Tai-Chung Huang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3173747/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Polatuzumab vedotin–based salvage immunochemotherapy as third-line or beyond treatment for patients with diffuse large B-cell lymphoma: a real-world experience. Annals of Hematology, 2022, 101, 349-358.	1.8	12
2	Investigating early progression of Hodgkin lymphoma in a two-center analysis. Journal of the Formosan Medical Association, 2022, , .	1.7	2
3	Epigenetic modulation of immune synaptic-cytoskeletal networks potentiates γδT cell-mediated cytotoxicity in lung cancer. Nature Communications, 2021, 12, 2163.	12.8	16
4	Safety, Feasibility, and Effects of Short-Term Calorie Reduction during Induction Chemotherapy in Patients with Diffuse Large B-Cell Lymphoma: A Pilot Study. Nutrients, 2021, 13, 3268.	4.1	6
5	A Clinicopathological Study of Cytomegalovirus Lymphadenitis and Tonsillitis and Their Association with Epstein–Barr Virus. Infectious Diseases and Therapy, 2021, 10, 2661-2675.	4.0	4
6	ASXL1 mutation confers poor prognosis in primary myelofibrosis patients with low JAK2V617F allele burden but not in those with high allele burden. Blood Cancer Journal, 2020, 10, 99.	6.2	5
7	Feasibility, Process, and Effects of Short-Term Calorie Reduction in Cancer Patients Receiving Chemotherapy: An Integrative Review. Nutrients, 2020, 12, 2823.	4.1	1
8	Correlative analysis of overall survival with clinical characteristics in 127 patients with mantle cell lymphoma: a multi-institutional cohort in Taiwan. International Journal of Hematology, 2020, 112, 385-394.	1.6	2
9	Next-Generation Sequencing Minimal Residual Disease of Mantle Cell Lymphoma in Autologous Stem Cell Grafts and Its Implication on Tumor Recurrence. Blood, 2020, 136, 22-23.	1.4	0
10	Clonal sequence tracking reveals TET2-mutated extranodal NK/T-cell lymphoma disseminated independent of Epstein Barr virus. Haematologica, 2019, 104, e489-e492.	3.5	1
11	Clinically validated machine learning algorithm for detecting residual diseases with multicolor flow cytometry analysis in acute myeloid leukemia and myelodysplastic syndrome. EBioMedicine, 2018, 37, 91-100.	6.1	54
12	Human adenine nucleotide translocases physically and functionally interact with respirasomes. Molecular Biology of the Cell, 2017, 28, 1489-1506.	2.1	37
13	A multi-omic analysis of human naÃ⁻ve CD4+ T cells. BMC Systems Biology, 2015, 9, 75.	3.0	43
14	Inhibition of Spleen Tyrosine Kinase Potentiates Paclitaxel-Induced Cytotoxicity in Ovarian Cancer Cells by Stabilizing Microtubules. Cancer Cell, 2015, 28, 82-96.	16.8	125
15	Ablation of Dicer leads to widespread perturbation of signaling pathways. Biochemical and Biophysical Research Communications, 2015, 463, 389-394.	2.1	7
16	Integrated analysis of CRLF2 signaling in acute lymphoblastic leukemia identifies Polo-like kinase 1 as a potential therapeutic target. Leukemia and Lymphoma, 2015, 56, 1524-1527.	1.3	2
17	Identification of miR-145 targets through an integrated omics analysis. Molecular BioSystems, 2015, 11, 197-207.	2.9	21
18	Differential Signaling through p190 and p210 Forms of BCR-ABL Fusion Proteins Revealed By Proteomic Analysis. Blood, 2015, 126, 3651-3651.	1.4	1

TAI-CHUNG HUANG

#	Article	IF	CITATIONS
19	Phosphoproteomic Profiling Reveals Epstein-Barr Virus Protein Kinase Integration of DNA Damage Response and Mitotic Signaling. PLoS Pathogens, 2015, 11, e1005346.	4.7	53
20	TSLP signaling pathway map: a platform for analysis of TSLP-mediated signaling. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau007-bau007.	3.0	71
21	A draft map of the human proteome. Nature, 2014, 509, 575-581.	27.8	1,948
22	Annotation of the Zebrafish Genome through an Integrated Transcriptomic and Proteomic Analysis. Molecular and Cellular Proteomics, 2014, 13, 3184-3198.	3.8	52
23	Regulation of PPAR-alpha pathway by Dicer revealed through proteomic analysis. Journal of Proteomics, 2014, 108, 306-315.	2.4	15
24	Identification of targets of miR-200b by a SILAC-based quantitative proteomic approach. EuPA Open Proteomics, 2014, 4, 10-17.	2.5	1
25	Proteomics for understanding miRNA biology. Proteomics, 2013, 13, 558-567.	2.2	21
26	The role of cardiolipin in defining the mammalian ANT interactome. FASEB Journal, 2013, 27, 1026.3.	0.5	0
27	TSLP Signaling Network Revealed by SILAC-Based Phosphoproteomics. Molecular and Cellular Proteomics, 2012, 11, M112.017764.	3.8	47
28	Regulation of Lipid Metabolism by Dicer Revealed through SILAC Mice. Journal of Proteome Research, 2012, 11, 2193-2205.	3.7	26
29	WT1 mutation in 470 adult patients with acute myeloid leukemia: stability during disease evolution and implication of its incorporation into a survival scoring system. Blood, 2010, 115, 5222-5231.	1.4	156
30	Identifying targets of miR-143 using a SILAC-based proteomic approach. Molecular BioSystems, 2010, 6, 1873.	2.9	58
31	Bone Marrow Hypoplasia Induced by Conditional Knockout of the RNase III Domain of Dicer-1. Blood, 2010, 116, 2226-2226.	1.4	0
32	Comparison of hypoplastic myelodysplastic syndrome (MDS) with normo-/hypercellular MDS by International Prognostic Scoring System, cytogenetic and genetic studies. Leukemia, 2008, 22, 544-550.	7.2	53
33	Hypotensive spinal cord infarction associated with vertebral body infarction after treatment with short-acting antihypertensive agent. Journal of the Formosan Medical Association, 2005, 104, 607-10.	1.7	4