

Hanna S Yuan

List of Publications by Year in descending order

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126907

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docs citations

94
times ranked

5137
citing authors

#	ARTICLE	IF	CITATIONS
1	Efficient Strategy to Design Protease Inhibitors: Application to Enterovirus 71 2A Protease. ACS Bio & Med Chem Au, 2022, 2, 437-449.	3.7	1
2	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
3	<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
4	Binding Proteins RNA-Binding Proteins in Bacterial and Mitochondrial RNA Decay. , 2021, , 517-526.		1
5	Synergistic Inhibition of SARS-CoV-2 Replication Using Disulfiram/Ebselen and Remdesivir. ACS Pharmacology and Translational Science, 2021, 4, 898-907.	4.9	49
6	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
7	Structures, Mechanisms, and Functions of His-Me Finger Nucleases. Trends in Biochemical Sciences, 2020, 45, 935-946.	7.5	14
8	Structural insights into CpG-specific DNA methylation by human DNA methyltransferase 3B. Nucleic Acids Research, 2020, 48, 3949-3961.	14.5	38
9	A unique exonuclease ExoG cleaves between RNA and DNA in mitochondrial DNA replication. Nucleic Acids Research, 2019, 47, 5405-5419.	14.5	17
10	Structural insights into nanoRNA degradation by human Rexo2. Rna, 2019, 25, 737-746.	3.5	13
11	RNA recognition motifs of disease-linked RNA-binding proteins contribute to amyloid formation. Scientific Reports, 2019, 9, 6171.	3.3	30
12	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
13	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
14	Structural insights into mitochondrial EndoG in response to oxidative stress. FASEB Journal, 2018, 32, lb69.	0.5	0
15	Structural Insights into a Unique Dimeric DEAD-Box Helicase CshA that Promotes RNA Decay. Structure, 2017, 25, 469-481.	3.3	19
16	Structural insights into RNA unwinding and degradation by RNase R. Nucleic Acids Research, 2017, 45, 12015-12024.	14.5	33
17	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
18	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

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19	Crystal structure of endonuclease G in complex with DNA reveals how it nonspecifically degrades DNA as a homodimer. <i>Nucleic Acids Research</i> , 2016, 44, gkw931.	14.5	12
20	Structural analysis of disease-related TDP-43 D169G mutation: linking enhanced stability and caspase cleavage efficiency to protein accumulation. <i>Scientific Reports</i> , 2016, 6, 21581.	3.3	70
21	Mitochondrial endonuclease G mediates breakdown of paternal mitochondria upon fertilization. <i>Science</i> , 2016, 353, 394-399.	12.6	148
22	Oxidative Stress Impairs Cell Death by Repressing the Nuclease Activity of Mitochondrial Endonuclease G. <i>Cell Reports</i> , 2016, 16, 279-287.	6.4	22
23	Aromatic residues in RNase T stack with nucleobases to guide the sequence-specific recognition and cleavage of nucleic acids. <i>Protein Science</i> , 2015, 24, 1934-1941.	7.6	10
24	The crystal structure of TDP-43 RRM1-DNA complex reveals the specific recognition for UG- and TG-rich nucleic acids. <i>Nucleic Acids Research</i> , 2014, 42, 4712-4722.	14.5	141
25	Structural Insights Into DNA Repair by RNase Tâ€™ An Exonuclease Processing 3â€™ End of Structured DNA in Repair Pathways. <i>PLoS Biology</i> , 2014, 12, e1001803.	5.6	23
26	Structure and function of TatD exonuclease in DNA repair. <i>Nucleic Acids Research</i> , 2014, 42, 10776-10785.	14.5	31
27	Full-length TDP-43 forms toxic amyloid oligomers that are present in frontotemporal lobar dementia-TDP patients. <i>Nature Communications</i> , 2014, 5, 4824.	12.8	153
28	Identification of Labile Zn Sites in Drug-Target Proteins. <i>Journal of the American Chemical Society</i> , 2013, 135, 14028-14031.	13.7	18
29	The Truncated C-terminal RNA Recognition Motif of TDP-43 Protein Plays a Key Role in Forming Proteinaceous Aggregates. <i>Journal of Biological Chemistry</i> , 2013, 288, 9049-9057.	3.4	84
30	Structural insights into RNase T in RNA maturation and DNA repair. <i>FASEB Journal</i> , 2013, 27, 988.1.	0.5	0
31	Structural Insights into Apoptotic DNA Degradation by CED-3 Protease Suppressor-6 (CPS-6) from <i>Caenorhabditis elegans</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 7110-7120.	3.4	11
32	Crystal structure of human polynucleotide phosphorylase: insights into its domain function in RNA binding and degradation. <i>Nucleic Acids Research</i> , 2012, 40, 4146-4157.	14.5	50
33	Recombination in the Nonstructural Gene Region in Type 2 Dengue Viruses. <i>Intervirology</i> , 2012, 55, 225-230.	2.8	3
34	How an exonuclease decides where to stop in trimming of nucleic acids: crystal structures of RNase Tâ€™ product complexes. <i>Nucleic Acids Research</i> , 2012, 40, 8144-8154.	14.5	33
35	Structural basis for RNA trimming by RNase T in stable RNA 3â€™-end maturation. <i>Nature Chemical Biology</i> , 2011, 7, 236-243.	8.0	33
36	Automatic noise removal and effect of NEX setting on magnetic resonance images. , 2011, , .		2

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37	Fis-protein induces rod-like DNA bending. <i>Chemical Physics Letters</i> , 2010, 500, 318-322.	2.6	0
38	Structural and biochemical characterization of CRN-5 and Rrp46: An exosome component participating in apoptotic DNA degradation. <i>Rna</i> , 2010, 16, 1748-1759.	3.5	13
39	Categorizing Host-Dependent RNA Viruses by Principal Component Analysis of Their Codon Usage Preferences. <i>Journal of Computational Biology</i> , 2009, 16, 1539-1547.	1.6	28
40	Crystal Structure of CRN-4: Implications for Domain Function in Apoptotic DNA Degradation. <i>Molecular and Cellular Biology</i> , 2009, 29, 448-457.	2.3	23
41	Structural and catalytic roles of residues located in $\hat{1}^{213}$ strand and the following $\hat{1}^2$ -turn loop in <i>Fibrobacter succinogenes</i> 1,3-1,4- $\hat{1}^2$ -d-glucanase. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2009, 1790, 231-239.	2.4	5
42	Practicability Study on the Improvement of the Indoor Location Tracking Accuracy with Active RFID. , 2009, , .		11
43	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. <i>Protein Science</i> , 2009, 11, 2947-2957.	7.6	51
44	Structural studies of the pigeon cytosolic NADP ⁺ -dependent malic enzyme. <i>Protein Science</i> , 2009, 11, 332-341.	7.6	69
45	Redesign of High-Affinity Nonspecific Nucleases with Altered Sequence Preference. <i>Journal of the American Chemical Society</i> , 2009, 131, 17345-17353.	13.7	13
46	Dynamic Indoor Localization Based on Active RFID for Healthcare Applications: A Shape Constraint Approach. , 2009, , .		12
47	Structural insights into TDP-43 in nucleic-acid binding and domain interactions. <i>Nucleic Acids Research</i> , 2009, 37, 1799-1808.	14.5	250
48	Accurate Location Tracking Based on Active RFID for Health and Safety Monitoring. , 2009, , .		7
49	Crystal structure of <i>Escherichia coli</i> PNPase: Central channel residues are involved in processive RNA degradation. <i>Rna</i> , 2008, 14, 2361-2371.	3.5	79
50	Structural and functional insights into human Tudor-SN, a key component linking RNA interference and editing. <i>Nucleic Acids Research</i> , 2008, 36, 3579-3589.	14.5	93
51	Distinguish Dengue Virus Serotypes via Codon Usage Patterns. , 2007, , .		0
52	The Conserved Asparagine in the HNH Motif Serves an Important Structural Role in Metal Finger Endonucleases. <i>Journal of Molecular Biology</i> , 2007, 368, 812-821.	4.2	38
53	Inhibition of IS2 transposition by factor for inversion stimulation. <i>FEMS Microbiology Letters</i> , 2007, 275, 98-105.	1.8	3
54	High-resolution Crystal Structure of a Truncated Cole7 Translocation Domain: Implications for Colicin Transport Across Membranes. <i>Journal of Molecular Biology</i> , 2006, 356, 22-31.	4.2	14

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55	S2c2-4 Nonspecific nucleases in cell defense and cell death(S2-c2: "Structural biology reveals) Tj ETQq1 1 0.784314 rgBT /Overlock 100 T Butsuri, 2006, 46, S128.	0.1	0
56	Crystal structural analysis and metal-dependent stability and activity studies of the ColE7 endonuclease domain in complex with DNA/Zn ²⁺ or inhibitor/Ni ²⁺ . Protein Science, 2006, 15, 269-280.	7.6	41
57	Structural basis for sequence-dependent DNA cleavage by nonspecific endonucleases. Nucleic Acids Research, 2006, 35, 584-594.	14.5	35
58	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
59	Structural and functional insight into sugar-nonspecific nucleases in host defense. Current Opinion in Structural Biology, 2005, 15, 126-134.	5.7	65
60	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
61	Stabilization and Enhancement of the Antiapoptotic Activity of Mcl-1 by TCTP. Molecular and Cellular Biology, 2005, 25, 3117-3126.	2.3	209
62	DNA Binding and Degradation by the HNH Protein ColE7. Structure, 2004, 12, 205-214.	3.3	58
63	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
64	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
65	Crystal Structure of a Natural Circularly Permuted Jellyroll Protein: 1,3-1,4-β-D-Glucanase from Fibrobacter succinogenes. Journal of Molecular Biology, 2003, 330, 607-620.	4.2	51
66	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
67	Mutagenesis of Trp54 and Trp203 Residues on Fibrobacter Succinogenes 1,3-1,4-β-D-Glucanase Significantly Affects Catalytic Activities of the Enzyme. Biochemistry, 2002, 41, 8759-8766.	2.5	18
68	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
69	The Crystal Structure of the Nuclease Domain of Colicin E7 Suggests a Mechanism for Binding to Double-stranded DNA by the HNH Endonucleases. Journal of Molecular Biology, 2002, 324, 227-236.	4.2	54
70	Structural basis of non-specific lipid binding in maize lipid-transfer protein complexes revealed by high-resolution X-ray crystallography1 Edited by D. Rees. Journal of Molecular Biology, 2001, 308, 263-278.	4.2	175
71	Crystallization and preliminary X-ray diffraction analysis of the 1,3-1,4-β-D-glucanase from Fibrobacter succinogenes. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1303-1306.	2.5	2
72	Directed Mutagenesis of Specific Active Site Residues on Fibrobacter succinogenes 1,3-1,4-β-D-Glucanase Significantly Affects Catalysis and Enzyme Structural Stability. Journal of Biological Chemistry, 2001, 276, 17895-17901.	3.4	21

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73	Structural analysis of the transcriptional activation region on fis: crystal structures of six fis mutants with different activation properties 1 Edited by R. Huber. Journal of Molecular Biology, 2000, 302, 1139-1151.	4.2	40
74	Quantitative phase determination for macromolecular crystals using stereoscopic multibeam imaging. Acta Crystallographica Section A: Foundations and Advances, 1999, 55, 933-938.	0.3	17
75	Expression, crystallization and preliminary X-ray diffraction studies of N-carbamyl-D-amino-acid amidohydrolase from Agrobacterium radiobacter. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 694-695.	2.5	7
76	Crystallization and preliminary crystallographic analysis of the Escherichia coli tyrosine aminotransferase. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1474-1477.	2.5	20
77	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
78	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
79	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
80	Conversion of a β -strand to an α -helix induced by a single-site mutation observed in the crystal structure of fis mutant pro ²⁶ Ala. Protein Science, 1998, 7, 1875-1883.	7.6	34
81	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
82	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
83	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
84	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
85	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
86	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
87	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
88	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
89	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
90	Stable carbocations. Part 267. Pagodane dication, a unique 2. π -aromatic cyclobutanoid system. Journal of the American Chemical Society, 1986, 108, 836-838.	13.7	38

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91	An x-ray study of $\text{FeH}(\text{dmpe})_2(\text{BH}_4)$: a compound containing a singly-bridged BH_4 ligand with a bent $\text{Fe}-\text{H}-\text{B}$ linkage. <i>Inorganica Chimica Acta</i> , 1986, 114, L27-L28.	2.4	45
92	Structures of the copper-containing Cu_4MgPh_6 and $[\text{Cu}_4\text{LiPh}_6]^-$ clusters: first example of a magnesium-containing transition-metal cluster compound. <i>Journal of the American Chemical Society</i> , 1985, 107, 1682-1684.	13.7	63