Yu-Chiao Chiu

List of Publications by Citations

51 papers	**900** citations	**18** h-index	**29** g-index
63 ext. papers	**1,247** ext. citations	**5.8** avg, IF	**4.2** L-index

#	Paper	IF	Citations
51	miRSystem: an integrated system for characterizing enriched functions and pathways of microRNA targets. *PLoS ONE*, **2012**, 7, e42390	3.7	217
50	Predicting drug response of tumors from integrated genomic profiles by deep neural networks. *BMC Medical Genomics*, **2019**, 12, 18	3.7	71
49	Amplification of distant estrogen response elements deregulates target genes associated with tamoxifen resistance in breast cancer. *Cancer Cell*, **2013**, 24, 197-212	24.3	42
48	A 3-microRNA scoring system for prognostication in de novo acute myeloid leukemia patients. *Leukemia*, **2015**, 29, 1051-9	10.7	41
47	Convolutional neural network models for cancer type prediction based on gene expression. *BMC Medical Genomics*, **2020**, 13, 44	3.7	38
46	DNMT3L promotes quiescence in postnatal spermatogonial progenitor cells. *Development (Cambridge)*, **2014**, 141, 2402-13	6.6	32
45	An mRNA expression signature for prognostication in de novo acute myeloid leukemia patients with normal karyotype. *Oncotarget*, **2015**, 6, 39098-110	3.3	31
44	Parameter optimization for constructing competing endogenous RNA regulatory network in glioblastoma multiforme and other cancers. *BMC Genomics*, **2015**, 16 Suppl 4, S1	4.5	29
43	Prognostic impacts and dynamic changes of cohesin complex gene mutations in de novo acute myeloid leukemia. *Blood Cancer Journal*, **2017**, 7, 663	7	26
42	The distinct biological implications of Asxl1 mutation and its roles in leukemogenesis revealed by a knock-in mouse model. *Journal of Hematology and Oncology*, **2017**, 10, 139	22.4	24
41	MicroRNA-769-3p down-regulates NDRG1 and enhances apoptosis in MCF-7 cells during reoxygenation. *Scientific Reports*, **2014**, 4, 5908	4.9	24
40	GSAE: an autoencoder with embedded gene-set nodes for genomics functional characterization. *BMC Systems Biology*, **2018**, 12, 142	3.5	24
39	Prognostic significance of NPM1 mutation-modulated microRNA-mRNA regulation in acute myeloid leukemia. *Leukemia*, **2016**, 30, 274-84	10.7	21
38	GATA2 zinc finger 1 mutations are associated with distinct clinico-biological features and outcomes different from GATA2 zinc finger 2 mutations in adult acute myeloid leukemia. *Blood Cancer Journal*, **2018**, 8, 87	7	20
37	Higher HOPX expression is associated with distinct clinical and biological features and predicts poor prognosis in acute myeloid leukemia. *Haematologica*, **2017**, 102, 1044-1053	6.6	19
36	Gene regulation, modulation, and their applications in gene expression data analysis. *Advances in Bioinformatics*, **2013**, 2013, 360678	5.5	19
35	Deep learning of pharmacogenomics resources: moving towards precision oncology. *Briefings in Bioinformatics*, **2020**, 21, 2066-2083	13.4	19

34	Differential network analysis reveals the genome-wide landscape of estrogen receptor modulation in hormonal cancers. *Scientific Reports*, **2016**, 6, 23035	4.9	19
33	A knock-in Npm1 mutation in mice results in myeloproliferation and implies a perturbation in hematopoietic microenvironment. *PLoS ONE*, **2012**, 7, e49769	3.7	18
32	Incorporation of long non-coding RNA expression profile in the 2017 ELN risk classification can improve prognostic prediction of acute myeloid leukemia patients. *EBioMedicine*, **2019**, 40, 240-250	8.8	17
31	The prognostic significance of global aberrant alternative splicing in patients with myelodysplastic syndrome. *Blood Cancer Journal*, **2018**, 8, 78	7	15
30	Differential correlation analysis of glioblastoma reveals immune ceRNA interactions predictive of patient survival. *BMC Bioinformatics*, **2017**, 18, 132	3.6	13
29	High expression of () confers poor prognosis in acute myeloid leukemia. *Oncotarget*, **2017**, 8, 72250-72259	5.3	13
28	Classification of Cancer Types Using Graph Convolutional Neural Networks. *Frontiers in Physics*, **2020**, 8,	3.9	12
27	scdNet: a computational tool for single-cell differential network analysis. *BMC Systems Biology*, **2018**, 12, 124	3.5	10
26	A simple gene set-based method accurately predicts the synergy of drug pairs. *BMC Systems Biology*, **2016**, 10 Suppl 3, 66	3.5	8
25	Knock-out of Hopx disrupts stemness and quiescence of hematopoietic stem cells in mice. *Oncogene*, **2020**, 39, 5112-5123	9.2	7
24	CeL-ID: cell line identification using RNA-seq data. *BMC Genomics*, **2019**, 20, 81	4.5	6
23	Predicting sites of epitranscriptome modifications using unsupervised representation learning based on generative adversarial networks. *Frontiers in Physics*, **2020**, 8,	3.9	6
22	GDF6-CD99 Signaling Regulates Src and Ewing Sarcoma Growth. *Cell Reports*, **2020**, 33, 108332	10.6	5
21	Identification of genes differentially expressed during the growth of Bambusa oldhamii. *Plant Physiology and Biochemistry*, **2013**, 63, 217-26	5.4	5
20	Modeling competing endogenous RNA regulatory networks in glioblastoma multiforme **2013**,		5
19	Prediction and interpretation of cancer survival using graph convolution neural networks. *Methods*, **2021**, 192, 120-130	4.6	5
18	Integrating resistance functions to predict response to induction chemotherapy in de novo acute myeloid leukemia. *European Journal of Haematology*, **2019**, 103, 417-425	3.8	4
17	Co-modulation analysis of gene regulation in breast cancer reveals complex interplay between ESR1 and ERBB2 genes. *BMC Genomics*, **2015**, 16 Suppl 7, S19	4.5	4

16	An ancestry informative marker panel design for individual ancestry estimation of Hispanic population using whole exome sequencing data. *BMC Genomics*, **2019**, 20, 1007	4.5	4
15	CancerSiamese: one-shot learning for predicting primary and metastatic tumor types unseen during model training. *BMC Bioinformatics*, **2021**, 22, 244	3.6	3
14	Predicting and characterizing a cancer dependency map of tumors with deep learning. *Science Advances*, **2021**, 7,	14.3	3
13	Genome-wide identification of key modulators of gene-gene interaction networks in breast cancer. *BMC Genomics*, **2017**, 18, 679	4.5	2
12	Analyzing Differential Regulatory Networks Modulated by Continuous-State Genomic Features in Glioblastoma Multiforme. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2018**, 15, 1754-1764	3	2
11	Androgen deprivation-induced elevated nuclear SIRT1 promotes prostate tumor cell survival by reactivation of AR signaling. *Cancer Letters*, **2021**, 505, 24-36	9.9	2
10	Analyzing differential regulatory networks modulated by continuous-state genomic features in glioblastoma multiforme **2015**,		1
9	Clinical and Prognostic Relevance of Expression of Homeodomain-Only Protein Homeobox (HOPX) in Acute Myeloid Leukemia. *Blood*, **2013**, 122, 3776-3776	2.2	1
8	CancerSiamese: one-shot learning for predicting primary and metastatic tumor types unseen during model training		1
7	Assessing the Heterogeneity of Cardiac Non-myocytes and the Effect of Cell Culture with Integrative Single Cell Analysis		1
6	Utilizing Cancer - Functional Gene Set - Compound Networks to Identify Putative Drugs for Breast Cancer. *Combinatorial Chemistry and High Throughput Screening*, **2018**, 21, 74-83	1.3	
5	The Clinical and Biological Implications of Early Clearance of Peripheral Blood Blasts after Induction Chemotherapy in Acute Myeloid Leukemia. *Blood*, **2018**, 132, 3991-3991	2.2	
4	Multi-omics analysis reveals the mutation and mismatch repair gene signatures associated with survival, protein expression, and copy number alterations in prostate cancer.. *Translational Cancer Research*, **2019**, 8, 1279-1288	0.3	
3	A Simple, Powerful, and Widely Applicable Micro-RNA Scoring System in Prognostication of De Novo Myeloid Leukemia Patients. *Blood*, **2014**, 124, 71-71	2.2	
2	The Clinical and Biological Characterization of De Novo Acute Myeloid Leukemia (AML) with GATA2 Mutation. *Blood*, **2015**, 126, 3822-3822	2.2	
1	Aberrant Patterns of Alternative Splicing Are Frequent Events and Harbor Prognostic Significance in Patients with Myelodysplastic Syndrome. *Blood*, **2016**, 128, 49-49	2.2	