

# Peter Jm Valk

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11458958/publications.pdf>

Version: 2024-02-01

56  
papers

7,613  
citations

218677

26  
h-index

189892

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 in a Hypermethylation Phenotype, Disrupt TET2 Function, and Impair Hematopoietic Differentiation. <i>Cancer Cell</i> , 2010, 18, 553-567.	16.8	2,328
2	Prognostically Useful Gene-Expression Profiles in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2004, 350, 1617-1628.	27.0	1,232
3	DNA Methylation Signatures Identify Biologically Distinct Subtypes in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2010, 17, 13-27.	16.8	737
4	Molecular Minimal Residual Disease in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2018, 378, 1189-1199.	27.0	605
5	High Prognostic Impact of Flow Cytometric Minimal Residual Disease Detection in Acute Myeloid Leukemia: Data From the HOVON/SAKK AML 42A Study. <i>Journal of Clinical Oncology</i> , 2013, 31, 3889-3897.	1.6	392
6	2021 Update on MRD in acute myeloid leukemia: a consensus document from the European LeukemiaNet MRD Working Party. <i>Blood</i> , 2021, 138, 2753-2767.	1.4	305
7	High <i>EVI1</i> Expression Predicts Outcome in Younger Adult Patients With Acute Myeloid Leukemia and Is Associated With Distinct Cytogenetic Abnormalities. <i>Journal of Clinical Oncology</i> , 2010, 28, 2101-2107.	1.6	222
8	Clinical, Molecular, and Prognostic Significance of WHO Type <i>inv(3)(q21q26.2)/t(3;3)(q21;q26.2)</i> and Various Other 3q Abnormalities in Acute Myeloid Leukemia. <i>Journal of Clinical Oncology</i> , 2010, 28, 3890-3898.	1.6	217
9	Identification of a 24-Gene Prognostic Signature That Improves the European LeukemiaNet Risk Classification of Acute Myeloid Leukemia: An International Collaborative Study. <i>Journal of Clinical Oncology</i> , 2013, 31, 1172-1181.	1.6	164
10	miR-196b directly targets both <i>HOXA9/MEIS1</i> oncogenes and <i>FAS</i> tumour suppressor in MLL-rearranged leukaemia. <i>Nature Communications</i> , 2012, 3, 688.	12.8	138
11	Molecular characterization of mutant <i>TP53</i> acute myeloid leukemia and high-risk myelodysplastic syndrome. <i>Blood</i> , 2022, 139, 2347-2354.	1.4	131
12	Epigenetic Identity in AML Depends on Disruption of Nonpromoter Regulatory Elements and Is Affected by Antagonistic Effects of Mutations in Epigenetic Modifiers. <i>Cancer Discovery</i> , 2017, 7, 868-883.	9.4	101
13	Gene Expression Profiling in Acute Myeloid Leukemia. <i>Journal of Clinical Oncology</i> , 2005, 23, 6296-6305.	1.6	99
14	Deregulated Expression of <i>EVI1</i> 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. <i>Journal of Clinical Oncology</i> , 2013, 31, 95-103.	1.6	95
15	Age-Specific Differences in Oncogenic Pathway Dysregulation in Patients With Acute Myeloid Leukemia. <i>Journal of Clinical Oncology</i> , 2009, 27, 5580-5586.	1.6	90
16	<i>CEBPA</i> mutations in 4708 patients with acute myeloid leukemia: differential impact of bZIP and TAD mutations on outcome. <i>Blood</i> , 2022, 139, 87-103.	1.4	82
17	Common and Overlapping Oncogenic Pathways Contribute to the Evolution of Acute Myeloid Leukemias. <i>Cancer Research</i> , 2011, 71, 4117-4129.	0.9	55
18	The evolving molecular genetic landscape in acute myeloid leukaemia. <i>Current Opinion in Hematology</i> , 2013, 20, 79-85.	2.5	53

#	ARTICLE	IF	CITATIONS
19	C/EBP $\beta$ deregulation results in differentiation arrest in acute myeloid leukemia. <i>Journal of Clinical Investigation</i> , 2012, 122, 4490-4504.	8.2	50
20	Characterization of the C3 YAC Contig from Proximal Mouse Chromosome 17 and Analysis of Allelic Expression of Genes Flanking the Imprinted <i>Igf2r</i> Gene. <i>Genomics</i> , 1997, 43, 285-297.	2.9	49
21	Next-generation sequencing in the diagnosis and minimal residual disease assessment of acute myeloid leukemia. <i>Haematologica</i> , 2019, 104, 868-871.	3.5	40
22	Absence of leukaemic $CD^{34}+$ cells in acute myeloid leukaemia is of high prognostic value: a longstanding controversy deciphered. <i>British Journal of Haematology</i> , 2015, 171, 227-238.	2.5	38
23	Systematic Profiling of <i>DNMT3A</i> Variants Reveals Protein Instability Mediated by the DCAF8 E3 Ubiquitin Ligase Adaptor. <i>Cancer Discovery</i> , 2022, 12, 220-235.	9.4	38
24	Large-scale identification of novel potential disease loci in mouse leukemia applying an improved strategy for cloning common virus integration sites. <i>Oncogene</i> , 2002, 21, 7247-7255.	5.9	37
25	Gene expression profiling in acute myeloid leukemia. <i>Current Opinion in Hematology</i> , 2005, 12, 76-81.	2.5	33
26	MEIS1-mediated transactivation of synaptotagmin-like 1 promotes CXCL12/CXCR4 signaling and leukemogenesis. <i>Journal of Clinical Investigation</i> , 2016, 126, 1664-1678.	8.2	30
27	The Peripheral Cannabinoid Receptor, Cb2, in Retrovirally-Induced Leukemic Transformation and Normal Hematopoiesis. <i>Leukemia and Lymphoma</i> , 1998, 32, 29-43.	1.3	27
28	HeatMapper: powerful combined visualization of gene expression profile correlations, genotypes, phenotypes and sample characteristics. <i>BMC Bioinformatics</i> , 2006, 7, 337.	2.6	27
29	Significance of Murine Retroviral Mutagenesis for Identification of Disease Genes in Human Acute Myeloid Leukemia. <i>Cancer Research</i> , 2006, 66, 622-626.	0.9	26
30	Double, but Not Single, CEBPA mutations Define a Subgroup of Acute Myeloid Leukemia with Favorable Outcome and a Distinct Gene Expression Profile. <i>Blood</i> , 2008, 112, 141-141.	1.4	24
31	The effect of oligonucleotide microarray data pre-processing on the analysis of patient-cohort studies. <i>BMC Bioinformatics</i> , 2006, 7, 105.	2.6	22
32	Digital PCR for <i>BCR-ABL1</i> Quantification in CML: Current Applications in Clinical Practice. <i>HemaSphere</i> , 2020, 4, e496.	2.7	17
33	Phenotyping of Evi1, Evi1/Cb2, and Evi12 Transformed Leukemias Isolated from a Novel Panel of Cas-Br-M Murine Leukemia Virus-Infected Mice. <i>Virology</i> , 2000, 268, 308-318.	2.4	13
34	SNPEXpress: integrated visualization of genome-wide genotypes, copy numbers and gene expression levels. <i>BMC Genomics</i> , 2008, 9, 41.	2.8	12
35	Impact of hospital experience on the quality of tyrosine kinase inhibitor response monitoring and consequence for chronic myeloid leukemia patient survival. <i>Haematologica</i> , 2017, 102, e486-e489.	3.5	10
36	Prospective Molecular MRD Detection By NGS: A Powerful Independent Predictor for Relapse and Survival in Adults with Newly Diagnosed AML. <i>Blood</i> , 2017, 130, LBA-5-LBA-5.	1.4	10

#	ARTICLE	IF	CITATIONS
37	Detection of CEBPA Double Mutants in Acute Myeloid Leukemia Using a Custom Gene Expression Array. <i>Genetic Testing and Molecular Biomarkers</i> , 2013, 17, 395-400.	0.7	8
38	A standardized microarray assay for the independent gene expression markers in AML: EVI1 and BAALC. <i>Experimental Hematology and Oncology</i> , 2013, 2, 7.	5.0	8
39	Molecular Minimal Residual Disease in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2018, 378, 2442-2443.	27.0	7
40	Omitting cytogenetic assessment from routine treatment response monitoring in chronic myeloid leukemia is safe. <i>European Journal of Haematology</i> , 2018, 100, 367-371.	2.2	6
41	Detection of Mutant NPM1 mRNA in Acute Myeloid Leukemia Using Custom Gene Expression Arrays. <i>Genetic Testing and Molecular Biomarkers</i> , 2013, 17, 295-300.	0.7	5
42	Whole Transcriptome Sequencing (RNAseq) As a Comprehensive, Cost-Efficient Diagnostic Tool for Acute Myeloid Leukemia. <i>Blood</i> , 2016, 128, 1701-1701.	1.4	4
43	Two Different EVI1 Expressing Poor-Risk AML Subgroups with Distinct Epigenetic Signatures Uncovered by Genome Wide DNA Methylation Profiling. <i>Blood</i> , 2008, 112, 757-757.	1.4	3
44	Epigenetic Signatures Identify New Clinically Relevant Subtypes and Define Gene Regulatory Patterns in Patients with Acute Myeloid Leukemia (AML). <i>Blood</i> , 2008, 112, 756-756.	1.4	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. <i>Blood</i> , 2021, 138, 4041-4041.	1.4	2
46	A Novel Subgroup of Poor Prognostic AML with Low CEBPA Expression, CEBPA Promoter Hypermethylation and DNMT3b Overexpression.. <i>Blood</i> , 2004, 104, 418-418.	1.4	1
47	High INDO (Indoleamine 2,3-Dioxygenase) mRNA Level in Blasts of Acute Myeloid Leukemic Patients Predicts Poor Clinical Outcome.. <i>Blood</i> , 2007, 110, 4297-4297.	1.4	1
48	High Prognostic Impact of Flowcytometric Minimal Residual Disease Detection In Acute Myeloid Leukemia: Prospective Data From the HOVON/SAKK 42a Study. <i>Blood</i> , 2010, 116, 760-760.	1.4	1
49	Extensive RAG-Mediated Rearrangements and Mutations in BCR-ABL1 and BCR-ABL1-like Adult Acute Lymphoblastic Leukemia. <i>Blood</i> , 2016, 128, 4067-4067.	1.4	1
50	DNMT3A Mutations Enhance CpG Mutagenesis through Deregulation of the Active DNA Demethylation Pathway. <i>Blood</i> , 2016, 128, 1076-1076.	1.4	1
51	Extensive Molecular Analysis Strongly Improves the Distinction Between AML and ALL in Adult Acute Leukemias of Ambiguous Lineage. <i>Blood</i> , 2014, 124, 1067-1067.	1.4	0
52	Changes of the Mutational Landscape in Relapsed Acute Myeloid Leukemia. <i>Blood</i> , 2016, 128, 599-599.	1.4	0
53	Archived Bone Marrow Smears Are an Excellent Source for NGS-Based Mutation Detection in Acute Myeloid Leukemia. <i>Blood</i> , 2018, 132, 2783-2783.	1.4	0
54	Does RAD21 Co-Mutation Have a Role in DNMT3A Mutated AML? Results of Harmony Alliance AML Database. <i>Blood</i> , 2021, 138, 608-608.	1.4	0

#	ARTICLE	IF	CITATIONS
55	Impact of Gender on Molecular AML Subclasses - a Harmony Alliance Study. Blood, 2021, 138, 3438-3438.	1.4	0
56	<i>TP53</i> Abnormalities Correlate with Immune Infiltration and Associate with Response to Flotetuzumab Immunotherapy in Acute Myeloid Leukemia. Blood, 2020, 136, 3-4.	1.4	0