Christopher A Miller

List of Publications by Year
in descending order

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		53794	40979
103	22,884	45	93
papers	citations	h-index	g-index

115	115	115	38663
all docs	docs citations	times ranked	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	Efficient Algorithms Unlock Understanding of Clonal Evolution in Cancer. Blood Cancer Discovery, 2022, 3, OF1-OF2.	5.0	0
7	Somatic Dnmt3a inactivation leads to slow, canonical DNA methylation loss in murine hematopoietic cells. IScience, 2022, 25, 104004.	4.1	2
8	Recurrent Transcriptional Responses in AML and MDS patients Treated with Decitabine. Experimental Hematology, 2022, , .	0.4	5
9	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. Cancer Genetics, 2022, 264-265, 90-99.	0.4	3
10	Convergent Clonal Evolution of Signaling Gene Mutations Is a Hallmark of Myelodysplastic Syndrome Progression. Blood Cancer Discovery, 2022, 3, 330-345.	5.0	10
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	Optimized polyepitope neoantigen DNA vaccines elicit neoantigen-specific immune responses in preclinical models and in clinical translation. Genome Medicine, 2021, 13, 56.	8.2	34
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	HPV transcript expression affects cervical cancer response to chemoradiation. JCI Insight, 2021, 6, .	5.0	12
18	U2af1 is a haplo-essential gene required for hematopoietic cancer cell survival in mice. Journal of Clinical Investigation, 2021, 131, .	8.2	9

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19	Tumor suppressor function of WT1 in acute promyelocytic leukemia. Haematologica, 2021, , .	3.5	4
20	Adverse Outcomes in Acute Myeloid Leukemia Are Associated with Tumor Cell-Mediated Immunosuppression. Blood, 2021, 138, 800-800.	1.4	0
21	Dnmt3a Inactivation Leads to Slow DNA Methylation Loss in Murine Hematopoietic Cells In Vivo. Blood, 2021, 138, 1087-1087.	1.4	0
22	Kdm6a deficiency restricted to mouse hematopoietic cells causes an age- and sex-dependent myelodysplastic syndrome-like phenotype. PLoS ONE, 2021, 16, e0255706.	2.5	4
23	HPV-EM: an accurate HPV detection and genotyping EM algorithm. Scientific Reports, 2020, 10, 14340.	3.3	3
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	pVACtools: A Computational Toolkit to Identify and Visualize Cancer Neoantigens. Cancer Immunology Research, 2020, 8, 409-420.	3.4	132
27	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
28	Molecular Profiling of Decitabine Response in MDS and AML Patients. Blood, 2020, 136, 40-40.	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	Detection of neoantigen-specific T cells following a personalized vaccine in a patient with glioblastoma. OncoImmunology, 2019, 8, e1561106.	4.6	50
31	Shared cell of origin in a patient with Erdheim-Chester disease and acute myeloid leukemia. Haematologica, 2019, 104, e373-e375.	3.5	13
32	Smc3 is required for mouse embryonic and adult hematopoiesis. Experimental Hematology, 2019, 70, 70-84.e6.	0.4	12
33	Exome analysis of treatmentâ€related <scp>AML</scp> after <scp>APL</scp> suggests secondary evolution. British Journal of Haematology, 2019, 185, 984-987.	2.5	1
34	DNMT3AR882 Alters the Epigenome of Hematopoietic Cells. Blood, 2019, 134, 112-112.	1.4	0
35	The Molecular Basis of Long First Remissions in Normal Karyotype AML Patients. Blood, 2019, 134, 3827-3827.	1.4	0
36	An â€œoff-the-shelfâ€•fratricide-resistant CAR-T for the treatment of T cell hematologic malignancies. Leukemia, 2018, 32, 1970-1983.	7.2	282

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37	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
38	Resistance-promoting effects of ependymoma treatment revealed through genomic analysis of multiple recurrences in a single patient. Journal of Physical Education and Sports Management, 2018, 4, a002444.	1.2	16
39	Cellular stressors contribute to the expansion of hematopoietic clones of varying leukemic potential. Nature Communications, 2018, 9, 455.	12.8	150
40	Biological and therapeutic implications of multisector sequencing in newly diagnosed glioblastoma. Neuro-Oncology, 2018, 20, 472-483.	1.2	42
41	Lenalidomide results in a durable complete remission in acute myeloid leukemia accompanied by persistence of somatic mutations and a T-cell infiltrate in the bone marrow. Haematologica, 2018, 103, e270-e273.	3.5	1
42	Somatic mutations and clonal hematopoiesis in congenital neutropenia. Blood, 2018, 131, 408-416.	1.4	91
43	A case of acute myeloid leukemia with promyelocytic features characterized by expression of a novel RARG-CPSF6 fusion. Blood Advances, 2018, 2, 1295-1299.	5.2	25
44	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	6.4	329
45	Immune Escape of Relapsed AML Cells after Allogeneic Transplantation. New England Journal of Medicine, 2018, 379, 2330-2341.	27.0	322
46	Mutation Clearance after Transplantation for Myelodysplastic Syndrome. New England Journal of Medicine, 2018, 379, 1028-1041.	27.0	93
47	The prognostic effects of somatic mutations in ER-positive breast cancer. Nature Communications, 2018, 9, 3476.	12.8	89
48	Discriminating a common somatic ASXL1 mutation (c.1934dup; p.G646Wfs*12) from artifact in myeloid malignancies using NGS. Leukemia, 2018, 32, 1874-1878.	7.2	18
49	Somatic mutations in benign breast disease tissue and risk of subsequent invasive breast cancer. British Journal of Cancer, 2018, 118, 1662-1664.	6.4	9
50	Clinical outcomes and differential effects of PI3K pathway mutation in obese versus non-obese patients with cervical cancer. Oncotarget, 2018, 9, 4061-4073.	1.8	14
51	Evidence for Complete Mutation Clearance in Normal Karyotype AML Patients with Very Long (> 5) Tj ETQq1 1 0.784314 rgBT /Overlo	1.4	0
52	ATRX in Diffuse Gliomas With its Mosaic/Heterogeneous Expression in a Subset. Brain Pathology, 2017, 27, 138-145.	4.1	16
53	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
54	Recurrent somatic mutations affecting B-cell receptor signaling pathway genes in follicular lymphoma. Blood, 2017, 129, 473-483.	1.4	147

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55	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. Experimental Hematology, 2017, 55, 19-33.	0.4	9
56	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
57	Haploinsufficiency for DNA methyltransferase 3A predisposes hematopoietic cells to myeloid malignancies. Journal of Clinical Investigation, 2017, 127, 3657-3674.	8.2	80
58	An Off-the-Shelfâ„¢ Fratricide-Resistant CAR-T for the Treatment of T Cell Hematologic Malignancies. Blood, 2017, 130, 844-844.	1.4	2
59	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. PLoS Medicine, 2016, 13, e1002174.	8.4	86
60	Visualizing tumor evolution with the fishplot package for R. BMC Genomics, 2016, 17, 880.	2.8	131
61	Cancer Immunogenomics: Computational Neoantigen Identification and Vaccine Design. Cold Spring Harbor Symposia on Quantitative Biology, 2016, 81, 105-111.	1.1	22
62	A common founding clone with TP53 and PTEN mutations gives rise to a concurrent germ cell tumor and acute megakaryoblastic leukemia. Journal of Physical Education and Sports Management, 2016, 2, a000687.	1.2	15
63	Rapid expansion of preexisting nonleukemic hematopoietic clones frequently follows induction therapy for de novo AML. Blood, 2016, 127, 893-897.	1.4	94
64	Immunogenomics of Hypermutated Glioblastoma: A Patient with Germline POLE Deficiency Treated with Checkpoint Blockade Immunotherapy. Cancer Discovery, 2016, 6, 1230-1236.	9.4	242
65	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. Cell Reports, 2016, 17, 249-260.	6.4	21
66	TP53 and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes. New England Journal of Medicine, 2016, 375, 2023-2036.	27.0	663
67	Impact of mutational profiles on response of primary oestrogen receptor-positive breast cancers to oestrogen deprivation. Nature Communications, 2016, 7, 13294.	12.8	34
68	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. Nature Communications, 2016, 7, 12498.	12.8	69
69	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
70	Clonal Evolution Revealed By Exome Sequencing in a Case of Primary Myelofibrosis Associated with Subsequent Development of Aggressive Systemic Mastocytosis/Mast Cell Leukemia. Blood, 2016, 128, 5496-5496.	1.4	0
71	Dynamic Changes in MDS Clonal Architecture Following Allogeneic Stem Cell Transplant. Blood, 2016, 128, 5506-5506.	1.4	0
72	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	6.2	174

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73	Genomic analysis of germ line and somatic variants in familial myelodysplasia/acute myeloid leukemia. Blood, 2015, 126, 2484-2490.	1.4	207
74	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
75	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83
76	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
77	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	12.8	243
78	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
79	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. Nature, 2015, 518, 552-555.	27.8	685
80	Dynamic Changes in the Clonal Structure of MDS and AML in Response to Epigenetic Therapy. Blood, 2015, 126, 610-610.	1.4	3
81	Dynamic Changes in Clonal Clearance with Decitabine Therapy in AML and MDS Patients. Blood, 2015, 126, 689-689.	1.4	1
82	Non-Malignant Oligoclonal Hematopoiesis Commonly Follows Cytoreductive Chemotherapy in Adult De Novo AML Patients. Blood, 2015, 126, 686-686.	1.4	0
83	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. PLoS Computational Biology, 2014, 10, e1003665.	3.2	400
84	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 379-392.	16.8	330
85	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	12.8	253
86	Age-related mutations associated with clonal hematopoietic expansion and malignancies. Nature Medicine, 2014, 20, 1472-1478.	30.7	1,533
87	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
88	DGIdb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.	19.0	443
89	Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.	27.8	3,695
90	Somatic neurofibromatosis type 1 (NF1) inactivation characterizes NF1-associated pilocytic astrocytoma. Genome Research, 2013, 23, 431-439.	5.5	99

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91	Genomic Landscapes and Clonality of De Novo AML. New England Journal of Medicine, 2013, 369, 1472-1473.	27.0	58
92	Background Mutations in Parental Cells Account for Most of the Genetic Heterogeneity of Induced Pluripotent Stem Cells. Cell Stem Cell, 2012, 10, 570-582.	11.1	199
93	Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature, 2012, 486, 353-360.	27.8	922
94	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	27.8	1,795
95	VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. Genome Research, 2012, 22, 568-576.	5.5	4,086
96	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	28.9	1,365
97	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
98	Long-range massively parallel mate pair sequencing detects distinct mutations and similar patterns of structural mutability in two breast cancer cell lines. Cancer Genetics, 2011, 204, 447-457.	0.4	16
99	ReadDepth: A Parallel R Package for Detecting Copy Number Alterations from Short Sequencing Reads. PLoS ONE, 2011, 6, e16327.	2.5	193
100	Discovering functional modules by identifying recurrent and mutually exclusive mutational patterns in tumors. BMC Medical Genomics, 2011, 4, 34.	1.5	119
101	BioStar: An Online Question & Answer Resource for the Bioinformatics Community. PLoS Computational Biology, 2011, 7, e1002216.	3.2	82
102	Pash 3.0: A versatile software package for read mapping and integrative analysis of genomic and epigenomic variation using massively parallel DNA sequencing. BMC Bioinformatics, 2010, 11, 572.	2.6	48
103	A sequence-level map of chromosomal breakpoints in the MCF-7 breast cancer cell line yields insights into the evolution of a cancer genome. Genome Research, 2009, 19, 167-177.	5.5	111