

# Raymond C Trievel

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

4,684  
citations

134610

34  
h-index

206121

51  
g-index

59  
all docs

59  
docs citations

59  
times ranked

6886  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular investigation of the tandem Tudor domain and plant homeodomain histone binding domains of the epigenetic regulator <sc>UHRF2</sc>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 835-847.	1.5	3
2	Investigating the structure of UHRF2 TTDâ€PHD with H3K9me3. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
3	Differential processing and localization of human Nocturnin controls metabolism of mRNA and nicotinamide adenine dinucleotide cofactors. <i>Journal of Biological Chemistry</i> , 2020, 295, 15112-15133.	1.6	6
4	An H3K9 methylation-dependent protein interaction regulates the non-enzymatic functions of a putative histone demethylase. <i>ELife</i> , 2020, 9, .	2.8	23
5	Structural and Functional Characterization of Sulfonium Carbonâ€Oxygen Hydrogen Bonding in the Deoxyamino Sugar Methyltransferase TylM1. <i>Biochemistry</i> , 2019, 58, 2152-2159.	1.2	0
6	A nonâ€enzymatic function associated with a putative histone demethylase regulates heterochromatin spreading and inheritance. <i>FASEB Journal</i> , 2019, 33, .	0.2	0
7	Structure, mechanism, and regulation of polycomb-repressive complex 2. <i>Journal of Biological Chemistry</i> , 2018, 293, 13805-13814.	1.6	60
8	Crystallographic and Computational Characterization of Methyl Tetrel Bonding in S-Adenosylmethionine-Dependent Methyltransferases. <i>Molecules</i> , 2018, 23, 2965.	1.7	29
9	Reply to â€Misreading chaperoneâ€substrate complexes from random noiseâ€™. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 990-991.	3.6	2
10	The structure of human Nocturnin reveals a conserved ribonuclease domain that represses target transcript translation and abundance in cells. <i>Nucleic Acids Research</i> , 2018, 46, 6257-6270.	6.5	22
11	Water-Mediated Carbonâ€Oxygen Hydrogen Bonding Facilitates <i>S</i>-Adenosylmethionine Recognition in the Reactivation Domain of Cobalamin-Dependent Methionine Synthase. <i>Biochemistry</i> , 2018, 57, 3733-3740.	1.2	16
12	The HIV-1 Tat Protein Is Monomethylated at Lysine 71 by the Lysine Methyltransferase KMT7. <i>Journal of Biological Chemistry</i> , 2016, 291, 16240-16248.	1.6	16
13	Measuring the Kinetics of Molecular Association by Isothermal Titration Calorimetry. <i>Methods in Enzymology</i> , 2016, 567, 181-213.	0.4	10
14	Visualizing chaperone-assisted protein folding. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 691-697.	3.6	52
15	Sulfurâ€Oxygen Chalcogen Bonding Mediates AdoMet Recognition in the Lysine Methyltransferase SET7/9. <i>ACS Chemical Biology</i> , 2016, 11, 748-754.	1.6	93
16	The LSD1 inhibitor RN-1 induces fetal hemoglobin synthesis and reduces disease pathology in sickle cell mice. <i>Blood</i> , 2015, 126, 386-396.	0.6	74
17	Frequent side chain methyl carbon-oxygen hydrogen bonding in proteins revealed by computational and stereochemical analysis of neutron structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 403-410.	1.5	42
18	Molecular basis for substrate recognition by lysine methyltransferases and demethylases. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1404-1415.	0.9	58

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19	Manipulating Unconventional CH-Based Hydrogen Bonding in a Methyltransferase via Noncanonical Amino Acid Mutagenesis. <i>ACS Chemical Biology</i> , 2014, 9, 1692-1697.	1.6	23
20	Crystal structure of <i>Saccharomyces cerevisiae</i> Aro8, a putative $\epsilon$ -amino adipate aminotransferase. <i>Protein Science</i> , 2013, 22, 1417-1424.	3.1	18
21	Conservation and Functional Importance of Carbon-Oxygen Hydrogen Bonding in AdoMet-Dependent Methyltransferases. <i>Journal of the American Chemical Society</i> , 2013, 135, 15536-15548.	6.6	92
22	Structural and Functional Analysis of JMJD2D Reveals Molecular Basis for Site-Specific Demethylation among JMJD2 Demethylases. <i>Structure</i> , 2013, 21, 98-108.	1.6	62
23	An overview of chromatin modifications. <i>Biopolymers</i> , 2013, 99, 95-97.	1.2	3
24	Carbon-Oxygen Hydrogen Bonding in Biological Structure and Function. <i>Journal of Biological Chemistry</i> , 2012, 287, 41576-41582.	1.6	251
25	Crystal Structure and Functional Analysis of JMJD5 Indicate an Alternate Specificity and Function. <i>Molecular and Cellular Biology</i> , 2012, 32, 4044-4052.	1.1	59
26	Crystal structure of homoisocitrate dehydrogenase from <i>Schizosaccharomyces pombe</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 661-666.	1.5	7
27	Purification and assay protocols for obtaining highly active Jumonji C demethylases. <i>Analytical Biochemistry</i> , 2012, 420, 48-53.	1.1	24
28	Direct Evidence for Methyl Group Coordination by Carbon-Oxygen Hydrogen Bonds in the Lysine Methyltransferase SET7/9. <i>Journal of Biological Chemistry</i> , 2011, 286, 18658-18663.	1.6	55
29	Structure and Function of Histone H3 Lysine 9 Methyltransferases and Demethylases. <i>ChemBioChem</i> , 2011, 12, 254-263.	1.3	75
30	Application of a high-throughput fluorescent acetyltransferase assay to identify inhibitors of homocitrate synthase. <i>Analytical Biochemistry</i> , 2011, 410, 133-140.	1.1	9
31	Substrate and product specificities of SET domain methyltransferases. <i>Epigenetics</i> , 2011, 6, 1059-1067.	1.3	117
32	Structural analysis of the core COMPASS family of histone H3K4 methylases from yeast to human. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20526-20531.	3.3	120
33	Structural Basis for L-Lysine Feedback Inhibition of Homocitrate Synthase*. <i>Journal of Biological Chemistry</i> , 2010, 285, 10446-10453.	1.6	28
34	SET7/9 Catalytic Mutants Reveal the Role of Active Site Water Molecules in Lysine Multiple Methylation. <i>Journal of Biological Chemistry</i> , 2010, 285, 31849-31858.	1.6	57
35	The Cellular Lysine Methyltransferase Set7/9-KMT7 Binds HIV-1 TAR RNA, Monomethylates the Viral Transactivator Tat, and Enhances HIV Transcription. <i>Cell Host and Microbe</i> , 2010, 7, 234-244.	5.1	88
36	Molecular Mechanisms of Lysine Methylation. <i>FASEB Journal</i> , 2010, 24, 78.3.	0.2	0

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37	Crystal Structure and Functional Analysis of Homocitrate Synthase, an Essential Enzyme in Lysine Biosynthesis. <i>Journal of Biological Chemistry</i> , 2009, 284, 35769-35780.	1.6	34
38	Regulation of H3K4 Trimethylation via Cps40 (Spp1) of COMPASS Is Monoubiquitination Independent: Implication for a Phe/Tyr Switch by the Catalytic Domain of Set1. <i>Molecular and Cellular Biology</i> , 2009, 29, 3478-3486.	1.1	54
39	WDR5, a complexed protein. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 678-680.	3.6	123
40	Histone modifying enzymes: Structures, mechanisms, and specificities. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2009, 1789, 58-68.	0.9	272
41	Structural Basis of Protein Lysine Methylation. <i>FASEB Journal</i> , 2009, 23, 89.1.	0.2	0
42	Structural origins for the product specificity of SET domain protein methyltransferases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20659-20664.	3.3	106
43	Kinetic Manifestation of Processivity during Multiple Methylations Catalyzed by SET Domain Protein Methyltransferases. <i>Biochemistry</i> , 2007, 46, 3905-3915.	1.2	44
44	Specificity and mechanism of JMJD2A, a trimethyllysine-specific histone demethylase. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 689-695.	3.6	247
45	Structural basis for the methylation site specificity of SET7/9. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 140-146.	3.6	149
46	Molecular recognition of histone H3 by the WD40 protein WDR5. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 698-703.	3.6	216
47	Histone-modifying enzymes: encrypting an enigmatic epigenetic code. <i>Current Opinion in Structural Biology</i> , 2006, 16, 753-760.	2.6	83
48	Catalytic Roles for Carbon-Oxygen Hydrogen Bonding in SET Domain Lysine Methyltransferases. <i>Journal of Biological Chemistry</i> , 2006, 281, 19280-19287.	1.6	76
49	A coupled fluorescent assay for histone methyltransferases. <i>Analytical Biochemistry</i> , 2005, 342, 86-92.	1.1	112
50	Structure, Specificity, and Mechanism of Protein Lysine Methylation by SET Domain Enzymes. , 2005, , 211-226.		0
51	Structural and functional analysis of SET8, a histone H4 Lys-20 methyltransferase. <i>Genes and Development</i> , 2005, 19, 1455-1465.	2.7	202
52	The SET-domain protein superfamily: protein lysine methyltransferases. <i>Genome Biology</i> , 2005, 6, 227.	13.9	661
53	Structure and Function of Histone Methyltransferases. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2004, 14, 147-170.	0.4	65
54	Mechanism of multiple lysine methylation by the SET domain enzyme Rubisco LSMT. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 545-552.	3.6	119

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55	Structure and Catalytic Mechanism of a SET Domain Protein Methyltransferase. <i>Cell</i> , 2002, 111, 91-103.	13.5	240
56	Application of a Fluorescent Histone Acetyltransferase Assay to Probe the Substrate Specificity of the Human p300/CBP-Associated Factor. <i>Analytical Biochemistry</i> , 2000, 287, 319-328.	1.1	87
57	Catalytic Mechanism and Function of Invariant Glutamic Acid 173 from the Histone Acetyltransferase GCN5 Transcriptional Coactivator. <i>Journal of Biological Chemistry</i> , 1999, 274, 18157-18160.	1.6	198