

# 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	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
2	Proteomic cellular signatures of kinase inhibitor-induced cardiotoxicity. <i>Scientific Data</i> , 2022, 9, 18.	2.4	2
3	Leveraging modeling and simulation to optimize the therapeutic window for epigenetic modifier drugs. , 2022, 235, 108162.		5
4	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
5	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
6	Protocol for Creating Antibodies with Complex Fluorescence Spectra. <i>Bioconjugate Chemistry</i> , 2021, 32, 1156-1166.	1.8	2
7	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
8	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
9	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
10	Transcriptomic profiling of human cardiac cells predicts protein kinase inhibitor-associated cardiotoxicity. <i>Nature Communications</i> , 2020, 11, 4809.	5.8	28
11	Wilm's tumor 1 promotes memory flexibility. <i>Nature Communications</i> , 2019, 10, 3756.	5.8	20
12	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
13	Highly Multiplexed, Quantitative Tissue Imaging at Cellular Resolution. <i>Current Pathobiology Reports</i> , 2019, 7, 109-118.	1.6	2
14	Mitochondrial origins of fractional control in regulated cell death. <i>Nature Communications</i> , 2019, 10, 1313.	5.8	30
15	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
16	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
17	Fluorescence Multiplexing with Spectral Imaging and Combinatorics. <i>ACS Combinatorial Science</i> , 2018, 20, 653-659.	3.8	15
18	Validating Antibodies for Quantitative Western Blot Measurements with Microwestern Array. <i>Scientific Reports</i> , 2018, 8, 11329.	1.6	14

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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. PLoS Computational Biology, 2018, 14, e1005985.	1.5	45
20	Analysis of copy number loss of the ErbB4 receptor tyrosine kinase in glioblastoma. PLoS ONE, 2018, 13, e0190664.	1.1	10
21	A Comparison of mRNA Sequencing with Random Primed and 3'-Directed Libraries. Scientific Reports, 2017, 7, 14626.	1.6	52
22	Cell size assays for mass cytometry. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2017, 91, 14-24.	1.1	48
23	Mechanistic Systems Modeling to Improve Understanding and Prediction of Cardiotoxicity Caused by Targeted Cancer Therapeutics. Frontiers in Physiology, 2017, 8, 651.	1.3	26
24	A Mechanistic Beta-Binomial Probability Model for mRNA Sequencing Data. PLoS ONE, 2016, 11, e0157828.	1.1	8
25	Drug response consistency in CCLE and CGP. Nature, 2016, 540, E9-E10.	13.7	64
26	A Temporal Logic Inference Approach for Model Discrimination. IEEE Life Sciences Letters, 2016, 2, 19-22.	1.2	13
27	Systems Pharmacology: An Overview. AAPS Advances in the Pharmaceutical Sciences Series, 2016, , 53-80.	0.2	7
28	Kinetic Models of Biochemical Signaling Networks. AAPS Advances in the Pharmaceutical Sciences Series, 2016, , 105-135.	0.2	1
29	Current Proteomic Methods to Investigate the Dynamics of Histone Turnover in the Central Nervous System. Methods in Enzymology, 2016, 574, 331-354.	0.4	4
30	Bistability in the Rac1, PAK, and RhoA Signaling Network Drives Actin Cytoskeleton Dynamics and Cell Motility Switches. Cell Systems, 2016, 2, 38-48.	2.9	159
31	Creating Complex Fluorophore Spectra on Antibodies Through Combinatorial Labeling. Translational Science, 2016, 2, .	0.0	1
32	Network pharmacodynamic models for customized cancer therapy. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2015, 7, 243-251.	6.6	11
33	Mitogen-Inducible Gene-6 Mediates Feedback Inhibition from Mutated BRAF towards the Epidermal Growth Factor Receptor and Thereby Limits Malignant Transformation. PLoS ONE, 2015, 10, e0129859.	1.1	8
34	Critical Role of Histone Turnover in Neuronal Transcription and Plasticity. Neuron, 2015, 87, 77-94.	3.8	257
35	Analytical reduction of combinatorial complexity arising from multiple protein modification sites. Journal of the Royal Society Interface, 2015, 12, 20141215.	1.5	9
36	Silence on the relevant literature and errors in implementation. Nature Biotechnology, 2015, 33, 336-339.	9.4	14

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37	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
38	Evaluating Strategies to Normalise Biological Replicates of Western Blot Data. <i>PLoS ONE</i> , 2014, 9, e87293.	1.1	174
39	Transcriptomes and shRNA Suppressors in a <i>TP53</i> Allele-Specific Model of Early-Onset Colon Cancer in African Americans. <i>Molecular Cancer Research</i> , 2014, 12, 1029-1041.	1.5	15
40	Dimerization-based control of cooperativity. <i>Molecular BioSystems</i> , 2014, 10, 1824-1832.	2.9	15
41	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
42	Bayesian multivariate Poisson abundance models for T-cell receptor data. <i>Journal of Theoretical Biology</i> , 2013, 326, 1-10.	0.8	6
43	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
44	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
45	ERK2 drives tumour cell migration in 3D microenvironments by suppressing expression of Rab17 and Liprin- $\beta$ 2. <i>Journal of Cell Science</i> , 2012, 125, 1465-77.	1.2	56
46	Mammalian protein expression noise: scaling principles and the implications for knockdown experiments. <i>Molecular BioSystems</i> , 2012, 8, 3068.	2.9	15
47	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
48	Novel Somatic Mutations to PI3K Pathway Genes in Metastatic Melanoma. <i>PLoS ONE</i> , 2012, 7, e43369.	1.1	87
49	NF $\kappa$ B and HIF display synergistic behaviour during hypoxic inflammation. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 1319-1329.	2.4	72
50	Linear Approaches to Intramolecular Förster Resonance Energy Transfer Probe Measurements for Quantitative Modeling. <i>PLoS ONE</i> , 2011, 6, e27823.	1.1	18
51	Biology using engineering tools. <i>Cell Cycle</i> , 2011, 10, 2069-2076.	1.3	18
52	Raf Family Kinases: Old Dogs Have Learned New Tricks. <i>Genes and Cancer</i> , 2011, 2, 232-260.	0.6	322
53	The Mammalian MAPK/ERK Pathway Exhibits Properties of a Negative Feedback Amplifier. <i>Science Signaling</i> , 2010, 3, ra90.	1.6	216
54	Ligand-Specific c-Fos Expression Emerges from the Spatiotemporal Control of ErbB Network Dynamics. <i>Cell</i> , 2010, 141, 884-896.	13.5	217

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55	Four-dimensional dynamics of MAPK information-processing systems. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2009, 1, 28-44.	6.6	67
56	Cell fate decisions are specified by the dynamic ERK interactome. <i>Nature Cell Biology</i> , 2009, 11, 1458-1464.	4.6	264
57	Endocytosis and signalling: A meeting with mathematics. <i>Molecular Oncology</i> , 2009, 3, 308-320.	2.1	30
58	Ligand-dependent responses of the ErbB signaling network: experimental and modeling analyses. <i>Molecular Systems Biology</i> , 2007, 3, 144.	3.2	203