

Cheryl A Keller

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

5,883
citations

186265
28
h-index

182427
51
g-index

67
all docs

67
docs citations

67
times ranked

10714
citing authors

#	ARTICLE	IF	CITATIONS
1	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444
2	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
3	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418.	9.6	410
4	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	27.8	259
5	The $\alpha 2$ Subunit of GABAA Receptors Is a Substrate for Palmitoylation by GODZ. <i>Journal of Neuroscience</i> , 2004, 24, 5881-5891.	3.6	225
6	Chromatin structure dynamics during the mitosis-to-G1 phase transition. <i>Nature</i> , 2019, 576, 158-162.	27.8	167
7	GODZ-Mediated Palmitoylation of GABAA Receptors Is Required for Normal Assembly and Function of GABAergic Inhibitory Synapses. <i>Journal of Neuroscience</i> , 2006, 26, 12758-12768.	3.6	148
8	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
9	Domain-focused CRISPR screen identifies HRI as a fetal hemoglobin regulator in human erythroid cells. <i>Science</i> , 2018, 361, 285-290.	12.6	119
10	Transcriptional Burst Initiation and Polymerase Pause Release Are Key Control Points of Transcriptional Regulation. <i>Molecular Cell</i> , 2019, 73, 519-532.e4.	9.7	118
11	The BET Protein BRD2 Cooperates with CTCF to Enforce Transcriptional and Architectural Boundaries. <i>Molecular Cell</i> , 2017, 66, 102-116.e7.	9.7	114
12	Comparative analysis of three-dimensional chromosomal architecture identifies a novel fetal hemoglobin regulatory element. <i>Genes and Development</i> , 2017, 31, 1704-1713.	5.9	113
13	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. <i>Genome Research</i> , 2011, 21, 1659-1671.	5.5	110
14	Genome accessibility is widely preserved and locally modulated during mitosis. <i>Genome Research</i> , 2015, 25, 213-225.	5.5	103
15	Occupancy by key transcription factors is a more accurate predictor of enhancer activity than histone modifications or chromatin accessibility. <i>Epigenetics and Chromatin</i> , 2015, 8, 16.	3.9	100
16	Functions of BET proteins in erythroid gene expression. <i>Blood</i> , 2015, 125, 2825-2834.	1.4	93
17	A hyperactive transcriptional state marks genome reactivation at the mitosis-to-G1 transition. <i>Genes and Development</i> , 2016, 30, 1423-1439.	5.9	92
18	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. <i>Genome Research</i> , 2014, 24, 1932-1944.	5.5	88

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19	Dynamic shifts in occupancy by TAL1 are guided by GATA factors and drive large-scale reprogramming of gene expression during hematopoiesis. <i>Genome Research</i> , 2014, 24, 1945-1962.	5.5	71
20	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. <i>Cell Reports</i> , 2021, 34, 108783.	6.4	53
21	Interrogating Histone Acetylation and BRD4 as Mitotic Bookmarks of Transcription. <i>Cell Reports</i> , 2019, 27, 400-415.e5.	6.4	52
22	Establishment of regulatory elements during erythro-megakaryopoiesis identifies hematopoietic lineage-commitment points. <i>Epigenetics and Chromatin</i> , 2018, 11, 22.	3.9	49
23	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. <i>Molecular Cell</i> , 2021, 81, 239-254.e8.	9.7	48
24	Loss-of-Function Mutations Reveal That the <i>Drosophila nautilus</i> Gene Is Not Essential for Embryonic Myogenesis or Viability. <i>Developmental Biology</i> , 2001, 231, 374-382.	2.0	44
25	The HRI-regulated transcription factor ATF4 activates BCL11A transcription to silence fetal hemoglobin expression. <i>Blood</i> , 2020, 135, 2121-2132.	1.4	42
26	Misexpression of <i>nautilus</i> Induces Myogenesis in Cardioblasts and Alters the Pattern of Somatic Muscle Fibers. <i>Developmental Biology</i> , 1997, 181, 197-212.	2.0	40
27	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , 2020, 30, 472-484.	5.5	38
28	Exploiting genetic variation to uncover rules of transcription factor binding and chromatin accessibility. <i>Nature Communications</i> , 2018, 9, 782.	12.8	36
29	Alteration of genome folding via contact domain boundary insertion. <i>Nature Genetics</i> , 2020, 52, 1076-1087.	21.4	35
30	Genome-Wide Organization of GATA1 and TAL1 Determined at High Resolution. <i>Molecular and Cellular Biology</i> , 2016, 36, 157-172.	2.3	32
31	CTCF and transcription influence chromatin structure re-configuration after mitosis. <i>Nature Communications</i> , 2021, 12, 5157.	12.8	32
32	S3norm: simultaneous normalization of sequencing depth and signal-to-noise ratio in epigenomic data. <i>Nucleic Acids Research</i> , 2020, 48, e43-e43.	14.5	31
33	Understanding heterogeneity of fetal hemoglobin induction through comparative analysis of F and A erythroblasts. <i>Blood</i> , 2020, 135, 1957-1968.	1.4	30
34	Frequent somatic <i>TET2</i> mutations in chronic NK-LGL leukemia with distinct patterns of cytopenias. <i>Blood</i> , 2021, 138, 662-673.	1.4	30
35	The E3 ligase adaptor molecule SPOP regulates fetal hemoglobin levels in adult erythroid cells. <i>Blood Advances</i> , 2019, 3, 1586-1597.	5.2	25
36	Protein Phosphatase 6C (PPP6C) Loss Significantly Raises Fetal Hemoglobin Levels and Reduces Cell Sickling. <i>Blood</i> , 2021, 138, 2031-2031.	1.4	18

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37	HRI depletion cooperates with pharmacologic inducers to elevate fetal hemoglobin and reduce sickle cell formation. Blood Advances, 2020, 4, 4560-4572.	5.2	15
38	Ubiquitination, proteasomes and GABAA receptors. Nature Cell Biology, 2001, 3, E232-E233.	10.3	14
39	Dual function NFI factors control fetal hemoglobin silencing in adult erythroid cells. Nature Genetics, 2022, 54, 874-884.	21.4	13
40	Dynamics of GATA1 binding and expression response in a GATA1-induced erythroid differentiation system. Genomics Data, 2015, 4, 1-7.	1.3	10
41	Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells. IUBMB Life, 2020, 72, 27-38.	3.4	8
42	Comparison of Expression and Epigenetic Profiles in Human and Mouse Erythropoiesis and Megakaryopoiesis Using a Systems Biology Model. Blood, 2015, 126, 2383-2383.	1.4	5
43	Identification and characterization of RBM12 as a novel regulator of fetal hemoglobin expression. Blood Advances, 2022, 6, 5956-5968.	5.2	5
44	SBR-Blood: systems biology repository for hematopoietic cells. Nucleic Acids Research, 2016, 44, D925-D931.	14.5	4
45	Effects of sheared chromatin length on ChIP-seq quality and sensitivity. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	3
46	HIC2 Controls Developmental Hemoglobin Switching By Repressing BCL11A Transcription. Blood, 2021, 138, 571-571.	1.4	2
47	Control of Fetal Hemoglobin Levels By NFI Transcription Factors. Blood, 2020, 136, 54-54.	1.4	2
48	De Novo DNA Methylation Is Associated with Granulopoiesis and Megakaryopoiesis but Not Erythropoiesis. Blood, 2016, 128, 3868-3868.	1.4	1
49	Epigenetics of Cellular Memory: Insights from the Chromatin Accessibility Landscape of the Mitotic Genome. Blood, 2014, 124, 4342-4342.	1.4	1
50	Isolated Changes in Chromatin Accessibility and Enhancer-Promoter Contacts at the β -Globin Locus Distinguish Fetal Hemoglobin Producing F-Cells from a-Cells. Blood, 2021, 138, 855-855.	1.4	1
51	Systems Biology in Heterogenous Tissues: Integrating Multiple *Omics Datasets to Understand Hematopoietic Differentiation. , 2019, , .		0
52	Enhancer Accessibility during Erythropoiesis and Megakaryopoiesis Correlates with Lineage-Specific Gene Expression. Blood, 2015, 126, 3576-3576.	1.4	0
53	Establishment of Enhancer Elements during Erythro-Megakaryopoiesis. Blood, 2016, 128, 1486-1486.	1.4	0
54	Mouse Erythroid Cells Originate from a Megakaryocyte Precursor in Common Myeloid Progenitors. Blood, 2019, 134, 337-337.	1.4	0

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55	Interrogating Post-Transcriptional Mechanisms of Fetal Hemoglobin Regulation. Blood, 2021, 138, 3079-3079.	1.4	0
56	A γ^2 -Globin Locus-Intrinsic Epigenetic Mechanism Underlies Fetal Globin Production in F-Cells. Blood, 2020, 136, 16-17.	1.4	0
57	Systematic Integration of Epigenomic Landscapes in Human and Mouse Blood Cells to Predict Activity and Targets of Regulatory Elements. FASEB Journal, 2022, 36, .	0.5	0