Cynthia Wolberger

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

115 papers	11,753 citations	52 h-index	108 g-index
134 ext. papers	13,092 ext. citations	14.1 avg, IF	6.33 L-index

#	Paper	IF	Citations
115	The ASCC2 CUE domain in the ALKBH3-ASCC DNA repair complex recognizes adjacent ubiquitins in K63-linked polyubiquitin.. *Journal of Biological Chemistry*, **2021**, 101545	5.4	0
114	Measuring DNA mechanics on the genome scale. *Nature*, **2021**, 589, 462-467	50.4	29
113	How structural biology transformed studies of transcription regulation. *Journal of Biological Chemistry*, **2021**, 296, 100741	5.4	4
112	Potent macrocycle inhibitors of the human SAGA deubiquitinating module.. *Cell Chemical Biology*, **2021**,	8.2	1
111	Comparison of Cross-Regulation by Different OTUB1:E2 Complexes. *Biochemistry*, **2020**, 59, 921-932	3.2	2
110	Structural basis for COMPASS recognition of an H2B-ubiquitinated nucleosome. *ELife*, **2020**, 9,	8.9	35
109	Activation and regulation of H2B-Ubiquitin-dependent histone methyltransferases. *Current Opinion in Structural Biology*, **2019**, 59, 98-106	8.1	22
108	Mechanism of Cross-talk between H2B Ubiquitination and H3 Methylation by Dot1L. *Cell*, **2019**, 176, 1490-1501.e12	56.2	97
107	FACT and Ubp10 collaborate to modulate H2B deubiquitination and nucleosome dynamics. *ELife*, **2019**, 8,	8.9	15
106	Semisynthesis of ubiquitinated histone H2B with a native or nonhydrolyzable linkage. *Methods in Enzymology*, **2019**, 618, 1-27	1.7	6
105	Hydrazide Mimics for Protein Lysine Acylation To Assess Nucleosome Dynamics and Deubiquitinase Action. *Journal of the American Chemical Society*, **2018**, 140, 9478-9485	16.4	21
104	Palladium prompted on-demand cysteine chemistry for the synthesis of challenging and uniquely modified proteins. *Nature Communications*, **2018**, 9, 3154	17.4	68
103	Competition Assay for Measuring Deubiquitinating Enzyme Substrate Affinity. *Methods in Molecular Biology*, **2018**, 1844, 59-70	1.4	2
102	OTUB1 non-catalytically stabilizes the E2 ubiquitin-conjugating enzyme UBE2E1 by preventing its autoubiquitination. *Journal of Biological Chemistry*, **2018**, 293, 18285-18295	5.4	14
101	Active site alanine mutations convert deubiquitinases into high-affinity ubiquitin-binding proteins. *EMBO Reports*, **2018**, 19,	6.5	22
100	Mutations that Allow SIR2 Orthologs to Function in a NAD-Depleted Environment. *Cell Reports*, **2017**, 18, 2310-2319	10.6	8
99	A Tunable Brake for HECT Ubiquitin Ligases. *Molecular Cell*, **2017**, 66, 345-357.e6	17.6	58

98	Total chemical synthesis of SUMO-2-Lys63-linked diubiquitin hybrid chains assisted by removable solubilizing tags. *Chemical Science*, **2017**, 8, 4027-4034	9.4	54
97	Recognition of ubiquitinated nucleosomes. *Current Opinion in Structural Biology*, **2017**, 42, 75-82	8.1	10
96	Not just Salk. *Science*, **2017**, 357, 1105-1106	33.3	3
95	A ubiquitin-dependent signalling axis specific for ALKBH-mediated DNA dealkylation repair. *Nature*, **2017**, 551, 389-393	50.4	52
94	RAP80, ubiquitin and SUMO in the DNA damage response. *Journal of Molecular Medicine*, **2017**, 95, 799-807	5.5	13
93	Enzymatic Analysis of PTEN Ubiquitylation by WWP2 and NEDD4-1 E3 Ligases. *Biochemistry*, **2016**, 55, 3658-66	3.2	28
92	Chemical Synthesis of Phosphorylated Histone H2A at Tyr57 Reveals Insight into the Inhibition Mode of the SAGA Deubiquitinating Module. *Angewandte Chemie*, **2016**, 128, 5056-5060	3.6	12
91	Structural basis for histone H2B deubiquitination by the SAGA DUB module. *Science*, **2016**, 351, 725-8	33.3	154
90	Structural basis for acyl-group discrimination by human Gcn5L2. *Acta Crystallographica Section D: Structural Biology*, **2016**, 72, 841-8	5.5	36
89	Chemical Synthesis of Phosphorylated Histone H2A at Tyr57 Reveals Insight into the Inhibition Mode of the SAGA Deubiquitinating Module. *Angewandte Chemie - International Edition*, **2016**, 55, 4972-6	16.4	50
88	SCIENTIFIC COMMUNITY. Preprints for the life sciences. *Science*, **2016**, 352, 899-901	33.3	68
87	The Substrate Specificity of Sirtuins. *Annual Review of Biochemistry*, **2016**, 85, 405-29	29.1	142
86	Role of E2-RING Interactions in Governing RNF4-Mediated Substrate Ubiquitination. *Journal of Molecular Biology*, **2016**, 428, 4639-4650	6.5	5
85	Nucleosome competition reveals processive acetylation by the SAGA HAT module. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E5461-70	11.5	36
84	Uncovering the role of Sgf73 in maintaining SAGA deubiquitinating module structure and activity. *Journal of Molecular Biology*, **2015**, 427, 1765-78	6.5	13
83	Structure of the yeast Bre1 RING domain. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 1185-90	4.2	7
82	Extracellular nicotinamide phosphoribosyltransferase (NAMPT) promotes M2 macrophage polarization in chronic lymphocytic leukemia. *Blood*, **2015**, 125, 111-23	2.2	117
81	Role of a non-canonical surface of Rad6 in ubiquitin conjugating activity. *Nucleic Acids Research*, **2015**, 43, 9039-50	20.1	16

80	A multilaboratory comparison of calibration accuracy and the performance of external references in analytical ultracentrifugation. *PLoS ONE*, **2015**, 10, e0126420	3.7	55
79	New insights into ubiquitin E3 ligase mechanism. *Nature Structural and Molecular Biology*, **2014**, 21, 301-7	17.6	367
78	Alternate deacylating specificities of the archaeal sirtuins Sir2Af1 and Sir2Af2. *Protein Science*, **2014** , 23, 1686-97	6.3	13
77	The bromodomain of Gcn5 regulates site specificity of lysine acetylation on histone H3. *Molecular and Cellular Proteomics*, **2014**, 13, 2896-910	7.6	50
76	Mechanisms for regulating deubiquitinating enzymes. *Protein Science*, **2014**, 23, 344-53	6.3	23
75	Characterization of the SUMO-binding activity of the myeloproliferative and mental retardation (MYM)-type zinc fingers in ZNF261 and ZNF198. *PLoS ONE*, **2014**, 9, e105271	3.7	18
74	Extracellular Nicotinamide Phosphoribosyltransferase (NAMPT) Shapes the CLL Microenvironment Promoting Macrophage M2 Polarization Via a Non-Enzymatic Mechanism. *Blood*, **2014**, 124, 3316-3316	2.2	
73	A conserved asparagine has a structural role in ubiquitin-conjugating enzymes. *Nature Chemical Biology*, **2013**, 9, 154-6	11.7	49
72	A new RING tossed into an old HAT. *Structure*, **2013**, 21, 1479-81	5.2	4
71	A new DUB makes linear ubiquitin a party to its own destruction. *Cell*, **2013**, 153, 1189-91	56.2	0
70	Architectural organization of the metabolic regulatory enzyme ghrelin O-acyltransferase. *Journal of Biological Chemistry*, **2013**, 288, 32211-32228	5.4	48
69	E2 ubiquitin-conjugating enzymes regulate the deubiquitinating activity of OTUB1. *Nature Structural and Molecular Biology*, **2013**, 20, 1033-9	17.6	76
68	A quantitative analysis of histone methylation and acetylation isoforms from their deuteroacetylated derivatives: application to a series of knockout mutants. *Journal of Mass Spectrometry*, **2013**, 48, 608-15	2.2	5
67	RNF4-Dependent Hybrid SUMO-Ubiquitin Chains are Signals for RAP80 and thereby Mediate the Recruitment of BRCA1 to Sites of DNA Damage. *FASEB Journal*, **2013**, 27, 782.7	0.9	
66	A role for intersubunit interactions in maintaining SAGA deubiquitinating module structure and activity. *Structure*, **2012**, 20, 1414-24	5.2	24
65	RNF4-dependent hybrid SUMO-ubiquitin chains are signals for RAP80 and thereby mediate the recruitment of BRCA1 to sites of DNA damage. *Science Signaling*, **2012**, 5, ra88	8.8	133
64	The mechanism of OTUB1-mediated inhibition of ubiquitination. *Nature*, **2012**, 483, 618-22	50.4	157
63	Biotinylation of lysine method identifies acetylated histone H3 lysine 79 in Saccharomyces cerevisiae as a substrate for Sir2. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, E916-25	11.5	16

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62	A new chapter in the transcription SAGA. *Current Opinion in Structural Biology*, **2011**, 21, 767-74	8.1	38
61	A spectrophotometric assay for conjugation of ubiquitin and ubiquitin-like proteins. *Analytical Biochemistry*, **2011**, 418, 102-10	3.1	65
60	Structure of Sir2Tm bound to a propionylated peptide. *Protein Science*, **2011**, 20, 131-9	6.3	16
59	Structural insights into the assembly and function of the SAGA deubiquitinating module. *Science*, **2010**, 328, 1025-9	33.3	166
58	Structure-based mechanism of ADP-ribosylation by sirtuins. *Journal of Biological Chemistry*, **2009**, 284, 33654-61	5.4	40
57	Side chain specificity of ADP-ribosylation by a sirtuin. *FEBS Journal*, **2009**, 276, 7159-76	5.7	24
56	Evidence for bidentate substrate binding as the basis for the K48 linkage specificity of otubain 1. *Journal of Molecular Biology*, **2009**, 386, 1011-23	6.5	102
55	Highly cooperative recruitment of Ets-1 and release of autoinhibition by Pax5. *Journal of Molecular Biology*, **2009**, 392, 452-64	6.5	20
54	The structure and conformation of Lys63-linked tetraubiquitin. *Journal of Molecular Biology*, **2009**, 392, 1117-24	6.5	93
53	Structural insights into intermediate steps in the Sir2 deacetylation reaction. *Structure*, **2008**, 16, 1368-77	5.2	104
52	Extracellular Nampt promotes macrophage survival via a nonenzymatic interleukin-6/STAT3 signaling mechanism. *Journal of Biological Chemistry*, **2008**, 283, 34833-43	5.4	150
51	Structural and functional studies of the Rap1 C-terminus reveal novel separation-of-function mutants. *Journal of Molecular Biology*, **2008**, 380, 520-31	6.5	30
50	The crystal structure of the tumor suppressor protein pp32 (Anp32a): structural insights into Anp32 family of proteins. *Protein Science*, **2007**, 16, 1308-15	6.3	35
49	N-lysine propionylation controls the activity of propionyl-CoA synthetase. *Journal of Biological Chemistry*, **2007**, 282, 30239-45	5.4	153
48	Nampt/PBEF/Visfatin regulates insulin secretion in beta cells as a systemic NAD biosynthetic enzyme. *Cell Metabolism*, **2007**, 6, 363-75	24.6	667
47	Crystal structure and solution NMR studies of Lys48-linked tetraubiquitin at neutral pH. *Journal of Molecular Biology*, **2007**, 367, 204-11	6.5	136
46	Identification of a new nicotinamide binding site in a sirtuin: a reassessment. *Molecular Cell*, **2007**, 28, 1102-3	17.6	2
45	Insights into the sirtuin mechanism from ternary complexes containing NAD+ and acetylated peptide. *Structure*, **2006**, 14, 1231-40	5.2	115

44	The structural basis of sirtuin substrate affinity. *Biochemistry*, **2006**, 45, 7511-21	3.2	80
43	The biochemistry of sirtuins. *Annual Review of Biochemistry*, **2006**, 75, 435-65	29.1	586
42	SIRT4 inhibits glutamate dehydrogenase and opposes the effects of calorie restriction in pancreatic beta cells. *Cell*, **2006**, 126, 941-54	56.2	915
41	Structure of Nampt/PBEF/visfatin, a mammalian NAD+ biosynthetic enzyme. *Nature Structural and Molecular Biology*, **2006**, 13, 661-2	17.6	204
40	Mms2-Ubc13 covalently bound to ubiquitin reveals the structural basis of linkage-specific polyubiquitin chain formation. *Nature Structural and Molecular Biology*, **2006**, 13, 915-20	17.6	261
39	Mechanism of sirtuin inhibition by nicotinamide: altering the NAD(+) cosubstrate specificity of a Sir2 enzyme. *Molecular Cell*, **2005**, 17, 855-68	17.6	358
38	How does the histone code work?. *Biochemistry and Cell Biology*, **2005**, 83, 468-76	3.6	170
37	Arm-domain interactions can provide high binding cooperativity. *Protein Science*, **2004**, 13, 2829-31	6.3	6
36	A conserved catalytic residue in the ubiquitin-conjugating enzyme family. *EMBO Journal*, **2004**, 23, 4876-4876	13	2
35	Regulated nucleosome mobility and the histone code. *Nature Structural and Molecular Biology*, **2004**, 11, 1037-43	17.6	284
34	Structural basis for the mechanism and regulation of Sir2 enzymes. *Molecular Cell*, **2004**, 13, 639-48	17.6	119
33	Insights into binding cooperativity of MATa1/MATalpha2 from the crystal structure of a MATa1 homeodomain-maltose binding protein chimera. *Protein Science*, **2003**, 12, 306-12	6.3	40
32	A conserved catalytic residue in the ubiquitin-conjugating enzyme family. *EMBO Journal*, **2003**, 22, 5241-50	13	134
31	Insights into nonspecific binding of homeodomains from a structure of MATalpha2 bound to DNA. *Proteins: Structure, Function and Bioinformatics*, **2003**, 51, 544-51	4.2	12
30	Structure of HoxA9 and Pbx1 bound to DNA: Hox hexapeptide and DNA recognition anterior to posterior. *Genes and Development*, **2003**, 17, 2060-72	12.6	161
29	Structural and thermodynamic characterization of the DNA binding properties of a triple alanine mutant of MATalpha2. *Structure*, **2002**, 10, 961-71	5.2	12
28	A core nucleosome surface crucial for transcriptional silencing. *Nature Genetics*, **2002**, 32, 273-9	36.3	102
27	A Hoogsteen base pair embedded in undistorted B-DNA. *Nucleic Acids Research*, **2002**, 30, 5244-52	20.1	59

26	SIR2 family of NAD(+)-dependent protein deacetylases. *Methods in Enzymology*, **2002**, 353, 282-300	1.7	43
25	Structural analysis of the autoinhibition of Ets-1 and its role in protein partnerships. *Journal of Biological Chemistry*, **2002**, 277, 45529-36	5.4	70
24	Structure of a Sir2 enzyme bound to an acetylated p53 peptide. *Molecular Cell*, **2002**, 10, 523-35	17.6	210
23	A standard reference frame for the description of nucleic acid base-pair geometry. *Journal of Molecular Biology*, **2001**, 313, 229-37	6.5	459
22	Recognition of specific DNA sequences. *Molecular Cell*, **2001**, 8, 937-46	17.6	277
21	Structural studies of Ets-1/Pax5 complex formation on DNA. *Molecular Cell*, **2001**, 8, 1267-76	17.6	159
20	Molecular insights into polyubiquitin chain assembly: crystal structure of the Mms2/Ubc13 heterodimer. *Cell*, **2001**, 105, 711-20	56.2	257
19	A phylogenetically conserved NAD+-dependent protein deacetylase activity in the Sir2 protein family. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 6658-63	11.5	622
18	Characterization of the N-terminal domain of the yeast transcriptional repressor Tup1. Proposal for an association model of the repressor complex Tup1 x Ssn6. *Journal of Biological Chemistry*, **2000**, 275, 9011-8	5.4	32
17	Characterization of the oligomeric states of wild type and mutant AraC. *Biochemistry*, **2000**, 39, 11593-601	3.2	25
16	Multiprotein-DNA complexes in transcriptional regulation. *Annual Review of Biophysics and Biomolecular Structure*, **1999**, 28, 29-56		92
15	Structure of a HoxB1-Pbx1 heterodimer bound to DNA: role of the hexapeptide and a fourth homeodomain helix in complex formation. *Cell*, **1999**, 96, 587-97	56.2	290
14	NMR studies of the pbx1 TALE homeodomain protein free in solution and bound to DNA: proposal for a mechanism of HoxB1-Pbx1-DNA complex assembly. *Journal of Molecular Biology*, **1999**, 291, 521-30	6.5	29
13	Combinatorial transcription factors. *Current Opinion in Genetics and Development*, **1998**, 8, 552-9	4.9	50
12	The structure of GABPalpha/beta: an ETS domain- ankyrin repeat heterodimer bound to DNA. *Science*, **1998**, 279, 1037-41	33.3	273
11	The 1.6 A crystal structure of the AraC sugar-binding and dimerization domain complexed with D-fucose. *Journal of Molecular Biology*, **1997**, 273, 226-37	6.5	53
10	Structural basis for ligand-regulated oligomerization of AraC. *Science*, **1997**, 276, 421-5	33.3	174
9	Homeodomain interactions. *Current Opinion in Structural Biology*, **1996**, 6, 62-8	8.1	118

8	Crystallization and preliminary X-ray diffraction studies of an a1/alpha 2/DNA ternary complex. *Proteins: Structure, Function and Bioinformatics*, **1995**, 21, 161-4	4.2	6
7	Transcription factor structure and DNA binding. *Current Opinion in Structural Biology*, **1993**, 3, 3-10	8.1	22
6	Crystal structure of a MAT alpha 2 homeodomain-operator complex suggests a general model for homeodomain-DNA interactions. *Cell*, **1991**, 67, 517-28	56.2	518
5	Crystallization and preliminary X-ray diffraction studies of a MAT alpha 2-DNA complex. *Journal of Molecular Biology*, **1991**, 217, 11-3	6.5	11
4	Structure of a phage 434 Cro/DNA complex. *Nature*, **1988**, 335, 789-95	50.4	187
3	Crystallization and X-ray diffraction studies of a 434 Cro-DNA complex. *Journal of Molecular Biology* , **1987**, 196, 951-4	6.5	7
2	Structural basis for COMPASS recognition of an H2B-ubiquitinated nucleosome		1
1	Active site alanine substitutions can convert deubiquitinating enzymes into avid ubiquitin-binding domains		1