Ross A. Dickins

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Oncogenic cooperation between TCF7-SPI1 and NRAS(G12D) requires β-catenin activity to drive T-cell acute lymphoblastic leukemia. Nature Communications, 2021, 12, 4164.	12.8	9
2	Acute myeloid leukemia maturation lineage influences residual disease and relapse following differentiation therapy. Nature Communications, 2021, 12, 6546.	12.8	7
3	Rerouting DOT1L inhibitors in leukemia. Blood, 2020, 136, 1900-1901.	1.4	2
4	The EMT modulator SNAI1 contributes to AML pathogenesis via its interaction with LSD1. Blood, 2020, 136, 957-973.	1.4	35
5	Interconversion between Tumorigenic and Differentiated States in Acute Myeloid Leukemia. Cell Stem Cell, 2019, 25, 258-272.e9.	11.1	60
6	Conserved IKAROS-regulated genes associated with B-progenitor acute lymphoblastic leukemia outcome. Journal of Experimental Medicine, 2017, 214, 773-791.	8.5	27
7	Metabolic gatekeeper function of B-lymphoid transcription factors. Nature, 2017, 542, 479-483.	27.8	175
8	Id2 and E Proteins Orchestrate the Initiation and Maintenance of MLL-Rearranged Acute Myeloid Leukemia. Cancer Cell, 2016, 30, 59-74.	16.8	29
9	PU.1 cooperates with IRF4 and IRF8 to suppress pre-B-cell leukemia. Leukemia, 2016, 30, 1375-1387.	7.2	53
10	Humanizing the Protease-Activated Receptor (PAR) Expression Profile in Mouse Platelets by Knocking PAR1 into the Par3 Locus Reveals PAR1 Expression Is Not Tolerated in Mouse Platelets. PLoS ONE, 2016, 11, e0165565.	2.5	16
11	Activated Notch counteracts Ikaros tumor suppression in mouse and human T-cell acute lymphoblastic leukemia. Leukemia, 2015, 29, 1301-1311.	7.2	27
12	A transgenic mouse model to inducibly target prosurvival Bcl2 proteins with selective BH3 peptides in vivo. Cell Death and Disease, 2015, 6, e1679-e1679.	6.3	1
13	A pooled shRNA screen for regulators of primary mammary stem and progenitor cells identifies roles for Asap1 and Prox1. BMC Cancer, 2015, 15, 221.	2.6	31
14	The class II PI 3-kinase, PI3KC2α, links platelet internal membrane structure to shear-dependent adhesive function. Nature Communications, 2015, 6, 6535.	12.8	67
15	Efficacy of Retinoids in IKZF1-Mutated BCR-ABL1 Acute Lymphoblastic Leukemia. Cancer Cell, 2015, 28, 343-356.	16.8	145
16	Pro-apoptotic Bim suppresses breast tumor cell metastasis and is a target gene of SNAI2. Oncogene, 2015, 34, 3926-3934.	5.9	27
17	Knockdown of PTHR1 in osteosarcoma cells decreases invasion and growth and increases tumor differentiation in vivo. Oncogene, 2015, 34, 2922-2933.	5.9	45
18	Stage-specific control of early B cell development by the transcription factor Ikaros. Nature Immunology, 2014, 15, 283-293.	14.5	194

Ross A. DICKINS

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19	MLL3 Is a Haploinsufficient 7q Tumor Suppressor in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 652-665.	16.8	274
20	Pax5 loss imposes a reversible differentiation block in B-progenitor acute lymphoblastic leukemia. Genes and Development, 2014, 28, 1337-1350.	5.9	73
21	Combined Targeting of JAK2 and Bcl-2/Bcl-xL to Cure Mutant JAK2-Driven Malignancies and Overcome Acquired Resistance to JAK2 Inhibitors. Cell Reports, 2013, 5, 1047-1059.	6.4	116
22	Modeling distinct osteosarcoma subtypes in vivo using Cre:lox and lineage-restricted transgenic shRNA. Bone, 2013, 55, 166-178.	2.9	65
23	Molecular and Biologic Analysis of Histone Deacetylase Inhibitors with Diverse Specificities. Molecular Cancer Therapeutics, 2013, 12, 2709-2721.	4.1	45
24	The genomic landscape of hypodiploid acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 242-252.	21.4	588
25	Variability of Inducible Expression across the Hematopoietic System of Tetracycline Transactivator Transgenic Mice. PLoS ONE, 2013, 8, e54009.	2.5	26
26	A pipeline for the generation of shRNA transgenic mice. Nature Protocols, 2012, 7, 374-393.	12.0	146
27	A Rapid and Scalable System for Studying Gene Function in Mice Using Conditional RNA Interference. Cell, 2011, 145, 145-158.	28.9	278
28	Functional Identification of Optimized RNAi Triggers Using a Massively Parallel Sensor Assay. Molecular Cell, 2011, 41, 733-746.	9.7	193
29	IL-10 Controls Cystatin C Synthesis and Blood Concentration in Response to Inflammation through Regulation of IFN Regulatory Factor 8 Expression. Journal of Immunology, 2011, 186, 3666-3673.	0.8	43
30	Dissecting the Unique Role of the Retinoblastoma Tumor Suppressor during Cellular Senescence. Cancer Cell, 2010, 17, 376-387.	16.8	323
31	Transgenic, inducible RNAi in megakaryocytes and platelets in mice. Journal of Thrombosis and Haemostasis, 2010, 8, 2751-2756.	3.8	11
32	Senescence of Activated Stellate Cells Limits Liver Fibrosis. Cell, 2008, 134, 657-667.	28.9	1,597
33	Senescence of Activated Stellate Cells Limits Liver Fibrosis. Cell, 2008, 135, 190.	28.9	8
34	ARF functions as a melanoma tumor suppressor by inducing p53-independent senescence. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10968-10973.	7.1	140
35	Tissue-specific and reversible RNA interference in transgenic mice. Nature Genetics, 2007, 39, 914-921.	21.4	170
36	Senescence and tumour clearance is triggered by p53 restoration in murine liver carcinomas. Nature, 2007, 445, 656-660.	27.8	2,159

Ross A. DICKINS

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37	Role of genomic instability and p53 in AID-induced c-myc–Igh translocations. Nature, 2006, 440, 105-109.	27.8	315
38	Trp53 loss during in vitro selection contributes to acquired Ara-C resistance in acute myeloid leukemia. Experimental Hematology, 2006, 34, 631-641.	0.4	36
39	Probing tumor phenotypes using stable and regulated synthetic microRNA precursors. Nature Genetics, 2005, 37, 1289-1295.	21.4	500
40	Drosophila Hfp negatively regulates dmyc and stg to inhibit cell proliferation. Development (Cambridge), 2004, 131, 1411-1423.	2.5	34
41	Generation and Analysis of Siah2 Mutant Mice. Molecular and Cellular Biology, 2003, 23, 9150-9161.	2.3	69
42	The Ubiquitin Ligase Component Siah1a Is Required for Completion of Meiosis I in Male Mice. Molecular and Cellular Biology, 2002, 22, 2294-2303.	2.3	99
43	Normal p53 Function in Primary Cells Deficient for Siah Genes. Molecular and Cellular Biology, 2002, 22, 8155-8164.	2.3	33
44	shRNA-seq data analysis with edgeR. F1000Research, 0, 3, 95.	1.6	43