Peter J M Valk

List of Publications by Year
in descending order

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147 papers	13,476 citations	34076 52 h-index	22808 112 g-index
147 all docs	147 docs citations	147 times ranked	13663 citing authors

#	Article	IF	Citations
1	CEBPA mutations in 4708 patients with acute myeloid leukemia: differential impact of bZIP and TAD mutations on outcome. Blood, 2022, 139, 87-103.	0.6	82
2	Systematic Profiling of DNMT3A Variants Reveals Protein Instability Mediated by the DCAF8 E3 Ubiquitin Ligase Adaptor. Cancer Discovery, 2022, 12, 220-235.	7.7	38
3	Molecular characterization of mutant TP53 acute myeloid leukemia and high-risk myelodysplastic syndrome. Blood, 2022, 139, 2347-2354.	0.6	131
4	Transplant in older adults with AML: genomic wheat and chaff. Blood, 2022, 139, 3459-3461.	0.6	1
5	Comprehensive diagnostics of acute myeloid leukemia by whole transcriptome RNA sequencing. Leukemia, 2021, 35, 47-61.	3.3	47
6	miRâ€15aâ€5p and miRâ€21â€5p contribute to chemoresistance in cytogenetically normal acute myeloid leukaemia by targeting PDCD4, ARL2 and BTG2. Journal of Cellular and Molecular Medicine, 2021, 25, 575-585.	1.6	30
7	Future Developments: Measurable Residual Disease. Hematologic Malignancies, 2021, , 317-337.	0.2	0
8	Genomic and evolutionary portraits of disease relapse in acute myeloid leukemia. Leukemia, 2021, 35, 2688-2692.	3.3	7
9	Addition of lenalidomide to intensive treatment in younger and middle-aged adults with newly diagnosed AML: the HOVON-SAKK-132 trial. Blood Advances, 2021, 5, 1110-1121.	2.5	33
10	PPM1D mutations appear in complete remission after exposure to chemotherapy without predicting emerging AML relapse. Leukemia, 2021, 35, 2693-2697.	3.3	2
11	Disruption of CSF-1R signaling inhibits growth of AML with inv(16). Blood Advances, 2021, 5, 1273-1277.	2.5	7
12	FLT3â€ITD mutations in acute myeloid leukaemia â€“ molecular characteristics, distribution and numerical variation. Molecular Oncology, 2021, 15, 2300-2317.	2.1	5
13	Sex disparity in acute myeloid leukaemia with FLT3 internal tandem duplication mutations: implications for prognosis. Molecular Oncology, 2021, 15, 2285-2299.	2.1	11
14	Molecular Minimal Residual Disease Detection in Acute Myeloid Leukemia. Cancers, 2021, 13, 5431.	1.7	18
15	2021 Update on MRD in acute myeloid leukemia: a consensus document from the European LeukemiaNet MRD Working Party. Blood, 2021, 138, 2753-2767.	0.6	305
16	Azacytidine Treatment for VEXAS Syndrome. HemaSphere, 2021, 5, e661.	1.2	45
17	TP53 abnormalities correlate with immune infiltration and associate with response to flotetuzumab immunotherapy in AML. Blood Advances, 2020, 4, 5011-5024.	2.5	85
18	RNA Targeting in Acute Myeloid Leukemia. ACS Pharmacology and Translational Science, 2020, 3, 1225-1232.	2.5	6

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19	Secondary CNL after SAA reveals insights in leukemic transformation of bone marrow failure syndromes. Blood Advances, 2020, 4, 5540-5546.	2.5	3
20	Digital PCR for BCRâ€ABL1 Quantification in CML: Current Applications in Clinical Practice. HemaSphere, 2020, 4, e496.	1.2	17
21	Reduced SLIT2 is Associated with Increased Cell Proliferation and Arsenic Trioxide Resistance in Acute Promyelocytic Leukemia. Cancers, 2020, 12, 3134.	1.7	7
22	Ibrutinib added to 10-day decitabine for older patients with AML and higher risk MDS. Blood Advances, 2020, 4, 4267-4277.	2.5	14
23	Immune landscapes predict chemotherapy resistance and immunotherapy response in acute myeloid leukemia. Science Translational Medicine, 2020, 12, .	5.8	117
24	Archived bone marrow smears are an excellent source for NGS-based mutation detection in acute myeloid leukemia. Leukemia, 2020, 34, 2220-2224.	3.3	4
25	Atypical 3q26/MECOM rearrangements genocopy inv(3)/t(3;3) in acute myeloid leukemia. Blood, 2020, 136, 224-234.	0.6	39
26	The neuropeptide receptor calcitonin receptor-like (CALCRL) is a potential therapeutic target in acute myeloid leukemia. Leukemia, 2019, 33, 2830-2841.	3.3	30
27	Next-generation sequencing in the diagnosis and minimal residual disease assessment of acute myeloid leukemia. Haematologica, 2019, 104, 868-871.	1.7	40
28	Altered NFE2 activity predisposes to leukemic transformation and myelosarcoma with AML-specific aberrations. Blood, 2019, 133, 1766-1777.	0.6	23
29	The Landscape of KMT2Aâ€PTD AML: Concurrent Mutations, Gene Expression Signatures, and Clinical Outcome. HemaSphere, 2019, 3, e181.	1.2	14
30	Genomic landscape and clonal evolution of acute myeloid leukemia with t(8;21): an international study on 331 patients. Blood, 2019, 133, 1140-1151.	0.6	96
31	CD34+CD38â^' leukemic stem cell frequency to predict outcome in acute myeloid leukemia. Leukemia, 2019, 33, 1102-1112.	3.3	130
32	Immune Landscapes Predict Chemotherapy Resistance and Anti-Leukemic Activity of Flotetuzumab, an Investigational CD123Ã—CD3 Bispecific DartÂ® Molecule, in Patients with Relapsed/Refractory Acute Myeloid Leukemia. Blood, 2019, 134, 460-460.	0.6	2
33	Durable Responses and Survival in High Risk AML and MDS Patients Treated with an Allogeneic Leukemia-Derived Dendritic Cell Vaccine. Blood, 2019, 134, 1381-1381.	0.6	5
34	Clinical and Functional Studies Reveal That TP73 Isoforms Levels Are Associated with Prognosis and RA-Resistance in Acute Promyelocytic Leukemia. Blood, 2019, 134, 2719-2719.	0.6	0
35	Clonal Evolution of Multiple Myeloma in Patients from Diagnosis to First Relapse, Who Were Treated in Subsequent Clinical Trials. Blood, 2019, 134, 1798-1798.	0.6	0
36	Allele-Specific Expression of GATA2 in AML with CEBPA Biallelic Mutations. Blood, 2019, 134, 1235-1235.	0.6	0

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37	Arsenic Trioxide Abrogate MN1 Mediated RA-Resistance in Acute Promyelocytic Leukemia. Blood, 2019, 134, 5166-5166.	0.6	0
38	Omitting cytogenetic assessment from routine treatment response monitoring in chronic myeloid leukemia is safe. European Journal of Haematology, 2018, 100, 367-371.	1.1	6
39	Molecular Minimal Residual Disease in Acute Myeloid Leukemia. New England Journal of Medicine, 2018, 378, 1189-1199.	13.9	605
40	MBD4 guards against methylation damage and germ line deficiency predisposes to clonal hematopoiesis and early-onset AML. Blood, 2018, 132, 1526-1534.	0.6	90
41	Next-Generation Sequencing Analysis of the Human TCRÎ³Î´+ T-Cell Repertoire Reveals Shifts in VÎ³- and VÎ´-Usage in Memory Populations upon Aging. Frontiers in Immunology, 2018, 9, 448.	2.2	31
42	Whole Transcriptome RNA Sequencing As a Comprehensive Diagnostic Tool for Acute Myeloid Leukemia. Blood, 2018, 132, 2762-2762.	0.6	0
43	A Leukemic Progression Model of Severe Congenital Neutropenia Uncovers a Novel Mechanism of AML Development Involving Elevated Inflammatory Responses, Mutation of CXXC4 and Decreased TET2 Levels. Blood, 2018, 132, 540-540.	0.6	1
44	Complex 3q26/EVI1 Rearrangements Genocopy Inv(3)/t(3;3) Acute Myeloid Leukemias By Enhancer Hijacking, EVI1 Overexpression, Absent MDS1-EVI1 and Low GATA2 Expression. Blood, 2018, 132, 2766-2766.	0.6	0
45	Slit-Robo Pathway Is Clinically Relevant and May Represent a Potential Target in Acute Promyelocytic Leukemia. Blood, 2018, 132, 1533-1533.	0.6	0
46	Metformintreatment Overcomes ATRA-Resistance in Acute Promyelocytic Leukemia and Increases FOXO3A Expression. Blood, 2018, 132, 1532-1532.	0.6	0
47	Therapeutic value of clofarabine in younger and middle-aged (18-65 years) adults with newly diagnosed AML. Blood, 2017, 129, 1636-1645.	0.6	77
48	Epigenetic Identity in AML Depends on Disruption of Nonpromoter Regulatory Elements and Is Affected by Antagonistic Effects of Mutations in Epigenetic Modifiers. Cancer Discovery, 2017, 7, 868-883.	7.7	101
49	Impact of hospital experience on the quality of tyrosine kinase inhibitor response monitoring and consequence for chronic myeloid leukemia patient survival. Haematologica, 2017, 102, e486-e489.	1.7	10
50	The application of an integrated clinical, cytogenetic, and molecular risk stratification for acute myeloid leukemia patients using a central laboratory in a Brazilian multicentric study. Blood Advances, 2017, 1, 86-89.	2.5	0
51	Review: Aberrant <scp>EVI</scp>1 expression in acute myeloid leukaemia. British Journal of Haematology, 2016, 172, 870-878.	1.2	60
52	MPL expression on AML blasts predicts peripheral blood neutropenia and thrombocytopenia. Blood, 2016, 128, 2253-2257.	0.6	34
53	Lack of splice factor and cohesin complex mutations in pediatric myelodysplastic syndrome. Haematologica, 2016, 101, e479-e481.	1.7	3
54	Distinct evolution and dynamics of epigenetic and genetic heterogeneity in acute myeloid leukemia. Nature Medicine, 2016, 22, 792-799.	15.2	322

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55	MLL-AF9 Expression in Hematopoietic Stem Cells Drives a Highly Invasive AML Expressing EMT-Related Genes Linked to Poor Outcome. Cancer Cell, 2016, 30, 43-58.	7.7	176
56	<scp>CD</scp>45<scp>RA</scp>, a specific marker for leukaemia stem cell subâ€populations in acute myeloid leukaemia. British Journal of Haematology, 2016, 173, 219-235.	1.2	47
57	A 4â€gene expression score associated with high levels of Wilms Tumorâ€1 (<scp>WT</scp>1) expression is an adverse prognostic factor in acute myeloid leukaemia. British Journal of Haematology, 2016, 172, 401-411.	1.2	14
58	A somatic mutation of GFI1B identified in leukemia alters cell fate via a SPI1 (PU.1) centered genetic regulatory network. Developmental Biology, 2016, 411, 277-286.	0.9	20
59	Molecular Minimal Residual Disease Detection in Acute Myeloid Leukemia. Blood, 2016, 128, SCI-30-SCI-30.	0.6	0
60	Expression profiling of adult acute lymphoblastic leukemia identifies a BCR-ABL1-like subgroup characterized by high non-response and relapse rates. Haematologica, 2015, 100, e261-e264.	1.7	82
61	Mutational spectrum of myeloid malignancies with inv(3)/t(3;3) reveals a predominant involvement of RAS/RTK signaling pathways. Blood, 2015, 125, 133-139.	0.6	86
62	Downregulation of the Wnt inhibitor CXXC5 predicts a better prognosis in acute myeloid leukemia. Blood, 2015, 125, 2985-2994.	0.6	42
63	RNA sequencing reveals a unique fusion of the lysine (K)-specific methyltransferase 2A and smooth muscle myosin heavy chain 11 in myelodysplastic syndrome and acute myeloid leukemia. Haematologica, 2015, 100, e1-e3l.	1.7	4
64	Integrated genome-wide genotyping and gene expression profiling reveals BCL11B as a putative oncogene in acute myeloid leukemia with 14q32 aberrations. Haematologica, 2014, 99, 848-857.	1.7	30
65	A Single Oncogenic Enhancer Rearrangement Causes Concomitant EVI1 and GATA2 Deregulation in Leukemia. Cell, 2014, 157, 369-381.	13.5	571
66	NrasG12D oncoprotein inhibits apoptosis of preleukemic cells expressing CbfÎ²-SMMHC via activation of MEK/ERK axis. Blood, 2014, 124, 426-436.	0.6	26
67	Two splice-factor mutant leukemia subgroups uncovered at the boundaries of MDS and AML using combined gene expression and DNA-methylation profiling. Blood, 2014, 123, 3327-3335.	0.6	52
68	Detection ofCEBPADouble Mutants in Acute Myeloid Leukemia Using a Custom Gene Expression Array. Genetic Testing and Molecular Biomarkers, 2013, 17, 395-400.	0.3	8
69	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.	0.8	164
70	Sox4 Is a Key Oncogenic Target in C/EBPÎ± Mutant Acute Myeloid Leukemia. Cancer Cell, 2013, 24, 575-588.	7.7	112
71	Deregulated Expression of EVI1 Defines a Poor Prognostic Subset of MLL-Rearranged Acute Myeloid Leukemias: A Study of the German-Austrian Acute Myeloid Leukemia Study Group and the Dutch-Belgian-Swiss HOVON/SAKK Cooperative Group. Journal of Clinical Oncology, 2013, 31, 95-103.	0.8	95
72	High Prognostic Impact of Flow Cytometric Minimal Residual Disease Detection in Acute Myeloid Leukemia: Data From the HOVON/SAKK AML 42A Study. Journal of Clinical Oncology, 2013, 31, 3889-3897.	0.8	392

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73	The evolving molecular genetic landscape in acute myeloid leukaemia. Current Opinion in Hematology, 2013, 20, 79-85.	1.2	53
74	Detection of MutantNPM1mRNA in Acute Myeloid Leukemia Using Custom Gene Expression Arrays. Genetic Testing and Molecular Biomarkers, 2013, 17, 295-300.	0.3	5
75	Genome-Wide Gene Expression Profiling, Genotyping, and Copy Number Analyses of Acute Myeloid Leukemia Using Affymetrix GeneChips. Methods in Molecular Biology, 2013, 1015, 155-177.	0.4	0
76	Base-Pair Resolution DNA Methylation Sequencing Reveals Profoundly Divergent Epigenetic Landscapes in Acute Myeloid Leukemia. PLoS Genetics, 2012, 8, e1002781.	1.5	263
77	miR-196b directly targets both HOXA9/MEIS1 oncogenes and FAS tumour suppressor in MLL-rearranged leukaemia. Nature Communications, 2012, 3, 688.	5.8	138
78	Autocrine activation of the MET receptor tyrosine kinase in acute myeloid leukemia. Nature Medicine, 2012, 18, 1118-1122.	15.2	162
79	Thrombopoietin/MPL participates in initiating and maintaining RUNX1-ETO acute myeloid leukemia via PI3K/AKT signaling. Blood, 2012, 120, 868-879.	0.6	47
80	Mutant DNMT3A: a marker of poor prognosis in acute myeloid leukemia. Blood, 2012, 119, 5824-5831.	0.6	221
81	Acquired mutations in ASXL1 in acute myeloid leukemia: prevalence and prognostic value. Haematologica, 2012, 97, 388-392.	1.7	143
82	Sequential gain of mutations in severe congenital neutropenia progressing to acute myeloid leukemia. Blood, 2012, 119, 5071-5077.	0.6	156
83	<scp>ID</scp>1 expression associates with other molecular markers and is not an independent prognostic factor in cytogenetically normal acute myeloid leukaemia. British Journal of Haematology, 2012, 158, 208-215.	1.2	9
84	C/EBPÎ³ deregulation results in differentiation arrest in acute myeloid leukemia. Journal of Clinical Investigation, 2012, 122, 4490-4504.	3.9	50
85	The HOXA/PBX3 Pathway Is an Attractive Therapeutic Target in MLL-Rearranged Acute Leukemia. Blood, 2012, 120, 3522-3522.	0.6	0
86	Identification of Sox4 As Key Oncogene in Leukemias with Mutated or Silenced C/EBPÎ±. Blood, 2012, 120, 114-114.	0.6	0
87	BAALC and EVI1 Prognostic Gene Expression in Adult Acute Myeloid Leukemia Using the Amlprofiler Custom Microarray. Blood, 2012, 120, 1420-1420.	0.6	0
88	Prognostic and Functional Relevance of Aberrant Microrna-9/9* Expression in Acute Myeloid Leukemia.. Blood, 2012, 120, 2542-2542.	0.6	0
89	The Impact of Novel Molecular Markers on Risk Stratification in Acute Myeloid Leukemia. Blood, 2012, 120, SCI-33-SCI-33.	0.6	1
90	Prognostic impact, concurrent genetic mutations, and gene expression features of AML with CEBPA mutations in a cohort of 1182 cytogenetically normal AML patients: further evidence for CEBPA double mutant AML as a distinctive disease entity. Blood, 2011, 117, 2469-2475.	0.6	341

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91	The Antioxidant Protein Peroxiredoxin 4 Is Epigenetically Down Regulated in Acute Promyelocytic Leukemia. PLoS ONE, 2011, 6, e16340.	1.1	36
92	Aberrant DNA hypermethylation signature in acute myeloid leukemia directed by EVI1. Blood, 2011, 117, 234-241.	0.6	94
93	Risk stratification of intermediate-risk acute myeloid leukemia: integrative analysis of a multitude of gene mutation and gene expression markers. Blood, 2011, 118, 1069-1076.	0.6	109
94	NUP98/NSD1 characterizes a novel poor prognostic group in acute myeloid leukemia with a distinct HOX gene expression pattern. Blood, 2011, 118, 3645-3656.	0.6	250
95	High BRE expression predicts favorable outcome in adult acute myeloid leukemia, in particular among MLL-AF9â€“positive patients. Blood, 2011, 118, 5613-5621.	0.6	32
96	Common and Overlapping Oncogenic Pathways Contribute to the Evolution of Acute Myeloid Leukemias. Cancer Research, 2011, 71, 4117-4129.	0.4	55
97	Characterization of CEBPA mutations and promoter hypermethylation in pediatric acute myeloid leukemia. Haematologica, 2011, 96, 384-392.	1.7	74
98	Preliminary Results From a Phase III Trial of Imatinib Versus Imatinib in Combination with Cytarabine in Patients with First Chronic Phase Myeloid Leukemia. Blood, 2011, 118, 2758-2758.	0.6	1
99	Retroviral Integration Mutagenesis in Mice and Comparative Analysis in Human AML Identify Reduced PTP4A3 Expression as a Prognostic Indicator. PLoS ONE, 2011, 6, e26537.	1.1	24
100	Methylated Retroviral Integration Mutagenesis (MRIM) in Mice and Comparative Analysis in Human AML Identify Reduced PTP4A3 Expression As a Prognostic Indicator. Blood, 2011, 118, 746-746.	0.6	0
101	A Single Microarray Assay for Simultaneous Diagnosis of t(15;17), t(8;21), Inv(16)/t(16;16), NPM1 Type A/B/D Mutation, CEBPA Double Mutation, and Aberrant Expression of BAALC or EVI1 in AML/APL Patients. Blood, 2011, 118, 4876-4876.	0.6	0
102	Linking the Glycolytic Enzyme HK3 to Neutrophil Differentiation of APL Cells Via PU.1. Blood, 2011, 118, 2425-2425.	0.6	0
103	Activation of a Mir-181-Targeting HOXA-PBX3 Homeobox Gene Signature Is Associated with Adverse Prognosis of Cytogenetically Abnormal Acute Myeloid Leukemia. Blood, 2011, 118, 236-236.	0.6	0
104	CEBPÎ± Is a Transcriptional Repressor of T-Cell Related Genes Explaining the Myeloid/T-Lymphoid Features of CEBPÎ±-Silenced AML. Blood, 2011, 118, 554-554.	0.6	4
105	Pim2 cooperates with PML-RARÎ± to induce acute myeloid leukemia in a bone marrow transplantation model. Blood, 2010, 115, 4507-4516.	0.6	12
106	A variant allele of Growth Factor Independence 1 (GFI1) is associated with acute myeloid leukemia. Blood, 2010, 115, 2462-2472.	0.6	46
107	DNA Methylation Signatures Identify Biologically Distinct Subtypes in Acute Myeloid Leukemia. Cancer Cell, 2010, 17, 13-27.	7.7	737
108	High VEGFC expression is associated with unique gene expression profiles and predicts adverse prognosis in pediatric and adult acute myeloid leukemia. Blood, 2010, 116, 1747-1754.	0.6	84

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109	High EVI1 Expression Predicts Outcome in Younger Adult Patients With Acute Myeloid Leukemia and Is Associated With Distinct Cytogenetic Abnormalities. Journal of Clinical Oncology, 2010, 28, 2101-2107.	0.8	222
110	Clinical, Molecular, and Prognostic Significance of WHO Type inv(3)(q21q26.2)/t(3;3)(q21;q26.2) and Various Other 3q Abnormalities in Acute Myeloid Leukemia. Journal of Clinical Oncology, 2010, 28, 3890-3898.	0.8	217
111	Harmonized Testing for BCR-ABL Kinase Domain Mutations In CML: Results of a Survey and First Control Round within 28 National Reference Laboratories In Europe. Blood, 2010, 116, 894-894.	0.6	1
112	Prediction of molecular subtypes in acute myeloid leukemia based on gene expression profiling. Haematologica, 2009, 94, 131-134.	1.7	300
113	Genes Predictive of Outcome and Novel Molecular Classification Schemes in Adult Acute Myeloid Leukemia. Cancer Treatment and Research, 2009, 145, 67-83.	0.2	17
114	Age-Specific Differences in Oncogenic Pathway Dysregulation in Patients With Acute Myeloid Leukemia. Journal of Clinical Oncology, 2009, 27, 5580-5586.	0.8	90
115	Genome-wide epigenetic analysis delineates a biologically distinct immature acute leukemia with myeloid/T-lymphoid features. Blood, 2009, 113, 2795-2804.	0.6	83
116	Double CEBPA mutations, but not single CEBPA mutations, define a subgroup of acute myeloid leukemia with a distinctive gene expression profile that is uniquely associated with a favorable outcome. Blood, 2009, 113, 3088-3091.	0.6	516
117	Gene expression profiling of minimally differentiated acute myeloid leukemia: M0 is a distinct entity subdivided by RUNX1 mutation status. Blood, 2009, 114, 3001-3007.	0.6	51
118	AML at older age: age-related gene expression profiles reveal a paradoxical down-regulation of p16INK4A mRNA with prognostic significance. Blood, 2009, 114, 2869-2877.	0.6	41
119	Polymorphisms in the Multidrug Resistance Gene MDR1 (ABCB1) Predict for Molecular Resistance in Patients with Newly Diagnosed Chronic Myeloid Leukemia (CML) Receiving High-Dose Imatinib.. Blood, 2009, 114, 2208-2208.	0.6	0
120	High EVI1 Expression Predicts Outcome in Younger Adult (15 to 60 years) Patients with Acute Myeloid Leukemia and Is Associated with Distinctive Cytogenetic Subgroups.. Blood, 2009, 114, 582-582.	0.6	1
121	VEGFC Predicts Poor Outcome in Pediatric as Well as Adult Acute Myeloid Leukemia: Insights in Associated Gene Expression Profiles.. Blood, 2009, 114, 997-997.	0.6	1
122	DNA Methylation Profiling Predicts Clinical Outcomes and Reveals Unique Insights Into the Molecular Complexity of Acute Myeloid Leukemia.. Blood, 2009, 114, 707-707.	0.6	0
123	SNPExpress: integrated visualization of genome-wide genotypes, copy numbers and gene expression levels. BMC Genomics, 2008, 9, 41.	1.2	12
124	MicroRNA expression profiling in relation to the genetic heterogeneity of acute myeloid leukemia. Blood, 2008, 111, 5078-5085.	0.6	376
125	High EVI1 levels predict adverse outcome in acute myeloid leukemia: prevalence of EVI1 overexpression and chromosome 3q26 abnormalities underestimated. Blood, 2008, 111, 4329-4337.	0.6	251
126	Mutant Wilmsâ€™ Tumor 1 (WT1) mRNA with Premature Termination Codons Is Sensitive to Nonsense-Mediated RNA Decay in Acute Myeloid Leukemia (AML). Blood, 2008, 112, 2538-2538.	0.6	1

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127	Distinct Gene Expression Profiling in AML in Elderly Versus Younger Patients. Blood, 2008, 112, 2546-2546.	0.6	8
128	Gene Expression Profiles with Signatures of Tumor Biology and Chemotherapy Sensitivity May Provide a Novel Approach to Maximize Response to Induction Therapy in Patients with Acute Myeloid Leukemia.. Blood, 2008, 112, 2252-2252.	0.6	0
129	A recurrent in-frame insertion in a CEBPA transactivation domain is a polymorphism rather than a mutation that does not affect gene expression profilingâ€“based clustering of AML. Blood, 2007, 109, 389-390.	0.6	36
130	Distinct gene expression profiles of acute myeloid/T-lymphoid leukemia with silenced CEBPA and mutations in NOTCH1. Blood, 2007, 110, 3706-3714.	0.6	180
131	Genetic vs. Epigenetic Disruption of the CEBPA Locus Yields Epigenomically and Biologically Distinct Leukemia Phenotypes.. Blood, 2007, 110, 2117-2117.	0.6	1
132	Essential role of Jun family transcription factors in PU.1 knockdownâ€“induced leukemic stem cells. Nature Genetics, 2006, 38, 1269-1277.	9.4	167
133	Tribbles homolog 2 inactivates C/EBPÎ± and causes acute myelogenous leukemia. Cancer Cell, 2006, 10, 401-411.	7.7	232
134	The effect of oligonucleotide microarray data pre-processing on the analysis of patient-cohort studies. BMC Bioinformatics, 2006, 7, 105.	1.2	22
135	HeatMapper: powerful combined visualization of gene expression profile correlations, genotypes, phenotypes and sample characteristics. BMC Bioinformatics, 2006, 7, 337.	1.2	27
136	Significance of Murine Retroviral Mutagenesis for Identification of Disease Genes in Human Acute Myeloid Leukemia. Cancer Research, 2006, 66, 622-626.	0.4	26
137	Tribbles Homolog 2 (Trib2) Inactivates C/EBPalpha and Causes Acute Myelogenous Leukemia.. Blood, 2006, 108, 776-776.	0.6	4
138	Myeloproliferative Disease in the Pathogenesis and Survival of Budd-Chiari Syndrome.. Blood, 2006, 108, 1480-1480.	0.6	1
139	Gene expression profiling in acute myeloid leukemia. Current Opinion in Hematology, 2005, 12, 76-81.	1.2	33
140	The Common Viral Insertion Site Evi12 Is Located in the 5â€²-Noncoding Region of Gnn, a Novel Gene with Enhanced Expression in Two Subclasses of Human Acute Myeloid Leukemia. Journal of Virology, 2005, 79, 5249-5258.	1.5	5
141	Gene Expression Profiling in Acute Myeloid Leukemia. Journal of Clinical Oncology, 2005, 23, 6296-6305.	0.8	99
142	Mutations in nucleophosmin (NPM1) in acute myeloid leukemia (AML): association with other gene abnormalities and previously established gene expression signatures and their favorable prognostic significance. Blood, 2005, 106, 3747-3754.	0.6	545
143	AML1-ETO fusion protein up-regulates TRKA mRNA expression in human CD34+ cells, allowing nerve growth factor-induced expansion. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4016-4021.	3.3	71
144	Prognostically Useful Gene-Expression Profiles in Acute Myeloid Leukemia. New England Journal of Medicine, 2004, 350, 1617-1628.	13.9	1,232

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145	Biallelic mutations in the CEBPA gene and low CEBPA expression levels as prognostic markers in intermediate-risk AML. The Hematology Journal, 2003, 4, 31-40.	2.0	198
146	Incidence and prognosis of c-KIT and FLT3 mutations in core binding factor (CBF) acute myeloid leukaemias. British Journal of Haematology, 2003, 121, 775-777.	1.2	283
147	High EVI1 expression predicts poor survival in acute myeloid leukemia: a study of 319 de novo AML patients. Blood, 2003, 101, 837-845.	0.6	324