Benjamin Haibe-Kains

List of Publications by Year
in descending order

233 papers	27,571 citations	9234 74 h-index	6630 156 g-index
282 all docs	282 docs citations	282 times ranked	36134 citing authors

#	Article	IF	Citations
1	Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach. Nature Communications, 2014, 5, 4006.	5.8	3,355
2	Gene Expression Profiling in Breast Cancer: Understanding the Molecular Basis of Histologic Grade To Improve Prognosis. Journal of the National Cancer Institute, 2006, 98, 262-272.	3.0	1,824
3	Similarity network fusion for aggregating data types on a genomic scale. Nature Methods, 2014, 11, 333-337.	9.0	1,392
4	Strong Time Dependence of the 76-Gene Prognostic Signature for Node-Negative Breast Cancer Patients in the TRANSBIG Multicenter Independent Validation Series. Clinical Cancer Research, 2007, 13, 3207-3214.	3.2	839
5	CD4+ follicular helper T cell infiltration predicts breast cancer survival. Journal of Clinical Investigation, 2013, 123, 2873-2892.	3.9	813
6	Meta-analysis of gene expression profiles in breast cancer: toward a unified understanding of breast cancer subtyping and prognosis signatures. Breast Cancer Research, 2008, 10, R65.	2.2	765
7	Biological Processes Associated with Breast Cancer Clinical Outcome Depend on the Molecular Subtypes. Clinical Cancer Research, 2008, 14, 5158-5165.	3.2	745
8	Definition of Clinically Distinct Molecular Subtypes in Estrogen Receptor–Positive Breast Carcinomas Through Genomic Grade. Journal of Clinical Oncology, 2007, 25, 1239-1246.	0.8	711
9	CT-based radiomic signature predicts distant metastasis in lung adenocarcinoma. Radiotherapy and Oncology, 2015, 114, 345-350.	0.3	576
10	Robust Radiomics Feature Quantification Using Semiautomatic Volumetric Segmentation. PLoS ONE, 2014, 9, e102107.	1.1	488
11	Inconsistency in large pharmacogenomic studies. Nature, 2013, 504, 389-393.	13.7	467
12	CD73 promotes anthracycline resistance and poor prognosis in triple negative breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11091-11096.	3.3	406
13	*survcomp*: an R/Bioconductor package for performance assessment and comparison of survival models. Bioinformatics, 2011, 27, 3206-3208.	1.8	384
14	Radiomic feature clusters and Prognostic Signatures specific for Lung and Head & Neck cancer. Scientific Reports, 2015, 5, 11044.	1.6	384
15	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. Nature Genetics, 2020, 52, 231-240.	9.4	365
16	*PIK3CA* mutations associated with gene signature of low mTORC1 signaling and better outcomes in estrogen receptor–positive breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10208-10213.	3.3	324
17	Elucidating Prognosis and Biology of Breast Cancer Arising in Young Women Using Gene Expression Profiling. Clinical Cancer Research, 2012, 18, 1341-1351.	3.2	303
18	Amplification of LAPTM4B and YWHAZ contributes to chemotherapy resistance and recurrence of breast cancer. Nature Medicine, 2010, 16, 214-218.	15.2	301

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19	Predicting prognosis using molecular profiling in estrogen receptor-positive breast cancer treated with tamoxifen. BMC Genomics, 2008, 9, 239.	1.2	300
20	A Three-Gene Model to Robustly Identify Breast Cancer Molecular Subtypes. Journal of the National Cancer Institute, 2012, 104, 311-325.	3.0	272
21	Spatially distinct tumor immune microenvironments stratify triple-negative breast cancers. Journal of Clinical Investigation, 2019, 129, 1785-1800.	3.9	266
22	Defining the biological basis of radiomic phenotypes in lung cancer. ELife, 2017, 6, .	2.8	258
23	Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy. Cell, 2021, 184, 226-242.e21.	13.5	258
24	Genefu: an R/Bioconductor package for computation of gene expression-based signatures in breast cancer. Bioinformatics, 2016, 32, 1097-1099.	1.8	255
25	PharmacoGx: an R package for analysis of large pharmacogenomic datasets. Bioinformatics, 2016, 32, 1244-1246.	1.8	249
26	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	5.8	240
27	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	13.5	236
28	Vulnerabilities of radiomic signature development: The need for safeguards. Radiotherapy and Oncology, 2019, 130, 2-9.	0.3	233
29	Transparency and reproducibility in artificial intelligence. Nature, 2020, 586, E14-E16.	13.7	233
30	microRNA-29c and microRNA-223 down-regulation has in vivo significance in chronic lymphocytic leukemia and improves disease risk stratification. Blood, 2009, 113, 5237-5245.	0.6	231
31	Global MicroRNA Expression Profiling Identifies MiR-210 Associated with Tumor Proliferation, Invasion and Poor Clinical Outcome in Breast Cancer. PLoS ONE, 2011, 6, e20980.	1.1	214
32	DNA methylation profiling reveals a predominant immune component in breast cancers. EMBO Molecular Medicine, 2011, 3, 726-741.	3.3	210
33	Gene regulatory networks and their applications: understanding biological and medical problems in terms of networks. Frontiers in Cell and Developmental Biology, 2014, 2, 38.	1.8	201
34	mRMRe: an R package for parallelized mRMR ensemble feature selection. Bioinformatics, 2013, 29, 2365-2368.	1.8	195
35	Gene Modules and Response to Neoadjuvant Chemotherapy in Breast Cancer Subtypes: A Pooled Analysis. Journal of Clinical Oncology, 2012, 30, 1996-2004.	0.8	194
36	A comparative study of survival models for breast cancer prognostication based on microarray data: does a single gene beat them all?. Bioinformatics, 2008, 24, 2200-2208.	1.8	192

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37	CD73 Is Associated with Poor Prognosis in High-Grade Serous Ovarian Cancer. Cancer Research, 2015, 75, 4494-4503.	0.4	186
38	A review of connectivity map and computational approaches in pharmacogenomics. Briefings in Bioinformatics, 2018, 19, bbw112.	3.2	182
39	Genomic Grade Index Is Associated With Response to Chemotherapy in Patients With Breast Cancer. Journal of Clinical Oncology, 2009, 27, 3185-3191.	0.8	173
40	ZNF143 provides sequence specificity to secure chromatin interactions at gene promoters. Nature Communications, 2015, 6, 6186.	5.8	173
41	Machine learning approaches to drug response prediction: challenges and recent progress. Npj Precision Oncology, 2020, 4, 19.	2.3	170
42	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170
43	Multifactorial Approach to Predicting Resistance to Anthracyclines. Journal of Clinical Oncology, 2011, 29, 1578-1586.	0.8	169
44	curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat013.	1.4	165
45	Metabolic regulation of dermal fibroblasts contributes to skin extracellular matrix homeostasis and fibrosis. Nature Metabolism, 2019, 1, 147-157.	5.1	150
46	Organoid Cultures as Preclinical Models of Non–Small Cell Lung Cancer. Clinical Cancer Research, 2020, 26, 1162-1174.	3.2	148
47	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity. Nature Cancer, 2021, 2, 157-173.	5.7	147
48	ONECUT2 is a driver of neuroendocrine prostate cancer. Nature Communications, 2019, 10, 278.	5.8	143
49	Adenosine 2B Receptor Expression on Cancer Cells Promotes Metastasis. Cancer Research, 2016, 76, 4372-4382.	0.4	130
50	PharmacoDB: an integrative database for mining in vitro anticancer drug screening studies. Nucleic Acids Research, 2018, 46, D994-D1002.	6.5	130
51	GLUT1 inhibition blocks growth of RB1-positive triple negative breast cancer. Nature Communications, 2020, 11, 4205.	5.8	130
52	Comparison of prognostic gene expression signatures for breast cancer. BMC Genomics, 2008, 9, 394.	1.2	123
53	Estrogen receptor negative/progesterone receptor positive breast cancer is not a reproducible subtype. Breast Cancer Research, 2013, 15, R68.	2.2	122
54	*APOBEC3B* expression in breast cancer reflects cellular proliferation, while a deletion polymorphism is associated with immune activation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2841-2846.	3.3	118

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55	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. Lancet Oncology, The, 2010, 11, 358-365.	5.1	116
56	Dr.VAE: improving drug response prediction via modeling of drug perturbation effects. Bioinformatics, 2019, 35, 3743-3751.	1.8	113
57	Comparative Meta-analysis of Prognostic Gene Signatures for Late-Stage Ovarian Cancer. Journal of the National Cancer Institute, 2014, 106, .	3.0	110
58	GeneSigDB: a manually curated database and resource for analysis of gene expression signatures. Nucleic Acids Research, 2012, 40, D1060-D1066.	6.5	108
59	Scoring of tumor-infiltrating lymphocytes: From visual estimation to machine learning. Seminars in Cancer Biology, 2018, 52, 151-157.	4.3	108
60	Angiogenic mRNA and microRNA Gene Expression Signature Predicts a Novel Subtype of Serous Ovarian Cancer. PLoS ONE, 2012, 7, e30269.	1.1	107
61	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. Neoplasia, 2010, 12, 727-739.	2.3	104
62	MicroRNA paraffin-based studies in osteosarcoma reveal reproducible independent prognostic profiles at 14q32. Genome Medicine, 2013, 5, 2.	3.6	96
63	MYC Interacts with the G9a Histone Methyltransferase to Drive Transcriptional Repression and Tumorigenesis. Cancer Cell, 2018, 34, 579-595.e8.	7.7	94
64	Evidence of galectin-1 involvement in glioma chemoresistanceâ˜†. Toxicology and Applied Pharmacology, 2008, 229, 172-183.	1.3	93
65	Consensus on Molecular Subtypes of High-Grade Serous Ovarian Carcinoma. Clinical Cancer Research, 2018, 24, 5037-5047.	3.2	93
66	Enhancing Reproducibility in Cancer Drug Screening: How Do We Move Forward?. Cancer Research, 2014, 74, 4016-4023.	0.4	90
67	Test set bias affects reproducibility of gene signatures. Bioinformatics, 2015, 31, 2318-2323.	1.8	90
68	Knocking Down Galectin 1 in Human Hs683 Glioblastoma Cells Impairs Both Angiogenesis and Endoplasmic Reticulum Stress Responses. Journal of Neuropathology and Experimental Neurology, 2008, 67, 456-469.	0.9	88
69	AutoDock and AutoDockTools for Protein-Ligand Docking: Beta-Site Amyloid Precursor Protein Cleaving Enzyme 1(BACE1) as a Case Study. Methods in Molecular Biology, 2017, 1598, 391-403.	0.4	88
70	Rac-specific guanine nucleotide exchange factor DOCK1 is a critical regulator of HER2-mediated breast cancer metastasis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7434-7439.	3.3	87
71	The molecular basis of breast cancer pathological phenotypes. Journal of Pathology, 2017, 241, 375-391.	2.1	86
72	A Genome-Wide Aberrant RNA Splicing in Patients with Acute Myeloid Leukemia Identifies Novel Potential Disease Markers and Therapeutic Targets. Clinical Cancer Research, 2014, 20, 1135-1145.	3.2	85

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73	4-IBP, a Ïƒ1 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. Neoplasia, 2007, 9, 358-369.	2.3	84
74	Loss of <i>Pgc-1α</i> expression in aging mouse muscle potentiates glucose intolerance and systemic inflammation. American Journal of Physiology - Endocrinology and Metabolism, 2014, 306, E157-E167.	1.8	84
75	Epigenetic Switchâ€"Induced Viral Mimicry Evasion in Chemotherapy-Resistant Breast Cancer. Cancer Discovery, 2020, 10, 1312-1329.	7.7	84
76	Medulloblastoma subgroups remain stable across primary and metastatic compartments. Acta Neuropathologica, 2015, 129, 449-457.	3.9	80
77	Software for the Integration of Multiomics Experiments in Bioconductor. Cancer Research, 2017, 77, e39-e42.	0.4	80
78	Revisiting inconsistency in large pharmacogenomic studies. F1000Research, 2016, 5, 2333.	0.8	79
79	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. Nature Communications, 2021, 12, 979.	5.8	77
80	Noncoding somatic and inherited single-nucleotide variants converge to promote ESR1 expression in breast cancer. Nature Genetics, 2016, 48, 1260-1266.	9.4	75
81	Predictive approaches for drug combination discovery in cancer. Briefings in Bioinformatics, 2018, 19, 263-276.	3.2	75
82	Improvement of the clinical applicability of the Genomic Grade Index through a qRT-PCR test performed on frozen and formalin-fixed paraffin-embedded tissues. BMC Genomics, 2009, 10, 424.	1.2	74
83	The gene regulatory network for breast cancer: integrated regulatory landscape of cancer hallmarks. Frontiers in Genetics, 2014, 5, 15.	1.1	74
84	CovidCTNet: an open-source deep learning approach to diagnose covid-19 using small cohort of CT images. Npj Digital Medicine, 2021, 4, 29.	5.7	74
85	Comparison and validation of genomic predictors for anticancer drug sensitivity. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 597-602.	2.2	70
86	Nucleolus and c-Myc: potential targets of cardenolide-mediated antitumor activity. Molecular Cancer Therapeutics, 2008, 7, 1285-1296.	1.9	69
87	Why imaging data alone is not enough: AI-based integration of imaging, omics, and clinical data. European Journal of Nuclear Medicine and Molecular Imaging, 2019, 46, 2722-2730.	3.3	69
88	The Gene expression Grade Index: a potential predictor of relapse for endocrine-treated breast cancer patients in the BIG 1â€"98 trial. BMC Medical Genomics, 2009, 2, 40.	0.7	67
89	Galectin 1 Proangiogenic and Promigratory Effects in the Hs683 Oligodendroglioma Model Are Partly Mediated through the Control of BEX2 Expression. Neoplasia, 2009, 11, 485-496.	2.3	63
90	Pan-cancer analysis of longitudinal metastatic tumors reveals genomic alterations and immune landscape dynamics associated with pembrolizumab sensitivity. Nature Communications, 2021, 12, 5137.	5.8	63

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91	Disruption of the anaphase-promoting complex confers resistance to TTK inhibitors in triple-negative breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1570-E1577.	3.3	62
92	A network model for angiogenesis in ovarian cancer. BMC Bioinformatics, 2015, 16, 115.	1.2	60
93	Radiomic Biomarkers to Refine Risk Models for Distant Metastasis in HPV-related Oropharyngeal Carcinoma. International Journal of Radiation Oncology Biology Physics, 2018, 102, 1107-1116.	0.4	57
94	Gene isoforms as expression-based biomarkers predictive of drug response in vitro. Nature Communications, 2017, 8, 1126.	5.8	54
95	Transfer of clinically relevant gene expression signatures in breast cancer: from Affymetrix microarray to Illumina RNA-Sequencing technology. BMC Genomics, 2014, 15, 1008.	1.2	52
96	Gene expression profiling identifies activated growth factor signaling in poor prognosis (Luminal-B) estrogen receptor positive breast cancer. BMC Medical Genomics, 2009, 2, 37.	0.7	51
97	Whole genomes define concordance of matched primary, xenograft, and organoid models of pancreas cancer. PLoS Computational Biology, 2019, 15, e1006596.	1.5	51
98	Revisiting inconsistency in large pharmacogenomic studies. F1000Research, 2016, 5, 2333.	0.8	51
99	BatchQC: interactive software for evaluating sample and batch effects in genomic data. Bioinformatics, 2016, 32, 3836-3838.	1.8	50
100	Identification of a microRNA signature associated with risk of distant metastasis in nasopharyngeal carcinoma. Oncotarget, 2015, 6, 4537-4550.	0.8	50
101	Statin-Induced Cancer Cell Death Can Be Mechanistically Uncoupled from Prenylation of RAS Family Proteins. Cancer Research, 2018, 78, 1347-1357.	0.4	49
102	Extensive rewiring of epithelial-stromal co-expression networks in breast cancer. Genome Biology, 2015, 16, 128.	3.8	48
103	Biomimetic hydrogel supports initiation and growth of patient-derived breast tumor organoids. Nature Communications, 2022, 13, 1466.	5.8	48
104	A fuzzy gene expression-based computational approach improves breast cancer prognostication. Genome Biology, 2010, 11, R18.	13.9	47
105	Characterization and Clinical Evaluation of CD10+ Stroma Cells in the Breast Cancer Microenvironment. Clinical Cancer Research, 2012, 18, 1004-1014.	3.2	46
106	Public data and open source tools for multi-assay genomic investigation of disease. Briefings in Bioinformatics, 2016, 17, 603-615.	3.2	46
107	UNBS5162, a Novel Naphthalimide That Decreases CXCL Chemokine Expression in Experimental Prostate Cancers. Neoplasia, 2008, 10, 573-586.	2.3	45
108	Single-cell chromatin accessibility profiling of glioblastoma identifies an invasive cancer stem cell population associated with lower survival. ELife, 2021, 10, .	2.8	45

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109	Proliferation and estrogen signaling can distinguish patients at risk for early versus late relapse among estrogen receptor positive breast cancers. Breast Cancer Research, 2013, 15, R86.	2.2	44
110	Ontogeny and Vulnerabilities of Drug-Tolerant Persisters in HER2+ Breast Cancer. Cancer Discovery, 2022, 12, 1022-1045.	7.7	43
111	PRMT inhibition induces a viral mimicry response in triple-negative breast cancer. Nature Chemical Biology, 2022, 18, 821-830.	3.9	43
112	Inference and validation of predictive gene networks from biomedical literature and gene expression data. Genomics, 2014, 103, 329-336.	1.3	40
113	Bidirectional terminators in Saccharomyces cerevisiae prevent cryptic transcription from invading neighboring genes. Nucleic Acids Research, 2017, 45, 6417-6426.	6.5	40
114	An imprinted non-coding genomic cluster at 14q32 defines clinically relevant molecular subtypes in osteosarcoma across multiple independent datasets. Journal of Hematology and Oncology, 2017, 10, 107.	6.9	38
115	An interim report on the investigator-initiated phase 2 study of pembrolizumab immunological response evaluation (INSPIRE). , 2019, 7, 72.		38
116	Quantification of ZAP70 mRNA in B Cells by Real-Time PCR Is a Powerful Prognostic Factor in Chronic Lymphocytic Leukemia. Clinical Chemistry, 2007, 53, 1757-1766.	1.5	36
117	NOTCH2 and FLT3 gene mis-splicings are common events in patients with acute myeloid leukemia (AML): new potential targets in AML. Blood, 2014, 123, 2816-2825.	0.6	36
118	The impact of the variation of imaging parameters on the robustness of Computed Tomography radiomic features: A review. Computers in Biology and Medicine, 2021, 133, 104400.	3.9	36
119	Molecular profiling of CD3âˆ'CD4+ T cells from patients with the lymphocytic variant of hypereosinophilic syndrome reveals targeting of growth control pathways. Blood, 2009, 114, 2969-2983.	0.6	34
120	Modeling invasive breast cancer: growth factors propel progression of HER2-positive premalignant lesions. Oncogene, 2012, 31, 3569-3583.	2.6	34
121	Integrative Pharmacogenomics Analysis of Patient-Derived Xenografts. Cancer Research, 2019, 79, 4539-4550.	0.4	34
122	Assessment of pharmacogenomic agreement. F1000Research, 2016, 5, 825.	0.8	34
123	Gene expression profiling reveals differences in microenvironment interaction between patients with chronic lymphocytic leukemia expressing high versus low ZAP70 mRNA. Haematologica, 2009, 94, 790-799.	1.7	33
124	Functional and genetic analysis of the colon cancer network. BMC Bioinformatics, 2014, 15, S6.	1.2	33
125	The Cdc42/Rac1 regulator CdGAP is a novel E-cadherin transcriptional co-repressor with Zeb2 in breast cancer. Oncogene, 2017, 36, 3490-3503.	2.6	33
126	Integrative Cancer Pharmacogenomics to Infer Large-Scale Drug Taxonomy. Cancer Research, 2017, 77, 3057-3069.	0.4	33

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127	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. Nature Biotechnology, 2017, 35, 1127-1128.	9.4	32
128	AXL knockdown gene signature reveals a drug repurposing opportunity for a class of antipsychotics to reduce growth and metastasis of triple-negative breast cancer. Oncotarget, 2019, 10, 2055-2067.	0.8	32
129	Assessment of modelling strategies for drug response prediction in cell lines and xenografts. Scientific Reports, 2020, 10, 2849.	1.6	31
130	Stem Cell-Like Gene Expression in Ovarian Cancer Predicts Type II Subtype and Prognosis. PLoS ONE, 2013, 8, e57799.	1.1	30
131	MetaGxData: Clinically Annotated Breast, Ovarian and Pancreatic Cancer Datasets and their Use in Generating a Multi-Cancer Gene Signature. Scientific Reports, 2019, 9, 8770.	1.6	29
132	Biological and therapeutic implications of a unique subtype of NPM1 mutated AML. Nature Communications, 2021, 12, 1054.	5.8	29
133	Predictive networks: a flexible, open source, web application for integration and analysis of human gene networks. Nucleic Acids Research, 2012, 40, D866-D875.	6.5	28
134	Significance Analysis of Prognostic Signatures. PLoS Computational Biology, 2013, 9, e1002875.	1.5	27
135	SYNERGxDB: an integrative pharmacogenomic portal to identify synergistic drug combinations for precision oncology. Nucleic Acids Research, 2020, 48, W494-W501.	6.5	27
136	A Comparative Study of Cluster Detection Algorithms in Protein–Protein Interaction for Drug Target Discovery and Drug Repurposing. Frontiers in Pharmacology, 2019, 10, 109.	1.6	26
137	IL6 Induces an IL22+ CD8+ T-cell Subset with Potent Antitumor Function. Cancer Immunology Research, 2020, 8, 321-333.	1.6	26
138	Drug sensitivity prediction from cell line-based pharmacogenomics data: guidelines for developing machine learning models. Briefings in Bioinformatics, 2021, 22, .	3.2	26
139	Minimising Immunohistochemical False Negative ER Classification Using a Complementary 23 Gene Expression Signature of ER Status. PLoS ONE, 2010, 5, e15031.	1.1	26
140	RamiGO: an R/Bioconductor package providing an AmiGO Visualize interface. Bioinformatics, 2013, 29, 666-668.	1.8	25
141	Long-term Temozolomide Treatment Induces Marked Amino Metabolism Modifications and an Increase in TMZ Sensitivity in Hs683 Oligodendroglioma Cells. Neoplasia, 2010, 12, 69-79.	2.3	24
142	Exploiting high-throughput cell line drug screening studies to identify candidate therapeutic agents in head and neck cancer. BMC Pharmacology & Toxicology, 2014, 15, 66.	1.0	23
143	Tissue specificity of in vitro drug sensitivity. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 158-166.	2.2	23
144	Modeling Cellular Response in Large-Scale Radiogenomic Databases to Advance Precision Radiotherapy. Cancer Research, 2019, 79, 6227-6237.	0.4	23

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145	Gene regulation by phorbol 12-myristate 13-acetate in MCF-7 and MDA-MB-231, two breast cancer cell lines exhibiting highly different phenotypes. Oncology Reports, 2004, 12, 701-7.	1.2	22
146	Safikhani et al. reply. Nature, 2016, 540, E2-E4.	13.7	22
147	Importance of collection in gene set enrichment analysis of drug response in cancer cell lines. Scientific Reports, 2014, 4, 4092.	1.6	21
148	Modeling germline mutations in pineoblastoma uncovers lysosome disruption-based therapy. Nature Communications, 2020, 11, 1825.	5.8	21
149	Administration of Hypoxia-Activated Prodrug Evofosfamide after Conventional Adjuvant Therapy Enhances Therapeutic Outcome and Targets Cancer-Initiating Cells in Preclinical Models of Colorectal Cancer. Clinical Cancer Research, 2018, 24, 2116-2127.	3.2	20
150	Identifying clusters of *cis*-regulatory elements underpinning TAD structures and lineage-specific regulatory networks. Genome Research, 2019, 29, 1733-1743.	2.4	19
151	The mevalonate pathway is an actionable vulnerability of t(4;14)-positive multiple myeloma. Leukemia, 2021, 35, 796-808.	3.3	19
152	Chromosomal instability as a prognostic marker in cervical cancer. BMC Cancer, 2015, 15, 361.	1.1	18
153	ABC: a tool to identify SNVs causing allele-specific transcription factor binding from ChIP-Seq experiments. Bioinformatics, 2015, 31, 3057-3059.	1.8	17
154	Low CD10 mRNA Expression Identifies High-Risk Ductal Carcinoma In Situ (DCIS). PLoS ONE, 2010, 5, e12100.	1.1	16
155	DNA replication stress: a source of APOBEC3B expression in breast cancer. Genome Biology, 2016, 17, 202.	3.8	16
156	Untangling statistical and biological models to understand network inference: the need for a genomics network ontology. Frontiers in Genetics, 2014, 5, 299.	1.1	15
157	Characterization of Conserved Toxicogenomic Responses in Chemically Exposed Hepatocytes across Species and Platforms. Environmental Health Perspectives, 2016, 124, 313-320.	2.8	15
158	PharmacoDB 2.0: improving scalability and transparency of *in vitro* pharmacogenomics analysis. Nucleic Acids Research, 2022, 50, D1348-D1357.	6.5	15
159	Novel Effects of Chromosome Y on Cardiac Regulation, Chromatin Remodeling, and Neonatal Programming in Male Mice. Endocrinology, 2013, 154, 4746-4756.	1.4	14
160	Assessment of Genetic Drift in Large Pharmacogenomic Studies. Cell Systems, 2020, 11, 393-401.e2.	2.9	14
161	Integrative Transcriptome Analyses Empower the Anti-COVID-19 Drug Arsenal. IScience, 2020, 23, 101697.	1.9	14
162	Prognostic microRNAs modulate the RHO adhesion pathway: A potential therapeutic target in undifferentiated pleomorphic sarcomas. Oncotarget, 2015, 6, 39127-39139.	0.8	14

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163	Genomic biomarkers for precision radiation medicine. Lancet Oncology, The, 2017, 18, e238.	5.1	12
164	Safikhani et al. reply. Nature, 2016, 540, E11-E12.	13.7	11
165	External validation and transfer learning of convolutional neural networks for computed tomography dental artifact classification. Physics in Medicine and Biology, 2020, 65, 035017.	1.6	11
166	Safikhani et al. reply. Nature, 2016, 540, E6-E8.	13.7	10
167	Transcriptome Analysis of Human Reninomas as an Approach to Understanding Juxtaglomerular Cell Biology. Hypertension, 2017, 69, 1145-1155.	1.3	10
168	Large organized chromatin lysine domains help distinguish primitive from differentiated cell populations. Nature Communications, 2021, 12, 499.	5.8	10
169	Prediction of Human Papillomavirus (HPV) Association of Oropharyngeal Cancer (OPC) Using Radiomics: The Impact of the Variation of CT Scanner. Cancers, 2021, 13, 2269.	1.7	10
170	Orchestrating and sharing large multimodal data for transparent and reproducible research. Nature Communications, 2021, 12, 5797.	5.8	10
171	Genome-wide DNA methylation patterns reveal clinically relevant predictive and prognostic subtypes in human osteosarcoma. Communications Biology, 2022, 5, 213.	2.0	10
172	Rational design and identification of immuno-oncology drug combinations. European Journal of Cancer, 2018, 95, 38-51.	1.3	9
173	Network science in clinical trials: A patient-centered approach. Seminars in Cancer Biology, 2018, 52, 135-150.	4.3	9
174	Automatic classification of dental artifact status for efficient image veracity checks: effects of image resolution and convolutional neural network depth. Physics in Medicine and Biology, 2020, 65, 015005.	1.6	9
175	ToxicoDB: an integrated database to mine and visualize large-scale toxicogenomic datasets. Nucleic Acids Research, 2020, 48, W455-W462.	6.5	9
176	MicroRNA-mRNA networks define translatable molecular outcome phenotypes in osteosarcoma. Scientific Reports, 2020, 10, 4409.	1.6	9
177	Centromeric cohesion failure invokes a conserved choreography of chromosomal mis-segregations in pancreatic neuroendocrine tumor. Genome Medicine, 2020, 12, 38.	3.6	9
178	Low residual proliferation after short-term letrozole therapy is an early predictive marker of response in high proliferative ER-positive breast cancer. Endocrine-Related Cancer, 2011, 18, 721-730.	1.6	8
179	Quantitative assessment and validation of network inference methods in bioinformatics. Frontiers in Genetics, 2014, 5, 221.	1.1	8
180	Personalized diagnosis of medulloblastoma subtypes across patients and model systems. Genomics, 2015, 106, 96-106.	1.3	8

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