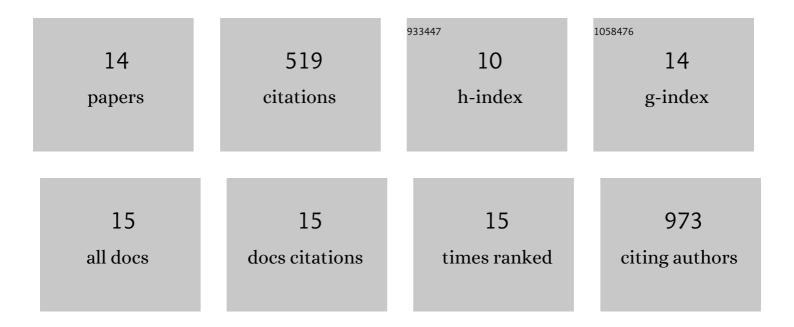
## Robert M Vaughan

List of Publications by Year in descending order

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POREDT M VALICHAN

#	Article	IF	CITATIONS
1	A DNA methylation reader complex that enhances gene transcription. Science, 2018, 362, 1182-1186.	12.6	181
2	Examining the Roles of H3K4 Methylation States with Systematically Characterized Antibodies. Molecular Cell, 2018, 72, 162-177.e7.	9.7	90
3	Chromatin Regulation through Ubiquitin and Ubiquitin-like Histone Modifications. Trends in Biochemical Sciences, 2021, 46, 258-269.	7.5	56
4	Chromatin structure and its chemical modifications regulate the ubiquitin ligase substrate selectivity of UHRF1. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8775-8780.	7.1	39
5	Comparative biochemical analysis of UHRF proteins reveals molecular mechanisms that uncouple UHRF2 from DNA methylation maintenance. Nucleic Acids Research, 2018, 46, 4405-4416.	14.5	25
6	A functional proteomics platform to reveal the sequence determinants of lysine methyltransferase substrate selectivity. Science Advances, 2018, 4, eaav2623.	10.3	25
7	A fluorescent carbapenem for structure function studies of penicillin-binding proteins, β-lactamases, and β-lactam sensors. Analytical Biochemistry, 2014, 463, 70-74.	2.4	17
8	A Read/Write Mechanism Connects p300 Bromodomain Function to H2A.Z Acetylation. IScience, 2019, 21, 773-788.	4.1	16
9	A trivalent nucleosome interaction by PHIP/BRWD2 is disrupted in neurodevelopmental disorders and cancer. Genes and Development, 2021, 35, 1642-1656.	5.9	16
10	Substrate Specificity Profiling of Histone-Modifying Enzymes by Peptide Microarray. Methods in Enzymology, 2016, 574, 31-52.	1.0	15
11	A physical basis for quantitative ChIP-sequencing. Journal of Biological Chemistry, 2020, 295, 15826-15837.	3.4	14
12	The finger loop of the SRA domain in the E3 ligase UHRF1 is a regulator of ubiquitin targeting and is required for the maintenance of DNA methylation. Journal of Biological Chemistry, 2019, 294, 15724-15732.	3.4	12
13	The histone and non-histone methyllysine reader activities of the UHRF1 tandem Tudor domain are dispensable for the propagation of aberrant DNA methylation patterning in cancer cells. Epigenetics and Chromatin, 2020, 13, 44.	3.9	10
14	A Degenerate Peptide Library Approach to Reveal Sequence Determinants of Methyllysine-Driven Protein Interactions. Frontiers in Cell and Developmental Biology, 2020, 8, 241.	3.7	3