

Gerd A Blobel

List of Publications by Year in descending order

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Version: 2024-02-01

133
papers

10,175
citations

71061

41
h-index

39638

94
g-index

141
all docs

141
docs citations

141
times ranked

16812
citing authors

#	ARTICLE	IF	CITATIONS
1	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
2	Activating RNAs associate with Mediator to enhance chromatin architecture and transcription. <i>Nature</i> , 2013, 494, 497-501.	13.7	759
3	Controlling Long-Range Genomic Interactions at a Native Locus by Targeted Tethering of a Looping Factor. <i>Cell</i> , 2012, 149, 1233-1244.	13.5	615
4	Proximity among Distant Regulatory Elements at the β^2 -Globin Locus Requires GATA-1 and FOG-1. <i>Molecular Cell</i> , 2005, 17, 453-462.	4.5	449
5	Role of SWI/SNF in acute leukemia maintenance and enhancer-mediated <i>Myc</i> regulation. <i>Genes and Development</i> , 2013, 27, 2648-2662.	2.7	394
6	Global regulation of erythroid gene expression by transcription factor GATA-1. <i>Blood</i> , 2004, 104, 3136-3147.	0.6	372
7	Reactivation of Developmentally Silenced Globin Genes by Forced Chromatin Looping. <i>Cell</i> , 2014, 158, 849-860.	13.5	370
8	GATA-1 and Erythropoietin Cooperate to Promote Erythroid Cell Survival by Regulating bcl-xL Expression. <i>Blood</i> , 1999, 94, 87-96.	0.6	338
9	Enhancer Regulation of Transcriptional Bursting Parameters Revealed by Forced Chromatin Looping. <i>Molecular Cell</i> , 2016, 62, 237-247.	4.5	296
10	A genome-editing strategy to treat β^2 -hemoglobinopathies that recapitulates a mutation associated with a benign genetic condition. <i>Nature Medicine</i> , 2016, 22, 987-990.	15.2	279
11	CREB-Binding Protein Acetylates Hematopoietic Transcription Factor GATA-1 at Functionally Important Sites. <i>Molecular and Cellular Biology</i> , 1999, 19, 3496-3505.	1.1	234
12	Unlinking an lncRNA from Its Associated cis Element. <i>Molecular Cell</i> , 2016, 62, 104-110.	4.5	216
13	Tissue-Specific Mitotic Bookmarking by Hematopoietic Transcription Factor GATA1. <i>Cell</i> , 2012, 150, 725-737.	13.5	215
14	Exchange of GATA Factors Mediates Transitions in Looped Chromatin Organization at a Developmentally Regulated Gene Locus. <i>Molecular Cell</i> , 2008, 29, 232-242.	4.5	192
15	Bromodomain protein Brd3 associates with acetylated GATA1 to promote its chromatin occupancy at erythroid target genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E159-68.	3.3	190
16	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.	2.4	184
17	Chromatin structure dynamics during the mitosis-to-G1 phase transition. <i>Nature</i> , 2019, 576, 158-162.	13.7	167
18	SCL and associated proteins distinguish active from repressive GATA transcription factor complexes. <i>Blood</i> , 2009, 113, 2191-2201.	0.6	158

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19	Long-range enhancer activity determines <i>Myc</i> sensitivity to Notch inhibitors in T cell leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4946-53.	3.3	151
20	Context-dependent regulation of GATA-1 by friend of GATA-1. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 476-481.	3.3	123
21	Domain-focused CRISPR screen identifies HRI as a fetal hemoglobin regulator in human erythroid cells. Science, 2018, 361, 285-290.	6.0	119
22	Transcriptional Burst Initiation and Polymerase Pause Release Are Key Control Points of Transcriptional Regulation. Molecular Cell, 2019, 73, 519-532.e4.	4.5	118
23	The BET Protein BRD2 Cooperates with CTCF to Enforce Transcriptional and Architectural Boundaries. Molecular Cell, 2017, 66, 102-116.e7.	4.5	114
24	Comparative analysis of three-dimensional chromosomal architecture identifies a novel fetal hemoglobin regulatory element. Genes and Development, 2017, 31, 1704-1713.	2.7	113
25	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671.	2.4	110
26	Structural Basis and Specificity of Acetylated Transcription Factor GATA1 Recognition by BET Family Bromodomain Protein Brd3. Molecular and Cellular Biology, 2011, 31, 2632-2640.	1.1	106
27	Genome accessibility is widely preserved and locally modulated during mitosis. Genome Research, 2015, 25, 213-225.	2.4	103
28	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.	1.8	100
29	A dynamic intron retention program in the mammalian megakaryocyte and erythrocyte lineages. Blood, 2016, 127, e24-e34.	0.6	94
30	Functions of BET proteins in erythroid gene expression. Blood, 2015, 125, 2825-2834.	0.6	93
31	A hyperactive transcriptional state marks genome reactivation at the mitosis-to-G1 transition. Genes and Development, 2016, 30, 1423-1439.	2.7	92
32	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. Genome Research, 2014, 24, 1932-1944.	2.4	88
33	A Dementia-Associated Risk Variant near TMEM106B Alters Chromatin Architecture and Gene Expression. American Journal of Human Genetics, 2017, 101, 643-663.	2.6	87
34	Acetylation of GATA-1 is required for chromatin occupancy. Blood, 2006, 108, 3736-3738.	0.6	76
35	Insight into the Architecture of the NuRD Complex. Journal of Biological Chemistry, 2014, 289, 21844-21855.	1.6	75
36	Dynamic enhancer-gene body contacts during transcription elongation. Genes and Development, 2015, 29, 1992-1997.	2.7	72

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37	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.	2.4	71
38	Forced chromatin looping raises fetal hemoglobin in adult sickle cells to higher levels than pharmacologic inducers. <i>Blood</i> , 2016, 128, 1139-1143.	0.6	69
39	The type 2 diabetes presumed causal variant within TCF7L2 resides in an element that controls the expression of ACSL5. <i>Diabetologia</i> , 2016, 59, 2360-2368.	2.9	68
40	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. <i>Cell Reports</i> , 2021, 34, 108783.	2.9	53
41	Testing the super-enhancer concept. <i>Nature Reviews Genetics</i> , 2021, 22, 749-755.	7.7	53
42	Interrogating Histone Acetylation and BRD4 as Mitotic Bookmarks of Transcription. <i>Cell Reports</i> , 2019, 27, 400-415.e5.	2.9	52
43	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. <i>Molecular Cell</i> , 2021, 81, 239-254.e8.	4.5	48
44	BRD4 orchestrates genome folding to promote neural crest differentiation. <i>Nature Genetics</i> , 2021, 53, 1480-1492.	9.4	48
45	Spatial Genome Re-organization between Fetal and Adult Hematopoietic Stem Cells. <i>Cell Reports</i> , 2019, 29, 4200-4211.e7.	2.9	46
46	CBP and p300: versatile coregulators with important roles in hematopoietic gene expression. <i>Journal of Leukocyte Biology</i> , 2002, 71, 545-56.	1.5	45
47	The HRI-regulated transcription factor ATF4 activates BCL11A transcription to silence fetal hemoglobin expression. <i>Blood</i> , 2020, 135, 2121-2132.	0.6	42
48	The interdependence of gene-regulatory elements and the 3D genome. <i>Journal of Cell Biology</i> , 2019, 218, 12-26.	2.3	41
49	The BRD3 ET domain recognizes a short peptide motif through a mechanism that is conserved across chromatin remodelers and transcriptional regulators. <i>Journal of Biological Chemistry</i> , 2018, 293, 7160-7175.	1.6	39
50	Characterization of BRD4 during Mammalian Postmeiotic Sperm Development. <i>Molecular and Cellular Biology</i> , 2015, 35, 1433-1448.	1.1	38
51	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , 2020, 30, 472-484.	2.4	38
52	The Role of Bromodomain and Extraterminal Motif (BET) Proteins in Chromatin Structure. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2017, 82, 37-43.	2.0	37
53	The Nucleosome Remodeling and Deacetylase Complex Has an Asymmetric, Dynamic, and Modular Architecture. <i>Cell Reports</i> , 2020, 33, 108450.	2.9	37
54	The tumour suppressor CHD5 forms a NuRD-type chromatin remodelling complex. <i>Biochemical Journal</i> , 2015, 468, 345-352.	1.7	36

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55	Exploiting genetic variation to uncover rules of transcription factor binding and chromatin accessibility. <i>Nature Communications</i> , 2018, 9, 782.	5.8	36
56	Alteration of genome folding via contact domain boundary insertion. <i>Nature Genetics</i> , 2020, 52, 1076-1087.	9.4	35
57	Function of GATA Factors in the Adult Mouse Liver. <i>PLoS ONE</i> , 2013, 8, e83723.	1.1	35
58	CTCF and transcription influence chromatin structure re-configuration after mitosis. <i>Nature Communications</i> , 2021, 12, 5157.	5.8	32
59	ZMYND8-regulated IRF8 transcription axis is an acute myeloid leukemia dependency. <i>Molecular Cell</i> , 2021, 81, 3604-3622.e10.	4.5	32
60	Disrupting the adult globin promoter alleviates promoter competition and reactivates fetal globin gene expression. <i>Blood</i> , 2022, 139, 2107-2118.	0.6	32
61	Understanding heterogeneity of fetal hemoglobin induction through comparative analysis of F and A erythroblasts. <i>Blood</i> , 2020, 135, 1957-1968.	0.6	30
62	Manipulating nuclear architecture. <i>Current Opinion in Genetics and Development</i> , 2014, 25, 1-7.	1.5	25
63	The E3 ligase adaptor molecule SPOP regulates fetal hemoglobin levels in adult erythroid cells. <i>Blood Advances</i> , 2019, 3, 1586-1597.	2.5	25
64	Circadian REV-ERBs repress E4bp4 to activate NAMPT-dependent NAD ⁺ biosynthesis and sustain cardiac function. , 2022, 1, 45-58.		25
65	Short Hairpin RNA Screen Reveals Bromodomain Proteins as Novel Targets in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2011, 20, 287-288.	7.7	22
66	Role of microRNAs in epigenetic silencing of the <i>CHD5</i> tumor suppressor gene in neuroblastomas. <i>Oncotarget</i> , 2016, 7, 15977-15985.	0.8	20
67	Protein Phosphatase 6C (PPP6C) Loss Significantly Raises Fetal Hemoglobin Levels and Reduces Cell Sickling. <i>Blood</i> , 2021, 138, 2031-2031.	0.6	18
68	Erythropoiesis provides a BRD's eye view of BET protein function. <i>Drug Discovery Today: Technologies</i> , 2016, 19, 23-28.	4.0	16
69	Comparative structure-function analysis of bromodomain and extraterminal motif (BET) proteins in a gene-complementation system. <i>Journal of Biological Chemistry</i> , 2020, 295, 1898-1914.	1.6	15
70	HRI depletion cooperates with pharmacologic inducers to elevate fetal hemoglobin and reduce sickle cell formation. <i>Blood Advances</i> , 2020, 4, 4560-4572.	2.5	15
71	Ubiquitin-Specific Protease 6 Functions as a Tumor Suppressor in Ewing Sarcoma through Immune Activation. <i>Cancer Research</i> , 2021, 81, 2171-2183.	0.4	14
72	Intrinsically disordered Meningioma-1 stabilizes the BAF complex to cause AML. <i>Molecular Cell</i> , 2021, 81, 2332-2348.e9.	4.5	14

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73	GWAS to Therapy by Genome Edits?. <i>Science</i> , 2013, 342, 206-207.	6.0	13
74	Comparative analysis of mitosis-specific antibodies for bulk purification of mitotic populations by fluorescence-activated cell sorting. <i>BioTechniques</i> , 2014, 56, 90-94.	0.8	13
75	Perturbing Chromatin Structure to Understand Mechanisms of Gene Expression. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2015, 80, 207-212.	2.0	13
76	Dual function NFI factors control fetal hemoglobin silencing in adult erythroid cells. <i>Nature Genetics</i> , 2022, 54, 874-884.	9.4	13
77	Detecting Long-Range Enhancer-Promoter Interactions by Quantitative Chromosome Conformation Capture. <i>Methods in Molecular Biology</i> , 2017, 1468, 51-62.	0.4	10
78	Engineering three-dimensional genome folding. <i>Nature Genetics</i> , 2021, 53, 602-611.	9.4	9
79	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.	1.5	8
80	The Identification and Structure of an N-Terminal PR Domain Show that FOG1 Is a Member of the PRDM Family of Proteins. <i>PLoS ONE</i> , 2014, 9, e106011.	1.1	7
81	An international effort to cure a global health problem: A report on the 19th Hemoglobin Switching Conference. <i>Experimental Hematology</i> , 2015, 43, 821-837.	0.2	7
82	Chromatin architecture underpinning transcription elongation. <i>Nucleus</i> , 2016, 7, 1-8.	0.6	7
83	A new bookmark of the mitotic genome in embryonic stem cells. <i>Nature Cell Biology</i> , 2016, 18, 1124-1125.	4.6	6
84	Robust erythroid differentiation system for rhesus hematopoietic progenitor cells allowing preclinical screening of genetic treatment strategies for the hemoglobinopathies. <i>Cytotherapy</i> , 2018, 20, 1278-1287.	0.3	6
85	Heterogeneity of fetal hemoglobin production in adult red blood cells. <i>Current Opinion in Hematology</i> , 2021, 28, 164-170.	1.2	6
86	Heme-Regulated Inhibitor (HRI) Activates Transcription Factor ATF4 to Promote BCL11A Transcription and Fetal Hemoglobin Silencing. <i>Blood</i> , 2019, 134, 814-814.	0.6	5
87	Identification and characterization of RBM12 as a novel regulator of fetal hemoglobin expression. <i>Blood Advances</i> , 2022, 6, 5956-5968.	2.5	5
88	Effects of sheared chromatin length on CHIP-seq quality and sensitivity. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
89	Histone H3 Lysine 9 Methylation and HP1 ³ Are Associated with Transcription Elongation through Mammalian Chromatin.. <i>Blood</i> , 2005, 106, 1734-1734.	0.6	3
90	Using Forced Chromatin Looping To Overcome Developmental Silencing Of Embryonic and Fetal β^2 -Type Globin Genes In Adult Erythroid Cells. <i>Blood</i> , 2013, 122, 433-433.	0.6	3

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91	Genome Editing Recreates Hereditary Persistence of Fetal Hemoglobin in Primary Human Erythroblasts. Blood, 2015, 126, 640-640.	0.6	3
92	Regulation of Fetal Hemoglobin Expression By the VHL-HIF1 α Oxygen Sensing System. Blood, 2021, 138, 574-574.	0.6	3
93	HIC2 Controls Developmental Hemoglobin Switching By Repressing BCL11A Transcription. Blood, 2021, 138, 571-571.	0.6	2
94	Control of Fetal Hemoglobin Levels By NFI Transcription Factors. Blood, 2020, 136, 54-54.	0.6	2
95	GATA-1 caught in the AKT. Blood, 2006, 107, 851a-852.	0.6	1
96	Editorial overview: Breaking open the mysteries of nuclear and chromatin organization. Current Opinion in Genetics and Development, 2021, 67, iii-vii.	1.5	1
97	Acetylation of GATA-1 Is Required for Chromatin Occupancy.. Blood, 2006, 108, 1179-1179.	0.6	1
98	Acetylation-Dependent Interaction of GATA-1 with the Potential Mitotic "Bookmarking" Protein Brd3.. Blood, 2010, 116, 2598-2598.	0.6	1
99	Defective Production, Turnover, and Secretion of the Platelet α -Granule Protein P-Selectin In Mice with Disrupted FOG1-NuRD Interaction. Blood, 2010, 116, 547-547.	0.6	1
100	Epigenetics of Cellular Memory: Insights from the Chromatin Accessibility Landscape of the Mitotic Genome. Blood, 2014, 124, 4342-4342.	0.6	1
101	A Dynamic Intron Retention Program in the Mammalian Megakaryocyte and Erythrocyte Lineages. Blood, 2015, 126, 2380-2380.	0.6	1
102	Isolated Changes in Chromatin Accessibility and Enhancer-Promoter Contacts at the β -Globin Locus Distinguish Fetal Hemoglobin Producing F-Cells from α -Cells. Blood, 2021, 138, 855-855.	0.6	1
103	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. Blood, 2020, 136, 54-54.	0.6	1
104	The Acetyltransferases CBP and p300: Molecular Integrators of Hematopoietic Transcription Involved in Chromosomal Translocations. , 0, , 497-517.		0
105	Kr β 4ppeling megakaryopoiesis. Blood, 2007, 110, 3823-3824.	0.6	0
106	A Cluster to Remember. Cell, 2013, 154, 718-720.	13.5	0
107	Charting a noncoding gene for β -globin activation. Blood, 2018, 132, 1865-1867.	0.6	0
108	Identification of Cyclin D3 as a Direct Transcriptional Target of E2A Using Damid.. Blood, 2004, 104, 1618-1618.	0.6	0

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109	Genetic Modeling of Chemical Antagonists: Genome Scale Validation of Hematopoietic Disease Drug Targets by In Vivo Functional Analysis.. Blood, 2004, 104, 2577-2577.	0.6	0
110	GATA-1 Directly Induces Physical Proximity between the LCR and $\hat{\beta}^2$ Globin Promoter in Erythroid Cells.. Blood, 2004, 104, 1612-1612.	0.6	0
111	Genomic Organization, Chromatin Structure, and Transcriptional Regulation of the Murine Alpha Hemoglobin Stabilizing Protein (AHSP) Gene.. Blood, 2005, 106, 3633-3633.	0.6	0
112	GATA-1 Represses PU.1/Sfpi-1 Gene Transcription in Erythro-Megakaryocytic Progenitors.. Blood, 2007, 110, 1226-1226.	0.6	0
113	A Potential Epigenetic Bookmarking Function for the Hematopoietic Transcription Factor GATA-1.. Blood, 2010, 116, 2601-2601.	0.6	0
114	Manipulating Higher Order Chromatin Structure of the $\hat{\beta}^2$ -Globin Locus by Targeted Tethering of a $\hat{\alpha}$ -looping Factor. Blood, 2010, 116, 647-647.	0.6	0
115	Lineage-Specific Mitotic Bookmarking by Hematopoietic Transcription Factor GATA1. Blood, 2011, 118, 547-547.	0.6	0
116	Linking Transcription Factor Pathways to Disease-Causing GATA1 Mutations. Blood, 2011, 118, 2371-2371.	0.6	0
117	Dissecting the Molecular Pathways That Underlie Disease-Causing GATA1 Mutations. Blood, 2012, 120, 3439-3439.	0.6	0
118	Controlling Long-Range Genomic Interactions to Reprogram the $\hat{\beta}^2$ -Globin Locus. Blood, 2012, 120, 280-280.	0.6	0
119	GATA1 and the BET Family Protein Brd3 Form a Mitotic Bookmarking Complex. Blood, 2012, 120, 282-282.	0.6	0
120	Hematopoietic Transcriptional Regulation At The Mitosis-G1 Transition. Blood, 2013, 122, 2440-2440.	0.6	0
121	Dissection of BET Protein Function in a Hematopoietic Differentiation Model. Blood, 2014, 124, 1574-1574.	0.6	0
122	Comparing Strategies to Reactivate Fetal Globin Expression for the Treatment of Beta-Globinopathies. Blood, 2014, 124, 333-333.	0.6	0
123	A Hyperactive Transcriptional State Marks Genome Reactivation during Mitotic Exit. Blood, 2015, 126, 48-48.	0.6	0
124	A Novel Regulatory Region of the p27 Locus Is Required for Normal Erythroid p27 Expression, and Produces a Long Noncoding RNA with No Detectable Function. Blood, 2015, 126, 1175-1175.	0.6	0
125	Deep Mining of Natural Genetic Variation in Erythroid Cells Reveals New Insights about In Vivo Transcription Factor Binding and Chromatin Accessibility. Blood, 2016, 128, 3879-3879.	0.6	0
126	The BET Protein BRD2 Cooperates with CTCF to Enforce a Transcriptional Boundary in Erythroid Cells. Blood, 2016, 128, 1034-1034.	0.6	0

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127	Comparison of Fetal and Adult Erythroid Chromosomal Architectures Identifies a Novel Fetal Hemoglobin Regulatory Region. <i>Blood</i> , 2017, 130, 774-774.	0.6	0
128	Heme-Regulated Inhibitor (HRI) Loss and Pharmacologic Treatments Cooperate to Strongly Elevate Fetal Hemoglobin and Reduce Sickle Cell Formation. <i>Blood</i> , 2018, 132, 721-721.	0.6	0
129	Understanding Heterogeneity of Fetal Hemoglobin Induction through Comparative Analysis of Stage-Matched F- and a-Cells. <i>Blood</i> , 2019, 134, 981-981.	0.6	0
130	Interrogating RNA Binding Proteins as Novel Regulators of Fetal Hemoglobin Expression. <i>Blood</i> , 2019, 134, 966-966.	0.6	0
131	Heme-Regulated Inhibitor (HRI) Depletion Cooperates with Pharmacologic Inducers to Strongly Elevate Fetal Hemoglobin and Reduce Sickle Cell Formation. <i>Blood</i> , 2019, 134, 3557-3557.	0.6	0
132	Interrogating Post-Transcriptional Mechanisms of Fetal Hemoglobin Regulation. <i>Blood</i> , 2021, 138, 3079-3079.	0.6	0
133	A β^2 -Globin Locus-Intrinsic Epigenetic Mechanism Underlies Fetal Globin Production in F-Cells. <i>Blood</i> , 2020, 136, 16-17.	0.6	0