

Choon Kiat Ong

List of Publications by Year in descending order

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89
papers

7,126
citations

109264

35
h-index

74108

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docs citations

98
times ranked

12396
citing authors

#	ARTICLE	IF	CITATIONS
1	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. <i>Nature</i> , 2011, 469, 539-542.	13.7	1,127
2	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 1116-1135.	7.7	637
3	Exome sequencing of gastric adenocarcinoma identifies recurrent somatic mutations in cell adhesion and chromatin remodeling genes. <i>Nature Genetics</i> , 2012, 44, 570-574.	9.4	560
4	Exome sequencing identifies distinct mutational patterns in liver fluke-associated and non-infection-related bile duct cancers. <i>Nature Genetics</i> , 2013, 45, 1474-1478.	9.4	426
5	Exome sequencing of liver fluke-associated cholangiocarcinoma. <i>Nature Genetics</i> , 2012, 44, 690-693.	9.4	412
6	Janus Kinase 3-Activating Mutations Identified in Natural Killer/T-cell Lymphoma. <i>Cancer Discovery</i> , 2012, 2, 591-597.	7.7	236
7	Genome-Wide Mutational Signatures of Aristolochic Acid and Its Application as a Screening Tool. <i>Science Translational Medicine</i> , 2013, 5, 197ra101.	5.8	233
8	Evolution of human papillomavirus type 18: an ancient phylogenetic root in Africa and intratype diversity reflect coevolution with human ethnic groups. <i>Journal of Virology</i> , 1993, 67, 6424-6431.	1.5	220
9	Oncogenic activation of the STAT3 pathway drives PD-L1 expression in natural killer/T-cell lymphoma. <i>Blood</i> , 2018, 132, 1146-1158.	0.6	218
10	Genetic drivers of oncogenic pathways in molecular subgroups of peripheral T-cell lymphoma. <i>Blood</i> , 2019, 133, 1664-1676.	0.6	184
11	Genomic and Transcriptomic Profiling of Combined Hepatocellular and Intrahepatic Cholangiocarcinoma Reveals Distinct Molecular Subtypes. <i>Cancer Cell</i> , 2019, 35, 932-947.e8.	7.7	182
12	Warburg metabolism in tumor-conditioned macrophages promotes metastasis in human pancreatic ductal adenocarcinoma. <i>Oncotmunology</i> , 2016, 5, e1191731.	2.1	178
13	Exome sequencing identifies highly recurrent MED12 somatic mutations in breast fibroadenoma. <i>Nature Genetics</i> , 2014, 46, 877-880.	9.4	172
14	Genomic landscapes of breast fibroepithelial tumors. <i>Nature Genetics</i> , 2015, 47, 1341-1345.	9.4	167
15	The draft genome of tropical fruit durian (<i>Durio zibethinus</i>). <i>Nature Genetics</i> , 2017, 49, 1633-1641.	9.4	150
16	Serglycin Is a Theranostic Target in Nasopharyngeal Carcinoma that Promotes Metastasis. <i>Cancer Research</i> , 2011, 71, 3162-3172.	0.4	133
17	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.	3.3	130
18	Reproducing the molecular subclassification of peripheral T-cell lymphoma by immunohistochemistry. <i>Blood</i> , 2019, 134, 2159-2170.	0.6	120

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19	Whole-genome reconstruction and mutational signatures in gastric cancer. <i>Genome Biology</i> , 2012, 13, R115.	13.9	116
20	Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in <i>Opisthorchis viverrini</i> Associated Cholangiocarcinoma. <i>EBioMedicine</i> , 2016, 8, 195-202.	2.7	94
21	Whole-Exome Sequencing Studies of Parathyroid Carcinomas Reveal Novel <i>PRUNE2</i> Mutations, Distinctive Mutational Spectra Related to APOBEC-Catalyzed DNA Mutagenesis and Mutational Enrichment in Kinases Associated With Cell Migration and Invasion. <i>Journal of Clinical Endocrinology and Metabolism</i> . 2015, 100, E360-E364.	1.8	86
22	Genomic and transcriptomic landscapes of Epstein-Barr virus in extranodal natural killer T-cell lymphoma. <i>Leukemia</i> , 2019, 33, 1451-1462.	3.3	86
23	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. <i>Lancet Oncology</i> , The, 2016, 17, 1240-1247.	5.1	84
24	Genetic and Structural Variation in the Gastric Cancer Kinome Revealed through Targeted Deep Sequencing. <i>Cancer Research</i> , 2011, 71, 29-39.	0.4	74
25	Mutational landscapes of tongue carcinoma reveal recurrent mutations in genes of therapeutic and prognostic relevance. <i>Genome Medicine</i> , 2015, 7, 98.	3.6	74
26	Avelumab for the treatment of relapsed or refractory extranodal NK/T-cell lymphoma: an open-label phase 2 study. <i>Blood</i> , 2020, 136, 2754-2763.	0.6	74
27	<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.	1.0	62
28	Overexpression of microRNA-21 regulating PDCD4 during tumorigenesis of liver fluke-associated cholangiocarcinoma contributes to tumor growth and metastasis. <i>Tumor Biology</i> , 2013, 34, 1579-1588.	0.8	61
29	Multiomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. <i>Journal of Clinical Investigation</i> , 2020, 130, 5833-5846.	3.9	58
30	Exome-wide Sequencing Shows Low Mutation Rates and Identifies Novel Mutated Genes in Seminomas. <i>European Urology</i> , 2015, 68, 77-83.	0.9	56
31	Expression of the PTTG1 Oncogene Is Associated with Aggressive Clear Cell Renal Cell Carcinoma. <i>Cancer Research</i> , 2012, 72, 4361-4371.	0.4	52
32	<i>SETD2</i> histone modifier loss in aggressive GI stromal tumours. <i>Gut</i> , 2016, 65, 1960-1972.	6.1	49
33	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study in multiple populations. <i>Lancet Oncology</i> , The, 2020, 21, 306-316.	5.1	49
34	Whole-genome sequencing identifies responders to Pembrolizumab in relapse/refractory natural-killer/T cell lymphoma. <i>Leukemia</i> , 2020, 34, 3413-3419.	3.3	42
35	Oncogenic activation of JAK3-STAT signaling confers clinical sensitivity to PRN371, a novel selective and potent JAK3 inhibitor, in natural killer/T-cell lymphoma. <i>Leukemia</i> , 2018, 32, 1147-1156.	3.3	41
36	Genomic Structure of Human OKL38 Gene and Its Differential Expression in Kidney Carcinogenesis. <i>Journal of Biological Chemistry</i> , 2004, 279, 743-754.	1.6	35

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37	Pathogenesis of cholangiocarcinoma: From genetics to signalling pathways. <i>Bailliere's Best Practice and Research in Clinical Gastroenterology</i> , 2015, 29, 233-244.	1.0	34
38	Identification Of Genomic Sequences Of Three Novel Human Papillomavirus Sequences In Cervical Smears Of Amazonian Indians. <i>Journal of Infectious Diseases</i> , 1994, 170, 1086-1088.	1.9	28
39	Pathogenesis and biomarkers of natural killer T cell lymphoma (NKTL). <i>Journal of Hematology and Oncology</i> , 2019, 12, 28.	6.9	27
40	Application of an ex-vivo drug sensitivity platform towards achieving complete remission in a refractory T-cell lymphoma. <i>Blood Cancer Journal</i> , 2020, 10, 9.	2.8	22
41	PRDM15 is a key regulator of metabolism critical to sustain B-cell lymphomagenesis. <i>Nature Communications</i> , 2020, 11, 3520.	5.8	20
42	A composite single-nucleotide polymorphism prediction signature for extranodal natural killer/T-cell lymphoma. <i>Blood</i> , 2021, 138, 452-463.	0.6	20
43	DNMT3A mutations define a unique biological and prognostic subgroup associated with cytotoxic T cells in PTCL-NOS. <i>Blood</i> , 2022, 140, 1278-1290.	0.6	20
44	First somatic mutation of E2F1 in a critical DNA binding residue discovered in well-differentiated papillary mesothelioma of the peritoneum. <i>Genome Biology</i> , 2011, 12, R96.	13.9	19
45	Molecular cloning, characterization and isolation of novel spliced variants of the human ortholog of a rat estrogen-regulated membrane-associated protein, UO-44. <i>Oncogene</i> , 2004, 23, 5707-5718.	2.6	18
46	Haem oxygenase 1 expression is associated with prognosis in cholangiocarcinoma patients and with drug sensitivity in xenografted mice. <i>Cell Proliferation</i> , 2016, 49, 90-101.	2.4	17
47	Genome-Wide miRNA Expression Profiling of Molecular Subgroups of Peripheral T-cell Lymphoma. <i>Clinical Cancer Research</i> , 2021, 27, 6039-6053.	3.2	17
48	Evaluation of the PIK3 pathway in peripheral T-cell lymphoma and NK/T-cell lymphoma. <i>British Journal of Haematology</i> , 2020, 189, 731-744.	1.2	17
49	Gene Expression Signatures for the Accurate Diagnosis of Peripheral T-Cell Lymphoma Entities in the Routine Clinical Practice. <i>Journal of Clinical Oncology</i> , 2022, 40, 4261-4275.	0.8	17
50	A clinicohaematological prognostic model for nasal-type natural killer/T-cell lymphoma: A multicenter study. <i>Scientific Reports</i> , 2019, 9, 14961.	1.6	16
51	Mutational Signatures in Mandibular Ameloblastoma Correlate with Smoking. <i>Journal of Dental Research</i> , 2019, 98, 652-658.	2.5	14
52	Whole-genome sequencing reveals potent therapeutic strategy for monomorphic epitheliotropic intestinal T-cell lymphoma. <i>Blood Advances</i> , 2020, 4, 4769-4774.	2.5	14
53	Fumarate Hydratase-deficient Cell Line NCCFH1 as a New In Vitro Model of Hereditary Papillary Renal Cell Carcinoma Type 2. <i>Anticancer Research</i> , 2015, 35, 6639-53.	0.5	14
54	Effect of Ang-2-VEGF-A Bispecific Antibody in Renal Cell Carcinoma. <i>Cancer Investigation</i> , 2015, 33, 378-386.	0.6	11

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55	The role of iron ions on microstructural and magnetic properties of MgCuZn ferrites prepared by sol-gel auto-combustion process. <i>Materials Research Bulletin</i> , 2019, 111, 195-201.	2.7	11
56	An Optimised Protocol Harnessing Laser Capture Microdissection for Transcriptomic Analysis of Matched Primary and Metastatic Colorectal Tumours. <i>Scientific Reports</i> , 2020, 10, 682.	1.6	11
57	CREBBP cooperates with the cell cycle machinery to attenuate chidamide sensitivity in relapsed/refractory diffuse large B-cell lymphoma. <i>Cancer Letters</i> , 2021, 521, 268-280.	3.2	10
58	Structural Characterization of Three Novel Rat OKL38 Transcripts, Their Tissue Distributions, and Their Regulation by Human Chorionic Gonadotropin. <i>Endocrinology</i> , 2004, 145, 4763-4774.	1.4	9
59	DDX3X loss is an adverse prognostic marker in diffuse large B-cell lymphoma and is associated with chemoresistance in aggressive non-Hodgkin lymphoma subtypes. <i>Molecular Cancer</i> , 2021, 20, 134.	7.9	9
60	Inhibition of placental growth factor in renal cell carcinoma. <i>Anticancer Research</i> , 2015, 35, 531-41.	0.5	8
61	Analytical and clinical validation of an amplicon-based next generation sequencing assay for ultrasensitive detection of circulating tumor DNA. <i>PLoS ONE</i> , 2022, 17, e0267389.	1.1	7
62	Whole exome sequencing identifies recessive germline mutations in FAM160A1 in familial NK/T cell lymphoma. <i>Blood Cancer Journal</i> , 2018, 8, 111.	2.8	5
63	Towards Next Generation Biomarkers in Natural Killer/T-Cell Lymphoma. <i>Life</i> , 2021, 11, 838.	1.1	4
64	A genomic augmented multivariate prognostic model for the survival of natural killer/T cell lymphoma patients from an international cohort. <i>American Journal of Hematology</i> , 2022, 97, 1159-1169.	2.0	4
65	T-Cell Lymphoma Clonality by Copy Number Variation Analysis of T-Cell Receptor Genes. <i>Cancers</i> , 2021, 13, 340.	1.7	3
66	Oncogenic activation of STAT3 pathway drives PD-L1 expression in natural killer/T cell lymphoma. <i>Journal of Clinical Oncology</i> , 2017, 35, 7549-7549.	0.8	3
67	Abstract 5184: Distinct mutational patterns in liver fluke-related and non-infection-related bile duct cancers revealed by whole exome sequencing. , 2014, , .		2
68	41 Genome-wide mutational signatures of aristolochic acid in urothelial cancer. <i>European Urology Supplements</i> , 2014, 13, e41-e41a.	0.1	1
69	Successful therapeutic rechallenge after a severe episode of high dose methotrexate induced choreoathetosis: A case report. <i>Molecular and Clinical Oncology</i> , 2019, 11, 354-358.	0.4	1
70	Checkpoint immunotherapy for NK/T cell lymphoma—Time for a showdown?. <i>Precision Clinical Medicine</i> , 2021, 4, 70-72.	1.3	1
71	Molecular Subgroups of Peripheral T-Cell Lymphoma Evolve By Distinct Genetic Pathways. <i>Blood</i> , 2016, 128, 4096-4096.	0.6	1
72	Generation of Non-Hodgkin Lymphoma Patient-Derived Xenografts and in Depth Characterization of a Monomorphic Epitheliotropic Intestinal T-Cell Lymphoma Model. <i>Blood</i> , 2016, 128, 4128-4128.	0.6	1

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73	Identification of mutations of the SWI/SNF complex gene PBRM1 by exome sequencing in renal carcinoma.. Journal of Clinical Oncology, 2011, 29, 4571-4571.	0.8	1
74	Genomic and proteomic characterization of ARID1A chromatin remodeller in ampullary tumors. American Journal of Cancer Research, 2017, 7, 484-502.	1.4	1
75	Super-Enhancer-Driven TOX2 Mediates Oncogenesis in Natural Killer/T Cell Lymphoma. Blood, 2020, 136, 17-17.	0.6	1
76	Misaligned sequencing reads from the GNAQ-pseudogene locus may yield GNAQ artefact variants. Nature Communications, 2022, 13, 458.	5.8	1
77	Evaluation of the PI3K pathway in peripheral t-cell lymphoma. Annals of Oncology, 2017, 28, v364.	0.6	0
78	Abstract 2805: Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. , 2011, , .		0
79	Abstract 1476: Serglycin in nasopharyngeal carcinoma: A metastasis regulator and prognostic indicator. , 2011, , .		0
80	Abstract 3823: Characterizing recurrent 18q rearrangements in gastric cancer. , 2011, , .		0
81	Abstract 3874: Mutational landscapes of oral tongue squamous cell carcinoma reveal recurrent mutations in genes of therapeutic and prognostic relevance. , 2015, , .		0
82	A Case of Two Young Brothers with Natural-Killer/T-Cell Lymphoma. Blood, 2016, 128, 5293-5293.	0.6	0
83	A Patient Derived Xenograft As a Preclinical Model for Monomorphic Epitheliotropic Intestinal T-Cell Lymphoma. Blood, 2018, 132, 2949-2949.	0.6	0
84	Pharmacogenomic Prediction of Bleomycin-Induced Pneumonitis in South East Asian Hodgkin Lymphoma Patients. Blood, 2018, 132, 4111-4111.	0.6	0
85	Whole-Genome Genomics Correlates of Response to Anti-PD1 Therapy in Relapsed/Refractory Natural Killer/T Cell Lymphoma. Blood, 2018, 132, 2915-2915.	0.6	0
86	Metagenomic discovery of a distinct inflammatory subtype of human angiosarcoma associated with human herpesvirus 7.. Journal of Clinical Oncology, 2019, 37, 11047-11047.	0.8	0
87	Ultrasensitive multiplex detection of structural rearrangements in <i>ALK</i> , <i>RET</i> , <i>ROS1</i> and <i>PD-L1</i> using a comprehensive next-generation sequencing assay.. Journal of Clinical Oncology, 2020, 38, 3572-3572.	0.8	0
88	No association between <i>ECSIT</i> germline mutations and hemophagocytic lymphohistiocytosis in natural killer/T-cell lymphoma. Haematologica, 2021, 106, 1737-1739.	1.7	0
89	Clinical Application of an Ex-Vivo Platform to Guide the Choice of Drug Combinations in Relapsed/Refractory Lymphoma; A Prospective Study. Blood, 2021, 138, 720-720.	0.6	0