

# Kristian Helin

## List of Publications by Year in descending order

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115  
papers

24,850  
citations

14614

66  
h-index

21474

114  
g-index

124  
all docs

124  
docs citations

124  
times ranked

28411  
citing authors

#	ARTICLE	IF	CITATIONS
1	UTX and JMJD3 are histone H3K27 demethylases involved in HOX gene regulation and development. <i>Nature</i> , 2007, 449, 731-734.	13.7	1,183
2	Genome-wide mapping of Polycomb target genes unravels their roles in cell fate transitions. <i>Genes and Development</i> , 2006, 20, 1123-1136.	2.7	1,098
3	EZH2 is downstream of the pRB-E2F pathway, essential for proliferation and amplified in cancer. <i>EMBO Journal</i> , 2003, 22, 5323-5335.	3.5	1,052
4	TET1 and hydroxymethylcytosine in transcription and DNA methylation fidelity. <i>Nature</i> , 2011, 473, 343-348.	13.7	905
5	Role of TET enzymes in DNA methylation, development, and cancer. <i>Genes and Development</i> , 2016, 30, 733-750.	2.7	781
6	Suz12 is essential for mouse development and for EZH2 histone methyltransferase activity. <i>EMBO Journal</i> , 2004, 23, 4061-4071.	3.5	778
7	The Polycomb group proteins bind throughout the INK4A-ARF locus and are disassociated in senescent cells. <i>Genes and Development</i> , 2007, 21, 525-530.	2.7	775
8	Transcriptional regulation by Polycomb group proteins. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1147-1155.	3.6	757
9	Molecular mechanisms and potential functions of histone demethylases. <i>Nature Reviews Molecular Cell Biology</i> , 2012, 13, 297-311.	16.1	708
10	The putative oncogene GASC1 demethylates tri- and dimethylated lysine 9 on histone H3. <i>Nature</i> , 2006, 442, 307-311.	13.7	670
11	A model for transmission of the H3K27me3 epigenetic mark. <i>Nature Cell Biology</i> , 2008, 10, 1291-1300.	4.6	656
12	Reduced H3K27me3 and DNA Hypomethylation Are Major Drivers of Gene Expression in K27M Mutant Pediatric High-Grade Gliomas. <i>Cancer Cell</i> , 2013, 24, 660-672.	7.7	633
13	The Polycomb Group Protein Suz12 Is Required for Embryonic Stem Cell Differentiation. <i>Molecular and Cellular Biology</i> , 2007, 27, 3769-3779.	1.1	628
14	Apaf-1 is a transcriptional target for E2F and p53. <i>Nature Cell Biology</i> , 2001, 3, 552-558.	4.6	552
15	Polycomb group proteins: navigators of lineage pathways led astray in cancer. <i>Nature Reviews Cancer</i> , 2009, 9, 773-784.	12.8	537
16	JARID2 regulates binding of the Polycomb repressive complex <sup>2</sup> to target genes in ES cells. <i>Nature</i> , 2010, 464, 306-310.	13.7	499
17	E2F target genes: unraveling the biology. <i>Trends in Biochemical Sciences</i> , 2004, 29, 409-417.	3.7	497
18	RBP2 Belongs to a Family of Demethylases, Specific for Tri- and Dimethylated Lysine 4 on Histone 3. <i>Cell</i> , 2007, 128, 1063-1076.	13.5	485

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19	Histone lysine demethylases as targets for anticancer therapy. <i>Nature Reviews Drug Discovery</i> , 2013, 12, 917-930.	21.5	413
20	Molecular Mechanisms Directing PRC2 Recruitment and H3K27 Methylation. <i>Molecular Cell</i> , 2019, 74, 8-18.	4.5	393
21	EZH2 is a potential therapeutic target for H3K27M-mutant pediatric gliomas. <i>Nature Medicine</i> , 2017, 23, 483-492.	15.2	392
22	Polycomb Complex 2 Is Required for <i>E-cadherin</i> Repression by the Snail1 Transcription Factor. <i>Molecular and Cellular Biology</i> , 2008, 28, 4772-4781.	1.1	390
23	Chromatin proteins and modifications as drug targets. <i>Nature</i> , 2013, 502, 480-488.	13.7	389
24	The H3K27me3 demethylase JMJD3 contributes to the activation of the <i>INK4A</i> locus in response to oncogene- and stress-induced senescence. <i>Genes and Development</i> , 2009, 23, 1171-1176.	2.7	384
25	Maintaining cell identity: PRC2-mediated regulation of transcription and cancer. <i>Nature Reviews Cancer</i> , 2016, 16, 803-810.	12.8	368
26	Gene Silencing Triggers Polycomb Repressive Complex 2 Recruitment to CpG Islands Genome Wide. <i>Molecular Cell</i> , 2014, 55, 347-360.	4.5	358
27	Fbxl10/Kdm2b Recruits Polycomb Repressive Complex 1 to CpG Islands and Regulates H2A Ubiquitylation. <i>Molecular Cell</i> , 2013, 49, 1134-1146.	4.5	351
28	Histone demethylases in development and disease. <i>Trends in Cell Biology</i> , 2010, 20, 662-671.	3.6	329
29	Characterization of an antagonistic switch between histone H3 lysine 27 methylation and acetylation in the transcriptional regulation of Polycomb group target genes. <i>Nucleic Acids Research</i> , 2010, 38, 4958-4969.	6.5	317
30	Chromatin Repressive Complexes in Stem Cells, Development, and Cancer. <i>Cell Stem Cell</i> , 2014, 14, 735-751.	5.2	301
31	Polycomb complexes act redundantly to repress genomic repeats and genes. <i>Genes and Development</i> , 2010, 24, 265-276.	2.7	298
32	Tet Proteins Connect the O-Linked N-acetylglucosamine Transferase Ogt to Chromatin in Embryonic Stem Cells. <i>Molecular Cell</i> , 2013, 49, 645-656.	4.5	285
33	DNA methylation: TET proteins "guardians of CpG islands?". <i>EMBO Reports</i> , 2012, 13, 28-35.	2.0	269
34	Histone methyltransferases in cancer. <i>Seminars in Cell and Developmental Biology</i> , 2010, 21, 209-220.	2.3	262
35	Role of the Polycomb Repressive Complex 2 in Acute Promyelocytic Leukemia. <i>Cancer Cell</i> , 2007, 11, 513-525.	7.7	228
36	Jarid2 Is Implicated in the Initial Xist-Induced Targeting of PRC2 to the Inactive X Chromosome. <i>Molecular Cell</i> , 2014, 53, 301-316.	4.5	221

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37	Loss of <i>TET2</i> in hematopoietic cells leads to DNA hypermethylation of active enhancers and induction of leukemogenesis. <i>Genes and Development</i> , 2015, 29, 910-922.	2.7	213
38	Polycomb Cbx family members mediate the balance between haematopoietic stem cell self-renewal and differentiation. <i>Nature Cell Biology</i> , 2013, 15, 353-362.	4.6	211
39	Jarid2 binds mono-ubiquitylated H2A lysine 119 to mediate crosstalk between Polycomb complexes PRC1 and PRC2. <i>Nature Communications</i> , 2016, 7, 13661.	5.8	207
40	The emerging functions of histone demethylases. <i>Current Opinion in Genetics and Development</i> , 2008, 18, 159-168.	1.5	201
41	ATAD2 Is a Novel Cofactor for MYC, Overexpressed and Amplified in Aggressive Tumors. <i>Cancer Research</i> , 2009, 69, 8491-8498.	0.4	201
42	A Functional Link between the Histone Demethylase PHF8 and the Transcription Factor ZNF711 in X-Linked Mental Retardation. <i>Molecular Cell</i> , 2010, 38, 165-178.	4.5	186
43	APAF1 is a key transcriptional target for p53 in the regulation of neuronal cell death. <i>Journal of Cell Biology</i> , 2001, 155, 207-216.	2.3	184
44	E2F-6: a novel member of the E2F family is an inhibitor of E2F-dependent transcription. <i>Oncogene</i> , 1998, 17, 611-623.	2.6	183
45	Jarid1b targets genes regulating development and is involved in neural differentiation. <i>EMBO Journal</i> , 2011, 30, 4586-4600.	3.5	183
46	Bypass of senescence by the polycomb group protein CBX8 through direct binding to the INK4A-ARF locus. <i>EMBO Journal</i> , 2007, 26, 1637-1648.	3.5	175
47	Accurate H3K27 methylation can be established de novo by SUZ12-directed PRC2. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 225-232.	3.6	162
48	The lncRNA MIR31HG regulates p16INK4A expression to modulate senescence. <i>Nature Communications</i> , 2015, 6, 6967.	5.8	161
49	Role of the Polycomb Repressive Complex 2 (PRC2) in Transcriptional Regulation and Cancer. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2016, 6, a026575.	2.9	151
50	NEK11 regulates CDC25A degradation and the IR-induced G2/M checkpoint. <i>Nature Cell Biology</i> , 2009, 11, 1247-1253.	4.6	122
51	Quantitative Mass Spectrometry of Histones H3.2 and H3.3 in Suz12-deficient Mouse Embryonic Stem Cells Reveals Distinct, Dynamic Post-translational Modifications at Lys-27 and Lys-36. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 838-850.	2.5	121
52	E2F-1-Induced p53-independent apoptosis in transgenic mice. <i>Oncogene</i> , 1998, 17, 143-155.	2.6	119
53	Optimizing sgRNA position markedly improves the efficiency of CRISPR/dCas9-mediated transcriptional repression. <i>Nucleic Acids Research</i> , 2016, 44, e141-e141.	6.5	118
54	Genome-wide profiling identifies a DNA methylation signature that associates with TET2 mutations in diffuse large B-cell lymphoma. <i>Haematologica</i> , 2013, 98, 1912-1920.	1.7	116

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55	The Histone Demethylase Jarid1b Ensures Faithful Mouse Development by Protecting Developmental Genes from Aberrant H3K4me3. <i>PLoS Genetics</i> , 2013, 9, e1003461.	1.5	114
56	Loss of the retinoblastoma protein-related p130 protein in small cell lung carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 6933-6938.	3.3	113
57	Non-core Subunits of the PRC2 Complex Are Collectively Required for Its Target-Site Specificity. <i>Molecular Cell</i> , 2019, 76, 423-436.e3.	4.5	108
58	E2F1 is crucial for E2Fâ€dependent apoptosis. <i>EMBO Reports</i> , 2005, 6, 661-668.	2.0	106
59	PRMT5 methylome profiling uncovers a direct link to splicing regulation in acute myeloid leukemia. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 999-1012.	3.6	105
60	Epigenetic control of IL-23 expression in keratinocytes is important for chronic skin inflammation. <i>Nature Communications</i> , 2018, 9, 1420.	5.8	88
61	Oncohistones: drivers of pediatric cancers. <i>Genes and Development</i> , 2017, 31, 2313-2324.	2.7	85
62	Continual removal of H3K9 promoter methylation by Jmjd2 demethylases is vital for <sc>ESC</sc> selfâ€renewal and early development. <i>EMBO Journal</i> , 2016, 35, 1550-1564.	3.5	84
63	Quantification of Differential Transcription Factor Activity and Multiomics-Based Classification into Activators and Repressors: diffTF. <i>Cell Reports</i> , 2019, 29, 3147-3159.e12.	2.9	84
64	Utx Is Required for Proper Induction of Ectoderm and Mesoderm during Differentiation of Embryonic Stem Cells. <i>PLoS ONE</i> , 2013, 8, e60020.	1.1	81
65	KDM4A regulates the maternal-to-zygotic transition by protecting broad H3K4me3 domains from H3K9me3 invasion in oocytes. <i>Nature Cell Biology</i> , 2020, 22, 380-388.	4.6	77
66	Middleâ€down hybrid chromatography/tandem mass spectrometry workflow for characterization of combinatorial postâ€translational modifications in histones. <i>Proteomics</i> , 2014, 14, 2200-2211.	1.3	76
67	Systems Level Analysis of Histone H3 Post-translational Modifications (PTMs) Reveals Features of PTM Crosstalk in Chromatin Regulation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2715-2729.	2.5	76
68	shRNA screening identifies JMJD1C as being required for leukemia maintenance. <i>Blood</i> , 2014, 123, 1870-1882.	0.6	73
69	ZFP57 maintains the parent-of-origin-specific expression of the imprinted genes and differentially affects non-imprinted targets in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , 2016, 44, 8165-8178.	6.5	73
70	Jmjd2/Kdm4 demethylases are required for expression of <i>Il3ra</i> and survival of acute myeloid leukemia cells. <i>Genes and Development</i> , 2016, 30, 1278-1288.	2.7	69
71	DNMT3A R882H mutant and Tet2 inactivation cooperate in the deregulation of DNA methylation control to induce lymphoid malignancies in mice. <i>Leukemia</i> , 2016, 30, 1388-1398.	3.3	67
72	The Histone Lysine Demethylase JMJD3/KDM6B Is Recruited to p53 Bound Promoters and Enhancer Elements in a p53 Dependent Manner. <i>PLoS ONE</i> , 2014, 9, e96545.	1.1	67

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73	TET2 binding to enhancers facilitates transcription factor recruitment in hematopoietic cells. <i>Genome Research</i> , 2019, 29, 564-575.	2.4	66
74	RSV-Induced H3K4 Demethylase KDM5B Leads to Regulation of Dendritic Cell-Derived Innate Cytokines and Exacerbates Pathogenesis In Vivo. <i>PLoS Pathogens</i> , 2015, 11, e1004978.	2.1	63
75	The Demethylase JMJD2C Localizes to H3K4me3-Positive Transcription Start Sites and Is Dispensable for Embryonic Development. <i>Molecular and Cellular Biology</i> , 2014, 34, 1031-1045.	1.1	62
76	Histone editing elucidates the functional roles of H3K27 methylation and acetylation in mammals. <i>Nature Genetics</i> , 2022, 54, 754-760.	9.4	59
77	PRMT5 Inhibition Modulates E2F1 Methylation and Gene-Regulatory Networks Leading to Therapeutic Efficacy in JAK2V617F-Mutant MPN. <i>Cancer Discovery</i> , 2020, 10, 1742-1757.	7.7	55
78	TET2 mutations are associated with hypermethylation at key regulatory enhancers in normal and malignant hematopoiesis. <i>Nature Communications</i> , 2021, 12, 6061.	5.8	47
79	Chromatin modifier HUSH co-operates with RNA decay factor NEXT to restrict transposable element expression. <i>Molecular Cell</i> , 2022, 82, 1691-1707.e8.	4.5	43
80	Complex-dependent histone acetyltransferase activity of KAT8 determines its role in transcription and cellular homeostasis. <i>Molecular Cell</i> , 2021, 81, 1749-1765.e8.	4.5	42
81	Tumor suppressor ASXL1 is essential for the activation of INK4B expression in response to oncogene activity and anti-proliferative signals. <i>Cell Research</i> , 2015, 25, 1205-1218.	5.7	41
82	The histone demethylase Jarid1b is required for hematopoietic stem cell self-renewal in mice. <i>Blood</i> , 2015, 125, 2075-2078.	0.6	40
83	The KDM4/JMJD2 histone demethylases are required for hematopoietic stem cell maintenance. <i>Blood</i> , 2019, 134, 1154-1158.	0.6	40
84	PR-DUB maintains the expression of critical genes through FOXK1/2- and ASXL1/2/3-dependent recruitment to chromatin and H2AK119ub1 deubiquitination. <i>Genome Research</i> , 2020, 30, 1119-1130.	2.4	36
85	MPP8 is essential for sustaining self-renewal of ground-state pluripotent stem cells. <i>Nature Communications</i> , 2021, 12, 3034.	5.8	35
86	Identification of recurrent FHL2-GLI2 oncogenic fusion in sclerosing stromal tumors of the ovary. <i>Nature Communications</i> , 2020, 11, 44.	5.8	34
87	Epigenetic Regulation of Angiogenesis by JARID1B-Induced Repression of HOXA5. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1645-1652.	1.1	33
88	A Functional Link between Nuclear RNA Decay and Transcriptional Control Mediated by the Polycomb Repressive Complex 2. <i>Cell Reports</i> , 2019, 29, 1800-1811.e6.	2.9	32
89	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells. <i>ELife</i> , 2019, 8, .	2.8	32
90	SATB2 preserves colon stem cell identity and mediates ileum-colon conversion via enhancer remodeling. <i>Cell Stem Cell</i> , 2022, 29, 101-115.e10.	5.2	31

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91	NEK11 Linking CHK1 and CDC25A in DNA damage checkpoint signaling. <i>Cell Cycle</i> , 2010, 9, 450-455.	1.3	29
92	Mutant FOXL2C134W Hijacks SMAD4 and SMAD2/3 to Drive Adult Granulosa Cell Tumors. <i>Cancer Research</i> , 2020, 80, 3466-3479.	0.4	29
93	PROSER1 mediates TET2 O-GlcNAcylation to regulate DNA demethylation on UTX-dependent enhancers and CpG islands. <i>Life Science Alliance</i> , 2022, 5, e202101228.	1.3	24
94	The SETDB1-TRIM28 Complex Suppresses Antitumor Immunity. <i>Cancer Immunology Research</i> , 2021, 9, 1413-1424.	1.6	24
95	Maternal expression of the JMJD2A/KDM4A histone demethylase is critical for pre-implantation development. <i>Development (Cambridge)</i> , 2017, 144, 3264-3277.	1.2	23
96	E2F activates late-G1 events but cannot replace E1A in inducing S phase in terminally differentiated skeletal muscle cells. <i>Oncogene</i> , 1999, 18, 5054-5062.	2.6	21
97	E2F1-mediated transcriptional inhibition of the plasminogen activator inhibitor type 1 gene. <i>FEBS Journal</i> , 2001, 268, 4969-4978.	0.2	20
98	Aggressiveness of non-EMT breast cancer cells relies on FBXO11 activity. <i>Molecular Cancer</i> , 2018, 17, 171.	7.9	20
99	SWI/SNF Subunits SMARCA4, SMARCD2 and DPF2 Collaborate in MLL-Rearranged Leukaemia Maintenance. <i>PLoS ONE</i> , 2015, 10, e0142806.	1.1	19
100	Human CDT1 Associates with CDC7 and Recruits CDC45 to Chromatin during S Phase. <i>Journal of Biological Chemistry</i> , 2009, 284, 3028-3036.	1.6	17
101	A Screen Identifies the Oncogenic Micro-RNA miR-378a-5p as a Negative Regulator of Oncogene-Induced Senescence. <i>PLoS ONE</i> , 2014, 9, e91034.	1.1	17
102	Isolation and characterization of DUSP11, a novel p53 target gene. <i>Journal of Cellular and Molecular Medicine</i> , 2009, 13, 2158-2170.	1.6	15
103	The Lysine Demethylase KDM5B Regulates Islet Function and Glucose Homeostasis. <i>Journal of Diabetes Research</i> , 2019, 2019, 1-15.	1.0	15
104	Targeting R1OK2 ATPase activity leads to decreased protein synthesis and cell death in acute myeloid leukemia. <i>Blood</i> , 2022, 139, 245-255.	0.6	13
105	The p53 Tumour Suppressor Protein. <i>Biotechnology and Genetic Engineering Reviews</i> , 2000, 17, 179-212.	2.4	10
106	The Role of Chromatin-Associated Proteins in Cancer. <i>Annual Review of Cancer Biology</i> , 2017, 1, 355-377.	2.3	10
107	CpG island reconfiguration for the establishment and synchronization of polycomb functions upon exit from naive pluripotency. <i>Molecular Cell</i> , 2022, 82, 1169-1185.e7.	4.5	10
108	BMP2/SMAD pathway activation in JAK2/p53-mutant megakaryocyte/erythroid progenitors promotes leukemic transformation. <i>Blood</i> , 2022, 139, 3630-3646.	0.6	9

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109	The histone demethylase Jarid1b mediates angiotensin II-induced endothelial dysfunction by controlling the 3'UTR of soluble epoxide hydrolase. <i>Acta Physiologica</i> , 2019, 225, e13168.	1.8	8
110	TET1: an epigenetic guardian of lymphomagenesis. <i>Nature Immunology</i> , 2015, 16, 592-594.	7.0	4
111	Regional tumour glutamine supply affects chromatin and cell identity. <i>Nature Cell Biology</i> , 2016, 18, 1027-1029.	4.6	4
112	Generation of locus-specific degradable tag knock-ins in mouse and human cell lines. <i>STAR Protocols</i> , 2021, 2, 100575.	0.5	4
113	Comprehensive and unbiased multiparameter high-throughput screening by compaRe finds effective and subtle drug responses in AML models. <i>ELife</i> , 2022, 11, .	2.8	2
114	ChIP-Sequencing of. <i>Methods in Molecular Biology</i> , 2021, 2272, 251-262.	0.4	1
115	Regulation of cell proliferation by the E2F transcription factors. <i>Biochemical Society Transactions</i> , 1999, 27, A64-A64.	1.6	0