

Dale B Wigley

List of Publications by Year in descending order

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98
papers

10,101
citations

50276

46
h-index

37204

96
g-index

104
all docs

104
docs citations

104
times ranked

6944
citing authors

#	ARTICLE	IF	CITATIONS
1	A conformational switch in response to Chi converts RecBCD from phage destruction to DNA repair. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 71-77.	8.2	55
2	The type 2 diabetes gene product STARD10 is a phosphoinositide-binding protein that controls insulin secretory granule biogenesis. <i>Molecular Metabolism</i> , 2020, 40, 101015.	6.5	22
3	INO80 and SWR1 complexes: the non-identical twins of chromatin remodelling. <i>Current Opinion in Structural Biology</i> , 2020, 61, 50-58.	5.7	36
4	Structure of the DNA-Bound Spacer Capture Complex of a Type II CRISPR-Cas System. <i>Molecular Cell</i> , 2019, 75, 90-101.e5.	9.7	35
5	CtIP forms a tetrameric dumbbell-shaped particle which bridges complex DNA end structures for double-strand break repair. <i>ELife</i> , 2019, 8, .	6.0	23
6	Structure and regulation of the human INO80 nucleosome complex. <i>Nature</i> , 2018, 556, 391-395.	27.8	148
7	Cryo-EM structures of the human INO80 chromatin-remodeling complex. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 37-44.	8.2	46
8	Structure and dynamics of the yeast SWR1-nucleosome complex. <i>Science</i> , 2018, 362, .	12.6	131
9	DNA translocation mechanism of an XPD family helicase. <i>ELife</i> , 2018, 7, .	6.0	38
10	Functional characterization and architecture of recombinant yeast SWR1 histone exchange complex. <i>Nucleic Acids Research</i> , 2017, 45, 7249-7260.	14.5	19
11	The structure and function of an RNA polymerase interaction domain in the PcrA/UvrD helicase. <i>Nucleic Acids Research</i> , 2017, 45, 3875-3887.	14.5	31
12	Production and Assay of Recombinant Multisubunit Chromatin Remodeling Complexes. <i>Methods in Enzymology</i> , 2017, 592, 27-47.	1.0	2
13	A glimpse into chromatin remodeling. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 498-500.	8.2	9
14	Crosstalk within a functional INO80 complex dimer regulates nucleosome sliding. <i>ELife</i> , 2017, 6, .	6.0	21
15	Chi hotspots trigger a conformational change in the helicase-like domain of AddAB to activate homologous recombination. <i>Nucleic Acids Research</i> , 2016, 44, 2727-2741.	14.5	6
16	Synergy and antagonism in regulation of recombinant human INO80 chromatin remodeling complex. <i>Nucleic Acids Research</i> , 2016, 44, 8179-8188.	14.5	30
17	Mechanism for nuclease regulation in RecBCD. <i>ELife</i> , 2016, 5, .	6.0	36
18	Structural basis for the inhibition of RecBCD by Gam and its synergistic antibacterial effect with quinolones. <i>ELife</i> , 2016, 5, .	6.0	50

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19	Structural features of Chi recognition in AddAB with implications for RecBCD. <i>Cell Cycle</i> , 2014, 13, 2812-2820.	2.6	11
20	Structural basis for translocation by AddAB helicase-nuclease and its arrest at χ sites. <i>Nature</i> , 2014, 508, 416-419.	27.8	43
21	Bacterial DNA repair: recent insights into the mechanism of RecBCD, AddAB and AdnAB. <i>Nature Reviews Microbiology</i> , 2013, 11, 9-13.	28.6	140
22	Insights into Chi recognition from the structure of an AddAB-type helicase-nuclease complex. <i>EMBO Journal</i> , 2012, 31, 1568-1578.	7.8	56
23	Interactions between the nucleosome histone core and Arp8 in the INO80 chromatin remodeling complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20883-20888.	7.1	47
24	Alteration of χ recognition by RecBCD reveals a regulated molecular latch and suggests a channel-bypass mechanism for biological control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8907-8912.	7.1	27
25	Molecular determinants responsible for recognition of the single-stranded DNA regulatory sequence, χ , by RecBCD enzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8901-8906.	7.1	52
26	Mechanistic Basis of χ Translocation in SF1B Helicases. <i>Cell</i> , 2009, 137, 849-859.	28.9	127
27	The RecB Nuclease Domain Binds to RecA-DNA Filaments: Implications for Filament Loading. <i>Journal of Molecular Biology</i> , 2009, 391, 269-274.	4.2	11
28	DNA binding to RecD: role of the 1B domain in SF1B helicase activity. <i>EMBO Journal</i> , 2008, 27, 2222-2229.	7.8	83
29	The 'glutamate switch' provides a link between ATPase activity and ligand binding in AAA+ proteins. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1223-1227.	8.2	105
30	Structural Basis of DNA Replication Origin Recognition by an ORC Protein. <i>Science</i> , 2007, 317, 1213-1216.	12.6	126
31	RecBCD: The Supercar of DNA Repair. <i>Cell</i> , 2007, 131, 651-653.	28.9	14
32	The Crystal Structure of χ -Gam Protein Suggests a Model for RecBCD Inhibition. <i>Journal of Molecular Biology</i> , 2007, 371, 25-33.	4.2	49
33	Structure and Mechanism of Helicases and Nucleic Acid Translocases. <i>Annual Review of Biochemistry</i> , 2007, 76, 23-50.	11.1	1,098
34	CeBRC-2 Stimulates D-loop Formation by RAD-51 and Promotes DNA Single-strand Annealing. <i>Journal of Molecular Biology</i> , 2006, 361, 231-242.	4.2	66
35	Biochemical Analysis of a DNA Replication Origin in the Archaeon <i>Aeropyrum pernix</i> . <i>Journal of Molecular Biology</i> , 2006, 363, 355-369.	4.2	48
36	Communication between subunits within an archaeal clamp-loader complex. <i>EMBO Journal</i> , 2006, 25, 2209-2218.	7.8	23

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37	Pumps, paradoxes and ploughshares: mechanism of the MCM2-7 DNA helicase. Trends in Biochemical Sciences, 2005, 30, 437-444.	7.5	146
38	Distinct roles for ATP binding and hydrolysis at individual subunits of an archaeal clamp loader. EMBO Journal, 2004, 23, 1360-1371.	7.8	44
39	Crystal structure of RecBCD enzyme reveals a machine for processing DNA breaks. Nature, 2004, 432, 187-193.	27.8	383
40	Conformational Changes Induced by Nucleotide Binding in Cdc6/ORC From Aeropyrum pernix. Journal of Molecular Biology, 2004, 343, 547-557.	4.2	73
41	NEW EMBO MEMBER'S REVIEW Multiple roles for ATP hydrolysis in nucleic acid modifying enzymes. EMBO Journal, 2003, 22, 4579-4583.	7.8	17
42	Biochemical analysis of components of the pre-replication complex of Archaeoglobus fulgidus. Nucleic Acids Research, 2003, 31, 4888-4898.	14.5	59
43	Structure of the single-strand annealing domain of human RAD52 protein. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13492-13497.	7.1	211
44	Biochemical characterisation of the clamp/clamp loader proteins from the euryarchaeon Archaeoglobus fulgidus. Nucleic Acids Research, 2002, 30, 4329-4338.	14.5	39
45	Restart of DNA replication in Gram-positive bacteria: functional characterisation of the Bacillus subtilis PriA initiator. Nucleic Acids Research, 2002, 30, 1593-1605.	14.5	50
46	Modularity and Specialization in Superfamily 1 and 2 Helicases. Journal of Bacteriology, 2002, 184, 1819-1826.	2.2	188
47	Structural Analysis of DNA Replication Fork Reversal by RecG. Cell, 2001, 107, 79-89.	28.9	276
48	Crystallization and preliminary X-ray analysis of RecG, a replication-fork reversal helicase from Thermotoga maritima complexed with a three-way DNA junction. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1695-1696.	2.5	10
49	Unwinding the "Gordian knot" of helicase action. Trends in Biochemical Sciences, 2001, 26, 47-54.	7.5	112
50	DNA helicases: One small step for PcrA, one giant leap for RecBC?. Current Biology, 2000, 10, R444-R446.	3.9	5
51	Structure of the zinc-binding domain of Bacillus stearothermophilus DNA primase. Structure, 2000, 8, 231-239.	3.3	75
52	High resolution refinement of β -galactosidase in a new crystal form reveals multiple metal-binding sites and provides a structural basis for Ca^{2+} complementation. Protein Science, 2000, 9, 1685-1699.	7.6	174
53	Uncoupling DNA translocation and helicase activity in PcrA: direct evidence for an active mechanism. EMBO Journal, 2000, 19, 3799-3810.	7.8	141
54	DNA ligases in the repair and replication of DNA. Mutation Research DNA Repair, 2000, 460, 301-318.	3.7	150

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55	Crystal Structure of T7 Gene 4 Ring Helicase Indicates a Mechanism for Sequential Hydrolysis of Nucleotides. <i>Cell</i> , 2000, 101, 589-600.	28.9	455
56	Demonstration of Unidirectional Single-Stranded DNA Translocation by PcrA Helicase: Measurement of Step Size and Translocation Speed. <i>Biochemistry</i> , 2000, 39, 205-212.	2.5	222
57	Mapping Protein-Protein Interactions within a Stable Complex of DNA Primase and DnaB Helicase from <i>Bacillus stearothermophilus</i> . <i>Biochemistry</i> , 2000, 39, 171-182.	2.5	103
58	Plasmid replication initiator protein RepD increases the processivity of PcrA DNA helicase. <i>Nucleic Acids Research</i> , 1999, 27, 1421-1428.	14.5	70
59	Symposia lectures. <i>Journal of Biosciences</i> , 1999, 24, 5-31.	1.1	0
60	Structure of the adenylation domain of an NAD ⁺ -dependent DNA ligase. <i>Structure</i> , 1999, 7, 35-42.	3.3	84
61	Crystal Structures of Complexes of PcrA DNA Helicase with a DNA Substrate Indicate an Inchworm Mechanism. <i>Cell</i> , 1999, 97, 75-84.	28.9	756
62	Functional domains of an ATP-dependent DNA ligase 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 285, 63-71.	4.2	56
63	Functional domains of an NAD ⁺ -dependent DNA ligase 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 285, 73-83.	4.2	77
64	DNA binding mediates conformational changes and metal ion coordination in the active site of PcrA helicase 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 290, 137-148.	4.2	110
65	Teaching a new dog old tricks?. <i>Structure</i> , 1998, 6, 543-548.	3.3	14
66	Conserved Themes but Novel Activities in Recombinases and Topoisomerases. <i>Cell</i> , 1998, 93, 149-152.	28.9	78
67	<i>Escherichia coli</i> ribosomal protein L3 stimulates the helicase activity of the <i>Bacillus stearothermophilus</i> PcrA helicase. <i>Nucleic Acids Research</i> , 1998, 26, 2374-2379.	14.5	22
68	X-Ray Crystallography Reveals a Large Conformational Change during Guanyl Transfer by mRNA Capping Enzymes. <i>Cell</i> , 1997, 89, 545-553.	28.9	260
69	The high-resolution crystal structure of a 24-kDa gyrase B fragment from <i>E. coli</i> complexed with one of the most potent coumarin inhibitors, clorobiocin. , 1997, 28, 41-52.		133
70	The high-resolution crystal structure of a 24-kDa gyrase B fragment from <i>E. coli</i> complexed with one of the most potent coumarin inhibitors, clorobiocin. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 28, 41-52.	2.6	5
71	Bacteriophage T7 DNA Ligase. <i>Journal of Biological Chemistry</i> , 1996, 271, 11083-11089.	3.4	34
72	Crystal Structure of an ATP-Dependent DNA Ligase from Bacteriophage T7. <i>Cell</i> , 1996, 85, 607-615.	28.9	261

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73	A wasp head with a relaxing bite. <i>Structure</i> , 1996, 4, 117-120.	3.3	9
74	Molecular mechanisms of durg inhibition of DNA gyrase. <i>BioEssays</i> , 1996, 18, 661-671.	2.5	72
75	Crystal structure of a DExx box DNA helicase. <i>Nature</i> , 1996, 384, 379-383.	27.8	429
76	A superior host strain for the over-expression of cloned genes using the T7 promoter based vectors. <i>Nucleic Acids Research</i> , 1995, 23, 2074-2075.	14.5	40
77	Three-dimensional Model of Escherichia coli Gyrase B Subunit Crystallized in Two-dimensions on Novobiocin-Linked Phospholipid Films. <i>Journal of Molecular Biology</i> , 1994, 236, 618-628.	4.2	40
78	Allosteric Activation in Bacillus stearothermophilus Lactate Dehydrogenase Investigated by an X-ray Crystallographic Analysis of a Mutant Designed to Prevent Tetramerization of the Enzyme. <i>Journal of Molecular Biology</i> , 1994, 238, 615-625.	4.2	29
79	Crystallization of Inhibitor Complexes of an N-Terminal 24 kDa Fragment of the DNA Gyrase B Protein. <i>Journal of Molecular Biology</i> , 1994, 241, 128-130.	4.2	52
80	The Third IgG-Binding Domain from Streptococcal Protein G. <i>Journal of Molecular Biology</i> , 1994, 243, 906-918.	4.2	324
81	Preliminary crystallographic analysis of 4-oxalocrotonate tautomerase reveals the oligomeric structure of the enzyme. <i>Journal of Molecular Biology</i> , 1994, 243, 799-801.	4.2	17
82	Analysis of Bacterial Immunoglobulin-Binding Proteins by X-Ray Crystallography. <i>ImmunoMethods</i> , 1993, 2, 9-15.	0.8	6
83	Structure and mechanism of Streptococcal protein G. <i>Biochemical Society Transactions</i> , 1993, 21, 333S-333S.	3.4	3
84	The structural consequences of exchanging tryptophan and tyrosine residues in B.stearothermophilus lactate dehydrogenase. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 611-615.	2.1	5
85	Structure of a ternary complex of an allosteric lactate dehydrogenase from Bacillus stearothermophilus at 2Å-5 Å... resolution. <i>Journal of Molecular Biology</i> , 1992, 223, 317-335.	4.2	137
86	Crystal structure of a streptococcal protein G domain bound to an Fab fragment. <i>Nature</i> , 1992, 359, 752-754.	27.8	179
87	Preliminary crystallographic analysis of the ATP-hydrolysing domain of the Escherichia coli DNA gyrase B protein. <i>Journal of Molecular Biology</i> , 1991, 217, 15-17.	4.2	24
88	Crystal structure of an N-terminal fragment of the DNA gyrase B protein. <i>Nature</i> , 1991, 351, 624-629.	27.8	551
89	Preliminary crystallographic analysis of the breakage-reunion domain of the Escherichia coli DNA gyrase a protein. <i>Journal of Molecular Biology</i> , 1990, 215, 493-495.	4.2	13
90	The serine acetyltransferase from Escherichia coli. <i>FEBS Letters</i> , 1990, 277, 267-271.	2.8	24

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91	Preliminary crystallographic analysis of 5-carboxymethyl-2-hydroxymuconate isomerase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1989, 210, 881-882.	4.2	4
92	Crystallization of a ternary complex of lactate dehydrogenase from <i>Bacillus stearothermophilus</i> . <i>Journal of Molecular Biology</i> , 1988, 204, 1041-1043.	4.2	6
93	Site-directed mutagenesis of <i>Bacillus stearothermophilus</i> lactate dehydrogenase. <i>Biochemical Society Transactions</i> , 1987, 15, 152-153.	3.4	5
94	Mapping motion in large proteins by single tryptophan probes inserted by site-directed mutagenesis: lactate dehydrogenase. <i>Biochemical Society Transactions</i> , 1987, 15, 991-993.	3.4	16
95	The greater strength of arginine: Carboxylate over lysine carboxylate ion pairs implications for the design of novel enzymes and drugs. <i>Biochemical and Biophysical Research Communications</i> , 1987, 149, 927-929.	2.1	20
96	The importance of arginine 171 in substrate binding by <i>Bacillus stearothermophilus</i> lactate dehydrogenase. <i>Biochemical and Biophysical Research Communications</i> , 1987, 146, 346-353.	2.1	46
97	Cloning, expression and complete nucleotide sequence of the <i>Bacillus stearothermophilus</i> -lactate dehydrogenase gene. <i>Gene</i> , 1986, 46, 47-55.	2.2	111
98	Site-directed mutagenesis reveals role of mobile arginine residue in lactate dehydrogenase catalysis. <i>Nature</i> , 1986, 324, 699-702.	27.8	180