

Avi Maayan

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

202
papers

24,795
citations

60
h-index

157
g-index

236
ext. papers

34,028
ext. citations

11
avg. IF

6.81
L-index

#	Paper	IF	Citations
202	Getting Started with the IDG KMC Datasets and Tools.. <i>Current Protocols</i> , 2022 , 2, e355		1
201	Gene and drug landing page aggregator.. <i>Bioinformatics Advances</i> , 2022 , 2, vbac013		
200	DrugShot: querying biomedical search terms to retrieve prioritized lists of small molecules.. <i>BMC Bioinformatics</i> , 2022 , 23, 76	3.6	0
199	Loss of proximal tubular transcription factor Kr̄pel-like factor 15 exacerbates kidney injury through loss of fatty acid oxidation. <i>Kidney International</i> , 2021 , 100, 1250-1267	9.9	4
198	Gene Set Knowledge Discovery with Enrichr. <i>Current Protocols</i> , 2021 , 1, e90		207
197	Appyters: Turning Jupyter Notebooks into data-driven web apps. <i>Patterns</i> , 2021 , 2, 100213	5.1	13
196	An Esrrb and Nanog Cell Fate Regulatory Module Controlled by Feed Forward Loop Interactions. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 630067	5.7	1
195	Transcriptome analysis of human dermal fibroblasts following red light phototherapy. <i>Scientific Reports</i> , 2021 , 11, 7315	4.9	1
194	KEA3: improved kinase enrichment analysis via data integration. <i>Nucleic Acids Research</i> , 2021 , 49, W304-W316	11.9	9
193	Kr̄pel-like factor 6-mediated loss of BCAA catabolism contributes to kidney injury in mice and humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
192	Connectivity Mapping Identifies BI-2536 as a Potential Drug to Treat Diabetic Kidney Disease. <i>Diabetes</i> , 2021 , 70, 589-602	0.9	4
191	Drugmonizome and Drugmonizome-ML: integration and abstraction of small molecule attributes for drug enrichment analysis and machine learning. <i>Database: the Journal of Biological Databases and Curation</i> , 2021 , 2021,	5	6
190	Prioritizing Pain-Associated Targets with Machine Learning. <i>Biochemistry</i> , 2021 , 60, 1430-1446	3.2	1
189	Predicting Lyme Disease From Patients' Peripheral Blood Mononuclear Cells Profiled With RNA-Sequencing. <i>Frontiers in Immunology</i> , 2021 , 12, 636289	8.4	2
188	Recent Progress in Lyme Disease and Remaining Challenges. <i>Frontiers in Medicine</i> , 2021 , 8, 666554	4.9	7
187	Systems Analysis Implicates WAVE2 Complex in the Pathogenesis of Developmental Left-Sided Obstructive Heart Defects. <i>JACC Basic To Translational Science</i> , 2020 , 5, 376-386	8.7	2
186	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. <i>Nucleic Acids Research</i> , 2020 , 48, W85-W93	20.1	9

185	Interoperable RNA-Seq analysis in the cloud. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020 , 1863, 194521	6	6
184	Genetic driver mutations introduced in identical cell-of-origin in murine glioblastoma reveal distinct immune landscapes but similar response to checkpoint blockade. <i>Glia</i> , 2020 , 68, 2148-2166	9	10
183	EnrichrBot: Twitter bot tracking tweets about human genes. <i>Bioinformatics</i> , 2020 , 36, 3932-3934	7.2	1
182	The COVID-19 Gene and Drug Set Library 2020 ,		4
181	The COVID-19 Drug and Gene Set Library. <i>Patterns</i> , 2020 , 1, 100090	5.1	36
180	Dermal sheath contraction powers stem cell niche relocation during hair cycle regression. <i>Science</i> , 2020 , 367, 161-166	33.3	39
179	LINCS Data Portal 2.0: next generation access point for perturbation-response signatures. <i>Nucleic Acids Research</i> , 2020 , 48, D431-D439	20.1	54
178	Chemokine Signatures of Pathogen-Specific T Cells II: Memory T Cells in Acute and Chronic Infection. <i>Journal of Immunology</i> , 2020 , 205, 2188-2206	5.3	3
177	Memory of Divisional History Directs the Continuous Process of Primitive Hematopoietic Lineage Commitment. <i>Stem Cell Reports</i> , 2020 , 14, 561-574	8	4
176	Chemokine Signatures of Pathogen-Specific T Cells I: Effector T Cells. <i>Journal of Immunology</i> , 2020 , 205, 2169-2187	5.3	9
175	Towards Intelligent Integration and Sharing of Stem Cell Research Data. <i>Studies in Health Technology and Informatics</i> , 2020 , 272, 334-337	0.5	2
174	Predicting opioid dependence from electronic health records with machine learning. <i>BioData Mining</i> , 2019 , 12, 3	4.3	33
173	ChEA3: transcription factor enrichment analysis by orthogonal omics integration. <i>Nucleic Acids Research</i> , 2019 , 47, W212-W224	20.1	134
172	Geneshot: search engine for ranking genes from arbitrary text queries. <i>Nucleic Acids Research</i> , 2019 , 47, W571-W577	20.1	26
171	modEnrichr: a suite of gene set enrichment analysis tools for model organisms. <i>Nucleic Acids Research</i> , 2019 , 47, W183-W190	20.1	22
170	Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. <i>Nature Cell Biology</i> , 2019 , 21, 560-567	23.4	43
169	A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. <i>Cell Systems</i> , 2019 , 9, 35-48.e5	10.6	46
168	Connectivity Mapping: Methods and Applications. <i>Annual Review of Biomedical Data Science</i> , 2019 , 2, 69-92	5.6	23

167	The Signaling Pathways Project, an integrated 'omics knowledgebase for mammalian cellular signaling pathways. <i>Scientific Data</i> , 2019 , 6, 252	8.2	38
166	Direct activation of PP2A for the treatment of tyrosine kinase inhibitor-resistant lung adenocarcinoma. <i>JCI Insight</i> , 2019 , 4,	9.9	25
165	Engineering a Hematopoietic Stem Cell Niche By Revitalizing Mesenchymal Stem Cells with Five Transcription Factors. <i>Blood</i> , 2019 , 134, 5004-5004	2.2	
164	FAIRshake: Toolkit to Evaluate the FAIRness of Research Digital Resources. <i>Cell Systems</i> , 2019 , 9, 417-421	10.6	17
163	Habenular TCF7L2 links nicotine addiction to diabetes. <i>Nature</i> , 2019 , 574, 372-377	50.4	47
162	Single-cell immune landscape of human atherosclerotic plaques. <i>Nature Medicine</i> , 2019 , 25, 1576-1588	50.5	247
161	Drug Gene Budger (DGB): an application for ranking drugs to modulate a specific gene based on transcriptomic signatures. <i>Bioinformatics</i> , 2019 , 35, 1247-1248	7.2	15
160	Mining data and metadata from the gene expression omnibus. <i>Biophysical Reviews</i> , 2019 , 11, 103-110	3.7	30
159	Dermal Condensate Niche Fate Specification Occurs Prior to Formation and Is Placode Progenitor Dependent. <i>Developmental Cell</i> , 2019 , 48, 32-48.e5	10.2	44
158	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018 , 17, 317-332	64.1	156
157	Datasets2Tools, repository and search engine for bioinformatics datasets, tools and canned analyses. <i>Scientific Data</i> , 2018 , 5, 180023	8.2	7
156	Massive mining of publicly available RNA-seq data from human and mouse. <i>Nature Communications</i> , 2018 , 9, 1366	17.4	242
155	L1000FWD: fireworks visualization of drug-induced transcriptomic signatures. <i>Bioinformatics</i> , 2018 , 34, 2150-2152	7.2	66
154	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	10.6	199
153	Cell-specific prediction and application of drug-induced gene expression profiles 2018 ,		1
152	Systematic analyses of drugs and disease indications in RepurposeDB reveal pharmacological, biological and epidemiological factors influencing drug repositioning. <i>Briefings in Bioinformatics</i> , 2018 , 19, 656-678	13.4	48
151	Effect of short-term liver X receptor activation on epidermal barrier features in mild to moderate atopic dermatitis: A randomized controlled trial. <i>Annals of Allergy, Asthma and Immunology</i> , 2018 , 120, 631-640.e11	3.2	19
150	SIRT6 haploinsufficiency induces BRAF melanoma cell resistance to MAPK inhibitors via IGF signalling. <i>Nature Communications</i> , 2018 , 9, 3440	17.4	51

149	Podocyte-Specific Induction of Krüppel-Like Factor 15 Restores Differentiation Markers and Attenuates Kidney Injury in Proteinuric Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2018 , 29, 2529-2545	12.7	19
148	Integration of pan-cancer transcriptomics with RPPA proteomics reveals mechanisms of epithelial-mesenchymal transition. <i>PLoS Computational Biology</i> , 2018 , 14, e1005911	5	23
147	Cell-specific prediction and application of drug-induced gene expression profiles. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018 , 23, 32-43	1.3	11
146	Transcriptomic analysis uncovers novel synergistic mechanisms in combination therapy for lupus nephritis. <i>Kidney International</i> , 2018 , 93, 416-429	9.9	21
145	Sustainable data and metadata management at the BD2K-LINCS Data Coordination and Integration Center. <i>Scientific Data</i> , 2018 , 5, 180117	8.2	15
144	BioJupies: Automated Generation of Interactive Notebooks for RNA-Seq Data Analysis in the Cloud. <i>Cell Systems</i> , 2018 , 7, 556-561.e3	10.6	98
143	Far away from the lamppost. <i>PLoS Biology</i> , 2018 , 16, e3000067	9.7	10
142	Cooperative Transcription Factor Induction Mediates Hemogenic Reprogramming. <i>Cell Reports</i> , 2018 , 25, 2821-2835.e7	10.6	21
141	Temporal proteomic profiling of postnatal human cortical development. <i>Translational Psychiatry</i> , 2018 , 8, 267	8.6	10
140	Data Portal for the Library of Integrated Network-based Cellular Signatures (LINCS) program: integrated access to diverse large-scale cellular perturbation response data. <i>Nucleic Acids Research</i> , 2018 , 46, D558-D566	20.1	84
139	eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks. <i>Nucleic Acids Research</i> , 2018 , 46, W171-W179	20.1	58
138	Integration of protein phosphorylation, acetylation, and methylation data sets to outline lung cancer signaling networks. <i>Science Signaling</i> , 2018 , 11,	8.8	29
137	Endothelial cells instruct liver specification of embryonic stem cell-derived endoderm through endothelial VEGFR2 signaling and endoderm epigenetic modifications. <i>Stem Cell Research</i> , 2018 , 30, 163-170	1.6	5
136	Krüppel-Like Factor 15 Mediates Glucocorticoid-Induced Restoration of Podocyte Differentiation Markers. <i>Journal of the American Society of Nephrology: JASN</i> , 2017 , 28, 166-184	12.7	48
135	Pharos: Collating protein information to shed light on the druggable genome. <i>Nucleic Acids Research</i> , 2017 , 45, D995-D1002	20.1	146
134	Differential cytokine contributions of perivascular haematopoietic stem cell niches. <i>Nature Cell Biology</i> , 2017 , 19, 214-223	23.4	254
133	Developing a framework for digital objects in the Big Data to Knowledge (BD2K) commons: Report from the Commons Framework Pilots workshop. <i>Journal of Biomedical Informatics</i> , 2017 , 71, 49-57	10.2	21
132	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. <i>Nature Communications</i> , 2017 , 8, 1186	17.4	38

131	Clustergrammer, a web-based heatmap visualization and analysis tool for high-dimensional biological data. <i>Scientific Data</i> , 2017 , 4, 170151	8.2	96
130	Complex systems biology. <i>Journal of the Royal Society Interface</i> , 2017 , 14,	4.1	32
129	Predicting age by mining electronic medical records with deep learning characterizes differences between chronological and physiological age. <i>Journal of Biomedical Informatics</i> , 2017 , 76, 59-68	10.2	20
128	Activation of tumor suppressor protein PP2A inhibits KRAS-driven tumor growth. <i>Journal of Clinical Investigation</i> , 2017 , 127, 2081-2090	15.9	106
127	Polycomb repressive complex 2 (PRC2) silences genes responsible for neurodegeneration. <i>Nature Neuroscience</i> , 2016 , 19, 1321-30	25.5	108
126	GEN3VA: aggregation and analysis of gene expression signatures from related studies. <i>BMC Bioinformatics</i> , 2016 , 17, 461	3.6	13
125	Extraction and analysis of signatures from the Gene Expression Omnibus by the crowd. <i>Nature Communications</i> , 2016 , 7, 12846	17.4	146
124	Glucocorticoid receptor isoforms direct distinct mitochondrial programs to regulate ATP production. <i>Scientific Reports</i> , 2016 , 6, 26419	4.9	26
123	The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	504
122	Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. <i>Nucleic Acids Research</i> , 2016 , 44, W90-7	20.1	3549
121	Signaling Networks among Stem Cell Precursors, Transit-Amplifying Progenitors, and their Niche in Developing Hair Follicles. <i>Cell Reports</i> , 2016 , 14, 3001-18	10.6	98
120	Fetal liver hematopoietic stem cell niches associate with portal vessels. <i>Science</i> , 2016 , 351, 176-80	33.3	147
119	Integrative radiogenomic analysis for multicentric radiophenotype in glioblastoma. <i>Oncotarget</i> , 2016 , 7, 11526-38	3.3	13
118	An open RNA-Seq data analysis pipeline tutorial with an example of reprocessing data from a recent Zika virus study. <i>F1000Research</i> , 2016 , 5, 1574	3.6	23
117	Regulatory consequences of neuronal ELAV-like protein binding to coding and non-coding RNAs in human brain. <i>ELife</i> , 2016 , 5,	8.9	86
116	Integrative Analysis of Sex-Specific microRNA Networks Following Stress in Mouse Nucleus Accumbens. <i>Frontiers in Molecular Neuroscience</i> , 2016 , 9, 144	6.1	31
115	L1000CDS: LINCS L1000 characteristic direction signatures search engine. <i>Npj Systems Biology and Applications</i> , 2016 , 2,	5	140
114	Drug-induced adverse events prediction with the LINCS L1000 data. <i>Bioinformatics</i> , 2016 , 32, 2338-45	7.2	95

113	Publisher's Note: Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction. <i>Computational Biology and Chemistry</i> , 2015 , 58, 104-19	3.6	2
112	GEO2Enrichr: browser extension and server app to extract gene sets from GEO and analyze them for biological functions. <i>Bioinformatics</i> , 2015 , 31, 3060-2	7.2	40
111	Morphine Regulated Synaptic Networks Revealed by Integrated Proteomics and Network Analysis. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2564-76	7.6	9
110	An Integrated Transcriptome Atlas of Embryonic Hair Follicle Progenitors, Their Niche, and the Developing Skin. <i>Developmental Cell</i> , 2015 , 34, 577-91	10.2	109
109	Dynamics of the discovery process of protein-protein interactions from low content studies. <i>BMC Systems Biology</i> , 2015 , 9, 26	3.5	13
108	Reprint of "Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction". <i>Computational Biology and Chemistry</i> , 2015 , 59 Pt B, 123-38	3.6	9
107	Principal Angle Enrichment Analysis (PAEA): Dimensionally Reduced Multivariate Gene Set Enrichment Analysis Tool 2015 , 2015, 256-262	0.8	8
106	Krüppel-like factor 6 regulates mitochondrial function in the kidney. <i>Journal of Clinical Investigation</i> , 2015 , 125, 1347-61	15.9	50
105	A Systems Approach Identifies Essential FOXO3 Functions at Key Steps of Terminal Erythropoiesis. <i>PLoS Genetics</i> , 2015 , 11, e1005526	6	40
104	Histone H3.3 and its proteolytically processed form drive a cellular senescence programme. <i>Nature Communications</i> , 2014 , 5, 5210	17.4	89
103	Synaptic, transcriptional and chromatin genes disrupted in autism. <i>Nature</i> , 2014 , 515, 209-15	50.4	1581
102	Lean Big Data integration in systems biology and systems pharmacology. <i>Trends in Pharmacological Sciences</i> , 2014 , 35, 450-60	13.2	67
101	A blueprint of cell identity. <i>Nature Biotechnology</i> , 2014 , 32, 1007-8	44.5	2
100	The characteristic direction: a geometrical approach to identify differentially expressed genes. <i>BMC Bioinformatics</i> , 2014 , 15, 79	3.6	103
99	Proteomics analysis of the non-muscle myosin heavy chain IIa-enriched actin-myosin complex reveals multiple functions within the podocyte. <i>PLoS ONE</i> , 2014 , 9, e100660	3.7	13
98	LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. <i>Nucleic Acids Research</i> , 2014 , 42, W449-60	20.1	204
97	Interconnected network motifs control podocyte morphology and kidney function. <i>Science Signaling</i> , 2014 , 7, ra12	8.8	44
96	Drug/Cell-line Browser: interactive canvas visualization of cancer drug/cell-line viability assay datasets. <i>Bioinformatics</i> , 2014 , 30, 3289-90	7.2	7

95	B-myb is an essential regulator of hematopoietic stem cell and myeloid progenitor cell development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 3122-7	11.5	29
94	Construction and validation of a regulatory network for pluripotency and self-renewal of mouse embryonic stem cells. <i>PLoS Computational Biology</i> , 2014 , 10, e1003777	5	64
93	DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. <i>Molecular Autism</i> , 2014 , 5, 22	6.5	89
92	Pathways of Toxicity. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2014 , 31, 53-61	4.3	59
91	A Systems Approach Identifies Essential FOXO3 Functions in Erythroblast Eucleation Process. <i>Blood</i> , 2014 , 124, 445-445	2.2	
90	Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. <i>BMC Bioinformatics</i> , 2013 , 14, 128	3.6	2715
89	Network2Canvas: network visualization on a canvas with enrichment analysis. <i>Bioinformatics</i> , 2013 , 29, 1872-8	7.2	32
88	Minimal differentiation of classical monocytes as they survey steady-state tissues and transport antigen to lymph nodes. <i>Immunity</i> , 2013 , 39, 599-610	32.3	511
87	Identification of small exonic CNV from whole-exome sequence data and application to autism spectrum disorder. <i>American Journal of Human Genetics</i> , 2013 , 93, 607-19	11	120
86	Transforming growth factor β signaling controls activities of human intestinal CD8(+)T suppressor cells. <i>Gastroenterology</i> , 2013 , 144, 601-612.e1	13.3	13
85	Biological and Quantitative Models for Stem Cell Self-Renewal and Differentiation 2013 , 427-441		
84	ELK1 transcription factor linked to dysregulated striatal mu opioid receptor signaling network and OPRM1 polymorphism in human heroin abusers. <i>Biological Psychiatry</i> , 2013 , 74, 511-9	7.9	27
83	Induction of a hemogenic program in mouse fibroblasts. <i>Cell Stem Cell</i> , 2013 , 13, 205-18	18	168
82	Renoprotective effect of combined inhibition of angiotensin-converting enzyme and histone deacetylase. <i>Journal of the American Society of Nephrology: JASN</i> , 2013 , 24, 801-11	12.7	41
81	Metasignatures identify two major subtypes of breast cancer. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2013 , 2, e35	4.5	13
80	ESCAPE: database for integrating high-content published data collected from human and mouse embryonic stem cells. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat045	5	62
79	Expression of HIV transgene aggravates kidney injury in diabetic mice. <i>Kidney International</i> , 2013 , 83, 626-34	9.9	43
78	RNA Sequencing Of Adult Bone Marrow Erythroid Populations Reveals Significant Transcriptional Deregluation In Foxo3 ^{-/-} Mutant Cells. <i>Blood</i> , 2013 , 122, 3416-3416	2.2	

77	Quantitative Approaches to Model Pluripotency and Differentiation in Stem Cells 2013 , 59-74		3
76	Sox2 in the dermal papilla niche controls hair growth by fine-tuning BMP signaling in differentiating hair shaft progenitors. <i>Developmental Cell</i> , 2012 , 23, 981-94	10.2	105
75	Oct4 links multiple epigenetic pathways to the pluripotency network. <i>Cell Research</i> , 2012 , 22, 155-67	24.7	128
74	Regulation of embryonic and induced pluripotency by aurora kinase-p53 signaling. <i>Cell Stem Cell</i> , 2012 , 11, 179-94	18	117
73	Genes2FANs: connecting genes through functional association networks. <i>BMC Bioinformatics</i> , 2012 , 13, 156	3.6	23
72	Sets2Networks: network inference from repeated observations of sets. <i>BMC Systems Biology</i> , 2012 , 6, 89	3.5	14
71	Colliding dynamical complex network models: biological attractors versus attractors from material physics. <i>Biophysical Journal</i> , 2012 , 103, 1816-7	2.9	3
70	Patterns and rates of exonic de novo mutations in autism spectrum disorders. <i>Nature</i> , 2012 , 485, 242-5	50.4	1300
69	Gene-expression profiles and transcriptional regulatory pathways that underlie the identity and diversity of mouse tissue macrophages. <i>Nature Immunology</i> , 2012 , 13, 1118-28	19.1	1361
68	A systems approach identifies HIPK2 as a key regulator of kidney fibrosis. <i>Nature Medicine</i> , 2012 , 18, 580-8	50.5	110
67	Nanog-dependent feedback loops regulate murine embryonic stem cell heterogeneity. <i>Nature Cell Biology</i> , 2012 , 14, 1139-47	23.4	129
66	Systems biology of kidney diseases. <i>Kidney International</i> , 2012 , 81, 22-39	9.9	60
65	Expression2Kinases: mRNA profiling linked to multiple upstream regulatory layers. <i>Bioinformatics</i> , 2012 , 28, 105-11	7.2	103
64	Network- and attribute-based classifiers can prioritize genes and pathways for autism spectrum disorders and intellectual disability. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2012 , 160C, 130-42	3.1	25
63	Activation of alternate prosurvival pathways accounts for acquired sunitinib resistance in U87MG glioma xenografts. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2012 , 343, 509-19	4.7	15
62	Kruppel-like factor 15 (KLF15) is a key regulator of podocyte differentiation. <i>Journal of Biological Chemistry</i> , 2012 , 287, 19122-35	5.4	73
61	Receptor heteromerization expands the repertoire of cannabinoid signaling in rodent neurons. <i>PLoS ONE</i> , 2012 , 7, e29239	3.7	59
60	Network Pharmacology to Aid the Drug Discovery Process 2012 , 161-172		1

59	Regulation of Primitive Erythroid Progenitor Development. <i>Blood</i> , 2012 , 120, 1211-1211	2.2	
58	Genes2WordCloud: a quick way to identify biological themes from gene lists and free text. <i>Source Code for Biology and Medicine</i> , 2011 , 6, 15	1.9	21
57	Sig2BioPAX: Java tool for converting flat files to BioPAX Level 3 format. <i>Source Code for Biology and Medicine</i> , 2011 , 6, 5	1.9	4
56	FNV: light-weight flash-based network and pathway viewer. <i>Bioinformatics</i> , 2011 , 27, 1181-2	7.2	4
55	Introduction to statistical methods to analyze large data sets: principal components analysis. <i>Science Signaling</i> , 2011 , 4, tr3	8.8	27
54	Introduction to statistical methods for analyzing large data sets: gene-set enrichment analysis. <i>Science Signaling</i> , 2011 , 4, tr4	8.8	22
53	Recovering protein-protein and domain-domain interactions from aggregation of IP-MS proteomics of coregulator complexes. <i>PLoS Computational Biology</i> , 2011 , 7, e1002319	5	13
52	Introduction to network analysis in systems biology. <i>Science Signaling</i> , 2011 , 4, tr5	8.8	79
51	Chronic morphine alters the presynaptic protein profile: identification of novel molecular targets using proteomics and network analysis. <i>PLoS ONE</i> , 2011 , 6, e25535	3.7	42
50	Primitive Erythroid Progenitors Are Regulated by Hypoxia and Display An Aerobic Glycolytic Metabolic Profile,. <i>Blood</i> , 2011 , 118, 3159-3159	2.2	
49	Mesenchymal and haematopoietic stem cells form a unique bone marrow niche. <i>Nature</i> , 2010 , 466, 829-304	30.4	2446
48	Global phosphorylation analysis of beta-arrestin-mediated signaling downstream of a seven transmembrane receptor (7TMR). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 15299-304	11.5	164
47	Flotillin-mediated endocytic events dictate cell type-specific responses to semaphorin 3A. <i>Journal of Neuroscience</i> , 2010 , 30, 15317-29	6.6	43
46	GATE: software for the analysis and visualization of high-dimensional time series expression data. <i>Bioinformatics</i> , 2010 , 26, 143-4	7.2	25
45	ChEA: transcription factor regulation inferred from integrating genome-wide ChIP-X experiments. <i>Bioinformatics</i> , 2010 , 26, 2438-44	7.2	533
44	Systems pharmacology of arrhythmias. <i>Science Signaling</i> , 2010 , 3, ra30	8.8	102
43	Microdynamics and criticality of adaptive regulatory networks. <i>Physical Review Letters</i> , 2010 , 104, 168704	7.4	12
42	Inferring the Sign of Kinase-Substrate Interactions by Combining Quantitative Phosphoproteomics with a Literature-Based Mammalian Kinome Network. <i>Proceedings-- IEEE International Symposium on Bioinformatics and Bioengineering</i> , 2010 , 2010, 180-184	1	2

41	Protein kinase target discovery from genome-wide messenger RNA expression profiling. <i>Mount Sinai Journal of Medicine</i> , 2010 , 77, 345-9		4
40	Lists2Networks: integrated analysis of gene/protein lists. <i>BMC Bioinformatics</i> , 2010 , 11, 87	3.6	34
39	SVM classifier to predict genes important for self-renewal and pluripotency of mouse embryonic stem cells. <i>BMC Systems Biology</i> , 2010 , 4, 173	3.5	16
38	Toward a complete in silico, multi-layered embryonic stem cell regulatory network. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010 , 2, 708-33	6.6	20
37	KEA: kinase enrichment analysis. <i>Bioinformatics</i> , 2009 , 25, 684-6	7.2	147
36	SNAVI: Desktop application for analysis and visualization of large-scale signaling networks. <i>BMC Systems Biology</i> , 2009 , 3, 10	3.5	23
35	Systems approach to explore components and interactions in the presynapse. <i>Proteomics</i> , 2009 , 9, 3303-15	4.5	43
34	Systems-level dynamic analyses of fate change in murine embryonic stem cells. <i>Nature</i> , 2009 , 462, 358-63	30.4	237
33	Mutation of SHOC2 promotes aberrant protein N-myristoylation and causes Noonan-like syndrome with loose anagen hair. <i>Nature Genetics</i> , 2009 , 41, 1022-6	36.3	291
32	Systems biology of stem cell fate and cellular reprogramming. <i>Nature Reviews Molecular Cell Biology</i> , 2009 , 10, 672-81	48.7	274
31	Neuro2A differentiation by Galphai/o pathway. <i>Science Signaling</i> , 2009 , 2, cm1	8.8	25
30	Insights into the organization of biochemical regulatory networks using graph theory analyses. <i>Journal of Biological Chemistry</i> , 2009 , 284, 5451-5	5.4	56
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7	BioJupies: Automated Generation of Interactive Notebooks for RNA-seq Data Analysis in the Cloud		2
6	Massive Mining of Publicly Available RNA-seq Data from Human and Mouse		7

5	Modulating the transcriptional landscape of SARS-CoV-2 as an effective method for developing antiviral compounds	15
4	Elysium: RNA-seq Alignment in the Cloud	4
3	piNET: a versatile web platform for downstream analysis and visualization of proteomics data	2
2	FAIRshake: toolkit to evaluate the findability, accessibility, interoperability, and reusability of research digital resources	2
1	Connecting omics signatures of diseases, drugs, and mechanisms of actions with iLINCS	21