

John N Weinstein

List of Publications by Year in descending order

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345
papers

136,762
citations

433

131
h-index

114

342
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366
all docs

366
docs citations

366
times ranked

119441
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature, 2008, 455, 1061-1068.	13.7	6,879
2	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	13.7	6,541
3	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	9.4	6,265
4	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	13.7	5,055
5	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	13.7	4,572
6	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	13.9	4,139
7	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
8	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
9	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
10	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
11	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	13.5	2,562
12	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	13.7	2,496
13	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
14	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318
15	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
16	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
17	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
18	Systematic variation in gene expression patterns in human cancer cell lines. Nature Genetics, 2000, 24, 227-235.	9.4	1,946

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19	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
20	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
21	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.	13.5	1,718
22	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	13.5	1,695
23	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
24	Exome Sequencing of Head and Neck Squamous Cell Carcinoma Reveals Inactivating Mutations in <i>NOTCH1</i> . <i>Science</i> , 2011, 333, 1154-1157.	6.0	1,568
25	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	13.5	1,485
26	Biomarkers in Cancer Staging, Prognosis and Treatment Selection. <i>Nature Reviews Cancer</i> , 2005, 5, 845-856.	12.8	1,465
27	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
28	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
29	A gene expression database for the molecular pharmacology of cancer. <i>Nature Genetics</i> , 2000, 24, 236-244.	9.4	1,357
30	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	13.5	1,242
31	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017, 543, 378-384.	13.7	1,158
32	An Information-Intensive Approach to the Molecular Pharmacology of Cancer. <i>Science</i> , 1997, 275, 343-349.	6.0	1,127
33	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	13.9	1,040
34	GoMiner: a resource for biological interpretation of genomic and proteomic data. <i>Genome Biology</i> , 2003, 4, R28.	13.9	1,038
35	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.	9.4	933
36	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, 279-290.	3.2	848

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37	Design of liposomes for enhanced local release of drugs by hyperthermia. <i>Science</i> , 1978, 202, 1290-1293.	6.0	845
38	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	2.9	801
39	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	6.0	781
40	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
41	A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. <i>European Urology</i> , 2020, 77, 420-433.	0.9	741
42	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
43	Co-occurring Genomic Alterations Define Major Subsets of <i>KRAS</i> -Mutant Lung Adenocarcinoma with Distinct Biology, Immune Profiles, and Therapeutic Vulnerabilities. <i>Cancer Discovery</i> , 2015, 5, 860-877.	7.7	696
44	Liposome-cell interaction: transfer and intracellular release of a trapped fluorescent marker. <i>Science</i> , 1977, 195, 489-492.	6.0	692
45	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	2.9	683
46	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
47	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
48	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
49	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	13.5	620
50	Chemosensitivity prediction by transcriptional profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 10787-10792.	3.3	619
51	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	2.9	605
52	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	7.7	532
53	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	2.9	523
54	TANRIC: An Interactive Open Platform to Explore the Function of lncRNAs in Cancer. <i>Cancer Research</i> , 2015, 75, 3728-3737.	0.4	518

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55	Predicting drug sensitivity and resistance. <i>Cancer Cell</i> , 2004, 6, 129-137.	7.7	496
56	Integrative Genomic Characterization of Oral Squamous Cell Carcinoma Identifies Frequent Somatic Drivers. <i>Cancer Discovery</i> , 2013, 3, 770-781.	7.7	484
57	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482
58	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
59	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, 14229-14234.	3.3	463
60	Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. <i>Journal of Clinical Investigation</i> , 2013, 123, 517-25.	3.9	462
61	A pan-cancer proteomic perspective on The Cancer Genome Atlas. <i>Nature Communications</i> , 2014, 5, 3887.	5.8	456
62	Nova regulates brain-specific splicing to shape the synapse. <i>Nature Genetics</i> , 2005, 37, 844-852.	9.4	447
63	TCPA: a resource for cancer functional proteomics data. <i>Nature Methods</i> , 2013, 10, 1046-1047.	9.0	446
64	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. <i>Cancer Cell</i> , 2017, 31, 820-832.e3.	7.7	433
65	Proteomic Profiling Identifies Dysregulated Pathways in Small Cell Lung Cancer and Novel Therapeutic Targets Including PARP1. <i>Cancer Discovery</i> , 2012, 2, 798-811.	7.7	432
66	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018, 8, 1548-1565.	7.7	422
67	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	2.9	416
68	Interactions of Liposomes with Mammalian Cells. <i>Annual Review of Biophysics and Bioengineering</i> , 1978, 7, 435-468.	5.3	408
69	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	2.9	407
70	ElemCor: accurate data analysis and enrichment calculation for high-resolution LC-MS stable isotope labeling experiments. <i>BMC Bioinformatics</i> , 2019, 20, 89.	1.2	402
71	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.	7.7	400
72	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396

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73	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, 609-620.	3.2	388
74	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. <i>Cell Reports</i> , 2019, 28, 1370-1384.e5.	2.9	382
75	Mutation analysis of 24 known cancer genes in the NCI-60 cell line set. <i>Molecular Cancer Therapeutics</i> , 2006, 5, 2606-2612.	1.9	374
76	Targeting to cells of fluorescent liposomes covalently coupled with monoclonal antibody or protein A. <i>Nature</i> , 1980, 288, 602-604.	13.7	367
77	TCGASpliceSeq a compendium of alternative mRNA splicing in cancer. <i>Nucleic Acids Research</i> , 2016, 44, D1018-D1022.	6.5	358
78	MicroRNAs modulate the chemosensitivity of tumor cells. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 1-9.	1.9	357
79	Liposomes and local hyperthermia: selective delivery of methotrexate to heated tumors. <i>Science</i> , 1979, 204, 188-191.	6.0	345
80	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. <i>Genome Research</i> , 2015, 25, 316-327.	2.4	343
81	Hydroxyurea as an inhibitor of human immunodeficiency virus-type 1 replication. <i>Science</i> , 1994, 266, 801-805.	6.0	341
82	Electric Power from Differences in Salinity: The Dialytic Battery. <i>Science</i> , 1976, 191, 557-559.	6.0	338
83	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	2.9	333
84	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	2.9	329
85	Inhibition of human immunodeficiency virus type-1 integrase by curcumin. <i>Biochemical Pharmacology</i> , 1995, 49, 1165-1170.	2.0	327
86	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	324
87	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	7.7	309
88	Neural computing in cancer drug development: predicting mechanism of action. <i>Science</i> , 1992, 258, 447-451.	6.0	302
89	Artificial neural networks improve the accuracy of cancer survival prediction. , 1997, 79, 857-862.		301
90	Transcript and protein expression profiles of the NCI-60 cancer cell panel: an integromic microarray study. <i>Molecular Cancer Therapeutics</i> , 2007, 6, 820-832.	1.9	289

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91	A strategy for predicting the chemosensitivity of human cancers and its application to drug discovery. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 13086-13091.	3.3	284
92	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	2.9	284
93	Membrane Transporters and Channels. Cancer Research, 2004, 64, 4294-4301.	0.4	281
94	CellMiner: a relational database and query tool for the NCI-60 cancer cell lines. BMC Genomics, 2009, 10, 277.	1.2	273
95	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
96	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	7.7	270
97	Assessing the clinical utility of cancer genomic and proteomic data across tumor types. Nature Biotechnology, 2014, 32, 644-652.	9.4	257
98	Meta-Analysis of the Luminal and Basal Subtypes of Bladder Cancer and the Identification of Signature Immunohistochemical Markers for Clinical Use. EBioMedicine, 2016, 12, 105-117.	2.7	257
99	Small-sample precision of ROC-related estimates. Bioinformatics, 2010, 26, 822-830.	1.8	256
100	Comprehensive molecular characterization of mitochondrial genomes in human cancers. Nature Genetics, 2020, 52, 342-352.	9.4	256
101	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). BMC Bioinformatics, 2005, 6, 168.	1.2	253
102	Gadd45, a p53-Responsive Stress Protein, Modifies DNA Accessibility on Damaged Chromatin. Molecular and Cellular Biology, 1999, 19, 1673-1685.	1.1	251
103	MicroRNA expression profiles for the NCI-60 cancer cell panel. Molecular Cancer Therapeutics, 2007, 6, 1483-1491.	1.9	247
104	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	2.9	245
105	Carboxyfluorescein as a probe for liposome-cell interactions effect of impurities, and purification of the dye. Biochimica Et Biophysica Acta - Biomembranes, 1981, 649, 133-137.	1.4	238
106	SpliceSeq: a resource for analysis and visualization of RNA-Seq data on alternative splicing and its functional impacts. Bioinformatics, 2012, 28, 2385-2387.	1.8	231
107	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
108	Karyotypic complexity of the NCI-60 drug-screening panel. Cancer Research, 2003, 63, 8634-47.	0.4	227

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109	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, 415-424.	0.4	226
110	VirusSeq: software to identify viruses and their integration sites using next-generation sequencing of human cancer tissue. <i>Bioinformatics</i> , 2013, 29, 266-267.	1.8	209
111	MedMiner: An Internet Text-Mining Tool for Biomedical Information, with Application to Gene Expression Profiling. <i>BioTechniques</i> , 1999, 27, 1210-1217.	0.8	208
112	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.	2.9	205
113	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	2.9	204
114	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, 2205-2214.	3.9	189
115	Comprehensive analysis of long non-coding RNAs in human breast cancer clinical subtypes. <i>Oncotarget</i> , 2014, 5, 9864-9876.	0.8	188
116	Landscape of DNA Virus Associations across Human Malignant Cancers: Analysis of 3,775 Cases Using RNA-Seq. <i>Journal of Virology</i> , 2013, 87, 8916-8926.	1.5	187
117	EDGAR: Extraction of Drugs, Genes And Relations from the Biomedical Literature. , 1999, , 517-28.		182
118	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	2.9	177
119	Molecular Modeling Studies of the DNA-Topoisomerase I Ternary Cleavable Complex with Camptothecin. <i>Journal of Medicinal Chemistry</i> , 1998, 41, 2216-2226.	2.9	175
120	Quantitative Structure-Antitumor Activity Relationships of Camptothecin Analogues: Cluster Analysis and Genetic Algorithm-Based Studies. <i>Journal of Medicinal Chemistry</i> , 2001, 44, 3254-3263.	2.9	171
121	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.	3.3	165
122	Selective Toxicity of NSC73306 in MDR1-Positive Cells as a New Strategy to Circumvent Multidrug Resistance in Cancer. <i>Cancer Research</i> , 2006, 66, 4808-4815.	0.4	162
123	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, 853-867.	1.9	157
124	A stromal gene signature associated with inflammatory breast cancer. <i>International Journal of Cancer</i> , 2008, 122, 1324-1332.	2.3	154
125	Profiling SLCO and SLC22 genes in the NCI-60 cancer cell lines to identify drug uptake transporters. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 3081-3091.	1.9	151
126	The glutaminase activity of l-asparaginase is not required for anticancer activity against ASNS-negative cells. <i>Blood</i> , 2014, 123, 3596-3606.	0.6	150

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127	PRADA: pipeline for RNA sequencing data analysis. <i>Bioinformatics</i> , 2014, 30, 2224-2226.	1.8	147
128	Diagnostic markers that distinguish colon and ovarian adenocarcinomas: identification by genomic, proteomic, and tissue array profiling. <i>Cancer Research</i> , 2003, 63, 5243-50.	0.4	144
129	Liposomes as drug carriers in cancer chemotherapy. , 1984, 24, 207-233.		142
130	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, 665-674.	3.2	142
131	DNA fingerprinting of the NCI-60 cell line panel. <i>Molecular Cancer Therapeutics</i> , 2009, 8, 713-724.	1.9	137
132	MatchMiner: a tool for batch navigation among gene and gene product identifiers. <i>Genome Biology</i> , 2003, 4, R27.	13.9	135
133	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.	2.9	134
134	mRNA and microRNA Expression Profiles of the NCI-60 Integrated with Drug Activities. <i>Molecular Cancer Therapeutics</i> , 2010, 9, 1080-1091.	1.9	132
135	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, 270-284.	1.4	131
136	Tissue-specific isoform switch and DNA hypomethylation of the pyruvate kinase PKM gene in human cancers. <i>Oncotarget</i> , 2014, 5, 8202-8210.	0.8	127
137	Molecular Interaction Maps of Bioregulatory Networks: A General Rubric for Systems Biology. <i>Molecular Biology of the Cell</i> , 2006, 17, 1-13.	0.9	126
138	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, 3842-3848.	3.2	124
139	Gene Expression Profile of the Clinically Aggressive Micropapillary Variant of Bladder Cancer. <i>European Urology</i> , 2016, 70, 611-620.	0.9	120
140	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	2.9	119
141	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, 4129-4140.	3.2	117
142	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, 1505-1515.	3.0	113
143	Invasive Bladder Cancer: Genomic Insights and Therapeutic Promise. <i>Clinical Cancer Research</i> , 2015, 21, 4514-4524.	3.2	110
144	Cancers as Wounds that Do Not Heal: Differences and Similarities between Renal Regeneration/Repair and Renal Cell Carcinoma. <i>Cancer Research</i> , 2006, 66, 7216-7224.	0.4	109

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145	The Pharmacology of Monoclonal Antibodies. <i>Annals of the New York Academy of Sciences</i> , 1987, 507, 199-210.	1.8	108
146	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, 189-199.	2.8	107
147	Dysregulation of EMT Drives the Progression to Clinically Aggressive Sarcomatoid Bladder Cancer. <i>Cell Reports</i> , 2019, 27, 1781-1793.e4.	2.9	102
148	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, 5603-5607.	3.3	101
149	Explore, Visualize, and Analyze Functional Cancer Proteomic Data Using the Cancer Proteome Atlas. <i>Cancer Research</i> , 2017, 77, e51-e54.	0.4	101
150	Asparagine synthetase as a causal, predictive biomarker for l-asparaginase activity in ovarian cancer cells. <i>Molecular Cancer Therapeutics</i> , 2006, 5, 2613-2623.	1.9	97
151	Mining and Visualizing Large Anticancer Drug Discovery Databases. <i>Journal of Chemical Information and Computer Sciences</i> , 2000, 40, 367-379.	2.8	95
152	Mistaken identifiers: gene name errors can be introduced inadvertently when using Excel in bioinformatics. <i>BMC Bioinformatics</i> , 2004, 5, 80.	1.2	95
153	Cell lines battle cancer. <i>Nature</i> , 2012, 483, 544-545.	13.7	95
154	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, 5163-5167.	3.3	94
155	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, 890-897.	2.9	94
156	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, 4089-4093.	3.3	93
157	Three microarray platforms: an analysis of their concordance in profiling gene expression. <i>BMC Genomics</i> , 2005, 6, 63.	1.2	93
158	The p53 Tumor Suppressor Network Is a Key Responder to Microenvironmental Components of Chronic Inflammatory Stress. <i>Cancer Research</i> , 2005, 65, 10255-10264.	0.4	93
159	Nonclassic Functions of Human Topoisomerase I: Genome-Wide and Pharmacologic Analyses. <i>Cancer Research</i> , 2007, 67, 8752-8761.	0.4	93
160	Pharmacogenomic analysis: correlating molecular substructure classes with microarray gene expression data. <i>Pharmacogenomics Journal</i> , 2002, 2, 259-271.	0.9	92
161	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.	13.9	91
162	Spotlight on molecular profiling: Integromic analysis of the NCI-60 cancer cell lines. <i>Molecular Cancer Therapeutics</i> , 2006, 5, 2601-2605.	1.9	91

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163	AMPK \pm Modulation in Cancer Progression: Multilayer Integrative Analysis of the Whole Transcriptome in Asian Gastric Cancer. <i>Cancer Research</i> , 2012, 72, 2512-2521.	0.4	91
164	Measurement of DNA Concentration as a Normalization Strategy for Metabolomic Data from Adherent Cell Lines. <i>Analytical Chemistry</i> , 2013, 85, 9536-9542.	3.2	90
165	Tumor Subtype-Specific Cancer $\text{\r{e}}$ Testis Antigens as Potential Biomarkers and Immunotherapeutic Targets for Cancers. <i>Cancer Immunology Research</i> , 2014, 2, 371-379.	1.6	90
166	VennMaster: Area-proportional Euler diagrams for functional GO analysis of microarrays. <i>BMC Bioinformatics</i> , 2008, 9, 67.	1.2	89
167	Monoclonal antibodies in the lymphatics: selective delivery to lymph node metastases of a solid tumor. <i>Science</i> , 1983, 222, 423-426.	6.0	88
168	Asparagine synthetase is a predictive biomarker of \langle scp>l</scp>-asparaginase activity in ovarian cancer cell lines. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 3123-3128.	1.9	88
169	A protein expression database for the molecular pharmacology of cancer. <i>Electrophoresis</i> , 1997, 18, 647-653.	1.3	87
170	Rapid mass spectrometric identification of proteins from two-dimensional polyacrylamide gels after in gel proteolytic digestion. <i>Electrophoresis</i> , 1997, 18, 391-402.	1.3	86
171	Charge clusters and the orientation of membrane proteins. <i>Journal of Membrane Biology</i> , 1982, 66, 203-212.	1.0	84
172	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, 8889-8893.	3.3	84
173	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, 241-251.	1.0	83
174	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
175	Assessment of Luminal and Basal Phenotypes in Bladder Cancer. <i>Scientific Reports</i> , 2020, 10, 9743.	1.6	83
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, 272-288.	1.4	82
177	Transcriptional regulation of mitotic genes by camptothecin-induced DNA damage: microarray analysis of dose- and time-dependent effects. <i>Cancer Research</i> , 2002, 62, 1688-95.	0.4	82
178	Integrative Analysis of Proteomic Signatures, Mutations, and Drug Responsiveness in the NCI 60 Cancer Cell Line Set. <i>Molecular Cancer Therapeutics</i> , 2010, 9, 257-267.	1.9	81
179	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, 1397-1405.	1.0	79
180	Charge-Mosaic Membranes: Enhanced Permeability and Negative Osmosis with a Symmetrical Salt. <i>Science</i> , 1968, 161, 70-72.	6.0	78

#	ARTICLE	IF	CITATIONS
181	Chk2 Molecular Interaction Map and Rationale for Chk2 Inhibitors: Fig. 1.. <i>Clinical Cancer Research</i> , 2006, 12, 2657-2661.	3.2	78
182	Metabolomics Reveals Attenuation of the SLC6A20 Kidney Transporter in Nonhuman Primate and Mouse Models of Type 2 Diabetes Mellitus. <i>Journal of Biological Chemistry</i> , 2011, 286, 19511-19522.	1.6	78
183	Transport properties of charge-mosaic membranes I. Theoretical models. <i>Desalination</i> , 1972, 11, 341-377.	4.0	77
184	Characterization of long non-coding RNA transcriptome in clear-cell renal cell carcinoma by next-generation deep sequencing. <i>Molecular Oncology</i> , 2015, 9, 32-43.	2.1	75
185	Predictive statistics and artificial intelligence in the U.S. National Cancer Institute's drug discovery program for cancer and AIDS. <i>Stem Cells</i> , 1994, 12, 13-22.	1.4	74
186	A survey of intragenic breakpoints in glioblastoma identifies a distinct subset associated with poor survival. <i>Genes and Development</i> , 2013, 27, 1462-1472.	2.7	74
187	Sequencing and analysis of 10,967 full-length cDNA clones from <i>Xenopus laevis</i> and <i>Xenopus tropicalis</i> reveals post-tetraploidization transcriptome remodeling. <i>Genome Research</i> , 2006, 16, 796-803.	2.4	73
188	Expression of human endogenous retrovirus-K is strongly associated with the basal-like breast cancer phenotype. <i>Scientific Reports</i> , 2017, 7, 41960.	1.6	73
189	Tumor-Specific Isoform Switch of the Fibroblast Growth Factor Receptor 2 Underlies the Mesenchymal and Malignant Phenotypes of Clear Cell Renal Cell Carcinomas. <i>Clinical Cancer Research</i> , 2013, 19, 2460-2472.	3.2	72
190	High-density lipoprotein recombinants: evidence for a bicycle tire micelle structure obtained by neutron scattering and electron microscopy. <i>FEBS Letters</i> , 1979, 104, 231-235.	1.3	69
191	Impact of p53 knockout and topotecan treatment on gene expression profiles in human colon carcinoma cells: a pharmacogenomic study. <i>Cancer Research</i> , 2003, 63, 2782-93.	0.4	69
192	Predicting cisplatin and trabectedin drug sensitivity in ovarian and colon cancers. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 10-18.	1.9	68
193	PurityEst: estimating purity of human tumor samples using next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, 2265-2266.	1.8	68
194	An Artifact in LC-MS/MS Measurement of Glutamine and Glutamic Acid: In-Source Cyclization to Pyroglutamic Acid. <i>Analytical Chemistry</i> , 2014, 86, 5633-5637.	3.2	68
195	Pharmacogenomics " Teaching Old Drugs New Tricks. <i>New England Journal of Medicine</i> , 2000, 343, 1408-1409.	13.9	67
196	Properties of Switch-like Bioregulatory Networks Studied by Simulation of the Hypoxia Response Control System. <i>Molecular Biology of the Cell</i> , 2004, 15, 3042-3052.	0.9	67
197	TransVar: a multilevel variant annotator for precision genomics. <i>Nature Methods</i> , 2015, 12, 1002-1003.	9.0	67
198	In vitro inhibition of human immunodeficiency virus (HIV) type 1 replication by C2 symmetry-based HIV protease inhibitors as single agents or in combinations. <i>Antimicrobial Agents and Chemotherapy</i> , 1992, 36, 926-933.	1.4	66

#	ARTICLE	IF	CITATIONS
199	AffyProbeMiner: a web resource for computing or retrieving accurately redefined Affymetrix probe sets. <i>Bioinformatics</i> , 2007, 23, 2385-2390.	1.8	66
200	Dihydroartemisinin accelerates c-MYC oncoprotein degradation and induces apoptosis in c-MYC-overexpressing tumor cells. <i>Biochemical Pharmacology</i> , 2010, 80, 22-30.	2.0	65
201	A Postgenomic Visual Icon. <i>Science</i> , 2008, 319, 1772-1773.	6.0	61
202	Relative differences in the binding free energies of human immunodeficiency virus 1 protease inhibitors: a thermodynamic cycle-perturbation approach.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 10287-10291.	3.3	59
203	'Omic' and hypothesis-driven research in the molecular pharmacology of cancer. <i>Current Opinion in Pharmacology</i> , 2002, 2, 361-365.	1.7	59
204	Monoclonal antibodies in the lymphatics: toward the diagnosis and therapy of tumor metastases. <i>Science</i> , 1982, 218, 1334-1337.	6.0	58
205	Dipyridamole potentiates the inhibition by 3'-azido-3'-deoxythymidine and other dideoxynucleosides of human immunodeficiency virus replication in monocyte-macrophages.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1989, 86, 3842-3846.	3.3	58
206	Exon Array Analyses across the NCI-60 Reveal Potential Regulation of TOP1 by Transcription Pausing at Guanosine Quartets in the First Intron. <i>Cancer Research</i> , 2010, 70, 2191-2203.	0.4	58
207	Global analysis of tRNA and translation factor expression reveals a dynamic landscape of translational regulation in human cancers. <i>Communications Biology</i> , 2018, 1, 234.	2.0	58
208	Signal pathway profiling of epithelial and stromal compartments of colonic carcinoma reveals epithelial-mesenchymal transition. <i>Oncogene</i> , 2008, 27, 323-331.	2.6	54
209	Genome-wide Analysis of Novel Splice Variants Induced by Topoisomerase I Poisoning Shows Preferential Occurrence in Genes Encoding Splicing Factors. <i>Cancer Research</i> , 2010, 70, 8055-8065.	0.4	54
210	BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. <i>Bioinformatics</i> , 2012, 28, 1923-1924.	1.8	54
211	Activation of Aminoflavone (NSC 686288) by a Sulfotransferase Is Required for the Antiproliferative Effect of the Drug and for Induction of Histone H3-H2AX. <i>Cancer Research</i> , 2006, 66, 9656-9664.	0.4	52
212	Identification of non-cross-resistant platinum compounds with novel cytotoxicity profiles using the NCI anticancer drug screen and clustered image map visualizations. <i>Critical Reviews in Oncology/Hematology</i> , 2005, 53, 25-34.	2.0	51
213	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2014, 157, 753.	13.5	51
214	Altered Expression and Splicing of <i>ESRP1</i> in Malignant Melanoma Correlates with Epithelial-Mesenchymal Status and Tumor-Associated Immune Cytolytic Activity. <i>Cancer Immunology Research</i> , 2016, 4, 552-561.	1.6	50
215	Voltage-dependent translocation of the asialoglycoprotein receptor across lipid membranes. <i>Nature</i> , 1980, 288, 333-338.	13.7	49
216	Multifactorial Regulation of E-Cadherin Expression: An Integrative Study. <i>Molecular Cancer Therapeutics</i> , 2010, 9, 1-16.	1.9	49

#	ARTICLE	IF	CITATIONS
217	Transcriptomic analysis of the NCI-60 cancer cell lines. <i>Comptes Rendus - Biologies</i> , 2003, 326, 909-920.	0.1	48
218	Human Apurinic/Apyrimidinic Endonuclease (Ape1) and Its N-terminal Truncated Form (AN34) Are Involved in DNA Fragmentation during Apoptosis. <i>Journal of Biological Chemistry</i> , 2003, 278, 37768-37776.	1.6	48
219	Detailed DNA methylation profiles of the E-cadherin promoter in the NCI-60 cancer cells. <i>Molecular Cancer Therapeutics</i> , 2007, 6, 391-403.	1.9	48
220	Fishing Expeditions. , 1998, 282, 627g-627.		48
221	Glutaminase Activity of <sc>L</sc>-Asparaginase Contributes to Durable Preclinical Activity against Acute Lymphoblastic Leukemia. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 1587-1592.	1.9	46
222	Inhibition of HIV-1 in Monocyte/Macrophage Cultures by 2,3-Dideoxycytidine-5-Triphosphate, Free and in Liposomes*. <i>AIDS Research and Human Retroviruses</i> , 1990, 6, 691-702.	0.5	45
223	Genes suppressed by DNA methylation in non-small cell lung cancer reveal the epigenetics of epithelial-mesenchymal transition. <i>BMC Genomics</i> , 2014, 15, 1079.	1.2	45
224	Transport properties of charge-mosaic membranes II. Experimental studies. <i>Desalination</i> , 1973, 12, 1-17.	4.0	44
225	Molecular targets in the National Cancer Institute drug screen. <i>Journal of Cancer Research and Clinical Oncology</i> , 1995, 121, 495-500.	1.2	43
226	Comparison of a Neural Net-Based QSAR Algorithm (PCANN) with Hologram- and Multiple Linear Regression-Based QSAR Approaches: Application to 1,4-Dihydropyridine-Based Calcium Channel Antagonists. <i>Journal of Chemical Information and Computer Sciences</i> , 2001, 41, 505-511.	2.8	43
227	Development of a robust classifier for quality control of reverse-phase protein arrays. <i>Bioinformatics</i> , 2015, 31, 912-918.	1.8	43
228	Charge-Mosaic Membranes: Dialytic Separation of Electrolytes from Nonelectrolytes and Amino Acids. <i>Science</i> , 1970, 169, 296-298.	6.0	42
229	Monoclonal Antibody Imaging of Human Melanoma. <i>Annals of Surgery</i> , 1986, 204, 223-235.	2.1	42
230	An Approach to Rapid Estimation of Relative Binding Affinities of Enzyme Inhibitors: Application to Peptidomimetic Inhibitors of the Human Immunodeficiency Virus Type 1 Protease. <i>Journal of Medicinal Chemistry</i> , 1996, 39, 705-712.	2.9	42
231	Quality assessment of microarrays: visualization of spatial artifacts and quantitation of regional biases. <i>BMC Bioinformatics</i> , 2005, 6, 166.	1.2	42
232	Depicting combinatorial complexity with the molecular interaction map notation. <i>Molecular Systems Biology</i> , 2006, 2, 51.	3.2	42
233	Evaluation of current methods used to analyze the expression profiles of ATP-binding cassette transporters yields an improved drug-discovery database. <i>Molecular Cancer Therapeutics</i> , 2009, 8, 2057-2066.	1.9	41
234	Discrimination techniques applied to the NCI in vitro anti-tumour drug screen: Predicting biochemical mechanism of action. <i>Statistics in Medicine</i> , 1994, 13, 719-730.	0.8	40

#	ARTICLE	IF	CITATIONS
235	Integromic Analysis of the NCI-60 Cancer Cell Lines. <i>Breast Disease</i> , 2004, 19, 11-22.	0.4	40
236	<i>NSD1</i> Inactivation and <i>SETD2</i> Mutation Drive a Convergence toward Loss of Function of H3K36 Writers in Clear Cell Renal Cell Carcinomas. <i>Cancer Research</i> , 2017, 77, 4835-4845.	0.4	40
237	Apoptotic susceptibility of cancer cells selected for camptothecin resistance: gene expression profiling, functional analysis, and molecular interaction mapping. <i>Cancer Research</i> , 2003, 63, 1000-11.	0.4	40
238	[38] Carboxyfluorescein leakage assay for lipoprotein-liposome interaction. <i>Methods in Enzymology</i> , 1986, 128, 657-668.	0.4	39
239	Discrepancies in drug sensitivity. <i>Nature</i> , 2013, 504, 381-383.	13.7	39
240	Transport properties of charge-mosaic membranes III. Piezodialysis. <i>Desalination</i> , 1973, 12, 19-33.	4.0	37
241	Chromosomal Instability Is Associated with Higher Expression of Genes Implicated in Epithelial-Mesenchymal Transition, Cancer Invasiveness, and Metastasis and with Lower Expression of Genes Involved in Cell Cycle Checkpoints, DNA Repair, and Chromatin Maintenance. <i>Neoplasia</i> , 2008, 10, 1222-IN26.	2.3	37
242	SpliceCenter: A suite of web-based bioinformatic applications for evaluating the impact of alternative splicing on RT-PCR, RNAi, microarray, and peptide-based studies. <i>BMC Bioinformatics</i> , 2008, 9, 313.	1.2	36
243	Mechanism of Catalysis by <i>Asparaginase</i> . <i>Biochemistry</i> , 2020, 59, 1927-1945.	1.2	36
244	High Resolution Copy Number Variation Data in the NCI-60 Cancer Cell Lines from Whole Genome Microarrays Accessible through CellMiner. <i>PLoS ONE</i> , 2014, 9, e92047.	1.1	36
245	Targeted metabolomic analysis of amino acid response to L-asparaginase in adherent cells. <i>Metabolomics</i> , 2014, 10, 909-919.	1.4	32
246	A Galaxy Implementation of Next-Generation Clustered Heatmaps for Interactive Exploration of Molecular Profiling Data. <i>Cancer Research</i> , 2017, 77, e23-e26.	0.4	32
247	Whole-Organ Genomic Characterization of Mucosal Field Effects Initiating Bladder Carcinogenesis. <i>Cell Reports</i> , 2019, 26, 2241-2256.e4.	2.9	31
248	Effect of Liposome Encapsulation of a Fluorescent Dye on Its Uptake by the Lymphatics of the Rat. <i>Pharmacology</i> , 1981, 23, 128-136.	0.9	31
249	Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. <i>F1000Research</i> , 2019, 8, 1750.	0.8	31
250	Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. <i>F1000Research</i> , 2019, 8, 1750.	0.8	31
251	Lipid Vesicle-Cell Interactions: Analysis of a Model for Transfer of Contents from Adsorbed Vesicles to Cells. <i>Membrane Biochemistry</i> , 1982, 4, 283-303.	0.6	30
252	Synergistic Drug Combinations in AIDS Therapy.. <i>Annals of the New York Academy of Sciences</i> , 1990, 616, 367-384.	1.8	29

#	ARTICLE	IF	CITATIONS
253	AbMiner: a bioinformatic resource on available monoclonal antibodies and corresponding gene identifiers for genomic, proteomic, and immunologic studies. BMC Bioinformatics, 2006, 7, 192.	1.2	29
254	A curated census of autophagy-modulating proteins and small molecules. Autophagy, 2014, 10, 1316-1326.	4.3	29
255	Molecular Interaction Maps--A Diagrammatic Graphical Language for Bioregulatory Networks. Science Signaling, 2004, 2004, pe8-pe8.	1.6	28
256	The macroscopic and microscopic pharmacology of monoclonal antibodies. International Journal of Immunopharmacology, 1992, 14, 457-463.	1.1	27
257	Exposing the cancer genome atlas as a SPARQL endpoint. Journal of Biomedical Informatics, 2010, 43, 998-1008.	2.5	27
258	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	5.8	27
259	Lysophosphatidylcholine in liposomal membranes. Enhanced permeability but little effect on transfer of a water-soluble fluorescent marker into human lymphocytes. Biochimica Et Biophysica Acta - Biomembranes, 1980, 597, 543-551.	1.4	26
260	Lymphatic Delivery of Monoclonal Antibodies: Potential for Detection and Treatment of Lymph Node Metastases. Cancer Investigation, 1985, 3, 85-95.	0.6	26
261	Application of the electrotopological state index to QSAR analysis of flavone derivatives as HIV-1 integrase inhibitors. Pharmaceutical Research, 1996, 13, 1892-1895.	1.7	26
262	Karyotypic "state" as a potential determinant for anticancer drug discovery. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2964-2969.	3.3	25
263	Catalytic Role of the Substrate Defines Specificity of Therapeutic L-Asparaginase. Journal of Molecular Biology, 2015, 427, 2867-2885.	2.0	25
264	Reconstitution of the hepatic asialoglycoprotein receptor with phospholipid vesicles.. Proceedings of the National Academy of Sciences of the United States of America, 1980, 77, 5087-5091.	3.3	24
265	Searching for Pharmacogenomic Markers: The Synergy between Omic and Hypothesis-Driven Research. Disease Markers, 2001, 17, 77-88.	0.6	24
266	Mapping the binding site of the nucleoside transporter protein: a 3D-QSAR study. BBA - Proteins and Proteomics, 1990, 1039, 356-366.	2.1	23
267	SpliceMiner: a high-throughput database implementation of the NCBI Evidence Viewer for microarray splice variant analysis. BMC Bioinformatics, 2007, 8, 75.	1.2	23
268	A user guide for the online exploration and visualization of PCAWG data. Nature Communications, 2020, 11, 3400.	5.8	23
269	Antitumor activity of selective hyperthermia in tumor-bearing rats using thermosensitive magnetoliposomes as a new hyperthermic material. Drug Delivery, 1997, 4, 37-42.	2.5	22
270	Molecular Targets in Cancer Drug Discovery: Cell-Based Profiling. Current Pharmaceutical Design, 2000, 6, 473-483.	0.9	22

#	ARTICLE	IF	CITATIONS
271	The bioinformatics of microarray gene expression profiling. <i>Cytometry</i> , 2002, 47, 46-49.	1.8	21
272	Opportunities and challenges in ovarian cancer research, a perspective from the 11th Ovarian cancer action/HHMT Forum, Lake Como, March 2007. <i>Gynecologic Oncology</i> , 2008, 108, 652-657.	0.6	21
273	Effect of dipyridamole on transport and phosphorylation of thymidine and 3-azido-2-deoxythymidine in human monocyte/macrophages. <i>Biochemical Pharmacology</i> , 1990, 40, 867-870.	2.0	20
274	New joint prediction algorithm (Q7-JASEP) improves the prediction of protein secondary structure. <i>Biochemistry</i> , 1991, 30, 11164-11172.	1.2	20
275	The EDGE hypothesis: Epigenetically directed genetic errors in repeat-containing proteins (RCPs) involved in evolution, neuroendocrine signaling, and cancer. <i>Frontiers in Neuroendocrinology</i> , 2008, 29, 428-444.	2.5	20
276	Asparagine synthetase: A new potential biomarker in ovarian cancer. <i>Drug News and Perspectives</i> , 2009, 22, 61.	1.9	20
277	Long non-coding RNA profiling links subgroup classification of endometrioid endometrial carcinomas with trithorax and polycomb complex aberrations. <i>Oncotarget</i> , 2015, 6, 39865-39876.	0.8	20
278	Multiplexing siRNAs to compress RNAi-based screen size in human cells. <i>Nucleic Acids Research</i> , 2007, 35, e57-e57.	6.5	19
279	Chromatin Challenges during DNA Replication: A Systems Representation. <i>Molecular Biology of the Cell</i> , 2008, 19, 1-7.	0.9	19
280	Liposomes as "targeted" drug carriers: a physical chemical perspective. <i>Pure and Applied Chemistry</i> , 1981, 53, 2241-2254.	0.9	18
281	Induction of IL-2 receptor expression in vivo: Response to concanavalin A. <i>Cellular Immunology</i> , 1988, 111, 420-432.	1.4	18
282	RedundancyMiner: De-replication of redundant GO categories in microarray and proteomics analysis. <i>BMC Bioinformatics</i> , 2011, 12, 52.	1.2	18
283	Identification of Common Prognostic Gene Expression Signatures with Biological Meanings from Microarray Gene Expression Datasets. <i>PLoS ONE</i> , 2012, 7, e45894.	1.1	18
284	Urothelial-to-Neural Plasticity Drives Progression to Small Cell Bladder Cancer. <i>IScience</i> , 2020, 23, 101201.	1.9	18
285	Voltage-dependent orientation of membrane proteins. <i>Journal of Cellular Biochemistry</i> , 1983, 22, 55-67.	1.2	17
286	Optimization of antigen presentation to T cell hybridomas by purified Ia molecules in planar membranes. <i>Journal of Immunological Methods</i> , 1987, 98, 29-41.	0.6	17
287	Effects of thymidine and uridine on the phosphorylation of 3'-azido-3'-deoxythymidine (zidovudine) in human mononuclear cells. <i>Antimicrobial Agents and Chemotherapy</i> , 1991, 35, 198-200.	1.4	17
288	Localized beta dosimetry of ¹³¹ I-labeled antibodies in follicular lymphoma. <i>Medical Physics</i> , 1992, 19, 97-104.	1.6	17

#	ARTICLE	IF	CITATIONS
289	Combination Gene Therapy: Synergistic Inhibition of Human Immunodeficiency Virus Tat and Rev Functions by a Single RNA Molecule. <i>Human Gene Therapy</i> , 2000, 11, 807-815.	1.4	17
290	Mutational Profiles Reveal an Aberrant TGF- β -CEA Regulated Pathway in Colon Adenomas. <i>PLoS ONE</i> , 2016, 11, e0153933.	1.1	17
291	The LeFE algorithm: embracing the complexity of gene expression in the interpretation of microarray data. <i>Genome Biology</i> , 2007, 8, R187.	13.9	16
292	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021, 34, 108707.	2.9	16
293	Compartmental analysis of light-induced proton movement in reconstituted bacteriorhodopsin vesicles. <i>Biochemistry</i> , 1982, 21, 3643-3650.	1.2	15
294	COMBO: A New Approach to the Analysis of Drug Combinations in Vitro. <i>Annals of the New York Academy of Sciences</i> , 1990, 616, 490-494.	1.8	15
295	In vitro anti-HIV-1 activity of HIV protease inhibitor KNI-272 in resting and activated cells: implications for its combined use with AZT or ddI. <i>Antiviral Research</i> , 1995, 28, 25-38.	1.9	14
296	<i>In vitro</i> differential sensitivity of melanomas to phenothiazines is based on the presence of codon 600 BRAF mutation. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 1337-1346.	1.9	14
297	Comparison of Methods for Sequential Screening of Large Compound Sets. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2006, 9, 115-122.	0.6	13
298	Concordance of Gene Expression and Functional Correlation Patterns across the NCI-60 Cell Lines and the Cancer Genome Atlas Glioblastoma Samples. <i>PLoS ONE</i> , 2012, 7, e40062.	1.1	13
299	Differential inhibition of 2'-deoxycytidine salvage as a possible mechanism for potentiation of the anti-human immunodeficiency virus activity of 2',3'-dideoxycytidine by dipyridamole. <i>Antimicrobial Agents and Chemotherapy</i> , 1991, 35, 1250-1253.	1.4	12
300	Effect of dipyridamole on zidovudine pharmacokinetics and short-term tolerance in asymptomatic human immunodeficiency virus-infected subjects. <i>Antimicrobial Agents and Chemotherapy</i> , 1994, 38, 1036-1040.	1.4	12
301	Connecting genes, drugs and diseases. <i>Nature Biotechnology</i> , 2006, 24, 1365-1366.	9.4	12
302	The origin of bladder cancer from mucosal field effects. <i>IScience</i> , 2022, 25, 104551.	1.9	12
303	Assessment of L-Asparaginase Pharmacodynamics in Mouse Models of Cancer. <i>Metabolites</i> , 2019, 9, 10.	1.3	11
304	Functional Categories Associated with Clusters of Genes That Are Co-Expressed across the NCI-60 Cancer Cell Lines. <i>PLoS ONE</i> , 2012, 7, e30317.	1.1	11
305	Neural network techniques for informatics of cancer drug discovery. <i>Methods in Enzymology</i> , 2000, 321, 369-395.	0.4	10
306	ZC3H12A Expression in Different Stages of Colorectal Cancer. <i>Oncoscience</i> , 2019, 6, 301-311.	0.9	10

#	ARTICLE	IF	CITATIONS
307	Site-Directed Mutagenesis of Tryptophan Residues to Conserved Hydrophobic Residues Inhibits the Processing of Human kb Cell Folate Receptor. Archives of Biochemistry and Biophysics, 1994, 315, 407-414.	1.4	9
308	Clinical significance of FBXO17 gene expression in high-grade glioma. BMC Cancer, 2018, 18, 773.	1.1	9
309	Definition of volume flow in the Kedem-Katchalsky formulation of electroosmosis. The Journal of Physical Chemistry, 1973, 77, 2710-2711.	2.9	8
310	Framework for Identifying Common Aberrations in DNA Copy Number Data. , 2007, , 122-136.		8
311	Is the Gene Expression Pattern of Lung Cancer Detected by Screening With Spiral Computed Tomography Different from That of Symptom-Detected Lung Cancer?. Clinical Cancer Research, 2004, 10, 5973-5974.	3.2	7
312	Network architecture of signaling from uncoupled helicase-polymerase to cell cycle checkpoints and trans-lesion DNA synthesis. Cell Cycle, 2009, 8, 2281-2299.	1.3	7
313	The Cancer Genome Atlas Project on Muscle-invasive Bladder Cancer. European Urology Focus, 2015, 1, 94-95.	1.6	7
314	SoS Notebook: an interactive multi-language data analysis environment. Bioinformatics, 2018, 34, 3768-3770.	1.8	7
315	Integrated transcriptomicâ€“genomic tool Texomer profiles cancer tissues. Nature Methods, 2019, 16, 401-404.	9.0	7
316	Secondary Structure of the Human Membrane-Associated Folate Binding Protein Using a Joint Prediction Approach. Journal of Biomolecular Structure and Dynamics, 1990, 7, 985-1001.	2.0	6
317	Antibody-Mediated Targeting of Liposomes. , 1982, , 185-202.		6
318	Compound NSC84167 selectively targets NRF2-activated pancreatic cancer by inhibiting asparagine synthesis pathway. Cell Death and Disease, 2021, 12, 693.	2.7	5
319	Predicting high-risk endometrioid carcinomas using proteins. Oncotarget, 2018, 9, 19704-19715.	0.8	5
320	Dipyridamole Potentiates the Activity of Zidovudine and Other Dideoxynucleosides against HIV-1 in Cultured Cells. Annals of the New York Academy of Sciences, 1990, 616, 613-616.	1.8	4
321	Information resources for liposome research: The drug discovery program of the u.s. national cancer institute. Journal of Liposome Research, 1995, 5, 837-844.	1.5	4
322	Antibody lymphoscintigraphy. Cancer Treatment and Research, 1990, 51, 365-385.	0.2	4
323	PathwaysWeb: a gene pathways API with directional interactions, expanded gene ontology, and versioning. Bioinformatics, 2016, 32, 312-314.	1.8	3
324	Response envelope analysis for quantitative evaluation of drug combinations. Bioinformatics, 2019, 35, 3761-3770.	1.8	3

#	ARTICLE	IF	CITATIONS
325	USE OF MONOCLONAL ANTIBODIES FOR DIAGNOSIS AND THERAPY OF TUMOR METASTASES IN LYMPH NODES. , 1983, , 337-342.		3
326	The Glutaminase Activity of L-Asparaginase Mediates Suppression of Asns Upregulation. Blood, 2018, 132, 3959-3959.	0.6	3
327	Dipyridamole mediated enhanced antiproliferative activity of 10-ethyl-10-deazaaminopterin (10-EDAM) against human lung cancer cell lines. Journal of Cellular Biochemistry, 1996, 63, 165-172.	1.2	2
328	<title>Analysis of gene expression data of the NCI 60 cancer cell lines using Bayesian hierarchical effects model</title>. , 2001, 4266, 228.		2
329	Linking Drugs and Genes: Pharmacogenomics, Pharmacoproteomics, Bioinformatics, and the NCI-60. , 2005, , 117-137.		2
330	Ontogenomic study of the relationship between number of gene splice variants and GO categorization. Bioinformatics, 2010, 26, 1945-1949.	1.8	2
331	MicroRNAs in Cancer Pharmacology and Therapeutics: Exploiting a Natural Synergy between "omic"™ and Hypothesis-Driven Research. Molecular Cancer Therapeutics, 2011, 10, 2021-2021.	1.9	2
332	Red Blood Cell-Encapsulation of L-Asparaginase Favorably Modulates Target Selectivity and Pharmacodynamics. Blood, 2016, 128, 1266-1266.	0.6	2
333	Piezodialysis: a comparison of theoretical treatments. Desalination, 1975, 16, 245-252.	4.0	1
334	VOLTAGE-DEPENDENT TRANSLOCATION OF HEPATIC BINDING PROTEIN. Annals of the New York Academy of Sciences, 1980, 358, 368-369.	1.8	1
335	Voltage-dependent Changes of a Membrane Protein in Lipid Model Membranes. Biophysical Journal, 1982, 37, 122-124.	0.2	1
336	A simple method for affinity purification of radiolabeled monoclonal antibodies. Nuclear Medicine and Biology, 1993, 20, 311-315.	0.3	1
337	Reply To Kenneth B. Yatai, Mark J. Dunning, Dennis Wang. Consensus Genomic Subtypes of Muscle-invasive Bladder Cancer: A Step in the Right Direction but Still a Long Way To Go. Eur Urol 2020;77:434-438. European Urology, 2020, 77, 436-438.	0.9	1
338	Antibody-Mediated Drug Delivery. , 1990, , 359-370.		1
339	The Glutaminase Activity Of L-Asparaginase Is Not Required For Anticancer Activity Against Asns-Negative Cell Lines. Blood, 2013, 122, 4912-4912.	0.6	1
340	Modulation of autophagy and its potential for cancer therapy. Drugs of the Future, 2011, 36, 919.	0.0	1
341	Genomic Assessment of Muscle-Invasive Bladder Cancer: Insights from the Cancer Genome Atlas (TCGA) Project. Molecular Pathology Library, 2018, , 43-64.	0.1	0
342	Lipid Model Membrane Studies on Immune Cytotoxic Mechanisms. Advances in Experimental Medicine and Biology, 1977, 84, 495-507.	0.8	0

#	ARTICLE	IF	CITATIONS
343	COMBO: New Concepts and Methods for Designing and Analyzing Experiments on Combination Therapy. , 1992, , 29-38.		0
344	Genome-Wide Mapping and Subtype Classification of Long Non-Coding RNA in Acute Myeloid Leukemia. Blood, 2014, 124, 2355-2355.	0.6	0
345	Whole-organ Genomic Characterization of Mucosal Field Effects Initiating Bladder Carcinogenesis. SSRN Electronic Journal, 0, , .	0.4	0