

Julio Saez-Rodriguez

List of Publications by Year in descending order

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Version: 2024-02-01

247
papers

26,447
citations

13068

68
h-index

9311

143
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. <i>Nephrology Dialysis Transplantation</i> , 2022, 37, 628-637.	0.4	6
2	Deficiency of myeloid PHD proteins aggravates atherogenesis via macrophage apoptosis and paracrine fibrotic signalling. <i>Cardiovascular Research</i> , 2022, 118, 1232-1246.	1.8	12
3	Transcriptomic Cross-species Analysis of Chronic Liver Disease Reveals Consistent Regulation Between Humans and Mice. <i>Hepatology Communications</i> , 2022, 6, 161-177.	2.0	24
4	MAGED2 controls vasopressin-induced aquaporin-2 expression in collecting duct cells. <i>Journal of Proteomics</i> , 2022, 252, 104424.	1.2	1
5	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. <i>Cell Reports Medicine</i> , 2022, 3, 100492.	3.3	33
6	FUNKI: interactive functional footprint-based analysis of omics data. <i>Bioinformatics</i> , 2022, 38, 2075-2076.	1.8	4
7	Stabilization but No Functional Influence of HIF-1 α Expression in the Intestinal Epithelium during <i>Salmonella Typhimurium</i> Infection. <i>Infection and Immunity</i> , 2022, 90, iai0022221.	1.0	7
8	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.	0.8	26
9	The spatial transcriptomic landscape of the healing mouse intestine following damage. <i>Nature Communications</i> , 2022, 13, 828.	5.8	43
10	decoupleR: ensemble of computational methods to infer biological activities from omics data. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	127
11	Patient-specific Boolean models of signalling networks guide personalised treatments. <i>ELife</i> , 2022, 11, .	2.8	38
12	Molecular consequences of SARS-CoV-2 liver tropism. <i>Nature Metabolism</i> , 2022, 4, 310-319.	5.1	98
13	Computational drug repurposing against SARS-CoV-2 reveals plasma membrane cholesterol depletion as key factor of antiviral drug activity. <i>PLoS Computational Biology</i> , 2022, 18, e1010021.	1.5	8
14	Explainable multiview framework for dissecting spatial relationships from highly multiplexed data. <i>Genome Biology</i> , 2022, 23, 97.	3.8	45
15	Mapping the epithelial-immune cell interactome upon infection in the gut and the upper airways. <i>Npj Systems Biology and Applications</i> , 2022, 8, 15.	1.4	3
16	Reducing lipid bilayer stress by monounsaturated fatty acids protects renal proximal tubules in diabetes. <i>ELife</i> , 2022, 11, .	2.8	18
17	Comparison of methods and resources for cell-cell communication inference from single-cell RNA-Seq data. <i>Nature Communications</i> , 2022, 13, .	5.8	143
18	Cancer-associated fibroblasts require proline synthesis by PYCR1 for the deposition of pro-tumorigenic extracellular matrix. <i>Nature Metabolism</i> , 2022, 4, 693-710.	5.1	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, .	5.8	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.	3.2	25
21	The Minimum Information about a Molecular Interaction Causal Statement (MI2CAST). <i>Bioinformatics</i> , 2021, 36, 5712-5718.	1.8	14
22	The tissue proteome in the multi-omic landscape of kidney disease. <i>Nature Reviews Nephrology</i> , 2021, 17, 205-219.	4.1	31
23	Dynamic 3D proteomes reveal protein functional alterations at high resolution in situ. <i>Cell</i> , 2021, 184, 545-559.e22.	13.5	82
24	Hepatocyte-specific NRF2 activation controls fibrogenesis and carcinogenesis in steatohepatitis. <i>Journal of Hepatology</i> , 2021, 74, 638-648.	1.8	84
25	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <i>Frontiers in Microbiology</i> , 2021, 12, 635781.	1.5	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.	1.8	15
27	Integrated intra- and intercellular signaling knowledge for multicellular omics analysis. <i>Molecular Systems Biology</i> , 2021, 17, e9923.	3.2	152
28	Consensus Transcriptional Landscape of Human End-Stage Heart Failure. <i>Journal of the American Heart Association</i> , 2021, 10, e019667.	1.6	36
29	Transcription Factor Activity Inference in Systemic Lupus Erythematosus. <i>Life</i> , 2021, 11, 299.	1.1	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.	2.8	17
31	Reusability and composability in process description maps: RAS-RAF-MEK-ERK signalling. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	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.	2.6	35
33	Deciphering the signaling network of breast cancer improves drug sensitivity prediction. <i>Cell Systems</i> , 2021, 12, 401-418.e12.	2.9	22
34	A comprehensive database for integrated analysis of omics data in autoimmune diseases. <i>BMC Bioinformatics</i> , 2021, 22, 343.	1.2	12
35	Advances in systems biology modeling: 10 years of crowdsourcing DREAM challenges. <i>Cell Systems</i> , 2021, 12, 636-653.	2.9	21
36	Macrophage beta2-adrenergic receptor is dispensable for the adipose tissue inflammation and function. <i>Molecular Metabolism</i> , 2021, 48, 101220.	3.0	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.	1.8	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.	1.9	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.	6.6	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.	3.6	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.	2.0	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.	1.8	4
43	Medial Arterial Calcification. <i>Journal of the American College of Cardiology</i> , 2021, 78, 1145-1165.	1.2	106
44	SREBP1-induced fatty acid synthesis depletes macrophages antioxidant defences to promote their alternative activation. <i>Nature Metabolism</i> , 2021, 3, 1150-1162.	5.1	29
45	Contextualization of causal regulatory networks from toxicogenomics data applied to drug-induced liver injury. <i>Toxicology Letters</i> , 2021, 350, 40-51.	0.4	0
46	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021, 17, e9730.	3.2	78
47	Norepinephrine promotes triglyceride storage in macrophages via beta2-adrenergic receptor activation. <i>FASEB Journal</i> , 2021, 35, e21266.	0.2	11
48	Decoding myofibroblast origins in human kidney fibrosis. <i>Nature</i> , 2021, 589, 281-286.	13.7	380
49	Systems approach reveals distinct and shared signaling networks of the four PGE ₂ receptors in T cells. <i>Science Signaling</i> , 2021, 14, eabc8579.	1.6	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.	3.2	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.	1.9	16
52	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	3.2	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.	0.9	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.	1.7	14

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55	Bringing data from curated pathway resources to Cytoscape with OmniPath. <i>Bioinformatics</i> , 2020, 36, 2632-2633.	1.8	30
56	A Functional Landscape of CKD Entities From Public Transcriptomic Data. <i>Kidney International Reports</i> , 2020, 5, 211-224.	0.4	14
57	Kinetic modelling of quantitative proteome data predicts metabolic reprogramming of liver cancer. <i>British Journal of Cancer</i> , 2020, 122, 233-244.	2.9	16
58	BIAS: Transparent reporting of biomedical image analysis challenges. <i>Medical Image Analysis</i> , 2020, 66, 101796.	7.0	59
59	CELLector: Genomics-Guided Selection of Cancer In Vitro Models. <i>Cell Systems</i> , 2020, 10, 424-432.e6.	2.9	35
60	Converting networks to predictive logic models from perturbation signalling data with CellNOpt. <i>Bioinformatics</i> , 2020, 36, 4523-4524.	1.8	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.	0.6	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.	2.9	19
63	Big Data Approaches in Heart Failure Research. <i>Current Heart Failure Reports</i> , 2020, 17, 213-224.	1.3	13
64	Inferring clonal composition from multiple tumor biopsies. <i>Npj Systems Biology and Applications</i> , 2020, 6, 27.	1.4	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.	3.0	66
66	Why do pathway methods work better than they should?. <i>FEBS Letters</i> , 2020, 594, 4189-4200.	1.3	19
67	Stratification and prediction of drug synergy based on target functional similarity. <i>Npj Systems Biology and Applications</i> , 2020, 6, 16.	1.4	37
68	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. <i>Cell</i> , 2020, 182, 685-712.e19.	13.5	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.	3.2	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.	3.8	216
71	Dysregulated mesenchymal PDGFR ² drives kidney fibrosis. <i>EMBO Molecular Medicine</i> , 2020, 12, e11021.	3.3	41
72	Personalized signaling models for personalized treatments. <i>Molecular Systems Biology</i> , 2020, 16, e9042.	3.2	36

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73	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
74	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. <i>Life Science Alliance</i> , 2020, 3, e202000867.	1.3	20
75	A statistical framework for assessing pharmacological responses and biomarkers using uncertainty estimates. <i>ELife</i> , 2020, 9, .	2.8	16
76	Novel plasma peptide markers involved in the pathology of CKD identified using mass spectrometric approach. <i>Journal of Molecular Medicine</i> , 2019, 97, 1451-1463.	1.7	10
77	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.	1.4	32
78	Benchmark and integration of resources for the estimation of human transcription factor activities. <i>Genome Research</i> , 2019, 29, 1363-1375.	2.4	552
79	Toward Explainable Anticancer Compound Sensitivity Prediction via Multimodal Attention-Based Convolutional Encoders. <i>Molecular Pharmaceutics</i> , 2019, 16, 4797-4806.	2.3	86
80	From expression footprints to causal pathways: contextualizing large signaling networks with CARNIVAL. <i>Npj Systems Biology and Applications</i> , 2019, 5, 40.	1.4	96
81	THU-471-Establishment of a short-termed orthotopic transplantation model in C57/B6 mice that recapitulates characteristic features of human intrahepatic cholangiocarcinoma. <i>Journal of Hepatology</i> , 2019, 70, e367-e368.	1.8	0
82	Assessment of network module identification across complex diseases. <i>Nature Methods</i> , 2019, 16, 843-852.	9.0	213
83	Reproducible biomedical benchmarking in the cloud: lessons from crowd-sourced data challenges. <i>Genome Biology</i> , 2019, 20, 195.	3.8	19
84	Modeling Cell-Cell Interactions from Spatial Molecular Data with Spatial Variance Component Analysis. <i>Cell Reports</i> , 2019, 29, 202-211.e6.	2.9	133
85	Signatures of cell death and proliferation in perturbation transcriptomics data from confounding factor to effective prediction. <i>Nucleic Acids Research</i> , 2019, 47, 10010-10026.	6.5	50
86	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.	5.8	240
87	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.	4.5	32
88	Hybrid parallel multimethod hyperheuristic for mixed-integer dynamic optimization problems in computational systems biology. <i>Journal of Supercomputing</i> , 2019, 75, 3471-3498.	2.4	3
89	Functional linkage of gene fusions to cancer cell fitness assessed by pharmacological and CRISPR-Cas9 screening. <i>Nature Communications</i> , 2019, 10, 2198.	5.8	92
90	MAPK pathway and B cells overactivation in multiple sclerosis revealed by phosphoproteomics and genomic analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9671-9676.	3.3	42

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91	Footprint-based functional analysis of multiomic data. <i>Current Opinion in Systems Biology</i> , 2019, 15, 82-90.	1.3	39
92	MEK1/2 inhibitor withdrawal reverses acquired resistance driven by BRAFV600E amplification whereas KRASG13D amplification promotes EMT-chemoresistance. <i>Nature Communications</i> , 2019, 10, 2030.	5.8	39
93	Big science and big data in nephrology. <i>Kidney International</i> , 2019, 95, 1326-1337.	2.6	56
94	Prioritization of cancer therapeutic targets using CRISPR-Cas9 screens. <i>Nature</i> , 2019, 568, 511-516.	13.7	886
95	Elastin imaging enables noninvasive staging and treatment monitoring of kidney fibrosis. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	56
96	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. <i>Nature Biotechnology</i> , 2019, 37, 314-322.	9.4	254
97	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>IScience</i> , 2019, 21, 664-680.	1.9	52
98	Literature and data-driven based inference of signalling interactions using time-course data. <i>IFAC-PapersOnLine</i> , 2019, 52, 52-57.	0.5	2
99	The authors reply. <i>Kidney International</i> , 2019, 96, 1422-1423.	2.6	0
100	Influence of Liver Fibrosis on Lobular Zonation. <i>Cells</i> , 2019, 8, 1556.	1.8	51
101	Metabolic rewiring of the hypertensive kidney. <i>Science Signaling</i> , 2019, 12, .	1.6	40
102	Elucidating essential kinases of endothelin signalling by logic modelling of phosphoproteomics data. <i>Molecular Systems Biology</i> , 2019, 15, e8828.	3.2	11
103	The proteome microenvironment determines the protective effect of preconditioning in cisplatin-induced acute kidney injury. <i>Kidney International</i> , 2019, 95, 333-349.	2.6	55
104	Prostaglandin E 2 signaling networks in T cells revealed through a systems approach. <i>FASEB Journal</i> , 2019, 33, lb258.	0.2	0
105	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , 2018, 50, e453-e453.	3.2	49
106	NADH Shuttling Couples Cytosolic Reductive Carboxylation of Glutamine with Glycolysis in Cells with Mitochondrial Dysfunction. <i>Molecular Cell</i> , 2018, 69, 581-593.e7.	4.5	171
107	Phosphoproteomics-Based Profiling of Kinase Activities in Cancer Cells. <i>Methods in Molecular Biology</i> , 2018, 1711, 103-132.	0.4	24
108	GDSCTools for mining pharmacogenomic interactions in cancer. <i>Bioinformatics</i> , 2018, 34, 1226-1228.	1.8	45

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109	Perturbation-response genes reveal signaling footprints in cancer gene expression. <i>Nature Communications</i> , 2018, 9, 20.	5.8	436
110	Post-translational regulation of metabolism in fumarate hydratase deficient cancer cells. <i>Metabolic Engineering</i> , 2018, 45, 149-157.	3.6	27
111	Transcription Factor Activities Enhance Markers of Drug Sensitivity in Cancer. <i>Cancer Research</i> , 2018, 78, 769-780.	0.4	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.	1.1	0
113	Adipocyte-secreted BMP8b mediates adrenergic-induced remodeling of the neuro-vascular network in adipose tissue. <i>Nature Communications</i> , 2018, 9, 4974.	5.8	104
114	Computational discovery of dynamic cell line specific Boolean networks from multiplex time-course data. <i>PLoS Computational Biology</i> , 2018, 14, e1006538.	1.5	25
115	In silico Prioritization of Transporter-Drug Relationships From Drug Sensitivity Screens. <i>Frontiers in Pharmacology</i> , 2018, 9, 1011.	1.6	23
116	Linking drug target and pathway activation for effective therapy using multi-task learning. <i>Scientific Reports</i> , 2018, 8, 8322.	1.6	34
117	A microfluidics platform for combinatorial drug screening on cancer biopsies. <i>Nature Communications</i> , 2018, 9, 2434.	5.8	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.	1.3	19
119	Alternative models for sharing confidential biomedical data. <i>Nature Biotechnology</i> , 2018, 36, 391-392.	9.4	56
120	Pathway-based dissection of the genomic heterogeneity of cancer hallmarks' acquisition with SLAPenrich. <i>Scientific Reports</i> , 2018, 8, 6713.	1.6	24
121	The germline genetic component of drug sensitivity in cancer cell lines. <i>Nature Communications</i> , 2018, 9, 3385.	5.8	38
122	Unsupervised correction of gene-independent cell responses to CRISPR-Cas9 targeting. <i>BMC Genomics</i> , 2018, 19, 604.	1.2	75
123	A systematic atlas of chaperome deregulation topologies across the human cancer landscape. <i>PLoS Computational Biology</i> , 2018, 14, e1005890.	1.5	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.	1.8	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.	2.4	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.	5.2	195
128	Mechanism-based biomarker discovery. <i>Drug Discovery Today</i> , 2017, 22, 1209-1215.	3.2	22
129	Drug Resistance Mechanisms in Colorectal Cancer Dissected with Cell Type-Specific Dynamic Logic Models. <i>Cancer Research</i> , 2017, 77, 3364-3375.	0.4	101
130	Stem cell-like transcriptional reprogramming mediates metastatic resistance to mTOR inhibition. <i>Oncogene</i> , 2017, 36, 2737-2749.	2.6	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.	1.8	11
132	Widespread Post-transcriptional Attenuation of Genomic Copy-Number Variation in Cancer. <i>Cell Systems</i> , 2017, 5, 386-398.e4.	2.9	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.	2.9	19
134	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. <i>Cell Reports</i> , 2017, 20, 2201-2214.	2.9	95
135	Logic Modeling in Quantitative Systems Pharmacology. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2017, 6, 499-511.	1.3	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.	2.9	17
137	Benchmarking substrate-based kinase activity inference using phosphoproteomic data. <i>Bioinformatics</i> , 2017, 33, 1845-1851.	1.8	64
138	Data-driven reverse engineering of signaling pathways using ensembles of dynamic models. <i>PLoS Computational Biology</i> , 2017, 13, e1005379.	1.5	41
139	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005297.	1.5	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.	1.1	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.	0.8	13
143	Logical Modeling and Dynamical Analysis of Cellular Networks. <i>Frontiers in Genetics</i> , 2016, 7, 94.	1.1	216
144	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016, 166, 740-754.	13.5	1,518

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145	OmniPath: guidelines and gateway for literature-curated signaling pathway resources. <i>Nature Methods</i> , 2016, 13, 966-967.	9.0	469
146	Fumarate is an epigenetic modifier that elicits epithelial-to-mesenchymal transition. <i>Nature</i> , 2016, 537, 544-547.	13.7	443
147	Looking beyond the cancer cell for effective drug combinations. <i>Genome Medicine</i> , 2016, 8, 125.	3.6	31
148	Crowdsourcing biomedical research: leveraging communities as innovation engines. <i>Nature Reviews Genetics</i> , 2016, 17, 470-486.	7.7	137
149	A CRISPR Dropout Screen Identifies Genetic Vulnerabilities and Therapeutic Targets in Acute Myeloid Leukemia. <i>Cell Reports</i> , 2016, 17, 1193-1205.	2.9	556
150	Efficient randomization of biological networks while preserving functional characterization of individual nodes. <i>BMC Bioinformatics</i> , 2016, 17, 542.	1.2	38
151	A computational method for designing diverse linear epitopes including citrullinated peptides with desired binding affinities to intravenous immunoglobulin. <i>BMC Bioinformatics</i> , 2016, 17, 155.	1.2	2
152	The orchestra of lipid-transfer proteins at the crossroads between metabolism and signaling. <i>Progress in Lipid Research</i> , 2016, 61, 30-39.	5.3	85
153	Transcriptional response networks for elucidating mechanisms of action of multitargeted agents. <i>Drug Discovery Today</i> , 2016, 21, 1063-1075.	3.2	28
154	Inferring causal molecular networks: empirical assessment through a community-based effort. <i>Nature Methods</i> , 2016, 13, 310-318.	9.0	209
155	Annexin A1 sustains tumor metabolism and cellular proliferation upon stable loss of HIF1A. <i>Oncotarget</i> , 2016, 7, 6693-6710.	0.8	12
156	Extended notions of sign consistency to relate experimental data to signaling and regulatory network topologies. <i>BMC Bioinformatics</i> , 2015, 16, 345.	1.2	12
157	Designing Experiments to Discriminate Families of Logic Models. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 131.	2.0	6
158	A Semi-Supervised Approach for Refining Transcriptional Signatures of Drug Response and Repositioning Predictions. <i>PLoS ONE</i> , 2015, 10, e0139446.	1.1	39
159	A single-cell model of PIP3 dynamics using chemical dimerization. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 2868-2876.	1.4	4
160	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	9.4	88
161	Cooperative development of logical modelling standards and tools with CoLoMoTo. <i>Bioinformatics</i> , 2015, 31, 1154-1159.	1.8	98
162	Integrative approaches for signalling and metabolic networks. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 844-845.	0.6	4

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163	Learning Boolean logic models of signaling networks with ASP. Theoretical Computer Science, 2015, 599, 79-101.	0.5	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.	3.3	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.	0.6	43
167	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	13.5	1,710
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