

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
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141
all docs

141
docs citations

141
times ranked

16812
citing authors

#	ARTICLE	IF	CITATIONS
1	Disrupting the adult globin promoter alleviates promoter competition and reactivates fetal globin gene expression. <i>Blood</i> , 2022, 139, 2107-2118.	0.6	32
2	Circadian REV-ERBs repress E4bp4 to activate NAMPT-dependent NAD ⁺ biosynthesis and sustain cardiac function. , 2022, 1, 45-58.		25
3	Identification and characterization of RBM12 as a novel regulator of fetal hemoglobin expression. <i>Blood Advances</i> , 2022, 6, 5956-5968.	2.5	5
4	Dual function NFI factors control fetal hemoglobin silencing in adult erythroid cells. <i>Nature Genetics</i> , 2022, 54, 874-884.	9.4	13
5	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. <i>Molecular Cell</i> , 2021, 81, 239-254.e8.	4.5	48
6	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
7	Distinct properties and functions of CTCF revealed by a rapidly inducible degron system. <i>Cell Reports</i> , 2021, 34, 108783.	2.9	53
8	Heterogeneity of fetal hemoglobin production in adult red blood cells. <i>Current Opinion in Hematology</i> , 2021, 28, 164-170.	1.2	6
9	Effects of sheared chromatin length on ChIP-seq quality and sensitivity. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
10	Editorial overview: Breaking open the mysteries of nuclear and chromatin organization. <i>Current Opinion in Genetics and Development</i> , 2021, 67, iii-vii.	1.5	1
11	Engineering three-dimensional genome folding. <i>Nature Genetics</i> , 2021, 53, 602-611.	9.4	9
12	Intrinsically disordered Meningioma-1 stabilizes the BAF complex to cause AML. <i>Molecular Cell</i> , 2021, 81, 2332-2348.e9.	4.5	14
13	CTCF and transcription influence chromatin structure re-configuration after mitosis. <i>Nature Communications</i> , 2021, 12, 5157.	5.8	32
14	Testing the super-enhancer concept. <i>Nature Reviews Genetics</i> , 2021, 22, 749-755.	7.7	53
15	ZMYND8-regulated IRF8 transcription axis is an acute myeloid leukemia dependency. <i>Molecular Cell</i> , 2021, 81, 3604-3622.e10.	4.5	32
16	BRD4 orchestrates genome folding to promote neural crest differentiation. <i>Nature Genetics</i> , 2021, 53, 1480-1492.	9.4	48
17	Protein Phosphatase 6C (PPP6C) Loss Significantly Raises Fetal Hemoglobin Levels and Reduces Cell Sickling. <i>Blood</i> , 2021, 138, 2031-2031.	0.6	18
18	Regulation of Fetal Hemoglobin Expression By the VHL-HIF1 α Oxygen Sensing System. <i>Blood</i> , 2021, 138, 574-574.	0.6	3

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19	Isolated Changes in Chromatin Accessibility and Enhancer-Promoter Contacts at the $\hat{\beta}^2$ -Globin Locus Distinguish Fetal Hemoglobin Producing F-Cells from a-Cells. <i>Blood</i> , 2021, 138, 855-855.	0.6	1
20	Interrogating Post-Transcriptional Mechanisms of Fetal Hemoglobin Regulation. <i>Blood</i> , 2021, 138, 3079-3079.	0.6	0
21	HIC2 Controls Developmental Hemoglobin Switching By Repressing BCL11A Transcription. <i>Blood</i> , 2021, 138, 571-571.	0.6	2
22	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
23	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
24	The Nucleosome Remodeling and Deacetylase Complex Has an Asymmetric, Dynamic, and Modular Architecture. <i>Cell Reports</i> , 2020, 33, 108450.	2.9	37
25	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
26	Alteration of genome folding via contact domain boundary insertion. <i>Nature Genetics</i> , 2020, 52, 1076-1087.	9.4	35
27	Understanding heterogeneity of fetal hemoglobin induction through comparative analysis of F and A erythroblasts. <i>Blood</i> , 2020, 135, 1957-1968.	0.6	30
28	The HRI-regulated transcription factor ATF4 activates BCL11A transcription to silence fetal hemoglobin expression. <i>Blood</i> , 2020, 135, 2121-2132.	0.6	42
29	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , 2020, 30, 472-484.	2.4	38
30	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. <i>Blood</i> , 2020, 136, 54-54.	0.6	1
31	A $\hat{\beta}^2$ -Globin Locus-Intrinsic Epigenetic Mechanism Underlies Fetal Globin Production in F-Cells. <i>Blood</i> , 2020, 136, 16-17.	0.6	0
32	Control of Fetal Hemoglobin Levels By NFI Transcription Factors. <i>Blood</i> , 2020, 136, 54-54.	0.6	2
33	Interrogating Histone Acetylation and BRD4 as Mitotic Bookmarks of Transcription. <i>Cell Reports</i> , 2019, 27, 400-415.e5.	2.9	52
34	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
35	Chromatin structure dynamics during the mitosis-to-G1 phase transition. <i>Nature</i> , 2019, 576, 158-162.	13.7	167
36	Spatial Genome Re-organization between Fetal and Adult Hematopoietic Stem Cells. <i>Cell Reports</i> , 2019, 29, 4200-4211.e7.	2.9	46

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37	The interdependence of gene-regulatory elements and the 3D genome. <i>Journal of Cell Biology</i> , 2019, 218, 12-26.	2.3	41
38	Transcriptional Burst Initiation and Polymerase Pause Release Are Key Control Points of Transcriptional Regulation. <i>Molecular Cell</i> , 2019, 73, 519-532.e4.	4.5	118
39	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
40	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
41	Interrogating RNA Binding Proteins as Novel Regulators of Fetal Hemoglobin Expression. <i>Blood</i> , 2019, 134, 966-966.	0.6	0
42	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
43	Exploiting genetic variation to uncover rules of transcription factor binding and chromatin accessibility. <i>Nature Communications</i> , 2018, 9, 782.	5.8	36
44	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
45	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
46	Charting a noncoding gene for $\hat{\beta}$ -globin activation. <i>Blood</i> , 2018, 132, 1865-1867.	0.6	0
47	Domain-focused CRISPR screen identifies HRI as a fetal hemoglobin regulator in human erythroid cells. <i>Science</i> , 2018, 361, 285-290.	6.0	119
48	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
49	The BET Protein BRD2 Cooperates with CTCF to Enforce Transcriptional and Architectural Boundaries. <i>Molecular Cell</i> , 2017, 66, 102-116.e7.	4.5	114
50	A Dementia-Associated Risk Variant near TMEM106B Alters Chromatin Architecture and Gene Expression. <i>American Journal of Human Genetics</i> , 2017, 101, 643-663.	2.6	87
51	Comparative analysis of three-dimensional chromosomal architecture identifies a novel fetal hemoglobin regulatory element. <i>Genes and Development</i> , 2017, 31, 1704-1713.	2.7	113
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	Detecting Long-Range Enhancer-Promoter Interactions by Quantitative Chromosome Conformation Capture. <i>Methods in Molecular Biology</i> , 2017, 1468, 51-62.	0.4	10
54	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

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55	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
56	Chromatin architecture underpinning transcription elongation. <i>Nucleus</i> , 2016, 7, 1-8.	0.6	7
57	A dynamic intron retention program in the mammalian megakaryocyte and erythrocyte lineages. <i>Blood</i> , 2016, 127, e24-e34.	0.6	94
58	Unlinking an lncRNA from Its Associated cis Element. <i>Molecular Cell</i> , 2016, 62, 104-110.	4.5	216
59	Enhancer Regulation of Transcriptional Bursting Parameters Revealed by Forced Chromatin Looping. <i>Molecular Cell</i> , 2016, 62, 237-247.	4.5	296
60	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
61	Erythropoiesis provides a BRD's eye view of BET protein function. <i>Drug Discovery Today: Technologies</i> , 2016, 19, 23-28.	4.0	16
62	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
63	A genome-editing strategy to treat β^0 -hemoglobinopathies that recapitulates a mutation associated with a benign genetic condition. <i>Nature Medicine</i> , 2016, 22, 987-990.	15.2	279
64	A new bookmark of the mitotic genome in embryonic stem cells. <i>Nature Cell Biology</i> , 2016, 18, 1124-1125.	4.6	6
65	A hyperactive transcriptional state marks genome reactivation at the mitosis-to-G1 transition. <i>Genes and Development</i> , 2016, 30, 1423-1439.	2.7	92
66	Deep Mining of Natural Genetic Variation in Erythroid Cells Reveals New Insights about In Vivo Transcription Factor Binding and Chromatin Accessibility. <i>Blood</i> , 2016, 128, 3879-3879.	0.6	0
67	The BET Protein BRD2 Cooperates with CTCF to Enforce a Transcriptional Boundary in Erythroid Cells. <i>Blood</i> , 2016, 128, 1034-1034.	0.6	0
68	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.	1.8	100
69	Functions of BET proteins in erythroid gene expression. <i>Blood</i> , 2015, 125, 2825-2834.	0.6	93
70	Characterization of BRD4 during Mammalian Postmeiotic Sperm Development. <i>Molecular and Cellular Biology</i> , 2015, 35, 1433-1448.	1.1	38
71	The tumour suppressor CHD5 forms a NuRD-type chromatin remodelling complex. <i>Biochemical Journal</i> , 2015, 468, 345-352.	1.7	36
72	Dynamic enhancer-gene body contacts during transcription elongation. <i>Genes and Development</i> , 2015, 29, 1992-1997.	2.7	72

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73	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
74	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
75	Genome accessibility is widely preserved and locally modulated during mitosis. <i>Genome Research</i> , 2015, 25, 213-225.	2.4	103
76	Genome Editing Recreates Hereditary Persistence of Fetal Hemoglobin in Primary Human Erythroblasts. <i>Blood</i> , 2015, 126, 640-640.	0.6	3
77	A Hyperactive Transcriptional State Marks Genome Reactivation during Mitotic Exit. <i>Blood</i> , 2015, 126, 48-48.	0.6	0
78	A Dynamic Intron Retention Program in the Mammalian Megakaryocyte and Erythrocyte Lineages. <i>Blood</i> , 2015, 126, 2380-2380.	0.6	1
79	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. <i>Blood</i> , 2015, 126, 1175-1175.	0.6	0
80	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
81	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
82	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. <i>Genome Research</i> , 2014, 24, 1932-1944.	2.4	88
83	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
84	Insight into the Architecture of the NuRD Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 21844-21855.	1.6	75
85	Manipulating nuclear architecture. <i>Current Opinion in Genetics and Development</i> , 2014, 25, 1-7.	1.5	25
86	Long-range enhancer activity determines <i>Myc</i> sensitivity to Notch inhibitors in T cell leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4946-53.	3.3	151
87	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
88	Reactivation of Developmentally Silenced Globin Genes by Forced Chromatin Looping. <i>Cell</i> , 2014, 158, 849-860.	13.5	370
89	Epigenetics of Cellular Memory: Insights from the Chromatin Accessibility Landscape of the Mitotic Genome. <i>Blood</i> , 2014, 124, 4342-4342.	0.6	1
90	Dissection of BET Protein Function in a Hematopoietic Differentiation Model. <i>Blood</i> , 2014, 124, 1574-1574.	0.6	0

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91	Comparing Strategies to Reactivate Fetal Globin Expression for the Treatment of Beta-Globinopathies. Blood, 2014, 124, 333-333.	0.6	0
92	A Cluster to Remember. Cell, 2013, 154, 718-720.	13.5	0
93	GWAS to Therapy by Genome Edits?. Science, 2013, 342, 206-207.	6.0	13
94	Activating RNAs associate with Mediator to enhance chromatin architecture and transcription. Nature, 2013, 494, 497-501.	13.7	759
95	Role of SWI/SNF in acute leukemia maintenance and enhancer-mediated <i>Myc</i> regulation. Genes and Development, 2013, 27, 2648-2662.	2.7	394
96	Using Forced Chromatin Looping To Overcome Developmental Silencing Of Embryonic and Fetal β^2 -Type Globin Genes In Adult Erythroid Cells. Blood, 2013, 122, 433-433.	0.6	3
97	Function of GATA Factors in the Adult Mouse Liver. PLoS ONE, 2013, 8, e83723.	1.1	35
98	Hematopoietic Transcriptional Regulation At The Mitosis-G1 Transition. Blood, 2013, 122, 2440-2440.	0.6	0
99	Tissue-Specific Mitotic Bookmarking by Hematopoietic Transcription Factor GATA1. Cell, 2012, 150, 725-737.	13.5	215
100	Controlling Long-Range Genomic Interactions at a Native Locus by Targeted Tethering of a Looping Factor. Cell, 2012, 149, 1233-1244.	13.5	615
101	Dissecting the Molecular Pathways That Underlie Disease-Causing GATA1 Mutations. Blood, 2012, 120, 3439-3439.	0.6	0
102	Controlling Long-Range Genomic Interactions to Reprogram the β^2 -Globin Locus. Blood, 2012, 120, 280-280.	0.6	0
103	GATA1 and the BET Family Protein Brd3 Form a Mitotic Bookmarking Complex. Blood, 2012, 120, 282-282.	0.6	0
104	Short Hairpin RNA Screen Reveals Bromodomain Proteins as Novel Targets in Acute Myeloid Leukemia. Cancer Cell, 2011, 20, 287-288.	7.7	22
105	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
106	Bromodomain protein Brd3 associates with acetylated GATA1 to promote its chromatin occupancy at erythroid target genes. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E159-68.	3.3	190
107	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671.	2.4	110
108	Lineage-Specific Mitotic Bookmarking by Hematopoietic Transcription Factor GATA1. Blood, 2011, 118, 547-547.	0.6	0

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109	Linking Transcription Factor Pathways to Disease-Causing GATA1 Mutations. <i>Blood</i> , 2011, 118, 2371-2371.	0.6	0
110	A Potential Epigenetic Bookmarking Function for the Hematopoietic Transcription Factor GATA-1.. <i>Blood</i> , 2010, 116, 2601-2601.	0.6	0
111	Acetylation-Dependent Interaction of GATA-1 with the Potential Mitotic "Bookmarking" Protein Brd3.. <i>Blood</i> , 2010, 116, 2598-2598.	0.6	1
112	Defective Production, Turnover, and Secretion of the Platelet Î±-Granule Protein P-Selectin In Mice with Disrupted FOG1-NuRD Interaction. <i>Blood</i> , 2010, 116, 547-547.	0.6	1
113	Manipulating Higher Order Chromatin Structure of the Î²-Globin Locus by Targeted Tethering of a "looping" Factor. <i>Blood</i> , 2010, 116, 647-647.	0.6	0
114	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
115	SCL and associated proteins distinguish active from repressive GATA transcription factor complexes. <i>Blood</i> , 2009, 113, 2191-2201.	0.6	158
116	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
117	KrÄppeling megakaryopoiesis. <i>Blood</i> , 2007, 110, 3823-3824.	0.6	0
118	GATA-1 Represses PU.1/Sfpi-1 Gene Transcription in Erythro-Megakaryocytic Progenitors.. <i>Blood</i> , 2007, 110, 1226-1226.	0.6	0
119	GATA-1 caught in the AKT. <i>Blood</i> , 2006, 107, 851a-852.	0.6	1
120	Acetylation of GATA-1 is required for chromatin occupancy. <i>Blood</i> , 2006, 108, 3736-3738.	0.6	76
121	Acetylation of GATA-1 Is Required for Chromatin Occupancy.. <i>Blood</i> , 2006, 108, 1179-1179.	0.6	1
122	Proximity among Distant Regulatory Elements at the Î²-Globin Locus Requires GATA-1 and FOG-1. <i>Molecular Cell</i> , 2005, 17, 453-462.	4.5	449
123	Histone H3 Lysine 9 Methylation and HP1Î³ Are Associated with Transcription Elongation through Mammalian Chromatin.. <i>Blood</i> , 2005, 106, 1734-1734.	0.6	3
124	Genomic Organization, Chromatin Structure, and Transcriptional Regulation of the Murine Alpha Hemoglobin Stabilizing Protein (AHSP) Gene.. <i>Blood</i> , 2005, 106, 3633-3633.	0.6	0
125	Context-dependent regulation of GATA-1 by friend of GATA-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 476-481.	3.3	123
126	Global regulation of erythroid gene expression by transcription factor GATA-1. <i>Blood</i> , 2004, 104, 3136-3147.	0.6	372

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127	Identification of Cyclin D3 as a Direct Transcriptional Target of E2A Using Damid.. Blood, 2004, 104, 1618-1618.	0.6	0
128	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
129	GATA-1 Directly Induces Physical Proximity between the LCR and $\hat{\nu}^2$ Globin Promoter in Erythroid Cells.. Blood, 2004, 104, 1612-1612.	0.6	0
130	CBP and p300: versatile coregulators with important roles in hematopoietic gene expression. Journal of Leukocyte Biology, 2002, 71, 545-56.	1.5	45
131	GATA-1 and Erythropoietin Cooperate to Promote Erythroid Cell Survival by Regulating bcl-xL Expression. Blood, 1999, 94, 87-96.	0.6	338
132	CREB-Binding Protein Acetylates Hematopoietic Transcription Factor GATA-1 at Functionally Important Sites. Molecular and Cellular Biology, 1999, 19, 3496-3505.	1.1	234
133	The Acetyltransferases CBP and p300: Molecular Integrators of Hematopoietic Transcription Involved in Chromosomal Translocations. , 0, , 497-517.		0