

Weng Khong Lim

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9283990/publications.pdf>

Version: 2024-02-01

49
papers

3,620
citations

236925

25
h-index

223800

46
g-index

56
all docs

56
docs citations

56
times ranked

7485
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 1116-1135.	9.4	637
2	Exome sequencing identifies distinct mutational patterns in liver fluke-related and non-infection-related bile duct cancers. <i>Nature Genetics</i> , 2013, 45, 1474-1478.	21.4	426
3	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.	12.8	240
4	Genome-Wide Mutational Signatures of Aristolochic Acid and Its Application as a Screening Tool. <i>Science Translational Medicine</i> , 2013, 5, 197ra101.	12.4	233
5	Exome sequencing identifies highly recurrent MED12 somatic mutations in breast fibroadenoma. <i>Nature Genetics</i> , 2014, 46, 877-880.	21.4	172
6	Genomic landscapes of breast fibroepithelial tumors. <i>Nature Genetics</i> , 2015, 47, 1341-1345.	21.4	167
7	Loss of tumor suppressor KDM6A amplifies PRC2-regulated transcriptional repression in bladder cancer and can be targeted through inhibition of EZH2. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	165
8	The DNA Structure-Specific Endonuclease MUS81 Mediates DNA Sensor STING-Dependent Host Rejection of Prostate Cancer Cells. <i>Immunity</i> , 2016, 44, 1177-1189.	14.3	162
9	The draft genome of tropical fruit durian (<i>Durio zibethinus</i>). <i>Nature Genetics</i> , 2017, 49, 1633-1641.	21.4	150
10	JAK-STAT and G-protein-coupled receptor signaling pathways are frequently altered in epitheliotropic intestinal T-cell lymphoma. <i>Leukemia</i> , 2016, 30, 1311-1319.	7.2	130
11	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. <i>Cell</i> , 2019, 179, 736-749.e15.	28.9	126
12	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	17.5	88
13	Mutational landscapes of tongue carcinoma reveal recurrent mutations in genes of therapeutic and prognostic relevance. <i>Genome Medicine</i> , 2015, 7, 98.	8.2	74
14	Activity of a heptad of transcription factors is associated with stem cell programs and clinical outcome in acute myeloid leukemia. <i>Blood</i> , 2013, 121, 2289-2300.	1.4	72
15	Association of <i>NOTCH2NLC</i> Repeat Expansions With Parkinson Disease. <i>JAMA Neurology</i> , 2020, 77, 1559.	9.0	66
16	An eleven gene molecular signature for extra-capsular spread in oral squamous cell carcinoma serves as a prognosticator of outcome in patients without nodal metastases. <i>Oral Oncology</i> , 2015, 51, 355-362.	1.5	64
17	<i>MED12</i> is frequently mutated in breast phyllodes tumours: a study of 112 cases. <i>Journal of Clinical Pathology</i> , 2015, 68, 685-691.	2.0	62
18	Beyond fitness tracking: The use of consumer-grade wearable data from normal volunteers in cardiovascular and lipidomics research. <i>PLoS Biology</i> , 2018, 16, e2004285.	5.6	57

#	ARTICLE	IF	CITATIONS
19	Germline Mutations in Cancer Predisposition Genes are Frequent in Sporadic Sarcomas. <i>Scientific Reports</i> , 2017, 7, 10660.	3.3	52
20	Recognizing the Continuous Nature of Expression Heterogeneity and Clinical Outcomes in Clear Cell Renal Cell Carcinoma. <i>Scientific Reports</i> , 2017, 7, 7342.	3.3	46
21	Integrated paired-end enhancer profiling and whole-genome sequencing reveals recurrent <i>CCNE1</i> and <i>IGF2</i> enhancer hijacking in primary gastric adenocarcinoma. <i>Gut</i> , 2020, 69, 1039-1052.	12.1	36
22	<i>NOTCH2NLC</i> GGC Repeat Expansions Are Associated with Sporadic Essential Tremor: Variable Disease Expressivity on Long-Term Follow-up. <i>Annals of Neurology</i> , 2020, 88, 614-618.	5.3	36
23	Pathogenesis of cholangiocarcinoma: From genetics to signalling pathways. <i>Bailliere's Best Practice and Research in Clinical Gastroenterology</i> , 2015, 29, 233-244.	2.4	34
24	Digital phenotyping by consumer wearables identifies sleep-associated markers of cardiovascular disease risk and biological aging. <i>Communications Biology</i> , 2019, 2, 361.	4.4	34
25	CD1d expression in renal cell carcinoma is associated with higher relapse rates, poorer cancer-specific and overall survival. <i>Journal of Clinical Pathology</i> , 2015, 68, 200-205.	2.0	32
26	MED12 protein expression in breast fibroepithelial lesions: correlation with mutation status and oestrogen receptor expression. <i>Journal of Clinical Pathology</i> , 2016, 69, 858-865.	2.0	26
27	Phenotypic bases of <i>NOTCH2NLC</i> GGC expansion positive neuronal intranuclear inclusion disease in a Southeast Asian cohort. <i>Clinical Genetics</i> , 2020, 98, 274-281.	2.0	25
28	Germline Pathogenic Variants in Homologous Recombination and DNA Repair Genes in an Asian Cohort of Young-Onset Colorectal Cancer. <i>JNCI Cancer Spectrum</i> , 2018, 2, pky054.	2.9	21
29	Family history assessment significantly enhances delivery of precision medicine in the genomics era. <i>Genome Medicine</i> , 2021, 13, 3.	8.2	19
30	Population genomics in South East Asia captures unexpectedly high carrier frequency for treatable inherited disorders. <i>Genetics in Medicine</i> , 2019, 21, 207-212.	2.4	18
31	Genetic Studies of Hypertrophic Cardiomyopathy in Singaporeans Identify Variants in <i>TNNI3</i> and <i>TNNT2</i> That Are Common in Chinese Patients. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, 424-434.	3.6	18
32	Implementation of genomics in medical practice to deliver precision medicine for an Asian population. <i>Npj Genomic Medicine</i> , 2019, 4, 12.	3.8	17
33	Low frequency variants associated with leukocyte telomere length in the Singapore Chinese population. <i>Communications Biology</i> , 2021, 4, 519.	4.4	15
34	Clinical relevance of screening checklists for detecting cancer predisposition syndromes in Asian childhood tumours. <i>Npj Genomic Medicine</i> , 2018, 3, 30.	3.8	13
35	Harnessing technology and molecular analysis to understand the development of cardiovascular diseases in Asia: a prospective cohort study (SingHEART). <i>BMC Cardiovascular Disorders</i> , 2019, 19, 259.	1.7	12
36	An Optimised Protocol Harnessing Laser Capture Microdissection for Transcriptomic Analysis of Matched Primary and Metastatic Colorectal Tumours. <i>Scientific Reports</i> , 2020, 10, 682.	3.3	11

#	ARTICLE	IF	CITATIONS
37	Germline hemizygous deletion of CDKN2A/CDKN2B locus in a patient presenting with Li-Fraumeni syndrome. <i>Npj Genomic Medicine</i> , 2016, 1, 16015.	3.8	9
38	NOTCH2NLC-linked neuronal intranuclear inclusion body disease and fragile X-associated tremor/ataxia syndrome. <i>Brain</i> , 2020, 143, e69-e69.	7.6	9
39	Evaluation of family health history collection methods impact on data and risk assessment outcomes. <i>Preventive Medicine Reports</i> , 2020, 18, 101072.	1.8	7
40	Variation in predicted COVID-19 risk among lemurs and lorises. <i>American Journal of Primatology</i> , 2021, 83, e23255.	1.7	7
41	Ligand-mediated PAI-1 inhibition in a mouse model of peritoneal carcinomatosis. <i>Cell Reports Medicine</i> , 2022, 3, 100526.	6.5	7
42	MicroRNAs dysregulated in breast cancer preferentially target key oncogenic pathways. <i>Molecular BioSystems</i> , 2011, 7, 2571.	2.9	6
43	Investigation into the origins of an ancient BRCA1 founder mutation identified among Chinese families in Singapore. <i>International Journal of Cancer</i> , 2021, 148, 637-645.	5.1	5
44	High Diagnostic Utility Incorporating a Targeted Neurodegeneration Gene Panel With MRI Brain Diagnostic Algorithms in Patients With Young-Onset Cognitive Impairment With Leukodystrophy. <i>Frontiers in Neurology</i> , 2021, 12, 631407.	2.4	3
45	Spectrum of Germline Mutations Within Fanconi Anemia-Associated Genes Across Populations of Varying Ancestry. <i>JNCI Cancer Spectrum</i> , 2021, 5, .	2.9	3
46	Abstract 5184: Distinct mutational patterns in liver fluke-related and non-infection-related bile duct cancers revealed by whole exome sequencing. , 2014, , .		2
47	Diffner E, Beck D, Gudgin E, et al. Activity of a heptad of transcription factors is associated with stem cell programs and clinical outcome in acute myeloid leukemia. <i>Blood</i> . 2013;121(12):2289-2300.. <i>Blood</i> , 2014, 123, 2901-2901.	1.4	0
48	Abstract 3874: Mutational landscapes of oral tongue squamous cell carcinoma reveal recurrent mutations in genes of therapeutic and prognostic relevance. , 2015, , .		0
49	Generating patient-derived ascites-dependent xenograft mouse models of peritoneal carcinomatosis. <i>STAR Protocols</i> , 2022, 3, 101548.	1.2	0