Edwin R Smith

List of Publications by Year in descending order

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FOWIN R SMITH

#	Article	IF	CITATIONS
1	AFF4, a Component of the ELL/P-TEFb Elongation Complex and a Shared Subunit of MLL Chimeras, Can Link Transcription Elongation to Leukemia. Molecular Cell, 2010, 37, 429-437.	9.7	504
2	The MLL3/MLL4 Branches of the COMPASS Family Function as Major Histone H3K4 Monomethylases at Enhancers. Molecular and Cellular Biology, 2013, 33, 4745-4754.	2.3	329
3	Global Analysis of H3K4 Methylation Defines MLL Family Member Targets and Points to a Role for MLL1-Mediated H3K4 Methylation in the Regulation of Transcriptional Initiation by RNA Polymerase II. Molecular and Cellular Biology, 2009, 29, 6074-6085.	2.3	308
4	Born to run: control of transcription elongation by RNA polymerase II. Nature Reviews Molecular Cell Biology, 2018, 19, 464-478.	37.0	304
5	The super elongation complex (SEC) and MLL in development and disease. Genes and Development, 2011, 25, 661-672.	5.9	289
6	Enhancer biology and enhanceropathies. Nature Structural and Molecular Biology, 2014, 21, 210-219.	8.2	259
7	PAF1, a Molecular Regulator of Promoter-Proximal Pausing by RNA Polymerase II. Cell, 2015, 162, 1003-1015.	28.9	196
8	The Chromatin Signaling Pathway: Diverse Mechanisms of Recruitment of Histone-Modifying Enzymes and Varied Biological Outcomes. Molecular Cell, 2010, 40, 689-701.	9.7	195
9	The COMPASS Family of H3K4 Methylases in Drosophila. Molecular and Cellular Biology, 2011, 31, 4310-4318.	2.3	195
10	Histone H3K4 monomethylation catalyzed by Trr and mammalian COMPASS-like proteins at enhancers is dispensable for development and viability. Nature Genetics, 2017, 49, 1647-1653.	21.4	168
11	The Mll2 branch of the COMPASS family regulates bivalent promoters in mouse embryonic stem cells. Nature Structural and Molecular Biology, 2013, 20, 1093-1097.	8.2	165
12	Dynamic transcriptional events in embryonic stem cells mediated by the super elongation complex (SEC). Genes and Development, 2011, 25, 1486-1498.	5.9	161
13	Characterization of Human Cyclin-Dependent Kinase 12 (CDK12) and CDK13 Complexes in C-Terminal Domain Phosphorylation, Gene Transcription, and RNA Processing. Molecular and Cellular Biology, 2015, 35, 928-938.	2.3	153
14	Resetting the epigenetic balance of Polycomb and COMPASS function at enhancers for cancer therapy. Nature Medicine, 2018, 24, 758-769.	30.7	125
15	<i>Drosophila</i> UTX Is a Histone H3 Lys27 Demethylase That Colocalizes with the Elongating Form of RNA Polymerase II. Molecular and Cellular Biology, 2008, 28, 1041-1046.	2.3	120
16	NELF Regulates a Promoter-Proximal Step Distinct from RNA Pol II Pause-Release. Molecular Cell, 2020, 78, 261-274.e5.	9.7	110
17	Therapeutic Targeting of MLL Degradation Pathways in MLL-Rearranged Leukemia. Cell, 2017, 168, 59-72.e13.	28.9	99
18	PAF1 regulation of promoter-proximal pause release via enhancer activation. Science, 2017, 357, 1294-1298.	12.6	95

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19	Zic2 Is an Enhancer-Binding Factor Required for Embryonic Stem Cell Specification. Molecular Cell, 2015, 57, 685-694.	9.7	92
20	TET2 coactivates gene expression through demethylation of enhancers. Science Advances, 2018, 4, eaau6986.	10.3	86
21	Targeting Processive Transcription Elongation via SEC Disruption for MYC-Induced Cancer Therapy. Cell, 2018, 175, 766-779.e17.	28.9	86
22	CATACOMB: An endogenous inducible gene that antagonizes H3K27 methylation activity of Polycomb repressive complex 2 via an H3K27M-like mechanism. Science Advances, 2019, 5, eaax2887.	10.3	86
23	Not All H3K4 Methylations Are Created Equal: Mll2/COMPASS Dependency in Primordial Germ Cell Specification. Molecular Cell, 2017, 65, 460-475.e6.	9.7	81
24	Uncoupling histone H3K4 trimethylation from developmental gene expression via an equilibrium of COMPASS, Polycomb and DNA methylation. Nature Genetics, 2020, 52, 615-625.	21.4	76
25	The Little Elongation Complex Regulates Small Nuclear RNA Transcription. Molecular Cell, 2011, 44, 954-965.	9.7	75
26	Analysis of dynamic changes in retinoid-induced transcription and epigenetic profiles of murine <i>Hox</i> clusters in ES cells. Genome Research, 2015, 25, 1229-1243.	5.5	64
27	Transcriptional elongation checkpoint control in development and disease. Genes and Development, 2013, 27, 1079-1088.	5.9	63
28	Regulation of the imprinted <i>Dlk1-Dio3</i> locus by allele-specific enhancer activity. Genes and Development, 2016, 30, 92-101.	5.9	55
29	An Mll4/COMPASS-Lsd1 epigenetic axis governs enhancer function and pluripotency transition in embryonic stem cells. Science Advances, 2018, 4, eaap8747.	10.3	55
30	DOT1L-controlled cell-fate determination and transcription elongation are independent of H3K79 methylation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27365-27373.	7.1	43
31	Aberrant activation of non-coding RNA targets of transcriptional elongation complexes contributes to TDP-43 toxicity. Nature Communications, 2018, 9, 4406.	12.8	40
32	Regulation of the transcriptional activity of poised RNA polymerase II by the elongation factor ELL. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8575-8579.	7.1	38
33	Acute perturbation strategies in interrogating RNA polymerase II elongation factor function in gene expression. Genes and Development, 2021, 35, 273-285.	5.9	25
34	A small UTX stabilization domain of Trr is conserved within mammalian MLL3-4/COMPASS and is sufficient to rescue loss of viability in null animals. Genes and Development, 2020, 34, 1493-1502.	5.9	14
35	Therapeutic targeting of transcriptional elongation in diffuse intrinsic pontine glioma. Neuro-Oncology, 2021, 23, 1348-1359.	1.2	12
36	The A, B, Gs of silencing. Genes and Development, 2007, 21, 1141-1144.	5.9	9

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37	A ChIP-exo screen of 887 Protein Capture Reagents Program transcription factor antibodies in human cells. Genome Research, 2021, 31, 1663-1679.	5.5	9
38	Histone Cross-Talk in Stem Cells. Science, 2009, 323, 221-222.	12.6	5