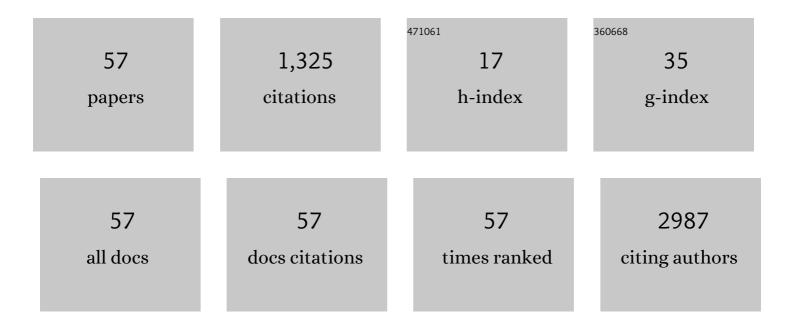
## Chung H Kok

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3919151/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Editorial: Molecular Mechanisms of Multiple Myeloma. Frontiers in Oncology, 2022, 12, 870123.	1.3	1
2	Outcomes following venetoclaxâ€based treatment in therapyâ€related myeloid neoplasms. American Journal of Hematology, 2022, 97, 1013-1022.	2.0	7
3	RNA-Based Targeted Gene Sequencing Improves the Diagnostic Yield of Mutant Detection in Chronic Myeloid Leukemia. Journal of Molecular Diagnostics, 2022, 24, 803-822.	1.2	2
4	CKLF and IL1B transcript levels at diagnosis are predictive of relapse in children with preâ€B ell acute lymphoblastic leukaemia. British Journal of Haematology, 2021, 193, 171-175.	1.2	2
5	Polycomb Factor PHF19 Controls Cell Growth and Differentiation Toward Erythroid Pathway in Chronic Myeloid Leukemia Cells. Frontiers in Cell and Developmental Biology, 2021, 9, 655201.	1.8	7
6	Clinical impact of <i>NPM1</i> -mutant molecular persistence after chemotherapy for acute myeloid leukemia. Blood Advances, 2021, 5, 5107-5111.	2.5	25
7	Distinct Senescent Bone Marrow Microenvironment in Therapy-Related Myeloid Neoplasms. Blood, 2021, 138, 2585-2585.	0.6	1
8	Highly Sensitive Droplet Digital PCR to Identify CML Patients with a High Probability of Achieving Treatment-Free Remission. Blood, 2021, 138, 2559-2559.	0.6	0
9	COVID-19 in Patients with Chronic Myeloid Leukemia: Poor Outcomes for Patients with Comorbidities, Older Age, Advanced Phase Disease, and Those from Low-Income Countries: An Update of the Candid Study. Blood, 2021, 138, 634-634.	0.6	5
10	Lineage of measurable residual disease in patients with chronic myeloid leukemia in treatment-free remission. Leukemia, 2020, 34, 1052-1061.	3.3	39
11	Integrated Bioinformatics Analysis Reveals Key Candidate Genes and Pathways Associated With Clinical Outcome in Hepatocellular Carcinoma. Frontiers in Genetics, 2020, 11, 814.	1.1	11
12	Successful treatmentâ€free remission in chronic myeloid leukaemia and its association with reduced immune suppressors and increased natural killer cells. British Journal of Haematology, 2020, 191, 433-441.	1.2	52
13	COVID-19 in Patients (pts) with Chronic Myeloid Leukemia (CML): Results from the International CML Foundation (iCMLf) CML and COVID-19 (CANDID) Study. Blood, 2020, 136, 46-47.	0.6	17
14	The Natural History of NPM1MUT Measurable Residual Disease (MRD) Positivity after Completion of Chemotherapy in Acute Myeloid Leukemia (AML). Blood, 2020, 136, 25-27.	0.6	4
15	Therapy-Related Myeloid Neoplasm Has a Distinct Pro-Inflammatory Bone Marrow Microenvironment and Delayed DNA Damage Repair. Blood, 2020, 136, 37-38.	0.6	0
16	Gene expression signature that predicts early molecular response failure in chronic-phase CML patients on frontline imatinib. Blood Advances, 2019, 3, 1610-1621.	2.5	27
17	A Combination of CD302 gene Expression and 3-Months BCR-ABL1 Level Predicts Inferior Achievement of Deep Molecular Response in CP-CML Patients Treated with Imatinib. Blood, 2019, 134, 663-663.	0.6	3
18	Pre-B acute lymphoblastic leukaemia recurrent fusion, EP300-ZNF384, is associated with a distinct gene expression. British Journal of Cancer, 2018, 118, 1000-1004.	2.9	28

Снимс Н Кок

#	Article	IF	CITATIONS
19	Long-term treatment-free remission of chronic myeloid leukemia with falling levels of residual leukemic cells. Leukemia, 2018, 32, 2572-2579.	3.3	66
20	Co-fuse: a new class discovery analysis tool to identify and prioritize recurrent fusion genes from RNA-sequencing data. Molecular Genetics and Genomics, 2018, 293, 1217-1229.	1.0	0
21	Modelling ponatinib resistance in tyrosine kinase inhibitor-naÃ <sup>-</sup> ve and dasatinib resistant <i>BCR-ABL1</i> + cell lines. Oncotarget, 2018, 9, 34735-34747.	0.8	12
22	Integration of Multiple Bioassays Using Machine Learning to Identify High-Risk CP-CML Patients Treated with Frontline Imatinib. Blood, 2018, 132, 1728-1728.	0.6	1
23	Increased peroxisome proliferator-activated receptor γ activity reduces imatinib uptake and efficacy in chronic myeloid leukemia mononuclear cells. Haematologica, 2017, 102, 843-853.	1.7	12
24	miR-155 as a potential target of IL-3 signaling in primary AML cells. Leukemia Research, 2017, 57, 57-59.	0.4	6
25	High prevalence of relapse in children with Philadelphia-like acute lymphoblastic leukemia despite risk-adapted treatment. Haematologica, 2017, 102, e490-e493.	1.7	52
26	Differential expression of MUC4, GPR110 and IL2RA defines two groups of CRLF2-rearranged acute lymphoblastic leukemia patients with distinct secondary lesions. Cancer Letters, 2017, 408, 92-101.	3.2	23
27	A Method for Next-Generation Sequencing of Paired Diagnostic and Remission Samples to Detect Mitochondrial DNA Mutations Associated with Leukemia. Journal of Molecular Diagnostics, 2017, 19, 711-721.	1.2	7
28	A novel somatic JAK2 kinase-domain mutation in pediatric acute lymphoblastic leukemia with rapid on-treatment development of LOH. Cancer Genetics, 2017, 216-217, 86-90.	0.2	10
29	In Vitro Modeling of Ph-like ALL Fusions Identifies Novel Kinase-Domain Mutations As Mode of TKI-Resistance - Implications for Targeted Therapy. Blood, 2016, 128, 3957-3957.	0.6	1
30	PTTG1 expression is associated with hyperproliferative disease and poor prognosis in multiple myeloma. Journal of Hematology and Oncology, 2015, 8, 106.	6.9	29
31	High Prevalence of Relapse in Australian Children with Ph-like Acute Lymphoblastic Leukemia Despite Risk Adapted Treatment. Blood, 2015, 126, 1419-1419.	0.6	1
32	A 20 Gene Expression Signature That Predicts Early Molecular Response Failure in Chronic Phase CML Patients Treated with Frontline Imatinib. Blood, 2015, 126, 596-596.	0.6	1
33	High Peroxisome Proliferator-Activated Receptor-Gamma (PPARγ) Transcriptional Activity Reduces Active Influx of Imatinib and Kinase Inhibition in CML Cells. Blood, 2015, 126, 2770-2770.	0.6	0
34	Interleukin-3-mediated regulation of β-catenin in myeloid transformation and acute myeloid leukemia. Journal of Leukocyte Biology, 2014, 96, 83-91.	1.5	13
35	Modeling Ponatinib Resistance in BCR-ABL1+ Cell Lines: Implications for Ponatinib Resistance in TKI-Resistant and TKI-naÃ <sup>-</sup> ve Patients. Blood, 2014, 124, 4515-4515.	0.6	1
36	Identification of an Epithelial-to-Mesenchymal Transition (EMT)-like Programme in t(4;14)-Positive Multiple Myeloma Reveals Novel Targets for Therapeutic Intervention. Blood, 2014, 124, 647-647.	0.6	1

Снимс Н Кок

#	Article	IF	CITATIONS
37	Whole Exome Sequencing of Acute Myeloid Leukaemia Patients Identifies Somatic and Germline Mutations in Fanconi Anaemia Genes. Blood, 2014, 124, 698-698.	0.6	0
38	High Plasma Levels of TGF-α and IL-6 at Diagnosis Predict Early Molecular Response Failure and Transformation in CML. Blood, 2014, 124, 1788-1788.	0.6	1
39	The preferential occurrence of <i><scp>FLT</scp>3</i> â€ <scp>TKD</scp> mutations in inv(16) <scp>AML</scp> and impact on survival outcome: a combined analysis of 1053 coreâ€binding factor <scp>AML</scp> patients. British Journal of Haematology, 2013, 160, 557-559.	1.2	11
40	Methylation of <i><scp>KLF</scp>5</i> contributes to reduced expression in acute myeloid leukaemia and is associated with poor overall survival. British Journal of Haematology, 2013, 161, 884-888.	1.2	18
41	HoxA9 regulated Bcl-2 expression mediates survival of myeloid progenitors and the severity of HoxA9-dependent leukemia. Oncotarget, 2013, 4, 1933-1947.	0.8	48
42	Role Of Peroxisome Proliferator-Activated Receptor Gamma (PPARγ) and Its Ligands In The Regulation Of Functional OCT-1 Activity In CML Cells. Blood, 2013, 122, 1470-1470.	0.6	0
43	Genome-wide gene expression profiling identifies overlap with malignant adrenocortical tumours and novel mechanisms of inefficient steroidogenesis in familial ACTH-independent macronodular adrenal hyperplasia. Endocrine-Related Cancer, 2012, 19, L19-L23.	1.6	6
44	Ecotopic viral integration site 1 (EVI1) regulates multiple cellular processes important for cancer and is a synergistic partner for FOS protein in invasive tumors. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2168-2173.	3.3	74
45	The GM-CSF receptor utilizes β-catenin and Tcf4 to specify macrophage lineage differentiation. Differentiation, 2012, 83, 47-59.	1.0	23
46	The granulocyte-associated transcription factor Krüppel-like factor 5 is silenced by hypermethylation in acute myeloid leukemia. Leukemia Research, 2012, 36, 110-116.	0.4	28
47	p53-Dependent Transcriptional Responses to Interleukin-3 Signaling. PLoS ONE, 2012, 7, e31428.	1.1	6
48	Global DNA Methylation Analysis Identifies Key Pathway Differences Between Poor (Low OCT-1 Activity) and Standard Risk CP-CML Patients At Diagnosis. Blood, 2012, 120, 3730-3730.	0.6	0
49	Methylation of the Proximal Promoter of GADD45A Is Common in Acute Myeloid Leukemia and Is Associated with Poor Survival Blood, 2012, 120, 2396-2396.	0.6	Ο
50	Heritable GATA2 mutations associated with familial myelodysplastic syndrome and acute myeloid leukemia. Nature Genetics, 2011, 43, 1012-1017.	9.4	524
51	Differential Lineage Involvement Between Very Low and Higher OCT-1 Activity Chronic-Phase CML Patients. Blood, 2011, 118, 1675-1675.	0.6	18
52	Non-Steroidal Anti-Inflammatory Drugs and Imatinib; Drug Interactions That May Impact Efficacy,. Blood, 2011, 118, 3501-3501.	0.6	0
53	Methylation of a Single CpG in the GADD45A Proximal Promoter Is Associated with Poor Survival in Acute Myeloid Leukemia,. Blood, 2011, 118, 3540-3540.	0.6	0
54	GATA2 is a New Predisposition Gene for Familial Myelodysplastic Syndrome (MDS) and Acute Myeloid Leukemia (AML). Blood, 2010, 116, LBA-3-LBA-3.	0.6	10

Снимс Н Кок

#	Article	IF	CITATIONS
55	Expression profiling of a hemopoietic cell survival transcriptome implicates osteopontin as a functional prognostic factor in AML. Blood, 2009, 114, 4859-4870.	0.6	52
56	Genetic regulators of myelopoiesis and leukemic signaling identified by gene profiling and linear modeling. Journal of Leukocyte Biology, 2006, 80, 433-447.	1.5	37
57	Highly sensitive droplet digital polymerase chain reaction for <i> <scp>BCR</scp> :: </i> <scp> <i>ABL1</i> messenger RNA </scp> identifies patients with chronic myeloid leukaemia with a low probability of achieving treatmentâ€free remission. British Journal of Haematology, 0, , .	1.2	2