Kuan-lin Huang

List of Publications by Year
in descending order

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		361413	223800
55	6,153	20	46
papers	citations	h-index	g-index

68	68	68	13801
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Modeling the Transmission of the SARS-CoV-2 Delta Variant in a Partially Vaccinated Population. Viruses, 2022, 14, 158.	3.3	6
2	Proteomic Analyses Identify Therapeutic Targets in Hepatocellular Carcinoma. Frontiers in Oncology, 2022, 12, 814120.	2.8	3
3	Modeling COVID-19 dynamic using a two-strain model with vaccination. Chaos, Solitons and Fractals, 2022, 157, 111927.	5.1	26
4	Abstract 5692: Tissue specificity of chromosome aneuploidy correlates with BRCA-associated cancer risk. Cancer Research, 2022, 82, 5692-5692.	0.9	0
5	Spatially interacting phosphorylation sites and mutations in cancer. Nature Communications, 2021, 12, 2313.	12.8	12
6	Diverse immune response of DNA damage repair-deficient tumors. Cell Reports Medicine, 2021, 2, 100276.	6.5	12
7	Phenome-wide and expression quantitative trait locus associations of coronavirus disease 2019 genetic risk loci. IScience, 2021, 24, 102550.	4.1	9
8	Analysis of sex-specific risk factors and clinical outcomes in COVID-19. Communications Medicine, 2021, 1, .	4.2	23
9	The Functional Hallmarks of Cancer Predisposition Genes. Cancer Management and Research, 2021, Volume 13, 4351-4357.	1.9	11
10	Genetic dependency of Alzheimerâ€™s disease-associated genes across cells and tissue types. Scientific Reports, 2021, 11, 12107.	3.3	5
11	Prediction of individual COVID-19 diagnosis using baseline demographics and lab data. Scientific Reports, 2021, 11, 13913.	3.3	3
12	Non-cancer-related pathogenic germline variants and expression consequences in ten-thousand cancer genomes. Genome Medicine, 2021, 13, 147.	8.2	4
13	Genomic Determinants of Homologous Recombination Deficiency across Human Cancers. Cancers, 2021, 13, 4572.	3.7	3
14	Pan-cancer proteogenomic investigations identify post-transcriptional kinase targets. Communications Biology, 2021, 4, 1112.	4.4	5
15	Analytical protocol to identify local ancestry-associated molecular features in cancer. STAR Protocols, 2021, 2, 100766.	1.2	2
16	Genomic and molecular features distinguish young adult cancer from later-onset cancer. Cell Reports, 2021, 37, 110005.	6.4	21
17	Pathogenic Germline Variants in Multiple Myeloma. Blood, 2021, 138, 399-399.	1.4	2
18	Shared Immunogenic Poly-Epitope Frameshift Mutations in Microsatellite Unstable Tumors. Cell, 2020, 183, 1634-1649.e17.	28.9	103

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19	Cooperation Between Distinct Cancer Driver Genes Underlies Intertumor Heterogeneity in Hepatocellular Carcinoma. Gastroenterology, 2020, 159, 2203-2220.e14.	1.3	47
20	Risk prediction of late-onset Alzheimerâ€™s disease implies an oligogenic architecture. Nature Communications, 2020, 11, 4799.	12.8	110
21	Cellular dependency analysis identifies genes implicated in Alzheimerâ€™s disease (AD) as potential treatment targets. Alzheimer's and Dementia, 2020, 16, e047523.	0.8	0
22	Ancestry-specific predisposing germline variants in cancer. Genome Medicine, 2020, 12, 51.	8.2	35
23	Ten Simple Rules for landing on the right job after your PhD or postdoc. PLoS Computational Biology, 2020, 16, e1007723.	3.2	4
24	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
25	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. Cancer Cell, 2020, 37, 639-654.e6.	16.8	151
26	Genotype concordance and polygenic risk score estimation across consumer genetic testing data. Annals of Human Genetics, 2020, 84, 352-356.	0.8	1
27	Abstract LB-329: Pancancer proteomic investigation identifies overexpressed kinases as novel cancer dependent targets. , 2020, , .		0
28	Abstract 2226: Precise stratification of immunotherapy outcomes using response-associated somatic mutations. , 2020, , .		0
29	AeQTL: eQTL analysis using region-based aggregation of rare genomic variants. , 2020, , .		0
30	CharGer: clinical Characterization of Germline variants. Bioinformatics, 2019, 35, 865-867.	4.1	39
31	Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability*. Molecular and Cellular Proteomics, 2019, 18, 1630-1650.	3.8	14
32	Mannose Phosphate Isomerase and Mannose Regulate Hepatic Stellate Cell Activation and Fibrosis in Zebrafish and Humans. Hepatology, 2019, 70, 2107-2122.	7.3	26
33	Functional analysis of BARD1 missense variants in homology-directed repair and damage sensitivity. PLoS Genetics, 2019, 15, e1008049.	3.5	23
34	Framework for microRNA variant annotation and prioritization using human population and disease datasets. Human Mutation, 2019, 40, 73-89.	2.5	18
35	Mass Spectrometryâ€“Based Proteomics Reveals Potential Roles of NEK9 and MAP2K4 in Resistance to PI3K Inhibition in Triple-Negative Breast Cancers. Cancer Research, 2018, 78, 2732-2746.	0.9	52
36	Pan-cancer analysis of somatic mutations across 21 neuroendocrine tumor types. Cell Research, 2018, 28, 601-604.	12.0	4

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37	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
38	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	28.9	620
39	Integrative omics analyses broaden treatment targets in human cancer. Genome Medicine, 2018, 10, 60.	8.2	17
40	Most popular public searches on gene names. Nature, 2018, 553, 405-405.	27.8	5
41	Abstract 5359: Regulatory germline variants in 10,389 adult cancers. Cancer Research, 2018, 78, 5359-5359.	0.9	13
42	Abstract 3424: Genomic alterations in clonal hematopoiesis. , 2018, , .		0
43	Characterization of Germline Variants in Multiple Myeloma. Blood, 2018, 132, 4499-4499.	1.4	0
44	Genome-wide association study identifies four novel loci associated with Alzheimerâ€™s endophenotypes and disease modifiers. Acta Neuropathologica, 2017, 133, 839-856.	7.7	199
45	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. Nature Neuroscience, 2017, 20, 1052-1061.	14.8	330
46	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. Genome Research, 2017, 27, 1450-1459.	5.5	15
47	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. Nature Communications, 2017, 8, 14864.	12.8	112
48	Breast tumors educate the proteome of stromal tissue in an individualized but coordinated manner. Science Signaling, 2017, 10, .	3.6	25
49	[O1â€“11â€“03]: CEREBROSPINAL FLUID ENDOPHENOTYPES PROVIDE INSIGHT INTO BIOLOGY UNDERLYING ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2017, 13, P218.	0.8	0
50	Pan-cancer methylation and expression profiling of adenocarcinomas revealed epigenetic silencing in the WNT signaling pathway. Neoplasma, 2016, 63, 208-14.	1.6	8
51	Chitinase-3-like 1 protein (CHI3L1) locus influences cerebrospinal fluid levels of YKL-40. BMC Neurology, 2016, 16, 217.	1.8	12
52	Proteogenomics connects somatic mutations to signalling in breast cancer. Nature, 2016, 534, 55-62.	27.8	1,384
53	Systematic discovery of complex insertions and deletions in human cancers. Nature Medicine, 2016, 22, 97-104.	30.7	93
54	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	12.8	243

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55	Yeast Tdh3 (Glyceraldehyde 3-Phosphate Dehydrogenase) Is a Sir2-Interacting Factor That Regulates Transcriptional Silencing and rDNA Recombination. PLoS Genetics, 2013, 9, e1003871.	3.5	53