

# Caroline Kisker

## List of Publications by Year in descending order

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134  
papers

10,500  
citations

30070

54  
h-index

34986

98  
g-index

145  
all docs

145  
docs citations

145  
times ranked

9754  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of ADP·AIF4 <sup>-</sup> -stabilized nitrogenase complex and its implications for signal transduction. <i>Nature</i> , 1997, 387, 370-376.	27.8	517
2	Molecular Basis of Sulfite Oxidase Deficiency from the Structure of Sulfite Oxidase. <i>Cell</i> , 1997, 91, 973-983.	28.9	507
3	Crystal Structure of DMSO Reductase: Redox-Linked Changes in Molybdopterin Coordination. <i>Science</i> , 1996, 272, 1615-1621.	12.6	498
4	MOLYBDENUM-COFACTOR-CONTAINING ENZYMES: Structure and Mechanism. <i>Annual Review of Biochemistry</i> , 1997, 66, 233-267.	11.1	489
5	Constitutive Activation of PKA Catalytic Subunit in Adrenal Cushing's Syndrome. <i>New England Journal of Medicine</i> , 2014, 370, 1019-1028.	27.0	355
6	Mouse Rev1 protein interacts with multiple DNA polymerases involved in translesion DNA synthesis. <i>EMBO Journal</i> , 2003, 22, 6621-6630.	7.8	322
7	Computed structures of core eukaryotic protein complexes. <i>Science</i> , 2021, 374, eabm4805.	12.6	316
8	Prokaryotic Nucleotide Excision Repair: The UvrABC System. <i>Chemical Reviews</i> , 2006, 106, 233-252.	47.7	294
9	Crystal Structure of Dimethyl Sulfoxide Reductase from <i>Rhodobacter capsulatus</i> at 1.88 Å Resolution. <i>Journal of Molecular Biology</i> , 1996, 263, 53-69.	4.2	284
10	High Affinity InhA Inhibitors with Activity against Drug-Resistant Strains of <i>Mycobacterium tuberculosis</i> . <i>ACS Chemical Biology</i> , 2006, 1, 43-53.	3.4	234
11	The Complex Formed Between Tet Repressor and Tetracycline-Mg <sup>2+</sup> Reveals Mechanism of Antibiotic Resistance. <i>Journal of Molecular Biology</i> , 1995, 247, 260-280.	4.2	214
12	Structural basis and mechanism of enoyl reductase inhibition by triclosan. <i>Journal of Molecular Biology</i> , 1999, 290, 859-865.	4.2	201
13	Crystal Structure of the FeS Cluster-Containing Nucleotide Excision Repair Helicase XPD. <i>PLoS Biology</i> , 2008, 6, e149.	5.6	195
14	Crystal Structures of the Active and Alloxanthine-Inhibited Forms of Xanthine Dehydrogenase from <i>Rhodobacter capsulatus</i> . <i>Structure</i> , 2002, 10, 115-125.	3.3	193
15	A Closer Look at the Active Site of $\Gamma^3$ -Class Carbonic Anhydrases: High-Resolution Crystallographic Studies of the Carbonic Anhydrase from <i>Methanosarcina thermophila</i> . <i>Biochemistry</i> , 2000, 39, 9222-9231.	2.5	175
16	Crystal structure of UvrB, a DNA helicase adapted for nucleotide excision repair. <i>EMBO Journal</i> , 1999, 18, 6899-6907.	7.8	167
17	Prokaryotic Nucleotide Excision Repair. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012591-a012591.	5.5	159
18	A Slow, Tight Binding Inhibitor of InhA, the Enoyl-Acyl Carrier Protein Reductase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 14330-14337.	3.4	155

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19	Crystal Structure and Deletion Analysis Show that the Accessory Subunit of Mammalian DNA Polymerase $\beta$ , Pol $\beta$ , Functions as a Homodimer. <i>Molecular Cell</i> , 2001, 7, 43-54.	9.7	135
20	The Crystal Structure of Plant Sulfite Oxidase Provides Insights into Sulfite Oxidation in Plants and Animals. <i>Structure</i> , 2003, 11, 1251-1263.	3.3	134
21	Functional Human Mitochondrial DNA Polymerase $\beta$ Forms a Heterotrimer. <i>Journal of Biological Chemistry</i> , 2006, 281, 374-382.	3.4	134
22	Different promoter affinities account for specificity in MYC-dependent gene regulation. <i>ELife</i> , 2016, 5, .	6.0	127
23	“Close-fitting sleeves”™: DNA damage recognition by the UvrABC nuclease system. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2005, 577, 92-117.	1.0	125
24	Error-Prone DNA Polymerases. <i>Cell</i> , 2001, 107, 9-12.	28.9	122
25	Lesion (in)tolerance reveals insights into DNA replication fidelity. <i>EMBO Journal</i> , 2004, 23, 1494-1505.	7.8	122
26	The Tetracycline Repressor—A Paradigm for a Biological Switch. <i>Angewandte Chemie - International Edition</i> , 2000, 39, 2042-2052.	13.8	118
27	Functional and structural studies of the nucleotide excision repair helicase XPD suggest a polarity for DNA translocation. <i>EMBO Journal</i> , 2012, 31, 494-502.	7.8	114
28	Specialization among Iron-Sulfur Cluster Helicases to Resolve G-quadruplex DNA Structures That Threaten Genomic Stability. <i>Journal of Biological Chemistry</i> , 2013, 288, 28217-28229.	3.4	113
29	A structural comparison of molybdenum cofactor-containing enzymes. <i>FEMS Microbiology Reviews</i> , 1998, 22, 503-521.	8.6	107
30	Slow-Onset Inhibition of the FabI Enoyl Reductase from <i>Francisella tularensis</i> : Residence Time and <i>in Vivo</i> Activity. <i>ACS Chemical Biology</i> , 2009, 4, 221-231.	3.4	106
31	Structural basis for DNA recognition and processing by UvrB. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 360-364.	8.2	101
32	Structure of Acyl Carrier Protein Bound to FabI, the FASII Enoyl Reductase from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 39285-39293.	3.4	101
33	The $\beta$ -Hairpin Motif of UvrB Is Essential for DNA Binding, Damage Processing, and UvrC-mediated Incisions. <i>Journal of Biological Chemistry</i> , 2002, 277, 1553-1559.	3.4	94
34	Novel Somatic Mutations in the Catalytic Subunit of the Protein Kinase A as a Cause of Adrenal Cushing's Syndrome: A European Multicentric Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014, 99, E2093-E2100.	3.6	92
35	DNA Binding Cooperativity of p53 Modulates the Decision between Cell-Cycle Arrest and Apoptosis. <i>Molecular Cell</i> , 2010, 38, 356-368.	9.7	89
36	Crystal Structure of <i>Mycobacterium tuberculosis</i> MenB, a Key Enzyme in Vitamin K2 Biosynthesis. <i>Journal of Biological Chemistry</i> , 2003, 278, 42352-42360.	3.4	86

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37	Structural insights into the first incision reaction during nucleotide excision repair. <i>EMBO Journal</i> , 2005, 24, 885-894.	7.8	84
38	Structural Basis of Assembly Chaperone- Mediated snRNP Formation. <i>Molecular Cell</i> , 2013, 49, 692-703.	9.7	82
39	In TFIIH, XPD Helicase Is Exclusively Devoted to DNA Repair. <i>PLoS Biology</i> , 2014, 12, e1001954.	5.6	79
40	<i>Staphylococcus aureus</i> FabI: Inhibition, Substrate Recognition, and Potential Implications for In Vivo Essentiality. <i>Structure</i> , 2012, 20, 802-813.	3.3	78
41	Isolated sulfite oxidase deficiency: identification of 12 novel SUOX mutations in 10 patients. <i>Human Mutation</i> , 2002, 20, 74-74.	2.5	74
42	<i>Chlamydia trachomatis</i> -containing vacuole serves as deubiquitination platform to stabilize Mcl-1 and to interfere with host defense. <i>ELife</i> , 2017, 6, .	6.0	74
43	Structural Insights into Sulfite Oxidase Deficiency. <i>Journal of Biological Chemistry</i> , 2005, 280, 33506-33515.	3.4	73
44	OmoMYC blunts promoter invasion by oncogenic MYC to inhibit gene expression characteristic of MYC-dependent tumors. <i>Oncogene</i> , 2017, 36, 1911-1924.	5.9	73
45	The nucleotide excision repair protein UvrB, a helicase-like enzyme with a catch. <i>Mutation Research DNA Repair</i> , 2000, 460, 277-300.	3.7	67
46	Crystal Structures of <i>Mycobacterium tuberculosis</i> KasA Show Mode of Action within Cell Wall Biosynthesis and its Inhibition by Thiolactomycin. <i>Structure</i> , 2009, 17, 1004-1013.	3.3	66
47	X-ray Absorption Spectroscopy of Chicken Sulfite Oxidase Crystals. <i>Inorganic Chemistry</i> , 1999, 38, 2539-2540.	4.0	63
48	PKA catalytic subunit mutations in adrenocortical Cushing's adenoma impair association with the regulatory subunit. <i>Nature Communications</i> , 2014, 5, 5680.	12.8	63
49	Rational Design of Broad Spectrum Antibacterial Activity Based on a Clinically Relevant Enoyl-Acyl Carrier Protein (ACP) Reductase Inhibitor. <i>Journal of Biological Chemistry</i> , 2014, 289, 15987-16005.	3.4	63
50	Structure and Mechanism of MbtI, the Salicylate Synthase from <i>Mycobacterium tuberculosis</i> . <i>Biochemistry</i> , 2007, 46, 954-964.	2.5	62
51	Mechanism of the Intramolecular Claisen Condensation Reaction Catalyzed by MenB, a Crotonase Superfamily Member. <i>Biochemistry</i> , 2011, 50, 9532-9544.	2.5	62
52	Interactions between UvrA and UvrB: the role of UvrB's domain 2 in nucleotide excision repair. <i>EMBO Journal</i> , 2004, 23, 2498-2509.	7.8	61
53	Proximity Mapping of the Tet Repressor-Tetracycline-Fe <sup>2+</sup> Complex by Hydrogen Peroxide Mediated Protein Cleavage. <i>Biochemistry</i> , 1995, 34, 22-31.	2.5	59
54	Raf Kinase Inhibitor Protein (RKIP) Dimer Formation Controls Its Target Switch from Raf1 to G Protein-coupled Receptor Kinase (GRK) 2. <i>Journal of Biological Chemistry</i> , 2012, 287, 23407-23417.	3.4	59

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55	Rational Optimization of Drug-Target Residence Time: Insights from Inhibitor Binding to the <i>Staphylococcus aureus</i> FabI Enzyme-Product Complex. <i>Biochemistry</i> , 2013, 52, 4217-4228.	2.5	58
56	Molybdopterin from molybdenum and tungsten enzymes. <i>Advances in Protein Chemistry</i> , 2001, 58, 47-94.	4.4	56
57	Structure of the C-terminal half of UvrC reveals an RNase H endonuclease domain with an Argonaute-like catalytic triad. <i>EMBO Journal</i> , 2007, 26, 613-622.	7.8	55
58	Role of XPD in cellular functions: To TFIIH and beyond. <i>DNA Repair</i> , 2016, 44, 136-142.	2.8	55
59	The molybdenum-cofactor: a crystallographic perspective. <i>Journal of Biological Inorganic Chemistry</i> , 1997, 2, 773-781.	2.6	53
60	Lysine 190 Is the Catalytic Base in MenF, the Menaquinone-Specific Isochorismate Synthase from <i>Escherichia coli</i> : Implications for an Enzyme Family. <i>Biochemistry</i> , 2007, 46, 946-953.	2.5	53
61	Michael Acceptor Based Antiplasmodial and Antitrypanosomal Cysteine Protease Inhibitors with Unusual Amino Acids. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 1951-1963.	6.4	48
62	Structural Basis for the Recognition of Mycolic Acid Precursors by KasA, a Condensing Enzyme and Drug Target from <i>Mycobacterium Tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 34190-34204.	3.4	48
63	Structural basis for the shielding function of the dynamic trypanosome variant surface glycoprotein coat. <i>Nature Microbiology</i> , 2017, 2, 1523-1532.	13.3	48
64	Structural insights into the recognition of cisplatin and AAF-dG lesion by Rad14 (XPA). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8272-8277.	7.1	46
65	Evaluating the Contribution of Transition-State Destabilization to Changes in the Residence Time of Triazole-Based InhA Inhibitors. <i>Journal of the American Chemical Society</i> , 2017, 139, 3417-3429.	13.7	46
66	Development of Modern InhA Inhibitors to Combat Drug Resistant Strains of <i>Mycobacterium tuberculosis</i> . <i>Current Topics in Medicinal Chemistry</i> , 2007, 7, 489-498.	2.1	42
67	Slow Onset Inhibition of Bacterial $\beta$ -Ketoacyl-acyl Carrier Protein Synthases by Thiolactomycin. <i>Journal of Biological Chemistry</i> , 2010, 285, 6161-6169.	3.4	42
68	Strand-specific Recognition of DNA Damages by XPD Provides Insights into Nucleotide Excision Repair Substrate Versatility. <i>Journal of Biological Chemistry</i> , 2014, 289, 3613-3624.	3.4	42
69	Differential Oligomerization of the Deubiquitinases USP25 and USP28 Regulates Their Activities. <i>Molecular Cell</i> , 2019, 74, 421-435.e10.	9.7	42
70	FANCM interacts with PCNA to promote replication traverse of DNA interstrand crosslinks. <i>Nucleic Acids Research</i> , 2016, 44, 3219-3232.	14.5	41
71	The structural and functional characterization of human RecQ4 reveals insights into its helicase mechanism. <i>Nature Communications</i> , 2017, 8, 15907.	12.8	41
72	Mechanism of Substrate and Inhibitor Binding of <i>Rhodobacter capsulatus</i> Xanthine Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2009, 284, 8768-8776.	3.4	40

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73	Structural Basis for the Recruitment of Ctf18-RFC to the Replisome. <i>Structure</i> , 2018, 26, 137-144.e3.	3.3	40
74	Structure of the Mouse Peptide N-Glycanase-HR23 Complex Suggests Co-evolution of the Endoplasmic Reticulum-associated Degradation and DNA Repair Pathways. <i>Journal of Biological Chemistry</i> , 2006, 281, 13751-13761.	3.4	39
75	Damage recognition in nucleotide excision DNA repair. <i>Current Opinion in Structural Biology</i> , 2012, 22, 88-93.	5.7	38
76	FadA5 a Thiolase from <i>Mycobacterium tuberculosis</i> : A Steroid-Binding Pocket Reveals the Potential for Drug Development against Tuberculosis. <i>Structure</i> , 2015, 23, 21-33.	3.3	38
77	Identification of Residues within UvrB That Are Important for Efficient DNA Binding and Damage Processing. <i>Journal of Biological Chemistry</i> , 2004, 279, 51574-51580.	3.4	37
78	Conserved salt-bridge competition triggered by phosphorylation regulates the protein interactome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13453-13458.	7.1	35
79	DNA Damage, Mutagenesis, and DNA Repair. <i>Journal of Nucleic Acids</i> , 2010, 2010, 1-1.	1.2	34
80	Global discovery of bacterial RNA-binding proteins by RNase-sensitive gradient profiles reports a new FinO domain protein. <i>Rna</i> , 2020, 26, 1448-1463.	3.5	34
81	The Q Motif of Fanconi Anemia Group J Protein (FANCI) DNA Helicase Regulates Its Dimerization, DNA Binding, and DNA Repair Function. <i>Journal of Biological Chemistry</i> , 2012, 287, 21699-21716.	3.4	33
82	In TFIIH the Arch domain of XPD is mechanistically essential for transcription and DNA repair. <i>Nature Communications</i> , 2020, 11, 1667.	12.8	32
83	The complex between ribonuclease T1 and 3'GMP suggests geometry of enzymic reaction path. An X-ray study. <i>FEBS Journal</i> , 1993, 218, 1005-1012.	0.2	31
84	A crystallographic view of the molybdenum cofactor. <i>Journal of the Chemical Society Dalton Transactions</i> , 1997, , 3909-3914.	1.1	31
85	Stereoselectivity of Enoyl-CoA Hydratase Results from Preferential Activation of One of Two Bound Substrate Conformers. <i>Chemistry and Biology</i> , 2002, 9, 1247-1255.	6.0	28
86	Characterizing septum inhibition in <i>Mycobacterium tuberculosis</i> for novel drug discovery. <i>Tuberculosis</i> , 2008, 88, 420-429.	1.9	28
87	High accuracy FIONA AFM hybrid imaging. <i>Ultramicroscopy</i> , 2011, 111, 350-355.	1.9	28
88	An Ordered Water Channel in <i>Staphylococcus aureus</i> FabI: Unraveling the Mechanism of Substrate Recognition and Reduction. <i>Biochemistry</i> , 2015, 54, 1943-1955.	2.5	27
89	The Structures of the C185S and C185A Mutants of Sulfite Oxidase Reveal Rearrangement of the Active Site. <i>Biochemistry</i> , 2010, 49, 3989-4000.	2.5	26
90	Repurposing a Library of Human Cathepsin L Ligands: Identification of Macrocyclic Lactams as Potent <i>Rhodesain</i> and <i>Trypanosoma brucei</i> Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 3350-3369.	6.4	26

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91	Structural basis for CDK7 activation by MAT1 and Cyclin H. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26739-26748.	7.1	26
92	Conservation and Divergence in Nucleotide Excision Repair Lesion Recognition. Journal of Biological Chemistry, 2016, 291, 18932-18946.	3.4	25
93	Correlating drug target kinetics and in vivo pharmacodynamics: long residence time inhibitors of the FabI enoyl-ACP reductase. Chemical Science, 2016, 7, 5945-5954.	7.4	24
94	A simple device for studying macromolecular crystals under moderate gas pressures (0.1–10 MPa). Journal of Applied Crystallography, 1996, 29, 608-613.	4.5	23
95	The XPD helicase: XPanDing archaeal XPD structures to get a grip on human DNA repair. Biological Chemistry, 2010, 391, 761-5.	2.5	21
96	Impact of Age-Associated Cyclopurine Lesions on DNA Repair Helicases. PLoS ONE, 2014, 9, e113293.	2.5	21
97	The intricate network between the p34 and p44 subunits is central to the activity of the transcription/DNA repair factor TFIIH. Nucleic Acids Research, 2017, 45, 10872-10883.	14.5	21
98	The 1.2 Å structure of the human sulfite oxidase cytochrome b5 domain. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1183-1191.	2.5	20
99	DNA Helicases in NER, BER, and MMR. Advances in Experimental Medicine and Biology, 2013, 767, 203-224.	1.6	20
100	The EM structure of human DNA polymerase $\beta$ reveals a localized contact between the catalytic and accessory subunits. EMBO Journal, 2007, 26, 4283-4291.	7.8	19
101	XPB helicase regulates DNA incision by the Thermoplasma acidophilum endonuclease Bax1. DNA Repair, 2012, 11, 286-293.	2.8	18
102	Structure of the Yersinia pestis FabV Enoyl-ACP Reductase and Its Interaction with Two 2-Pyridone Inhibitors. Structure, 2012, 20, 89-100.	3.3	18
103	Elucidation of the Protonation States of the Catalytic Residues in KasA: Implications for Inhibitor Design. Biochemistry, 2011, 50, 5743-5756.	2.5	17
104	The TFIIH subunits p44/p62 act as a damage sensor during nucleotide excision repair. Nucleic Acids Research, 2020, 48, 12689-12696.	14.5	17
105	Catabolism of the Cholesterol Side Chain in Mycobacterium tuberculosis Is Controlled by a Redox-Sensitive Thiol Switch. ACS Infectious Diseases, 2017, 3, 666-675.	3.8	16
106	Single molecule analysis reveals monomeric XPA bends DNA and undergoes episodic linear diffusion during damage search. Nature Communications, 2020, 11, 1356.	12.8	16
107	On-Bead Screening of a Combinatorial Fumaric Acid Derived Peptide Library Yields Antiplasmodial Cysteine Protease Inhibitors with Unusual Peptide Sequences. Journal of Medicinal Chemistry, 2009, 52, 5662-5672.	6.4	15
108	Interaction between Salt-inducible Kinase 2 (SIK2) and p97/Valosin-containing Protein (VCP) Regulates Endoplasmic Reticulum (ER)-associated Protein Degradation in Mammalian Cells. Journal of Biological Chemistry, 2013, 288, 33861-33872.	3.4	15

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109	X-ray crystallographic and calorimetric studies of the effects of the mutation Trp59 Tyr in ribonuclease T1. FEBS Journal, 1994, 220, 527-534.	0.2	14
110	Biophysical and Functional Analyses Suggest That Adenovirus E4-ORF3 Protein Requires Higher-order Multimerization to Function against Promyelocytic Leukemia Protein Nuclear Bodies. Journal of Biological Chemistry, 2012, 287, 22573-22583.	3.4	14
111	How to limit the speed of a motor: the intricate regulation of the XPB ATPase and translocase in TFIIH. Nucleic Acids Research, 2020, 48, 12282-12296.	14.5	14
112	Structural analysis of missense mutations causing isolated sulfite oxidase deficiency. Dalton Transactions, 2005, , 3459.	3.3	13
113	Comparing crystallographic and solution structures of nitrogenase complexes. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 727-728.	2.5	12
114	Bax1 Is a Novel Endonuclease. Journal of Biological Chemistry, 2009, 284, 32272-32278.	3.4	12
115	Crystallographic Characterization of an Exocyclic DNA Adduct: 3,N4-etheno-2'-deoxycytidine in the Dodecamer 5'-CGCGAATTTCGCG-3'. Journal of Molecular Biology, 2003, 329, 685-697.	4.2	11
116	The Structure of the TFIIH p34 Subunit Reveals a Von Willebrand Factor A Like Fold. PLoS ONE, 2014, 9, e102389.	2.5	10
117	Nucleotide Excision Repair from Bacteria to Humans: Structure-Function Studies. , 2011, , 267-296.		10
118	Structural Basis of Substrate Recognition and Covalent Inhibition of Cdu1 from <i>Chlamydia trachomatis</i> . ChemMedChem, 2018, 13, 2014-2023.	3.2	8
119	Molecular dynamics of Mycobacterium tuberculosis KasA: implications for inhibitor and substrate binding and consequences for drug design. Journal of Computer-Aided Molecular Design, 2011, 25, 1053-1069.	2.9	7
120	Selectivity of Pyridone- and Diphenyl Ether-Based Inhibitors for the <i>Yersinia pestis</i> FabV Enoyl-ACP Reductase. Biochemistry, 2016, 55, 2992-3006.	2.5	6
121	Three targets in one complex: A molecular perspective of TFIIH in cancer therapy. DNA Repair, 2021, 105, 103143.	2.8	6
122	Rationalizing the Binding Kinetics for the Inhibition of the <i>Burkholderia pseudomallei</i> FabI1 Enoyl-ACP Reductase. Biochemistry, 2017, 56, 1865-1878.	2.5	5
123	A structural comparison of molybdenum cofactor-containing enzymes. FEMS Microbiology Reviews, 1998, 22, 503-521.	8.6	5
124	Crystallizing the 6S and 8S spliceosomal assembly intermediates: a complex project. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2040-2053.	2.5	4
125	Mechanistic insights into the enzymatic activity and inhibition of the replicative polymerase exonuclease domain from Mycobacterium tuberculosis. DNA Repair, 2019, 74, 17-25.	2.8	4
126	The Interaction Efficiency of XPD-p44 With Bulky DNA Damages Depends on the Structure of the Damage. Frontiers in Cell and Developmental Biology, 2021, 9, 617160.	3.7	4



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127	A Long Residence Time Enoyl-Reductase Inhibitor Explores an Extended Binding Region with Isoenzyme-Dependent Tautomer Adaptation and Differential Substrate-Binding Loop Closure. ACS Infectious Diseases, 2021, 7, 746-758.	3.8	4
128	Transcriptional pausing to scout ahead for DNA damage. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3905-3906.	7.1	3
129	When One Protein Does the Job of Many. Structure, 2007, 15, 1163-1165.	3.3	2
130	Cesium based phasing of macromolecules: a general easy to use approach for solving the phase problem. Scientific Reports, 2021, 11, 17038.	3.3	1
131	A simple pressure cell and delivery system for the preparation of Xe derivatives for protein crystallography. Review of Scientific Instruments, 1996, 67, 3365-3365.	1.3	0
132	Third EU-US workshop on "Nucleotide excision repair and crosslink repair" From molecules to mankind, Smolenice Castle, Slovak Republic, May 7th-11th 2017. DNA Repair, 2017, 58, 62-66.	2.8	0
133	Structural Features of Bypass Polymerases. , 2005, , .		0
134	Targeting the Enoyl-Reductase Enzyme (FabI): Modern Drug Discovery Effects to Combat Tularemia. FASEB Journal, 2008, 22, 791.6.	0.5	0