David Shechter

List of Publications by Year
in descending order

39 papers	3,933 citations	257450 24 h-index	330143 37 g-index
46 all docs	46 docs citations	46 times ranked	5672 citing authors

#	ARTICLE	IF	CITATIONS
1	Type I and II PRMTs inversely regulate post-transcriptional intron detention through Sm and CHTOP methylation. ELife, 2022, 11, .	6.0	20
2	Independent transcriptomic and proteomic regulation by type I and II protein arginine methyltransferases. IScience, 2021, 24, 102971.	4.1	20
3	A Binary Arginine Methylation Switch on Histone H3 Arginine 2 Regulates Its Interaction with WDR5. Biochemistry, 2020, 59, 3696-3708.	2.5	21
4	Structure of a single-chain H2A/H2B dimer. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 194-198.	0.8	1
5	Rinf Regulates Pluripotency Network Genes and Tet Enzymes in Embryonic Stem Cells. Cell Reports, 2019, 28, 1993-2003.e5.	6.4	18
6	Introduction to the multi-author review on methylation in cellular physiology. Cellular and Molecular Life Sciences, 2019, 76, 2871-2872.	5.4	5
7	Cellular consequences of arginine methylation. Cellular and Molecular Life Sciences, 2019, 76, 2933-2956.	5.4	99
8	Chromatin Characterization inXenopus laevisCell-Free Egg Extracts and Embryos. Cold Spring Harbor Protocols, 2019, 2019, pdb.prot099879.	0.3	5
9	Sarcosine Is Uniquely Modulated by Aging and Dietary Restriction in Rodents and Humans. Cell Reports, 2018, 25, 663-676.e6.	6.4	43
10	A TGFÎ2-PRMT5-MEP50 axis regulates cancer cell invasion through histone H3 and H4 arginine methylation coupled transcriptional activation and repression. Oncogene, 2017, 36, 373-386.	5.9	150
11	Fly Fishing for Histones: Catch and Release by Histone Chaperone Intrinsically Disordered Regions and Acidic Stretches. Journal of Molecular Biology, 2017, 429, 2401-2426.	4.2	62
12	A simplified characterization of S-adenosyl-<scp>l</scp>-methionine-consuming enzymes with 1-Step EZ-MTase: a universal and straightforward coupled-assay for in vitro and in vivo setting. Chemical Science, 2017, 8, 6601-6612.	7.4	18
13	Dynamic intramolecular regulation of the histone chaperone nucleoplasmin controls histone binding and release. Nature Communications, 2017, 8, 2215.	12.8	23
14	Chromatin assembly and transcriptional cross-talk in Xenopus laevis oocyte and egg extracts. International Journal of Developmental Biology, 2016, 60, 315-320.	0.6	12
15	Chaperone-mediated chromatin assembly and transcriptional regulation in Xenopus laevis. International Journal of Developmental Biology, 2016, 60, 271-276.	0.6	3
16	Pax6 associates with H3K4-specific histone methyltransferases Mll1, Mll2, and Set1a and regulates H3K4 methylation at promoters and enhancers. Epigenetics and Chromatin, 2016, 9, 37.	3.9	25
17	The PRMT5 arginine methyltransferase: many roles in development, cancer and beyond. Cellular and Molecular Life Sciences, 2015, 72, 2041-2059.	5.4	364
18	Histone H2A and H4 N-terminal Tails Are Positioned by the MEP50 WD Repeat Protein for Efficient Methylation by the PRMT5 Arginine Methyltransferase. Journal of Biological Chemistry, 2015, 290, 9674-9689.	3.4	75

#	ARTICLE	IF	CITATIONS
19	Developmentally Regulated Post-translational Modification of Nucleoplasmin Controls Histone Sequestration and Deposition. Cell Reports, 2015, 10, 1735-1748.	6.4	41
20	Phosphorylation and arginine methylation mark histone H2A prior to deposition during Xenopus laevis development. Epigenetics and Chromatin, 2014, 7, 22.	3.9	26
21	Seeing Beyond the Double Helix. Journal of Pediatric Ophthalmology and Strabismus, 2014, 51, 268-268.	0.7	1
22	Structure of the Arginine Methyltransferase PRMT5-MEP50 Reveals a Mechanism for Substrate Specificity. PLoS ONE, 2013, 8, e57008.	2.5	109
23	Protein Arginine Methyltransferase Prmt5-Mep50 Methylates Histones H2A and H4 and the Histone Chaperone Nucleoplasmin in Xenopus laevis Eggs. Journal of Biological Chemistry, 2011, 286, 42221-42231.	3.4	49
24	Analysis of histones and chromatin in Xenopus laevis egg and oocyte extracts. Methods, 2010, 51, 3-10.	3.8	16
25	A distinct H2A.X isoform is enriched in<i>Xenopus laevis</i>eggs and early embryos and is phosphorylated in the absence of a checkpoint. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 749-754.	7.1	56
26	Analysis of Histones in Xenopus laevis. Journal of Biological Chemistry, 2009, 284, 1075-1085.	3.4	43
27	Analysis of Histones in Xenopus laevis. Journal of Biological Chemistry, 2009, 284, 1064-1074.	3.4	66
28	WSTF regulates the H2A.X DNA damage response via a novel tyrosine kinase activity. Nature, 2009, 457, 57-62.	27.8	360
29	Extraction, purification and analysis of histones. Nature Protocols, 2007, 2, 1445-1457.	12.0	879
30	A lasting marriage: histones and DNA tie a knot that is here to stay. Nature Reviews Genetics, 2007, 8, S23-S23.	16.3	2
31	ATM and ATR Check in on Origins: A Dynamic Model for Origin Selection and Activation. Cell Cycle, 2005, 4, 238-240.	2.6	38
32	ATM and ATR check in on origins: a dynamic model for origin selection and activation. Cell Cycle, 2005, 4, 235-8.	2.6	25
33	MCM proteins and checkpoint kinases get together at the fork. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10845-10846.	7.1	33
34	DNA Unwinding Is an MCM Complex-dependent and ATP Hydrolysis-dependent Process. Journal of Biological Chemistry, 2004, 279, 45586-45593.	3.4	44
35	ATR and ATM regulate the timing of DNA replication origin firing. Nature Cell Biology, 2004, 6, 648-655.	10.3	333
36	Regulation of DNA replication by ATR: signaling in response to DNA intermediates. DNA Repair, 2004, 3, 901-908.	2.8	170

#	Article	IF	Citations
37	An ATR- and Cdc7-Dependent DNA Damage Checkpoint that Inhibits Initiation of DNA Replication. Molecular Cell, 2003, 11, 203-213.	9.7	331
38	The Intrinsic DNA Helicase Activity of Methanobacterium thermoautotrophicum Î"H Minichromosome Maintenance Protein. Journal of Biological Chemistry, 2000, 275, 15049-15059.	3.4	133
39	Clamp loading, unloading and intrinsic stability of the PCNA, Î² and gp45 sliding clamps of human, E. coli and T4 replicases. Genes To Cells, 1996, 1, 101-113.	1.2	207