Hanna S Yuan

List of Publications by Year
in descending order

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92	3,737	126907	144013
papers	citations	33 h-index	57 g-index

94	94	94	5137
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural insights into TDP-43 in nucleic-acid binding and domain interactions. Nucleic Acids Research, 2009, 37, 1799-1808.	14.5	250
2	Stabilization and Enhancement of the Antiapoptotic Activity of Mcl-1 by TCTP. Molecular and Cellular Biology, 2005, 25, 3117-3126.	2.3	209
3	The crystal structure of the DNase domain of colicin E7 in complex with its inhibitor Im7 protein. Structure, 1999, 7, 91-102.	3.3	193
4	Structural basis of non-specific lipid binding in maize lipid-transfer protein complexes revealed by high-resolution X-ray crystallography1 1Edited by D. Rees. Journal of Molecular Biology, 2001, 308, 263-278.	4.2	175
5	Full-length TDP-43 forms toxic amyloid oligomers that are present in frontotemporal lobar dementia-TDP patients. Nature Communications, 2014, 5, 4824.	12.8	153
6	Mitochondrial endonuclease G mediates breakdown of paternal mitochondria upon fertilization. Science, 2016, 353, 394-399.	12.6	148
7	The molecular structure of wild-type and a mutant Fis protein: relationship between mutational changes and recombinational enhancer function or DNA binding.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 9558-9562.	7.1	147
8	The crystal structure of TDP-43 RRM1-DNA complex reveals the specific recognition for UG- and TG-rich nucleic acids. Nucleic Acids Research, 2014, 42, 4712-4722.	14.5	141
9	Structural and functional insights into human Tudor-SN, a key component linking RNA interference and editing. Nucleic Acids Research, 2008, 36, 3579-3589.	14.5	93
10	DNA binding and cleavage by the periplasmic nuclease Vvn: a novel structure with a known active site. EMBO Journal, 2003, 22, 4014-4025.	7.8	92
11	The Truncated C-terminal RNA Recognition Motif of TDP-43 Protein Plays a Key Role in Forming Proteinaceous Aggregates. Journal of Biological Chemistry, 2013, 288, 9049-9057.	3.4	84
12	Crystal structure of Escherichia coli PNPase: Central channel residues are involved in processive RNA degradation. Rna, 2008, 14, 2361-2371.	3.5	79
13	Multi-targeting of functional cysteines in multiple conserved SARS-CoV-2 domains by clinically safe Zn-ejectors. Chemical Science, 2020, 11, 9904-9909.	7.4	73
14	Structural analysis of disease-related TDP-43 D169G mutation: linking enhanced stability and caspase cleavage efficiency to protein accumulation. Scientific Reports, 2016, 6, 21581.	3.3	70
15	Structural studies of the pigeon cytosolic NADP+-dependent malic enzyme. Protein Science, 2009, 11, 332-341.	7.6	69
16	Stable carbocations. 273. [1.1.1.1]- and [2.2.1.1]Pagodane dications: frozen two-electron Woodward-Hoffmann transition-state models. Journal of the American Chemical Society, 1988, 110, 7764-7772.	13.7	65
17	Structural and functional insight into sugar-nonspecific nucleases in host defense. Current Opinion in Structural Biology, 2005, 15, 126-134.	5.7	65
18	Structures of the copper-containing Cu4MgPh6 and [Cu4LiPh6]- clusters: first example of a magnesium-containing transition-metal cluster compound. Journal of the American Chemical Society, 1985, 107, 1682-1684.	13.7	63

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19	DNA Binding and Degradation by the HNH Protein ColE7. Structure, 2004, 12, 205-214.	3.3	58
20	The Crystal Structure of the Nuclease Domain of Colicin E7 Suggests a Mechanism for Binding to Double-stranded DNA by the Hâ€“Nâ€“H Endonucleases. Journal of Molecular Biology, 2002, 324, 227-236.	4.2	54
21	The transactivation region of the Fis protein that controls site-specific DNA inversion contains extended mobile beta -hairpin arms. EMBO Journal, 1997, 16, 6860-6873.	7.8	52
22	The zinc ion in the HNH motif of the endonuclease domain of colicin E7 is not required for DNA binding but is essential for DNA hydrolysis. Nucleic Acids Research, 2002, 30, 1670-1678.	14.5	52
23	The crystal structure of the immunity protein of colicin E7 suggests a possible colicin-interacting surface.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 6437-6442.	7.1	51
24	Crystal Structure of a Natural Circularly Permuted Jellyroll Protein: 1,3-1,4-Î²-d-Glucanase from Fibrobacter succinogenes. Journal of Molecular Biology, 2003, 330, 607-620.	4.2	51
25	Metal ions and phosphate binding in the H-N-H motif: Crystal structures of the nuclease domain of ColE7/Im7 in complex with a phosphate ion and different divalent metal ions. Protein Science, 2009, 11, 2947-2957.	7.6	51
26	Crystal structure of human polynucleotide phosphorylase: insights into its domain function in RNA binding and degradation. Nucleic Acids Research, 2012, 40, 4146-4157.	14.5	50
27	Synergistic Inhibition of SARS-CoV-2 Replication Using Disulfiram/Ebselen and Remdesivir. ACS Pharmacology and Translational Science, 2021, 4, 898-907.	4.9	49
28	An x-ray study of FeH(dmpe)2(BH4): a compound containing a singly-bridged BH4 ligand with a bent Feî—¸Hî—¸B linkage. Inorganica Chimica Acta, 1986, 114, L27-L28.	2.4	45
29	Crystal structural analysis and metal-dependent stability and activity studies of the ColE7 endonuclease domain in complex with DNA/Zn2+ or inhibitor/Ni2+. Protein Science, 2006, 15, 269-280.	7.6	41
30	Structural analysis of the transcriptional activation region on fis: crystal structures of six fis mutants with different activation properties 1 1Edited by R. Huber. Journal of Molecular Biology, 2000, 302, 1139-1151.	4.2	40
31	Identification of an Essential Cleavage Site in ColE7 Required for Import and Killing of Cells. Journal of Biological Chemistry, 2005, 280, 24663-24668.	3.4	40
32	Stable carbocations. Part 267. Pagodane dication, a unique 2.pi.-aromatic cyclobutanoid system. Journal of the American Chemical Society, 1986, 108, 836-838.	13.7	38
33	The Conserved Asparagine in the HNH Motif Serves an Important Structural Role in Metal Finger Endonucleases. Journal of Molecular Biology, 2007, 368, 812-821.	4.2	38
34	Structural insights into CpG-specific DNA methylation by human DNA methyltransferase 3B. Nucleic Acids Research, 2020, 48, 3949-3961.	14.5	38
35	Using an Old Drug to Target a New Drug Site: Application of Disulfiram to Target the Zn-Site in HCV NS5A Protein. Journal of the American Chemical Society, 2016, 138, 3856-3862.	13.7	36
36	Structural basis for sequence-dependent DNA cleavage by nonspecific endonucleases. Nucleic Acids Research, 2006, 35, 584-594.	14.5	35

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37	Conversion of a Î²â€strand to anÎ±â€helix induced by a singleâ€site mutation observed in the crystal structure of fis mutant pro²⁶Ala. Protein Science, 1998, 7, 1875-1883.	7.6	34
38	Structural basis for RNA trimming by RNase T in stable RNA 3â€²-end maturation. Nature Chemical Biology, 2011, 7, 236-243.	8.0	33
39	How an exonuclease decides where to stop in trimming of nucleic acids: crystal structures of RNase Tâ€“product complexes. Nucleic Acids Research, 2012, 40, 8144-8154.	14.5	33
40	Structural insights into RNA unwinding and degradation by RNase R. Nucleic Acids Research, 2017, 45, 12015-12024.	14.5	33
41	Structure and function of TatD exonuclease in DNA repair. Nucleic Acids Research, 2014, 42, 10776-10785.	14.5	31
42	RNA recognition motifs of disease-linked RNA-binding proteins contribute to amyloid formation. Scientific Reports, 2019, 9, 6171.	3.3	30
43	Categorizing Host-Dependent RNA Viruses by Principal Component Analysis of Their Codon Usage Preferences. Journal of Computational Biology, 2009, 16, 1539-1547.	1.6	28
44	The Critical Roles of Polyamines in Regulating ColE7 Production and Restricting ColE7 Uptake of the Colicin-producing Escherichia coli. Journal of Biological Chemistry, 2006, 281, 13083-13091.	3.4	23
45	Crystal Structure of CRN-4: Implications for Domain Function in Apoptotic DNA Degradation. Molecular and Cellular Biology, 2009, 29, 448-457.	2.3	23
46	Structural Insights Into DNA Repair by RNase Tâ€”An Exonuclease Processing 3â€² End of Structured DNA in Repair Pathways. PLoS Biology, 2014, 12, e1001803.	5.6	23
47	Oxidative Stress Impairs Cell Death by Repressing the Nuclease Activity of Mitochondrial Endonuclease G. Cell Reports, 2016, 16, 279-287.	6.4	22
48	Directed Mutagenesis of Specific Active Site Residues onFibrobacter succinogenes1,3â€“1,4-Î²-d-Glucanase Significantly Affects Catalysis and Enzyme Structural Stability. Journal of Biological Chemistry, 2001, 276, 17895-17901.	3.4	21
49	Crystallization and preliminary crystallographic analysis of the Escherichia coli tyrosine aminotransferase. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1474-1477.	2.5	20
50	Identification of Inhibitors for the DEDDh Family of Exonucleases and a Unique Inhibition Mechanism by Crystal Structure Analysis of CRN-4 Bound with 2-Morpholin-4-ylethanesulfonate (MES). Journal of Medicinal Chemistry, 2016, 59, 8019-8029.	6.4	19
51	Structural Insights into a Unique Dimeric DEAD-Box Helicase CshA that Promotes RNA Decay. Structure, 2017, 25, 469-481.	3.3	19
52	Mutagenesis of Trp54 and Trp203 Residues on Fibrobacter Succinogenes 1,3â^'1,4-Î²-d-Glucanase Significantly Affects Catalytic Activities of the Enzyme. Biochemistry, 2002, 41, 8759-8766.	2.5	18
53	Identification of Labile Zn Sites in Drug-Target Proteins. Journal of the American Chemical Society, 2013, 135, 14028-14031.	13.7	18
54	Quantitative phase determination for macromolecular crystals using stereoscopic multibeam imaging. Acta Crystallographica Section A: Foundations and Advances, 1999, 55, 933-938.	0.3	17

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55	A unique exonuclease ExoG cleaves between RNA and DNA in mitochondrial DNA replication. Nucleic Acids Research, 2019, 47, 5405-5419.	14.5	17
56	THE STRUCTURE OF FIS MUTANT PRO61ALA ILLUSTRATES THAT THE KINK WITHIN THE LONG ALPHA-HELIX IS NOT DUE TO THE PRESENCE OF THE PROLINE RESIDUE. , 1994, 269, 28947-54.		17
57	A novel role of ImmE7 in the autoregulatory expression of the ColE7 operon and identification of possible RNase active sites in the crystal structure of dimeric ImmE7. EMBO Journal, 1997, 16, 1444-1454.	7.8	16
58	Determination of the absolute configuration of (+)-neopentyl-1-d alcohol by neutron and x-ray diffraction analysis.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 12872-12876.	7.1	15
59	High-resolution Crystal Structure of a Truncated ColE7 Translocation Domain: Implications for Colicin Transport Across Membranes. Journal of Molecular Biology, 2006, 356, 22-31.	4.2	14
60	Crystal structure of dimeric human PNPase reveals why disease-linked mutants suffer from low RNA import and degradation activities. Nucleic Acids Research, 2018, 46, 8630-8640.	14.5	14
61	Structures, Mechanisms, and Functions of His-Me Finger Nucleases. Trends in Biochemical Sciences, 2020, 45, 935-946.	7.5	14
62	Redesign of High-Affinity Nonspecific Nucleases with Altered Sequence Preference. Journal of the American Chemical Society, 2009, 131, 17345-17353.	13.7	13
63	Structural and biochemical characterization of CRN-5 and Rrp46: An exosome component participating in apoptotic DNA degradation. Rna, 2010, 16, 1748-1759.	3.5	13
64	Tudor staphylococcal nuclease is a structure-specific ribonuclease that degrades RNA at unstructured regions during microRNA decay. Rna, 2018, 24, 739-748.	3.5	13
65	Structural insights into nanoRNA degradation by human Rexo2. Rna, 2019, 25, 737-746.	3.5	13
66	Involvement of colicin in the limited protection of the colicin producing cells against bacteriophage. Biochemical and Biophysical Research Communications, 2004, 318, 81-87.	2.1	12
67	Dynamic Indoor Localization Based on Active RFID for Healthcare Applications: A Shape Constraint Approach. , 2009, , .		12
68	Crystal structure of endonuclease G in complex with DNA reveals how it nonspecifically degrades DNA as a homodimer. Nucleic Acids Research, 2016, 44, gkw931.	14.5	12
69	<scp>Frontotemporal dementia</scp>â€linked <scp>P112H</scp> mutation of <scp>TDP</scp>â€43 induces protein structural change and impairs its <scp>RNA</scp> binding function. Protein Science, 2021, 30, 350-365.	7.6	12
70	Practicability Study on the Improvement of the Indoor Location Tracking Accuracy with Active RFID. , 2009, , .		11
71	Structural Insights into Apoptotic DNA Degradation by CED-3 Protease Suppressor-6 (CPS-6) from Caenorhabditis elegans. Journal of Biological Chemistry, 2012, 287, 7110-7120.	3.4	11
72	Aromatic residues in RNase T stack with nucleobases to guide the sequence-specific recognition and cleavage of nucleic acids. Protein Science, 2015, 24, 1934-1941.	7.6	10

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73	Determination of the absolute configuration of (-)-(2R)-succinic-2-d acid by neutron diffraction study: unambiguous proof of the absolute stereochemistry of the NAD+/NADH interconversion.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 2889-2893.	7.1	8
74	Expression, crystallization and preliminary X-ray diffraction studies ofN-carbamyl-D-amino-acid amidohydrolase fromAgrobacterium radiobacter. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 694-695.	2.5	7
75	Hierarchical Order of Critical Residues on the Immunity-Determining Region of the Im7 Protein Which Confer Specific Immunity to Its Cognate Colicin. Biochemical and Biophysical Research Communications, 1999, 264, 69-75.	2.1	7
76	Accurate Location Tracking Based on Active RFID for Health and Safety Monitoring. , 2009, , .		7
77	Structural and catalytic roles of residues located in Î²13 strand and the following Î²-turn loop in Fibrobacter succinogenes 1,3-1,4-Î²-d-glucanase. Biochimica Et Biophysica Acta - General Subjects, 2009, 1790, 231-239.	2.4	5
78	Dimeric assembly of human Suv3 helicase promotes its <scp>RNA</scp> unwinding function in mitochondrial <scp>RNA</scp> degradosome for <scp>RNA</scp> decay. Protein Science, 2022, 31, e4312.	7.6	5
79	Characterization of the specific cleavage of ceiE7-mRNA of the bactericidal ColE7 operon. Biochemical and Biophysical Research Communications, 2002, 299, 613-620.	2.1	4
80	Crystallization and preliminary X-ray crystallographic analysis of ImmE7 protein of colicin E7. Proteins: Structure, Function and Bioinformatics, 1995, 23, 588-590.	2.6	3
81	Inhibition of IS2transposition by factor for inversion stimulation. FEMS Microbiology Letters, 2007, 275, 98-105.	1.8	3
82	Recombination in the Nonstructural Gene Region in Type 2 Dengue Viruses. Intervirology, 2012, 55, 225-230.	2.8	3
83	Crystallization and preliminary X-ray diffraction analysis of malic enzyme from pigeon liver. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1930-1932.	2.5	2
84	Crystallization and preliminary X-ray diffraction analysis of the 1,3-1,4-Î²-D-glucanase fromFibrobacter succinogenes. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1303-1306.	2.5	2
85	Automatic noise removal and effect of NEX setting on magnetic resonance images. , 2011, , .		2
86	Binding Proteins | RNA-Binding Proteins in Bacterial and Mitochondrial RNA Decay. , 2021, , 517-526.		1
87	Efficient Strategy to Design Protease Inhibitors: Application to Enterovirus 71 2A Protease. ACS Bio & Med Chem Au, 2022, 2, 437-449.	3.7	1
88	S2c2-4 Nonspecific nucleases in cell defense and cell death(S2-c2: "Structural biology reveals) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 147 Butsuri, 2006, 46, S128.	0.1	0
89	Distinguish Dengue Virus Serotypes via Codon Usage Patterns. , 2007, , .		0
90	Fis-protein induces rod-like DNA bending. Chemical Physics Letters, 2010, 500, 318-322.	2.6	0

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91	Structural insights into RNase T in RNA maturation and DNA repair. FASEB Journal, 2013, 27, 988.1.	0.5	0
92	Structural insights into mitochondrial EndoG in response to oxidative stress. FASEB Journal, 2018, 32, lb69.	0.5	0