Hsueh-Fen Juan

List of Publications by Year in Descending Order

142 papers	7,231 citations	34 h-index	83 g-index
152 ext. papers	8,327 ext. citations	6.1 avg, IF	5.11 L-index

#	Paper	IF	Citations
142	Single-cell RNA sequencing uncovers the individual alteration of intestinal mucosal immunocytes in knockout mice.. *IScience*, **2022**, 25, 103738	6.1	
141	Quantitative phosphoproteomics reveals ectopic ATP synthase on mesenchymal stem cells to promote tumor progression via ERK/c-Fos pathway activation.. *Molecular and Cellular Proteomics*, **2022**, 100237	7.6	0
140	A Single-Cell Network-Based Drug Repositioning Strategy for Post-COVID-19 Pulmonary Fibrosis. *Pharmaceutics*, **2022**, 14, 971	6.4	0
139	Stratification of lncRNA modulation networks in breast cancer.. *BMC Medical Genomics*, **2022**, 14, 300	3.7	
138	Identification of cell states using super-enhancer RNA. *BMC Genomics*, **2021**, 22, 787	4.5	
137	Targeting protein interaction networks in mitochondrial dynamics for cancer therapy. *Drug Discovery Today*, **2021**,	8.8	2
136	Identification of a gut microbiota member that ameliorates DSS-induced colitis in intestinal barrier enhanced Dusp6-deficient mice. *Cell Reports*, **2021**, 37, 110016	10.6	3
135	Connecting MHC-I-binding motifs with HLA alleles via deep learning. *Communications Biology*, **2021**, 4, 1194	6.7	2
134	Inhibitor development of MTH1 via high-throughput screening with fragment based library and MTH1 substrate binding cavity. *Bioorganic Chemistry*, **2021**, 110, 104813	5.1	1
133	Proteomic Analysis Reveals That Metformin Suppresses PSMD2, STIP1, and CAP1 for Preventing Gastric Cancer AGS Cell Proliferation and Migration. *ACS Omega*, **2021**, 6, 14208-14219	3.9	1
132	Loss of Fis1 impairs proteostasis during skeletal muscle aging in Drosophila. *Aging Cell*, **2021**, 20, e13379	9.9	1
131	DockCoV2: a drug database against SARS-CoV-2. *Nucleic Acids Research*, **2021**, 49, D1152-D1159	20.1	17
130	LncTx: A network-based method to repurpose drugs acting on the survival-related lncRNAs in lung cancer. *Computational and Structural Biotechnology Journal*, **2021**, 19, 3990-4002	6.8	1
129	Modular signature of long non-coding RNA association networks as a prognostic biomarker in lung cancer. *BMC Medical Genomics*, **2021**, 14, 290	3.7	1
128	BI-2536 Promotes Neuroblastoma Cell Death via Minichromosome Maintenance Complex Components 2 and 10.. *Pharmaceuticals*, **2021**, 15,	5.2	2
127	Enhancement of the IFN-βInduced host signature informs repurposed drugs for COVID-19. *Heliyon*, **2020**, 6, e05646	3.6	7
126	Phosphoproteome Analysis Reveals Dynamic Heat Shock Protein 27 Phosphorylation in Tanshinone IIA-Induced Cell Death. *Journal of Proteome Research*, **2020**, 19, 1620-1634	5.6	6

125	Quantitative Phosphoproteomics Reveals Cell Alignment and Mitochondrial Length Change under Cyclic Stretching in Lung Cells. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	3
124	ZNF322A-mediated protein phosphorylation induces autophagosome formation through modulation of IRS1-AKT glucose uptake and HSP-elicited UPR in lung cancer. *Journal of Biomedical Science*, **2020**, 27, 75	13.3	3
123	C1GALT1 is associated with poor survival and promotes soluble Ephrin A1-mediated cell migration through activation of EPHA2 in gastric cancer. *Oncogene*, **2020**, 39, 2724-2740	9.2	10
122	Characterizing the cancer-associated microbiome with small RNA sequencing data. *Biochemical and Biophysical Research Communications*, **2020**, 522, 776-782	3.4	3
121	Multiomics Reveals Ectopic ATP Synthase Blockade Induces Cancer Cell Death via a lncRNA-mediated Phospho-signaling Network. *Molecular and Cellular Proteomics*, **2020**, 19, 1805-1825	7.6	5
120	Multiresolution Imaging Using Bioluminescence Resonance Energy Transfer Identifies Distinct Biodistribution Profiles of Extracellular Vesicles and Exomeres with Redirected Tropism. *Advanced Science*, **2020**, 7, 2001467	13.6	24
119	Quantitative Proteomics of Th-MYCN Transgenic Mice Reveals Aurora Kinase Inhibitor Altered Metabolic Pathways and Enhanced ACADM To Suppress Neuroblastoma Progression. *Journal of Proteome Research*, **2019**, 18, 3850-3866	5.6	5
118	Perturbational Gene-Expression Signatures for Combinatorial Drug Discovery. *IScience*, **2019**, 15, 291-306.	6.1	16
117	Proteomic Techniques and Their Applications **2019**, 81-99		0
116	Therapeutic Targeting of Non-oncogene Dependencies in High-risk Neuroblastoma. *Clinical Cancer Research*, **2019**, 25, 4063-4078	12.9	10
115	Combinatorial targeting of MTHFD2 and PAICS in purine synthesis as a novel therapeutic strategy. *Cell Death and Disease*, **2019**, 10, 786	9.8	7
114	Activation of Aryl Hydrocarbon Receptor by Kynurenine Impairs Progression and Metastasis of Neuroblastoma. *Cancer Research*, **2019**, 79, 5550-5562	10.1	18
113	Investigating the role of super-enhancer RNAs underlying embryonic stem cell differentiation. *BMC Genomics*, **2019**, 20, 896	4.5	9
112	RNA-Binding Proteomics Reveals MATR3 Interacting with lncRNA SNHG1 To Enhance Neuroblastoma Progression. *Journal of Proteome Research*, **2019**, 18, 406-416	5.6	14
111	Introduction to Cancer Systems Biology **2018**, 1-9		
110	High-risk, Expression-Based Prognostic Long Noncoding RNA Signature in Neuroblastoma. *JNCI Cancer Spectrum*, **2018**, 2, pky015	4.6	12
109	C1GALT1 predicts poor prognosis and is a potential therapeutic target in head and neck cancer. *Oncogene*, **2018**, 37, 5780-5793	9.2	24
108	Transcriptome Analysis: Library Construction **2018**, 11-22		

107	Quantitative Proteome: The Isobaric Tags for Relative and Absolute Quantitation (iTRAQ) **2018**, 23-37		
106	Phosphoproteome: Sample Preparation **2018**, 39-48		
105	Proteomic Data Analysis: Functional Enrichment **2018**, 63-74		
104	Pathway and Network Analysis **2018**, 91-102		
103	Docking Simulation **2018**, 129-143		
102	A Large-Scale Gene Expression Intensity-Based Similarity Metric for Drug Repositioning. *IScience*, **2018**, 7, 40-52	6.1	8
101	Dynamics of alternative polyadenylation in human preimplantation embryos. *Biochemical and Biophysical Research Communications*, **2018**, 504, 727-733	3.4	3
100	MCM2-regulated functional networks in lung cancer by multi-dimensional proteomic approach. *Scientific Reports*, **2017**, 7, 13302	4.9	23
99	Cdc7-Dbf4-mediated phosphorylation of HSP90-S164 stabilizes HSP90-HCLK2-MRN complex to enhance ATR/ATM signaling that overcomes replication stress in cancer. *Scientific Reports*, **2017**, 7, 17024	4.9	12
98	DynaPho: a web platform for inferring the dynamics of time-series phosphoproteomics. *Bioinformatics*, **2017**, 33, 3664-3666	7.2	7
97	Quantitative proteomics in lung cancer. *Journal of Biomedical Science*, **2017**, 24, 37	13.3	54
96	3'UTR polymorphisms of carbonic anhydrase IX determine the miR-34a targeting efficiency and prognosis of hepatocellular carcinoma. *Scientific Reports*, **2017**, 7, 4466	4.9	37
95	GALNT6 expression enhances aggressive phenotypes of ovarian cancer cells by regulating EGFR activity. *Oncotarget*, **2017**, 8, 42588-42601	3.3	23
94	Identification of lncRNA functions in lung cancer based on associated protein-protein interaction modules. *Scientific Reports*, **2016**, 6, 35939	4.9	16
93	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). *Autophagy*, **2016**, 12, 1-222	10.2	3838
92	Novel Utilization of Terminators in the Design of Biologically Adjustable Synthetic Filters. *ACS Synthetic Biology*, **2016**, 5, 365-74	5.7	8
91	Co-expression analysis identifies long noncoding RNA SNHG1 as a novel predictor for event-free survival in neuroblastoma. *Oncotarget*, **2016**, 7, 58022-58037	3.3	49
90	Unveiling MYCN regulatory networks in neuroblastoma via integrative analysis of heterogeneous genomics data. *Oncotarget*, **2016**, 7, 36293-36310	3.3	26

89	Mucin glycosylating enzyme GALNT2 suppresses malignancy in gastric adenocarcinoma by reducing MET phosphorylation. *Oncotarget*, **2016**, 7, 11251-62	3.3	28
88	Integrating transcriptomics and proteomics to show that tanshinone IIA suppresses cell growth by blocking glucose metabolism in gastric cancer cells. *BMC Genomics*, **2015**, 16, 41	4.5	29
87	Circadian systems biology in Metazoa. *Briefings in Bioinformatics*, **2015**, 16, 1008-24	13.4	2
86	Integrating Phosphoproteomics and Bioinformatics to Study Brassinosteroid-Regulated Phosphorylation Dynamics in Arabidopsis. *BMC Genomics*, **2015**, 16, 533	4.5	36
85	Functional Analysis and Characterization of Differential Coexpression Networks. *Scientific Reports*, **2015**, 5, 13295	4.9	39
84	Knockdown of GALNT1 suppresses malignant phenotype of hepatocellular carcinoma by suppressing EGFR signaling. *Oncotarget*, **2015**, 6, 5650-65	3.3	34
83	Temporal Phosphoproteome Dynamics Induced by an ATP Synthase Inhibitor Citreoviridin. *Molecular and Cellular Proteomics*, **2015**, 14, 3284-98	7.6	15
82	Quantitative proteomics reveals middle infrared radiation-interfered networks in breast cancer cells. *Journal of Proteome Research*, **2015**, 14, 1250-62	5.6	9
81	Dissecting the human protein-protein interaction network via phylogenetic decomposition. *Scientific Reports*, **2014**, 4, 7153	4.9	18
80	MicroRNA-mediated networks underlie immune response regulation in papillary thyroid carcinoma. *Scientific Reports*, **2014**, 4, 6495	4.9	23
79	Deciphering molecular determinants of chemotherapy in gastrointestinal malignancy using systems biology approaches. *Drug Discovery Today*, **2014**, 19, 1402-9	8.8	6
78	Mirin: identifying microRNA regulatory modules in protein-protein interaction networks. *Bioinformatics*, **2014**, 30, 2527-8	7.2	6
77	A histone deacetylase inhibitor YCW1 with antitumor and antimetastasis properties enhances cisplatin activity against non-small cell lung cancer in preclinical studies. *Cancer Letters*, **2014**, 346, 84-93	9.9	17
76	Aryl hydrocarbon receptor downregulates MYCN expression and promotes cell differentiation of neuroblastoma. *PLoS ONE*, **2014**, 9, e88795	3.7	22
75	Predicting the severity and prognosis of trismus after intensity-modulated radiation therapy for oral cancer patients by magnetic resonance imaging. *PLoS ONE*, **2014**, 9, e92561	3.7	16
74	FBXO7 Y52C polymorphism as a potential protective factor in Parkinson's disease. *PLoS ONE*, **2014**, 9, e101392	3.7	8
73	Identification of microRNA 395a in 24-epibrassinolide-regulated root growth of Arabidopsis thaliana using microRNA arrays. *International Journal of Molecular Sciences*, **2013**, 14, 14270-86	6.3	11
72	Quantitative proteomics reveals diverse roles of miR-148a from gastric cancer progression to neurological development. *Journal of Proteome Research*, **2013**, 12, 3993-4004	5.6	16

71	MicroRNA-regulated protein-protein interaction networks and their functions in breast cancer. *International Journal of Molecular Sciences*, **2013**, 14, 11560-606	6.3	49
70	ValidNESs: a database of validated leucine-rich nuclear export signals. *Nucleic Acids Research*, **2013**, 41, D338-43	20.1	58
69	Middle infrared radiation induces G2/M cell cycle arrest in A549 lung cancer cells. *PLoS ONE*, **2013**, 8, e54117	3.7	22
68	Differential microRNA regulation correlates with alternative polyadenylation pattern between breast cancer and normal cells. *PLoS ONE*, **2013**, 8, e56958	3.7	20
67	Quantitative proteomic analysis of human lung tumor xenografts treated with the ectopic ATP synthase inhibitor citreoviridin. *PLoS ONE*, **2013**, 8, e70642	3.7	19
66	Link clustering reveals structural characteristics and biological contexts in signed molecular networks. *PLoS ONE*, **2013**, 8, e67089	3.7	7
65	Discovering Drug Targets for Cancer Therapy **2012**, 299-322		
64	MicroRNA Regulation in Cellular Networks **2012**, 35-46		
63	Disease Modules in Protein–Protein Interaction Networks **2012**, 47-54		
62	Discovery of biomarkers for gastric cancer: a proteomics approach. *Journal of Proteomics*, **2012**, 75, 3081-97	3.9	71
61	Crosstalk between transcription factors and microRNAs in human protein interaction network. *BMC Systems Biology*, **2012**, 6, 18	3.5	43
60	Helicobacter pylori disrupts host cell membranes, initiating a repair response and cell proliferation. *International Journal of Molecular Sciences*, **2012**, 13, 10176-92	6.3	14
59	Phosphoproteomic analysis of Rhodopseudomonas palustris reveals the role of pyruvate phosphate dikinase phosphorylation in lipid production. *Journal of Proteome Research*, **2012**, 11, 5362-75	5.6	27
58	Combination of RGD compound and low-dose paclitaxel induces apoptosis in human glioblastoma cells. *PLoS ONE*, **2012**, 7, e37935	3.7	8
57	Calreticulin mediates nerve growth factor-induced neuronal differentiation. *Journal of Molecular Neuroscience*, **2012**, 47, 571-81	3.3	13
56	Corrigendum to Silencing of miR-124 induces neuroblastoma SK-N-SH cell differentiation, cell cycle arrest and apoptosis through promoting AHR [FEBS Lett. 585 (2011) 3582–3586]. *FEBS Letters*, **2012**, 586, 107-107	3.8	
55	Systems biology of meridians, acupoints, and chinese herbs in disease. *Evidence-based Complementary and Alternative Medicine*, **2012**, 2012, 372670	2.3	14
54	Revealing the anti-tumor effect of artificial miRNA p-27-5p on human breast carcinoma cell line T-47D. *International Journal of Molecular Sciences*, **2012**, 13, 6352-69	6.3	4

53	Revealing the molecular mechanism of gastric cancer marker annexin A4 in cancer cell proliferation using exon arrays. *PLoS ONE*, **2012**, 7, e44615	3.7	27
52	Ectopic ATP synthase blockade suppresses lung adenocarcinoma growth by activating the unfolded protein response. *Cancer Research*, **2012**, 72, 4696-706	10.1	57
51	Profiling lipid-protein interactions using nonquenched fluorescent liposomal nanovesicles and proteome microarrays. *Molecular and Cellular Proteomics*, **2012**, 11, 1177-90	7.6	29
50	Introduction to Systems Biology **2012**, 3-16		
49	Lengthening of 3'UTR increases with morphological complexity in animal evolution. *Bioinformatics*, **2012**, 28, 3178-81	7.2	31
48	Gene Network Construction for Molecular Regulation **2012**, 17-33		
47	Systems Biology **2012**,		2
46	Identification of 14-3-3⬚in human gastric cancer cells and its potency as a diagnostic and prognostic biomarker. *Proteomics*, **2011**, 11, 2423-39	4.8	34
45	Revealing the functions of the transketolase enzyme isoforms in Rhodopseudomonas palustris using a systems biology approach. *PLoS ONE*, **2011**, 6, e28329	3.7	9
44	Insulin-like growth factor II mRNA-binding protein 3 expression predicts unfavorable prognosis in patients with neuroblastoma. *Cancer Science*, **2011**, 102, 2191-8	6.9	21
43	Silencing of miR-124 induces neuroblastoma SK-N-SH cell differentiation, cell cycle arrest and apoptosis through promoting AHR. *FEBS Letters*, **2011**, 585, 3582-6	3.8	59
42	Integrative network analysis reveals active microRNAs and their functions in gastric cancer. *BMC Systems Biology*, **2011**, 5, 99	3.5	69
41	Coregulation of transcription factors and microRNAs in human transcriptional regulatory network. *BMC Bioinformatics*, **2011**, 12 Suppl 1, S41	3.6	62
40	ATP13A2 variability in Taiwanese Parkinson's disease. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2011**, 156B, 720-9	3.5	17
39	The effect of narrow bandwidth infrared radiation on the growth of Escherichia coli. *Applied Physics Letters*, **2011**, 99, 163704	3.4	7
38	A novel sialyltransferase inhibitor suppresses FAK/paxillin signaling and cancer angiogenesis and metastasis pathways. *Cancer Research*, **2011**, 71, 473-83	10.1	85
37	Reviewing ligand-based rational drug design: the search for an ATP synthase inhibitor. *International Journal of Molecular Sciences*, **2011**, 12, 5304-18	6.3	39
36	Ganoderma lucidum Polysaccharides Induce Macrophage-Like Differentiation in Human Leukemia THP-1 Cells via Caspase and p53 Activation. *Evidence-based Complementary and Alternative Medicine*, **2011**, 2011, 358717	2.3	29

35	Notch1 expression predicts an unfavorable prognosis and serves as a therapeutic target of patients with neuroblastoma. *Clinical Cancer Research*, **2010**, 16, 4411-20	12.9	35
34	Dynamic functional modules in co-expressed protein interaction networks of dilated cardiomyopathy. *BMC Systems Biology*, **2010**, 4, 138	3.5	36
33	Essential core of protein-protein interaction network in Escherichia coli. *Journal of Proteome Research*, **2009**, 8, 1925-31	5.6	27
32	Predicting essential genes based on network and sequence analysis. *Molecular BioSystems*, **2009**, 5, 1672-8		83
31	MeInfoText: associated gene methylation and cancer information from text mining. *BMC Bioinformatics*, **2008**, 9, 22	3.6	28
30	TCMGeneDIT: a database for associated traditional Chinese medicine, gene and disease information using text mining. *BMC Complementary and Alternative Medicine*, **2008**, 8, 58	4.7	83
29	Breast tumor microenvironment: proteomics highlights the treatments targeting secretome. *Journal of Proteome Research*, **2008**, 7, 1379-87	5.6	49
28	Targeting therapy for breast carcinoma by ATP synthase inhibitor aurovertin B. *Journal of Proteome Research*, **2008**, 7, 1433-44	5.6	87
27	Prediction of human miRNAs using tissue-selective motifs in 3' UTRs. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 17061-6	11.5	12
26	Identification of GRP75 as an independent favorable prognostic marker of neuroblastoma by a proteomics analysis. *Clinical Cancer Research*, **2008**, 14, 6237-45	12.9	26
25	Cytotoxicity and proteomics analyses of OSU03013 in lung cancer. *Clinical Cancer Research*, **2008**, 14, 1823-30	12.9	11
24	Characterization of microRNA-regulated protein-protein interaction network. *Proteomics*, **2008**, 8, 1975-9	4.8	92
23	Annexin A4: A novel molecular marker for gastric cancer with Helicobacter pylori infection using proteomics approach. *Proteomics - Clinical Applications*, **2008**, 2, 619-34	3.1	39
22	Comparative analysis of differentially expressed genes in normal and white spot syndrome virus infected Penaeus monodon. *BMC Genomics*, **2007**, 8, 120	4.5	92
21	Ganoderma lucidum polysaccharides in human monocytic leukemia cells: from gene expression to network construction. *BMC Genomics*, **2007**, 8, 411	4.5	47
20	An apoptosis-related gene network induced by novel compound-cRGD in human breast cancer cells. *FEBS Letters*, **2007**, 581, 3517-22	3.8	10
19	Bioinformatics: microarray data clustering and functional classification. *Methods in Molecular Biology*, **2007**, 382, 405-16	1.4	21
18	RINGdb: an integrated database for G protein-coupled receptors and regulators of G protein signaling. *BMC Genomics*, **2006**, 7, 317	4.5	3

List of Publications

17	An agent-based system to discover protein-protein interactions, identify protein complexes and proteins with multiple peptide mass fingerprints. *Journal of Computational Chemistry*, **2006**, 27, 1020-32[3.5]		2
16	Quantitative proteomic and genomic profiling reveals metastasis-related protein expression patterns in gastric cancer cells. *Journal of Proteome Research*, **2006**, 5, 2727-42	5.6	68
15	Proteomics analysis of a novel compound: cyclic RGD in breast carcinoma cell line MCF-7. *Proteomics*, **2006**, 6, 2991-3000	4.8	18
14	Lipopolysaccharide-stimulated responses in rat aortic endothelial cells by a systems biology approach. *Proteomics*, **2006**, 6, 5915-28	4.8	16
13	A proteomics study of the mung bean epicotyl regulated by brassinosteroids under conditions of chilling stress. *Cellular and Molecular Biology Letters*, **2006**, 11, 264-78	8.1	40
12	MultiProtIdent: identifying proteins using database search and protein-protein interactions. *Journal of Proteome Research*, **2005**, 4, 690-7	5.6	1
11	A new application of microwave technology to proteomics. *Proteomics*, **2005**, 5, 840-2	4.8	90
10	GeneNetwork: an interactive tool for reconstruction of genetic networks using microarray data. *Bioinformatics*, **2004**, 20, 3691-3	7.2	50
9	ProteMiner-SSM: a web server for efficient analysis of similar protein tertiary substructures. *Nucleic Acids Research*, **2004**, 32, W76-82	20.1	14
8	Small molecules targeting severe acute respiratory syndrome human coronavirus. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 10012-7	11.5	368
7	Immunomodulatory effect of decoy receptor 3 on the differentiation and function of bone marrow-derived dendritic cells in nonobese diabetic mice: from regulatory mechanism to clinical implication. *Journal of Leukocyte Biology*, **2004**, 75, 293-306	6.5	28
6	Identification of tumor-associated plasma biomarkers using proteomic techniques: from mouse to human. *Proteomics*, **2004**, 4, 2766-75	4.8	76
5	Incremental generation of summarized clustering hierarchy for protein family analysis. *Bioinformatics*, **2004**, 20, 2586-96	7.2	3
4	Biomic study of human myeloid leukemia cells differentiation to macrophages using DNA array, proteomic, and bioinformatic analytical methods. *Electrophoresis*, **2002**, 23, 2490-504	3.6	54
3	Bioinformatics, functional genomics, and proteomics study of Bacillus sp. *Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences*, **2002**, 771, 261-87	3.2	19
2	Comparison of three classes of snake neurotoxins by homology modeling and computer simulation graphics. *Biochemical and Biophysical Research Communications*, **1999**, 257, 500-10	3.4	9
1	Identification of Cell States Using Super-Enhancer RNA		1