

# 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	Experimental and computational technologies to dissect the kidney at the single-cell level. Nephrology Dialysis Transplantation, 2022, 37, 628-637.	0.7	6
2	Deficiency of myeloid PHD proteins aggravates atherogenesis via macrophage apoptosis and paracrine fibrotic signalling. Cardiovascular Research, 2022, 118, 1232-1246.	3.8	12
3	Transcriptomic Cross-Species Analysis of Chronic Liver Disease Reveals Consistent Regulation Between Humans and Mice. Hepatology Communications, 2022, 6, 161-177.	4.3	24
4	MAGED2 controls vasopressin-induced aquaporin-2 expression in collecting duct cells. Journal of Proteomics, 2022, 252, 104424.	2.4	1
5	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. Cell Reports Medicine, 2022, 3, 100492.	6.5	33
6	FUNKI: interactive functional footprint-based analysis of omics data. Bioinformatics, 2022, 38, 2075-2076.	4.1	4
7	Stabilization but No Functional Influence of HIF-1 $\alpha$ Expression in the Intestinal Epithelium during Salmonella Typhimurium Infection. Infection and Immunity, 2022, 90, iai0022221.	2.2	7
8	Two heads are better than one: current landscape of integrating QSP and machine learning. Journal of Pharmacokinetics and Pharmacodynamics, 2022, 49, 5-18.	1.8	26
9	The spatial transcriptomic landscape of the healing mouse intestine following damage. Nature Communications, 2022, 13, 828.	12.8	43
10	decoupleR: ensemble of computational methods to infer biological activities from omics data. Bioinformatics Advances, 2022, 2, .	2.4	127
11	Patient-specific Boolean models of signalling networks guide personalised treatments. ELife, 2022, 11, .	6.0	38
12	Molecular consequences of SARS-CoV-2 liver tropism. Nature Metabolism, 2022, 4, 310-319.	11.9	98
13	Computational drug repurposing against SARS-CoV-2 reveals plasma membrane cholesterol depletion as key factor of antiviral drug activity. PLoS Computational Biology, 2022, 18, e1010021.	3.2	8
14	Explainable multiview framework for dissecting spatial relationships from highly multiplexed data. Genome Biology, 2022, 23, 97.	8.8	45
15	Mapping the epithelial-immune cell interactome upon infection in the gut and the upper airways. Npj Systems Biology and Applications, 2022, 8, 15.	3.0	3
16	Reducing lipid bilayer stress by monounsaturated fatty acids protects renal proximal tubules in diabetes. ELife, 2022, 11, .	6.0	18
17	Comparison of methods and resources for cell-cell communication inference from single-cell RNA-Seq data. Nature Communications, 2022, 13, .	12.8	143
18	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

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19	Imbalanced gut microbiota fuels hepatocellular carcinoma development by shaping the hepatic inflammatory microenvironment. <i>Nature Communications</i> , 2022, 13, .	12.8	68
20	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
21	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). <i>Bioinformatics</i> , 2021, 36, 5712-5718.	4.1	14
22	The tissue proteome in the multi-omic landscape of kidney disease. <i>Nature Reviews Nephrology</i> , 2021, 17, 205-219.	9.6	31
23	Dynamic 3D proteomes reveal protein functional alterations at high resolution in situ. <i>Cell</i> , 2021, 184, 545-559.e22.	28.9	82
24	Hepatocyte-specific NRF2 activation controls fibrogenesis and carcinogenesis in steatohepatitis. <i>Journal of Hepatology</i> , 2021, 74, 638-648.	3.7	84
25	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <i>Frontiers in Microbiology</i> , 2021, 12, 635781.	3.5	51
26	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
27	Integrated intra- and intercellular signaling knowledge for multicellular omics analysis. <i>Molecular Systems Biology</i> , 2021, 17, e9923.	7.2	152
28	Consensus Transcriptional Landscape of Human End-Stage Heart Failure. <i>Journal of the American Heart Association</i> , 2021, 10, e019667.	3.7	36
29	Transcription Factor Activity Inference in Systemic Lupus Erythematosus. <i>Life</i> , 2021, 11, 299.	2.4	5
30	How will artificial intelligence and bioinformatics change our understanding of IgA Nephropathy in the next decade?. <i>Seminars in Immunopathology</i> , 2021, 43, 739-752.	6.1	17
31	Reusability and composability in process description maps: RAS→RAF→MEK→ERK signalling. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	3
32	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
33	Deciphering the signaling network of breast cancer improves drug sensitivity prediction. <i>Cell Systems</i> , 2021, 12, 401-418.e12.	6.2	22
34	A comprehensive database for integrated analysis of omics data in autoimmune diseases. <i>BMC Bioinformatics</i> , 2021, 22, 343.	2.6	12
35	Advances in systems biology modeling: 10 years of crowdsourcing DREAM challenges. <i>Cell Systems</i> , 2021, 12, 636-653.	6.2	21
36	Macrophage beta2-adrenergic receptor is dispensable for the adipose tissue inflammation and function. <i>Molecular Metabolism</i> , 2021, 48, 101220.	6.5	11

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37	SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. <i>Bioinformatics</i> , 2021, 37, 3702-3706.	4.1	6
38	New insights into the mechanisms underlying 5-fluorouracil-induced intestinal toxicity based on transcriptomic and metabolomic responses in human intestinal organoids. <i>Archives of Toxicology</i> , 2021, 95, 2691-2718.	4.2	20
39	Deep spatial profiling of human COVID-19 brains reveals neuroinflammation with distinct microanatomical microglia-T-cell interactions. <i>Immunity</i> , 2021, 54, 1594-1610.e11.	14.3	210
40	Prediction of combination therapies based on topological modeling of the immune signaling network in multiple sclerosis. <i>Genome Medicine</i> , 2021, 13, 117.	8.2	10
41	Integration of temporal single cell cellular stress response activity with logic-ODE modeling reveals activation of ATF4-CHOP axis as a critical predictor of drug-induced liver injury. <i>Biochemical Pharmacology</i> , 2021, 190, 114591.	4.4	14
42	Partial Inhibition of the 6-Phosphofructo-2-Kinase/Fructose-2,6-Bisphosphatase-3 (PFKFB3) Enzyme in Myeloid Cells Does Not Affect Atherosclerosis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 695684.	3.7	4
43	Medial Arterial Calcification. <i>Journal of the American College of Cardiology</i> , 2021, 78, 1145-1165.	2.8	106
44	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
45	Contextualization of causal regulatory networks from toxicogenomics data applied to drug-induced liver injury. <i>Toxicology Letters</i> , 2021, 350, 40-51.	0.8	0
46	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021, 17, e9730.	7.2	78
47	Norepinephrine promotes triglyceride storage in macrophages via beta $\alpha$ -adrenergic receptor activation. <i>FASEB Journal</i> , 2021, 35, e21266.	0.5	11
48	Decoding myofibroblast origins in human kidney fibrosis. <i>Nature</i> , 2021, 589, 281-286.	27.8	380
49	Systems approach reveals distinct and shared signaling networks of the four PGE <sub>2</sub> receptors in T cells. <i>Science Signaling</i> , 2021, 14, eabc8579.	3.6	5
50	Cell-to-cell and type-to-type heterogeneity of signaling networks: insights from the crowd. <i>Molecular Systems Biology</i> , 2021, 17, e10402.	7.2	9
51	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
52	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
53	Transfer of regulatory knowledge from human to mouse for functional genomics analysis. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194431.	1.9	98
54	Quantitative Systems Toxicology Modeling To Address Key Safety Questions in Drug Development: A Focus of the TransQST Consortium. <i>Chemical Research in Toxicology</i> , 2020, 33, 7-9.	3.3	14

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55	Bringing data from curated pathway resources to Cytoscape with OmniPath. <i>Bioinformatics</i> , 2020, 36, 2632-2633.	4.1	30
56	A Functional Landscape of CKD Entities From Public Transcriptomic Data. <i>Kidney International Reports</i> , 2020, 5, 211-224.	0.8	14
57	Kinetic modelling of quantitative proteome data predicts metabolic reprogramming of liver cancer. <i>British Journal of Cancer</i> , 2020, 122, 233-244.	6.4	16
58	BIAS: Transparent reporting of biomedical image analysis challenges. <i>Medical Image Analysis</i> , 2020, 66, 101796.	11.6	59
59	CELLector: Genomics-Guided Selection of Cancer In Vitro Models. <i>Cell Systems</i> , 2020, 10, 424-432.e6.	6.2	35
60	Converting networks to predictive logic models from perturbation signalling data with CellNOpt. <i>Bioinformatics</i> , 2020, 36, 4523-4524.	4.1	17
61	Increased CXCL4 expression in hematopoietic cells links inflammation and progression of bone marrow fibrosis in MPN. <i>Blood</i> , 2020, 136, 2051-2064.	1.4	56
62	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. <i>Cell Systems</i> , 2020, 11, 186-195.e9.	6.2	19
63	Big Data Approaches in Heart Failure Research. <i>Current Heart Failure Reports</i> , 2020, 17, 213-224.	3.3	13
64	Inferring clonal composition from multiple tumor biopsies. <i>Npj Systems Biology and Applications</i> , 2020, 6, 27.	3.0	5
65	Only Hyperuricemia with Crystalluria, but not Asymptomatic Hyperuricemia, Drives Progression of Chronic Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 2773-2792.	6.1	66
66	Why do pathway methods work better than they should?. <i>FEBS Letters</i> , 2020, 594, 4189-4200.	2.8	19
67	Stratification and prediction of drug synergy based on target functional similarity. <i>Npj Systems Biology and Applications</i> , 2020, 6, 16.	3.0	37
68	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. <i>Cell</i> , 2020, 182, 685-712.e19.	28.9	825
69	Patient-specific logic models of signaling pathways from screenings on cancer biopsies to prioritize personalized combination therapies. <i>Molecular Systems Biology</i> , 2020, 16, e8664.	7.2	60
70	Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data. <i>Genome Biology</i> , 2020, 21, 36.	8.8	216
71	Dysregulated mesenchymal PDGFR $\beta$ drives kidney fibrosis. <i>EMBO Molecular Medicine</i> , 2020, 12, e11021.	6.9	41
72	Personalized signaling models for personalized treatments. <i>Molecular Systems Biology</i> , 2020, 16, e9042.	7.2	36

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73	<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
74	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. Life Science Alliance, 2020, 3, e202000867.	2.8	20
75	A statistical framework for assessing pharmacological responses and biomarkers using uncertainty estimates. ELife, 2020, 9, .	6.0	16
76	Novel plasma peptide markers involved in the pathology of CKD identified using mass spectrometric approach. Journal of Molecular Medicine, 2019, 97, 1451-1463.	3.9	10
77	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. Npj Systems Biology and Applications, 2019, 5, 20.	3.0	32
78	Benchmark and integration of resources for the estimation of human transcription factor activities. Genome Research, 2019, 29, 1363-1375.	5.5	552
79	Toward Explainable Anticancer Compound Sensitivity Prediction via Multimodal Attention-Based Convolutional Encoders. Molecular Pharmaceutics, 2019, 16, 4797-4806.	4.6	86
80	From expression footprints to causal pathways: contextualizing large signaling networks with CARNIVAL. Npj Systems Biology and Applications, 2019, 5, 40.	3.0	96
81	THU-471-Establishment of a short-termed orthotopic transplantation model in C57/B6 mice that recapitulates characteristic features of human intrahepatic cholangiocarcinoma. Journal of Hepatology, 2019, 70, e367-e368.	3.7	0
82	Assessment of network module identification across complex diseases. Nature Methods, 2019, 16, 843-852.	19.0	213
83	Reproducible biomedical benchmarking in the cloud: lessons from crowd-sourced data challenges. Genome Biology, 2019, 20, 195.	8.8	19
84	Modeling Cell-Cell Interactions from Spatial Molecular Data with Spatial Variance Component Analysis. Cell Reports, 2019, 29, 202-211.e6.	6.4	133
85	Signatures of cell death and proliferation in perturbation transcriptomics dataâ€”from confounding factor to effective prediction. Nucleic Acids Research, 2019, 47, 10010-10026.	14.5	50
86	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
87	Analysis of the Human Kinome and Phosphatome by Mass Cytometry Reveals Overexpression-Induced Effects on Cancer-Related Signaling. Molecular Cell, 2019, 74, 1086-1102.e5.	9.7	32
88	Hybrid parallel multimethod hyperheuristic for mixed-integer dynamic optimization problems in computational systems biology. Journal of Supercomputing, 2019, 75, 3471-3498.	3.6	3
89	Functional linkage of gene fusions to cancer cell fitness assessed by pharmacological and CRISPR-Cas9 screening. Nature Communications, 2019, 10, 2198.	12.8	92
90	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

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91	Footprint-based functional analysis of multiomic data. Current Opinion in Systems Biology, 2019, 15, 82-90.	2.6	39
92	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
93	Big science and big data in nephrology. Kidney International, 2019, 95, 1326-1337.	5.2	56
94	Prioritization of cancer therapeutic targets using CRISPR-Cas9 screens. Nature, 2019, 568, 511-516.	27.8	886
95	Elastin imaging enables noninvasive staging and treatment monitoring of kidney fibrosis. Science Translational Medicine, 2019, 11, .	12.4	56
96	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. Nature Biotechnology, 2019, 37, 314-322.	17.5	254
97	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680.	4.1	52
98	Literature and data-driven based inference of signalling interactions using time-course data. IFAC-PapersOnLine, 2019, 52, 52-57.	0.9	2
99	The authors reply. Kidney International, 2019, 96, 1422-1423.	5.2	0
100	Influence of Liver Fibrosis on Lobular Zonation. Cells, 2019, 8, 1556.	4.1	51
101	Metabolic rewiring of the hypertensive kidney. Science Signaling, 2019, 12, .	3.6	40
102	Elucidating essential kinases of endothelin signalling by logic modelling of phosphoproteomics data. Molecular Systems Biology, 2019, 15, e8828.	7.2	11
103	The proteome microenvironment determines the protective effect of preconditioning in cisplatin-induced acute kidney injury. Kidney International, 2019, 95, 333-349.	5.2	55
104	Prostaglandin E 2 signaling networks in T cells revealed through a systems approach. FASEB Journal, 2019, 33, lb258.	0.5	0
105	Whither systems medicine?. Experimental and Molecular Medicine, 2018, 50, e453-e453.	7.7	49
106	NADH Shuttling Couples Cytosolic Reductive Carboxylation of Glutamine with Glycolysis in Cells with Mitochondrial Dysfunction. Molecular Cell, 2018, 69, 581-593.e7.	9.7	171
107	Phosphoproteomics-Based Profiling of Kinase Activities in Cancer Cells. Methods in Molecular Biology, 2018, 1711, 103-132.	0.9	24
108	GDSCTools for mining pharmacogenomic interactions in cancer. Bioinformatics, 2018, 34, 1226-1228.	4.1	45

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109	Perturbation-response genes reveal signaling footprints in cancer gene expression. <i>Nature Communications</i> , 2018, 9, 20.	12.8	436
110	Post-translational regulation of metabolism in fumarate hydratase deficient cancer cells. <i>Metabolic Engineering</i> , 2018, 45, 149-157.	7.0	27
111	Transcription Factor Activities Enhance Markers of Drug Sensitivity in Cancer. <i>Cancer Research</i> , 2018, 78, 769-780.	0.9	161
112	Embracing the Dark Side: Computational Approaches to Unveil the Functionality of Genes Lacking Biological Annotation in Drug-Induced Liver Injury. <i>Frontiers in Genetics</i> , 2018, 9, 527.	2.3	0
113	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
114	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
115	In silico Prioritization of Transporter-Drug Relationships From Drug Sensitivity Screens. <i>Frontiers in Pharmacology</i> , 2018, 9, 1011.	3.5	23
116	Linking drug target and pathway activation for effective therapy using multi-task learning. <i>Scientific Reports</i> , 2018, 8, 8322.	3.3	34
117	A microfluidics platform for combinatorial drug screening on cancer biopsies. <i>Nature Communications</i> , 2018, 9, 2434.	12.8	177
118	How to find the right drug for each patient? Advances and challenges in pharmacogenomics. <i>Current Opinion in Systems Biology</i> , 2018, 10, 53-62.	2.6	19
119	Alternative models for sharing confidential biomedical data. <i>Nature Biotechnology</i> , 2018, 36, 391-392.	17.5	56
120	Pathway-based dissection of the genomic heterogeneity of cancer hallmarks' acquisition with SLAPenrich. <i>Scientific Reports</i> , 2018, 8, 6713.	3.3	24
121	The germline genetic component of drug sensitivity in cancer cell lines. <i>Nature Communications</i> , 2018, 9, 3385.	12.8	38
122	Unsupervised correction of gene-independent cell responses to CRISPR-Cas9 targeting. <i>BMC Genomics</i> , 2018, 19, 604.	2.8	75
123	A systematic atlas of chaperome deregulation topologies across the human cancer landscape. <i>PLoS Computational Biology</i> , 2018, 14, e1005890.	3.2	46
124	Abstract 3886: A large cancer pharmacogenomics combination screen powering crowd-sourced advancement of computational drug synergy predictions. , 2018, , .		0
125	caspo: a toolbox for automated reasoning on the response of logical signaling networks families. <i>Bioinformatics</i> , 2017, 33, 947-950.	4.1	16
126	Genome-wide chemical mutagenesis screens allow unbiased saturation of the cancer genome and identification of drug resistance mutations. <i>Genome Research</i> , 2017, 27, 613-625.	5.5	20



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127	Gli1 + Mesenchymal Stromal Cells Are a Key Driver of Bone Marrow Fibrosis and an Important Cellular Therapeutic Target. <i>Cell Stem Cell</i> , 2017, 20, 785-800.e8.	11.1	195
128	Mechanism-based biomarker discovery. <i>Drug Discovery Today</i> , 2017, 22, 1209-1215.	6.4	22
129	Drug Resistance Mechanisms in Colorectal Cancer Dissected with Cell Type-Specific Dynamic Logic Models. <i>Cancer Research</i> , 2017, 77, 3364-3375.	0.9	101
130	Stem cell-like transcriptional reprogramming mediates metastatic resistance to mTOR inhibition. <i>Oncogene</i> , 2017, 36, 2737-2749.	5.9	34
131	System-Wide Quantitative Proteomics of the Metabolic Syndrome in Mice: Genotypic and Dietary Effects. <i>Journal of Proteome Research</i> , 2017, 16, 831-841.	3.7	11
132	Widespread Post-transcriptional Attenuation of Genomic Copy-Number Variation in Cancer. <i>Cell Systems</i> , 2017, 5, 386-398.e4.	6.2	102
133	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. <i>Cell Systems</i> , 2017, 5, 485-497.e3.	6.2	19
134	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. <i>Cell Reports</i> , 2017, 20, 2201-2214.	6.4	95
135	Logic Modeling in Quantitative Systems Pharmacology. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2017, 6, 499-511.	2.5	25
136	Systems Pharmacology Dissection of Cholesterol Regulation Reveals Determinants of Large Pharmacodynamic Variability between Cell Lines. <i>Cell Systems</i> , 2017, 5, 604-619.e7.	6.2	17
137	Benchmarking substrate-based kinase activity inference using phosphoproteomic data. <i>Bioinformatics</i> , 2017, 33, 1845-1851.	4.1	64
138	Data-driven reverse engineering of signaling pathways using ensembles of dynamic models. <i>PLoS Computational Biology</i> , 2017, 13, e1005379.	3.2	41
139	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005297.	3.2	51
140	Abstract A44: A landscape of pharmacogenomic interactions in cancer. , 2017, , .		9
141	A parallel metaheuristic for large mixed-integer dynamic optimization problems, with applications in computational biology. <i>PLoS ONE</i> , 2017, 12, e0182186.	2.5	10
142	Integrated transcriptomic and proteomic analysis identifies protein kinase CK2 as a key signaling node in an inflammatory cytokine network in ovarian cancer cells. <i>Oncotarget</i> , 2016, 7, 15648-15661.	1.8	13
143	Logical Modeling and Dynamical Analysis of Cellular Networks. <i>Frontiers in Genetics</i> , 2016, 7, 94.	2.3	216
144	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016, 166, 740-754.	28.9	1,518

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145	OmniPath: guidelines and gateway for literature-curated signaling pathway resources. Nature Methods, 2016, 13, 966-967.	19.0	469
146	Fumarate is an epigenetic modifier that elicits epithelial-to-mesenchymal transition. Nature, 2016, 537, 544-547.	27.8	443
147	Looking beyond the cancer cell for effective drug combinations. Genome Medicine, 2016, 8, 125.	8.2	31
148	Crowdsourcing biomedical research: leveraging communities as innovation engines. Nature Reviews Genetics, 2016, 17, 470-486.	16.3	137
149	A CRISPR Dropout Screen Identifies Genetic Vulnerabilities and Therapeutic Targets in Acute Myeloid Leukemia. Cell Reports, 2016, 17, 1193-1205.	6.4	556
150	Efficient randomization of biological networks while preserving functional characterization of individual nodes. BMC Bioinformatics, 2016, 17, 542.	2.6	38
151	A computational method for designing diverse linear epitopes including citrullinated peptides with desired binding affinities to intravenous immunoglobulin. BMC Bioinformatics, 2016, 17, 155.	2.6	2
152	The orchestra of lipid-transfer proteins at the crossroads between metabolism and signaling. Progress in Lipid Research, 2016, 61, 30-39.	11.6	85
153	Transcriptional response networks for elucidating mechanisms of action of multitargeted agents. Drug Discovery Today, 2016, 21, 1063-1075.	6.4	28
154	Inferring causal molecular networks: empirical assessment through a community-based effort. Nature Methods, 2016, 13, 310-318.	19.0	209
155	Annexin A1 sustains tumor metabolism and cellular proliferation upon stable loss of HIF1A. Oncotarget, 2016, 7, 6693-6710.	1.8	12
156	Extended notions of sign consistency to relate experimental data to signaling and regulatory network topologies. BMC Bioinformatics, 2015, 16, 345.	2.6	12
157	Designing Experiments to Discriminate Families of Logic Models. Frontiers in Bioengineering and Biotechnology, 2015, 3, 131.	4.1	6
158	A Semi-Supervised Approach for Refining Transcriptional Signatures of Drug Response and Repositioning Predictions. PLoS ONE, 2015, 10, e0139446.	2.5	39
159	A single-cell model of PIP3 dynamics using chemical dimerization. Bioorganic and Medicinal Chemistry, 2015, 23, 2868-2876.	3.0	4
160	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	17.5	88
161	Cooperative development of logical modelling standards and tools with CoLoMoTo. Bioinformatics, 2015, 31, 1154-1159.	4.1	98
162	Integrative approaches for signalling and metabolic networks. Integrative Biology (United Kingdom), 2015, 7, 844-845.	1.3	4

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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	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
165	BioPreDyn-bench: a suite of benchmark problems for dynamic modelling in systems biology. BMC Systems Biology, 2015, 9, 8.	3.0	61
166	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
167	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	28.9	1,710
168	Modeling Signaling Networks to Advance New Cancer Therapies. Annual Review of Biomedical Engineering, 2015, 17, 143-163.	12.3	34
169	Large-scale models of signal propagation in human cells derived from discovery phosphoproteomic data. Nature Communications, 2015, 6, 8033.	12.8	79
170	Reverse engineering of logic-based differential equation models using a mixed-integer dynamic optimization approach. Bioinformatics, 2015, 31, 2999-3007.	4.1	21
171	Pharmacogenomic agreement between two cancer cell line data sets. Nature, 2015, 528, 84-87.	27.8	358
172	Signaling networks in MS: A systems-based approach to developing new pharmacological therapies. Multiple Sclerosis Journal, 2015, 21, 138-146.	3.0	24
173	DREAMTools: a Python package for scoring collaborative challenges. F1000Research, 2015, 4, 1030.	1.6	14
174	A Crispr/Cas9 Drop-out Screen Identifies Genome-Wide Genetic Vulnerabilities in Acute Myeloid Leukaemia. Blood, 2015, 126, 554-554.	1.4	1
175	DREAMTools: a Python package for scoring collaborative challenges. F1000Research, 2015, 4, 1030.	1.6	16
176	Phosphoproteomic analyses reveal novel cross-talk modulation mechanisms between two signaling pathways in yeast. Molecular Systems Biology, 2014, 10, 767.	7.2	58
177	Exhaustively characterizing feasible logic models of a signaling network using Answer Set Programming. Bioinformatics, 2014, 30, 1942-1942.	4.1	1
178	Fast randomization of large genomic datasets while preserving alteration counts. Bioinformatics, 2014, 30, i617-i623.	4.1	36
179	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
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