

Belinda M Giardine

List of Publications by Year in descending order

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Version: 2024-02-01

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	Galaxy: A platform for interactive large-scale genome analysis. <i>Genome Research</i> , 2005, 15, 1451-1455.	5.5	1,795
2	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.6	1,283
3	Integrative annotation of chromatin elements from ENCODE data. <i>Nucleic Acids Research</i> , 2013, 41, 827-841.	14.5	490
4	HbVar: A relational database of human hemoglobin variants and thalassemia mutations at the globin gene server. <i>Human Mutation</i> , 2002, 19, 225-233.	2.5	400
5	Complete Khoisan and Bantu genomes from southern Africa. <i>Nature</i> , 2010, 463, 943-947.	27.8	400
6	Updates of the HbVar database of human hemoglobin variants and thalassemia mutations. <i>Nucleic Acids Research</i> , 2014, 42, D1063-D1069.	14.5	361
7	The UCSC Genome Browser database: extensions and updates 2011. <i>Nucleic Acids Research</i> , 2012, 40, D918-D923.	14.5	294
8	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	27.8	259
9	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007, 17, 1797-1808.	5.5	237
10	Mulan: Multiple-sequence local alignment and visualization for studying function and evolution. <i>Genome Research</i> , 2005, 15, 184-194.	5.5	218
11	Erythroid GATA1 function revealed by genome-wide analysis of transcription factor occupancy, histone modifications, and mRNA expression. <i>Genome Research</i> , 2009, 19, 2172-2184.	5.5	184
12	Chromatin structure dynamics during the mitosis-to-G1 phase transition. <i>Nature</i> , 2019, 576, 158-162.	27.8	167
13	Systematic documentation and analysis of human genetic variation in hemoglobinopathies using the microattribution approach. <i>Nature Genetics</i> , 2011, 43, 295-301.	21.4	142
14	The value of data. <i>Nature Genetics</i> , 2011, 43, 281-283.	21.4	126
15	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
16	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
17	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
18	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

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19	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
20	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. <i>Genome Research</i> , 2011, 21, 1659-1671.	5.5	110
21	Genome accessibility is widely preserved and locally modulated during mitosis. <i>Genome Research</i> , 2015, 25, 213-225.	5.5	103
22	Functions of BET proteins in erythroid gene expression. <i>Blood</i> , 2015, 125, 2825-2834.	1.4	93
23	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
24	PhenCode: connecting ENCODE data with mutations and phenotype. <i>Human Mutation</i> , 2007, 28, 554-562.	2.5	79
25	Clinically relevant updates of the HbVar database of human hemoglobin variants and thalassemia mutations. <i>Nucleic Acids Research</i> , 2021, 49, D1192-D1196.	14.5	62
26	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. <i>Cell Reports</i> , 2021, 34, 108783.	6.4	53
27	Interrogating Histone Acetylation and BRD4 as Mitotic Bookmarks of Transcription. <i>Cell Reports</i> , 2019, 27, 400-415.e5.	6.4	52
28	Establishment of regulatory elements during erythro-megakaryopoiesis identifies hematopoietic lineage-commitment points. <i>Epigenetics and Chromatin</i> , 2018, 11, 22.	3.9	49
29	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. <i>Molecular Cell</i> , 2021, 81, 239-254.e8.	9.7	48
30	GALA, a Database for Genomic Sequence Alignments and Annotations. <i>Genome Research</i> , 2003, 13, 732-741.	5.5	45
31	The HRI-regulated transcription factor ATF4 activates BCL11A transcription to silence fetal hemoglobin expression. <i>Blood</i> , 2020, 135, 2121-2132.	1.4	42
32	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , 2020, 30, 472-484.	5.5	38
33	DATABASES OF HUMAN HEMOGLOBIN VARIANTS AND OTHER RESOURCES AT THE GLOBIN GENE SERVER. <i>Hemoglobin</i> , 2001, 25, 183-193.	0.8	35
34	Alteration of genome folding via contact domain boundary insertion. <i>Nature Genetics</i> , 2020, 52, 1076-1087.	21.4	35
35	CTCF and transcription influence chromatin structure re-configuration after mitosis. <i>Nature Communications</i> , 2021, 12, 5157.	12.8	32
36	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

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37	Understanding heterogeneity of fetal hemoglobin induction through comparative analysis of F and A erythroblasts. <i>Blood</i> , 2020, 135, 1957-1968.	1.4	30
38	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
39	HRI depletion cooperates with pharmacologic inducers to elevate fetal hemoglobin and reduce sickle cell formation. <i>Blood Advances</i> , 2020, 4, 4560-4572.	5.2	15
40	Dual function NFI factors control fetal hemoglobin silencing in adult erythroid cells. <i>Nature Genetics</i> , 2022, 54, 874-884.	21.4	13
41	Dynamics of GATA1 binding and expression response in a GATA1-induced erythroid differentiation system. <i>Genomics Data</i> , 2015, 4, 1-7.	1.3	10
42	Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells. <i>IUBMB Life</i> , 2020, 72, 27-38.	3.4	8
43	S3V2-IDEAS: a package for normalizing, denoising and integrating epigenomic datasets across different cell types. <i>Bioinformatics</i> , 2021, 37, 3011-3013.	4.1	5
44	Heme-Regulated Inhibitor (HRI) Activates Transcription Factor ATF4 to Promote BCL11A Transcription and Fetal Hemoglobin Silencing. <i>Blood</i> , 2019, 134, 814-814.	1.4	5
45	Identification and characterization of RBM12 as a novel regulator of fetal hemoglobin expression. <i>Blood Advances</i> , 2022, 6, 5956-5968.	5.2	5
46	Effects of sheared chromatin length on CHIP-seq quality and sensitivity. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	3
47	HIC2 Controls Developmental Hemoglobin Switching By Repressing BCL11A Transcription. <i>Blood</i> , 2021, 138, 571-571.	1.4	2
48	Control of Fetal Hemoglobin Levels By NFI Transcription Factors. <i>Blood</i> , 2020, 136, 54-54.	1.4	2
49	Epigenetics of Cellular Memory: Insights from the Chromatin Accessibility Landscape of the Mitotic Genome. <i>Blood</i> , 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. <i>Blood</i> , 2021, 138, 855-855.	1.4	1
51	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. <i>Blood</i> , 2020, 136, 54-54.	1.4	1
52	Systems Biology in Heterogenous Tissues: Integrating Multiple *Omics Datasets to Understand Hematopoietic Differentiation. , 2019, , .		0
53	A Hyperactive Transcriptional State Marks Genome Reactivation during Mitotic Exit. <i>Blood</i> , 2015, 126, 48-48.	1.4	0
54	The BET Protein BRD2 Cooperates with CTCF to Enforce a Transcriptional Boundary in Erythroid Cells. <i>Blood</i> , 2016, 128, 1034-1034.	1.4	0

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55	Comparison of Fetal and Adult Erythroid Chromosomal Architectures Identifies a Novel Fetal Hemoglobin Regulatory Region. <i>Blood</i> , 2017, 130, 774-774.	1.4	0
56	Mouse Erythroid Cells Originate from a Megakaryocyte Precursor in Common Myeloid Progenitors. <i>Blood</i> , 2019, 134, 337-337.	1.4	0
57	Understanding Heterogeneity of Fetal Hemoglobin Induction through Comparative Analysis of Stage-Matched F- and a-Cells. <i>Blood</i> , 2019, 134, 981-981.	1.4	0
58	Interrogating Post-Transcriptional Mechanisms of Fetal Hemoglobin Regulation. <i>Blood</i> , 2021, 138, 3079-3079.	1.4	0
59	A β^2 -Globin Locus-Intrinsic Epigenetic Mechanism Underlies Fetal Globin Production in F-Cells. <i>Blood</i> , 2020, 136, 16-17.	1.4	0
60	Systematic Integration of Epigenomic Landscapes in Human and Mouse Blood Cells to Predict Activity and Targets of Regulatory Elements. <i>FASEB Journal</i> , 2022, 36, .	0.5	0