

# Julio Saez-Rodriguez

## List of Publications by Year in descending order

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247  
papers

26,447  
citations

13099

68  
h-index

9103

144  
g-index

339  
all docs

339  
docs citations

339  
times ranked

34219  
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic identification of genomic markers of drug sensitivity in cancer cells. Nature, 2012, 483, 570-575.	27.8	2,173
2	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	28.9	1,710
3	A Landscape of Pharmacogenomic Interactions in Cancer. Cell, 2016, 166, 740-754.	28.9	1,518
4	Prioritization of cancer therapeutic targets using CRISPR-Cas9 screens. Nature, 2019, 568, 511-516.	27.8	886
5	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. Cell, 2020, 182, 685-712.e19.	28.9	825
6	A community effort to assess and improve drug sensitivity prediction algorithms. Nature Biotechnology, 2014, 32, 1202-1212.	17.5	653
7	A CRISPR Dropout Screen Identifies Genetic Vulnerabilities and Therapeutic Targets in Acute Myeloid Leukemia. Cell Reports, 2016, 17, 1193-1205.	6.4	556
8	Benchmark and integration of resources for the estimation of human transcription factor activities. Genome Research, 2019, 29, 1363-1375.	5.5	552
9	Critical assessment of automated flow cytometry data analysis techniques. Nature Methods, 2013, 10, 228-238.	19.0	509
10	OmniPath: guidelines and gateway for literature-curated signaling pathway resources. Nature Methods, 2016, 13, 966-967.	19.0	469
11	Structural and functional analysis of cellular networks with CellNetAnalyzer. BMC Systems Biology, 2007, 1, 2.	3.0	454
12	Fumarate is an epigenetic modifier that elicits epithelial-to-mesenchymal transition. Nature, 2016, 537, 544-547.	27.8	443
13	Perturbation-response genes reveal signaling footprints in cancer gene expression. Nature Communications, 2018, 9, 20.	12.8	436
14	Machine Learning Prediction of Cancer Cell Sensitivity to Drugs Based on Genomic and Chemical Properties. PLoS ONE, 2013, 8, e61318.	2.5	406
15	Decoding myofibroblast origins in human kidney fibrosis. Nature, 2021, 589, 281-286.	27.8	380
16	Pharmacogenomic agreement between two cancer cell line data sets. Nature, 2015, 528, 84-87.	27.8	358
17	Evaluation of methods for modeling transcription factor sequence specificity. Nature Biotechnology, 2013, 31, 126-134.	17.5	341
18	Towards a Rigorous Assessment of Systems Biology Models: The DREAM3 Challenges. PLoS ONE, 2010, 5, e9202.	2.5	337

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19	A methodology for the structural and functional analysis of signaling and regulatory networks. BMC Bioinformatics, 2006, 7, 56.	2.6	330
20	A Logical Model Provides Insights into T Cell Receptor Signaling. PLoS Computational Biology, 2007, 3, e163.	3.2	311
21	Discrete logic modelling as a means to link protein signalling networks with functional analysis of mammalian signal transduction. Molecular Systems Biology, 2009, 5, 331.	7.2	308
22	Logic-Based Models for the Analysis of Cell Signaling Networks. Biochemistry, 2010, 49, 3216-3224.	2.5	306
23	A community computational challenge to predict the activity of pairs of compounds. Nature Biotechnology, 2014, 32, 1213-1222.	17.5	264
24	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. Nature Biotechnology, 2019, 37, 314-322.	17.5	254
25	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
26	Logical Modeling and Dynamical Analysis of Cellular Networks. Frontiers in Genetics, 2016, 7, 94.	2.3	216
27	Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data. Genome Biology, 2020, 21, 36.	8.8	216
28	Assessment of network module identification across complex diseases. Nature Methods, 2019, 16, 843-852.	19.0	213
29	Transforming Boolean models to continuous models: methodology and application to T-cell receptor signaling. BMC Systems Biology, 2009, 3, 98.	3.0	212
30	Deep spatial profiling of human COVID-19 brains reveals neuroinflammation with distinct microanatomical microglia-T-cell interactions. Immunity, 2021, 54, 1594-1610.e11.	14.3	210
31	Transcriptional data: a new gateway to drug repositioning?. Drug Discovery Today, 2013, 18, 350-357.	6.4	209
32	Inferring causal molecular networks: empirical assessment through a community-based effort. Nature Methods, 2016, 13, 310-318.	19.0	209
33	CellNOptR: a flexible toolkit to train protein signaling networks to data using multiple logic formalisms. BMC Systems Biology, 2012, 6, 133.	3.0	198
34	Gli1 + Mesenchymal Stromal Cells Are a Key Driver of Bone Marrow Fibrosis and an Important Cellular Therapeutic Target. Cell Stem Cell, 2017, 20, 785-800.e8.	11.1	195
35	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
36	A microfluidics platform for combinatorial drug screening on cancer biopsies. Nature Communications, 2018, 9, 2434.	12.8	177

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37	NADH Shuttling Couples Cytosolic Reductive Carboxylation of Glutamine with Glycolysis in Cells with Mitochondrial Dysfunction. <i>Molecular Cell</i> , 2018, 69, 581-593.e7.	9.7	171
38	The Logic of EGFR/ErbB Signaling: Theoretical Properties and Analysis of High-Throughput Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000438.	3.2	164
39	Transcription Factor Activities Enhance Markers of Drug Sensitivity in Cancer. <i>Cancer Research</i> , 2018, 78, 769-780.	0.9	161
40	Integrated intra- and intercellular signaling knowledge for multicellular omics analysis. <i>Molecular Systems Biology</i> , 2021, 17, e9923.	7.2	152
41	Fuzzy Logic Analysis of Kinase Pathway Crosstalk in TNF/EGF/Insulin-Induced Signaling. <i>PLoS Computational Biology</i> , 2009, 5, e1000340.	3.2	145
42	SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. <i>BMC Systems Biology</i> , 2013, 7, 135.	3.0	145
43	Path2Models: large-scale generation of computational models from biochemical pathway maps. <i>BMC Systems Biology</i> , 2013, 7, 116.	3.0	145
44	Comparison of methods and resources for cell-cell communication inference from single-cell RNA-Seq data. <i>Nature Communications</i> , 2022, 13, .	12.8	143
45	Crowdsourcing biomedical research: leveraging communities as innovation engines. <i>Nature Reviews Genetics</i> , 2016, 17, 470-486.	16.3	137
46	Modeling Cell-Cell Interactions from Spatial Molecular Data with Spatial Variance Component Analysis. <i>Cell Reports</i> , 2019, 29, 202-211.e6.	6.4	133
47	Comparing Signaling Networks between Normal and Transformed Hepatocytes Using Discrete Logical Models. <i>Cancer Research</i> , 2011, 71, 5400-5411.	0.9	132
48	MEIGO: an open-source software suite based on metaheuristics for global optimization in systems biology and bioinformatics. <i>BMC Bioinformatics</i> , 2014, 15, 136.	2.6	131
49	decoupleR: ensemble of computational methods to infer biological activities from omics data. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	127
50	Training Signaling Pathway Maps to Biochemical Data with Constrained Fuzzy Logic: Quantitative Analysis of Liver Cell Responses to Inflammatory Stimuli. <i>PLoS Computational Biology</i> , 2011, 7, e1001099.	3.2	113
51	Identifying Drug Effects via Pathway Alterations using an Integer Linear Programming Optimization Formulation on Phosphoproteomic Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000591.	3.2	112
52	BioServices: a common Python package to access biological Web Services programmatically. <i>Bioinformatics</i> , 2013, 29, 3241-3242.	4.1	109
53	Medial Arterial Calcification. <i>Journal of the American College of Cardiology</i> , 2021, 78, 1145-1165.	2.8	106
54	Adipocyte-secreted BMP8b mediates adrenergic-induced remodeling of the neuro-vascular network in adipose tissue. <i>Nature Communications</i> , 2018, 9, 4974.	12.8	104

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55	Crowdsourcing Network Inference: The DREAM Predictive Signaling Network Challenge <b>Meeting Information:</b> The DREAM4 Predictive Signaling Network Challenge took place in the summer of 2009. Results were presented at the DREAM4 conference, December 2009, The Broad Institute of MIT and Harvard, Cambridge, Massachusetts.. Science Signaling, 2011, 4, mr7.	3.6	102
56	Widespread Post-transcriptional Attenuation of Genomic Copy-Number Variation in Cancer. Cell Systems, 2017, 5, 386-398.e4.	6.2	102
57	Drug Resistance Mechanisms in Colorectal Cancer Dissected with Cell Typeâ€“Specific Dynamic Logic Models. Cancer Research, 2017, 77, 3364-3375.	0.9	101
58	Cooperative development of logical modelling standards and tools with CoLoMoTo. Bioinformatics, 2015, 31, 1154-1159.	4.1	98
59	Transfer of regulatory knowledge from human to mouse for functional genomics analysis. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194431.	1.9	98
60	Molecular consequences of SARS-CoV-2 liver tropism. Nature Metabolism, 2022, 4, 310-319.	11.9	98
61	From expression footprints to causal pathways: contextualizing large signaling networks with CARNIVAL. Npj Systems Biology and Applications, 2019, 5, 40.	3.0	96
62	Networks Inferred from Biochemical Data Reveal Profound Differences in Toll-like Receptor and Inflammatory Signaling between Normal and Transformed Hepatocytes. Molecular and Cellular Proteomics, 2010, 9, 1849-1865.	3.8	95
63	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. Cell Reports, 2017, 20, 2201-2214.	6.4	95
64	Functional linkage of gene fusions to cancer cell fitness assessed by pharmacological and CRISPR-Cas9 screening. Nature Communications, 2019, 10, 2198.	12.8	92
65	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	17.5	88
66	Toward Explainable Anticancer Compound Sensitivity Prediction via Multimodal Attention-Based Convolutional Encoders. Molecular Pharmaceutics, 2019, 16, 4797-4806.	4.6	86
67	The orchestra of lipid-transfer proteins at the crossroads between metabolism and signaling. Progress in Lipid Research, 2016, 61, 30-39.	11.6	85
68	Hepatocyte-specific NRF2 activation controls fibrogenesis and carcinogenesis in steatohepatitis. Journal of Hepatology, 2021, 74, 638-648.	3.7	84
69	Bridging the layers: towards integration of signal transduction, regulation and metabolism into mathematical models. Molecular BioSystems, 2013, 9, 1576.	2.9	83
70	Dynamic 3D proteomes reveal protein functional alterations at high resolution in situ. Cell, 2021, 184, 545-559.e22.	28.9	82
71	Large-scale models of signal propagation in human cells derived from discovery phosphoproteomic data. Nature Communications, 2015, 6, 8033.	12.8	79
72	Dissecting the puzzle of life: modularization of signal transduction networks. Computers and Chemical Engineering, 2005, 29, 619-629.	3.8	78

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73	A domain-oriented approach to the reduction of combinatorial complexity in signal transduction networks. BMC Bioinformatics, 2006, 7, 34.	2.6	78
74	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. Molecular Systems Biology, 2021, 17, e9730.	7.2	78
75	Unsupervised correction of gene-independent cell responses to CRISPR-Cas9 targeting. BMC Genomics, 2018, 19, 604.	2.8	75
76	Creating and analyzing pathway and protein interaction compendia for modelling signal transduction networks. BMC Systems Biology, 2012, 6, 29.	3.0	71
77	A Rapidly Reversible Chemical Dimerizer System to Study Lipid Signaling in Living Cells. Angewandte Chemie - International Edition, 2014, 53, 6720-6723.	13.8	70
78	Empirical inference of circuitry and plasticity in a kinase signaling network. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7719-7724.	7.1	69
79	Imbalanced gut microbiota fuels hepatocellular carcinoma development by shaping the hepatic inflammatory microenvironment. Nature Communications, 2022, 13, .	12.8	68
80	Only Hyperuricemia with Crystalluria, but not Asymptomatic Hyperuricemia, Drives Progression of Chronic Kidney Disease. Journal of the American Society of Nephrology: JASN, 2020, 31, 2773-2792.	6.1	66
81	Flexible informatics for linking experimental data to mathematical models via <i>DataRail</i>. Bioinformatics, 2008, 24, 840-847.	4.1	64
82	DvD: An R/Cytoscape pipeline for drug repurposing using public repositories of gene expression data. Bioinformatics, 2013, 29, 132-134.	4.1	64
83	Benchmarking substrate-based kinase activity inference using phosphoproteomic data. Bioinformatics, 2017, 33, 1845-1851.	4.1	64
84	Exhaustively characterizing feasible logic models of a signaling network using Answer Set Programming. Bioinformatics, 2013, 29, 2320-2326.	4.1	62
85	Network topology and parameter estimation: from experimental design methods to gene regulatory network kinetics using a community based approach. BMC Systems Biology, 2014, 8, 13.	3.0	62
86	Systems biology—An engineering perspective. Journal of Biotechnology, 2007, 129, 329-351.	3.8	61
87	BioPreDyn-bench: a suite of benchmark problems for dynamic modelling in systems biology. BMC Systems Biology, 2015, 9, 8.	3.0	61
88	Modular analysis of signal transduction networks. IEEE Control Systems, 2004, 24, 35-52.	0.8	60
89	Phosphoproteomics data classify hematological cancer cell lines according to tumor type and sensitivity to kinase inhibitors. Genome Biology, 2013, 14, R37.	9.6	60
90	Patient-specific logic models of signaling pathways from screenings on cancer biopsies to prioritize personalized combination therapies. Molecular Systems Biology, 2020, 16, e8664.	7.2	60

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91	Reduction of mathematical models of signal transduction networks: simulation-based approach applied to EGF receptor signalling. IET Systems Biology, 2004, 1, 159-169.	2.0	59
92	BIAS: Transparent reporting of biomedical image analysis challenges. Medical Image Analysis, 2020, 66, 101796.	11.6	59
93	Phosphoproteomic analyses reveal novel cross-modulation mechanisms between two signaling pathways in yeast. Molecular Systems Biology, 2014, 10, 767.	7.2	58
94	Alternative models for sharing confidential biomedical data. Nature Biotechnology, 2018, 36, 391-392.	17.5	56
95	Big science and big data in nephrology. Kidney International, 2019, 95, 1326-1337.	5.2	56
96	Elastin imaging enables noninvasive staging and treatment monitoring of kidney fibrosis. Science Translational Medicine, 2019, 11, .	12.4	56
97	Increased CXCL4 expression in hematopoietic cells links inflammation and progression of bone marrow fibrosis in MPN. Blood, 2020, 136, 2051-2064.	1.4	56
98	The proteome microenvironment determines the protective effect of preconditioning in cisplatin-induced acute kidney injury. Kidney International, 2019, 95, 333-349.	5.2	55
99	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
100	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680.	4.1	52
101	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. PLoS Computational Biology, 2017, 13, e1005297.	3.2	51
102	Influence of Liver Fibrosis on Lobular Zonation. Cells, 2019, 8, 1556.	4.1	51
103	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. Frontiers in Microbiology, 2021, 12, 635781.	3.5	51
104	Signatures of cell death and proliferation in perturbation transcriptomics data from confounding factor to effective prediction. Nucleic Acids Research, 2019, 47, 10010-10026.	14.5	50
105	Whither systems medicine?. Experimental and Molecular Medicine, 2018, 50, e453-e453.	7.7	49
106	Cancer-associated fibroblasts require proline synthesis by PYCR1 for the deposition of pro-tumorigenic extracellular matrix. Nature Metabolism, 2022, 4, 693-710.	11.9	49
107	Using chemical reaction network theory to discard a kinetic mechanism hypothesis. IET Systems Biology, 2005, 152, 243.	2.0	47
108	State-time spectrum of signal transduction logic models. Physical Biology, 2012, 9, 045003.	1.8	47

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109	Network based elucidation of drug response: from modulators to targets. BMC Systems Biology, 2013, 7, 139.	3.0	47
110	A systematic atlas of chaperome deregulation topologies across the human cancer landscape. PLoS Computational Biology, 2018, 14, e1005890.	3.2	46
111	GDSCTools for mining pharmacogenomic interactions in cancer. Bioinformatics, 2018, 34, 1226-1228.	4.1	45
112	Explainable multiview framework for dissecting spatial relationships from highly multiplexed data. Genome Biology, 2022, 23, 97.	8.8	45
113	Identification of drug-specific pathways based on gene expression data: application to drug induced lung injury. Integrative Biology (United Kingdom), 2015, 7, 904-920.	1.3	43
114	The spatial transcriptomic landscape of the healing mouse intestine following damage. Nature Communications, 2022, 13, 828.	12.8	43
115	MAPK pathway and B cells overactivation in multiple sclerosis revealed by phosphoproteomics and genomic analysis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9671-9676.	7.1	42
116	Data-driven reverse engineering of signaling pathways using ensembles of dynamic models. PLoS Computational Biology, 2017, 13, e1005379.	3.2	41
117	Dysregulated mesenchymal PDGFR $\alpha$ drives kidney fibrosis. EMBO Molecular Medicine, 2020, 12, e11021.	6.9	41
118	Metabolic rewiring of the hypertensive kidney. Science Signaling, 2019, 12, .	3.6	40
119	PIP <sub>3</sub> Induces the Recycling of Receptor Tyrosine Kinases. Science Signaling, 2014, 7, ra5.	3.6	39
120	A Semi-Supervised Approach for Refining Transcriptional Signatures of Drug Response and Repositioning Predictions. PLoS ONE, 2015, 10, e0139446.	2.5	39
121	Footprint-based functional analysis of multiomic data. Current Opinion in Systems Biology, 2019, 15, 82-90.	2.6	39
122	MEK1/2 inhibitor withdrawal reverses acquired resistance driven by BRAFV600E amplification whereas KRASG13D amplification promotes EMT-chemoresistance. Nature Communications, 2019, 10, 2030.	12.8	39
123	Efficient randomization of biological networks while preserving functional characterization of individual nodes. BMC Bioinformatics, 2016, 17, 542.	2.6	38
124	The germline genetic component of drug sensitivity in cancer cell lines. Nature Communications, 2018, 9, 3385.	12.8	38
125	Patient-specific Boolean models of signalling networks guide personalised treatments. ELife, 2022, 11, .	6.0	38
126	Stratification and prediction of drug synergy based on target functional similarity. Npj Systems Biology and Applications, 2020, 6, 16.	3.0	37



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127	Fast randomization of large genomic datasets while preserving alteration counts. <i>Bioinformatics</i> , 2014, 30, i617-i623.	4.1	36
128	Consensus Transcriptional Landscape of Human End-stage Heart Failure. <i>Journal of the American Heart Association</i> , 2021, 10, e019667.	3.7	36
129	Personalized signaling models for personalized treatments. <i>Molecular Systems Biology</i> , 2020, 16, e9042.	7.2	36
130	CySBGN: A Cytoscape plug-in to integrate SBGN maps. <i>BMC Bioinformatics</i> , 2013, 14, 17.	2.6	35
131	CELLector: Genomics-Guided Selection of Cancer In-Vitro Models. <i>Cell Systems</i> , 2020, 10, 424-432.e6.	6.2	35
132	Differential expression of microRNA miR-150-5p in IgA nephropathy as a potential mediator and marker of disease progression. <i>Kidney International</i> , 2021, 99, 1127-1139.	5.2	35
133	Modeling Signaling Networks Using High-throughput Phospho-proteomics. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 19-57.	1.6	35
134	Automatic decomposition of kinetic models of signaling networks minimizing the retroactivity among modules. <i>Bioinformatics</i> , 2008, 24, i213-i219.	4.1	34
135	Integrating literature-constrained and data-driven inference of signalling networks. <i>Bioinformatics</i> , 2012, 28, 2311-2317.	4.1	34
136	Modeling Signaling Networks to Advance New Cancer Therapies. <i>Annual Review of Biomedical Engineering</i> , 2015, 17, 143-163.	12.3	34
137	Stem cell-like transcriptional reprogramming mediates metastatic resistance to mTOR inhibition. <i>Oncogene</i> , 2017, 36, 2737-2749.	5.9	34
138	Linking drug target and pathway activation for effective therapy using multi-task learning. <i>Scientific Reports</i> , 2018, 8, 8322.	3.3	34
139	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. <i>Cell Reports Medicine</i> , 2022, 3, 100492.	6.5	33
140	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. <i>Npj Systems Biology and Applications</i> , 2019, 5, 20.	3.0	32
141	Analysis of the Human Kinome and Phosphatome by Mass Cytometry Reveals Overexpression-Induced Effects on Cancer-Related Signaling. <i>Molecular Cell</i> , 2019, 74, 1086-1102.e5.	9.7	32
142	Looking beyond the cancer cell for effective drug combinations. <i>Genome Medicine</i> , 2016, 8, 125.	8.2	31
143	The tissue proteome in the multi-omic landscape of kidney disease. <i>Nature Reviews Nephrology</i> , 2021, 17, 205-219.	9.6	31
144	Bringing data from curated pathway resources to Cytoscape with OmniPath. <i>Bioinformatics</i> , 2020, 36, 2632-2633.	4.1	30

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145	SREBP1-induced fatty acid synthesis depletes macrophages antioxidant defences to promote their alternative activation. <i>Nature Metabolism</i> , 2021, 3, 1150-1162.	11.9	29
146	Transcriptional response networks for elucidating mechanisms of action of multitargeted agents. <i>Drug Discovery Today</i> , 2016, 21, 1063-1075.	6.4	28
147	Post-translational regulation of metabolism in fumarate hydratase deficient cancer cells. <i>Metabolic Engineering</i> , 2018, 45, 149-157.	7.0	27
148	Dynamics of Proximal Signaling Events after TCR/CD8-Mediated Induction of Proliferation or Apoptosis in Mature CD8+ T Cells. <i>Journal of Immunology</i> , 2008, 180, 6703-6712.	0.8	26
149	Two heads are better than one: current landscape of integrating QSP and machine learning. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2022, 49, 5-18.	1.8	26
150	Logic Modeling in Quantitative Systems Pharmacology. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2017, 6, 499-511.	2.5	25
151	Computational discovery of dynamic cell line specific Boolean networks from multiplex time-course data. <i>PLoS Computational Biology</i> , 2018, 14, e1006538.	3.2	25
152	Setting the basis of best practices and standards for curation and annotation of logical models in biology—highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. <i>Briefings in Bioinformatics</i> , 2021, 22, 1848-1859.	6.5	25
153	Mapping the human phosphatome on growth pathways. <i>Molecular Systems Biology</i> , 2012, 8, 603.	7.2	24
154	Signaling networks in MS: A systems-based approach to developing new pharmacological therapies. <i>Multiple Sclerosis Journal</i> , 2015, 21, 138-146.	3.0	24
155	Phosphoproteomics-Based Profiling of Kinase Activities in Cancer Cells. <i>Methods in Molecular Biology</i> , 2018, 1711, 103-132.	0.9	24
156	Pathway-based dissection of the genomic heterogeneity of cancer hallmarks—acquisition with SLAPenrich. <i>Scientific Reports</i> , 2018, 8, 6713.	3.3	24
157	Transcriptomic Cross-Species Analysis of Chronic Liver Disease Reveals Consistent Regulation Between Humans and Mice. <i>Hepatology Communications</i> , 2022, 6, 161-177.	4.3	24
158	In silico Prioritization of Transporter-Drug Relationships From Drug Sensitivity Screens. <i>Frontiers in Pharmacology</i> , 2018, 9, 1011.	3.5	23
159	Mechanism-based biomarker discovery. <i>Drug Discovery Today</i> , 2017, 22, 1209-1215.	6.4	22
160	Deciphering the signaling network of breast cancer improves drug sensitivity prediction. <i>Cell Systems</i> , 2021, 12, 401-418.e12.	6.2	22
161	Reverse engineering of logic-based differential equation models using a mixed-integer dynamic optimization approach. <i>Bioinformatics</i> , 2015, 31, 2999-3007.	4.1	21
162	Advances in systems biology modeling: 10 years of crowdsourcing DREAM challenges. <i>Cell Systems</i> , 2021, 12, 636-653.	6.2	21

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163	Learning Boolean logic models of signaling networks with ASP. Theoretical Computer Science, 2015, 599, 79-101.	0.9	20
164	Genome-wide chemical mutagenesis screens allow unbiased saturation of the cancer genome and identification of drug resistance mutations. Genome Research, 2017, 27, 613-625.	5.5	20
165	New insights into the mechanisms underlying 5-fluorouracil-induced intestinal toxicity based on transcriptomic and metabolomic responses in human intestinal organoids. Archives of Toxicology, 2021, 95, 2691-2718.	4.2	20
166	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. Life Science Alliance, 2020, 3, e202000867.	2.8	20
167	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. Cell Systems, 2017, 5, 485-497.e3.	6.2	19
168	How to find the right drug for each patient? Advances and challenges in pharmacogenomics. Current Opinion in Systems Biology, 2018, 10, 53-62.	2.6	19
169	Reproducible biomedical benchmarking in the cloud: lessons from crowd-sourced data challenges. Genome Biology, 2019, 20, 195.	8.8	19
170	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. Cell Systems, 2020, 11, 186-195.e9.	6.2	19
171	Why do pathway methods work better than they should?. FEBS Letters, 2020, 594, 4189-4200.	2.8	19
172	A model integration approach linking signalling and gene-regulatory logic with kinetic metabolic models. BioSystems, 2014, 124, 26-38.	2.0	18
173	Reducing lipid bilayer stress by monounsaturated fatty acids protects renal proximal tubules in diabetes. ELife, 2022, 11, .	6.0	18
174	Systems Pharmacology Dissection of Cholesterol Regulation Reveals Determinants of Large Pharmacodynamic Variability between Cell Lines. Cell Systems, 2017, 5, 604-619.e7.	6.2	17
175	Converting networks to predictive logic models from perturbation signalling data with CellNOpt. Bioinformatics, 2020, 36, 4523-4524.	4.1	17
176	How will artificial intelligence and bioinformatics change our understanding of IgA Nephropathy in the next decade?. Seminars in Immunopathology, 2021, 43, 739-752.	6.1	17
177	Visual setup of logical models of signaling and regulatory networks with ProMoT. BMC Bioinformatics, 2006, 7, 506.	2.6	16
178	caspo: a toolbox for automated reasoning on the response of logical signaling networks families. Bioinformatics, 2017, 33, 947-950.	4.1	16
179	Kinetic modelling of quantitative proteome data predicts metabolic reprogramming of liver cancer. British Journal of Cancer, 2020, 122, 233-244.	6.4	16
180	DREAMTools: a Python package for scoring collaborative challenges. F1000Research, 2015, 4, 1030.	1.6	16

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181	A statistical framework for assessing pharmacological responses and biomarkers using uncertainty estimates. <i>ELife</i> , 2020, 9, .	6.0	16
182	The human hepatocyte TXG-MAPr: gene co-expression network modules to support mechanism-based risk assessment. <i>Archives of Toxicology</i> , 2021, 95, 3745-3775.	4.2	16
183	Construction of large signaling pathways using an adaptive perturbation approach with phosphoproteomic data. <i>Molecular BioSystems</i> , 2012, 8, 1571.	2.9	15
184	PHONEMeS: Efficient Modeling of Signaling Networks Derived from Large-Scale Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2021, 20, 2138-2144.	3.7	15
185	Non Linear Programming (NLP) Formulation for Quantitative Modeling of Protein Signal Transduction Pathways. <i>PLoS ONE</i> , 2012, 7, e50085.	2.5	14
186	DREAMTools: a Python package for scoring collaborative challenges. <i>F1000Research</i> , 2015, 4, 1030.	1.6	14
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