

List of Publications by Year in descending order

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55
papers

2,239
citations

218677

26
h-index

243625

44
g-index

56
all docs

56
docs citations

56
times ranked

3034
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for DNA targeting by the Tn7 transposon. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 143-151.	8.2	29
2	A dissipative pathway for the structural evolution of DNA fibres. <i>Nature Chemistry</i> , 2021, 13, 843-849.	13.6	60
3	Exo1 recruits Cdc5 polo kinase to MutL ³ to ensure efficient meiotic crossover formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30577-30588.	7.1	28
4	Distinct surfaces on Cdc5/PLK Polo-box domain orchestrate combinatorial substrate recognition during cell division. <i>Scientific Reports</i> , 2020, 10, 3379.	3.3	9
5	Evaluation of pre- and post-fusion Human metapneumovirus F proteins as subunit vaccine candidates in mice. <i>Vaccine</i> , 2020, 38, 2122-2127.	3.8	12
6	Role of Era in assembly and homeostasis of the ribosomal small subunit. <i>Nucleic Acids Research</i> , 2019, 47, 8301-8317.	14.5	34
7	Structural consequences of the interaction of RbgA with a 50S ribosomal subunit assembly intermediate. <i>Nucleic Acids Research</i> , 2019, 47, 10414-10425.	14.5	38
8	Structures of a dimodular nonribosomal peptide synthetase reveal conformational flexibility. <i>Science</i> , 2019, 366, .	12.6	99
9	<i>Streptomyces</i> IHF uses multiple interfaces to bind DNA. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 129405.	2.4	2
10	Identification of an XRCC1 DNA binding activity essential for retention at sites of DNA damage. <i>Scientific Reports</i> , 2019, 9, 3095.	3.3	13
11	Binding of the regulatory domain of MutL to the sliding γ^2 -clamp is species specific. <i>Nucleic Acids Research</i> , 2019, 47, 4831-4842.	14.5	11
12	Supramolecular arrangement of the full-length Zika virus NS5. <i>PLoS Pathogens</i> , 2019, 15, e1007656.	4.7	38
13	The More the Merrier: When Four Interfaces Are Better Than One. <i>Structure</i> , 2019, 27, 1483-1484.	3.3	0
14	Characterization of platelet factor 4 amino acids that bind pathogenic antibodies in heparin-induced thrombocytopenia. <i>Journal of Thrombosis and Haemostasis</i> , 2019, 17, 389-399.	3.8	33
15	The endonuclease domain of <i>Bacillus subtilis</i> MutL is functionally asymmetric. <i>DNA Repair</i> , 2019, 73, 1-6.	2.8	6
16	Direct binding and internalization of diverse extracellular nucleic acid species through the collagenous domain of class A scavenger receptors. <i>Immunology and Cell Biology</i> , 2018, 96, 922-934.	2.3	6
17	FHA domains: Phosphopeptide binding and beyond. <i>Progress in Biophysics and Molecular Biology</i> , 2017, 127, 105-110.	2.9	49
18	Large-scale production of recombinant Saw1 in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2017, 133, 75-80.	1.3	3

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19	The cryo-EM structure of YjeQ bound to the 30S subunit suggests a fidelity checkpoint function for this protein in ribosome assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3396-E3403.	7.1	33
20	Molecular basis of human CD22 function and therapeutic targeting. <i>Nature Communications</i> , 2017, 8, 764.	12.8	114
21	Complementary uses of small angle X-ray scattering and X-ray crystallography. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1623-1630.	2.3	4
22	Rifampin phosphotransferase is an unusual antibiotic resistance kinase. <i>Nature Communications</i> , 2016, 7, 11343.	12.8	36
23	AND™ logic gates at work: Crystal structure of Rad53 bound to Dbf4 and Cdc7. <i>Scientific Reports</i> , 2016, 6, 34237.	3.3	17
24	Structural and functional characterization of KEOPS dimerization by Pcc1 and its role in t ⁶ A biosynthesis. <i>Nucleic Acids Research</i> , 2016, 44, 6971-6980.	14.5	26
25	A naturally occurring transcript variant of MARCO reveals the SRCR domain is critical for function. <i>Immunology and Cell Biology</i> , 2016, 94, 646-655.	2.3	24
26	Mismatch repair in Gram-positive bacteria. <i>Research in Microbiology</i> , 2016, 167, 4-12.	2.1	45
27	Insights from a decade of biophysical studies on MutL: Roles in strand discrimination and mismatch removal. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 117, 149-156.	2.9	35
28	Conformational toggling controls target site choice for the heteromeric transposase element Tn7. <i>Nucleic Acids Research</i> , 2015, 43, 10734-10745.	14.5	18
29	The sliding clamp tethers the endonuclease domain of MutL to DNA. <i>Nucleic Acids Research</i> , 2015, 43, 10746-10759.	14.5	45
30	Higher-Order Assembly of BRCC36/KIAA0157 Is Required for DUB Activity and Biological Function. <i>Molecular Cell</i> , 2015, 59, 970-983.	9.7	44
31	A Novel Non-canonical Forkhead-associated (FHA) Domain-binding Interface Mediates the Interaction between Rad53 and Dbf4 Proteins. <i>Journal of Biological Chemistry</i> , 2014, 289, 2589-2599.	3.4	21
32	Dimeric Structure of Pseudokinase RNase L Bound to 2-5A Reveals a Basis for Interferon-Induced Antiviral Activity. <i>Molecular Cell</i> , 2014, 53, 221-234.	9.7	123
33	Mlh1-Mlh3, a Meiotic Crossover and DNA Mismatch Repair Factor, Is a Msh2-Msh3-stimulated Endonuclease. <i>Journal of Biological Chemistry</i> , 2014, 289, 5664-5673.	3.4	124
34	Characterization of the defects in the ATP lid of E. coli MutL that cause transient hypermutability. <i>DNA Repair</i> , 2013, 12, 864-869.	2.8	5
35	Trapping and visualizing intermediate steps in the mismatch repair pathway <i>in vivo</i> . <i>Molecular Microbiology</i> , 2013, 90, 680-698.	2.5	28
36	A novel nucleoid-associated protein specific to the actinobacteria. <i>Nucleic Acids Research</i> , 2013, 41, 4171-4184.	14.5	41

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37	Dbf4: The whole is greater than the sum of its parts. <i>Cell Cycle</i> , 2013, 12, 1180-1188.	2.6	23
38	Functional Characterization Of Dbf4 Interactions With DNA Replication And Checkpoint Factors. <i>FASEB Journal</i> , 2013, 27, 542.10.	0.5	0
39	<i>Saccharomyces cerevisiae</i> Dbf4 Has Unique Fold Necessary for Interaction with Rad53 Kinase. <i>Journal of Biological Chemistry</i> , 2012, 287, 2378-2387.	3.4	22
40	The Functions of MutL in Mismatch Repair. <i>Progress in Molecular Biology and Translational Science</i> , 2012, 110, 41-70.	1.7	40
41	Crystal Structure of the Minimalist Max-E47 Protein Chimera. <i>PLoS ONE</i> , 2012, 7, e32136.	2.5	12
42	The Role of MukE in Assembling a Functional MukBEF Complex. <i>Journal of Molecular Biology</i> , 2011, 412, 578-590.	4.2	20
43	The endonuclease domain of MutL interacts with the β sliding clamp. <i>DNA Repair</i> , 2011, 10, 87-93.	2.8	61
44	Acyldepsipeptide Antibiotics Induce the Formation of a Structured Axial Channel in ClpP: A Model for the ClpX/ClpA-Bound State of ClpP. <i>Chemistry and Biology</i> , 2010, 17, 959-969.	6.0	168
45	Structure of the Endonuclease Domain of MutL: Unlicensed to Cut. <i>Molecular Cell</i> , 2010, 39, 145-151.	9.7	122
46	Structural insights into the cooperative binding of SeqA to a tandem GATC repeat. <i>Nucleic Acids Research</i> , 2009, 37, 3143-3152.	14.5	17
47	The PMS2 Subunit of Human MutL β Contains a Metal Ion Binding Domain of the Iron-Dependent Repressor Protein Family. <i>Journal of Molecular Biology</i> , 2008, 382, 610-627.	4.2	55
48	MukE and MukF Form Two Distinct High Affinity Complexes. <i>Journal of Biological Chemistry</i> , 2007, 282, 14373-14378.	3.4	8
49	Crystal structure of a SeqA β filament: implications for DNA replication and chromosome organization. <i>EMBO Journal</i> , 2005, 24, 1502-1511.	7.8	48
50	Structure of the MutL C-terminal domain: a model of intact MutL and its roles in mismatch repair. <i>EMBO Journal</i> , 2004, 23, 4134-4145.	7.8	163
51	Insights into negative modulation of <i>E. coli</i> replication initiation from the structure of SeqA β -hemimethylated DNA complex. <i>Nature Structural Biology</i> , 2002, 9, 839-43.	9.7	29
52	Crystallization and preliminary X-ray analysis of the hydroperoxidase I C-terminal domain from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 853-855.	2.5	5
53	Structural and biochemical features distinguish the foot-and-mouth disease virus leader proteinase from other papain-like enzymes 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 302, 1227-1240.	4.2	62
54	The structures of picornaviral proteinases. <i>Virus Research</i> , 1999, 62, 159-168.	2.2	105

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55	Conformation of the hypervariable region L3 without the key proline residue. Protein Science, 1996, 5, 167-169.	7.6	20