Marjorie Brand

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Dynamic changes in transcription factor complexes during erythroid differentiation revealed by quantitative proteomics. Nature Structural and Molecular Biology, 2004, 11, 73-80.	3.6	199
2	Activator-Mediated Recruitment of the MLL2 Methyltransferase Complex to the β-Globin Locus. Molecular Cell, 2007, 27, 573-584.	4.5	122
3	Differential genomic targeting of the transcription factor TAL1 in alternate haematopoietic lineages. EMBO Journal, 2011, 30, 494-509.	3.5	120
4	UTX inhibition as selective epigenetic therapy against TAL1-driven T-cell acute lymphoblastic leukemia. Genes and Development, 2016, 30, 508-521.	2.7	104
5	Single-Cell Proteomics Reveal that Quantitative Changes in Co-expressed Lineage-Specific Transcription Factors Determine Cell Fate. Cell Stem Cell, 2019, 24, 812-820.e5.	5.2	99
6	Analysis of epigenetic modifications of chromatin at specific gene loci by native chromatin immunoprecipitation of nucleosomes isolated using hydroxyapatite chromatography. Nature Protocols, 2008, 3, 398-409.	5.5	92
7	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. Molecular Cell, 2020, 78, 960-974.e11.	4.5	83
8	UTX demethylase activity is required for satellite cell–mediated muscle regeneration. Journal of Clinical Investigation, 2016, 126, 1555-1565.	3.9	74
9	Micro-RNA Profiling of Exosomes from Marrow-Derived Mesenchymal Stromal Cells in Patients with Acute Myeloid Leukemia: Implications in Leukemogenesis. Stem Cell Reviews and Reports, 2017, 13, 817-825.	5.6	65
10	Trichostatin A Enhances Vascular Repair by Injected Human Endothelial Progenitors through Increasing the Expression of TAL1-Dependent Genes. Cell Stem Cell, 2014, 14, 644-657.	5.2	48
11	Polycomb/Trithorax Antagonism: Cellular Memory in Stem Cell Fate and Function. Cell Stem Cell, 2019, 24, 518-533.	5.2	48
12	A phosphorylation switch on RbBP5 regulates histone H3 Lys4 methylation. Genes and Development, 2015, 29, 123-128.	2.7	42
13	Molecular Basis for DPY-30 Association to COMPASS-like and NURF Complexes. Structure, 2014, 22, 1821-1830.	1.6	40
14	Epigenetic Activation of Pro-angiogenic Signaling Pathways in Human Endothelial Progenitors Increases Vasculogenesis. Stem Cell Reports, 2017, 9, 1573-1587.	2.3	36
15	Adipogenic Mesenchymal Stromal Cells from Bone Marrow and Their Hematopoietic Supportive Role: Towards Understanding the Permissive Marrow Microenvironment in Acute Myeloid Leukemia. Stem Cell Reviews and Reports, 2016, 12, 235-244.	5.6	34
16	Single-cell profiling of human bone marrow progenitors reveals mechanisms of failing erythropoiesis in Diamond-Blackfan anemia. Science Translational Medicine, 2021, 13, eabf0113.	5.8	32
17	Structural Analysis of the Ash2L/Dpy-30 Complex Reveals a Heterogeneity in H3K4 Methylation. Structure, 2018, 26, 1594-1603.e4.	1.6	26
18	A non-canonical role for the proneural gene <i>Neurog1</i> as a negative regulator of neocortical neurogenesis. Development (Cambridge), 2018, 145, .	1.2	24

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19	Lineage commitment of hematopoietic stem cells and progenitors: insights from recent single cell and lineage tracing technologies. Experimental Hematology, 2020, 88, 1-6.	0.2	21
20	Alteration of CTCF-associated chromatin neighborhood inhibits TAL1-driven oncogenic transcription program and leukemogenesis. Nucleic Acids Research, 2020, 48, 3119-3133.	6.5	19
21	<scp>KMT</scp> 1 family methyltransferases regulate heterochromatin–nuclear periphery tethering via histone and nonâ€histone protein methylation. EMBO Reports, 2019, 20, .	2.0	18
22	Negative elongation factor regulates muscle progenitor expansion for efficient myofiber repair and stem cell pool repopulation. Developmental Cell, 2021, 56, 1014-1029.e7.	3.1	18
23	Lentiviral-mediated Knockdown During Ex Vivo Erythropoiesis of Human Hematopoietic Stem Cells. Journal of Visualized Experiments, 2011, , .	0.2	14
24	Single-cell fate decisions of bipotential hematopoietic progenitors. Current Opinion in Hematology, 2020, 27, 232-240.	1.2	13
25	Recapitulation of erythropoiesis in congenital dyserythropoietic anemia type I (CDA-I) identifies defects in differentiation and nucleolar abnormalities. Haematologica, 2021, 106, 2960-2970.	1.7	10
26	Recombinant Human Collagen Hydrogel Rapidly Reduces Methylglyoxal Adducts within Cardiomyocytes and Improves Borderzone Contractility after Myocardial Infarction in Mice. Advanced Functional Materials, 2022, 32, .	7.8	9
27	An international effort to cure a global health problem: A report on the 19th Hemoglobin Switching Conference. Experimental Hematology, 2015, 43, 821-837.	0.2	7
28	Proteomic/transcriptomic analysis of erythropoiesis. Current Opinion in Hematology, 2021, 28, 150-157.	1.2	5
29	Chromatin and transcription factor profiling in rare stem cell populations using CUT&Tag. STAR Protocols, 2021, 2, 100751.	0.5	5
30	Absolute quantification of transcription factors in human erythropoiesis using selected reaction monitoring mass spectrometry. STAR Protocols, 2020, 1, 100216.	0.5	4
31	TFII-I/Gtf2i and Erythro-Megakaryopoiesis. Frontiers in Physiology, 2020, 11, 590180.	1.3	3
32	Splicing of Ezh1 gets muscle out of stressful situations. Nature Structural and Molecular Biology, 2017, 24, 435-437.	3.6	2
33	Epigenetic plasticity of erythroid progenitors. Blood, 2021, 138, 1646-1648.	0.6	1
34	Pharmacologic control of chromatin looping. Blood, 2015, 126, 569-570.	0.6	0
35	Understanding Erythropoiesis Using Quantitative Proteomics and Single Cell Mass Cytometry. Blood, 2019, 134, SCI-21-SCI-21.	0.6	Ο
36	Single-Cell Transcriptional Landscapes of Human Bone Marrow Reveal Distinct Erythroid Phenotypes Underpinned By Genotype in Diamond-Blackfan Anemia. Blood, 2020, 136, 1-2.	0.6	0