Timothy J Ley

List of Publications by Year
in descending order

134 papers	28,615 citations	41344 49 h-index	25787 108 g-index
136 all docs	136 docs citations	136 times ranked	35058 citing authors

#	Article	IF	Citations
1	Genetic and Transcriptional Contributions to Relapse in Normal Karyotype Acute Myeloid Leukemia. Blood Cancer Discovery, 2022, 3, 32-49.	5.0	14
2	DNMT3Aovergrowth syndrome is associated with the development of hematopoietic malignancies in children and young adults. Blood, 2022, 139, 461-464.	1.4	9
3	Failure to Detect Mutations in U2AF1 due to Changes in the GRCh38 Reference Sequence. Journal of Molecular Diagnostics, 2022, 24, 219-223.	2.8	13
4	Focal disruption of DNA methylation dynamics at enhancers in IDH-mutant AML cells. Leukemia, 2022, 36, 935-945.	7.2	18
5	Decitabine salvage for <i>TP53</i>-mutated, relapsed/refractory acute myeloid leukemia after cytotoxic induction therapy. Haematologica, 2022, 107, 1709-1713.	3.5	2
6	Somatic Dnmt3a inactivation leads to slow, canonical DNA methylation loss in murine hematopoietic cells. IScience, 2022, 25, 104004.	4.1	2
7	Physicianâ€scientists in the United States at 2020: Trends and concerns. FASEB Journal, 2022, 36, e22253.	0.5	15
8	Recurrent Transcriptional Responses in AML and MDS patients Treated with Decitabine. Experimental Hematology, 2022, , .	0.4	5
9	Convergent Clonal Evolution of Signaling Gene Mutations Is a Hallmark of Myelodysplastic Syndrome Progression. Blood Cancer Discovery, 2022, 3, 330-345.	5.0	10
10	IL-1Î² expression in bone marrow dendritic cells is induced by TLR2 agonists and regulates HSC function. Blood, 2022, 140, 1607-1620.	1.4	4
11	Enhanced Efficacy and Increased Long-Term Toxicity of CNS-Directed, AAV-Based Combination Therapy for Krabbe Disease. Molecular Therapy, 2021, 29, 691-701.	8.2	27
12	Genome Sequencing as an Alternative to Cytogenetic Analysis in Myeloid Cancers. New England Journal of Medicine, 2021, 384, 924-935.	27.0	170
13	Dnmt3a deficiency in the skin causes focal, canonical DNA hypomethylation and a cellular proliferation phenotype. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2022760118.	7.1	6
14	Co-evolution of tumor and immune cells during progression of multiple myeloma. Nature Communications, 2021, 12, 2559.	12.8	68
15	Tumor suppressor function of Gata2 in acute promyelocytic leukemia. Blood, 2021, 138, 1148-1161.	1.4	14
16	Functional and epigenetic phenotypes of humans and mice with DNMT3A Overgrowth Syndrome. Nature Communications, 2021, 12, 4549.	12.8	21
17	Impact of a 40-Gene Targeted Panel Test on Physician Decision Making for Patients With Acute Myeloid Leukemia. JCO Precision Oncology, 2021, 5, 191-203.	3.0	4
18	Tumor suppressor function of WT1 in acute promyelocytic leukemia. Haematologica, 2021, , .	3.5	4

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19	Adverse Outcomes in Acute Myeloid Leukemia Are Associated with Tumor Cell-Mediated Immunosuppression. Blood, 2021, 138, 800-800.	1.4	0
20	Immunosuppression and outcomes in adult patients with de novo acute myeloid leukemia with normal karyotypes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	24
21	Dnmt3a Inactivation Leads to Slow DNA Methylation Loss in Murine Hematopoietic Cells In Vivo. Blood, 2021, 138, 1087-1087.	1.4	0
22	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. Haematologica, 2020, 105, 1559-1566.	3.5	32
23	Long non-coding RNA RAMS11 promotes metastatic colorectal cancer progression. Nature Communications, 2020, 11, 2156.	12.8	83
24	Remethylation of Dnmt3a ^{â^'/â^'} hematopoietic cells is associated with partial correction of gene dysregulation and reduced myeloid skewing. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3123-3134.	7.1	27
25	The clonal evolution of metastatic colorectal cancer. Science Advances, 2020, 6, eaay9691.	10.3	41
26	Signaling Gene Mutations Are Characterized By Diverse Patterns of Expansion and Contraction during Progression from MDS to Secondary AML. Blood, 2020, 136, 2-3.	1.4	0
27	Molecular Profiling of Decitabine Response in MDS and AML Patients. Blood, 2020, 136, 40-40.	1.4	0
28	Comparison of Deep Whole Exome Versus Targeted Gene Sequencing for Assessment of Persistent Molecular Disease in Acute Myeloid Leukemia Samples. Blood, 2020, 136, 6-7.	1.4	0
29	A general approach for detecting expressed mutations in AML cells using single cell RNA-sequencing. Nature Communications, 2019, 10, 3660.	12.8	147
30	Sequencing of Tumor DNA to Guide Cancer Risk Assessment and Therapy. JAMA - Journal of the American Medical Association, 2018, 319, 1497.	7.4	9
31	Cellular stressors contribute to the expansion of hematopoietic clones of varying leukemic potential. Nature Communications, 2018, 9, 455.	12.8	150
32	Immune Escape of Relapsed AML Cells after Allogeneic Transplantation. New England Journal of Medicine, 2018, 379, 2330-2341.	27.0	322
33	Mutation Clearance after Transplantation for Myelodysplastic Syndrome. New England Journal of Medicine, 2018, 379, 1028-1041.	27.0	93
34	MIR142 Loss-of-Function Mutations Derepress ASH1L to Increase HOXA Gene Expression and Promote Leukemogenesis. Cancer Research, 2018, 78, 3510-3521.	0.9	39
35	DNMT3AR882-associated hypomethylation patterns are maintained in primary AML xenografts, but not in the DNMT3AR882C OCI-AML3 leukemia cell line. Blood Cancer Journal, 2018, 8, 38.	6.2	7
36	Subclones dominate at MDS progression following allogeneic hematopoietic cell transplant. JCI Insight, 2018, 3, .	5.0	48

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37	Decitabine inTP53-Mutated AML. New England Journal of Medicine, 2017, 376, 796-798.	27.0	45
38	CpG Island Hypermethylation Mediated by DNMT3A Is a Consequence of AML Progression. Cell, 2017, 168, 801-816.e13.	28.9	177
39	Mutational landscape and response are conserved in peripheral blood of AML and MDS patients during decitabine therapy. Blood, 2017, 129, 1397-1401.	1.4	24
40	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. Experimental Hematology, 2017, 55, 19-33.	0.4	9
41	Haploinsufficiency for DNA methyltransferase 3A predisposes hematopoietic cells to myeloid malignancies. Journal of Clinical Investigation, 2017, 127, 3657-3674.	8.2	80
42	Visualizing tumor evolution with the fishplot package for R. BMC Genomics, 2016, 17, 880.	2.8	131
43	Rapid expansion of preexisting nonleukemic hematopoietic clones frequently follows induction therapy for de novo AML. Blood, 2016, 127, 893-897.	1.4	94
44	TP53 and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes. New England Journal of Medicine, 2016, 375, 2023-2036.	27.0	663
45	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. Experimental Hematology, 2016, 44, 603-613.	0.4	44
46	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. Blood, 2016, 128, 448-448.	1.4	3
47	Clonal Evolution of Acute Myeloid Leukemia Following Allogeneic Stem Cell Transplantation. Blood, 2016, 128, 1528-1528.	1.4	4
48	DNMT3A-Dependent DNA Methylation May Act As a Tumor Suppressor-Not a Tumor Promoter-during AML Progression. Blood, 2016, 128, 1050-1050.	1.4	3
49	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	6.2	174
50	Genomic analysis of germ line and somatic variants in familial myelodysplasia/acute myeloid leukemia. Blood, 2015, 126, 2484-2490.	1.4	207
51	Genetic Heterogeneity of Induced Pluripotent Stem Cells: Results from 24 Clones Derived from a Single C57BL/6 Mouse. PLoS ONE, 2015, 10, e0120585.	2.5	12
52	Whole Exome Sequencing Reveals the Order of Genetic Changes during Malignant Transformation and Metastasis in a Single Patient with NF1-plexiform Neurofibroma. Clinical Cancer Research, 2015, 21, 4201-4211.	7.0	39
53	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. JAMA - Journal of the American Medical Association, 2015, 314, 811.	7.4	302
54	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. Nature, 2015, 518, 552-555.	27.8	685

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55	PML-RARA requires DNA methyltransferase 3A to initiate acute promyelocytic leukemia. Journal of Clinical Investigation, 2015, 126, 85-98.	8.2	36
56	Recurrent Somatic Genomic Alterations in Follicular NHL (FL) Revealed By Exome and Custom-Capture Next Generation Sequencing. Blood, 2015, 126, 574-574.	1.4	2
57	Dynamic Changes in the Clonal Structure of MDS and AML in Response to Epigenetic Therapy. Blood, 2015, 126, 610-610.	1.4	3
58	Dynamic Changes in Clonal Clearance with Decitabine Therapy in AML and MDS Patients. Blood, 2015, 126, 689-689.	1.4	1
59	Reprogramming of Leukemic and Pre-Leukemic Cells from Primary Human De Novo Acute Myeloid Leukemia Samples into Induced Pluripotent Stem (iPS) Cells. Blood, 2015, 126, 1862-1862.	1.4	0
60	Detection of Clonal Hematopoiesis in Cytopenic Patients Using Targeted Sequencing. Blood, 2015, 126, 1654-1654.	1.4	0
61	Non-Malignant Oligoclonal Hematopoiesis Commonly Follows Cytoreductive Chemotherapy in Adult De Novo AML Patients. Blood, 2015, 126, 686-686.	1.4	0
62	Clonal Architectures and Driver Mutations in Metastatic Melanomas. PLoS ONE, 2014, 9, e111153.	2.5	69
63	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. PLoS Computational Biology, 2014, 10, e1003665.	3.2	400
64	Clonal Architecture of Secondary Acute Myeloid Leukemia Defined by Single-Cell Sequencing. PLoS Genetics, 2014, 10, e1004462.	3.5	115
65	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 379-392.	16.8	330
66	Age-related mutations associated with clonal hematopoietic expansion and malignancies. Nature Medicine, 2014, 20, 1472-1478.	30.7	1,533
67	The R882H DNMT3A Mutation Associated with AML Dominantly Inhibits Wild-Type DNMT3A by Blocking Its Ability to Form Active Tetramers. Cancer Cell, 2014, 25, 442-454.	16.8	374
68	Caspase-9 is required for normal hematopoietic development and protection from alkylator-induced DNA damage in mice. Blood, 2014, 124, 3887-3895.	1.4	20
69	Whole-Genome Bisulfite Sequencing of Primary AML Cells with the DNMT3A R882H Mutation Identifies Regions of Focal Hypomethylation That Are Associated with Open Chromatin. Blood, 2014, 124, 608-608.	1.4	3
70	DNMT3A R882H Overexpression Acts in a Dominant Negative Manner to Cause DNA Hypomethylation and Increased Susceptibility to Hematopoietic Malignancies in Transgenic Mice. Blood, 2014, 124, 609-609.	1.4	1
71	Myeloproliferative Disease and Myeloid Leukemia in Dnmt3a Haploinsufficient Mice. Blood, 2014, 124, 890-890.	1.4	1
72	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

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73	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
74	DGIdb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.	19.0	443
75	Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.	27.8	3,695
76	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
77	Notch signaling in acute promyelocytic leukemia. Leukemia, 2013, 27, 1548-1557.	7.2	28
78	Genomic Landscapes and Clonality of De Novo AML. New England Journal of Medicine, 2013, 369, 1472-1473.	27.0	58
79	Genomic impact of transient low-dose decitabine treatment on primary AML cells. Blood, 2013, 121, 1633-1643.	1.4	137
80	DNMT3A R882H Overexpression Leads To Hematopoietic and Skin Alterations In Transgenic Mice. Blood, 2013, 122, 479-479.	1.4	4
81	The Role Of Early TP53 Mutations On The Evolution Of Therapy-Related AML. Blood, 2013, 122, 5-5.	1.4	5
82	Subclonal â€œskewingâ€•Of De Novo AML Samples After Engraftment In Immunodeficient Mice. Blood, 2013, 122, 609-609.	1.4	0
83	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. Bioinformatics, 2012, 28, 311-317.	4.1	566
84	Recurrent mutations in the U2AF1 splicing factor in myelodysplastic syndromes. Nature Genetics, 2012, 44, 53-57.	21.4	513
85	Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098.	27.0	688
86	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	27.8	1,795
87	Expression and Function of PML-RARA in the Hematopoietic Progenitor Cells of Ctsg-PML-RARA Mice. PLoS ONE, 2012, 7, e46529.	2.5	15
88	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	28.9	1,365
89	Functional Hematopoietic Cells Derived From Mouse Embryonic Stem Cells.. Blood, 2012, 120, 2304-2304.	1.4	0
90	Dysregulation of the Imprinted DLK1-DIO3 Locus in Promyelocytic Leukemia. Blood, 2012, 120, 3500-3500.	1.4	0

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91	Clonal Evolution Revealed by Whole Genome Sequencing in a Case of Primary Myelofibrosis Transformed to Secondary Acute Myeloid Leukemia. Blood, 2012, 120, 706-706.	1.4	1
92	Whole Genome Sequencing Reveals Novel Recurring Somatic Mutations Affecting HUWE1 and DIAPH2 Genes in Multiple Myeloma. Blood, 2012, 120, 320-320.	1.4	0
93	In Vitro Decitabine Treatment Demonstrates Heterogeneous Changes in Methylation and Gene Expression in Primary AML Samples.. Blood, 2012, 120, 2527-2527.	1.4	0
94	Use of Whole-Genome Sequencing to Diagnose a Cryptic Fusion Oncogene. JAMA - Journal of the American Medical Association, 2011, 305, 1577.	7.4	233
95	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. Journal of Clinical Investigation, 2011, 121, 1445-1455.	8.2	91
96	DNMT3A Mutations in Acute Myeloid Leukemia. Blood, 2011, 118, SCI-31-SCI-31.	1.4	3
97	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
98	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	27.8	1,077
99	DNMT3AMutations in Acute Myeloid Leukemia. New England Journal of Medicine, 2010, 363, 2424-2433.	27.0	1,777
100	Recurrent DNMT3A Mutations In Patients with Myelodysplastic Syndrome. Blood, 2010, 116, 608-608.	1.4	0
101	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
102	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. New England Journal of Medicine, 2009, 361, 1058-1066.	27.0	2,009
103	High throughput digital quantification of mRNA abundance in primary human acute myeloid leukemia samples. Journal of Clinical Investigation, 2009, 119, 1714-1726.	8.2	130
104	Chromatin Immunoprecipitation of GFP-Tagged PML-Rara Coupled to High-Throughput Next Generation Sequencing.. Blood, 2009, 114, 1276-1276.	1.4	1
105	MCL1 Haploinsufficiency Protects Mice From MYC-Induced Acute Myeloid Leukemia.. Blood, 2009, 114, 764-764.	1.4	11
106	Comprehensive Evaluation of MicroRNA Genes and Gene Expression Using Next Generation Sequencing in a Patient with Acute Myelogenous Leukemia.. Blood, 2009, 114, 271-271.	1.4	2
107	Latent Murine Herpesvirus-4 Infection Arms NK Cells.. Blood, 2009, 114, 3678-3678.	1.4	0
108	DNA Sequencing of a Murine Acute Promyelocytic Leukemia (APL) Genome Using Next Generation Technology.. Blood, 2009, 114, 3965-3965.	1.4	0

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109	POU4F1 Is Associated with t(8;21) AML and Contributes Directly to Its Unique Transcriptional Signature.. Blood, 2009, 114, 2623-2623.	1.4	6
110	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	27.8	1,275
111	The Gender Gap in NIH Grant Applications. Science, 2008, 322, 1472-1474.	12.6	206
112	IL-12 Stimulates Interferon-Gamma Mediated Inhibition of Tumor-Induced Regulatory T Cell Proliferation and Enhances Tumor Clearance. Blood, 2008, 112, 2558-2558.	1.4	1
113	A Protease-Resistant PML-RARÎ± Has Increased Leukemogenic Potential in a Murine Model of Acute Promyelocytic Leukemia (APL).. Blood, 2008, 112, 930-930.	1.4	0
114	G-CSFSR Mutations Present in Patients with Severe Congenital Neutropenia Cooperate with PML-RARÎ± To Induce Acute Myeloid Leukemia in Mice.. Blood, 2007, 110, 2193-2193.	1.4	8
115	CXCR4/SDF-1 Is a Key Regulator for Leukemia Migration and Homing to the BM: Impact of AMD3100 on In Vivo Response to Chemotherapy.. Blood, 2006, 108, 569-569.	1.4	2
116	RETROSPECTIVE: Stanley Joel Korsmeyer (1950-2005). Science, 2005, 308, 803-804.	12.6	2
117	Reduced PU.1 expression causes myeloid progenitor expansion and increased leukemia penetrance in mice expressing PML-RARÂ. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12513-12518.	7.1	81
118	The Physician-Scientist Career Pipeline in 2005. JAMA - Journal of the American Medical Association, 2005, 294, 1343.	7.4	317
119	AMD3100 Mobilizes Acute Promyelocytic Leukemia Cells from the Bone Marrow into the Peripheral Blood and Sensitizes Leukemia Cells to Chemotherapy.. Blood, 2005, 106, 246-246.	1.4	6
120	Transcriptome Analysis of Murine Myeloid Development.. Blood, 2005, 106, 2724-2724.	1.4	0
121	Identification of PML-RARa Target Genes Using Microarray and ChIP-on-Chip Analysis.. Blood, 2005, 106, 2994-2994.	1.4	0
122	Genomic DNA Copy Number Alterations Present in AML Bone Marrow Samples with Normal Cytogenetics.. Blood, 2004, 104, 142-142.	1.4	4
123	Orphan Granzymes Downstream from Granzyme B Are Important for Tumor Clearance In Vivo and in Vitro.. Blood, 2004, 104, 2653-2653.	1.4	0
124	Neutrophil Elastase Is Important for Several Activities of PML-RARÎ± in Early Myeloid Cells.. Blood, 2004, 104, 486-486.	1.4	0
125	A pilot study of high-throughput, sequence-based mutational profiling of primary human acute myeloid leukemia cell genomes. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 14275-14280.	7.1	55
126	High-penetrance mouse model of acute promyelocytic leukemia with very low levels of PML-RARÎ± expression. Blood, 2003, 102, 1857-1865.	1.4	139

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127	1998 ASCI Presidential Address. Journal of Clinical Investigation, 2003, 112, S9-11.	8.2	1
128	Removing Career Obstacles for Young Physician-Scientists â€" Loan-Repayment Programs. New England Journal of Medicine, 2002, 346, 368-372.	27.0	96
129	Sudden death among patients with acute promyelocytic leukemia treated with arsenic trioxide. Blood, 2001, 98, 266-271.	1.4	233
130	The Physicianâ€Scientist: Career Issues and Challenges at the Year 2000. FASEB Journal, 2000, 14, 221-230.	0.5	206
131	Independent formation of DnaseI hypersensitive sites in the murine Î²-globin locus control region. Blood, 2000, 95, 3600-3604.	1.4	34
132	Seed Versus Soil: The Importance of the Target Cell for Transgenic Models of Human Leukemias. Blood, 1999, 93, 2143-2148.	1.4	56
133	Reduced beta-Globin Gene Expression in Adult Mice Containing Deletions of Locus Control Region 5' HS-2 or 5' HS-3a. Annals of the New York Academy of Sciences, 1998, 850, 45-53.	3.8	15
134	Granzyme B Plays a Critical Role in Cytotoxic Lymphocyte-induced Apoptosis. Immunological Reviews, 1995, 146, 211-221.	6.0	69