

James M Allan

List of Publications by Year in descending order

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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	Genome-wide association study identifies risk loci for progressive chronic lymphocytic leukemia. Nature Communications, 2021, 12, 665.	12.8	9
2	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
3	Genome-wide association study identifies susceptibility loci for acute myeloid leukemia. Nature Communications, 2021, 12, 6233.	12.8	17
4	Insight into genetic predisposition to chronic lymphocytic leukemia from integrative epigenomics. Nature Communications, 2019, 10, 3615.	12.8	32
5	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
6	Genetic susceptibility to breast cancer in lymphoma survivors. Blood, 2019, 133, 1004-1006.	1.4	1
7	Identification of four novel associations for B-cell acute lymphoblastic leukaemia risk. Nature Communications, 2019, 10, 5348.	12.8	58
8	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Blood Cancer Journal, 2019, 9, 1.	6.2	40
9	Mutant TET2 Allele Dosage Affects Response to 5-Azacidine in Acute Myeloid Leukemia. Blood, 2019, 134, 113-113.	1.4	1
10	Identification of New Risk Loci and Regulatory Mechanisms Influencing Genetic Susceptibility to Acute Lymphoblastic Leukaemia. Blood, 2019, 134, 650-650.	1.4	0
11	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. Nature Communications, 2018, 9, 1340.	12.8	58
12	The Oncogenic Transcription Factor RUNX1/ETO Corrupts Cell Cycle Regulation to Drive Leukemic Transformation. Cancer Cell, 2018, 34, 626-642.e8.	16.8	81
13	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
14	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
15	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
16	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	12.8	75
17	Telomere length is a critical determinant for survival in multiple myeloma. British Journal of Haematology, 2017, 178, 94-98.	2.5	26
18	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

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19	A genome-wide association study identifies risk loci for childhood acute lymphoblastic leukemia at 10q26.13 and 12q23.1. <i>Leukemia</i> , 2017, 31, 573-579.	7.2	69
20	Functional characterisation of a novel ovarian cancer cell line, NUOC-1. <i>Oncotarget</i> , 2017, 8, 26832-26844.	1.8	3
21	Genetic Predisposition to Chronic Lymphocytic Leukemia Is Mediated by a BMF Super-Enhancer Polymorphism. <i>Cell Reports</i> , 2016, 16, 2061-2067.	6.4	58
22	Whole-exome Sequence Analysis Implicates Rare IL17REL Variants in Familial and Sporadic Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 20-27.	1.9	13
23	Does radiation-induced <i>c-MYC</i> amplification initiate breast oncogenesis?. <i>Molecular and Cellular Oncology</i> , 2016, 3, e1010950.	0.7	6
24	Targeting Ikk β in CLL: Inhibition of Non-Canonical NF- κ B Signaling Decreases Survival and Proliferation of CD40L-Stimulated Primary CLL Cells. <i>Blood</i> , 2016, 128, 3959-3959.	1.4	0
25	Inhibition of ATR in Combination with Nucleoside Analogues Eradicates Acute Myeloid Leukaemia in an Orthotopic Murine Xenograft Model. <i>Blood</i> , 2016, 128, 4031-4031.	1.4	0
26	The 9p21.3 risk of childhood acute lymphoblastic leukaemia is explained by a rare high-impact variant in CDKN2A. <i>Scientific Reports</i> , 2015, 5, 15065.	3.3	24
27	Cytarabine preferentially induces mutation at specific sequences in the genome which are identifiable in relapsed acute myeloid leukaemia. <i>Leukemia</i> , 2015, 29, 491-494.	7.2	10
28	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. <i>Lancet Diabetes and Endocrinology</i> , 2015, 3, 243-253.	11.4	115
29	<i>c-MYC</i> is a radiosensitive locus in human breast cells. <i>Oncogene</i> , 2015, 34, 4985-4994.	5.9	23
30	Common variation at 12q24.13 (OAS3) influences chronic lymphocytic leukemia risk. <i>Leukemia</i> , 2015, 29, 748-751.	7.2	24
31	Common cancer-associated imbalances in the DNA damage response confer sensitivity to single agent ATR inhibition. <i>Oncotarget</i> , 2015, 6, 32396-32409.	1.8	59
32	Second Malignant Neoplasms and Cardiovascular Disease Following Radiotherapy. <i>Health Physics</i> , 2014, 106, 229-246.	0.5	27
33	Telomere dysfunction accurately predicts clinical outcome in chronic lymphocytic leukaemia, even in patients with early stage disease. <i>British Journal of Haematology</i> , 2014, 167, 214-223.	2.5	73
34	A genome-wide association study identifies multiple susceptibility loci for chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2014, 46, 56-60.	21.4	166
35	Ras pathway mutations are prevalent in relapsed childhood acute lymphoblastic leukemia and confer sensitivity to MEK inhibition. <i>Blood</i> , 2014, 124, 3420-3430.	1.4	209
36	Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. <i>Nature Genetics</i> , 2013, 45, 1221-1225.	21.4	143

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37	Aetiology, genetics and prevention of secondary neoplasms in adult cancer survivors. <i>Nature Reviews Clinical Oncology</i> , 2013, 10, 289-301.	27.6	207
38	Searching for clarity in therapy-related myelodysplastic syndrome/acute myeloid leukemia prognostication. <i>Leukemia and Lymphoma</i> , 2013, 54, 447-448.	1.3	0
39	Variation at 10p12.2 and 10p14 influences risk of childhood B-cell acute lymphoblastic leukemia and phenotype. <i>Blood</i> , 2013, 122, 3298-3307.	1.4	147
40	The Genomic Landscape Of Lineage Switch Acute Leukemia. <i>Blood</i> , 2013, 122, 2552-2552.	1.4	2
41	Second Malignant Neoplasms and Cardiovascular Disease Following Radiotherapy. <i>Journal of the National Cancer Institute</i> , 2012, 104, 357-370.	6.3	187
42	A functional variant in the core promoter of the CD95 cell death receptor gene predicts prognosis in acute promyelocytic leukemia. <i>Blood</i> , 2012, 119, 196-205.	1.4	24
43	Common genetic variation contributes significantly to the risk of childhood B-cell precursor acute lymphoblastic leukemia. <i>Leukemia</i> , 2012, 26, 2212-2215.	7.2	42
44	MHC variation and risk of childhood B-cell precursor acute lymphoblastic leukemia. <i>Blood</i> , 2011, 117, 1633-1640.	1.4	24
45	DNA mismatch repair status affects cellular response to Ara-C and other anti-leukemic nucleoside analogs. <i>Leukemia</i> , 2011, 25, 1046-1049.	7.2	19
46	The Angiogenic Factor Angiopoietin-1 Is Regulated by the Acute Myeloid Leukemia Fusion Protein AML1/ETO. <i>Blood</i> , 2011, 118, 2426-2426.	1.4	0
47	AML1/ETO Confers a Mutator Phenotype In Acute Myeloid Leukemia Associated with Downregulation of the Base-Excision-Repair Gene OGG1,. <i>Blood</i> , 2011, 118, 3441-3441.	1.4	0
48	Genome-wide homozygosity signatures and childhood acute lymphoblastic leukemia risk. <i>Blood</i> , 2010, 115, 4472-4477.	1.4	36
49	Genetic variation in the folate metabolic pathway and risk of childhood leukemia. <i>Blood</i> , 2010, 115, 3923-3929.	1.4	85
50	Melanocortin 1 receptor (MC1R), pigmentary characteristics and sun exposure: Findings from a case-control study of diffuse large B-cell and follicular lymphoma. <i>Cancer Epidemiology</i> , 2010, 34, 136-141.	1.9	6
51	Non-Homologous End-Joining Gene Profiling Reveals Distinct Expression Patterns Associated with Lymphoma and Multiple Myeloma. <i>British Journal of Haematology</i> , 2010, 149, 258-262.	2.5	15
52	A polymorphism in the 3' UTR of <i>IRF4</i> linked to susceptibility and pathogenesis in chronic lymphocytic leukaemia and Hodgkin lymphoma has limited impact in multiple myeloma. <i>British Journal of Haematology</i> , 2010, 150, 371-373.	2.5	8
53	Variant IRF4/MUM1 associates with CD38 status and treatment-free survival in chronic lymphocytic leukaemia. <i>Leukemia</i> , 2010, 24, 877-881.	7.2	18
54	Common variants at 2q37.3, 8q24.21, 15q21.3 and 16q24.1 influence chronic lymphocytic leukemia risk. <i>Nature Genetics</i> , 2010, 42, 132-136.	21.4	223

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55	Variation in CDKN2A at 9p21.3 influences childhood acute lymphoblastic leukemia risk. <i>Nature Genetics</i> , 2010, 42, 492-494.	21.4	248
56	Testicular Cancer Survivorship: Research Strategies and Recommendations. <i>Journal of the National Cancer Institute</i> , 2010, 102, 1114-1130.	6.3	260
57	The t(8;21) Fusion Protein AML1/ETO Promotes Susceptibility to Mutation In Acute Myeloid Leukemia.. <i>Blood</i> , 2010, 116, 3368-3368.	1.4	0
58	A Functional Polymorphism In the CD95 Cell Death Receptor Associated with Prognosis In Acute Promyelocytic Leukemia. <i>Blood</i> , 2010, 116, 756-756.	1.4	0
59	Cellular Response to Cytarabine Is Modulated by the DNA Mismatch Repair Pathway: Implications for Treatment of Acute Myeloid Leukemia. <i>Blood</i> , 2010, 116, 1819-1819.	1.4	0
60	Polymorphisms in the nucleotide excision repair gene ERCC2/XPD and risk of non-Hodgkin lymphoma. <i>Cancer Epidemiology</i> , 2009, 33, 257-260.	1.9	21
61	Loci on 7p12.2, 10q21.2 and 14q11.2 are associated with risk of childhood acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2009, 41, 1006-1010.	21.4	445
62	Association of Molecular Markers With Toxicity Outcomes in a Randomized Trial of Chemotherapy for Advanced Colorectal Cancer: The FOCUS Trial. <i>Journal of Clinical Oncology</i> , 2009, 27, 5519-5528.	1.6	120
63	Genome-wide association study to identify novel loci associated with therapy-related myeloid leukemia susceptibility. <i>Blood</i> , 2009, 113, 5575-5582.	1.4	93
64	MLH1 $\hat{\sim}$ 93G>A promoter polymorphism and risk of mismatch repair deficient colorectal cancer. <i>International Journal of Cancer</i> , 2008, 123, 2456-2459.	5.1	44
65	Influence of DNA repair gene polymorphisms on the initial repair of MMS–induced DNA damage in human lymphocytes as measured by the alkaline comet assay. <i>Environmental and Molecular Mutagenesis</i> , 2008, 49, 669-675.	2.2	7
66	A genome-wide association study identifies six susceptibility loci for chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2008, 40, 1204-1210.	21.4	329
67	Risk of Leukemia Among Survivors of Testicular Cancer: A Population-based Study of 42,722 Patients. <i>Annals of Epidemiology</i> , 2008, 18, 416-421.	1.9	55
68	The Genetics of Cancer Survivorship. <i>Hematology/Oncology Clinics of North America</i> , 2008, 22, 257-269.	2.2	2
69	MDM2 SNP309 and TP53 Arg72Pro interact to alter therapy-related acute myeloid leukemia susceptibility. <i>Blood</i> , 2008, 112, 741-749.	1.4	90
70	Genetic variation in genes expressed in the germinal center and risk of B cell lymphoma among Caucasians. <i>Haematologica</i> , 2008, 93, 1597-1600.	3.5	7
71	GENETIC SUSCEPTIBILITY TO RADIOGENIC CANCER IN HUMANS. <i>Health Physics</i> , 2008, 95, 677-686.	0.5	20
72	A Genome-Wide Analysis to Identify Novel Susceptibility Loci for Therapy-Related Acute Myeloid Leukemia. <i>Blood</i> , 2008, 112, 432-432.	1.4	1

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73	A common genetic variant in XPD associates with risk of 5q- and 7q-deleted acute myeloid leukemia. <i>Blood</i> , 2007, 109, 1233-1236.	1.4	23
74	RAG1 and BRCA2 polymorphisms in non-Hodgkin lymphoma. <i>Blood</i> , 2007, 109, 5522-5523.	1.4	4
75	Polymorphic MLH1 and risk of cancer after methylating chemotherapy for Hodgkin lymphoma. <i>Journal of Medical Genetics</i> , 2007, 45, 142-146.	3.2	37
76	RAD51 homologous recombination repair gene haplotypes and risk of acute myeloid leukaemia. <i>Leukemia Research</i> , 2007, 31, 169-174.	0.8	33
77	Cancer Survivorshipâ€™ Genetic Susceptibility and Second Primary Cancers: Research Strategies and Recommendations. <i>Journal of the National Cancer Institute</i> , 2006, 98, 15-25.	6.3	295
78	Molar pregnancy, childhood cancer and genomic imprinting â€“ is there a link?. <i>Human Fertility</i> , 2006, 9, 171-174.	1.7	7
79	Deregulation of homologous recombination DNA repair in alkylating agent-treated stem cell clones: a possible role in the aetiology of chemotherapy-induced leukaemia. <i>Oncogene</i> , 2006, 25, 1709-1720.	5.9	24
80	Acute Myeloid Leukemia Following Hodgkin Lymphoma: A Population-Based Study of 35â€™511 Patients. <i>Journal of the National Cancer Institute</i> , 2006, 98, 215-218.	6.3	84
81	Breast cancer risk following radiotherapy for Hodgkin lymphoma: modification by other risk factors. <i>Blood</i> , 2005, 106, 3358-3365.	1.4	101
82	Mechanisms of therapy-related carcinogenesis. <i>Nature Reviews Cancer</i> , 2005, 5, 943-955.	28.4	245
83	Genetic susceptibility to iatrogenic malignancy. <i>Pharmacogenomics</i> , 2005, 6, 615-628.	1.3	12
84	Risk of Non-Hodgkin Lymphoma Associated with Polymorphisms in Folate-Metabolizing Genes. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2005, 14, 2999-3003.	2.5	72
85	Application of DNA pooling to large studies of disease. <i>Statistics in Medicine</i> , 2004, 23, 3841-3850.	1.6	5
86	Genetic variation in XPD predicts treatment outcome and risk of acute myeloid leukemia following chemotherapy. <i>Blood</i> , 2004, 104, 3872-3877.	1.4	108
87	Poor metabolizer status at the cytochrome p450 2c19 and 2d6 loci does not modulate susceptibility to therapy-related acute myeloid leukaemia. <i>British Journal of Haematology</i> , 2003, 121, 192-194.	2.5	8
88	Gastric marginal zone lymphoma is associated with polymorphisms in genes involved in inflammatory response and antioxidative capacity. <i>Blood</i> , 2003, 102, 1007-1011.	1.4	79
89	Polymorphic variation in GSTP1 modulates outcome following therapy for multiple myeloma. <i>Blood</i> , 2003, 102, 2345-2350.	1.4	90
90	Functional FAS promoter polymorphisms are associated with increased risk of acute myeloid leukemia. <i>Cancer Research</i> , 2003, 63, 4327-30.	0.9	168

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91	An intron splice acceptor polymorphism in hMSH2 and risk of leukemia after treatment with chemotherapeutic alkylating agents. <i>Clinical Cancer Research</i> , 2003, 9, 3012-20.	7.0	63
92	Genetic alterations in bronchial mucosa and plasma DNA from individuals at high risk of lung cancer. <i>International Journal of Cancer</i> , 2001, 91, 359-365.	5.1	49
93	Polymorphisms of 5,10-methylenetetrahydrofolate reductase and risk of gastric cancer in a Chinese population: A case-control study. <i>International Journal of Cancer</i> , 2001, 95, 332-336.	5.1	119
94	Polymorphism in glutathione <i>S</i> -transferase P1 is associated with susceptibility to chemotherapy-induced leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 11592-11597.	7.1	233
95	The effect of hOGG1 and glutathione peroxidase I genotypes and 3p chromosomal loss on 8-hydroxydeoxyguanosine levels in lung cancer. <i>Carcinogenesis</i> , 2000, 21, 167-172.	2.8	73
96	DNA repair methyltransferase (Mgmt) knockout mice are sensitive to the lethal effects of chemotherapeutic alkylating agents. <i>Mutagenesis</i> , 1999, 14, 339-347.	2.6	129
97	3-methyladenine DNA glycosylases: structure, function, and biological importance. <i>BioEssays</i> , 1999, 21, 668-676.	2.5	173
98	3-methyladenine DNA glycosylases: structure, function, and biological importance. <i>BioEssays</i> , 1999, 21, 668-676.	2.5	3
99	A Chemical and Genetic Approach Together Define the Biological Consequences of 3-Methyladenine Lesions in the Mammalian Genome. <i>Journal of Biological Chemistry</i> , 1998, 273, 5412-5418.	3.4	115
100	Detection of DNA damage by <i>Escherichia coli</i> UvrB-binding competition assay is limited by the stability of the UvrB-DNA complex. <i>Carcinogenesis</i> , 1997, 18, 1407-1413.	2.8	4
101	Base excision repair deficient mice lacking the Aag 3-methyladenine DNA glycosylase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 13087-13092.	7.1	215
102	The <i>Escherichia coli</i> DNA repair protein UvrA can re-associate with the UvrB: aflatoxin B1-DNA complex in vitro. <i>Mutation Research DNA Repair</i> , 1996, 362, 261-268.	3.7	6
103	The use of purified DNA repair proteins to detect DNA damage. <i>Mutation Research - Environmental Mutagenesis and Related Subjects Including Methodology</i> , 1994, 313, 165-174.	0.4	6