

Eric Y Chuang

List of Publications by Year in descending order

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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	Altered gut microbiota and inflammatory cytokine responses in patients with Parkinson's disease. <i>Journal of Neuroinflammation</i> , 2019, 16, 129.	3.1	283
2	miRSystem: An Integrated System for Characterizing Enriched Functions and Pathways of MicroRNA Targets. <i>PLoS ONE</i> , 2012, 7, e42390.	1.1	277
3	Identification of a Novel Biomarker, <i>SEMA5A</i> , for Non-Small Cell Lung Carcinoma in Nonsmoking Women. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 2590-2597.	1.1	270
4	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
5	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
6	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
7	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
8	Deregulated microRNAs in triple-negative breast cancer revealed by deep sequencing. <i>Molecular Cancer</i> , 2015, 14, 36.	7.9	100
9	Radiogenomics: Radiobiology Enters the Era of Big Data and Team Science. <i>International Journal of Radiation Oncology Biology Physics</i> , 2014, 89, 709-713.	0.4	99
10	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
11	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.	1.7	70
12	Integrated Analyses of Copy Number Variations and Gene Expression in Lung Adenocarcinoma. <i>PLoS ONE</i> , 2011, 6, e24829.	1.1	68
13	Concurrent Gene Signatures for Han Chinese Breast Cancers. <i>PLoS ONE</i> , 2013, 8, e76421.	1.1	65
14	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
15	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
16	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.	1.6	54
17	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
18	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

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19	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
20	MicroRNA-449a Enhances Radiosensitivity in CL1-0 Lung Adenocarcinoma Cells. <i>PLoS ONE</i> , 2013, 8, e62383.	1.1	40
21	Identification of Gene Expression Biomarkers for Predicting Radiation Exposure. <i>Scientific Reports</i> , 2014, 4, 6293.	1.6	39
22	Prognostic impacts and dynamic changes of cohesin complex gene mutations in <i>de novo</i> acute myeloid leukemia. <i>Blood Cancer Journal</i> , 2017, 7, 663.	2.8	39
23	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
24	DBCAT: Database of CpG Islands and Analytical Tools for Identifying Comprehensive Methylation Profiles in Cancer Cells. <i>Journal of Computational Biology</i> , 2011, 18, 1013-1017.	0.8	37
25	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
26	The hypoxia-responsive lncRNA <i>NDRG-OT1</i> promotes NDRG1 degradation via ubiquitin-mediated proteolysis in breast cancer cells. <i>Oncotarget</i> , 2018, 9, 10470-10482.	0.8	33
27	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
28	Transcription of <i>Tnfrsf3</i> Is Regulated by NF- κ B and p38 via C/EBP β in Activated Macrophages. <i>PLoS ONE</i> , 2013, 8, e73153.	1.1	32
29	ADAM9 Up-Regulates N-Cadherin via miR-218 Suppression in Lung Adenocarcinoma Cells. <i>PLoS ONE</i> , 2014, 9, e94065.	1.1	32
30	MicroRNA-769-3p Down-regulates NDRG1 and Enhances Apoptosis in MCF-7 Cells During Reoxygenation. <i>Scientific Reports</i> , 2014, 4, 5908.	1.6	31
31	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
32	c-Abl regulates Early Growth Response Protein (EGR1) in response to oxidative stress. <i>Oncogene</i> , 2005, 24, 8085-8092.	2.6	29
33	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
34	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
35	Identification of regulatory SNPs associated with genetic modifications in lung adenocarcinoma. <i>BMC Research Notes</i> , 2015, 8, 92.	0.6	27
36	Transcriptional signature of flavopiridol-induced tumor cell death. <i>Molecular Cancer Therapeutics</i> , 2004, 3, 861-72.	1.9	27

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37	Down-Regulation of NDRG1 Promotes Migration of Cancer Cells during Reoxygenation. PLoS ONE, 2011, 6, e24375.	1.1	26
38	SHANK3 Regulates Intestinal Barrier Function Through Modulating ZO-1 Expression Through the PKC μ -dependent Pathway. Inflammatory Bowel Diseases, 2017, 23, 1730-1740.	0.9	26
39	Identification of Prognostic Genes for Recurrent Risk Prediction in Triple Negative Breast Cancer Patients in Taiwan. PLoS ONE, 2011, 6, e28222.	1.1	25
40	Gene Regulation, Modulation, and Their Applications in Gene Expression Data Analysis. Advances in Bioinformatics, 2013, 2013, 1-11.	5.7	25
41	CellExpress: a comprehensive microarray-based cancer cell line and clinical sample gene expression analysis online system. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	25
42	Distinct Effects of Ionizing Radiation on In vivo Murine Kidney and Brain Normal Tissue Gene Expression. Clinical Cancer Research, 2006, 12, 3823-3830.	3.2	24
43	Circulating mRNA Profiling in Esophageal Squamous Cell Carcinoma Identifies FAM84B As A Biomarker In Predicting Pathological Response to Neoadjuvant Chemoradiation. Scientific Reports, 2015, 5, 10291.	1.6	24
44	Duodenal Ulcer-related Antigens from Helicobacter pylori. Molecular and Cellular Proteomics, 2007, 6, 1018-1026.	2.5	23
45	Comparison of DNA stabilizers and storage conditions on preserving fecal microbiota profiles. Journal of the Formosan Medical Association, 2020, 119, 1791-1798.	0.8	23
46	Utilizing Multiple in Silico Analyses to Identify Putative Causal SCN5A Variants in Brugada Syndrome. Scientific Reports, 2014, 4, 3850.	1.6	21
47	Liver Gene Expression Profiles Correlate with Virus Infection and Response to Interferon Therapy in Chronic Hepatitis B Patients. Scientific Reports, 2016, 6, 31349.	1.6	21
48	Whole-genome de novo sequencing reveals unique genes that contributed to the adaptive evolution of the Mikado pheasant. GigaScience, 2018, 7, .	3.3	21
49	Identification of Methylation-Driven, Differentially Expressed STXBP6 as a Novel Biomarker in Lung Adenocarcinoma. Scientific Reports, 2017, 7, 42573.	1.6	20
50	Different effects of long noncoding RNA <i>NDRG1-OT1</i> fragments on <i>NDRG1</i> transcription in breast cancer cells under hypoxia. RNA Biology, 2018, 15, 1487-1498.	1.5	20
51	Aryl Hydrocarbon Receptor Activates NDRG1 Transcription under Hypoxia in Breast Cancer Cells. Scientific Reports, 2016, 6, 20808.	1.6	19
52	The extracellular SEMA domain attenuates intracellular apoptotic signaling of semaphorin 6A in lung cancer cells. Oncogenesis, 2018, 7, 95.	2.1	17
53	iCCâ€”an integrated analysis package of gene expression and copy number alteration. BMC Bioinformatics, 2017, 18, 35.	1.2	16
54	Differential correlation analysis of glioblastoma reveals immune ceRNA interactions predictive of patient survival. BMC Bioinformatics, 2017, 18, 132.	1.2	16

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55	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
56	Genetic loci associated with an earlier age at onset in multiplex schizophrenia. Scientific Reports, 2017, 7, 6486.	1.6	15
57	Effects of hypoxia on radiation-responsive stress-activated protein kinase, p53, and caspase 3 signals in TK6 human lymphoblastoid cells. Cancer Research, 2005, 65, 579-86.	0.4	15
58	An automated microfluidic DNA microarray platform for genetic variant detection in inherited arrhythmic diseases. Analyst, The, 2018, 143, 1367-1377.	1.7	14
59	GSTM3 variant is a novel genetic modifier in Brugada syndrome, a disease with risk of sudden cardiac death. EBioMedicine, 2020, 57, 102843.	2.7	14
60	A risk prediction model of gene signatures in ovarian cancer through bagging of GA-XGBoost models. Journal of Advanced Research, 2021, 30, 113-122.	4.4	14
61	Identification of reproducible gene expression signatures in lung adenocarcinoma. BMC Bioinformatics, 2013, 14, 371.	1.2	13
62	anamiR: integrated analysis of MicroRNA and gene expression profiling. BMC Bioinformatics, 2019, 20, 239.	1.2	13
63	MicroRNA-107 enhances radiosensitivity by suppressing granulin in PC-3 prostate cancer cells. Scientific Reports, 2020, 10, 14584.	1.6	13
64	Rare variants discovery by extensive whole-genome sequencing of the Han Chinese population in Taiwan: Applications to cardiovascular medicine. Journal of Advanced Research, 2021, 30, 147-158.	4.4	13
65	An Artificial Intelligence-Enabled ECG Algorithm for the Prediction and Localization of Angiography-Proven Coronary Artery Disease. Biomedicines, 2022, 10, 394.	1.4	13
66	Abnormal Gene Expression Profiles in Unaffected Parents of Patients with Hereditary-Type Retinoblastoma. Cancer Research, 2006, 66, 3428-3433.	0.4	12
67	Radiation-Induced Changes in Gene-Expression Profiles for the SCC VII Tumor Cells Grown In Vitro and In Vivo. Antioxidants and Redox Signaling, 2006, 8, 1263-1272.	2.5	12
68	Validation and Disease Risk Assessment of Previously Reported Genome-Wide Genetic Variants Associated With Brugada Syndrome. Circulation Genomic and Precision Medicine, 2020, 13, e002797.	1.6	12
69	Uremic Toxin-Producing Bacteroides Species Preval in the Gut Microbiota of Taiwanese CKD Patients: An Analysis Using the New Taiwan Microbiome Baseline. Frontiers in Cellular and Infection Microbiology, 2022, 12, 726256.	1.8	12
70	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
71	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
72	Identification of Genes with Consistent Methylation Levels across Different Human Tissues. Scientific Reports, 2015, 4, 4351.	1.6	11

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73	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
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	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
76	Rare variants: data types and analysis strategies. <i>Annals of Translational Medicine</i> , 2021, 9, 961-961.	0.7	10
77	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
78	EasyMAP: A user-friendly online platform for analyzing 16S ribosomal DNA sequencing data. <i>New Biotechnology</i> , 2021, 63, 37-44.	2.4	10
79	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
80	DNA (cytosine-5)-methyltransferase 1 as a mediator of mutant p53-determined p16ink4A down-regulation. <i>Journal of Biomedical Science</i> , 2008, 15, 163-168.	2.6	9
81	Prediction consistency and clinical presentations of breast cancer molecular subtypes for Han Chinese population. <i>Journal of Translational Medicine</i> , 2012, 10, S10.	1.8	9
82	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.	1.3	9
83	A model-based circular binary segmentation algorithm for the analysis of array CGH data. <i>BMC Research Notes</i> , 2011, 4, 394.	0.6	8
84	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
85	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
86	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
87	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
88	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
89	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
90	Semaphorin 5A suppresses the proliferation and migration of lung adenocarcinoma cells. <i>International Journal of Oncology</i> , 2020, 56, 165-177.	1.4	6

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91	Modeling competing endogenous RNA regulatory networks in glioblastoma multiforme. , 2013, , .		5
92	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
93	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
94	Macrophage Migration Inhibitory Factor Acts as the Potential Target of a Newly Synthesized Compound, 1-(9- β -methyl-3- β -carbazole)-3, 4-dihydro- β -carboline. <i>Scientific Reports</i> , 2019, 9, 2147.	1.6	5
95	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
96	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
97	The Gut Microbiome, Seleno-Compounds, and Acute Myocardial Infarction. <i>Journal of Clinical Medicine</i> , 2022, 11, 1462.	1.0	5
98	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
99	Comparisons and performance evaluations of RNA-seq alignment tools. , 2014, , .		4
100	Estrogen receptor status prediction by gene component regression: a comparative study. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 9, 149.	0.1	4
101	Genome-wide identification of key modulators of gene-gene interaction networks in breast cancer. <i>BMC Genomics</i> , 2017, 18, 679.	1.2	4
102	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
103	Using proteomic profiling to characterize protein signatures of different thymoma subtypes. <i>BMC Cancer</i> , 2019, 19, 796.	1.1	4
104	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
105	Putative effectors for prognosis in lung adenocarcinoma are ethnic and gender specific. <i>Oncotarget</i> , 2015, 6, 19483-19499.	0.8	4
106	Evaluation of Hybridization Conditions for Spotted Oligonucleotide-Based DNA Microarrays. <i>Molecular Biotechnology</i> , 2005, 29, 221-224.	1.3	3
107	Refinement of breast cancer risk prediction with concordant leading edge subsets from prognostic gene signatures. <i>Breast Cancer Research and Treatment</i> , 2014, 147, 353-370.	1.1	3
108	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

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109	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
110	Risk Factors and Genetic Biomarkers of Multiple Primary Cancers in Esophageal Cancer Patients. <i>Frontiers in Oncology</i> , 2020, 10, 585621.	1.3	3
111	Evolutionary Trajectories and Genomic Divergence in Localized Breast Cancers after Ipsilateral Breast Tumor Recurrence. <i>Cancers</i> , 2021, 13, 1821.	1.7	3
112	Overexpression of methylation-driven DCC suppresses proliferation of lung cancer cells. <i>Translational Cancer Research</i> , 2016, 5, 169-175.	0.4	3
113	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
114	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
115	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
116	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
117	Verifying expressed transcript variants by detecting and assembling stretches of consecutive exons. <i>Nucleic Acids Research</i> , 2010, 38, e187-e187.	6.5	2
118	In vivo THz fiber-scanning mammography of early breast cancer in mice. , 2011, , .		2
119	Targeting the gut microbiome for non-communicable diseases: present and future. <i>Annals of Translational Medicine</i> , 2021, 9, 361-361.	0.7	2
120	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
121	MiDSytem: A comprehensive online system for de novo assembly and analysis of microbial genomes. <i>New Biotechnology</i> , 2021, 65, 42-52.	2.4	2
122	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
123	Analyzing differential regulatory networks modulated by continuous-state genomic features in glioblastoma multiforme. , 2015, , .		1
124	High-performance deep learning pipeline predicts individuals in mixtures of DNA using sequencing data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	1
125	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
126	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.	0.6	1

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127	Next-Generation Sequencing in the Genetics of Human Atrial Fibrillation. <i>Acta Cardiologica Sinica</i> , 2013, 29, 317-22.	0.1	1
128	The extended concurrent genes signature for disease-free survival in breast cancer. <i>Journal of the Formosan Medical Association</i> , 2022, , .	0.8	1
129	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
130	Development of a normalization algorithm for array comparative genomic hybridization. , 2006, , .		0
131	Comparison of triple negative breast cancer between Asian and western data sets. , 2010, , .		0
132	Using gene sets to identify putative drugs for breast cancer. , 2012, , .		0
133	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.	0.1	0
134	Patho-finder â€” A fast and accurate program for pathogen identification through RNA-seq. , 2015, , .		0
135	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
136	ATTRACTIVE â€” An Auto-Updating Database for Experimental Protocols in Regenerative Medicine. <i>IEEE Access</i> , 2021, 9, 75202-75210.	2.6	0
137	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
138	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
139	MutScape: an analytical toolkit for probing the mutational landscape in cancer genomics. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab099.	1.5	0
140	A major milestone for Translational Cancer Research: indexing in PubMed/PubMed Central. <i>Translational Cancer Research</i> , 2022, 11, 1-2.	0.4	0
141	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