

John A Tainer

List of Publications by Year in descending order

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369
papers

40,141
citations

1457

107
h-index

3394

183
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396
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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.	2.4	1,026
2	Structural Biology of Rad50 ATPase. Cell, 2000, 101, 789-800.	13.5	886
3	DNA-bound structures and mutants reveal abasic DNA binding by APE1 DNA repair and coordination. Nature, 2000, 403, 451-456.	13.7	689
4	Structure of Nitric Oxide Synthase Oxygenase Dimer with Pterin and Substrate. Science, 1998, 279, 2121-2126.	6.0	676
5	Accurate assessment of mass, models and resolution by small-angle scattering. Nature, 2013, 496, 477-481.	13.7	670
6	Type IV pilus structure and bacterial pathogenicity. Nature Reviews Microbiology, 2004, 2, 363-378.	13.6	662
7	Robust, high-throughput solution structural analyses by small angle X-ray scattering (SAXS). Nature Methods, 2009, 6, 606-612.	9.0	610
8	XPD Helicase Structures and Activities: Insights into the Cancer and Aging Phenotypes from XPD Mutations. Cell, 2008, 133, 789-800.	13.5	593
9	Electrostatic recognition between superoxide and copper, zinc superoxide dismutase. Nature, 1983, 306, 287-290.	13.7	541
10	A nucleotide-flipping mechanism from the structure of human uracil-DNA glycosylase bound to DNA. Nature, 1996, 384, 87-92.	13.7	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.	4.6	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.	13.7	505
13	Accurate SAXS Profile Computation and its Assessment by Contrast Variation Experiments. Biophysical Journal, 2013, 105, 962-974.	0.2	489
14	Structure of the fibre-forming protein pilin at 2.6 Å... resolution. Nature, 1995, 378, 32-38.	13.7	488
15	The Rad50 zinc-hook is a structure joining Mre11 complexes in DNA recombination and repair. Nature, 2002, 418, 562-566.	13.7	485
16	DNA Double-Strand Break Repair Pathway Choice Is Directed by Distinct MRE11 Nuclease Activities. Molecular Cell, 2014, 53, 7-18.	4.5	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.	13.5	456
18	Structural Biochemistry and Interaction Architecture of the DNA Double-Strand Break Repair Mre11 Nuclease and Rad50-ATPase. Cell, 2001, 105, 473-485.	13.5	448

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19	Characterizing flexible and intrinsically unstructured biological macromolecules by SAS using the Porodâ€Debye law. <i>Biopolymers</i> , 2011, 95, 559-571.	1.2	440
20	Mre11 Dimers Coordinate DNA End Bridging and Nuclease Processing in Double-Strand-Break Repair. <i>Cell</i> , 2008, 135, 97-109.	13.5	427
21	FoXS, FoXSDock and MultiFoXS: Single-state and multi-state structural modeling of proteins and their complexes based on SAXS profiles. <i>Nucleic Acids Research</i> , 2016, 44, W424-W429.	6.5	427
22	Active and inhibited human catalase structures: ligand and NADPH binding and catalytic mechanism 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 296, 295-309.	2.0	388
23	Structure and function of the multifunctional DNA-repair enzyme exonuclease III. <i>Nature</i> , 1995, 374, 381-386.	13.7	378
24	Nickel Superoxide Dismutase Structure and Mechanism. <i>Biochemistry</i> , 2004, 43, 8038-8047.	1.2	373
25	Crystal structure and mutational analysis of human uracil-DNA glycosylase: Structural basis for specificity and catalysis. <i>Cell</i> , 1995, 80, 869-878.	13.5	361
26	Type IV Pilus Structure by Cryo-Electron Microscopy and Crystallography: Implications for Pilus Assembly and Functions. <i>Molecular Cell</i> , 2006, 23, 651-662.	4.5	358
27	Mre11â€Rad50â€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.. <i>Biochemistry and Cell Biology</i> , 2007, 85, 509-520.	0.9	351
28	The Structure of Nitric Oxide Synthase Oxygenase Domain and Inhibitor Complexes. <i>Science</i> , 1997, 278, 425-431.	6.0	345
29	Microbial metalloproteomes are largely uncharacterized. <i>Nature</i> , 2010, 466, 779-782.	13.7	330
30	Crystal Structures of a Schistosomal Drug and Vaccine Target: Glutathione S-Transferase from <i>Schistosoma japonica</i> and its Complex with the Leading Antischistosomal Drug Praziquantel. <i>Journal of Molecular Biology</i> , 1995, 246, 21-27.	2.0	309
31	The MRE11â€RAD50â€NBS1 Complex Conducts the Orchestration of Damage Signaling and Outcomes to Stress in DNA Replication and Repair. <i>Annual Review of Biochemistry</i> , 2018, 87, 263-294.	5.0	303
32	Identification of a New Cryptochrome Class. <i>Molecular Cell</i> , 2003, 11, 59-67.	4.5	301
33	SUMO-targeted ubiquitin ligases in genome stability. <i>EMBO Journal</i> , 2007, 26, 4089-4101.	3.5	301
34	MutY catalytic core, mutant and bound adenine structures define specificity for DNA repair enzyme superfamily. <i>Nature Structural Biology</i> , 1998, 5, 1058-1064.	9.7	297
35	Structure of the DNA Repair Enzyme Endonuclease IV and Its DNA Complex. <i>Cell</i> , 1999, 98, 397-408.	13.5	277
36	DNA binding and nucleotide flipping by the human DNA repair protein AGT. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 714-720.	3.6	275

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37	ModBase, a database of annotated comparative protein structure models and associated resources. <i>Nucleic Acids Research</i> , 2014, 42, D336-D346.	6.5	275
38	Structure of a designed protein cage that self-assembles into a highly porous cube. <i>Nature Chemistry</i> , 2014, 6, 1065-1071.	6.6	267
39	Type IV Pilin Structure and Assembly. <i>Molecular Cell</i> , 2003, 11, 1139-1150.	4.5	260
40	Structure of the DNA Repair and Replication Endonuclease and Exonuclease FEN-1. <i>Cell</i> , 1998, 95, 135-146.	13.5	257
41	Crystal structure of human uracil-DNA glycosylase in complex with a protein inhibitor: Protein mimicry of DNA. <i>Cell</i> , 1995, 82, 701-708.	13.5	253
42	Structural Basis for FEN-1 Substrate Specificity and PCNA-Mediated Activation in DNA Replication and Repair. <i>Cell</i> , 2004, 116, 39-50.	13.5	253
43	Structural Basis for Isozyme-specific Regulation of Electron Transfer in Nitric-oxide Synthase. <i>Journal of Biological Chemistry</i> , 2004, 279, 37918-37927.	1.6	244
44	Full-length archaeal Rad51 structure and mutants: mechanisms for RAD51 assembly and control by BRCA2. <i>EMBO Journal</i> , 2003, 22, 4566-4576.	3.5	239
45	Human Flap Endonuclease Structures, DNA Double-Base Flipping, and a Unified Understanding of the FEN1 Superfamily. <i>Cell</i> , 2011, 145, 198-211.	13.5	238
46	Crystal Structure and Mutational Analysis of the Human CDK2 Kinase Complex with Cell Cycle-Regulatory Protein CksHs1. <i>Cell</i> , 1996, 84, 863-874.	13.5	237
47	Abasic site recognition by two apurinic/aprimidinic endonuclease families in DNA base excision repair: the 3' ends justify the means. <i>Mutation Research DNA Repair</i> , 2000, 460, 211-229.	3.8	230
48	Exploring the repeat protein universe through computational protein design. <i>Nature</i> , 2015, 528, 580-584.	13.7	227
49	Evolution and mechanism from structures of an ADP-ribosylating toxin and NAD complex. <i>Nature Structural Biology</i> , 1999, 6, 932-936.	9.7	223
50	Evolution of CuZn superoxide dismutase and the Greek Key β^2 -barrel structural motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 1989, 5, 322-336.	1.5	214
51	Implementation and performance of SIBYLS: a dual endstation small-angle X-ray scattering and macromolecular crystallography beamline at the Advanced Light Source. <i>Journal of Applied Crystallography</i> , 2013, 46, 1-13.	1.9	208
52	Anchored plasticity opens doors for selective inhibitor design in nitric oxide synthase. <i>Nature Chemical Biology</i> , 2008, 4, 700-707.	3.9	205
53	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 710-728.	1.1	205
54	MDB: the Metalloprotein Database and Browser at The Scripps Research Institute. <i>Nucleic Acids Research</i> , 2002, 30, 379-382.	6.5	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.	1.6	202
56	A SIM-ultaneous role for SUMO and ubiquitin. <i>Trends in Biochemical Sciences</i> , 2008, 33, 201-208.	3.7	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.	3.3	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.	4.5	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.	1.3	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.	1.3	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.	2.6	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.	1.6	189
63	Mechanism and Regulation of DNA-Protein Crosslink Repair by the DNA-Dependent Metalloprotease SPRTN. <i>Molecular Cell</i> , 2016, 64, 688-703.	4.5	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.	1.9	187
65	A structural model for regulation of NHEJ by DNA-PKcs autophosphorylation. <i>DNA Repair</i> , 2010, 9, 1307-1314.	1.3	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.	0.4	184
67	ALS Mutants of Human Superoxide Dismutase Form Fibrous Aggregates Via Framework Destabilization. <i>Journal of Molecular Biology</i> , 2003, 332, 601-615.	2.0	183
68	Cancer, cadmium and genome integrity. <i>Nature Genetics</i> , 2003, 34, 239-241.	9.4	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.	4.5	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.	0.4	176
71	Human Mitochondrial Manganese Superoxide Dismutase Polymorphic Variant Ile58Thr Reduces Activity by Destabilizing the Tetrameric Interfaceâ€™. <i>Biochemistry</i> , 1996, 35, 4287-4297.	1.2	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.	1.6	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.	2.0	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.	5.7	168
76	Structure and mechanism of the RuvB holliday junction branch migration motor. <i>Journal of Molecular Biology</i> , 2001, 311, 297-310.	2.0	157
77	Human ABH3 structure and key residues for oxidative demethylation to reverse DNA/RNA damage. <i>EMBO Journal</i> , 2006, 25, 3389-3397.	3.5	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.	1.3	154
79	Structural basis for endothelial nitric oxide synthase binding to calmodulin. <i>EMBO Journal</i> , 2003, 22, 766-775.	3.5	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.	1.6	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.	3.6	149
82	Metal-binding sites in proteins. <i>Current Opinion in Biotechnology</i> , 1991, 2, 582-591.	3.3	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.	2.6	145
84	HU multimerization shift controls nucleoid compaction. <i>Science Advances</i> , 2016, 2, e1600650.	4.7	144
85	Structures of the Ni ²⁺ -Hydroxy-L-Arginine Complex of Inducible Nitric Oxide Synthase Oxygenase Dimer with Active and Inactive Pterins. <i>Biochemistry</i> , 2000, 39, 4608-4621.	1.2	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.	2.0	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.	4.5	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.	4.5	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.	1.3	135
90	DNA double-strand break repair from head to tail. <i>Current Opinion in Structural Biology</i> , 2002, 12, 115-122.	2.6	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.	3.6	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.	2.6	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.	3.3	130
94	Structural Tuning of the Fluorescent Protein iLOV for Improved Photostability. <i>Journal of Biological Chemistry</i> , 2012, 287, 22295-22304.	1.6	130
95	ATP-driven Rad50 conformations regulate DNA tethering, end resection, and ATM checkpoint signaling. <i>EMBO Journal</i> , 2014, 33, 482-500.	3.5	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.	2.0	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.	2.0	124
98	Structural Characterization of Zinc-deficient Human Superoxide Dismutase and Implications for ALS. <i>Journal of Molecular Biology</i> , 2007, 373, 877-890.	2.0	122
99	Flipping of alkylated DNA damage bridges base and nucleotide excision repair. <i>Nature</i> , 2009, 459, 808-813.	13.7	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.	1.2	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.	1.2	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 Edited by D. C. Rees. <i>Journal of Molecular Biology</i> , 1999, 287, 331-346.	2.0	120
103	Envisioning the molecular choreography of DNA base excision repair. <i>Current Opinion in Structural Biology</i> , 1999, 9, 37-47.	2.6	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.	1.5	118
105	Lessons learned from structural results on uracil-DNA glycosylase. <i>Mutation Research DNA Repair</i> , 2000, 460, 183-199.	3.8	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.	6.5	117
107	Unusual Trigonal-Planar Copper Configuration Revealed in the Atomic Structure of Yeast Copper-Zinc Superoxide Dismutase. <i>Biochemistry</i> , 1996, 35, 2316-2321.	1.2	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.	1.0	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.	9.0	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.	3.3	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.	1.5	108
113	Type-4 pilus-structure: outside to inside and top to bottom "aminireview. <i>Gene</i> , 1997, 192, 165-169.	1.0	107
114	Structural Chemistry of a Green Fluorescent Protein Zn Biosensor. <i>Journal of the American Chemical Society</i> , 2002, 124, 3522-3524.	6.6	105
115	XLF Regulates Filament Architecture of the XRCC4-Ligase IV Complex. <i>Structure</i> , 2010, 18, 1431-1442.	1.6	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.	1.3	100
117	Probing the Active Site of Human Manganese Superoxide Dismutase: The Role of Glutamine 143,. <i>Biochemistry</i> , 1998, 37, 4731-4739.	1.2	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.	3.3	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.	4.5	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.	1.6	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.	1.2	93
122	DNA apurinic-apyrimidinic site binding and excision by endonuclease IV. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 515-522.	3.6	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.	1.4	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.	0.9	91
125	Human DNA Ligase III Recognizes DNA Ends by Dynamic Switching between Two DNA-Bound States. <i>Biochemistry</i> , 2010, 49, 6165-6176.	1.2	90
126	A new structural framework for integrating replication protein A into DNA processing machinery. <i>Nucleic Acids Research</i> , 2013, 41, 2313-2327.	6.5	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.	1.6	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.	2.0	87
129	Substrate specificity of prostate-specific antigen (PSA). <i>Chemistry and Biology</i> , 1998, 5, 475-488.	6.2	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.	3.3	86
131	The Rad50 Signature Motif: Essential to ATP Binding and Biological Function. <i>Journal of Molecular Biology</i> , 2004, 335, 937-951.	2.0	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.	3.5	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.	3.6	83
134	Improving small-angle X-ray scattering data for structural analyses of the RNA world. <i>Rna</i> , 2010, 16, 638-646.	1.6	83
135	Metals in biology: defining metalloproteomes. <i>Current Opinion in Biotechnology</i> , 2012, 23, 89-95.	3.3	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.	1.3	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.	5.8	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.	2.0	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.	3.6	79
140	Atomic and residue hydrophilicity in the context of folded protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 536-547.	1.5	78
141	Structural biochemistry of a type 2 RNase H: RNA primer recognition and removal during DNA replication Edited by K. Morikawa. <i>Journal of Molecular Biology</i> , 2001, 307, 541-556.	2.0	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.	1.6	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.	2.0	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.	3.8	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.	1.5	76
146	Crystallographic Structures of Discosoma Red Fluorescent Protein with Immature and Mature Chromophores: Linking Peptide Bond Trans [→] Cis Isomerization and Acylimine Formation in Chromophore Maturation. <i>Biochemistry</i> , 2005, 44, 9833-9840.	1.2	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.	0.4	76
148	Kinetic Analysis of Product Inhibition in Human Manganese Superoxide Dismutase. <i>Biochemistry</i> , 2001, 40, 12051-12058.	1.2	75
149	Selective small molecule PARC inhibitor causes replication fork stalling and cancer cell death. <i>Nature Communications</i> , 2019, 10, 5654.	5.8	75
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