James M Allan

List of Publications by Year
in descending order

103 papers	6,902 citations	57758 44 h-index	60623 81 g-index
108 all docs	108 docs citations	108 times ranked	10124 citing authors

#	Article	IF	Citations
1	Loci on 7p12.2, 10q21.2 and 14q11.2 are associated with risk of childhood acute lymphoblastic leukemia. Nature Genetics, 2009, 41, 1006-1010.	21.4	445
2	A genome-wide association study identifies six susceptibility loci for chronic lymphocytic leukemia. Nature Genetics, 2008, 40, 1204-1210.	21.4	329
3	Cancer Survivorshipâ€"Genetic Susceptibility and Second Primary Cancers: Research Strategies and Recommendations. Journal of the National Cancer Institute, 2006, 98, 15-25.	6.3	295
4	Testicular Cancer Survivorship: Research Strategies and Recommendations. Journal of the National Cancer Institute, 2010, 102, 1114-1130.	6.3	260
5	Variation in CDKN2A at 9p21.3 influences childhood acute lymphoblastic leukemia risk. Nature Genetics, 2010, 42, 492-494.	21.4	248
6	Mechanisms of therapy-related carcinogenesis. Nature Reviews Cancer, 2005, 5, 943-955.	28.4	245
7	Polymorphism in glutathione S -transferase P1 is associated with susceptibility to chemotherapy-induced leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 11592-11597.	7.1	233
8	Common variants at 2q37.3, 8q24.21, 15q21.3 and 16q24.1 influence chronic lymphocytic leukemia risk. Nature Genetics, 2010, 42, 132-136.	21.4	223
9	Base excision repair deficient mice lacking the Aag alkyladenine DNA glycosylase. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 13087-13092.	7.1	215
10	Ras pathway mutations are prevalent in relapsed childhood acute lymphoblastic leukemia and confer sensitivity to MEK inhibition. Blood, 2014, 124, 3420-3430.	1.4	209
11	Aetiology, genetics and prevention of secondary neoplasms in adult cancer survivors. Nature Reviews Clinical Oncology, 2013, 10, 289-301.	27.6	207
12	Second Malignant Neoplasms and Cardiovascular Disease Following Radiotherapy. Journal of the National Cancer Institute, 2012, 104, 357-370.	6.3	187
13	3-methyladenine DNA glycosylases: structure, function, and biological importance. BioEssays, 1999, 21, 668-676.	2.5	173
14	Functional FAS promoter polymorphisms are associated with increased risk of acute myeloid leukemia. Cancer Research, 2003, 63, 4327-30.	0.9	168
15	A genome-wide association study identifies multiple susceptibility loci for chronic lymphocytic leukemia. Nature Genetics, 2014, 46, 56-60.	21.4	166
16	Variation at 10p12.2 and 10p14 influences risk of childhood B-cell acute lymphoblastic leukemia and phenotype. Blood, 2013, 122, 3298-3307.	1.4	147
17	Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. Nature Genetics, 2013, 45, 1221-1225.	21.4	143
18	DNA repair methyltransferase (Mgmt) knockout mice are sensitive to the lethal effects of chemotherapeutic alkylating agents. Mutagenesis, 1999, 14, 339-347.	2.6	129

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19	Association of Molecular Markers With Toxicity Outcomes in a Randomized Trial of Chemotherapy for Advanced Colorectal Cancer: The FOCUS Trial. Journal of Clinical Oncology, 2009, 27, 5519-5528.	1.6	120
20	Polymorphisms of 5,10-methylenetetrahydrofolate reductase and risk of gastric cancer in a Chinese population: A case-control study. International Journal of Cancer, 2001, 95, 332-336.	5.1	119
21	A Chemical and Genetic Approach Together Define the Biological Consequences of 3-Methyladenine Lesions in the Mammalian Genome. Journal of Biological Chemistry, 1998, 273, 5412-5418.	3.4	115
22	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2015, 3, 243-253.	11.4	115
23	Genetic variation in XPD predicts treatment outcome and risk of acute myeloid leukemia following chemotherapy. Blood, 2004, 104, 3872-3877.	1.4	108
24	Breast cancer risk following radiotherapy for Hodgkin lymphoma: modification by other risk factors. Blood, 2005, 106, 3358-3365.	1.4	101
25	Genome-wide association study to identify novel loci associated with therapy-related myeloid leukemia susceptibility. Blood, 2009, 113, 5575-5582.	1.4	93
26	Polymorphic variation in GSTP1 modulates outcome following therapy for multiple myeloma. Blood, 2003, 102, 2345-2350.	1.4	90
27	MDM2 SNP309 and TP53 Arg72Pro interact to alter therapy-related acute myeloid leukemia susceptibility. Blood, 2008, 112, 741-749.	1.4	90
28	Genetic variation in the folate metabolic pathway and risk of childhood leukemia. Blood, 2010, 115, 3923-3929.	1.4	85
29	Acute Myeloid Leukemia Following Hodgkin Lymphoma: A Population-Based Study of 35â€‰511 Patients. Journal of the National Cancer Institute, 2006, 98, 215-218.	6.3	84
30	The Oncogenic Transcription Factor RUNX1/ETO Corrupts Cell Cycle Regulation to Drive Leukemic Transformation. Cancer Cell, 2018, 34, 626-642.e8.	16.8	81
31	Gastric marginal zone lymphoma is associated with polymorphisms in genes involved in inflammatory response and antioxidative capacity. Blood, 2003, 102, 1007-1011.	1.4	79
32	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	12.8	75
33	The effect of hOGG1 and glutathione peroxidase I genotypes and 3p chromosomal loss on 8-hydroxydeoxyguanosine levels in lung cancer. Carcinogenesis, 2000, 21, 167-172.	2.8	73
34	Telomere dysfunction accurately predicts clinical outcome in chronic lymphocytic leukaemia, even in patients with early stage disease. British Journal of Haematology, 2014, 167, 214-223.	2.5	73
35	Risk of Non-Hodgkin Lymphoma Associated with Polymorphisms in Folate-Metabolizing Genes. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 2999-3003.	2.5	72
36	A genome-wide association study identifies risk loci for childhood acute lymphoblastic leukemia at 10q26.13 and 12q23.1. Leukemia, 2017, 31, 573-579.	7.2	69

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37	An intron splice acceptor polymorphism in hMSH2 and risk of leukemia after treatment with chemotherapeutic alkylating agents. Clinical Cancer Research, 2003, 9, 3012-20.	7.0	63
38	Common cancer-associated imbalances in the DNA damage response confer sensitivity to single agent ATR inhibition. Oncotarget, 2015, 6, 32396-32409.	1.8	59
39	Genetic Predisposition to Chronic Lymphocytic Leukemia Is Mediated by a BMF Super-Enhancer Polymorphism. Cell Reports, 2016, 16, 2061-2067.	6.4	58
40	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. Nature Communications, 2018, 9, 1340.	12.8	58
41	Identification of four novel associations for B-cell acute lymphoblastic leukaemia risk. Nature Communications, 2019, 10, 5348.	12.8	58
42	Risk of Leukemia Among Survivors of Testicular Cancer: A Population-based Study of 42,722 Patients. Annals of Epidemiology, 2008, 18, 416-421.	1.9	55
43	Genetic alterations in bronchial mucosa and plasma DNA from individuals at high risk of lung cancer. International Journal of Cancer, 2001, 91, 359-365.	5.1	49
44	MLH1 â^'93G>A promoter polymorphism and risk of mismatch repair deficient colorectal cancer. International Journal of Cancer, 2008, 123, 2456-2459.	5.1	44
45	Common genetic variation contributes significantly to the risk of childhood B-cell precursor acute lymphoblastic leukemia. Leukemia, 2012, 26, 2212-2215.	7.2	42
46	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Blood Cancer Journal, 2019, 9, 1.	6.2	40
47	Polymorphic MLH1 and risk of cancer after methylating chemotherapy for Hodgkin lymphoma. Journal of Medical Genetics, 2007, 45, 142-146.	3.2	37
48	Genome-wide homozygosity signatures and childhood acute lymphoblastic leukemia risk. Blood, 2010, 115, 4472-4477.	1.4	36
49	RAD51 homologous recombination repair gene haplotypes and risk of acute myeloid leukaemia. Leukemia Research, 2007, 31, 169-174.	0.8	33
50	Insight into genetic predisposition to chronic lymphocytic leukemia from integrative epigenomics. Nature Communications, 2019, 10, 3615.	12.8	32
51	Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. Scientific Reports, 2017, 7, 41071.	3.3	31
52	Inhibition of ATR acutely sensitizes acute myeloid leukemia cells to nucleoside analogs that target ribonucleotide reductase. Blood Advances, 2018, 2, 1157-1169.	5.2	28
53	Second Malignant Neoplasms and Cardiovascular Disease Following Radiotherapy. Health Physics, 2014, 106, 229-246.	0.5	27
54	Telomere length is a critical determinant for survival in multiple myeloma. British Journal of Haematology, 2017, 178, 94-98.	2.5	26

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55	Deregulation of homologous recombination DNA repair in alkylating agent-treated stem cell clones: a possible role in the aetiology of chemotherapy-induced leukaemia. Oncogene, 2006, 25, 1709-1720.	5.9	24
56	MHC variation and risk of childhood B-cell precursor acute lymphoblastic leukemia. Blood, 2011, 117, 1633-1640.	1.4	24
57	A functional variant in the core promoter of the CD95 cell death receptor gene predicts prognosis in acute promyelocytic leukemia. Blood, 2012, 119, 196-205.	1.4	24
58	The 9p21.3 risk of childhood acute lymphoblastic leukaemia is explained by a rare high-impact variant in CDKN2A. Scientific Reports, 2015, 5, 15065.	3.3	24
59	Common variation at 12q24.13 (OAS3) influences chronic lymphocytic leukemia risk. Leukemia, 2015, 29, 748-751.	7.2	24
60	A common genetic variant in XPD associates with risk of 5q- and 7q-deleted acute myeloid leukemia. Blood, 2007, 109, 1233-1236.	1.4	23
61	c-MYC is a radiosensitive locus in human breast cells. Oncogene, 2015, 34, 4985-4994.	5.9	23
62	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
63	Polymorphisms in the nucleotide excision repair gene ERCC2/XPD and risk of non-Hodgkin lymphoma. Cancer Epidemiology, 2009, 33, 257-260.	1.9	21
64	GENETIC SUSCEPTIBILITY TO RADIOGENIC CANCER IN HUMANS. Health Physics, 2008, 95, 677-686.	0.5	20
65	DNA mismatch repair status affects cellular response to Ara-C and other anti-leukemic nucleoside analogs. Leukemia, 2011, 25, 1046-1049.	7.2	19
66	Variant IRF4/MUM1 associates with CD38 status and treatment-free survival in chronic lymphocytic leukaemia. Leukemia, 2010, 24, 877-881.	7.2	18
67	Genome-wide association study identifies susceptibility loci for acute myeloid leukemia. Nature Communications, 2021, 12, 6233.	12.8	17
68	Nonâ€Homologous Endâ€Joining Gene Profiling Reveals Distinct Expression Patterns Associated with Lymphoma and Multiple Myeloma. British Journal of Haematology, 2010, 149, 258-262.	2.5	15
69	Whole-exome Sequence Analysis Implicates Rare Il17REL Variants in Familial and Sporadic Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2016, 22, 20-27.	1.9	13
70	Genetic susceptibility to iatrogenic malignancy. Pharmacogenomics, 2005, 6, 615-628.	1.3	12
71	Cytarabine preferentially induces mutation at specific sequences in the genome which are identifiable in relapsed acute myeloid leukaemia. Leukemia, 2015, 29, 491-494.	7.2	10
72	Genome-wide association study identifies risk loci for progressive chronic lymphocytic leukemia. Nature Communications, 2021, 12, 665.	12.8	9

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73	Poor metabolizer status at the cytochrome p450 2c19 and 2d6 loci does not modulate susceptibility to therapy-related acute myeloid leukaemia. British Journal of Haematology, 2003, 121, 192-194.	2.5	8
74	A polymorphism in the 3â€² UTR of IRF4 linked to susceptibility and pathogenesis in chronic lymphocytic leukaemia and Hodgkin lymphoma has limited impact in multiple myeloma. British Journal of Haematology, 2010, 150, 371-373.	2.5	8
75	Pharmacogenetic association of MBL2 and CD95 polymorphisms with grade 3 infection following adjuvant therapy for breast cancer with doxorubicin and cyclophosphamide. European Journal of Cancer, 2017, 71, 15-24.	2.8	8
76	Genome-Wide Association Analyses Identify Variants in IRF4 Associated With Acute Myeloid Leukemia and Myelodysplastic Syndrome Susceptibility. Frontiers in Genetics, 2021, 12, 554948.	2.3	8
77	Molar pregnancy, childhood cancer and genomic imprinting â€“ is there a link?. Human Fertility, 2006, 9, 171-174.	1.7	7
78	Influence of DNA repair gene polymorphisms on the initial repair of MMSâ€induced DNA damage in human lymphocytes as measured by the alkaline comet assay. Environmental and Molecular Mutagenesis, 2008, 49, 669-675.	2.2	7
79	Genetic variation in genes expressed in the germinal center and risk of B cell lymphoma among Caucasians. Haematologica, 2008, 93, 1597-1600.	3.5	7
80	The use of purified DNA repair proteins to detect DNA damage. Mutation Research - Environmental Mutagenesis and Related Subjects Including Methodology, 1994, 313, 165-174.	0.4	6
81	The Escherichia coli DNA repair protein UvrA can re-associate with the UvrB: aflatoxin B1-DNA complex in vitro. Mutation Research DNA Repair, 1996, 362, 261-268.	3.7	6
82	Melanocortin 1 receptor (MC1R), pigmentary characteristics and sun exposure: Findings from a caseâ€“control study of diffuse large B-cell and follicular lymphoma. Cancer Epidemiology, 2010, 34, 136-141.	1.9	6
83	Does radiation-induced c-MYC amplification initiate breast oncogenesis?. Molecular and Cellular Oncology, 2016, 3, e1010950.	0.7	6
84	Application of DNA pooling to large studies of disease. Statistics in Medicine, 2004, 23, 3841-3850.	1.6	5
85	Detection of DNA damage by Escherichia coli UvrB-binding competition assay is limited by the stability of the UvrB-DNA complex. Carcinogenesis, 1997, 18, 1407-1413.	2.8	4
86	RAG1 and BRCA2 polymorphisms in non-Hodgkin lymphoma. Blood, 2007, 109, 5522-5523.	1.4	4
87	3â€methyladenine DNA glycosylases: structure, function, and biological importance. BioEssays, 1999, 21, 668-676.	2.5	3
88	Functional characterisation of a novel ovarian cancer cell line, NUOC-1. Oncotarget, 2017, 8, 26832-26844.	1.8	3
89	The Genetics of Cancer Survivorship. Hematology/Oncology Clinics of North America, 2008, 22, 257-269.	2.2	2
90	The Genomic Landscape Of Lineage Switch Acute Leukemia. Blood, 2013, 122, 2552-2552.	1.4	2

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91	Genetic susceptibility to breast cancer in lymphoma survivors. Blood, 2019, 133, 1004-1006.	1.4	1
92	A Genome-Wide Analysis to Identify Novel Susceptibility Loci for Therapy-Related Acute Myeloid Leukemia. Blood, 2008, 112, 432-432.	1.4	1
93	Mutant TET2 Allele Dosage Affects Response to 5-Azacitidine in Acute Myeloid Leukemia. Blood, 2019, 134, 113-113.	1.4	1
94	Searching for clarity in therapy-related myelodysplastic syndrome/acute myeloid leukemia prognostication. Leukemia and Lymphoma, 2013, 54, 447-448.	1.3	0
95	The t(8;21) Fusion Protein AML1/ETO Promotes Susceptibility to Mutation In Acute Myeloid Leukemia.. Blood, 2010, 116, 3368-3368.	1.4	0
96	A Functional Polymorphism In the CD95 Cell Death Receptor Associated with Prognosis In Acute Promyelocytic Leukemia. Blood, 2010, 116, 756-756.	1.4	0
97	Cellular Response to Cytarabine Is Modulated by the DNA Mismatch Repair Pathway: Implications for Treatment of Acute Myeloid Leukemia. Blood, 2010, 116, 1819-1819.	1.4	0
98	The Angiogenic Factor Angiopoietin-1 Is Regulated by the Acute Myeloid Leukemia Fusion Protein AML1/ETO. Blood, 2011, 118, 2426-2426.	1.4	0
99	AML1/ETO Confers a Mutator Phenotype In Acute Myeloid Leukemia Associated with Downregulation of the Base-Excision-Repair Gene OGG1,. Blood, 2011, 118, 3441-3441.	1.4	0
100	Targeting Ikkî± in CLL: Inhibition of Non-Canonical NF-Îºb Signaling Decreases Survival and Proliferation of CD40L-Stimulated Primary CLL Cells. Blood, 2016, 128, 3959-3959.	1.4	0
101	Inhibition of ATR in Combination with Nucleoside Analogues Eradicates Acute Myeloid Leukaemia in an Orthotopic Murine Xenograft Model. Blood, 2016, 128, 4031-4031.	1.4	0
102	Genome Wide Association Analyses Identify Pleiotropic Variants Associated with Acute Myeloid Leukemia (AML) and Myelodysplastic Syndrome (MDS) Susceptibility. Blood, 2018, 132, 1500-1500.	1.4	0
103	Identification of New Risk Loci and Regulatory Mechanisms Influencing Genetic Susceptibility to Acute Lymphoblastic Leukaemia. Blood, 2019, 134, 650-650.	1.4	0