

Robert J Klose

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

13,396
citations

76031

42
h-index

139680

61
g-index

76
all docs

76
docs citations

76
times ranked

18034
citing authors

#	ARTICLE	IF	CITATIONS
1	Live-cell single particle tracking of PRC1 reveals a highly dynamic system with low target site occupancy. <i>Nature Communications</i> , 2021, 12, 887.	5.8	49
2	Getting under the skin of Polycomb-dependent gene regulation. <i>Genes and Development</i> , 2021, 35, 301-303.	2.7	4
3	BAP1 constrains pervasive H2AK119ub1 to control the transcriptional potential of the genome. <i>Genes and Development</i> , 2021, 35, 749-770.	2.7	38
4	The molecular principles of gene regulation by Polycomb repressive complexes. <i>Nature Reviews Molecular Cell Biology</i> , 2021, 22, 815-833.	16.1	207
5	Variant PCGF1-PRC1 links PRC2 recruitment with differentiation-associated transcriptional inactivation at target genes. <i>Nature Communications</i> , 2021, 12, 5341.	5.8	25
6	PRC1 drives Polycomb-mediated gene repression by controlling transcription initiation and burst frequency. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 811-824.	3.6	62
7	PRC1 Catalytic Activity Is Central to Polycomb System Function. <i>Molecular Cell</i> , 2020, 77, 857-874.e9.	4.5	184
8	Distinct contributions of DNA methylation and histone acetylation to the genomic occupancy of transcription factors. <i>Genome Research</i> , 2020, 30, 1393-1406.	2.4	41
9	Identifying proteins bound to native mitotic ESC chromosomes reveals chromatin repressors are important for compaction. <i>Nature Communications</i> , 2020, 11, 4118.	5.8	26
10	Understanding the interplay between CpG island-associated gene promoters and H3K4 methylation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194567.	0.9	82
11	Analysis of Genome Architecture during SCNT Reveals a Role of Cohesin in Impeding Minor ZGA. <i>Molecular Cell</i> , 2020, 79, 234-250.e9.	4.5	39
12	ATACing DNA Methylation during Differentiation. <i>Molecular Cell</i> , 2020, 77, 1159-1161.	4.5	4
13	CDK-Mediator and FBXL19 prime developmental genes for activation by promoting atypical regulatory interactions. <i>Nucleic Acids Research</i> , 2020, 48, 2942-2955.	6.5	9
14	Cohesin Disrupts Polycomb-Dependent Chromosome Interactions in Embryonic Stem Cells. <i>Cell Reports</i> , 2020, 30, 820-835.e10.	2.9	129
15	KDM2 proteins constrain transcription from CpG island gene promoters independently of their histone demethylase activity. <i>Nucleic Acids Research</i> , 2019, 47, 9005-9023.	6.5	26
16	Synergy between Variant PRC1 Complexes Defines Polycomb-Mediated Gene Repression. <i>Molecular Cell</i> , 2019, 74, 1020-1036.e8.	4.5	200
17	Biochemical Identification of Nonmethylated DNA by BioCAP-Seq. <i>Methods in Molecular Biology</i> , 2018, 1766, 15-29.	0.4	2
18	Polycomb repressive complex 1 shapes the nucleosome landscape but not accessibility at target genes. <i>Genome Research</i> , 2018, 28, 1494-1507.	2.4	72

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19	FBXL19 recruits CDK-Mediator to CpG islands of developmental genes priming them for activation during lineage commitment. <i>ELife</i> , 2018, 7, .	2.8	22
20	MLL-AF4 Spreading Identifies Binding Sites that Are Distinct from Super-Enhancers and that Govern Sensitivity to DOT1L Inhibition in Leukemia. <i>Cell Reports</i> , 2017, 18, 482-495.	2.9	69
21	The SET1 Complex Selects Actively Transcribed Target Genes via Multivalent Interaction with CpG Island Chromatin. <i>Cell Reports</i> , 2017, 20, 2313-2327.	2.9	86
22	The pioneer factor OCT4 requires the chromatin remodeller BRG1 to support gene regulatory element function in mouse embryonic stem cells. <i>ELife</i> , 2017, 6, .	2.8	215
23	PCGF6-PRC1 suppresses premature differentiation of mouse embryonic stem cells by regulating germ cell-related genes. <i>ELife</i> , 2017, 6, .	2.8	99
24	RYBP stimulates PRC1 to shape chromatin-based communication between Polycomb repressive complexes. <i>ELife</i> , 2016, 5, .	2.8	111
25	Protection of CpG islands from DNA methylation is DNA-encoded and evolutionarily conserved. <i>Nucleic Acids Research</i> , 2016, 44, 6693-6706.	6.5	80
26	Successful transmission and transcriptional deployment of a human chromosome via mouse male meiosis. <i>ELife</i> , 2016, 5, .	2.8	4
27	Histone demethylases in chromatin biology and beyond. <i>EMBO Reports</i> , 2015, 16, 1620-1639.	2.0	172
28	Targeting Polycomb systems to regulate gene expression: modifications to a complex story. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 643-649.	16.1	314
29	Understanding the relationship between DNA methylation and histone lysine methylation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1362-1372.	0.9	430
30	Variant PRC1 Complex-Dependent H2A Ubiquitylation Drives PRC2 Recruitment and Polycomb Domain Formation. <i>Cell</i> , 2014, 157, 1445-1459.	13.5	613
31	5-Carboxy-8-hydroxyquinoline is a broad spectrum 2-oxoglutarate oxygenase inhibitor which causes iron translocation. <i>Chemical Science</i> , 2013, 4, 3110.	3.7	142
32	ZF-CxxC domain-containing proteins, CpG islands and the chromatin connection. <i>Biochemical Society Transactions</i> , 2013, 41, 727-740.	1.6	209
33	Chromatin Sampling – An Emerging Perspective on Targeting Polycomb Repressor Proteins. <i>PLoS Genetics</i> , 2013, 9, e1003717.	1.5	109
34	Epigenetic conservation at gene regulatory elements revealed by non-methylated DNA profiling in seven vertebrates. <i>ELife</i> , 2013, 2, e00348.	2.8	192
35	Bio-CAP: a versatile and highly sensitive technique to purify and characterise regions of non-methylated DNA. <i>Nucleic Acids Research</i> , 2012, 40, e32-e32.	6.5	27
36	Recognition of CpG Island Chromatin by KDM2A Requires Direct and Specific Interaction with Linker DNA. <i>Molecular and Cellular Biology</i> , 2012, 32, 479-489.	1.1	40

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37	KDM2B links the Polycomb Repressive Complex 1 (PRC1) to recognition of CpG islands. <i>ELife</i> , 2012, 1, e00205.	2.8	414
38	Plant Growth Regulator Daminozide Is a Selective Inhibitor of Human KDM2/7 Histone Demethylases. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 6639-6643.	2.9	125
39	The oncometabolite 2-hydroxyglutarate inhibits histone lysine demethylases. <i>EMBO Reports</i> , 2011, 12, 463-469.	2.0	851
40	CpG island chromatin. <i>Epigenetics</i> , 2011, 6, 147-152.	1.3	128
41	Jarid2 is a PRC2 component in embryonic stem cells required for multi-lineage differentiation and recruitment of PRC1 and RNA Polymerase II to developmental regulators. <i>Nature Cell Biology</i> , 2010, 12, 618-624.	4.6	274
42	Quantitative High-Throughput Screening Identifies 8-Hydroxyquinolines as Cell-Active Histone Demethylase Inhibitors. <i>PLoS ONE</i> , 2010, 5, e15535.	1.1	194
43	PHF8, a gene associated with cleft lip/palate and mental retardation, encodes for an N ^ε -dimethyl lysine demethylase. <i>Human Molecular Genetics</i> , 2010, 19, 217-222.	1.4	153
44	CpG Islands Recruit a Histone H3 Lysine 36 Demethylase. <i>Molecular Cell</i> , 2010, 38, 179-190.	4.5	273
45	Histone lysine methylation: an epigenetic modification?. <i>Epigenomics</i> , 2010, 2, 151-161.	1.0	21
46	Phosphorylation of MeCP2 at Serine 80 regulates its chromatin association and neurological function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4882-4887.	3.3	200
47	Dynamic protein methylation in chromatin biology. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 407-22.	2.4	185
48	MeCP2 Binding to DNA Depends upon Hydration at Methyl-CpG. <i>Molecular Cell</i> , 2008, 29, 525-531.	4.5	252
49	Demethylation of Histone H3K36 and H3K9 by Rph1: a Vestige of an H3K9 Methylation System in <i>Saccharomyces cerevisiae</i> ?. <i>Molecular and Cellular Biology</i> , 2007, 27, 3951-3961.	1.1	79
50	The Retinoblastoma Binding Protein RBP2 Is an H3K4 Demethylase. <i>Cell</i> , 2007, 128, 889-900.	13.5	399
51	PLU-1 Is an H3K4 Demethylase Involved in Transcriptional Repression and Breast Cancer Cell Proliferation. <i>Molecular Cell</i> , 2007, 25, 801-812.	4.5	431
52	Regulation of histone methylation by demethyliminination and demethylation. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 307-318.	16.1	764
53	Histone H3 Arg2 methylation provides alternative directions for COMPASS. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1058-1060.	3.6	7
54	Yeast Jhd2p is a histone H3 Lys4 trimethyl demethylase. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 243-245.	3.6	111

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55	The trithorax-group protein Lid is a histone H3 trimethyl-Lys4 demethylase. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 341-343.	3.6	100
56	JmjC-domain-containing proteins and histone demethylation. <i>Nature Reviews Genetics</i> , 2006, 7, 715-727.	7.7	1,096
57	The transcriptional repressor JHDM3A demethylates trimethyl histone H3 lysine ⁹ and lysine ³⁶ . <i>Nature</i> , 2006, 442, 312-316.	13.7	563
58	Genomic DNA methylation: the mark and its mediators. <i>Trends in Biochemical Sciences</i> , 2006, 31, 89-97.	3.7	2,190
59	DNA Binding Selectivity of MeCP2 Due to a Requirement for A/T Sequences Adjacent to Methyl-CpG. <i>Molecular Cell</i> , 2005, 19, 667-678.	4.5	322
60	MeCP2 Behaves as an Elongated Monomer That Does Not Stably Associate with the Sin3a Chromatin Remodeling Complex. <i>Journal of Biological Chemistry</i> , 2004, 279, 46490-46496.	1.6	75