Belinda M Giardine

List of Publications by Year
in descending order

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60 papers	8,076 citations	136950 32 h-index	182427 51 g-index
69 all docs	69 docs citations	69 times ranked	15261 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	Clinically relevant updates of the HbVar database of human hemoglobin variants and thalassemia mutations. Nucleic Acids Research, 2021, 49, D1192-D1196.	14.5	62
5	ZNF410ÂUniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. Molecular Cell, 2021, 81, 239-254.e8.	9.7	48
6	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. Cell Reports, 2021, 34, 108783.	6.4	53
7	Effects of sheared chromatin length on ChIP-seq quality and sensitivity. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	3
8	S3V2-IDEAS: a package for normalizing, denoising and integrating epigenomic datasets across different cell types. Bioinformatics, 2021, 37, 3011-3013.	4.1	5
9	CTCF and transcription influence chromatin structure re-configuration after mitosis. Nature Communications, 2021, 12, 5157.	12.8	32
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	Alteration of genome folding via contact domain boundary insertion. Nature Genetics, 2020, 52, 1076-1087.	21.4	35
17	Understanding heterogeneity of fetal hemoglobin induction through comparative analysis of F and A erythroblasts. Blood, 2020, 135, 1957-1968.	1.4	30
18	The HRI-regulated transcription factor ATF4 activates BCL11A transcription to silence fetal hemoglobin expression. Blood, 2020, 135, 2121-2132.	1.4	42

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19	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. Genome Research, 2020, 30, 472-484.	5.5	38
20	S3norm: simultaneous normalization of sequencing depth and signal-to-noise ratio in epigenomic data. Nucleic Acids Research, 2020, 48, e43-e43.	14.5	31
21	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. Blood, 2020, 136, 54-54.	1.4	1
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	Heme-Regulated Inhibitor (HRI) Activates Transcription Factor ATF4 to Promote BCL11A Transcription and Fetal Hemoglobin Silencing. Blood, 2019, 134, 814-814.	1.4	5
31	Understanding Heterogeneity of Fetal Hemoglobin Induction through Comparative Analysis of Stage-Matched F- and a-Cells. Blood, 2019, 134, 981-981.	1.4	0
32	Establishment of regulatory elements during erythro-megakaryopoiesis identifies hematopoietic lineage-commitment points. Epigenetics and Chromatin, 2018, 11, 22.	3.9	49
33	Domain-focused CRISPR screen identifies HRI as a fetal hemoglobin regulator in human erythroid cells. Science, 2018, 361, 285-290.	12.6	119
34	The BET Protein BRD2 Cooperates with CTCF to Enforce Transcriptional and Architectural Boundaries. Molecular Cell, 2017, 66, 102-116.e7.	9.7	114
35	Comparative analysis of three-dimensional chromosomal architecture identifies a novel fetal hemoglobin regulatory element. Genes and Development, 2017, 31, 1704-1713.	5.9	113
36	Comparison of Fetal and Adult Erythroid Chromosomal Architectures Identifies a Novel Fetal Hemoglobin Regulatory Region. Blood, 2017, 130, 774-774.	1.4	0

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37	A hyperactive transcriptional state marks genome reactivation at the mitosisâ€“G1 transition. Genes and Development, 2016, 30, 1423-1439.	5.9	92
38	The BET Protein BRD2 Cooperates with CTCF to Enforce a Transcriptional Boundary in Erythroid Cells. Blood, 2016, 128, 1034-1034.	1.4	0
39	Functions of BET proteins in erythroid gene expression. Blood, 2015, 125, 2825-2834.	1.4	93
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	Genome accessibility is widely preserved and locally modulated during mitosis. Genome Research, 2015, 25, 213-225.	5.5	103
42	A Hyperactive Transcriptional State Marks Genome Reactivation during Mitotic Exit. Blood, 2015, 126, 48-48.	1.4	0
43	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	27.8	259
44	Updates of the HbVar database of human hemoglobin variants and thalassemia mutations. Nucleic Acids Research, 2014, 42, D1063-D1069.	14.5	361
45	Epigenetics of Cellular Memory: Insights from the Chromatin Accessibility Landscape of the Mitotic Genome. Blood, 2014, 124, 4342-4342.	1.4	1
46	Integrative annotation of chromatin elements from ENCODE data. Nucleic Acids Research, 2013, 41, 827-841.	14.5	490
47	The UCSC Genome Browser database: extensions and updates 2011. Nucleic Acids Research, 2012, 40, D918-D923.	14.5	294
48	Systematic documentation and analysis of human genetic variation in hemoglobinopathies using the microattribution approach. Nature Genetics, 2011, 43, 295-301.	21.4	142
49	The value of data. Nature Genetics, 2011, 43, 281-283.	21.4	126
50	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671.	5.5	110
51	Complete Khoisan and Bantu genomes from southern Africa. Nature, 2010, 463, 943-947.	27.8	400
52	Erythroid GATA1 function revealed by genome-wide analysis of transcription factor occupancy, histone modifications, and mRNA expression. Genome Research, 2009, 19, 2172-2184.	5.5	184
53	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
54	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283

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55	PhenCode: connecting ENCODE data with mutations and phenotype. Human Mutation, 2007, 28, 554-562.	2.5	79
56	Mulan: Multiple-sequence local alignment and visualization for studying function and evolution. Genome Research, 2005, 15, 184-194.	5.5	218
57	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	5.5	1,795
58	GALA, a Database for Genomic Sequence Alignments and Annotations. Genome Research, 2003, 13, 732-741.	5.5	45
59	HbVar: A relational database of human hemoglobin variants and thalassemia mutations at the globin gene server. Human Mutation, 2002, 19, 225-233.	2.5	400
60	DATABASES OF HUMAN HEMOGLOBIN VARIANTS AND OTHER RESOURCES AT THE GLOBIN GENE SERVER. Hemoglobin, 2001, 25, 183-193.	0.8	35