

Christoph W MÃ¼ller

List of Publications by Year in descending order

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116
papers

11,470
citations

36303

51
h-index

30087

103
g-index

134
all docs

134
docs citations

134
times ranked

14132
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis of DNA methylation-dependent site selectivity of the Epstein-Barr virus lytic switch protein ZEBRA/Zta/BZLF1. <i>Nucleic Acids Research</i> , 2022, 50, 490-511.	14.5	8
2	Mechanism of RNA polymerase I selection by transcription factor UAF. <i>Science Advances</i> , 2022, 8, eabn5725.	10.3	9
3	Structural insights into nuclear transcription by eukaryotic DNA-dependent RNA polymerases. <i>Nature Reviews Molecular Cell Biology</i> , 2022, 23, 603-622.	37.0	44
4	An integrated model for termination of RNA polymerase III transcription. <i>Science Advances</i> , 2022, 8, .	10.3	14
5	Cryo-EM structures of human RNA polymerase III in its unbound and transcribing states. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 210-219.	8.2	59
6	Cryo-EM structures of human RNA polymerase I. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 997-1008.	8.2	28
7	A modular platform for automated cryo-FIB workflows. <i>ELife</i> , 2021, 10, .	6.0	65
8	Structure of the TFIIIC subcomplex β_2 provides insights into RNA polymerase III pre-initiation complex formation. <i>Nature Communications</i> , 2020, 11, 4905.	12.8	16
9	In-cell architecture of the nuclear pore and snapshots of its turnover. <i>Nature</i> , 2020, 586, 796-800.	27.8	139
10	Structural basis for RNA polymerase III transcription repression by Maf1. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 229-232.	8.2	37
11	Molecular basis of tRNA recognition by the Elongator complex. <i>Science Advances</i> , 2019, 5, eaaw2326.	10.3	44
12	Unleashing the Power of ASH1L Methyltransferase. <i>Structure</i> , 2019, 27, 727-728.	3.3	7
13	Molecular insight into RNA polymerase I promoter recognition and promoter melting. <i>Nature Communications</i> , 2019, 10, 5543.	12.8	33
14	Structural Basis for the Activation of the Deubiquitinase Calypso by the Polycomb Protein ASX. <i>Structure</i> , 2019, 27, 528-536.e4.	3.3	19
15	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. <i>ELife</i> , 2019, 8, .	6.0	36
16	Molecular mechanism of promoter opening by RNA polymerase III. <i>Nature</i> , 2018, 553, 295-300.	27.8	101
17	Pervasive Protein Thermal Stability Variation during the Cell Cycle. <i>Cell</i> , 2018, 173, 1495-1507.e18.	28.9	183
18	Structural asymmetry in the eukaryotic Elongator complex. <i>FEBS Letters</i> , 2018, 592, 502-515.	2.8	29

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19	The signalling conformation of the insulin receptor ectodomain. <i>Nature Communications</i> , 2018, 9, 4420.	12.8	98
20	The cryo-EM resolution revolution and transcription complexes. <i>Current Opinion in Structural Biology</i> , 2018, 52, 8-15.	5.7	31
21	Molecular architecture of polycomb repressive complexes. <i>Biochemical Society Transactions</i> , 2017, 45, 193-205.	3.4	153
22	Architecture of the yeast Elongator complex. <i>EMBO Reports</i> , 2017, 18, 264-279.	4.5	75
23	The LOTUS domain is a conserved DEAD-box RNA helicase regulator essential for the recruitment of Vasa to the germ plasm and nuage. <i>Genes and Development</i> , 2017, 31, 939-952.	5.9	61
24	Structural insights into transcription initiation by yeast RNA polymerase I. <i>EMBO Journal</i> , 2017, 36, 2698-2709.	7.8	58
25	RNA polymerase I and III: similar yet unique. <i>Current Opinion in Structural Biology</i> , 2017, 47, 88-94.	5.7	68
26	Editorial overview: Protein-nucleic acid interactions: An expanding universe. <i>Current Opinion in Structural Biology</i> , 2017, 47, iv-v.	5.7	1
27	RNA polymerase III initiation on coligo DNA templates containing loops of variable sequence, size and nucleotide chemistry. <i>Gene</i> , 2017, 612, 49-54.	2.2	1
28	A synthetic biology approach to probing nucleosome symmetry. <i>ELife</i> , 2017, 6, .	6.0	16
29	Transcribing <scp>RNA</scp> polymerase <scp>III</scp> observed by electron cryomicroscopy. <i>FEBS Journal</i> , 2016, 283, 2811-2819.	4.7	18
30	Molecular Structures of Transcribing RNA Polymerase I. <i>Molecular Cell</i> , 2016, 64, 1135-1143.	9.7	85
31	A bromodomain-DNA interaction facilitates acetylation-dependent bivalent nucleosome recognition by the BET protein BRDT. <i>Nature Communications</i> , 2016, 7, 13855.	12.8	103
32	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. <i>Nature Methods</i> , 2016, 13, 515-520.	19.0	49
33	Structural basis for tRNA modification by Elp3 from <i>Dehalococcoides mccartyi</i> . <i>Nature Structural and Molecular Biology</i> , 2016, 23, 794-802.	8.2	59
34	Specialization versus conservation: How Pol I and Pol III use the conserved architecture of the pre-initiation complex for specialized transcription. <i>Transcription</i> , 2016, 7, 127-132.	3.1	9
35	Complex Interdependence Regulates Heterotypic Transcription Factor Distribution and Coordinates Cardiogenesis. <i>Cell</i> , 2016, 164, 999-1014.	28.9	179
36	The Combination of X-Ray Crystallography and Cryo-Electron Microscopy Provides Insight into the Overall Architecture of the Dodecameric Rvb1/Rvb2 Complex. <i>PLoS ONE</i> , 2016, 11, e0146457.	2.5	14

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37	Xlink Analyzer: Software for analysis and visualization of cross-linking data in the context of three-dimensional structures. <i>Journal of Structural Biology</i> , 2015, 189, 177-183.	2.8	156
38	Structure of the Kti11/Kti13 Heterodimer and Its Double Role in Modifications of tRNA and Eukaryotic Elongation Factor 2. <i>Structure</i> , 2015, 23, 149-160.	3.3	36
39	The Crystal Structure of the <i>Drosophila</i> Germline Inducer Oskar Identifies Two Domains with Distinct Vasa Helicase- and RNA-Binding Activities. <i>Cell Reports</i> , 2015, 12, 587-598.	6.4	76
40	Architecture of TFIIC and its role in RNA polymerase III pre-initiation complex assembly. <i>Nature Communications</i> , 2015, 6, 7387.	12.8	57
41	Molecular structures of unbound and transcribing RNA polymerase III. <i>Nature</i> , 2015, 528, 231-236.	27.8	167
42	Enzyme- ϵ -chromatin complex visualized. <i>Nature</i> , 2014, 514, 572-573.	27.8	2
43	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <i>Nucleic Acids Research</i> , 2014, 42, 13525-13533.	14.5	55
44	Solving the RNA polymerase I structural puzzle. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2570-2582.	2.5	23
45	Histone H2A monoubiquitination promotes histone H3 methylation in Polycomb repression. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 569-571.	8.2	376
46	Crystal structure of the 14-subunit RNA polymerase AI . <i>Nature</i> , 2013, 502, 644-649.	27.8	179
47	Structural basis for targeting the chromatin repressor Sfmtb to Polycomb response elements. <i>Genes and Development</i> , 2013, 27, 2367-2379.	5.9	53
48	Structural insights into Elongator function. <i>Current Opinion in Structural Biology</i> , 2013, 23, 235-242.	5.7	52
49	Structure of a Truncation Mutant of the Nuclear Export Factor CRM1 Provides Insights into the Auto-Inhibitory Role of Its C-Terminal Helix. <i>Structure</i> , 2013, 21, 1338-1349.	3.3	15
50	Bacterial Expression, Purification, and Crystallization of Tyrosine Phosphorylated STAT Proteins. <i>Methods in Molecular Biology</i> , 2013, 967, 301-317.	0.9	3
51	RNA polymerase III-specific general transcription factor IIIC contains a heterodimer resembling TFIIF Rap30/Rap74. <i>Nucleic Acids Research</i> , 2013, 41, 9183-9196.	14.5	23
52	Structural and Functional Characterization of a Phosphatase Domain within Yeast General Transcription Factor IIIC. <i>Journal of Biological Chemistry</i> , 2013, 288, 15110-15120.	3.4	13
53	Elongator. <i>Transcription</i> , 2012, 3, 273-276.	3.1	28
54	The Elongator subcomplex Elp456 is a hexameric RecA-like ATPase. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 314-320.	8.2	85

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55	Mass Spectrometry Reveals Stable Modules in holo and apo RNA Polymerases I and III. <i>Structure</i> , 2011, 19, 90-100.	3.3	47
56	Recognizing and remodeling the nucleosome. <i>Current Opinion in Structural Biology</i> , 2011, 21, 335-341.	5.7	25
57	Human importin alpha and RNA do not compete for binding to influenza A virus nucleoprotein. <i>Virology</i> , 2011, 409, 84-90.	2.4	27
58	Analyzing RNA polymerase III by electron cryomicroscopy. <i>RNA Biology</i> , 2011, 8, 760-765.	3.1	12
59	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. <i>Journal of Biological Chemistry</i> , 2011, 286, 23388-23396.	3.4	61
60	Insights into the Function of the CRM1 Cofactor RanBP3 from the Structure of Its Ran-Binding Domain. <i>PLoS ONE</i> , 2011, 6, e17011.	2.5	18
61	WD40 proteins propel cellular networks. <i>Trends in Biochemical Sciences</i> , 2010, 35, 565-574.	7.5	518
62	Solving the NES problem. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1288-1289.	8.2	3
63	Conformational flexibility of RNA polymerase III during transcriptional elongation. <i>EMBO Journal</i> , 2010, 29, 3762-3772.	7.8	64
64	Full Repression of RNA Polymerase III Transcription Requires Interaction between Two Domains of Its Negative Regulator Maf1. <i>Journal of Biological Chemistry</i> , 2010, 285, 35719-35727.	3.4	13
65	Structural Basis of TBX5â€™DNA Recognition: The T-Box Domain in Its DNA-Bound and -Unbound Form. <i>Journal of Molecular Biology</i> , 2010, 400, 71-81.	4.2	46
66	A systematic screen for proteinâ€™lipid interactions in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2010, 6, 430.	7.2	146
67	Molecular recognition of histone lysine methylation by the Polycomb group repressor dSfmbt. <i>EMBO Journal</i> , 2009, 28, 1965-1977.	7.8	77
68	Cooperative binding of two acetylation marks on a histone tail by a single bromodomain. <i>Nature</i> , 2009, 461, 664-668.	27.8	395
69	Structure of the <i>Drosophila</i> nucleosome core particle highlights evolutionary constraints on the H2Aâ€™H2B histone dimer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1-7.	2.6	55
70	Structural basis for LEAFY floral switch function and similarity with helix-turn-helix proteins. <i>EMBO Journal</i> , 2008, 27, 2628-2637.	7.8	97
71	Insights into Transcription Initiation and Termination from the Electron Microscopy Structure of Yeast RNA Polymerase III. <i>Molecular Cell</i> , 2007, 25, 813-823.	9.7	74
72	Structural and functional analyses of methylâ€™lysine binding by the malignant brain tumour repeat protein Sex comb on midleg. <i>EMBO Reports</i> , 2007, 8, 1031-1037.	4.5	61

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73	Solution Study of the NF- κ B p50-DNA Complex by UV Laser Protein-DNA Cross-linking. <i>Photochemistry and Photobiology</i> , 2007, 77, 592-596.	2.5	2
74	Structural Basis of Lytic Cycle Activation by the Epstein-Barr Virus ZEBRA Protein. <i>Molecular Cell</i> , 2006, 21, 565-572.	9.7	82
75	Structure of the κ ,60/ κ ,91 Subcomplex of Yeast Transcription Factor IIIC: Insights into Preinitiation Complex Assembly. <i>Molecular Cell</i> , 2006, 24, 221-232.	9.7	32
76	Expression, proteolytic analysis, reconstitution, and crystallization of the κ ,60/ κ ,91 subcomplex of yeast TFIIIC. <i>Protein Expression and Purification</i> , 2006, 45, 255-261.	1.3	3
77	Expression, purification, crystallization and preliminary X-ray analysis of a C-terminal fragment of the Epstein-Barr virus ZEBRA protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 210-214.	0.7	4
78	HDAC6-controlled polyubiquitin chain turnover. <i>EMBO Journal</i> , 2006, 25, 3357-3366.	7.8	248
79	Karyopherin flexibility in nucleocytoplasmic transport. <i>Current Opinion in Structural Biology</i> , 2006, 16, 237-244.	5.7	186
80	Interaction of influenza virus proteins with nucleosomes. <i>Virology</i> , 2005, 332, 329-336.	2.4	54
81	The Histone Fold Subunits of Drosophila CHRAC Facilitate Nucleosome Sliding through Dynamic DNA Interactions. <i>Molecular and Cellular Biology</i> , 2005, 25, 9886-9896.	2.3	71
82	The Histone Octamer Is Invisible When NF- κ B Binds to the Nucleosome. <i>Journal of Biological Chemistry</i> , 2004, 279, 42374-42382.	3.4	60
83	Architecture of CRM1/Exportin1 Suggests How Cooperativity Is Achieved during Formation of a Nuclear Export Complex. <i>Molecular Cell</i> , 2004, 16, 761-775.	9.7	119
84	Structure of an Activated Dictyostelium STAT in Its DNA-Unbound Form. <i>Molecular Cell</i> , 2004, 13, 791-804.	9.7	60
85	Structure of the GCM domain-DNA complex: a DNA-binding domain with a novel fold and mode of target site recognition. <i>EMBO Journal</i> , 2003, 22, 1835-1845.	7.8	71
86	Crystal structure of the M1 protein-binding domain of the influenza A virus nuclear export protein (NEP/NS2). <i>EMBO Journal</i> , 2003, 22, 4646-4655.	7.8	174
87	Crystal Structure and Functional Analysis of a Nucleosome Recognition Module of the Remodeling Factor ISWI. <i>Molecular Cell</i> , 2003, 12, 449-460.	9.7	239
88	Solution Study of the NF- κ B p50-DNA Complex by UV Laser Protein-DNA Cross-linking. <i>Photochemistry and Photobiology</i> , 2003, 77, 592.	2.5	16
89	X-Ray Crystal Structure of STAT Proteins and Structure-Activity Relationships. , 2003, , 311-325.		1
90	The GCM domain is a Zn-coordinating DNA-binding domain. <i>FEBS Letters</i> , 2002, 528, 95-100.	2.8	26

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91	Structure of the DNA-Bound T-Box Domain of Human TBX3, a Transcription Factor Responsible for Ulnar-Mammary Syndrome. <i>Structure</i> , 2002, 10, 343-356.	3.3	105
92	Comparison of ARM and HEAT protein repeats. <i>Journal of Molecular Biology</i> , 2001, 309, 1-18.	4.2	464
93	Crystal structure of the ankyrin repeat domain of Bcl-3: a unique member of the IkappaB protein family. <i>EMBO Journal</i> , 2001, 20, 6180-6190.	7.8	68
94	Transcription factors: global and detailed views. <i>Current Opinion in Structural Biology</i> , 2001, 11, 26-32.	5.7	54
95	Nuclear import factors importin β and importin β_2 undergo mutually induced conformational changes upon association. <i>FEBS Letters</i> , 2000, 484, 291-298.	2.8	48
96	Different TBX5 interactions in heart and limb defined by Holt-Oram syndrome mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 2919-2924.	7.1	354
97	Structure of importin- β_2 bound to the IBB domain of importin- β . <i>Nature</i> , 1999, 399, 221-229.	27.8	530
98	A firm hand on NF κ B: structures of the I κ B μ -NF κ B complex. <i>Structure</i> , 1999, 7, R1-R6.	3.3	30
99	Structure of the specificity domain of the Dorsal homologue Gambif1 bound to DNA. <i>Structure</i> , 1999, 7, 841-852.	3.3	26
100	Three-dimensional structure of the Stat3 β homodimer bound to DNA. <i>Nature</i> , 1998, 394, 145-151.	27.8	780
101	Expression of a tyrosine phosphorylated, DNA binding Stat3 β dimer in bacteria. <i>FEBS Letters</i> , 1998, 441, 141-147.	2.8	42
102	Preparation and Properties of Oligodeoxynucleotides Containing 5-Iodouracil and 5-Bromo- and 5-Iodocytosine. <i>Bioconjugate Chemistry</i> , 1997, 8, 757-761.	3.6	21
103	Engineering of diffraction-quality crystals of the NF κ B P52 homodimer:DNA complex. <i>FEBS Letters</i> , 1997, 405, 373-377.	2.8	23
104	Crystallographic structure of the T domain μ -DNA complex of the Brachyury transcription factor. <i>Nature</i> , 1997, 389, 884-888.	27.8	318
105	Structure of the human NF-kappa B p52 homodimer-DNA complex at 2.1A resolution. <i>EMBO Journal</i> , 1997, 16, 7078-7090.	7.8	126
106	Adenylate kinase motions during catalysis: an energetic counterweight balancing substrate binding. <i>Structure</i> , 1996, 4, 147-156.	3.3	403
107	Comparison of two different DNA-binding modes of the NF κ B p50 homodimer. <i>Nature Structural Biology</i> , 1996, 3, 224-227.	9.7	22
108	Structure of the NF κ B p50 homodimer bound to DNA. <i>Nature</i> , 1995, 373, 311-317.	27.8	531

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109	The structure of the NF- κ B p50:DNA-complex a starting point for analyzing the Rel family. FEBS Letters, 1995, 369, 113-117.	2.8	32
110	Crystal structures of two mutants of adenylate kinase from Escherichia coli that modify the Gly-loop. Proteins: Structure, Function and Bioinformatics, 1993, 15, 42-49.	2.6	34
111	Delineation of two functional regions of transcription factor TFIIIB. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 5628-5632.	7.1	93
112	Structure of the complex between adenylate kinase from Escherichia coli and the inhibitor Ap5A refined at 1.9 Å... resolution. Journal of Molecular Biology, 1992, 224, 159-177.	4.2	491
113	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.	1.5	2
114	Induced-fit movements in adenylate kinases. Journal of Molecular Biology, 1990, 213, 627-630.	4.2	194
115	Crystallization of proteins under microgravity. FEBS Letters, 1989, 259, 194-198.	2.8	31
116	Structure of the complex of adenylate kinase from Escherichia coli with the inhibitor P ₁ ,P ₅ -di(adenosine-5'- ϵ -)pentaphosphate. Journal of Molecular Biology, 1988, 202, 909-912.	4.2	75