

Benjamin Haibe-Kains

List of Publications by Year in Descending Order

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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.

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	Signaling by the tyrosine kinase Yes promotes liver cancer development.. <i>Science Signaling</i> , 2022 , 15, eabj4743	8.8	1
232	Biomimetic hydrogel supports initiation and growth of patient-derived breast tumor organoids.. <i>Nature Communications</i> , 2022 , 13, 1466	17.4	6
231	Genome-wide DNA methylation patterns reveal clinically relevant predictive and prognostic subtypes in human osteosarcoma.. <i>Communications Biology</i> , 2022 , 5, 213	6.7	1
230	PRMT inhibition induces a viral mimicry response in triple-negative breast cancer.. <i>Nature Chemical Biology</i> , 2022 ,	11.7	3
229	Evaluation of statistical approaches for association testing in noisy drug screening data.. <i>BMC Bioinformatics</i> , 2022 , 23, 188	3.6	1
228	REFLECTions on Combination Therapies Empowered by Data Sharing. <i>Cancer Discovery</i> , 2022 , 12, 1416-1418	11.8	0
227	Assessing therapy response in patient-derived xenografts. <i>Science Translational Medicine</i> , 2021 , 13, eabf4969	17.5	2
226	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
225	Orchestrating and sharing large multimodal data for transparent and reproducible research. <i>Nature Communications</i> , 2021 , 12, 5797	17.4	0
224	Automated detection of dental artifacts for large-scale radiomic analysis in radiation oncology. <i>Physics and Imaging in Radiation Oncology</i> , 2021 , 18, 41-47	3.1	1
223	Prediction of Human Papillomavirus (HPV) Association of Oropharyngeal Cancer (OPC) Using Radiomics: The Impact of the Variation of CT Scanner. <i>Cancers</i> , 2021 , 13,	6.6	2
222	Novel subtypes of -mutated AML with distinct outcome. <i>Molecular and Cellular Oncology</i> , 2021 , 8, 1924600	6.0	0
221	Using real-word data to evaluate the effects of broadening eligibility criteria in oncology trials. <i>Cancer Cell</i> , 2021 , 39, 750-752	24.3	1
220	The impact of the variation of imaging parameters on the robustness of Computed Tomography radiomic features: A review. <i>Computers in Biology and Medicine</i> , 2021 , 133, 104400	7	7
219	Consistency of in vitro drug sensitivities within pharmacological classes. <i>University of Toronto Journal of Undergraduate Life Sciences</i> , 2021 , 15, 12	0	0
218	The mevalonate pathway is an actionable vulnerability of t(4;14)-positive multiple myeloma. <i>Leukemia</i> , 2021 , 35, 796-808	10.7	6
217	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity.. <i>Nature Cancer</i> , 2021 , 2, 157-173	15.4	31

216	Single-cell chromatin accessibility profiling of glioblastoma identifies an invasive cancer stem cell population associated with lower survival. <i>ELife</i> , 2021 , 10,	8.9	9
215	Large organized chromatin lysine domains help distinguish primitive from differentiated cell populations. <i>Nature Communications</i> , 2021 , 12, 499	17.4	3
214	Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy. <i>Cell</i> , 2021 , 184, 226-243.e2168	46.2	168
213	CovidCTNet: an open-source deep learning approach to diagnose covid-19 using small cohort of CT images. <i>Npj Digital Medicine</i> , 2021 , 4, 29	15.7	29
212	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , 2021 , 12, 979	17.4	23
211	Biological and therapeutic implications of a unique subtype of NPM1 mutated AML. <i>Nature Communications</i> , 2021 , 12, 1054	17.4	7
210	Pan-cancer analysis of longitudinal metastatic tumors reveals genomic alterations and immune landscape dynamics associated with pembrolizumab sensitivity. <i>Nature Communications</i> , 2021 , 12, 5137	17.4	5
209	Drug sensitivity prediction from cell line-based pharmacogenomics data: guidelines for developing machine learning models. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3
208	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021 , 184, 5031-5052.e26	56.2	26
207	Ontogeny and Vulnerabilities of Drug-Tolerant Persisters in HER2+ Breast Cancer.. <i>Cancer Discovery</i> , 2021 ,	24.4	4
206	Integrative Transcriptome Analyses Empower the Anti-COVID-19 Drug Arsenal. <i>IScience</i> , 2020 , 23, 101697.	107.1	11
205	85: The Role of Cytokine Signaling in the Reversal of Chronic Lymphedema. <i>Radiotherapy and Oncology</i> , 2020 , 150, S38-S39	5.3	
204	ToxicoDB: an integrated database to mine and visualize large-scale toxicogenomic datasets. <i>Nucleic Acids Research</i> , 2020 , 48, W455-W462	20.1	3
203	Machine learning approaches to drug response prediction: challenges and recent progress. <i>Npj Precision Oncology</i> , 2020 , 4, 19	9.8	50
202	Epigenetic Switch-Induced Viral Mimicry Evasion in Chemotherapy-Resistant Breast Cancer. <i>Cancer Discovery</i> , 2020 , 10, 1312-1329	24.4	34
201	MicroRNA-mRNA networks define translatable molecular outcome phenotypes in osteosarcoma. <i>Scientific Reports</i> , 2020 , 10, 4409	4.9	6
200	Assessment of modelling strategies for drug response prediction in cell lines and xenografts. <i>Scientific Reports</i> , 2020 , 10, 2849	4.9	8
199	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. <i>Nature Genetics</i> , 2020 , 52, 231-240	36.3	148

198	IL6 Induces an IL22 CD8 T-cell Subset with Potent Antitumor Function. <i>Cancer Immunology Research</i> , 2020 , 8, 321-333	12.5	10
197	Centromeric cohesion failure invokes a conserved choreography of chromosomal mis-segregations in pancreatic neuroendocrine tumor. <i>Genome Medicine</i> , 2020 , 12, 38	14.4	1
196	Radiomic response evaluation of recurrent or metastatic head and neck squamous cell cancer (R/M HNSCC) patients receiving pembrolizumab on KEYNOTE-012 study.. <i>Journal of Clinical Oncology</i> , 2020 , 38, 6545-6545	2.2	1
195	SYNERGxDB: an integrative pharmacogenomic portal to identify synergistic drug combinations for precision oncology. <i>Nucleic Acids Research</i> , 2020 , 48, W494-W501	20.1	11
194	Organoid Cultures as Preclinical Models of Non-Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 1162-1174	12.9	58
193	Automatic classification of dental artifact status for efficient image veracity checks: effects of image resolution and convolutional neural network depth. <i>Physics in Medicine and Biology</i> , 2020 , 65, 015005	2.8	7
192	External validation and transfer learning of convolutional neural networks for computed tomography dental artifact classification. <i>Physics in Medicine and Biology</i> , 2020 , 65, 035017	3.8	5
191	Pathway-Based Drug Response Prediction Using Similarity Identification in Gene Expression. <i>Frontiers in Genetics</i> , 2020 , 11, 1016	4.5	2
190	Nonesterified Fatty Acids and Depression in Cancer Patients and Caregivers. <i>Current Developments in Nutrition</i> , 2020 , 4, nzaa156	0.4	
189	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020 , 586, E14-E16	50.4	85
188	Assessment of Genetic Drift in Large Pharmacogenomic Studies. <i>Cell Systems</i> , 2020 , 11, 393-401.e2	10.6	3
187	Meta-gene markers predict meningioma recurrence with high accuracy. <i>Scientific Reports</i> , 2020 , 10, 18028	3.9	1
186	GLUT1 inhibition blocks growth of RB1-positive triple negative breast cancer. <i>Nature Communications</i> , 2020 , 11, 4205	17.4	41
185	Modeling germline mutations in pineoblastoma uncovers lysosome disruption-based therapy. <i>Nature Communications</i> , 2020 , 11, 1825	17.4	7
184	Creating reproducible pharmacogenomic analysis pipelines. <i>Scientific Data</i> , 2019 , 6, 166	8.2	1
183	Identifying clusters of -regulatory elements underpinning TAD structures and lineage-specific regulatory networks. <i>Genome Research</i> , 2019 , 29, 1733-1743	9.7	9
182	Modeling Cellular Response in Large-Scale Radiogenomic Databases to Advance Precision Radiotherapy. <i>Cancer Research</i> , 2019 , 79, 6227-6237	10.1	15
181	ONECUT2 is a driver of neuroendocrine prostate cancer. <i>Nature Communications</i> , 2019 , 10, 278	17.4	72

180	SIGN: similarity identification in gene expression. <i>Bioinformatics</i> , 2019 , 35, 4830-4833	7.2	1
179	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> , 2019 , 46, 2722-2730	8.8	34
178	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019 , 10, 2674	17.4	119
177	MetaGxData: Clinically Annotated Breast, Ovarian and Pancreatic Cancer Datasets and their Use in Generating a Multi-Cancer Gene Signature. <i>Scientific Reports</i> , 2019 , 9, 8770	4.9	15
176	Integrative Pharmacogenomics Analysis of Patient-Derived Xenografts. <i>Cancer Research</i> , 2019 , 79, 4539-4550	18	
175	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> , 2019 , 10, 2055-2067	3.3	15
174	A Comparative Study of Cluster Detection Algorithms in Protein-Protein Interaction for Drug Target Discovery and Drug Repurposing. <i>Frontiers in Pharmacology</i> , 2019 , 10, 109	5.6	15
173	Dr.VAE: improving drug response prediction via modeling of drug perturbation effects. <i>Bioinformatics</i> , 2019 , 35, 3743-3751	7.2	55
172	An interim report on the investigator-initiated phase 2 study of pembrolizumab immunological response evaluation (INSPIRE) 2019 , 7, 72		16
171	Network-based approach to identify principal isoforms among four cancer types. <i>Molecular Omics</i> , 2019 , 15, 117-129	4.4	3
170	Spatially distinct tumor immune microenvironments stratify triple-negative breast cancers. <i>Journal of Clinical Investigation</i> , 2019 , 129, 1785-1800	15.9	125
169	Applications of Computational Systems Biology in Cancer Signaling Pathways 2019 , 513-537		
168	Meta-Analysis of 1,200 Transcriptomic Profiles Identifies a Prognostic Model for Pancreatic Ductal Adenocarcinoma. <i>JCO Clinical Cancer Informatics</i> , 2019 , 3, 1-16	5.2	7
167	Vulnerabilities of radiomic signature development: The need for safeguards. <i>Radiotherapy and Oncology</i> , 2019 , 130, 2-9	5.3	137
166	Metabolic regulation of dermal fibroblasts contributes to skin extracellular matrix homeostasis and fibrosis. <i>Nature Metabolism</i> , 2019 , 1, 147-157	14.6	79
165	Whole genomes define concordance of matched primary, xenograft, and organoid models of pancreas cancer. <i>PLoS Computational Biology</i> , 2019 , 15, e1006596	5	29
164	A review of connectivity map and computational approaches in pharmacogenomics. <i>Briefings in Bioinformatics</i> , 2018 , 19, 506-523	13.4	101
163	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> , 2018 , 24, 2116-2127	12.9	14

162	Radiomic Biomarkers to Refine Risk Models for Distant Metastasis in HPV-related Oropharyngeal Carcinoma. <i>International Journal of Radiation Oncology Biology Physics</i> , 2018 , 102, 1107-1116	4	30
161	Rational design and identification of immuno-oncology drug combinations. <i>European Journal of Cancer</i> , 2018 , 95, 38-51	7.5	7
160	CrosstalkNet: A Visualization Tool for Differential Co-expression Networks and Communities. <i>Cancer Research</i> , 2018 , 78, 2140-2143	10.1	1
159	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> , 2018 , 115, E1570-E1577	11.5	32
158	Tissue specificity of in vitro drug sensitivity. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2018 , 25, 158-166	8.6	15
157	Network science in clinical trials: A patient-centered approach. <i>Seminars in Cancer Biology</i> , 2018 , 52, 135-150	15.0	6
156	PharmacDB: an integrative database for mining in vitro anticancer drug screening studies. <i>Nucleic Acids Research</i> , 2018 , 46, D994-D1002	20.1	82
155	Predictive approaches for drug combination discovery in cancer. <i>Briefings in Bioinformatics</i> , 2018 , 19, 263-276	13.4	41
154	Scoring of tumor-infiltrating lymphocytes: From visual estimation to machine learning. <i>Seminars in Cancer Biology</i> , 2018 , 52, 151-157	12.7	71
153	Consensus on Molecular Subtypes of High-Grade Serous Ovarian Carcinoma. <i>Clinical Cancer Research</i> , 2018 , 24, 5037-5047	12.9	43
152	Gene expression signatures prognostic for relapse in stage I testicular germ cell tumours. <i>BJU International</i> , 2018 , 122, 814-822	5.6	3
151	Orchestrating a community-developed computational workshop and accompanying training materials. <i>F1000Research</i> , 2018 , 7, 1656	3.6	1
150	Statin-Induced Cancer Cell Death Can Be Mechanistically Uncoupled from Prenylation of RAS Family Proteins. <i>Cancer Research</i> , 2018 , 78, 1347-1357	10.1	29
149	The Antiarrhythmic Drug, Dronedarone, Demonstrates Cytotoxic Effects in Breast Cancer Independent of Thyroid Hormone Receptor Alpha 1 (THR1) Antagonism. <i>Scientific Reports</i> , 2018 , 8, 16562	4.9	4
148	MYC Interacts with the G9a Histone Methyltransferase to Drive Transcriptional Repression and Tumorigenesis. <i>Cancer Cell</i> , 2018 , 34, 579-595.e8	24.3	52
147	The Cdc42/Rac1 regulator CdGAP is a novel E-cadherin transcriptional co-repressor with Zeb2 in breast cancer. <i>Oncogene</i> , 2017 , 36, 3490-3503	9.2	28
146	Transcriptome Analysis of Human Reninomas as an Approach to Understanding Juxtaglomerular Cell Biology. <i>Hypertension</i> , 2017 , 69, 1145-1155	8.5	5
145	Genomic biomarkers for precision radiation medicine. <i>Lancet Oncology, The</i> , 2017 , 18, e238	21.7	5

144	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> , 2017 , 1598, 391-403	1.4	40
143	Bidirectional terminators in <i>Saccharomyces cerevisiae</i> prevent cryptic transcription from invading neighboring genes. <i>Nucleic Acids Research</i> , 2017 , 45, 6417-6426	20.1	24
142	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. <i>Cancer Research</i> , 2017 , 77, 3057-3069	10.1	20
141	Integrative cancer pharmacogenomics to establish drug mechanism of action: drug repurposing. <i>Pharmacogenomics</i> , 2017 , 18, 1469-1472	2.6	2
140	Gene isoforms as expression-based biomarkers predictive of drug response in vitro. <i>Nature Communications</i> , 2017 , 8, 1126	17.4	34
139	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. <i>Nature Biotechnology</i> , 2017 , 35, 1127-1128	44.5	23
138	Software for the Integration of Multiomics Experiments in Bioconductor. <i>Cancer Research</i> , 2017 , 77, e39-e42	1.4	53
137	Study of Meta-analysis strategies for network inference using information-theoretic approaches. <i>BioData Mining</i> , 2017 , 10, 15	4.3	0
136	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> , 2017 , 10, 107	22.4	26
135	The molecular basis of breast cancer pathological phenotypes. <i>Journal of Pathology</i> , 2017 , 241, 375-391	9.4	62
134	Older adults with heart failure treated with carvedilol, bisoprolol, or metoprolol tartrate: risk of mortality. <i>Pharmacoepidemiology and Drug Safety</i> , 2017 , 26, 81-90	2.6	3
133	Defining the biological basis of radiomic phenotypes in lung cancer. <i>ELife</i> , 2017 , 6,	8.9	158
132	Author response: Defining the biological basis of radiomic phenotypes in lung cancer 2017 ,		5
131	Public data and open source tools for multi-assay genomic investigation of disease. <i>Briefings in Bioinformatics</i> , 2016 , 17, 603-15	13.4	38
130	Noncoding somatic and inherited single-nucleotide variants converge to promote ESR1 expression in breast cancer. <i>Nature Genetics</i> , 2016 , 48, 1260-6	36.3	53
129	BatchQC: interactive software for evaluating sample and batch effects in genomic data. <i>Bioinformatics</i> , 2016 , 32, 3836-3838	7.2	31
128	MM2S: personalized diagnosis of medulloblastoma patients and model systems. <i>Source Code for Biology and Medicine</i> , 2016 , 11, 6	1.9	1
127	PharmacoGx: an R package for analysis of large pharmacogenomic datasets. <i>Bioinformatics</i> , 2016 , 32, 1244-6	7.2	127

126	Genefu: an R/Bioconductor package for computation of gene expression-based signatures in breast cancer. <i>Bioinformatics</i> , 2016 , 32, 1097-9	7.2	150
125	Assessment of pharmacogenomic agreement. <i>F1000Research</i> , 2016 , 5, 825	3.6	25
124	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , 2016 , 5, 2333	3.6	49
123	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , 2016 , 5, 2333	3.6	35
122	Characterization of Conserved Toxicogenomic Responses in Chemically Exposed Hepatocytes across Species and Platforms. <i>Environmental Health Perspectives</i> , 2016 , 124, 313-20	8.4	12
121	Study of Meta-analysis Strategies for Network Inference Using Information-Theoretic Approaches 2016 ,		1
120	Safikhani et al. reply. <i>Nature</i> , 2016 , 540, E2-E4	50.4	14
119	Safikhani et al. reply. <i>Nature</i> , 2016 , 540, E6-E8	50.4	9
118	Safikhani et al. reply. <i>Nature</i> , 2016 , 540, E11-E12	50.4	8
117	Adenosine 2B Receptor Expression on Cancer Cells Promotes Metastasis. <i>Cancer Research</i> , 2016 , 76, 4372-82	10.1	94
116	DNA replication stress: a source of APOBEC3B expression in breast cancer. <i>Genome Biology</i> , 2016 , 17, 202	18.3	14
115	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> , 2015 , 112, 2841-6	11.5	95
114	Using shRNA experiments to validate gene regulatory networks. <i>Genomics Data</i> , 2015 , 4, 123-6		
113	CT-based radiomic signature predicts distant metastasis in lung adenocarcinoma. <i>Radiotherapy and Oncology</i> , 2015 , 114, 345-50	5.3	444
112	Test set bias affects reproducibility of gene signatures. <i>Bioinformatics</i> , 2015 , 31, 2318-23	7.2	59
111	Chromosomal instability as a prognostic marker in cervical cancer. <i>BMC Cancer</i> , 2015 , 15, 361	4.8	12
110	CD73 is associated with poor prognosis in high-grade serous ovarian cancer. <i>Cancer Research</i> , 2015 , 75, 4494-503	10.1	142
109	Extensive rewiring of epithelial-stromal co-expression networks in breast cancer. <i>Genome Biology</i> , 2015 , 16, 128	18.3	31

108	Radiomic feature clusters and prognostic signatures specific for Lung and Head & Neck cancer. <i>Scientific Reports</i> , 2015 , 5, 11044	4.9	292
107	A network model for angiogenesis in ovarian cancer. <i>BMC Bioinformatics</i> , 2015 , 16, 115	3.6	47
106	Personalized diagnosis of medulloblastoma subtypes across patients and model systems. <i>Genomics</i> , 2015 , 106, 96-106	4.3	7
105	ABC: a tool to identify SNVs causing allele-specific transcription factor binding from CHIP-Seq experiments. <i>Bioinformatics</i> , 2015 , 31, 3057-9	7.2	11
104	Medulloblastoma subgroups remain stable across primary and metastatic compartments. <i>Acta Neuropathologica</i> , 2015 , 129, 449-57	14.3	58
103	ZNF143 provides sequence specificity to secure chromatin interactions at gene promoters. <i>Nature Communications</i> , 2015 , 2, 6186	17.4	123
102	Identification of a microRNA signature associated with risk of distant metastasis in nasopharyngeal carcinoma. <i>Oncotarget</i> , 2015 , 6, 4537-50	3.3	40
101	Prognostic microRNAs modulate the RHO adhesion pathway: A potential therapeutic target in undifferentiated pleomorphic sarcomas. <i>Oncotarget</i> , 2015 , 6, 39127-39	3.3	13
100	Comparative meta-analysis of prognostic gene signatures for late-stage ovarian cancer. <i>Journal of the National Cancer Institute</i> , 2014 , 106,	9.7	77
99	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> , 2014 , 20, 1135-45	12.9	65
98	Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach. <i>Nature Communications</i> , 2014 , 5, 4006	17.4	2330
97	Similarity network fusion for aggregating data types on a genomic scale. <i>Nature Methods</i> , 2014 , 11, 333-7	11.6	849
96	Enhancing reproducibility in cancer drug screening: how do we move forward?. <i>Cancer Research</i> , 2014 , 74, 4016-23	10.1	64
95	Functional and genetic analysis of the colon cancer network. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 6, S6	3.6	28
94	Inference and validation of predictive gene networks from biomedical literature and gene expression data. <i>Genomics</i> , 2014 , 103, 329-36	4.3	28
93	Loss of Pgc-1 β expression in aging mouse muscle potentiates glucose intolerance and systemic inflammation. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2014 , 306, E157-67	6	65
92	NOTCH2 and FLT3 gene mis-splicings are common events in patients with acute myeloid leukemia (AML): new potential targets in AML. <i>Blood</i> , 2014 , 123, 2816-25	2.2	28
91	Importance of collection in gene set enrichment analysis of drug response in cancer cell lines. <i>Scientific Reports</i> , 2014 , 4, 4092	4.9	14

90	Robust Radiomics feature quantification using semiautomatic volumetric segmentation. <i>PLoS ONE</i> , 2014 , 9, e102107	3.7	363
89	Gene regulatory networks and their applications: understanding biological and medical problems in terms of networks. <i>Frontiers in Cell and Developmental Biology</i> , 2014 , 2, 38	5.7	86
88	The gene regulatory network for breast cancer: integrated regulatory landscape of cancer hallmarks. <i>Frontiers in Genetics</i> , 2014 , 5, 15	4.5	42
87	Quantitative assessment and validation of network inference methods in bioinformatics. <i>Frontiers in Genetics</i> , 2014 , 5, 221	4.5	8
86	Exploiting high-throughput cell line drug screening studies to identify candidate therapeutic agents in head and neck cancer. <i>BMC Pharmacology & Toxicology</i> , 2014 , 15, 66	2.6	21
85	Untangling statistical and biological models to understand network inference: the need for a genomics network ontology. <i>Frontiers in Genetics</i> , 2014 , 5, 299	4.5	11
84	Relevance of different prior knowledge sources for inferring gene interaction networks. <i>Frontiers in Genetics</i> , 2014 , 5, 177	4.5	5
83	Transfer of clinically relevant gene expression signatures in breast cancer: from Affymetrix microarray to Illumina RNA-Sequencing technology. <i>BMC Genomics</i> , 2014 , 15, 1008	4.5	45
82	MicroRNA paraffin-based studies in osteosarcoma reveal reproducible independent prognostic profiles at 14q32. <i>Genome Medicine</i> , 2013 , 5, 2	14.4	69
81	Genome-wide gene expression profiling to predict resistance to anthracyclines in breast cancer patients. <i>Genomics Data</i> , 2013 , 1, 7-10		3
80	mRMRe: an R package for parallelized mRMR ensemble feature selection. <i>Bioinformatics</i> , 2013 , 29, 2365-82	7.2	117
79	Inconsistency in large pharmacogenomic studies. <i>Nature</i> , 2013 , 504, 389-93	50.4	360
78	Novel effects of chromosome Y on cardiac regulation, chromatin remodeling, and neonatal programming in male mice. <i>Endocrinology</i> , 2013 , 154, 4746-56	4.8	12
77	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> , 2013 , 110, 11091-6	11.5	303
76	Significance analysis of prognostic signatures. <i>PLoS Computational Biology</i> , 2013 , 9, e1002875	5	22
75	RamiGO: an R/Bioconductor package providing an AmiGO visualize interface. <i>Bioinformatics</i> , 2013 , 29, 666-8	7.2	23
74	curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat013	5	123
73	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> , 2013 , 110, 7434-9	11.5	73

72	Estrogen receptor negative/progesterone receptor positive breast cancer is not a reproducible subtype. <i>Breast Cancer Research</i> , 2013 , 15, R68	8.3	92
71	Comparison and validation of genomic predictors for anticancer drug sensitivity. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013 , 20, 597-602	8.6	52
70	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> , 2013 , 15, R86	8.3	33
69	Network statistics of genetically-driven gene co-expression modules in mouse crosses. <i>Frontiers in Genetics</i> , 2013 , 4, 291	4.5	3
68	CD4+ follicular helper T cell infiltration predicts breast cancer survival. <i>Journal of Clinical Investigation</i> , 2013 , 123, 2873-92	15.9	554
67	Stem cell-like gene expression in ovarian cancer predicts type II subtype and prognosis. <i>PLoS ONE</i> , 2013 , 8, e57799	3.7	28
66	Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian cancer. <i>PLoS ONE</i> , 2012 , 7, e30269	3.7	84
65	Predictive networks: a flexible, open source, web application for integration and analysis of human gene networks. <i>Nucleic Acids Research</i> , 2012 , 40, D866-75	20.1	26
64	Elucidating prognosis and biology of breast cancer arising in young women using gene expression profiling. <i>Clinical Cancer Research</i> , 2012 , 18, 1341-51	12.9	239
63	Modeling invasive breast cancer: growth factors propel progression of HER2-positive premalignant lesions. <i>Oncogene</i> , 2012 , 31, 3569-83	9.2	28
62	A three-gene model to robustly identify breast cancer molecular subtypes. <i>Journal of the National Cancer Institute</i> , 2012 , 104, 311-25	9.7	218
61	Characterization and clinical evaluation of CD10+ stroma cells in the breast cancer microenvironment. <i>Clinical Cancer Research</i> , 2012 , 18, 1004-14	12.9	39
60	Gene modules and response to neoadjuvant chemotherapy in breast cancer subtypes: a pooled analysis. <i>Journal of Clinical Oncology</i> , 2012 , 30, 1996-2004	2.2	167
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16	CREAM: Clustering of genomic REgions Analysis Method		4
15	Revisiting inconsistency in large pharmacogenomic studies		4
14	Integrative pharmacogenomics to infer large-scale drug taxonomy		3
13	Tissue specificity of in vitro drug sensitivity		1
12	Software for the integration of multi-omics experiments in Bioconductor		3
11	Gene isoforms as expression-based biomarkers predictive of drug response in vitro		3
10	Consensus on Molecular Subtypes of Ovarian Cancer		2
9	Machine learning-based prediction of response to PARP inhibition across cancer types		2
8	The impact of the variation of imaging factors on the robustness of Computed Tomography Radiomic Features: A review		1
7	KuLGap: A Selective Measure for Assessing Therapy Response in Patient-Derived Xenografts		1
6	Orchestrating and sharing large multimodal data for transparent and reproducible research		2
5	Whole Genomes Define Concordance of Matched Primary, Xenograft, and Organoid Models of Pancreas Cancer		2
4	Meta-analysis of 1,200 transcriptomic profiles identifies a prognostic model for pancreatic ductal adenocarcinoma		2
3	Single-cell chromatin accessibility in glioblastoma delineates cancer stem cell heterogeneity predictive of survival		3
2	Modeling cellular response in large-scale radiogenomic databases to advance precision radiotherapy		2
1	Integrative Pharmacogenomics Analysis of Patient Derived Xenografts		1

