

Christoph W MÃ¼ller

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8223212/publications.pdf>

Version: 2024-02-01

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	Three-dimensional structure of the Stat3 ^{Δ2} homodimer bound to DNA. <i>Nature</i> , 1998, 394, 145-151.	27.8	780
2	Structure of the NF- κ B p50 homodimer bound to DNA. <i>Nature</i> , 1995, 373, 311-317.	27.8	531
3	Structure of importin- β^2 bound to the IBB domain of importin- α . <i>Nature</i> , 1999, 399, 221-229.	27.8	530
4	WD40 proteins propel cellular networks. <i>Trends in Biochemical Sciences</i> , 2010, 35, 565-574.	7.5	518
5	Structure of the complex between adenylate kinase from <i>Escherichia coli</i> and the inhibitor Ap5A refined at 1.9 Å... resolution. <i>Journal of Molecular Biology</i> , 1992, 224, 159-177.	4.2	491
6	Comparison of ARM and HEAT protein repeats. <i>Journal of Molecular Biology</i> , 2001, 309, 1-18.	4.2	464
7	Adenylate kinase motions during catalysis: an energetic counterweight balancing substrate binding. <i>Structure</i> , 1996, 4, 147-156.	3.3	403
8	Cooperative binding of two acetylation marks on a histone tail by a single bromodomain. <i>Nature</i> , 2009, 461, 664-668.	27.8	395
9	Histone H2A monoubiquitination promotes histone H3 methylation in Polycomb repression. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 569-571.	8.2	376
10	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
11	Crystallographic structure of the T domain-DNA complex of the Brachyury transcription factor. <i>Nature</i> , 1997, 389, 884-888.	27.8	318
12	HDAC6-p97/VCP controlled polyubiquitin chain turnover. <i>EMBO Journal</i> , 2006, 25, 3357-3366.	7.8	248
13	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
14	Induced-fit movements in adenylate kinases. <i>Journal of Molecular Biology</i> , 1990, 213, 627-630.	4.2	194
15	Karyopherin flexibility in nucleocytoplasmic transport. <i>Current Opinion in Structural Biology</i> , 2006, 16, 237-244.	5.7	186
16	Pervasive Protein Thermal Stability Variation during the Cell Cycle. <i>Cell</i> , 2018, 173, 1495-1507.e18.	28.9	183
17	Crystal structure of the 14-subunit RNA polymerase α . <i>Nature</i> , 2013, 502, 644-649.	27.8	179
18	Complex Interdependence Regulates Heterotypic Transcription Factor Distribution and Coordinates Cardiogenesis. <i>Cell</i> , 2016, 164, 999-1014.	28.9	179

#	ARTICLE	IF	CITATIONS
19	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
20	Molecular structures of unbound and transcribing RNA polymerase III. <i>Nature</i> , 2015, 528, 231-236.	27.8	167
21	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
22	Molecular architecture of polycomb repressive complexes. <i>Biochemical Society Transactions</i> , 2017, 45, 193-205.	3.4	153
23	A systematic screen for protein-lipid interactions in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2010, 6, 430.	7.2	146
24	In-cell architecture of the nuclear pore and snapshots of its turnover. <i>Nature</i> , 2020, 586, 796-800.	27.8	139
25	Structure of the human NF-kappa B p52 homodimer-DNA complex at 2.1 Å resolution. <i>EMBO Journal</i> , 1997, 16, 7078-7090.	7.8	126
26	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
27	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
28	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
29	Molecular mechanism of promoter opening by RNA polymerase III. <i>Nature</i> , 2018, 553, 295-300.	27.8	101
30	The signalling conformation of the insulin receptor ectodomain. <i>Nature Communications</i> , 2018, 9, 4420.	12.8	98
31	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
32	Delineation of two functional regions of transcription factor TFIIB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 5628-5632.	7.1	93
33	The Elongator subcomplex Elp456 is a hexameric RecA-like ATPase. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 314-320.	8.2	85
34	Molecular Structures of Transcribing RNA Polymerase I. <i>Molecular Cell</i> , 2016, 64, 1135-1143.	9.7	85
35	Structural Basis of Lytic Cycle Activation by the Epstein-Barr Virus ZEBRA Protein. <i>Molecular Cell</i> , 2006, 21, 565-572.	9.7	82
36	Molecular recognition of histone lysine methylation by the Polycomb group repressor dSfmbt. <i>EMBO Journal</i> , 2009, 28, 1965-1977.	7.8	77

#	ARTICLE	IF	CITATIONS
37	The Crystal Structure of the Drosophila 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
38	Structure of the complex of adenylate kinase from Escherichia coli with the inhibitor P1,P5-di(adenosine-5'-pentaphosphate). <i>Journal of Molecular Biology</i> , 1988, 202, 909-912.	4.2	75
39	Architecture of the yeast Elongator complex. <i>EMBO Reports</i> , 2017, 18, 264-279.	4.5	75
40	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
41	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
42	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
43	Crystal structure of the ankyrin repeat domain of Bcl-3: a unique member of the I κ B protein family. <i>EMBO Journal</i> , 2001, 20, 6180-6190.	7.8	68
44	RNA polymerase I and III: similar yet unique. <i>Current Opinion in Structural Biology</i> , 2017, 47, 88-94.	5.7	68
45	A modular platform for automated cryo-FIB workflows. <i>ELife</i> , 2021, 10, .	6.0	65
46	Conformational flexibility of RNA polymerase III during transcriptional elongation. <i>EMBO Journal</i> , 2010, 29, 3762-3772.	7.8	64
47	Structural and functional analyses of methyllysine binding by the malignant brain tumour repeat protein Sex comb on midleg. <i>EMBO Reports</i> , 2007, 8, 1031-1037.	4.5	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. <i>Journal of Biological Chemistry</i> , 2011, 286, 23388-23396.	3.4	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. <i>Genes and Development</i> , 2017, 31, 939-952.	5.9	61
50	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
51	Structure of an Activated Dictyostelium STAT in Its DNA-Unbound Form. <i>Molecular Cell</i> , 2004, 13, 791-804.	9.7	60
52	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
53	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
54	Structural insights into transcription initiation by yeast RNA polymerase I. <i>EMBO Journal</i> , 2017, 36, 2698-2709.	7.8	58

#	ARTICLE	IF	CITATIONS
55	Architecture of TFIIIC and its role in RNA polymerase III pre-initiation complex assembly. <i>Nature Communications</i> , 2015, 6, 7387.	12.8	57
56	Structure of the <i>Drosophila</i> nucleosome core particle highlights evolutionary constraints on the H2A-H2B histone dimer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1-7.	2.6	55
57	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
58	Transcription factors: global and detailed views. <i>Current Opinion in Structural Biology</i> , 2001, 11, 26-32.	5.7	54
59	Interaction of influenza virus proteins with nucleosomes. <i>Virology</i> , 2005, 332, 329-336.	2.4	54
60	Structural basis for targeting the chromatin repressor Sfmtb to Polycomb response elements. <i>Genes and Development</i> , 2013, 27, 2367-2379.	5.9	53
61	Structural insights into Elongator function. <i>Current Opinion in Structural Biology</i> , 2013, 23, 235-242.	5.7	52
62	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. <i>Nature Methods</i> , 2016, 13, 515-520.	19.0	49
63	Nuclear import factors importin β_1 and importin β_2 undergo mutually induced conformational changes upon association. <i>FEBS Letters</i> , 2000, 484, 291-298.	2.8	48
64	Mass Spectrometry Reveals Stable Modules in holo and apo RNA Polymerases I and III. <i>Structure</i> , 2011, 19, 90-100.	3.3	47
65	Structural Basis of TBX5 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	Molecular basis of tRNA recognition by the Elongator complex. <i>Science Advances</i> , 2019, 5, eaaw2326.	10.3	44
67	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
68	Expression of a tyrosine phosphorylated, DNA binding Stat3 β dimer in bacteria. <i>FEBS Letters</i> , 1998, 441, 141-147.	2.8	42
69	Structural basis for RNA polymerase III transcription repression by Maf1. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 229-232.	8.2	37
70	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
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. <i>ELife</i> , 2019, 8, .	6.0	36
72	Crystal structures of two mutants of adenylate kinase from <i>Escherichia coli</i> that modify the Gly-loop. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 42-49.	2.6	34

#	ARTICLE	IF	CITATIONS
73	Molecular insight into RNA polymerase I promoter recognition and promoter melting. <i>Nature Communications</i> , 2019, 10, 5543.	12.8	33
74	The structure of the NF- κ B p50:DNA-complex a starting point for analyzing the Rel family. <i>FEBS Letters</i> , 1995, 369, 113-117.	2.8	32
75	Structure of the κ ,60/ κ ,91 Subcomplex of Yeast Transcription Factor III C: Insights into Preinitiation Complex Assembly. <i>Molecular Cell</i> , 2006, 24, 221-232.	9.7	32
76	Crystallization of proteins under microgravity. <i>FEBS Letters</i> , 1989, 259, 194-198.	2.8	31
77	The cryo-EM resolution revolution and transcription complexes. <i>Current Opinion in Structural Biology</i> , 2018, 52, 8-15.	5.7	31
78	A firm hand on NF- κ B: structures of the κ B1 \pm â€œNF- κ B complex. <i>Structure</i> , 1999, 7, R1-R6.	3.3	30
79	Structural asymmetry in the eukaryotic Elongator complex. <i>FEBS Letters</i> , 2018, 592, 502-515.	2.8	29
80	Elongator. <i>Transcription</i> , 2012, 3, 273-276.	3.1	28
81	Cryo-EM structures of human RNA polymerase I. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 997-1008.	8.2	28
82	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
83	Structure of the specificity domain of the Dorsal homologue Gambif1 bound to DNA. <i>Structure</i> , 1999, 7, 841-852.	3.3	26
84	The GCM domain is a Zn-coordinating DNA-binding domain. <i>FEBS Letters</i> , 2002, 528, 95-100.	2.8	26
85	Recognizing and remodeling the nucleosome. <i>Current Opinion in Structural Biology</i> , 2011, 21, 335-341.	5.7	25
86	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
87	RNA polymerase III-specific general transcription factor III C contains a heterodimer resembling TFIIF Rap30/Rap74. <i>Nucleic Acids Research</i> , 2013, 41, 9183-9196.	14.5	23
88	Solving the RNA polymerase I structural puzzle. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2570-2582.	2.5	23
89	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
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	Transcribing <scp>RNA</scp> polymerase <scp>III</scp> observed by electron cryomicroscopy. <i>FEBS Journal</i> , 2016, 283, 2811-2819.	4.7	18
93	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
94	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
95	Structure of the TFIIIC subcomplex β , γ provides insights into RNA polymerase III pre-initiation complex formation. <i>Nature Communications</i> , 2020, 11, 4905.	12.8	16
96	A synthetic biology approach to probing nucleosome symmetry. <i>ELife</i> , 2017, 6, .	6.0	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. <i>Structure</i> , 2013, 21, 1338-1349.	3.3	15
98	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
99	An integrated model for termination of RNA polymerase III transcription. <i>Science Advances</i> , 2022, 8, .	10.3	14
100	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
101	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
102	Analyzing RNA polymerase III by electron cryomicroscopy. <i>RNA Biology</i> , 2011, 8, 760-765.	3.1	12
103	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
104	Mechanism of RNA polymerase I selection by transcription factor UAF. <i>Science Advances</i> , 2022, 8, eabn5725.	10.3	9
105	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
106	Unleashing the Power of ASH1L Methyltransferase. <i>Structure</i> , 2019, 27, 727-728.	3.3	7
107	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
108	Expression, proteolytic analysis, reconstitution, and crystallization of the β , γ , δ subcomplex of yeast TFIIIC. <i>Protein Expression and Purification</i> , 2006, 45, 255-261.	1.3	3

#	ARTICLE	IF	CITATIONS
109	Solving the NES problem. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1288-1289.	8.2	3
110	Bacterial Expression, Purification, and Crystallization of Tyrosine Phosphorylated STAT Proteins. <i>Methods in Molecular Biology</i> , 2013, 967, 301-317.	0.9	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. <i>Journal of Crystal Growth</i> , 1992, 122, 385-392.	1.5	2
112	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
113	Enzyme-chromatin complex visualized. <i>Nature</i> , 2014, 514, 572-573.	27.8	2
114	Editorial overview: Protein-nucleic acid interactions: An expanding universe. <i>Current Opinion in Structural Biology</i> , 2017, 47, iv-v.	5.7	1
115	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
116	X-Ray Crystal Structure of STAT Proteins and Structure-Activity Relationships. , 2003, , 311-325.		1