

# Caroline Kisker

## List of Publications by Citations

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133  
papers

8,509  
citations

50  
h-index

90  
g-index

144  
ext. papers

9,598  
ext. citations

10.1  
avg, IF

5.62  
L-index

#	Paper	IF	Citations
133	Structure of ADP x AIF4(-)-stabilized nitrogenase complex and its implications for signal transduction. <i>Nature</i> , <b>1997</b> , 387, 370-6	50.4	452
132	Molecular basis of sulfite oxidase deficiency from the structure of sulfite oxidase. <i>Cell</i> , <b>1997</b> , 91, 973-83	56.2	438
131	Molybdenum-cofactor-containing enzymes: structure and mechanism. <i>Annual Review of Biochemistry</i> , <b>1997</b> , 66, 233-67	29.1	423
130	Crystal structure of DMSO reductase: redox-linked changes in molybdopterin coordination. <i>Science</i> , <b>1996</b> , 272, 1615-21	33.3	417
129	Mouse Rev1 protein interacts with multiple DNA polymerases involved in translesion DNA synthesis. <i>EMBO Journal</i> , <b>2003</b> , 22, 6621-30	13	288
128	Constitutive activation of PKA catalytic subunit in adrenal Cushing's syndrome. <i>New England Journal of Medicine</i> , <b>2014</b> , 370, 1019-28	59.2	284
127	Crystal structure of dimethyl sulfoxide reductase from <i>Rhodobacter capsulatus</i> at 1.88 Å resolution. <i>Journal of Molecular Biology</i> , <b>1996</b> , 263, 53-69	6.5	248
126	Prokaryotic nucleotide excision repair: the UvrABC system. <i>Chemical Reviews</i> , <b>2006</b> , 106, 233-52	68.1	239
125	High affinity InhA inhibitors with activity against drug-resistant strains of <i>Mycobacterium tuberculosis</i> . <i>ACS Chemical Biology</i> , <b>2006</b> , 1, 43-53	4.9	210
124	The complex formed between Tet repressor and tetracycline-Mg <sup>2+</sup> reveals mechanism of antibiotic resistance. <i>Journal of Molecular Biology</i> , <b>1995</b> , 247, 260-80	6.5	187
123	Structural basis and mechanism of enoyl reductase inhibition by triclosan. <i>Journal of Molecular Biology</i> , <b>1999</b> , 290, 859-65	6.5	179
122	Crystal structure of the FeS cluster-containing nucleotide excision repair helicase XPD. <i>PLoS Biology</i> , <b>2008</b> , 6, e149	9.7	177
121	Crystal structures of the active and alloxanthine-inhibited forms of xanthine dehydrogenase from <i>Rhodobacter capsulatus</i> . <i>Structure</i> , <b>2002</b> , 10, 115-25	5.2	165
120	Crystal structure of UvrB, a DNA helicase adapted for nucleotide excision repair. <i>EMBO Journal</i> , <b>1999</b> , 18, 6899-907	13	156
119	A closer look at the active site of gamma-class carbonic anhydrases: high-resolution crystallographic studies of the carbonic anhydrase from <i>Methanosarcina thermophila</i> . <i>Biochemistry</i> , <b>2000</b> , 39, 9222-31	3.2	149
118	A slow, tight binding inhibitor of InhA, the enoyl-acyl carrier protein reductase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 14330-7	5.4	126
117	Crystal structure and deletion analysis show that the accessory subunit of mammalian DNA polymerase gamma, Pol gamma B, functions as a homodimer. <i>Molecular Cell</i> , <b>2001</b> , 7, 43-54	17.6	126

116	Functional human mitochondrial DNA polymerase gamma forms a heterotrimer. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 374-82	5.4	117
115	Prokaryotic nucleotide excision repair. <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2013</b> , 5, a012591	10.2	116
114	The crystal structure of plant sulfite oxidase provides insights into sulfite oxidation in plants and animals. <i>Structure</i> , <b>2003</b> , 11, 1251-63	5.2	116
113	Lesion (in)tolerance reveals insights into DNA replication fidelity. <i>EMBO Journal</i> , <b>2004</b> , 23, 1494-505	13	110
112	Error-prone DNA polymerases: novel structures and the benefits of infidelity. <i>Cell</i> , <b>2001</b> , 107, 9-12	56.2	109
111	'Close-fitting sleeves': DNA damage recognition by the UvrABC nuclease system. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , <b>2005</b> , 577, 92-117	3.3	106
110	Slow-onset inhibition of the FabI enoyl reductase from <i>Francisella tularensis</i> : residence time and in vivo activity. <i>ACS Chemical Biology</i> , <b>2009</b> , 4, 221-31	4.9	98
109	The Tetracycline Repressor-A Paradigm for a Biological Switch. <i>Angewandte Chemie - International Edition</i> , <b>2000</b> , 39, 2042-2052	16.4	98
108	Functional and structural studies of the nucleotide excision repair helicase XPD suggest a polarity for DNA translocation. <i>EMBO Journal</i> , <b>2012</b> , 31, 494-502	13	95
107	A structural comparison of molybdenum cofactor-containing enzymes. <i>FEMS Microbiology Reviews</i> , <b>1998</b> , 22, 503-21	15.1	95
106	Structural basis for DNA recognition and processing by UvrB. <i>Nature Structural and Molecular Biology</i> , <b>2006</b> , 13, 360-4	17.6	91
105	Different promoter affinities account for specificity in MYC-dependent gene regulation. <i>ELife</i> , <b>2016</b> , 5,	8.9	90
104	Specialization among iron-sulfur cluster helicases to resolve G-quadruplex DNA structures that threaten genomic stability. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 28217-29	5.4	89
103	Structure of acyl carrier protein bound to FabI, the FASII enoyl reductase from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 39285-39293	5.4	87
102	The beta-hairpin motif of UvrB is essential for DNA binding, damage processing, and UvrC-mediated incisions. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 1553-9	5.4	86
101	Crystal structure of <i>Mycobacterium tuberculosis</i> MenB, a key enzyme in vitamin K2 biosynthesis. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 42352-60	5.4	75
100	DNA binding cooperativity of p53 modulates the decision between cell-cycle arrest and apoptosis. <i>Molecular Cell</i> , <b>2010</b> , 38, 356-68	17.6	69
99	<i>Staphylococcus aureus</i> FabI: inhibition, substrate recognition, and potential implications for in vivo essentiality. <i>Structure</i> , <b>2012</b> , 20, 802-13	5.2	68

98	Structural insights into the first incision reaction during nucleotide excision repair. <i>EMBO Journal</i> , <b>2005</b> , 24, 885-94	13	68
97	Structural basis of assembly chaperone- mediated snRNP formation. <i>Molecular Cell</i> , <b>2013</b> , 49, 692-703	17.6	67
96	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> , <b>2014</b> , 99, E2093-100	5.6	67
95	Isolated sulfite oxidase deficiency: identification of 12 novel SUOX mutations in 10 patients. <i>Human Mutation</i> , <b>2002</b> , 20, 74	4.7	66
94	Structural insights into sulfite oxidase deficiency. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 33506-15	5.4	66
93	OmoMYC blunts promoter invasion by oncogenic MYC to inhibit gene expression characteristic of MYC-dependent tumors. <i>Oncogene</i> , <b>2017</b> , 36, 1911-1924	9.2	57
92	In TFIIH, XPD helicase is exclusively devoted to DNA repair. <i>PLoS Biology</i> , <b>2014</b> , 12, e1001954	9.7	57
91	The nucleotide excision repair protein UvrB, a helicase-like enzyme with a catch. <i>Mutation Research DNA Repair</i> , <b>2000</b> , 460, 277-300		57
90	Structure and mechanism of MbtI, the salicylate synthase from <i>Mycobacterium tuberculosis</i> . <i>Biochemistry</i> , <b>2007</b> , 46, 954-64	3.2	54
89	Proximity mapping of the Tet repressor-tetracycline-Fe <sup>2+</sup> complex by hydrogen peroxide mediated protein cleavage. <i>Biochemistry</i> , <b>1995</b> , 34, 22-31	3.2	54
88	Interactions between UvrA and UvrB: the role of UvrB's domain 2 in nucleotide excision repair. <i>EMBO Journal</i> , <b>2004</b> , 23, 2498-509	13	52
87	Crystal structures of <i>Mycobacterium tuberculosis</i> KasA show mode of action within cell wall biosynthesis and its inhibition by thiolactomycin. <i>Structure</i> , <b>2009</b> , 17, 1004-13	5.2	51
86	Computed structures of core eukaryotic protein complexes. <i>Science</i> , <b>2021</b> , 374, eabm4805	33.3	51
85	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> , <b>2012</b> , 287, 23407-17	5.4	50
84	Rational optimization of drug-target residence time: insights from inhibitor binding to the <i>Staphylococcus aureus</i> FabI enzyme-product complex. <i>Biochemistry</i> , <b>2013</b> , 52, 4217-28	3.2	50
83	X-ray Absorption Spectroscopy of Chicken Sulfite Oxidase Crystals. <i>Inorganic Chemistry</i> , <b>1999</b> , 38, 2539-2540	5.4	50
82	PKA catalytic subunit mutations in adrenocortical Cushing's adenoma impair association with the regulatory subunit. <i>Nature Communications</i> , <b>2014</b> , 5, 5680	17.4	49
81	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> , <b>2007</b> , 46, 946-53	3.2	47

80	Molybdopterin from molybdenum and tungsten enzymes. <i>Advances in Protein Chemistry</i> , <b>2001</b> , 58, 47-94		47
79	Structure of the C-terminal half of UvrC reveals an RNase H endonuclease domain with an Argonaute-like catalytic triad. <i>EMBO Journal</i> , <b>2007</b> , 26, 613-22	13	46
78	The molybdenum-cofactor: a crystallographic perspective. <i>Journal of Biological Inorganic Chemistry</i> , <b>1997</b> , 2, 773-781	3.7	45
77	Michael acceptor based antiplasmodial and antitrypanosomal cysteine protease inhibitors with unusual amino acids. <i>Journal of Medicinal Chemistry</i> , <b>2010</b> , 53, 1951-63	8.3	43
76	Role of XPD in cellular functions: To TFIIH and beyond. <i>DNA Repair</i> , <b>2016</b> , 44, 136-142	4.3	43
75	Mechanism of the intramolecular Claisen condensation reaction catalyzed by MenB, a crotonase superfamily member. <i>Biochemistry</i> , <b>2011</b> , 50, 9532-44	3.2	41
74	-containing vacuole serves as deubiquitination platform to stabilize Mcl-1 and to interfere with host defense. <i>ELife</i> , <b>2017</b> , 6,	8.9	41
73	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> , <b>2014</b> , 289, 15987-6005	5.4	39
72	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> , <b>2015</b> , 112, 8272-7	11.5	38
71	FANCM interacts with PCNA to promote replication traverse of DNA interstrand crosslinks. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 3219-32	20.1	38
70	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> , <b>2017</b> , 139, 3417-3429	16.4	37
69	Development of modern InhA inhibitors to combat drug resistant strains of Mycobacterium tuberculosis. <i>Current Topics in Medicinal Chemistry</i> , <b>2007</b> , 7, 489-98	3	37
68	Strand-specific recognition of DNA damages by XPD provides insights into nucleotide excision repair substrate versatility. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 3613-24	5.4	36
67	Mechanism of Substrate and Inhibitor Binding of Rhodobacter capsulatus Xanthine Dehydrogenase. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 8768-76	5.4	33
66	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> , <b>2006</b> , 281, 13751-13761	5.4	33
65	Structural basis for the shielding function of the dynamic trypanosome variant surface glycoprotein coat. <i>Nature Microbiology</i> , <b>2017</b> , 2, 1523-1532	26.6	32
64	FadA5 a thiolase from Mycobacterium tuberculosis: a steroid-binding pocket reveals the potential for drug development against tuberculosis. <i>Structure</i> , <b>2015</b> , 23, 21-33	5.2	31
63	Damage recognition in nucleotide excision DNA repair. <i>Current Opinion in Structural Biology</i> , <b>2012</b> , 22, 88-93	8.1	31

62	Slow onset inhibition of bacterial beta-ketoacyl-acyl carrier protein synthases by thiolactomycin. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 6161-9	5.4	30
61	Identification of residues within UvrB that are important for efficient DNA binding and damage processing. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 51574-80	5.4	29
60	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> , <b>2012</b> , 287, 21699-716	5.4	28
59	A crystallographic view of the molybdenum cofactor $\square$ <i>Journal of the Chemical Society Dalton Transactions</i> , <b>1997</b> , 3909-3914		28
58	The complex between ribonuclease T1 and 3'GMP suggests geometry of enzymic reaction path. An X-ray study. <i>FEBS Journal</i> , <b>1993</b> , 218, 1005-12		28
57	Stereoselectivity of enoyl-CoA hydratase results from preferential activation of one of two bound substrate conformers. <i>Chemistry and Biology</i> , <b>2002</b> , 9, 1247-55		27
56	DNA damage, mutagenesis, and DNA repair. <i>Journal of Nucleic Acids</i> , <b>2010</b> , 2010, 182894	2.3	26
55	High accuracy FIONA-AFM hybrid imaging. <i>Ultramicroscopy</i> , <b>2011</b> , 111, 350-5	3.1	25
54	The structures of the C185S and C185A mutants of sulfite oxidase reveal rearrangement of the active site. <i>Biochemistry</i> , <b>2010</b> , 49, 3989-4000	3.2	25
53	Characterizing septum inhibition in Mycobacterium tuberculosis for novel drug discovery. <i>Tuberculosis</i> , <b>2008</b> , 88, 420-9	2.6	25
52	Structural basis for the recognition of mycolic acid precursors by KasA, a condensing enzyme and drug target from Mycobacterium tuberculosis. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 34190-34204	5.4	23
51	The structural and functional characterization of human RecQ4 reveals insights into its helicase mechanism. <i>Nature Communications</i> , <b>2017</b> , 8, 15907	17.4	22
50	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> , <b>2017</b> , 114, 13453-13458	11.5	21
49	Global discovery of bacterial RNA-binding proteins by RNase-sensitive gradient profiles reports a new FinO domain protein. <i>Rna</i> , <b>2020</b> , 26, 1448-1463	5.8	21
48	Differential Oligomerization of the Deubiquitinases USP25 and USP28 Regulates Their Activities. <i>Molecular Cell</i> , <b>2019</b> , 74, 421-435.e10	17.6	20
47	Conservation and Divergence in Nucleotide Excision Repair Lesion Recognition. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 18932-46	5.4	20
46	Structural Basis for the Recruitment of Ctf18-RFC to the Replisome. <i>Structure</i> , <b>2018</b> , 26, 137-144.e3	5.2	20
45	Impact of age-associated cyclopurine lesions on DNA repair helicases. <i>PLoS ONE</i> , <b>2014</b> , 9, e113293	3.7	19

44	Correlating Drug-Target Kinetics and Pharmacodynamics: Long Residence Time Inhibitors of the FabI Enoyl-ACP Reductase. <i>Chemical Science</i> , <b>2016</b> , 7, 5945-5954	9.4	19
43	An ordered water channel in Staphylococcus aureus FabI: unraveling the mechanism of substrate recognition and reduction. <i>Biochemistry</i> , <b>2015</b> , 54, 1943-55	3.2	18
42	The EM structure of human DNA polymerase gamma reveals a localized contact between the catalytic and accessory subunits. <i>EMBO Journal</i> , <b>2007</b> , 26, 4283-91	13	18
41	DNA Helicases in NER, BER, and MMR. <i>Advances in Experimental Medicine and Biology</i> , <b>2013</b> , 767, 203-24	3.6	17
40	The XPD helicase: XPanDing archaeal XPD structures to get a grip on human DNA repair. <i>Biological Chemistry</i> , <b>2010</b> , 391, 761-5	4.5	17
39	XPB helicase regulates DNA incision by the Thermoplasma acidophilum endonuclease Bax1. <i>DNA Repair</i> , <b>2012</b> , 11, 286-93	4.3	16
38	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> , <b>2017</b> , 45, 10872-10883	20.1	16
37	The 1.2 Å structure of the human sulfite oxidase cytochrome b(5) domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2003</b> , 59, 1183-91		16
36	In TFIIH the Arch domain of XPD is mechanistically essential for transcription and DNA repair. <i>Nature Communications</i> , <b>2020</b> , 11, 1667	17.4	15
35	Repurposing a Library of Human Cathepsin L Ligands: Identification of Macrocyclic Lactams as Potent Rhodesain and Trypanosoma brucei Inhibitors. <i>Journal of Medicinal Chemistry</i> , <b>2018</b> , 61, 3350-3369	8.3	15
34	Structure of the Yersinia pestis FabV enoyl-ACP reductase and its interaction with two 2-pyridone inhibitors. <i>Structure</i> , <b>2012</b> , 20, 89-100	5.2	15
33	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> , <b>2009</b> , 52, 5662-72	8.3	15
32	Elucidation of the protonation states of the catalytic residues in mtKasA: implications for inhibitor design. <i>Biochemistry</i> , <b>2011</b> , 50, 5743-56	3.2	14
31	A simple device for studying macromolecular crystals under moderate gas pressures (0.1–10 MPa). <i>Journal of Applied Crystallography</i> , <b>1996</b> , 29, 608-613	3.8	14
30	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> , <b>2012</b> , 287, 22573-83	5.4	13
29	Comparing crystallographic and solution structures of nitrogenase complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1999</b> , 55, 727-8		12
28	X-ray crystallographic and calorimetric studies of the effects of the mutation Trp59-->Tyr in ribonuclease T1. <i>FEBS Journal</i> , <b>1994</b> , 220, 527-34		12
27	Bax1 is a novel endonuclease: implications for archaeal nucleotide excision repair. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 32272-8	5.4	11

26	Structural analysis of missense mutations causing isolated sulfite oxidase deficiency. <i>Dalton Transactions</i> , <b>2005</b> , 3459-63	4.3	11
25	Crystallographic characterization of an exocyclic DNA adduct: 3,N4-etheno-2'-deoxycytidine in the dodecamer 5'-CGCGAATepsilonCGCG-3'. <i>Journal of Molecular Biology</i> , <b>2003</b> , 329, 685-97	6.5	11
24	Catabolism of the Cholesterol Side Chain in Mycobacterium tuberculosis Is Controlled by a Redox-Sensitive Thiol Switch. <i>ACS Infectious Diseases</i> , <b>2017</b> , 3, 666-675	5.5	10
23	The structure of the TFIIH p34 subunit reveals a von Willebrand factor A like fold. <i>PLoS ONE</i> , <b>2014</b> , 9, e102389	3.7	10
22	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> , <b>2013</b> , 288, 33861-33872	5.4	10
21	Single molecule analysis reveals monomeric XPA bends DNA and undergoes episodic linear diffusion during damage search. <i>Nature Communications</i> , <b>2020</b> , 11, 1356	17.4	8
20	Nucleotide Excision Repair from Bacteria to Humans: StructureFunction Studies <b>2011</b> , 267-296		7
19	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> , <b>2020</b> , 117, 26739-26748	11.5	7
18	The TFIIH subunits p44/p62 act as a damage sensor during nucleotide excision repair. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 12689-12696	20.1	7
17	Rationalizing the Binding Kinetics for the Inhibition of the Burkholderia pseudomallei FabI Enoyl-ACP Reductase. <i>Biochemistry</i> , <b>2017</b> , 56, 1865-1878	3.2	5
16	Structural Basis of Substrate Recognition and Covalent Inhibition of Cdu1 from Chlamydia trachomatis. <i>ChemMedChem</i> , <b>2018</b> , 13, 2014-2023	3.7	5
15	Molecular dynamics of Mycobacterium tuberculosis KasA: implications for inhibitor and substrate binding and consequences for drug design. <i>Journal of Computer-Aided Molecular Design</i> , <b>2011</b> , 25, 1053-69 <sup>2</sup>	4.2	5
14	How to limit the speed of a motor: the intricate regulation of the XPB ATPase and translocase in TFIIH. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 12282-12296	20.1	5
13	Selectivity of Pyridone- and Diphenyl Ether-Based Inhibitors for the Yersinia pestis FabV Enoyl-ACP Reductase. <i>Biochemistry</i> , <b>2016</b> , 55, 2992-3006	3.2	5
12	Crystallizing the 6S and 8S spliceosomal assembly intermediates: a complex project. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 2040-53		2
11	Transcriptional pausing to scout ahead for DNA damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 3905-6	11.5	2
10	When one protein does the job of many. <i>Structure</i> , <b>2007</b> , 15, 1163-5	5.2	2
9	Mechanistic insights into the enzymatic activity and inhibition of the replicative polymerase exonuclease domain from Mycobacterium tuberculosis. <i>DNA Repair</i> , <b>2019</b> , 74, 17-25	4.3	2

8	The TFIIH subunits p44/p62 act as a damage sensor during nucleotide excision repair		1
7	Three targets in one complex: A molecular perspective of TFIIH in cancer therapy. <i>DNA Repair</i> , <b>2021</b> , 105, 103143	4.3	1
6	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> , <b>2021</b> , 9, 617160	5.7	0
5	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> , <b>2021</b> , 7, 746-758	5.5	0
4	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> , <b>2017</b> , 58, 62-66	4.3	
3	A simple pressure cell and delivery system for the preparation of Xe derivatives for protein crystallography. <i>Review of Scientific Instruments</i> , <b>1996</b> , 67, 3365-3365	1.7	
2	Targeting the Enoyl-Reductase Enzyme (FabI): Modern Drug Discovery Effects to Combat Tularemia. <i>FASEB Journal</i> , <b>2008</b> , 22, 791.6	0.9	
1	Cesium based phasing of macromolecules: a general easy to use approach for solving the phase problem. <i>Scientific Reports</i> , <b>2021</b> , 11, 17038	4.9	