

# John A Tainer

## List of Publications by Year in descending order

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369  
papers

40,141  
citations

1463

107  
h-index

3407

183  
g-index

396  
all docs

396  
docs citations

396  
times ranked

32117  
citing authors

#	ARTICLE	IF	CITATIONS
1	X-ray solution scattering (SAXS) combined with crystallography and computation: defining accurate macromolecular structures, conformations and assemblies in solution. Quarterly Reviews of Biophysics, 2007, 40, 191-285.	5.7	1,026
2	Structural Biology of Rad50 ATPase. Cell, 2000, 101, 789-800.	28.9	886
3	DNA-bound structures and mutants reveal abasic DNA binding by APE1 DNA repair and coordination. Nature, 2000, 403, 451-456.	27.8	689
4	Structure of Nitric Oxide Synthase Oxygenase Dimer with Pterin and Substrate. Science, 1998, 279, 2121-2126.	12.6	676
5	Accurate assessment of mass, models and resolution by small-angle scattering. Nature, 2013, 496, 477-481.	27.8	670
6	Type IV pilus structure and bacterial pathogenicity. Nature Reviews Microbiology, 2004, 2, 363-378.	28.6	662
7	Robust, high-throughput solution structural analyses by small angle X-ray scattering (SAXS). Nature Methods, 2009, 6, 606-612.	19.0	610
8	XPD Helicase Structures and Activities: Insights into the Cancer and Aging Phenotypes from XPD Mutations. Cell, 2008, 133, 789-800.	28.9	593
9	Electrostatic recognition between superoxide and copper, zinc superoxide dismutase. Nature, 1983, 306, 287-290.	27.8	541
10	A nucleotide-flipping mechanism from the structure of human uracil-DNA glycosylase bound to DNA. Nature, 1996, 384, 87-92.	27.8	520
11	PD-L1-mediated gasdermin C expression switches apoptosis to pyroptosis in cancer cells and facilitates tumour necrosis. Nature Cell Biology, 2020, 22, 1264-1275.	10.3	508
12	The reactivity of anti-peptide antibodies is a function of the atomic mobility of sites in a protein. Nature, 1984, 312, 127-134.	27.8	505
13	Accurate SAXS Profile Computation and its Assessment by Contrast Variation Experiments. Biophysical Journal, 2013, 105, 962-974.	0.5	489
14	Structure of the fibre-forming protein pilin at 2.6 Å... resolution. Nature, 1995, 378, 32-38.	27.8	488
15	The Rad50 zinc-hook is a structure joining Mre11 complexes in DNA recombination and repair. Nature, 2002, 418, 562-566.	27.8	485
16	DNA Double-Strand Break Repair Pathway Choice Is Directed by Distinct MRE11 Nuclease Activities. Molecular Cell, 2014, 53, 7-18.	9.7	466
17	The structure of human mitochondrial manganese superoxide dismutase reveals a novel tetrameric interface of two 4-helix bundles. Cell, 1992, 71, 107-118.	28.9	456
18	Structural Biochemistry and Interaction Architecture of the DNA Double-Strand Break Repair Mre11 Nuclease and Rad50-ATPase. Cell, 2001, 105, 473-485.	28.9	448

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19	Characterizing flexible and intrinsically unstructured biological macromolecules by SAS using the Porod-Debye law. Biopolymers, 2011, 95, 559-571.	2.4	440
20	Mre11 Dimers Coordinate DNA End Bridging and Nuclease Processing in Double-Strand-Break Repair. Cell, 2008, 135, 97-109.	28.9	427
21	FoXS, FoXSDock and MultiFoXS: Single-state and multi-state structural modeling of proteins and their complexes based on SAXS profiles. Nucleic Acids Research, 2016, 44, W424-W429.	14.5	427
22	Active and inhibited human catalase structures: ligand and NADPH binding and catalytic mechanism 1 Edited by R. Huber. Journal of Molecular Biology, 2000, 296, 295-309.	4.2	388
23	Structure and function of the multifunctional DNA-repair enzyme exonuclease III. Nature, 1995, 374, 381-386.	27.8	378
24	Nickel Superoxide Dismutase Structure and Mechanism. Biochemistry, 2004, 43, 8038-8047.	2.5	373
25	Crystal structure and mutational analysis of human uracil-DNA glycosylase: Structural basis for specificity and catalysis. Cell, 1995, 80, 869-878.	28.9	361
26	Type IV Pilus Structure by Cryo-Electron Microscopy and Crystallography: Implications for Pilus Assembly and Functions. Molecular Cell, 2006, 23, 651-662.	9.7	358
27	Mre11a-Rad50a-Nbs1 is a keystone complex connecting DNA repair machinery, double-strand break signaling, and the chromatin template This paper is one of a selection of papers published in this Special Issue, entitled 28th International West Coast Chromatin and Chromosome Conference, and has undergone the Journal's usual peer review process.. Biochemistry and Cell Biology, 2007, 85, 509-520.	2.0	351
28	The Structure of Nitric Oxide Synthase Oxygenase Domain and Inhibitor Complexes. Science, 1997, 278, 425-431.	12.6	345
29	Microbial metalloproteomes are largely uncharacterized. Nature, 2010, 466, 779-782.	27.8	330
30	Crystal Structures of a Schistosomal Drug and Vaccine Target: Glutathione S-Transferase from Schistosoma japonica and its Complex with the Leading Antischistosomal Drug Praziquantel. Journal of Molecular Biology, 1995, 246, 21-27.	4.2	309
31	The MRE11-RAD50-NBS1 Complex Conducts the Orchestration of Damage Signaling and Outcomes to Stress in DNA Replication and Repair. Annual Review of Biochemistry, 2018, 87, 263-294.	11.1	303
32	Identification of a New Cryptochrome Class. Molecular Cell, 2003, 11, 59-67.	9.7	301
33	SUMO-targeted ubiquitin ligases in genome stability. EMBO Journal, 2007, 26, 4089-4101.	7.8	301
34	MutY catalytic core, mutant and bound adenine structures define specificity for DNA repair enzyme superfamily. Nature Structural Biology, 1998, 5, 1058-1064.	9.7	297
35	Structure of the DNA Repair Enzyme Endonuclease IV and Its DNA Complex. Cell, 1999, 98, 397-408.	28.9	277
36	DNA binding and nucleotide flipping by the human DNA repair protein AGT. Nature Structural and Molecular Biology, 2004, 11, 714-720.	8.2	275

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37	ModBase, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2014, 42, D336-D346.	14.5	275
38	Structure of a designed protein cage that self-assembles into a highly porous cube. Nature Chemistry, 2014, 6, 1065-1071.	13.6	267
39	Type IV Pilin Structure and Assembly. Molecular Cell, 2003, 11, 1139-1150.	9.7	260
40	Structure of the DNA Repair and Replication Endonuclease and Exonuclease FEN-1. Cell, 1998, 95, 135-146.	28.9	257
41	Crystal structure of human uracil-DNA glycosylase in complex with a protein inhibitor: Protein mimicry of DNA. Cell, 1995, 82, 701-708.	28.9	253
42	Structural Basis for FEN-1 Substrate Specificity and PCNA-Mediated Activation in DNA Replication and Repair. Cell, 2004, 116, 39-50.	28.9	253
43	Structural Basis for Isozyme-specific Regulation of Electron Transfer in Nitric-oxide Synthase. Journal of Biological Chemistry, 2004, 279, 37918-37927.	3.4	244
44	Full-length archaeal Rad51 structure and mutants: mechanisms for RAD51 assembly and control by BRCA2. EMBO Journal, 2003, 22, 4566-4576.	7.8	239
45	Human Flap Endonuclease Structures, DNA Double-Base Flipping, and a Unified Understanding of the FEN1 Superfamily. Cell, 2011, 145, 198-211.	28.9	238
46	Crystal Structure and Mutational Analysis of the Human CDK2 Kinase Complex with Cell Cycle-Regulatory Protein CksHs1. Cell, 1996, 84, 863-874.	28.9	237
47	Abasic site recognition by two apurinic/apyrimidinic endonuclease families in DNA base excision repair: the 3' ends justify the means. Mutation Research DNA Repair, 2000, 460, 211-229.	3.7	230
48	Exploring the repeat protein universe through computational protein design. Nature, 2015, 528, 580-584.	27.8	227
49	Evolution and mechanism from structures of an ADP-ribosylating toxin and NAD complex. Nature Structural Biology, 1999, 6, 932-936.	9.7	223
50	Evolution of CuZn superoxide dismutase and the Greek Key $\beta^2$ -barrel structural motif. Proteins: Structure, Function and Bioinformatics, 1989, 5, 322-336.	2.6	214
51	Implementation and performance of SIBYLS: a dual endstation small-angle X-ray scattering and macromolecular crystallography beamline at the Advanced Light Source. Journal of Applied Crystallography, 2013, 46, 1-13.	4.5	208
52	Anchored plasticity opens doors for selective inhibitor design in nitric oxide synthase. Nature Chemical Biology, 2008, 4, 700-707.	8.0	205
53	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. Acta Crystallographica Section D: Structural Biology, 2017, 73, 710-728.	2.3	205
54	MDB: the Metalloprotein Database and Browser at The Scripps Research Institute. Nucleic Acids Research, 2002, 30, 379-382.	14.5	203

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55	A Role for Acidic Residues in Di-leucine Motif-based Targeting to the Endocytic Pathway. <i>Journal of Biological Chemistry</i> , 1995, 270, 19989-19997.	3.4	202
56	A SIM-ultaneous role for SUMO and ubiquitin. <i>Trends in Biochemical Sciences</i> , 2008, 33, 201-208.	7.5	201
57	Mechanism and energetics of green fluorescent protein chromophore synthesis revealed by trapped intermediate structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12111-12116.	7.1	194
58	Recognition of RNA Polymerase II and Transcription Bubbles by XPG, CSB, and TFIIH: Insights for Transcription-Coupled Repair and Cockayne Syndrome. <i>Molecular Cell</i> , 2005, 20, 187-198.	9.7	194
59	The intricate structural chemistry of base excision repair machinery: Implications for DNA damage recognition, removal, and repair. <i>DNA Repair</i> , 2007, 6, 410-428.	2.8	194
60	Mre11â€“Rad50â€“Nbs1 conformations and the control of sensing, signaling, and effector responses at DNA double-strand breaks. <i>DNA Repair</i> , 2010, 9, 1299-1306.	2.8	194
61	Rad50/SMC proteins and ABC transporters: unifying concepts from high-resolution structures. <i>Current Opinion in Structural Biology</i> , 2003, 13, 249-255.	5.7	193
62	Ku and DNA-dependent Protein Kinase Dynamic Conformations and Assembly Regulate DNA Binding and the Initial Non-homologous End Joining Complex. <i>Journal of Biological Chemistry</i> , 2010, 285, 1414-1423.	3.4	189
63	Mechanism and Regulation of DNA-Protein Crosslink Repair by the DNA-Dependent Metalloprotease SPRTN. <i>Molecular Cell</i> , 2016, 64, 688-703.	9.7	189
64	Emerging critical roles of Feâ€“S clusters in DNA replication and repair. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2015, 1853, 1253-1271.	4.1	187
65	A structural model for regulation of NHEJ by DNA-PKcs autophosphorylation. <i>DNA Repair</i> , 2010, 9, 1307-1314.	2.8	186
66	DNA base damage recognition and removal: New twists and grooves. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2005, 577, 55-76.	1.0	184
67	ALS Mutants of Human Superoxide Dismutase Form Fibrous Aggregates Via Framework Destabilization. <i>Journal of Molecular Biology</i> , 2003, 332, 601-615.	4.2	183
68	Cancer, cadmium and genome integrity. <i>Nature Genetics</i> , 2003, 34, 239-241.	21.4	179
69	Super-Resolution in Solution X-Ray Scattering and Its Applications to Structural Systems Biology. <i>Annual Review of Biophysics</i> , 2013, 42, 415-441.	10.0	179
70	High-Throughput SAXS for the Characterization of Biomolecules in Solution: A Practical Approach. <i>Methods in Molecular Biology</i> , 2014, 1091, 245-258.	0.9	176
71	Human Mitochondrial Manganese Superoxide Dismutase Polymorphic Variant Ile58Thr Reduces Activity by Destabilizing the Tetrameric Interfaceâ€“,â€“. <i>Biochemistry</i> , 1996, 35, 4287-4297.	2.5	173
72	Human dUTP pyrophosphatase: uracil recognition by a Î² hairpin and active sites formed by three separate subunits. <i>Structure</i> , 1996, 4, 1077-1092.	3.3	171

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73	Human glutathione transferase A4-4 crystal structures and mutagenesis reveal the basis of high catalytic efficiency with toxic lipid peroxidation products. <i>Journal of Molecular Biology</i> , 1999, 288, 427-439.	4.2	171
74	DNA REPAIR MECHANISMS FOR THE RECOGNITION AND REMOVAL OF DAMAGED DNA BASES. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1999, 28, 101-128.	18.3	170
75	A first-in-class polymerase theta inhibitor selectively targets homologous-recombination-deficient tumors. <i>Nature Cancer</i> , 2021, 2, 598-610.	13.2	168
76	Structure and mechanism of the RuvB holliday junction branch migration motor. <i>Journal of Molecular Biology</i> , 2001, 311, 297-310.	4.2	157
77	Human ABH3 structure and key residues for oxidative demethylation to reverse DNA/RNA damage. <i>EMBO Journal</i> , 2006, 25, 3389-3397.	7.8	157
78	DNA binding, nucleotide flipping, and the helix-turn-helix motif in base repair by O6-alkylguanine-DNA alkyltransferase and its implications for cancer chemotherapy. <i>DNA Repair</i> , 2007, 6, 1100-1115.	2.8	154
79	Structural basis for endothelial nitric oxide synthase binding to calmodulin. <i>EMBO Journal</i> , 2003, 22, 766-775.	7.8	151
80	XRCC4 Protein Interactions with XRCC4-like Factor (XLF) Create an Extended Grooved Scaffold for DNA Ligation and Double Strand Break Repair. <i>Journal of Biological Chemistry</i> , 2011, 286, 32638-32650.	3.4	151
81	ABC ATPase signature helices in Rad50 link nucleotide state to Mre11 interface for DNA repair. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 423-431.	8.2	149
82	Metal-binding sites in proteins. <i>Current Opinion in Biotechnology</i> , 1991, 2, 582-591.	6.6	146
83	Bridging the solution divide: comprehensive structural analyses of dynamic RNA, DNA, and protein assemblies by small-angle X-ray scattering. <i>Current Opinion in Structural Biology</i> , 2010, 20, 128-137.	5.7	145
84	HU multimerization shift controls nucleoid compaction. <i>Science Advances</i> , 2016, 2, e1600650.	10.3	144
85	Structures of the N <sup>6</sup> -Hydroxy-L-Arginine Complex of Inducible Nitric Oxide Synthase Oxygenase Dimer with Active and Inactive Pterins. <i>Biochemistry</i> , 2000, 39, 4608-4621.	2.5	143
86	Crystal structure and novel recognition motif of Rho ADP-ribosylating C3 exoenzyme from <i>Clostridium botulinum</i> : structural insights for recognition specificity and catalysis. <i>Journal of Molecular Biology</i> , 2001, 305, 95-107.	4.2	142
87	A Flexible Interface between DNA Ligase and PCNA Supports Conformational Switching and Efficient Ligation of DNA. <i>Molecular Cell</i> , 2006, 24, 279-291.	9.7	142
88	Conserved XPB Core Structure and Motifs for DNA Unwinding: Implications for Pathway Selection of Transcription or Excision Repair. <i>Molecular Cell</i> , 2006, 22, 27-37.	9.7	140
89	XPB and XPD helicases in TFIIH orchestrate DNA duplex opening and damage verification to coordinate repair with transcription and cell cycle via CAK kinase. <i>DNA Repair</i> , 2011, 10, 697-713.	2.8	135
90	DNA double-strand break repair from head to tail. <i>Current Opinion in Structural Biology</i> , 2002, 12, 115-122.	5.7	133

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91	WRN exonuclease structure and molecular mechanism imply an editing role in DNA end processing. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 414-422.	8.2	131
92	Evolving SAXS versatility: solution X-ray scattering for macromolecular architecture, functional landscapes, and integrative structural biology. <i>Current Opinion in Structural Biology</i> , 2019, 58, 197-213.	5.7	131
93	Cloning, expression, and characterization of a nitric oxide synthase protein from <i>Deinococcus radiodurans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 107-112.	7.1	130
94	Structural Tuning of the Fluorescent Protein iLOV for Improved Photostability. <i>Journal of Biological Chemistry</i> , 2012, 287, 22295-22304.	3.4	130
95	ATP-driven Rad50 conformations regulate DNA tethering, end resection, and ATM checkpoint signaling. <i>EMBO Journal</i> , 2014, 33, 482-500.	7.8	129
96	Superoxide Dismutase from the Eukaryotic Thermophile <i>Alvinella pompejana</i> : Structures, Stability, Mechanism, and Insights into Amyotrophic Lateral Sclerosis. <i>Journal of Molecular Biology</i> , 2009, 385, 1534-1555.	4.2	126
97	The interdependence of protein surface topography and bound water molecules revealed by surface accessibility and fractal density measures. <i>Journal of Molecular Biology</i> , 1992, 228, 13-22.	4.2	124
98	Structural Characterization of Zinc-deficient Human Superoxide Dismutase and Implications for ALS. <i>Journal of Molecular Biology</i> , 2007, 373, 877-890.	4.2	122
99	Flipping of alkylated DNA damage bridges base and nucleotide excision repair. <i>Nature</i> , 2009, 459, 808-813.	27.8	121
100	Consequences of the loss of O-linked glycosylation of meningococcal type IV pilin on piliation and pilus-mediated adhesion. <i>Molecular Microbiology</i> , 1998, 27, 705-715.	2.5	120
101	Crystal Structure of Y34F Mutant Human Mitochondrial Manganese Superoxide Dismutase and the Functional Role of Tyrosine 34,. <i>Biochemistry</i> , 1998, 37, 4722-4730.	2.5	120
102	Protein mimicry of DNA from crystal structures of the uracil-DNA glycosylase inhibitor protein and its complex with <i>Escherichia coli</i> uracil-DNA glycosylase 1 1Edited by D. C. Rees. <i>Journal of Molecular Biology</i> , 1999, 287, 331-346.	4.2	120
103	Envisioning the molecular choreography of DNA base excision repair. <i>Current Opinion in Structural Biology</i> , 1999, 9, 37-47.	5.7	119
104	The role of arginine 143 in the electrostatics and mechanism of Cu, Zn superoxide dismutase: Computational and experimental evaluation by mutational analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 19, 24-34.	2.6	118
105	Lessons learned from structural results on uracil-DNA glycosylase. <i>Mutation Research DNA Repair</i> , 2000, 460, 183-199.	3.7	117
106	Translocation and deletion breakpoints in cancer genomes are associated with potential non-B DNA-forming sequences. <i>Nucleic Acids Research</i> , 2016, 44, 5673-5688.	14.5	117
107	Unusual Trigonal-Planar Copper Configuration Revealed in the Atomic Structure of Yeast CopperâˆŽZinc Superoxide Dismutaseâ€¢. <i>Biochemistry</i> , 1996, 35, 2316-2321.	2.5	116
108	Mre11 and Rad50 from <i>Pyrococcus furiosus</i> : Cloning and Biochemical Characterization Reveal an Evolutionarily Conserved Multiprotein Machine. <i>Journal of Bacteriology</i> , 2000, 182, 6036-6041.	2.2	116



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109	Identification of critical active-site residues in the multifunctional human DNA repair enzyme HAP1. <i>Nature Structural Biology</i> , 1995, 2, 561-568.	9.7	113
110	Comprehensive macromolecular conformations mapped by quantitative SAXS analyses. <i>Nature Methods</i> , 2013, 10, 453-454.	19.0	112
111	Functional motifs in the (6-4) photolyase crystal structure make a comparative framework for DNA repair photolyases and clock cryptochromes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6962-6967.	7.1	110
112	Screening a peptidyl database for potential ligands to proteins with side-chain flexibility. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 33, 74-87.	2.6	108
113	Type-4 pilus-structure: outside to inside and top to bottom “aminireview. <i>Gene</i> , 1997, 192, 165-169.	2.2	107
114	Structural Chemistry of a Green Fluorescent Protein Zn Biosensor. <i>Journal of the American Chemical Society</i> , 2002, 124, 3522-3524.	13.7	105
115	XLF Regulates Filament Architecture of the XRCC4-Ligase IV Complex. <i>Structure</i> , 2010, 18, 1431-1442.	3.3	104
116	Structural insights into NHEJ: Building up an integrated picture of the dynamic DSB repair super complex, one component and interaction at a time. <i>DNA Repair</i> , 2014, 17, 110-120.	2.8	100
117	Probing the Active Site of Human Manganese Superoxide Dismutase: The Role of Glutamine 143,. <i>Biochemistry</i> , 1998, 37, 4731-4739.	2.5	96
118	DNA charge transport as a first step in coordinating the detection of lesions by repair proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1856-1861.	7.1	95
119	Insights into Flal Functions in Archaeal Motor Assembly and Motility from Structures, Conformations, and Genetics. <i>Molecular Cell</i> , 2013, 49, 1069-1082.	9.7	94
120	Base excision repair enzyme family portrait: integrating the structure and chemistry of an entire DNA repair pathway. <i>Structure</i> , 1997, 5, 1543-1550.	3.3	93
121	Crystallographic structure reveals phosphorylated pilin from <i>Neisseria</i> : phosphoserine sites modify type IV pilus surface chemistry and fibre morphology. <i>Molecular Microbiology</i> , 1999, 31, 743-752.	2.5	93
122	DNA apurinic-apyrimidinic site binding and excision by endonuclease IV. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 515-522.	8.2	93
123	Envisioning the dynamics and flexibility of Mre11-Rad50-Nbs1 complex to decipher its roles in DNA replication and repair. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 117, 182-193.	2.9	93
124	XRCC4 and XLF form long helical protein filaments suitable for DNA end protection and alignment to facilitate DNA double strand break repair. <i>Biochemistry and Cell Biology</i> , 2013, 91, 31-41.	2.0	91
125	Human DNA Ligase III Recognizes DNA Ends by Dynamic Switching between Two DNA-Bound States. <i>Biochemistry</i> , 2010, 49, 6165-6176.	2.5	90
126	A new structural framework for integrating replication protein A into DNA processing machinery. <i>Nucleic Acids Research</i> , 2013, 41, 2313-2327.	14.5	88



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127	Conserved Structural Chemistry for Incision Activity in Structurally Non-homologous Apurinic/Apyrimidinic Endonuclease APE1 and Endonuclease IV DNA Repair Enzymes. <i>Journal of Biological Chemistry</i> , 2013, 288, 8445-8455.	3.4	88
128	The Structure of the CRISPR-Associated Protein Csa3 Provides Insight into the Regulation of the CRISPR/Cas System. <i>Journal of Molecular Biology</i> , 2011, 405, 939-955.	4.2	87
129	Substrate specificity of prostate-specific antigen (PSA). <i>Chemistry and Biology</i> , 1998, 5, 475-488.	6.0	86
130	Unraveling the three-metal-ion catalytic mechanism of the DNA repair enzyme endonuclease IV. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1465-1470.	7.1	86
131	The Rad50 Signature Motif: Essential to ATP Binding and Biological Function. <i>Journal of Molecular Biology</i> , 2004, 335, 937-951.	4.2	85
132	Hexameric structures of the archaeal secretion ATPase GspE and implications for a universal secretion mechanism. <i>EMBO Journal</i> , 2007, 26, 878-890.	7.8	85
133	Structures of endonuclease V with DNA reveal initiation of deaminated adenine repair. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 138-143.	8.2	83
134	Improving small-angle X-ray scattering data for structural analyses of the RNA world. <i>Rna</i> , 2010, 16, 638-646.	3.5	83
135	Metals in biology: defining metalloproteomes. <i>Current Opinion in Biotechnology</i> , 2012, 23, 89-95.	6.6	82
136	The cutting edges in DNA repair, licensing, and fidelity: DNA and RNA repair nucleases sculpt DNA to measure twice, cut once. <i>DNA Repair</i> , 2014, 19, 95-107.	2.8	82
137	Phosphate steering by Flap Endonuclease 1 promotes 5' flap specificity and incision to prevent genome instability. <i>Nature Communications</i> , 2017, 8, 15855.	12.8	81
138	Insights into Lou Gehrig's Disease from the Structure and Instability of the A4V Mutant of Human Cu,Zn Superoxide Dismutase. <i>Journal of Molecular Biology</i> , 2002, 324, 247-256.	4.2	79
139	Dissection of DNA double-strand-break repair using novel single-molecule forceps. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 482-487.	8.2	79
140	Atomic and residue hydrophilicity in the context of folded protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 536-547.	2.6	78
141	Structural biochemistry of a type 2 RNase H: RNA primer recognition and removal during DNA replication <sup>11</sup> Edited by K. Morikawa. <i>Journal of Molecular Biology</i> , 2001, 307, 541-556.	4.2	77
142	Report of the wwPDB Small-Angle Scattering Task Force: Data Requirements for Biomolecular Modeling and the PDB. <i>Structure</i> , 2013, 21, 875-881.	3.3	77
143	Crystal Structure of the Human Cell Cycle Protein CksHs1: Single Domain Fold with Similarity to Kinase N-lobe Domain. <i>Journal of Molecular Biology</i> , 1995, 249, 835-842.	4.2	76
144	Conserved structural motifs governing the stoichiometric repair of alkylated DNA by O6-alkylguanine-DNA alkyltransferase. <i>Mutation Research DNA Repair</i> , 2000, 460, 151-163.	3.7	76

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145	The ARTT motif and a unified structural understanding of substrate recognition in ADP-ribosylating bacterial toxins and eukaryotic ADP-ribosyltransferases. <i>International Journal of Medical Microbiology</i> , 2001, 291, 523-529.	3.6	76
146	Crystallographic Structures of Discosoma Red Fluorescent Protein with Immature and Mature Chromophores: Linking Peptide Bond Trans $\rightarrow$ Cis Isomerization and Acylimine Formation in Chromophore Maturation,. <i>Biochemistry</i> , 2005, 44, 9833-9840.	2.5	76
147	MacroBac: New Technologies for Robust and Efficient Large-Scale Production of Recombinant Multiprotein Complexes. <i>Methods in Enzymology</i> , 2017, 592, 1-26.	1.0	76
148	Kinetic Analysis of Product Inhibition in Human Manganese Superoxide Dismutase. <i>Biochemistry</i> , 2001, 40, 12051-12058.	2.5	75
149	Selective small molecule PARC inhibitor causes replication fork stalling and cancer cell death. <i>Nature Communications</i> , 2019, 10, 5654.	12.8	75
150	Proliferating cell nuclear antigen loaded onto double-stranded DNA: dynamics, minor groove interactions and functional implications. <i>Nucleic Acids Research</i> , 2006, 34, 6023-6033.	14.5	73
151	Understanding GFP Chromophore Biosynthesis: Controlling Backbone Cyclization and Modifying Post-translational Chemistry,. <i>Biochemistry</i> , 2005, 44, 1960-1970.	2.5	72
152	The R-factor gap in macromolecular crystallography: an untapped potential for insights on accurate structures. <i>FEBS Journal</i> , 2014, 281, 4046-4060.	4.7	72
153	Defining the Role of Arginine 96 in Green Fluorescent Protein Fluorophore Biosynthesis. <i>Biochemistry</i> , 2005, 44, 16211-16220.	2.5	71
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