

# Hanna S Yuan

## List of Publications by Year in Descending Order

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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

32  
h-index

53  
g-index

94  
ext. papers

3,397  
ext. citations

9.5  
avg, IF

4.82  
L-index

| #  | Paper  | IF   | Citations |
|----|--|------|-----------|
| 89 | Dimeric assembly of human Suv3 helicase promotes its RNA unwinding function in mitochondrial RNA degradosome for RNA decay.. <i>Protein Science</i> , <b>2022</b> , 31, e4312  | 6.3  | 1         |
| 88 | Synergistic Inhibition of SARS-CoV-2 Replication Using Disulfiram/Ebselen and Remdesivir. <i>ACS Pharmacology and Translational Science</i> , <b>2021</b> , 4, 898-907   | 5.9  | 20        |
| 87 | Frontotemporal dementia-linked P112H mutation of TDP-43 induces protein structural change and impairs its RNA binding function. <i>Protein Science</i> , <b>2021</b> , 30, 350-365   | 6.3  | 2         |
| 86 | Binding Proteins   RNA-Binding Proteins in Bacterial and Mitochondrial RNA Decay <b>2021</b> , 517-526   |      | 1         |
| 85 | Structures, Mechanisms, and Functions of His-Me Finger Nucleases. <i>Trends in Biochemical Sciences</i> , <b>2020</b> , 45, 935-946  | 10.3 | 4         |
| 84 | Structural insights into CpG-specific DNA methylation by human DNA methyltransferase 3B. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 3949-3961   | 20.1 | 16        |
| 83 | Multi-targeting of functional cysteines in multiple conserved SARS-CoV-2 domains by clinically safe Zn-ejectors. <i>Chemical Science</i> , <b>2020</b> , 11, 9904-9909   | 9.4  | 40        |
| 82 | A unique exonuclease ExoG cleaves between RNA and DNA in mitochondrial DNA replication. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 5405-5419  | 20.1 | 10        |
| 81 | Structural insights into nanoRNA degradation by human Rexo2. <i>Rna</i> , <b>2019</b> , 25, 737-746  | 5.8  | 9         |
| 80 | RNA recognition motifs of disease-linked RNA-binding proteins contribute to amyloid formation. <i>Scientific Reports</i> , <b>2019</b> , 9, 6171   | 4.9  | 17        |
| 79 | Tudor staphylococcal nuclease is a structure-specific ribonuclease that degrades RNA at unstructured regions during microRNA decay. <i>Rna</i> , <b>2018</b> , 24, 739-748   | 5.8  | 8         |
| 78 | Crystal structure of dimeric human PNPase reveals why disease-linked mutants suffer from low RNA import and degradation activities. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 8630-8640  | 20.1 | 10        |
| 77 | Structural insights into mitochondrial EndoG in response to oxidative stress. <i>FASEB Journal</i> , <b>2018</b> , 32, lb69  | 0.9  |           |
| 76 | Structural Insights into a Unique Dimeric DEAD-Box Helicase CshA that Promotes RNA Decay. <i>Structure</i> , <b>2017</b> , 25, 469-481   | 5.2  | 16        |
| 75 | Structural insights into RNA unwinding and degradation by RNase R. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 12015-12024   | 20.1 | 20        |
| 74 | 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> , <b>2016</b> , 59, 8019-29 | 8.3  | 11        |
| 73 | Crystal structure of endonuclease G in complex with DNA reveals how it nonspecifically degrades DNA as a homodimer. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 10480-10490  | 20.1 | 12        |

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|----|--|------|-----|
| 72 | Structural analysis of disease-related TDP-43 D169G mutation: linking enhanced stability and caspase cleavage efficiency to protein accumulation. <i>Scientific Reports</i> , <b>2016</b> , 6, 21581 | 4.9  | 47  |
| 71 | Mitochondrial endonuclease G mediates breakdown of paternal mitochondria upon fertilization. <i>Science</i> , <b>2016</b> , 353, 394-9   | 33.3 | 107 |
| 70 | Oxidative Stress Impairs Cell Death by Repressing the Nuclease Activity of Mitochondrial Endonuclease G. <i>Cell Reports</i> , <b>2016</b> , 16, 279-287   | 10.6 | 17  |
| 69 | 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> , <b>2016</b> , 138, 3856-62       | 16.4 | 26  |
| 68 | Aromatic residues in RNase T stack with nucleobases to guide the sequence-specific recognition and cleavage of nucleic acids. <i>Protein Science</i> , <b>2015</b> , 24, 1934-41                     | 6.3  | 9   |
| 67 | Full-length TDP-43 forms toxic amyloid oligomers that are present in frontotemporal lobar dementia-TDP patients. <i>Nature Communications</i> , <b>2014</b> , 5, 4824                                | 17.4 | 107 |
| 66 | 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> , <b>2014</b> , 42, 4712-22                       | 20.1 | 87  |
| 65 | Structural insights into DNA repair by RNase T—an exonuclease processing 3' end of structured DNA in repair pathways. <i>PLoS Biology</i> , <b>2014</b> , 12, e1001803                               | 9.7  | 18  |
| 64 | Structure and function of TatD exonuclease in DNA repair. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 10776-85   | 20.1 | 17  |
| 63 | Identification of labile Zn sites in drug-target proteins. <i>Journal of the American Chemical Society</i> , <b>2013</b> , 135, 14028-31   | 16.4 | 15  |
| 62 | 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> , <b>2013</b> , 288, 9049-57           | 5.4  | 70  |
| 61 | Structural insights into RNase T in RNA maturation and DNA repair. <i>FASEB Journal</i> , <b>2013</b> , 27, 988.1  | 0.9  |     |
| 60 | 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> , <b>2012</b> , 287, 7110-20   | 5.4  | 11  |
| 59 | Crystal structure of human polynucleotide phosphorylase: insights into its domain function in RNA binding and degradation. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 4146-57                 | 20.1 | 46  |
| 58 | Recombination in the nonstructural gene region in type 2 dengue viruses. <i>Intervirology</i> , <b>2012</b> , 55, 225-30   | 2.5  | 3   |
| 57 | How an exonuclease decides where to stop in trimming of nucleic acids: crystal structures of RNase T-product complexes. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 8144-54                    | 20.1 | 25  |
| 56 | Structural basis for RNA trimming by RNase T in stable RNA 3' end maturation. <i>Nature Chemical Biology</i> , <b>2011</b> , 7, 236-43   | 11.7 | 28  |
| 55 | Structural and biochemical characterization of CRN-5 and Rrp46: an exosome component participating in apoptotic DNA degradation. <i>Rna</i> , <b>2010</b> , 16, 1748-59                              | 5.8  | 8   |

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|----|---|------|-----|
| 54 | Fis-protein induces rod-like DNA bending. <i>Chemical Physics Letters</i> , <b>2010</b> , 500, 318-322  | 2.5  |     |
| 53 | Categorizing host-dependent RNA viruses by principal component analysis of their codon usage preferences. <i>Journal of Computational Biology</i> , <b>2009</b> , 16, 1539-47   | 1.7  | 24  |
| 52 | Crystal structure of CRN-4: implications for domain function in apoptotic DNA degradation. <i>Molecular and Cellular Biology</i> , <b>2009</b> , 29, 448-57   | 4.8  | 19  |
| 51 | Structural and catalytic roles of residues located in beta13 strand and the following beta-turn loop in <i>Fibrobacter succinogenes</i> 1,3-1,4-beta-D-glucanase. <i>Biochimica Et Biophysica Acta - General Subjects</i> , <b>2009</b> , 1790, 231-9 | 4    | 5   |
| 50 | Practicability Study on the Improvement of the Indoor Location Tracking Accuracy with Active RFID <b>2009</b> ,   |      | 9   |
| 49 | Redesign of high-affinity nonspecific nucleases with altered sequence preference. <i>Journal of the American Chemical Society</i> , <b>2009</b> , 131, 17345-53   | 16.4 | 12  |
| 48 | Dynamic Indoor Localization Based on Active RFID for Healthcare Applications: A Shape Constraint Approach <b>2009</b> ,   |      | 10  |
| 47 | Structural insights into TDP-43 in nucleic-acid binding and domain interactions. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 1799-808   | 20.1 | 212 |
| 46 | Accurate Location Tracking Based on Active RFID for Health and Safety Monitoring <b>2009</b> ,  |      | 7   |
| 45 | Crystal structure of <i>Escherichia coli</i> PNPase: central channel residues are involved in processive RNA degradation. <i>Rna</i> , <b>2008</b> , 14, 2361-71  | 5.8  | 74  |
| 44 | Structural and functional insights into human Tudor-SN, a key component linking RNA interference and editing. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, 3579-89   | 20.1 | 76  |
| 43 | Inhibition of IS2 transposition by factor for inversion stimulation. <i>FEMS Microbiology Letters</i> , <b>2007</b> , 275, 98-105   | 2.9  | 2   |
| 42 | Structural basis for sequence-dependent DNA cleavage by nonspecific endonucleases. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, 584-94   | 20.1 | 32  |
| 41 | The conserved asparagine in the HNH motif serves an important structural role in metal finger endonucleases. <i>Journal of Molecular Biology</i> , <b>2007</b> , 368, 812-21  | 6.5  | 34  |
| 40 | The critical roles of polyamines in regulating ColE7 production and restricting ColE7 uptake of the colicin-producing <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 13083-13091                               | 5.4  | 22  |
| 39 | High-resolution crystal structure of a truncated ColE7 translocation domain: implications for colicin transport across membranes. <i>Journal of Molecular Biology</i> , <b>2006</b> , 356, 22-31  | 6.5  | 11  |
| 38 | 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> , <b>2006</b> , 46, S128                    | 0    |     |
| 37 | Crystal structural analysis and metal-dependent stability and activity studies of the ColE7 endonuclease domain in complex with DNA/Zn <sup>2+</sup> or inhibitor/Ni <sup>2+</sup> . <i>Protein Science</i> , <b>2006</b> , 15, 269-80                | 6.3  | 35  |

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|----|--|------|-----|
| 36 | Structural and functional insight into sugar-nonspecific nucleases in host defense. <i>Current Opinion in Structural Biology</i> , <b>2005</b> , 15, 126-34  | 8.1  | 59  |
| 35 | Identification of an essential cleavage site in ColE7 required for import and killing of cells. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 24663-8  | 5.4  | 37  |
| 34 | Stabilization and enhancement of the antiapoptotic activity of mcl-1 by TCTP. <i>Molecular and Cellular Biology</i> , <b>2005</b> , 25, 3117-26  | 4.8  | 193 |
| 33 | DNA binding and degradation by the HNH protein ColE7. <i>Structure</i> , <b>2004</b> , 12, 205-14  | 5.2  | 55  |
| 32 | Involvement of colicin in the limited protection of the colicin producing cells against bacteriophage. <i>Biochemical and Biophysical Research Communications</i> , <b>2004</b> , 318, 81-7  | 3.4  | 9   |
| 31 | DNA binding and cleavage by the periplasmic nuclease Vvn: a novel structure with a known active site. <i>EMBO Journal</i> , <b>2003</b> , 22, 4014-25  | 13   | 81  |
| 30 | Crystal structure of a natural circularly permuted jellyroll protein: 1,3-1,4-beta-D-glucanase from <i>Fibrobacter succinogenes</i> . <i>Journal of Molecular Biology</i> , <b>2003</b> , 330, 607-20  | 6.5  | 49  |
| 29 | 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> , <b>2002</b> , 11, 2947-57                          | 6.3  | 45  |
| 28 | Structural studies of the pigeon cytosolic NADP(+)-dependent malic enzyme. <i>Protein Science</i> , <b>2002</b> , 11, 332-41   | 6.3  | 65  |
| 27 | 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> , <b>2002</b> , 30, 1670-8   | 20.1 | 47  |
| 26 | Mutagenesis of Trp(54) and Trp(203) residues on <i>Fibrobacter succinogenes</i> 1,3-1,4-beta-D-glucanase significantly affects catalytic activities of the enzyme. <i>Biochemistry</i> , <b>2002</b> , 41, 8759-66   | 3.2  | 18  |
| 25 | Characterization of the specific cleavage of <i>ceiE7</i> -mRNA of the bactericidal ColE7 operon. <i>Biochemical and Biophysical Research Communications</i> , <b>2002</b> , 299, 613-20   | 3.4  | 4   |
| 24 | 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> , <b>2002</b> , 324, 227-36   | 6.5  | 52  |
| 23 | Crystallization and preliminary X-ray diffraction analysis of the 1,3-1,4-beta-D-glucanase from <i>Fibrobacter succinogenes</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2001</b> , 57, 1303-6                           |      | 1   |
| 22 | Directed mutagenesis of a specific active site residues on <i>Fibrobacter succinogenes</i> 1,3-1,4-beta-D-glucanase significantly affects catalysis and enzyme structural stability. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 17895-901 | 5.4  | 18  |
| 21 | 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> , <b>2001</b> , 308, 263-78  | 6.5  | 145 |
| 20 | 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> , <b>2000</b> , 302, 1139-51  | 6.5  | 36  |
| 19 | Quantitative phase determination for macromolecular crystals using stereoscopic multibeam imaging. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>1999</b> , 55, 933-938   |      | 4   |

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|----|---|------|-----|
| 18 | Expression, crystallization and preliminary X-ray diffraction studies of N-carbamyl-D-amino-acid amidohydrolase from <i>Agrobacterium radiobacter</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1999</b> , 55, 694-5   |      | 6   |
| 17 | Crystallization and preliminary crystallographic analysis of the <i>Escherichia coli</i> tyrosine aminotransferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1999</b> , 55, 1474-7  |      | 16  |
| 16 | Crystallization and preliminary x-ray diffraction analysis of malic enzyme from pigeon liver. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1999</b> , 55, 1930-2  |      | 2   |
| 15 | The crystal structure of the DNase domain of colicin E7 in complex with its inhibitor Im7 protein. <i>Structure</i> , <b>1999</b> , 7, 91-102   | 5.2  | 176 |
| 14 | Hierarchical order of critical residues on the immunity-determining region of the Im7 protein which confer specific immunity to its cognate colicin. <i>Biochemical and Biophysical Research Communications</i> , <b>1999</b> , 264, 69-75  | 3.4  | 7   |
| 13 | 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> , <b>1998</b> , 7, 1875-83   | 6.3  | 32  |
| 12 | The transactivation region of the fis protein that controls site-specific DNA inversion contains extended mobile beta-hairpin arms. <i>EMBO Journal</i> , <b>1997</b> , 16, 6860-73   | 13   | 47  |
| 11 | 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> , <b>1997</b> , 16, 1444-54   | 13   | 16  |
| 10 | 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> , <b>1996</b> , 93, 6437-42   | 11.5 | 48  |
| 9  | Crystallization and preliminary X-ray crystallographic analysis of ImmE7 protein of colicin E7. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 588-90  | 4.2  | 2   |
| 8  | 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> , <b>1994</b> , 91, 12872-6  | 11.5 | 12  |
| 7  | 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> , <b>1994</b> , 269, 28947-54  | 5.4  | 17  |
| 6  | 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> , <b>1991</b> , 88, 9558-62   | 11.5 | 138 |
| 5  | 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> , <b>1988</b> , 110, 7764-7772   | 16.4 | 53  |
| 4  | Determination of the absolute configuration of (-)-(2R)-succinic-2-d acid by neutron diffraction study: unambiguous proof of the absolute stereochemistry of the NAD <sup>+</sup> /NADH interconversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1988</b> , 85, 2889-93 | 11.5 | 6   |
| 3  | An x-ray study of FeH(dmpe) <sub>2</sub> (BH <sub>4</sub> ): a compound containing a singly-bridged BH <sub>4</sub> ligand with a bent Fe-H-B linkage. <i>Inorganica Chimica Acta</i> , <b>1986</b> , 114, L27-L28  | 2.7  | 40  |
| 2  | Stable carbocations. Part 267. Pagodane dication, a unique 2.π-aromatic cyclobutanoid system. <i>Journal of the American Chemical Society</i> , <b>1986</b> , 108, 836-838  | 16.4 | 29  |
| 1  | Structures of the copper-containing Cu <sub>4</sub> MgPh <sub>6</sub> and [Cu <sub>4</sub> LiPh <sub>6</sub> ]- clusters: first example of a magnesium-containing transition-metal cluster compound. <i>Journal of the American Chemical Society</i> , <b>1985</b> , 107, 1682-1684   | 16.4 | 53  |

