

Eric Y Chuang

List of Publications by Citations

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

125 papers	2,657 citations	26 h-index	48 g-index
143 ext. papers	3,257 ext. citations	5.6 avg, IF	4.68 L-index

#	Paper	IF	Citations
125	miRSystem: an integrated system for characterizing enriched functions and pathways of microRNA targets. <i>PLoS ONE</i> , 2012 , 7, e42390	3.7	217
124	Identification of a novel biomarker, SEMA5A, for non-small cell lung carcinoma in nonsmoking women. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 2590-7	4	213
123	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, 361-71	24.3	157
122	Gene expression profiling of breast, prostate, and glioma cells following single versus fractionated doses of radiation. <i>Cancer Research</i> , 2007 , 67, 3845-52	10.1	150
121	Nuclear factor-kappaB is an important modulator of the altered gene expression profile and malignant phenotype in squamous cell carcinoma. <i>Cancer Research</i> , 2004 , 64, 6511-23	10.1	149
120	Altered gut microbiota and inflammatory cytokine responses in patients with Parkinson's disease. <i>Journal of Neuroinflammation</i> , 2019 , 16, 129	10.1	137
119	Deregulated microRNAs in triple-negative breast cancer revealed by deep sequencing. <i>Molecular Cancer</i> , 2015 , 14, 36	42.1	86
118	Profiling microdissected epithelium and stroma to model genomic signatures for cervical carcinogenesis accommodating for covariates. <i>Cancer Research</i> , 2007 , 67, 7113-23	10.1	76
117	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	25.5	65
116	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, 5390-5	11.5	61
115	High-sensitivity in vivo THz transmission imaging of early human breast cancer in a subcutaneous xenograft mouse model. <i>Optics Express</i> , 2011 , 19, 21552-62	3.3	60
114	Integrated analyses of copy number variations and gene expression in lung adenocarcinoma. <i>PLoS ONE</i> , 2011 , 6, e24829	3.7	55
113	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	10.1	50
112	Disease-targeted sequencing of ion channel genes identifies de novo mutations in patients with non-familial Brugada syndrome. <i>Scientific Reports</i> , 2014 , 4, 6733	4.9	40
111	Concurrent gene signatures for han chinese breast cancers. <i>PLoS ONE</i> , 2013 , 8, e76421	3.7	40
110	MicroRNA-449a enhances radiosensitivity in CL1-0 lung adenocarcinoma cells. <i>PLoS ONE</i> , 2013 , 8, e62383	3.7	37
109	Identification of gene expression biomarkers for predicting radiation exposure. <i>Scientific Reports</i> , 2014 , 4, 6293	4.9	31

108	An mRNA expression signature for prognostication in de novo acute myeloid leukemia patients with normal karyotype. <i>Oncotarget</i> , 2015 , 6, 39098-110	3.3	31
107	Parameter optimization for constructing competing endogenous RNA regulatory network in glioblastoma multiforme and other cancers. <i>BMC Genomics</i> , 2015 , 16 Suppl 4, S1	4.5	29
106	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	5.8	29
105	DBCAT: database of CpG islands and analytical tools for identifying comprehensive methylation profiles in cancer cells. <i>Journal of Computational Biology</i> , 2011 , 18, 1013-7	1.7	29
104	c-Abl regulates early growth response protein (EGR1) in response to oxidative stress. <i>Oncogene</i> , 2005 , 24, 8085-92	9.2	28
103	ADAM9 up-regulates N-cadherin via miR-218 suppression in lung adenocarcinoma cells. <i>PLoS ONE</i> , 2014 , 9, e94065	3.7	28
102	Prognostic impacts and dynamic changes of cohesin complex gene mutations in de novo acute myeloid leukemia. <i>Blood Cancer Journal</i> , 2017 , 7, 663	7	26
101	Transcriptional signature of flavopiridol-induced tumor cell death. <i>Molecular Cancer Therapeutics</i> , 2004 , 3, 861-72	6.1	26
100	MicroRNA-769-3p down-regulates NDRG1 and enhances apoptosis in MCF-7 cells during reoxygenation. <i>Scientific Reports</i> , 2014 , 4, 5908	4.9	24
99	Distinct effects of ionizing radiation on in vivo murine kidney and brain normal tissue gene expression. <i>Clinical Cancer Research</i> , 2006 , 12, 3823-30	12.9	24
98	Genome-wide screening identifies a KCNIP1 copy number variant as a genetic predictor for atrial fibrillation. <i>Nature Communications</i> , 2016 , 7, 10190	17.4	23
97	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	4.6	22
96	Transcription of Tnfaip3 is regulated by NF- κ B and p38 via C/EBP β in activated macrophages. <i>PLoS ONE</i> , 2013 , 8, e73153	3.7	21
95	Down-regulation of NDRG1 promotes migration of cancer cells during reoxygenation. <i>PLoS ONE</i> , 2011 , 6, e24375	3.7	21
94	Identification of prognostic genes for recurrent risk prediction in triple negative breast cancer patients in Taiwan. <i>PLoS ONE</i> , 2011 , 6, e28222	3.7	21
93	The hypoxia-responsive lncRNA promotes NDRG1 degradation via ubiquitin-mediated proteolysis in breast cancer cells. <i>Oncotarget</i> , 2018 , 9, 10470-10482	3.3	20
92	Gene regulation, modulation, and their applications in gene expression data analysis. <i>Advances in Bioinformatics</i> , 2013 , 2013, 360678	5.5	19
91	Differential network analysis reveals the genome-wide landscape of estrogen receptor modulation in hormonal cancers. <i>Scientific Reports</i> , 2016 , 6, 23035	4.9	19

90	Utilizing multiple in silico analyses to identify putative causal SCN5A variants in Brugada syndrome. <i>Scientific Reports</i> , 2014 , 4, 3850	4.9	18
89	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	4.9	18
88	Duodenal ulcer-related antigens from <i>Helicobacter pylori</i> : immunoproteome and protein microarray approaches. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1018-26	7.6	18
87	ADAM9 enhances CDCP1 by inhibiting miR-1 through EGFR signaling activation in lung cancer metastasis. <i>Oncotarget</i> , 2017 , 8, 47365-47378	3.3	18
86	Identification of Methylation-Driven, Differentially Expressed STXBP6 as a Novel Biomarker in Lung Adenocarcinoma. <i>Scientific Reports</i> , 2017 , 7, 42573	4.9	17
85	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	4.9	17
84	SHANK3 Regulates Intestinal Barrier Function Through Modulating ZO-1 Expression Through the PKC-dependent Pathway. <i>Inflammatory Bowel Diseases</i> , 2017 , 23, 1730-1740	4.5	16
83	Identification of regulatory SNPs associated with genetic modifications in lung adenocarcinoma. <i>BMC Research Notes</i> , 2015 , 8, 92	2.3	15
82	Differential correlation analysis of glioblastoma reveals immune ceRNA interactions predictive of patient survival. <i>BMC Bioinformatics</i> , 2017 , 18, 132	3.6	13
81	Aryl Hydrocarbon Receptor Activates NDRG1 Transcription under Hypoxia in Breast Cancer Cells. <i>Scientific Reports</i> , 2016 , 6, 20808	4.9	13
80	Different effects of long noncoding RNA NDRG1-OT1 fragments on NDRG1 transcription in breast cancer cells under hypoxia. <i>RNA Biology</i> , 2018 , 15, 1487-1498	4.8	13
79	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	10.1	13
78	Identification of reproducible gene expression signatures in lung adenocarcinoma. <i>BMC Bioinformatics</i> , 2013 , 14, 371	3.6	12
77	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, 1263-72	8.4	12
76	iGC-an integrated analysis package of gene expression and copy number alteration. <i>BMC Bioinformatics</i> , 2017 , 18, 35	3.6	11
75	SNP rs10248565 in HDAC9 as a novel genomic aberration biomarker of lung adenocarcinoma in non-smoking women. <i>Journal of Biomedical Science</i> , 2014 , 21, 24	13.3	11
74	Abnormal gene expression profiles in unaffected parents of patients with hereditary-type retinoblastoma. <i>Cancer Research</i> , 2006 , 66, 3428-33	10.1	11
73	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,	5	11

72	Semaphorin 6A Attenuates the Migration Capability of Lung Cancer Cells via the NRF2/HMOX1 Axis. <i>Scientific Reports</i> , 2019 , 9, 13302	4.9	10
71	Identification of genes with consistent methylation levels across different human tissues. <i>Scientific Reports</i> , 2014 , 4, 4351	4.9	10
70	Comparison of DNA stabilizers and storage conditions on preserving fecal microbiota profiles. <i>Journal of the Formosan Medical Association</i> , 2020 , 119, 1791-1798	3.2	10
69	An automated microfluidic DNA microarray platform for genetic variant detection in inherited arrhythmic diseases. <i>Analyst, The</i> , 2018 , 143, 1367-1377	5	10
68	SLCO3A1, A novel crohn's disease-associated gene, regulates nf- κ B activity and associates with intestinal perforation. <i>PLoS ONE</i> , 2014 , 9, e100515	3.7	10
67	Multiclass prediction with partial least square regression for gene expression data: applications in breast cancer intrinsic taxonomy. <i>BioMed Research International</i> , 2013 , 2013, 248648	3	9
66	GSTM3 variant is a novel genetic modifier in Brugada syndrome, a disease with risk of sudden cardiac death. <i>EBioMedicine</i> , 2020 , 57, 102843	8.8	9
65	anamiR: integrated analysis of MicroRNA and gene expression profiling. <i>BMC Bioinformatics</i> , 2019 , 20, 239	3.6	8
64	Identifying the functions and biomarkers of and aqueous extracts in hepatic cells. <i>Chinese Medicine</i> , 2019 , 14, 10	4.7	8
63	Genome-Wide Copy Number Variation Association Study of Atrial Fibrillation Related Thromboembolic Stroke. <i>Journal of Clinical Medicine</i> , 2019 , 8,	5.1	8
62	A simple gene set-based method accurately predicts the synergy of drug pairs. <i>BMC Systems Biology</i> , 2016 , 10 Suppl 3, 66	3.5	8
61	Identification of a liver cirrhosis signature in plasma for predicting hepatocellular carcinoma risk in a population-based cohort of hepatitis B carriers. <i>Molecular Carcinogenesis</i> , 2014 , 53, 58-66	5	8
60	A model-based circular binary segmentation algorithm for the analysis of array CGH data. <i>BMC Research Notes</i> , 2011 , 4, 394	2.3	8
59	The extracellular SEMA domain attenuates intracellular apoptotic signaling of semaphorin 6A in lung cancer cells. <i>Oncogenesis</i> , 2018 , 7, 95	6.6	8
58	Development of a prediction model for radiosensitivity using the expression values of genes and long non-coding RNAs. <i>Oncotarget</i> , 2016 , 7, 26739-50	3.3	7
57	Whole-genome de novo sequencing reveals unique genes that contributed to the adaptive evolution of the Mikado pheasant. <i>GigaScience</i> , 2018 , 7,	7.6	6
56	Genetic loci associated with an earlier age at onset in multiplex schizophrenia. <i>Scientific Reports</i> , 2017 , 7, 6486	4.9	6
55	DNA (cytosine-5)-methyltransferase 1 as a mediator of mutant p53-determined p16(ink4A) down-regulation. <i>Journal of Biomedical Science</i> , 2008 , 15, 163-8	13.3	6

54	Prediction consistency and clinical presentations of breast cancer molecular subtypes for Han Chinese population. <i>Journal of Translational Medicine</i> , 2012 , 10 Suppl 1, S10	8.5	5
53	Modeling competing endogenous RNA regulatory networks in glioblastoma multiforme 2013 ,		5
52	MicroRNA-107 enhances radiosensitivity by suppressing granulin in PC-3 prostate cancer cells. <i>Scientific Reports</i> , 2020 , 10, 14584	4.9	5
51	Hypoxia-Induced Promotes the Proliferation and Migration of Breast Cancer Cells by Sponging. <i>Frontiers in Oncology</i> , 2021 , 11, 658151	5.3	5
50	Macrophage Migration Inhibitory Factor Acts as the Potential Target of a Newly Synthesized Compound, 1-(9-methyl-3H-carbazole)-3, 4-dihydro-carboline. <i>Scientific Reports</i> , 2019 , 9, 2147	4.9	5
49	Validation and Disease Risk Assessment of Previously Reported Genome-Wide Genetic Variants Associated With Brugada Syndrome: SADS-TW BrS Registry. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002797	5.2	4
48	Estrogen receptor status prediction by gene component regression: a comparative study. <i>International Journal of Data Mining and Bioinformatics</i> , 2014 , 9, 149-71	0.5	4
47	Co-modulation analysis of gene regulation in breast cancer reveals complex interplay between ESR1 and ERBB2 genes. <i>BMC Genomics</i> , 2015 , 16 Suppl 7, S19	4.5	4
46	Comparisons and performance evaluations of RNA-seq alignment tools 2014 ,		4
45	Putative effectors for prognosis in lung adenocarcinoma are ethnic and gender specific. <i>Oncotarget</i> , 2015 , 6, 19483-99	3.3	4
44	Regulatory Mechanisms and Functional Roles of Hypoxia-Induced Long Non-Coding RNA in Breast Cancer Cells. <i>Frontiers in Oncology</i> , 2021 , 11, 663114	5.3	4
43	EasyMAP: A user-friendly online platform for analyzing 16S ribosomal DNA sequencing data. <i>New Biotechnology</i> , 2021 , 63, 37-44	6.4	4
42	Deep Sequencing Reveals a MicroRNA Expression Signature in Triple-Negative Breast Cancer. <i>Methods in Molecular Biology</i> , 2018 , 1699, 99-111	1.4	3
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,	5	3
40	Evaluation of hybridization conditions for spotted oligonucleotide-based DNA microarrays. <i>Molecular Biotechnology</i> , 2005 , 29, 221-4	3	3
39	Mitomycin C treatment induces resistance and enhanced migration via phosphorylated Akt in aggressive lung cancer cells. <i>Oncotarget</i> , 2016 , 7, 79995-80007	3.3	3
38	Overexpression of methylation-driven DCC suppresses proliferation of lung cancer cells. <i>Translational Cancer Research</i> , 2016 , 5, 169-175	0.3	3
37	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	3	3

36	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	13	3
35	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	5.3	3
34	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,	5.1	3
33	Genome-wide identification of key modulators of gene-gene interaction networks in breast cancer. <i>BMC Genomics</i> , 2017 , 18, 679	4.5	2
32	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	3	2
31	Refinement of breast cancer risk prediction with concordant leading edge subsets from prognostic gene signatures. <i>Breast Cancer Research and Treatment</i> , 2014 , 147, 353-70	4.4	2
30	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	0.3	2
29	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,	5	2
28	Dual immuno-renal targeting of 7-benzylidenenaltrexone alleviates lupus nephritis via FcRIIB and HO-1. <i>Journal of Molecular Medicine</i> , 2018 , 96, 413-425	5.5	1
27	Analyzing differential regulatory networks modulated by continuous-state genomic features in glioblastoma multiforme 2015 ,		1
26	In vivo THz fiber-scanning mammography of early breast cancer in mice 2011 ,		1
25	Verifying expressed transcript variants by detecting and assembling stretches of consecutive exons. <i>Nucleic Acids Research</i> , 2010 , 38, e187	20.1	1
24	Join Classifier of Type and Index Mutation on Lung Cancer DNA Using Sequential Labeling Model. <i>IEEE Access</i> , 2022 , 10, 9004-9021	3.5	1
23	Next-Generation Sequencing in the Genetics of Human Atrial Fibrillation. <i>Acta Cardiologica Sinica</i> , 2013 , 29, 317-22	1.1	1
22	Novel Tumor-Specific Antigens for Immunotherapy Identified From Multi-omics Profiling in Thymic Carcinomas. <i>Frontiers in Immunology</i> , 2021 , 12, 748820	8.4	1
21	Semaphorin 5A suppresses the proliferation and migration of lung adenocarcinoma cells. <i>International Journal of Oncology</i> , 2020 , 56, 165-177	4.4	1
20	Evolutionary Trajectories and Genomic Divergence in Localized Breast Cancers after Ipsilateral Breast Tumor Recurrence. <i>Cancers</i> , 2021 , 13,	6.6	1
19	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	13	1

18	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	7.8	1
17	MiDSysTEM: A comprehensive online system for de novo assembly and analysis of microbial genomes. <i>New Biotechnology</i> , 2021 , 65, 42-52	6.4	1
16	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	7	1
15	Uremic Toxin-Producing 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	5.9	1
14	Using proteomic profiling to characterize protein signatures of different thymoma subtypes. <i>BMC Cancer</i> , 2019 , 19, 796	4.8	0
13	Lidocaine and Bupivacaine Downregulate MYB and lncRNA by Upregulating in MCF-7 Cells.. <i>Frontiers in Medicine</i> , 2021 , 8, 732817	4.9	0
12	Prediction of Breast Cancer Recurrence Using a Deep Convolutional Neural Network Without Region-of-Interest Labeling. <i>Frontiers in Oncology</i> , 2021 , 11, 734015	5.3	0
11	Risk Factors and Genetic Biomarkers of Multiple Primary Cancers in Esophageal Cancer Patients. <i>Frontiers in Oncology</i> , 2020 , 10, 585621	5.3	0
10	Differential whole-genome doubling and homologous recombination deficiencies across breast cancer subtypes from the Taiwanese population. <i>Communications Biology</i> , 2021 , 4, 1052	6.7	0
9	Predicting Breast Cancer Gene Expression Signature by Applying Deep Convolutional Neural Networks From Unannotated Pathological Images.. <i>Frontiers in Oncology</i> , 2021 , 11, 769447	5.3	0
8	Prevalence of sudden arrhythmic death syndrome-related genetic mutations in an Asian cohort of whole genome sequence. <i>Europace</i> , 2020 , 22, 1287-1297	3.9	
7	Concurrent analysis of copy number variation and gene expression: application in paired non-smoking female lung cancer patients. <i>International Journal of Data Mining and Bioinformatics</i> , 2013 , 8, 92-104	0.5	
6	MutScape: an analytical toolkit for probing the mutational landscape in cancer genomics. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab099	3.7	
5	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	1.3	
4	A Simple, Powerful, and Widely Applicable Micro-RNA Scoring System in Prognostication of De Novo Myeloid Leukemia Patients. <i>Blood</i> , 2014 , 124, 71-71	2.2	
3	The Clinical and Biological Characterization of De Novo Acute Myeloid Leukemia (AML) with GATA2 Mutation. <i>Blood</i> , 2015 , 126, 3822-3822	2.2	
2	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	1.7	
1	ATTRACTIVE [An Auto-Updating Database for Experimental Protocols in Regenerative Medicine. <i>IEEE Access</i> , 2021 , 9, 75202-75210	3.5	

