

# Kuan-lin Huang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5046859/publications.pdf>

Version: 2024-02-01

55  
papers

6,153  
citations

361413

20  
h-index

223800

46  
g-index

68  
all docs

68  
docs citations

68  
times ranked

13801  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	27.8	1,966
2	Proteogenomics connects somatic mutations to signalling in breast cancer. <i>Nature</i> , 2016, 534, 55-62.	27.8	1,384
3	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	28.9	620
4	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. <i>Nature Neuroscience</i> , 2017, 20, 1052-1061.	14.8	330
5	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	28.9	272
6	Patterns and functional implications of rare germline variants across 12 cancer types. <i>Nature Communications</i> , 2015, 6, 10086.	12.8	243
7	Genome-wide association study identifies four novel loci associated with Alzheimer's endophenotypes and disease modifiers. <i>Acta Neuropathologica</i> , 2017, 133, 839-856.	7.7	199
8	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020, 37, 639-654.e6.	16.8	151
9	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. <i>Nature Communications</i> , 2017, 8, 14864.	12.8	112
10	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. <i>Nature Communications</i> , 2020, 11, 4799.	12.8	110
11	Shared Immunogenic Poly-Epitope Frameshift Mutations in Microsatellite Unstable Tumors. <i>Cell</i> , 2020, 183, 1634-1649.e17.	28.9	103
12	Systematic discovery of complex insertions and deletions in human cancers. <i>Nature Medicine</i> , 2016, 22, 97-104.	30.7	93
13	Yeast Tdh3 (Glyceraldehyde 3-Phosphate Dehydrogenase) Is a Sir2-Interacting Factor That Regulates Transcriptional Silencing and rDNA Recombination. <i>PLoS Genetics</i> , 2013, 9, e1003871.	3.5	53
14	Mass Spectrometry-Based Proteomics Reveals Potential Roles of NEK9 and MAP2K4 in Resistance to PI3K Inhibition in Triple-Negative Breast Cancers. <i>Cancer Research</i> , 2018, 78, 2732-2746.	0.9	52
15	Cooperation Between Distinct Cancer Driver Genes Underlies Intertumor Heterogeneity in Hepatocellular Carcinoma. <i>Gastroenterology</i> , 2020, 159, 2203-2220.e14.	1.3	47
16	CharGer: clinical Characterization of Germline variants. <i>Bioinformatics</i> , 2019, 35, 865-867.	4.1	39
17	Ancestry-specific predisposing germline variants in cancer. <i>Genome Medicine</i> , 2020, 12, 51.	8.2	35
18	Mannose Phosphate Isomerase and Mannose Regulate Hepatic Stellate Cell Activation and Fibrosis in Zebrafish and Humans. <i>Hepatology</i> , 2019, 70, 2107-2122.	7.3	26

#	ARTICLE	IF	CITATIONS
19	Modeling COVID-19 dynamic using a two-strain model with vaccination. <i>Chaos, Solitons and Fractals</i> , 2022, 157, 111927.	5.1	26
20	Breast tumors educate the proteome of stromal tissue in an individualized but coordinated manner. <i>Science Signaling</i> , 2017, 10, .	3.6	25
21	Functional analysis of BARD1 missense variants in homology-directed repair and damage sensitivity. <i>PLoS Genetics</i> , 2019, 15, e1008049.	3.5	23
22	Analysis of sex-specific risk factors and clinical outcomes in COVID-19. <i>Communications Medicine</i> , 2021, 1, .	4.2	23
23	Genomic and molecular features distinguish young adult cancer from later-onset cancer. <i>Cell Reports</i> , 2021, 37, 110005.	6.4	21
24	Framework for microRNA variant annotation and prioritization using human population and disease datasets. <i>Human Mutation</i> , 2019, 40, 73-89.	2.5	18
25	Integrative omics analyses broaden treatment targets in human cancer. <i>Genome Medicine</i> , 2018, 10, 60.	8.2	17
26	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. <i>Genome Research</i> , 2017, 27, 1450-1459.	5.5	15
27	Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1630-1650.	3.8	14
28	Abstract 5359: Regulatory germline variants in 10,389 adult cancers. <i>Cancer Research</i> , 2018, 78, 5359-5359.	0.9	13
29	Chitinase-3-like 1 protein (CHI3L1) locus influences cerebrospinal fluid levels of YKL-40. <i>BMC Neurology</i> , 2016, 16, 217.	1.8	12
30	Spatially interacting phosphorylation sites and mutations in cancer. <i>Nature Communications</i> , 2021, 12, 2313.	12.8	12
31	Diverse immune response of DNA damage repair-deficient tumors. <i>Cell Reports Medicine</i> , 2021, 2, 100276.	6.5	12
32	The Functional Hallmarks of Cancer Predisposition Genes. <i>Cancer Management and Research</i> , 2021, Volume 13, 4351-4357.	1.9	11
33	Phenome-wide and expression quantitative trait locus associations of coronavirus disease 2019 genetic risk loci. <i>IScience</i> , 2021, 24, 102550.	4.1	9
34	Pan-cancer methylation and expression profiling of adenocarcinomas revealed epigenetic silencing in the WNT signaling pathway. <i>Neoplasia</i> , 2016, 63, 208-14.	1.6	8
35	Modeling the Transmission of the SARS-CoV-2 Delta Variant in a Partially Vaccinated Population. <i>Viruses</i> , 2022, 14, 158.	3.3	6
36	Most popular public searches on gene names. <i>Nature</i> , 2018, 553, 405-405.	27.8	5

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37	Genetic dependency of Alzheimer's disease-associated genes across cells and tissue types. <i>Scientific Reports</i> , 2021, 11, 12107.	3.3	5
38	Pan-cancer proteogenomic investigations identify post-transcriptional kinase targets. <i>Communications Biology</i> , 2021, 4, 1112.	4.4	5
39	Pan-cancer analysis of somatic mutations across 21 neuroendocrine tumor types. <i>Cell Research</i> , 2018, 28, 601-604.	12.0	4
40	Ten Simple Rules for landing on the right job after your PhD or postdoc. <i>PLoS Computational Biology</i> , 2020, 16, e1007723.	3.2	4
41	Non-cancer-related pathogenic germline variants and expression consequences in ten-thousand cancer genomes. <i>Genome Medicine</i> , 2021, 13, 147.	8.2	4
42	Prediction of individual COVID-19 diagnosis using baseline demographics and lab data. <i>Scientific Reports</i> , 2021, 11, 13913.	3.3	3
43	Genomic Determinants of Homologous Recombination Deficiency across Human Cancers. <i>Cancers</i> , 2021, 13, 4572.	3.7	3
44	Proteomic Analyses Identify Therapeutic Targets in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2022, 12, 814120.	2.8	3
45	Analytical protocol to identify local ancestry-associated molecular features in cancer. <i>STAR Protocols</i> , 2021, 2, 100766.	1.2	2
46	Pathogenic Germline Variants in Multiple Myeloma. <i>Blood</i> , 2021, 138, 399-399.	1.4	2
47	Genotype concordance and polygenic risk score estimation across consumer genetic testing data. <i>Annals of Human Genetics</i> , 2020, 84, 352-356.	0.8	1
48	[O11]: CEREBROSPINAL FLUID ENDOPHENOTYPES PROVIDE INSIGHT INTO BIOLOGY UNDERLYING ALZHEIMER'S DISEASE. <i>Alzheimer's and Dementia</i> , 2017, 13, P218.	0.8	0
49	Cellular dependency analysis identifies genes implicated in Alzheimer's disease (AD) as potential treatment targets. <i>Alzheimer's and Dementia</i> , 2020, 16, e047523.	0.8	0
50	Abstract 3424: Genomic alterations in clonal hematopoiesis. , 2018, , .		0
51	Characterization of Germline Variants in Multiple Myeloma. <i>Blood</i> , 2018, 132, 4499-4499.	1.4	0
52	Abstract LB-329: Pancancer proteomic investigation identifies overexpressed kinases as novel cancer dependent targets. , 2020, , .		0
53	Abstract 2226: Precise stratification of immunotherapy outcomes using response-associated somatic mutations. , 2020, , .		0
54	AeQTL: eQTL analysis using region-based aggregation of rare genomic variants. , 2020, , .		0

#	ARTICLE	IF	CITATIONS
55	Abstract 5692: Tissue specificity of chromosome aneuploidy correlates with BRCA-associated cancer risk. <i>Cancer Research</i> , 2022, 82, 5692-5692.	0.9	0