Cheryl A Keller

List of Publications by Year
in descending order

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	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
2	Identification and characterization of RBM12 as a novel regulator ofÂfetal hemoglobin expression. Blood Advances, 2022, 6, 5956-5968.	5.2	5
3	Dual function NFI factors control fetal hemoglobin silencing in adult erythroid cells. Nature Genetics, 2022, 54, 874-884.	21.4	13
4	ZNF410ÂUniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. Molecular Cell, 2021, 81, 239-254.e8.	9.7	48
5	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. Cell Reports, 2021, 34, 108783.	6.4	53
6	Frequent somatic TET2 mutations in chronic NK-LGL leukemia with distinct patterns of cytopenias. Blood, 2021, 138, 662-673.	1.4	30
7	Effects of sheared chromatin length on ChIP-seq quality and sensitivity. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	3
8	CTCF and transcription influence chromatin structure re-configuration after mitosis. Nature Communications, 2021, 12, 5157.	12.8	32
9	Protein Phosphatase 6C (PPP6C) Loss Significantly Raises Fetal Hemoglobin Levels and Reduces Cell Sickling. Blood, 2021, 138, 2031-2031.	1.4	18
10	Isolated Changes in Chromatin Accessibility and Enhancer-Promoter Contacts at the Î²-Globin Locus Distinguish Fetal Hemoglobin Producing F-Cells from a-Cells. Blood, 2021, 138, 855-855.	1.4	1
11	Interrogating Post-Transcriptional Mechanisms of Fetal Hemoglobin Regulation. Blood, 2021, 138, 3079-3079.	1.4	0
12	HIC2 Controls Developmental Hemoglobin Switching By Repressing BCL11A Transcription. Blood, 2021, 138, 571-571.	1.4	2
13	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
14	HRI depletion cooperates with pharmacologic inducers to elevate fetal hemoglobin and reduce sickle cell formation. Blood Advances, 2020, 4, 4560-4572.	5.2	15
15	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
16	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
17	Alteration of genome folding via contact domain boundary insertion. Nature Genetics, 2020, 52, 1076-1087.	21.4	35
18	Understanding heterogeneity of fetal hemoglobin induction through comparative analysis of F and A erythroblasts. Blood, 2020, 135, 1957-1968.	1.4	30

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19	The HRI-regulated transcription factor ATF4 activates BCL11A transcription to silence fetal hemoglobin expression. Blood, 2020, 135, 2121-2132.	1.4	42
20	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. Genome Research, 2020, 30, 472-484.	5.5	38
21	S3norm: simultaneous normalization of sequencing depth and signal-to-noise ratio in epigenomic data. Nucleic Acids Research, 2020, 48, e43-e43.	14.5	31
22	A Î²-Globin Locus-Intrinsic Epigenetic Mechanism Underlies Fetal Globin Production in F-Cells. Blood, 2020, 136, 16-17.	1.4	0
23	Control of Fetal Hemoglobin Levels By NFI Transcription Factors. Blood, 2020, 136, 54-54.	1.4	2
24	Interrogating Histone Acetylation and BRD4 as Mitotic Bookmarks of Transcription. Cell Reports, 2019, 27, 400-415.e5.	6.4	52
25	Systems Biology in Heterogenous Tissues: Integrating Multiple *Omics Datasets to Understand Hematopoietic Differentiation. , 2019, , .		0
26	The E3 ligase adaptor molecule SPOP regulates fetal hemoglobin levels in adult erythroid cells. Blood Advances, 2019, 3, 1586-1597.	5.2	25
27	Chromatin structure dynamics during the mitosis-to-G1 phase transition. Nature, 2019, 576, 158-162.	27.8	167
28	Transcriptional Burst Initiation and Polymerase Pause Release Are Key Control Points of Transcriptional Regulation. Molecular Cell, 2019, 73, 519-532.e4.	9.7	118
29	Mouse Erythroid Cells Originate from a Megakaryocyte Precursor in Common Myeloid Progenitors. Blood, 2019, 134, 337-337.	1.4	0
30	Exploiting genetic variation to uncover rules of transcription factor binding and chromatin accessibility. Nature Communications, 2018, 9, 782.	12.8	36
31	Establishment of regulatory elements during erythro-megakaryopoiesis identifies hematopoietic lineage-commitment points. Epigenetics and Chromatin, 2018, 11, 22.	3.9	49
32	Domain-focused CRISPR screen identifies HRI as a fetal hemoglobin regulator in human erythroid cells. Science, 2018, 361, 285-290.	12.6	119
33	The BET Protein BRD2 Cooperates with CTCF to Enforce Transcriptional and Architectural Boundaries. Molecular Cell, 2017, 66, 102-116.e7.	9.7	114
34	Comparative analysis of three-dimensional chromosomal architecture identifies a novel fetal hemoglobin regulatory element. Genes and Development, 2017, 31, 1704-1713.	5.9	113
35	A hyperactive transcriptional state marks genome reactivation at the mitosisâ€“G1 transition. Genes and Development, 2016, 30, 1423-1439.	5.9	92
36	Genome-Wide Organization of GATA1 and TAL1 Determined at High Resolution. Molecular and Cellular Biology, 2016, 36, 157-172.	2.3	32

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37	SBR-Blood: systems biology repository for hematopoietic cells. Nucleic Acids Research, 2016, 44, D925-D931.	14.5	4
38	De Novo DNA Methylation Is Associated with Granulopoiesis and Megakaryopoiesis but Not Erythropoiesis. Blood, 2016, 128, 3868-3868.	1.4	1
39	Establishment of Enhancer Elements during Erythro-Megakaryopoiesis. Blood, 2016, 128, 1486-1486.	1.4	0
40	Occupancy by key transcription factors is a more accurate predictor of enhancer activity than histone modifications or chromatin accessibility. Epigenetics and Chromatin, 2015, 8, 16.	3.9	100
41	Functions of BET proteins in erythroid gene expression. Blood, 2015, 125, 2825-2834.	1.4	93
42	Dynamics of GATA1 binding and expression response in a GATA1-induced erythroid differentiation system. Genomics Data, 2015, 4, 1-7.	1.3	10
43	Genome accessibility is widely preserved and locally modulated during mitosis. Genome Research, 2015, 25, 213-225.	5.5	103
44	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
45	Enhancer Accessibility during Erythropoiesis and Megakaryopoiesis Correlates with Lineage-Specific Gene Expression. Blood, 2015, 126, 3576-3576.	1.4	0
46	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. Genome Research, 2014, 24, 1932-1944.	5.5	88
47	Dynamic shifts in occupancy by TAL1 are guided by GATA factors and drive large-scale reprogramming of gene expression during hematopoiesis. Genome Research, 2014, 24, 1945-1962.	5.5	71
48	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	27.8	259
49	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
50	Epigenetics of Cellular Memory: Insights from the Chromatin Accessibility Landscape of the Mitotic Genome. Blood, 2014, 124, 4342-4342.	1.4	1
51	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	9.6	410
52	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671.	5.5	110
53	GODZ-Mediated Palmitoylation of GABAA Receptors Is Required for Normal Assembly and Function of GABAergic Inhibitory Synapses. Journal of Neuroscience, 2006, 26, 12758-12768.	3.6	148
54	The Â2 Subunit of GABAA Receptors Is a Substrate for Palmitoylation by GODZ. Journal of Neuroscience, 2004, 24, 5881-5891.	3.6	225

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55	Loss-of-Function Mutations Reveal That the Drosophila nautilus Gene Is Not Essential for Embryonic Myogenesis or Viability. Developmental Biology, 2001, 231, 374-382.	2.0	44
56	Ubiquitination, proteasomes and GABAA receptors. Nature Cell Biology, 2001, 3, E232-E233.	10.3	14
57	Misexpression ofnautilusInduces Myogenesis in Cardioblasts and Alters the Pattern of Somatic Muscle Fibers. Developmental Biology, 1997, 181, 197-212.	2.0	40