Maria Rodriguez Martinez

List of Publications by Year
in descending order

49 papers	**2,484** citations	331259 **21** h-index	264894 **42** g-index
52 all docs	**52** docs citations	**52** times ranked	**4488** citing authors

#	Article	IF	Citations
1	A Single-Cell Atlas of the Tumor and Immune Ecosystem of Human Breast Cancer. Cell, 2019, 177, 1330-1345.e18.	13.5	547
2	Elucidating Compound Mechanism of Action by Network Perturbation Analysis. Cell, 2015, 162, 441-451.	13.5	278
3	Observational consequences of a landscape. Journal of High Energy Physics, 2006, 2006, 039-039.	1.6	206
4	Input–output robustness in simple bacterial signaling systems. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19931-19935.	3.3	170
5	Transient transcriptional responses to stress are generated by opposing effects of mRNA production and degradation. Molecular Systems Biology, 2008, 4, 223.	3.2	169
6	Development of input connections in neural cultures. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13758-13763.	3.3	163
7	Toward Explainable Anticancer Compound Sensitivity Prediction via Multimodal Attention-Based Convolutional Encoders. Molecular Pharmaceutics, 2019, 16, 4797-4806.	2.3	86
8	Cosmology of a Brane Radiating Gravitons into the Extra Dimension. Physical Review Letters, 2002, 89, 171301.	2.9	82
9	TITAN: T-cell receptor specificity prediction with bimodal attention networks. Bioinformatics, 2021, 37, i237-i244.	1.8	73
10	Diagnostics and correction of batch effects in large‐scale proteomic studies: a tutorial. Molecular Systems Biology, 2021, 17, e10240.	3.2	57
11	Brane cosmology with a bulk scalar field. Physical Review D, 2001, 64, .	1.6	56
12	High-throughput validation of ceRNA regulatory networks. BMC Genomics, 2017, 18, 418.	1.2	46
13	PaccMannRL: De novo generation of hit-like anticancer molecules from transcriptomic data via reinforcement learning. IScience, 2021, 24, 102269.	1.9	42
14	PaccMann: a web service for interpretable anticancer compound sensitivity prediction. Nucleic Acids Research, 2020, 48, W502-W508.	6.5	38
15	Quorum percolation in living neural networks. Europhysics Letters, 2010, 89, 18008.	0.7	37
16	Quantitative modeling of the terminal differentiation of B cells and mechanisms of lymphomagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2672-2677.	3.3	37
17	Constraining Lorentz violations with gamma ray bursts. Journal of Cosmology and Astroparticle Physics, 2006, 2006, 006-006.	1.9	36
18	CellCycleTRACER accounts for cell cycle and volume in mass cytometry data. Nature Communications, 2018, 9, 632.	5.8	36

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19	The number of titrated microRNA species dictates ceRNA regulation. Nucleic Acids Research, 2018, 46, 4354-4369.	6.5	32
20	GRB 051221A and tests of Lorentz symmetry. Journal of Cosmology and Astroparticle Physics, 2006, 2006, 017-017.	1.9	27
21	Depletion of FOXM1 via MET Targeting Underlies Establishment of a DNA Damageâ€"Induced Senescence Program in Gastric Cancer. Clinical Cancer Research, 2016, 22, 5322-5336.	3.2	27
22	A Probabilistic Model of the Germinal Center Reaction. Frontiers in Immunology, 2019, 10, 689.	2.2	23
23	PIMKL: Pathway-Induced Multiple Kernel Learning. Npj Systems Biology and Applications, 2019, 5, 8.	1.4	21
24	Network-based Biased Tree Ensembles (NetBiTE) for Drug Sensitivity Prediction and Drug Sensitivity Biomarker Identification in Cancer. Scientific Reports, 2019, 9, 15918.	1.6	20
25	DeStress: Deep Learning for Unsupervised Identification of Mental Stress in Firefighters from Heart-Rate Variability (HRV) Data. Studies in Computational Intelligence, 2021, , 93-105.	0.7	18
26	Convergent network effects along the axis of gene expression during prostate cancer progression. Genome Biology, 2020, 21, 302.	3.8	17
27	Computational Model Reveals a Stochastic Mechanism behind Germinal Center Clonal Bursts. Cells, 2020, 9, 1448.	1.8	16
28	Multiscale Modeling of Germinal Center Recapitulates the Temporal Transition From Memory B Cells to Plasma Cells Differentiation as Regulated by Antigen Affinity-Based Tfh Cell Help. Frontiers in Immunology, 2020, 11, 620716.	2.2	16
29	Data-driven molecular design for discovery and synthesis of novel ligands: a case study on SARS-CoV-2. Machine Learning: Science and Technology, 2021, 2, 025024.	2.4	16
30	PaccMannRL: Designing Anticancer Drugs From Transcriptomic Data via Reinforcement Learning. Lecture Notes in Computer Science, 2020, , 231-233.	1.0	16
31	On the feasibility of deep learning applications using raw mass spectrometry data. Bioinformatics, 2021, 37, i245-i253.	1.8	10
32	Fluctuating brane in a dilatonic bulk. Physical Review D, 2003, 67, .	1.6	9
33	Messenger RNA fluctuations and regulatory RNAs shape the dynamics of a negative feedback loop. Physical Review E, 2010, 81, 031924.	0.8	9
34	Context-specific interaction networks from vector representation of words. Nature Machine Intelligence, 2019, 1, 181-190.	8.3	9
35	Pan-cancer analysis of somatic mutations and epigenetic alterations in insulated neighbourhood boundaries. PLoS ONE, 2020, 15, e0227180.	1.1	8
36	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. Bioinformatics, 2021, 37, 3702-3706.	1.8	6

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37	Inferring clonal composition from multiple tumor biopsies. Npj Systems Biology and Applications, 2020, 6, 27.	1.4	5
38	COSIFER: a Python package for the consensus inference of molecular interaction networks. Bioinformatics, 2021, 37, 2070-2072.	1.8	4
39	The Multiple Dimensions of Networks in Cancer: A Perspective. Symmetry, 2021, 13, 1559.	1.1	4
40	DECODE: a computational pipeline to discover T cell receptor binding rules. Bioinformatics, 2022, 38, i246-i254.	1.8	4
41	Defining perturbations on submanifolds. Physical Review D, 2003, 68, .	1.6	3
42	FPGA Accelerated Analysis of Boolean Gene Regulatory Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 2141-2147.	1.9	1
43	Stabilized Reconstruction of Signaling Networks from Single-Cell Cue-Response Data. Scientific Reports, 2020, 10, 1233.	1.6	1
44	Multi-Scale Modeling Recapitulates the Effect of Genetic Alterations Associated With Diffuse Large B-Cell Lymphoma in the Germinal Center Dynamics. Frontiers in Systems Biology, 2022, 2, .	0.5	1
45	PCfun: a hybrid computational framework for systematic characterization of protein complex function. Briefings in Bioinformatics, 0, , .	3.2	1
46	General relativistic interaction of massless fields in cylindrical waves. Physical Review D, 2003, 68, .	1.6	0
47	Gamma-Ray Bursts and New Physics. Progress of Theoretical Physics Supplement, 2006, 163, 23-37.	0.2	0
48	Identifying the Potential Mechanism of Action of SNPs Associated With Breast Cancer Susceptibility With GVITamIN. Frontiers in Bioengineering and Biotechnology, 2020, 8, 798.	2.0	0
49	Abstract 5231: Highly conserved ceRNA regulatory interactions cooperate with genomic variability to modulate drivers of tumorigenesis.. , 2013, , .		0