

Wei Yang

List of Publications by Year in descending order

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146
papers

14,483
citations

18482

62
h-index

20358

116
g-index

153
all docs

153
docs citations

153
times ranked

11583
citing authors

#	ARTICLE	IF	CITATIONS
1	Autophosphorylation transforms DNA-PK from protecting to processing DNA ends. <i>Molecular Cell</i> , 2022, 82, 177-189.e4.	9.7	44
2	Flexibility of telomerase in binding the RNA template and DNA telomeric repeat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	8
3	Structure of human <i>BCCIP</i> and implications for binding and modification of partner proteins. <i>Protein Science</i> , 2021, 30, 693-699.	7.6	3
4	Structure of an activated DNA-PK and its implications for NHEJ. <i>Molecular Cell</i> , 2021, 81, 801-810.e3.	9.7	77
5	Multiple deprotonation paths of the nucleophile 3'-OH in the DNA synthesis reaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2103990118.	7.1	11
6	Novel <i>Escherichia coli</i> active site <i>dnaE</i> alleles with altered base and sugar selectivity. <i>Molecular Microbiology</i> , 2021, 116, 909-925.	2.5	3
7	SARS-CoV-2: from its discovery to genome structure, transcription, and replication. <i>Cell and Bioscience</i> , 2021, 11, 136.	4.8	140
8	Inner workings of RAG recombinase and its specialization for adaptive immunity. <i>Current Opinion in Structural Biology</i> , 2021, 71, 79-86.	5.7	9
9	Mismatch-bound human MutL complex triggers DNA incisions and activates mismatch repair. <i>Cell Research</i> , 2021, 31, 542-553.	12.0	26
10	Molecular-level understanding of the hTAS2R1 receptor-bitter tasting tetra-peptide binding: a structural biology study based on computational approaches. <i>New Journal of Chemistry</i> , 2021, 45, 21369-21381.	2.8	1
11	Different mechanisms for translocation by monomeric and hexameric helicases. <i>Current Opinion in Structural Biology</i> , 2020, 61, 25-32.	5.7	37
12	A fast and high-quality charge model for the next generation general AMBER force field. <i>Journal of Chemical Physics</i> , 2020, 153, 114502.	3.0	195
13	How a B family DNA polymerase has been evolved to copy RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21274-21280.	7.1	10
14	Cutting antiparallel DNA strands in a single active site. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 119-126.	8.2	25
15	How mouse RAG recombinase avoids DNA transposition. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 127-133.	8.2	16
16	Replisome structure suggests mechanism for continuous fork progression and post-replication repair. <i>DNA Repair</i> , 2019, 81, 102658.	2.8	18
17	Novel Human Aminopeptidase N Inhibitors: Discovery and Optimization of Subsite Binding Interactions. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 7185-7209.	6.4	17
18	Evolution of Inosine-Specific Endonuclease V from Bacterial DNase to Eukaryotic RNase. <i>Molecular Cell</i> , 2019, 76, 44-56.e3.	9.7	29

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19	Structures and operating principles of the replisome. <i>Science</i> , 2019, 363, .	12.6	119
20	Discovery of High Affinity Receptors for Dityrosine through Inverse Virtual Screening and Docking and Molecular Dynamics. <i>International Journal of Molecular Sciences</i> , 2019, 20, 115.	4.1	24
21	Translesion and Repair DNA Polymerases: Diverse Structure and Mechanism. <i>Annual Review of Biochemistry</i> , 2018, 87, 239-261.	11.1	169
22	Cracking the DNA Code for V(D)J Recombination. <i>Molecular Cell</i> , 2018, 70, 358-370.e4.	9.7	61
23	Structure of HIV-1 reverse transcriptase cleaving RNA in an RNA/DNA hybrid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 507-512.	7.1	39
24	Generation of AMBER force field parameters for zinc centres of M1 and M17 family aminopeptidases. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 2595-2604.	3.5	13
25	Bypassing a 8,5- ϵ^2 -cyclo-2 α^2 -deoxyadenosine lesion by human DNA polymerase β at atomic resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10660-10665.	7.1	14
26	Mapping the Pathway and Dynamics of Bestatin Inhibition of the <i>Plasmodium falciparum</i> M1 Aminopeptidase β . <i>ChemMedChem</i> , 2018, 13, 2504-2513.	3.2	9
27	Cation trafficking propels RNA hydrolysis. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 715-721.	8.2	39
28	Template and primer requirements for DNA Pol β -mediated end joining. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7747-7752.	7.1	28
29	Mouse DNA polymerase β lacking the forty-two amino acids encoded by exon-2 is catalytically inactive in vitro. <i>DNA Repair</i> , 2017, 50, 71-76.	2.8	4
30	M1 aminopeptidases as drug targets: broad applications or therapeutic niche?. <i>FEBS Journal</i> , 2017, 284, 1473-1488.	4.7	53
31	Probing the structural requirements for thyroid hormone receptor inhibitory activity of sulfonynitrophenylthiazoles (SNPTs) using 2D-QSAR and 3D-QSAR approaches. <i>Medicinal Chemistry Research</i> , 2017, 26, 344-360.	2.4	2
32	How DNA polymerases catalyse replication and repair with contrasting fidelity. <i>Nature Reviews Chemistry</i> , 2017, 1, .	30.2	54
33	Detection of Reaction Intermediates in Mg ²⁺ -Dependent DNA Synthesis and RNA Degradation by Time-Resolved X-Ray Crystallography. <i>Methods in Enzymology</i> , 2017, 592, 283-327.	1.0	16
34	A new paradigm of DNA synthesis: three-metal-ion catalysis. <i>Cell and Bioscience</i> , 2016, 6, 51.	4.8	54
35	Capture of a third Mg ²⁺ is essential for catalyzing DNA synthesis. <i>Science</i> , 2016, 352, 1334-1337.	12.6	142
36	In silico study on β -aminoketone derivatives as thyroid hormone receptor inhibitors: a combined 3D-QSAR and molecular docking study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1-13.	3.5	4

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37	Structure-based approach for the study of thyroid hormone receptor binding affinity and subtype selectivity. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 2251-2267.	3.5	8
38	Rapid generation of novel models of RAG1 deficiency by CRISPR/Cas9-induced mutagenesis in murine zygotes. <i>Oncotarget</i> , 2016, 7, 12962-12974.	1.8	11
39	Posttranslational Regulation of Human DNA Polymerase δ . <i>Journal of Biological Chemistry</i> , 2015, 290, 27332-27344.	3.4	13
40	Mut δ generates both expansions and contractions in a mouse model of the Fragile X-associated disorders. <i>Human Molecular Genetics</i> , 2015, 24, ddv408.	2.9	52
41	A DNA-hairpin model for repeat-addition processivity in telomere synthesis. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 844-847.	8.2	27
42	Crystal structure of the V(D)J recombinase RAG1-RAG2. <i>Nature</i> , 2015, 518, 507-511.	27.8	145
43	Structural analysis of selective agonists of thyroid hormone receptor β using 3D-QSAR and molecular docking. <i>Journal of the Taiwan Institute of Chemical Engineers</i> , 2015, 49, 1-18.	5.3	15
44	How a homolog of high-fidelity replicases conducts mutagenic DNA synthesis. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 298-303.	8.2	41
45	Molecular determinants of thyroid hormone receptor selectivity in a series of phosphonic acid derivatives: 3D-QSAR analysis and molecular docking. <i>Chemico-Biological Interactions</i> , 2015, 240, 324-335.	4.0	9
46	Assembly Pathway and Characterization of the RAG1/2-DNA Paired and Signal-end Complexes. <i>Journal of Biological Chemistry</i> , 2015, 290, 14618-14625.	3.4	15
47	Tripartite DNA Lesion Recognition and Verification by XPC, TFIIH, and XPA in Nucleotide Excision Repair. <i>Molecular Cell</i> , 2015, 59, 1025-1034.	9.7	131
48	3D-QSAR, molecular docking and molecular dynamics studies of a series of ROR γ inhibitors. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 1929-1940.	3.5	20
49	Human Pol δ purified with accessory subunits is active in translesion DNA synthesis and complements Pol β in cisplatin bypass. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2954-2959.	7.1	154
50	Correlation of Phenotype/Genotype in a Cohort of 23 Xeroderma Pigmentosum-Variant Patients Reveals 12 New Disease-Causing <i>POLH</i> Mutations. <i>Human Mutation</i> , 2014, 35, 117-128.	2.5	41
51	The Steric Gate of DNA Polymerase δ Regulates Ribonucleotide Incorporation and Deoxyribonucleotide Fidelity. <i>Journal of Biological Chemistry</i> , 2014, 289, 9136-9145.	3.4	34
52	Variants of mouse DNA polymerase δ reveal a mechanism of efficient and accurate translesion synthesis past a benzo[<i>a</i>]pyrene dG adduct. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1789-1794.	7.1	33
53	Structure and Dynamics of Apical Membrane Antigen 1 from <i>Plasmodium falciparum</i> FVO. <i>Biochemistry</i> , 2014, 53, 7310-7320.	2.5	23
54	The histone-fold complex MHF is remodeled by FANCM to recognize branched DNA and protect genome stability. <i>Cell Research</i> , 2014, 24, 560-575.	12.0	24

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55	Calcium Inhibition of Ribonuclease H1 Two-Metal Ion Catalysis. <i>Journal of the American Chemical Society</i> , 2014, 136, 3137-3144.	13.7	52
56	Structural and mechanistic studies of polymerase β -bypass of phenanthriplatin DNA damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9133-9138.	7.1	55
57	Molecular basis for unidirectional scaffold switching of human Plk4 in centriole biogenesis. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 696-703.	8.2	94
58	An Overview of Y-Family DNA Polymerases and a Case Study of Human DNA Polymerase β . <i>Biochemistry</i> , 2014, 53, 2793-2803.	2.5	153
59	Novel insights from structural analysis of lentiviral and gammaretroviral reverse transcriptases in complex with RNA/DNA hybrids. <i>Retrovirology</i> , 2013, 10, .	2.0	0
60	Complexes of HIV-1 RT, NNRTI and RNA/DNA hybrid reveal a structure compatible with RNA degradation. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 230-236.	8.2	78
61	The Histone Mark H3K36me3 Regulates Human DNA Mismatch Repair through Its Interaction with MutS β . <i>Cell</i> , 2013, 153, 590-600.	28.9	504
62	Mechanism of somatic hypermutation at the WA motif by human DNA polymerase β . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8146-8151.	7.1	75
63	MuB is an AAA+ ATPase that forms helical filaments to control target selection for DNA transposition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2441-50.	7.1	40
64	Examining the Role of the HIV-1 Reverse Transcriptase p51 Subunit in Positioning and Hydrolysis of RNA/DNA Hybrids. <i>Journal of Biological Chemistry</i> , 2013, 288, 16177-16184.	3.4	16
65	Reply to "Structural requirements for RNA degradation by HIV-1 reverse transcriptase". <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1342-1343.	8.2	4
66	Mechanism of the nucleotidyl-transfer reaction in DNA polymerase revealed by time-resolved protein crystallography. <i>Biophysics (Nagoya-shi, Japan)</i> , 2013, 9, 31-36.	0.4	5
67	Watching DNA Polymerase β Make a Phosphodiester Bond. <i>Seibutsu Butsuri</i> , 2013, 53, 254-257.	0.1	1
68	Visualization of Nucleotidyl Transfer Reaction by Human DNA Polymerase β Using Time Resolved Protein Crystallography. <i>Nihon Kessho Gakkaishi</i> , 2013, 55, 42-46.	0.0	0
69	Critical amino acids in Escherichia coli UmuC responsible for sugar discrimination and base-substitution fidelity. <i>Nucleic Acids Research</i> , 2012, 40, 6144-6157.	14.5	36
70	Structural basis of human DNA polymerase β -mediated chemoresistance to cisplatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7269-7274.	7.1	142
71	Assembly of prototype foamy virus strand transfer complexes on product DNA bypassing catalysis of integration. <i>Protein Science</i> , 2012, 21, 1849-1857.	7.6	32
72	Escherichia coli UmuC active site mutants: Effects on translesion DNA synthesis, mutagenesis and cell survival. <i>DNA Repair</i> , 2012, 11, 726-732.	2.8	22

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73	Mechanism of mismatch recognition revealed by human MutS $\hat{1}$ bound to unpaired DNA loops. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 72-78.	8.2	136
74	Watching DNA polymerase $\hat{1}$ make a phosphodiester bond. <i>Nature</i> , 2012, 487, 196-201.	27.8	231
75	Investigation on the binding mode of benzothiophene analogues as potent factor IXa (FIXa) inhibitors in thrombosis by CoMFA, docking and molecular dynamic studies. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2011, 26, 792-804.	5.2	9
76	Nucleases: diversity of structure, function and mechanism. <i>Quarterly Reviews of Biophysics</i> , 2011, 44, 1-93.	5.7	489
77	Catalytic Mechanism of RNA Backbone Cleavage by Ribonuclease H from Quantum Mechanics/Molecular Mechanics Simulations. <i>Journal of the American Chemical Society</i> , 2011, 133, 8934-8941.	13.7	164
78	Dynamic communication between androgen and coactivator: Mutually induced conformational perturbations in androgen receptor ligand-binding domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1154-1171.	2.6	22
79	Surviving the Sun: Repair and bypass of DNA UV lesions. <i>Protein Science</i> , 2011, 20, 1781-1789.	7.6	49
80	Structure and mechanism of human DNA polymerase $\hat{1}$. <i>Nature</i> , 2010, 465, 1044-1048.	27.8	300
81	Autoinhibition of DNA cleavage mediated by RAG1 and RAG2 is overcome by an epigenetic signal in V(D)J recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22487-22492.	7.1	52
82	Mechanism of MicroRNA-Target Interaction: Molecular Dynamics Simulations and Thermodynamics Analysis. <i>PLoS Computational Biology</i> , 2010, 6, e1000866.	3.2	76
83	DNA Scissors Device Used to Measure MutS Binding to DNA Mis-pairs. <i>Journal of the American Chemical Society</i> , 2010, 132, 4352-4357.	13.7	53
84	Topoisomerases and site-specific recombinases: similarities in structure and mechanism. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2010, 45, 520-534.	5.2	37
85	Lessons Learned from UvrD Helicase: Mechanism for Directional Movement. <i>Annual Review of Biophysics</i> , 2010, 39, 367-385.	10.0	48
86	Discovery of estrogen receptor modulators: a review of virtual screening and SAR efforts. <i>Expert Opinion on Drug Discovery</i> , 2010, 5, 21-31.	5.0	15
87	Identification of a residue critical for the excision of 3'-blocking ends in apurinic/apyrimidinic endonucleases of the Xth family. <i>Nucleic Acids Research</i> , 2009, 37, 1829-1842.	14.5	27
88	Structural and functional modules in RNA interference. <i>Current Opinion in Structural Biology</i> , 2009, 19, 286-293.	5.7	50
89	Structural Insight into Translesion Synthesis by DNA Pol II. <i>Cell</i> , 2009, 139, 1279-1289.	28.9	94
90	Initial Stages of V(D)J Recombination: The Organization of RAG1/2 and RSS DNA in the Postcleavage Complex. <i>Molecular Cell</i> , 2009, 35, 217-227.	9.7	44

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91	Structure and mechanism for DNA lesion recognition. <i>Cell Research</i> , 2008, 18, 184-197.	12.0	121
92	Specific recognition of RNA/DNA hybrid and enhancement of human RNase H1 activity by HBD. <i>EMBO Journal</i> , 2008, 27, 1172-1181.	7.8	91
93	An equivalent metal ion in one- and two-metal-ion catalysis. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1228-1231.	8.2	99
94	Protein-nucleic acid complexes: large, small, old, and new. <i>Current Opinion in Structural Biology</i> , 2008, 18, 67-69.	5.7	3
95	Here Comes the Sun: Recognition of UV-Damaged DNA. <i>Cell</i> , 2008, 135, 1172-1174.	28.9	13
96	RAG2 PHD finger couples histone H3 lysine 4 trimethylation with V(D)J recombination. <i>FASEB Journal</i> , 2008, 22, 600.2.	0.5	2
97	The plant homeodomain finger of RAG2 recognizes histone H3 methylated at both lysine-4 and arginine-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18993-18998.	7.1	186
98	What a difference a decade makes: Insights into translesion DNA synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15591-15598.	7.1	338
99	Mechanism of Template-independent Nucleotide Incorporation Catalyzed by a Template-dependent DNA Polymerase. <i>Journal of Molecular Biology</i> , 2007, 365, 590-602.	4.2	48
100	Structure of Human RNase H1 Complexed with an RNA/DNA Hybrid: Insight into HIV Reverse Transcription. <i>Molecular Cell</i> , 2007, 28, 264-276.	9.7	282
101	Crystal structure of T4 endonuclease VII resolving a Holliday junction. <i>Nature</i> , 2007, 449, 616-620.	27.8	112
102	RAG2 PHD finger couples histone H3 lysine 4 trimethylation with V(D)J recombination. <i>Nature</i> , 2007, 450, 1106-1110.	27.8	429
103	Human MutL \pm : The jack of all trades in MMR is also an endonuclease. <i>DNA Repair</i> , 2007, 6, 135-139.	2.8	23
104	UvrD Helicase Unwinds DNA One Base Pair at a Time by a Two-Part Power Stroke. <i>Cell</i> , 2006, 127, 1349-1360.	28.9	342
105	Poor base stacking at DNA lesions may initiate recognition by many repair proteins. <i>DNA Repair</i> , 2006, 5, 654-666.	2.8	95
106	Making and Breaking Nucleic Acids: Two-Mg ²⁺ -Ion Catalysis and Substrate Specificity. <i>Molecular Cell</i> , 2006, 22, 5-13.	9.7	495
107	Stepwise analyses of metal ions in RNase H catalysis from substrate destabilization to product release. <i>EMBO Journal</i> , 2006, 25, 1924-1933.	7.8	225
108	Crystal structure of a SeqA ϵ N filament: implications for DNA replication and chromosome organization. <i>EMBO Journal</i> , 2005, 24, 1502-1511.	7.8	48

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109	Fidelity of Dpo4: effect of metal ions, nucleotide selection and pyrophosphorolysis. <i>EMBO Journal</i> , 2005, 24, 2957-2967.	7.8	170
110	Structure of a repair enzyme interrogating undamaged DNA elucidates recognition of damaged DNA. <i>Nature</i> , 2005, 434, 612-618.	27.8	316
111	MutH Complexed with Hemi- and Unmethylated DNAs: Coupling Base Recognition and DNA Cleavage. <i>Molecular Cell</i> , 2005, 20, 155-166.	9.7	76
112	Crystal Structures of RNase H Bound to an RNA/DNA Hybrid: Substrate Specificity and Metal-Dependent Catalysis. <i>Cell</i> , 2005, 121, 1005-1016.	28.9	552
113	Portraits of a Y-family DNA polymerase. <i>FEBS Letters</i> , 2005, 579, 868-872.	2.8	72
114	Crystal structure of a benzo[a]pyrene diol epoxide adduct in a ternary complex with a DNA polymerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2265-2269.	7.1	176
115	Proliferating Cell Nuclear Antigen-dependent Coordination of the Biological Functions of Human DNA Polymerase η . <i>Journal of Biological Chemistry</i> , 2004, 279, 48360-48368.	3.4	83
116	Investigating the Role of the Little Finger Domain of Y-family DNA Polymerases in Low Fidelity Synthesis and Translesion Replication. <i>Journal of Biological Chemistry</i> , 2004, 279, 32932-32940.	3.4	122
117	The MLH1 D132H variant is associated with susceptibility to sporadic colorectal cancer. <i>Nature Genetics</i> , 2004, 36, 694-699.	21.4	92
118	Structure of the MutL C-terminal domain: a model of intact MutL and its roles in mismatch repair. <i>EMBO Journal</i> , 2004, 23, 4134-4145.	7.8	163
119	Snapshots of Replication through an Abasic Lesion. <i>Molecular Cell</i> , 2004, 13, 751-762.	9.7	186
120	Damage repair DNA polymerases Y. <i>Current Opinion in Structural Biology</i> , 2003, 13, 23-30.	5.7	138
121	Pruning DNA. <i>Structure</i> , 2003, 11, 365-366.	3.3	6
122	Replication of a cis- γ syn thymine dimer at atomic resolution. <i>Nature</i> , 2003, 424, 1083-1087.	27.8	212
123	Tetramerization and DNA Ligase IV Interaction of the DNA Double-strand Break Repair Protein XRCC4 are Mutually Exclusive. <i>Journal of Molecular Biology</i> , 2003, 334, 215-228.	4.2	67
124	Monovalent cation dependence and preference of GHKL ATPases and kinases 1. <i>FEBS Letters</i> , 2003, 544, 268-273.	2.8	38
125	In vitro and in vivo studies of MutS, MutL and MutH mutants: correlation of mismatch repair and DNA recombination. <i>DNA Repair</i> , 2003, 2, 387-405.	2.8	109
126	Crystal Structure and Biochemical Analysis of the MutS \cdot ADP \cdot Beryllium Fluoride Complex Suggests a Conserved Mechanism for ATP Interactions in Mismatch Repair. <i>Journal of Biological Chemistry</i> , 2003, 278, 16088-16094.	3.4	47

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127	Yeast POL5 Is an Evolutionarily Conserved Regulator of rDNA Transcription Unrelated to Any Known DNA Polymerases. <i>Cell Cycle</i> , 2003, 2, 120-122.	2.6	15
128	Histidine Kinases. , 2003, , 219-236.		1
129	Insights into negative modulation of E. coli replication initiation from the structure of SeqA-hemimethylated DNA complex. <i>Nature Structural Biology</i> , 2002, 9, 839-43.	9.7	29
130	Structure-based interpretation of missense mutations in Y-family DNA polymerases and their implications for polymerase function and lesion bypass. <i>DNA Repair</i> , 2002, 1, 343-358.	2.8	71
131	Evidence for sequential action of two ATPase active sites in yeast Msh2-Msh6. <i>DNA Repair</i> , 2002, 1, 743-753.	2.8	80
132	Disruption of the helix-u-turn-helix motif of MutS protein: loss of subunit dimerization, mismatch binding and ATP hydrolysis. <i>Journal of Molecular Biology</i> , 2001, 305, 805-816.	4.2	43
133	Composite Active Site of an ABC ATPase. <i>Molecular Cell</i> , 2001, 7, 1-12.	9.7	242
134	Crystal Structure of a Y-Family DNA Polymerase in Action. <i>Cell</i> , 2001, 107, 91-102.	28.9	588
135	A Ku Bridge over Broken DNA. <i>Structure</i> , 2001, 9, 881-884.	3.3	40
136	Asymmetric Recognition of DNA Local Distortion. <i>Journal of Biological Chemistry</i> , 2001, 276, 46225-46229.	3.4	67
137	Crystal structures of mismatch repair protein MutS and its complex with a substrate DNA. <i>Nature</i> , 2000, 407, 703-710.	27.8	605
138	Structure and function of mismatch repair proteins. <i>Mutation Research DNA Repair</i> , 2000, 460, 245-256.	3.7	98
139	Oligomerization of a MutS Mismatch Repair Protein from <i>Thermus aquaticus</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 23673-23678.	3.4	51
140	Transformation of MutL by ATP Binding and Hydrolysis. <i>Cell</i> , 1999, 97, 85-97.	28.9	374
141	Crystal Structure and ATPase Activity of MutL. <i>Cell</i> , 1998, 95, 541-552.	28.9	352
142	Site-specific recombination in plane view. <i>Structure</i> , 1997, 5, 1401-1406.	3.3	42
143	Recombining the structures of HIV integrase, RuvC and RNase H. <i>Structure</i> , 1995, 3, 131-134.	3.3	243
144	Crystal structure of the site-specific recombinase ϕ 31 resolvase complexed with a 34 bp cleavage site. <i>Cell</i> , 1995, 82, 193-207.	28.9	259

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145	Crystallization and characterization of human chorionic gonadotropin in chemically deglycosylated and enzymically desialylated states. <i>Biochemistry</i> , 1989, 28, 9239-9243.	2.5	64
146	Two-Metal-Ion-Dependent Catalysis in Nucleic Acid Enzymes. , 0, , 415-436.		0