

John N Weinstein

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Compound NSC84167 selectively targets NRF2-activated pancreatic cancer by inhibiting asparagine synthesis pathway. <i>Cell Death and Disease</i> , 2021 , 12, 693	9.8	2
339	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021 , 34, 108707	10.6	7
338	Mechanism of Catalysis by L-Asparaginase. <i>Biochemistry</i> , 2020 , 59, 1927-1945	3.2	14
337	Assessment of Luminal and Basal Phenotypes in Bladder Cancer. <i>Scientific Reports</i> , 2020 , 10, 9743	4.9	24
336	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020 , 11, 3400	17.4	7
335	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
334	Comprehensive molecular characterization of mitochondrial genomes in human cancers. <i>Nature Genetics</i> , 2020 , 52, 342-352	36.3	105
333	Urothelial-to-Neural Plasticity Drives Progression to Small Cell Bladder Cancer. <i>iScience</i> , 2020 , 23, 101206.1	10.6	7
332	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020 , 11, 4748	17.4	10
331	A Consensus Molecular Classification of Muscle-invasive Bladder Cancer. <i>European Urology</i> , 2020 , 77, 420-433	10.2	309
330	Glutaminase Activity of L-Asparaginase Contributes to Durable Preclinical Activity against Acute Lymphoblastic Leukemia. <i>Molecular Cancer Therapeutics</i> , 2019 , 18, 1587-1592	6.1	22
329	Dysregulation of EMT Drives the Progression to Clinically Aggressive Sarcomatoid Bladder Cancer. <i>Cell Reports</i> , 2019 , 27, 1781-1793.e4	10.6	53
328	Response envelope analysis for quantitative evaluation of drug combinations. <i>Bioinformatics</i> , 2019 , 35, 3761-3770	7.2	3
327	Integrated transcriptomic-genomic tool Texomer profiles cancer tissues. <i>Nature Methods</i> , 2019 , 16, 401-406	10.6	4
326	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
325	Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. <i>F1000Research</i> , 2019 , 8,	3.6	11
324	Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. <i>F1000Research</i> , 2019 , 8, 1750	3.6	13

323	ZC3H12A Expression in Different Stages of Colorectal Cancer. <i>Oncoscience</i> , 2019 , 6, 301-311	0.8	5
322	Whole-Organ Genomic Characterization of Mucosal Field Effects Initiating Bladder Carcinogenesis. <i>Cell Reports</i> , 2019 , 26, 2241-2256.e4	10.6	15
321	ElemCor: accurate data analysis and enrichment calculation for high-resolution LC-MS stable isotope labeling experiments. <i>BMC Bioinformatics</i> , 2019 , 20, 89	3.6	57
320	Assessment of L-Asparaginase Pharmacodynamics in Mouse Models of Cancer. <i>Metabolites</i> , 2019 , 9,	5.6	7
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 Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
317	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
316	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.e12	56.2	133
315	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
314	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15	56.2	560
313	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
312	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018 , 173, 355-370.e14	56.2	342
311	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
310	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
309	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018 , 23, 194-212.e6	10.6	146
308	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
307	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5	10.6	295
306	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

305	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
304	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 172-180.e3	10.6	66
303	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-226.e3	10.6	56
302	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
301	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018 , 23, 255-269.e4	10.6	112
300	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121
299	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10	24.3	150
298	Genomic Assessment of Muscle-Invasive Bladder Cancer: Insights from the Cancer Genome Atlas (TCGA) Project. <i>Molecular Pathology Library</i> , 2018 , 43-64		
297	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
296	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
295	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
294	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
293	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
292	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
291	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327
290	Clinical significance of FBXO17 gene expression in high-grade glioma. <i>BMC Cancer</i> , 2018 , 18, 773	4.8	4
289	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406.e10	10.6	200
288	The Glutaminase Activity of L-Asparaginase Mediates Suppression of Asns Upregulation. <i>Blood</i> , 2018 , 132, 3959-3959	2.2	2

287	Predicting high-risk endometrioid carcinomas using proteins. <i>Oncotarget</i> , 2018 , 9, 19704-19715	3.3	5
286	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	6.7	37
285	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
284	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018 , 362,	33.3	392
283	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018 , 8, 1548-1565	24.4	258
282	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018 , 25, 1304-1317.e5	10.6	152
281	SoS Notebook: an interactive multi-language data analysis environment. <i>Bioinformatics</i> , 2018 , 34, 3768-3770	37.0	5
280	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017 , 543, 378-384	50.4	755
279	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
278	Expression of human endogenous retrovirus-K is strongly associated with the basal-like breast cancer phenotype. <i>Scientific Reports</i> , 2017 , 7, 41960	4.9	42
277	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
276	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. <i>Cancer Cell</i> , 2017 , 31, 820-832.e3	32.3	286
275	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
274	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017 , 18, 2780-2794	10.6	247
273	Explore, Visualize, and Analyze Functional Cancer Proteomic Data Using the Cancer Proteome Atlas. <i>Cancer Research</i> , 2017 , 77, e51-e54	10.1	50
272	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e25	25.2	961
271	Inactivation and 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	10.1	23
270	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391

269	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203. e13896		
268	A Galaxy Implementation of Next-Generation Clustered Heatmaps for Interactive Exploration of Molecular Profiling Data. <i>Cancer Research</i> , 2017 , 77, e23-e26	10.1	22
267	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965. e28	56.2	451
266	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
265	PathwaysWeb: a gene pathways API with directional interactions, expanded gene ontology, and versioning. <i>Bioinformatics</i> , 2016 , 32, 312-4	7.2	3
264	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140
263	TCGASpliceSeq a compendium of alternative mRNA splicing in cancer. <i>Nucleic Acids Research</i> , 2016 , 44, D1018-22	20.1	181
262	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016 , 374, 135-45	59.2	753
261	Red Blood Cell-Encapsulation of L-Asparaginase Favorably Modulates Target Selectivity and Pharmacodynamics. <i>Blood</i> , 2016 , 128, 1266-1266	2.2	1
260	Mutational Profiles Reveal an Aberrant TGF- β -ECEA Regulated Pathway in Colon Adenomas. <i>PLoS ONE</i> , 2016 , 11, e0153933	3.7	13
259	Cancer Bioinformatics 2016 , 1-14		
258	Gene Expression Profile of the Clinically Aggressive Micropapillary Variant of Bladder Cancer. <i>European Urology</i> , 2016 , 70, 611-620	10.2	92
257	Altered Expression and Splicing of ESRP1 in Malignant Melanoma Correlates with Epithelial-Mesenchymal Status and Tumor-Associated Immune Cytolytic Activity. <i>Cancer Immunology Research</i> , 2016 , 4, 552-61	12.5	39
256	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736. e3	36.3	324
255	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016 , 48, 607-16	36.3	613
254	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
253	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96	56.2	1807
252	TANRIC: An Interactive Open Platform to Explore the Function of lncRNAs in Cancer. <i>Cancer Research</i> , 2015 , 75, 3728-37	10.1	354

251	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
250	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
249	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25	56.2	1713
248	TransVar: a multilevel variant annotator for precision genomics. <i>Nature Methods</i> , 2015 , 12, 1002-3	21.6	40
247	Invasive Bladder Cancer: Genomic Insights and Therapeutic Promise. <i>Clinical Cancer Research</i> , 2015 , 21, 4514-24	12.9	85
246	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
245	Catalytic Role of the Substrate Defines Specificity of Therapeutic L-Asparaginase. <i>Journal of Molecular Biology</i> , 2015 , 427, 2867-85	6.5	21
244	Development of a robust classifier for quality control of reverse-phase protein arrays. <i>Bioinformatics</i> , 2015 , 31, 912-8	7.2	33
243	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	7.9	63
242	Update on The Cancer Genome Atlas Project on Muscle-invasive Bladder Cancer. <i>European Urology Focus</i> , 2015 , 1, 94-95	5.1	4
241	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
240	Long non-coding RNA profiling links subgroup classification of endometrioid endometrial carcinomas with trithorax and polycomb complex aberrations. <i>Oncotarget</i> , 2015 , 6, 39865-76	3.3	16
239	Targeted metabolomic analysis of amino acid response to L-asparaginase in adherent cells. <i>Metabolomics</i> , 2014 , 10, 909-919	4.7	25
238	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014 , 507, 315-22	50.4	1963
237	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
236	An artifact in LC-MS/MS measurement of glutamine and glutamic acid: in-source cyclization to pyroglutamic acid. <i>Analytical Chemistry</i> , 2014 , 86, 5633-7	7.8	50
235	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014 , 513, 202-9	50.4	3659
234	The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , 2014 , 26, 319-330	24.3	521

233	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014 , 511, 543-50	50.4	3310
232	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
231	Assessing the clinical utility of cancer genomic and proteomic data across tumor types. <i>Nature Biotechnology</i> , 2014 , 32, 644-52	44.5	205
230	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
229	A pan-cancer proteomic perspective on The Cancer Genome Atlas. <i>Nature Communications</i> , 2014 , 5, 3887-9	17.4	324
228	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
227	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	4.5	37
226	A curated census of autophagy-modulating proteins and small molecules: candidate targets for cancer therapy. <i>Autophagy</i> , 2014 , 10, 1316-26	10.2	27
225	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90	56.2	1660
224	Tumor subtype-specific cancer-testis antigens as potential biomarkers and immunotherapeutic targets for cancers. <i>Cancer Immunology Research</i> , 2014 , 2, 371-9	12.5	64
223	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2014 , 157, 753	56.2	29
222	PRADA: pipeline for RNA sequencing data analysis. <i>Bioinformatics</i> , 2014 , 30, 2224-6	7.2	117
221	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	3.7	31
220	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
219	Comprehensive analysis of long non-coding RNAs in human breast cancer clinical subtypes. <i>Oncotarget</i> , 2014 , 5, 9864-76	3.3	156
218	Genome-Wide Mapping and Subtype Classification of Long Non-Coding RNA in Acute Myeloid Leukemia. <i>Blood</i> , 2014 , 124, 2355-2355	2.2	
217	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
216	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2	2900

215	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013 , 45, 1113-20	36.3	3933
214	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
213	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
212	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013 , 497, 67-73	50.4	2800
211	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
210	TCPA: a resource for cancer functional proteomics data. <i>Nature Methods</i> , 2013 , 10, 1046-7	21.6	288
209	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, 2460-72	12.9	61
208	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
207	A survey of intragenic breakpoints in glioblastoma identifies a distinct subset associated with poor survival. <i>Genes and Development</i> , 2013 , 27, 1462-72	12.6	50
206	Integrative genomic characterization of oral squamous cell carcinoma identifies frequent somatic drivers. <i>Cancer Discovery</i> , 2013 , 3, 770-81	24.4	391
205	Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. <i>Journal of Clinical Investigation</i> , 2013 , 123, 517-25	15.9	371
204	The Glutaminase Activity Of L-Asparaginase Is Not Required For Anticancer Activity Against Asns-Negative Cell Lines. <i>Blood</i> , 2013 , 122, 4912-4912	2.2	1
203	BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. <i>Bioinformatics</i> , 2012 , 28, 1923-4	7.2	52
202	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
201	Identification of common prognostic gene expression signatures with biological meanings from microarray gene expression datasets. <i>PLoS ONE</i> , 2012 , 7, e45894	3.7	15
200	AMPK γ 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
199	PurityEst: estimating purity of human tumor samples using next-generation sequencing data. <i>Bioinformatics</i> , 2012 , 28, 2265-6	7.2	54
198	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

197	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	3.7	10
196	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	3.7	12
195	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011 , 474, 609-15	50.4	5210
194	Exome sequencing of head and neck squamous cell carcinoma reveals inactivating mutations in NOTCH1. <i>Science</i> , 2011 , 333, 1154-7	33.3	1331
193	RedundancyMiner: De-replication of redundant GO categories in microarray and proteomics analysis. <i>BMC Bioinformatics</i> , 2011 , 12, 52	3.6	13
192	MicroRNAs in cancer pharmacology and therapeutics: exploiting a natural synergy between '-omic' and hypothesis-driven research. <i>Molecular Cancer Therapeutics</i> , 2011 , 10, 2021	6.1	1
191	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, 19511-22	5.4	59
190	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
189	Ontogenomic study of the relationship between number of gene splice variants and GO categorization. <i>Bioinformatics</i> , 2010 , 26, 1945-9	7.2	1
188	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, 8055-65	10.1	49
187	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, 2191-203	10.1	54
186	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
185	Small-sample precision of ROC-related estimates. <i>Bioinformatics</i> , 2010 , 26, 822-30	7.2	195
184	Multifactorial regulation of E-cadherin expression: an integrative study. <i>Molecular Cancer Therapeutics</i> , 2010 , 9, 1-16	6.1	43
183	Dihydroartemisinin accelerates c-MYC oncoprotein degradation and induces apoptosis in c-MYC-overexpressing tumor cells. <i>Biochemical Pharmacology</i> , 2010 , 80, 22-30	6	60
182	Exposing the cancer genome atlas as a SPARQL endpoint. <i>Journal of Biomedical Informatics</i> , 2010 , 43, 998-1008	10.2	20
181	DNA fingerprinting of the NCI-60 cell line panel. <i>Molecular Cancer Therapeutics</i> , 2009 , 8, 713-24	6.1	123
180	Network architecture of signaling from uncoupled helicase-polymerase to cell cycle checkpoints and trans-lesion DNA synthesis. <i>Cell Cycle</i> , 2009 , 8, 2281-99	4.7	7

179	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, 2057-66	6.1	34
178	CellMiner: a relational database and query tool for the NCI-60 cancer cell lines. <i>BMC Genomics</i> , 2009 , 10, 277	4.5	165
177	Asparagine synthetase: a new potential biomarker in ovarian cancer. <i>Drug News and Perspectives</i> , 2009 , 22, 61-4		9
176	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008 , 455, 1061-8	50.4	5669
175	Signal pathway profiling of epithelial and stromal compartments of colonic carcinoma reveals epithelial-mesenchymal transition. <i>Oncogene</i> , 2008 , 27, 323-31	9.2	51
174	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, 428-44	8.9	19
173	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, 652-7	4.9	19
172	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	3.6	36
171	VennMaster: area-proportional Euler diagrams for functional GO analysis of microarrays. <i>BMC Bioinformatics</i> , 2008 , 9, 67	3.6	81
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6	Definition of volume flow in the Kedem-Katchalsky formulation of electroosmosis. <i>The Journal of Physical Chemistry</i> , 1973 , 77, 2710-2711		7
5	Transport properties of charge-mosaic membranes I. Theoretical models. <i>Desalination</i> , 1972 , 11, 341-377	10.3	56
4	Charge-mosaic membranes: dialytic separation of electrolytes from nonelectrolytes and amino acids. <i>Science</i> , 1970 , 169, 296-8	33.3	36
3	Charge-mosaic membranes: enhanced permeability and negative osmosis with a symmetrical salt. <i>Science</i> , 1968 , 161, 70-2	33.3	62
2	Comprehensive Molecular Characterization of Mitochondrial Genomes in Human Cancers		6
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