

Edwin R Smith

List of Publications by Year in descending order

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Version: 2024-02-01

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 | 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 |
| 2 | Therapeutic targeting of transcriptional elongation in diffuse intrinsic pontine glioma. <i>Neuro-Oncology</i> , 2021, 23, 1348-1359. | 0.6 | 12 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| 7 | 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 |
| 8 | 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 |
| 9 | 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 |
| 10 | TET2 coactivates gene expression through demethylation of enhancers. <i>Science Advances</i> , 2018, 4, eaau6986. | 4.7 | 86 |
| 11 | 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 |
| 12 | Targeting Processive Transcription Elongation via SEC Disruption for MYC-Induced Cancer Therapy. <i>Cell</i> , 2018, 175, 766-779.e17. | 13.5 | 86 |
| 13 | 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 |
| 14 | 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 |
| 15 | 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 |
| 16 | Therapeutic Targeting of MLL Degradation Pathways in MLL-Rearranged Leukemia. <i>Cell</i> , 2017, 168, 59-72.e13. | 13.5 | 99 |
| 17 | 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 |
| 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 | 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 |
| 20 | 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 |
| 21 | Zic2 Is an Enhancer-Binding Factor Required for Embryonic Stem Cell Specification. <i>Molecular Cell</i> , 2015, 57, 685-694. | 4.5 | 92 |
| 22 | PAF1, a Molecular Regulator of Promoter-Proximal Pausing by RNA Polymerase II. <i>Cell</i> , 2015, 162, 1003-1015. | 13.5 | 196 |
| 23 | 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 |
| 24 | Enhancer biology and enhanceropathies. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 210-219. | 3.6 | 259 |
| 25 | 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 |
| 26 | 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 |
| 27 | Transcriptional elongation checkpoint control in development and disease. <i>Genes and Development</i> , 2013, 27, 1079-1088. | 2.7 | 63 |
| 28 | The Little Elongation Complex Regulates Small Nuclear RNA Transcription. <i>Molecular Cell</i> , 2011, 44, 954-965. | 4.5 | 75 |
| 29 | The COMPASS Family of H3K4 Methylases in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 4310-4318. | 1.1 | 195 |
| 30 | 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 |
| 31 | The super elongation complex (SEC) and MLL in development and disease. <i>Genes and Development</i> , 2011, 25, 661-672. | 2.7 | 289 |
| 32 | 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 |
| 33 | 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 |
| 34 | Histone Cross-Talk in Stem Cells. <i>Science</i> , 2009, 323, 221-222. | 6.0 | 5 |
| 35 | 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 |
| 36 | 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 |

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|----|--|-----|-----------|
| 37 | <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 |
| 38 | The A, B, Gs of silencing. <i>Genes and Development</i> , 2007, 21, 1141-1144. | 2.7 | 9 |