

# Benjamin Haibe-Kains

## List of Publications by Citations

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233  
papers

19,041  
citations

64  
h-index

136  
g-index

282  
ext. papers

23,945  
ext. citations

10.7  
avg, IF

6.39  
L-index

#	Paper	IF	Citations
233	Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach. <i>Nature Communications</i> , <b>2014</b> , 5, 4006	17.4	2330
232	Gene expression profiling in breast cancer: understanding the molecular basis of histologic grade to improve prognosis. <i>Journal of the National Cancer Institute</i> , <b>2006</b> , 98, 262-72	9.7	1485
231	Similarity network fusion for aggregating data types on a genomic scale. <i>Nature Methods</i> , <b>2014</b> , 11, 333-7	11.6	849
230	Strong time dependence of the 76-gene prognostic signature for node-negative breast cancer patients in the TRANSBIG multicenter independent validation series. <i>Clinical Cancer Research</i> , <b>2007</b> , 13, 3207-14	12.9	759
229	Meta-analysis of gene expression profiles in breast cancer: toward a unified understanding of breast cancer subtyping and prognosis signatures. <i>Breast Cancer Research</i> , <b>2008</b> , 10, R65	8.3	658
228	Definition of clinically distinct molecular subtypes in estrogen receptor-positive breast carcinomas through genomic grade. <i>Journal of Clinical Oncology</i> , <b>2007</b> , 25, 1239-46	2.2	650
227	Biological processes associated with breast cancer clinical outcome depend on the molecular subtypes. <i>Clinical Cancer Research</i> , <b>2008</b> , 14, 5158-65	12.9	641
226	CD4+ follicular helper T cell infiltration predicts breast cancer survival. <i>Journal of Clinical Investigation</i> , <b>2013</b> , 123, 2873-92	15.9	554
225	CT-based radiomic signature predicts distant metastasis in lung adenocarcinoma. <i>Radiotherapy and Oncology</i> , <b>2015</b> , 114, 345-50	5.3	444
224	Robust Radiomics feature quantification using semiautomatic volumetric segmentation. <i>PLoS ONE</i> , <b>2014</b> , 9, e102107	3.7	363
223	Inconsistency in large pharmacogenomic studies. <i>Nature</i> , <b>2013</b> , 504, 389-93	50.4	360
222	CD73 promotes anthracycline resistance and poor prognosis in triple negative breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 11091-6	11.5	303
221	PIK3CA mutations associated with gene signature of low mTORC1 signaling and better outcomes in estrogen receptor-positive breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 10208-13	11.5	293
220	Radiomic feature clusters and prognostic signatures specific for Lung and Head & Neck cancer. <i>Scientific Reports</i> , <b>2015</b> , 5, 11044	4.9	292
219	Predicting prognosis using molecular profiling in estrogen receptor-positive breast cancer treated with tamoxifen. <i>BMC Genomics</i> , <b>2008</b> , 9, 239	4.5	272
218	survcomp: an R/Bioconductor package for performance assessment and comparison of survival models. <i>Bioinformatics</i> , <b>2011</b> , 27, 3206-8	7.2	267
217	Amplification of LAPT4B and YWHAZ contributes to chemotherapy resistance and recurrence of breast cancer. <i>Nature Medicine</i> , <b>2010</b> , 16, 214-8	50.5	262

216	Elucidating prognosis and biology of breast cancer arising in young women using gene expression profiling. <i>Clinical Cancer Research</i> , <b>2012</b> , 18, 1341-51	12.9	239
215	A three-gene model to robustly identify breast cancer molecular subtypes. <i>Journal of the National Cancer Institute</i> , <b>2012</b> , 104, 311-25	9.7	218
214	microRNA-29c and microRNA-223 down-regulation has in vivo significance in chronic lymphocytic leukemia and improves disease risk stratification. <i>Blood</i> , <b>2009</b> , 113, 5237-45	2.2	204
213	Global microRNA expression profiling identifies MiR-210 associated with tumor proliferation, invasion and poor clinical outcome in breast cancer. <i>PLoS ONE</i> , <b>2011</b> , 6, e20980	3.7	175
212	DNA methylation profiling reveals a predominant immune component in breast cancers. <i>EMBO Molecular Medicine</i> , <b>2011</b> , 3, 726-41	12	167
211	Gene modules and response to neoadjuvant chemotherapy in breast cancer subtypes: a pooled analysis. <i>Journal of Clinical Oncology</i> , <b>2012</b> , 30, 1996-2004	2.2	167
210	Defining the biological basis of radiomic phenotypes in lung cancer. <i>ELife</i> , <b>2017</b> , 6,	8.9	158
209	A comparative study of survival models for breast cancer prognostication based on microarray data: does a single gene beat them all?. <i>Bioinformatics</i> , <b>2008</b> , 24, 2200-8	7.2	157
208	Genomic grade index is associated with response to chemotherapy in patients with breast cancer. <i>Journal of Clinical Oncology</i> , <b>2009</b> , 27, 3185-91	2.2	153
207	Genefu: an R/Bioconductor package for computation of gene expression-based signatures in breast cancer. <i>Bioinformatics</i> , <b>2016</b> , 32, 1097-9	7.2	150
206	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. <i>Nature Genetics</i> , <b>2020</b> , 52, 231-240	36.3	148
205	Multifactorial approach to predicting resistance to anthracyclines. <i>Journal of Clinical Oncology</i> , <b>2011</b> , 29, 1578-86	2.2	143
204	CD73 is associated with poor prognosis in high-grade serous ovarian cancer. <i>Cancer Research</i> , <b>2015</b> , 75, 4494-503	10.1	142
203	Vulnerabilities of radiomic signature development: The need for safeguards. <i>Radiotherapy and Oncology</i> , <b>2019</b> , 130, 2-9	5.3	137
202	PharmacGx: an R package for analysis of large pharmacogenomic datasets. <i>Bioinformatics</i> , <b>2016</b> , 32, 1244-6	7.2	127
201	Spatially distinct tumor immune microenvironments stratify triple-negative breast cancers. <i>Journal of Clinical Investigation</i> , <b>2019</b> , 129, 1785-1800	15.9	125
200	ZNF143 provides sequence specificity to secure chromatin interactions at gene promoters. <i>Nature Communications</i> , <b>2015</b> , 2, 6186	17.4	123
199	curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2013</b> , 2013, bat013	5	123

198	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , <b>2019</b> , 10, 2674	17.4	119
197	mRMRe: an R package for parallelized mRMR ensemble feature selection. <i>Bioinformatics</i> , <b>2013</b> , 29, 2365-82	7.8	117
196	Comparison of prognostic gene expression signatures for breast cancer. <i>BMC Genomics</i> , <b>2008</b> , 9, 394	4.5	110
195	A review of connectivity map and computational approaches in pharmacogenomics. <i>Briefings in Bioinformatics</i> , <b>2018</b> , 19, 506-523	13.4	101
194	Assessment of an RNA interference screen-derived mitotic and ceramide pathway metagene as a predictor of response to neoadjuvant paclitaxel for primary triple-negative breast cancer: a retrospective analysis of five clinical trials. <i>Lancet Oncology</i> , <b>2010</b> , 11, 358-65	21.7	97
193	APOBEC3B expression in breast cancer reflects cellular proliferation, while a deletion polymorphism is associated with immune activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 2841-6	11.5	95
192	Adenosine 2B Receptor Expression on Cancer Cells Promotes Metastasis. <i>Cancer Research</i> , <b>2016</b> , 76, 4372-82	10.1	94
191	Estrogen receptor negative/progesterone receptor positive breast cancer is not a reproducible subtype. <i>Breast Cancer Research</i> , <b>2013</b> , 15, R68	8.3	92
190	GeneSigDB: a manually curated database and resource for analysis of gene expression signatures. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D1060-6	20.1	89
189	Gene regulatory networks and their applications: understanding biological and medical problems in terms of networks. <i>Frontiers in Cell and Developmental Biology</i> , <b>2014</b> , 2, 38	5.7	86
188	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , <b>2020</b> , 586, E14-E16	50.4	85
187	Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian cancer. <i>PLoS ONE</i> , <b>2012</b> , 7, e30269	3.7	84
186	Long-term in vitro treatment of human glioblastoma cells with temozolomide increases resistance in vivo through up-regulation of GLUT transporter and aldo-keto reductase enzyme AKR1C expression. <i>Neoplasia</i> , <b>2010</b> , 12, 727-39	6.4	83
185	PharmacoDB: an integrative database for mining in vitro anticancer drug screening studies. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D994-D1002	20.1	82
184	Evidence of galectin-1 involvement in glioma chemoresistance. <i>Toxicology and Applied Pharmacology</i> , <b>2008</b> , 229, 172-83	4.6	81
183	Metabolic regulation of dermal fibroblasts contributes to skin extracellular matrix homeostasis and fibrosis. <i>Nature Metabolism</i> , <b>2019</b> , 1, 147-157	14.6	79
182	Comparative meta-analysis of prognostic gene signatures for late-stage ovarian cancer. <i>Journal of the National Cancer Institute</i> , <b>2014</b> , 106,	9.7	77
181	Rac-specific guanine nucleotide exchange factor DOCK1 is a critical regulator of HER2-mediated breast cancer metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 7434-9	11.5	73

180	ONECUT2 is a driver of neuroendocrine prostate cancer. <i>Nature Communications</i> , <b>2019</b> , 10, 278	17.4	72
179	Knocking down galectin 1 in human hs683 glioblastoma cells impairs both angiogenesis and endoplasmic reticulum stress responses. <i>Journal of Neuropathology and Experimental Neurology</i> , <b>2008</b> , 67, 456-69	3.1	72
178	4-IBP, a sigma1 receptor agonist, decreases the migration of human cancer cells, including glioblastoma cells, in vitro and sensitizes them in vitro and in vivo to cytotoxic insults of proapoptotic and proautophagic drugs. <i>Neoplasia</i> , <b>2007</b> , 9, 358-69	6.4	72
177	Scoring of tumor-infiltrating lymphocytes: From visual estimation to machine learning. <i>Seminars in Cancer Biology</i> , <b>2018</b> , 52, 151-157	12.7	71
176	MicroRNA paraffin-based studies in osteosarcoma reveal reproducible independent prognostic profiles at 14q32. <i>Genome Medicine</i> , <b>2013</b> , 5, 2	14.4	69
175	Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy. <i>Cell</i> , <b>2021</b> , 184, 226-243.e2168	33.2	68
174	Improvement of the clinical applicability of the Genomic Grade Index through a qRT-PCR test performed on frozen and formalin-fixed paraffin-embedded tissues. <i>BMC Genomics</i> , <b>2009</b> , 10, 424	4.5	67
173	A genome-wide aberrant RNA splicing in patients with acute myeloid leukemia identifies novel potential disease markers and therapeutic targets. <i>Clinical Cancer Research</i> , <b>2014</b> , 20, 1135-45	12.9	65
172	Loss of Pgc-1 $\alpha$ expression in aging mouse muscle potentiates glucose intolerance and systemic inflammation. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , <b>2014</b> , 306, E157-67	6	65
171	Enhancing reproducibility in cancer drug screening: how do we move forward?. <i>Cancer Research</i> , <b>2014</b> , 74, 4016-23	10.1	64
170	The molecular basis of breast cancer pathological phenotypes. <i>Journal of Pathology</i> , <b>2017</b> , 241, 375-391	9.4	62
169	Test set bias affects reproducibility of gene signatures. <i>Bioinformatics</i> , <b>2015</b> , 31, 2318-23	7.2	59
168	Medulloblastoma subgroups remain stable across primary and metastatic compartments. <i>Acta Neuropathologica</i> , <b>2015</b> , 129, 449-57	14.3	58
167	The Gene expression Grade Index: a potential predictor of relapse for endocrine-treated breast cancer patients in the BIG 1-98 trial. <i>BMC Medical Genomics</i> , <b>2009</b> , 2, 40	3.7	58
166	Galectin 1 proangiogenic and promigratory effects in the Hs683 oligodendroglioma model are partly mediated through the control of BEX2 expression. <i>Neoplasia</i> , <b>2009</b> , 11, 485-96	6.4	58
165	Organoid Cultures as Preclinical Models of Non-Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 1162-1174	12.9	58
164	Dr.VAE: improving drug response prediction via modeling of drug perturbation effects. <i>Bioinformatics</i> , <b>2019</b> , 35, 3743-3751	7.2	55
163	Noncoding somatic and inherited single-nucleotide variants converge to promote ESR1 expression in breast cancer. <i>Nature Genetics</i> , <b>2016</b> , 48, 1260-6	36.3	53

162	Software for the Integration of Multiomics Experiments in Bioconductor. <i>Cancer Research</i> , <b>2017</b> , 77, e39-e42	4.2	53
161	Comparison and validation of genomic predictors for anticancer drug sensitivity. <i>Journal of the American Medical Informatics Association: JAMIA</i> , <b>2013</b> , 20, 597-602	8.6	52
160	Nucleolus and c-Myc: potential targets of cardenolide-mediated antitumor activity. <i>Molecular Cancer Therapeutics</i> , <b>2008</b> , 7, 1285-96	6.1	52
159	MYC Interacts with the G9a Histone Methyltransferase to Drive Transcriptional Repression and Tumorigenesis. <i>Cancer Cell</i> , <b>2018</b> , 34, 579-595.e8	24.3	52
158	Machine learning approaches to drug response prediction: challenges and recent progress. <i>Npj Precision Oncology</i> , <b>2020</b> , 4, 19	9.8	50
157	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , <b>2016</b> , 5, 2333	3.6	49
156	A network model for angiogenesis in ovarian cancer. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 115	3.6	47
155	Transfer of clinically relevant gene expression signatures in breast cancer: from Affymetrix microarray to Illumina RNA-Sequencing technology. <i>BMC Genomics</i> , <b>2014</b> , 15, 1008	4.5	45
154	Consensus on Molecular Subtypes of High-Grade Serous Ovarian Carcinoma. <i>Clinical Cancer Research</i> , <b>2018</b> , 24, 5037-5047	12.9	43
153	UNBS5162, a novel naphthalimide that decreases CXCL chemokine expression in experimental prostate cancers. <i>Neoplasia</i> , <b>2008</b> , 10, 573-86	6.4	43
152	The gene regulatory network for breast cancer: integrated regulatory landscape of cancer hallmarks. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 15	4.5	42
151	Predictive approaches for drug combination discovery in cancer. <i>Briefings in Bioinformatics</i> , <b>2018</b> , 19, 263-276	13.4	41
150	GLUT1 inhibition blocks growth of RB1-positive triple negative breast cancer. <i>Nature Communications</i> , <b>2020</b> , 11, 4205	17.4	41
149	AutoDock and AutoDockTools for Protein-Ligand Docking: Beta-Site Amyloid Precursor Protein Cleaving Enzyme 1(BACE1) as a Case Study. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1598, 391-403	1.4	40
148	Identification of a microRNA signature associated with risk of distant metastasis in nasopharyngeal carcinoma. <i>Oncotarget</i> , <b>2015</b> , 6, 4537-50	3.3	40
147	Gene expression profiling identifies activated growth factor signaling in poor prognosis (Luminal-B) estrogen receptor positive breast cancer. <i>BMC Medical Genomics</i> , <b>2009</b> , 2, 37	3.7	39
146	Characterization and clinical evaluation of CD10+ stroma cells in the breast cancer microenvironment. <i>Clinical Cancer Research</i> , <b>2012</b> , 18, 1004-14	12.9	39
145	Public data and open source tools for multi-assay genomic investigation of disease. <i>Briefings in Bioinformatics</i> , <b>2016</b> , 17, 603-15	13.4	38

144	A fuzzy gene expression-based computational approach improves breast cancer prognostication. <i>Genome Biology</i> , <b>2010</b> , 11, R18	18.3	36
143	Quantification of ZAP70 mRNA in B cells by real-time PCR is a powerful prognostic factor in chronic lymphocytic leukemia. <i>Clinical Chemistry</i> , <b>2007</b> , 53, 1757-66	5.5	35
142	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , <b>2016</b> , 5, 2333	3.6	35
141	Gene isoforms as expression-based biomarkers predictive of drug response in vitro. <i>Nature Communications</i> , <b>2017</b> , 8, 1126	17.4	34
140	Why imaging data alone is not enough: AI-based integration of imaging, omics, and clinical data. <i>European Journal of Nuclear Medicine and Molecular Imaging</i> , <b>2019</b> , 46, 2722-2730	8.8	34
139	Epigenetic Switch-Induced Viral Mimicry Evasion in Chemotherapy-Resistant Breast Cancer. <i>Cancer Discovery</i> , <b>2020</b> , 10, 1312-1329	24.4	34
138	Proliferation and estrogen signaling can distinguish patients at risk for early versus late relapse among estrogen receptor positive breast cancers. <i>Breast Cancer Research</i> , <b>2013</b> , 15, R86	8.3	33
137	Disruption of the anaphase-promoting complex confers resistance to TTK inhibitors in triple-negative breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E1570-E1577	11.5	32
136	BatchQC: interactive software for evaluating sample and batch effects in genomic data. <i>Bioinformatics</i> , <b>2016</b> , 32, 3836-3838	7.2	31
135	Extensive rewiring of epithelial-stromal co-expression networks in breast cancer. <i>Genome Biology</i> , <b>2015</b> , 16, 128	18.3	31
134	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
133	Radiomic Biomarkers to Refine Risk Models for Distant Metastasis in HPV-related Oropharyngeal Carcinoma. <i>International Journal of Radiation Oncology Biology Physics</i> , <b>2018</b> , 102, 1107-1116	4	30
132	Molecular profiling of CD3-CD4+ T cells from patients with the lymphocytic variant of hypereosinophilic syndrome reveals targeting of growth control pathways. <i>Blood</i> , <b>2009</b> , 114, 2969-83	2.2	30
131	Whole genomes define concordance of matched primary, xenograft, and organoid models of pancreas cancer. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1006596	5	29
130	CovidCTNet: an open-source deep learning approach to diagnose covid-19 using small cohort of CT images. <i>Npj Digital Medicine</i> , <b>2021</b> , 4, 29	15.7	29
129	Statin-Induced Cancer Cell Death Can Be Mechanistically Uncoupled from Prenylation of RAS Family Proteins. <i>Cancer Research</i> , <b>2018</b> , 78, 1347-1357	10.1	29
128	The Cdc42/Rac1 regulator CdGAP is a novel E-cadherin transcriptional co-repressor with Zeb2 in breast cancer. <i>Oncogene</i> , <b>2017</b> , 36, 3490-3503	9.2	28
127	Functional and genetic analysis of the colon cancer network. <i>BMC Bioinformatics</i> , <b>2014</b> , 15 Suppl 6, S6	3.6	28

126	Inference and validation of predictive gene networks from biomedical literature and gene expression data. <i>Genomics</i> , <b>2014</b> , 103, 329-36	4.3	28
125	NOTCH2 and FLT3 gene mis-splicings are common events in patients with acute myeloid leukemia (AML): new potential targets in AML. <i>Blood</i> , <b>2014</b> , 123, 2816-25	2.2	28
124	Modeling invasive breast cancer: growth factors propel progression of HER2-positive premalignant lesions. <i>Oncogene</i> , <b>2012</b> , 31, 3569-83	9.2	28
123	Stem cell-like gene expression in ovarian cancer predicts type II subtype and prognosis. <i>PLoS ONE</i> , <b>2013</b> , 8, e57799	3.7	28
122	Gene expression profiling reveals differences in microenvironment interaction between patients with chronic lymphocytic leukemia expressing high versus low ZAP70 mRNA. <i>Haematologica</i> , <b>2009</b> , 94, 790-9	6.6	27
121	An imprinted non-coding genomic cluster at 14q32 defines clinically relevant molecular subtypes in osteosarcoma across multiple independent datasets. <i>Journal of Hematology and Oncology</i> , <b>2017</b> , 10, 107	22.4	26
120	Predictive networks: a flexible, open source, web application for integration and analysis of human gene networks. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D866-75	20.1	26
119	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , <b>2021</b> , 184, 5031-5052.e26	56.2	26
118	Assessment of pharmacogenomic agreement. <i>F1000Research</i> , <b>2016</b> , 5, 825	3.6	25
117	Bidirectional terminators in <i>Saccharomyces cerevisiae</i> prevent cryptic transcription from invading neighboring genes. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 6417-6426	20.1	24
116	Minimising immunohistochemical false negative ER classification using a complementary 23 gene expression signature of ER status. <i>PLoS ONE</i> , <b>2010</b> , 5, e15031	3.7	24
115	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 1127-1128	44.5	23
114	RamiGO: an R/Bioconductor package providing an AmiGO visualize interface. <i>Bioinformatics</i> , <b>2013</b> , 29, 666-8	7.2	23
113	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , <b>2021</b> , 12, 979	17.4	23
112	Significance analysis of prognostic signatures. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1002875	5	22
111	Long-term temozolomide treatment induces marked amino metabolism modifications and an increase in TMZ sensitivity in Hs683 oligodendroglioma cells. <i>Neoplasia</i> , <b>2010</b> , 12, 69-79	6.4	22
110	Exploiting high-throughput cell line drug screening studies to identify candidate therapeutic agents in head and neck cancer. <i>BMC Pharmacology &amp; Toxicology</i> , <b>2014</b> , 15, 66	2.6	21
109	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. <i>Cancer Research</i> , <b>2017</b> , 77, 3057-3069	10.1	20



108	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , <b>2021</b> , 27, 1885-1892	50.5	19
107	Integrative Pharmacogenomics Analysis of Patient-Derived Xenografts. <i>Cancer Research</i> , <b>2019</b> , 79, 4539-4550	18	
106	Gene regulation by phorbol 12-myristate 13-acetate in MCF-7 and MDA-MB-231, two breast cancer cell lines exhibiting highly different phenotypes. <i>Oncology Reports</i> , <b>2004</b> , 12, 701-7	3.5	18
105	An interim report on the investigator-initiated phase 2 study of pembrolizumab immunological response evaluation (INSPIRE) <b>2019</b> , 7, 72		16
104	Modeling Cellular Response in Large-Scale Radiogenomic Databases to Advance Precision Radiotherapy. <i>Cancer Research</i> , <b>2019</b> , 79, 6227-6237	10.1	15
103	MetaGxData: Clinically Annotated Breast, Ovarian and Pancreatic Cancer Datasets and their Use in Generating a Multi-Cancer Gene Signature. <i>Scientific Reports</i> , <b>2019</b> , 9, 8770	4.9	15
102	AXL knockdown gene signature reveals a drug repurposing opportunity for a class of antipsychotics to reduce growth and metastasis of triple-negative breast cancer. <i>Oncotarget</i> , <b>2019</b> , 10, 2055-2067	3.3	15
101	A Comparative Study of Cluster Detection Algorithms in Protein-Protein Interaction for Drug Target Discovery and Drug Repurposing. <i>Frontiers in Pharmacology</i> , <b>2019</b> , 10, 109	5.6	15
100	Tissue specificity of in vitro drug sensitivity. <i>Journal of the American Medical Informatics Association: JAMIA</i> , <b>2018</b> , 25, 158-166	8.6	15
99	Administration of Hypoxia-Activated Prodrug Evofosfamide after Conventional Adjuvant Therapy Enhances Therapeutic Outcome and Targets Cancer-Initiating Cells in Preclinical Models of Colorectal Cancer. <i>Clinical Cancer Research</i> , <b>2018</b> , 24, 2116-2127	12.9	14
98	Importance of collection in gene set enrichment analysis of drug response in cancer cell lines. <i>Scientific Reports</i> , <b>2014</b> , 4, 4092	4.9	14
97	Safikhani et al. reply. <i>Nature</i> , <b>2016</b> , 540, E2-E4	50.4	14
96	DNA replication stress: a source of APOBEC3B expression in breast cancer. <i>Genome Biology</i> , <b>2016</b> , 17, 202	18.3	14
95	Prognostic microRNAs modulate the RHO adhesion pathway: A potential therapeutic target in undifferentiated pleomorphic sarcomas. <i>Oncotarget</i> , <b>2015</b> , 6, 39127-39	3.3	13
94	Chromosomal instability as a prognostic marker in cervical cancer. <i>BMC Cancer</i> , <b>2015</b> , 15, 361	4.8	12
93	Novel effects of chromosome Y on cardiac regulation, chromatin remodeling, and neonatal programming in male mice. <i>Endocrinology</i> , <b>2013</b> , 154, 4746-56	4.8	12
92	Low CD10 mRNA expression identifies high-risk ductal carcinoma in situ (DCIS). <i>PLoS ONE</i> , <b>2010</b> , 5, e121007	12	
91	Characterization of Conserved Toxicogenomic Responses in Chemically Exposed Hepatocytes across Species and Platforms. <i>Environmental Health Perspectives</i> , <b>2016</b> , 124, 313-20	8.4	12

90	Integrative Transcriptome Analyses Empower the Anti-COVID-19 Drug Arsenal. <i>iScience</i> , <b>2020</b> , 23, 101697-1	7.1	11
89	ABC: a tool to identify SNVs causing allele-specific transcription factor binding from ChIP-Seq experiments. <i>Bioinformatics</i> , <b>2015</b> , 31, 3057-9	7.2	11
88	Untangling statistical and biological models to understand network inference: the need for a genomics network ontology. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 299	4.5	11
87	SYNERGxDB: an integrative pharmacogenomic portal to identify synergistic drug combinations for precision oncology. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, W494-W501	20.1	11
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36	Orchestrating and sharing large multimodal data for transparent and reproducible research	2
35	Whole Genomes Define Concordance of Matched Primary, Xenograft, and Organoid Models of Pancreas Cancer	2
34	Meta-analysis of 1,200 transcriptomic profiles identifies a prognostic model for pancreatic ductal adenocarcinoma	2
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