

# Avi Maayan

## List of Publications by Citations

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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	Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, W90-7	20.1	3549
201	Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 128	3.6	2715
200	Mesenchymal and haematopoietic stem cells form a unique bone marrow niche. <i>Nature</i> , <b>2010</b> , 466, 829-34	36.4	2446
199	Synaptic, transcriptional and chromatin genes disrupted in autism. <i>Nature</i> , <b>2014</b> , 515, 209-15	50.4	1581
198	Gene-expression profiles and transcriptional regulatory pathways that underlie the identity and diversity of mouse tissue macrophages. <i>Nature Immunology</i> , <b>2012</b> , 13, 1118-28	19.1	1361
197	Patterns and rates of exonic de novo mutations in autism spectrum disorders. <i>Nature</i> , <b>2012</b> , 485, 242-5	50.4	1300
196	Functional atlas of the integrin adhesome. <i>Nature Cell Biology</i> , <b>2007</b> , 9, 858-67	23.4	899
195	ChEA: transcription factor regulation inferred from integrating genome-wide ChIP-X experiments. <i>Bioinformatics</i> , <b>2010</b> , 26, 2438-44	7.2	533
194	Minimal differentiation of classical monocytes as they survey steady-state tissues and transport antigen to lymph nodes. <i>Immunity</i> , <b>2013</b> , 39, 599-610	32.3	511
193	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> , <b>2016</b> , 2016,	5	504
192	Mutation of SHOC2 promotes aberrant protein N-myristoylation and causes Noonan-like syndrome with loose anagen hair. <i>Nature Genetics</i> , <b>2009</b> , 41, 1022-6	36.3	291
191	Systems biology of stem cell fate and cellular reprogramming. <i>Nature Reviews Molecular Cell Biology</i> , <b>2009</b> , 10, 672-81	48.7	274
190	Formation of regulatory patterns during signal propagation in a Mammalian cellular network. <i>Science</i> , <b>2005</b> , 309, 1078-83	33.3	268
189	Differential cytokine contributions of perivascular haematopoietic stem cell niches. <i>Nature Cell Biology</i> , <b>2017</b> , 19, 214-223	23.4	254
188	Single-cell immune landscape of human atherosclerotic plaques. <i>Nature Medicine</i> , <b>2019</b> , 25, 1576-1588	50.5	247
187	Massive mining of publicly available RNA-seq data from human and mouse. <i>Nature Communications</i> , <b>2018</b> , 9, 1366	17.4	242
186	Systems-level dynamic analyses of fate change in murine embryonic stem cells. <i>Nature</i> , <b>2009</b> , 462, 358-63	30.4	237

185	Gene Set Knowledge Discovery with Enrichr. <i>Current Protocols</i> , <b>2021</b> , 1, e90		207
184	LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W449-60	20.1	204
183	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , <b>2018</b> , 6, 13-24	10.6	199
182	Induction of a hemogenic program in mouse fibroblasts. <i>Cell Stem Cell</i> , <b>2013</b> , 13, 205-18	18	168
181	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> , <b>2010</b> , 107, 15299-304	11.5	164
180	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , <b>2018</b> , 17, 317-332	64.1	156
179	Fetal liver hematopoietic stem cell niches associate with portal vessels. <i>Science</i> , <b>2016</b> , 351, 176-80	33.3	147
178	KEA: kinase enrichment analysis. <i>Bioinformatics</i> , <b>2009</b> , 25, 684-6	7.2	147
177	Pharos: Collating protein information to shed light on the druggable genome. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D995-D1002	20.1	146
176	Extraction and analysis of signatures from the Gene Expression Omnibus by the crowd. <i>Nature Communications</i> , <b>2016</b> , 7, 12846	17.4	146
175	L1000CDS: LINCS L1000 characteristic direction signatures search engine. <i>Npj Systems Biology and Applications</i> , <b>2016</b> , 2,	5	140
174	ChEA3: transcription factor enrichment analysis by orthogonal omics integration. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, W212-W224	20.1	134
173	Nanog-dependent feedback loops regulate murine embryonic stem cell heterogeneity. <i>Nature Cell Biology</i> , <b>2012</b> , 14, 1139-47	23.4	129
172	Oct4 links multiple epigenetic pathways to the pluripotency network. <i>Cell Research</i> , <b>2012</b> , 22, 155-67	24.7	128
171	Identification of small exonic CNV from whole-exome sequence data and application to autism spectrum disorder. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 607-19	11	120
170	Regulation of embryonic and induced pluripotency by aurora kinase-p53 signaling. <i>Cell Stem Cell</i> , <b>2012</b> , 11, 179-94	18	117
169	Design logic of a cannabinoid receptor signaling network that triggers neurite outgrowth. <i>Science</i> , <b>2008</b> , 320, 903-9	33.3	114
168	Genes2Networks: connecting lists of gene symbols using mammalian protein interactions databases. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 372	3.6	114

167	A systems approach identifies HIPK2 as a key regulator of kidney fibrosis. <i>Nature Medicine</i> , <b>2012</b> , 18, 580-8	50.5	110
166	An Integrated Transcriptome Atlas of Embryonic Hair Follicle Progenitors, Their Niche, and the Developing Skin. <i>Developmental Cell</i> , <b>2015</b> , 34, 577-91	10.2	109
165	Polycomb repressive complex 2 (PRC2) silences genes responsible for neurodegeneration. <i>Nature Neuroscience</i> , <b>2016</b> , 19, 1321-30	25.5	108
164	Activation of tumor suppressor protein PP2A inhibits KRAS-driven tumor growth. <i>Journal of Clinical Investigation</i> , <b>2017</b> , 127, 2081-2090	15.9	106
163	Sox2 in the dermal papilla niche controls hair growth by fine-tuning BMP signaling in differentiating hair shaft progenitors. <i>Developmental Cell</i> , <b>2012</b> , 23, 981-94	10.2	105
162	The characteristic direction: a geometrical approach to identify differentially expressed genes. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 79	3.6	103
161	Expression2Kinases: mRNA profiling linked to multiple upstream regulatory layers. <i>Bioinformatics</i> , <b>2012</b> , 28, 105-11	7.2	103
160	Systems pharmacology of arrhythmias. <i>Science Signaling</i> , <b>2010</b> , 3, ra30	8.8	102
159	Signaling Networks among Stem Cell Precursors, Transit-Amplifying Progenitors, and their Niche in Developing Hair Follicles. <i>Cell Reports</i> , <b>2016</b> , 14, 3001-18	10.6	98
158	BioJupies: Automated Generation of Interactive Notebooks for RNA-Seq Data Analysis in the Cloud. <i>Cell Systems</i> , <b>2018</b> , 7, 556-561.e3	10.6	98
157	Clustergrammer, a web-based heatmap visualization and analysis tool for high-dimensional biological data. <i>Scientific Data</i> , <b>2017</b> , 4, 170151	8.2	96
156	Drug-induced adverse events prediction with the LINCS L1000 data. <i>Bioinformatics</i> , <b>2016</b> , 32, 2338-45	7.2	95
155	Histone H3.3 and its proteolytically processed form drive a cellular senescence programme. <i>Nature Communications</i> , <b>2014</b> , 5, 5210	17.4	89
154	DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. <i>Molecular Autism</i> , <b>2014</b> , 5, 22	6.5	89
153	Regulatory consequences of neuronal ELAV-like protein binding to coding and non-coding RNAs in human brain. <i>ELife</i> , <b>2016</b> , 5,	8.9	86
152	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> , <b>2018</b> , 46, D558-D566	20.1	84
151	Network analysis of FDA approved drugs and their targets. <i>Mount Sinai Journal of Medicine</i> , <b>2007</b> , 74, 27-32		81
150	Introduction to network analysis in systems biology. <i>Science Signaling</i> , <b>2011</b> , 4, tr5	8.8	79

149	Kruppel-like factor 15 (KLF15) is a key regulator of podocyte differentiation. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 19122-35	5.4	73
148	Toward predictive models of mammalian cells. <i>Annual Review of Biophysics and Biomolecular Structure</i> , <b>2005</b> , 34, 319-49		69
147	Lean Big Data integration in systems biology and systems pharmacology. <i>Trends in Pharmacological Sciences</i> , <b>2014</b> , 35, 450-60	13.2	67
146	L1000FWD: fireworks visualization of drug-induced transcriptomic signatures. <i>Bioinformatics</i> , <b>2018</b> , 34, 2150-2152	7.2	66
145	Construction and validation of a regulatory network for pluripotency and self-renewal of mouse embryonic stem cells. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003777	5	64
144	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> , <b>2013</b> , 2013, bat045	5	62
143	Systems biology of kidney diseases. <i>Kidney International</i> , <b>2012</b> , 81, 22-39	9.9	60
142	Receptor heteromerization expands the repertoire of cannabinoid signaling in rodent neurons. <i>PLoS ONE</i> , <b>2012</b> , 7, e29239	3.7	59
141	Pathways of Toxicity. <i>ALTEX: Alternatives To Animal Experimentation</i> , <b>2014</b> , 31, 53-61	4.3	59
140	eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, W171-W179	20.1	58
139	Insights into the organization of biochemical regulatory networks using graph theory analyses. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 5451-5	5.4	56
138	LINCS Data Portal 2.0: next generation access point for perturbation-response signatures. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D431-D439	20.1	54
137	SIRT6 haploinsufficiency induces BRAF melanoma cell resistance to MAPK inhibitors via IGF signalling. <i>Nature Communications</i> , <b>2018</b> , 9, 3440	17.4	51
136	Kruppel-like factor 6 regulates mitochondrial function in the kidney. <i>Journal of Clinical Investigation</i> , <b>2015</b> , 125, 1347-61	15.9	50
135	Kruppel-Like Factor 15 Mediates Glucocorticoid-Induced Restoration of Podocyte Differentiation Markers. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2017</b> , 28, 166-184	12.7	48
134	Systematic analyses of drugs and disease indications in RepurposeDB reveal pharmacological, biological and epidemiological factors influencing drug repositioning. <i>Briefings in Bioinformatics</i> , <b>2018</b> , 19, 656-678	13.4	48
133	Habenular TCF7L2 links nicotine addiction to diabetes. <i>Nature</i> , <b>2019</b> , 574, 372-377	50.4	47
132	A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. <i>Cell Systems</i> , <b>2019</b> , 9, 35-48.e5	10.6	46

131	Interconnected network motifs control podocyte morphology and kidney function. <i>Science Signaling</i> , <b>2014</b> , 7, ra12	8.8	44
130	Dermal Condensate Niche Fate Specification Occurs Prior to Formation and Is Placode Progenitor Dependent. <i>Developmental Cell</i> , <b>2019</b> , 48, 32-48.e5	10.2	44
129	Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. <i>Nature Cell Biology</i> , <b>2019</b> , 21, 560-567	23.4	43
128	Expression of HIV transgene aggravates kidney injury in diabetic mice. <i>Kidney International</i> , <b>2013</b> , 83, 626-34	9.9	43
127	Flotillin-mediated endocytic events dictate cell type-specific responses to semaphorin 3A. <i>Journal of Neuroscience</i> , <b>2010</b> , 30, 15317-29	6.6	43
126	Systems approach to explore components and interactions in the presynapse. <i>Proteomics</i> , <b>2009</b> , 9, 3303-15	4.5	43
125	Chronic morphine alters the presynaptic protein profile: identification of novel molecular targets using proteomics and network analysis. <i>PLoS ONE</i> , <b>2011</b> , 6, e25535	3.7	42
124	Renoprotective effect of combined inhibition of angiotensin-converting enzyme and histone deacetylase. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2013</b> , 24, 801-11	12.7	41
123	GEO2Enrichr: browser extension and server app to extract gene sets from GEO and analyze them for biological functions. <i>Bioinformatics</i> , <b>2015</b> , 31, 3060-2	7.2	40
122	Ordered cyclic motifs contribute to dynamic stability in biological and engineered networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 19235-40	11.5	40
121	A Systems Approach Identifies Essential FOXO3 Functions at Key Steps of Terminal Erythropoiesis. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005526	6	40
120	Dermal sheath contraction powers stem cell niche relocation during hair cycle regression. <i>Science</i> , <b>2020</b> , 367, 161-166	33.3	39
119	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. <i>Nature Communications</i> , <b>2017</b> , 8, 1186	17.4	38
118	The Signaling Pathways Project, an integrated 'omics knowledgebase for mammalian cellular signaling pathways. <i>Scientific Data</i> , <b>2019</b> , 6, 252	8.2	38
117	The COVID-19 Drug and Gene Set Library. <i>Patterns</i> , <b>2020</b> , 1, 100090	5.1	36
116	Retinoic acid utilizes CREB and USF1 in a transcriptional feed-forward loop in order to stimulate MKP1 expression in human immunodeficiency virus-infected podocytes. <i>Molecular and Cellular Biology</i> , <b>2008</b> , 28, 5785-94	4.8	35
115	Lists2Networks: integrated analysis of gene/protein lists. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 87	3.6	34
114	Predicting opioid dependence from electronic health records with machine learning. <i>BioData Mining</i> , <b>2019</b> , 12, 3	4.3	33

113	Network2Canvas: network visualization on a canvas with enrichment analysis. <i>Bioinformatics</i> , <b>2013</b> , 29, 1872-8	7.2	32
112	Complex systems biology. <i>Journal of the Royal Society Interface</i> , <b>2017</b> , 14,	4.1	32
111	Network integration and graph analysis in mammalian molecular systems biology. <i>IET Systems Biology</i> , <b>2008</b> , 2, 206-21	1.4	31
110	Integrative Analysis of Sex-Specific microRNA Networks Following Stress in Mouse Nucleus Accumbens. <i>Frontiers in Molecular Neuroscience</i> , <b>2016</b> , 9, 144	6.1	31
109	Mining data and metadata from the gene expression omnibus. <i>Biophysical Reviews</i> , <b>2019</b> , 11, 103-110	3.7	30
108	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> , <b>2014</b> , 111, 3122-7	11.5	29
107	Integration of protein phosphorylation, acetylation, and methylation data sets to outline lung cancer signaling networks. <i>Science Signaling</i> , <b>2018</b> , 11,	8.8	29
106	ELK1 transcription factor linked to dysregulated striatal mu opioid receptor signaling network and OPRM1 polymorphism in human heroin abusers. <i>Biological Psychiatry</i> , <b>2013</b> , 74, 511-9	7.9	27
105	Introduction to statistical methods to analyze large data sets: principal components analysis. <i>Science Signaling</i> , <b>2011</b> , 4, tr3	8.8	27
104	Functions of bifans in context of multiple regulatory motifs in signaling networks. <i>Biophysical Journal</i> , <b>2008</b> , 94, 2566-79	2.9	27
103	Geneshot: search engine for ranking genes from arbitrary text queries. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, W571-W577	20.1	26
102	Glucocorticoid receptor isoforms direct distinct mitochondrial programs to regulate ATP production. <i>Scientific Reports</i> , <b>2016</b> , 6, 26419	4.9	26
101	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> , <b>2012</b> , 160C, 130-42	3.1	25
100	GATE: software for the analysis and visualization of high-dimensional time series expression data. <i>Bioinformatics</i> , <b>2010</b> , 26, 143-4	7.2	25
99	Neuro2A differentiation by Galphai/o pathway. <i>Science Signaling</i> , <b>2009</b> , 2, cm1	8.8	25
98	AVIS: AJAX viewer of interactive signaling networks. <i>Bioinformatics</i> , <b>2007</b> , 23, 2803-5	7.2	25
97	Direct activation of PP2A for the treatment of tyrosine kinase inhibitor-resistant lung adenocarcinoma. <i>JCI Insight</i> , <b>2019</b> , 4,	9.9	25
96	Integration of pan-cancer transcriptomics with RPPA proteomics reveals mechanisms of epithelial-mesenchymal transition. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005911	5	23



95	Connectivity Mapping: Methods and Applications. <i>Annual Review of Biomedical Data Science</i> , <b>2019</b> , 2, 69-92	5.6	23
94	Genes2FANs: connecting genes through functional association networks. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 156	3.6	23
93	SNAVI: Desktop application for analysis and visualization of large-scale signaling networks. <i>BMC Systems Biology</i> , <b>2009</b> , 3, 10	3.5	23
92	Toward stem cell systems biology: from molecules to networks and landscapes. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , <b>2008</b> , 73, 211-5	3.9	23
91	An open RNA-Seq data analysis pipeline tutorial with an example of reprocessing data from a recent Zika virus study. <i>F1000Research</i> , <b>2016</b> , 5, 1574	3.6	23
90	modEnrichr: a suite of gene set enrichment analysis tools for model organisms. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, W183-W190	20.1	22
89	Introduction to statistical methods for analyzing large data sets: gene-set enrichment analysis. <i>Science Signaling</i> , <b>2011</b> , 4, tr4	8.8	22
88	Proximity of intracellular regulatory networks to monotone systems. <i>IET Systems Biology</i> , <b>2008</b> , 2, 103-114	11.4	22
87	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> , <b>2017</b> , 71, 49-57	10.2	21
86	Genes2WordCloud: a quick way to identify biological themes from gene lists and free text. <i>Source Code for Biology and Medicine</i> , <b>2011</b> , 6, 15	1.9	21
85	Connecting omics signatures of diseases, drugs, and mechanisms of actions with iLINCS		21
84	Transcriptomic analysis uncovers novel synergistic mechanisms in combination therapy for lupus nephritis. <i>Kidney International</i> , <b>2018</b> , 93, 416-429	9.9	21
83	Cooperative Transcription Factor Induction Mediates Hemogenic Reprogramming. <i>Cell Reports</i> , <b>2018</b> , 25, 2821-2835.e7	10.6	21
82	Predicting age by mining electronic medical records with deep learning characterizes differences between chronological and physiological age. <i>Journal of Biomedical Informatics</i> , <b>2017</b> , 76, 59-68	10.2	20
81	Toward a complete in silico, multi-layered embryonic stem cell regulatory network. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , <b>2010</b> , 2, 708-33	6.6	20
80	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> , <b>2018</b> , 120, 631-640.e11	3.2	19
79	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> , <b>2018</b> , 29, 2529-2545	12.7	19
78	Multiple kinases and system robustness: a link between Cdc37 and genome integrity. <i>Cell Cycle</i> , <b>2007</b> , 6, 3145-7	4.7	17



77	FAIRshake: Toolkit to Evaluate the FAIRness of Research Digital Resources. <i>Cell Systems</i> , <b>2019</b> , 9, 417-421	10.6	17
76	SVM classifier to predict genes important for self-renewal and pluripotency of mouse embryonic stem cells. <i>BMC Systems Biology</i> , <b>2010</b> , 4, 173	3.5	16
75	Activation of alternate prosurvival pathways accounts for acquired sunitinib resistance in U87MG glioma xenografts. <i>Journal of Pharmacology and Experimental Therapeutics</i> , <b>2012</b> , 343, 509-19	4.7	15
74	Modulating the transcriptional landscape of SARS-CoV-2 as an effective method for developing antiviral compounds		15
73	Drug Gene Budger (DGB): an application for ranking drugs to modulate a specific gene based on transcriptomic signatures. <i>Bioinformatics</i> , <b>2019</b> , 35, 1247-1248	7.2	15
72	Sustainable data and metadata management at the BD2K-LINCS Data Coordination and Integration Center. <i>Scientific Data</i> , <b>2018</b> , 5, 180117	8.2	15
71	Sets2Networks: network inference from repeated observations of sets. <i>BMC Systems Biology</i> , <b>2012</b> , 6, 89	3.5	14
70	From components to regulatory motifs in signalling networks. <i>Briefings in Functional Genomics &amp; Proteomics</i> , <b>2006</b> , 5, 57-61		14
69	Dynamics of the discovery process of protein-protein interactions from low content studies. <i>BMC Systems Biology</i> , <b>2015</b> , 9, 26	3.5	13
68	GEN3VA: aggregation and analysis of gene expression signatures from related studies. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 461	3.6	13
67	Transforming growth factor $\beta$ signaling controls activities of human intestinal CD8(+)T suppressor cells. <i>Gastroenterology</i> , <b>2013</b> , 144, 601-612.e1	13.3	13
66	Proteomics analysis of the non-muscle myosin heavy chain IIA-enriched actin-myosin complex reveals multiple functions within the podocyte. <i>PLoS ONE</i> , <b>2014</b> , 9, e100660	3.7	13
65	Metasignatures identify two major subtypes of breast cancer. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , <b>2013</b> , 2, e35	4.5	13
64	Recovering protein-protein and domain-domain interactions from aggregation of IP-MS proteomics of coregulator complexes. <i>PLoS Computational Biology</i> , <b>2011</b> , 7, e1002319	5	13
63	Integrative radiogenomic analysis for multicentric radiophenotype in glioblastoma. <i>Oncotarget</i> , <b>2016</b> , 7, 11526-38	3.3	13
62	Appyters: Turning Jupyter Notebooks into data-driven web apps. <i>Patterns</i> , <b>2021</b> , 2, 100213	5.1	13
61	Microdynamics and criticality of adaptive regulatory networks. <i>Physical Review Letters</i> , <b>2010</b> , 104, 168704	7.4	12
60	Cell-specific prediction and application of drug-induced gene expression profiles. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2018</b> , 23, 32-43	1.3	11

59	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> , <b>2020</b> , 68, 2148-2166	9	10
58	The cognitive phenotype of Down syndrome: insights from intracellular network analysis. <i>NeuroRx</i> , <b>2006</b> , 3, 396-406		10
57	Far away from the lamppost. <i>PLoS Biology</i> , <b>2018</b> , 16, e3000067	9.7	10
56	Temporal proteomic profiling of postnatal human cortical development. <i>Translational Psychiatry</i> , <b>2018</b> , 8, 267	8.6	10
55	Morphine Regulated Synaptic Networks Revealed by Integrated Proteomics and Network Analysis. <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 2564-76	7.6	9
54	Reprint of "Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction". <i>Computational Biology and Chemistry</i> , <b>2015</b> , 59 Pt B, 123-38	3.6	9
53	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, W85-W93	20.1	9
52	Chemokine Signatures of Pathogen-Specific T Cells I: Effector T Cells. <i>Journal of Immunology</i> , <b>2020</b> , 205, 2169-2187	5.3	9
51	KEA3: improved kinase enrichment analysis via data integration. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, W304-W316	13.1	9
50	Principal Angle Enrichment Analysis (PAEA): Dimensionally Reduced Multivariate Gene Set Enrichment Analysis Tool <b>2015</b> , 2015, 256-262	0.8	8
49	Datasets2Tools, repository and search engine for bioinformatics datasets, tools and canned analyses. <i>Scientific Data</i> , <b>2018</b> , 5, 180023	8.2	7
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