Torsten Haferlach

List of Publications by Year
in descending order

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125 papers	14,914 citations	41344 49 h-index	19190 118 g-index
127 all docs	127 docs citations	127 times ranked	12762 citing authors

#	Article	IF	Citations
1	Next-generation diagnostics for precision oncology: Preanalytical considerations, technical challenges, and available technologies. Seminars in Cancer Biology, 2022, 84, 3-15.	9.6	12
2	Analytical demands to use whole-genome sequencing in precision oncology. Seminars in Cancer Biology, 2022, 84, 16-22.	9.6	22
3	Indeterminate and oncogenic potential: CHIP vs CHOP mutations in AML with NPM1 alteration. Leukemia, 2022, 36, 394-402.	7.2	24
4	Aberrant somatic hypermutation of CCND1 generates non-coding drivers of mantle cell lymphomagenesis. Cancer Gene Therapy, 2022, , .	4.6	1
5	CCL22 mutations drive natural killer cell lymphoproliferative disease by deregulating microenvironmental crosstalk. Nature Genetics, 2022, 54, 637-648.	21.4	13
6	The 5th edition of the World Health Organization Classification of Haematolymphoid Tumours: Myeloid and Histiocytic/DendriticÂNeoplasms. Leukemia, 2022, 36, 1703-1719.	7.2	1,211
7	AML, NOS and AML-MRC as defined by multilineage dysplasia share a common mutation pattern which is distinct from AML-MRC as defined by MDS-related cytogenetics. Leukemia, 2022, 36, 1939-1942.	7.2	9
8	Rare germline alterations of myeloperoxidase predispose to myeloid neoplasms. Leukemia, 2022, 36, 2086-2096.	7.2	2
9	Clinical relevance of molecular characteristics in Burkitt lymphoma differs according to age. Nature Communications, 2022, 13, .	12.8	28
10	Precision Medicine in Hematology 2021: Definitions, Tools, Perspectives, and Open Questions. HemaSphere, 2021, 5, e536.	2.7	11
11	The time has come for next-generation sequencing in routine diagnostic workup in hematology. Haematologica, 2021, 106, 659-661.	3.5	3
12	Machine learning integrates genomic signatures for subclassification beyond primary and secondary acute myeloid leukemia. Blood, 2021, 138, 1885-1895.	1.4	32
13	How artificial intelligence might disrupt diagnostics in hematology in the near future. Oncogene, 2021, 40, 4271-4280.	5.9	34
14	Genome Sequencing in Myeloid Cancers. New England Journal of Medicine, 2021, 384, e106.	27.0	13
15	Splicing factor gene mutations in acute myeloid leukemia offer additive value if incorporated in current risk classification. Blood Advances, 2021, 5, 3254-3265.	5.2	30
16	Maturation State-Specific Alternative Splicing in FLT3-ITD and NPM1 Mutated AML. Cancers, 2021, 13, 3929.	3.7	5
17	A geno-clinical decision model for the diagnosis of myelodysplastic syndromes. Blood Advances, 2021, 5, 4361-4369.	5.2	9
18	The combination of WGS and RNA-Seq is superior to conventional diagnostic tests in multiple myeloma: Ready for prime time?. Cancer Genetics, 2020, 242, 15-24.	0.4	32

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19	The power and potential of integrated diagnostics in acute myeloid leukaemia. British Journal of Haematology, 2020, 188, 36-48.	2.5	44
20	Progress in the molecular diagnostics of hematologic neoplasia. Best Practice and Research in Clinical Haematology, 2020, 33, 101198.	1.7	0
21	Whole transcriptome sequencing detects a large number of novel fusion transcripts in patients with AML and MDS. Blood Advances, 2020, 4, 5393-5401.	5.2	29
22	Hematologistâ€Ł evel Classification of Mature Bâ€Cell Neoplasm Using Deep Learning on Multiparameter Flow Cytometry Data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 1073-1080.	1.5	32
23	WGS and WTS in leukaemia: A tool for diagnostics?. Best Practice and Research in Clinical Haematology, 2020, 33, 101190.	1.7	7
24	Molecular landscape and clonal architecture of adult myelodysplastic/myeloproliferative neoplasms. Blood, 2020, 136, 1851-1862.	1.4	112
25	Artificial Intelligence Substantially Supports Chromosome Banding Analysis Maintaining Its Strengths in Hematologic Diagnostics Even in the Era of Newer Technologies. Blood, 2020, 136, 47-48.	1.4	6
26	A Personalized Clinical-Decision Tool to Improve the Diagnostic Accuracy of Myelodysplastic Syndromes. Blood, 2020, 136, 33-35.	1.4	2
27	Machine Learning (ML) Can Successfully Support Microscopic Differential Counts of Peripheral Blood Smears in a High Throughput Hematology Laboratory. Blood, 2020, 136, 45-46.	1.4	4
28	Employment of Machine Learning Models Yields Highly Accurate Hematological Disease Prediction from Raw Flow Cytometry Matrix Data without the Need for Visualization or Human Intervention. Blood, 2020, 136, 11-11.	1.4	2
29	Creating a Variant Database for the American Society of Hematalogy By Consensus Variant Classification of Common Genes Associated with Hematologic Malignancies. Blood, 2020, 136, 4-5.	1.4	2
30	Correlation of Mutation Patterns with Patient Age in 2656 Cases with 11 Different Hematological Malignancies. Blood, 2020, 136, 16-17.	1.4	1
31	The Molecular Pathology of Myelodysplastic Syndrome. Pathobiology, 2019, 86, 24-29.	3.8	30
32	â€œSomaticâ€•and â€œpathogenicâ€• is the classification strategy applicable in times of large-scale sequencing?. Haematologica, 2019, 104, 1515-1520.	3.5	9
33	Dark-matter matters: Discriminating subtle blood cancers using the darkest DNA. PLoS Computational Biology, 2019, 15, e1007332.	3.2	7
34	DNMT3A mutations are over-represented in young adults with NPM1 mutated AML and prompt a distinct co-mutational pattern. Leukemia, 2019, 33, 2741-2746.	7.2	15
35	More than a fusion gene: the RUNX1-RUNX1T1 AML. Blood, 2019, 133, 1006-1007.	1.4	9
36	Genomic subtyping and therapeutic targeting of acute erythroleukemia. Nature Genetics, 2019, 51, 694-704.	21.4	97

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37	Clonal Hematopoiesis with Oncogenic Potential (CHOP): Separation from CHIP and Roads to AML. International Journal of Molecular Sciences, 2019, 20, 789.	4.1	50
38	Molecular characterization of AML with RUNX1â€RUNX1T1 at diagnosis and relapse reveals net loss of coâ€mutations. HemaSphere, 2019, 3, e178.	2.7	8
39	Comprehensive genetic diagnosis of acute myeloid leukemia by next-generation sequencing. Haematologica, 2019, 104, 277-287.	3.5	33
40	Application of RNA Sequencing Detects a Large Number of Novel Fusion Transcripts in Patients with AML and MDS. Blood, 2019, 134, 887-887.	1.4	1
41	Comprehensive Analysis of MYC Translocations in Multiple Myeloma By Whole Genome Sequencing and Whole Transcriptome Sequencing. Blood, 2019, 134, 1774-1774.	1.4	2
42	Challenging Blast Counts By Machine Learning Techniques and Genome Sequencing for Discriminating AML and MDS. Blood, 2019, 134, 4663-4663.	1.4	2
43	Geno-Clinical Model for the Diagnosis of Bone Marrow Myeloid Neoplasms. Blood, 2019, 134, 4238-4238.	1.4	2
44	A Personalized Prediction Model to Risk Stratify Patients with Acute Myeloid Leukemia (AML) Using Artificial Intelligence. Blood, 2019, 134, 2091-2091.	1.4	11
45	A Novel Machine Learning Based in silico Pathogenicity Predictor for Missense Variants in a Hematological Setting. Blood, 2019, 134, 2090-2090.	1.4	4
46	Integrated Transcriptomic and Genomic Sequencing Identifies Prognostic Constellations of Driver Mutations in Acute Myeloid Leukemia and Myelodysplastic Syndromes. Blood, 2019, 134, LBA-4-LBA-4.	1.4	20
47	Minimal residual disease (MRD) monitoring and mutational landscape in AML with RUNX1-RUNX1T1: a study on 134 patients. Leukemia, 2018, 32, 2270-2274.	7.2	18
48	Minimal/measurable residual disease in AML: a consensus document from the European LeukemiaNet MRD Working Party. Blood, 2018, 131, 1275-1291.	1.4	796
49	The mutational landscape of 18 investigated genes clearly separates four subtypes of myelodysplastic/myeloproliferative neoplasms. Haematologica, 2018, 103, e192-e195.	3.5	39
50	Efficacy of azacitidine is independent of molecular and clinical characteristics - an analysis of 128 patients with myelodysplastic syndromes or acute myeloid leukemia and a review of the literature. Oncotarget, 2018, 9, 27882-27894.	1.8	60
51	NPM1 mutated AML can relapse with wild-type NPM1: persistent clonal hematopoiesis can drive relapse. Blood Advances, 2018, 2, 3118-3125.	5.2	62
52	Consequences of mutant TET2 on clonality and subclonal hierarchy. Leukemia, 2018, 32, 1751-1761.	7.2	54
53	Molecular patterns in cytopenia patients with or without evidence of myeloid neoplasmâ€"a comparison of 756 cases. Leukemia, 2018, 32, 2295-2298.	7.2	18
54	Acute myeloid leukemias with ring sideroblasts show a unique molecular signature straddling secondary acute myeloid leukemia and de novo acute myeloid leukemia. Haematologica, 2017, 102, e125-e128.	3.5	6

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55	Response and progression on midostaurin in advanced systemic mastocytosis: KIT D816V and other molecular markers. Blood, 2017, 130, 137-145.	1.4	97
56	Dynamics of clonal evolution in myelodysplastic syndromes. Nature Genetics, 2017, 49, 204-212.	21.4	348
57	Proposed Terminology and Classification of Pre-Malignant Neoplastic Conditions: A Consensus Proposal. EBioMedicine, 2017, 26, 17-24.	6.1	24
58	Molecular analysis of myelodysplastic syndrome with isolated deletion of the long arm of chromosome 5 reveals a specific spectrum of molecular mutations with prognostic impact: a study on 123 patients and 27 genes. Haematologica, 2017, 102, 1502-1510.	3.5	41
59	BCRâ€ABL1â€positive and JAK2 V617Fâ€positive clones in 23 patients with both aberrations reveal biologic and clinical importance. British Journal of Haematology, 2017, 176, 135-139.	2.5	21
60	Proposed minimal diagnostic criteria for myelodysplastic syndromes (MDS) and potential pre-MDS conditions. Oncotarget, 2017, 8, 73483-73500.	1.8	153
61	Ultra-deep sequencing leads to earlier and more sensitive detection of the tyrosine kinase inhibitor resistance mutation T315I in chronic myeloid leukemia. Haematologica, 2016, 101, 830-838.	3.5	42
62	Integrating clinical features and genetic lesions in the risk assessment of patients with chronic myelomonocytic leukemia. Blood, 2016, 128, 1408-1417.	1.4	249
63	Application of an <scp>NGS</scp>â€based 28â€gene panel in myeloproliferative neoplasms reveals distinct mutation patterns in essential thrombocythaemia, primary myelofibrosis and polycythaemia vera. British Journal of Haematology, 2016, 175, 419-426.	2.5	65
64	Molecular subtypes of NPM1 mutations have different clinical profiles, specific patterns of accompanying molecular mutations and varying outcomes in intermediate risk acute myeloid leukemia. Haematologica, 2016, 101, e55-e58.	3.5	51
65	Karyotype evolution and acquisition of FLT3 or RAS pathway alterations drive progression of myelodysplastic syndrome to acute myeloid leukemia. Haematologica, 2015, 100, e487-e490.	3.5	31
66	Refractory anemia with ring sideroblasts and marked thrombocytosis cases harbor mutations in SF3B1 or other spliceosome genes accompanied by JAK2V617F and ASXL1 mutations. Haematologica, 2015, 100, e125-e127.	3.5	68
67	Mutational profiling in patients with MDS: Ready for every-day use in the clinic?. Best Practice and Research in Clinical Haematology, 2015, 28, 32-42.	1.7	23
68	Why germline variations in ALL can matter. Lancet Oncology, The, 2015, 16, 1577-1578.	10.7	1
69	Next-generation deep sequencing improves detection of BCR-ABL1 kinase domain mutations emerging under tyrosine kinase inhibitor treatment of chronic myeloid leukemia patients in chronic phase. Journal of Cancer Research and Clinical Oncology, 2015, 141, 887-899.	2.5	67
70	A robust molecular pattern for myelodysplastic syndromes in two independent cohorts investigated by nextâ€generation sequencing can be revealed by comparative bioinformatic analyses. British Journal of Haematology, 2014, 167, 278-281.	2.5	2
71		0.6	0
72	In memoriam Professor Helmut LÃ¶ffler. Annals of Hematology, 2014, 93, 721-722.	1.8	0

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73	Investigation of 305 patients with myelodysplastic syndromes and 20q deletion for associated cytogenetic and molecular genetic lesions and their prognostic impact. British Journal of Haematology, 2014, 164, 822-833.	2.5	44
74	Perspective on how to approach molecular diagnostics in acute myeloid leukemia and myelodysplastic syndromes in the era of next-generation sequencing. Leukemia and Lymphoma, 2014, 55, 1725-1734.	1.3	18
75	Specific molecular mutation patterns delineate chronic neutrophilic leukemia, atypical chronic myeloid leukemia, and chronic myelomonocytic leukemia. Haematologica, 2014, 99, e244-e246.	3.5	90
76	Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. Nature Genetics, 2013, 45, 1232-1237.	21.4	334
77	Patients with therapy-related myelodysplastic syndromes and acute myeloid leukemia share genetic features but can be separated by blast counts and cytogenetic risk profiles into prognostically relevant subgroups. Leukemia and Lymphoma, 2013, 54, 639-642.	1.3	13
78	Unraveling the complexity of tyrosine kinase inhibitorâ€“resistant populations by ultra-deep sequencing of the BCR-ABL kinase domain. Blood, 2013, 122, 1634-1648.	1.4	152
79	Nextâ€generation sequencing â€“ feasibility and practicality in haematology. British Journal of Haematology, 2013, 160, 736-753.	2.5	54
80	Comprehensive mutational profiling in advanced systemic mastocytosis. Blood, 2013, 122, 2460-2466.	1.4	222
81	<scp>CEBPA</scp> doubleâ€mutated acute myeloid leukaemia harbours concomitant molecular mutations in 76Â·8% of cases with <scp>TET</scp>2 and <scp>GATA</scp>2 alterations impacting prognosis. British Journal of Haematology, 2013, 161, 649-658.	2.5	59
82	Robustness of Amplicon Deep Sequencing Underlines Its Utility in Clinical Applications. Journal of Molecular Diagnostics, 2013, 15, 473-484.	2.8	48
83	Multilineage dysplasia does not influence prognosis in CEBPA-mutated AML, supporting the WHO proposal to classify these patients as a unique entity. Blood, 2012, 119, 4719-4722.	1.4	62
84	A novel hierarchical prognostic model of AML solely based on molecular mutations. Blood, 2012, 120, 2963-2972.	1.4	235
85	SRSF2 mutations in 275 cases with chronic myelomonocytic leukemia (CMML). Blood, 2012, 120, 3080-3088.	1.4	272
86	Molecular genetics in myelodysplastic syndromes. Leukemia Research, 2012, 36, 1459-1462.	0.8	25
87	Diversity of the juxtamembrane and TKD1 mutations (Exons 13â€“15) in the FLT3 gene with regards to mutant load, sequence, length, localization, and correlation with biological data. Genes Chromosomes and Cancer, 2012, 51, 910-924.	2.8	76
88	Amount of bone marrow blasts is strongly correlated to NPM1 and FLT3-ITD mutation rate in AML with normal karyotype. Leukemia Research, 2012, 36, 51-58.	0.8	18
89	Prognoses of MDS subtypes RARS, RCMD and RCMD-RS are comparable but cytogenetics separates a subgroup with inferior clinical course. Leukemia Research, 2012, 36, 826-831.	0.8	14
90	Mixed Phenotype Acute Leukemia, T/Myeloid, NOS (MPAL-TM) Has a High DNMT3A Mutation Frequency and Carries Further Genetic Features of Both AML and T-ALL: Results of a Comprehensive Next-Generation Sequencing Study Analyzing 32 Genes. Blood, 2012, 120, 403-403.	1.4	12

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91	RUNX1 mutations are frequent in de novo AML with noncomplex karyotype and confer an unfavorable prognosis. Blood, 2011, 117, 2348-2357.	1.4	231
92	Molecular Genetics of Adult Acute Myeloid Leukemia: Prognostic and Therapeutic Implications. Journal of Clinical Oncology, 2011, 29, 475-486.	1.6	510
93	Whole-exome sequencing identifies somatic mutations of BCOR in acute myeloid leukemia with normal karyotype. Blood, 2011, 118, 6153-6163.	1.4	227
94	Frequent pathway mutations of splicing machinery in myelodysplasia. Nature, 2011, 478, 64-69.	27.8	1,764
95	R453Plus1Toolbox: an R/Bioconductor package for analyzing Roche 454 Sequencing data. Bioinformatics, 2011, 27, 1162-1163.	4.1	20
96	Monitoring of Minimal Residual Disease Using Next-Generation Deep-Sequencing in 460 Acute Myeloid Leukemia Cases identifies RUNX1 Mutated Patients with Resistant Disease. Blood, 2011, 118, 747-747.	1.4	7
97	Multilineage dysplasia has no impact on biologic, clinicopathologic, and prognostic features of AML with mutated nucleophosmin (NPM1). Blood, 2010, 115, 3776-3786.	1.4	109
98	IDH1 mutations are detected in 6.6% of 1414 AML patients and are associated with intermediate risk karyotype and unfavorable prognosis in adults younger than 60 years and unmutated NPM1 status. Blood, 2010, 116, 5486-5496.	1.4	175
99	Associations between imatinib resistance conferring mutations and Philadelphia positive clonal cytogenetic evolution in CML. Genes Chromosomes and Cancer, 2010, 49, 910-918.	2.8	12
100	Clinical utility of multiparameter flow cytometry in the diagnosis of 1013 patients with suspected myelodysplastic syndrome. Cancer, 2010, 116, 4549-4563.	4.1	99
101	Clinical Utility of Microarray-Based Gene Expression Profiling in the Diagnosis and Subclassification of Leukemia: Report From the International Microarray Innovations in Leukemia Study Group. Journal of Clinical Oncology, 2010, 28, 2529-2537.	1.6	567
102	Next-Generation Sequencing Technology Reveals a Characteristic Pattern of Molecular Mutations in 72.8% of Chronic Myelomonocytic Leukemia by Detecting Frequent Alterations in TET2, CBL, RAS, and RUNX1. Journal of Clinical Oncology, 2010, 28, 3858-3865.	1.6	283
103	Age-Related Risk Profile and Chemotherapy Dose Response in Acute Myeloid Leukemia: A Study by the German Acute Myeloid Leukemia Cooperative Group. Journal of Clinical Oncology, 2009, 27, 61-69.	1.6	315
104	Minimal residual disease levels assessed by NPM1 mutationâ€“specific RQ-PCR provide important prognostic information in AML. Blood, 2009, 114, 2220-2231.	1.4	307
105	Microarray-based classifiers and prognosis models identify subgroups with distinct clinical outcomes and high risk of AML transformation of myelodysplastic syndrome. Blood, 2009, 114, 1063-1072.	1.4	152
106	NPM1 mutations and cytoplasmic nucleophosmin are mutually exclusive of recurrent genetic abnormalities: a comparative analysis of 2562 patients with acute myeloid leukemia. Haematologica, 2008, 93, 439-442.	3.5	74
107	Prognostic relevance of FLT3-TKD mutations in AML: the combination mattersâ€”an analysis of 3082 patients. Blood, 2008, 111, 2527-2537.	1.4	354
108	Trisomy 13 is strongly associated with AML1/RUNX1 mutations and increased FLT3 expression in acute myeloid leukemia. Blood, 2007, 110, 1308-1316.	1.4	106

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109	KIT-D816 mutations in AML1-ETO-positive AML are associated with impaired event-free and overall survival. Blood, 2006, 107, 1791-1799.	1.4	362
110	Implications of NRAS mutations in AML: a study of 2502 patients. Blood, 2006, 107, 3847-3853.	1.4	273
111	Nucleophosmin gene mutations are predictors of favorable prognosis in acute myelogenous leukemia with a normal karyotype. Blood, 2005, 106, 3733-3739.	1.4	645
112	Modern diagnostics in acute leukemias. Critical Reviews in Oncology/Hematology, 2005, 56, 223-234.	4.4	70
113	AML M3 and AML M3 variant each have a distinct gene expression signature but also share patterns different from other genetically defined AML subtypes. Genes Chromosomes and Cancer, 2005, 43, 113-127.	2.8	42
114	Double Induction Containing Two Courses Versus One Course of High- Dose AraC/ Mitoxantrone (HAM) and Autologous Stem Cell Transplantation Versus Prolonged Maintenance for Acute Myeloid Leukemia (AML).. Blood, 2005, 106, 272-272.	1.4	1
115	Risk assessment by monitoring expression levels of partial tandem duplications in the MLL gene in acute myeloid leukemia during therapy. Haematologica, 2005, 90, 881-9.	3.5	58
116	Determination of relapse risk based on assessment of minimal residual disease during complete remission by multiparameter flow cytometry in unselected patients with acute myeloid leukemia. Blood, 2004, 104, 3078-3085.	1.4	249
117	A new prognostic score for patients with acute myeloid leukemia based on cytogenetics and early blast clearance in trials of the German AML Cooperative Group. Haematologica, 2004, 89, 408-18.	3.5	38
118	Morphologic Dysplasia in De Novo Acute Myeloid Leukemia (AML) Is Related to Unfavorable Cytogenetics but Has No Independent Prognostic Relevance Under the Conditions of Intensive Induction Therapy: Results of a Multiparameter Analysis From the German AML Cooperative Group Studies. Journal of Clinical Oncology, 2003, 21, 256-265.	1.6	166
119	New score predicting for prognosis in PML-RARA+, AML1-ETO+, or CBFBMYH11+ acute myeloid leukemia based on quantification of fusion transcripts. Blood, 2003, 102, 2746-2755.	1.4	208
120	Acute myeloid leukemias with reciprocal rearrangements can be distinguished by specific gene expression profiles. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10008-10013.	7.1	246
121	Distinct genetic patterns can be identified in acute monoblastic and acute monocytic leukaemia (FAB) Tj ETQq1 1 0.784314 rgBT /Ov	2.5	48
122	Analysis of FLT3 length mutations in 1003 patients with acute myeloid leukemia: correlation to cytogenetics, FAB subtype, and prognosis in the AMLCG study and usefulness as a marker for the detection of minimal residual disease. Blood, 2002, 100, 59-66.	1.4	893
123	Patients with de novo acute myeloid leukaemia and complex karyotype aberrations show a poor prognosis despite intensive treatment: a study of 90 patients. British Journal of Haematology, 2001, 112, 118-126.	2.5	155
124	Proliferative activity of leukaemic blasts and cytosine arabinoside pharmacodynamics are associated with cytogenetically defined prognostic subgroups in acute myeloid leukaemia. British Journal of Haematology, 2001, 113, 975-982.	2.5	29
125	Semiquantitative reverse transcription polymerase chain reaction analysis for detection of bcr/abl rearrangement using RNA extracts from bone marrow aspirates compared with glass slide smears after 0, 2 and 4 d of storage. British Journal of Haematology, 2001, 115, 583-587.	2.5	3