

Choon Kiat Ong

List of Publications by Year in descending order

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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 | Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. <i>Nature</i> , 2011, 469, 539-542. | 27.8 | 1,127 |
| 2 | Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 1116-1135. | 9.4 | 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. | 21.4 | 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. | 21.4 | 426 |
| 5 | Exome sequencing of liver fluke-associated cholangiocarcinoma. <i>Nature Genetics</i> , 2012, 44, 690-693. | 21.4 | 412 |
| 6 | Janus Kinase 3-Activating Mutations Identified in Natural Killer/T-cell Lymphoma. <i>Cancer Discovery</i> , 2012, 2, 591-597. | 9.4 | 236 |
| 7 | 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 |
| 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. | 3.4 | 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. | 1.4 | 218 |
| 10 | Genetic drivers of oncogenic pathways in molecular subgroups of peripheral T-cell lymphoma. <i>Blood</i> , 2019, 133, 1664-1676. | 1.4 | 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. | 16.8 | 182 |
| 12 | Warburg metabolism in tumor-conditioned macrophages promotes metastasis in human pancreatic ductal adenocarcinoma. <i>Oncotmunology</i> , 2016, 5, e1191731. | 4.6 | 178 |
| 13 | Exome sequencing identifies highly recurrent MED12 somatic mutations in breast fibroadenoma. <i>Nature Genetics</i> , 2014, 46, 877-880. | 21.4 | 172 |
| 14 | Genomic landscapes of breast fibroepithelial tumors. <i>Nature Genetics</i> , 2015, 47, 1341-1345. | 21.4 | 167 |
| 15 | The draft genome of tropical fruit durian (<i>Durio zibethinus</i>). <i>Nature Genetics</i> , 2017, 49, 1633-1641. | 21.4 | 150 |
| 16 | Serglycin Is a Theranostic Target in Nasopharyngeal Carcinoma that Promotes Metastasis. <i>Cancer Research</i> , 2011, 71, 3162-3172. | 0.9 | 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. | 7.2 | 130 |
| 18 | Reproducing the molecular subclassification of peripheral T-cell lymphoma by immunohistochemistry. <i>Blood</i> , 2019, 134, 2159-2170. | 1.4 | 120 |

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|----|---|------|-----------|
| 19 | Whole-genome reconstruction and mutational signatures in gastric cancer. <i>Genome Biology</i> , 2012, 13, R115. | 9.6 | 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. | 6.1 | 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. | 3.6 | 86 |
| 22 | Genomic and transcriptomic landscapes of Epstein-Barr virus in extranodal natural killer T-cell lymphoma. <i>Leukemia</i> , 2019, 33, 1451-1462. | 7.2 | 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. | 10.7 | 84 |
| 24 | Genetic and Structural Variation in the Gastric Cancer Kinome Revealed through Targeted Deep Sequencing. <i>Cancer Research</i> , 2011, 71, 29-39. | 0.9 | 74 |
| 25 | 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 |
| 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. | 1.4 | 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. | 2.0 | 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. | 1.8 | 61 |
| 29 | Multiomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. <i>Journal of Clinical Investigation</i> , 2020, 130, 5833-5846. | 8.2 | 58 |
| 30 | Exome-wide Sequencing Shows Low Mutation Rates and Identifies Novel Mutated Genes in Seminomas. <i>European Urology</i> , 2015, 68, 77-83. | 1.9 | 56 |
| 31 | Expression of the PTTG1 Oncogene Is Associated with Aggressive Clear Cell Renal Cell Carcinoma. <i>Cancer Research</i> , 2012, 72, 4361-4371. | 0.9 | 52 |
| 32 | <i>SETD2</i> histone modifier loss in aggressive GI stromal tumours. <i>Gut</i> , 2016, 65, 1960-1972. | 12.1 | 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. | 10.7 | 49 |
| 34 | Whole-genome sequencing identifies responders to Pembrolizumab in relapse/refractory natural-killer/T cell lymphoma. <i>Leukemia</i> , 2020, 34, 3413-3419. | 7.2 | 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. | 7.2 | 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. | 3.4 | 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. | 2.4 | 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. | 4.0 | 28 |
| 39 | Pathogenesis and biomarkers of natural killer T cell lymphoma (NKTL). <i>Journal of Hematology and Oncology</i> , 2019, 12, 28. | 17.0 | 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. | 6.2 | 22 |
| 41 | PRDM15 is a key regulator of metabolism critical to sustain B-cell lymphomagenesis. <i>Nature Communications</i> , 2020, 11, 3520. | 12.8 | 20 |
| 42 | A composite single-nucleotide polymorphism prediction signature for extranodal natural killer/T-cell lymphoma. <i>Blood</i> , 2021, 138, 452-463. | 1.4 | 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. | 1.4 | 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. | 9.6 | 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. | 5.9 | 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. | 5.3 | 17 |
| 47 | Genome-Wide miRNA Expression Profiling of Molecular Subgroups of Peripheral T-cell Lymphoma. <i>Clinical Cancer Research</i> , 2021, 27, 6039-6053. | 7.0 | 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. | 2.5 | 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. | 1.6 | 17 |
| 50 | A clinicohaematological prognostic model for nasal-type natural killer/T-cell lymphoma: A multicenter study. <i>Scientific Reports</i> , 2019, 9, 14961. | 3.3 | 16 |
| 51 | Mutational Signatures in Mandibular Ameloblastoma Correlate with Smoking. <i>Journal of Dental Research</i> , 2019, 98, 652-658. | 5.2 | 14 |
| 52 | Whole-genome sequencing reveals potent therapeutic strategy for monomorphic epitheliotropic intestinal T-cell lymphoma. <i>Blood Advances</i> , 2020, 4, 4769-4774. | 5.2 | 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. | 1.1 | 14 |
| 54 | Effect of Ang-2-VEGF-A Bispecific Antibody in Renal Cell Carcinoma. <i>Cancer Investigation</i> , 2015, 33, 378-386. | 1.3 | 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. | 5.2 | 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. | 3.3 | 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. | 7.2 | 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. | 2.8 | 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. | 19.2 | 9 |
| 60 | Inhibition of placental growth factor in renal cell carcinoma. <i>Anticancer Research</i> , 2015, 35, 531-41. | 1.1 | 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. | 2.5 | 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. | 6.2 | 5 |
| 63 | Towards Next Generation Biomarkers in Natural Killer/T-Cell Lymphoma. <i>Life</i> , 2021, 11, 838. | 2.4 | 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. | 4.1 | 4 |
| 65 | T-Cell Lymphoma Clonality by Copy Number Variation Analysis of T-Cell Receptor Genes. <i>Cancers</i> , 2021, 13, 340. | 3.7 | 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. | 1.6 | 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. | 1.0 | 1 |
| 70 | Checkpoint immunotherapy for NK/T cell lymphoma—Time for a showdown?. <i>Precision Clinical Medicine</i> , 2021, 4, 70-72. | 3.3 | 1 |
| 71 | Molecular Subgroups of Peripheral T-Cell Lymphoma Evolve By Distinct Genetic Pathways. <i>Blood</i> , 2016, 128, 4096-4096. | 1.4 | 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. | 1.4 | 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. | 1.6 | 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. | 1.4 | 1 |
| 76 | Misaligned sequencing reads from the GNAQ-pseudogene locus may yield GNAQ artefact variants. Nature Communications, 2022, 13, 458. | 12.8 | 1 |
| 77 | Evaluation of the PI3K pathway in peripheral t-cell lymphoma. Annals of Oncology, 2017, 28, v364. | 1.2 | 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. | 1.4 | 0 |
| 83 | A Patient Derived Xenograft As a Preclinical Model for Monomorphic Epitheliotropic Intestinal T-Cell Lymphoma. Blood, 2018, 132, 2949-2949. | 1.4 | 0 |
| 84 | Pharmacogenomic Prediction of Bleomycin-Induced Pneumonitis in South East Asian Hodgkin Lymphoma Patients. Blood, 2018, 132, 4111-4111. | 1.4 | 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. | 1.4 | 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. | 1.6 | 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. | 1.6 | 0 |
| 88 | No association between <i>ECSIT</i> germline mutations and hemophagocytic lymphohistiocytosis in natural killer/T-cell lymphoma. Haematologica, 2021, 106, 1737-1739. | 3.5 | 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. | 1.4 | 0 |