

Caroline Kisker

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Computed structures of core eukaryotic protein complexes. <i>Science</i> , 2021 , 374, eabm4805	33.3	51
132	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	5.7	0
131	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	5.5	0
130	Cesium based phasing of macromolecules: a general easy to use approach for solving the phase problem. <i>Scientific Reports</i> , 2021 , 11, 17038	4.9	
129	Three targets in one complex: A molecular perspective of TFIIH in cancer therapy. <i>DNA Repair</i> , 2021 , 105, 103143	4.3	1
128	Single molecule analysis reveals monomeric XPA bends DNA and undergoes episodic linear diffusion during damage search. <i>Nature Communications</i> , 2020 , 11, 1356	17.4	8
127	In TFIIH the Arch domain of XPD is mechanistically essential for transcription and DNA repair. <i>Nature Communications</i> , 2020 , 11, 1667	17.4	15
126	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	20.1	5
125	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	11.5	7
124	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	5.8	21
123	The TFIIH subunits p44/p62 act as a damage sensor during nucleotide excision repair. <i>Nucleic Acids Research</i> , 2020 , 48, 12689-12696	20.1	7
122	Differential Oligomerization of the Deubiquitinases USP25 and USP28 Regulates Their Activities. <i>Molecular Cell</i> , 2019 , 74, 421-435.e10	17.6	20
121	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	4.3	2
120	Repurposing a Library of Human Cathepsin L Ligands: Identification of Macrocyclic Lactams as Potent Rhodesain and <i>Trypanosoma brucei</i> Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 3350-3369	8.3	15
119	Structural Basis of Substrate Recognition and Covalent Inhibition of Cdu1 from <i>Chlamydia trachomatis</i> . <i>ChemMedChem</i> , 2018 , 13, 2014-2023	3.7	5
118	Structural Basis for the Recruitment of Ctf18-RFC to the Replisome. <i>Structure</i> , 2018 , 26, 137-144.e3	5.2	20
117	Rationalizing the Binding Kinetics for the Inhibition of the <i>Burkholderia pseudomallei</i> FabI Enoyl-ACP Reductase. <i>Biochemistry</i> , 2017 , 56, 1865-1878	3.2	5

116	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	16.4	37
115	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	20.1	16
114	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	4.3	
113	Structural basis for the shielding function of the dynamic trypanosome variant surface glycoprotein coat. <i>Nature Microbiology</i> , 2017 , 2, 1523-1532	26.6	32
112	Catabolism of the Cholesterol Side Chain in Mycobacterium tuberculosis Is Controlled by a Redox-Sensitive Thiol Switch. <i>ACS Infectious Diseases</i> , 2017 , 3, 666-675	5.5	10
111	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	11.5	21
110	The structural and functional characterization of human RecQ4 reveals insights into its helicase mechanism. <i>Nature Communications</i> , 2017 , 8, 15907	17.4	22
109	OmoMYC blunts promoter invasion by oncogenic MYC to inhibit gene expression characteristic of MYC-dependent tumors. <i>Oncogene</i> , 2017 , 36, 1911-1924	9.2	57
108	-containing vacuole serves as deubiquitination platform to stabilize Mcl-1 and to interfere with host defense. <i>ELife</i> , 2017 , 6,	8.9	41
107	Conservation and Divergence in Nucleotide Excision Repair Lesion Recognition. <i>Journal of Biological Chemistry</i> , 2016 , 291, 18932-46	5.4	20
106	FANCM interacts with PCNA to promote replication traverse of DNA interstrand crosslinks. <i>Nucleic Acids Research</i> , 2016 , 44, 3219-32	20.1	38
105	Different promoter affinities account for specificity in MYC-dependent gene regulation. <i>ELife</i> , 2016 , 5,	8.9	90
104	Role of XPD in cellular functions: To TFIIH and beyond. <i>DNA Repair</i> , 2016 , 44, 136-142	4.3	43
103	Selectivity of Pyridone- and Diphenyl Ether-Based Inhibitors for the Yersinia pestis FabV Enoyl-ACP Reductase. <i>Biochemistry</i> , 2016 , 55, 2992-3006	3.2	5
102	Correlating Drug-Target Kinetics and Pharmacodynamics: Long Residence Time Inhibitors of the FabI Enoyl-ACP Reductase. <i>Chemical Science</i> , 2016 , 7, 5945-5954	9.4	19
101	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, 8272-7	11.5	38
100	An ordered water channel in Staphylococcus aureus FabI: unraveling the mechanism of substrate recognition and reduction. <i>Biochemistry</i> , 2015 , 54, 1943-55	3.2	18
99	FadA5 a thiolase from Mycobacterium tuberculosis: a steroid-binding pocket reveals the potential for drug development against tuberculosis. <i>Structure</i> , 2015 , 23, 21-33	5.2	31

98	Crystallizing the 6S and 8S spliceosomal assembly intermediates: a complex project. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 2040-53		2
97	Strand-specific recognition of DNA damages by XPD provides insights into nucleotide excision repair substrate versatility. <i>Journal of Biological Chemistry</i> , 2014 , 289, 3613-24	5.4	36
96	Constitutive activation of PKA catalytic subunit in adrenal Cushing's syndrome. <i>New England Journal of Medicine</i> , 2014 , 370, 1019-28	59.2	284
95	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, 15987-6005	5.4	39
94	The structure of the TFIIF p34 subunit reveals a von Willebrand factor A like fold. <i>PLoS ONE</i> , 2014 , 9, e102389	3.7	10
93	Impact of age-associated cyclopurine lesions on DNA repair helicases. <i>PLoS ONE</i> , 2014 , 9, e113293	3.7	19
92	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, 3905-6	11.5	2
91	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, E2093-100	5.6	67
90	PKA catalytic subunit mutations in adrenocortical Cushing's adenoma impair association with the regulatory subunit. <i>Nature Communications</i> , 2014 , 5, 5680	17.4	49
89	In TFIIF, XPD helicase is exclusively devoted to DNA repair. <i>PLoS Biology</i> , 2014 , 12, e1001954	9.7	57
88	Structural basis of assembly chaperone-mediated snRNP formation. <i>Molecular Cell</i> , 2013 , 49, 692-703	17.6	67
87	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	5.4	23
86	DNA Helicases in NER, BER, and MMR. <i>Advances in Experimental Medicine and Biology</i> , 2013 , 767, 203-24	3.6	17
85	Prokaryotic nucleotide excision repair. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013 , 5, a012591	10.2	116
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> , 2013 , 52, 4217-28	3.2	50
83	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	5.4	10
82	Specialization among iron-sulfur cluster helicases to resolve G-quadruplex DNA structures that threaten genomic stability. <i>Journal of Biological Chemistry</i> , 2013 , 288, 28217-29	5.4	89
81	XPB helicase regulates DNA incision by the <i>Thermoplasma acidophilum</i> endonuclease Bax1. <i>DNA Repair</i> , 2012 , 11, 286-93	4.3	16

80	Damage recognition in nucleotide excision DNA repair. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 88-93	8.1	31
79	Structure of the Yersinia pestis FabV enoyl-ACP reductase and its interaction with two 2-pyridone inhibitors. <i>Structure</i> , 2012 , 20, 89-100	5.2	15
78	Staphylococcus aureus FabI: inhibition, substrate recognition, and potential implications for in vivo essentiality. <i>Structure</i> , 2012 , 20, 802-13	5.2	68
77	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, 23407-17	5.4	50
76	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	13	95
75	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, 21699-716	5.4	28
74	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, 22573-83	5.4	13
73	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> , 2011 , 25, 1053-69	4.2	5
72	High accuracy FIONA-AFM hybrid imaging. <i>Ultramicroscopy</i> , 2011 , 111, 350-5	3.1	25
71	Mechanism of the intramolecular Claisen condensation reaction catalyzed by MenB, a crotonase superfamily member. <i>Biochemistry</i> , 2011 , 50, 9532-44	3.2	41
70	Elucidation of the protonation states of the catalytic residues in mtKasA: implications for inhibitor design. <i>Biochemistry</i> , 2011 , 50, 5743-56	3.2	14
69	Nucleotide Excision Repair from Bacteria to Humans: StructureFunction Studies 2011 , 267-296		7
68	DNA damage, mutagenesis, and DNA repair. <i>Journal of Nucleic Acids</i> , 2010 , 2010, 182894	2.3	26
67	The XPD helicase: XPanDing archaeal XPD structures to get a grip on human DNA repair. <i>Biological Chemistry</i> , 2010 , 391, 761-5	4.5	17
66	Slow onset inhibition of bacterial beta-ketoacyl-acyl carrier protein synthases by thiolactomycin. <i>Journal of Biological Chemistry</i> , 2010 , 285, 6161-9	5.4	30
65	The structures of the C185S and C185A mutants of sulfite oxidase reveal rearrangement of the active site. <i>Biochemistry</i> , 2010 , 49, 3989-4000	3.2	25
64	DNA binding cooperativity of p53 modulates the decision between cell-cycle arrest and apoptosis. <i>Molecular Cell</i> , 2010 , 38, 356-68	17.6	69
63	A slow, tight binding inhibitor of InhA, the enoyl-acyl carrier protein reductase from Mycobacterium tuberculosis. <i>Journal of Biological Chemistry</i> , 2010 , 285, 14330-7	5.4	126

62	Michael acceptor based antiplasmodial and antitrypanosomal cysteine protease inhibitors with unusual amino acids. <i>Journal of Medicinal Chemistry</i> , 2010 , 53, 1951-63	8.3	43
61	Bax1 is a novel endonuclease: implications for archaeal nucleotide excision repair. <i>Journal of Biological Chemistry</i> , 2009 , 284, 32272-8	5.4	11
60	Mechanism of Substrate and Inhibitor Binding of Rhodobacter capsulatus Xanthine Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2009 , 284, 8768-76	5.4	33
59	Crystal structures of Mycobacterium tuberculosis KasA show mode of action within cell wall biosynthesis and its inhibition by thiolactomycin. <i>Structure</i> , 2009 , 17, 1004-13	5.2	51
58	Slow-onset inhibition of the FabI enoyl reductase from Francisella tularensis: residence time and in vivo activity. <i>ACS Chemical Biology</i> , 2009 , 4, 221-31	4.9	98
57	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, 5662-72	8.3	15
56	Characterizing septum inhibition in Mycobacterium tuberculosis for novel drug discovery. <i>Tuberculosis</i> , 2008 , 88, 420-9	2.6	25
55	Crystal structure of the FeS cluster-containing nucleotide excision repair helicase XPD. <i>PLoS Biology</i> , 2008 , 6, e149	9.7	177
54	Targeting the Enoyl-Reductase Enzyme (FabI): Modern Drug Discovery Effects to Combat Tularemia. <i>FASEB Journal</i> , 2008 , 22, 791.6	0.9	
53	Lysine 190 is the catalytic base in MenF, the menaquinone-specific isochorismate synthase from Escherichia coli: implications for an enzyme family. <i>Biochemistry</i> , 2007 , 46, 946-53	3.2	47
52	Structure and mechanism of MbtI, the salicylate synthase from Mycobacterium tuberculosis. <i>Biochemistry</i> , 2007 , 46, 954-64	3.2	54
51	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, 613-22	13	46
50	The EM structure of human DNA polymerase gamma reveals a localized contact between the catalytic and accessory subunits. <i>EMBO Journal</i> , 2007 , 26, 4283-91	13	18
49	When one protein does the job of many. <i>Structure</i> , 2007 , 15, 1163-5	5.2	2
48	Development of modern InhA inhibitors to combat drug resistant strains of Mycobacterium tuberculosis. <i>Current Topics in Medicinal Chemistry</i> , 2007 , 7, 489-98	3	37
47	Functional human mitochondrial DNA polymerase gamma forms a heterotrimer. <i>Journal of Biological Chemistry</i> , 2006 , 281, 374-82	5.4	117
46	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	5.4	33
45	Structure of acyl carrier protein bound to FabI, the FASII enoyl reductase from Escherichia coli. <i>Journal of Biological Chemistry</i> , 2006 , 281, 39285-39293	5.4	87

44	High affinity InhA inhibitors with activity against drug-resistant strains of Mycobacterium tuberculosis. <i>ACS Chemical Biology</i> , 2006 , 1, 43-53	4.9	210
43	Prokaryotic nucleotide excision repair: the UvrABC system. <i>Chemical Reviews</i> , 2006 , 106, 233-52	68.1	239
42	Structural basis for DNA recognition and processing by UvrB. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 360-4	17.6	91
41	Structural analysis of missense mutations causing isolated sulfite oxidase deficiency. <i>Dalton Transactions</i> , 2005 , 3459-63	4.3	11
40	Structural insights into the first incision reaction during nucleotide excision repair. <i>EMBO Journal</i> , 2005 , 24, 885-94	13	68
39	'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	3.3	106
38	Structural insights into sulfite oxidase deficiency. <i>Journal of Biological Chemistry</i> , 2005 , 280, 33506-15	5.4	66
37	Identification of residues within UvrB that are important for efficient DNA binding and damage processing. <i>Journal of Biological Chemistry</i> , 2004 , 279, 51574-80	5.4	29
36	Lesion (in)tolerance reveals insights into DNA replication fidelity. <i>EMBO Journal</i> , 2004 , 23, 1494-505	13	110
35	Interactions between UvrA and UvrB: the role of UvrB's domain 2 in nucleotide excision repair. <i>EMBO Journal</i> , 2004 , 23, 2498-509	13	52
34	The crystal structure of plant sulfite oxidase provides insights into sulfite oxidation in plants and animals. <i>Structure</i> , 2003 , 11, 1251-63	5.2	116
33	The 1.2 Å structure of the human sulfite oxidase cytochrome b(5) domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 1183-91		16
32	Mouse Rev1 protein interacts with multiple DNA polymerases involved in translesion DNA synthesis. <i>EMBO Journal</i> , 2003 , 22, 6621-30	13	288
31	Crystallographic characterization of an exocyclic DNA adduct: 3,N4-etheno-2'-deoxycytidine in the dodecamer 5'-CGCGAATepsilonCGCG-3'. <i>Journal of Molecular Biology</i> , 2003 , 329, 685-97	6.5	11
30	Crystal structure of Mycobacterium tuberculosis MenB, a key enzyme in vitamin K2 biosynthesis. <i>Journal of Biological Chemistry</i> , 2003 , 278, 42352-60	5.4	75
29	Crystal structures of the active and alloxanthine-inhibited forms of xanthine dehydrogenase from <i>Rhodobacter capsulatus</i> . <i>Structure</i> , 2002 , 10, 115-25	5.2	165
28	Isolated sulfite oxidase deficiency: identification of 12 novel SUOX mutations in 10 patients. <i>Human Mutation</i> , 2002 , 20, 74	4.7	66
27	Stereoselectivity of enoyl-CoA hydratase results from preferential activation of one of two bound substrate conformers. <i>Chemistry and Biology</i> , 2002 , 9, 1247-55		27

26	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, 1553-9	5.4	86
25	Molybdopterin from molybdenum and tungsten enzymes. <i>Advances in Protein Chemistry</i> , 2001 , 58, 47-94		47
24	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> , 2001 , 7, 43-54	17.6	126
23	Error-prone DNA polymerases: novel structures and the benefits of infidelity. <i>Cell</i> , 2001 , 107, 9-12	56.2	109
22	The Tetracycline Repressor-A Paradigm for a Biological Switch. <i>Angewandte Chemie - International Edition</i> , 2000 , 39, 2042-2052	16.4	98
21	The nucleotide excision repair protein UvrB, a helicase-like enzyme with a catch. <i>Mutation Research DNA Repair</i> , 2000 , 460, 277-300		57
20	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> , 2000 , 39, 9222-31	3.2	149
19	Comparing crystallographic and solution structures of nitrogenase complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 727-8		12
18	Crystal structure of UvrB, a DNA helicase adapted for nucleotide excision repair. <i>EMBO Journal</i> , 1999 , 18, 6899-907	13	156
17	X-ray Absorption Spectroscopy of Chicken Sulfite Oxidase Crystals. <i>Inorganic Chemistry</i> , 1999 , 38, 2539-2540	5.4	50
16	Structural basis and mechanism of enoyl reductase inhibition by triclosan. <i>Journal of Molecular Biology</i> , 1999 , 290, 859-65	6.5	179
15	A structural comparison of molybdenum cofactor-containing enzymes. <i>FEMS Microbiology Reviews</i> , 1998 , 22, 503-21	15.1	95
14	A crystallographic view of the molybdenum cofactor. <i>Journal of the Chemical Society Dalton Transactions</i> , 1997 , 3909-3914		28
13	Molybdenum-cofactor-containing enzymes: structure and mechanism. <i>Annual Review of Biochemistry</i> , 1997 , 66, 233-67	29.1	423
12	Molecular basis of sulfite oxidase deficiency from the structure of sulfite oxidase. <i>Cell</i> , 1997 , 91, 973-83	56.2	438
11	Structure of ADP x AIF4(-)-stabilized nitrogenase complex and its implications for signal transduction. <i>Nature</i> , 1997 , 387, 370-6	50.4	452
10	The molybdenum-cofactor: a crystallographic perspective. <i>Journal of Biological Inorganic Chemistry</i> , 1997 , 2, 773-781	3.7	45
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	6.5	248

8	Crystal structure of DMSO reductase: redox-linked changes in molybdopterin coordination. <i>Science</i> , 1996 , 272, 1615-21	33.3	417
7	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	1.7	
6	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	3.8	14
5	Proximity mapping of the Tet repressor-tetracycline-Fe ²⁺ complex by hydrogen peroxide mediated protein cleavage. <i>Biochemistry</i> , 1995 , 34, 22-31	3.2	54
4	The complex formed between Tet repressor and tetracycline-Mg ²⁺ reveals mechanism of antibiotic resistance. <i>Journal of Molecular Biology</i> , 1995 , 247, 260-80	6.5	187
3	X-ray crystallographic and calorimetric studies of the effects of the mutation Trp59→Tyr in ribonuclease T1. <i>FEBS Journal</i> , 1994 , 220, 527-34		12
2	The complex between ribonuclease T1 and 3'GMP suggests geometry of enzymic reaction path. An X-ray study. <i>FEBS Journal</i> , 1993 , 218, 1005-12		28
1	The TFIIH subunits p44/p62 act as a damage sensor during nucleotide excision repair		1