

# Alistair M Chalk

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

7,679  
citations

218677  
26  
h-index

302126  
39  
g-index

41  
all docs

41  
docs citations

41  
times ranked

11686  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
2	Antisense Transcription in the Mammalian Transcriptome. <i>Science</i> , 2005, 309, 1564-1566.	12.6	1,553
3	RNA editing by ADAR1 prevents MDA5 sensing of endogenous dsRNA as nonself. <i>Science</i> , 2015, 349, 1115-1120.	12.6	661
4	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
5	Disease-specific, neurosphere-derived cells as models for brain disorders. <i>DMM Disease Models and Mechanisms</i> , 2010, 3, 785-798.	2.4	175
6	Rapid SNP diagnostics using asymmetric isothermal amplification and a new mismatch-suppression technology. <i>Nature Methods</i> , 2007, 4, 257-262.	19.0	161
7	Improved and automated prediction of effective siRNA. <i>Biochemical and Biophysical Research Communications</i> , 2004, 319, 264-274.	2.1	129
8	Genome-wide detection and analysis of hippocampus core promoters using DeepCAGE. <i>Genome Research</i> , 2009, 19, 255-265.	5.5	128
9	BET inhibitors induce apoptosis through a MYC independent mechanism and synergise with CDK inhibitors to kill osteosarcoma cells. <i>Scientific Reports</i> , 2015, 5, 10120.	3.3	103
10	A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. <i>Genomics</i> , 2008, 91, 281-288.	2.9	92
11	A Cross-Study Transcriptional Analysis of Parkinson's Disease. <i>PLoS ONE</i> , 2009, 4, e4955.	2.5	81
12	The majority of A-to-I RNA editing is not required for mammalian homeostasis. <i>Genome Biology</i> , 2019, 20, 268.	8.8	68
13	Alternate transcription of the Toll-like receptor signaling cascade. <i>Genome Biology</i> , 2006, 7, R10.	9.6	66
14	Modeling distinct osteosarcoma subtypes in vivo using Cre:lox and lineage-restricted transgenic shRNA. <i>Bone</i> , 2013, 55, 166-178.	2.9	65
15	Protein recoding by ADAR1-mediated RNA editing is not essential for normal development and homeostasis. <i>Genome Biology</i> , 2017, 18, 166.	8.8	64
16	Systematic Screening Identifies Dual PI3K and mTOR Inhibition as a Conserved Therapeutic Vulnerability in Osteosarcoma. <i>Clinical Cancer Research</i> , 2015, 21, 3216-3229.	7.0	58
17	siRNADB: a database of siRNA sequences. <i>Nucleic Acids Research</i> , 2004, 33, D131-D134.	14.5	57
18	<scp>ADAR1</scp>, inosine and the immune sensing system: distinguishing self from non-€self. <i>Wiley Interdisciplinary Reviews RNA</i> , 2016, 7, 157-172.	6.4	54

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19	Adenosine-to-inosine RNA editing by ADAR1 is essential for normal murine erythropoiesis. <i>Experimental Hematology</i> , 2016, 44, 947-963.	0.4	52
20	Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. <i>Genome Biology</i> , 2006, 7, R5.	9.6	48
21	The Rothmund-Thomson syndrome helicase RECQL4 is essential for hematopoiesis. <i>Journal of Clinical Investigation</i> , 2014, 124, 3551-3565.	8.2	48
22	Knockdown of PTHR1 in osteosarcoma cells decreases invasion and growth and increases tumor differentiation in vivo. <i>Oncogene</i> , 2015, 34, 2922-2933.	5.9	45
23	Srsf2 P95H initiates myeloid bias and myelodysplastic/myeloproliferative syndrome from hemopoietic stem cells. <i>Blood</i> , 2018, 132, 608-621.	1.4	45
24	Computational antisense oligo prediction with a neural network model. <i>Bioinformatics</i> , 2002, 18, 1567-1575.	4.1	41
25	Activation of PTHrP-cAMP-CREB1 signaling following p53 loss is essential for osteosarcoma initiation and maintenance. <i>ELife</i> , 2016, 5, .	6.0	38
26	RNAi Screen Indicates Widespread Biological Function for Human Natural Antisense Transcripts. <i>PLoS ONE</i> , 2010, 5, e13177.	2.5	35
27	Wnt inhibitory factor 1 (WIF1) is a marker of osteoblastic differentiation stage and is not silenced by DNA methylation in osteosarcoma. <i>Bone</i> , 2015, 73, 223-232.	2.9	27
28	Differential regulation of osteoadherin (OSAD) by TGF- $\beta$ 1 and BMP-2. <i>Biochemical and Biophysical Research Communications</i> , 2006, 349, 1057-1064.	2.1	25
29	Profiled support vector machines for antisense oligonucleotide efficacy prediction. <i>BMC Bioinformatics</i> , 2004, 5, 135.	2.6	24
30	The characterization of distinct populations of murine skeletal cells that have different roles in B lymphopoiesis. <i>Blood</i> , 2021, 138, 304-317.	1.4	20
31	The SKI proto-oncogene enhances the in vivo repopulation of hematopoietic stem cells and causes myeloproliferative disease. <i>Haematologica</i> , 2014, 99, 647-655.	3.5	18
32	siRNA specificity searching incorporating mismatch tolerance data. <i>Bioinformatics</i> , 2008, 24, 1316-1317.	4.1	17
33	Hematopoietic stem and progenitor cell-restricted Cdx2 expression induces transformation to myelodysplasia and acute leukemia. <i>Nature Communications</i> , 2020, 11, 3021.	12.8	15
34	Focusing on RISC assembly in mammalian cells. <i>Biochemical and Biophysical Research Communications</i> , 2008, 368, 703-708.	2.1	13
35	Defining the functions of adenosine-to-inosine RNA editing through hematology. <i>Current Opinion in Hematology</i> , 2019, 26, 241-248.	2.5	6
36	Sfixem--graphical sequence feature display in Java. <i>Bioinformatics</i> , 2004, 20, 2488-2490.	4.1	4

#	ARTICLE	IF	CITATIONS
37	siRNAdb: a database of siRNA sequences. Nucleic Acids Research, 2005, 33, 1737-1737.	14.5	4
38	Genome-wide screening identifies cell-cycle control as a synthetic lethal pathway with SRSF2P95H mutation. Blood Advances, 2022, 6, 2092-2106.	5.2	3
39	Gene expression profiling to define the cell intrinsic role of the SKI proto-oncogene in hematopoiesis and myeloid neoplasms. Genomics Data, 2014, 2, 189-191.	1.3	1
40	Using CAGE Data for Quantitative Expression. , 2009, , 101-121.		0