Klaus H Metzeler

List of Publications by Year
in descending order

179 papers	9,627 citations	44069 48 h-index	39675 94 g-index
186 all docs	186 docs citations	186 times ranked	11454 citing authors

#	Article	IF	Citations
1	Stem cell gene expression programs influence clinical outcome in human leukemia. Nature Medicine, 2011, 17, 1086-1093.	30.7	894
2	IDH1 and IDH2 Gene Mutations Identify Novel Molecular Subsets Within De Novo Cytogenetically Normal Acute Myeloid Leukemia: A Cancer and Leukemia Group B Study. Journal of Clinical Oncology, 2010, 28, 2348-2355.	1.6	699
3	A 17-gene stemness score for rapid determination of risk in acute leukaemia. Nature, 2016, 540, 433-437.	27.8	617
4	Spectrum and prognostic relevance of driver gene mutations in acute myeloid leukemia. Blood, 2016, 128, 686-698.	1.4	456
5	Prognostic Significance of the European LeukemiaNet Standardized System for Reporting Cytogenetic and Molecular Alterations in Adults With Acute Myeloid Leukemia. Journal of Clinical Oncology, 2012, 30, 4515-4523.	1.6	363
6	An 86-probe-set gene-expression signature predicts survival in cytogenetically normal acute myeloid leukemia. Blood, 2008, 112, 4193-4201.	1.4	357
7	TET2 Mutations Improve the New European LeukemiaNet Risk Classification of Acute Myeloid Leukemia: A Cancer and Leukemia Group B Study. Journal of Clinical Oncology, 2011, 29, 1373-1381.	1.6	291
8	Acute Myeloid Leukemia With Biallelic CEBPA Gene Mutations and Normal Karyotype Represents a Distinct Genetic Entity Associated With a Favorable Clinical Outcome. Journal of Clinical Oncology, 2010, 28, 570-577.	1.6	274
9	ASXL1 mutations identify a high-risk subgroup of older patients with primary cytogenetically normal AML within the ELN Favorable genetic category. Blood, 2011, 118, 6920-6929.	1.4	246
10	Age-Related Prognostic Impact of Different Types of DNMT3A Mutations in Adults With Primary Cytogenetically Normal Acute Myeloid Leukemia. Journal of Clinical Oncology, 2012, 30, 742-750.	1.6	244
11	RUNX1 Mutations Are Associated With Poor Outcome in Younger and Older Patients With Cytogenetically Normal Acute Myeloid Leukemia and With Distinct Gene and MicroRNA Expression Signatures. Journal of Clinical Oncology, 2012, 30, 3109-3118.	1.6	242
12	Coexpression profile of leukemic stem cell markers for combinatorial targeted therapy in AML. Leukemia, 2019, 33, 64-74.	7.2	212
13	FLT3 internal tandem duplication associates with adverse outcome and gene- and microRNA-expression signatures in patients 60 years of age or older with primary cytogenetically normal acute myeloid leukemia: a Cancer and Leukemia Group B study. Blood, 2010, 116, 3622-3626.	1.4	201
14	Blockade of the PD-1/PD-L1 axis augments lysis of AML cells by the CD33/CD3 BiTE antibody construct AMG 330: reversing a T-cell-induced immune escape mechanism. Leukemia, 2016, 30, 484-491.	7.2	201
15	DNMT3A mutations and response to the hypomethylating agent decitabine in acute myeloid leukemia. Leukemia, 2012, 26, 1106-1107.	7.2	188
16	Prognostic Significance of Expression of a Single MicroRNA, miR-181a, in Cytogenetically Normal Acute Myeloid Leukemia: A Cancer and Leukemia Group B Study. Journal of Clinical Oncology, 2010, 28, 5257-5264.	1.6	176
17	CD33 target validation and sustained depletion of AML blasts in long-term cultures by the bispecific T-cellâ€“engaging antibody AMG 330. Blood, 2014, 123, 356-365.	1.4	168
18	Clinical Role of microRNAs in Cytogenetically Normal Acute Myeloid Leukemia: miR-155 Upregulation Independently Identifies High-Risk Patients. Journal of Clinical Oncology, 2013, 31, 2086-2093.	1.6	165

#	Article	IF	Citations
19	Validation and refinement of the revised 2017 European LeukemiaNet genetic risk stratification of acute myeloid leukemia. Leukemia, 2020, 34, 3161-3172.	7.2	141
20	Adults with Philadelphia chromosomeâ€“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
21	Epigenetics Meets Genetics in Acute Myeloid Leukemia: Clinical Impact of a Novel Seven-Gene Score. Journal of Clinical Oncology, 2014, 32, 548-556.	1.6	134
22	ERG Expression Is an Independent Prognostic Factor and Allows Refined Risk Stratification in Cytogenetically Normal Acute Myeloid Leukemia: A Comprehensive Analysis of ERG, MN1, and BAALC Transcript Levels Using Oligonucleotide Microarrays. Journal of Clinical Oncology, 2009, 27, 5031-5038.	1.6	119
23	BAALC and ERG expression levels are associated with outcome and distinct gene and microRNA expression profiles in older patients with de novo cytogenetically normal acute myeloid leukemia: a Cancer and Leukemia Group B study. Blood, 2010, 116, 5660-5669.	1.4	110
24	Persistence of pre-leukemic clones during first remission and risk of relapse in acute myeloid leukemia. Leukemia, 2018, 32, 1598-1608.	7.2	106
25	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
26	Age-Specific Differences in Oncogenic Pathway Dysregulation in Patients With Acute Myeloid Leukemia. Journal of Clinical Oncology, 2009, 27, 5580-5586.	1.6	90
27	Combined Molecular and Clinical Prognostic Index for Relapse and Survival in Cytogenetically Normal Acute Myeloid Leukemia. Journal of Clinical Oncology, 2014, 32, 1586-1594.	1.6	87
28	Ten-year outcome of patients with acute myeloid leukemia not treated with allogeneic transplantation in first complete remission. Blood Advances, 2018, 2, 1645-1650.	5.2	85
29	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
30	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
31	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
32	An Advanced Preclinical Mouse Model for Acute Myeloid Leukemia Using Patients' Cells of Various Genetic Subgroups and In Vivo Bioluminescence Imaging. PLoS ONE, 2015, 10, e0120925.	2.5	78
33	Genome-wide methylation profiling in decitabine-treated patients with acute myeloid leukemia. Blood, 2012, 120, 2466-2474.	1.4	74
34	Bifunctional PD-1 Ã— Î±CD3 Ã— Î±CD33 fusion protein reverses adaptive immune escape in acute myeloid leukemia. Blood, 2018, 132, 2484-2494.	1.4	73
35	Activity of a heptad of transcription factors is associated with stem cell programs and clinical outcome in acute myeloid leukemia. Blood, 2013, 121, 2289-2300.	1.4	72
36	Prognostic and biologic significance of DNMT3B expression in older patients with cytogenetically normal primary acute myeloid leukemia. Leukemia, 2015, 29, 567-575.	7.2	69

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37	miR-3151 interplays with its host gene BAALC and independently affects outcome of patients with cytogenetically normal acute myeloid leukemia. Blood, 2012, 120, 249-258.	1.4	64
38	Dual PI3K/mTOR inhibition shows antileukemic activity in MLL-rearranged acute myeloid leukemia. Leukemia, 2015, 29, 828-838.	7.2	63
39	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
40	High expression of lymphoid enhancer-binding factor-1 (LEF1) is a novel favorable prognostic factor in cytogenetically normal acute myeloid leukemia. Blood, 2012, 120, 2118-2126.	1.4	62
41	Overexpression of CDX2 perturbs HOX gene expression in murine progenitors depending on its N-terminal domain and is closely correlated with deregulated HOX gene expression in human acute myeloid leukemia. Blood, 2008, 111, 309-319.	1.4	61
42	Tyrosine kinase inhibition increases the cell surface localization of FLT3-ITD and enhances FLT3-directed immunotherapy of acute myeloid leukemia. Leukemia, 2018, 32, 313-322.	7.2	61
43	The clinical mutatome of core binding factor leukemia. Leukemia, 2020, 34, 1553-1562.	7.2	60
44	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
45	CHIP and hips: clonal hematopoiesis is common in patients undergoing hip arthroplasty and is associated with autoimmune disease. Blood, 2021, 138, 1727-1732.	1.4	58
46	Loss of KDM6A confers drug resistance in acute myeloid leukemia. Leukemia, 2020, 34, 50-62.	7.2	56
47	Preclinical efficacy of maternal embryonic leucine-zipper kinase (MELK) inhibition in acute myeloid leukemia. Oncotarget, 2014, 5, 12371-12382.	1.8	56
48	Low expression of MN1 associates with better treatment response in older patients with de novo cytogenetically normal acute myeloid leukemia. Blood, 2011, 118, 4188-4198.	1.4	52
49	SPARC promotes leukemic cell growth and predicts acute myeloid leukemia outcome. Journal of Clinical Investigation, 2014, 124, 1512-1524.	8.2	52
50	A stem cell-like gene expression signature associates with inferior outcomes and a distinct microRNA expression profile in adults with primary cytogenetically normal acute myeloid leukemia. Leukemia, 2013, 27, 2023-2031.	7.2	50
51	Genetic heterogeneity of cytogenetically normal AML with mutations of CEBPA. Blood Advances, 2018, 2, 2724-2731.	5.2	46
52	GAS6 expression identifies high-risk adult AML patients: potential implications for therapy. Leukemia, 2014, 28, 1252-1258.	7.2	45
53	ZBTB7A mutations in acute myeloid leukaemia with t(8;21) translocation. Nature Communications, 2016, 7, 11733.	12.8	45
54	inv(16)/t(16;16) acute myeloid leukemia with nonâ€“type A CBFB-MYH11 fusions associate with distinct clinical and genetic features and lack KIT mutations. Blood, 2013, 121, 385-391.	1.4	39

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55	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
56	Characterization of a Novel FLT3 BiTE Molecule for the Treatment of Acute Myeloid Leukemia. Molecular Cancer Therapeutics, 2020, 19, 1875-1888.	4.1	34
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	Direct modulation of the bone marrow mesenchymal stromal cell compartment by azacitidine enhances healthy hematopoiesis. Blood Advances, 2018, 2, 3447-3461.	5.2	31
59	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
60	The neuropeptide receptor calcitonin receptor-like (CALCRL) is a potential therapeutic target in acute myeloid leukemia. Leukemia, 2019, 33, 2830-2841.	7.2	30
61	Therapeutic management of neuro-oncologic patients - potential relevance of CSF liquid biopsy. Theranostics, 2020, 10, 856-866.	10.0	25
62	Prognostic gene mutations and distinct gene- and microRNA-expression signatures in acute myeloid leukemia with a sole trisomy 8. Leukemia, 2014, 28, 1754-1758.	7.2	24
63	An Intrinsic Î³-Aminobutyric Acid (GABA)ergic System in the Adrenal Cortex: Findings from Human and Rat Adrenal Glands and the NCI-H295R Cell Line. Endocrinology, 2004, 145, 2402-2411.	2.8	23
64	Idiopathic hyperammonemia (IHA) after dose-dense induction chemotherapy for acute myeloid leukemia: Case report and review of the literature. Leukemia Research, 2009, 33, e69-e72.	0.8	23
65	Loss-of-function mutations in the histone methyltransferase EZH2 promote chemotherapy resistance in AML. Scientific Reports, 2021, 11, 5838.	3.3	22
66	Comparison of Treatment Recommendations by Molecular Tumor Boards Worldwide. JCO Precision Oncology, 2018, 2, 1-14.	3.0	21
67	Clinical outcome and gene- and microRNA-expression profiling according to the Wilms tumor 1 (WT1) single nucleotide polymorphism rs16754 in adult de novo cytogenetically normal acute myeloid leukemia: a Cancer and Leukemia Group B study. Haematologica, 2011, 96, 1488-1495.	3.5	20
68	Validating Comprehensive Next-Generation Sequencing Results for Precision Oncology: The NCT/DKTK Molecularly Aided Stratification for Tumor Eradication Research Experience. JCO Precision Oncology, 2018, 2, 1-13.	3.0	20
69	The MLL partial tandem duplication in adults aged 60 years and older with de novo cytogenetically normal acute myeloid leukemia. Leukemia, 2012, 26, 1713-1717.	7.2	19
70	Clinical and preclinical characterization of CD99 isoforms in acute myeloid leukemia. Haematologica, 2020, 105, 999-1012.	3.5	19
71	High expression ofMZB1predicts 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
72	Molecular Genetic Characterization of Individual Cancer Cells Isolated via Single-Cell Printing. PLoS ONE, 2016, 11, e0163455.	2.5	18

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73	Clonal hematopoiesis and preleukemiaâ€"Genetics, biology, and clinical implications. Genes Chromosomes and Cancer, 2019, 58, 828-838.	2.8	18
74	Identification of BCL-XL as highly active survival factor and promising therapeutic target in colorectal cancer. Cell Death and Disease, 2020, 11, 875.	6.3	17
75	An Immune Risk Score Predicts Survival of Patients with Acute Myeloid Leukemia Receiving Chemotherapy. Clinical Cancer Research, 2021, 27, 255-266.	7.0	17
76	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
77	Gene mutations and clonal architecture in myelodysplastic syndromes and changes upon progression to acute myeloid leukaemia and under treatment. British Journal of Haematology, 2018, 182, 830-842.	2.5	16
78	Differences in expression and function of LEF1 isoforms in normal versus leukemic hematopoiesis. Leukemia, 2020, 34, 1027-1037.	7.2	16
79	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
80	Clinical Relevance of RUNX1 and CBFB Alterations in Acute Myeloid Leukemia and Other Hematological Disorders. Advances in Experimental Medicine and Biology, 2017, 962, 175-199.	1.6	15
81	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
82	Plasticity in growth behavior of patients' acute myeloid leukemia stem cells growing in mice. Haematologica, 2020, 105, 2855-2860.	3.5	15
83	Relapse of acute myeloid leukemia after allogeneic stem cell transplantation is associated with gain of WT1 alterations and high mutation load. Haematologica, 2018, 103, e581-e584.	3.5	14
84	Characteristics and outcome of patients with core-binding factor acute myeloid leukemia and FLT3-ITD: results from an international collaborative study. Haematologica, 2022, 107, 836-843.	3.5	14
85	In rare acute myeloid leukemia patients harboring both RUNX1 and NPM1 mutations, RUNX1 mutations are unusual in structure and present in the germline. Haematologica, 2013, 98, e92-e94.	3.5	13
86	The new and recurrent FLT3 juxtamembrane deletion mutation shows a dominant negative effect on the wild-type FLT3 receptor. Scientific Reports, 2016, 6, 28032.	3.3	13
87	Universal Genomic Testing: The next step in oncological decision-making or a dead end street?. European Journal of Cancer, 2017, 82, 72-79.	2.8	13
88	Implementation of Precision Oncology for Patients with Metastatic Breast Cancer in an Interdisciplinary MTB Setting. Diagnostics, 2021, 11, 733.	2.6	13
89	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
90	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

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91	ASXL genes and RUNX1: an intimate connection?. Blood, 2014, 124, 1382-1383.	1.4	11
92	Therapy of older persons with acute myeloid leukaemia. Leukemia Research, 2017, 60, 1-10.	0.8	11
93	NGS-guided precision oncology in metastatic breast and gynecological cancer: first experiences at the CCC Munich LMU. Archives of Gynecology and Obstetrics, 2021, 303, 1331-1345.	1.7	11
94	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
95	Double Drop-Off Droplet Digital PCR. Journal of Molecular Diagnostics, 2021, 23, 975-985.	2.8	10
96	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
97	Allelic Imbalance of Recurrently Mutated Genes in Acute Myeloid Leukaemia. Scientific Reports, 2019, 9, 11796.	3.3	9
98	Persistence of pre-leukemic clones during first remission and risk of relapse in acute myeloid leukemia. Leukemia, 2017, , .	7.2	8
99	Patients with spontaneous remission of high-risk MDS and AML show persistent preleukemic clonal hematopoiesis. Blood Advances, 2019, 3, 2696-2699.	5.2	8
100	<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
101	Clonal hematopoiesis of indeterminate potential in older patients having received an allogeneic stem cell transplantation from young donors. Bone Marrow Transplantation, 2020, 55, 665-668.	2.4	7
102	Myelodysplastic syndromes: Biological and therapeutic consequences of the evolving molecular aberrations landscape. Neoplasia, 2021, 23, 1101-1109.	5.3	6
103	NPM1 Variant Allele Frequency and Outcomes in AML. Blood, 2018, 132, 1486-1486.	1.4	6
104	DNA Methylation Profiling of AML Reveals Epigenetic Subgroups with Distinct Clinical Outcome. Blood, 2019, 134, 2715-2715.	1.4	6
105	Evaluation Of CD33 Expression and Functional Analysis Of The CD33/CD3 Bispecific BiTEÂ® Antibody AMG 330 In Primary AML Samples. Blood, 2013, 122, 239-239.	1.4	6
106	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
107	Diagnostic applications of next generation sequencing: working towards quality standards/Diagnostische Anwendung von Next Generation Sequencing: Auf dem Weg zu QualitÃtsstandards. Laboratoriums Medizin, 2012, 36, .	0.6	4
108	The ParaHox gene Cdx4 induces acute erythroid leukemia in mice. Blood Advances, 2019, 3, 3729-3739.	5.2	4

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109	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
110	PTPN11 mutations and Outcomes in Adult Patients with Acute Myeloid Leukemia. Blood, 2020, 136, 4-5.	1.4	4
111	Targeting AML Using an Fc-Engineered BST1/CD157 Monoclonal Antibody. Blood, 2014, 124, 987-987.	1.4	4
112	An 86-Probe Gene Expression Signature Can Predict Survival in AML with Normal Karyotype Independently of FLT3 ITD and NPM1 Mutation Status - A Collaborative Study from the AMLCG and CALGB Study Groups.. Blood, 2007, 110, 596-596.	1.4	4
113	Association between a Prognostic Gene Signature and Functional Gene Sets. Bioinformatics and Biology Insights, 2008, 2, BBI.S1018.	2.0	3
114	Applications and data analysis of next-generation sequencing. Laboratoriums Medizin, 2013, 37, .	0.6	3
115	Response assessment in acute myeloid leukemia by flow cytometry supersedes cytomorphology at time of aplasia, amends cases without molecular residual disease marker and serves as an independent prognostic marker at time of aplasia and post-induction. Haematologica, 2019, 104, e510-e513.	3.5	3
116	Development of a Bifunctional Checkpoint Inhibitory T Cell Engager (CiTE) to Reverse Adaptive Immune Escape in AML. Blood, 2018, 132, 4069-4069.	1.4	3
117	Ivosidenib Improves Overall Survival Relative to Standard Therapies in Relapsed or Refractory Mutant IDH1 AML: Results from Matched Comparisons to Historical Controls. Blood, 2020, 136, 18-19.	1.4	3
118	Cisplatin-Based Chemotherapy for Pulmonary Metastasized Germ Cell Tumors of the Testis â€“ Be Aware of Acute Respiratory Distress Syndrome. Oncology Research and Treatment, 2009, 32, 125-128.	1.2	2
119	Sole Trisomy 8 In Patients (pts) with De Novo Acute Myeloid Leukemia (AML) Is Associated with Age-Independent Poor Outcome That Is Modified by Molecular Markers and with Unique Gene- and Microrna (miR)-Signatures: a Cancer and Leukemia Group B (CALGB) Study. Blood, 2010, 116, 577-577.	1.4	2
120	Prognostic Utility of the European LeukemiaNet (ELN) Genetic-Risk Classification in Adults with De Novo Acute Myeloid Leukemia (AML): A Study of 1,550 Patients (Pts). Blood, 2011, 118, 414-414.	1.4	2
121	Analysis of Cooperating Genetic Events in MLLT3-MLL Rearranged Acute Myeloid Leukemia (AML) by Targeted Next-Generation Sequencing of 16 Leukemia-Related Genes Reveals Frequent Mutations Affecting Growth Factor Signalling Pathways and Provides Evidence for Clonal Heterogeneity. Blood, 2012, 120, 1379-1379.	1.4	2
122	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
123	Genetic Profiling By Targeted, Deep Resequencing Confirms That a Murine Xenograft Model Of Acute Myeloid Leukemia (AML) Recapitulates The Mutational Landscape Of The Human Disease and Provides Evidence For Clonal Heterogeneity and Clonal Evolution. Blood, 2013, 122, 49-49.	1.4	2
124	Evolving Exhaustion of T Cells during the Course of the Disease in AML Can be Abrogated By CD33 BiTE Â® Construct Mediated Cytotoxicity. Blood, 2021, 138, 1172-1172.	1.4	2
125	High Prevalence of CHF and Diabetes in AML Long-Term Survivors - a Patient Forever?. Blood, 2021, 138, 4127-4127.	1.4	2
126	Harmony Alliance Provides a Machine Learning Researching Tool to Predict the Risk of Relapse after First Remission in AML Patients Treated without Allogeneic Haematopoietic Stem Cell Transplantation. Blood, 2021, 138, 4041-4041.	1.4	2

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127	Quality of Life and Life Satisfaction in AML Long-Term Survivors: Primary Results of the AMLCG-Survivorship Study. Blood, 2021, 138, 2289-2289.	1.4	2
128	Extramedullary Clonal Hematopoiesis with Indeterminate Potential. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, e696-e698.	0.4	1
129	Impact of DNMT3A mutations on Clinical Response to the Hypomethylating Agent Decitabine in Older Patients (pts) with Acute Myeloid Leukemia (AML). Blood, 2011, 118, 944-944.	1.4	1
130	The Clinical Role of Micrornas (miRs) in Cytogenetically Normal (CN) Acute Myeloid Leukemia (AML): miR-155 Upregulation Independently Identifies High-Risk Patients (Pts). Blood, 2012, 120, 1387-1387.	1.4	1
131	SPARC contributes to Leukemia Growth and Aggressive Disease in Acute Myeloid Leukemia (AML). Blood, 2012, 120, 773-773.	1.4	1
132	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
133	PS29MRC - a Novel Predictive Score for Response to Therapy in Acute Myeloid Leukemia. Blood, 2016, 128, 1209-1209.	1.4	1
134	Dual Inhibition Of PI3K and mTOR Shows Preferential Antileukemic Activity In MLL-Rearranged AML. Blood, 2013, 122, 818-818.	1.4	1
135	Genetic Evolution of Cytogenetically Normal Acute Myeloid Leukemia (CN-AML) during Therapy and Relapse: An Exome Sequencing Study of 47 Cases. Blood, 2014, 124, 17-17.	1.4	1
136	The Mutatome of CBFB/MYH11-rearranged Acute Myeloid Leukemia (AML). Blood, 2014, 124, 14-14.	1.4	1
137	Characterization of Somatic Mosaicism and Mutational Profiling of Clonal Hematopoiesis Compared to MDS and sAML Depicts Diversities of Clonal Evolution. Blood, 2021, 138, 3278-3278.	1.4	1
138	miR-3151 Interplays With its Host Gene BAALC and Independently Impacts on Outcome of Older Patients With Cytogenetically Normal Acute Myeloid Leukemia by Direct Deregulation of TP53. Clinical Lymphoma, Myeloma and Leukemia, 2014, 14, S157.	0.4	0
139	Diffner E, Beck D, Gudgin E, et al. Activity of a heptad of transcription factors is associated with stem cell programs and clinical outcome in acute myeloid leukemia. Blood. 2013;121(12):2289-2300.. Blood, 2014, 123, 2901-2901.	1.4	0
140	A fluorescence in situ hybridizationâ€based screen allows rapid detection of adverse cytogenetic alterations in patients with acute myeloid leukemia. Genes Chromosomes and Cancer, 2017, 56, 632-638.	2.8	0
141	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
142	Neuroendocrine properties of human adrenocortical cells: GABA production and functional GABAB receptors in the NCI-H295R cell line. Experimental and Clinical Endocrinology and Diabetes, 2003, 111, .	1.2	0
143	HHV-6 Reactivation after Autologous Stem Cell Transplantation Is Associated with Prolonged Hospitalization but Not with Delayed Engraftment.. Blood, 2004, 104, 3168-3168.	1.4	0
144	Prognosis of AML with Unfavourable Cytogenetics Treated with Intensive Double Induction Chemotherapy: An Analysis of 342 Patients from the German AMLCG-2000 Study.. Blood, 2006, 108, 2006-2006.	1.4	0

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145	Age-specific differences in oncogenic pathway deregulation and chemosensitivity in patients with acute myeloid leukemia: Strategies to maximize response to induction chemotherapy. Journal of Clinical Oncology, 2009, 27, 7013-7013.	1.6	0
146	High Expression of Lymphoid Enhancer-Binding Factor 1 (LEF1) Is a Novel, Favorable Prognostic Marker in Cytogenetically Normal AML and Is Associated with Upregulation of T-Lymphoid Lineage Markers in AML Blasts.. Blood, 2009, 114, 398-398.	1.4	0
147	Gene Expression Analysis of Independent Data Sets Identifies HBG1 to Be Associated with Outcome in Cytogenetically Normal AML.. Blood, 2009, 114, 2613-2613.	1.4	0
148	Mutations In the Tet Oncogene Family Member 2 (TET2) Gene Refine the New European LeukemiaNet Risk Classification of Primary, Cytogenetically Normal Acute Myeloid Leukemia (CN-AML) In Adults: A Cancer and Leukemia Group B (CALGB) Study. Blood, 2010, 116, 98-98.	1.4	0
149	Poor Outcome of RUNX1-Mutated (RUNX1-mut) Patients (Pts) with Primary, Cytogenetically Normal Acute Myeloid Leukemia (CN-AML) and Associated Gene- and MicroRNA (miR) Expression Signatures,. Blood, 2011, 118, 3454-3454.	1.4	0
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151	MiR-3151, a Novel MicroRNA Embedded in BAALC, Is Only Weakly Co-Expressed with Its Host Gene and Independently Impacts on the Clinical Outcome of Older Patients (Pts) with De Novo Cytogenetically Normal Acute Myeloid Leukemia (CN-AML). Blood, 2011, 118, 1462-1462.	1.4	0
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