

# Susan E Tsutakawa

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Robust, high-throughput solution structural analyses by small angle X-ray scattering (SAXS). <i>Nature Methods</i> , 2009, 6, 606-612.	19.0	610
2	Human Flap Endonuclease Structures, DNA Double-Base Flipping, and a Unified Understanding of the FEN1 Superfamily. <i>Cell</i> , 2011, 145, 198-211.	28.9	238
3	Exploring the repeat protein universe through computational protein design. <i>Nature</i> , 2015, 528, 580-584.	27.8	227
4	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
5	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
6	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
7	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
8	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
9	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
10	Solution X-ray scattering combined with computational modeling reveals multiple conformations of covalently bound ubiquitin on PCNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17672-17677.	7.1	61
11	Unpairing and gating: sequence-independent substrate recognition by FEN superfamily nucleases. <i>Trends in Biochemical Sciences</i> , 2012, 37, 74-84.	7.5	60
12	Transcription preinitiation complex structure and dynamics provide insight into genetic diseases. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 397-406.	8.2	60
13	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.	2.9	45
14	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.	14.5	42
15	Structurally Distinct Ubiquitin- and Sumo-Modified PCNA: Implications for Their Distinct Roles in the DNA Damage Response. <i>Structure</i> , 2015, 23, 724-733.	3.3	39
16	Transient and stabilized complexes of Nsp7, Nsp8, and Nsp12 in SARS-CoV-2 replication. <i>Biophysical Journal</i> , 2021, 120, 3152-3165.	0.5	39
17	Human XPG nuclease structure, assembly, and activities with insights for neurodegeneration and cancer from pathogenic mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14127-14138.	7.1	37
18	Envisioning how the prototypic molecular machine TFIIH functions in transcription initiation and DNA repair. <i>DNA Repair</i> , 2020, 96, 102972.	2.8	36

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19	Single-molecule FRET unveils induced-fit mechanism for substrate selectivity in flap endonuclease 1. <i>ELife</i> , 2017, 6, .	6.0	35
20	Efficient production of oxidized terpenoids via engineering fusion proteins of terpene synthase and cytochrome P450. <i>Metabolic Engineering</i> , 2021, 64, 41-51.	7.0	33
21	Target highlights in <scp>CASP14</scp>: Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1647-1672.	2.6	27
22	EXO5-DNA structure and BLM interactions direct DNA resection critical for ATR-dependent replication restart. <i>Molecular Cell</i> , 2021, 81, 2989-3006.e9.	9.7	26
23	Small angle X-ray scattering-assisted protein structure prediction in CASP13 and emergence of solution structure differences. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1298-1314.	2.6	24
24	Small angle X-ray scattering and cross-linking for data assisted protein structure prediction in CASP 12 with prospects for improved accuracy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 202-214.	2.6	23
25	Double strand binding single strand incision mechanism for human flap endonuclease: Implications for the superfamily. <i>Mechanisms of Ageing and Development</i> , 2012, 133, 195-202.	4.6	17
26	Conformational Dynamics in the Interaction of SARS-CoV-2 Papain-like Protease with Human Interferon-Stimulated Gene 15 Protein. <i>Journal of Physical Chemistry Letters</i> , 2021, 12, 5608-5615.	4.6	14
27	Breaking the Rules: Protein Sculpting in NEIL2 Regulation. <i>Structure</i> , 2021, 29, 1-2.	3.3	9
28	The Role of XPB/Ssl2 dsDNA Translocase Processivity in Transcription Start-site Scanning. <i>Journal of Molecular Biology</i> , 2021, 433, 166813.	4.2	8
29	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.	1.0	4
30	Decoding Cancer Variants of Unknown Significance for Helicase Nuclease RPA Complexes Orchestrating DNA Repair During Transcription and Replication. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 791792.	3.5	4
31	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.	1.0	2
32	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.	0.9	1