Amit U Sinha

List of Publications by Year
in descending order

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25 papers	3,892 citations	516710 16 h-index	677142 22 g-index
25 all docs	25 docs citations	25 times ranked	6651 citing authors

#	Article	IF	Citations
1	MLL1 and DOT1L cooperate with meningioma-1 to induce acute myeloid leukemia. Journal of Clinical Investigation, 2016, 126, 1438-1450.	8.2	33
2	MLL-AF9â€“ and HOXA9-mediated acute myeloid leukemia stem cell self-renewal requires JMJD1C. Journal of Clinical Investigation, 2016, 126, 997-1011.	8.2	69
3	DOT1L inhibits SIRT1-mediated epigenetic silencing to maintain leukemic gene expression in MLL-rearranged leukemia. Nature Medicine, 2015, 21, 335-343.	30.7	200
4	AF10 Regulates Progressive H3K79 Methylation and HOX Gene Expression in Diverse AML Subtypes. Cancer Cell, 2014, 26, 896-908.	16.8	153
5	Mutations in epigenetic regulators including SETD2 are gained during relapse in paediatric acute lymphoblastic leukaemia. Nature Communications, 2014, 5, 3469.	12.8	171
6	Leukemic transformation by the MLL-AF6 fusion oncogene requires the H3K79 methyltransferase Dot1l. Blood, 2013, 121, 2533-2541.	1.4	149
7	Myeloid Leukemia Cells With MLL partial Tandem Duplication Are Sensitive To Pharmacological Inhibition Of The H3K79 Methyltransferase DOT1L. Blood, 2013, 122, 1256-1256.	1.4	35
8	Regulation Of Normal and Malignant Hoxa Gene Expression Through Higher H3K79 Methylated States. Blood, 2013, 122, 2492-2492.	1.4	2
9	Genome-Wide RNAi Screen Identifies The Mechanistic Role For DOT1L In MLL-Rearranged Leukemia. Blood, 2013, 122, 598-598.	1.4	4
10	Haploinsufficiency of Dnmt1 impairs leukemia stem cell function through derepression of bivalent chromatin domains. Genes and Development, 2012, 26, 344-349.	5.9	121
11	Polycomb repressive complex 2 is required for MLL-AF9 leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5028-5033.	7.1	198
12	iCanPlot: Visual Exploration of High-Throughput Omics Data Using Interactive Canvas Plotting. PLoS ONE, 2012, 7, e31690.	2.5	9
13	Chromatin-modifying enzymes as modulators of reprogramming. Nature, 2012, 483, 598-602.	27.8	583
14	The Interaction Between DOT1L and AF10 Is Required for H3K79 Dimethylation and MLL-AF9 Leukemia. Blood, 2012, 120, 401-401.	1.4	0
15	MLL-Rearranged Leukemia Is Dependent on Aberrant H3K79 Methylation by DOT1L. Cancer Cell, 2011, 20, 66-78.	16.8	791
16	eXframe: reusable framework for storage, analysis and visualization of genomics experiments. BMC Bioinformatics, 2011, 12, 452.	2.6	5
17	Haploinsufficiency of Dnmt1 Impairs Leukemia Stem Cell Function Through Derepression of Bivalent Chromatin Domains,. Blood, 2011, 118, 3459-3459.	1.4	3
18	MLL-Rearranged B Lymphoblastic Leukemias Selectively Express the Immunoregulatory Carbohydrate-Binding Protein Galectin-1. Clinical Cancer Research, 2010, 16, 2122-2130.	7.0	39

#	Article	IF	Citations
19	The Wnt/Î²-Catenin Pathway Is Required for the Development of Leukemia Stem Cells in AML. Science, 2010, 327, 1650-1653.	12.6	675
20	Dissecting microregulation of a master regulatory network. BMC Genomics, 2008, 9, 88.	2.8	36
21	H3K79 Methylation Profiles Define Murine and Human MLL-AF4 Leukemias. Cancer Cell, 2008, 14, 355-368.	16.8	494
22	Sensitivity analysis for reversal distance and breakpoint reuse in genome rearrangements. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 37-48.	0.7	5
23	Identifying Functional Binding Motifs of Tumor Protein p53 Using Support Vector Machines. , 2007, , .		3
24	Cinteny: flexible analysis and visualization of synteny and genome rearrangements in multiple organisms. BMC Bioinformatics, 2007, 8, 82.	2.6	112
25	SENSITIVITY ANALYSIS FOR REVERSAL DISTANCE AND BREAKPOINT REUSE IN GENOME REARRANGEMENTS. , 2007, , .		2