

Malcolm F White

List of Publications by Year in descending order

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155
papers

12,796
citations

32410

55
h-index

32181

105
g-index

170
all docs

170
docs citations

170
times ranked

10918
citing authors

#	ARTICLE	IF	CITATIONS
1	Life Sciences New Talent collection. Royal Society Open Science, 2022, 9, 211981.	1.1	0
2	Cyclic Nucleotide Signaling in Phage Defense and Counter-Defense. Annual Review of Virology, 2022, 9, 451-468.	3.0	37
3	The CRISPR ancillary effector Can2 is a dual-specificity nuclease potentiating type III CRISPR defence. Nucleic Acids Research, 2021, 49, 2777-2789.	6.5	46
4	Cyclic oligoadenylate signaling and regulation by ring nucleases during type III CRISPR defense. Rna, 2021, 27, 855-867.	1.6	31
5	Specificity and sensitivity of an RNA targeting type III CRISPR complex coupled with a NucC endonuclease effector. Nucleic Acids Research, 2021, 49, 13122-13134.	6.5	38
6	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. Nature Reviews Microbiology, 2020, 18, 67-83.	13.6	1,427
7	Fuse to defuse: a self-limiting ribonuclease-ring nuclease fusion for type III CRISPR defence. Nucleic Acids Research, 2020, 48, 6149-6156.	6.5	18
8	Facile and scalable expression and purification of transcription factor IIIH (TFIIH) core complex. Protein Expression and Purification, 2020, 174, 105660.	0.6	0
9	Regulation of the RNA and DNA nuclease activities required for Pyrococcus furiosus Type III-B CRISPR-Cas immunity. Nucleic Acids Research, 2020, 48, 4418-4434.	6.5	34
10	Bacteria SAVED from Viruses. Cell, 2020, 182, 5-6.	13.5	5
11	An anti-CRISPR viral ring nuclease subverts type III CRISPR immunity. Nature, 2020, 577, 572-575.	13.7	139
12	Structure and mechanism of a Type III CRISPR defence DNA nuclease activated by cyclic oligoadenylate. Nature Communications, 2020, 11, 500.	5.8	97
13	The dynamic interplay of host and viral enzymes in type III CRISPR-mediated cyclic nucleotide signalling. ELife, 2020, 9, .	2.8	41
14	Tetramerisation of the CRISPR ring nuclease Crn3/Csx3 facilitates cyclic oligoadenylate cleavage. ELife, 2020, 9, .	2.8	22
15	Cyclic oligoadenylate signalling mediates Mycobacterium tuberculosis CRISPR defence. Nucleic Acids Research, 2019, 47, 9259-9270.	6.5	55
16	Asymmetric base-pair opening drives helicase unwinding dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22471-22477.	3.3	15
17	Investigation of the cyclic oligoadenylate signaling pathway of type III CRISPR systems. Methods in Enzymology, 2019, 616, 191-218.	0.4	36
18	A Type III CRISPR Ancillary Ribonuclease Degrades Its Cyclic Oligoadenylate Activator. Journal of Molecular Biology, 2019, 431, 2894-2899.	2.0	68

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19	Prespacer processing and specific integration in a Type I-A CRISPR system. <i>Nucleic Acids Research</i> , 2018, 46, 1007-1020.	6.5	70
20	Ring nucleases deactivate type III CRISPR ribonucleases by degrading cyclic oligoadenylate. <i>Nature</i> , 2018, 562, 277-280.	13.7	105
21	Control of cyclic oligoadenylate synthesis in a type III CRISPR system. <i>ELife</i> , 2018, 7, .	2.8	131
22	DNA repair in the archaea—“an emerging picture. <i>FEMS Microbiology Reviews</i> , 2018, 42, 514-526.	3.9	49
23	A type III-B CRISPR-Cas effector complex mediating massive target DNA destruction. <i>Nucleic Acids Research</i> , 2017, 45, gkw1274.	6.5	67
24	High-affinity RNA binding by a hyperthermophilic single-stranded DNA-binding protein. <i>Extremophiles</i> , 2017, 21, 369-379.	0.9	14
25	DNA-Interacting Characteristics of the Archaeal Rudiviral Protein SIRV2_Gp1. <i>Viruses</i> , 2017, 9, 190.	1.5	10
26	Cpf1 shape-shifts for streamlined CRISPR cleavage. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 365-366.	3.6	3
27	Taking a molecular motor for a spin: helicase mechanism studied by spin labeling and PELDOR. <i>Nucleic Acids Research</i> , 2016, 44, 954-968.	6.5	13
28	Multiple nucleic acid cleavage modes in divergent type III CRISPR systems. <i>Nucleic Acids Research</i> , 2016, 44, 1789-1799.	6.5	53
29	Mechanism of DNA loading by the DNA repair helicase XPD. <i>Nucleic Acids Research</i> , 2016, 44, 2806-2815.	6.5	37
30	Functional Characterization of a Conserved Archaeal Viral Operon Revealing Single-Stranded DNA Binding, Annealing and Nuclease Activities. <i>Journal of Molecular Biology</i> , 2015, 427, 2179-2191.	2.0	32
31	Biogenesis pathways of RNA guides in archaeal and bacterial CRISPR-Cas adaptive immunity. <i>FEMS Microbiology Reviews</i> , 2015, 39, 428-441.	3.9	223
32	The structural basis of DNA binding by the single-stranded DNA-binding protein from <i>Sulfolobus solfataricus</i> . <i>Biochemical Journal</i> , 2015, 465, 337-346.	1.7	29
33	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 722-736.	13.6	2,081
34	Expression and Purification of the CMR (Type III-B) Complex in <i>Sulfolobus solfataricus</i> . <i>Methods in Molecular Biology</i> , 2015, 1311, 185-194.	0.4	4
35	Binding dynamics of a monomeric SSB protein to DNA: a single-molecule multi-process approach. <i>Nucleic Acids Research</i> , 2015, 43, 10907-10924.	6.5	25
36	Intrinsic sequence specificity of the Cas1 integrase directs new spacer acquisition. <i>ELife</i> , 2015, 4, .	2.8	104

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37	Crystal "Unengineering": Reducing the Crystallisability of <i>Sulfolobus solfataricus</i> Hjc. Australian Journal of Chemistry, 2014, 67, 1818.	0.5	2
38	CRISPR-mediated targeted mRNA degradation in the archaeon <i>Sulfolobus solfataricus</i> . Nucleic Acids Research, 2014, 42, 5280-5288.	6.5	93
39	Single-molecule characterization of Fen1 and Fen1/PCNA complexes acting on flap substrates. Nucleic Acids Research, 2014, 42, 1857-1872.	6.5	40
40	Backbone and side-chain 1H, 13C and 15N resonance assignments of the OB domain of the single stranded DNA binding protein from <i>Sulfolobus solfataricus</i> and chemical shift mapping of the DNA-binding interface. Biomolecular NMR Assignments, 2014, 8, 243-246.	0.4	9
41	Protein-Protein Interactions Leading to Recruitment of the Host DNA Sliding Clamp by the Hyperthermophilic <i>Sulfolobus islandicus</i> Rod-Shaped Virus 2. Journal of Virology, 2014, 88, 7105-7108.	1.5	16
42	Cas6 specificity and CRISPR RNA loading in a complex CRISPR-Cas system. Nucleic Acids Research, 2014, 42, 6532-6541.	6.5	50
43	crRNA Biogenesis. , 2013, , 115-144.		5
44	Structure of the CRISPR Interference Complex CSM Reveals Key Similarities with Cascade. Molecular Cell, 2013, 52, 124-134.	4.5	181
45	Hot and crispy: CRISPR-Cas systems in the hyperthermophile <i>Sulfolobus solfataricus</i> . Biochemical Society Transactions, 2013, 41, 1422-1426.	1.6	28
46	CRISPR interference: a structural perspective. Biochemical Journal, 2013, 453, 155-166.	1.7	113
47	Structure of a dimeric crenarchaeal Cas6 enzyme with an atypical active site for CRISPR RNA processing. Biochemical Journal, 2013, 452, 223-230.	1.7	32
48	Crenarchaeal chromatin proteins Cren7 and Sul7 compact DNA by inducing rigid bends. Nucleic Acids Research, 2013, 41, 196-205.	6.5	39
49	Protein-induced changes in DNA structure and dynamics observed with noncovalent site-directed spin labeling and PELDOR. Nucleic Acids Research, 2013, 41, e11-e11.	6.5	29
50	Structure of the archaeal Cascade subunit Csa5. RNA Biology, 2013, 10, 762-769.	1.5	24
51	crRNA Biogenesis. , 2013, , 115-144.		5
52	Displacement of the canonical single-stranded DNA-binding protein in the Thermoproteales. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E398-405.	3.3	34
53	Alba shapes the archaeal genome using a delicate balance of bridging and stiffening the DNA. Nature Communications, 2012, 3, 1328.	5.8	76
54	<i>Staphylococcus aureus</i> DinG, a helicase that has evolved into a nuclease. Biochemical Journal, 2012, 442, 77-84.	1.7	20

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55	Postcards from the Edge. <i>Advances in Virus Research</i> , 2012, 82, 33-62.	0.9	40
56	The CRISPR Associated Protein Cas4 Is a 5â€² to 3â€² DNA Exonuclease with an Iron-Sulfur Cluster. <i>PLoS ONE</i> , 2012, 7, e47232.	1.1	101
57	Structure and Mechanism of the CMR Complex for CRISPR-Mediated Antiviral Immunity. <i>Molecular Cell</i> , 2012, 45, 303-313.	4.5	279
58	Ironâ€”sulphur clusters in nucleic acid processing enzymes. <i>Current Opinion in Structural Biology</i> , 2012, 22, 94-100.	2.6	126
59	The evolution and mechanisms of nucleotide excision repair proteins. <i>Research in Microbiology</i> , 2011, 162, 19-26.	1.0	73
60	Structural and Functional Characterization of an Archaeal Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR)-associated Complex for Antiviral Defense (CASCADE). <i>Journal of Biological Chemistry</i> , 2011, 286, 21643-21656.	1.6	183
61	Recognition of Archaeal CRISPR RNA: No P in the alindromic Repeat?. <i>Structure</i> , 2011, 19, 142-144.	1.6	7
62	Homologous recombination in the archaea: the means justify the ends. <i>Biochemical Society Transactions</i> , 2011, 39, 15-19.	1.6	60
63	hSSB1 rapidly binds at the sites of DNA double-strand breaks and is required for the efficient recruitment of the MRN complex. <i>Nucleic Acids Research</i> , 2011, 39, 1692-1702.	6.5	70
64	A Dimeric Rep Protein Initiates Replication of a Linear Archaeal Virus Genome: Implications for the Rep Mechanism and Viral Replication. <i>Journal of Virology</i> , 2011, 85, 925-931.	1.5	36
65	hSSB1 interacts directly with the MRN complex stimulating its recruitment to DNA double-strand breaks and its endo-nuclease activity. <i>Nucleic Acids Research</i> , 2011, 39, 3643-3651.	6.5	70
66	Dimerâ€”dimer stacking interactions are important for nucleic acid binding by the archaeal chromatin protein Alba. <i>Biochemical Journal</i> , 2010, 427, 49-55.	1.7	26
67	Archaeal Chromatin Organization. , 2010, , 205-217.		10
68	The Scottish Structural Proteomics Facility: targets, methods and outputs. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 167-180.	1.2	107
69	Extensive Lysine Methylation in Hyperthermophilic Crenarchaea: Potential Implications for Protein Stability and Recombinant Enzymes. <i>Archaea</i> , 2010, 2010, 1-6.	2.3	86
70	PCNA and XPF cooperate to distort DNA substrates. <i>Nucleic Acids Research</i> , 2010, 38, 1664-1675.	6.5	23
71	The helicase XPD unwinds bubble structures and is not stalled by DNA lesions removed by the nucleotide excision repair pathway. <i>Nucleic Acids Research</i> , 2010, 38, 931-941.	6.5	58
72	The XBP-Bax1 Helicase-Nuclease Complex Unwinds and Cleaves DNA. <i>Journal of Biological Chemistry</i> , 2010, 285, 11013-11022.	1.6	31

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73	Reactions to UV damage in the model archaeon <i>Sulfolobus solfataricus</i> . <i>Biochemical Society Transactions</i> , 2009, 37, 36-41.	1.6	36
74	Structure, function and evolution of the XPD family of iron-sulfur-containing DNA helicases. <i>Biochemical Society Transactions</i> , 2009, 37, 547-551.	1.6	96
75	The crenarchaeal DNA damage-inducible transcription factor B paralogue TFB3 is a general activator of transcription. <i>Molecular Microbiology</i> , 2009, 72, 1487-1499.	1.2	27
76	AcsD catalyzes enantioselective citrate desymmetrization in siderophore biosynthesis. <i>Nature Chemical Biology</i> , 2009, 5, 174-182.	3.9	67
77	Structural and Functional Characterisation of a Conserved Archaeal RadA Paralog with Antirecombinase Activity. <i>Journal of Molecular Biology</i> , 2009, 389, 661-673.	2.0	45
78	RecA family proteins in archaea: RadA and its cousins. <i>Biochemical Society Transactions</i> , 2009, 37, 102-107.	1.6	58
79	DNA Damage: from Causes to Cures. <i>Biochemical Society Transactions</i> , 2009, 37, 479-481.	1.6	1
80	The Mre11 protein interacts with both Rad50 and the HerA bipolar helicase and is recruited to DNA following gamma irradiation in the archaeon <i>Sulfolobus acidocaldarius</i> . <i>BMC Molecular Biology</i> , 2008, 9, 25.	3.0	62
81	Purification, crystallization and data collection of <i>Pectobacterium chrysanthemi</i> AcsD, a type A siderophore synthetase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 1052-1055.	0.7	4
82	Unusual Chromophore and Cross-Links in Ranasmurfin: A Blue Protein from the Foam Nests of a Tropical Frog. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 7853-7856.	7.2	20
83	Single-stranded DNA-binding protein hSSB1 is critical for genomic stability. <i>Nature</i> , 2008, 453, 677-681.	13.7	220
84	The Major Architects of Chromatin: Architectural Proteins in Bacteria, Archaea and Eukaryotes. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2008, 43, 393-418.	2.3	194
85	The Archaeal XPB Protein is a ssDNA-Dependent ATPase with a Novel Partner. <i>Journal of Molecular Biology</i> , 2008, 376, 634-644.	2.0	31
86	Structure of the DNA Repair Helicase XPD. <i>Cell</i> , 2008, 133, 801-812.	13.5	490
87	TarO: a target optimisation system for structural biology. <i>Nucleic Acids Research</i> , 2008, 36, W190-W196.	6.5	79
88	Structure of the DNA Repair Helicase Hel308 Reveals DNA Binding and Autoinhibitory Domains. <i>Journal of Biological Chemistry</i> , 2008, 283, 5118-5126.	1.6	81
89	PCNA stimulates catalysis by structure-specific nucleases using two distinct mechanisms: substrate targeting and catalytic step. <i>Nucleic Acids Research</i> , 2008, 36, 6720-6727.	6.5	25
90	CC1, a Novel Crenarchaeal DNA Binding Protein. <i>Journal of Bacteriology</i> , 2007, 189, 403-409.	1.0	36

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91	The <i>Sulfolobus solfataricus</i> radA paralogue sso0777 is DNA damage inducible and positively regulated by the Sta1 protein. <i>Nucleic Acids Research</i> , 2007, 35, 6788-6797.	6.5	22
92	Responses of hyperthermophilic crenarchaea to UV irradiation. <i>Genome Biology</i> , 2007, 8, R220.	13.9	118
93	Expression, purification, crystallization, data collection and preliminary biochemical characterization of methicillin-resistant <i>Staphylococcus aureus</i> Sar2028, an aspartate/tyrosine/phenylalanine pyridoxal-5-P-phosphate-dependent aminotransferase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 452-456.	0.7	5
94	Purification, crystallization and data collection of methicillin-resistant <i>Staphylococcus aureus</i> Sar2676, a pantothenate synthetase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 488-491.	0.7	4
95	Equal rates of repair of DNA photoproducts in transcribed and non-transcribed strands in <i>Sulfolobus solfataricus</i> . <i>Molecular Microbiology</i> , 2007, 63, 521-529.	1.2	30
96	An acetylase with relaxed specificity catalyses protein N-terminal acetylation in <i>Sulfolobus solfataricus</i> . <i>Molecular Microbiology</i> , 2007, 64, 1540-1548.	1.2	36
97	PCNA Activates the Holliday Junction Endonuclease Hjc. <i>Journal of Molecular Biology</i> , 2006, 364, 243-247.	2.0	15
98	The DNA Repair Helicases XPD and FancJ Have Essential Iron-Sulfur Domains. <i>Molecular Cell</i> , 2006, 23, 801-808.	4.5	298
99	Overexpression, purification, crystallization and data collection of <i>Sulfolobus solfataricus</i> Sso6206, a novel highly conserved protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 228-230.	0.7	0
100	Structure of the heterotrimeric PCNA from <i>Sulfolobus solfataricus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 944-948.	0.7	61
101	Crystallization of Ranasmurfin, a blue-coloured protein from <i>Polypedates leucomystax</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1124-1126.	0.7	7
102	Structure of an XPF endonuclease with and without DNA suggests a model for substrate recognition. <i>EMBO Journal</i> , 2005, 24, 895-905.	3.5	105
103	Obligate Heterodimerization of the Archaeal Alba2 Protein with Alba1 Provides a Mechanism for Control of DNA Packaging. <i>Structure</i> , 2005, 13, 963-971.	1.6	70
104	Conformational flexibility revealed by the crystal structure of a crenarchaeal RadA. <i>Nucleic Acids Research</i> , 2005, 33, 1465-1473.	6.5	32
105	An Archaeal Endonuclease Displays Key Properties of Both Eukaryal XPF-ERCC1 and Mus81. <i>Journal of Biological Chemistry</i> , 2005, 280, 5924-5928.	1.6	42
106	DNA end-directed and processive nuclease activities of the archaeal XPF enzyme. <i>Nucleic Acids Research</i> , 2005, 33, 6662-6670.	6.5	19
107	The Endonuclease Hje Catalyses Rapid, Multiple Turnover Resolution of Holliday junctions. <i>Journal of Molecular Biology</i> , 2005, 350, 1-6.	2.0	25
108	DNA Damage Detection by an Archaeal Single-stranded DNA-binding Protein. <i>Journal of Molecular Biology</i> , 2005, 353, 507-516.	2.0	56

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109	Archaeal DNA replication and repair. <i>Current Opinion in Microbiology</i> , 2005, 8, 669-676.	2.3	134
110	Substrate recognition and catalysis by the Holliday junction resolving enzyme Hje. <i>Nucleic Acids Research</i> , 2004, 32, 5442-5451.	6.5	41
111	Physical and functional interaction of the archaeal single-stranded DNA-binding protein SSB with RNA polymerase. <i>Nucleic Acids Research</i> , 2004, 32, 1065-1074.	6.5	48
112	Insights into ssDNA recognition by the OB fold from a structural and thermodynamic study of <i>Sulfolobus</i> SSB protein. <i>EMBO Journal</i> , 2003, 22, 2561-2570.	3.5	122
113	An archaeal XPF repair endonuclease dependent on a heterotrimeric PCNA. <i>Molecular Microbiology</i> , 2003, 48, 361-371.	1.2	78
114	Crystallization and preliminary X-ray diffraction studies of Hje, a Holliday junction resolving enzyme from <i>Sulfolobus solfataricus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 171-173.	2.5	7
115	Transcriptional response to DNA damage in the archaeon <i>Sulfolobus solfataricus</i> . <i>Nucleic Acids Research</i> , 2003, 31, 6127-6138.	6.5	33
116	Archaeal DNA repair: paradigms and puzzles. <i>Biochemical Society Transactions</i> , 2003, 31, 690-3.	1.6	33
117	Recruitment of intron-encoded and co-opted proteins in splicing of the b13 group I intron RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 128-133.	3.3	46
118	Holliday Junction Resolution Is Modulated by Archaeal Chromatin Components in Vitro. <i>Journal of Biological Chemistry</i> , 2002, 277, 2992-2996.	1.6	20
119	Mechanistic implications for <i>Escherichia coli</i> cofactor-dependent phosphoglycerate mutase based on the high-resolution crystal structure of a vanadate complex. <i>Journal of Molecular Biology</i> , 2002, 316, 1071-1081.	2.0	56
120	The Interaction of Alba, a Conserved Archaeal Chromatin Protein, with Sir2 and Its Regulation by Acetylation. <i>Science</i> , 2002, 296, 148-151.	6.0	271
121	Holding it together: chromatin in the Archaea. <i>Trends in Genetics</i> , 2002, 18, 621-626.	2.9	124
122	Structure of Alba: an archaeal chromatin protein modulated by acetylation. <i>EMBO Journal</i> , 2002, 21, 4654-4662.	3.5	146
123	Distortion of DNA junctions imposed by the binding of resolving enzymes: a fluorescence study. <i>Journal of Molecular Biology</i> , 2001, 313, 751-764.	2.0	36
124	Multiple Holliday junction resolving enzyme activities in the Crenarchaeota and Euryarchaeota. <i>FEBS Letters</i> , 2001, 491, 243-246.	1.3	12
125	Overexpression, purification, crystallization and data collection of a single-stranded DNA-binding protein from <i>Sulfolobus solfataricus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1290-1292.	2.5	4
126	Preliminary crystallographic studies of the double-stranded DNA-binding protein Sso10b from <i>Sulfolobus solfataricus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1893-1894.	2.5	4

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127	High Resolution Structure of the Phosphohistidine-activated Form of Escherichia coli Cofactor-dependent Phosphoglycerate Mutase. <i>Journal of Biological Chemistry</i> , 2001, 276, 3247-3253.	1.6	63
128	Identification and properties of the crenarchaeal single-stranded DNA binding protein from <i>Sulfolobus solfataricus</i> . <i>Nucleic Acids Research</i> , 2001, 29, 914-920.	6.5	122
129	Structure of Hjc, a Holliday junction resolvase, from <i>Sulfolobus solfataricus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 5509-5514.	3.3	85
130	A Novel Member of the Bacterial-Archaeal Regulator Family Is a Nonspecific DNA-binding Protein and Induces Positive Supercoiling. <i>Journal of Biological Chemistry</i> , 2001, 276, 10745-10752.	1.6	27
131	The junction-resolving enzymes. <i>Nature Reviews Molecular Cell Biology</i> , 2001, 2, 433-443.	16.1	59
132	Resolving the relationships of resolving enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 9351-9353.	3.3	70
133	A Conserved Nuclease Domain in the Archaeal Holliday Junction Resolving Enzyme Hjc. <i>Journal of Biological Chemistry</i> , 2000, 275, 25540-25546.	1.6	50
134	Site-directed Mutagenesis of the Yeast Resolving Enzyme Cce1 Reveals Catalytic Residues and Relationship with the Intron-splicing Factor Mrs1. <i>Journal of Biological Chemistry</i> , 2000, 275, 23725-23728.	1.6	16
135	An archaeal holliday junction resolving enzyme from <i>Sulfolobus solfataricus</i> exhibits unique properties. <i>Journal of Molecular Biology</i> , 2000, 295, 193-202.	2.0	51
136	Two holliday junction resolving enzymes in <i>Sulfolobus solfataricus</i> 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 2000, 297, 923-932.	2.0	64
137	Nucleosome mobilization catalysed by the yeast SWI/SNF complex. <i>Nature</i> , 1999, 400, 784-787.	13.7	306
138	The two analogous phosphoglycerate mutases of <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1999, 455, 344-348.	1.3	90
139	Sequence and Functional-Group Specificity for Cleavage of DNA Junctions by RuvC of <i>Escherichia coli</i> . <i>Biochemistry</i> , 1999, 38, 11349-11358.	1.2	36
140	Quantitation of Metal Ion and DNA Junction Binding to the Holliday Junction Endonuclease Cce1. <i>Biochemistry</i> , 1999, 38, 16613-16619.	1.2	20
141	Dissection of the Sequence Specificity of the Holliday Junction Endonuclease CCE1. <i>Biochemistry</i> , 1998, 37, 7733-7740.	1.2	50
142	Interaction of the resolving enzyme YDC2 with the four-way DNA junction. <i>Nucleic Acids Research</i> , 1998, 26, 5609-5616.	6.5	32
143	Characterization of a Holliday Junction-Resolving Enzyme from <i>Schizosaccharomyces pombe</i> . <i>Molecular and Cellular Biology</i> , 1997, 17, 6465-6471.	1.1	67
144	111 A Holliday junction endonuclease from fission yeast. <i>Biochemical Society Transactions</i> , 1997, 25, S645-S645.	1.6	0

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145	112 Sequence specificity of CCE1. <i>Biochemical Society Transactions</i> , 1997, 25, S646-S646.	1.6	2
146	The resolving enzyme CCE1 of yeast opens the structure of the four-way DNA junction 1 1 Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 1997, 266, 122-134.	2.0	88
147	Recognition and manipulation of branched DNA structure by junction-resolving enzymes 1 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1997, 269, 647-664.	2.0	101
148	The Structure-selectivity and Sequence-preference of the Junction-resolving Enzyme CCE1 of <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1996, 257, 330-341.	2.0	97
149	Crystallization and Preliminary X-ray Analysis of Recombinant 1-Aminocyclopropane-1-carboxylate Synthase from Apple. <i>Journal of Molecular Biology</i> , 1994, 243, 947-949.	2.0	11
150	Expression of apple 1-aminocyclopropane-1-carboxylate synthase in <i>Escherichia coli</i> : kinetic characterization of wild-type and active-site mutant forms.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 12428-12432.	3.3	82
151	Development of a mutagenesis, expression and purification system for yeast phosphoglycerate mutase. Investigation of the role of active-site His181. <i>FEBS Journal</i> , 1992, 207, 709-714.	0.2	54
152	Mutase versus synthase: the phosphoglycerate mutase family studied by protein engineering. <i>Biochemical Society Transactions</i> , 1990, 18, 257-257.	1.6	7
153	Sequence of the gene encoding phosphoglycerate mutase from <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 1988, 229, 383-387.	1.3	41
154	DNA Repair. , 0, , 171-183.		1
155	Recombination Machinery: Holliday Junction-Resolving Enzymes. , 0, , 405-412.		0