Choon Kiat Ong

List of Publications by Year
in descending order

89 papers	7,126 citations	109321 35 h-index	74163 75 g-index
98 all docs	98 docs citations	98 times ranked	12396 citing authors

#	Article	IF	Citations
1	Misaligned sequencing reads from the GNAQ-pseudogene locus may yield GNAQ artefact variants. Nature Communications, 2022, 13, 458.	12.8	1
2	Analytical and clinical validation of an amplicon-based next generation sequencing assay for ultrasensitive detection of circulating tumor DNA. PLoS ONE, 2022, 17, e0267389.	2.5	7
3	DNMT3A mutations define a unique biological and prognostic subgroup associated with cytotoxic T cells in PTCL-NOS. Blood, 2022, 140, 1278-1290.	1.4	20
4	A genomicâ€augmented multivariate prognostic model for the survival of naturalâ€killer/Tâ€cell lymphoma patients from an international cohort. American Journal of Hematology, 2022, 97, 1159-1169.	4.1	4
5	Gene Expression Signatures for the Accurate Diagnosis of Peripheral T-Cell Lymphoma Entities in the Routine Clinical Practice. Journal of Clinical Oncology, 2022, 40, 4261-4275.	1.6	17
6	Checkpoint immunotherapy for NK/T cell lymphomaâ€"Time for a showdown?. Precision Clinical Medicine, 2021, 4, 70-72.	3.3	1
7	T-Cell Lymphoma Clonality by Copy Number Variation Analysis of T-Cell Receptor Genes. Cancers, 2021, 13, 340.	3.7	3
8	A composite single-nucleotide polymorphism prediction signature for extranodal natural killer/T-cell lymphoma. Blood, 2021, 138, 452-463.	1.4	20
9	Genome-Wide miRNA Expression Profiling of Molecular Subgroups of Peripheral T-cell Lymphoma. Clinical Cancer Research, 2021, 27, 6039-6053.	7.0	17
10	Towards Next Generation Biomarkers in Natural Killer/T-Cell Lymphoma. Life, 2021, 11, 838.	2.4	4
11	CREBBP cooperates with the cell cycle machinery to attenuate chidamide sensitivity in relapsed/refractory diffuse large B-cell lymphoma. Cancer Letters, 2021, 521, 268-280.	7.2	10
12	DDX3X loss is an adverse prognostic marker in diffuse large B-cell lymphoma and is associated with chemoresistance in aggressive non-Hodgkin lymphoma subtypes. Molecular Cancer, 2021, 20, 134.	19.2	9
13	No association between ECSIT germline mutations and hemophagocytic lymphohistiocytosis in natural killer/T-cell lymphoma. Haematologica, 2021, 106, 1737-1739.	3.5	0
14	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.	1.4	0
15	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study in multiple populations. Lancet Oncology, The, 2020, 21, 306-316.	10.7	49
16	PRDM15 is a key regulator of metabolism critical to sustain B-cell lymphomagenesis. Nature Communications, 2020, 11, 3520.	12.8	20
17	Avelumab for the treatment of relapsed or refractory extranodal NK/T-cell lymphoma: an open-label phase 2 study. Blood, 2020, 136, 2754-2763.	1.4	74
18	Whole-genome sequencing identifies responders to Pembrolizumab in relapse/refractory natural-killer/T cell lymphoma. Leukemia, 2020, 34, 3413-3419.	7.2	42

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19	Whole-genome sequencing reveals potent therapeutic strategy for monomorphic epitheliotropic intestinal T-cell lymphoma. Blood Advances, 2020, 4, 4769-4774.	5.2	14
20	Application of an ex-vivo drug sensitivity platform towards achieving complete remission in a refractory T-cell lymphoma. Blood Cancer Journal, 2020, 10, 9.	6.2	22
21	An Optimised Protocol Harnessing Laser Capture Microdissection for Transcriptomic AnalysisÂon Matched Primary and Metastatic Colorectal Tumours. Scientific Reports, 2020, 10, 682.	3.3	11
22	Evaluation of the PIK3 pathway in peripheral Tâ€cell lymphoma and NK/Tâ€cell lymphoma. British Journal of Haematology, 2020, 189, 731-744.	2.5	17
23	Multiomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. Journal of Clinical Investigation, 2020, 130, 5833-5846.	8.2	58
24	Ultrasensitive multiplex detection of structural rearrangements in ALK, RET, ROS1 and PD-L1 using a comprehensive next-generation sequencing assay.. Journal of Clinical Oncology, 2020, 38, 3572-3572.	1.6	0
25	Super-Enhancer-Driven TOX2 Mediates Oncogenesis in Natural Killer/T Cell Lymphoma. Blood, 2020, 136, 17-17.	1.4	1
26	A clinicohaematological prognostic model for nasal-type natural killer/T-cell lymphoma: A multicenter study. Scientific Reports, 2019, 9, 14961.	3.3	16
27	Reproducing the molecular subclassification of peripheral T-cell lymphomaâ€“NOS by immunohistochemistry. Blood, 2019, 134, 2159-2170.	1.4	120
28	Successful therapeutic rechallenge after a severe episode of high dose methotrexateâ€‘induced choreoathetosis: A case report. Molecular and Clinical Oncology, 2019, 11, 354-358.	1.0	1
29	Genomic and Transcriptomic Profiling of Combined Hepatocellular and Intrahepatic Cholangiocarcinoma Reveals Distinct Molecular Subtypes. Cancer Cell, 2019, 35, 932-947.e8.	16.8	182
30	Mutational Signatures in Mandibular Ameloblastoma Correlate with Smoking. Journal of Dental Research, 2019, 98, 652-658.	5.2	14
31	Pathogenesis and biomarkers of natural killer T cell lymphoma (NKTL). Journal of Hematology and Oncology, 2019, 12, 28.	17.0	27
32	Genetic drivers of oncogenic pathways in molecular subgroups of peripheral T-cell lymphoma. Blood, 2019, 133, 1664-1676.	1.4	184
33	The role of iron ions on microstructural and magnetic properties of MgCuZn ferrites prepared by sol-gel auto-combustion process. Materials Research Bulletin, 2019, 111, 195-201.	5.2	11
34	Genomic and transcriptomic landscapes of Epstein-Barr virus in extranodal natural killer T-cell lymphoma. Leukemia, 2019, 33, 1451-1462.	7.2	86
35	Metagenomic discovery of a distinct inflammatory subtype of human angiosarcoma associated with human herpesvirus 7.. Journal of Clinical Oncology, 2019, 37, 11047-11047.	1.6	0
36	Oncogenic activation of JAK3-STAT signaling confers clinical sensitivity to PRN371, a novel selective and potent JAK3 inhibitor, in natural killer/T-cell lymphoma. Leukemia, 2018, 32, 1147-1156.	7.2	41

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37	Whole exome sequencing identifies recessive germline mutations in FAM160A1 in familial NK/T cell lymphoma. Blood Cancer Journal, 2018, 8, 111.	6.2	5
38	Oncogenic activation of the STAT3 pathway drives PD-L1 expression in natural killer/T-cell lymphoma. Blood, 2018, 132, 1146-1158.	1.4	218
39	A Patient Derived Xenograft As a Preclinical Model for Monomorphic Epitheliotropic Intestinal T-Cell Lymphoma. Blood, 2018, 132, 2949-2949.	1.4	0
40	Pharmacogenomic Prediction of Bleomycin-Induced Pneumonitis in South East Asian Hodgkin Lymphoma Patients. Blood, 2018, 132, 4111-4111.	1.4	0
41	Whole-Genome Genomics Correlates of Response to Anti-PD1 Therapy in Relapsed/Refractory Natural Killer/T Cell Lymphoma. Blood, 2018, 132, 2915-2915.	1.4	0
42	The draft genome of tropical fruit durian (Durio zibethinus). Nature Genetics, 2017, 49, 1633-1641.	21.4	150
43	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. Cancer Discovery, 2017, 7, 1116-1135.	9.4	637
44	Evaluation of the PI3K pathway in peripheral t-cell lymphoma. Annals of Oncology, 2017, 28, v364.	1.2	0
45	Oncogenic activation of STAT3 pathway drives PD-L1 expression in natural killer/T cell lymphoma.. Journal of Clinical Oncology, 2017, 35, 7549-7549.	1.6	3
46	Genomic and proteomic characterization of ARID1A chromatin remodeller in ampullary tumors. American Journal of Cancer Research, 2017, 7, 484-502.	1.4	1
47	Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in Opisthorchis viverrini Associated Cholangiocarcinoma. EBioMedicine, 2016, 8, 195-202.	6.1	94
48	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. Lancet Oncology, The, 2016, 17, 1240-1247.	10.7	84
49	Haem oxygenase 1 expression is associated with prognosis in cholangiocarcinoma patients and with drug sensitivity in xenografted mice. Cell Proliferation, 2016, 49, 90-101.	5.3	17
50	Warburg metabolism in tumor-conditioned macrophages promotes metastasis in human pancreatic ductal adenocarcinoma. OncoImmunology, 2016, 5, e1191731.	4.6	178
51	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
52	SETD2histone modifier loss in aggressive GI stromal tumours. Gut, 2016, 65, 1960-1972.	12.1	49
53	Molecular Subgroups of Peripheral T-Cell Lymphoma Evolve By Distinct Genetic Pathways. Blood, 2016, 128, 4096-4096.	1.4	1
54	Generation of Non-Hodgkin Lymphoma Patient-Derived Xenografts and in Depth Characterization of a Monomorphic Epitheliotropic Intestinal T-Cell Lymphoma Model. Blood, 2016, 128, 4128-4128.	1.4	1

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55	A Case of Two Young Brothers with Natural-Killer/T-Cell Lymphoma. Blood, 2016, 128, 5293-5293.	1.4	0
56	Mutational landscapes of tongue carcinoma reveal recurrent mutations in genes of therapeutic and prognostic relevance. Genome Medicine, 2015, 7, 98.	8.2	74
57	MED12 is frequently mutated in breast phyllodes tumours: a study of 112 cases. Journal of Clinical Pathology, 2015, 68, 685-691.	2.0	62
58	Exome-wide Sequencing Shows Low Mutation Rates and Identifies Novel Mutated Genes in Seminomas. European Urology, 2015, 68, 77-83.	1.9	56
59	Whole-Exome Sequencing Studies of Parathyroid Carcinomas Reveal NovelPRUNE2Mutations, Distinctive Mutational Spectra Related to APOBEC-Catalyzed DNA Mutagenesis and Mutational Enrichment in Kinases Associated With Cell Migration and Invasion. Journal of Clinical Endocrinology and Metabolism, 2015, 100, E360-E364.	3.6	86
60	Pathogenesis of cholangiocarcinoma: From genetics to signalling pathways. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2015, 29, 233-244.	2.4	34
61	Effect of Ang-2-VEGF-A Bispecific Antibody in Renal Cell Carcinoma. Cancer Investigation, 2015, 33, 378-386.	1.3	11
62	Genomic landscapes of breast fibroepithelial tumors. Nature Genetics, 2015, 47, 1341-1345.	21.4	167
63	Abstract 3874: Mutational landscapes of oral tongue squamous cell carcinoma reveal recurrent mutations in genes of therapeutic and prognostic relevance. , 2015, , .		0
64	Inhibition of placental growth factor in renal cell carcinoma. Anticancer Research, 2015, 35, 531-41.	1.1	8
65	Fumarate Hydratase-deficient Cell Line NCCFH1 as a New In Vitro Model of Hereditary Papillary Renal Cell Carcinoma Type 2. Anticancer Research, 2015, 35, 6639-53.	1.1	14
66	Exome sequencing identifies highly recurrent MED12 somatic mutations in breast fibroadenoma. Nature Genetics, 2014, 46, 877-880.	21.4	172
67	41 Genome-wide mutational signatures of aristolochic acid in urothelial cancer. European Urology Supplements, 2014, 13, e41-e41a.	0.1	1
68	Abstract 5184: Distinct mutational patterns in liver fluke-related and non-infection-related bile duct cancers revealed by whole exome sequencing. , 2014, , .		2
69	Overexpression of microRNA-21 regulating PDCD4 during tumorigenesis of liver fluke-associated cholangiocarcinoma contributes to tumor growth and metastasis. Tumor Biology, 2013, 34, 1579-1588.	1.8	61
70	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
71	Genome-Wide Mutational Signatures of Aristolochic Acid and Its Application as a Screening Tool. Science Translational Medicine, 2013, 5, 197ra101.	12.4	233
72	Expression of the PTTG1 Oncogene Is Associated with Aggressive Clear Cell Renal Cell Carcinoma. Cancer Research, 2012, 72, 4361-4371.	0.9	52

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73	Janus Kinase 3â€“Activating Mutations Identified in Natural Killer/T-cell Lymphoma. Cancer Discovery, 2012, 2, 591-597.	9.4	236
74	Exome sequencing of gastric adenocarcinoma identifies recurrent somatic mutations in cell adhesion and chromatin remodeling genes. Nature Genetics, 2012, 44, 570-574.	21.4	560
75	Exome sequencing of liver flukeâ€“associated cholangiocarcinoma. Nature Genetics, 2012, 44, 690-693.	21.4	412
76	Whole-genome reconstruction and mutational signatures in gastric cancer. Genome Biology, 2012, 13, R115.	9.6	116
77	First somatic mutation of E2F1 in a critical DNA binding residue discovered in well-differentiated papillary mesothelioma of the peritoneum. Genome Biology, 2011, 12, R96.	9.6	19
78	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. Nature, 2011, 469, 539-542.	27.8	1,127
79	Serglycin Is a Theranostic Target in Nasopharyngeal Carcinoma that Promotes Metastasis. Cancer Research, 2011, 71, 3162-3172.	0.9	133
80	Genetic and Structural Variation in the Gastric Cancer Kinome Revealed through Targeted Deep Sequencing. Cancer Research, 2011, 71, 29-39.	0.9	74
81	Abstract 2805: Exome sequencing identifies frequent mutation of the SWI/SNF complex genePBRM1in renal carcinoma. , 2011, , .		0
82	Abstract 1476: Serglycin in nasopharyngeal carcinoma: A metastasis regulator and prognostic indicator. , 2011, , .		0
83	Abstract 3823: Characterizing recurrent 18q rearrangements in gastric cancer. , 2011, , .		0
84	Identification of mutations of the SWI/SNF complex gene PBRM1 by exome sequencing in renal carcinoma.. Journal of Clinical Oncology, 2011, 29, 4571-4571.	1.6	1
85	Structural Characterization of Three Novel Rat OKL38 Transcripts, Their Tissue Distributions, and Their Regulation by Human Chorionic Gonadotropin. Endocrinology, 2004, 145, 4763-4774.	2.8	9
86	Genomic Structure of Human OKL38 Gene and Its Differential Expression in Kidney Carcinogenesis. Journal of Biological Chemistry, 2004, 279, 743-754.	3.4	35
87	Molecular cloning, characterization and isolation of novel spliced variants of the human ortholog of a rat estrogen-regulated membrane-associated protein, UO-44. Oncogene, 2004, 23, 5707-5718.	5.9	18
88	Identification Of Genomic Sequences Of Three Novel Human Papillomavirus Sequences In Cervical Smears Of Amazonian Indians. Journal of Infectious Diseases, 1994, 170, 1086-1088.	4.0	28
89	Evolution of human papillomavirus type 18: an ancient phylogenetic root in Africa and intratype diversity reflect coevolution with human ethnic groups. Journal of Virology, 1993, 67, 6424-6431.	3.4	220