Gary D Bader

List of Publications by Citations

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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.

276	46,921	85	216
papers	citations	h-index	g-index

342	58,522	13.7	7.15
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
276	An automated method for finding molecular complexes in large protein interaction networks. *BMC Bioinformatics*, **2003**, 4, 2	3.6	3136
275	Systematic identification of protein complexes in Saccharomyces cerevisiae by mass spectrometry. *Nature*, **2002**, 415, 180-3	50.4	3069
274	The GeneMANIA prediction server: biological network integration for gene prioritization and predicting gene function. *Nucleic Acids Research*, **2010**, 38, W214-20	20.1	2164
273	Integration of biological networks and gene expression data using Cytoscape. *Nature Protocols*, **2007**, 2, 2366-82	18.8	1798
272	Global mapping of the yeast genetic interaction network. *Science*, **2004**, 303, 808-13	33.3	1700
271	Systematic genetic analysis with ordered arrays of yeast deletion mutants. *Science*, **2001**, 294, 2364-8	33.3	1676
270	The genetic landscape of a cell. *Science*, **2010**, 327, 425-31	33.3	1627
269	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
268	A draft map of the human proteome. *Nature*, **2014**, 509, 575-81	50.4	1520
267	Functional impact of global rare copy number variation in autism spectrum disorders. *Nature*, **2010**, 466, 368-72	50.4	1499
266	Enrichment map: a network-based method for gene-set enrichment visualization and interpretation. *PLoS ONE*, **2010**, 5, e13984	3.7	1264
265	A travel guide to Cytoscape plugins. *Nature Methods*, **2012**, 9, 1069-76	21.6	983
264	BIND: the Biomolecular Interaction Network Database. *Nucleic Acids Research*, **2003**, 31, 248-50	20.1	862
263	Pathway Commons, a web resource for biological pathway data. *Nucleic Acids Research*, **2011**, 39, D685-90	20.1	786
262	Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. *Cancer Cell*, **2015**, 27, 728-43	24.3	672
261	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
260	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. *Nature*, **2012**, 488, 49-56	50.4	596

259	A combined experimental and computational strategy to define protein interaction networks for peptide recognition modules. *Science*, **2002**, 295, 321-4	33.3	582
258	Cytoscape Web: an interactive web-based network browser. *Bioinformatics*, **2010**, 26, 2347-8	7.2	547
257	Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap. *Nature Protocols*, **2019**, 14, 482-517	18.8	515
256	Intertumoral Heterogeneity within Medulloblastoma Subgroups. *Cancer Cell*, **2017**, 31, 737-754.e6	24.3	511
255	The HUPO PSIQs molecular interaction format--a community standard for the representation of protein interaction data. *Nature Biotechnology*, **2004**, 22, 177-83	44.5	504
254	The BioPAX community standard for pathway data sharing. *Nature Biotechnology*, **2010**, 28, 935-42	44.5	499
253	Biological network exploration with Cytoscape 3. *Current Protocols in Bioinformatics*, **2014**, 47, 8.13.1-24	24.2	490
252	Genome sequencing of SHH medulloblastoma predicts genotype-related response to smoothened inhibition. *Cancer Cell*, **2014**, 25, 393-405	24.3	469
251	Single cell RNA sequencing of human liver reveals distinct intrahepatic macrophage populations. *Nature Communications*, **2018**, 9, 4383	17.4	452
250	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. *Nature*, **2014**, 506, 445-50	50.4	434
249	Analyzing yeast protein-protein interaction data obtained from different sources. *Nature Biotechnology*, **2002**, 20, 991-7	44.5	431
248	GeneMANIA Cytoscape plugin: fast gene function predictions on the desktop. *Bioinformatics*, **2010**, 26, 2927-8	7.2	413
247	Delineation of two clinically and molecularly distinct subgroups of posterior fossa ependymoma. *Cancer Cell*, **2011**, 20, 143-57	24.3	395
246	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. *Nature*, **2014**, 511, 428-34	50.4	377
245	Comprehensive identification of mutational cancer driver genes across 12 tumor types. *Scientific Reports*, **2013**, 3, 2650	4.9	350
244	A specificity map for the PDZ domain family. *PLoS Biology*, **2008**, 6, e239	9.7	348
243	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. *BMC Bioinformatics*, **2011**, 12, 436	3.6	337
242	NetPath: a public resource of curated signal transduction pathways. *Genome Biology*, **2010**, 11, R3	18.3	331

241	Pathguide: a pathway resource list. *Nucleic Acids Research*, **2006**, 34, D504-6	20.1	326
240	GeneMANIA update 2018. *Nucleic Acids Research*, **2018**, 46, W60-W64	20.1	309
239	GeneMANIA prediction server 2013 update. *Nucleic Acids Research*, **2013**, 41, W115-22	20.1	280
238	Tracing the origins of relapse in acute myeloid leukaemia to stem cells. *Nature*, **2017**, 547, 104-108	50.4	274
237	Too many roads not taken. *Nature*, **2011**, 470, 163-5	50.4	271
236	A reference map of the human binary protein interactome. *Nature*, **2020**, 580, 402-408	50.4	269
235	Cytoscape.js: a graph theory library for visualisation and analysis. *Bioinformatics*, **2016**, 32, 309-11	7.2	261
234	Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. *Cell*, **2016**, 164, 293-309	56.2	259
233	Single cell-derived clonal analysis of human glioblastoma links functional and genomic heterogeneity. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 851-6	11.5	251
232	Quantitative analysis of fitness and genetic interactions in yeast on a genome scale. *Nature Methods*, **2010**, 7, 1017-24	21.6	251
231	Pathway and network analysis of cancer genomes. *Nature Methods*, **2015**, 12, 615-621	21.6	235
230	The minimum information required for reporting a molecular interaction experiment (MIMIx). *Nature Biotechnology*, **2007**, 25, 894-8	44.5	229
229	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. *Nature Methods*, **2011**, 8, 528-9	21.6	227
228	Divergent clonal selection dominates medulloblastoma at recurrence. *Nature*, **2016**, 529, 351-7	50.4	206
227	Broadening the horizon--level 2.5 of the HUPO-PSI format for molecular interactions. *BMC Biology*, **2007**, 5, 44	7.3	204
226	Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. *Molecular Systems Biology*, **2013**, 9, 637	12.2	192
225	Inhibition of the Mitochondrial Protease ClpP as a Therapeutic Strategy for Human Acute Myeloid Leukemia. *Cancer Cell*, **2015**, 27, 864-76	24.3	191
224	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186

223	Quiescent sox2(+) cells drive hierarchical growth and relapse in sonic hedgehog subgroup medulloblastoma. *Cancer Cell*, **2014**, 26, 33-47	24.3	181
222	GeneMANIA: Fast gene network construction and function prediction for Cytoscape. *F1000Research*, **2014**, 3, 153	3.6	176
221	Mapping the cellular response to small molecules using chemogenomic fitness signatures. *Science*, **2014**, 344, 208-11	33.3	174
220	PreBIND and Textomy--mining the biomedical literature for protein-protein interactions using a support vector machine. *BMC Bioinformatics*, **2003**, 4, 11	3.6	174
219	Attenuation of miR-126 activity expands HSC in vivo without exhaustion. *Cell Stem Cell*, **2012**, 11, 799-811	18	164
218	BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. *Bioinformatics*, **2000**, 16, 465-77	7.2	156
217	Comparative analysis reveals conserved protein phosphorylation networks implicated in multiple diseases. *Science Signaling*, **2009**, 2, ra39	8.8	152
216	Computational prediction of protein-protein interactions. *Molecular Biotechnology*, **2008**, 38, 1-17	3	152
215	Single-cell transcriptomic profiling of the aging mouse brain. *Nature Neuroscience*, **2019**, 22, 1696-1708	25.5	152
214	A comparative transcriptomic analysis reveals conserved features of stem cell pluripotency in planarians and mammals. *Stem Cells*, **2012**, 30, 1734-45	5.8	151
213	Bayesian modeling of the yeast SH3 domain interactome predicts spatiotemporal dynamics of endocytosis proteins. *PLoS Biology*, **2009**, 7, e1000218	9.7	151
212	Functional complexes between YAP2 and ZO-2 are PDZ domain-dependent, and regulate YAP2 nuclear localization and signalling. *Biochemical Journal*, **2010**, 432, 461-72	3.8	143
211	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. *Cancer Cell*, **2016**, 30, 891-908	24.3	135
210	A predictive model for drug bioaccumulation and bioactivity in Caenorhabditis elegans. *Nature Chemical Biology*, **2010**, 6, 549-57	11.7	132
209	Computational approaches to identify functional genetic variants in cancer genomes. *Nature Methods*, **2013**, 10, 723-9	21.6	129
208	AutoAnnotate: A Cytoscape app for summarizing networks with semantic annotations. *F1000Research*, **2016**, 5, 1717	3.6	126
207	Inhibition of Dopamine Receptor D4 Impedes Autophagic Flux, Proliferation, and Survival of Glioblastoma Stem Cells. *Cancer Cell*, **2016**, 29, 859-873	24.3	124
206	Germ-line DNA copy number variation frequencies in a large North American population. *Human Genetics*, **2007**, 122, 345-53	6.3	122

205	miR-126 Regulates Distinct Self-Renewal Outcomes in Normal and Malignant Hematopoietic Stem Cells. *Cancer Cell*, **2016**, 29, 214-28	24.3	118
204	Molecular subgroups of atypical teratoid rhabdoid tumours in children: an integrated genomic and clinicopathological analysis. *Lancet Oncology, The*, **2015**, 16, 569-82	21.7	117
203	The mutational landscape of phosphorylation signaling in cancer. *Scientific Reports*, **2013**, 3, 2651	4.9	116
202	A regression framework incorporating quantitative and negative interaction data improves quantitative prediction of PDZ domain-peptide interaction from primary sequence. *Bioinformatics*, **2011**, 27, 383-90	7.2	110
201	Bringing order to protein disorder through comparative genomics and genetic interactions. *Genome Biology*, **2011**, 12, R14	18.3	105
200	Dynamic interaction networks in a hierarchically organized tissue. *Molecular Systems Biology*, **2010**, 6, 417	12.2	104
199	An improved method for scoring protein-protein interactions using semantic similarity within the gene ontology. *BMC Bioinformatics*, **2010**, 11, 562	3.6	104
198	Cytoscape app store. *Bioinformatics*, **2013**, 29, 1350-1	7.2	102
197	Functional genomics and proteomics: charting a multidimensional map of the yeast cell. *Trends in Cell Biology*, **2003**, 13, 344-56	18.3	102
196	Transfer learning for biomedical named entity recognition with neural networks. *Bioinformatics*, **2018**, 34, 4087-4094	7.2	98
195	Developmental Emergence of Adult Neural Stem Cells as Revealed by Single-Cell Transcriptional Profiling. *Cell Reports*, **2017**, 21, 3970-3986	10.6	96
194	The biology/disease-driven human proteome project (B/D-HPP): enabling protein research for the life sciences community. *Journal of Proteome Research*, **2013**, 12, 23-7	5.6	87
193	Enrichment Map - a Cytoscape app to visualize and explore OMICs pathway enrichment results. *F1000Research*, **2014**, 3, 141	3.6	87
192	Coevolution of PDZ domain-ligand interactions analyzed by high-throughput phage display and deep sequencing. *Molecular BioSystems*, **2010**, 6, 1782-90		85
191	cPath: open source software for collecting, storing, and querying biological pathways. *BMC Bioinformatics*, **2006**, 7, 497	3.6	83
190	Pathway information for systems biology. *FEBS Letters*, **2005**, 579, 1815-20	3.8	83
189	Functional genomic landscape of cancer-intrinsic evasion of killing by T cells. *Nature*, **2020**, 586, 120-126	50.4	82
188	Spatial heterogeneity in medulloblastoma. *Nature Genetics*, **2017**, 49, 780-788	36.3	80

187	Combined deletion of Pten and p53 in mammary epithelium accelerates triple-negative breast cancer with dependency on eEF2K. *EMBO Molecular Medicine*, **2014**, 6, 1542-60	12	80
186	Mapping the Hsp90 genetic interaction network in Candida albicans reveals environmental contingency and rewired circuitry. *PLoS Genetics*, **2012**, 8, e1002562	6	80
185	Positive selection of tyrosine loss in metazoan evolution. *Science*, **2009**, 325, 1686-8	33.3	80
184	ASCL1 Reorganizes Chromatin to Direct Neuronal Fate and Suppress Tumorigenicity of Glioblastoma Stem Cells. *Cell Stem Cell*, **2017**, 21, 209-224.e7	18	78
183	A Progesterone-CXCR4 Axis Controls Mammary Progenitor Cell Fate in the Adult Gland. *Stem Cell Reports*, **2015**, 4, 529	8	78
182	How to visually interpret biological data using networks. *Nature Biotechnology*, **2009**, 27, 921-4	44.5	78
181	Long read nanopore sequencing for detection of HLA and CYP2D6 variants and haplotypes. *F1000Research*, **2015**, 4, 17	3.6	75
180	Computational prediction of cancer-gene function. *Nature Reviews Cancer*, **2007**, 7, 23-34	31.3	73
179	Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. *Nature Communications*, **2015**, 6, 8554	17.4	71
178	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. *Nucleic Acids Research*, **2020**, 48, D489-D497	20.1	71
177	Musashi-2 attenuates AHR signalling to expand human haematopoietic stem cells. *Nature*, **2016**, 532, 508-511	50.4	71
176	The Biomolecular Interaction Network Database in PSI-MI 2.5. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, baq037	5	70
175	The multiple-specificity landscape of modular peptide recognition domains. *Molecular Systems Biology*, **2011**, 7, 484	12.2	67
174	DRYGIN: a database of quantitative genetic interaction networks in yeast. *Nucleic Acids Research*, **2010**, 38, D502-7	20.1	67
173	WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. *Source Code for Biology and Medicine*, **2011**, 6, 7	1.9	66
172	RB1 deficiency in triple-negative breast cancer induces mitochondrial protein translation. *Journal of Clinical Investigation*, **2016**, 126, 3739-3757	15.9	65
171	SBML Level 3: an extensible format for the exchange and reuse of biological models. *Molecular Systems Biology*, **2020**, 16, e9110	12.2	65
170	IL-7 coordinates proliferation, differentiation and Tcra recombination during thymocyte selection. *Nature Immunology*, **2015**, 16, 397-405	19.1	64

169	NetMatch: a Cytoscape plugin for searching biological networks. *Bioinformatics*, **2007**, 23, 910-2	7.2	62
168	Chromatin is an ancient innovation conserved between Archaea and Eukarya. *ELife*, **2012**, 1, e00078	8.9	60
167	Seventeen-gene signature from enriched Her2/Neu mammary tumor-initiating cells predicts clinical outcome for human HER2+:ER□breast cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 5832-7	11.5	58
166	The reactome pathway knowledgebase 2022. *Nucleic Acids Research*, **2021**,	20.1	57
165	EAG2 potassium channel with evolutionarily conserved function as a brain tumor target. *Nature Neuroscience*, **2015**, 18, 1236-46	25.5	56
164	Comprehensive Analysis of the Human SH3 Domain Family Reveals a Wide Variety of Non-canonical Specificities. *Structure*, **2017**, 25, 1598-1610.e3	5.2	56
163	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. *Frontiers in Bioengineering and Biotechnology*, **2015**, 3, 19	5.8	56
162	Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. *Proteomics*, **2010**, 10, 1316-27	4.8	53
161	Evolutionary constraint and disease associations of post-translational modification sites in human genomes. *PLoS Genetics*, **2015**, 11, e1004919	6	52
160	Visualizing gene-set enrichment results using the Cytoscape plug-in enrichment map. *Methods in Molecular Biology*, **2011**, 781, 257-77	1.4	51
159	MIMP: predicting the impact of mutations on kinase-substrate phosphorylation. *Nature Methods*, **2015**, 12, 531-3	21.6	50
158	Long read nanopore sequencing for detection of HLA and CYP2D6 variants and haplotypes. *F1000Research*, **2015**, 4, 17	3.6	50
157	HOX gene complement and expression in the planarian Schmidtea mediterranea. *EvoDevo*, **2016**, 7, 7	3.2	49
156	Patient Similarity Networks for Precision Medicine. *Journal of Molecular Biology*, **2018**, 430, 2924-2938	6.5	48
155	From bytes to bedside: data integration and computational biology for translational cancer research. *PLoS Computational Biology*, **2007**, 3, e12	5	48
154	SH3 interactome conserves general function over specific form. *Molecular Systems Biology*, **2013**, 9, 652	12.2	47
153	Using biological pathway data with paxtools. *PLoS Computational Biology*, **2013**, 9, e1003194	5	47
152	Rapid evolution of functional complexity in a domain family. *Science Signaling*, **2009**, 2, ra50	8.8	47

151	Leveraging increased cytoplasmic nucleoside kinase activity to target mtDNA and oxidative phosphorylation in AML. *Blood*, **2017**, 129, 2657-2666	2.2	43
150	Cardioprotective Signature of Short-Term Caloric Restriction. *PLoS ONE*, **2015**, 10, e0130658	3.7	43
149	Intercellular network structure and regulatory motifs in the human hematopoietic system. *Molecular Systems Biology*, **2014**, 10, 741	12.2	41
148	Protein complexes are central in the yeast genetic landscape. *PLoS Computational Biology*, **2011**, 7, e1001092	3	41
147	Exploring biological networks with Cytoscape software. *Current Protocols in Bioinformatics*, **2008**, Chapter 8, Unit 8.13	24.2	41
146	Ectopic miR-125a Expression Induces Long-Term Repopulating Stem Cell Capacity in Mouse and Human Hematopoietic Progenitors. *Cell Stem Cell*, **2016**, 19, 383-96	18	40
145	Sphingolipid Modulation Activates Proteostasis Programs to Govern Human Hematopoietic Stem Cell Self-Renewal. *Cell Stem Cell*, **2019**, 25, 639-653.e7	18	40
144	Identification of CDC25 as a Common Therapeutic Target for Triple-Negative Breast Cancer. *Cell Reports*, **2018**, 23, 112-126	10.6	38
143	MUSI: an integrated system for identifying multiple specificity from very large peptide or nucleic acid data sets. *Nucleic Acids Research*, **2012**, 40, e47	20.1	38
142	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF-B Signaling. *Cell Systems*, **2017**, 5, 564-577.e12	10.6	37
141	Compound prioritization methods increase rates of chemical probe discovery in model organisms. *Chemistry and Biology*, **2011**, 18, 1273-83		37
140	SeqHound: biological sequence and structure database as a platform for bioinformatics research. *BMC Bioinformatics*, **2002**, 3, 32	3.6	37
139	Relapse-Fated Latent Diagnosis Subclones in Acute B Lineage Leukemia Are Drug Tolerant and Possess Distinct Metabolic Programs. *Cancer Discovery*, **2020**, 10, 568-587	24.4	37
138	Integrative pathway dissection of molecular mechanisms of moxLDL-induced vascular smooth muscle phenotype transformation. *BMC Cardiovascular Disorders*, **2013**, 13, 4	2.3	36
137	Domain-mediated protein interaction prediction: From genome to network. *FEBS Letters*, **2012**, 586, 2751-63	3.8	35
136	netDx: interpretable patient classification using integrated patient similarity networks. *Molecular Systems Biology*, **2019**, 15, e8497	12.2	34
135	EPIC: software toolkit for elution profile-based inference of protein complexes. *Nature Methods*, **2019**, 16, 737-742	21.6	34
134	A comprehensive manually curated reaction map of RANKL/RANK-signaling pathway. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, bar021	5	33

133	Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in Escherichia coli. *Bioinformatics*, **2015**, 31, 306-10	7.2	31
132	Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. *Genome Medicine*, **2016**, 8, 55	14.4	31
131	Proteome scanning to predict PDZ domain interactions using support vector machines. *BMC Bioinformatics*, **2010**, 11, 507	3.6	31
130	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity.. *Nature Cancer*, **2021**, 2, 157-173	15.4	31
129	A Progesterone-CXCR4 Axis Controls Mammary Progenitor Cell Fate in the Adult Gland. *Stem Cell Reports*, **2015**, 4, 313-322	8	29
128	Towards reliable named entity recognition in the biomedical domain. *Bioinformatics*, **2020**, 36, 280-286	7.2	29
127	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. *F1000Research*, **2019**, 8,	3.6	28
126	Metabolic adaptation to chronic inhibition of mitochondrial protein synthesis in acute myeloid leukemia cells. *PLoS ONE*, **2013**, 8, e58367	3.7	28
125	NetSlim: high-confidence curated signaling maps. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, bar032	5	27
124	Predicting PDZ domain mediated protein interactions from structure. *BMC Bioinformatics*, **2013**, 14, 27	3.6	25
123	HyperModules: identifying clinically and phenotypically significant network modules with disease mutations for biomarker discovery. *Bioinformatics*, **2014**, 30, 2230-2	7.2	25
122	A clinically applicable integrative molecular classification of meningiomas. *Nature*, **2021**, 597, 119-125	50.4	25
121	Canadian Open Genetics Repository (COGR): a unified clinical genomics database as a community resource for standardising and sharing genetic interpretations. *Journal of Medical Genetics*, **2015**, 52, 438-45	5.8	23
120	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. *F1000Research*, **2019**, 8, 296	3.6	23
119	Generation of mature compact ventricular cardiomyocytes from human pluripotent stem cells. *Nature Communications*, **2021**, 12, 3155	17.4	23
118	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. *Nature Communications*, **2021**, 12, 979	17.4	23
117	The mitochondrial peptidase, neurolysin, regulates respiratory chain supercomplex formation and is necessary for AML viability. *Science Translational Medicine*, **2020**, 12,	17.5	22
116	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. *Cancer Research*, **2017**, 77, 3057-3069	10.1	20

115	Powerful gene set analysis in GWAS with the Generalized Berk-Jones statistic. *PLoS Genetics*, **2019**, 15, e1007530	6	20
114	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nature Communications*, **2020**, 11, 312	17.4	20
113	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. *Journal of Cell Biology*, **2018**, 217, 2951-2974	7.3	20
112	Functional genomics of intracellular peptide recognition domains with combinatorial biology methods. *Current Opinion in Chemical Biology*, **2003**, 7, 97-102	9.7	20
111	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data. *PLoS Computational Biology*, **2020**, 16, e1008205	5	20
110	The Mitochondrial Transacylase, Tafazzin, Regulates for AML Stemness by Modulating Intracellular Levels of Phospholipids. *Cell Stem Cell*, **2019**, 24, 621-636.e16	18	19
109	Antitumor activity of the novel multi-kinase inhibitor EC-70124 in triple negative breast cancer. *Oncotarget*, **2015**, 6, 27923-37	3.3	19
108	Single-Cell Profiling Shows Murine Forebrain Neural Stem Cells Reacquire a Developmental State when Activated for Adult Neurogenesis. *Cell Reports*, **2020**, 32, 108022	10.6	18
107	Transcriptomic analysis reveals abnormal muscle repair and remodeling in survivors of critical illness with sustained weakness. *Scientific Reports*, **2016**, 6, 29334	4.9	18
106	A roadmap for the Human Developmental Cell Atlas. *Nature*, **2021**, 597, 196-205	50.4	18
105	Rewiring of the Human Mitochondrial Interactome during Neuronal Reprogramming Reveals Regulators of the Respirasome and Neurogenesis. *IScience*, **2019**, 19, 1114-1132	6.1	17
104	Systems analysis reveals down-regulation of a network of pro-survival miRNAs drives the apoptotic response in dilated cardiomyopathy. *Molecular BioSystems*, **2015**, 11, 239-51		17
103	Generation of Functional Liver Sinusoidal Endothelial Cells from Human Pluripotent Stem-Cell-Derived Venous Angioblasts. *Cell Stem Cell*, **2020**, 27, 254-269.e9	18	17
102	scClustViz Single-cell RNAseq cluster assessment and visualization. *F1000Research*, **2018**, 7, 1522	3.6	17
101	Distinct fibroblast functional states drive clinical outcomes in ovarian cancer and are regulated by TCF21. *Journal of Experimental Medicine*, **2020**, 217,	16.6	17
100	Disrupting Mitochondrial Copper Distribution Inhibits Leukemic Stem Cell Self-Renewal. *Cell Stem Cell*, **2020**, 26, 926-937.e10	18	16
99	Dynamic interplay between locus-specific DNA methylation and hydroxymethylation regulates distinct biological pathways in prostate carcinogenesis. *Clinical Epigenetics*, **2016**, 8, 32	7.7	16
98	Inferring interaction type in gene regulatory networks using co-expression data. *Algorithms for Molecular Biology*, **2015**, 10, 23	1.8	16

97	Metabolomic profiling in liver of adiponectin-knockout mice uncovers lysophospholipid metabolism as an important target of adiponectin action. *Biochemical Journal*, **2015**, 469, 71-82	3.8	16
96	microRNA-143/145 loss induces Ras signaling to promote aggressive Pten-deficient basal-like breast cancer. *JCI Insight*, **2017**, 2,	9.9	16
95	Response to Comment on "Positive Selection of Tyrosine Loss in Metazoan Evolution". *Science*, **2011**, 332, 917-917	33.3	15
94	scClustViz - Single-cell RNAseq cluster assessment and visualization. *F1000Research*, **2018**, 7,	3.6	15
93	Phosphorylation sites of higher stoichiometry are more conserved. *Nature Methods*, **2012**, 9, 317; author reply 318	21.6	14
92	The health care and life sciences community profile for dataset descriptions. *PeerJ*, **2016**, 4, e2331	3.1	14
91	DeCLUTR: Deep Contrastive Learning for Unsupervised Textual Representations **2021**,		14
90	CD200 expression marks leukemia stem cells in human AML. *Blood Advances*, **2020**, 4, 5402-5413	7.8	13
89	BraInMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. *Cell Systems* , **2020**, 10, 333-350.e14	10.6	13
88	Nanoparticle Uptake in a Spontaneous and Immunocompetent Woodchuck Liver Cancer Model. *ACS Nano*, **2020**, 14, 4698-4715	16.7	13
87	Highlights of B/D-HPP and HPP Resource Pillar Workshops at 12th Annual HUPO World Congress of Proteomics: September 14-18, 2013, Yokohama, Japan. *Proteomics*, **2014**, 14, 975-88	4.8	13
86	Multiple genetic interaction experiments provide complementary information useful for gene function prediction. *PLoS Computational Biology*, **2012**, 8, e1002559	5	13
85	NetMatchStar: an enhanced Cytoscape network querying app. *F1000Research*, **2015**, 4, 479	3.6	13
84	Identification of CD146 as a marker enriched for tumor-propagating capacity reveals targetable pathways in primary human sarcoma. *Oncotarget*, **2015**, 6, 40283-94	3.3	13
83	A reference map of the human protein interactome		13
82	Wnt activation as a therapeutic strategy in medulloblastoma. *Nature Communications*, **2020**, 11, 4323	17.4	13
81	Integrated analysis of proteome, phosphotyrosine-proteome, tyrosine-kinome, and tyrosine-phosphatome in acute myeloid leukemia. *Proteomics*, **2017**, 17, 1600361	4.8	12
80	Detecting microRNAs of high influence on protein functional interaction networks: a prostate cancer case study. *BMC Systems Biology*, **2012**, 6, 112	3.5	12

79	Disruption of Abi1/Hssh3bp1 expression induces prostatic intraepithelial neoplasia in the conditional Abi1/Hssh3bp1 KO mice. *Oncogenesis*, **2012**, 1, e26	6.6	12
78	Large-scale survey and database of high affinity ligands for peptide recognition modules. *Molecular Systems Biology*, **2020**, 16, e9310	12.2	11
77	Social Network: a Cytoscape app for visualizing co-publication networks. *F1000Research*, **2015**, 4, 481	3.6	10
76	Single-Cell, Single-Nucleus, and Spatial RNA Sequencing of the Human Liver Identifies Cholangiocyte and Mesenchymal Heterogeneity. *Hepatology Communications*, **2021**,	6	10
75	Medulloblastoma Arises from the Persistence of a Rare and Transient Sox2 Granule Neuron Precursor. *Cell Reports*, **2020**, 31, 107511	10.6	10
74	Bmi1 regulates human glioblastoma stem cells through activation of differential gene networks in CD133+ brain tumor initiating cells. *Journal of Neuro-Oncology*, **2019**, 143, 417-428	4.8	9
73	Network Assessor: an automated method for quantitative assessment of a network's potential for gene function prediction. *Frontiers in Genetics*, **2014**, 5, 123	4.5	9
72	Cytoscape ESP: simple search of complex biological networks. *Bioinformatics*, **2008**, 24, 1465-6	7.2	9
71	Sphingosine-1-phosphate receptor 3 potentiates inflammatory programs in normal and leukemia stem cells to promote differentiation. *Blood Cancer Discovery*, **2021**, 2, 32-53	7	9
70	Exploring targets of TET2-mediated methylation reprogramming as potential discriminators of prostate cancer progression. *Clinical Epigenetics*, **2019**, 11, 54	7.7	8
69	Potential therapeutic targets for lung repair during human lung perfusion. *European Respiratory Journal*, **2020**, 55,	13.6	8
68	Prediction and experimental characterization of nsSNPs altering human PDZ-binding motifs. *PLoS ONE*, **2014**, 9, e94507	3.7	8
67	Mitochondrial carrier homolog 2 is necessary for AML survival. *Blood*, **2020**, 136, 81-92	2.2	8
66	The Cytoscape app article collection. *F1000Research*, **2014**, 3, 138	3.6	8
65	NetMatchStar: an enhanced Cytoscape network querying app. *F1000Research*, **2015**, 4, 479	3.6	8
64	Coordinate microRNA-mediated regulation of protein complexes in prostate cancer. *PLoS ONE*, **2013**, 8, e84261	3.7	8
63	Specifications of Standards in Systems and Synthetic Biology. *Journal of Integrative Bioinformatics*, **2015**, 12, 258	3.8	8
62	Surveilling and Tracking COVID-19 Patients Using a Portable Quantum Dot Smartphone Device. *Nano Letters*, **2021**, 21, 5209-5216	11.5	8

61	Induction of rod versus cone photoreceptor-specific progenitors from retinal precursor cells. *Stem Cell Research*, **2018**, 33, 215-227	1.6	8
60	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. *Journal of Integrative Bioinformatics*, **2016**, 13, 1-7	3.8	7
59	Specifications of Standards in Systems and Synthetic Biology. *Journal of Integrative Bioinformatics*, **2015**, 12, 1-3	3.8	7
58	The transcriptional landscape of Shh medulloblastoma. *Nature Communications*, **2021**, 12, 1749	17.4	7
57	Biological and therapeutic implications of a unique subtype of NPM1 mutated AML. *Nature Communications*, **2021**, 12, 1054	17.4	7
56	Global neuroscience and mental health research: a bibliometrics case study. *Scientometrics*, **2016**, 109, 515-531	3	6
55	Single-Cell RNA Sequencing: A New Window into Cell Scale Dynamics. *Biophysical Journal*, **2018**, 115, 429-435	2.9	6
54	Meeting report from the first meetings of the Computational Modeling in Biology Network (COMBINE). *Standards in Genomic Sciences*, **2011**, 5, 230-42		6
53	BioPAX □biological pathway data exchange format **2006**,		6
52	Social Network: a Cytoscape app for visualizing co-publication networks. *F1000Research*, **2015**, 4, 481	3.6	6
51	Dynamics of the cell-free DNA methylome of metastatic prostate cancer during androgen-targeting treatment. *Epigenomics*, **2020**, 12, 1317-1332	4.4	6
50	Tutorial: guidelines for annotating single-cell transcriptomic maps using automated and manual methods. *Nature Protocols*, **2021**, 16, 2749-2764	18.8	6
49	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2017. *Journal of Integrative Bioinformatics*, **2018**, 15,	3.8	5
48	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2019. *Journal of Integrative Bioinformatics*, **2019**, 16,	3.8	5
47	Displaying chemical information on a biological network using Cytoscape. *Methods in Molecular Biology*, **2011**, 781, 363-76	1.4	5
46	Nicotinamide phosphoribosyltransferase inhibitors selectively induce apoptosis of AML stem cells by disrupting lipid homeostasis. *Cell Stem Cell*, **2021**, 28, 1851-1867.e8	18	5
45	GESTODIFFERENT: a Cytoscape plugin for the generation and the identification of gene regulatory networks describing a stochastic cell differentiation process. *Bioinformatics*, **2013**, 29, 513-4	7.2	4
44	Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. *Molecular Systems Biology*, **2014**, 10, 637	12.2	4

43	The BioPAX Validator. *Bioinformatics*, **2013**, 29, 2659-60	7.2	4
42	Pathway enrichment analysis of -omics data		4
41	Single-cell transcriptomics of the aged mouse brain reveals convergent, divergent and unique aging signatures		4
40	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNAsequencing data		4
39	Single Cell, Single Nucleus and Spatial RNA Sequencing of the Human Liver Identifies Hepatic Stellate Cell and Cholangiocyte Heterogeneity		4
38	Distinct DNA methylation patterns associated with treatment resistance in metastatic castration resistant prostate cancer. *Scientific Reports*, **2021**, 11, 6630	4.9	4
37	Comparative analysis of co-expression networks reveals molecular changes during the cancer progression. *IFMBE Proceedings*, **2015**, 1481-1487	0.2	3
36	Predicting physiologically relevant SH3 domain mediated protein-protein interactions in yeast. *Bioinformatics*, **2016**, 32, 1865-72	7.2	3
35	A brief history of COMBINE **2017**,		3
34	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. *Journal of Integrative Bioinformatics*, **2016**, 13, 289	3.8	3
33	Molecular atlas of the human brain vasculature at the single-cell level		3
32	Integrative pharmacogenomics to infer large-scale drug taxonomy		3
31	The human brain vasculature shows a distinct expression pattern of SARS-CoV-2 entry factors		3
30	Control of tissue development and cell diversity by cell cycle-dependent transcriptional filtering. *ELife*, **2021**, 10,	8.9	3
29	Meta-analysis of gene expression profiles of lean and obese PCOS to identify differentially regulated pathways and risk of comorbidities. *Computational and Structural Biotechnology Journal*, **2020**, 18, 1735-1745	6.8	2
28	Chemogenomic Profiling: Understanding the Cellular Response to Drug **2013**, 153-176		2
27	A Shared Transcriptional Identity for Forebrain and Dentate Gyrus Neural Stem Cells from Embryogenesis to Adulthood.. *ENeuro*, **2022**,	3.9	2
26	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. *F1000Research*,8, 296	3.6	2

25	Towards reliable named entity recognition in the biomedical domain		2
24	ARGLU1 is a Glucocorticoid Receptor Coactivator and Splicing Modulator Important in Stress Hormone Signaling and Brain Development		2
23	SBGN Bricks Ontology as a tool to describe recurring concepts in molecular networks. *Briefings in Bioinformatics*, **2021**, 22,	13.4	2
22	Automated Computational Inference of Multi-protein Assemblies from Biochemical Co-purification Data. *Methods in Molecular Biology*, **2018**, 1764, 391-399	1.4	1
21	Hypophosphorylated pRb knock-in mice exhibit hallmarks of aging and vitamin C-preventable diabetes.. *EMBO Journal*, **2022**, e106825	13	1
20	Nicotinamide Phosphoribosyltransferase Inhibitors Induce Apoptosis of AML Stem Cells through Dysregulation of Lipid Metabolism. *Blood*, **2020**, 136, 25-26	2.2	1
19	netDx: Software for building interpretable patient classifiers by multi-Qmic data integration using patient similarity networks. *F1000Research*, **2020**, 9, 1239	3.6	1
18	Macromolecular Connectivity Landscape of Mammalian Brain. *SSRN Electronic Journal*,	1	1
17	Capturing scientific knowledge in computable form		1
16	BIONIC: Biological Network Integration using Convolutions		1
15	netDx: Software for building interpretable patient classifiers by multi-Qmic data integration using patient similarity networks. *F1000Research*, **2020**, 9, 1239	3.6	1
14	A flexible search system for high-accuracy identification of biological entities and molecules. *Journal of Open Source Software*, **2021**, 6, 3756	5.2	0
13	A microfluidic platform enables comprehensive gene expression profiling of mouse retinal stem cells. *Lab on A Chip*, **2021**, 21, 4464-4476	7.2	0
12	Identification of the global miR-130a targetome reveals a role for TBL1XR1 in hematopoietic stem cell self-renewal and t(8;21) AML.. *Cell Reports*, **2022**, 38, 110481	10.6	0
11	Temporal profiling of therapy resistance in human medulloblastoma identifies novel targetable drivers of recurrence. *Science Advances*, **2021**, 7, eabi5568	14.3	0
10	OpenPIP: An Open-source Platform for Hosting, Visualizing and Analyzing Protein Interaction Data. *Journal of Molecular Biology*, **2022**, 167603	6.5	0
9	GreedyPlus: An Algorithm for the Alignment of Interface Interaction Networks. *Scientific Reports*, **2015**, 5, 12074	4.9	
8	MG-108 Beyond the ACMG 56: Parental choices and initial results from a comprehensive whole genome sequencing-based search for predictive genomic variants in children. *Journal of Medical Genetics*, **2015**, 52, A3.2-A4	5.8	

7	Protein Interaction Databases433-459	
6	IPO11 Regulates the Nuclear Import of BZW1/2 and Is Necessary for AML Cells and Stem Cells. *Blood*, **2020**, 136, 22-23	2.2
5	The Metabolic Enzyme Hexokinase 2 Localizes to the Nucleus in AML and Normal Hematopoietic Stem/Progenitor Cells to Maintain Stemness. *Blood*, **2020**, 136, 1-2	2.2
4	A Stemness-Based Screen Identifies PLK1 Inhibitors for Targeting Leukemia Stem Cells in AML. *Blood*, **2020**, 136, 34-35	2.2
3	Interaction Databases **2001**, 399-416	
2	Peptide Recognition Module Networks: Combining Phage Display with Two-Hybrid Analysis to Define Protein-Protein Interactions **2003**, 311-315	
1	Interaction Databases399-413	