

# Gary D Bader

## List of Publications by Year in descending order

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Version: 2024-02-01

274  
papers

66,009  
citations

<sup>2669</sup>  
95  
h-index

<sup>906</sup>  
241  
g-index

343  
all docs

343  
docs citations

343  
times ranked

81025  
citing authors

#	ARTICLE	IF	CITATIONS
1	The reactome pathway knowledgebase 2022. <i>Nucleic Acids Research</i> , 2022, 50, D687-D692.	6.5	924
2	Single-Cell, Single-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
3	Hypophosphorylated pRb knock-in mice exhibit hallmarks of aging and vitamin C-preventable diabetes. <i>EMBO Journal</i> , 2022, 41, e106825.	3.5	13
4	A Shared Transcriptional Identity for Forebrain and Dentate Gyrus Neural Stem Cells from Embryogenesis to Adulthood. <i>ENeuro</i> , 2022, 9, ENEURO.0271-21.2021.	0.9	15
5	IPO11 regulates the nuclear import of BZW1/2 and is necessary for AML cells and stem cells. <i>Leukemia</i> , 2022, 36, 1283-1295.	3.3	8
6	Identification of the global miR-130a targetome reveals a role for TBL1XR1 in hematopoietic stem cell self-renewal and t(8;21) AML. <i>Cell Reports</i> , 2022, 38, 110481.	2.9	4
7	OpenPIP: An Open-source Platform for Hosting, Visualizing and Analyzing Protein Interaction Data. <i>Journal of Molecular Biology</i> , 2022, 434, 167603.	2.0	3
8	PLAG1 dampens protein synthesis to promote human hematopoietic stem cell self-renewal. <i>Blood</i> , 2022, 140, 992-1008.	0.6	11
9	The metabolic enzyme hexokinase 2 localizes to the nucleus in AML and normal haematopoietic stem and progenitor cells to maintain stemness. <i>Nature Cell Biology</i> , 2022, 24, 872-884.	4.6	25
10	Uncovering the Contribution of Moderate-Penetrance Susceptibility Genes to Breast Cancer by Whole-Exome Sequencing and Targeted Enrichment Sequencing of Candidate Genes in Women of European Ancestry. <i>Cancers</i> , 2022, 14, 3363.	1.7	2
11	DeCLUTR: Deep Contrastive Learning for Unsupervised Textual Representations. , 2021, , .		94
12	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
13	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , 2021, 12, 979.	5.8	77
14	Biological and therapeutic implications of a unique subtype of NPM1 mutated AML. <i>Nature Communications</i> , 2021, 12, 1054.	5.8	29
15	Distinct DNA methylation patterns associated with treatment resistance in metastatic castration resistant prostate cancer. <i>Scientific Reports</i> , 2021, 11, 6630.	1.6	8
16	SBGN Bricks Ontology as a tool to describe recurring concepts in molecular networks. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
17	The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , 2021, 12, 1749.	5.8	47
18	Tutorial: guidelines for annotating single-cell transcriptomic maps using automated and manual methods. <i>Nature Protocols</i> , 2021, 16, 2749-2764.	5.5	100

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19	Generation of mature compact ventricular cardiomyocytes from human pluripotent stem cells. <i>Nature Communications</i> , 2021, 12, 3155.	5.8	93
20	scNetViz: from single cells to networks using Cytoscape. <i>F1000Research</i> , 2021, 10, 448.	0.8	1
21	Surveilling and Tracking COVID-19 Patients Using a Portable Quantum Dot Smartphone Device. <i>Nano Letters</i> , 2021, 21, 5209-5216.	4.5	38
22	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
23	Control of tissue development and cell diversity by cell cycle-dependent transcriptional filtering. <i>ELife</i> , 2021, 10, .	2.8	7
24	A clinically applicable integrative molecular classification of meningiomas. <i>Nature</i> , 2021, 597, 119-125.	13.7	180
25	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	13.7	114
26	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
27	A microfluidic platform enables comprehensive gene expression profiling of mouse retinal stem cells. <i>Lab on A Chip</i> , 2021, 21, 4464-4476.	3.1	3
28	A flexible search system for high-accuracy identification of biological entities and molecules. <i>Journal of Open Source Software</i> , 2021, 6, 3756.	2.0	1
29	Author-sourced capture of pathway knowledge in computable form using Biofactoid. <i>ELife</i> , 2021, 10, .	2.8	11
30	Temporal profiling of therapy resistance in human medulloblastoma identifies novel targetable drivers of recurrence. <i>Science Advances</i> , 2021, 7, eabi5568.	4.7	8
31	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. <i>Nucleic Acids Research</i> , 2020, 48, D489-D497.	6.5	161
32	Towards reliable named entity recognition in the biomedical domain. <i>Bioinformatics</i> , 2020, 36, 280-286.	1.8	51
33	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
34	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
35	Functional genomic landscape of cancer-intrinsic evasion of killing by T cells. <i>Nature</i> , 2020, 586, 120-126.	13.7	249
36	Wnt activation as a therapeutic strategy in medulloblastoma. <i>Nature Communications</i> , 2020, 11, 4323.	5.8	34

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37	Dynamics of the cell-free DNA methylome of metastatic prostate cancer during androgen-targeting treatment. <i>Epigenomics</i> , 2020, 12, 1317-1332.	1.0	15
38	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2020, 16, e1008205.	1.5	49
39	CD200 expression marks leukemia stem cells in human AML. <i>Blood Advances</i> , 2020, 4, 5402-5413.	2.5	31
40	BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020, 10, 333-350.e14.	2.9	48
41	Disrupting Mitochondrial Copper Distribution Inhibits Leukemic Stem Cell Self-Renewal. <i>Cell Stem Cell</i> , 2020, 26, 926-937.e10.	5.2	35
42	The mitochondrial peptidase, neurolysin, regulates respiratory chain supercomplex formation and is necessary for AML viability. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	33
43	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
44	Meta-analysis of gene expression profiles of lean and obese PCOS to identify differentially regulated pathways and risk of comorbidities. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1735-1745.	1.9	10
45	Potential therapeutic targets for lung repair during human <i>ex vivo</i> lung perfusion. <i>European Respiratory Journal</i> , 2020, 55, 1902222.	3.1	31
46	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	5.8	30
47	Nanoparticle Uptake in a Spontaneous and Immunocompetent Woodchuck Liver Cancer Model. <i>ACS Nano</i> , 2020, 14, 4698-4715.	7.3	20
48	A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408.	13.7	724
49	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
50	netDx: Software for building interpretable patient classifiers by multi-'omic data integration using patient similarity networks. <i>F1000Research</i> , 2020, 9, 1239.	0.8	2
51	Medulloblastoma Arises from the Persistence of a Rare and Transient Sox2+ Granule Neuron Precursor. <i>Cell Reports</i> , 2020, 31, 107511.	2.9	35
52	Nicotinamide Phosphoribosyltransferase Inhibitors Induce Apoptosis of AML Stem Cells through Dysregulation of Lipid Metabolism. <i>Blood</i> , 2020, 136, 25-26.	0.6	1
53	Mitochondrial carrier homolog 2 is necessary for AML survival. <i>Blood</i> , 2020, 136, 81-92.	0.6	19
54	<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

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55	Large-scale survey and database of high affinity ligands for peptide recognition modules. <i>Molecular Systems Biology</i> , 2020, 16, e9310.	3.2	22
56	netDx: Software for building interpretable patient classifiers by multi-'omic data integration using patient similarity networks. <i>F1000Research</i> , 2020, 9, 1239.	0.8	2
57	IPO11 Regulates the Nuclear Import of BZW1/2 and Is Necessary for AML Cells and Stem Cells. <i>Blood</i> , 2020, 136, 22-23.	0.6	0
58	The Metabolic Enzyme Hexokinase 2 Localizes to the Nucleus in AML and Normal Hematopoietic Stem/Progenitor Cells to Maintain Stemness. <i>Blood</i> , 2020, 136, 1-2.	0.6	0
59	A Stemness-Based Screen Identifies PLK1 Inhibitors for Targeting Leukemia Stem Cells in AML. <i>Blood</i> , 2020, 136, 34-35.	0.6	0
60	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data. , 2020, 16, e1008205.		0
61	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data. , 2020, 16, e1008205.		0
62	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data. , 2020, 16, e1008205.		0
63	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data. , 2020, 16, e1008205.		0
64	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data. , 2020, 16, e1008205.		0
65	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data. , 2020, 16, e1008205.		0
66	EPIC: software toolkit for elution profile-based inference of protein complexes. <i>Nature Methods</i> , 2019, 16, 737-742.	9.0	67
67	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2019. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	7
68	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
69	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
70	Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap. <i>Nature Protocols</i> , 2019, 14, 482-517.	5.5	1,172
71	Bmi1 regulates human glioblastoma stem cells through activation of differential gene networks in CD133+ brain tumor initiating cells. <i>Journal of Neuro-Oncology</i> , 2019, 143, 417-428.	1.4	13
72	Exploring targets of TET2-mediated methylation reprogramming as potential discriminators of prostate cancer progression. <i>Clinical Epigenetics</i> , 2019, 11, 54.	1.8	20

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73	Powerful gene set analysis in GWAS with the Generalized Berk-Jones statistic. <i>PLoS Genetics</i> , 2019, 15, e1007530.	1.5	35
74	netDx: interpretable patient classification using integrated patient similarity networks. <i>Molecular Systems Biology</i> , 2019, 15, e8497.	3.2	65
75	The Mitochondrial Transacylase, Tafazzin, Regulates AML Stemness by Modulating Intracellular Levels of Phospholipids. <i>Cell Stem Cell</i> , 2019, 24, 621-636.e16.	5.2	32
76	Single-cell transcriptomic profiling of the aging mouse brain. <i>Nature Neuroscience</i> , 2019, 22, 1696-1708.	7.1	432
77	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
78	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
79	Identification of CDC25 as a Common Therapeutic Target for Triple-Negative Breast Cancer. <i>Cell Reports</i> , 2018, 23, 112-126.	2.9	58
80	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2017. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	7
81	Automated Computational Inference of Multi-protein Assemblies from Biochemical Co-purification Data. <i>Methods in Molecular Biology</i> , 2018, 1764, 391-399.	0.4	1
82	Induction of rod versus cone photoreceptor-specific progenitors from retinal precursor cells. <i>Stem Cell Research</i> , 2018, 33, 215-227.	0.3	10
83	Single cell RNA sequencing of human liver reveals distinct intrahepatic macrophage populations. <i>Nature Communications</i> , 2018, 9, 4383.	5.8	958
84	Single-Cell RNA Sequencing: A New Window into Cell Scale Dynamics. <i>Biophysical Journal</i> , 2018, 115, 429-435.	0.2	9
85	Transfer learning for biomedical named entity recognition with neural networks. <i>Bioinformatics</i> , 2018, 34, 4087-4094.	1.8	154
86	Patient Similarity Networks for Precision Medicine. <i>Journal of Molecular Biology</i> , 2018, 430, 2924-2938.	2.0	93
87	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. <i>Journal of Cell Biology</i> , 2018, 217, 2951-2974.	2.3	35
88	GeneMANIA update 2018. <i>Nucleic Acids Research</i> , 2018, 46, W60-W64.	6.5	698
89	The Cytoscape Automation app article collection. <i>F1000Research</i> , 2018, 7, 800.	0.8	17
90	scClustViz "Single-cell RNAseq cluster assessment and visualization. <i>F1000Research</i> , 2018, 7, 1522.	0.8	32

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91	scClustViz â€“ Single-cell RNAseq cluster assessment and visualization. F1000Research, 2018, 7, 1522.	0.8	28
92	Integrated analysis of proteome, phosphotyrosineâ€proteome, tyrosineâ€kinome, and tyrosineâ€phosphatome in acute myeloid leukemia. Proteomics, 2017, 17, 1600361.	1.3	17
93	Spatial heterogeneity in medulloblastoma. Nature Genetics, 2017, 49, 780-788.	9.4	112
94	Intertumoral Heterogeneity within Medulloblastoma Subgroups. Cancer Cell, 2017, 31, 737-754.e6.	7.7	836
95	Leveraging increased cytoplasmic nucleoside kinase activity to target mtDNA and oxidative phosphorylation in AML. Blood, 2017, 129, 2657-2666.	0.6	61
96	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. Cancer Research, 2017, 77, 3057-3069.	0.4	33
97	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
98	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
99	Comprehensive Analysis of the Human SH3 Domain Family Reveals a Wide Variety of Non-canonical Specificities. Structure, 2017, 25, 1598-1610.e3.	1.6	105
100	ASCL1 Reorganizes Chromatin to Direct Neuronal Fate and Suppress Tumorigenicity of Glioblastoma Stem Cells. Cell Stem Cell, 2017, 21, 209-224.e7.	5.2	150
101	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF- $\kappa$ B Signaling. Cell Systems, 2017, 5, 564-577.e12.	2.9	44
102	Tracing the origins of relapse in acute myeloid leukaemia to stem cells. Nature, 2017, 547, 104-108.	13.7	424
103	Developmental Emergence of Adult Neural Stem Cells as Revealed by Single-Cell Transcriptional Profiling. Cell Reports, 2017, 21, 3970-3986.	2.9	171
104	A brief history of COMBINE. , 2017, , .		6
105	microRNA-143/145 loss induces Ras signaling to promote aggressive Pten-deficient basal-like breast cancer. JCI Insight, 2017, 2, .	2.3	22
106	Cytoscape.js: a graph theory library for visualisation and analysis. Bioinformatics, 2016, 32, 309-311.	1.8	531
107	Transcriptomic analysis reveals abnormal muscle repair and remodeling in survivors of critical illness with sustained weakness. Scientific Reports, 2016, 6, 29334.	1.6	32
108	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. Cancer Cell, 2016, 30, 891-908.	7.7	191

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109	Musashi-2 attenuates AHR signalling to expand human haematopoietic stem cells. <i>Nature</i> , 2016, 532, 508-511.	13.7	101
110	Global neuroscience and mental health research: a bibliometrics case study. <i>Scientometrics</i> , 2016, 109, 515-531.	1.6	26
111	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
112	Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. <i>Genome Medicine</i> , 2016, 8, 55.	3.6	51
113	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 1-7.	1.0	12
114	Dynamic interplay between locus-specific DNA methylation and hydroxymethylation regulates distinct biological pathways in prostate carcinogenesis. <i>Clinical Epigenetics</i> , 2016, 8, 32.	1.8	20
115	HOX gene complement and expression in the planarian <i>Schmidtea mediterranea</i> . <i>EvoDevo</i> , 2016, 7, 7.	1.3	72
116	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
117	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016, 529, 351-357.	13.7	266
118	Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. <i>Cell</i> , 2016, 164, 293-309.	13.5	399
119	Predicting physiologically relevant SH3 domain mediated protein-protein interactions in yeast. <i>Bioinformatics</i> , 2016, 32, 1865-1872.	1.8	6
120	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
121	RB1 deficiency in triple-negative breast cancer induces mitochondrial protein translation. <i>Journal of Clinical Investigation</i> , 2016, 126, 3739-3757.	3.9	107
122	AutoAnnotate: A Cytoscape app for summarizing networks with semantic annotations. <i>F1000Research</i> , 2016, 5, 1717.	0.8	249
123	Ten Simple Rules for Developing Public Biological Databases. <i>PLoS Computational Biology</i> , 2016, 12, e1005128.	1.5	27
124	The health care and life sciences community profile for dataset descriptions. <i>PeerJ</i> , 2016, 4, e2331.	0.9	18
125	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 289.	1.0	7
126	Specifications of Standards in Systems and Synthetic Biology. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 1-3.	1.0	11



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127	MG-108â€¦Beyond the ACMG 56: Parental choices and initial results from a comprehensive whole genome sequencing-based search for predictive genomic variants in children. <i>Journal of Medical Genetics</i> , 2015, 52, A3.2-A4.	1.5	0
128	Inferring interaction type in gene regulatory networks using co-expression data. <i>Algorithms for Molecular Biology</i> , 2015, 10, 23.	0.3	22
129	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
130	Cardioprotective Signature of Short-Term Caloric Restriction. <i>PLoS ONE</i> , 2015, 10, e0130658.	1.1	47
131	Metabolomic profiling in liver of adiponectin-knockout mice uncovers lysophospholipid metabolism as an important target of adiponectin action. <i>Biochemical Journal</i> , 2015, 469, 71-82.	1.7	20
132	Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. <i>Cancer Cell</i> , 2015, 27, 728-743.	7.7	933
133	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
134	Canadian Open Genetics Repository (COGR): a unified clinical genomics database as a community resource for standardising and sharing genetic interpretations. <i>Journal of Medical Genetics</i> , 2015, 52, 438-445.	1.5	27
135	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
136	GreedyPlus: An Algorithm for the Alignment of Interface Interaction Networks. <i>Scientific Reports</i> , 2015, 5, 12074.	1.6	0
137	Evolutionary Constraint and Disease Associations of Post-Translational Modification Sites in Human Genomes. <i>PLoS Genetics</i> , 2015, 11, e1004919.	1.5	69
138	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015, 12, 615-621.	9.0	297
139	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
140	IL-7 coordinates proliferation, differentiation and Tcra recombination during thymocyte Î²-selection. <i>Nature Immunology</i> , 2015, 16, 397-405.	7.0	93
141	MIMP: predicting the impact of mutations on kinase-substrate phosphorylation. <i>Nature Methods</i> , 2015, 12, 531-533.	9.0	75
142	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
143	EAG2 potassium channel with evolutionarily conserved function as a brain tumor target. <i>Nature Neuroscience</i> , 2015, 18, 1236-1246.	7.1	74
144	Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. <i>Nature Communications</i> , 2015, 6, 8554.	5.8	102

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145	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
146	Systems analysis reveals down-regulation of a network of pro-survival miRNAs drives the apoptotic response in dilated cardiomyopathy. <i>Molecular BioSystems</i> , 2015, 11, 239-251.	2.9	23
147	Long read nanopore sequencing for detection of HLA and CYP2D6 variants and haplotypes. <i>F1000Research</i> , 2015, 4, 17.	0.8	55
148	Long read nanopore sequencing for detection of HLA and CYP2D6 variants and haplotypes. <i>F1000Research</i> , 2015, 4, 17.	0.8	96
149	NetMatchStar: an enhanced Cytoscape network querying App. <i>F1000Research</i> , 2015, 4, 479.	0.8	17
150	NetMatchStar: an enhanced Cytoscape network querying App. <i>F1000Research</i> , 2015, 4, 479.	0.8	11
151	Social Network: a Cytoscape app for visualizing co-authorship networks. <i>F1000Research</i> , 2015, 4, 481.	0.8	12
152	Antitumor activity of the novel multi-kinase inhibitor EC-70124 in triple negative breast cancer. <i>Oncotarget</i> , 2015, 6, 27923-27937.	0.8	24
153	Identification of CD146 as a marker enriched for tumor-propagating capacity reveals targetable pathways in primary human sarcoma. <i>Oncotarget</i> , 2015, 6, 40283-40294.	0.8	15
154	Specifications of Standards in Systems and Synthetic Biology. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 258.	1.0	14
155	Social Network: a Cytoscape app for visualizing co-publication networks. <i>F1000Research</i> , 2015, 4, 481.	0.8	6
156	Prediction and Experimental Characterization of nsSNPs Altering Human PDZ-Binding Motifs. <i>PLoS ONE</i> , 2014, 9, e94507.	1.1	10
157	Enrichment Map – a Cytoscape app to visualize and explore OMICs pathway enrichment results. <i>F1000Research</i> , 2014, 3, 141.	0.8	128
158	Network Assessor: An automated method for quantitative assessment of a network's potential for gene function prediction. <i>Frontiers in Genetics</i> , 2014, 5, 123.	1.1	10
159	Combined deletion of p53 and p16 in mammary epithelium accelerates triple negative breast cancer with dependency on E2K. <i>EMBO Molecular Medicine</i> , 2014, 6, 1542-1560.	3.3	91
160	Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. <i>Molecular Systems Biology</i> , 2014, 10, .	3.2	4
161	HyperModules: identifying clinically and phenotypically significant network modules with disease mutations for biomarker discovery. <i>Bioinformatics</i> , 2014, 30, 2230-2232.	1.8	28
162	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. <i>Science</i> , 2014, 344, 208-211.	6.0	217

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163	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. <i>Nature</i> , 2014, 506, 445-450.	13.7	521
164	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothed Inhibition. <i>Cancer Cell</i> , 2014, 25, 393-405.	7.7	627
165	A draft map of the human proteome. <i>Nature</i> , 2014, 509, 575-581.	13.7	1,948
166	Highlights of B/D-HPP and HPP Resource Pillar Workshops at 12th Annual HUPO World Congress of Proteomics. <i>Proteomics</i> , 2014, 14, 975-988.	1.3	13
167	Intercellular network structure and regulatory motifs in the human hematopoietic system. <i>Molecular Systems Biology</i> , 2014, 10, 741.	3.2	57
168	Biological Network Exploration with Cytoscape 3. <i>Current Protocols in Bioinformatics</i> , 2014, 47, 8.13.1-24.	25.8	780
169	Enhancer hijacking activates GF1 family oncogenes in medulloblastoma. <i>Nature</i> , 2014, 511, 428-434.	13.7	520
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