Susan E Tsutakawa

List of Publications by Year
in descending order

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32 papers	2,528 citations	361413 20 h-index	414414 32 g-index
40 all docs	40 docs citations	40 times ranked	3773 citing authors

#	Article	IF	Citations
1	Universally Accessible Structural Data on Macromolecular Conformation, Assembly, and Dynamics by Small Angle X-Ray for Insights. Methods in Molecular Biology, 2022, 2444, 43-68.	0.9	1
2	Uncovering DNA-PKcs ancient phylogeny, unique sequence motifs and insights for human disease. Progress in Biophysics and Molecular Biology, 2021, 163, 87-108.	2.9	45
3	Breaking the Rules: Protein Sculpting in NEIL2 Regulation. Structure, 2021, 29, 1-2.	3.3	9
4	Efficient production of oxidized terpenoids via engineering fusion proteins of terpene synthase and cytochrome P450. Metabolic Engineering, 2021, 64, 41-51.	7.0	33
5	Conformational Dynamics in the Interaction of SARS-CoV-2 Papain-like Protease with Human Interferon-Stimulated Gene 15 Protein. Journal of Physical Chemistry Letters, 2021, 12, 5608-5615.	4.6	14
6	EXO5-DNA structure and BLM interactions direct DNA resection critical for ATR-dependent replication restart. Molecular Cell, 2021, 81, 2989-3006.e9.	9.7	26
7	Transient and stabilized complexes of Nsp7, Nsp8, and Nsp12 in SARS-CoV-2 replication. Biophysical Journal, 2021, 120, 3152-3165.	0.5	39
8	Target highlights in <scp>CASP14</scp>: Analysis of models by structure providers. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1647-1672.	2.6	27
9	The Role of XPB/Ssl2 dsDNA Translocase Processivity in Transcription Start-site Scanning. Journal of Molecular Biology, 2021, 433, 166813.	4.2	8
10	An efficient chemical screening method for structure-based inhibitors to nucleic acid enzymes targeting the DNA repair-replication interface and SARS CoV-2. Methods in Enzymology, 2021, 661, 407-431.	1.0	2
11	An efficient chemical screening method for structure-based inhibitors to nucleic acid enzymes targeting the DNA repair-replication interface and SARS CoV-2. Methods in Enzymology, 2021, 661, 407-431.	1.0	4
12	Decoding Cancer Variants of Unknown Significance for Helicaseâ€“Nucleaseâ€“RPA Complexes Orchestrating DNA Repair During Transcription and Replication. Frontiers in Molecular Biosciences, 2021, 8, 791792.	3.5	4
13	Envisioning how the prototypic molecular machine TFIIH functions in transcription initiation and DNA repair. DNA Repair, 2020, 96, 102972.	2.8	36
14	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.	7.1	37
15	Small angle Xâ€ray scatteringâ€assisted protein structure prediction in CASP13 and emergence of solution structure differences. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1298-1314.	2.6	24
16	Transcription preinitiation complex structure and dynamics provide insight into genetic diseases. Nature Structural and Molecular Biology, 2019, 26, 397-406.	8.2	60
17	Small angle Xâ€ray scattering and crossâ€linking for data assisted protein structure prediction in CASP 12 with prospects for improved accuracy. Proteins: Structure, Function and Bioinformatics, 2018, 86, 202-214.	2.6	23
18	Dissection of DNA double-strand-break repair using novel single-molecule forceps. Nature Structural and Molecular Biology, 2018, 25, 482-487.	8.2	79

#	ARTICLE	IF	CITATIONS
19	Phosphate steering by Flap Endonuclease 1 promotes 5â€²-flap specificity and incision to prevent genome instability. Nature Communications, 2017, 8, 15855.	12.8	81
20	Single-molecule FRET unveils induced-fit mechanism for substrate selectivity in flap endonuclease 1. ELife, 2017, 6, .	6.0	35
21	Mechanism and Regulation of DNA-Protein Crosslink Repair by the DNA-Dependent Metalloprotease SPRTN. Molecular Cell, 2016, 64, 688-703.	9.7	189
22	Structurally Distinct Ubiquitin- and Sumo-Modified PCNA: Implications for Their Distinct Roles in the DNA Damage Response. Structure, 2015, 23, 724-733.	3.3	39
23	Exploring the repeat protein universe through computational protein design. Nature, 2015, 528, 580-584.	27.8	227
24	High-Throughput SAXS for the Characterization of Biomolecules in Solution: A Practical Approach. Methods in Molecular Biology, 2014, 1091, 245-258.	0.9	176
25	A new structural framework for integrating replication protein A into DNA processing machinery. Nucleic Acids Research, 2013, 41, 2313-2327.	14.5	88
26	Flap endonucleases pass 5â€²-flaps through a flexible arch using a disorder-thread-order mechanism to confer specificity for free 5â€²-ends. Nucleic Acids Research, 2012, 40, 4507-4519.	14.5	42
27	Double strand bindingâ€"single strand incision mechanism for human flap endonuclease: Implications for the superfamily. Mechanisms of Ageing and Development, 2012, 133, 195-202.	4.6	17
28	Unpairing and gating: sequence-independent substrate recognition by FEN superfamily nucleases. Trends in Biochemical Sciences, 2012, 37, 74-84.	7.5	60
29	Human Flap Endonuclease Structures, DNA Double-Base Flipping, and a Unified Understanding of the FEN1 Superfamily. Cell, 2011, 145, 198-211.	28.9	238
30	Solution X-ray scattering combined with computational modeling reveals multiple conformations of covalently bound ubiquitin on PCNA. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17672-17677.	7.1	61
31	Robust, high-throughput solution structural analyses by small angle X-ray scattering (SAXS). Nature Methods, 2009, 6, 606-612.	19.0	610
32	Recognition of RNA Polymerase II and Transcription Bubbles by XPG, CSB, and TFIIH: Insights for Transcription-Coupled Repair and Cockayne Syndrome. Molecular Cell, 2005, 20, 187-198.	9.7	194