Peter Jm Valk

List of Publications by Year
in descending order

56 papers	7,613 citations	218381 26 h-index	189595 50 g-index
59 all docs	59 docs citations	59 times ranked	10200 citing authors

#	Article	IF	Citations
1	Leukemic IDH1 and IDH2 Mutations Result inÂa Hypermethylation Phenotype, Disrupt TET2 Function, and Impair Hematopoietic Differentiation. Cancer Cell, 2010, 18, 553-567.	7.7	2,328
2	Prognostically Useful Gene-Expression Profiles in Acute Myeloid Leukemia. New England Journal of Medicine, 2004, 350, 1617-1628.	13.9	1,232
3	DNA Methylation Signatures Identify Biologically Distinct Subtypes in Acute Myeloid Leukemia. Cancer Cell, 2010, 17, 13-27.	7.7	737
4	Molecular Minimal Residual Disease in Acute Myeloid Leukemia. New England Journal of Medicine, 2018, 378, 1189-1199.	13.9	605
5	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
6	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
7	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
8	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
9	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
10	miR-196b directly targets both HOXA9/MEIS1 oncogenes and FAS tumour suppressor in MLL-rearranged leukaemia. Nature Communications, 2012, 3, 688.	5.8	138
11	Molecular characterization of mutant TP53 acute myeloid leukemia and high-risk myelodysplastic syndrome. Blood, 2022, 139, 2347-2354.	0.6	131
12	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
13	Gene Expression Profiling in Acute Myeloid Leukemia. Journal of Clinical Oncology, 2005, 23, 6296-6305.	0.8	99
14	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
15	Age-Specific Differences in Oncogenic Pathway Dysregulation in Patients With Acute Myeloid Leukemia. Journal of Clinical Oncology, 2009, 27, 5580-5586.	0.8	90
16	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
17	Common and Overlapping Oncogenic Pathways Contribute to the Evolution of Acute Myeloid Leukemias. Cancer Research, 2011, 71, 4117-4129.	0.4	55
18	The evolving molecular genetic landscape in acute myeloid leukaemia. Current Opinion in Hematology, 2013, 20, 79-85.	1.2	53

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19	C/EBPÎ³ deregulation results in differentiation arrest in acute myeloid leukemia. Journal of Clinical Investigation, 2012, 122, 4490-4504.	3.9	50
20	Characterization of the C3 YAC Contig from Proximal Mouse Chromosome 17 and Analysis of Allelic Expression of Genes Flanking the Imprinted Igf2r Gene. Genomics, 1997, 43, 285-297.	1.3	49
21	Next-generation sequencing in the diagnosis and minimal residual disease assessment of acute myeloid leukemia. Haematologica, 2019, 104, 868-871.	1.7	40
22	Absence of leukaemic <scp>CD</scp>34⁺ cells in acute myeloid leukaemia is of high prognostic value: a longstanding controversy deciphered. British Journal of Haematology, 2015, 171, 227-238.	1.2	38
23	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
24	Large-scale identification of novel potential disease loci in mouse leukemia applying an improved strategy for cloning common virus integration sites. Oncogene, 2002, 21, 7247-7255.	2.6	37
25	Gene expression profiling in acute myeloid leukemia. Current Opinion in Hematology, 2005, 12, 76-81.	1.2	33
26	MEIS1-mediated transactivation of synaptotagmin-like 1 promotes CXCL12/CXCR4 signaling and leukemogenesis. Journal of Clinical Investigation, 2016, 126, 1664-1678.	3.9	30
27	The Peripheral Cannabinoid Receptor, Cb2, in Retrovirally-Induced Leukemic Transformation and Normal Hematopoiesis. Leukemia and Lymphoma, 1998, 32, 29-43.	0.6	27
28	HeatMapper: powerful combined visualization of gene expression profile correlations, genotypes, phenotypes and sample characteristics. BMC Bioinformatics, 2006, 7, 337.	1.2	27
29	Significance of Murine Retroviral Mutagenesis for Identification of Disease Genes in Human Acute Myeloid Leukemia. Cancer Research, 2006, 66, 622-626.	0.4	26
30	Double, but Not Single, CEBPA mutations Define a Subgroup of Acute Myeloid Leukemia with Favorable Outcome and a Distinct Gene Expression Profile. Blood, 2008, 112, 141-141.	0.6	24
31	The effect of oligonucleotide microarray data pre-processing on the analysis of patient-cohort studies. BMC Bioinformatics, 2006, 7, 105.	1.2	22
32	Digital PCR for BCRâ€ABL1 Quantification in CML: Current Applications in Clinical Practice. HemaSphere, 2020, 4, e496.	1.2	17
33	Phenotyping of Evi1, Evi11/Cb2, and Evi12 Transformed Leukemias Isolated from a Novel Panel of Cas-Br-M Murine Leukemia Virus-Infected Mice. Virology, 2000, 268, 308-318.	1.1	13
34	SNPExpress: integrated visualization of genome-wide genotypes, copy numbers and gene expression levels. BMC Genomics, 2008, 9, 41.	1.2	12
35	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
36	Prospective Molecular MRD Detection By NGS: A Powerful Independent Predictor for Relapse and Survival in Adults with Newly Diagnosed AML. Blood, 2017, 130, LBA-5-LBA-5.	0.6	10

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37	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
38	A standardized microarray assay for the independent gene expression markers in AML: EVI1 and BAALC. Experimental Hematology and Oncology, 2013, 2, 7.	2.0	8
39	Molecular Minimal Residual Disease in Acute Myeloid Leukemia. New England Journal of Medicine, 2018, 378, 2442-2443.	13.9	7
40	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
41	Detection of MutantNPM1mRNA in Acute Myeloid Leukemia Using Custom Gene Expression Arrays. Genetic Testing and Molecular Biomarkers, 2013, 17, 295-300.	0.3	5
42	Whole Transcriptome Sequencing (RNAseq) As a Comprehensive, Cost-Efficient Diagnostic Tool for Acute Myeloid Leukemia. Blood, 2016, 128, 1701-1701.	0.6	4
43	Two Different EVI1 Expressing Poor-Risk AML Subgroups with Distinct Epigenetic Signatures Uncovered by Genome Wide DNA Methylation Profiling. Blood, 2008, 112, 757-757.	0.6	3
44	Epigenetic Signatures Identify New Clinically Relevant Subtypes and Define Gene Regulatory Patterns in Patients with Acute Myeloid Leukemia (AML). Blood, 2008, 112, 756-756.	0.6	2
45	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.	0.6	2
46	A Novel Subgroup of Poor Prognostic AML with Low CEBPA Expression, CEBPA Promoter Hypermethylation and DNMT3b Overexpression.. Blood, 2004, 104, 418-418.	0.6	1
47	High INDO (Indoleamine 2,3-Dioxygenase) mRNA Level in Blasts of Acute Myeloid Leukemic Patients Predicts Poor Clinical Outcome.. Blood, 2007, 110, 4297-4297.	0.6	1
48	High Prognostic Impact of Flowcytometric Minimal Residual Disease Detection In Acute Myeloid Leukemia: Prospective Data From the HOVON/SAKK 42a Study. Blood, 2010, 116, 760-760.	0.6	1
49	Extensive RAG-Mediated Rearrangements and Mutations in BCR-ABL1 and BCR-ABL1-like Adult Acute Lymphoblastic Leukemia. Blood, 2016, 128, 4067-4067.	0.6	1
50	DNMT3A Mutations Enhance CpG Mutagenesis through Deregulation of the Active DNA Demethylation Pathway. Blood, 2016, 128, 1076-1076.	0.6	1
51	Extensive Molecular Analysis Strongly Improves the Distinction Between AML and ALL in Adult Acute Leukemias of Ambiguous Lineage. Blood, 2014, 124, 1067-1067.	0.6	0
52	Changes of the Mutational Landscape in Relapsed Acute Myeloid Leukemia. Blood, 2016, 128, 599-599.	0.6	0
53	Archived Bone Marrow Smears Are an Excellent Source for NGS-Based Mutation Detection in Acute Myeloid Leukemia. Blood, 2018, 132, 2783-2783.	0.6	0
54	Does RAD21 Co-Mutation Have a Role in DNMT3A Mutated AML? Results of Harmony Alliance AML Database. Blood, 2021, 138, 608-608.	0.6	0

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55	Impact of Gender on Molecular AML Subclasses - a Harmony Alliance Study. Blood, 2021, 138, 3438-3438.	0.6	0
56	TP53 Abnormalities Correlate with Immune Infiltration and Associate with Response to Flotetuzumab Immunotherapy in Acute Myeloid Leukemia. Blood, 2020, 136, 3-4.	0.6	0