

John A Tainer

List of Publications by Year in descending order

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Version: 2024-02-01

369
papers

40,141
citations

1457

107
h-index

3394

183
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396
docs citations

396
times ranked

32117
citing authors

#	ARTICLE	IF	CITATIONS
1	Stress Responses as Master Keys to Epigenomic Changes in Transcriptome and Metabolome for Cancer Etiology and Therapeutics. <i>Molecular and Cellular Biology</i> , 2022, 42, MCB0048321.	1.1	1
2	Distinct sequence features underlie microdeletions and gross deletions in the human genome. <i>Human Mutation</i> , 2022, 43, 328-346.	1.1	3
3	Robust Computational Approaches to Defining Insights on the Interface of with Replication and Transcription in Cancer. <i>Methods in Molecular Biology</i> , 2022, 2444, 1-13.	0.4	1
4	Monitoring Nuclease Activity by X-Ray Scattering Interferometry Using Gold Nanoparticle-Conjugated DNA. <i>Methods in Molecular Biology</i> , 2022, 2444, 183-205.	0.4	5
5	Universally Accessible Structural Data on Macromolecular Conformation, Assembly, and Dynamics by Small Angle X-Ray for Insights. <i>Methods in Molecular Biology</i> , 2022, 2444, 43-68.	0.4	1
6	Cleavage-defective Topoisomerase I mutants sharply increase G-quadruplex-associated genomic instability. <i>Microbial Cell</i> , 2022, 9, 52-68.	1.4	3
7	Vitamin E Enhances Cancer Immunotherapy by Reinvigorating Dendritic Cells via Targeting Checkpoint SHP1. <i>Cancer Discovery</i> , 2022, 12, 1742-1759.	7.7	35
8	Uncovering DNA-PKcs ancient phylogeny, unique sequence motifs and insights for human disease. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 87-108.	1.4	45
9	Heparin-mediated dimerization of follistatin. <i>Experimental Biology and Medicine</i> , 2021, 246, 467-482.	1.1	3
10	Visualizing functional dynamicity in the DNA-dependent protein kinase holoenzyme DNA-PK complex by integrating SAXS with cryo-EM. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 74-86.	1.4	13
11	Fragment- and structure-based drug discovery for developing therapeutic agents targeting the DNA Damage Response. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 130-142.	1.4	21
12	A collagen glucosyltransferase drives lung adenocarcinoma progression in mice. <i>Communications Biology</i> , 2021, 4, 482.	2.0	16
13	A first-in-class polymerase theta inhibitor selectively targets homologous-recombination-deficient tumors. <i>Nature Cancer</i> , 2021, 2, 598-610.	5.7	168
14	X-ray scattering reveals disordered linkers and dynamic interfaces in complexes and mechanisms for <sc>DNA</sc> double-strand break repair impacting cell and cancer biology. <i>Protein Science</i> , 2021, 30, 1735-1756.	3.1	19
15	Autism-Associated Vigilin Depletion Impairs DNA Damage Repair. <i>Molecular and Cellular Biology</i> , 2021, 41, e0008221.	1.1	8
16	EXO5-DNA structure and BLM interactions direct DNA resection critical for ATR-dependent replication restart. <i>Molecular Cell</i> , 2021, 81, 2989-3006.e9.	4.5	26
17	GRB2 enforces homology-directed repair initiation by MRE11. <i>Science Advances</i> , 2021, 7, .	4.7	21
18	Targeting SARS-CoV-2 Nsp3 macrodomain structure with insights from human poly(ADP-ribose) glycohydrolase (PARG) structures with inhibitors. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 171-186.	1.4	39

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19	The renaissance in biophysics and molecular biology enabled by the interface of DNA repair and replication with cancer. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 1-4.	1.4	0
20	An effective human uracil-DNA glycosylase inhibitor targets the open pre-catalytic active site conformation. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 143-159.	1.4	14
21	Direct interaction of DNA repair protein tyrosyl DNA phosphodiesterase 1 and the DNA ligase III catalytic domain is regulated by phosphorylation of its flexible N-terminus. <i>Journal of Biological Chemistry</i> , 2021, 297, 100921.	1.6	6
22	Target highlights in <sc>CASP14</sc>: Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1647-1672.	1.5	27
23	Heritable pattern of oxidized DNA base repair coincides with pre-targeting of repair complexes to open chromatin. <i>Nucleic Acids Research</i> , 2021, 49, 221-243.	6.5	29
24	An atypical BRCTâ€“BRCT interaction with the XRCC1 scaffold protein compacts human DNA Ligase III± within a flexible DNA repair complex. <i>Nucleic Acids Research</i> , 2021, 49, 306-321.	6.5	21
25	Aberrant RNA methylation triggers recruitment of an alkylation repair complex. <i>Molecular Cell</i> , 2021, 81, 4228-4242.e8.	4.5	18
26	An efficient chemical screening method for structure-based inhibitors to nucleic acid enzymes targeting the DNA repair-replication interface and SARS CoV-2. <i>Methods in Enzymology</i> , 2021, 661, 407-431.	0.4	2
27	Translesion polymerase eta both facilitates DNA replication and promotes increased human genetic variation at common fragile sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	20
28	An efficient chemical screening method for structure-based inhibitors to nucleic acid enzymes targeting the DNA repair-replication interface and SARS CoV-2. <i>Methods in Enzymology</i> , 2021, 661, 407-431.	0.4	4
29	Decoding Cancer Variants of Unknown Significance for Helicaseâ€“Nucleaseâ€“RPA Complexes Orchestrating DNA Repair During Transcription and Replication. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 791792.	1.6	4
30	Function and Molecular Mechanism of the DNA Damage Response in Immunity and Cancer Immunotherapy. <i>Frontiers in Immunology</i> , 2021, 12, 797880.	2.2	35
31	The structure of the periplasmic FlaGâ€“FlaF complex and its essential role for archaeal swimming motility. <i>Nature Microbiology</i> , 2020, 5, 216-225.	5.9	32
32	Mechanism of efficient double-strand break repair by a long non-coding RNA. <i>Nucleic Acids Research</i> , 2020, 48, 10953-10972.	6.5	43
33	Envisioning how the prototypic molecular machine TFIIF functions in transcription initiation and DNA repair. <i>DNA Repair</i> , 2020, 96, 102972.	1.3	36
34	Histone Acetyltransferase MOF Orchestrates Outcomes at the Crossroad of Oncogenesis, DNA Damage Response, Proliferation, and Stem Cell Development. <i>Molecular and Cellular Biology</i> , 2020, 40, .	1.1	37
35	XRCC1 promotes replication restart, nascent fork degradation and mutagenic DNA repair in BRCA2-deficient cells. <i>NAR Cancer</i> , 2020, 2, zcaa013.	1.6	36
36	PD-L1-mediated gasdermin C expression switches apoptosis to pyroptosis in cancer cells and facilitates tumour necrosis. <i>Nature Cell Biology</i> , 2020, 22, 1264-1275.	4.6	508

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37	Human XPG nuclease structure, assembly, and activities with insights for neurodegeneration and cancer from pathogenic mutations. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14127-14138.	3.3	37
38	Replication-Based Rearrangements Are a Common Mechanism for SNCA Duplication in Parkinson's Disease. Movement Disorders, 2020, 35, 868-876.	2.2	9
39	Small angle X-ray scattering-assisted protein structure prediction in CASP13 and emergence of solution structure differences. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1298-1314.	1.5	24
40	Flexible Tethering of ASPP Proteins Facilitates PP-1c Catalysis. Structure, 2019, 27, 1485-1496.e4.	1.6	23
41	DNA damage response mechanisms and structures fundamental to cancer research progress. Progress in Biophysics and Molecular Biology, 2019, 147, 1-3.	1.4	0
42	SLX4IP acts with SLX4 and XPF-ERCC1 to promote interstrand crosslink repair. Nucleic Acids Research, 2019, 47, 10181-10201.	6.5	26
43	Evolving SAXS versatility: solution X-ray scattering for macromolecular architecture, functional landscapes, and integrative structural biology. Current Opinion in Structural Biology, 2019, 58, 197-213.	2.6	131
44	Transcription preinitiation complex structure and dynamics provide insight into genetic diseases. Nature Structural and Molecular Biology, 2019, 26, 397-406.	3.6	60
45	Cancer mutational burden is shaped by G4 DNA, replication stress and mitochondrial dysfunction. Progress in Biophysics and Molecular Biology, 2019, 147, 47-61.	1.4	35
46	Formylglycine-generating enzyme binds substrate directly at a mononuclear Cu(I) center to initiate O ₂ activation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5370-5375.	3.3	38
47	Selective small molecule PARC inhibitor causes replication fork stalling and cancer cell death. Nature Communications, 2019, 10, 5654.	5.8	75
48	Charge Transport Communication through DNA by Protein Fe-S Clusters: How Far Is Not Too Far?. ACS Central Science, 2019, 5, 7-9.	5.3	2
49	RNA Modifications: Reversal Mechanisms and Cancer. Biochemistry, 2019, 58, 312-329.	1.2	41
50	Pro-metastatic collagen lysyl hydroxylase dimer assemblies stabilized by Fe ²⁺ -binding. Nature Communications, 2018, 9, 512.	5.8	34
51	Small angle X-ray scattering and cross-linking for data assisted protein structure prediction in CASP 12 with prospects for improved accuracy. Proteins: Structure, Function and Bioinformatics, 2018, 86, 202-214.	1.5	23
52	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.	5.0	303
53	Structural Control of Nonnative Ligand Binding in Engineered Mutants of Phosphoenolpyruvate Carboxykinase. Biochemistry, 2018, 57, 6688-6700.	1.2	5
54	Dissection of DNA double-strand-break repair using novel single-molecule forceps. Nature Structural and Molecular Biology, 2018, 25, 482-487.	3.6	79

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55	Robust Production, Crystallization, Structure Determination, and Analysis of [Fe-S] Proteins: Uncovering Control of Electron Shuttling and Gating in the Respiratory Metabolism of Molybdopterin Guanine Dinucleotide Enzymes. <i>Methods in Enzymology</i> , 2018, 599, 157-196.	0.4	11
56	Targeting Allostery with Avatars to Design Inhibitors Assessed by Cell Activity: Dissecting MRE11 Endo- and Exonuclease Activities. <i>Methods in Enzymology</i> , 2018, 601, 205-241.	0.4	20
57	Microhomology-mediated end joining is activated in irradiated human cells due to phosphorylation-dependent formation of the XRCC1 repair complex. <i>Nucleic Acids Research</i> , 2017, 45, gkw1262.	6.5	62
58	Structural and functional characterization of the PNKP-XRCC4-LigIV DNA repair complex. <i>Nucleic Acids Research</i> , 2017, 45, 6238-6251.	6.5	39
59	Hybrid Methods Reveal Multiple Flexibly Linked DNA Polymerases within the Bacteriophage T7 Replisome. <i>Structure</i> , 2017, 25, 157-166.	1.6	17
60	What Combined Measurements From Structures and Imaging Tell Us About DNA Damage Responses. <i>Methods in Enzymology</i> , 2017, 592, 417-455.	0.4	10
61	Uncovering the secrets of protein interactions with the DNA enforcing genomic stability. <i>Progress in Biophysics and Molecular Biology</i> , 2017, 127, 89-92.	1.4	0
62	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
63	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
64	Charging of Proteins in Native Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 332-340.	1.2	27
65	Coiled coils unspring protein origami. <i>Nature Biotechnology</i> , 2017, 35, 1044-1045.	9.4	2
66	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
67	High Resolution Distance Distributions Determined by X-Ray and Neutron Scattering. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1009, 167-181.	0.8	5
68	Single-molecule FRET unveils induced-fit mechanism for substrate selectivity in flap endonuclease 1. <i>ELife</i> , 2017, 6, .	2.8	35
69	The nucleotide-dependent interaction of FlaH and FlaI is essential for assembly and function of the archaeal motor. <i>Molecular Microbiology</i> , 2016, 99, 674-685.	1.2	47
70	Designing and defining dynamic protein cage nanoassemblies in solution. <i>Science Advances</i> , 2016, 2, e1501855.	4.7	37
71	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
72	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

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73	An Intrinsically Disordered APLF Links Ku, DNA-PKcs, and XRCC4-DNA Ligase IV in an Extended Flexible Non-homologous End Joining Complex. <i>Journal of Biological Chemistry</i> , 2016, 291, 26987-27006.	1.6	61
74	HU multimerization shift controls nucleoid compaction. <i>Science Advances</i> , 2016, 2, e1600650.	4.7	144
75	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
76	Defining NADH-Driven Allostery Regulating Apoptosis-Inducing Factor. <i>Structure</i> , 2016, 24, 2067-2079.	1.6	39
77	The ATPase Motor Turns for Type IV Pilus Assembly. <i>Structure</i> , 2016, 24, 1857-1859.	1.6	10
78	Noncoding RNA joins Ku and DNA-PKcs for DNA-break resistance in breast cancer. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 509-510.	3.6	12
79	RNF8 E3 Ubiquitin Ligase Stimulates Ubc13 E2 Conjugating Activity That Is Essential for DNA Double Strand Break Signaling and BRCA1 Tumor Suppressor Recruitment. <i>Journal of Biological Chemistry</i> , 2016, 291, 9396-9410.	1.6	26
80	Perchlorate Reductase Is Distinguished by Active Site Aromatic Gate Residues. <i>Journal of Biological Chemistry</i> , 2016, 291, 9190-9202.	1.6	71
81	Cell-free expression of functional receptor tyrosine kinases. <i>Scientific Reports</i> , 2015, 5, 12896.	1.6	23
82	Modeling Macromolecular Motions by X-Ray-Scattering-Constrained Molecular Dynamics. <i>Biophysical Journal</i> , 2015, 108, 2421-2423.	0.2	5
83	FlaF Is a β -Sandwich Protein that Anchors the Archaeum in the Archaeal Cell Envelope by Binding the S-Layer Protein. <i>Structure</i> , 2015, 23, 863-872.	1.6	60
84	Structurally Distinct Ubiquitin- and Sumo-Modified PCNA: Implications for Their Distinct Roles in the DNA Damage Response. <i>Structure</i> , 2015, 23, 724-733.	1.6	39
85	Exploring the repeat protein universe through computational protein design. <i>Nature</i> , 2015, 528, 580-584.	13.7	227
86	Human DNA ligase III bridges two DNA ends to promote specific intermolecular DNA end joining. <i>Nucleic Acids Research</i> , 2015, 43, 7021-7031.	6.5	25
87	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
88	Emerging critical roles of Fe-S clusters in DNA replication and repair. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2015, 1853, 1253-1271.	1.9	187
89	The Salmonella Type III Secretion System Virulence Effector Forms a New Hexameric Chaperone Assembly for Export of Effector/Chaperone Complexes. <i>Journal of Bacteriology</i> , 2015, 197, 672-675.	1.0	11
90	Bending Forks and Wagging Dogsâ€™ tails about the DNA 3' Tail. <i>Molecular Cell</i> , 2015, 58, 972-973.	4.5	1

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91	Dynamic structures in DNA damage responses & cancer. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 117, 129-133.	1.4	3
92	DNA repair without flipping out. <i>Nature</i> , 2015, 527, 168-169.	13.7	3
93	Structural, Functional, and Immunogenic Insights on Cu,Zn Superoxide Dismutase Pathogenic Virulence Factors from <i>Neisseria meningitidis</i> and <i>Brucella abortus</i> . <i>Journal of Bacteriology</i> , 2015, 197, 3834-3847.	1.0	24
94	An AAA+ ATPase Clamshell Targets Transposition. <i>Cell</i> , 2015, 162, 701-703.	13.5	1
95	Archaeal Genome Guardians Give Insights into Eukaryotic DNA Replication and Damage Response Proteins. <i>Archaea</i> , 2014, 2014, 1-24.	2.3	15
96	A structure-specific nucleic acid-binding domain conserved among DNA repair proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7618-7623.	3.3	34
97	The Rad50 hook domain regulates DNA damage signaling and tumorigenesis. <i>Genes and Development</i> , 2014, 28, 451-462.	2.7	43
98	Methods for Using New Conceptual Tools and Parameters to Assess RNA Structure by Small-Angle X-Ray Scattering. <i>Methods in Enzymology</i> , 2014, 549, 235-263.	0.4	31
99	The Râ€factor gap in macromolecular crystallography: an untapped potential for insights on accurate structures. <i>FEBS Journal</i> , 2014, 281, 4046-4060.	2.2	72
100	Mechanistic insights into the role of Hop2-Mnd1 in meiotic homologous DNA pairing. <i>Nucleic Acids Research</i> , 2014, 42, 906-917.	6.5	52
101	ModBase, a database of annotated comparative protein structure models and associated resources. <i>Nucleic Acids Research</i> , 2014, 42, D336-D346.	6.5	275
102	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
103	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
104	DNA Double-Strand Break Repair Pathway Choice Is Directed by Distinct MRE11 Nuclease Activities. <i>Molecular Cell</i> , 2014, 53, 7-18.	4.5	466
105	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
106	ATP-driven Rad50 conformations regulate DNA tethering, end resection, and ATM checkpoint signaling. <i>EMBO Journal</i> , 2014, 33, 482-500.	3.5	129
107	Aggregation propensities of superoxide dismutase G93 hotspot mutants mirror ALS clinical phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4568-76.	3.3	64
108	Intact Functional Fourteen-subunit Respiratory Membrane-bound [NiFe]-Hydrogenase Complex of the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 19364-19372.	1.6	37

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109	How substrate specificity is imposed on a histone demethylase—lessons from KDM2A. <i>Genes and Development</i> , 2014, 28, 1735-1738.	2.7	11
110	Interfacial Residues Promote an Optimal Alignment of the Catalytic Center in Human Soluble Guanylate Cyclase: Heterodimerization Is Required but Not Sufficient for Activity. <i>Biochemistry</i> , 2014, 53, 2153-2165.	1.2	39
111	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
112	<scp>RNF</scp> 4 interacts with both <scp>SUMO</scp> and nucleosomes to promote the <scp>DNA</scp> damage response. <i>EMBO Reports</i> , 2014, 15, 601-608.	2.0	45
113	Accurate SAXS Profile Computation and its Assessment by Contrast Variation Experiments. <i>Biophysical Journal</i> , 2013, 105, 962-974.	0.2	489
114	Probing DNA by 2-OG-Dependent Dioxygenase. <i>Cell</i> , 2013, 155, 1448-1450.	13.5	7
115	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
116	Sculpting of DNA at Abasic Sites by DNA Glycosylase Homolog Mag2. <i>Structure</i> , 2013, 21, 154-166.	1.6	8
117	The Disordered C-Terminal Domain of Human DNA Glycosylase NEIL1 Contributes to Its Stability via Intramolecular Interactions. <i>Journal of Molecular Biology</i> , 2013, 425, 2359-2371.	2.0	41
118	Insights into Flh1 Functions in Archaeal Motor Assembly and Motility from Structures, Conformations, and Genetics. <i>Molecular Cell</i> , 2013, 49, 1069-1082.	4.5	94
119	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
120	Accurate assessment of mass, models and resolution by small-angle scattering. <i>Nature</i> , 2013, 496, 477-481.	13.7	670
121	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
122	Developing advanced X-ray scattering methods combined with crystallography and computation. <i>Methods</i> , 2013, 59, 363-371.	1.9	22
123	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
124	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
125	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
126	Comprehensive macromolecular conformations mapped by quantitative SAXS analyses. <i>Nature Methods</i> , 2013, 10, 453-454.	9.0	112

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127	A Mutation in the FHA Domain of <i>Coprinus cinereus</i> Nbs1 Leads to Spo11-Independent Meiotic Recombination and Chromosome Segregation. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1927-1943.	0.8	27
128	DNA conformations in mismatch repair probed in solution by X-ray scattering from gold nanocrystals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17308-17313.	3.3	53
129	Flap endonucleases pass 5'-flaps through a flexible arch using a disorder-thread-order mechanism to confer specificity for free 5'-ends. <i>Nucleic Acids Research</i> , 2012, 40, 4507-4519.	6.5	42
130	Mre11 ATLD17/18 mutation retains Tel1/ATM activity but blocks DNA double-strand break repair. <i>Nucleic Acids Research</i> , 2012, 40, 11435-11449.	6.5	20
131	Structure of mammalian poly(ADP-ribose) glycohydrolase reveals a flexible tyrosine clasp as a substrate-binding element. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 653-656.	3.6	60
132	Anacardic Acid Inhibits the Catalytic Activity of Matrix Metalloproteinase-2 and Matrix Metalloproteinase-9. <i>Molecular Pharmacology</i> , 2012, 82, 614-622.	1.0	53
133	Combining H/D exchange mass spectroscopy and computational docking reveals extended DNA-binding surface on uracil-DNA glycosylase. <i>Nucleic Acids Research</i> , 2012, 40, 6070-6081.	6.5	28
134	MRE11 facilitates the removal of human topoisomerase II complexes from genomic DNA. <i>Biology Open</i> , 2012, 1, 863-873.	0.6	58
135	Repair complexes of FEN1 endonuclease, DNA, and Rad9-Hus1-Rad1 are distinguished from their PCNA counterparts by functionally important stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8528-8533.	3.3	45
136	Alkyltransferase-like protein (At1) distinguishes alkylated guanines for DNA repair using cation- π interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18755-18760.	3.3	19
137	The Wonders of Flap Endonucleases: Structure, Function, Mechanism and Regulation. <i>Sub-Cellular Biochemistry</i> , 2012, 62, 301-326.	1.0	46
138	Structure of an Essential Type IV Pilus Biogenesis Protein Provides Insights into Pilus and Type II Secretion Systems. <i>Journal of Molecular Biology</i> , 2012, 419, 110-124.	2.0	29
139	At1 Regulates Choice between Global Genome and Transcription-Coupled Repair of O6-Alkylguanines. <i>Molecular Cell</i> , 2012, 47, 50-60.	4.5	31
140	Structural basis for recognition of 5'-phosphotyrosine adducts by Tdp2. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1372-1377.	3.6	53
141	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
142	Kinetic and Stoichiometric Characterisation of Streptavidin-Binding Aptamers. <i>ChemBioChem</i> , 2012, 13, 829-836.	1.3	24
143	Structural Tuning of the Fluorescent Protein iLOV for Improved Photostability. <i>Journal of Biological Chemistry</i> , 2012, 287, 22295-22304.	1.6	130
144	Metals in biology: defining metalloproteomes. <i>Current Opinion in Biotechnology</i> , 2012, 23, 89-95.	3.3	82

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145	Double strand bindingâ€“single strand incision mechanism for human flap endonuclease: Implications for the superfamily. <i>Mechanisms of Ageing and Development</i> , 2012, 133, 195-202.	2.2	17
146	Unpairing and gating: sequence-independent substrate recognition by FEN superfamily nucleases. <i>Trends in Biochemical Sciences</i> , 2012, 37, 74-84.	3.7	60
147	ATP-Stimulated, DNA-Mediated Redox Signaling by XPD, a DNA Repair and Transcription Helicase. <i>Journal of the American Chemical Society</i> , 2011, 133, 16378-16381.	6.6	55
148	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
149	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
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