

# Stephen A Shinsky

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/208901/publications.pdf>

Version: 2024-02-01

19  
papers

909  
citations

623574

14  
h-index

839398

18  
g-index

19  
all docs

19  
docs citations

19  
times ranked

1496  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Taf14 YEATS domain is a reader of histone crotonylation. <i>Nature Chemical Biology</i> , 2016, 12, 396-398.	3.9	195
2	Histone deacetylase 10 structure and molecular function as a polyamine deacetylase. <i>Nature Communications</i> , 2017, 8, 15368.	5.8	139
3	Biochemical Reconstitution and Phylogenetic Comparison of Human SET1 Family Core Complexes Involved in Histone Methylation. <i>Journal of Biological Chemistry</i> , 2015, 290, 6361-6375.	1.6	92
4	Recognition of Histone Crotonylation by Taf14 Links Metabolic State to Gene Expression. <i>Molecular Cell</i> , 2019, 76, 909-921.e3.	4.5	83
5	Structure/Function Analysis of Recurrent Mutations in SETD2 Protein Reveals a Critical and Conserved Role for a SET Domain Residue in Maintaining Protein Stability and Histone H3 Lys-36 Trimethylation. <i>Journal of Biological Chemistry</i> , 2016, 291, 21283-21295.	1.6	64
6	Targeted Disruption of the Interaction between WD-40 Repeat Protein 5 (WDR5) and Mixed Lineage Leukemia (MLL)/SET1 Family Proteins Specifically Inhibits MLL1 and SETd1A Methyltransferase Complexes. <i>Journal of Biological Chemistry</i> , 2016, 291, 22357-22372.	1.6	56
7	Histone peptide microarray screen of chromo and Tudor domains defines new histone lysine methylation interactions. <i>Epigenetics and Chromatin</i> , 2017, 10, 12.	1.8	47
8	A Non-Active-Site SET Domain Surface Crucial for the Interaction of MLL1 and the RbBP5/Ash2L Heterodimer within MLL Family Core Complexes. <i>Journal of Molecular Biology</i> , 2014, 426, 2283-2299.	2.0	46
9	Chromatin condensation and recruitment of PHD finger proteins to histone H3K4me3 are mutually exclusive. <i>Nucleic Acids Research</i> , 2016, 44, 6102-6112.	6.5	30
10	Automethylation Activities within the Mixed Lineage Leukemia-1 (MLL1) Core Complex Reveal Evidence Supporting a "Two-active Site" Model for Multiple Histone H3 Lysine 4 Methylation. <i>Journal of Biological Chemistry</i> , 2014, 289, 868-884.	1.6	27
11	Polyamine Deacetylase Structure and Catalysis: Prokaryotic Acetylpolyamine Amidohydrolase and Eukaryotic HDAC10. <i>Biochemistry</i> , 2018, 57, 3105-3114.	1.2	27
12	Unique Role of the WD-40 Repeat Protein 5 (WDR5) Subunit within the Mixed Lineage Leukemia 3 (MLL3) Histone Methyltransferase Complex. <i>Journal of Biological Chemistry</i> , 2015, 290, 25819-25833.	1.6	25
13	Discovery of the cryptic function of terpene cyclases as aromatic prenyltransferases. <i>Nature Communications</i> , 2020, 11, 3958.	5.8	22
14	Stepwise Conversion of a Binding Protein to a Fluorescent Switch: Application to <i>Thermoanaerobacter tengcongensis</i> Ribose Binding Protein. <i>Biochemistry</i> , 2013, 52, 600-612.	1.2	19
15	Characterization of the Grp94/OS-9 Chaperone-Lectin Complex. <i>Journal of Molecular Biology</i> , 2014, 426, 3590-3605.	2.0	15
16	First Fluorescent Acetylspermidine Deacetylation Assay for HDAC10 Identifies Selective Inhibitors with Cellular Target Engagement**. <i>ChemBioChem</i> , 2022, 23, .	1.3	9
17	Structure and Function of the Acetylpolyamine Amidohydrolase from the Deep Earth Halophile <i>Marinobacter subterranei</i> . <i>Biochemistry</i> , 2019, 58, 3755-3766.	1.2	8
18	Structure of Sesquisabinene Synthase 1, a Terpenoid Cyclase That Generates a Strained [3.1.0] Bridged-Bicyclic Product. <i>ACS Chemical Biology</i> , 2019, 14, 1011-1019.	1.6	5

#	ARTICLE	IF	CITATIONS
19	A Non-Active Site Set Domain Surface that is Crucial for Di-Methylation of Histone H3 Lysine 4 by the Mixed Lineage Leukemia-1 (MLL1) Core Complex. Biophysical Journal, 2014, 106, 477a.	0.2	0