Tzu-Pin Lu

List of Publications by Year
in descending order

149 papers	2,560 citations	331538 21 h-index	243529 44 g-index
158 all docs	158 docs citations	158 times ranked	4702 citing authors

#	Article	IF	Citations
1	Altered gut microbiota and inflammatory cytokine responses in patients with Parkinson's disease. Journal of Neuroinflammation, 2019, 16, 129.	3.1	283
2	miRSystem: An Integrated System for Characterizing Enriched Functions and Pathways of MicroRNA Targets. PLoS ONE, 2012, 7, e42390.	1.1	277
3	Identification of a Novel Biomarker, *SEMA5A*, for Non–Small Cell Lung Carcinoma in Nonsmoking Women. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2590-2597.	1.1	270
4	Long-term changes of gut microbiota, antibiotic resistance, and metabolic parameters after Helicobacter pylori eradication: a multicentre, open-label, randomised trial. Lancet Infectious Diseases, The, 2019, 19, 1109-1120.	4.6	127
5	Prenatal smoke exposure, DNA methylation, and childhood atopic dermatitis. Clinical and Experimental Allergy, 2013, 43, 535-543.	1.4	89
6	ADAM9 Promotes Lung Cancer Metastases to Brain by a Plasminogen Activator-Based Pathway. Cancer Research, 2014, 74, 5229-5243.	0.4	70
7	Integrated Analyses of Copy Number Variations and Gene Expression in Lung Adenocarcinoma. PLoS ONE, 2011, 6, e24829.	1.1	68
8	Preoperative sarcopenia is associated with poor overall survival in pancreatic cancer patients following pancreaticoduodenectomy. European Radiology, 2021, 31, 2472-2481.	2.3	55
9	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
10	Clinicopathologic Characterization of GREB1-rearranged Uterine Sarcomas With Variable Sex-Cord Differentiation. American Journal of Surgical Pathology, 2019, 43, 928-942.	2.1	43
11	Disparity in Tumor Immune Microenvironment of Breast Cancer and Prognostic Impact: Asian Versus Western Populations. Oncologist, 2020, 25, e16-e23.	1.9	40
12	Identification of Gene Expression Biomarkers for Predicting Radiation Exposure. Scientific Reports, 2014, 4, 6293.	1.6	39
13	Tumor-Infiltrating Leukocyte Composition and Prognostic Power in Hepatitis B- and Hepatitis C-Related Hepatocellular Carcinomas. Genes, 2019, 10, 630.	1.0	38
14	ADAM9 promotes lung cancer progression through vascular remodeling by VEGFA, ANGPT2, and PLAT. Scientific Reports, 2017, 7, 15108.	1.6	37
15	Differential network analysis reveals the genome-wide landscape of estrogen receptor modulation in hormonal cancers. Scientific Reports, 2016, 6, 23035.	1.6	31
16	Hypoxia-Induced MALAT1 Promotes the Proliferation and Migration of Breast Cancer Cells by Sponging MiR-3064-5p. Frontiers in Oncology, 2021, 11, 658151.	1.3	29
17	Genomewide copy number analysis of Müllerian adenosarcoma identified chromosomal instability in the aggressive subgroup. Modern Pathology, 2016, 29, 1070-1082.	2.9	28
18	Identification of regulatory SNPs associated with genetic modifications in lung adenocarcinoma. BMC Research Notes, 2015, 8, 92.	0.6	27

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19	Gene-gene interaction: the curse of dimensionality. Annals of Translational Medicine, 2019, 7, 813-813.	0.7	27
20	Down-Regulation of NDRG1 Promotes Migration of Cancer Cells during Reoxygenation. PLoS ONE, 2011, 6, e24375.	1.1	26
21	Predictive biomarkers for treatment selection: statistical considerations. Biomarkers in Medicine, 2015, 9, 1121-1135.	0.6	25
22	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
23	Identification of theranostic factors for patients developing metastasis after surgery for early-stage lung adenocarcinoma. Theranostics, 2021, 11, 3661-3675.	4.6	25
24	Prognostic significance of NPM1 mutation-modulated microRNAâˆ’mRNA regulation in acute myeloid leukemia. Leukemia, 2016, 30, 274-284.	3.3	24
25	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
26	Utilizing Multiple in Silico Analyses to Identify Putative Causal SCN5A Variants in Brugada Syndrome. Scientific Reports, 2014, 4, 3850.	1.6	21
27	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
28	Whole-genome de novo sequencing reveals unique genes that contributed to the adaptive evolution of the Mikado pheasant. GigaScience, 2018, 7, .	3.3	21
29	Identification of Methylation-Driven, Differentially Expressed STXBP6 as a Novel Biomarker in Lung Adenocarcinoma. Scientific Reports, 2017, 7, 42573.	1.6	20
30	<i>SP110</i>Polymorphisms Are Genetic Markers for Vulnerability to Latent and Active Tuberculosis Infection in Taiwan. Disease Markers, 2018, 2018, 1-12.	0.6	20
31	A 4-lncRNA scoring system for prognostication of adult myelodysplastic syndromes. Blood Advances, 2017, 1, 1505-1516.	2.5	19
32	Developing a Prognostic Gene Panel of Epithelial Ovarian Cancer Patients by a Machine Learning Model. Cancers, 2019, 11, 270.	1.7	19
33	Development of a prediction model for breast cancer based on the national cancer registry in Taiwan. Breast Cancer Research, 2019, 21, 92.	2.2	18
34	Transcriptome Changes in Relation to Manic Episode. Frontiers in Psychiatry, 2019, 10, 280.	1.3	18
35	Clinical Relevance of Liver Kinase B1(LKB1) Protein and Gene Expression in Breast Cancer. Scientific Reports, 2016, 6, 21374.	1.6	17
36	The extracellular SEMA domain attenuates intracellular apoptotic signaling of semaphorin 6A in lung cancer cells. Oncogenesis, 2018, 7, 95.	2.1	17

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37	iGC—an integrated analysis package of gene expression and copy number alteration. BMC Bioinformatics, 2017, 18, 35.	1.2	16
38	Differential correlation analysis of glioblastoma reveals immune ceRNA interactions predictive of patient survival. BMC Bioinformatics, 2017, 18, 132.	1.2	16
39	Distinct Signaling Pathways After Higher or Lower Doses of Radiation in Three Closely Related Human Lymphoblast Cell Lines. International Journal of Radiation Oncology Biology Physics, 2010, 76, 212-219.	0.4	15
40	Genetic loci associated with an earlier age at onset in multiplex schizophrenia. Scientific Reports, 2017, 7, 6486.	1.6	15
41	Nonintubated Versus Intubated Uniportal Thoracoscopic Segmentectomy for Lung Tumors. Annals of Thoracic Surgery, 2021, 111, 1182-1189.	0.7	15
42	An automated microfluidic DNA microarray platform for genetic variant detection in inherited arrhythmic diseases. Analyst, The, 2018, 143, 1367-1377.	1.7	14
43	CDH1, DLEC1 and SFRP5 methylation panel as a prognostic marker for advanced epithelial ovarian cancer. Epigenomics, 2018, 10, 1397-1413.	1.0	14
44	Clinical-Genomic Models of Node-Positive Breast Cancer: Training, Testing, and Validation. International Journal of Radiation Oncology Biology Physics, 2019, 105, 637-648.	0.4	14
45	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
46	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
47	Identification of reproducible gene expression signatures in lung adenocarcinoma. BMC Bioinformatics, 2013, 14, 371.	1.2	13
48	Epithelioid Trophoblastic Tumor Around an Abdominal Cesarean Scar: A Pathologic and Molecular Genetic Analysis. International Journal of Gynecological Pathology, 2017, 36, 562-567.	0.9	13
49	anamiR: integrated analysis of MicroRNA and gene expression profiling. BMC Bioinformatics, 2019, 20, 239.	1.2	13
50	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
51	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
52	Uremic Toxin-Producing Bacteroides Species Prevail 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
53	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
54	Identification of Genes with Consistent Methylation Levels across Different Human Tissues. Scientific Reports, 2015, 4, 4351.	1.6	11

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55	Thoracoscopic Wedge Resection Versus Segmentectomy for cT1N0 Lung Adenocarcinoma. Annals of Surgical Oncology, 2021, 28, 8398-8411.	0.7	11
56	Cost-sensitive performance metric for comparing multiple ordinal classifiers. Artificial Intelligence Research, 2015, 5, 135-143.	0.3	10
57	Development of a Gene-Based Prediction Model for Recurrence of Colorectal Cancer Using an Ensemble Learning Algorithm. Frontiers in Oncology, 2021, 11, 631056.	1.3	10
58	Regulatory Mechanisms and Functional Roles of Hypoxia-Induced Long Non-Coding RNA MTORT1 in Breast Cancer Cells. Frontiers in Oncology, 2021, 11, 663114.	1.3	10
59	EasyMAP: A user-friendly online platform for analyzing 16S ribosomal DNA sequencing data. New Biotechnology, 2021, 63, 37-44.	2.4	10
60	Elucidation of a Causal Relationship Between Platelet Count and Hypertension: A Bi-Directional Mendelian Randomization Study. Frontiers in Cardiovascular Medicine, 2021, 8, 743075.	1.1	10
61	Impact of Ancestral Differences and Reassessment of the Classification of Previously Reported Pathogenic Variants in Patients With Brugada Syndrome in the Genomic Era: A SADS-TW BrS Registry. Frontiers in Genetics, 2018, 9, 680.	1.1	9
62	Development of a prediction model for radiosensitivity using the expression values of genes and long non-coding RNAs. Oncotarget, 2016, 7, 26739-26750.	0.8	8
63	Genome-wide methylation profiles in coronary artery ectasia. Clinical Science, 2017, 131, 583-594.	1.8	8
64	High prevalence of APOA1/C3/A4/A5 alterations in luminal breast cancers among young women in East Asia. Npj Breast Cancer, 2021, 7, 88.	2.3	8
65	Population-Based Cohort Study Reveals Distinct Associations Between Female Lung Cancer and Breast Cancer in Taiwan. JCO Clinical Cancer Informatics, 2018, 2, 1-14.	1.0	7
66	VariED: the first integrated database of gene annotation and expression profiles for variants related to human diseases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	7
67	A new clinical-genomic model to predict 10-year recurrence risk in primary operable breast cancer patients. Scientific Reports, 2020, 10, 4861.	1.6	7
68	First-time offenders for recreational ketamine use under a new penalty system in Taiwan: incidence, recidivism and mortality in national cohorts from 2009 to 2017. Addiction, 2021, 116, 1770-1781.	1.7	7
69	Molecular subtyping of breast cancer intrinsic taxonomy with oligonucleotide microarray and NanoString nCounter. Bioscience Reports, 2021, 41, .	1.1	7
70	The impact of Taiwan's implementation of a nationwide harm reduction program in 2006 on the use of various illicit drugs: trend analysis of first-time offenders from 2001 to 2017. Harm Reduction Journal, 2021, 18, 117.	1.3	7
71	Probabilistic prioritization of candidate pathway association with pathway score. BMC Bioinformatics, 2018, 19, 391.	1.2	6
72	Text-mining in cancer research may help identify effective treatments. Translational Lung Cancer Research, 2019, 8, S460-S463.	1.3	6

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73	RNASeqR: An R Package for Automated Two-Group RNA-Seq Analysis Workflow. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2023-2031.	1.9	6
74	Association test using Copy Number Profile Curves (CONCUR) enhances power in rare copy number variant analysis. PLoS Computational Biology, 2020, 16, e1007797.	1.5	6
75	Loss of SFRP1 expression is a key progression event in gastrointestinal stromal tumor pathogenesis. Human Pathology, 2021, 107, 69-79.	1.1	6
76	Gene-set integrative analysis of multi-omics data using tensor-based association test. Bioinformatics, 2021, 37, 2259-2265.	1.8	6
77	Subgroup identification for treatment selection in biomarker adaptive design. BMC Medical Research Methodology, 2015, 15, 105.	1.4	5
78	Establishment of a New Ovarian Cancer Cell Line CA5171. Reproductive Sciences, 2015, 22, 725-734.	1.1	5
79	An evaluation of the 25 by 25 goal for premature cardiovascular disease mortality in Taiwan: an age-period-cohort analysis, population attributable fraction and national population-based study. Heart Asia, 2017, 9, e010905.	1.1	5
80	CNVIntegrate: the first multi-ethnic database for identifying copy number variations associated with cancer. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	5
81	Statin-induced microRNAome alterations modulating inflammation pathways of peripheral blood mononuclear cells in patients with hypercholesterolemia. Bioscience Reports, 2020, 40, .	1.1	5
82	Application of graphical lasso in estimating network structure in gene set. Annals of Translational Medicine, 2020, 8, 1556-1556.	0.7	5
83	Distinct Survival Outcomes in Subgroups of Stage III Pancreatic Cancer Patients: Taiwan Cancer Registry and Surveillance, Epidemiology and End Results registry. Annals of Surgical Oncology, 2021, , 1.	0.7	5
84	Thoracoscopic Lobectomy Versus Sublobar Resection for pStage I Geriatric Non-Small Cell Lung Cancer. Frontiers in Oncology, 2021, 11, 777590.	1.3	5
85	Primary Tumor Resection for Stage IV Non-small-cell Lung Cancer Without Progression After First-Line Epidermal Growth Factor Receptor-Tyrosine Kinase Inhibitor Treatment: A Retrospective Case–Control Study. Annals of Surgical Oncology, 2022, 29, 4873-4884.	0.7	5
86	Race-Specific Genetic Profiles of Homologous Recombination Deficiency in Multiple Cancers. Journal of Personalized Medicine, 2021, 11, 1287.	1.1	5
87	Comparisons and performance evaluations of RNA-seq alignment tools. , 2014, , .		4
88	Gene-set Analysis with CGI Information for Differential DNA Methylation Profiling. Scientific Reports, 2016, 6, 24666.	1.6	4
89	Translating Gene Signatures Into a Pathologic Feature: Tumor Necrosis Predicts Disease Relapse in Operable and Stage I Lung Adenocarcinoma. JCO Precision Oncology, 2018, 2, 1-13.	1.5	4
90	Using proteomic profiling to characterize protein signatures of different thymoma subtypes. BMC Cancer, 2019, 19, 796.	1.1	4

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91	Long-term outcomes and left ventricular diastolic function of sarcomere mutation-positive and mutation-negative patients with hypertrophic cardiomyopathy: a prospective cohort study. European Heart Journal Cardiovascular Imaging, 2020, , .	0.5	4
92	Predicting Colon Cancer-Specific Survival for the Asian Population Using National Cancer Registry Data from Taiwan. Annals of Surgical Oncology, 2022, 29, 853-863.	0.7	4
93	Incidence of chronic thromboembolic pulmonary hypertension in Taiwan. Journal of the Formosan Medical Association, 2021, 120, 1740-1748.	0.8	4
94	Residual risk stratification of Taiwanese breast cancers following curative therapies with the extended concurrent genes signature. Breast Cancer Research and Treatment, 2021, 186, 475-485.	1.1	4
95	Putative effectors for prognosis in lung adenocarcinoma are ethnic and gender specific. Oncotarget, 2015, 6, 19483-19499.	0.8	4
96	Develop and Apply Electrocardiography-Based Risk Score to Identify Community-Based Elderly Individuals at High-Risk of Mortality. Frontiers in Cardiovascular Medicine, 2021, 8, 738061.	1.1	4
97	A DNA Damage Response Gene Panel for Different Histologic Types of Epithelial Ovarian Carcinomas and Their Outcomes. Biomedicines, 2021, 9, 1384.	1.4	4
98	Mitochondrial DNA methylation profiling of the human prefrontal cortex and nucleus accumbens: correlations with aging and drug use. Clinical Epigenetics, 2022, 14, .	1.8	4
99	A Composite Model for Subgroup Identification and Prediction via Bicluster Analysis. PLoS ONE, 2014, 9, e111318.	1.1	3
100	Evolutionary Trajectories and Genomic Divergence in Localized Breast Cancers after Ipsilateral Breast Tumor Recurrence. Cancers, 2021, 13, 1821.	1.7	3
101	Pulmonary â€œInflammatory Leiomyosarcomasâ€•Are Indolent Tumors With Diploid Genomes and No Convincing Rhabdomyoblastic Differentiation. American Journal of Surgical Pathology, 2022, 46, 424-433.	2.1	3
102	Overcoming the challenges of imputation of rare variants in a Taiwanese cohort. Translational Cancer Research, 2020, 9, 4065-4069.	0.4	3
103	Novel Tumor-Specific Antigens for Immunotherapy Identified From Multi-omics Profiling in Thymic Carcinomas. Frontiers in Immunology, 2021, 12, 748820.	2.2	3
104	Lidocaine and Bupivacaine Downregulate MYB and DANCR lncRNA by Upregulating miR-187-5p in MCF-7 Cells. Frontiers in Medicine, 2021, 8, 732817.	1.2	3
105	Identification of drug-induced toxicity biomarkers for treatment determination. Pharmaceutical Statistics, 2015, 14, 284-293.	0.7	2
106	Utilizing gene expression profiles to characterize tumor infiltrating lymphocytes in cancers. Annals of Translational Medicine, 2019, 7, S289-S289.	0.7	2
107	Development of a semi-structured, multifaceted, computer-aided questionnaire for outbreak investigation: e-Outbreak Platform. Biomedical Journal, 2020, 43, 318-324.	1.4	2
108	Targeted Sequencing of Taiwanese Breast Cancer with Risk Stratification by the Concurrent Genes Signature: A Feasibility Study. Journal of Personalized Medicine, 2021, 11, 613.	1.1	2

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109	An Integrative Co-localization (INCO) Analysis for SNV and CNV Genomic Features With an Application to Taiwan Biobank Data. Frontiers in Genetics, 2021, 12, 709555.	1.1	2
110	Differential whole-genome doubling and homologous recombination deficiencies across breast cancer subtypes from the Taiwanese population. Communications Biology, 2021, 4, 1052.	2.0	2
111	MiDSystem: A comprehensive online system for de novo assembly and analysis of microbial genomes. New Biotechnology, 2021, 65, 42-52.	2.4	2
112	SEAGLE: A Scalable Exact Algorithm for Large-Scale Set-Based Gene-Environment Interaction Tests in Biobank Data. Frontiers in Genetics, 2021, 12, 710055.	1.1	2
113	Leveraging well-annotated databases for deep learning in biomedical research. Translational Cancer Research, 2020, 9, 7682-7684.	0.4	2
114	Non-Intubated Versus Intubated Video-Assisted Thoracic Surgery in Patients Aged 75 Years and Older: A Propensity Matching Study. Frontiers in Surgery, 2022, 9, 880007.	0.6	2
115	Concurrent analysis of copy number variations and expression profiles to identify genes associated with tumorigenesis and survival outcome in lung adenocarcinoma. , 2010, , .		1
116	Transcript annotation tool (TransAT): an R package for retrieving annotations for transcript-specific genetic variants. BMC Bioinformatics, 2021, 22, 350.	1.2	1
117	High-performance deep learning pipeline predicts individuals in mixtures of DNA using sequencing data. Briefings in Bioinformatics, 2021, 22, .	3.2	1
118	Fungal Spore Richness in School Classrooms is Related to Surrounding Forest in a Season-Dependent Manner. Microbial Ecology, 2022, 84, 351-362.	1.4	1
119	Abstract 4028: Identification of universal survival predictors in lung adenocarcinoma.. Cancer Research, 2013, 73, 4028-4028.	0.4	1
120	Prognostic value of a new clinical-genomic model to predict 10-year risk of recurrence in patients with operable breast cancer.. Journal of Clinical Oncology, 2019, 37, 530-530.	0.8	1
121	Recurrence risk stratification by Dutch clinical risk criteria for early-stage luminal breast cancer patients in Taiwan: A population-based analysis.. Journal of Clinical Oncology, 2020, 38, e12509-e12509.	0.8	1
122	Genome-Wide Association Study (GWAS) on Metabolic Syndrome in Subjects with Abdominal Obesity in a Taiwanese Population.. , 2020, , .		1
123	ASO Author Reflections: Identification of Prognostic Factors for Stage-III Pancreatic Ductal Adenocarcinoma patients.. Annals of Surgical Oncology, 2022, 29, 1616-1617.	0.7	1
124	The extended concurrent genes signature for disease-free survival in breast cancer. Journal of the Formosan Medical Association, 2022, , .	0.8	1
125	Concurrent analysis of copy number variation and gene expression: Application in paired non-smoking female lung cancer patients. , 2010, , .		0
126	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

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127	Biomarkers of susceptibility. , 2014, , 975-982.		0
128	MA03.03 High Risk for Second Primary Lung Cancer in Taiwanese Early-Onset Female Breast Cancer Patients. Journal of Thoracic Oncology, 2017, 12, S353-S354.	0.5	0
129	Abstract PS6-51: Identification of a low-risk luminal breast cancer cohort that may not benefit from multi-gene testing. , 2021, , .		0
130	ASO Visual Abstract: Thoracoscopic Wedge Resection Versus Segmentectomy for cT1N0 Lung Adenocarcinoma. Annals of Surgical Oncology, 2021, 28, 488-489.	0.7	0
131	Risk evaluation of early-stage hormone receptor-positive and human epidermal growth factor receptor 2-negative breast cancer patients: a population-based study from Taiwan. Breast Cancer Research and Treatment, 2021, 189, 807-815.	1.1	0
132	ASO Visual Abstract: Predicting Colon Cancer-Specific Survival for the Asian Population Using National Cancer Registry Data from Taiwan. Annals of Surgical Oncology, 2021, 28, 649-649.	0.7	0
133	ASO Author Reflections: Robust Prediction Models for Colon Cancer in Asian Patients. Annals of Surgical Oncology, 2022, 29, 864-865.	0.7	0
134	Abstract 2944: Genome-wide transcriptional modulation screening in non-smoking female lung cancer in Taiwan. , 2010, , .		0
135	Abstract 112: Concurrent analysis between copy number variation and gene expression of non-smoking lung cancer females in Taiwan. , 2010, , .		0
136	Abstract 2208: Overexpression of NDRG1 inhibits cell migration of breast cancer cells via reactive oxygen species during reoxygenation. , 2011, , .		0
137	Abstract 4852: Performances evaluation of algorithms for identifying differentially expressed genes in RNA-seq data. , 2015, , .		0
138	Low correlation of lncRNA and target gene expression in microarray data. Translational Cancer Research, 2016, 5, 160-168.	0.4	0
139	Abstract 2265: An integrated analysis of gene mutations and gene sets for predicting paclitaxel response in lung adenocarcinoma. , 2016, , .		0
140	Abstract 4490: Comparisons of genetic alterations of breast cancer between East and West: Special emphases on young patients with ER+/HER2- tumors. , 2016, , .		0
141	Abstract 5284: Characterizing the differences of allelic imbalance between tumor and normal tissues by next-generation sequencing. , 2016, , .		0
142	Abstract 1507: Investigation of estrogen receptor-modulated association between immune activities and patient survival in breast cancer. , 2016, , .		0
143	A 6-Lncrna Scoring System for Prognostication of Adult Myelodysplastic Syndromes. Blood, 2016, 128, 4344-4344.	0.6	0
144	Abstract 4017: Clinical-genomic models of node-positive breast cancer: training, testing, and validation. , 2019, , .		0

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145	ASO Visual Abstract: Distinct Survival Outcomes for Subgroups of Stage 3 Pancreatic Cancer Patients: Taiwan Cancer Registry and Surveillance, Epidemiology, and End Results Registry. Annals of Surgical Oncology, 2022, , 1.	0.7	0
146	Extracellular domain of semaphorin 5A serves a tumor‑suppressing role by activating interferon signaling pathways in lung adenocarcinoma cells. International Journal of Oncology, 2022, 60, .	1.4	0
147	Editorial: Current Status and Future Challenges of Biobank Data Analysis. Frontiers in Genetics, 2022, 13, 882611.	1.1	0
148	Abstract 4017: Clinical-genomic models of node-positive breast cancer: training, testing, and validation. , 2019, , .		0
149	ASO Visual Abstract: Primary Tumor Resection for Stage IV Non-Small-Cell Lung Cancer Without Progression After First-Line Epidermal Growth Factor Receptor-Tyrosine Kinase Inhibitor Treatment: A Retrospective Case-Control Study. Annals of Surgical Oncology, 2022, , .	0.7	0