Cynthia Wolberger

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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	SIRT4 inhibits glutamate dehydrogenase and opposes the effects of calorie restriction in pancreatic beta cells. *Cell*, **2006**, 126, 941-54	56.2	915
114	Nampt/PBEF/Visfatin regulates insulin secretion in beta cells as a systemic NAD biosynthetic enzyme. *Cell Metabolism*, **2007**, 6, 363-75	24.6	667
113	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
112	The biochemistry of sirtuins. *Annual Review of Biochemistry*, **2006**, 75, 435-65	29.1	586
111	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
110	A standard reference frame for the description of nucleic acid base-pair geometry. *Journal of Molecular Biology*, **2001**, 313, 229-37	6.5	459
109	New insights into ubiquitin E3 ligase mechanism. *Nature Structural and Molecular Biology*, **2014**, 21, 301-7	17.6	367
108	Mechanism of sirtuin inhibition by nicotinamide: altering the NAD(+) cosubstrate specificity of a Sir2 enzyme. *Molecular Cell*, **2005**, 17, 855-68	17.6	358
107	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
106	Regulated nucleosome mobility and the histone code. *Nature Structural and Molecular Biology*, **2004**, 11, 1037-43	17.6	284
105	Recognition of specific DNA sequences. *Molecular Cell*, **2001**, 8, 937-46	17.6	277
104	The structure of GABPalpha/beta: an ETS domain- ankyrin repeat heterodimer bound to DNA. *Science*, **1998**, 279, 1037-41	33.3	273
103	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
102	Molecular insights into polyubiquitin chain assembly: crystal structure of the Mms2/Ubc13 heterodimer. *Cell*, **2001**, 105, 711-20	56.2	257
101	Structure of a Sir2 enzyme bound to an acetylated p53 peptide. *Molecular Cell*, **2002**, 10, 523-35	17.6	210
100	Structure of Nampt/PBEF/visfatin, a mammalian NAD+ biosynthetic enzyme. *Nature Structural and Molecular Biology*, **2006**, 13, 661-2	17.6	204
99	Structure of a phage 434 Cro/DNA complex. *Nature*, **1988**, 335, 789-95	50.4	187

98	Structural basis for ligand-regulated oligomerization of AraC. *Science*, **1997**, 276, 421-5	33.3	174
97	How does the histone code work?. *Biochemistry and Cell Biology*, **2005**, 83, 468-76	3.6	170
96	Structural insights into the assembly and function of the SAGA deubiquitinating module. *Science*, **2010**, 328, 1025-9	33.3	166
95	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
94	Structural studies of Ets-1/Pax5 complex formation on DNA. *Molecular Cell*, **2001**, 8, 1267-76	17.6	159
93	The mechanism of OTUB1-mediated inhibition of ubiquitination. *Nature*, **2012**, 483, 618-22	50.4	157
92	Structural basis for histone H2B deubiquitination by the SAGA DUB module. *Science*, **2016**, 351, 725-8	33.3	154
91	N-lysine propionylation controls the activity of propionyl-CoA synthetase. *Journal of Biological Chemistry*, **2007**, 282, 30239-45	5.4	153
90	Extracellular Nampt promotes macrophage survival via a nonenzymatic interleukin-6/STAT3 signaling mechanism. *Journal of Biological Chemistry*, **2008**, 283, 34833-43	5.4	150
89	The Substrate Specificity of Sirtuins. *Annual Review of Biochemistry*, **2016**, 85, 405-29	29.1	142
88	Crystal structure and solution NMR studies of Lys48-linked tetraubiquitin at neutral pH. *Journal of Molecular Biology*, **2007**, 367, 204-11	6.5	136
87	A conserved catalytic residue in the ubiquitin-conjugating enzyme family. *EMBO Journal*, **2003**, 22, 5241-50	19	134
86	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
85	Structural basis for the mechanism and regulation of Sir2 enzymes. *Molecular Cell*, **2004**, 13, 639-48	17.6	119
84	Homeodomain interactions. *Current Opinion in Structural Biology*, **1996**, 6, 62-8	8.1	118
83	Extracellular nicotinamide phosphoribosyltransferase (NAMPT) promotes M2 macrophage polarization in chronic lymphocytic leukemia. *Blood*, **2015**, 125, 111-23	2.2	117
82	Insights into the sirtuin mechanism from ternary complexes containing NAD+ and acetylated peptide. *Structure*, **2006**, 14, 1231-40	5.2	115
81	Structural insights into intermediate steps in the Sir2 deacetylation reaction. *Structure*, **2008**, 16, 1368-77	5.2	104

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79	A core nucleosome surface crucial for transcriptional silencing. *Nature Genetics*, **2002**, 32, 273-9	36.3	102
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77	The structure and conformation of Lys63-linked tetraubiquitin. *Journal of Molecular Biology*, **2009**, 392, 1117-24	6.5	93
76	Multiprotein-DNA complexes in transcriptional regulation. *Annual Review of Biophysics and Biomolecular Structure*, **1999**, 28, 29-56		92
75	The structural basis of sirtuin substrate affinity. *Biochemistry*, **2006**, 45, 7511-21	3.2	80
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73	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
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70	A spectrophotometric assay for conjugation of ubiquitin and ubiquitin-like proteins. *Analytical Biochemistry*, **2011**, 418, 102-10	3.1	65
69	A Hoogsteen base pair embedded in undistorted B-DNA. *Nucleic Acids Research*, **2002**, 30, 5244-52	20.1	59
68	A Tunable Brake for HECT Ubiquitin Ligases. *Molecular Cell*, **2017**, 66, 345-357.e6	17.6	58
67	A multilaboratory comparison of calibration accuracy and the performance of external references in analytical ultracentrifugation. *PLoS ONE*, **2015**, 10, e0126420	3.7	55
66	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
65	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
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63	The bromodomain of Gcn5 regulates site specificity of lysine acetylation on histone H3. *Molecular and Cellular Proteomics*, **2014**, 13, 2896-910	7.6	50

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59	Architectural organization of the metabolic regulatory enzyme ghrelin O-acyltransferase. *Journal of Biological Chemistry*, **2013**, 288, 32211-32228	5.4	48
58	SIR2 family of NAD(+)-dependent protein deacetylases. *Methods in Enzymology*, **2002**, 353, 282-300	1.7	43
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36	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
35	Role of a non-canonical surface of Rad6 in ubiquitin conjugating activity. *Nucleic Acids Research*, **2015**, 43, 9039-50	20.1	16
34	Structure of Sir2Tm bound to a propionylated peptide. *Protein Science*, **2011**, 20, 131-9	6.3	16
33	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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30	Uncovering the role of Sgf73 in maintaining SAGA deubiquitinating module structure and activity. *Journal of Molecular Biology*, **2015**, 427, 1765-78	6.5	13
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17	Semisynthesis of ubiquitinated histone H2B with a native or nonhydrolyzable linkage. *Methods in Enzymology*, **2019**, 618, 1-27	1.7	6
16	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
15	Role of E2-RING Interactions in Governing RNF4-Mediated Substrate Ubiquitination. *Journal of Molecular Biology*, **2016**, 428, 4639-4650	6.5	5
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13	How structural biology transformed studies of transcription regulation. *Journal of Biological Chemistry*, **2021**, 296, 100741	5.4	4
12	Not just Salk. *Science*, **2017**, 357, 1105-1106	33.3	3
11	Comparison of Cross-Regulation by Different OTUB1:E2 Complexes. *Biochemistry*, **2020**, 59, 921-932	3.2	2
10	Identification of a new nicotinamide binding site in a sirtuin: a reassessment. *Molecular Cell*, **2007**, 28, 1102-3	17.6	2
9	A conserved catalytic residue in the ubiquitin-conjugating enzyme family. *EMBO Journal*, **2004**, 23, 4876-4876	13	2

8	Competition Assay for Measuring Deubiquitinating Enzyme Substrate Affinity. *Methods in Molecular Biology*, **2018**, 1844, 59-70	1.4	2
7	Structural basis for COMPASS recognition of an H2B-ubiquitinated nucleosome		1
6	Active site alanine substitutions can convert deubiquitinating enzymes into avid ubiquitin-binding domains		1
5	Potent macrocycle inhibitors of the human SAGA deubiquitinating module.. *Cell Chemical Biology*, **2021**,	8.2	1
4	A new DUB makes linear ubiquitin a party to its own destruction. *Cell*, **2013**, 153, 1189-91	56.2	0
3	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
2	Extracellular Nicotinamide Phosphoribosyltransferase (NAMPT) Shapes the CLL Microenvironment Promoting Macrophage M2 Polarization Via a Non-Enzymatic Mechanism. *Blood*, **2014**, 124, 3316-3316	2.2	
1	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	