Jeffery M Klco

List of Publications by Year
in descending order

95 papers	12,735 citations	87888 38 h-index	69250 77 g-index
96 all docs	96 docs citations	96 times ranked	17446 citing authors

#	Article	IF	Citations
1	CAR T cells redirected to cell surface GRP78 display robust anti-acute myeloid leukemia activity and do not target hematopoietic progenitor cells. Nature Communications, 2022, 13, 587.	12.8	41
2	Phase Separation Mediates NUP98 Fusion Oncoprotein Leukemic Transformation. Cancer Discovery, 2022, 12, 1152-1169.	9.4	68
3	Integrated Genomic Analysis Identifies UBTF Tandem Duplications as a Recurrent Lesion in Pediatric Acute Myeloid Leukemia. Blood Cancer Discovery, 2022, 3, 194-207.	5.0	38
4	Molecular basis of ETV6-mediated predisposition to childhood acute lymphoblastic leukemia. Blood, 2021, 137, 364-373.	1.4	37
5	Advances in germline predisposition to acute leukaemias and myeloid neoplasms. Nature Reviews Cancer, 2021, 21, 122-137.	28.4	91
6	SequencErr: measuring and suppressing sequencer errors in next-generation sequencing data. Genome Biology, 2021, 22, 37.	8.8	15
7	The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. Nature Communications, 2021, 12, 985.	12.8	31
8	Pediatric MDS and bone marrow failure-associated germline mutations in SAMD9 and SAMD9L impair multiple pathways in primary hematopoietic cells. Leukemia, 2021, 35, 3232-3244.	7.2	32
9	Activity of venetoclax against relapsed acute undifferentiated leukemia. Cancer, 2021, 127, 2608-2611.	4.1	0
10	Enhancer Hijacking Drives Oncogenic BCL11B Expression in Lineage-Ambiguous Stem Cell Leukemia. Cancer Discovery, 2021, 11, 2846-2867.	9.4	83
11	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. Cancer Discovery, 2021, 11, 3008-3027.	9.4	88
12	The RUNX1 database (RUNX1db): establishment of an expert curated RUNX1 registry and genomics database as a public resource for familial platelet disorder with myeloid malignancy. Haematologica, 2021, 106, 3004-3007.	3.5	29
13	Abstract 633: Thiopurines and mismatch repair deficiency cooperate to fuel TP53 mutagenesis and ALL relapse. , 2021, , .		0
14	Abstract 642: Genomes for Kids: Comprehensive DNA and RNA sequencing defining the scope of actionable mutations in pediatric cancer. , 2021, , .		0
15	Chemotherapy and mismatch repair deficiency cooperate to fuel TP53 mutagenesis and ALL relapse. Nature Cancer, 2021, 2, 819-834.	13.2	24
16	Integrative Genomic Analysis of Pediatric Myeloid-Related Acute Leukemias Identifies Novel Subtypes and Prognostic Indicators. Blood Cancer Discovery, 2021, 2, 586-599.	5.0	21
17	Rational biomarker development for the early and minimally invasive monitoring of AML. Blood Advances, 2021, 5, 4515-4520.	5.2	6
18	Poster: ALL-144: Oncogenic Deregulation of BCL11B in Lineage Ambiguous Leukemia. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, S207.	0.4	0

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19	Serial assessment of measurable residual disease in medulloblastoma liquid biopsies. Cancer Cell, 2021, 39, 1519-1530.e4.	16.8	64
20	Integrated Genomic Analysis Identifies UBTF Tandem Duplications As a Subtype-Defining Lesion in Pediatric Acute Myeloid Leukemia. Blood, 2021, 138, LBA-4-LBA-4.	1.4	0
21	A six-gene leukemic stem cell score identifies high risk pediatric acute myeloid leukemia. Leukemia, 2020, 34, 735-745.	7.2	56
22	Mechanistic insights and potential therapeutic approaches for NUP98-rearranged hematologic malignancies. Blood, 2020, 136, 2275-2289.	1.4	58
23	Safety, pharmacokinetics, and pharmacodynamics of panobinostat in children, adolescents, and young adults with relapsed acute myeloid leukemia. Cancer, 2020, 126, 4800-4805.	4.1	12
24	Venetoclax in combination with cytarabine with or without idarubicin in children with relapsed or refractory acute myeloid leukaemia: a phase 1, dose-escalation study. Lancet Oncology, The, 2020, 21, 551-560.	10.7	92
25	Enhancer Hijacking of BCL11B Defines a Subtype of Lineage Ambiguous Acute Leukemia. Blood, 2020, 136, LBA-3-LBA-3.	1.4	2
26	Clofarabine Can Replace Anthracyclines and Etoposide in Remission Induction Therapy for Childhood Acute Myeloid Leukemia: The AML08 Multicenter, Randomized Phase III Trial. Journal of Clinical Oncology, 2019, 37, 2072-2081.	1.6	34
27	Integrative Analysis of Pediatric Acute Leukemia Identifies Immature Subtypes That Span a T Lineage and Myeloid Continuum with Distinct Prognoses. Blood, 2019, 134, 918-918.	1.4	1
28	Comprehensive Genomic Profiling of Pediatric Therapy-Related Myeloid Neoplasms Identifies Mecom Dysregulation to be Associated with Poor Outcome. Blood, 2019, 134, 1394-1394.	1.4	2
29	Safety and activity of venetoclax in combination with high-dose cytarabine in children with relapsed or refractory acute myeloid leukemia.. Journal of Clinical Oncology, 2019, 37, 10004-10004.	1.6	3
30	NUP98-KDM5A Fusion Induces Hematopoietic Cell Proliferation and Alters Myelo-Erythropoietic Differentiation. Blood, 2019, 134, 3775-3775.	1.4	1
31	Venetoclax in Combination with High-Dose Chemotherapy Is Active and Well-Tolerated in Children with Relapsed or Refractory Acute Myeloid Leukemia. Blood, 2019, 134, 178-178.	1.4	0
32	TAK1 restricts spontaneous NLRP3 activation and cell death to control myeloid proliferation. Journal of Experimental Medicine, 2018, 215, 1023-1034.	8.5	167
33	Clinical cancer genomic profiling by three-platform sequencing of whole genome, whole exome and transcriptome. Nature Communications, 2018, 9, 3962.	12.8	142
34	Immune Escape of Relapsed AML Cells after Allogeneic Transplantation. New England Journal of Medicine, 2018, 379, 2330-2341.	27.0	322
35	Germline SAMD9 and SAMD9L mutations are associated with extensive genetic evolution and diverse hematologic outcomes. JCI Insight, 2018, 3, .	5.0	71
36	Donor-derived MDS/AML in families with germline GATA2 mutation. Blood, 2018, 132, 1994-1998.	1.4	48

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37	Clonal dynamics of donor-derived myelodysplastic syndrome after unrelated hematopoietic cell transplantation for high-risk pediatric B-lymphoblastic leukemia. Journal of Physical Education and Sports Management, 2018, 4, a002980.	1.2	7
38	Novel V1551L Mutation in SAMD9L Inhibits Cell Cycle Progression and Results in Pancytopenia That Progresses to MDS with Monosomy 7. Blood, 2018, 132, 3863-3863.	1.4	1
39	Hematolymphoid System. Molecular Pathology Library, 2018, , 89-136.	0.1	0
40	Development of a Data Portal for Aggregation and Analysis of Genomics Data in Familial Platelet Disorder with Predisposition to Myeloid Malignancy - the RUNX1.DB. Blood, 2018, 132, 5241-5241.	1.4	0
41	The Mutational Profile of Pediatric Therapy-Related Myeloid Neoplasms. Blood, 2018, 132, 2775-2775.	1.4	1
42	Transcriptome profiling of patient derived xenograft models established from pediatric acute myeloid leukemia patients confirm maintenance of FLT3-ITD mutation. Leukemia and Lymphoma, 2017, 58, 247-250.	1.3	5
43	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. Experimental Hematology, 2017, 55, 19-33.	0.4	9
44	The genomic landscape of pediatric myelodysplastic syndromes. Nature Communications, 2017, 8, 1557.	12.8	143
45	Haploinsufficiency for DNA methyltransferase 3A predisposes hematopoietic cells to myeloid malignancies. Journal of Clinical Investigation, 2017, 127, 3657-3674.	8.2	80
46	Rapid expansion of preexisting nonleukemic hematopoietic clones frequently follows induction therapy for de novo AML. Blood, 2016, 127, 893-897.	1.4	94
47	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	21.4	215
48	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
49	The Genomic Landscape of Pediatric Myelodysplastic Syndromes. Blood, 2016, 128, 956-956.	1.4	1
50	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	6.2	174
51	Enforced differentiation of Dnmt3a-null bone marrow leads to failure with c-Kit mutations driving leukemic transformation. Blood, 2015, 125, 619-628.	1.4	86
52	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
53	Epigenomic analysis of the HOX gene loci reveals mechanisms that may control canonical expression patterns in AML and normal hematopoietic cells. Leukemia, 2015, 29, 1279-1289.	7.2	96
54	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

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55	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. Nature, 2015, 518, 552-555.	27.8	685
56	DNMT3A R882H Can Cooperate with FLT3-ITD to Cause AML in Mice. Blood, 2015, 126, 2458-2458.	1.4	0
57	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
58	Non-Malignant Oligoclonal Hematopoiesis Commonly Follows Cytoreductive Chemotherapy in Adult De Novo AML Patients. Blood, 2015, 126, 686-686.	1.4	0
59	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 379-392.	16.8	330
60	Enforced Differentiation of Dnmt3a-Null Bone Marrow Leads to Failure with c-Kit Mutations Driving Leukemic Transformation. Blood, 2014, 124, 837-837.	1.4	0
61	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
62	Notch signaling in acute promyelocytic leukemia. Leukemia, 2013, 27, 1548-1557.	7.2	28
63	Genomic impact of transient low-dose decitabine treatment on primary AML cells. Blood, 2013, 121, 1633-1643.	1.4	137
64	Functional Early Hematopoietic Progenitor Cells Derived From Mouse Embryonic Stem Cells and Induced Pluripotent Stem Cells. Blood, 2013, 122, 2421-2421.	1.4	1
65	Comprehensive Analysis Of HOX Gene Expression and DNA Methylation From 189 Primary AMLs Demonstrates Canonical Patterns Associated With Hematopoietic Stem/Progenitors and Recurrent AML Mutations. Blood, 2013, 122, 2496-2496.	1.4	2
66	DNMT3A R882H Overexpression Leads To Hematopoietic and Skin Alterations In Transgenic Mice. Blood, 2013, 122, 479-479.	1.4	4
67	Subclonal â€œskewingâ€•Of De Novo AML Samples After Engraftment In Immunodeficient Mice. Blood, 2013, 122, 609-609.	1.4	0
68	Expression and Function of PML-RARA in the Hematopoietic Progenitor Cells of Ctsg-PML-RARA Mice. PLoS ONE, 2012, 7, e46529.	2.5	15
69	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	28.9	1,365
70	Functional Hematopoietic Cells Derived From Mouse Embryonic Stem Cells.. Blood, 2012, 120, 2304-2304.	1.4	0
71	Deep Digital Sequencing Identifies an AML Subclone with Enhanced in Vitro and in Vivo Growth Properties Associated with Disease Relapse. Blood, 2012, 120, 407-407.	1.4	0
72	In Vitro Decitabine Treatment Demonstrates Heterogeneous Changes in Methylation and Gene Expression in Primary AML Samples.. Blood, 2012, 120, 2527-2527.	1.4	0

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73	Rara haploinsufficiency modestly influences the phenotype of acute promyelocytic leukemia in mice. Blood, 2011, 117, 2460-2468.	1.4	17
74	Use of classic and novel immunohistochemical markers in the diagnosis of cutaneous myeloid sarcoma. Journal of Cutaneous Pathology, 2011, 38, 945-953.	1.3	30
75	Combination decitabine, arsenic trioxide, and ascorbic acid for the treatment of myelodysplastic syndrome and acute myeloid leukemia: A phase I study. American Journal of Hematology, 2011, 86, 796-800.	4.1	39
76	Use of Whole-Genome Sequencing to Diagnose a Cryptic Fusion Oncogene. JAMA - Journal of the American Medical Association, 2011, 305, 1577.	7.4	233
77	Immunohistochemical Analysis of Monocytic Leukemias. American Journal of Clinical Pathology, 2011, 135, 720-730.	0.7	21
78	Transcription factor MIST1 in terminal differentiation of mouse and human plasma cells. Physiological Genomics, 2011, 43, 174-186.	2.3	23
79	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
80	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
81	Bone marrow biopsy in patients with hepatitis C virus infection: Spectrum of findings and diagnostic utility. American Journal of Hematology, 2010, 85, 106-110.	4.1	33
82	Molecular Pathology of Myeloproliferative Neoplasms. American Journal of Clinical Pathology, 2010, 133, 602-615.	0.7	28
83	Complement factor 5a receptor chimeras reveal the importance of lipidâ€facing residues in transport competence. FEBS Journal, 2009, 276, 2786-2800.	4.7	2
84	The spectrum of adult Bâ€lymphoid leukemias with BCRâ€ABL: Molecular diagnostic, cytogenetic, and clinical laboratory perspectives. American Journal of Hematology, 2008, 83, 901-907.	4.1	9
85	Structure of the Complement Factor 5a Receptor-Ligand Complex Studied by Disulfide Trapping and Molecular Modeling. Journal of Biological Chemistry, 2008, 283, 7763-7775.	3.4	25
86	Dimerization/oligomerization in G proteinâ€coupled receptors (GPCRs) involve the participation of all transmembrane domains. FASEB Journal, 2007, 21, A613.	0.5	0
87	Genetic Analysis of the First and Third Extracellular Loops of the C5a Receptor Reveals an Essential WXFG Motif in the First Loop. Journal of Biological Chemistry, 2006, 281, 12010-12019.	3.4	57
88	Essential role for the second extracellular loop in C5a receptor activation. Nature Structural and Molecular Biology, 2005, 12, 320-326.	8.2	147
89	pVHL Modification by NEDD8 Is Required for Fibronectin Matrix Assembly and Suppression of Tumor Development. Molecular and Cellular Biology, 2004, 24, 3251-3261.	2.3	156
90	Inhibition of vascular endothelial growth factor with a sequence-specific hypoxia response element antagonist. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16768-16773.	7.1	211

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91	C5a Receptor Oligomerization. Journal of Biological Chemistry, 2003, 278, 35345-35353.	3.4	102
92	Gene expression profiling in a renal cell carcinoma cell line: dissecting VHL and hypoxia-dependent pathways. Molecular Cancer Research, 2003, 1, 453-62.	3.4	94
93	Inhibition of HIF is necessary for tumor suppression by the von Hippel-Lindau protein. Cancer Cell, 2002, 1, 237-246.	16.8	695
94	von Hippel-Lindau protein mutants linked to type 2C VHL disease preserve the ability to downregulate HIF. Human Molecular Genetics, 2001, 10, 1019-1027.	2.9	341
95	Suppression of tumor growth through disruption of hypoxia-inducible transcription. Nature Medicine, 2000, 6, 1335-1340.	30.7	726