Weng Khong Lim

List of Publications by Year
in descending order

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

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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	Ligand-mediated PAI-1 inhibition in a mouse model of peritoneal carcinomatosis. Cell Reports Medicine, 2022, 3, 100526.	6.5	7
2	Generating patient-derived ascites-dependent xenograft mouse models of peritoneal carcinomatosis. STAR Protocols, 2022, 3, 101548.	1.2	0
3	Investigation into the origins of an ancient BRCA1 founder mutation identified among Chinese families in Singapore. International Journal of Cancer, 2021, 148, 637-645.	5.1	5
4	Family history assessment significantly enhances delivery of precision medicine in the genomics era. Genome Medicine, 2021, 13, 3.	8.2	19
5	High Diagnostic Utility Incorporating a Targeted Neurodegeneration Gene Panel With MRI Brain Diagnostic Algorithms in Patients With Young-Onset Cognitive Impairment With Leukodystrophy. Frontiers in Neurology, 2021, 12, 631407.	2.4	3
6	Variation in predicted COVIDâ€19 risk among lemurs and lorises. American Journal of Primatology, 2021, 83, e23255.	1.7	7
7	Low frequency variants associated with leukocyte telomere length in the Singapore Chinese population. Communications Biology, 2021, 4, 519.	4.4	15
8	Spectrum of Germline Mutations Within Fanconi Anemiaâ€“Associated Genes Across Populations of Varying Ancestry. JNCI Cancer Spectrum, 2021, 5, .	2.9	3
9	Integrated paired-end enhancer profiling and whole-genome sequencing reveals recurrent CCNE1 and IGF2 enhancer hijacking in primary gastric adenocarcinoma. Gut, 2020, 69, 1039-1052.	12.1	36
10	NOTCH2NLC-linked neuronal intranuclear inclusion body disease and fragile X-associated tremor/ataxia syndrome. Brain, 2020, 143, e69-e69.	7.6	9
11	Association of NOTCH2NLC Repeat Expansions With Parkinson Disease. JAMA Neurology, 2020, 77, 1559.	9.0	66
12	Genetic Studies of Hypertrophic Cardiomyopathy in Singaporeans Identify Variants in TNNI3 and TNNT2 That Are Common in Chinese Patients. Circulation Genomic and Precision Medicine, 2020, 13, 424-434.	3.6	18
13	<scp>NOTCH2NLC GGC</scp> Repeat Expansions Are Associated with Sporadic Essential Tremor: Variable Disease Expressivity on Longâ€Term Followâ€up. Annals of Neurology, 2020, 88, 614-618.	5.3	36
14	Evaluation of family health history collection methods impact on data and risk assessment outcomes. Preventive Medicine Reports, 2020, 18, 101072.	1.8	7
15	Phenotypic bases of <scp>NOTCH2NLC GGC</scp> expansion positive neuronal intranuclear inclusion disease in a Southeast Asian cohort. Clinical Genetics, 2020, 98, 274-281.	2.0	25
16	An Optimised Protocol Harnessing Laser Capture Microdissection for Transcriptomic AnalysisÂon Matched Primary and Metastatic Colorectal Tumours. Scientific Reports, 2020, 10, 682.	3.3	11
17	Population genomics in South East Asia captures unexpectedly high carrier frequency for treatable inherited disorders. Genetics in Medicine, 2019, 21, 207-212.	2.4	18
18	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15.	28.9	126

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19	Digital phenotyping by consumer wearables identifies sleep-associated markers of cardiovascular disease risk and biological aging. Communications Biology, 2019, 2, 361.	4.4	34
20	Implementation of genomics in medical practice to deliver precision medicine for an Asian population. Npj Genomic Medicine, 2019, 4, 12.	3.8	17
21	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
22	Harnessing technology and molecular analysis to understand the development of cardiovascular diseases in Asia: a prospective cohort study (SingHEART). BMC Cardiovascular Disorders, 2019, 19, 259.	1.7	12
23	Clinical relevance of screening checklists for detecting cancer predisposition syndromes in Asian childhood tumours. Npj Genomic Medicine, 2018, 3, 30.	3.8	13
24	Germline Pathogenic Variants in Homologous Recombination and DNA Repair Genes in an Asian Cohort of Young-Onset Colorectal Cancer. JNCI Cancer Spectrum, 2018, 2, pky054.	2.9	21
25	Beyond fitness tracking: The use of consumer-grade wearable data from normal volunteers in cardiovascular and lipidomics research. PLoS Biology, 2018, 16, e2004285.	5.6	57
26	Loss of tumor suppressor KDM6A amplifies PRC2-regulated transcriptional repression in bladder cancer and can be targeted through inhibition of EZH2. Science Translational Medicine, 2017, 9, .	12.4	165
27	The draft genome of tropical fruit durian (Durio zibethinus). Nature Genetics, 2017, 49, 1633-1641.	21.4	150
28	Germline Mutations in Cancer Predisposition Genes are Frequent in Sporadic Sarcomas. Scientific Reports, 2017, 7, 10660.	3.3	52
29	Recognizing the Continuous Nature of Expression Heterogeneity and Clinical Outcomes in Clear Cell Renal Cell Carcinoma. Scientific Reports, 2017, 7, 7342.	3.3	46
30	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. Cancer Discovery, 2017, 7, 1116-1135.	9.4	637
31	Germline hemizygous deletion of CDKN2Aâ€“CDKN2B locus in a patient presenting with Liâ€“Fraumeni syndrome. Npj Genomic Medicine, 2016, 1, 16015.	3.8	9
32	MED12 protein expression in breast fibroepithelial lesions: correlation with mutation status and oestrogen receptor expression. Journal of Clinical Pathology, 2016, 69, 858-865.	2.0	26
33	The DNA Structure-Specific Endonuclease MUS81 Mediates DNA Sensor STING-Dependent Host Rejection of Prostate Cancer Cells. Immunity, 2016, 44, 1177-1189.	14.3	162
34	JAK-STAT and G-protein-coupled receptor signaling pathways are frequently altered in epitheliotropic intestinal T-cell lymphoma. Leukemia, 2016, 30, 1311-1319.	7.2	130
35	Mutational landscapes of tongue carcinoma reveal recurrent mutations in genes of therapeutic and prognostic relevance. Genome Medicine, 2015, 7, 98.	8.2	74
36	MED12 is frequently mutated in breast phyllodes tumours: a study of 112 cases. Journal of Clinical Pathology, 2015, 68, 685-691.	2.0	62

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37	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	17.5	88
38	Pathogenesis of cholangiocarcinoma: From genetics to signalling pathways. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2015, 29, 233-244.	2.4	34
39	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. Oral Oncology, 2015, 51, 355-362.	1.5	64
40	CD1d expression in renal cell carcinoma is associated with higher relapse rates, poorer cancer-specific and overall survival. Journal of Clinical Pathology, 2015, 68, 200-205.	2.0	32
41	Genomic landscapes of breast fibroepithelial tumors. Nature Genetics, 2015, 47, 1341-1345.	21.4	167
42	Abstract 3874: Mutational landscapes of oral tongue squamous cell carcinoma reveal recurrent mutations in genes of therapeutic and prognostic relevance. , 2015, , .		0
43	Exome sequencing identifies highly recurrent MED12 somatic mutations in breast fibroadenoma. Nature Genetics, 2014, 46, 877-880.	21.4	172
44	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. Blood. 2013;121(12):2289-2300.. Blood, 2014, 123, 2901-2901.	1.4	0
45	Abstract 5184: Distinct mutational patterns in liver fluke-related and non-infection-related bile duct cancers revealed by whole exome sequencing. , 2014, , .		2
46	Exome sequencing identifies distinct mutational patterns in liver flukeâ€“related and non-infection-related bile duct cancers. Nature Genetics, 2013, 45, 1474-1478.	21.4	426
47	Genome-Wide Mutational Signatures of Aristolochic Acid and Its Application as a Screening Tool. Science Translational Medicine, 2013, 5, 197ra101.	12.4	233
48	Activity of a heptad of transcription factors is associated with stem cell programs and clinical outcome in acute myeloid leukemia. Blood, 2013, 121, 2289-2300.	1.4	72
49	MicroRNAs dysregulated in breast cancer preferentially target key oncogenic pathways. Molecular BioSystems, 2011, 7, 2571.	2.9	6