Tobias Herold

List of Publications by Year
in descending order

118 papers	5,576 citations	109321 35 h-index	88630 70 g-index
130 all docs	130 docs citations	130 times ranked	11137 citing authors

#	Article	IF	Citations
1	Elevated levels of IL-6 and CRP predict the need for mechanical ventilation in COVID-19. Journal of Allergy and Clinical Immunology, 2020, 146, 128-136.e4.	2.9	783
2	A 17-gene stemness score for rapid determination of risk in acute leukaemia. Nature, 2016, 540, 433-437.	27.8	617
3	Spectrum and prognostic relevance of driver gene mutations in acute myeloid leukemia. Blood, 2016, 128, 686-698.	1.4	456
4	Coexpression profile of leukemic stem cell markers for combinatorial targeted therapy in AML. Leukemia, 2019, 33, 64-74.	7.2	212
5	COVID-19 severity and mortality in patients with chronic lymphocytic leukemia: a joint study by ERIC, the European Research Initiative on CLL, and CLL Campus. Leukemia, 2020, 34, 2354-2363.	7.2	198
6	Identification of a 24-Gene Prognostic Signature That Improves the European LeukemiaNet Risk Classification of Acute Myeloid Leukemia: An International Collaborative Study. Journal of Clinical Oncology, 2013, 31, 1172-1181.	1.6	164
7	GPR56 identifies primary human acute myeloid leukemia cells with high repopulating potential in vivo. Blood, 2016, 127, 2018-2027.	1.4	148
8	RIPK3 Restricts Myeloid Leukemogenesis by Promoting Cell Death and Differentiation of Leukemia Initiating Cells. Cancer Cell, 2016, 30, 75-91.	16.8	144
9	Validation and refinement of the revised 2017 European LeukemiaNet genetic risk stratification of acute myeloid leukemia. Leukemia, 2020, 34, 3161-3172.	7.2	141
10	GATA2 zinc finger 1 mutations associated with biallelic CEBPA mutations define a unique genetic entity of acute myeloid leukemia. Blood, 2012, 120, 395-403.	1.4	137
11	Adults with Philadelphia chromosome–like acute lymphoblastic leukemia frequently have *IGH-CRLF2* and *JAK2* mutations, persistence of minimal residual disease and poor prognosis. Haematologica, 2017, 102, 130-138.	3.5	136
12	miR-22 has a potent anti-tumour role with therapeutic potential in acute myeloid leukaemia. Nature Communications, 2016, 7, 11452.	12.8	113
13	Persistence of pre-leukemic clones during first remission and risk of relapse in acute myeloid leukemia. Leukemia, 2018, 32, 1598-1608.	7.2	106
14	Genetics of acute myeloid leukemia in the elderly: mutation spectrum and clinical impact in intensively treated patients aged 75 years or older. Haematologica, 2018, 103, 1853-1861.	3.5	96
15	A 29-gene and cytogenetic score for the prediction of resistance to induction treatment in acute myeloid leukemia. Haematologica, 2018, 103, 456-465.	3.5	84
16	RUNX1 mutations in cytogenetically normal acute myeloid leukemia are associated with a poor prognosis and up-regulation of lymphoid genes. Haematologica, 2012, 97, 1909-1915.	3.5	82
17	Isolated trisomy 13 defines a homogeneous AML subgroup with high frequency of mutations in spliceosome genes and poor prognosis. Blood, 2014, 124, 1304-1311.	1.4	81
18	Dual PI3K/mTOR inhibition shows antileukemic activity in MLL-rearranged acute myeloid leukemia. Leukemia, 2015, 29, 828-838.	7.2	63

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19	Evolution of Cytogenetically Normal Acute Myeloid Leukemia During Therapy and Relapse: An Exome Sequencing Study of 50 Patients. Clinical Cancer Research, 2018, 24, 1716-1726.	7.0	63
20	Ph-like Acute Lymphoblastic Leukemia in Older Adults. New England Journal of Medicine, 2014, 371, 2235-2235.	27.0	62
21	The clinical mutatome of core binding factor leukemia. Leukemia, 2020, 34, 1553-1562.	7.2	60
22	Activating FLT3 Mutants Show Distinct Gain-of-Function Phenotypes In Vitro and a Characteristic Signaling Pathway Profile Associated with Prognosis in Acute Myeloid Leukemia. PLoS ONE, 2014, 9, e89560.	2.5	60
23	An eight-gene expression signature for the prediction of survival and time to treatment in chronic lymphocytic leukemia. Leukemia, 2011, 25, 1639-1645.	7.2	59
24	Genomic 5-hydroxymethylcytosine levels correlate with TET2 mutations and a distinct global gene expression pattern in secondary acute myeloid leukemia. Leukemia, 2011, 25, 1649-1652.	7.2	57
25	COVID-19 severity and mortality in patients with CLL: an update of the international ERIC and Campus CLL study. Leukemia, 2021, 35, 3444-3454.	7.2	57
26	Preclinical efficacy of maternal embryonic leucine-zipper kinase (MELK) inhibition in acute myeloid leukemia. Oncotarget, 2014, 5, 12371-12382.	1.8	56
27	Adeno-associated virus serotypes 1 to 5 mediated tumor cell directed gene transfer and improvement of transduction efficiency. Journal of Gene Medicine, 2005, 7, 1429-1438.	2.8	51
28	IL-8 as mediator in the microenvironment-leukaemia network in acute myeloid leukaemia. Scientific Reports, 2016, 5, 18411.	3.3	51
29	Exome sequencing identifies recurring FLT3 N676K mutations in core-binding factor leukemia. Blood, 2013, 122, 1761-1769.	1.4	48
30	Eradication of Acute Myeloid Leukemia with FLT3 Ligand–Targeted miR-150 Nanoparticles. Cancer Research, 2016, 76, 4470-4480.	0.9	48
31	Genetic heterogeneity of cytogenetically normal AML with mutations of CEBPA. Blood Advances, 2018, 2, 2724-2731.	5.2	46
32	ZBTB7A mutations in acute myeloid leukaemia with t(8;21) translocation. Nature Communications, 2016, 7, 11733.	12.8	45
33	Hypoxia regulates proliferation of acute myeloid leukemia and sensitivity against chemotherapy. Leukemia Research, 2015, 39, 779-785.	0.8	43
34	The homeobox gene CDX2 is aberrantly expressed and associated with an inferior prognosis in patients with acute lymphoblastic leukemia. Leukemia, 2009, 23, 649-655.	7.2	38
35	A four-gene LincRNA expression signature predicts risk in multiple cohorts of acute myeloid leukemia patients. Leukemia, 2018, 32, 263-272.	7.2	36
36	Venetoclax with azacitidine targets refractory MDS but spares healthy hematopoiesis at tailored dose. Experimental Hematology and Oncology, 2019, 8, 9.	5.0	36

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37	Dynamics of SARS-CoV-2 shedding in the respiratory tract depends on the severity of disease in COVID-19 patients. European Respiratory Journal, 2021, 58, 2002724.	6.7	34
38	Priority-Lasso: a simple hierarchical approach to the prediction of clinical outcome using multi-omics data. BMC Bioinformatics, 2018, 19, 322.	2.6	33
39	Clonal heterogeneity of FLT3-ITD detected by high-throughput amplicon sequencing correlates with adverse prognosis in acute myeloid leukemia. Oncotarget, 2018, 9, 30128-30145.	1.8	33
40	Clinical presentation and differential splicing of SRSF2, U2AF1 and SF3B1 mutations in patients with acute myeloid leukemia. Leukemia, 2020, 34, 2621-2634.	7.2	31
41	The neuropeptide receptor calcitonin receptor-like (CALCRL) is a potential therapeutic target in acute myeloid leukemia. Leukemia, 2019, 33, 2830-2841.	7.2	30
42	Ph-like acute lymphoblastic leukemia in older adults. New England Journal of Medicine, 2014, 371, 2235.	27.0	30
43	Breakthrough infection of Trichosporon asahii during posaconazole treatment in a patient with acute myeloid leukaemia. European Journal of Clinical Microbiology and Infectious Diseases, 2007, 26, 843-845.	2.9	27
44	Integrative Analysis of Lincrna Expression and Clinical Annotations Reveals a Signature of 17 Genes with Prognostic Significance in Acute Myeloid Leukemia (AML). Blood, 2014, 124, 483-483.	1.4	27
45	RNA Splicing Alterations Induce a Cellular Stress Response Associated with Poor Prognosis in Acute Myeloid Leukemia. Clinical Cancer Research, 2020, 26, 3597-3607.	7.0	26
46	TET1 promotes growth of T-cell acute lymphoblastic leukemia and can be antagonized via PARP inhibition. Leukemia, 2021, 35, 389-403.	7.2	26
47	Philadelphia-Like Acute Lymphoblastic Leukemia in Adults. Current Oncology Reports, 2017, 19, 31.	4.0	25
48	Silencing of GATA3 defines a novel stem cell-like subgroup of ETP-ALL. Journal of Hematology and Oncology, 2016, 9, 95.	17.0	23
49	SAMHD1 is a key regulator of the lineage-specific response of acute lymphoblastic leukaemias to nelarabine. Communications Biology, 2020, 3, 324.	4.4	23
50	Loss-of-function mutations in the histone methyltransferase EZH2 promote chemotherapy resistance in AML. Scientific Reports, 2021, 11, 5838.	3.3	22
51	Sequential therapy combining clofarabine and T-cell-replete HLA-haploidentical haematopoietic SCT is feasible and shows efficacy in the treatment of refractory or relapsed aggressive lymphoma. Bone Marrow Transplantation, 2015, 50, 679-684.	2.4	21
52	Clinical and preclinical characterization of CD99 isoforms in acute myeloid leukemia. Haematologica, 2020, 105, 999-1012.	3.5	19
53	High expression of *MZB1* predicts adverse prognosis in chronic lymphocytic leukemia, follicular lymphoma and diffuse large B-cell lymphoma and is associated with a unique gene expression signature. Leukemia and Lymphoma, 2013, 54, 1652-1657.	1.3	18
54	HER2 expression and markers of phosphoinositide-3-kinase pathway activation define a favorable subgroup of metastatic pulmonary adenocarcinomas. Lung Cancer, 2015, 88, 34-41.	2.0	17

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55	An Immune Risk Score Predicts Survival of Patients with Acute Myeloid Leukemia Receiving Chemotherapy. Clinical Cancer Research, 2021, 27, 255-266.	7.0	17
56	Differential impact of *IDH1*/*2* mutational subclasses on outcome in adult AML: results from a large multicenter study. Blood Advances, 2022, 6, 1394-1405.	5.2	17
57	Expression analysis of genes located in the minimally deleted regions of 13q14 and 11q22â€23 in chronic lymphocytic leukemiaâ€"unexpected expression pattern of the RHO GTPase activator *ARHGAP20*. Genes Chromosomes and Cancer, 2011, 50, 546-558.	2.8	16
58	RUNX1/ETO blocks selectin-mediated adhesion via epigenetic silencing of PSGL-1. Oncogenesis, 2015, 4, e146-e146.	4.9	16
59	High Expression of the Endoplasmic Reticulum Protein MZB1 predicts Inferior Prognosis in Chronic Lymphocytic Leukemia, Follicular Lymphoma and Diffuse Large B-Cell Lymphoma and Is Associated with a Unique Gene Expression Profile,. Blood, 2011, 118, 3657-3657.	1.4	16
60	Acute myeloid leukemia with del(9q) is characterized by frequent mutations of *NPM1*, *DNMT3A, WT1* and low expression of *TLE4*. Genes Chromosomes and Cancer, 2017, 56, 75-86.	2.8	15
61	Plasticity in growth behavior of patients' acute myeloid leukemia stem cells growing in mice. Haematologica, 2020, 105, 2855-2860.	3.5	15
62	Progressive multifocal leukoencephalopathy after treatment with rituximab, fludarabine and cyclophosphamide in a patient with chronic lymphocytic leukemia. Leukemia and Lymphoma, 2012, 53, 169-172.	1.3	14
63	A 4â€gene expression score associated with high levels of *Wilms Tumorâ€1 (WT1)* expression is an adverse prognostic factor in acute myeloid leukaemia. British Journal of Haematology, 2016, 172, 401-411.	2.5	14
64	Extracorporeal Membrane Oxygenation in Predominantly Leuco- and Thrombocytopenic Haematologic/Oncologic Patients with Acute Respiratory Distress Syndrome - a Single-Centre Experience. Oncology Research and Treatment, 2018, 41, 539-543.	1.2	14
65	Fusion gene detection by RNA sequencing complements diagnostics of acute myeloid leukemia and identifies recurring NRIP1-MIR99AHG rearrangements. Haematologica, 2021, , .	3.5	13
66	Close correlation of copy number aberrations detected by nextâ€generation sequencing with results from routine cytogenetics in acute myeloid leukemia. Genes Chromosomes and Cancer, 2016, 55, 553-567.	2.8	12
67	Complement cascade gene expression defines novel prognostic subgroups of acute myeloid leukemia. Experimental Hematology, 2016, 44, 1039-1043.e10.	0.4	12
68	Nuclear factor of activated T-cells, NFATC1, governs FLT3ITD-driven hematopoietic stem cell transformation and a poor prognosis in AML. Journal of Hematology and Oncology, 2019, 12, 72.	17.0	12
69	Lowâ€density lipoprotein receptor (LDLR) is an independent adverse prognostic factor in acute myeloid leukaemia. British Journal of Haematology, 2021, 192, 494-503.	2.5	12
70	The target cell of transformation is distinct from the leukemia stem cell in murine CALM/AF10 leukemia models. Leukemia, 2016, 30, 1166-1176.	7.2	10
71	In vivo inducible reverse genetics in patientsâ€™ tumors to identify individual therapeutic targets. Nature Communications, 2021, 12, 5655.	12.8	10
72	Mediation analysis reveals common mechanisms of RUNX1 point mutations and RUNX1/RUNX1T1 fusions influencing survival of patients with acute myeloid leukemia. Scientific Reports, 2018, 8, 11293.	3.3	9

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73	Allelic Imbalance of Recurrently Mutated Genes in Acute Myeloid Leukaemia. Scientific Reports, 2019, 9, 11796.	3.3	9
74	MLKL promotes cellular differentiation in myeloid leukemia by facilitating the release of G-CSF. Cell Death and Differentiation, 2021, 28, 3235-3250.	11.2	9
75	Persistence of pre-leukemic clones during first remission and risk of relapse in acute myeloid leukemia. Leukemia, 2017, , .	7.2	8
76	Subtype assignment of CLL based on B-cell subset associated gene signatures from normal bone marrow â€" A proof of concept study. PLoS ONE, 2018, 13, e0193249.	2.5	8
77	<scp>HERVs</scp> characterize normal and leukemia stem cells and represent a source of shared epitopes for cancer immunotherapy. American Journal of Hematology, 2022, 97, 1200-1214.	4.1	8
78	Added predictive value of omics data: specific issues related to validation illustrated by two case studies. BMC Medical Research Methodology, 2014, 14, 117.	3.1	6
79	NPM1 Variant Allele Frequency and Outcomes in AML. Blood, 2018, 132, 1486-1486.	1.4	6
80	DNA Methylation Profiling of AML Reveals Epigenetic Subgroups with Distinct Clinical Outcome. Blood, 2019, 134, 2715-2715.	1.4	6
81	The retinoic acid receptor co-factor NRIP1 is uniquely upregulated and represents a therapeutic target in acute myeloid leukemia with chromosome 3q rearrangements. Haematologica, 2022, 107, 1758-1772.	3.5	6
82	Inducible transgene expression in PDX models in vivo identifies KLF4 as a therapeutic target for B-ALL. Biomarker Research, 2020, 8, 46.	6.8	5
83	Acute Myeloid Leukemia With Isolated Trisomy 13 Is a Genetically Homogenous Entity With a High Frequency Of Mutations In Genes Encoding Components Of The Splicing Machinery and Extremely Poor Prognosis. Blood, 2013, 122, 608-608.	1.4	5
84	The long non-coding RNA <i>Cancer Susceptibility 15</i> (<i>CASC15</i>) is induced by isocitrate dehydrogenase (IDH) mutations and maintains an immature phenotype in adult acute myeloid leukemia. Haematologica, 2020, 105, e448-453.	3.5	5
85	The ParaHox gene Cdx4 induces acute erythroid leukemia in mice. Blood Advances, 2019, 3, 3729-3739.	5.2	4
86	Clinical and molecular relevance of genetic variants in the non-coding transcriptome of patients with cytogenetically normal acute myeloid leukemia. Haematologica, 2022, 107, 1034-1044.	3.5	4
87	RNA and protein expression of herpesvirus entry mediator (HVEM) is associated with molecular markers, immunity-related pathways and relapse-free survival of patients with AML. Cancer Immunology, Immunotherapy, 2015, 64, 1505-1515.	4.2	3
88	Exome Sequencing Identifies Recurring FLT3 N676K Mutations in Core Binding Factor Leukemia. Blood, 2012, 120, 404-404.	1.4	3
89	Activating FLT3 Mutations Display a Wide Range Of Transforming Potential and a Characteristic Pathway Profile Associated With Prognosis In Acute Myeloid Leukemia. Blood, 2013, 122, 1312-1312.	1.4	3
90	Targeted Treatment of FLT3 -Overexpressing Acute Myeloid Leukemia with MiR-150 Nanoparticles Guided By Conjugated FLT3 Ligand Peptides. Blood, 2015, 126, 3784-3784.	1.4	2

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91	DNMT3A Mutations Associate with Shorter Survival and Modulate the Prognostic Impact of Mutated NPM1: an Analysis Based on Comprehensive Mutational Screening of 660 AML Patients Treated on German AML Cooperative Group (AMLCG) Trials. Blood, 2015, 126, 3815-3815.	1.4	2
92	Worldwide Examination of Patients with CLL Hospitalized for COVID-19. Blood, 2020, 136, 45-49.	1.4	2
93	BCR-ABL1-like Acute Lymphoblastic Leukemia Is Associated with IKZF1 and JAK2 Alterations and inferior Outcome in Adults. Blood, 2014, 124, 3787-3787.	1.4	1
94	PS29MRC - a Novel Predictive Score for Response to Therapy in Acute Myeloid Leukemia. Blood, 2016, 128, 1209-1209.	1.4	1
95	Alterations Of The Chemokine Microenvironment In Chronic Lymphocytic Leukemia. Blood, 2013, 122, 1619-1619.	1.4	1
96	The Mutatome of CBFB/MYH11-rearranged Acute Myeloid Leukemia (AML). Blood, 2014, 124, 14-14.	1.4	1
97	A CRISPR/Cas9 Library Screen in Patients' Leukemia Cells In Vivo. Blood, 2019, 134, 3945-3945.	1.4	1
98	Adverse stem cell clones within a single patient's tumor predict clinical outcome in AML patients. Journal of Hematology and Oncology, 2022, 15, 25.	17.0	1
99	Specific effects of somatic GATA2 zinc finger mutations on erythroid differentiation. Experimental Hematology, 2022, 108, 26-35.	0.4	1
100	PS929ÂKLF4 EXERTS A TUMOR SUPPRESSOR FUNCTION IN PATIENTS' B‐ALL CELLS GROWING IN MICE AND IS RE‐UPREGULATED BY AZACYTIDIN. HemaSphere, 2019, 3, 418-419.	2.7	0
101	A Clinically Applicable Gene Expression based Score predicts Resistance to Induction Treatment in Acute Myeloid Leukemia. Blood Advances, 2021, 5, 4752-4761.	5.2	0
102	Role of Microenvironment-Associated Chemokines and Cytokines for Binet Stage A CLL Patients Included in a Prospective Trial (CLL1 trial) of the German CLL Study Group (GCLLSG): sll2Ralpha Is An Independent Predictor of Progression-Free Survival (PFS),. Blood, 2011, 118, 3869-3869.	1.4	0
103	Copy Number Alteration (CNA) Analysis in Targeted Sequencing Data from Acute Myeloid Leukemia (AML) Patients with Chromosome 9q Deletion. Blood, 2014, 124, 1058-1058.	1.4	0
104	Targeted, Deep Sequencing of Adult AML Patients Treated on the AMLCG-2008 Trial Detects Clonal Heterogeneity in 52% of Patients at Initial Diagnosis and Reveals Patterns of Clonal Evolution. Blood, 2014, 124, 697-697.	1.4	0
105	Genetic Characterization of Patients with Monoallelic and Biallelic CEBPA Mutations Using a Targeted Sequencing Approach Reveals Differences in the Spectrum of Cooperating Mutations. Blood, 2014, 124, 2385-2385.	1.4	0
106	Identification of TET1â₤miR-22â₤CREB-MYC Signaling Reveals Potent Tumor-Suppressor Role of Mir-22 in Acute Myeloid Leukemia. Blood, 2014, 124, 886-886.	1.4	0
107	A 16-Gene Signature Associated with High Levels of Wilms Tumor-1 (WT1) Expression Is an Adverse Prognostic Factor in Acute Myeloid Leukemia. Blood, 2014, 124, 1021-1021.	1.4	0
108	Analysis of the Tissue-Specific Expression Requirements and Identification of Cooperating Mutations for Leukemogenesis in an Inducible CALM/AF10 Knock-in Mouse Model. Blood, 2014, 124, 126-126.	1.4	0

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109	Normal B-Cell Gene Expression Signatures Classifies Chronic Lymphocytic Leukemia into Distinct Subtypes - Indication of Plasticity. Blood, 2016, 128, 2017-2017.	1.4	0
110	High Expression of ARMCX1 Predicts Poor Survival in Intensively Treated Older Acute Myeloid Leukemia Patients (â‰¥ 60 years). Blood, 2016, 128, 2840-2840.	1.4	0
111	PF210 CLINICAL ASPECTS AND DIFFERENTIAL SPLICING IN ACUTE MYELOID LEUKEMIA PATIENTS WITH SRSF2, U2AF1 AND SF3B1 MUTATIONS. HemaSphere, 2019, 3, 57.	2.7	0
112	Gene Fusion Detection By RNA-Seq in Acute Myeloid Leukemia (AML). Blood, 2019, 134, 4655-4655.	1.4	0
113	Identification of Recurrent Alternative RNA Splicing in Adverse-Risk Acute Myeloid Leukemia. Blood, 2019, 134, 457-457.	1.4	0
114	Single Cell Clones Derived from a Patient's AML Xenograft Display Genetic and Functional Heterogeneity. Blood, 2019, 134, 1450-1450.	1.4	0
115	Prospective Identification of Acute Myeloid Leukemia Patients Who Benefit from Gene-Expression Based Risk Stratification. Blood, 2019, 134, 1397-1397.	1.4	0
116	CSF3R T618I Collaborates with RUNX1-RUNX1T1 to Expand Human Haematopoietic Stem and Progenitor Cells. Blood, 2021, 138, 2233-2233.	1.4	0
117	In Vivo CRISPR-Cas9 Screens in PDX Models Reveals ADAM10 As Novel Therapeutic Target in Acute Leukemia. Blood, 2021, 138, 708-708.	1.4	0
118	Streamlining preclinical in vivo treatment trials by multiplexing genetically labelled PDX models in a single mouse. Klinische Padiatrie, 2022, , .	0.6	0