

Eric Y Chuang

List of Publications by Year in descending order

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Version: 2024-02-01

141
papers

3,724
citations

185998

28
h-index

155451

55
g-index

143
all docs

143
docs citations

143
times ranked

7024
citing authors

#	ARTICLE	IF	CITATIONS
1	A major milestone for Translational Cancer Research: indexing in PubMed/PubMed Central. <i>Translational Cancer Research</i> , 2022, 11, 1-2.	0.4	0
2	Join Classifier of Type and Index Mutation on Lung Cancer DNA Using Sequential Labeling Model. <i>IEEE Access</i> , 2022, 10, 9004-9021.	2.6	3
3	Extracellular domain of semaphorin 5A serves a tumor-suppressing role by activating interferon signaling pathways in lung adenocarcinoma cells. <i>International Journal of Oncology</i> , 2022, 60, .	1.4	0
4	An Artificial Intelligence-Enabled ECG Algorithm for the Prediction and Localization of Angiography-Proven Coronary Artery Disease. <i>Biomedicines</i> , 2022, 10, 394.	1.4	13
5	The extended concurrent genes signature for disease-free survival in breast cancer. <i>Journal of the Formosan Medical Association</i> , 2022, , .	0.8	1
6	The Gut Microbiome, Seleno-Compounds, and Acute Myocardial Infarction. <i>Journal of Clinical Medicine</i> , 2022, 11, 1462.	1.0	5
7	To compare the performance of prokaryotic taxonomy classifiers using curated 16S full-length rRNA sequences. <i>Computers in Biology and Medicine</i> , 2022, 145, 105416.	3.9	10
8	Uremic Toxin-Producing Bacteroides Species Prevail in the Gut Microbiota of Taiwanese CKD Patients: An Analysis Using the New Taiwan Microbiome Baseline. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 726256.	1.8	12
9	Identification of Genetic Variations in the NAD-Related Pathways for Patients with Major Depressive Disorder: A Case-Control Study in Taiwan. <i>Journal of Clinical Medicine</i> , 2022, 11, 3622.	1.0	1
10	RNASeqR: An R Package for Automated Two-Group RNA-Seq Analysis Workflow. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2023-2031.	1.9	6
11	Rare variants discovery by extensive whole-genome sequencing of the Han Chinese population in Taiwan: Applications to cardiovascular medicine. <i>Journal of Advanced Research</i> , 2021, 30, 147-158.	4.4	13
12	A risk prediction model of gene signatures in ovarian cancer through bagging of GA-XGBoost models. <i>Journal of Advanced Research</i> , 2021, 30, 113-122.	4.4	14
13	CNVIntegrate: the first multi-ethnic database for identifying copy number variations associated with cancer. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	5
14	Development of a Gene-Based Prediction Model for Recurrence of Colorectal Cancer Using an Ensemble Learning Algorithm. <i>Frontiers in Oncology</i> , 2021, 11, 631056.	1.3	10
15	Targeting the gut microbiome for non-communicable diseases: present and future. <i>Annals of Translational Medicine</i> , 2021, 9, 361-361.	0.7	2
16	Evolutionary Trajectories and Genomic Divergence in Localized Breast Cancers after Ipsilateral Breast Tumor Recurrence. <i>Cancers</i> , 2021, 13, 1821.	1.7	3
17	Hypoxia-Induced MALAT1 Promotes the Proliferation and Migration of Breast Cancer Cells by Sponging MiR-3064-5p. <i>Frontiers in Oncology</i> , 2021, 11, 658151.	1.3	29
18	Rare variants: data types and analysis strategies. <i>Annals of Translational Medicine</i> , 2021, 9, 961-961.	0.7	10

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19	Regulatory Mechanisms and Functional Roles of Hypoxia-Induced Long Non-Coding RNA MTORT1 in Breast Cancer Cells. <i>Frontiers in Oncology</i> , 2021, 11, 663114.	1.3	10
20	EasyMAP: A user-friendly online platform for analyzing 16S ribosomal DNA sequencing data. <i>New Biotechnology</i> , 2021, 63, 37-44.	2.4	10
21	High prevalence of APOA1/C3/A4/A5 alterations in luminal breast cancers among young women in East Asia. <i>Npj Breast Cancer</i> , 2021, 7, 88.	2.3	8
22	High-performance deep learning pipeline predicts individuals in mixtures of DNA using sequencing data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	1
23	Differential whole-genome doubling and homologous recombination deficiencies across breast cancer subtypes from the Taiwanese population. <i>Communications Biology</i> , 2021, 4, 1052.	2.0	2
24	MiDSysTEM: A comprehensive online system for de novo assembly and analysis of microbial genomes. <i>New Biotechnology</i> , 2021, 65, 42-52.	2.4	2
25	ATTRACTIVE "An Auto-Updating Database for Experimental Protocols in Regenerative Medicine. <i>IEEE Access</i> , 2021, 9, 75202-75210.	2.6	0
26	Prediction of Breast Cancer Recurrence Using a Deep Convolutional Neural Network Without Region-of-Interest Labeling. <i>Frontiers in Oncology</i> , 2021, 11, 734015.	1.3	5
27	MutScape: an analytical toolkit for probing the mutational landscape in cancer genomics. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab099.	1.5	0
28	Novel Tumor-Specific Antigens for Immunotherapy Identified From Multi-omics Profiling in Thymic Carcinomas. <i>Frontiers in Immunology</i> , 2021, 12, 748820.	2.2	3
29	Lidocaine and Bupivacaine Downregulate MYB and DANCR lncRNA by Upregulating miR-187-5p in MCF-7 Cells. <i>Frontiers in Medicine</i> , 2021, 8, 732817.	1.2	3
30	Predicting Breast Cancer Gene Expression Signature by Applying Deep Convolutional Neural Networks From Unannotated Pathological Images. <i>Frontiers in Oncology</i> , 2021, 11, 769447.	1.3	5
31	GSTM3 variant is a novel genetic modifier in Brugada syndrome, a disease with risk of sudden cardiac death. <i>EBioMedicine</i> , 2020, 57, 102843.	2.7	14
32	MicroRNA-107 enhances radiosensitivity by suppressing granulin in PC-3 prostate cancer cells. <i>Scientific Reports</i> , 2020, 10, 14584.	1.6	13
33	The puzzle of genetics in Brugada syndrome: a disease with a high risk of sudden cardiac death in young people. <i>Annals of Palliative Medicine</i> , 2020, 9, 4394-4397.	0.5	0
34	Validation and Disease Risk Assessment of Previously Reported Genome-Wide Genetic Variants Associated With Brugada Syndrome. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002797.	1.6	12
35	Prevalence of sudden arrhythmic death syndrome-related genetic mutations in an Asian cohort of whole genome sequence. <i>Europace</i> , 2020, 22, 1287-1297.	0.7	3
36	Comparison of DNA stabilizers and storage conditions on preserving fecal microbiota profiles. <i>Journal of the Formosan Medical Association</i> , 2020, 119, 1791-1798.	0.8	23

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37	Risk Factors and Genetic Biomarkers of Multiple Primary Cancers in Esophageal Cancer Patients. <i>Frontiers in Oncology</i> , 2020, 10, 585621.	1.3	3
38	IL-27/IL-27RA signaling may modulate inflammation and progression of benign prostatic hyperplasia via suppressing the LPS/TLR4 pathway. <i>Translational Cancer Research</i> , 2020, 9, 4618-4634.	0.4	2
39	Semaphorin 5A suppresses the proliferation and migration of lung adenocarcinoma cells. <i>International Journal of Oncology</i> , 2020, 56, 165-177.	1.4	6
40	Using proteomic profiling to characterize protein signatures of different thymoma subtypes. <i>BMC Cancer</i> , 2019, 19, 796.	1.1	4
41	VariED: the first integrated database of gene annotation and expression profiles for variants related to human diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	7
42	Altered gut microbiota and inflammatory cytokine responses in patients with Parkinson's disease. <i>Journal of Neuroinflammation</i> , 2019, 16, 129.	3.1	283
43	Long-term changes of gut microbiota, antibiotic resistance, and metabolic parameters after <i>Helicobacter pylori</i> eradication: a multicentre, open-label, randomised trial. <i>Lancet Infectious Diseases</i> , 2019, 19, 1109-1120.	4.6	127
44	Semaphorin 6A Attenuates the Migration Capability of Lung Cancer Cells via the NRF2/HMOX1 Axis. <i>Scientific Reports</i> , 2019, 9, 13302.	1.6	33
45	anamiR: integrated analysis of MicroRNA and gene expression profiling. <i>BMC Bioinformatics</i> , 2019, 20, 239.	1.2	13
46	Identifying the functions and biomarkers of <i>Codonopsis pilosula</i> and <i>Astragalus membranaceus</i> aqueous extracts in hepatic cells. <i>Chinese Medicine</i> , 2019, 14, 10.	1.6	8
47	Genome-Wide Copy Number Variation Association Study of Atrial Fibrillation Related Thromboembolic Stroke. <i>Journal of Clinical Medicine</i> , 2019, 8, 332.	1.0	11
48	Macrophage Migration Inhibitory Factor Acts as the Potential Target of a Newly Synthesized Compound, 1-(9-methyl-3-carbazole)-3, 4-dihydro-1 ² -carboline. <i>Scientific Reports</i> , 2019, 9, 2147.	1.6	5
49	miR-338-5p inhibits cell proliferation, colony formation, migration and cisplatin resistance in esophageal squamous cancer cells by targeting FERMT2. <i>Carcinogenesis</i> , 2019, 40, 883-892.	1.3	38
50	Role of artificial intelligence in integrated analysis of multi-omics and imaging data in cancer research. <i>Translational Cancer Research</i> , 2019, 8, E7-E10.	0.4	3
51	Dual immuno-renal targeting of 7-benzylidenenaltrexone alleviates lupus nephritis via Fc γ RIIB and HO-1. <i>Journal of Molecular Medicine</i> , 2018, 96, 413-425.	1.7	4
52	An automated microfluidic DNA microarray platform for genetic variant detection in inherited arrhythmic diseases. <i>Analyst</i> , 2018, 143, 1367-1377.	1.7	14
53	Analyzing Differential Regulatory Networks Modulated by Continuous-State Genomic Features in Glioblastoma Multiforme. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1754-1764.	1.9	3
54	Deep Sequencing Reveals a MicroRNA Expression Signature in Triple-Negative Breast Cancer. <i>Methods in Molecular Biology</i> , 2018, 1699, 99-111.	0.4	5

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55	Global Expression Profiling Identifies a Novel Hyaluronan Synthases 2 Gene in the Pathogenesis of Lower Extremity Varicose Veins. <i>Journal of Clinical Medicine</i> , 2018, 7, 537.	1.0	5
56	CellExpress: a comprehensive microarray-based cancer cell line and clinical sample gene expression analysis online system. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	25
57	Different effects of long noncoding RNA <i>NDRG1-OT1</i> fragments on <i>NDRG1</i> transcription in breast cancer cells under hypoxia. <i>RNA Biology</i> , 2018, 15, 1487-1498.	1.5	20
58	The extracellular SEMA domain attenuates intracellular apoptotic signaling of semaphorin 6A in lung cancer cells. <i>Oncogenesis</i> , 2018, 7, 95.	2.1	17
59	The hypoxia-responsive lncRNA <i>NDRG-OT1</i> promotes <i>NDRG1</i> degradation via ubiquitin-mediated proteolysis in breast cancer cells. <i>Oncotarget</i> , 2018, 9, 10470-10482.	0.8	33
60	Whole-genome de novo sequencing reveals unique genes that contributed to the adaptive evolution of the Mikado pheasant. <i>GigaScience</i> , 2018, 7, .	3.3	21
61	Utilizing Cancer - Functional Gene Set - Compound Networks to Identify Putative Drugs for Breast Cancer. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2018, 21, 74-83.	0.6	0
62	iGC – an integrated analysis package of gene expression and copy number alteration. <i>BMC Bioinformatics</i> , 2017, 18, 35.	1.2	16
63	Identification of Methylation-Driven, Differentially Expressed STXBP6 as a Novel Biomarker in Lung Adenocarcinoma. <i>Scientific Reports</i> , 2017, 7, 42573.	1.6	20
64	Differential correlation analysis of glioblastoma reveals immune ceRNA interactions predictive of patient survival. <i>BMC Bioinformatics</i> , 2017, 18, 132.	1.2	16
65	SHANK3 Regulates Intestinal Barrier Function Through Modulating ZO-1 Expression Through the PKC μ -dependent Pathway. <i>Inflammatory Bowel Diseases</i> , 2017, 23, 1730-1740.	0.9	26
66	Genetic loci associated with an earlier age at onset in multiplex schizophrenia. <i>Scientific Reports</i> , 2017, 7, 6486.	1.6	15
67	Prognostic impacts and dynamic changes of cohesin complex gene mutations in de novo acute myeloid leukemia. <i>Blood Cancer Journal</i> , 2017, 7, 663.	2.8	39
68	Genome-wide identification of key modulators of gene-gene interaction networks in breast cancer. <i>BMC Genomics</i> , 2017, 18, 679.	1.2	4
69	ADAM9 enhances CDCP1 by inhibiting miR-1 through EGFR signaling activation in lung cancer metastasis. <i>Oncotarget</i> , 2017, 8, 47365-47378.	0.8	29
70	Development of a prediction model for radiosensitivity using the expression values of genes and long non-coding RNAs. <i>Oncotarget</i> , 2016, 7, 26739-26750.	0.8	8
71	Differential network analysis reveals the genome-wide landscape of estrogen receptor modulation in hormonal cancers. <i>Scientific Reports</i> , 2016, 6, 23035.	1.6	31
72	Liver Gene Expression Profiles Correlate with Virus Infection and Response to Interferon Therapy in Chronic Hepatitis B Patients. <i>Scientific Reports</i> , 2016, 6, 31349.	1.6	21

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73	Aryl Hydrocarbon Receptor Activates NDRG1 Transcription under Hypoxia in Breast Cancer Cells. <i>Scientific Reports</i> , 2016, 6, 20808.	1.6	19
74	A simple gene set-based method accurately predicts the synergy of drug pairs. <i>BMC Systems Biology</i> , 2016, 10, 66.	3.0	10
75	Genome-wide screening identifies a KCNIP1 copy number variant as a genetic predictor for atrial fibrillation. <i>Nature Communications</i> , 2016, 7, 10190.	5.8	37
76	Mitomycin C treatment induces resistance and enhanced migration via phosphorylated Akt in aggressive lung cancer cells. <i>Oncotarget</i> , 2016, 7, 79995-80007.	0.8	4
77	Overexpression of methylation-driven DCC suppresses proliferation of lung cancer cells. <i>Translational Cancer Research</i> , 2016, 5, 169-175.	0.4	3
78	Applying gene set analysis to characterize the activities of immune cells in estrogen receptor positive breast cancer. <i>Translational Cancer Research</i> , 2016, 5, 176-185.	0.4	1
79	Patho-finder "A fast and accurate program for pathogen identification through RNA-seq. , , .		0
80	Co-modulation analysis of gene regulation in breast cancer reveals complex interplay between ESR1 and ERBB2 genes. <i>BMC Genomics</i> , 2015, 16, S19.	1.2	7
81	Parameter optimization for constructing competing endogenous RNA regulatory network in glioblastoma multiforme and other cancers. <i>BMC Genomics</i> , 2015, 16, S1.	1.2	43
82	Circulating mRNA Profiling in Esophageal Squamous Cell Carcinoma Identifies FAM84B As A Biomarker In Predicting Pathological Response to Neoadjuvant Chemoradiation. <i>Scientific Reports</i> , 2015, 5, 10291.	1.6	24
83	Analyzing differential regulatory networks modulated by continuous-state genomic features in glioblastoma multiforme. , 2015, , .		1
84	Next-generation sequencing of nine atrial fibrillation candidate genes identified novel de novo mutations in patients with extreme trait of atrial fibrillation. <i>Journal of Medical Genetics</i> , 2015, 52, 28-36.	1.5	49
85	Deregulated microRNAs in triple-negative breast cancer revealed by deep sequencing. <i>Molecular Cancer</i> , 2015, 14, 36.	7.9	100
86	Identification of regulatory SNPs associated with genetic modifications in lung adenocarcinoma. <i>BMC Research Notes</i> , 2015, 8, 92.	0.6	27
87	Identification of Genes with Consistent Methylation Levels across Different Human Tissues. <i>Scientific Reports</i> , 2015, 4, 4351.	1.6	11
88	Putative effectors for prognosis in lung adenocarcinoma are ethnic and gender specific. <i>Oncotarget</i> , 2015, 6, 19483-19499.	0.8	4
89	An mRNA expression signature for prognostication in <i>de novo</i> acute myeloid leukemia patients with normal karyotype. <i>Oncotarget</i> , 2015, 6, 39098-39110.	0.8	42
90	The Clinical and Biological Characterization of De Novo Acute Myeloid Leukemia (AML) with GATA2 Mutation. <i>Blood</i> , 2015, 126, 3822-3822.	0.6	0

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91	SLCO3A1, a Novel Crohn's Disease-Associated Gene, Regulates NF- κ B Activity and Associates with Intestinal Perforation. PLoS ONE, 2014, 9, e100515.	1.1	15
92	Comparisons and performance evaluations of RNA-seq alignment tools. , 2014, , .		4
93	Identification of a liver cirrhosis signature in plasma for predicting hepatocellular carcinoma risk in a population-based cohort of hepatitis B carriers. Molecular Carcinogenesis, 2014, 53, 58-66.	1.3	9
94	Radiogenomics: Radiobiology Enters the Era of Big Data and Team Science. International Journal of Radiation Oncology Biology Physics, 2014, 89, 709-713.	0.4	99
95	Refinement of breast cancer risk prediction with concordant leading edge subsets from prognostic gene signatures. Breast Cancer Research and Treatment, 2014, 147, 353-370.	1.1	3
96	SNP rs10248565 in HDAC9 as a novel genomic aberration biomarker of lung adenocarcinoma in non-smoking women. Journal of Biomedical Science, 2014, 21, 24.	2.6	11
97	Estrogen receptor status prediction by gene component regression: a comparative study. International Journal of Data Mining and Bioinformatics, 2014, 9, 149.	0.1	4
98	MicroRNA-769-3p Down-regulates NDRG1 and Enhances Apoptosis in MCF-7 Cells During Reoxygenation. Scientific Reports, 2014, 4, 5908.	1.6	31
99	Identification of Gene Expression Biomarkers for Predicting Radiation Exposure. Scientific Reports, 2014, 4, 6293.	1.6	39
100	Utilizing Multiple in Silico Analyses to Identify Putative Causal SCN5A Variants in Brugada Syndrome. Scientific Reports, 2014, 4, 3850.	1.6	21
101	Disease-Targeted Sequencing of Ion Channel Genes identifies de novo mutations in Patients with Non-Familial Brugada Syndrome. Scientific Reports, 2014, 4, 6733.	1.6	54
102	ADAM9 Up-Regulates N-Cadherin via miR-218 Suppression in Lung Adenocarcinoma Cells. PLoS ONE, 2014, 9, e94065.	1.1	32
103	A Simple, Powerful, and Widely Applicable Micro-RNA Scoring System in Prognostication of De Novo Myeloid Leukemia Patients. Blood, 2014, 124, 71-71.	0.6	1
104	Identification of reproducible gene expression signatures in lung adenocarcinoma. BMC Bioinformatics, 2013, 14, 371.	1.2	13
105	Concurrent analysis of copy number variation and gene expression: application in paired non-smoking female lung cancer patients. International Journal of Data Mining and Bioinformatics, 2013, 8, 92.	0.1	0
106	Multiclass Prediction with Partial Least Square Regression for Gene Expression Data: Applications in Breast Cancer Intrinsic Taxonomy. BioMed Research International, 2013, 2013, 1-9.	0.9	11
107	Modeling competing endogenous RNA regulatory networks in glioblastoma multiforme. , 2013, , .		5
108	Gene Regulation, Modulation, and Their Applications in Gene Expression Data Analysis. Advances in Bioinformatics, 2013, 2013, 1-11.	5.7	25

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109	Transcription of Tnfaip3 Is Regulated by NF- κ B and p38 via C/EBP β in Activated Macrophages. PLoS ONE, 2013, 8, e73153.	1.1	32
110	MicroRNA-449a Enhances Radiosensitivity in CL1-0 Lung Adenocarcinoma Cells. PLoS ONE, 2013, 8, e62383.	1.1	40
111	Concurrent Gene Signatures for Han Chinese Breast Cancers. PLoS ONE, 2013, 8, e76421.	1.1	65
112	Next-Generation Sequencing in the Genetics of Human Atrial Fibrillation. Acta Cardiologica Sinica, 2013, 29, 317-22.	0.1	1
113	Using gene sets to identify putative drugs for breast cancer. , 2012, , .		0
114	Prediction consistency and clinical presentations of breast cancer molecular subtypes for Han Chinese population. Journal of Translational Medicine, 2012, 10, S10.	1.8	9
115	miRSystem: An Integrated System for Characterizing Enriched Functions and Pathways of MicroRNA Targets. PLoS ONE, 2012, 7, e42390.	1.1	277
116	In vivo THz fiber-scanning mammography of early breast cancer in mice. , 2011, , .		2
117	High-sensitivity in vivo THz transmission imaging of early human breast cancer in a subcutaneous xenograft mouse model. Optics Express, 2011, 19, 21552.	1.7	70
118	Down-Regulation of NDRG1 Promotes Migration of Cancer Cells during Reoxygenation. PLoS ONE, 2011, 6, e24375.	1.1	26
119	Integrated Analyses of Copy Number Variations and Gene Expression in Lung Adenocarcinoma. PLoS ONE, 2011, 6, e24829.	1.1	68
120	Identification of Prognostic Genes for Recurrent Risk Prediction in Triple Negative Breast Cancer Patients in Taiwan. PLoS ONE, 2011, 6, e28222.	1.1	25
121	DBCAT: Database of CpG Islands and Analytical Tools for Identifying Comprehensive Methylation Profiles in Cancer Cells. Journal of Computational Biology, 2011, 18, 1013-1017.	0.8	37
122	A model-based circular binary segmentation algorithm for the analysis of array CGH data. BMC Research Notes, 2011, 4, 394.	0.6	8
123	Verifying expressed transcript variants by detecting and assembling stretches of consecutive exons. Nucleic Acids Research, 2010, 38, e187-e187.	6.5	2
124	Identification of a Novel Biomarker, <i>SEMA5A</i> , for Non-Small Cell Lung Carcinoma in Nonsmoking Women. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2590-2597.	1.1	270
125	Comparison of triple negative breast cancer between Asian and western data sets. , 2010, , .		0
126	DNA (cytosine-5)-methyltransferase 1 as a mediator of mutant p53-determined p16ink4A down-regulation. Journal of Biomedical Science, 2008, 15, 163-168.	2.6	9

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127	Duodenal Ulcer-related Antigens from <i>Helicobacter pylori</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1018-1026.	2.5	23
128	Profiling Microdissected Epithelium and Stroma to Model Genomic Signatures for Cervical Carcinogenesis Accommodating for Covariates. <i>Cancer Research</i> , 2007, 67, 7113-7123.	0.4	87
129	Gene Expression Profiling of Breast, Prostate, and Glioma Cells following Single versus Fractionated Doses of Radiation. <i>Cancer Research</i> , 2007, 67, 3845-3852.	0.4	167
130	Development of a normalization algorithm for array comparative genomic hybridization. , 2006, , .		0
131	Distinct Effects of Ionizing Radiation on In vivo Murine Kidney and Brain Normal Tissue Gene Expression. <i>Clinical Cancer Research</i> , 2006, 12, 3823-3830.	3.2	24
132	Abnormal Gene Expression Profiles in Unaffected Parents of Patients with Hereditary-Type Retinoblastoma. <i>Cancer Research</i> , 2006, 66, 3428-3433.	0.4	12
133	Radiation-Induced Changes in Gene-Expression Profiles for the SCC VII Tumor Cells Grown In Vitro and In Vivo. <i>Antioxidants and Redox Signaling</i> , 2006, 8, 1263-1272.	2.5	12
134	Evaluation of Hybridization Conditions for Spotted Oligonucleotide-Based DNA Microarrays. <i>Molecular Biotechnology</i> , 2005, 29, 221-224.	1.3	3
135	c-Abl regulates Early Growth Response Protein (EGR1) in response to oxidative stress. <i>Oncogene</i> , 2005, 24, 8085-8092.	2.6	29
136	Effects of hypoxia on radiation-responsive stress-activated protein kinase, p53, and caspase 3 signals in TK6 human lymphoblastoid cells. <i>Cancer Research</i> , 2005, 65, 579-86.	0.4	15
137	Nuclear Factor- κ B is an Important Modulator of the Altered Gene Expression Profile and Malignant Phenotype in Squamous Cell Carcinoma. <i>Cancer Research</i> , 2004, 64, 6511-6523.	0.4	159
138	Distinct effects on gene expression of chemical and genetic manipulation of the cancer epigenome revealed by a multimodality approach. <i>Cancer Cell</i> , 2004, 6, 361-371.	7.7	172
139	Transcriptional signature of flavopiridol-induced tumor cell death. <i>Molecular Cancer Therapeutics</i> , 2004, 3, 861-72.	1.9	27
140	Semiquinone radical intermediate in catecholic estrogen-mediated cytotoxicity and mutagenesis: Chemoprevention strategies with antioxidants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5390-5395.	3.3	63
141	Gene expression analysis of esophageal squamous cell carcinoma reveals consistent molecular profiles related to a family history of upper gastrointestinal cancer. <i>Cancer Research</i> , 2003, 63, 3872-6.	0.4	63