

# 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	The Interaction Efficiency of XPD-p44 With Bulky DNA Damages Depends on the Structure of the Damage. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 617160.	3.7	4
2	A Long Residence Time Enoyl-Reductase Inhibitor Explores an Extended Binding Region with Isoenzyme-Dependent Tautomer Adaptation and Differential Substrate-Binding Loop Closure. <i>ACS Infectious Diseases</i> , 2021, 7, 746-758.	3.8	4
3	Cesium based phasing of macromolecules: a general easy to use approach for solving the phase problem. <i>Scientific Reports</i> , 2021, 11, 17038.	3.3	1
4	Three targets in one complex: A molecular perspective of TFIIH in cancer therapy. <i>DNA Repair</i> , 2021, 105, 103143.	2.8	6
5	Computed structures of core eukaryotic protein complexes. <i>Science</i> , 2021, 374, eabm4805.	12.6	316
6	Structural basis for CDK7 activation by MAT1 and Cyclin H. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26739-26748.	7.1	26
7	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
8	The TFIIH subunits p44/p62 act as a damage sensor during nucleotide excision repair. <i>Nucleic Acids Research</i> , 2020, 48, 12689-12696.	14.5	17
9	Single molecule analysis reveals monomeric XPA bends DNA and undergoes episodic linear diffusion during damage search. <i>Nature Communications</i> , 2020, 11, 1356.	12.8	16
10	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
11	How to limit the speed of a motor: the intricate regulation of the XPB ATPase and translocase in TFIIH. <i>Nucleic Acids Research</i> , 2020, 48, 12282-12296.	14.5	14
12	Differential Oligomerization of the Deubiquitinases USP25 and USP28 Regulates Their Activities. <i>Molecular Cell</i> , 2019, 74, 421-435.e10.	9.7	42
13	Mechanistic insights into the enzymatic activity and inhibition of the replicative polymerase exonuclease domain from <i>Mycobacterium tuberculosis</i> . <i>DNA Repair</i> , 2019, 74, 17-25.	2.8	4
14	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
15	Structural Basis for the Recruitment of Ctf18-RFC to the Replisome. <i>Structure</i> , 2018, 26, 137-144.e3.	3.3	40
16	Structural Basis of Substrate Recognition and Covalent Inhibition of Cdu1 from <i>Chlamydia trachomatis</i> . <i>ChemMedChem</i> , 2018, 13, 2014-2023.	3.2	8
17	Rationalizing the Binding Kinetics for the Inhibition of the <i>Burkholderia pseudomallei</i> FabI1 Enoyl-ACP Reductase. <i>Biochemistry</i> , 2017, 56, 1865-1878.	2.5	5
18	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

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19	The intricate network between the p34 and p44 subunits is central to the activity of the transcription/DNA repair factor TFIIH. <i>Nucleic Acids Research</i> , 2017, 45, 10872-10883.	14.5	21
20	Third EU-US workshop on "Nucleotide excision repair and crosslink repair" From molecules to mankind, Smolenice Castle, Slovak Republic, May 7th-11th 2017. <i>DNA Repair</i> , 2017, 58, 62-66.	2.8	0
21	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
22	Catabolism of the Cholesterol Side Chain in <i>Mycobacterium tuberculosis</i> Is Controlled by a Redox-Sensitive Thiol Switch. <i>ACS Infectious Diseases</i> , 2017, 3, 666-675.	3.8	16
23	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
24	The structural and functional characterization of human RecQ4 reveals insights into its helicase mechanism. <i>Nature Communications</i> , 2017, 8, 15907.	12.8	41
25	OncMYC 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
26	<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
27	Different promoter affinities account for specificity in MYC-dependent gene regulation. <i>ELife</i> , 2016, 5, .	6.0	127
28	Role of XPD in cellular functions: To TFIIH and beyond. <i>DNA Repair</i> , 2016, 44, 136-142.	2.8	55
29	Selectivity of Pyridone- and Diphenyl Ether-Based Inhibitors for the <i>Yersinia pestis</i> FabV Enoyl-ACP Reductase. <i>Biochemistry</i> , 2016, 55, 2992-3006.	2.5	6
30	Correlating drug-target kinetics and in vivo pharmacodynamics: long residence time inhibitors of the FabI enoyl-ACP reductase. <i>Chemical Science</i> , 2016, 7, 5945-5954.	7.4	24
31	Conservation and Divergence in Nucleotide Excision Repair Lesion Recognition. <i>Journal of Biological Chemistry</i> , 2016, 291, 18932-18946.	3.4	25
32	FANCM interacts with PCNA to promote replication traverse of DNA interstrand crosslinks. <i>Nucleic Acids Research</i> , 2016, 44, 3219-3232.	14.5	41
33	Crystallizing the 6S and 8S spliceosomal assembly intermediates: a complex project. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2040-2053.	2.5	4
34	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
35	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
36	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

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37	The Structure of the TFIIH p34 Subunit Reveals a Von Willebrand Factor A Like Fold. <i>PLoS ONE</i> , 2014, 9, e102389.	2.5	10
38	Impact of Age-Associated Cyclopurine Lesions on DNA Repair Helicases. <i>PLoS ONE</i> , 2014, 9, e113293.	2.5	21
39	Transcriptional pausing to scout ahead for DNA damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3905-3906.	7.1	3
40	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
41	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
42	In TFIIH, XPD Helicase Is Exclusively Devoted to DNA Repair. <i>PLoS Biology</i> , 2014, 12, e1001954.	5.6	79
43	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
44	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
45	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
46	Structural Basis of Assembly Chaperone-Mediated snRNP Formation. <i>Molecular Cell</i> , 2013, 49, 692-703.	9.7	82
47	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
48	DNA Helicases in NER, BER, and MMR. <i>Advances in Experimental Medicine and Biology</i> , 2013, 767, 203-224.	1.6	20
49	Prokaryotic Nucleotide Excision Repair. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012591-a012591.	5.5	159
50	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
51	Interaction between Salt-inducible Kinase 2 (SIK2) and p97/Valosin-containing Protein (VCP) Regulates Endoplasmic Reticulum (ER)-associated Protein Degradation in Mammalian Cells. <i>Journal of Biological Chemistry</i> , 2013, 288, 33861-33872.	3.4	15
52	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
53	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
54	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

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55	Biophysical and Functional Analyses Suggest That Adenovirus E4-ORF3 Protein Requires Higher-order Multimerization to Function against Promyelocytic Leukemia Protein Nuclear Bodies. <i>Journal of Biological Chemistry</i> , 2012, 287, 22573-22583.	3.4	14
56	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
57	XPB helicase regulates DNA incision by the <i>Thermoplasma acidophilum</i> endonuclease Bax1. <i>DNA Repair</i> , 2012, 11, 286-293.	2.8	18
58	Damage recognition in nucleotide excision DNA repair. <i>Current Opinion in Structural Biology</i> , 2012, 22, 88-93.	5.7	38
59	Structure of the <i>Yersinia pestis</i> FabV Enoyl-ACP Reductase and Its Interaction with Two 2-Pyridone Inhibitors. <i>Structure</i> , 2012, 20, 89-100.	3.3	18
60	<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
61	Mechanism of the Intramolecular Claisen Condensation Reaction Catalyzed by MenB, a Crotonase Superfamily Member. <i>Biochemistry</i> , 2011, 50, 9532-9544.	2.5	62
62	Elucidation of the Protonation States of the Catalytic Residues in <i>Mt</i> KasA: Implications for Inhibitor Design. <i>Biochemistry</i> , 2011, 50, 5743-5756.	2.5	17
63	Molecular dynamics of <i>Mycobacterium tuberculosis</i> KasA: implications for inhibitor and substrate binding and consequences for drug design. <i>Journal of Computer-Aided Molecular Design</i> , 2011, 25, 1053-1069.	2.9	7
64	High accuracy FIONA AFM hybrid imaging. <i>Ultramicroscopy</i> , 2011, 111, 350-355.	1.9	28
65	Nucleotide Excision Repair from Bacteria to Humans: Structure-Function Studies. , 2011, , 267-296.		10
66	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
67	DNA Damage, Mutagenesis, and DNA Repair. <i>Journal of Nucleic Acids</i> , 2010, 2010, 1-1.	1.2	34
68	The XPD helicase: XPanDing archaeal XPD structures to get a grip on human DNA repair. <i>Biological Chemistry</i> , 2010, 391, 761-5.	2.5	21
69	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
70	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
71	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
72	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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73	Bax1 Is a Novel Endonuclease. <i>Journal of Biological Chemistry</i> , 2009, 284, 32272-32278.	3.4	12
74	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
75	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
76	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
77	On-Bead Screening of a Combinatorial Fumaric Acid Derived Peptide Library Yields Antiplasmodial Cysteine Protease Inhibitors with Unusual Peptide Sequences. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 5662-5672.	6.4	15
78	Characterizing septum inhibition in <i>Mycobacterium tuberculosis</i> for novel drug discovery. <i>Tuberculosis</i> , 2008, 88, 420-429.	1.9	28
79	Crystal Structure of the FeS Cluster-Containing Nucleotide Excision Repair Helicase XPD. <i>PLoS Biology</i> , 2008, 6, e149.	5.6	195
80	Targeting the Enoyl-Reductase Enzyme (FabI): Modern Drug Discovery Effects to Combat Tularemia. <i>FASEB Journal</i> , 2008, 22, 791.6.	0.5	0
81	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
82	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
83	Structure and Mechanism of MbtI, the Salicylate Synthase from <i>Mycobacterium tuberculosis</i> . <i>Biochemistry</i> , 2007, 46, 954-964.	2.5	62
84	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
85	The EM structure of human DNA polymerase $\beta$ reveals a localized contact between the catalytic and accessory subunits. <i>EMBO Journal</i> , 2007, 26, 4283-4291.	7.8	19
86	When One Protein Does the Job of Many. <i>Structure</i> , 2007, 15, 1163-1165.	3.3	2
87	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
88	Prokaryotic Nucleotide Excision Repair: The UvrABC System. <i>Chemical Reviews</i> , 2006, 106, 233-252.	47.7	294
89	Structural basis for DNA recognition and processing by UvrB. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 360-364.	8.2	101
90	Functional Human Mitochondrial DNA Polymerase $\beta$ Forms a Heterotrimer. <i>Journal of Biological Chemistry</i> , 2006, 281, 374-382.	3.4	134

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91	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
92	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
93	Structural insights into the first incision reaction during nucleotide excision repair. <i>EMBO Journal</i> , 2005, 24, 885-894.	7.8	84
94	“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
95	Structural Insights into Sulfite Oxidase Deficiency. <i>Journal of Biological Chemistry</i> , 2005, 280, 33506-33515.	3.4	73
96	Structural analysis of missense mutations causing isolated sulfite oxidase deficiency. <i>Dalton Transactions</i> , 2005, , 3459.	3.3	13
97	Structural Features of Bypass Polymerases. , 2005, , .		0
98	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
99	Lesion (in)tolerance reveals insights into DNA replication fidelity. <i>EMBO Journal</i> , 2004, 23, 1494-1505.	7.8	122
100	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
101	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
102	The 1.2Å... structure of the human sulfite oxidase cytochrome b5 domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1183-1191.	2.5	20
103	Mouse Rev1 protein interacts with multiple DNA polymerases involved in translesion DNA synthesis. <i>EMBO Journal</i> , 2003, 22, 6621-6630.	7.8	322
104	Crystallographic Characterization of an Exocyclic DNA Adduct: 3,N4-etheno-2-deoxycytidine in the Dodecamer 5'-CGCGAATTTCGCG-3'. <i>Journal of Molecular Biology</i> , 2003, 329, 685-697.	4.2	11
105	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
106	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
107	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
108	Isolated sulfite oxidase deficiency: identification of 12 novel SUOX mutations in 10 patients. <i>Human Mutation</i> , 2002, 20, 74-74.	2.5	74



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109	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
110	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
111	Error-Prone DNA Polymerases. <i>Cell</i> , 2001, 107, 9-12.	28.9	122
112	Molybdopterin from molybdenum and tungsten enzymes. <i>Advances in Protein Chemistry</i> , 2001, 58, 47-94.	4.4	56
113	The Tetracycline Repressor—A Paradigm for a Biological Switch. <i>Angewandte Chemie - International Edition</i> , 2000, 39, 2042-2052.	13.8	118
114	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
115	A Closer Look at the Active Site of $\beta$ -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
116	Comparing crystallographic and solution structures of nitrogenase complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 727-728.	2.5	12
117	Crystal structure of UvrB, a DNA helicase adapted for nucleotide excision repair. <i>EMBO Journal</i> , 1999, 18, 6899-6907.	7.8	167
118	X-ray Absorption Spectroscopy of Chicken Sulfite Oxidase Crystals. <i>Inorganic Chemistry</i> , 1999, 38, 2539-2540.	4.0	63
119	Structural basis and mechanism of enoyl reductase inhibition by triclosan. <i>Journal of Molecular Biology</i> , 1999, 290, 859-865.	4.2	201
120	A structural comparison of molybdenum cofactor-containing enzymes. <i>FEMS Microbiology Reviews</i> , 1998, 22, 503-521.	8.6	107
121	A structural comparison of molybdenum cofactor-containing enzymes. <i>FEMS Microbiology Reviews</i> , 1998, 22, 503-521.	8.6	5
122	A crystallographic view of the molybdenum cofactor. <i>Journal of the Chemical Society Dalton Transactions</i> , 1997, , 3909-3914.	1.1	31
123	MOLYBDENUM-COFACTOR-CONTAINING ENZYMES: Structure and Mechanism. <i>Annual Review of Biochemistry</i> , 1997, 66, 233-267.	11.1	489
124	Molecular Basis of Sulfite Oxidase Deficiency from the Structure of Sulfite Oxidase. <i>Cell</i> , 1997, 91, 973-983.	28.9	507
125	Structure of ADP $\cdot$ AlF $_4$ -stabilized nitrogenase complex and its implications for signal transduction. <i>Nature</i> , 1997, 387, 370-376.	27.8	517
126	The molybdenum-cofactor: a crystallographic perspective. <i>Journal of Biological Inorganic Chemistry</i> , 1997, 2, 773-781.	2.6	53



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127	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
128	Crystal Structure of DMSO Reductase: Redox-Linked Changes in Molybdopterin Coordination. <i>Science</i> , 1996, 272, 1615-1621.	12.6	498
129	A simple pressure cell and delivery system for the preparation of Xe derivatives for protein crystallography. <i>Review of Scientific Instruments</i> , 1996, 67, 3365-3365.	1.3	0
130	A simple device for studying macromolecular crystals under moderate gas pressures (0.1–10 MPa). <i>Journal of Applied Crystallography</i> , 1996, 29, 608-613.	4.5	23
131	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
132	The Complex Formed Between Tet Repressor and Tetracycline-Mg <sup>2+</sup>   <i>ihbop</i>   +Reveals Mechanism of Antibiotic Resistance. <i>Journal of Molecular Biology</i> , 1995, 247, 260-280.	4.2	214
133	X-ray crystallographic and calorimetric studies of the effects of the mutation Trp59 Tyr in ribonuclease T1. <i>FEBS Journal</i> , 1994, 220, 527-534.	0.2	14
134	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