase inhibitor-induced cardiotoxicity. <i>Scientific Data</i> , 2022, 9, 18.	2.4	2
57	Kinetic Models of Biochemical Signaling Networks. <i>AAPS Advances in the Pharmaceutical Sciences Series</i> , 2016, , 105-135.	0.2	1
58	Creating Complex Fluorophore Spectra on Antibodies Through Combinatorial Labeling. <i>Translational Science</i> , 2016, 2, .	0.0	1