

John N Weinstein

List of Publications by Citations

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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.

340
papers

95,988
citations

126
h-index

309
g-index

366
ext. papers

120,135
ext. citations

15
avg, IF

8.91
L-index

#	Paper	IF	Citations
340	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008 , 455, 1061-8	50.4	5669
339	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011 , 474, 609-15	50.4	5210
338	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013 , 45, 1113-20	36.3	3933
337	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014 , 513, 202-9	50.4	3659
336	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014 , 511, 543-50	50.4	3310
335	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. <i>New England Journal of Medicine</i> , 2013 , 368, 2059-74	59.2	3137
334	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2	2900
333	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013 , 497, 67-73	50.4	2800
332	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014 , 507, 315-22	50.4	1963
331	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
330	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96	56.2	1807
329	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
328	Systematic variation in gene expression patterns in human cancer cell lines. <i>Nature Genetics</i> , 2000 , 24, 227-35	36.3	1739
327	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25	56.2	1713
326	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90	56.2	1660
325	Exome sequencing of head and neck squamous cell carcinoma reveals inactivating mutations in NOTCH1. <i>Science</i> , 2011 , 333, 1154-7	33.3	1331
324	Biomarkers in cancer staging, prognosis and treatment selection. <i>Nature Reviews Cancer</i> , 2005 , 5, 845-56	31.3	1278

323	A gene expression database for the molecular pharmacology of cancer. <i>Nature Genetics</i> , 2000 , 24, 236-446.3	46.3	1173
322	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140
321	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
320	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
319	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11	56.2	1072
318	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
317	An information-intensive approach to the molecular pharmacology of cancer. <i>Science</i> , 1997 , 275, 343-9	33.3	1009
316	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e25	56.2	961
315	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , 2014 , 158, 929-944	56.2	935
314	GoMiner: a resource for biological interpretation of genomic and proteomic data. <i>Genome Biology</i> , 2003 , 4, R28	18.3	934
313	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203.e13	56.2	13896
312	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018 , 173, 291-304.e6	56.2	888
311	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
310	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
309	Design of liposomes for enhanced local release of drugs by hyperthermia. <i>Science</i> , 1978 , 202, 1290-3	33.3	763
308	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017 , 543, 378-384	50.4	755
307	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016 , 374, 135-45	59.2	753
306	An epithelial-mesenchymal transition gene signature predicts resistance to EGFR and PI3K inhibitors and identifies Axl as a therapeutic target for overcoming EGFR inhibitor resistance. <i>Clinical Cancer Research</i> , 2013 , 19, 279-90	12.9	649

305	Liposome-cell interaction: transfer and intracellular release of a trapped fluorescent marker. <i>Science</i> , 1977 , 195, 489-92	33.3	641
304	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016 , 48, 607-16	36.3	613
303	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15	56.2	560
302	Chemosensitivity prediction by transcriptional profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 10787-92	11.5	534
301	The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , 2014 , 26, 319-330	24.3	521
300	Co-occurring genomic alterations define major subsets of KRAS-mutant lung adenocarcinoma with distinct biology, immune profiles, and therapeutic vulnerabilities. <i>Cancer Discovery</i> , 2015 , 5, 860-77	24.4	476
299	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
298	Predicting drug sensitivity and resistance: profiling ABC transporter genes in cancer cells. <i>Cancer Cell</i> , 2004 , 6, 129-37	24.3	432
297	Proteomic profiling of the NCI-60 cancer cell lines using new high-density reverse-phase lysate microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 14229-34	11.5	415
296	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405
295	Nova regulates brain-specific splicing to shape the synapse. <i>Nature Genetics</i> , 2005 , 37, 844-52	36.3	397
294	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018 , 362,	33.3	392
293	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391
292	Integrative genomic characterization of oral squamous cell carcinoma identifies frequent somatic drivers. <i>Cancer Discovery</i> , 2013 , 3, 770-81	24.4	391
291	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	43	377
290	Interactions of liposomes with mammalian cells. <i>Annual Review of Biophysics and Bioengineering</i> , 1978 , 7, 435-68		374
289	Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. <i>Journal of Clinical Investigation</i> , 2013 , 123, 517-25	15.9	371
288	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018 , 23, 181-193.e7	10.6	366

287	TANRIC: An Interactive Open Platform to Explore the Function of lncRNAs in Cancer. <i>Cancer Research</i> , 2015 , 75, 3728-37	10.1	354
286	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
285	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018 , 173, 355-370.e14	56.2	342
284	Targeting to cells of fluorescent liposomes covalently coupled with monoclonal antibody or protein A. <i>Nature</i> , 1980 , 288, 602-4	50.4	330
283	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327
282	A pan-cancer proteomic perspective on The Cancer Genome Atlas. <i>Nature Communications</i> , 2014 , 5, 3887	17.4	324
281	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736	24.3	324
280	Proteomic profiling identifies dysregulated pathways in small cell lung cancer and novel therapeutic targets including PARP1. <i>Cancer Discovery</i> , 2012 , 2, 798-811	24.4	323
279	Mutation analysis of 24 known cancer genes in the NCI-60 cell line set. <i>Molecular Cancer Therapeutics</i> , 2006 , 5, 2606-12	6.1	322
278	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
277	MicroRNAs modulate the chemosensitivity of tumor cells. <i>Molecular Cancer Therapeutics</i> , 2008 , 7, 1-9	6.1	318
276	Liposomes and local hyperthermia: selective delivery of methotrexate to heated tumors. <i>Science</i> , 1979 , 204, 188-91	33.3	315
275	A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. <i>European Urology</i> , 2020 , 77, 420-433	10.2	309
274	Hydroxyurea as an inhibitor of human immunodeficiency virus-type 1 replication. <i>Science</i> , 1994 , 266, 801-5	33.3	303
273	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5	10.6	295
272	TCPA: a resource for cancer functional proteomics data. <i>Nature Methods</i> , 2013 , 10, 1046-7	21.6	288
271	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. <i>Cancer Cell</i> , 2017 , 31, 820-832.e3	24.3	286
270	Electric power from differences in salinity: the dialytic battery. <i>Science</i> , 1976 , 191, 557-9	33.3	286

269	Inhibition of human immunodeficiency virus type-1 integrase by curcumin. <i>Biochemical Pharmacology</i> , 1995 , 49, 1165-70	6	280
268	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
267	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018 , 33, 706-720.e9	24.3	275
266	Neural computing in cancer drug development: predicting mechanism of action. <i>Science</i> , 1992 , 258, 447-513	3.3	269
265	Transcript and protein expression profiles of the NCI-60 cancer cell panel: an integromic microarray study. <i>Molecular Cancer Therapeutics</i> , 2007 , 6, 820-32	6.1	263
264	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018 , 8, 1548-1565	24.4	258
263	A Patient-Derived, Pan-Cancer EMT Signature Identifies Global Molecular Alterations and Immune Target Enrichment Following Epithelial-to-Mesenchymal Transition. <i>Clinical Cancer Research</i> , 2016 , 22, 609-20	12.9	254
262	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017 , 18, 2780-2794	10.6	247
261	A strategy for predicting the chemosensitivity of human cancers and its application to drug discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 13086-91	11.5	245
260	Artificial neural networks improve the accuracy of cancer survival prediction. <i>Cancer</i> , 1997 , 79, 857-62	6.4	244
259	Membrane transporters and channels: role of the transportome in cancer chemosensitivity and chemoresistance. <i>Cancer Research</i> , 2004 , 64, 4294-301	10.1	244
258	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. <i>Genome Research</i> , 2015 , 25, 316-27	9.7	240
257	High-Throughput GoMiner, an 'industrial-strength' integrative gene ontology tool for interpretation of multiple-microarray experiments, with application to studies of Common Variable Immune Deficiency (CVID). <i>BMC Bioinformatics</i> , 2005 , 6, 168	3.6	237
256	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018 , 23, 227-238.e3	10.6	235
255	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
254	Gadd45, a p53-responsive stress protein, modifies DNA accessibility on damaged chromatin. <i>Molecular and Cellular Biology</i> , 1999 , 19, 1673-85	4.8	228
253	Carboxyfluorescein as a probe for liposome-cell interactions effect of impurities, and purification of the dye. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1981 , 649, 133-137	3.8	218
252	MicroRNA expression profiles for the NCI-60 cancer cell panel. <i>Molecular Cancer Therapeutics</i> , 2007 , 6, 1483-91	6.1	215

251	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
250	Assessing the clinical utility of cancer genomic and proteomic data across tumor types. <i>Nature Biotechnology</i> , 2014 , 32, 644-52	44.5	205
249	Karyotypic complexity of the NCI-60 drug-screening panel. <i>Cancer Research</i> , 2003 , 63, 8634-47	10.1	205
248	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406	10.6	200
247	Integrating global gene expression and radiation survival parameters across the 60 cell lines of the National Cancer Institute Anticancer Drug Screen. <i>Cancer Research</i> , 2008 , 68, 415-24	10.1	197
246	Small-sample precision of ROC-related estimates. <i>Bioinformatics</i> , 2010 , 26, 822-30	7.2	195
245	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
244	TCGASpliceSeq a compendium of alternative mRNA splicing in cancer. <i>Nucleic Acids Research</i> , 2016 , 44, D1018-22	20.1	181
243	VirusSeq: software to identify viruses and their integration sites using next-generation sequencing of human cancer tissue. <i>Bioinformatics</i> , 2013 , 29, 266-7	7.2	175
242	MedMiner: an Internet text-mining tool for biomedical information, with application to gene expression profiling. <i>BioTechniques</i> , 1999 , 27, 1210-4, 1216-7	2.5	169
241	Meta-Analysis of the Luminal and Basal Subtypes of Bladder Cancer and the Identification of Signature Immunohistochemical Markers for Clinical Use. <i>EBioMedicine</i> , 2016 , 12, 105-117	8.8	169
240	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
239	CellMiner: a relational database and query tool for the NCI-60 cancer cell lines. <i>BMC Genomics</i> , 2009 , 10, 277	4.5	165
238	Generation of a drug resistance profile by quantitation of mdr-1/P-glycoprotein in the cell lines of the National Cancer Institute Anticancer Drug Screen. <i>Journal of Clinical Investigation</i> , 1995 , 95, 2205-14	15.9	164
237	Molecular modeling studies of the DNA-topoisomerase I ternary cleavable complex with camptothecin. <i>Journal of Medicinal Chemistry</i> , 1998 , 41, 2216-26	8.3	163
236	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. <i>Cell Reports</i> , 2019 , 28, 1370-1384.e5	10.6	161
235	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018 , 6, 282-300.e2	10.6	159
234	Quantitative structure-antitumor activity relationships of camptothecin analogues: cluster analysis and genetic algorithm-based studies. <i>Journal of Medicinal Chemistry</i> , 2001 , 44, 3254-63	8.3	159

233	Comprehensive analysis of long non-coding RNAs in human breast cancer clinical subtypes. <i>Oncotarget</i> , 2014 , 5, 9864-76	3.3	156
232	Landscape of DNA virus associations across human malignant cancers: analysis of 3,775 cases using RNA-Seq. <i>Journal of Virology</i> , 2013 , 87, 8916-26	6.6	153
231	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018 , 25, 1304-1317.e5	10.6	152
230	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10	24.3	150
229	Selective toxicity of NSC73306 in MDR1-positive cells as a new strategy to circumvent multidrug resistance in cancer. <i>Cancer Research</i> , 2006 , 66, 4808-15	10.1	148
228	Targeting cancer micrometastases with monoclonal antibodies: a binding-site barrier. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995 , 92, 8999-9003	11.5	148
227	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018 , 23, 297-312.e12	10.6	147
226	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018 , 23, 194-212.e6	10.6	146
225	SpliceSeq: a resource for analysis and visualization of RNA-Seq data on alternative splicing and its functional impacts. <i>Bioinformatics</i> , 2012 , 28, 2385-7	7.2	144
224	Integrating data on DNA copy number with gene expression levels and drug sensitivities in the NCI-60 cell line panel. <i>Molecular Cancer Therapeutics</i> , 2006 , 5, 853-67	6.1	140
223	A stromal gene signature associated with inflammatory breast cancer. <i>International Journal of Cancer</i> , 2008 , 122, 1324-32	7.5	134
222	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.e32	10.2	133
221	UPLC-ESI-TOFMS-based metabolomics and gene expression dynamics inspector self-organizing metabolomic maps as tools for understanding the cellular response to ionizing radiation. <i>Analytical Chemistry</i> , 2008 , 80, 665-74	7.8	131
220	Profiling SLCO and SLC22 genes in the NCI-60 cancer cell lines to identify drug uptake transporters. <i>Molecular Cancer Therapeutics</i> , 2008 , 7, 3081-91	6.1	130
219	Liposomes as drug carriers in cancer chemotherapy 1984 , 24, 207-33		129
218	Diagnostic markers that distinguish colon and ovarian adenocarcinomas: identification by genomic, proteomic, and tissue array profiling. <i>Cancer Research</i> , 2003 , 63, 5243-50	10.1	125
217	DNA fingerprinting of the NCI-60 cell line panel. <i>Molecular Cancer Therapeutics</i> , 2009 , 8, 713-24	6.1	123
216	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121

215	MatchMiner: a tool for batch navigation among gene and gene product identifiers. <i>Genome Biology</i> , 2003 , 4, R27	18.3	120
214	mRNA and microRNA expression profiles of the NCI-60 integrated with drug activities. <i>Molecular Cancer Therapeutics</i> , 2010 , 9, 1080-91	6.1	118
213	PRADA: pipeline for RNA sequencing data analysis. <i>Bioinformatics</i> , 2014 , 30, 2224-6	7.2	117
212	Phase transition release, a new approach to the interaction of proteins with lipid vesicles. Application to lipoproteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1981 , 647, 270-84	3.8	117
211	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018 , 23, 255-269.e4	10.6	112
210	Identification of epidermal growth factor receptor and c-erbB2 pathway inhibitors by correlation with gene expression patterns. <i>Journal of the National Cancer Institute</i> , 1997 , 89, 1505-15	9.7	107
209	The glutaminase activity of L-asparaginase is not required for anticancer activity against ASNS-negative cells. <i>Blood</i> , 2014 , 123, 3596-606	2.2	105
208	Comprehensive molecular characterization of mitochondrial genomes in human cancers. <i>Nature Genetics</i> , 2020 , 52, 342-352	36.3	105
207	Molecular interaction maps of bioregulatory networks: a general rubric for systems biology. <i>Molecular Biology of the Cell</i> , 2006 , 17, 1-13	3.5	104
206	Tissue-specific isoform switch and DNA hypomethylation of the pyruvate kinase PKM gene in human cancers. <i>Oncotarget</i> , 2014 , 5, 8202-10	3.3	101
205	Mining the NCI anticancer drug discovery databases: genetic function approximation for the QSAR study of anticancer ellipticine analogues. <i>Journal of Chemical Information and Computer Sciences</i> , 1998 , 38, 189-99		100
204	Squamous cell carcinoma of the oral tongue in young non-smokers is genomically similar to tumors in older smokers. <i>Clinical Cancer Research</i> , 2014 , 20, 3842-8	12.9	96
203	The pharmacology of monoclonal antibodies. <i>Annals of the New York Academy of Sciences</i> , 1987 , 507, 199-210	6.5	96
202	Liposome-lymphocyte interaction: saturable sites for transfer and intracellular release of liposome contents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1977 , 74, 5603-7	14.5	96
201	Gene Expression Profile of the Clinically Aggressive Micropapillary Variant of Bladder Cancer. <i>European Urology</i> , 2016 , 70, 611-620	10.2	92
200	Cancers as wounds that do not heal: differences and similarities between renal regeneration/repair and renal cell carcinoma. <i>Cancer Research</i> , 2006 , 66, 7216-24	10.1	91
199	Next-generation sequencing of translocation renal cell carcinoma reveals novel RNA splicing partners and frequent mutations of chromatin-remodeling genes. <i>Clinical Cancer Research</i> , 2014 , 20, 4129-40	12.9	89
198	The p53 tumor suppressor network is a key responder to microenvironmental components of chronic inflammatory stress. <i>Cancer Research</i> , 2005 , 65, 10255-64	10.1	89

197	Three-dimensional quantitative structure-activity relationship (QSAR) of HIV integrase inhibitors: a comparative molecular field analysis (CoMFA) study. <i>Journal of Medicinal Chemistry</i> , 1995 , 38, 890-7	8.3	89
196	EDGAR: extraction of drugs, genes and relations from the biomedical literature. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2000 , 517-28	1.3	87
195	Lateral diffusion of surface immunoglobulin, Thy-1 antigen, and a lipid probe in lymphocyte plasma membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1979 , 76, 5163-7	11.5	86
194	Receptor-mediated endocytosis of antibody-opsonized liposomes by tumor cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1980 , 77, 4089-93	11.5	86
193	Invasive Bladder Cancer: Genomic Insights and Therapeutic Promise. <i>Clinical Cancer Research</i> , 2015 , 21, 4514-24	12.9	85
192	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018 , 7, 422-437.e7	10.6	85
191	Nonclassic functions of human topoisomerase I: genome-wide and pharmacologic analyses. <i>Cancer Research</i> , 2007 , 67, 8752-61	10.1	84
190	Pharmacogenomic analysis: correlating molecular substructure classes with microarray gene expression data. <i>Pharmacogenomics Journal</i> , 2002 , 2, 259-71	3.5	84
189	A protein expression database for the molecular pharmacology of cancer. <i>Electrophoresis</i> , 1997 , 18, 647-53	3.8	83
188	Three microarray platforms: an analysis of their concordance in profiling gene expression. <i>BMC Genomics</i> , 2005 , 6, 63	4.5	83
187	Mining and visualizing large anticancer drug discovery databases. <i>Journal of Chemical Information and Computer Sciences</i> , 2000 , 40, 367-79		83
186	AMPK β modulation in cancer progression: multilayer integrative analysis of the whole transcriptome in Asian gastric cancer. <i>Cancer Research</i> , 2012 , 72, 2512-21	10.1	82
185	VennMaster: area-proportional Euler diagrams for functional GO analysis of microarrays. <i>BMC Bioinformatics</i> , 2008 , 9, 67	3.6	81
184	Spotlight on molecular profiling: "Integromic" analysis of the NCI-60 cancer cell lines. <i>Molecular Cancer Therapeutics</i> , 2006 , 5, 2601-5	6.1	81
183	Comparing cDNA and oligonucleotide array data: concordance of gene expression across platforms for the NCI-60 cancer cells. <i>Genome Biology</i> , 2003 , 4, R82	18.3	81
182	Asparagine synthetase as a causal, predictive biomarker for L-asparaginase activity in ovarian cancer cells. <i>Molecular Cancer Therapeutics</i> , 2006 , 5, 2613-23	6.1	80
181	Charge clusters and the orientation of membrane proteins. <i>Journal of Membrane Biology</i> , 1982 , 66, 203-12	12.3	80
180	Rapid mass spectrometric identification of proteins from two-dimensional polyacrylamide gels after in gel proteolytic digestion. <i>Electrophoresis</i> , 1997 , 18, 391-402	3.6	78

179	Mining the National Cancer Institute Anticancer Drug Discovery Database: cluster analysis of ellipticine analogs with p53-inverse and central nervous system-selective patterns of activity. <i>Molecular Pharmacology</i> , 1998 , 53, 241-51	4.3	78
178	Elimination of infectious human immunodeficiency virus from human T-cell cultures by synergistic action of CD4-Pseudomonas exotoxin and reverse transcriptase inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990 , 87, 8889-93	11.5	77
177	Chk2 molecular interaction map and rationale for Chk2 inhibitors. <i>Clinical Cancer Research</i> , 2006 , 12, 2657-61	12.9	76
176	Antibody-mediated targeting of liposomes. Binding to lymphocytes does not ensure incorporation of vesicle contents into the cells. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1978 , 509, 272-88	3.8	75
175	Integrative analysis of proteomic signatures, mutations, and drug responsiveness in the NCI 60 cancer cell line set. <i>Molecular Cancer Therapeutics</i> , 2010 , 9, 257-67	6.1	74
174	Analysis of ATP-binding cassette transporter expression in drug-selected cell lines by a microarray dedicated to multidrug resistance. <i>Molecular Pharmacology</i> , 2004 , 66, 1397-405	4.3	73
173	Measurement of DNA concentration as a normalization strategy for metabolomic data from adherent cell lines. <i>Analytical Chemistry</i> , 2013 , 85, 9536-42	7.8	72
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