Christoph W MÃ¼ller

List of Publications by Year
in descending order

116 papers	11,470 citations	36203 51 h-index	30010 103 g-index
134 all docs	134 docs citations	134 times ranked	14132 citing authors

#	Article	IF	Citations
1	Three-dimensional structure of the Stat3Î² homodimer bound to DNA. Nature, 1998, 394, 145-151.	13.7	780
2	Structure of the NF-ÎºB p50 homodimer bound to DNA. Nature, 1995, 373, 311-317.	13.7	531
3	Structure of importin-Î² bound to the IBB domain of importin-Î±. Nature, 1999, 399, 221-229.	13.7	530
4	WD40 proteins propel cellular networks. Trends in Biochemical Sciences, 2010, 35, 565-574.	3.7	518
5	Structure of the complex between adenylate kinase from Escherichia coli and the inhibitor Ap5A refined at 1.9 Ã… resolution. Journal of Molecular Biology, 1992, 224, 159-177.	2.0	491
6	Comparison of ARM and HEAT protein repeats. Journal of Molecular Biology, 2001, 309, 1-18.	2.0	464
7	Adenylate kinase motions during catalysis: an energetic counterweight balancing substrate binding. Structure, 1996, 4, 147-156.	1.6	403
8	Cooperative binding of two acetylation marks on a histone tail by a single bromodomain. Nature, 2009, 461, 664-668.	13.7	395
9	Histone H2A monoubiquitination promotes histone H3 methylation in Polycomb repression. Nature Structural and Molecular Biology, 2014, 21, 569-571.	3.6	376
10	Different TBX5 interactions in heart and limb defined by Holt-Oram syndrome mutations. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 2919-2924.	3.3	354
11	Crystallographic structure of the T domainâ€“DNA complex of the Brachyury transcription factor. Nature, 1997, 389, 884-888.	13.7	318
12	HDAC6â€“p97/VCP controlled polyubiquitin chain turnover. EMBO Journal, 2006, 25, 3357-3366.	3.5	248
13	Crystal Structure and Functional Analysis of a Nucleosome Recognition Module of the Remodeling Factor ISWI. Molecular Cell, 2003, 12, 449-460.	4.5	239
14	Induced-fit movements in adenylate kinases. Journal of Molecular Biology, 1990, 213, 627-630.	2.0	194
15	Karyopherin flexibility in nucleocytoplasmic transport. Current Opinion in Structural Biology, 2006, 16, 237-244.	2.6	186
16	Pervasive Protein Thermal Stability Variation during the Cell Cycle. Cell, 2018, 173, 1495-1507.e18.	13.5	183
17	Crystal structure of the 14-subunit RNA polymeraseÂ I. Nature, 2013, 502, 644-649.	13.7	179
18	Complex Interdependence Regulates Heterotypic Transcription Factor Distribution and Coordinates Cardiogenesis. Cell, 2016, 164, 999-1014.	13.5	179

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19	Crystal structure of the M1 protein-binding domain of the influenza A virus nuclear export protein (NEP/NS2). EMBO Journal, 2003, 22, 4646-4655.	3.5	174
20	Molecular structures of unbound and transcribing RNA polymerase III. Nature, 2015, 528, 231-236.	13.7	167
21	Xlink Analyzer: Software for analysis and visualization of cross-linking data in the context of three-dimensional structures. Journal of Structural Biology, 2015, 189, 177-183.	1.3	156
22	Molecular architecture of polycomb repressive complexes. Biochemical Society Transactions, 2017, 45, 193-205.	1.6	153
23	A systematic screen for proteinâ€“lipid interactions in <i>Saccharomyces cerevisiae</i>. Molecular Systems Biology, 2010, 6, 430.	3.2	146
24	In-cell architecture of the nuclear pore and snapshots of its turnover. Nature, 2020, 586, 796-800.	13.7	139
25	Structure of the human NF-kappa B p52 homodimer-DNA complex at 2.1Aresolution. EMBO Journal, 1997, 16, 7078-7090.	3.5	126
26	Architecture of CRM1/Exportin1 Suggests How Cooperativity Is Achieved during Formation of a Nuclear Export Complex. Molecular Cell, 2004, 16, 761-775.	4.5	119
27	Structure of the DNA-Bound T-Box Domain of Human TBX3, a Transcription Factor Responsible for Ulnar-Mammary Syndrome. Structure, 2002, 10, 343-356.	1.6	105
28	A bromodomainâ€“DNA interaction facilitates acetylation-dependent bivalent nucleosome recognition by the BET protein BRDT. Nature Communications, 2016, 7, 13855.	5.8	103
29	Molecular mechanism of promoter opening by RNA polymerase III. Nature, 2018, 553, 295-300.	13.7	101
30	The signalling conformation of the insulin receptor ectodomain. Nature Communications, 2018, 9, 4420.	5.8	98
31	Structural basis for LEAFY floral switch function and similarity with helix-turn-helix proteins. EMBO Journal, 2008, 27, 2628-2637.	3.5	97
32	Delineation of two functional regions of transcription factor TFIIB.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 5628-5632.	3.3	93
33	The Elongator subcomplex Elp456 is a hexameric RecA-like ATPase. Nature Structural and Molecular Biology, 2012, 19, 314-320.	3.6	85
34	Molecular Structures of Transcribing RNA Polymerase I. Molecular Cell, 2016, 64, 1135-1143.	4.5	85
35	Structural Basis of Lytic Cycle Activation by the Epstein-Barr Virus ZEBRA Protein. Molecular Cell, 2006, 21, 565-572.	4.5	82
36	Molecular recognition of histone lysine methylation by the Polycomb group repressor dSfmbt. EMBO Journal, 2009, 28, 1965-1977.	3.5	77

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37	The Crystal Structure of the Drosophila Germline Inducer Oskar Identifies Two Domains with Distinct Vasa Helicase- and RNA-Binding Activities. Cell Reports, 2015, 12, 587-598.	2.9	76
38	Structure of the complex of adenylate kinase from Escherichia coli with the inhibitor P1,P5-di(adenosine-5â€²-)pentaphosphate. Journal of Molecular Biology, 1988, 202, 909-912.	2.0	75
39	Architecture of the yeast Elongator complex. EMBO Reports, 2017, 18, 264-279.	2.0	75
40	Insights into Transcription Initiation and Termination from the Electron Microscopy Structure of Yeast RNA Polymerase III. Molecular Cell, 2007, 25, 813-823.	4.5	74
41	Structure of the GCM domain-DNA complex: a DNA-binding domain with a novel fold and mode of target site recognition. EMBO Journal, 2003, 22, 1835-1845.	3.5	71
42	The Histone Fold Subunits of Drosophila CHRAC Facilitate Nucleosome Sliding through Dynamic DNA Interactions. Molecular and Cellular Biology, 2005, 25, 9886-9896.	1.1	71
43	Crystal structure of the ankyrin repeat domain of Bcl-3: a unique member of the IkappaB protein family. EMBO Journal, 2001, 20, 6180-6190.	3.5	68
44	RNA polymerase I and III: similar yet unique. Current Opinion in Structural Biology, 2017, 47, 88-94.	2.6	68
45	A modular platform for automated cryo-FIB workflows. ELife, 2021, 10, .	2.8	65
46	Conformational flexibility of RNA polymerase III during transcriptional elongation. EMBO Journal, 2010, 29, 3762-3772.	3.5	64
47	Structural and functional analyses of methylâ€lysine binding by the malignant brain tumour repeat protein Sex comb on midleg. EMBO Reports, 2007, 8, 1031-1037.	2.0	61
48	Chromatin-modifying Complex Component Nurf55/p55 Associates with Histones H3 and H4 and Polycomb Repressive Complex 2 Subunit Su(z)12 through Partially Overlapping Binding Sites. Journal of Biological Chemistry, 2011, 286, 23388-23396.	1.6	61
49	The LOTUS domain is a conserved DEAD-box RNA helicase regulator essential for the recruitment of Vasa to the germ plasm and nuage. Genes and Development, 2017, 31, 939-952.	2.7	61
50	The Histone Octamer Is Invisible When NF-Î°B Binds to the Nucleosome. Journal of Biological Chemistry, 2004, 279, 42374-42382.	1.6	60
51	Structure of an Activated Dictyostelium STAT in Its DNA-Unbound Form. Molecular Cell, 2004, 13, 791-804.	4.5	60
52	Structural basis for tRNA modification by Elp3 from Dehalococcoides mccartyi. Nature Structural and Molecular Biology, 2016, 23, 794-802.	3.6	59
53	Cryo-EM structures of human RNA polymerase III in its unbound and transcribing states. Nature Structural and Molecular Biology, 2021, 28, 210-219.	3.6	59
54	Structural insights into transcription initiation by yeast RNA polymerase I. EMBO Journal, 2017, 36, 2698-2709.	3.5	58

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55	Architecture of TFIIIC and its role in RNA polymerase III pre-initiation complex assembly. Nature Communications, 2015, 6, 7387.	5.8	57
56	Structure of the <i>Drosophila</i> nucleosome core particle highlights evolutionary constraints on the H2Aâ€H2B histone dimer. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1-7.	1.5	55
57	An integrated approach for genome annotation of the eukaryotic thermophile Chaetomium thermophilum. Nucleic Acids Research, 2014, 42, 13525-13533.	6.5	55
58	Transcription factors: global and detailed views. Current Opinion in Structural Biology, 2001, 11, 26-32.	2.6	54
59	Interaction of influenza virus proteins with nucleosomes. Virology, 2005, 332, 329-336.	1.1	54
60	Structural basis for targeting the chromatin repressor Sfmbt to Polycomb response elements. Genes and Development, 2013, 27, 2367-2379.	2.7	53
61	Structural insights into Elongator function. Current Opinion in Structural Biology, 2013, 23, 235-242.	2.6	52
62	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. Nature Methods, 2016, 13, 515-520.	9.0	49
63	Nuclear import factors importin Î± and importin Î² undergo mutually induced conformational changes upon association. FEBS Letters, 2000, 484, 291-298.	1.3	48
64	Mass Spectrometry Reveals Stable Modules in holo and apo RNA Polymerases I and III. Structure, 2011, 19, 90-100.	1.6	47
65	Structural Basis of TBX5â€“DNA Recognition: The T-Box Domain in Its DNA-Bound and -Unbound Form. Journal of Molecular Biology, 2010, 400, 71-81.	2.0	46
66	Molecular basis of tRNA recognition by the Elongator complex. Science Advances, 2019, 5, eaaw2326.	4.7	44
67	Structural insights into nuclear transcription by eukaryotic DNA-dependent RNA polymerases. Nature Reviews Molecular Cell Biology, 2022, 23, 603-622.	16.1	44
68	Expression of a tyrosine phosphorylated, DNA binding Stat3Î² dimer in bacteria. FEBS Letters, 1998, 441, 141-147.	1.3	42
69	Structural basis for RNA polymerase III transcription repression by Maf1. Nature Structural and Molecular Biology, 2020, 27, 229-232.	3.6	37
70	Structure of the Kti11/Kti13 Heterodimer and Its Double Role in Modifications of tRNA and Eukaryotic Elongation Factor 2. Structure, 2015, 23, 149-160.	1.6	36
71	The cryo-EM structure of a 12-subunit variant of RNA polymerase I reveals dissociation of the A49-A34.5 heterodimer and rearrangement of subunit A12.2. ELife, 2019, 8, .	2.8	36
72	Crystal structures of two mutants of adenylate kinase fromEscherichia coli that modify the Gly-loop. Proteins: Structure, Function and Bioinformatics, 1993, 15, 42-49.	1.5	34

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73	Molecular insight into RNA polymerase I promoter recognition and promoter melting. Nature Communications, 2019, 10, 5543.	5.8	33
74	The structure of the NF-Î°B p50:DNA-complex a starting point for analyzing the Rel family. FEBS Letters, 1995, 369, 113-117.	1.3	32
75	Structure of the Ï„60/Î"Ï„91 Subcomplex of Yeast Transcription Factor IIIC: Insights into Preinitiation Complex Assembly. Molecular Cell, 2006, 24, 221-232.	4.5	32
76	Crystallization of proteins under microgravity. FEBS Letters, 1989, 259, 194-198.	1.3	31
77	The cryo-EM resolution revolution and transcription complexes. Current Opinion in Structural Biology, 2018, 52, 8-15.	2.6	31
78	A firm hand on NFÎ°B: structures of the IÎ°BÎ±â€"NFÎ°B complex. Structure, 1999, 7, R1-R6.	1.6	30
79	Structural asymmetry in the eukaryotic Elongator complex. FEBS Letters, 2018, 592, 502-515.	1.3	29
80	Elongator. Transcription, 2012, 3, 273-276.	1.7	28
81	Cryo-EM structures of human RNA polymerase I. Nature Structural and Molecular Biology, 2021, 28, 997-1008.	3.6	28
82	Human importin alpha and RNA do not compete for binding to influenza A virus nucleoprotein. Virology, 2011, 409, 84-90.	1.1	27
83	Structure of the specificity domain of the Dorsal homologue Gambif1 bound to DNA. Structure, 1999, 7, 841-852.	1.6	26
84	The GCM domain is a Zn-coordinating DNA-binding domain. FEBS Letters, 2002, 528, 95-100.	1.3	26
85	Recognizing and remodeling the nucleosome. Current Opinion in Structural Biology, 2011, 21, 335-341.	2.6	25
86	Engineering of diffraction-quality crystals of the NF-Î°B P52 homodimer:DNA complex. FEBS Letters, 1997, 405, 373-377.	1.3	23
87	RNA polymerase III-specific general transcription factor IIIC contains a heterodimer resembling TFIIF Rap30/Rap74. Nucleic Acids Research, 2013, 41, 9183-9196.	6.5	23
88	Solving the RNA polymerase I structural puzzle. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2570-2582.	2.5	23
89	Comparison of two different DMA-binding modes of the NF-Î°B p50 homodimer. Nature Structural Biology, 1996, 3, 224-227.	9.7	22
90	Preparation and Properties of Oligodeoxynucleotides Containing 5-Iodouracil and 5-Bromo- and 5-Iodocytosine. Bioconjugate Chemistry, 1997, 8, 757-761.	1.8	21

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91	Structural Basis for the Activation of the Deubiquitinase Calypso by the Polycomb Protein ASX. Structure, 2019, 27, 528-536.e4.	1.6	19
92	Transcribing <scp>RNA</scp> polymerase <scp>III</scp> observed by electron cryomicroscopy. FEBS Journal, 2016, 283, 2811-2819.	2.2	18
93	Insights into the Function of the CRM1 Cofactor RanBP3 from the Structure of Its Ran-Binding Domain. PLoS ONE, 2011, 6, e17011.	1.1	18
94	Solution Study of the NF-Îºb p50â€“DNA Complex by UV Laser Proteinâ€“DNA Cross-linkingÂ¶. Photochemistry and Photobiology, 2003, 77, 592.	1.3	16
95	Structure of the TFIIIC subcomplex Ï„A provides insights into RNA polymerase III pre-initiation complex formation. Nature Communications, 2020, 11, 4905.	5.8	16
96	A synthetic biology approach to probing nucleosome symmetry. ELife, 2017, 6, .	2.8	16
97	Structure of a Truncation Mutant of the Nuclear Export Factor CRM1 Provides Insights into the Auto-Inhibitory Role of Its C-Terminal Helix. Structure, 2013, 21, 1338-1349.	1.6	15
98	The Combination of X-Ray Crystallography and Cryo-Electron Microscopy Provides Insight into the Overall Architecture of the Dodecameric Rvb1/Rvb2 Complex. PLoS ONE, 2016, 11, e0146457.	1.1	14
99	An integrated model for termination of RNA polymerase III transcription. Science Advances, 2022, 8, .	4.7	14
100	Full Repression of RNA Polymerase III Transcription Requires Interaction between Two Domains of Its Negative Regulator Maf1. Journal of Biological Chemistry, 2010, 285, 35719-35727.	1.6	13
101	Structural and Functional Characterization of a Phosphatase Domain within Yeast General Transcription Factor IIIC. Journal of Biological Chemistry, 2013, 288, 15110-15120.	1.6	13
102	Analyzing RNA polymerase III by electron cryomicroscopy. RNA Biology, 2011, 8, 760-765.	1.5	12
103	Specialization versus conservation: How Pol I and Pol III use the conserved architecture of the pre-initiation complex for specialized transcription. Transcription, 2016, 7, 127-132.	1.7	9
104	Mechanism of RNA polymerase I selection by transcription factor UAF. Science Advances, 2022, 8, eabn5725.	4.7	9
105	Structural basis of DNA methylation-dependent site selectivity of the Epsteinâ€“Barr virus lytic switch protein ZEBRA/Zta/BZLF1. Nucleic Acids Research, 2022, 50, 490-511.	6.5	8
106	Unleashing the Power of ASH1L Methyltransferase. Structure, 2019, 27, 727-728.	1.6	7
107	Expression, purification, crystallization and preliminary X-ray analysis of a C-terminal fragment of the Epsteinâ€“Barr virus ZEBRA protein. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 210-214.	0.7	4
108	Expression, proteolytic analysis, reconstitution, and crystallization of the Ï„60/Ï„91 subcomplex of yeast TFIIIC. Protein Expression and Purification, 2006, 45, 255-261.	0.6	3

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109	Solving the NES problem. Nature Structural and Molecular Biology, 2010, 17, 1288-1289.	3.6	3
110	Bacterial Expression, Purification, and Crystallization of Tyrosine Phosphorylated STAT Proteins. Methods in Molecular Biology, 2013, 967, 301-317.	0.4	3
111	Highly ordered crystals of channel-forming membrane proteins, of nucleoside-monophosphate kinases, of FAD-containing oxidoreductases and of sugar-processing enzymes and their mutants. Journal of Crystal Growth, 1992, 122, 385-392.	0.7	2
112	Solution Study of the NF-ÎºB p50-DNA Complex by UV Laser Protein-DNA Cross-linkingÂ¶. Photochemistry and Photobiology, 2007, 77, 592-596.	1.3	2
113	Enzymeâ€“chromatin complex visualized. Nature, 2014, 514, 572-573.	13.7	2
114	Editorial overview: Proteinâ€“nucleic acid interactions: An expanding universe. Current Opinion in Structural Biology, 2017, 47, iv-v.	2.6	1
115	RNA polymerase III initiation on coligo DNA templates containing loops of variable sequence, size and nucleotide chemistry. Gene, 2017, 612, 49-54.	1.0	1
116	X-Ray Crystal Structure of STAT Proteins and Structure-Activity Relationships. , 2003, , 311-325.		1