

Avi Ma'ayan

List of Publications by Year in descending order

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Version: 2024-02-01

211
papers

40,238
citations

13068

68
h-index

3476

182
g-index

236
all docs

236
docs citations

236
times ranked

59969
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, W90-W97. | 6.5 | 7,240 |
| 2 | Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. <i>BMC Bioinformatics</i> , 2013, 14, 128. | 1.2 | 5,305 |
| 3 | Mesenchymal and haematopoietic stem cells form a unique bone marrow niche. <i>Nature</i> , 2010, 466, 829-834. | 13.7 | 2,935 |
| 4 | Synaptic, transcriptional and chromatin genes disrupted in autism. <i>Nature</i> , 2014, 515, 209-215. | 13.7 | 2,254 |
| 5 | Gene-expression profiles and transcriptional regulatory pathways that underlie the identity and diversity of mouse tissue macrophages. <i>Nature Immunology</i> , 2012, 13, 1118-1128. | 7.0 | 1,731 |
| 6 | Patterns and rates of exonic de novo mutations in autism spectrum disorders. <i>Nature</i> , 2012, 485, 242-245. | 13.7 | 1,597 |
| 7 | Gene Set Knowledge Discovery with Enrichr. <i>Current Protocols</i> , 2021, 1, e90. | 1.3 | 1,464 |
| 8 | 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, baw100. | 1.4 | 1,085 |
| 9 | Functional atlas of the integrin adhesome. <i>Nature Cell Biology</i> , 2007, 9, 858-867. | 4.6 | 1,033 |
| 10 | ChEA: transcription factor regulation inferred from integrating genome-wide CHIP-X experiments. <i>Bioinformatics</i> , 2010, 26, 2438-2444. | 1.8 | 822 |
| 11 | Minimal Differentiation of Classical Monocytes as They Survey Steady-State Tissues and Transport Antigen to Lymph Nodes. <i>Immunity</i> , 2013, 39, 599-610. | 6.6 | 656 |
| 12 | Single-cell immune landscape of human atherosclerotic plaques. <i>Nature Medicine</i> , 2019, 25, 1576-1588. | 15.2 | 540 |
| 13 | ChEA3: transcription factor enrichment analysis by orthogonal omics integration. <i>Nucleic Acids Research</i> , 2019, 47, W212-W224. | 6.5 | 512 |
| 14 | Massive mining of publicly available RNA-seq data from human and mouse. <i>Nature Communications</i> , 2018, 9, 1366. | 5.8 | 507 |
| 15 | Mutation of SHOC2 promotes aberrant protein N-myristoylation and causes Noonan-like syndrome with loose anagen hair. <i>Nature Genetics</i> , 2009, 41, 1022-1026. | 9.4 | 358 |
| 16 | Differential cytokine contributions of perivascular haematopoietic stem cell niches. <i>Nature Cell Biology</i> , 2017, 19, 214-223. | 4.6 | 332 |
| 17 | Systems biology of stem cell fate and cellular reprogramming. <i>Nature Reviews Molecular Cell Biology</i> , 2009, 10, 672-681. | 16.1 | 330 |
| 18 | Formation of Regulatory Patterns During Signal Propagation in a Mammalian Cellular Network. <i>Science</i> , 2005, 309, 1078-1083. | 6.0 | 329 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | 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. | 2.9 | 327 |
| 20 | LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. <i>Nucleic Acids Research</i> , 2014, 42, W449-W460. | 6.5 | 280 |
| 21 | Systems-level dynamic analyses of fate change in murine embryonic stem cells. <i>Nature</i> , 2009, 462, 358-362. | 13.7 | 277 |
| 22 | Pharos: Collating protein information to shed light on the druggable genome. <i>Nucleic Acids Research</i> , 2017, 45, D995-D1002. | 6.5 | 271 |
| 23 | Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 317-332. | 21.5 | 263 |
| 24 | L1000CDS2: LINCS L1000 characteristic direction signatures search engine. <i>Npj Systems Biology and Applications</i> , 2016, 2, . | 1.4 | 250 |
| 25 | BioJupies: Automated Generation of Interactive Notebooks for RNA-Seq Data Analysis in the Cloud. <i>Cell Systems</i> , 2018, 7, 556-561.e3. | 2.9 | 217 |
| 26 | Extraction and analysis of signatures from the Gene Expression Omnibus by the crowd. <i>Nature Communications</i> , 2016, 7, 12846. | 5.8 | 204 |
| 27 | An Integrated Transcriptome Atlas of Embryonic Hair Follicle Progenitors, Their Niche, and the Developing Skin. <i>Developmental Cell</i> , 2015, 34, 577-591. | 3.1 | 197 |
| 28 | KEA: kinase enrichment analysis. <i>Bioinformatics</i> , 2009, 25, 684-686. | 1.8 | 196 |
| 29 | Induction of a Hemogenic Program in Mouse Fibroblasts. <i>Cell Stem Cell</i> , 2013, 13, 205-218. | 5.2 | 195 |
| 30 | Fetal liver hematopoietic stem cell niches associate with portal vessels. <i>Science</i> , 2016, 351, 176-180. | 6.0 | 193 |
| 31 | Global phosphorylation analysis of β -arrestin ¹ -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, 15299-15304. | 3.3 | 182 |
| 32 | Polycomb repressive complex 2 (PRC2) silences genes responsible for neurodegeneration. <i>Nature Neuroscience</i> , 2016, 19, 1321-1330. | 7.1 | 178 |
| 33 | Clustergrammer, a web-based heatmap visualization and analysis tool for high-dimensional biological data. <i>Scientific Data</i> , 2017, 4, 170151. | 2.4 | 176 |
| 34 | Signaling Networks among Stem Cell Precursors, Transit-Amplifying Progenitors, and their Niche in Developing Hair Follicles. <i>Cell Reports</i> , 2016, 14, 3001-3018. | 2.9 | 160 |
| 35 | Drug-induced adverse events prediction with the LINCS L1000 data. <i>Bioinformatics</i> , 2016, 32, 2338-2345. | 1.8 | 155 |
| 36 | Activation of tumor suppressor protein PP2A inhibits KRAS-driven tumor growth. <i>Journal of Clinical Investigation</i> , 2017, 127, 2081-2090. | 3.9 | 155 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | Oct4 links multiple epigenetic pathways to the pluripotency network. <i>Cell Research</i> , 2012, 22, 155-167. | 5.7 | 149 |
| 38 | The characteristic direction: a geometrical approach to identify differentially expressed genes. <i>BMC Bioinformatics</i> , 2014, 15, 79. | 1.2 | 148 |
| 39 | Design Logic of a Cannabinoid Receptor Signaling Network That Triggers Neurite Outgrowth. <i>Science</i> , 2008, 320, 903-909. | 6.0 | 143 |
| 40 | 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. | 6.5 | 143 |
| 41 | Regulation of Embryonic and Induced Pluripotency by Aurora Kinase-p53 Signaling. <i>Cell Stem Cell</i> , 2012, 11, 179-194. | 5.2 | 142 |
| 42 | Nanog-dependent feedback loops regulate murine embryonic stem cell heterogeneity. <i>Nature Cell Biology</i> , 2012, 14, 1139-1147. | 4.6 | 141 |
| 43 | Expression2Kinases: mRNA profiling linked to multiple upstream regulatory layers. <i>Bioinformatics</i> , 2012, 28, 105-111. | 1.8 | 137 |
| 44 | 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, 607-619. | 2.6 | 136 |
| 45 | A systems approach identifies HIPK2 as a key regulator of kidney fibrosis. <i>Nature Medicine</i> , 2012, 18, 580-588. | 15.2 | 131 |
| 46 | Genes2Networks: connecting lists of gene symbols using mammalian protein interactions databases. <i>BMC Bioinformatics</i> , 2007, 8, 372. | 1.2 | 130 |
| 47 | Regulatory consequences of neuronal ELAV-like protein binding to coding and non-coding RNAs in human brain. <i>ELife</i> , 2016, 5, . | 2.8 | 128 |
| 48 | 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, 981-994. | 3.1 | 127 |
| 49 | eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks. <i>Nucleic Acids Research</i> , 2018, 46, W171-W179. | 6.5 | 127 |
| 50 | Histone H3.3 and its proteolytically processed form drive a cellular senescence programme. <i>Nature Communications</i> , 2014, 5, 5210. | 5.8 | 119 |
| 51 | Systems Pharmacology of Arrhythmias. <i>Science Signaling</i> , 2010, 3, ra30. | 1.6 | 118 |
| 52 | LINCS Data Portal 2.0: next generation access point for perturbation-response signatures. <i>Nucleic Acids Research</i> , 2020, 48, D431-D439. | 6.5 | 112 |
| 53 | DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. <i>Molecular Autism</i> , 2014, 5, 22. | 2.6 | 111 |
| 54 | L1000FWD: fireworks visualization of drug-induced transcriptomic signatures. <i>Bioinformatics</i> , 2018, 34, 2150-2152. | 1.8 | 109 |

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|----|--|------|-----------|
| 55 | Network analysis of FDA approved drugs and their targets. Mount Sinai Journal of Medicine, 2007, 74, 27-32. | 1.9 | 108 |
| 56 | Introduction to Network Analysis in Systems Biology. Science Signaling, 2011, 4, tr5. | 1.6 | 108 |
| 57 | A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. Cell Systems, 2019, 9, 35-48.e5. | 2.9 | 95 |
| 58 | Dermal Condensate Niche Fate Specification Occurs Prior to Formation and Is Placode Progenitor Dependent. Developmental Cell, 2019, 48, 32-48.e5. | 3.1 | 91 |
| 59 | ESCAPE: database for integrating high-content published data collected from human and mouse embryonic stem cells. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat045. | 1.4 | 88 |
| 60 | Construction and Validation of a Regulatory Network for Pluripotency and Self-Renewal of Mouse Embryonic Stem Cells. PLoS Computational Biology, 2014, 10, e1003777. | 1.5 | 88 |
| 61 | Krüppel-like Factor 15 (KLF15) Is a Key Regulator of Podocyte Differentiation. Journal of Biological Chemistry, 2012, 287, 19122-19135. | 1.6 | 87 |
| 62 | Toward Predictive Models of Mammalian Cells. Annual Review of Biophysics and Biomolecular Structure, 2005, 34, 319-349. | 18.3 | 85 |
| 63 | Lean Big Data integration in systems biology and systems pharmacology. Trends in Pharmacological Sciences, 2014, 35, 450-460. | 4.0 | 85 |
| 64 | The Signaling Pathways Project, an integrated omics knowledgebase for mammalian cellular signaling pathways. Scientific Data, 2019, 6, 252. | 2.4 | 82 |
| 65 | Systematic analyses of drugs and disease indications in RepurposeDB reveal pharmacological, biological and epidemiological factors influencing drug repositioning. Briefings in Bioinformatics, 2018, 19, 656-678. | 3.2 | 81 |
| 66 | Habenular TCF7L2 links nicotine addiction to diabetes. Nature, 2019, 574, 372-377. | 13.7 | 81 |
| 67 | SIRT6 haploinsufficiency induces BRAFV600E melanoma cell resistance to MAPK inhibitors via IGF signalling. Nature Communications, 2018, 9, 3440. | 5.8 | 80 |
| 68 | Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. Nature Communications, 2017, 8, 1186. | 5.8 | 78 |
| 69 | Dermal sheath contraction powers stem cell niche relocation during hair cycle regression. Science, 2020, 367, 161-166. | 6.0 | 77 |
| 70 | Pathways of Toxicity. ALTEX: Alternatives To Animal Experimentation, 2014, 31, 53-61. | 0.9 | 75 |
| 71 | Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. Nature Cell Biology, 2019, 21, 560-567. | 4.6 | 74 |
| 72 | Systems biology of kidney diseases. Kidney International, 2012, 81, 22-39. | 2.6 | 72 |

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|----|---|-----|-----------|
| 73 | Insights into the Organization of Biochemical Regulatory Networks Using Graph Theory Analyses. <i>Journal of Biological Chemistry</i> , 2009, 284, 5451-5455. | 1.6 | 71 |
| 74 | Receptor Heteromerization Expands the Repertoire of Cannabinoid Signaling in Rodent Neurons. <i>PLoS ONE</i> , 2012, 7, e29239. | 1.1 | 69 |
| 75 | Mining data and metadata from the gene expression omnibus. <i>Biophysical Reviews</i> , 2019, 11, 103-110. | 1.5 | 67 |
| 76 | Predicting opioid dependence from electronic health records with machine learning. <i>BioData Mining</i> , 2019, 12, 3. | 2.2 | 65 |
| 77 | Krüppel-like factor 6 regulates mitochondrial function in the kidney. <i>Journal of Clinical Investigation</i> , 2015, 125, 1347-1361. | 3.9 | 65 |
| 78 | Complex systems biology. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20170391. | 1.5 | 64 |
| 79 | modEnrichr: a suite of gene set enrichment analysis tools for model organisms. <i>Nucleic Acids Research</i> , 2019, 47, W183-W190. | 6.5 | 62 |
| 80 | The COVID-19 Drug and Gene Set Library. <i>Patterns</i> , 2020, 1, 100090. | 3.1 | 61 |
| 81 | Appyters: Turning Jupyter Notebooks into data-driven web apps. <i>Patterns</i> , 2021, 2, 100213. | 3.1 | 58 |
| 82 | 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. | 3.0 | 57 |
| 83 | Geneshot: search engine for ranking genes from arbitrary text queries. <i>Nucleic Acids Research</i> , 2019, 47, W571-W577. | 6.5 | 57 |
| 84 | KEA3: improved kinase enrichment analysis via data integration. <i>Nucleic Acids Research</i> , 2021, 49, W304-W316. | 6.5 | 55 |
| 85 | Recent Progress in Lyme Disease and Remaining Challenges. <i>Frontiers in Medicine</i> , 2021, 8, 666554. | 1.2 | 55 |
| 86 | A Systems Approach Identifies Essential FOXO3 Functions at Key Steps of Terminal Erythropoiesis. <i>PLoS Genetics</i> , 2015, 11, e1005526. | 1.5 | 55 |
| 87 | DrugShot: querying biomedical search terms to retrieve prioritized lists of small molecules. <i>BMC Bioinformatics</i> , 2022, 23, 76. | 1.2 | 55 |
| 88 | Expression of HIV transgene aggravates kidney injury in diabetic mice. <i>Kidney International</i> , 2013, 83, 626-634. | 2.6 | 53 |
| 89 | Interconnected Network Motifs Control Podocyte Morphology and Kidney Function. <i>Science Signaling</i> , 2014, 7, ra12. | 1.6 | 53 |
| 90 | Chronic Morphine Alters the Presynaptic Protein Profile: Identification of Novel Molecular Targets Using Proteomics and Network Analysis. <i>PLoS ONE</i> , 2011, 6, e25535. | 1.1 | 51 |

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| 91 | GEO2Enrich: browser extension and server app to extract gene sets from GEO and analyze them for biological functions. <i>Bioinformatics</i> , 2015, 31, 3060-3062. | 1.8 | 50 |
| 92 | Systems approach to explore components and interactions in the presynapse. <i>Proteomics</i> , 2009, 9, 3303-3315. | 1.3 | 47 |
| 93 | Flotillin-Mediated Endocytic Events Dictate Cell Type-Specific Responses to Semaphorin 3A. <i>Journal of Neuroscience</i> , 2010, 30, 15317-15329. | 1.7 | 47 |
| 94 | 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> , 2008, 105, 19235-19240. | 3.3 | 46 |
| 95 | Renoprotective Effect of Combined Inhibition of Angiotensin-Converting Enzyme and Histone Deacetylase. <i>Journal of the American Society of Nephrology: JASN</i> , 2013, 24, 801-811. | 3.0 | 46 |
| 96 | 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> , 2008, 28, 5785-5794. | 1.1 | 45 |
| 97 | B- <i>myb</i> 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, 3122-3127. | 3.3 | 44 |
| 98 | Direct activation of PP2A for the treatment of tyrosine kinase inhibitor-resistant lung adenocarcinoma. <i>JCI Insight</i> , 2019, 4, . | 2.3 | 43 |
| 99 | Network integration and graph analysis in mammalian molecular systems biology. <i>IET Systems Biology</i> , 2008, 2, 206-221. | 0.8 | 42 |
| 100 | Introduction to Statistical Methods to Analyze Large Data Sets: Principal Components Analysis. <i>Science Signaling</i> , 2011, 4, tr3. | 1.6 | 40 |
| 101 | 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, 511-519. | 0.7 | 40 |
| 102 | Integration of protein phosphorylation, acetylation, and methylation data sets to outline lung cancer signaling networks. <i>Science Signaling</i> , 2018, 11, . | 1.6 | 40 |
| 103 | Connectivity Mapping: Methods and Applications. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 69-92. | 2.8 | 39 |
| 104 | Lists2Networks: Integrated analysis of gene/protein lists. <i>BMC Bioinformatics</i> , 2010, 11, 87. | 1.2 | 38 |
| 105 | Glucocorticoid receptor isoforms direct distinct mitochondrial programs to regulate ATP production. <i>Scientific Reports</i> , 2016, 6, 26419. | 1.6 | 38 |
| 106 | Functions of Bifans in Context of Multiple Regulatory Motifs in Signaling Networks. <i>Biophysical Journal</i> , 2008, 94, 2566-2579. | 0.2 | 37 |
| 107 | Proximity of intracellular regulatory networks to monotone systems. <i>IET Systems Biology</i> , 2008, 2, 103. | 0.8 | 35 |
| 108 | Integrative Analysis of Sex-Specific microRNA Networks Following Stress in Mouse Nucleus Accumbens. <i>Frontiers in Molecular Neuroscience</i> , 2016, 9, 144. | 1.4 | 35 |

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|-----|--|-----|-----------|
| 109 | Network2Canvas: network visualization on a canvas with enrichment analysis. <i>Bioinformatics</i> , 2013, 29, 1872-1878. | 1.8 | 34 |
| 110 | Kr γ 4ppl-like factor 6 α -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, . | 3.3 | 34 |
| 111 | Integration of pan-cancer transcriptomics with RPPA proteomics reveals mechanisms of epithelial-mesenchymal transition. <i>PLoS Computational Biology</i> , 2018, 14, e1005911. | 1.5 | 33 |
| 112 | FAIRshake: Toolkit to Evaluate the FAIRness of Research Digital Resources. <i>Cell Systems</i> , 2019, 9, 417-421. | 2.9 | 33 |
| 113 | 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, 130-142. | 0.7 | 32 |
| 114 | Podocyte-Specific Induction of Kr γ 4ppl-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. | 3.0 | 32 |
| 115 | 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. | 0.8 | 30 |
| 116 | Chemokine Signatures of Pathogen-Specific T Cells I: Effector T Cells. <i>Journal of Immunology</i> , 2020, 205, 2169-2187. | 0.4 | 30 |
| 117 | Neuro2A Differentiation by G β Pathway. <i>Science Signaling</i> , 2009, 2, cm1. | 1.6 | 29 |
| 118 | GATE: software for the analysis and visualization of high-dimensional time series expression data. <i>Bioinformatics</i> , 2010, 26, 143-144. | 1.8 | 29 |
| 119 | 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. | 1.8 | 29 |
| 120 | Toward Stem Cell Systems Biology: From Molecules to Networks and Landscapes. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2008, 73, 211-215. | 2.0 | 28 |
| 121 | SNAVI: Desktop application for analysis and visualization of large-scale signaling networks. <i>BMC Systems Biology</i> , 2009, 3, 10. | 3.0 | 28 |
| 122 | Genes2FANs: connecting genes through functional association networks. <i>BMC Bioinformatics</i> , 2012, 13, 156. | 1.2 | 28 |
| 123 | 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. | 2.5 | 28 |
| 124 | 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. | 2.5 | 28 |
| 125 | Loss of proximal tubular transcription factor Kr γ 4ppl-like factor 15 exacerbates kidney injury through loss of fatty acid oxidation. <i>Kidney International</i> , 2021, 100, 1250-1267. | 2.6 | 28 |
| 126 | AVIS: AJAX viewer of interactive signaling networks. <i>Bioinformatics</i> , 2007, 23, 2803-2805. | 1.8 | 27 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 127 | Cooperative Transcription Factor Induction Mediates Hemogenic Reprogramming. <i>Cell Reports</i> , 2018, 25, 2821-2835.e7. | 2.9 | 27 |
| 128 | Effect of short-term liver X receptor activation on epidermal barrier features in mild to moderate atopic dermatitis. <i>Annals of Allergy, Asthma and Immunology</i> , 2018, 120, 631-640.e11. | 0.5 | 26 |
| 129 | Transcriptomic analysis uncovers novel synergistic mechanisms in combination therapy for lupus nephritis. <i>Kidney International</i> , 2018, 93, 416-429. | 2.6 | 26 |
| 130 | SigCom LINCS: data and metadata search engine for a million gene expression signatures. <i>Nucleic Acids Research</i> , 2022, 50, W697-W709. | 6.5 | 26 |
| 131 | Introduction to Statistical Methods for Analyzing Large Data Sets: Gene-Set Enrichment Analysis. <i>Science Signaling</i> , 2011, 4, tr4. | 1.6 | 24 |
| 132 | Systems pharmacology meets predictive, preventive, personalized and participatory medicine. <i>Pharmacogenomics</i> , 2013, 14, 119-122. | 0.6 | 24 |
| 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. | 2.5 | 24 |
| 134 | SVM classifier to predict genes important for self-renewal and pluripotency of mouse embryonic stem cells. <i>BMC Systems Biology</i> , 2010, 4, 173. | 3.0 | 23 |
| 135 | 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. | 1.7 | 23 |
| 136 | Sustainable data and metadata management at the BD2K-LINCS Data Coordination and Integration Center. <i>Scientific Data</i> , 2018, 5, 180117. | 2.4 | 22 |
| 137 | Temporal proteomic profiling of postnatal human cortical development. <i>Translational Psychiatry</i> , 2018, 8, 267. | 2.4 | 22 |
| 138 | Toward a complete <i>in silico</i> , multi-layered embryonic stem cell regulatory network. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 708-733. | 6.6 | 21 |
| 139 | Multiple Kinases and System Robustness: A Link Between Cdc37 and Genome Integrity. <i>Cell Cycle</i> , 2007, 6, 3145-3147. | 1.3 | 20 |
| 140 | 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, . | 1.4 | 19 |
| 141 | piNET: a versatile web platform for downstream analysis and visualization of proteomics data. <i>Nucleic Acids Research</i> , 2020, 48, W85-W93. | 6.5 | 18 |
| 142 | Metasignatures Identify Two Major Subtypes of Breast Cancer. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2013, 2, 1-10. | 1.3 | 17 |
| 143 | GEN3VA: aggregation and analysis of gene expression signatures from related studies. <i>BMC Bioinformatics</i> , 2016, 17, 461. | 1.2 | 17 |
| 144 | Interoperable RNA-Seq analysis in the cloud. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194521. | 0.9 | 17 |

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|-----|---|-----|-----------|
| 145 | Recovering Protein-Protein and Domain-Domain Interactions from Aggregation of IP-MS Proteomics of Coregulator Complexes. PLoS Computational Biology, 2011, 7, e1002319. | 1.5 | 16 |
| 146 | Activation of Alternate Prosurvival Pathways Accounts for Acquired Sunitinib Resistance in U87MG Glioma Xenografts. Journal of Pharmacology and Experimental Therapeutics, 2012, 343, 509-519. | 1.3 | 16 |
| 147 | Transforming Growth Factor \hat{I}^2 Signaling Controls Activities of Human Intestinal CD8+T Suppressor Cells. Gastroenterology, 2013, 144, 601-612.e1. | 0.6 | 16 |
| 148 | Morphine Regulated Synaptic Networks Revealed by Integrated Proteomics and Network Analysis. Molecular and Cellular Proteomics, 2015, 14, 2564-2576. | 2.5 | 16 |
| 149 | From components to regulatory motifs in signalling networks. Briefings in Functional Genomics & Proteomics, 2006, 5, 57-61. | 3.8 | 15 |
| 150 | Sets2Networks: network inference from repeated observations of sets. BMC Systems Biology, 2012, 6, 89. | 3.0 | 15 |
| 151 | Systems Analysis Implicates WAVE2-Complex in the Pathogenesis of Developmental Left-Sided Obstructive Heart Defects. JACC Basic To Translational Science, 2020, 5, 376-386. | 1.9 | 15 |
| 152 | Integrative radiogenomic analysis for multicentric radiophenotype in glioblastoma. Oncotarget, 2016, 7, 11526-11538. | 0.8 | 15 |
| 153 | Cell-specific prediction and application of drug-induced gene expression profiles. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 32-43. | 0.7 | 15 |
| 154 | Proteomics Analysis of the Non-Muscle Myosin Heavy Chain Ila-Enriched Actin-Myosin Complex Reveals Multiple Functions within the Podocyte. PLoS ONE, 2014, 9, e100660. | 1.1 | 14 |
| 155 | Reprint of "Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction". Computational Biology and Chemistry, 2015, 59, 123-138. | 1.1 | 14 |
| 156 | Cell-specific prediction and application of drug-induced gene expression profiles. , 2018, , . | | 14 |
| 157 | Microdynamics and Criticality of Adaptive Regulatory Networks. Physical Review Letters, 2010, 104, 168701. | 2.9 | 13 |
| 158 | Dynamics of the discovery process of protein-protein interactions from low content studies. BMC Systems Biology, 2015, 9, 26. | 3.0 | 13 |
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