Hanna S Yuan

List of Publications by Citations

Source: https://exaly.com/author-pdf/2237166/hanna-s-yuan-publications-by-citations.pdf

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

89
papers

3,041
citations

94
ext. papers

3,041
32
h-index

9-index

9.5
avg, IF

L-index

#	Paper	IF	Citations
89	Structural insights into TDP-43 in nucleic-acid binding and domain interactions. <i>Nucleic Acids Research</i> , 2009 , 37, 1799-808	20.1	212
88	Stabilization and enhancement of the antiapoptotic activity of mcl-1 by TCTP. <i>Molecular and Cellular Biology</i> , 2005 , 25, 3117-26	4.8	193
87	The crystal structure of the DNase domain of colicin E7 in complex with its inhibitor Im7 protein. <i>Structure</i> , 1999 , 7, 91-102	5.2	176
86	Structural basis of non-specific lipid binding in maize lipid-transfer protein complexes revealed by high-resolution X-ray crystallography. <i>Journal of Molecular Biology</i> , 2001 , 308, 263-78	6.5	145
85	The molecular structure of wild-type and a mutant Fis protein: relationship between mutational changes and recombinational enhancer function or DNA binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991 , 88, 9558-62	11.5	138
84	Mitochondrial endonuclease G mediates breakdown of paternal mitochondria upon fertilization. <i>Science</i> , 2016 , 353, 394-9	33.3	107
83	Full-length TDP-43 forms toxic amyloid oligomers that are present in frontotemporal lobar dementia-TDP patients. <i>Nature Communications</i> , 2014 , 5, 4824	17.4	107
82	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, 4712-22	20.1	87
81	DNA binding and cleavage by the periplasmic nuclease Vvn: a novel structure with a known active site. <i>EMBO Journal</i> , 2003 , 22, 4014-25	13	81
80	Structural and functional insights into human Tudor-SN, a key component linking RNA interference and editing. <i>Nucleic Acids Research</i> , 2008 , 36, 3579-89	20.1	76
79	Crystal structure of Escherichia coli PNPase: central channel residues are involved in processive RNA degradation. <i>Rna</i> , 2008 , 14, 2361-71	5.8	74
78	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, 9049-57	5.4	70
77	Structural studies of the pigeon cytosolic NADP(+)-dependent malic enzyme. <i>Protein Science</i> , 2002 , 11, 332-41	6.3	65
76	Structural and functional insight into sugar-nonspecific nucleases in host defense. <i>Current Opinion in Structural Biology</i> , 2005 , 15, 126-34	8.1	59
75	DNA binding and degradation by the HNH protein ColE7. Structure, 2004 , 12, 205-14	5.2	55
74	Stable carbocations. 273. [1.1.1.1]- and [2.2.1.1]Pagodane dications: frozen two-electron Woodward-Hoffmann transition-state models. <i>Journal of the American Chemical Society</i> , 1988 , 110, 770	54 ¹⁶ 7772	53
73	Structures of the copper-containing Cu4MgPh6 and [Cu4LiPh6]- clusters: first example of a magnesium-containing transition-metal cluster compound. <i>Journal of the American Chemical Society</i> , 1985 , 107, 1682-1684	16.4	53

72	The crystal structure of the nuclease domain of colicin E7 suggests a mechanism for binding to double-stranded DNA by the H-N-H endonucleases. <i>Journal of Molecular Biology</i> , 2002 , 324, 227-36	6.5	52
71	Crystal structure of a natural circularly permuted jellyroll protein: 1,3-1,4-beta-D-glucanase from Fibrobacter succinogenes. <i>Journal of Molecular Biology</i> , 2003 , 330, 607-20	6.5	49
70	The crystal structure of the immunity protein of colicin E7 suggests a possible colicin-interacting surface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996 , 93, 6437-	-4 2 .5	48
69	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	4.9	47
68	The transactivation region of the fis protein that controls site-specific DNA inversion contains extended mobile beta-hairpin arms. <i>EMBO Journal</i> , 1997 , 16, 6860-73	13	47
67	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. <i>Nucleic Acids Research</i> , 2002 , 30, 1670-8	20.1	47
66	Crystal structure of human polynucleotide phosphorylase: insights into its domain function in RNA binding and degradation. <i>Nucleic Acids Research</i> , 2012 , 40, 4146-57	20.1	46
65	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> , 2002 , 11, 2947-57	6.3	45
64	An x-ray study of FeH(dmpe)2(BH4): a compound containing a singly-bridged BH4 ligand with a bent Fe?H?B linkage. <i>Inorganica Chimica Acta</i> , 1986 , 114, L27-L28	2.7	40
63	Multi-targeting of functional cysteines in multiple conserved SARS-CoV-2 domains by clinically safe Zn-ejectors. <i>Chemical Science</i> , 2020 , 11, 9904-9909	9.4	40
62	Identification of an essential cleavage site in ColE7 required for import and killing of cells. <i>Journal of Biological Chemistry</i> , 2005 , 280, 24663-8	5.4	37
61	Structural analysis of the transcriptional activation region on Fis: crystal structures of six Fis mutants with different activation properties. <i>Journal of Molecular Biology</i> , 2000 , 302, 1139-51	6.5	36
60	Crystal structural analysis and metal-dependent stability and activity studies of the ColE7 endonuclease domain in complex with DNA/Zn2+ or inhibitor/Ni2+. <i>Protein Science</i> , 2006 , 15, 269-80	6.3	35
59	The conserved asparagine in the HNH motif serves an important structural role in metal finger endonucleases. <i>Journal of Molecular Biology</i> , 2007 , 368, 812-21	6.5	34
58	Conversion of a beta-strand to an alpha-helix induced by a single-site mutation observed in the crystal structure of Fis mutant Pro26Ala. <i>Protein Science</i> , 1998 , 7, 1875-83	6.3	32
57	Structural basis for sequence-dependent DNA cleavage by nonspecific endonucleases. <i>Nucleic Acids Research</i> , 2007 , 35, 584-94	20.1	32
56	Stable carbocations. Part 267. Pagodane dication, a unique 2.piaromatic cyclobutanoid system. Journal of the American Chemical Society, 1986 , 108, 836-838	16.4	29
55	Structural basis for RNA trimming by RNase T in stable RNA 3@end maturation. <i>Nature Chemical Biology</i> , 2011 , 7, 236-43	11.7	28

54	Using an Old Drug to Target a New Drug Site: Application of Disulfiram to Target the Zn-Site in HCV NS5A Protein. <i>Journal of the American Chemical Society</i> , 2016 , 138, 3856-62	16.4	26
53	How an exonuclease decides where to stop in trimming of nucleic acids: crystal structures of RNase T-product complexes. <i>Nucleic Acids Research</i> , 2012 , 40, 8144-54	20.1	25
52	Categorizing host-dependent RNA viruses by principal component analysis of their codon usage preferences. <i>Journal of Computational Biology</i> , 2009 , 16, 1539-47	1.7	24
51	The critical roles of polyamines in regulating ColE7 production and restricting ColE7 uptake of the colicin-producing Escherichia coli. <i>Journal of Biological Chemistry</i> , 2006 , 281, 13083-13091	5.4	22
50	Structural insights into RNA unwinding and degradation by RNase R. <i>Nucleic Acids Research</i> , 2017 , 45, 12015-12024	20.1	20
49	Synergistic Inhibition of SARS-CoV-2 Replication Using Disulfiram/Ebselen and Remdesivir. <i>ACS Pharmacology and Translational Science</i> , 2021 , 4, 898-907	5.9	20
48	Crystal structure of CRN-4: implications for domain function in apoptotic DNA degradation. <i>Molecular and Cellular Biology</i> , 2009 , 29, 448-57	4.8	19
47	Structural insights into DNA repair by RNase Tan exonuclease processing 3@nd of structured DNA in repair pathways. <i>PLoS Biology</i> , 2014 , 12, e1001803	9.7	18
46	Directed mutagenesis of apecific active site residues on Fibrobacter succinogenes 1,3-1,4-beta -D-glucanase significantly affects catalysis and enzyme structural stability. <i>Journal of Biological Chemistry</i> , 2001 , 276, 17895-901	5.4	18
45	Mutagenesis of Trp(54) and Trp(203) residues on Fibrobacter succinogenes 1,3-1,4-beta-D-glucanase significantly affects catalytic activities of the enzyme. <i>Biochemistry</i> , 2002 , 41, 8759-66	3.2	18
44	RNA recognition motifs of disease-linked RNA-binding proteins contribute to amyloid formation. <i>Scientific Reports</i> , 2019 , 9, 6171	4.9	17
43	Oxidative Stress Impairs Cell Death by Repressing the Nuclease Activity of Mitochondrial Endonuclease G. <i>Cell Reports</i> , 2016 , 16, 279-287	10.6	17
42	Structure and function of TatD exonuclease in DNA repair. <i>Nucleic Acids Research</i> , 2014 , 42, 10776-85	20.1	17
41	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. <i>Journal of Biological Chemistry</i> , 1994 , 269, 28947-54	5.4	17
40	Structural Insights into a Unique Dimeric DEAD-Box Helicase CshA that Promotes RNA Decay. <i>Structure</i> , 2017 , 25, 469-481	5.2	16
39	Structural insights into CpG-specific DNA methylation by human DNA methyltransferase 3B. <i>Nucleic Acids Research</i> , 2020 , 48, 3949-3961	20.1	16
38	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. <i>EMBO Journal</i> , 1997 , 16, 1444-54	13	16
37	Crystallization and preliminary crystallographic analysis of the Escherichia coli tyrosine aminotransferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1474-7		16

36	Identification of labile Zn sites in drug-target proteins. <i>Journal of the American Chemical Society</i> , 2013 , 135, 14028-31	16.4	15
35	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, 10480-10490	20.1	12
34	Redesign of high-affinity nonspecific nucleases with altered sequence preference. <i>Journal of the American Chemical Society</i> , 2009 , 131, 17345-53	16.4	12
33	Determination of the absolute configuration of (+)-neopentyl-1-d alcohol by neutron and x-ray diffraction analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994 , 91, 12872-6	11.5	12
32	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). <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 8019-29	8.3	11
31	Structural insights into apoptotic DNA degradation by CED-3 protease suppressor-6 (CPS-6) from Caenorhabditis elegans. <i>Journal of Biological Chemistry</i> , 2012 , 287, 7110-20	5.4	11
30	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	6.5	11
29	A unique exonuclease ExoG cleaves between RNA and DNA in mitochondrial DNA replication. <i>Nucleic Acids Research</i> , 2019 , 47, 5405-5419	20.1	10
28	Crystal structure of dimeric human PNPase reveals why disease-linked mutants suffer from low RNA import and degradation activities. <i>Nucleic Acids Research</i> , 2018 , 46, 8630-8640	20.1	10
27	Dynamic Indoor Localization Based on Active RFID for Healthcare Applications: A Shape Constraint Approach 2009 ,		10
27 26		5.8	9
	Approach 2009 ,	5.8 6.3	
26	Approach 2009, Structural insights into nanoRNA degradation by human Rexo2. <i>Rna</i> , 2019, 25, 737-746 Aromatic residues in RNase T stack with nucleobases to guide the sequence-specific recognition		9
26 25	Approach 2009, Structural insights into nanoRNA degradation by human Rexo2. <i>Rna</i> , 2019, 25, 737-746 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, 1934-41 Practicability Study on the Improvement of the Indoor Location Tracking Accuracy with Active RFID		9
26 25 24	Approach 2009, Structural insights into nanoRNA degradation by human Rexo2. <i>Rna</i> , 2019, 25, 737-746 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, 1934-41 Practicability Study on the Improvement of the Indoor Location Tracking Accuracy with Active RFID 2009, Involvement of colicin in the limited protection of the colicin producing cells against bacteriophage.	6.3	9 9
26 25 24 23	Approach 2009, Structural insights into nanoRNA degradation by human Rexo2. <i>Rna</i> , 2019, 25, 737-746 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, 1934-41 Practicability Study on the Improvement of the Indoor Location Tracking Accuracy with Active RFID 2009, Involvement of colicin in the limited protection of the colicin producing cells against bacteriophage. <i>Biochemical and Biophysical Research Communications</i> , 2004, 318, 81-7 Tudor staphylococcal nuclease is a structure-specific ribonuclease that degrades RNA at	6.3	9 9 9
26 25 24 23 22	Approach 2009, Structural insights into nanoRNA degradation by human Rexo2. <i>Rna</i> , 2019, 25, 737-746 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, 1934-41 Practicability Study on the Improvement of the Indoor Location Tracking Accuracy with Active RFID 2009, Involvement of colicin in the limited protection of the colicin producing cells against bacteriophage. <i>Biochemical and Biophysical Research Communications</i> , 2004, 318, 81-7 Tudor staphylococcal nuclease is a structure-specific ribonuclease that degrades RNA at unstructured regions during microRNA decay. <i>Rna</i> , 2018, 24, 739-748 Structural and biochemical characterization of CRN-5 and Rrp46: an exosome component	6. ₃ 3. ₄ 5. ₈	9 9 9 9 8

18	Expression, crystallization and preliminary X-ray diffraction studies of N-carbamyl-D-amino-acid amidohydrolase from Agrobacterium radiobacter. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 694-5		6
17	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988 , 85, 2889-93	11.5	6
16	Structural and catalytic roles of residues located in beta13 strand and the following beta-turn loop in Fibrobacter succinogenes 1,3-1,4-beta-D-glucanase. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2009 , 1790, 231-9	4	5
15	Structures, Mechanisms, and Functions of His-Me Finger Nucleases. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 935-946	10.3	4
14	Characterization of the specific cleavage of ceiE7-mRNA of the bactericidal ColE7 operon. <i>Biochemical and Biophysical Research Communications</i> , 2002 , 299, 613-20	3.4	4
13	Quantitative phase determination for macromolecular crystals using stereoscopic multibeam imaging. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1999 , 55, 933-938		4
12	Recombination in the nonstructural gene region in type 2 dengue viruses. <i>Intervirology</i> , 2012 , 55, 225-30	02.5	3
11	Inhibition of IS2 transposition by factor for inversion stimulation. <i>FEMS Microbiology Letters</i> , 2007 , 275, 98-105	2.9	2
10	Crystallization and preliminary x-ray diffraction analysis of malic enzyme from pigeon liver. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1930-2		2
9	Crystallization and preliminary X-ray crystallographic analysis of ImmE7 protein of colicin E7. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 23, 588-90	4.2	2
8	Frontotemporal dementia-linked P112H mutation of TDP-43 induces protein structural change and impairs its RNA binding function. <i>Protein Science</i> , 2021 , 30, 350-365	6.3	2
7	Crystallization and preliminary X-ray diffraction analysis of the 1,3-1,4-beta-D-glucanase from Fibrobacter succinogenes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 1303-6		1
6	Binding Proteins RNA-Binding Proteins in Bacterial and Mitochondrial RNA Decay 2021 , 517-526		1
5	Dimeric assembly of human Suv3 helicase promotes its RNA unwinding function in mitochondrial RNA degradosome for RNA decay <i>Protein Science</i> , 2022 , 31, e4312	6.3	1
4	Fis-protein induces rod-like DNA bending. <i>Chemical Physics Letters</i> , 2010 , 500, 318-322	2.5	
3	S2c2-4 Nonspecific nucleases in cell defense and cell death(S2-c2: "Structural biology reveals macromolecular interaction",Symposia,Abstract,Meeting Program of EABS & BSJ 2006). <i>Seibutsu Butsuri</i> , 2006 , 46, S128	О	
2	Structural insights into mitochondrial EndoG in response to oxidative stress. <i>FASEB Journal</i> , 2018 , 32, lb69	0.9	
1	Structural insights into RNase T in RNA maturation and DNA repair. FASEB Journal, 2013, 27, 988.1	0.9	