

Gary D Bader

List of Publications by Year in descending order

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274
papers

66,009
citations

2669

95
h-index

906

241
g-index

343
all docs

343
docs citations

343
times ranked

81025
citing authors

#	ARTICLE	IF	CITATIONS
1	An automated method for finding molecular complexes in large protein interaction networks. BMC Bioinformatics, 2003, 4, 2.	1.2	4,773
2	Systematic identification of protein complexes in Saccharomyces cerevisiae by mass spectrometry. Nature, 2002, 415, 180-183.	13.7	3,445
3	The GeneMANIA prediction server: biological network integration for gene prioritization and predicting gene function. Nucleic Acids Research, 2010, 38, W214-W220.	6.5	3,436
4	Integration of biological networks and gene expression data using Cytoscape. Nature Protocols, 2007, 2, 2366-2382.	5.5	2,275
5	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
6	A draft map of the human proteome. Nature, 2014, 509, 575-581.	13.7	1,948
7	Systematic Genetic Analysis with Ordered Arrays of Yeast Deletion Mutants. Science, 2001, 294, 2364-2368.	6.0	1,946
8	The Genetic Landscape of a Cell. Science, 2010, 327, 425-431.	6.0	1,937
9	Global Mapping of the Yeast Genetic Interaction Network. Science, 2004, 303, 808-813.	6.0	1,908
10	Enrichment Map: A Network-Based Method for Gene-Set Enrichment Visualization and Interpretation. PLoS ONE, 2010, 5, e13984.	1.1	1,883
11	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	13.7	1,803
12	A travel guide to Cytoscape plugins. Nature Methods, 2012, 9, 1069-1076.	9.0	1,289
13	Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap. Nature Protocols, 2019, 14, 482-517.	5.5	1,172
14	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
15	Pathway Commons, a web resource for biological pathway data. Nucleic Acids Research, 2011, 39, D685-D690.	6.5	980
16	BIND: the Biomolecular Interaction Network Database. Nucleic Acids Research, 2003, 31, 248-250.	6.5	969
17	Single cell RNA sequencing of human liver reveals distinct intrahepatic macrophage populations. Nature Communications, 2018, 9, 4383.	5.8	958
18	Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. Cancer Cell, 2015, 27, 728-743.	7.7	933

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19	The reactome pathway knowledgebase 2022. <i>Nucleic Acids Research</i> , 2022, 50, D687-D692.	6.5	924
20	Intertumoral Heterogeneity within Medulloblastoma Subgroups. <i>Cancer Cell</i> , 2017, 31, 737-754.e6.	7.7	836
21	Biological Network Exploration with Cytoscape 3. <i>Current Protocols in Bioinformatics</i> , 2014, 47, 8.13.1-24.	25.8	780
22	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012, 488, 49-56.	13.7	761
23	A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408.	13.7	724
24	GeneMANIA update 2018. <i>Nucleic Acids Research</i> , 2018, 46, W60-W64.	6.5	698
25	A Combined Experimental and Computational Strategy to Define Protein Interaction Networks for Peptide Recognition Modules. <i>Science</i> , 2002, 295, 321-324.	6.0	668
26	Cytoscape Web: an interactive web-based network browser. <i>Bioinformatics</i> , 2010, 26, 2347-2348.	1.8	648
27	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. <i>Cancer Cell</i> , 2014, 25, 393-405.	7.7	627
28	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	9.4	613
29	The HUPO PSI's Molecular Interaction formatâ€”a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004, 22, 177-183.	9.4	581
30	GeneMANIA Cytoscape plugin: fast gene function predictions on the desktop. <i>Bioinformatics</i> , 2010, 26, 2927-2928.	1.8	552
31	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. <i>BMC Bioinformatics</i> , 2011, 12, 436.	1.2	541
32	Cytoscape.js: a graph theory library for visualisation and analysis. <i>Bioinformatics</i> , 2016, 32, 309-311.	1.8	531
33	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. <i>Nature</i> , 2014, 506, 445-450.	13.7	521
34	Enhancer hijacking activates GF11 family oncogenes in medulloblastoma. <i>Nature</i> , 2014, 511, 428-434.	13.7	520
35	Analyzing yeast proteinâ€”protein interaction data obtained from different sources. <i>Nature Biotechnology</i> , 2002, 20, 991-997.	9.4	508
36	Delineation of Two Clinically and Molecularly Distinct Subgroups of Posterior Fossa Ependymoma. <i>Cancer Cell</i> , 2011, 20, 143-157.	7.7	494

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37	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010, 11, R3.	13.9	456
38	Comprehensive identification of mutational cancer driver genes across 12 tumor types. <i>Scientific Reports</i> , 2013, 3, 2650.	1.6	437
39	Single-cell transcriptomic profiling of the aging mouse brain. <i>Nature Neuroscience</i> , 2019, 22, 1696-1708.	7.1	432
40	Tracing the origins of relapse in acute myeloid leukaemia to stem cells. <i>Nature</i> , 2017, 547, 104-108.	13.7	424
41	A Specificity Map for the PDZ Domain Family. <i>PLoS Biology</i> , 2008, 6, e239.	2.6	410
42	Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. <i>Cell</i> , 2016, 164, 293-309.	13.5	399
43	Pathguide: a Pathway Resource List. <i>Nucleic Acids Research</i> , 2006, 34, D504-D506.	6.5	397
44	GeneMANIA Prediction Server 2013 Update. <i>Nucleic Acids Research</i> , 2013, 41, W115-W122.	6.5	343
45	Too many roads not taken. <i>Nature</i> , 2011, 470, 163-165.	13.7	341
46	Single cell-derived clonal analysis of human glioblastoma links functional and genomic heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 851-856.	3.3	321
47	Quantitative analysis of fitness and genetic interactions in yeast on a genome scale. <i>Nature Methods</i> , 2010, 7, 1017-1024.	9.0	319
48	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015, 12, 615-621.	9.0	297
49	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
50	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	9.4	274
51	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	9.0	274
52	Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. <i>Molecular Systems Biology</i> , 2013, 9, 637.	3.2	267
53	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016, 529, 351-357.	13.7	266
54	Inhibition of the Mitochondrial Protease ClpP as a Therapeutic Strategy for Human Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2015, 27, 864-876.	7.7	265

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55	Functional genomic landscape of cancer-intrinsic evasion of killing by T cells. <i>Nature</i> , 2020, 586, 120-126.	13.7	249
56	AutoAnnotate: A Cytoscape app for summarizing networks with semantic annotations. <i>F1000Research</i> , 2016, 5, 1717.	0.8	249
57	GeneMANIA: Fast gene network construction and function prediction for Cytoscape. <i>F1000Research</i> , 2014, 3, 153.	0.8	242
58	Quiescent Sox2+ Cells Drive Hierarchical Growth and Relapse in Sonic Hedgehog Subgroup Medulloblastoma. <i>Cancer Cell</i> , 2014, 26, 33-47.	7.7	241
59	PreBIND and Textomy—mining the biomedical literature for protein-protein interactions using a support vector machine. <i>BMC Bioinformatics</i> , 2003, 4, 11.	1.2	239
60	Broadening the horizon “ level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , 2007, 5, 44.	1.7	237
61	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. <i>Science</i> , 2014, 344, 208-211.	6.0	217
62	miR-126 Regulates Distinct Self-Renewal Outcomes in Normal and Malignant Hematopoietic Stem Cells. <i>Cancer Cell</i> , 2016, 29, 214-228.	7.7	216
63	Computational Prediction of Protein-Protein Interactions. <i>Molecular Biotechnology</i> , 2008, 38, 1-17.	1.3	201
64	Attenuation of miR-126 Activity Expands HSC In Vivo without Exhaustion. <i>Cell Stem Cell</i> , 2012, 11, 799-811.	5.2	197
65	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. <i>Cancer Cell</i> , 2016, 30, 891-908.	7.7	191
66	A Comparative Transcriptomic Analysis Reveals Conserved Features of Stem Cell Pluripotency in Planarians and Mammals. <i>Stem Cells</i> , 2012, 30, 1734-1745.	1.4	181
67	Functional complexes between YAP2 and ZO-2 are PDZ domain-dependent, and regulate YAP2 nuclear localization and signalling. <i>Biochemical Journal</i> , 2010, 432, 461-478.	1.7	180
68	A clinically applicable integrative molecular classification of meningiomas. <i>Nature</i> , 2021, 597, 119-125.	13.7	180
69	<sc>SBML</sc> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
70	BIND—a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. <i>Bioinformatics</i> , 2000, 16, 465-477.	1.8	175
71	Bayesian Modeling of the Yeast SH3 Domain Interactome Predicts Spatiotemporal Dynamics of Endocytosis Proteins. <i>PLoS Biology</i> , 2009, 7, e1000218.	2.6	172
72	Comparative Analysis Reveals Conserved Protein Phosphorylation Networks Implicated in Multiple Diseases. <i>Science Signaling</i> , 2009, 2, ra39.	1.6	171

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73	Developmental Emergence of Adult Neural Stem Cells as Revealed by Single-Cell Transcriptional Profiling. <i>Cell Reports</i> , 2017, 21, 3970-3986.	2.9	171
74	Inhibition of Dopamine Receptor D4 Impedes Autophagic Flux, Proliferation, and Survival of Glioblastoma Stem Cells. <i>Cancer Cell</i> , 2016, 29, 859-873.	7.7	169
75	A predictive model for drug bioaccumulation and bioactivity in <i>Caenorhabditis elegans</i> . <i>Nature Chemical Biology</i> , 2010, 6, 549-557.	3.9	164
76	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013, 10, 723-729.	9.0	161
77	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. <i>Nucleic Acids Research</i> , 2020, 48, D489-D497.	6.5	161
78	Cytoscape App Store. <i>Bioinformatics</i> , 2013, 29, 1350-1351.	1.8	154
79	Transfer learning for biomedical named entity recognition with neural networks. <i>Bioinformatics</i> , 2018, 34, 4087-4094.	1.8	154
80	An improved method for scoring protein-protein interactions using semantic similarity within the gene ontology. <i>BMC Bioinformatics</i> , 2010, 11, 562.	1.2	153
81	ASCL1 Reorganizes Chromatin to Direct Neuronal Fate and Suppress Tumorigenicity of Glioblastoma Stem Cells. <i>Cell Stem Cell</i> , 2017, 21, 209-224.e7.	5.2	150
82	The mutational landscape of phosphorylation signaling in cancer. <i>Scientific Reports</i> , 2013, 3, 2651.	1.6	149
83	Molecular subgroups of atypical teratoid rhabdoid tumours in children: an integrated genomic and clinicopathological analysis. <i>Lancet Oncology</i> , The, 2015, 16, 569-582.	5.1	147
84	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity. <i>Nature Cancer</i> , 2021, 2, 157-173.	5.7	147
85	Bringing order to protein disorder through comparative genomics and genetic interactions. <i>Genome Biology</i> , 2011, 12, R14.	13.9	129
86	Enrichment Map – a Cytoscape app to visualize and explore OMICs pathway enrichment results. <i>F1000Research</i> , 2014, 3, 141.	0.8	128
87	Germ-line DNA copy number variation frequencies in a large North American population. <i>Human Genetics</i> , 2007, 122, 345-353.	1.8	127
88	Functional genomics and proteomics: charting a multidimensional map of the yeast cell. <i>Trends in Cell Biology</i> , 2003, 13, 344-356.	3.6	126
89	Dynamic interaction networks in a hierarchically organized tissue. <i>Molecular Systems Biology</i> , 2010, 6, 417.	3.2	122
90	WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. <i>Source Code for Biology and Medicine</i> , 2011, 6, 7.	1.7	120

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91	A regression framework incorporating quantitative and negative interaction data improves quantitative prediction of PDZ domainâ€“peptide interaction from primary sequence. <i>Bioinformatics</i> , 2011, 27, 383-390.	1.8	114
92	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	13.7	114
93	Spatial heterogeneity in medulloblastoma. <i>Nature Genetics</i> , 2017, 49, 780-788.	9.4	112
94	cPath: open source software for collecting, storing, and querying biological pathways. <i>BMC Bioinformatics</i> , 2006, 7, 497.	1.2	108
95	Pathway information for systems biology. <i>FEBS Letters</i> , 2005, 579, 1815-1820.	1.3	107
96	Coevolution of PDZ domainâ€“ligand interactions analyzed by high-throughput phage display and deep sequencing. <i>Molecular BioSystems</i> , 2010, 6, 1782.	2.9	107
97	RB1 deficiency in triple-negative breast cancer induces mitochondrial protein translation. <i>Journal of Clinical Investigation</i> , 2016, 126, 3739-3757.	3.9	107
98	Comprehensive Analysis of the Human SH3 Domain Family Reveals a Wide Variety of Non-canonical Specificities. <i>Structure</i> , 2017, 25, 1598-1610.e3.	1.6	105
99	Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. <i>Nature Communications</i> , 2015, 6, 8554.	5.8	102
100	Musashi-2 attenuates AHR signalling to expand human haematopoietic stem cells. <i>Nature</i> , 2016, 532, 508-511.	13.7	101
101	The Biology/Disease-driven Human Proteome Project (B/D-HPP): Enabling Protein Research for the Life Sciences Community. <i>Journal of Proteome Research</i> , 2013, 12, 23-27.	1.8	100
102	Tutorial: guidelines for annotating single-cell transcriptomic maps using automated and manual methods. <i>Nature Protocols</i> , 2021, 16, 2749-2764.	5.5	100
103	Mapping the Hsp90 Genetic Interaction Network in <i>Candida albicans</i> Reveals Environmental Contingency and Rewired Circuitry. <i>PLoS Genetics</i> , 2012, 8, e1002562.	1.5	98
104	Singleâ€“Cell, Singleâ€“Nucleus, and Spatial RNA Sequencing of the Human Liver Identifies Cholangiocyte and Mesenchymal Heterogeneity. <i>Hepatology Communications</i> , 2022, 6, 821-840.	2.0	98
105	Long read nanopore sequencing for detection of HLA and CYP2D6 variants and haplotypes. <i>F1000Research</i> , 2015, 4, 17.	0.8	96
106	The Biomolecular Interaction Network Database in PSI-MI 2.5. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, baq037.	1.4	95
107	DeCLUTR: Deep Contrastive Learning for Unsupervised Textual Representations. , 2021, , .		94
108	How to visually interpret biological data using networks. <i>Nature Biotechnology</i> , 2009, 27, 921-924.	9.4	93

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109	IL-7 coordinates proliferation, differentiation and Tcr α recombination during thymocyte β 2-selection. <i>Nature Immunology</i> , 2015, 16, 397-405.	7.0	93
110	Patient Similarity Networks for Precision Medicine. <i>Journal of Molecular Biology</i> , 2018, 430, 2924-2938.	2.0	93
111	Generation of mature compact ventricular cardiomyocytes from human pluripotent stem cells. <i>Nature Communications</i> , 2021, 12, 3155.	5.8	93
112	Positive Selection of Tyrosine Loss in Metazoan Evolution. <i>Science</i> , 2009, 325, 1686-1688.	6.0	91
113	Combined deletion of p53 and p21 in mammary epithelium accelerates triple-negative breast cancer with dependency on p53. <i>EMBO Molecular Medicine</i> , 2014, 6, 1542-1560.	3.3	91
114	Computational prediction of cancer-gene function. <i>Nature Reviews Cancer</i> , 2007, 7, 23-34.	12.8	81
115	Sphingolipid Modulation Activates Proteostasis Programs to Govern Human Hematopoietic Stem Cell Self-Renewal. <i>Cell Stem Cell</i> , 2019, 25, 639-653.e7.	5.2	79
116	The multiple specificity landscape of modular peptide recognition domains. <i>Molecular Systems Biology</i> , 2011, 7, 484.	3.2	78
117	Chromatin is an ancient innovation conserved between Archaea and Eukarya. <i>ELife</i> , 2012, 1, e00078.	2.8	78
118	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , 2021, 12, 979.	5.8	77
119	NetMatch: a Cytoscape plugin for searching biological networks. <i>Bioinformatics</i> , 2007, 23, 910-912.	1.8	75
120	DRYGIN: a database of quantitative genetic interaction networks in yeast. <i>Nucleic Acids Research</i> , 2010, 38, D502-D507.	6.5	75
121	MIMP: predicting the impact of mutations on kinase-substrate phosphorylation. <i>Nature Methods</i> , 2015, 12, 531-533.	9.0	75
122	EAG2 potassium channel with evolutionarily conserved function as a brain tumor target. <i>Nature Neuroscience</i> , 2015, 18, 1236-1246.	7.1	74
123	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 19.	2.0	72
124	HOX gene complement and expression in the planarian <i>Schmidtea mediterranea</i> . <i>EvoDevo</i> , 2016, 7, 7.	1.3	72
125	Relapse-Fated Latent Diagnosis Subclones in Acute B Lineage Leukemia Are Drug Tolerant and Possess Distinct Metabolic Programs. <i>Cancer Discovery</i> , 2020, 10, 568-587.	7.7	72
126	Evolutionary Constraint and Disease Associations of Post-Translational Modification Sites in Human Genomes. <i>PLoS Genetics</i> , 2015, 11, e1004919.	1.5	69

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127	Visualizing Gene-Set Enrichment Results Using the Cytoscape Plug-in Enrichment Map. <i>Methods in Molecular Biology</i> , 2011, 781, 257-277.	0.4	68
128	Seventeen-gene signature from enriched Her2/Neu mammary tumor-initiating cells predicts clinical outcome for human HER2 ⁺ breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5832-5837.	3.3	67
129	EPIC: software toolkit for elution profile-based inference of protein complexes. <i>Nature Methods</i> , 2019, 16, 737-742.	9.0	67
130	netDx: interpretable patient classification using integrated patient similarity networks. <i>Molecular Systems Biology</i> , 2019, 15, e8497.	3.2	65
131	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013, 9, 652.	3.2	61
132	Leveraging increased cytoplasmic nucleoside kinase activity to target mtDNA and oxidative phosphorylation in AML. <i>Blood</i> , 2017, 129, 2657-2666.	0.6	61
133	Exploring Biological Networks with Cytoscape Software. <i>Current Protocols in Bioinformatics</i> , 2008, 23, Unit 8.13.	25.8	60
134	Identification of CDC25 as a Common Therapeutic Target for Triple-Negative Breast Cancer. <i>Cell Reports</i> , 2018, 23, 112-126.	2.9	58
135	Rapid Evolution of Functional Complexity in a Domain Family. <i>Science Signaling</i> , 2009, 2, ra50.	1.6	57
136	Protein Complexes are Central in the Yeast Genetic Landscape. <i>PLoS Computational Biology</i> , 2011, 7, e1001092.	1.5	57
137	Using Biological Pathway Data with Paxtools. <i>PLoS Computational Biology</i> , 2013, 9, e1003194.	1.5	57
138	Intercellular network structure and regulatory motifs in the human hematopoietic system. <i>Molecular Systems Biology</i> , 2014, 10, 741.	3.2	57
139	Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. <i>Proteomics</i> , 2010, 10, 1316-1327.	1.3	55
140	Long read nanopore sequencing for detection of HLA and CYP2D6 variants and haplotypes. <i>F1000Research</i> , 2015, 4, 17.	0.8	55
141	From Bytes to Bedside: Data Integration and Computational Biology for Translational Cancer Research. <i>PLoS Computational Biology</i> , 2007, 3, e12.	1.5	52
142	Ectopic miR-125a Expression Induces Long-Term Repopulating Stem Cell Capacity in Mouse and Human Hematopoietic Progenitors. <i>Cell Stem Cell</i> , 2016, 19, 383-396.	5.2	52
143	Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. <i>Genome Medicine</i> , 2016, 8, 55.	3.6	51
144	Towards reliable named entity recognition in the biomedical domain. <i>Bioinformatics</i> , 2020, 36, 280-286.	1.8	51

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145	Distinct fibroblast functional states drive clinical outcomes in ovarian cancer and are regulated by TCF21. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	51
146	Generation of Functional Liver Sinusoidal Endothelial Cells from Human Pluripotent Stem-Cell-Derived Venous Angioblasts. <i>Cell Stem Cell</i> , 2020, 27, 254-269.e9.	5.2	50
147	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2020, 16, e1008205.	1.5	49
148	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , 2019, 8, 296.	0.8	49
149	Domain-mediated protein interaction prediction: From genome to network. <i>FEBS Letters</i> , 2012, 586, 2751-2763.	1.3	48
150	Integrative pathway dissection of molecular mechanisms of oxLDL-induced vascular smooth muscle phenotype transformation. <i>BMC Cardiovascular Disorders</i> , 2013, 13, 4.	0.7	48
151	BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020, 10, 333-350.e14.	2.9	48
152	Cardioprotective Signature of Short-Term Caloric Restriction. <i>PLoS ONE</i> , 2015, 10, e0130658.	1.1	47
153	The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , 2021, 12, 1749.	5.8	47
154	MUSI: an integrated system for identifying multiple specificity from very large peptide or nucleic acid data sets. <i>Nucleic Acids Research</i> , 2012, 40, e47-e47.	6.5	45
155	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , 2019, 8, 296.	0.8	45
156	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF- κ B Signaling. <i>Cell Systems</i> , 2017, 5, 564-577.e12.	2.9	44
157	Nicotinamide phosphoribosyltransferase inhibitors selectively induce apoptosis of AML stem cells by disrupting lipid homeostasis. <i>Cell Stem Cell</i> , 2021, 28, 1851-1867.e8.	5.2	43
158	Compound Prioritization Methods Increase Rates of Chemical Probe Discovery in Model Organisms. <i>Chemistry and Biology</i> , 2011, 18, 1273-1283.	6.2	41
159	SeqHound: biological sequence and structure database as a platform for bioinformatics research. <i>BMC Bioinformatics</i> , 2002, 3, 32.	1.2	40
160	Single-Cell Profiling Shows Murine Forebrain Neural Stem Cells Reacquire a Developmental State when Activated for Adult Neurogenesis. <i>Cell Reports</i> , 2020, 32, 108022.	2.9	40
161	A comprehensive manually curated reaction map of RANKL/RANK-signaling pathway. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar021-bar021.	1.4	39
162	Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2015, 31, 306-310.	1.8	38

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163	A Progesterone-CXCR4 Axis Controls Mammary Progenitor Cell Fate in the Adult Gland. <i>Stem Cell Reports</i> , 2015, 4, 313-322.	2.3	38
164	Rewiring of the Human Mitochondrial Interactome during Neuronal Reprogramming Reveals Regulators of the Respirasome and Neurogenesis. <i>IScience</i> , 2019, 19, 1114-1132.	1.9	38
165	Surveilling and Tracking COVID-19 Patients Using a Portable Quantum Dot Smartphone Device. <i>Nano Letters</i> , 2021, 21, 5209-5216.	4.5	38
166	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. <i>Journal of Cell Biology</i> , 2018, 217, 2951-2974.	2.3	35
167	Powerful gene set analysis in GWAS with the Generalized Berk-Jones statistic. <i>PLoS Genetics</i> , 2019, 15, e1007530.	1.5	35
168	Disrupting Mitochondrial Copper Distribution Inhibits Leukemic Stem Cell Self-Renewal. <i>Cell Stem Cell</i> , 2020, 26, 926-937.e10.	5.2	35
169	Medulloblastoma Arises from the Persistence of a Rare and Transient Sox2+ Granule Neuron Precursor. <i>Cell Reports</i> , 2020, 31, 107511.	2.9	35
170	Sphingosine-1-Phosphate Receptor 3 Potentiates Inflammatory Programs in Normal and Leukemia Stem Cells to Promote Differentiation. <i>Blood Cancer Discovery</i> , 2021, 2, 32-53.	2.6	35
171	Wnt activation as a therapeutic strategy in medulloblastoma. <i>Nature Communications</i> , 2020, 11, 4323.	5.8	34
172	Proteome scanning to predict PDZ domain interactions using support vector machines. <i>BMC Bioinformatics</i> , 2010, 11, 507.	1.2	33
173	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. <i>Cancer Research</i> , 2017, 77, 3057-3069.	0.4	33
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