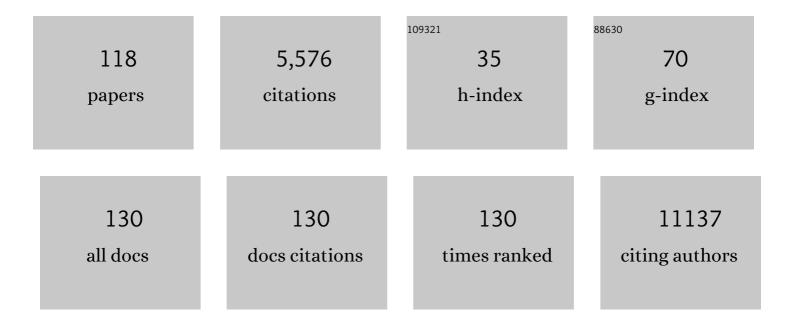
Tobias Herold

List of Publications by Year in descending order

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TORIAS HEDOLD

#	Article	IF	CITATIONS
1	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
2	Differential impact of <i>IDH1</i> / <i>2</i> mutational subclasses on outcome in adult AML: results from a large multicenter study. Blood Advances, 2022, 6, 1394-1405.	5.2	17
3	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
4	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
5	Specific effects of somatic GATA2 zinc finger mutations on erythroid differentiation. Experimental Hematology, 2022, 108, 26-35.	0.4	1
6	Streamlining preclinical in vivo treatment trials by multiplexing genetically labelled PDX models in a single mouse. Klinische Padiatrie, 2022, , .	0.6	0
7	<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
8	TET1 promotes growth of T-cell acute lymphoblastic leukemia and can be antagonized via PARP inhibition. Leukemia, 2021, 35, 389-403.	7.2	26
9	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
10	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
11	Loss-of-function mutations in the histone methyltransferase EZH2 promote chemotherapy resistance in AML. Scientific Reports, 2021, 11, 5838.	3.3	22
12	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
13	Fusion gene detection by RNA sequencing complements diagnostics of acute myeloid leukemia and identifies recurring NRIP1-MIR99AHG rearrangements. Haematologica, 2021, , .	3.5	13
14	In vivo inducible reverse genetics in patients' tumors to identify individual therapeutic targets. Nature Communications, 2021, 12, 5655.	12.8	10
15	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
16	An Immune Risk Score Predicts Survival of Patients with Acute Myeloid Leukemia Receiving Chemotherapy. Clinical Cancer Research, 2021, 27, 255-266.	7.0	17
17	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
18	CSF3R T618I Collaborates with RUNX1-RUNX1T1 to Expand Human Haematopoietic Stem and Progenitor Cells. Blood, 2021, 138, 2233-2233.	1.4	0

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19	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
20	The clinical mutatome of core binding factor leukemia. Leukemia, 2020, 34, 1553-1562.	7.2	60
21	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
22	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
23	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
24	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
25	SAMHD1 is a key regulator of the lineage-specific response of acute lymphoblastic leukaemias to nelarabine. Communications Biology, 2020, 3, 324.	4.4	23
26	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
27	Validation and refinement of the revised 2017 European LeukemiaNet genetic risk stratification of acute myeloid leukemia. Leukemia, 2020, 34, 3161-3172.	7.2	141
28	Clinical and preclinical characterization of CD99 isoforms in acute myeloid leukemia. Haematologica, 2020, 105, 999-1012.	3.5	19
29	Plasticity in growth behavior of patients' acute myeloid leukemia stem cells growing in mice. Haematologica, 2020, 105, 2855-2860.	3.5	15
30	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
31	Worldwide Examination of Patients with CLL Hospitalized for COVID-19. Blood, 2020, 136, 45-49.	1.4	2
32	Coexpression profile of leukemic stem cell markers for combinatorial targeted therapy in AML. Leukemia, 2019, 33, 64-74.	7.2	212
33	Allelic Imbalance of Recurrently Mutated Genes in Acute Myeloid Leukaemia. Scientific Reports, 2019, 9, 11796.	3.3	9
34	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
35	The neuropeptide receptor calcitonin receptor-like (CALCRL) is a potential therapeutic target in acute myeloid leukemia. Leukemia, 2019, 33, 2830-2841.	7.2	30
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	The ParaHox gene Cdx4 induces acute erythroid leukemia in mice. Blood Advances, 2019, 3, 3729-3739.	5.2	4
38	PS929ÂKLF4 EXERTS A TUMOR SUPPRESSOR FUNCTION IN PATIENTS' Bâ€ALL CELLS GROWING IN MICE AND REâ€UPREGULATED BY AZACYTIDIN. HemaSphere, 2019, 3, 418-419.) S 2.7	0
39	DNA Methylation Profiling of AML Reveals Epigenetic Subgroups with Distinct Clinical Outcome. Blood, 2019, 134, 2715-2715.	1.4	6
40	PF210 CLINICAL ASPECTS AND DIFFERENTIAL SPLICING IN ACUTE MYELOID LEUKEMIA PATIENTS WITH SRSF2, U2AF1 AND SF3B1 MUTATIONS. HemaSphere, 2019, 3, 57.	2.7	0
41	Gene Fusion Detection By RNA-Seq in Acute Myeloid Leukemia (AML). Blood, 2019, 134, 4655-4655.	1.4	0
42	Identification of Recurrent Alternative RNA Splicing in Adverse-Risk Acute Myeloid Leukemia. Blood, 2019, 134, 457-457.	1.4	0
43	Single Cell Clones Derived from a Patient's AML Xenograft Display Genetic and Functional Heterogeneity. Blood, 2019, 134, 1450-1450.	1.4	0
44	A CRISPR/Cas9 Library Screen in Patients' Leukemia Cells In Vivo. Blood, 2019, 134, 3945-3945.	1.4	1
45	Prospective Identification of Acute Myeloid Leukemia Patients Who Benefit from Gene-Expression Based Risk Stratification. Blood, 2019, 134, 1397-1397.	1.4	Ο
46	Persistence of pre-leukemic clones during first remission and risk of relapse in acute myeloid leukemia. Leukemia, 2018, 32, 1598-1608.	7.2	106
47	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
48	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
49	A four-gene LincRNA expression signature predicts risk in multiple cohorts of acute myeloid leukemia patients. Leukemia, 2018, 32, 263-272.	7.2	36
50	Priority-Lasso: a simple hierarchical approach to the prediction of clinical outcome using multi-omics data. BMC Bioinformatics, 2018, 19, 322.	2.6	33
51	Genetic heterogeneity of cytogenetically normal AML with mutations of CEBPA. Blood Advances, 2018, 2, 2724-2731.	5.2	46
52	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
53	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
54	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

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55	NPM1 Variant Allele Frequency and Outcomes in AML. Blood, 2018, 132, 1486-1486.	1.4	6
56	Subtype assignment of CLL based on B-cell subset associated gene signatures from normal bone marrow – A proof of concept study. PLoS ONE, 2018, 13, e0193249.	2.5	8
57	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
58	Philadelphia-Like Acute Lymphoblastic Leukemia in Adults. Current Oncology Reports, 2017, 19, 31.	4.0	25
59	Adults with Philadelphia chromosome–like acute lymphoblastic leukemia frequently have <i>IGH-CRLF2</i> and <i>JAK2</i> mutations, persistence of minimal residual disease and poor prognosis. Haematologica, 2017, 102, 130-138.	3.5	136
60	Acute myeloid leukemia with del(9q) is characterized by frequent mutations of <i>NPM1</i> , <i>DNMT3A, WT1</i> and low expression of <i>TLE4</i> . Genes Chromosomes and Cancer, 2017, 56, 75-86.	2.8	15
61	Persistence of pre-leukemic clones during first remission and risk of relapse in acute myeloid leukemia. Leukemia, 2017, , .	7.2	8
62	RIPK3 Restricts Myeloid Leukemogenesis by Promoting Cell Death and Differentiation of Leukemia Initiating Cells. Cancer Cell, 2016, 30, 75-91.	16.8	144
63	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
64	IL-8 as mediator in the microenvironment-leukaemia network in acute myeloid leukaemia. Scientific Reports, 2016, 5, 18411.	3.3	51
65	A 17-gene stemness score for rapid determination of risk in acute leukaemia. Nature, 2016, 540, 433-437.	27.8	617
66	Spectrum and prognostic relevance of driver gene mutations in acute myeloid leukemia. Blood, 2016, 128, 686-698.	1.4	456
67	Silencing of GATA3 defines a novel stem cell-like subgroup of ETP-ALL. Journal of Hematology and Oncology, 2016, 9, 95.	17.0	23
68	Complement cascade gene expression defines novel prognostic subgroups of acute myeloid leukemia. Experimental Hematology, 2016, 44, 1039-1043.e10.	0.4	12
69	GPR56 identifies primary human acute myeloid leukemia cells with high repopulating potential in vivo. Blood, 2016, 127, 2018-2027.	1.4	148
70	ZBTB7A mutations in acute myeloid leukaemia with t(8;21) translocation. Nature Communications, 2016, 7, 11733.	12.8	45
71	miR-22 has a potent anti-tumour role with therapeutic potential in acute myeloid leukaemia. Nature Communications, 2016, 7, 11452.	12.8	113
72	Eradication of Acute Myeloid Leukemia with FLT3 Ligand–Targeted miR-150 Nanoparticles. Cancer Research, 2016, 76, 4470-4480.	0.9	48

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73	A 4â€gene expression score associated with high levels of <i>Wilms Tumorâ€1 (<scp>WT</scp>1)</i> expression is an adverse prognostic factor in acute myeloid leukaemia. British Journal of Haematology, 2016, 172, 401-411.	2.5	14
74	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
75	PS29MRC - a Novel Predictive Score for Response to Therapy in Acute Myeloid Leukemia. Blood, 2016, 128, 1209-1209.	1.4	1
76	Normal B-Cell Gene Expression Signatures Classifies Chronic Lymphocytic Leukemia into Distinct Subtypes - Indication of Plasticity. Blood, 2016, 128, 2017-2017.	1.4	0
77	High Expression of ARMCX1 Predicts Poor Survival in Intensively Treated Older Acute Myeloid Leukemia Patients (≥ 60 years). Blood, 2016, 128, 2840-2840.	1.4	0
78	RUNX1/ETO blocks selectin-mediated adhesion via epigenetic silencing of PSGL-1. Oncogenesis, 2015, 4, e146-e146.	4.9	16
79	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
80	Hypoxia regulates proliferation of acute myeloid leukemia and sensitivity against chemotherapy. Leukemia Research, 2015, 39, 779-785.	0.8	43
81	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
82	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
83	Dual PI3K/mTOR inhibition shows antileukemic activity in MLL-rearranged acute myeloid leukemia. Leukemia, 2015, 29, 828-838.	7.2	63
84	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
85	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
86	Ph-like Acute Lymphoblastic Leukemia in Older Adults. New England Journal of Medicine, 2014, 371, 2235-2235.	27.0	62
87	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
88	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
89	Ph-like acute lymphoblastic leukemia in older adults. New England Journal of Medicine, 2014, 371, 2235.	27.0	30
90	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

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91	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
92	Preclinical efficacy of maternal embryonic leucine-zipper kinase (MELK) inhibition in acute myeloid leukemia. Oncotarget, 2014, 5, 12371-12382.	1.8	56
93	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
94	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
95	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
96	Identification of TET1⊣miR-22⊣CREB-MYC Signaling Reveals Potent Tumor-Suppressor Role of Mir-22 in Acute Myeloid Leukemia. Blood, 2014, 124, 886-886.	1.4	0
97	The Mutatome of CBFB/MYH11-rearranged Acute Myeloid Leukemia (AML). Blood, 2014, 124, 14-14.	1.4	1
98	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
99	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
100	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
101	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
102	High expression of <i>MZB1</i> 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
103	Exome sequencing identifies recurring FLT3 N676K mutations in core-binding factor leukemia. Blood, 2013, 122, 1761-1769.	1.4	48
104	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
105	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
106	Alterations Of The Chemokine Microenvironment In Chronic Lymphocytic Leukemia. Blood, 2013, 122, 1619-1619.	1.4	1
107	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
108	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

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109	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
110	Exome Sequencing Identifies Recurring FLT3 N676K Mutations in Core Binding Factor Leukemia. Blood, 2012, 120, 404-404.	1.4	3
111	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
112	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
113	Expression analysis of genes located in the minimally deleted regions of 13q14 and 11q22â€23 in chronic lymphocytic leukemia—unexpected expression pattern of the RHO GTPase activator <i>ARHGAP20</i> . Genes Chromosomes and Cancer, 2011, 50, 546-558.	2.8	16
114	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): sIl2Ralpha Is An Independent Predictor of Progression-Free Survival (PFS),. Blood, 2011, 118, 3869-3869.	1.4	0
115	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
116	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
117	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
118	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