Robert E Kingston

List of Publications by Year
in descending order

76 papers	14,826 citations	47006 47 h-index	76900 74 g-index
80 all docs	80 docs citations	80 times ranked	14768 citing authors

#	Article	IF	Citations
1	HERVH-derived lncRNAs negatively regulate chromatin targeting and remodeling mediated by CHD7. Life Science Alliance, 2022, 5, e202101127.	2.8	3
2	TRACE generates fluorescent human reporter cell lines to characterize epigenetic pathways. Molecular Cell, 2022, 82, 479-491.e7.	9.7	7
3	Context-specific Polycomb mechanisms in development. Nature Reviews Genetics, 2022, 23, 680-695.	16.3	40
4	Elongin A associates with actively transcribed genes and modulates enhancer RNA levels with limited impact on transcription elongation rate inÂvivo. Journal of Biological Chemistry, 2021, 296, 100202.	3.4	15
5	Elongin A regulates transcription inÂvivo through enhanced RNA polymerase processivity. Journal of Biological Chemistry, 2021, 296, 100170.	3.4	7
6	Full methylation of H3K27 by PRC2 is dispensable for initial embryoid body formation but required to maintain differentiated cell identity. Development (Cambridge), 2021, 148, .	2.5	11
7	A Polycomb domain found in committed cells impairs differentiation when introduced into PRC1 in pluripotent cells. Molecular Cell, 2021, 81, 4677-4691.e8.	9.7	20
8	Modulating mesendoderm competence during human germ layer differentiation. Cell Reports, 2021, 37, 109990.	6.4	11
9	S-phase Enriched Non-coding RNAs Regulate Gene Expression and Cell Cycle Progression. Cell Reports, 2020, 31, 107629.	6.4	11
10	De Novo Variants in the ATPase Module of MORC2 Cause a Neurodevelopmental Disorder with Growth Retardation and Variable Craniofacial Dysmorphism. American Journal of Human Genetics, 2020, 107, 352-363.	6.2	64
11	lncRNA DIGIT and BRD3 protein form phase-separated condensates to regulate endoderm differentiation. Nature Cell Biology, 2020, 22, 1211-1222.	10.3	100
12	The CBX family of proteins in transcriptional repression and memory. Journal of Biosciences, 2020, 45, 1.	1.1	32
13	The CBX family of proteins in transcriptional repression and memory. Journal of Biosciences, 2020, 45, .	1.1	8
14	Xist RNA antagonizes the SWI/SNF chromatin remodeler BRG1 on the inactive X chromosome. Nature Structural and Molecular Biology, 2019, 26, 96-109.	8.2	54
15	Phase separation of Polycomb-repressive complex 1 is governed by a charged disordered region of CBX2. Genes and Development, 2019, 33, 799-813.	5.9	264
16	A conserved genetic interaction between Spt6 and Set2 regulates H3K36 methylation. Nucleic Acids Research, 2019, 47, 3888-3903.	14.5	33
17	Dynamics of activating and repressive histone modifications in Drosophila neural stem cell lineages and brain tumors. Development (Cambridge), 2019, 146, .	2.5	7
18	Beyond the Histone Code: A Physical Map of Chromatin States. Molecular Cell, 2018, 69, 5-7.	9.7	10

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19	Dynamic condensates activate transcription. Science, 2018, 361, 329-330.	12.6	64
20	Prostaglandin E2 Stimulates CREB-Mediated Modification of Histone Variant Nucleosomes at Enhancers to Promote Hematopoietic Stem Cell Fate. Blood, 2018, 132, 530-530.	1.4	1
21	Polycomb Repressive Complex 1 Generates Discrete Compacted Domains that Change during Differentiation. Molecular Cell, 2017, 65, 432-446.e5.	9.7	287
22	Mutation of a nucleosome compaction region disrupts Polycomb-mediated axial patterning. Science, 2017, 355, 1081-1084.	12.6	133
23	Hyperactivation of HUSH complex function by Charcotâ€"Marieâ€"Tooth disease mutation in MORC2. Nature Genetics, 2017, 49, 1035-1044.	21.4	105
24	Widespread changes in nucleosome accessibility without changes in nucleosome occupancy during a rapid transcriptional induction. Genes and Development, 2017, 31, 451-462.	5.9	90
25	Multitasking by Polycomb response elements. Genes and Development, 2017, 31, 1069-1072.	5.9	8
26	Polycomb Repressive Complex 2 Methylates Elongin A to Regulate Transcription. Molecular Cell, 2017, 68, 872-884.e6.	9.7	50
27	Enhanced chromatin accessibility of the dosage compensated Drosophila male X-chromosome requires the CLAMP zinc finger protein. PLoS ONE, 2017, 12, e0186855.	2.5	29
28	MNase titration reveals differences between nucleosome occupancy and chromatin accessibility. Nature Communications, 2016, 7, 11485.	12.8	185
29	Regulated large-scale nucleosome density patterns and precise nucleosome positioning correlate with V(D)J recombination. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6427-E6436.	7.1	31
30	Structural, super-resolution microscopy analysis of paraspeckle nuclear body organization. Journal of Cell Biology, 2016, 214, 817-830.	5.2	262
31	CAT7 and cat7l Long Non-coding RNAs Tune Polycomb Repressive Complex 1 Function during Human and Zebrafish Development. Journal of Biological Chemistry, 2016, 291, 19558-19572.	3.4	32
32	Molecular Dissection of Chromatin Maturation via Click Chemistry. Current Protocols in Molecular Biology, 2016, 114, 21.33.1-21.33.11.	2.9	1
33	Chromatin topology is coupled to Polycomb group protein subnuclear organization. Nature Communications, 2016, 7, 10291.	12.8	176
34	Enhancer regions show high histone H3.3 turnover that changes during differentiation. ELife, 2016, 5, .	6.0	86
35	Nucleosomal occupancy changes locally over key regulatory regions during cell differentiation and reprogramming. Nature Communications, 2014, 5, 4719.	12.8	80
36	The Long Noncoding RNAs NEAT1 and MALAT1 Bind Active Chromatin Sites. Molecular Cell, 2014, 55, 791-802.	9.7	578

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37	Transcriptional Regulation by Trithorax-Group Proteins. Cold Spring Harbor Perspectives in Biology, 2014, 6, a019349-a019349.	5.5	103
38	A Chromatin-Dependent Role of the Fragile X Mental Retardation Protein FMRP in the DNA Damage Response. Cell, 2014, 157, 869-881.	28.9	151
39	H3K27 modifications define segmental regulatory domains in the Drosophila bithorax complex. ELife, 2014, 3, e02833.	6.0	111
40	Multiplexed Illumina sequencing libraries from picogram quantities of DNA. BMC Genomics, 2013, 14, 466.	2.8	74
41	High-resolution Xist binding maps reveal two-step spreading during X-chromosome inactivation. Nature, 2013, 504, 465-469.	27.8	351
42	Occupying Chromatin: Polycomb Mechanisms for Getting to Genomic Targets, Stopping Transcriptional Traffic, and Staying Put. Molecular Cell, 2013, 49, 808-824.	9.7	638
43	Variable Requirements for DNA-Binding Proteins at Polycomb-Dependent Repressive Regions in Human HOX Clusters. Molecular and Cellular Biology, 2013, 33, 3274-3285.	2.3	30
44	Epigenetic mechanism: silent nucleosomal structures and nonâ€coding RNAs.. FASEB Journal, 2013, 27, 456.2.	0.5	0
45	Chromatin remodeling by the CHD7 protein is impaired by mutations that cause human developmental disorders. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19238-19243.	7.1	102
46	Histone Variant H2A.Bbd Is Associated with Active Transcription and mRNA Processing in Human Cells. Molecular Cell, 2012, 47, 596-607.	9.7	92
47	The fragile X mental retardation protein FMRP plays a role in the DNA damage response. FASEB Journal, 2012, 26, 88.1.	0.5	1
48	Compaction of chromatin by diverse Polycomb group proteins requires localized regions of high charge. Genes and Development, 2011, 25, 2210-2221.	5.9	211
49	The genomic binding sites of a noncoding RNA. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20497-20502.	7.1	377
50	Structural Basis of Silencing: Sir3 BAH Domain in Complex with a Nucleosome at 3.0 Ã… Resolution. Science, 2011, 334, 977-982.	12.6	241
51	A Region of the Human HOXD Cluster that Confers Polycomb-Group Responsiveness. Cell, 2010, 140, 99-110.	28.9	289
52	Interaction of HP1 and Brg1/Brm with the Globular Domain of Histone H3 Is Required for HP1-Mediated Repression. PLoS Genetics, 2009, 5, e1000769.	3.5	74
53	Mechanisms of Polycomb gene silencing: knowns and unknowns. Nature Reviews Molecular Cell Biology, 2009, 10, 697-708.	37.0	1,185
54	Purification of Proteins Associated with Specific Genomic Loci. Cell, 2009, 136, 175-186.	28.9	462

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55	Analysis of a Polycomb Group Protein Defines Regions That Link Repressive Activity on Nucleosomal Templates to In Vivo Function. Molecular and Cellular Biology, 2005, 25, 6578-6591.	2.3	72
56	Requirement for Sex Comb on Midleg Protein Interactions in Drosophila Polycomb Group Repression. Genetics, 2004, 167, 1225-1239.	2.9	55
57	Division of labor in Polycomb group repression. Trends in Biochemical Sciences, 2004, 29, 478-485.	7.5	206
58	Chromatin Compaction by a Polycomb Group Protein Complex. Science, 2004, 306, 1574-1577.	12.6	736
59	Propagation of Silencing. Molecular Cell, 2004, 13, 415-425.	9.7	95
60	Regulation of Polycomb group complexes by the sequence-specific DNA binding proteins Zeste and GAGA. Genes and Development, 2003, 17, 2741-2746.	5.9	74
61	Native and Recombinant Polycomb Group Complexes Establish a Selective Block to Template Accessibility To Repress Transcription In Vitro. Molecular and Cellular Biology, 2002, 22, 7919-7928.	2.3	94
62	The Core of the Polycomb Repressive Complex Is Compositionally and Functionally Conserved in Flies and Humans. Molecular and Cellular Biology, 2002, 22, 6070-6078.	2.3	360
63	Histone Methyltransferase Activity of a Drosophila Polycomb Group Repressor Complex. Cell, 2002, 111, 197-208.	28.9	1,416
64	Reconstitution of a Functional Core Polycomb Repressive Complex. Molecular Cell, 2001, 8, 545-556.	9.7	345
65	Specifying transcription. Nature, 2001, 414, 859-861.	27.8	6
66	Mechanisms of transcriptional memory. Nature Reviews Molecular Cell Biology, 2001, 2, 409-421.	37.0	345
67	A Drosophila Polycomb group complex includes Zeste and dTAFII proteins. Nature, 2001, 412, 655-660.	27.8	349
68	Purification and characterization of mSin3A-containing Brg1 and hBrm chromatin remodeling complexes. Genes and Development, 2001, 15, 603-618.	5.9	251
69	A shared but complex bridge. Nature, 1999, 399, 199-200.	27.8	26
70	Stabilization of Chromatin Structure by PRC1, a Polycomb Complex. Cell, 1999, 98, 37-46.	28.9	735
71	Chromatin deacetylation by an ATP-dependent nucleosome remodelling complex. Nature, 1998, 395, 917-921.	27.8	620
72	The C-terminal hydrophobic repeat ofSchizosaccharomyces pombe heat shock factor is not required for heat-induced DNA-binding. , 1998, 14, 733-746.		1

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73	A snapshot of a dynamic nuclear building block. Nature Structural Biology, 1997, 4, 763-766.	9.7	9
74	Nucleosome disruption and enhancement of activator binding by a human SW1/SNF complex. Nature, 1994, 370, 477-481.	27.8	744
75	Facilitated binding of TATA-binding protein to nucleosomal DNA. Nature, 1994, 370, 481-485.	27.8	598
76	Activation in vitro of sequence-specific DNA binding by a human regulatory factor. Nature, 1988, 335, 372-375.	27.8	291