# Peter J M Valk

List of Publications by Year
in descending order

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

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Prognostically Useful Gene-Expression Profiles in Acute Myeloid Leukemia. New England Journal of Medicine, 2004, 350, 1617-1628. | 13.9 | 1,232 |
| 2 | DNA Methylation Signatures Identify Biologically Distinct Subtypes in Acute Myeloid Leukemia. Cancer Cell, 2010, 17, 13-27. | 7.7 | 737 |
| 3 | Molecular Minimal Residual Disease in Acute Myeloid Leukemia. New England Journal of Medicine, 2018, 378, 1189-1199. | 13.9 | 605 |
| 4 | A Single Oncogenic Enhancer Rearrangement Causes Concomitant EVI1 and GATA2 Deregulation in Leukemia. Cell, 2014, 157, 369-381. | 13.5 | 571 |
| 5 | 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 |
| 6 | 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 |
| 7 | 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 |
| 8 | MicroRNA expression profiling in relation to the genetic heterogeneity of acute myeloid leukemia. Blood, 2008, 111, 5078-5085. | 0.6 | 376 |
| 9 | 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 |
| 10 | 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 |
| 11 | Distinct evolution and dynamics of epigenetic and genetic heterogeneity in acute myeloid leukemia. Nature Medicine, 2016, 22, 792-799. | 15.2 | 322 |
| 12 | 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 |
| 13 | Prediction of molecular subtypes in acute myeloid leukemia based on gene expression profiling. Haematologica, 2009, 94, 131-134. | 1.7 | 300 |
| 14 | 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 |
| 15 | Base-Pair Resolution DNA Methylation Sequencing Reveals Profoundly Divergent Epigenetic Landscapes in Acute Myeloid Leukemia. PLoS Genetics, 2012, 8, e1002781. | 1.5 | 263 |
| 16 | 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 |
| 17 | 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 |
| 18 | Tribbles homolog 2 inactivates C/EBPα and causes acute myelogenous leukemia. Cancer Cell, 2006, 10, 401-411. | 7.7 | 232 |

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|---|---------|-----|-----------|
| 19 | 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 |
| 20 | Mutant DNMT3A: a marker of poor prognosis in acute myeloid leukemia. Blood, 2012, 119, 5824-5831. | 0.6 | 221 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | Essential role of Jun family transcription factors in PU.1 knockdown–induced leukemic stem cells. Nature Genetics, 2006, 38, 1269-1277. | 9.4 | 167 |
| 26 | 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 |
| 27 | Autocrine activation of the MET receptor tyrosine kinase in acute myeloid leukemia. Nature Medicine, 2012, 18, 1118-1122. | 15.2 | 162 |
| 28 | Sequential gain of mutations in severe congenital neutropenia progressing to acute myeloid leukemia. Blood, 2012, 119, 5071-5077. | 0.6 | 156 |
| 29 | Acquired mutations in ASXL1 in acute myeloid leukemia: prevalence and prognostic value. Haematologica, 2012, 97, 388-392. | 1.7 | 143 |
| 30 | miR-196b directly targets both HOXA9/MEIS1 oncogenes and FAS tumour suppressor in MLL-rearranged leukaemia. Nature Communications, 2012, 3, 688. | 5.8 | 138 |
| 31 | Molecular characterization of mutant *TP53* acute myeloid leukemia and high-risk myelodysplastic syndrome. Blood, 2022, 139, 2347-2354. | 0.6 | 131 |
| 32 | CD34+CD38− leukemic stem cell frequency to predict outcome in acute myeloid leukemia. Leukemia, 2019, 33, 1102-1112. | 3.3 | 130 |
| 33 | Immune landscapes predict chemotherapy resistance and immunotherapy response in acute myeloid leukemia. Science Translational Medicine, 2020, 12, . | 5.8 | 117 |
| 34 | Sox4 Is a Key Oncogenic Target in C/EBPα Mutant Acute Myeloid Leukemia. Cancer Cell, 2013, 24, 575-588. | 7.7 | 112 |
| 35 | 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 |
| 36 | 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 |

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|---|---------|-----|-----------|
| 37 | Gene Expression Profiling in Acute Myeloid Leukemia. Journal of Clinical Oncology, 2005, 23, 6296-6305. | 0.8 | 99 |
| 38 | 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 |
| 39 | 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 |
| 40 | Aberrant DNA hypermethylation signature in acute myeloid leukemia directed by EVI1. Blood, 2011, 117, 234-241. | 0.6 | 94 |
| 41 | Age-Specific Differences in Oncogenic Pathway Dysregulation in Patients With Acute Myeloid Leukemia. Journal of Clinical Oncology, 2009, 27, 5580-5586. | 0.8 | 90 |
| 42 | 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 |
| 43 | 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 |
| 44 | TP53 abnormalities correlate with immune infiltration and associate with response to flotetuzumab immunotherapy in AML. Blood Advances, 2020, 4, 5011-5024. | 2.5 | 85 |
| 45 | 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 |
| 46 | Genome-wide epigenetic analysis delineates a biologically distinct immature acute leukemia with myeloid/T-lymphoid features. Blood, 2009, 113, 2795-2804. | 0.6 | 83 |
| 47 | 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 |
| 48 | *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 |
| 49 | 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 |
| 50 | Characterization of CEBPA mutations and promoter hypermethylation in pediatric acute myeloid leukemia. Haematologica, 2011, 96, 384-392. | 1.7 | 74 |
| 51 | 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 |
| 52 | Review: Aberrant *EVI1* expression in acute myeloid leukaemia. British Journal of Haematology, 2016, 172, 870-878. | 1.2 | 60 |
| 53 | Common and Overlapping Oncogenic Pathways Contribute to the Evolution of Acute Myeloid Leukemias. Cancer Research, 2011, 71, 4117-4129. | 0.4 | 55 |
| 54 | The evolving molecular genetic landscape in acute myeloid leukaemia. Current Opinion in Hematology, 2013, 20, 79-85. | 1.2 | 53 |

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|---|---------|----|-----------| 
| 55 | 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 |
| 56 | 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 |
| 57 | C/EBPÎ³ deregulation results in differentiation arrest in acute myeloid leukemia. Journal of Clinical Investigation, 2012, 122, 4490-4504. | 3.9 | 50 |
| 58 | Thrombopoietin/MPL participates in initiating and maintaining RUNX1-ETO acute myeloid leukemia via PI3K/AKT signaling. Blood, 2012, 120, 868-879. | 0.6 | 47 |
| 59 | <scp>CD</scp>45<scp>RA</scp>, a specific marker for leukaemia stem cell sub€populations in acute myeloid leukaemia. British Journal of Haematology, 2016, 173, 219-235. | 1.2 | 47 |
| 60 | Comprehensive diagnostics of acute myeloid leukemia by whole transcriptome RNA sequencing. Leukemia, 2021, 35, 47-61. | 3.3 | 47 |
| 61 | A variant allele of Growth Factor Independence 1 (GFI1) is associated with acute myeloid leukemia. Blood, 2010, 115, 2462-2472. | 0.6 | 46 |
| 62 | Azacytidine Treatment for VEXAS Syndrome. HemaSphere, 2021, 5, e661. | 1.2 | 45 |
| 63 | Downregulation of the Wnt inhibitor CXXC5 predicts a better prognosis in acute myeloid leukemia. Blood, 2015, 125, 2985-2994. | 0.6 | 42 |
| 64 | 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 |
| 65 | Next-generation sequencing in the diagnosis and minimal residual disease assessment of acute myeloid leukemia. Haematologica, 2019, 104, 868-871. | 1.7 | 40 |
| 66 | Atypical 3q26/MECOM rearrangements genocopy inv(3)/t(3;3) in acute myeloid leukemia. Blood, 2020, 136, 224-234. | 0.6 | 39 |
| 67 | Systematic Profiling of <i>DNMT3A</i> Variants Reveals Protein Instability Mediated by the DCAF8 E3 Ubiquitin Ligase Adaptor. Cancer Discovery, 2022, 12, 220-235. | 7.7 | 38 |
| 68 | A recurrent in-frame insertion in a CEBPA transactivation domain is a polymorphism rather than a mutation that does not affect gene expression profiling€"based clustering of AML. Blood, 2007, 109, 389-390. | 0.6 | 36 |
| 69 | The Antioxidant Protein Peroxiredoxin 4 Is Epigenetically Down Regulated in Acute Promyelocytic Leukemia. PLoS ONE, 2011, 6, e16340. | 1.1 | 36 |
| 70 | MPL expression on AML blasts predicts peripheral blood neutropenia and thrombocytopenia. Blood, 2016, 128, 2253-2257. | 0.6 | 34 |
| 71 | Gene expression profiling in acute myeloid leukemia. Current Opinion in Hematology, 2005, 12, 76-81. | 1.2 | 33 |
| 72 | 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 |

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|---|---------|-----|-----------|
| 73 | 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 |
| 74 | 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 |
| 75 | 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 |
| 76 | The neuropeptide receptor calcitonin receptor-like (CALCRL) is a potential therapeutic target in acute myeloid leukemia. Leukemia, 2019, 33, 2830-2841. | 3.3 | 30 |
| 77 | 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 |
| 78 | HeatMapper: powerful combined visualization of gene expression profile correlations, genotypes, phenotypes and sample characteristics. BMC Bioinformatics, 2006, 7, 337. | 1.2 | 27 |
| 79 | Significance of Murine Retroviral Mutagenesis for Identification of Disease Genes in Human Acute Myeloid Leukemia. Cancer Research, 2006, 66, 622-626. | 0.4 | 26 |
| 80 | NrasG12D oncoprotein inhibits apoptosis of preleukemic cells expressing CbfÎ²-SMMHC via activation of MEK/ERK axis. Blood, 2014, 124, 426-436. | 0.6 | 26 |
| 81 | 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 |
| 82 | Altered NFE2 activity predisposes to leukemic transformation and myelosarcoma with AML-specific aberrations. Blood, 2019, 133, 1766-1777. | 0.6 | 23 |
| 83 | The effect of oligonucleotide microarray data pre-processing on the analysis of patient-cohort studies. BMC Bioinformatics, 2006, 7, 105. | 1.2 | 22 |
| 84 | 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 |
| 85 | Molecular Minimal Residual Disease Detection in Acute Myeloid Leukemia. Cancers, 2021, 13, 5431. | 1.7 | 18 |
| 86 | 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 |
| 87 | Digital PCR for <i>BCRâ€ABL1</i> Quantification in CML: Current Applications in Clinical Practice. HemaSphere, 2020, 4, e496. | 1.2 | 17 |
| 88 | 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. | 1.2 | 14 |
| 89 | The Landscape of <i>KMT2A</i>â€PTD AML: Concurrent Mutations, Gene Expression Signatures, and Clinical Outcome. HemaSphere, 2019, 3, e181. | 1.2 | 14 |
| 90 | Ibrutinib added to 10-day decitabine for older patients with AML and higher risk MDS. Blood Advances, 2020, 4, 4267-4277. | 2.5 | 14 |

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| 91 | SNPExpress: integrated visualization of genome-wide genotypes, copy numbers and gene expression levels. BMC Genomics, 2008, 9, 41. | 1.2 | 12 |
| 92 | Pim2 cooperates with PML-RARÎ± to induce acute myeloid leukemia in a bone marrow transplantation model. Blood, 2010, 115, 4507-4516. | 0.6 | 12 |
| 93 | Sex disparity in acute myeloid leukaemia with <i>FLT3</i> internal tandem duplication mutations: implications for prognosis. Molecular Oncology, 2021, 15, 2285-2299. | 2.1 | 11 |
| 94 | 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 |
| 95 | <i><scp>ID</scp>1</i> 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 |
| 96 | 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 |
| 97 | Distinct Gene Expression Profiling in AML in Elderly Versus Younger Patients. Blood, 2008, 112, 2546-2546. | 0.6 | 8 |
| 98 | Reduced SLIT2 is Associated with Increased Cell Proliferation and Arsenic Trioxide Resistance in Acute Promyelocytic Leukemia. Cancers, 2020, 12, 3134. | 1.7 | 7 |
| 99 | Genomic and evolutionary portraits of disease relapse in acute myeloid leukemia. Leukemia, 2021, 35, 2688-2692. | 3.3 | 7 |
| 100 | Disruption of CSF-1R signaling inhibits growth of AML with inv(16). Blood Advances, 2021, 5, 1273-1277. | 2.5 | 7 |
| 101 | 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 |
| 102 | RNA Targeting in Acute Myeloid Leukemia. ACS Pharmacology and Translational Science, 2020, 3, 1225-1232. | 2.5 | 6 |
| 103 | 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 |
| 104 | Detection of MutantNPM1mRNA in Acute Myeloid Leukemia Using Custom Gene Expression Arrays. Genetic Testing and Molecular Biomarkers, 2013, 17, 295-300. | 0.3 | 5 |
| 105 | FLT3â€‘ITD mutations in acute myeloid leukaemia â€" molecular characteristics, distribution and numerical variation. Molecular Oncology, 2021, 15, 2300-2317. | 2.1 | 5 |
| 106 | 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 |
| 107 | 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 |
| 108 | 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 |

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|---|---------|----|----------|
| 109 | Tribbles Homolog 2 (Trib2) Inactivates C/EBPalpha and Causes Acute Myelogenous Leukemia.. Blood, 2006, 108, 776-776. | 0.6 | 4 |
| 110 | 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 |
| 111 | Lack of splice factor and cohesin complex mutations in pediatric myelodysplastic syndrome. Haematologica, 2016, 101, e479-e481. | 1.7 | 3 |
| 112 | Secondary CNL after SAA reveals insights in leukemic transformation of bone marrow failure syndromes. Blood Advances, 2020, 4, 5540-5546. | 2.5 | 3 |
| 113 | PPM1D mutations appear in complete remission after exposure to chemotherapy without predicting emerging AML relapse. Leukemia, 2021, 35, 2693-2697. | 3.3 | 2 |
| 114 | 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 |
| 115 | Genetic vs. Epigenetic Disruption of the CEBPA Locus Yields Epigenomically and Biologically Distinct Leukemia Phenotypes.. Blood, 2007, 110, 2117-2117. | 0.6 | 1 |
| 116 | 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 |
| 117 | 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 |
| 118 | Myeloproliferative Disease in the Pathogenesis and Survival of Budd-Chiari Syndrome.. Blood, 2006, 108, 1480-1480. | 0.6 | 1 |
| 119 | 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 |
| 120 | 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 |
| 121 | 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 |
| 122 | The Impact of Novel Molecular Markers on Risk Stratification in Acute Myeloid Leukemia. Blood, 2012, 120, SCI-33-SCI-33. | 0.6 | 1 |
| 123 | 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 |
| 124 | Transplant in older adults with AML: genomic wheat and chaff. Blood, 2022, 139, 3459-3461. | 0.6 | 1 |
| 125 | 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 |
| 126 | Future Developments: Measurable Residual Disease. Hematologic Malignancies, 2021, , 317-337. | 0.2 | 0 |

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|---|---------|-----|-----------|
| 127 | 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 |
| 128 | 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 |
| 129 | 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 |
| 130 | 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 |
| 131 | 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 |
| 132 | Linking the Glycolytic Enzyme HK3 to Neutrophil Differentiation of APL Cells Via PU.1. Blood, 2011, 118, 2425-2425. | 0.6 | 0 |
| 133 | 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 |
| 134 | The HOXA/PBX3 Pathway Is an Attractive Therapeutic Target in MLL-Rearranged Acute Leukemia. Blood, 2012, 120, 3522-3522. | 0.6 | 0 |
| 135 | Identification of Sox4 As Key Oncogene in Leukemias with Mutated or Silenced C/EBPÎ±. Blood, 2012, 120, 114-114. | 0.6 | 0 |
| 136 | BAALC and EVI1 Prognostic Gene Expression in Adult Acute Myeloid Leukemia Using the Amlprofiler Custom Microarray. Blood, 2012, 120, 1420-1420. | 0.6 | 0 |
| 137 | Prognostic and Functional Relevance of Aberrant Microrna-9/9* Expression in Acute Myeloid Leukemia.. Blood, 2012, 120, 2542-2542. | 0.6 | 0 |
| 138 | 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 |
| 139 | Molecular Minimal Residual Disease Detection in Acute Myeloid Leukemia. Blood, 2016, 128, SCI-30-SCI-30. | 0.6 | 0 |
| 140 | Whole Transcriptome RNA Sequencing As a Comprehensive Diagnostic Tool for Acute Myeloid Leukemia. Blood, 2018, 132, 2762-2762. | 0.6 | 0 |
| 141 | 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 |
| 142 | Slit-Robo Pathway Is Clinically Relevant and May Represent a Potential Target in Acute Promyelocytic Leukemia. Blood, 2018, 132, 1533-1533. | 0.6 | 0 |
| 143 | Metformintreatment Overcomes ATRA-Resistance in Acute Promyelocytic Leukemia and Increases FOXO3A Expression. Blood, 2018, 132, 1532-1532. | 0.6 | 0 |
| 144 | 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 |

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|---|---------|-----|-----------|
| 145 | 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 |
| 146 | Allele-Specific Expression of GATA2 in AML with CEBPA Biallelic Mutations. Blood, 2019, 134, 1235-1235. | 0.6 | 0 |
| 147 | Arsenic Trioxide Abrogate MN1 Mediated RA-Resistance in Acute Promyelocytic Leukemia. Blood, 2019, 134, 5166-5166. | 0.6 | 0 |