

# Timothy J Ley

## List of Publications by Year in descending order

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134  
papers

28,615  
citations

41344

49  
h-index

25787

108  
g-index

136  
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136  
docs citations

136  
times ranked

35058  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2013, 368, 2059-2074.	27.0	4,139
2	Mutational landscape and significance across 12 major cancer types. <i>Nature</i> , 2013, 502, 333-339.	27.8	3,695
3	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. <i>New England Journal of Medicine</i> , 2009, 361, 1058-1066.	27.0	2,009
4	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. <i>Nature</i> , 2012, 481, 506-510.	27.8	1,795
5	<i>DNMT3A</i> Mutations in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2010, 363, 2424-2433.	27.0	1,777
6	Age-related mutations associated with clonal hematopoietic expansion and malignancies. <i>Nature Medicine</i> , 2014, 20, 1472-1478.	30.7	1,533
7	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. <i>Cell</i> , 2012, 150, 264-278.	28.9	1,365
8	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. <i>Nature</i> , 2008, 456, 66-72.	27.8	1,275
9	Genome remodelling in a basal-like breast cancer metastasis and xenograft. <i>Nature</i> , 2010, 464, 999-1005.	27.8	1,077
10	Clonal Architecture of Secondary Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2012, 366, 1090-1098.	27.0	688
11	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. <i>Nature</i> , 2015, 518, 552-555.	27.8	685
12	<i>TP53</i> and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes. <i>New England Journal of Medicine</i> , 2016, 375, 2023-2036.	27.0	663
13	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. <i>Bioinformatics</i> , 2012, 28, 311-317.	4.1	566
14	Recurrent mutations in the U2AF1 splicing factor in myelodysplastic syndromes. <i>Nature Genetics</i> , 2012, 44, 53-57.	21.4	513
15	DGIdb: mining the druggable genome. <i>Nature Methods</i> , 2013, 10, 1209-1210.	19.0	443
16	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. <i>PLoS Computational Biology</i> , 2014, 10, e1003665.	3.2	400
17	The R882H DNMT3A Mutation Associated with AML Dominantly Inhibits Wild-Type DNMT3A by Blocking Its Ability to Form Active Tetramers. <i>Cancer Cell</i> , 2014, 25, 442-454.	16.8	374
18	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2014, 25, 379-392.	16.8	330

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19	Immune Escape of Relapsed AML Cells after Allogeneic Transplantation. <i>New England Journal of Medicine</i> , 2018, 379, 2330-2341.	27.0	322
20	The Physician-Scientist Career Pipeline in 2005. <i>JAMA - Journal of the American Medical Association</i> , 2005, 294, 1343.	7.4	317
21	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. <i>JAMA - Journal of the American Medical Association</i> , 2015, 314, 811.	7.4	302
22	Sudden death among patients with acute promyelocytic leukemia treated with arsenic trioxide. <i>Blood</i> , 2001, 98, 266-271.	1.4	233
23	Use of Whole-Genome Sequencing to Diagnose a Cryptic Fusion Oncogene. <i>JAMA - Journal of the American Medical Association</i> , 2011, 305, 1577.	7.4	233
24	Genomic analysis of germ line and somatic variants in familial myelodysplasia/acute myeloid leukemia. <i>Blood</i> , 2015, 126, 2484-2490.	1.4	207
25	The Physician-Scientist: Career Issues and Challenges at the Year 2000. <i>FASEB Journal</i> , 2000, 14, 221-230.	0.5	206
26	The Gender Gap in NIH Grant Applications. <i>Science</i> , 2008, 322, 1472-1474.	12.6	206
27	CpG Island Hypermethylation Mediated by DNMT3A Is a Consequence of AML Progression. <i>Cell</i> , 2017, 168, 801-816.e13.	28.9	177
28	Optimizing Cancer Genome Sequencing and Analysis. <i>Cell Systems</i> , 2015, 1, 210-223.	6.2	174
29	Genome Sequencing as an Alternative to Cytogenetic Analysis in Myeloid Cancers. <i>New England Journal of Medicine</i> , 2021, 384, 924-935.	27.0	170
30	Cellular stressors contribute to the expansion of hematopoietic clones of varying leukemic potential. <i>Nature Communications</i> , 2018, 9, 455.	12.8	150
31	A general approach for detecting expressed mutations in AML cells using single cell RNA-sequencing. <i>Nature Communications</i> , 2019, 10, 3660.	12.8	147
32	High-penetrance mouse model of acute promyelocytic leukemia with very low levels of PML-RAR $\alpha$ expression. <i>Blood</i> , 2003, 102, 1857-1865.	1.4	139
33	Genomic impact of transient low-dose decitabine treatment on primary AML cells. <i>Blood</i> , 2013, 121, 1633-1643.	1.4	137
34	Visualizing tumor evolution with the fishplot package for R. <i>BMC Genomics</i> , 2016, 17, 880.	2.8	131
35	High throughput digital quantification of mRNA abundance in primary human acute myeloid leukemia samples. <i>Journal of Clinical Investigation</i> , 2009, 119, 1714-1726.	8.2	130
36	Clonal Architecture of Secondary Acute Myeloid Leukemia Defined by Single-Cell Sequencing. <i>PLoS Genetics</i> , 2014, 10, e1004462.	3.5	115

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37	Removing Career Obstacles for Young Physician-Scientists â€” Loan-Repayment Programs. <i>New England Journal of Medicine</i> , 2002, 346, 368-372.	27.0	96
38	Rapid expansion of preexisting nonleukemic hematopoietic clones frequently follows induction therapy for de novo AML. <i>Blood</i> , 2016, 127, 893-897.	1.4	94
39	Mutation Clearance after Transplantation for Myelodysplastic Syndrome. <i>New England Journal of Medicine</i> , 2018, 379, 1028-1041.	27.0	93
40	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. <i>Journal of Clinical Investigation</i> , 2011, 121, 1445-1455.	8.2	91
41	Long non-coding RNA RAMS11 promotes metastatic colorectal cancer progression. <i>Nature Communications</i> , 2020, 11, 2156.	12.8	83
42	Reduced PU.1 expression causes myeloid progenitor expansion and increased leukemia penetrance in mice expressing PML-RAR $\alpha$ . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12513-12518.	7.1	81
43	Haploinsufficiency for DNA methyltransferase 3A predisposes hematopoietic cells to myeloid malignancies. <i>Journal of Clinical Investigation</i> , 2017, 127, 3657-3674.	8.2	80
44	Granzyme B Plays a Critical Role in Cytotoxic Lymphocyte-induced Apoptosis. <i>Immunological Reviews</i> , 1995, 146, 211-221.	6.0	69
45	Clonal Architectures and Driver Mutations in Metastatic Melanomas. <i>PLoS ONE</i> , 2014, 9, e111153.	2.5	69
46	Co-evolution of tumor and immune cells during progression of multiple myeloma. <i>Nature Communications</i> , 2021, 12, 2559.	12.8	68
47	Genomic Landscapes and Clonality of De Novo AML. <i>New England Journal of Medicine</i> , 2013, 369, 1472-1473.	27.0	58
48	Seed Versus Soil: The Importance of the Target Cell for Transgenic Models of Human Leukemias. <i>Blood</i> , 1999, 93, 2143-2148.	1.4	56
49	A pilot study of high-throughput, sequence-based mutational profiling of primary human acute myeloid leukemia cell genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 14275-14280.	7.1	55
50	Subclones dominate at MDS progression following allogeneic hematopoietic cell transplant. <i>JCI Insight</i> , 2018, 3, .	5.0	48
51	Decitabine in TP53-Mutated AML. <i>New England Journal of Medicine</i> , 2017, 376, 796-798.	27.0	45
52	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. <i>Experimental Hematology</i> , 2016, 44, 603-613.	0.4	44
53	The clonal evolution of metastatic colorectal cancer. <i>Science Advances</i> , 2020, 6, eaay9691.	10.3	41
54	Whole Exome Sequencing Reveals the Order of Genetic Changes during Malignant Transformation and Metastasis in a Single Patient with NF1-plexiform Neurofibroma. <i>Clinical Cancer Research</i> , 2015, 21, 4201-4211.	7.0	39

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55	<i>MIR142</i> Loss-of-Function Mutations Derepress <i>ASH1L</i> to Increase <i>HOXA</i> Gene Expression and Promote Leukemogenesis. <i>Cancer Research</i> , 2018, 78, 3510-3521.	0.9	39
56	PML-RARA requires DNA methyltransferase 3A to initiate acute promyelocytic leukemia. <i>Journal of Clinical Investigation</i> , 2015, 126, 85-98.	8.2	36
57	Independent formation of DnaseI hypersensitive sites in the murine $\beta$ -globin locus control region. <i>Blood</i> , 2000, 95, 3600-3604.	1.4	34
58	Obesity is a risk factor for acute promyelocytic leukemia: evidence from population and cross-sectional studies and correlation with FLT3 mutations and polyunsaturated fatty acid metabolism. <i>Haematologica</i> , 2020, 105, 1559-1566.	3.5	32
59	Notch signaling in acute promyelocytic leukemia. <i>Leukemia</i> , 2013, 27, 1548-1557.	7.2	28
60	Remethylation of <i>Dnmt3a</i> hematopoietic cells is associated with partial correction of gene dysregulation and reduced myeloid skewing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3123-3134.	7.1	27
61	Enhanced Efficacy and Increased Long-Term Toxicity of CNS-Directed, AAV-Based Combination Therapy for Krabbe Disease. <i>Molecular Therapy</i> , 2021, 29, 691-701.	8.2	27
62	Mutational landscape and response are conserved in peripheral blood of AML and MDS patients during decitabine therapy. <i>Blood</i> , 2017, 129, 1397-1401.	1.4	24
63	Immunosuppression and outcomes in adult patients with de novo acute myeloid leukemia with normal karyotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	24
64	Functional and epigenetic phenotypes of humans and mice with DNMT3A Overgrowth Syndrome. <i>Nature Communications</i> , 2021, 12, 4549.	12.8	21
65	Caspase-9 is required for normal hematopoietic development and protection from alkylator-induced DNA damage in mice. <i>Blood</i> , 2014, 124, 3887-3895.	1.4	20
66	Focal disruption of DNA methylation dynamics at enhancers in IDH-mutant AML cells. <i>Leukemia</i> , 2022, 36, 935-945.	7.2	18
67	Reduced beta-Globin Gene Expression in Adult Mice Containing Deletions of Locus Control Region 5' HS-2 or 5' HS-3a. <i>Annals of the New York Academy of Sciences</i> , 1998, 850, 45-53.	3.8	15
68	Expression and Function of PML-RARA in the Hematopoietic Progenitor Cells of Ctsg-PML-RARA Mice. <i>PLoS ONE</i> , 2012, 7, e46529.	2.5	15
69	Physician-scientists in the United States at 2020: Trends and concerns. <i>FASEB Journal</i> , 2022, 36, e22253.	0.5	15
70	Tumor suppressor function of <i>Gata2</i> in acute promyelocytic leukemia. <i>Blood</i> , 2021, 138, 1148-1161.	1.4	14
71	Genetic and Transcriptional Contributions to Relapse in Normal Karyotype Acute Myeloid Leukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 32-49.	5.0	14
72	Failure to Detect Mutations in U2AF1 due to Changes in the GRCh38 Reference Sequence. <i>Journal of Molecular Diagnostics</i> , 2022, 24, 219-223.	2.8	13

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73	Genetic Heterogeneity of Induced Pluripotent Stem Cells: Results from 24 Clones Derived from a Single C57BL/6 Mouse. <i>PLoS ONE</i> , 2015, 10, e0120585.	2.5	12
74	MCL1 Haploinsufficiency Protects Mice From MYC-Induced Acute Myeloid Leukemia.. <i>Blood</i> , 2009, 114, 764-764.	1.4	11
75	Convergent Clonal Evolution of Signaling Gene Mutations Is a Hallmark of Myelodysplastic Syndrome Progression. <i>Blood Cancer Discovery</i> , 2022, 3, 330-345.	5.0	10
76	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. <i>Experimental Hematology</i> , 2017, 55, 19-33.	0.4	9
77	Sequencing of Tumor DNA to Guide Cancer Risk Assessment and Therapy. <i>JAMA - Journal of the American Medical Association</i> , 2018, 319, 1497.	7.4	9
78	<i>DNMT3A</i> overgrowth syndrome is associated with the development of hematopoietic malignancies in children and young adults. <i>Blood</i> , 2022, 139, 461-464.	1.4	9
79	G-CSFSR Mutations Present in Patients with Severe Congenital Neutropenia Cooperate with PML-RAR $\alpha$ To Induce Acute Myeloid Leukemia in Mice.. <i>Blood</i> , 2007, 110, 2193-2193.	1.4	8
80	DNMT3AR882-associated hypomethylation patterns are maintained in primary AML xenografts, but not in the DNMT3AR882C OCI-AML3 leukemia cell line. <i>Blood Cancer Journal</i> , 2018, 8, 38.	6.2	7
81	Dnmt3a deficiency in the skin causes focal, canonical DNA hypomethylation and a cellular proliferation phenotype. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2022760118.	7.1	6
82	AMD3100 Mobilizes Acute Promyelocytic Leukemia Cells from the Bone Marrow into the Peripheral Blood and Sensitizes Leukemia Cells to Chemotherapy.. <i>Blood</i> , 2005, 106, 246-246.	1.4	6
83	POU4F1 Is Associated with t(8;21) AML and Contributes Directly to Its Unique Transcriptional Signature.. <i>Blood</i> , 2009, 114, 2623-2623.	1.4	6
84	The Role Of Early TP53 Mutations On The Evolution Of Therapy-Related AML. <i>Blood</i> , 2013, 122, 5-5.	1.4	5
85	Recurrent Transcriptional Responses in AML and MDS patients Treated with Decitabine. <i>Experimental Hematology</i> , 2022, , .	0.4	5
86	Impact of a 40-Gene Targeted Panel Test on Physician Decision Making for Patients With Acute Myeloid Leukemia. <i>JCO Precision Oncology</i> , 2021, 5, 191-203.	3.0	4
87	Genomic DNA Copy Number Alterations Present in AML Bone Marrow Samples with Normal Cytogenetics.. <i>Blood</i> , 2004, 104, 142-142.	1.4	4
88	DNMT3A R882H Overexpression Leads To Hematopoietic and Skin Alterations In Transgenic Mice. <i>Blood</i> , 2013, 122, 479-479.	1.4	4
89	Tumor suppressor function of <i>WT1</i> in acute promyelocytic leukemia. <i>Haematologica</i> , 2021, , .	3.5	4
90	Clonal Evolution of Acute Myeloid Leukemia Following Allogeneic Stem Cell Transplantation. <i>Blood</i> , 2016, 128, 1528-1528.	1.4	4

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91	IL-1 $\beta$ expression in bone marrow dendritic cells is induced by TLR2 agonists and regulates HSC function. <i>Blood</i> , 2022, 140, 1607-1620.	1.4	4
92	Whole-Genome Bisulfite Sequencing of Primary AML Cells with the DNMT3A R882H Mutation Identifies Regions of Focal Hypomethylation That Are Associated with Open Chromatin. <i>Blood</i> , 2014, 124, 608-608.	1.4	3
93	Dynamic Changes in the Clonal Structure of MDS and AML in Response to Epigenetic Therapy. <i>Blood</i> , 2015, 126, 610-610.	1.4	3
94	Obesity As a Risk Factor for Acute Promyelocytic Leukemia. Results from Population and Case-Control Studies Across Western Countries and Correlation with Gene Expression in the TCGA. <i>Blood</i> , 2016, 128, 448-448.	1.4	3
95	DNMT3A Mutations in Acute Myeloid Leukemia. <i>Blood</i> , 2011, 118, SCI-31-SCI-31.	1.4	3
96	DNMT3A-Dependent DNA Methylation May Act As a Tumor Suppressor-Not a Tumor Promoter-during AML Progression. <i>Blood</i> , 2016, 128, 1050-1050.	1.4	3
97	RETROSPECTIVE: Stanley Joel Korsmeyer (1950-2005). <i>Science</i> , 2005, 308, 803-804.	12.6	2
98	CXCR4/SDF-1 Is a Key Regulator for Leukemia Migration and Homing to the BM: Impact of AMD3100 on In Vivo Response to Chemotherapy. <i>Blood</i> , 2006, 108, 569-569.	1.4	2
99	Recurrent Somatic Genomic Alterations in Follicular NHL (FL) Revealed By Exome and Custom-Capture Next Generation Sequencing. <i>Blood</i> , 2015, 126, 574-574.	1.4	2
100	Comprehensive Evaluation of MicroRNA Genes and Gene Expression Using Next Generation Sequencing in a Patient with Acute Myelogenous Leukemia. <i>Blood</i> , 2009, 114, 271-271.	1.4	2
101	Decitabine salvage for TP53-mutated, relapsed/refractory acute myeloid leukemia after cytotoxic induction therapy. <i>Haematologica</i> , 2022, 107, 1709-1713.	3.5	2
102	Somatic Dnmt3a inactivation leads to slow, canonical DNA methylation loss in murine hematopoietic cells. <i>Science</i> , 2022, 25, 104004.	4.1	2
103	IL-12 Stimulates Interferon-Gamma Mediated Inhibition of Tumor-Induced Regulatory T Cell Proliferation and Enhances Tumor Clearance. <i>Blood</i> , 2008, 112, 2558-2558.	1.4	1
104	DNMT3A R882H Overexpression Acts in a Dominant Negative Manner to Cause DNA Hypomethylation and Increased Susceptibility to Hematopoietic Malignancies in Transgenic Mice. <i>Blood</i> , 2014, 124, 609-609.	1.4	1
105	Dynamic Changes in Clonal Clearance with Decitabine Therapy in AML and MDS Patients. <i>Blood</i> , 2015, 126, 689-689.	1.4	1
106	Chromatin Immunoprecipitation of GFP-Tagged PML-Rara Coupled to High-Throughput Next Generation Sequencing. <i>Blood</i> , 2009, 114, 1276-1276.	1.4	1
107	Clonal Evolution Revealed by Whole Genome Sequencing in a Case of Primary Myelofibrosis Transformed to Secondary Acute Myeloid Leukemia. <i>Blood</i> , 2012, 120, 706-706.	1.4	1
108	Myeloproliferative Disease and Myeloid Leukemia in Dnmt3a Haploinsufficient Mice. <i>Blood</i> , 2014, 124, 890-890.	1.4	1

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109	1998 ASCI Presidential Address. Journal of Clinical Investigation, 2003, 112, S9-11.	8.2	1
110	Orphan Granzymes Downstream from Granzyme B Are Important for Tumor Clearance In Vivo and in Vitro.. Blood, 2004, 104, 2653-2653.	1.4	0
111	Neutrophil Elastase Is Important for Several Activities of PML-RAR $\alpha$ in Early Myeloid Cells.. Blood, 2004, 104, 486-486.	1.4	0
112	Transcriptome Analysis of Murine Myeloid Development.. Blood, 2005, 106, 2724-2724.	1.4	0
113	Identification of PML-RAR $\alpha$ Target Genes Using Microarray and ChIP-on-Chip Analysis.. Blood, 2005, 106, 2994-2994.	1.4	0
114	A Protease-Resistant PML-RAR $\alpha$ Has Increased Leukemogenic Potential in a Murine Model of Acute Promyelocytic Leukemia (APL).. Blood, 2008, 112, 930-930.	1.4	0
115	Latent Murine Herpesvirus-4 Infection Arms NK Cells.. Blood, 2009, 114, 3678-3678.	1.4	0
116	DNA Sequencing of a Murine Acute Promyelocytic Leukemia (APL) Genome Using Next Generation Technology.. Blood, 2009, 114, 3965-3965.	1.4	0
117	Recurrent DNMT3A Mutations In Patients with Myelodysplastic Syndrome. Blood, 2010, 116, 608-608.	1.4	0
118	The NK Cell MicroRNA Transcriptome Defined by Next-Generation Sequencing Identifies IL-15-Signaled Alterations In Mature MiR-223 Expression, and MiR-223 as a Potential Regulator of Murine Granzyme B. Blood, 2010, 116, 104-104.	1.4	0
119	Activation of Notch Signaling Is An Early Event in the Development of PML-Rara-Induced Acute Promyelocytic Leukemia (APL). Blood, 2011, 118, 2468-2468.	1.4	0
120	Functional Hematopoietic Cells Derived From Mouse Embryonic Stem Cells.. Blood, 2012, 120, 2304-2304.	1.4	0
121	Dysregulation of the Imprinted DLK1-DIO3 Locus in Promyelocytic Leukemia. Blood, 2012, 120, 3500-3500.	1.4	0
122	Whole Genome Sequencing Reveals Novel Recurring Somatic Mutations Affecting HUWE1 and DIAPH2 Genes in Multiple Myeloma. Blood, 2012, 120, 320-320.	1.4	0
123	In Vitro Decitabine Treatment Demonstrates Heterogeneous Changes in Methylation and Gene Expression in Primary AML Samples.. Blood, 2012, 120, 2527-2527.	1.4	0
124	Subclonal "skewing" Of De Novo AML Samples After Engraftment In Immunodeficient Mice. Blood, 2013, 122, 609-609.	1.4	0
125	Rare Hematopoietic Subclones Harboring Leukemogenic TP53 Mutations Are Detectable Via Error-Corrected Sequencing in Healthy Elderly Individuals. Blood, 2014, 124, 2907-2907.	1.4	0
126	Whole Genome Bisulfite Sequencing of Purified Mouse Promyelocytes Reveals Differentially Methylated Regions in Cells Expressing PML-Rara. Blood, 2014, 124, 3531-3531.	1.4	0



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127	Reprogramming of Leukemic and Pre-Leukemic Cells from Primary Human De Novo Acute Myeloid Leukemia Samples into Induced Pluripotent Stem (iPS) Cells. <i>Blood</i> , 2015, 126, 1862-1862.	1.4	0
128	Detection of Clonal Hematopoiesis in Cytopenic Patients Using Targeted Sequencing. <i>Blood</i> , 2015, 126, 1654-1654.	1.4	0
129	Non-Malignant Oligoclonal Hematopoiesis Commonly Follows Cytoreductive Chemotherapy in Adult De Novo AML Patients. <i>Blood</i> , 2015, 126, 686-686.	1.4	0
130	Adverse Outcomes in Acute Myeloid Leukemia Are Associated with Tumor Cell-Mediated Immunosuppression. <i>Blood</i> , 2021, 138, 800-800.	1.4	0
131	<i>Dnmt3a</i> Inactivation Leads to Slow DNA Methylation Loss in Murine Hematopoietic Cells <i>In Vivo</i> . <i>Blood</i> , 2021, 138, 1087-1087.	1.4	0
132	Signaling Gene Mutations Are Characterized By Diverse Patterns of Expansion and Contraction during Progression from MDS to Secondary AML. <i>Blood</i> , 2020, 136, 2-3.	1.4	0
133	Molecular Profiling of Decitabine Response in MDS and AML Patients. <i>Blood</i> , 2020, 136, 40-40.	1.4	0
134	Comparison of Deep Whole Exome Versus Targeted Gene Sequencing for Assessment of Persistent Molecular Disease in Acute Myeloid Leukemia Samples. <i>Blood</i> , 2020, 136, 6-7.	1.4	0