

Emily J Rendleman

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,817
citations

331670

21
h-index

526287

27
g-index

27
all docs

27
docs citations

27
times ranked

3487
citing authors

#	ARTICLE	IF	CITATIONS
1	BMAL1 drives muscle repair through control of hypoxic NAD ⁺ regeneration in satellite cells. <i>Genes and Development</i> , 2022, 36, 149-166.	5.9	13
2	A synthetic lethality screen reveals ING5 as a genetic dependency of catalytically dead Set1A/COMPASS in mouse embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118385119.	7.1	3
3	Acute perturbation strategies in interrogating RNA polymerase II elongation factor function in gene expression. <i>Genes and Development</i> , 2021, 35, 273-285.	5.9	25
4	Therapeutic targeting of transcriptional elongation in diffuse intrinsic pontine glioma. <i>Neuro-Oncology</i> , 2021, 23, 1348-1359.	1.2	12
5	SPT5 stabilization of promoter-proximal RNA polymerase II. <i>Molecular Cell</i> , 2021, 81, 4413-4424.e5.	9.7	46
6	A trivalent nucleosome interaction by PHIP/BRWD2 is disrupted in neurodevelopmental disorders and cancer. <i>Genes and Development</i> , 2021, 35, 1642-1656.	5.9	16
7	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.	7.1	43
8	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.	5.9	14
9	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.	21.4	76
10	NELF Regulates a Promoter-Proximal Step Distinct from RNA Pol II Pause-Release. <i>Molecular Cell</i> , 2020, 78, 261-274.e5.	9.7	110
11	Coordinated regulation of cellular identity-associated H3K4me3 breadth by the COMPASS family. <i>Science Advances</i> , 2020, 6, eaaz4764.	10.3	37
12	Chromatin Hyperacetylation Impacts Chromosome Folding by Forming a Nuclear Subcompartment. <i>Molecular Cell</i> , 2020, 78, 112-126.e12.	9.7	62
13	Posttranslational Regulation of the Exon Skipping Machinery Controls Aberrant Splicing in Leukemia. <i>Cancer Discovery</i> , 2020, 10, 1388-1409.	9.4	37
14	Î²-Catenin/Tcf7l2-dependent transcriptional regulation of GLUT1 gene expression by Zic family proteins in colon cancer. <i>Science Advances</i> , 2019, 5, eaax0698.	10.3	28
15	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.	10.3	86
16	USP7 Cooperates with NOTCH1 to Drive the Oncogenic Transcriptional Program in T-Cell Leukemia. <i>Clinical Cancer Research</i> , 2019, 25, 222-239.	7.0	66
17	Regulation of MLL/COMPASS stability through its proteolytic cleavage by taspase1 as a possible approach for clinical therapy of leukemia. <i>Genes and Development</i> , 2019, 33, 61-74.	5.9	26
18	An Mll4/COMPASS-Lsd1 epigenetic axis governs enhancer function and pluripotency transition in embryonic stem cells. <i>Science Advances</i> , 2018, 4, eaap8747.	10.3	55

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19	TET2 coactivates gene expression through demethylation of enhancers. <i>Science Advances</i> , 2018, 4, eaau6986.	10.3	86
20	Targeting Processive Transcription Elongation via SEC Disruption for MYC-Induced Cancer Therapy. <i>Cell</i> , 2018, 175, 766-779.e17.	28.9	86
21	Resetting the epigenetic balance of Polycomb and COMPASS function at enhancers for cancer therapy. <i>Nature Medicine</i> , 2018, 24, 758-769.	30.7	125
22	Therapeutic targeting of polycomb and BET bromodomain proteins in diffuse intrinsic pontine gliomas. <i>Nature Medicine</i> , 2017, 23, 493-500.	30.7	332
23	SET1A/COMPASS and shadow enhancers in the regulation of homeotic gene expression. <i>Genes and Development</i> , 2017, 31, 787-801.	5.9	48
24	A cryptic Tudor domain links BRWD2/PHIP to COMPASS-mediated histone H3K4 methylation. <i>Genes and Development</i> , 2017, 31, 2003-2014.	5.9	54
25	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.	21.4	168
26	Histone H3K4 methylation-dependent and -independent functions of Set1A/COMPASS in embryonic stem cell self-renewal and differentiation. <i>Genes and Development</i> , 2017, 31, 1732-1737.	5.9	68
27	PAF1 regulation of promoter-proximal pause release via enhancer activation. <i>Science</i> , 2017, 357, 1294-1298.	12.6	95