

# Edwin R Smith

## List of Publications by Year in descending order

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38  
papers

4,796  
citations

168829

31  
h-index

340414

39  
g-index

40  
all docs

40  
docs citations

40  
times ranked

8169  
citing authors

#	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. <i>Molecular Cell</i> , 2010, 37, 429-437.	4.5	504
2	The MLL3/MLL4 Branches of the COMPASS Family Function as Major Histone H3K4 Monomethylases at Enhancers. <i>Molecular and Cellular Biology</i> , 2013, 33, 4745-4754.	1.1	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. <i>Molecular and Cellular Biology</i> , 2009, 29, 6074-6085.	1.1	308
4	Born to run: control of transcription elongation by RNA polymerase II. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 464-478.	16.1	304
5	The super elongation complex (SEC) and MLL in development and disease. <i>Genes and Development</i> , 2011, 25, 661-672.	2.7	289
6	Enhancer biology and enhanceropathies. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 210-219.	3.6	259
7	PAF1, a Molecular Regulator of Promoter-Proximal Pausing by RNA Polymerase II. <i>Cell</i> , 2015, 162, 1003-1015.	13.5	196
8	The Chromatin Signaling Pathway: Diverse Mechanisms of Recruitment of Histone-Modifying Enzymes and Varied Biological Outcomes. <i>Molecular Cell</i> , 2010, 40, 689-701.	4.5	195
9	The COMPASS Family of H3K4 Methylases in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 4310-4318.	1.1	195
10	Histone H3K4 monomethylation catalyzed by Trr and mammalian COMPASS-like proteins at enhancers is dispensable for development and viability. <i>Nature Genetics</i> , 2017, 49, 1647-1653.	9.4	168
11	The Mll2 branch of the COMPASS family regulates bivalent promoters in mouse embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1093-1097.	3.6	165
12	Dynamic transcriptional events in embryonic stem cells mediated by the super elongation complex (SEC). <i>Genes and Development</i> , 2011, 25, 1486-1498.	2.7	161
13	Characterization of Human Cyclin-Dependent Kinase 12 (CDK12) and CDK13 Complexes in C-Terminal Domain Phosphorylation, Gene Transcription, and RNA Processing. <i>Molecular and Cellular Biology</i> , 2015, 35, 928-938.	1.1	153
14	Resetting the epigenetic balance of Polycomb and COMPASS function at enhancers for cancer therapy. <i>Nature Medicine</i> , 2018, 24, 758-769.	15.2	125
15	<i>Drosophila</i> UTX Is a Histone H3 Lys27 Demethylase That Colocalizes with the Elongating Form of RNA Polymerase II. <i>Molecular and Cellular Biology</i> , 2008, 28, 1041-1046.	1.1	120
16	NELF Regulates a Promoter-Proximal Step Distinct from RNA Pol II Pause-Release. <i>Molecular Cell</i> , 2020, 78, 261-274.e5.	4.5	110
17	Therapeutic Targeting of MLL Degradation Pathways in MLL-Rearranged Leukemia. <i>Cell</i> , 2017, 168, 59-72.e13.	13.5	99
18	PAF1 regulation of promoter-proximal pause release via enhancer activation. <i>Science</i> , 2017, 357, 1294-1298.	6.0	95

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19	Zic2 Is an Enhancer-Binding Factor Required for Embryonic Stem Cell Specification. <i>Molecular Cell</i> , 2015, 57, 685-694.	4.5	92
20	TET2 coactivates gene expression through demethylation of enhancers. <i>Science Advances</i> , 2018, 4, eaau6986.	4.7	86
21	Targeting Processive Transcription Elongation via SEC Disruption for MYC-Induced Cancer Therapy. <i>Cell</i> , 2018, 175, 766-779.e17.	13.5	86
22	CATACOMB: An endogenous inducible gene that antagonizes H3K27 methylation activity of Polycomb repressive complex 2 via an H3K27M-like mechanism. <i>Science Advances</i> , 2019, 5, eaax2887.	4.7	86
23	Not All H3K4 Methylations Are Created Equal: Mll2/COMPASS Dependency in Primordial Germ Cell Specification. <i>Molecular Cell</i> , 2017, 65, 460-475.e6.	4.5	81
24	Uncoupling histone H3K4 trimethylation from developmental gene expression via an equilibrium of COMPASS, Polycomb and DNA methylation. <i>Nature Genetics</i> , 2020, 52, 615-625.	9.4	76
25	The Little Elongation Complex Regulates Small Nuclear RNA Transcription. <i>Molecular Cell</i> , 2011, 44, 954-965.	4.5	75
26	Analysis of dynamic changes in retinoid-induced transcription and epigenetic profiles of murine <i>Hox</i> clusters in ES cells. <i>Genome Research</i> , 2015, 25, 1229-1243.	2.4	64
27	Transcriptional elongation checkpoint control in development and disease. <i>Genes and Development</i> , 2013, 27, 1079-1088.	2.7	63
28	Regulation of the imprinted <i>Dlk1-Dio3</i> locus by allele-specific enhancer activity. <i>Genes and Development</i> , 2016, 30, 92-101.	2.7	55
29	An Mll4/COMPASS-Lsd1 epigenetic axis governs enhancer function and pluripotency transition in embryonic stem cells. <i>Science Advances</i> , 2018, 4, eaap8747.	4.7	55
30	DOT1L-controlled cell-fate determination and transcription elongation are independent of H3K79 methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27365-27373.	3.3	43
31	Aberrant activation of non-coding RNA targets of transcriptional elongation complexes contributes to TDP-43 toxicity. <i>Nature Communications</i> , 2018, 9, 4406.	5.8	40
32	Regulation of the transcriptional activity of poised RNA polymerase II by the elongation factor ELL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8575-8579.	3.3	38
33	Acute perturbation strategies in interrogating RNA polymerase II elongation factor function in gene expression. <i>Genes and Development</i> , 2021, 35, 273-285.	2.7	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. <i>Genes and Development</i> , 2020, 34, 1493-1502.	2.7	14
35	Therapeutic targeting of transcriptional elongation in diffuse intrinsic pontine glioma. <i>Neuro-Oncology</i> , 2021, 23, 1348-1359.	0.6	12
36	The A, B, Gs of silencing. <i>Genes and Development</i> , 2007, 21, 1141-1144.	2.7	9

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37	A ChIP-exo screen of 887 Protein Capture Reagents Program transcription factor antibodies in human cells. <i>Genome Research</i> , 2021, 31, 1663-1679.	2.4	9
38	Histone Cross-Talk in Stem Cells. <i>Science</i> , 2009, 323, 221-222.	6.0	5