

Robert E Kingston

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

14,826
citations

53939

47
h-index

87275

74
g-index

80
all docs

80
docs citations

80
times ranked

16440
citing authors

#	ARTICLE	IF	CITATIONS
1	HERVH-derived lncRNAs negatively regulate chromatin targeting and remodeling mediated by CHD7. <i>Life Science Alliance</i> , 2022, 5, e202101127.	1.3	3
2	TRACE generates fluorescent human reporter cell lines to characterize epigenetic pathways. <i>Molecular Cell</i> , 2022, 82, 479-491.e7.	4.5	7
3	Context-specific Polycomb mechanisms in development. <i>Nature Reviews Genetics</i> , 2022, 23, 680-695.	7.7	40
4	Elongin A associates with actively transcribed genes and modulates enhancer RNA levels with limited impact on transcription elongation rate in vivo. <i>Journal of Biological Chemistry</i> , 2021, 296, 100202.	1.6	15
5	Elongin A regulates transcription in vivo through enhanced RNA polymerase processivity. <i>Journal of Biological Chemistry</i> , 2021, 296, 100170.	1.6	7
6	Full methylation of H3K27 by PRC2 is dispensable for initial embryoid body formation but required to maintain differentiated cell identity. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	11
7	A Polycomb domain found in committed cells impairs differentiation when introduced into PRC1 in pluripotent cells. <i>Molecular Cell</i> , 2021, 81, 4677-4691.e8.	4.5	20
8	Modulating mesendoderm competence during human germ layer differentiation. <i>Cell Reports</i> , 2021, 37, 109990.	2.9	11
9	S-phase Enriched Non-coding RNAs Regulate Gene Expression and Cell Cycle Progression. <i>Cell Reports</i> , 2020, 31, 107629.	2.9	11
10	De Novo Variants in the ATPase Module of MORC2 Cause a Neurodevelopmental Disorder with Growth Retardation and Variable Craniofacial Dysmorphism. <i>American Journal of Human Genetics</i> , 2020, 107, 352-363.	2.6	64
11	lncRNA DIGIT and BRD3 protein form phase-separated condensates to regulate endoderm differentiation. <i>Nature Cell Biology</i> , 2020, 22, 1211-1222.	4.6	100
12	The CBX family of proteins in transcriptional repression and memory. <i>Journal of Biosciences</i> , 2020, 45, 1.	0.5	32
13	The CBX family of proteins in transcriptional repression and memory. <i>Journal of Biosciences</i> , 2020, 45, .	0.5	8
14	Xist RNA antagonizes the SWI/SNF chromatin remodeler BRG1 on the inactive X chromosome. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 96-109.	3.6	54
15	Phase separation of Polycomb-repressive complex 1 is governed by a charged disordered region of CBX2. <i>Genes and Development</i> , 2019, 33, 799-813.	2.7	264
16	A conserved genetic interaction between Spt6 and Set2 regulates H3K36 methylation. <i>Nucleic Acids Research</i> , 2019, 47, 3888-3903.	6.5	33
17	Dynamics of activating and repressive histone modifications in <i>Drosophila</i> neural stem cell lineages and brain tumors. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	7
18	Beyond the Histone Code: A Physical Map of Chromatin States. <i>Molecular Cell</i> , 2018, 69, 5-7.	4.5	10

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19	Dynamic condensates activate transcription. <i>Science</i> , 2018, 361, 329-330.	6.0	64
20	Prostaglandin E2 Stimulates CREB-Mediated Modification of Histone Variant Nucleosomes at Enhancers to Promote Hematopoietic Stem Cell Fate. <i>Blood</i> , 2018, 132, 530-530.	0.6	1
21	Polycomb Repressive Complex 1 Generates Discrete Compacted Domains that Change during Differentiation. <i>Molecular Cell</i> , 2017, 65, 432-446.e5.	4.5	287
22	Mutation of a nucleosome compaction region disrupts Polycomb-mediated axial patterning. <i>Science</i> , 2017, 355, 1081-1084.	6.0	133
23	Hyperactivation of HUSH complex function by Charcot-Marie-Tooth disease mutation in MORC2. <i>Nature Genetics</i> , 2017, 49, 1035-1044.	9.4	105
24	Widespread changes in nucleosome accessibility without changes in nucleosome occupancy during a rapid transcriptional induction. <i>Genes and Development</i> , 2017, 31, 451-462.	2.7	90
25	Multitasking by Polycomb response elements. <i>Genes and Development</i> , 2017, 31, 1069-1072.	2.7	8
26	Polycomb Repressive Complex 2 Methylates Elongin A to Regulate Transcription. <i>Molecular Cell</i> , 2017, 68, 872-884.e6.	4.5	50
27	Enhanced chromatin accessibility of the dosage compensated Drosophila male X-chromosome requires the CLAMP zinc finger protein. <i>PLoS ONE</i> , 2017, 12, e0186855.	1.1	29
28	MNase titration reveals differences between nucleosome occupancy and chromatin accessibility. <i>Nature Communications</i> , 2016, 7, 11485.	5.8	185
29	Regulated large-scale nucleosome density patterns and precise nucleosome positioning correlate with V(D)J recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6427-E6436.	3.3	31
30	Structural, super-resolution microscopy analysis of paraspeckle nuclear body organization. <i>Journal of Cell Biology</i> , 2016, 214, 817-830.	2.3	262
31	CAT7 and cat7l Long Non-coding RNAs Tune Polycomb Repressive Complex 1 Function during Human and Zebrafish Development. <i>Journal of Biological Chemistry</i> , 2016, 291, 19558-19572.	1.6	32
32	Molecular Dissection of Chromatin Maturation via Click Chemistry. <i>Current Protocols in Molecular Biology</i> , 2016, 114, 21.33.1-21.33.11.	2.9	1
33	Chromatin topology is coupled to Polycomb group protein subnuclear organization. <i>Nature Communications</i> , 2016, 7, 10291.	5.8	176
34	Enhancer regions show high histone H3.3 turnover that changes during differentiation. <i>ELife</i> , 2016, 5, .	2.8	86
35	Nucleosomal occupancy changes locally over key regulatory regions during cell differentiation and reprogramming. <i>Nature Communications</i> , 2014, 5, 4719.	5.8	80
36	The Long Noncoding RNAs NEAT1 and MALAT1 Bind Active Chromatin Sites. <i>Molecular Cell</i> , 2014, 55, 791-802.	4.5	578

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37	Transcriptional Regulation by Trithorax-Group Proteins. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a019349-a019349.	2.3	103
38	A Chromatin-Dependent Role of the Fragile X Mental Retardation Protein FMRP in the DNA Damage Response. <i>Cell</i> , 2014, 157, 869-881.	13.5	151
39	H3K27 modifications define segmental regulatory domains in the <i>Drosophila</i> bithorax complex. <i>ELife</i> , 2014, 3, e02833.	2.8	111
40	Multiplexed Illumina sequencing libraries from picogram quantities of DNA. <i>BMC Genomics</i> , 2013, 14, 466.	1.2	74
41	High-resolution Xist binding maps reveal two-step spreading during X-chromosome inactivation. <i>Nature</i> , 2013, 504, 465-469.	13.7	351
42	Occupying Chromatin: Polycomb Mechanisms for Getting to Genomic Targets, Stopping Transcriptional Traffic, and Staying Put. <i>Molecular Cell</i> , 2013, 49, 808-824.	4.5	638
43	Variable Requirements for DNA-Binding Proteins at Polycomb-Dependent Repressive Regions in Human HOX Clusters. <i>Molecular and Cellular Biology</i> , 2013, 33, 3274-3285.	1.1	30
44	Epigenetic mechanism: silent nucleosomal structures and non-coding RNAs. <i>FASEB Journal</i> , 2013, 27, 456.2.	0.2	0
45	Chromatin remodeling by the CHD7 protein is impaired by mutations that cause human developmental disorders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19238-19243.	3.3	102
46	Histone Variant H2A.Bbd Is Associated with Active Transcription and mRNA Processing in Human Cells. <i>Molecular Cell</i> , 2012, 47, 596-607.	4.5	92
47	The fragile X mental retardation protein FMRP plays a role in the DNA damage response. <i>FASEB Journal</i> , 2012, 26, 88.1.	0.2	1
48	Compaction of chromatin by diverse Polycomb group proteins requires localized regions of high charge. <i>Genes and Development</i> , 2011, 25, 2210-2221.	2.7	211
49	The genomic binding sites of a noncoding RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20497-20502.	3.3	377
50	Structural Basis of Silencing: Sir3 BAH Domain in Complex with a Nucleosome at 3.0 Å... Resolution. <i>Science</i> , 2011, 334, 977-982.	6.0	241
51	A Region of the Human HOXD Cluster that Confers Polycomb-Group Responsiveness. <i>Cell</i> , 2010, 140, 99-110.	13.5	289
52	Interaction of HP1 and Brg1/Brm with the Globular Domain of Histone H3 Is Required for HP1-Mediated Repression. <i>PLoS Genetics</i> , 2009, 5, e1000769.	1.5	74
53	Mechanisms of Polycomb gene silencing: knowns and unknowns. <i>Nature Reviews Molecular Cell Biology</i> , 2009, 10, 697-708.	16.1	1,185
54	Purification of Proteins Associated with Specific Genomic Loci. <i>Cell</i> , 2009, 136, 175-186.	13.5	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. <i>Molecular and Cellular Biology</i> , 2005, 25, 6578-6591.	1.1	72
56	Requirement for Sex Comb on Midleg Protein Interactions in <i>Drosophila</i> Polycomb Group Repression. <i>Genetics</i> , 2004, 167, 1225-1239.	1.2	55
57	Division of labor in Polycomb group repression. <i>Trends in Biochemical Sciences</i> , 2004, 29, 478-485.	3.7	206
58	Chromatin Compaction by a Polycomb Group Protein Complex. <i>Science</i> , 2004, 306, 1574-1577.	6.0	736
59	Propagation of Silencing. <i>Molecular Cell</i> , 2004, 13, 415-425.	4.5	95
60	Regulation of Polycomb group complexes by the sequence-specific DNA binding proteins Zeste and GAGA. <i>Genes and Development</i> , 2003, 17, 2741-2746.	2.7	74
61	Native and Recombinant Polycomb Group Complexes Establish a Selective Block to Template Accessibility To Repress Transcription In Vitro. <i>Molecular and Cellular Biology</i> , 2002, 22, 7919-7928.	1.1	94
62	The Core of the Polycomb Repressive Complex Is Compositionally and Functionally Conserved in Flies and Humans. <i>Molecular and Cellular Biology</i> , 2002, 22, 6070-6078.	1.1	360
63	Histone Methyltransferase Activity of a <i>Drosophila</i> Polycomb Group Repressor Complex. <i>Cell</i> , 2002, 111, 197-208.	13.5	1,416
64	Reconstitution of a Functional Core Polycomb Repressive Complex. <i>Molecular Cell</i> , 2001, 8, 545-556.	4.5	345
65	Specifying transcription. <i>Nature</i> , 2001, 414, 859-861.	13.7	6
66	Mechanisms of transcriptional memory. <i>Nature Reviews Molecular Cell Biology</i> , 2001, 2, 409-421.	16.1	345
67	A <i>Drosophila</i> Polycomb group complex includes Zeste and dTAFII proteins. <i>Nature</i> , 2001, 412, 655-660.	13.7	349
68	Purification and characterization of mSin3A-containing Brg1 and hBrm chromatin remodeling complexes. <i>Genes and Development</i> , 2001, 15, 603-618.	2.7	251
69	A shared but complex bridge. <i>Nature</i> , 1999, 399, 199-200.	13.7	26
70	Stabilization of Chromatin Structure by PRC1, a Polycomb Complex. <i>Cell</i> , 1999, 98, 37-46.	13.5	735
71	Chromatin deacetylation by an ATP-dependent nucleosome remodelling complex. <i>Nature</i> , 1998, 395, 917-921.	13.7	620
72	The C-terminal hydrophobic repeat of <i>Schizosaccharomyces pombe</i> 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. <i>Nature Structural Biology</i> , 1997, 4, 763-766.	9.7	9
74	Nucleosome disruption and enhancement of activator binding by a human SW1/SNF complex. <i>Nature</i> , 1994, 370, 477-481.	13.7	744
75	Facilitated binding of TATA-binding protein to nucleosomal DNA. <i>Nature</i> , 1994, 370, 481-485.	13.7	598
76	Activation in vitro of sequence-specific DNA binding by a human regulatory factor. <i>Nature</i> , 1988, 335, 372-375.	13.7	291