

# Gary D Bader

## List of Publications by Year in Descending Order

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**Version:** 2024-04-25

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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  
papers

46,921  
citations

85  
h-index

216  
g-index

342  
ext. papers

58,522  
ext. citations

13.7  
avg, IF

7.15  
L-index

#	Paper	IF	Citations
276	Hypophosphorylated pRb knock-in mice exhibit hallmarks of aging and vitamin C-preventable diabetes.. <i>EMBO Journal</i> , <b>2022</b> , e106825	13	1
275	A Shared Transcriptional Identity for Forebrain and Dentate Gyrus Neural Stem Cells from Embryogenesis to Adulthood.. <i>ENeuro</i> , <b>2022</b> ,	3.9	2
274	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> , <b>2022</b> , 38, 110481	10.6	0
273	OpenPIP: An Open-source Platform for Hosting, Visualizing and Analyzing Protein Interaction Data. <i>Journal of Molecular Biology</i> , <b>2022</b> , 167603	6.5	0
272	Sphingosine-1-phosphate receptor 3 potentiates inflammatory programs in normal and leukemia stem cells to promote differentiation. <i>Blood Cancer Discovery</i> , <b>2021</b> , 2, 32-53	7	9
271	Single-Cell, Single-Nucleus, and Spatial RNA Sequencing of the Human Liver Identifies Cholangiocyte and Mesenchymal Heterogeneity. <i>Hepatology Communications</i> , <b>2021</b> ,	6	10
270	A flexible search system for high-accuracy identification of biological entities and molecules. <i>Journal of Open Source Software</i> , <b>2021</b> , 6, 3756	5.2	0
269	A microfluidic platform enables comprehensive gene expression profiling of mouse retinal stem cells. <i>Lab on A Chip</i> , <b>2021</b> , 21, 4464-4476	7.2	0
268	The reactome pathway knowledgebase 2022. <i>Nucleic Acids Research</i> , <b>2021</b> ,	20.1	57
267	The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , <b>2021</b> , 12, 1749	17.4	7
266	Tutorial: guidelines for annotating single-cell transcriptomic maps using automated and manual methods. <i>Nature Protocols</i> , <b>2021</b> , 16, 2749-2764	18.8	6
265	Generation of mature compact ventricular cardiomyocytes from human pluripotent stem cells. <i>Nature Communications</i> , <b>2021</b> , 12, 3155	17.4	23
264	Surveilling and Tracking COVID-19 Patients Using a Portable Quantum Dot Smartphone Device. <i>Nano Letters</i> , <b>2021</b> , 21, 5209-5216	11.5	8
263	DeCLUTR: Deep Contrastive Learning for Unsupervised Textual Representations <b>2021</b> ,		14
262	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity.. <i>Nature Cancer</i> , <b>2021</b> , 2, 157-173	15.4	31
261	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , <b>2021</b> , 12, 979	17.4	23
260	Biological and therapeutic implications of a unique subtype of NPM1 mutated AML. <i>Nature Communications</i> , <b>2021</b> , 12, 1054	17.4	7

259	Distinct DNA methylation patterns associated with treatment resistance in metastatic castration resistant prostate cancer. <i>Scientific Reports</i> , <b>2021</b> , 11, 6630	4.9	4
258	SBGN Bricks Ontology as a tool to describe recurring concepts in molecular networks. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	2
257	Nicotinamide phosphoribosyltransferase inhibitors selectively induce apoptosis of AML stem cells by disrupting lipid homeostasis. <i>Cell Stem Cell</i> , <b>2021</b> , 28, 1851-1867.e8	18	5
256	Control of tissue development and cell diversity by cell cycle-dependent transcriptional filtering. <i>ELife</i> , <b>2021</b> , 10,	8.9	3
255	A clinically applicable integrative molecular classification of meningiomas. <i>Nature</i> , <b>2021</b> , 597, 119-125	50.4	25
254	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , <b>2021</b> , 597, 196-205	50.4	18
253	Temporal profiling of therapy resistance in human medulloblastoma identifies novel targetable drivers of recurrence. <i>Science Advances</i> , <b>2021</b> , 7, eabi5568	14.3	0
252	CD200 expression marks leukemia stem cells in human AML. <i>Blood Advances</i> , <b>2020</b> , 4, 5402-5413	7.8	13
251	BraInMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , <b>2020</b> , 10, 333-350.e14	10.6	13
250	Disrupting Mitochondrial Copper Distribution Inhibits Leukemic Stem Cell Self-Renewal. <i>Cell Stem Cell</i> , <b>2020</b> , 26, 926-937.e10	18	16
249	The mitochondrial peptidase, neurolysin, regulates respiratory chain supercomplex formation and is necessary for AML viability. <i>Science Translational Medicine</i> , <b>2020</b> , 12,	17.5	22
248	Generation of Functional Liver Sinusoidal Endothelial Cells from Human Pluripotent Stem-Cell-Derived Venous Angioblasts. <i>Cell Stem Cell</i> , <b>2020</b> , 27, 254-269.e9	18	17
247	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> , <b>2020</b> , 18, 1735-1745	6.8	2
246	Potential therapeutic targets for lung repair during human lung perfusion. <i>European Respiratory Journal</i> , <b>2020</b> , 55,	13.6	8
245	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , <b>2020</b> , 11, 312	17.4	20
244	Nanoparticle Uptake in a Spontaneous and Immunocompetent Woodchuck Liver Cancer Model. <i>ACS Nano</i> , <b>2020</b> , 14, 4698-4715	16.7	13
243	A reference map of the human binary protein interactome. <i>Nature</i> , <b>2020</b> , 580, 402-408	50.4	269
242	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D489-D497	20.1	71

241	IPO11 Regulates the Nuclear Import of BZW1/2 and Is Necessary for AML Cells and Stem Cells. <i>Blood</i> , <b>2020</b> , 136, 22-23	2.2	
240	The Metabolic Enzyme Hexokinase 2 Localizes to the Nucleus in AML and Normal Hematopoietic Stem/Progenitor Cells to Maintain Stemness. <i>Blood</i> , <b>2020</b> , 136, 1-2	2.2	
239	A Stemness-Based Screen Identifies PLK1 Inhibitors for Targeting Leukemia Stem Cells in AML. <i>Blood</i> , <b>2020</b> , 136, 34-35	2.2	
238	Nicotinamide Phosphoribosyltransferase Inhibitors Induce Apoptosis of AML Stem Cells through Dysregulation of Lipid Metabolism. <i>Blood</i> , <b>2020</b> , 136, 25-26	2.2	1
237	Mitochondrial carrier homolog 2 is necessary for AML survival. <i>Blood</i> , <b>2020</b> , 136, 81-92	2.2	8
236	SBML Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , <b>2020</b> , 16, e9110	12.2	65
235	Large-scale survey and database of high affinity ligands for peptide recognition modules. <i>Molecular Systems Biology</i> , <b>2020</b> , 16, e9310	12.2	11
234	netDx: Software for building interpretable patient classifiers by multi-omic data integration using patient similarity networks. <i>F1000Research</i> , <b>2020</b> , 9, 1239	3.6	1
233	Medulloblastoma Arises from the Persistence of a Rare and Transient Sox2 Granule Neuron Precursor. <i>Cell Reports</i> , <b>2020</b> , 31, 107511	10.6	10
232	Towards reliable named entity recognition in the biomedical domain. <i>Bioinformatics</i> , <b>2020</b> , 36, 280-286	7.2	29
231	Single-Cell Profiling Shows Murine Forebrain Neural Stem Cells Reacquire a Developmental State when Activated for Adult Neurogenesis. <i>Cell Reports</i> , <b>2020</b> , 32, 108022	10.6	18
230	Distinct fibroblast functional states drive clinical outcomes in ovarian cancer and are regulated by TCF21. <i>Journal of Experimental Medicine</i> , <b>2020</b> , 217,	16.6	17
229	Functional genomic landscape of cancer-intrinsic evasion of killing by T cells. <i>Nature</i> , <b>2020</b> , 586, 120-126	50.4	82
228	Wnt activation as a therapeutic strategy in medulloblastoma. <i>Nature Communications</i> , <b>2020</b> , 11, 4323	17.4	13
227	Dynamics of the cell-free DNA methylome of metastatic prostate cancer during androgen-targeting treatment. <i>Epigenomics</i> , <b>2020</b> , 12, 1317-1332	4.4	6
226	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1008205	5	20
225	Relapse-Fated Latent Diagnosis Subclones in Acute B Lineage Leukemia Are Drug Tolerant and Possess Distinct Metabolic Programs. <i>Cancer Discovery</i> , <b>2020</b> , 10, 568-587	24.4	37
224	netDx: Software for building interpretable patient classifiers by multi-omic data integration using patient similarity networks. <i>F1000Research</i> , <b>2020</b> , 9, 1239	3.6	1

223	Rewiring of the Human Mitochondrial Interactome during Neuronal Reprogramming Reveals Regulators of the Respirasome and Neurogenesis. <i>iScience</i> , <b>2019</b> , 19, 1114-1132	6.1	17
222	Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap. <i>Nature Protocols</i> , <b>2019</b> , 14, 482-517	18.8	515
221	Bmi1 regulates human glioblastoma stem cells through activation of differential gene networks in CD133+ brain tumor initiating cells. <i>Journal of Neuro-Oncology</i> , <b>2019</b> , 143, 417-428	4.8	9
220	Exploring targets of TET2-mediated methylation reprogramming as potential discriminators of prostate cancer progression. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 54	7.7	8
219	Powerful gene set analysis in GWAS with the Generalized Berk-Jones statistic. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1007530	6	20
218	netDx: interpretable patient classification using integrated patient similarity networks. <i>Molecular Systems Biology</i> , <b>2019</b> , 15, e8497	12.2	34
217	The Mitochondrial Transacylase, Tafazzin, Regulates for AML Stemness by Modulating Intracellular Levels of Phospholipids. <i>Cell Stem Cell</i> , <b>2019</b> , 24, 621-636.e16	18	19
216	EPIC: software toolkit for elution profile-based inference of protein complexes. <i>Nature Methods</i> , <b>2019</b> , 16, 737-742	21.6	34
215	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2019. <i>Journal of Integrative Bioinformatics</i> , <b>2019</b> , 16,	3.8	5
214	Sphingolipid Modulation Activates Proteostasis Programs to Govern Human Hematopoietic Stem Cell Self-Renewal. <i>Cell Stem Cell</i> , <b>2019</b> , 25, 639-653.e7	18	40
213	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , <b>2019</b> , 8,	3.6	28
212	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , <b>2019</b> , 8, 296	3.6	23
211	Single-cell transcriptomic profiling of the aging mouse brain. <i>Nature Neuroscience</i> , <b>2019</b> , 22, 1696-1708	25.5	152
210	Identification of CDC25 as a Common Therapeutic Target for Triple-Negative Breast Cancer. <i>Cell Reports</i> , <b>2018</b> , 23, 112-126	10.6	38
209	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2017. <i>Journal of Integrative Bioinformatics</i> , <b>2018</b> , 15,	3.8	5
208	Automated Computational Inference of Multi-protein Assemblies from Biochemical Co-purification Data. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1764, 391-399	1.4	1
207	Single-Cell RNA Sequencing: A New Window into Cell Scale Dynamics. <i>Biophysical Journal</i> , <b>2018</b> , 115, 429-435	2.9	6
206	Transfer learning for biomedical named entity recognition with neural networks. <i>Bioinformatics</i> , <b>2018</b> , 34, 4087-4094	7.2	98

205	Patient Similarity Networks for Precision Medicine. <i>Journal of Molecular Biology</i> , <b>2018</b> , 430, 2924-2938	6.5	48
204	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. <i>Journal of Cell Biology</i> , <b>2018</b> , 217, 2951-2974	7.3	20
203	GeneMANIA update 2018. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, W60-W64	20.1	309
202	scClustViz - Single-cell RNAseq cluster assessment and visualization. <i>F1000Research</i> , <b>2018</b> , 7,	3.6	15
201	scClustViz Single-cell RNAseq cluster assessment and visualization. <i>F1000Research</i> , <b>2018</b> , 7, 1522	3.6	17
200	Induction of rod versus cone photoreceptor-specific progenitors from retinal precursor cells. <i>Stem Cell Research</i> , <b>2018</b> , 33, 215-227	1.6	8
199	Single cell RNA sequencing of human liver reveals distinct intrahepatic macrophage populations. <i>Nature Communications</i> , <b>2018</b> , 9, 4383	17.4	452
198	Integrated analysis of proteome, phosphotyrosine-proteome, tyrosine-kinome, and tyrosine-phosphatome in acute myeloid leukemia. <i>Proteomics</i> , <b>2017</b> , 17, 1600361	4.8	12
197	Spatial heterogeneity in medulloblastoma. <i>Nature Genetics</i> , <b>2017</b> , 49, 780-788	36.3	80
196	Intertumoral Heterogeneity within Medulloblastoma Subgroups. <i>Cancer Cell</i> , <b>2017</b> , 31, 737-754.e6	24.3	511
195	Leveraging increased cytoplasmic nucleoside kinase activity to target mtDNA and oxidative phosphorylation in AML. <i>Blood</i> , <b>2017</b> , 129, 2657-2666	2.2	43
194	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. <i>Cancer Research</i> , <b>2017</b> , 77, 3057-3069	10.1	20
193	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , <b>2017</b> , 551, 92-94	50.4	643
192	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , <b>2017</b> , 49, 1767-1778	36.3	186
191	Comprehensive Analysis of the Human SH3 Domain Family Reveals a Wide Variety of Non-canonical Specificities. <i>Structure</i> , <b>2017</b> , 25, 1598-1610.e3	5.2	56
190	ASCL1 Reorganizes Chromatin to Direct Neuronal Fate and Suppress Tumorigenicity of Glioblastoma Stem Cells. <i>Cell Stem Cell</i> , <b>2017</b> , 21, 209-224.e7	18	78
189	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF- $\kappa$ B Signaling. <i>Cell Systems</i> , <b>2017</b> , 5, 564-577.e12	10.6	37
188	Tracing the origins of relapse in acute myeloid leukaemia to stem cells. <i>Nature</i> , <b>2017</b> , 547, 104-108	50.4	274

187	Developmental Emergence of Adult Neural Stem Cells as Revealed by Single-Cell Transcriptional Profiling. <i>Cell Reports</i> , <b>2017</b> , 21, 3970-3986	10.6	96
186	A brief history of COMBINE <b>2017</b> ,		3
185	microRNA-143/145 loss induces Ras signaling to promote aggressive Pten-deficient basal-like breast cancer. <i>JCI Insight</i> , <b>2017</b> , 2,	9.9	16
184	Cytoscape.js: a graph theory library for visualisation and analysis. <i>Bioinformatics</i> , <b>2016</b> , 32, 309-11	7.2	261
183	Global neuroscience and mental health research: a bibliometrics case study. <i>Scientometrics</i> , <b>2016</b> , 109, 515-531	3	6
182	Ectopic miR-125a Expression Induces Long-Term Repopulating Stem Cell Capacity in Mouse and Human Hematopoietic Progenitors. <i>Cell Stem Cell</i> , <b>2016</b> , 19, 383-96	18	40
181	Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. <i>Genome Medicine</i> , <b>2016</b> , 8, 55	14.4	31
180	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. <i>Journal of Integrative Bioinformatics</i> , <b>2016</b> , 13, 1-7	3.8	7
179	Dynamic interplay between locus-specific DNA methylation and hydroxymethylation regulates distinct biological pathways in prostate carcinogenesis. <i>Clinical Epigenetics</i> , <b>2016</b> , 8, 32	7.7	16
178	HOX gene complement and expression in the planarian <i>Schmidtea mediterranea</i> . <i>EvoDevo</i> , <b>2016</b> , 7, 7	3.2	49
177	Inhibition of Dopamine Receptor D4 Impedes Autophagic Flux, Proliferation, and Survival of Glioblastoma Stem Cells. <i>Cancer Cell</i> , <b>2016</b> , 29, 859-873	24.3	124
176	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , <b>2016</b> , 529, 351-7	50.4	206
175	Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. <i>Cell</i> , <b>2016</b> , 164, 293-309	56.2	259
174	Predicting physiologically relevant SH3 domain mediated protein-protein interactions in yeast. <i>Bioinformatics</i> , <b>2016</b> , 32, 1865-72	7.2	3
173	miR-126 Regulates Distinct Self-Renewal Outcomes in Normal and Malignant Hematopoietic Stem Cells. <i>Cancer Cell</i> , <b>2016</b> , 29, 214-28	24.3	118
172	RB1 deficiency in triple-negative breast cancer induces mitochondrial protein translation. <i>Journal of Clinical Investigation</i> , <b>2016</b> , 126, 3739-3757	15.9	65
171	AutoAnnotate: A Cytoscape app for summarizing networks with semantic annotations. <i>F1000Research</i> , <b>2016</b> , 5, 1717	3.6	126
170	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. <i>Journal of Integrative Bioinformatics</i> , <b>2016</b> , 13, 289	3.8	3

169	The health care and life sciences community profile for dataset descriptions. <i>PeerJ</i> , <b>2016</b> , 4, e2331	3.1	14
168	Transcriptomic analysis reveals abnormal muscle repair and remodeling in survivors of critical illness with sustained weakness. <i>Scientific Reports</i> , <b>2016</b> , 6, 29334	4.9	18
167	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. <i>Cancer Cell</i> , <b>2016</b> , 30, 891-908	24.3	135
166	Musashi-2 attenuates AHR signalling to expand human haematopoietic stem cells. <i>Nature</i> , <b>2016</b> , 532, 508-511	50.4	71
165	GreedyPlus: An Algorithm for the Alignment of Interface Interaction Networks. <i>Scientific Reports</i> , <b>2015</b> , 5, 12074	4.9	
164	Evolutionary constraint and disease associations of post-translational modification sites in human genomes. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1004919	6	52
163	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , <b>2015</b> , 12, 615-621	21.6	235
162	Molecular subgroups of atypical teratoid rhabdoid tumours in children: an integrated genomic and clinicopathological analysis. <i>Lancet Oncology</i> , <b>2015</b> , 16, 569-82	21.7	117
161	IL-7 coordinates proliferation, differentiation and Tcra recombination during thymocyte selection. <i>Nature Immunology</i> , <b>2015</b> , 16, 397-405	19.1	64
160	MIMP: predicting the impact of mutations on kinase-substrate phosphorylation. <i>Nature Methods</i> , <b>2015</b> , 12, 531-3	21.6	50
159	Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in Escherichia coli. <i>Bioinformatics</i> , <b>2015</b> , 31, 306-10	7.2	31
158	EAG2 potassium channel with evolutionarily conserved function as a brain tumor target. <i>Nature Neuroscience</i> , <b>2015</b> , 18, 1236-46	25.5	56
157	Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. <i>Nature Communications</i> , <b>2015</b> , 6, 8554	17.4	71
156	Comparative analysis of co-expression networks reveals molecular changes during the cancer progression. <i>IFMBE Proceedings</i> , <b>2015</b> , 1481-1487	0.2	3
155	A Progesterone-CXCR4 Axis Controls Mammary Progenitor Cell Fate in the Adult Gland. <i>Stem Cell Reports</i> , <b>2015</b> , 4, 313-322	8	29
154	Systems analysis reveals down-regulation of a network of pro-survival miRNAs drives the apoptotic response in dilated cardiomyopathy. <i>Molecular BioSystems</i> , <b>2015</b> , 11, 239-51		17
153	Specifications of Standards in Systems and Synthetic Biology. <i>Journal of Integrative Bioinformatics</i> , <b>2015</b> , 12, 1-3	3.8	7
152	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. <i>Journal of Medical Genetics</i> , <b>2015</b> , 52, A3.2-A4	5.8	



151	A Progesterone-CXCR4 Axis Controls Mammary Progenitor Cell Fate in the Adult Gland. <i>Stem Cell Reports</i> , <b>2015</b> , 4, 529	8	78
150	Inferring interaction type in gene regulatory networks using co-expression data. <i>Algorithms for Molecular Biology</i> , <b>2015</b> , 10, 23	1.8	16
149	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2015</b> , 3, 19	5.8	56
148	Cardioprotective Signature of Short-Term Caloric Restriction. <i>PLoS ONE</i> , <b>2015</b> , 10, e0130658	3.7	43
147	Metabolomic profiling in liver of adiponectin-knockout mice uncovers lysophospholipid metabolism as an important target of adiponectin action. <i>Biochemical Journal</i> , <b>2015</b> , 469, 71-82	3.8	16
146	Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. <i>Cancer Cell</i> , <b>2015</b> , 27, 728-43	24.3	672
145	Inhibition of the Mitochondrial Protease ClpP as a Therapeutic Strategy for Human Acute Myeloid Leukemia. <i>Cancer Cell</i> , <b>2015</b> , 27, 864-76	24.3	191
144	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> , <b>2015</b> , 52, 438-45	5.8	23
143	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> , <b>2015</b> , 112, 851-6	11.5	251
142	Long read nanopore sequencing for detection of HLA and CYP2D6 variants and haplotypes. <i>F1000Research</i> , <b>2015</b> , 4, 17	3.6	50
141	Long read nanopore sequencing for detection of HLA and CYP2D6 variants and haplotypes. <i>F1000Research</i> , <b>2015</b> , 4, 17	3.6	75
140	NetMatchStar: an enhanced Cytoscape network querying app. <i>F1000Research</i> , <b>2015</b> , 4, 479	3.6	13
139	NetMatchStar: an enhanced Cytoscape network querying app. <i>F1000Research</i> , <b>2015</b> , 4, 479	3.6	8
138	Social Network: a Cytoscape app for visualizing co-publication networks. <i>F1000Research</i> , <b>2015</b> , 4, 481	3.6	10
137	Antitumor activity of the novel multi-kinase inhibitor EC-70124 in triple negative breast cancer. <i>Oncotarget</i> , <b>2015</b> , 6, 27923-37	3.3	19
136	Identification of CD146 as a marker enriched for tumor-propagating capacity reveals targetable pathways in primary human sarcoma. <i>Oncotarget</i> , <b>2015</b> , 6, 40283-94	3.3	13
135	Specifications of Standards in Systems and Synthetic Biology. <i>Journal of Integrative Bioinformatics</i> , <b>2015</b> , 12, 258	3.8	8
134	Social Network: a Cytoscape app for visualizing co-publication networks. <i>F1000Research</i> , <b>2015</b> , 4, 481	3.6	6

133	Mapping the cellular response to small molecules using chemogenomic fitness signatures. <i>Science</i> , <b>2014</b> , 344, 208-11	33.3	174
132	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. <i>Nature</i> , <b>2014</b> , 506, 445-50	50.4	434
131	Genome sequencing of SHH medulloblastoma predicts genotype-related response to smoothed inhibition. <i>Cancer Cell</i> , <b>2014</b> , 25, 393-405	24.3	469
130	A draft map of the human proteome. <i>Nature</i> , <b>2014</b> , 509, 575-81	50.4	1520
129	Highlights of B/D-HPP and HPP Resource Pillar Workshops at 12th Annual HUPO World Congress of Proteomics: September 14-18, 2013, Yokohama, Japan. <i>Proteomics</i> , <b>2014</b> , 14, 975-88	4.8	13
128	Intercellular network structure and regulatory motifs in the human hematopoietic system. <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 741	12.2	41
127	Biological network exploration with Cytoscape 3. <i>Current Protocols in Bioinformatics</i> , <b>2014</b> , 47, 8.13.1-24	24.2	490
126	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. <i>Nature</i> , <b>2014</b> , 511, 428-34	50.4	377
125	Quiescent sox2(+) cells drive hierarchical growth and relapse in sonic hedgehog subgroup medulloblastoma. <i>Cancer Cell</i> , <b>2014</b> , 26, 33-47	24.3	181
124	Prediction and experimental characterization of nsSNPs altering human PDZ-binding motifs. <i>PLoS ONE</i> , <b>2014</b> , 9, e94507	3.7	8
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