

# Shang-Te Danny Hsu

## List of Publications by Year in descending order

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104  
papers

4,467  
citations

108046

37  
h-index

134545

62  
g-index

118  
all docs

118  
docs citations

118  
times ranked

6628  
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct shifts in site-specific glycosylation pattern of SARS-CoV-2 spike proteins associated with arising mutations in the D614G and Alpha variants. <i>Glycobiology</i> , 2022, 32, 60-72.	1.3	16
2	Sialic acid-containing glycolipids mediate binding and viral entry of SARS-CoV-2. <i>Nature Chemical Biology</i> , 2022, 18, 81-90.	3.9	141
3	The catalytic activity of TCPTP is auto-regulated by its intrinsically disordered tail and activated by Integrin alpha-1. <i>Nature Communications</i> , 2022, 13, 94.	5.8	16
4	BARD1 is an ATPase activating protein for OLA1. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2022, 1866, 130099.	1.1	1
5	Oxidation of catalytic cysteine of human deubiquitinase BAP1 triggers misfolding and aggregation in addition to functional loss. <i>Biochemical and Biophysical Research Communications</i> , 2022, 599, 57-62.	1.0	1
6	Impacts of Cancer-associated Mutations on the Structure-Activity Relationship of BAP1. <i>Journal of Molecular Biology</i> , 2022, 434, 167553.	2.0	4
7	Tumor suppressor BAP1 nuclear import is governed by transportin-1. <i>Journal of Cell Biology</i> , 2022, 221, .	2.3	5
8	Direct Visualization of a 26 kDa Protein by Cryo-Electron Microscopy Aided by a Small Scaffold Protein. <i>Biochemistry</i> , 2021, 60, 1075-1079.	1.2	8
9	Cross-over Loop Cysteine C152 Acts as an Antioxidant to Maintain the Folding Stability and Deubiquitinase Activity of UCH-L1 Under Oxidative Stress. <i>Journal of Molecular Biology</i> , 2021, 433, 166879.	2.0	6
10	Tying up the Loose Ends: A Mathematically Knotted Protein. <i>Frontiers in Chemistry</i> , 2021, 9, 663241.	1.8	7
11	Converging experimental and computational views of the knotting mechanism of a small knotted protein. <i>Biophysical Journal</i> , 2021, 120, 2276-2286.	0.2	12
12	Structural polymorphism and substrate promiscuity of a ribosome-associated molecular chaperone. <i>Magnetic Resonance</i> , 2021, 2, 375-386.	0.8	1
13	Generation and Characterization of a Spike Glycoprotein Domain A-Specific Neutralizing Single-Chain Variable Fragment against Porcine Epidemic Diarrhea Virus. <i>Vaccines</i> , 2021, 9, 833.	2.1	4
14	Effect of SARS-CoV-2 B.1.1.7 mutations on spike protein structure and function. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 731-739.	3.6	124
15	D614G mutation in the SARS-CoV-2 spike protein enhances viral fitness by desensitizing it to temperature-dependent denaturation. <i>Journal of Biological Chemistry</i> , 2021, 297, 101238.	1.6	46
16	Structure-guided antibody cocktail for prevention and treatment of COVID-19. <i>PLoS Pathogens</i> , 2021, 17, e1009704.	2.1	12
17	Targeting protein tyrosine phosphatase PTP-PEST (PTPN12) for therapeutic intervention in acute myocardial infarction. <i>Cardiovascular Research</i> , 2020, 116, 1032-1046.	1.8	13
18	Protein knots provide mechano-resilience to an AAA+ protease-mediated proteolysis with profound ATP energy expenses. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140330.	1.1	10

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19	Cryo-EM analysis of a feline coronavirus spike protein reveals a unique structure and camouflaging glycans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1438-1446.	3.3	94
20	Untying a Knotted SPOUT RNA Methyltransferase by Circular Permutation Results in a Domain-Swapped Dimer. <i>Structure</i> , 2019, 27, 1224-1233.e4.	1.6	18
21	Untying a Protein Knot by Circular Permutation. <i>Journal of Molecular Biology</i> , 2019, 431, 857-863.	2.0	18
22	A High-Throughput Interbacterial Competition Screen Identifies ClpAP in Enhancing Recipient Susceptibility to Type VI Secretion System-Mediated Attack by <i>Agrobacterium tumefaciens</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3077.	1.5	15
23	A Natively Monomeric Deubiquitinase UCH-L1 Forms Highly Dynamic but Defined Metastable Oligomeric Folding Intermediates. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 2433-2437.	2.1	13
24	Soluble Siglec-14 glycan-recognition protein is generated by alternative splicing and suppresses myeloid inflammatory responses. <i>Journal of Biological Chemistry</i> , 2018, 293, 19645-19658.	1.6	32
25	How Native and Non-Native Cations Bind and Modulate the Properties of GTP/ATP. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 3311-3320.	2.3	9
26	Comparative folding analyses of unknotted versus trefoil-knotted ornithine transcarbamylases suggest stabilizing effects of protein knots. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 822-829.	1.0	14
27	Dissecting the Structure-Activity Relationship of Galectin-Ligand Interactions. <i>International Journal of Molecular Sciences</i> , 2018, 19, 392.	1.8	58
28	Topologically knotted deubiquitinases exhibit unprecedented mechanostability to withstand the proteolysis by an AAA+ protease. <i>Scientific Reports</i> , 2018, 8, 7076.	1.6	31
29	Entropic stabilization of a deubiquitinase provides conformational plasticity and slow unfolding kinetics beneficial for functioning on the proteasome. <i>Scientific Reports</i> , 2017, 7, 45174.	1.6	14
30	Lactose Binding Induces Opposing Dynamics Changes in Human Galectins Revealed by NMR-Based Hydrogen-Deuterium Exchange. <i>Molecules</i> , 2017, 22, 1357.	1.7	13
31	Familial Mutations and Post-translational Modifications of UCH-L1 in Parkinson's Disease and Neurodegenerative Disorders. <i>Current Protein and Peptide Science</i> , 2017, 18, 733-745.	0.7	25
32	Moenomycin Biosynthesis: Structure and Mechanism of Action of the Prenyltransferase MoeN5. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 4716-4720.	7.2	19
33	Protein knotting through concatenation significantly reduces folding stability. <i>Scientific Reports</i> , 2016, 6, 39357.	1.6	5
34	Folding analysis of the most complex Stevedore's protein knot. <i>Scientific Reports</i> , 2016, 6, 31514.	1.6	32
35	The Knotted Protein UCH-L1 Exhibits Partially Unfolded Forms under Native Conditions that Share Common Structural Features with Its Kinetic Folding Intermediates. <i>Journal of Molecular Biology</i> , 2016, 428, 2507-2520.	2.0	44
36	Dual thio-digalactoside-binding modes of human galectins as the structural basis for the design of potent and selective inhibitors. <i>Scientific Reports</i> , 2016, 6, 29457.	1.6	70

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37	A novel transition pathway of ligand-induced topological conversion from hybrid forms to parallel forms of human telomeric G-quadruplexes. <i>Nucleic Acids Research</i> , 2016, 44, 3958-3968.	6.5	30
38	Interfacial Enzyme Function Visualized Using Neutron, X-Ray, and Light-Scattering Methods. , 2016, , 149-190.		1
39	NMR assignments of the peptidyl-prolyl cis $\leftrightarrow$ trans isomerase domain of trigger factor from <i>E. coli</i> . <i>Biomolecular NMR Assignments</i> , 2016, 10, 149-152.	0.4	3
40	A Multivalent Marine Lectin from <i>Crenomytilus grayanus</i> Possesses Anti-cancer Activity through Recognizing Globotriose Gb3. <i>Journal of the American Chemical Society</i> , 2016, 138, 4787-4795.	6.6	51
41	Structures of Trypanosome Vacuolar Soluble Pyrophosphatases: Antiparasitic Drug Targets. <i>ACS Chemical Biology</i> , 2016, 11, 1362-1371.	1.6	15
42	Comparative analysis of the folding dynamics and kinetics of an engineered knotted protein and its variants derived from HP0242 of <i>Helicobacter pylori</i> . <i>Journal of Physics Condensed Matter</i> , 2015, 27, 354106.	0.7	23
43	Site-Specific Solid-State NMR Studies of $\alpha$ -Trigger Factor in Complex with the Large Ribosomal Subunit...50S. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 4367-4369.	7.2	42
44	Unraveling the Folding Mechanism of the Smallest Knotted Protein, MJ0366. <i>Journal of Physical Chemistry B</i> , 2015, 119, 4359-4370.	1.2	44
45	Random-Coil Behavior of Chemically Denatured Topologically Knotted Proteins Revealed by Small-Angle X-ray Scattering. <i>Journal of Physical Chemistry B</i> , 2015, 119, 5437-5443.	1.2	20
46	Key Residues of Outer Membrane Protein OprI Involved in Hexamer Formation and Bacterial Susceptibility to Cationic Antimicrobial Peptides. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 6210-6222.	1.4	8
47	NMR assignments of the C-terminal domain of human galectin-8. <i>Biomolecular NMR Assignments</i> , 2015, 9, 427-430.	0.4	3
48	Conformational Transition of a Hairpin Structure to G-Quadruplex within the <i>WNT1</i> Gene Promoter. <i>Journal of the American Chemical Society</i> , 2015, 137, 210-218.	6.6	51
49	Solution structure and tandem DNA recognition of the C-terminal effector domain of PmrA from <i>Klebsiella pneumoniae</i> . <i>Nucleic Acids Research</i> , 2014, 42, 4080-4093.	6.5	24
50	Structural basis of sodium $\leftrightarrow$ potassium exchange of a human telomeric DNA quadruplex without topological conversion. <i>Nucleic Acids Research</i> , 2014, 42, 4723-4733.	6.5	52
51	Backbone NMR assignments of a topologically knotted protein in urea-denatured state. <i>Biomolecular NMR Assignments</i> , 2014, 8, 439-442.	0.4	10
52	NMR assignments of PI3-SH3 domain aided by protonless NMR spectroscopy. <i>Biomolecular NMR Assignments</i> , 2014, 8, 291-295.	0.4	0
53	NMR assignments of a hypothetical pseudo-knotted protein HP0242 from <i>Helicobacter pylori</i> . <i>Biomolecular NMR Assignments</i> , 2014, 8, 287-289.	0.4	2
54	Backbone NMR assignments of a topologically knotted protein in urea-denatured state. <i>Biomolecular NMR Assignments</i> , 2014, 8, 283-285.	0.4	11

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55	Nucleotide Contributions to the Structural Integrity and DNA Replication Initiation Activity of Noncoding Y RNA. <i>Biochemistry</i> , 2014, 53, 5848-5863.	1.2	17
56	Self-Assembly of MinE on the Membrane Underlies Formation of the MinE Ring to Sustain Function of the Escherichia coli Min System. <i>Journal of Biological Chemistry</i> , 2014, 289, 21252-21266.	1.6	18
57	Unfolding Kinetics of Human Telomeric G-Quadruplexes Studied by NMR Spectroscopy. <i>Journal of Physical Chemistry B</i> , 2014, 118, 931-936.	1.2	11
58	Structure, function and inhibition of ent-kaurene synthase from Bradyrhizobium japonicum. <i>Scientific Reports</i> , 2014, 4, 6214.	1.6	44
59	A Nanobody Binding to Non-Amyloidogenic Regions of the Protein Human Lysozyme Enhances Partial Unfolding but Inhibits Amyloid Fibril Formation. <i>Journal of Physical Chemistry B</i> , 2013, 117, 13245-13258.	1.2	42
60	Crystal Structure of Vaccinia Viral A27 Protein Reveals a Novel Structure Critical for Its Function and Complex Formation with A26 Protein. <i>PLoS Pathogens</i> , 2013, 9, e1003563.	2.1	32
61	Residue-Specific Annotation of Disorder-to-Order Transition and Cathepsin Inhibition of a Propeptide-Like Crammer from <i>D. melanogaster</i> . <i>PLoS ONE</i> , 2013, 8, e54187.	1.1	0
62	A molten globule-to-ordered structure transition of <i>Drosophila melanogaster</i> crammer is required for its ability to inhibit cathepsin. <i>Biochemical Journal</i> , 2012, 442, 563-572.	1.7	8
63	Functional Dynamics of Proteins. <i>Computational and Mathematical Methods in Medicine</i> , 2012, 2012, 1-3.	0.7	1
64	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments of human muscle acylphosphatase. <i>Biomolecular NMR Assignments</i> , 2012, 6, 27-29.	0.4	16
65	The Effect of Parkinson's-Disease-Associated Mutations on the Deubiquitinating Enzyme UCH-L1. <i>Journal of Molecular Biology</i> , 2011, 407, 261-272.	2.0	61
66	Experimental free energy surfaces reveal the mechanisms of maintenance of protein solubility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 21057-21062.	3.3	65
67	Backbone assignments of the 26 kDa neuron-specific ubiquitin carboxyl-terminal hydrolase L1 (UCH-L1). <i>Biomolecular NMR Assignments</i> , 2010, 4, 41-43.	0.4	9
68	Folding Study of Venus Reveals a Strong Ion Dependence of Its Yellow Fluorescence under Mildly Acidic Conditions. <i>Journal of Biological Chemistry</i> , 2010, 285, 4859-4869.	1.6	19
69	Transient Tertiary Structure Formation within the Ribosome Exit Port. <i>Journal of the American Chemical Society</i> , 2010, 132, 16928-16937.	6.6	69
70	Local Cooperativity in an Amyloidogenic State of Human Lysozyme Observed at Atomic Resolution. <i>Journal of the American Chemical Society</i> , 2010, 132, 15580-15588.	6.6	55
71	Towards Multiparametric Fluorescent Imaging of Amyloid Formation: Studies of a YFP Model of $\beta$ -Synuclein Aggregation. <i>Journal of Molecular Biology</i> , 2010, 395, 627-642.	2.0	72
72	Structure and Properties of a Complex of $\beta$ -Synuclein and a Single-Domain Camelid Antibody. <i>Journal of Molecular Biology</i> , 2010, 402, 326-343.	2.0	164

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73	Small molecule-mediated inhibition of translation by targeting a native RNA G-quadruplex. <i>Organic and Biomolecular Chemistry</i> , 2010, 8, 2771.	1.5	101
74	Probing ribosome-nascent chain complexes produced in vivo by NMR spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22239-22244.	3.3	81
75	<sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C assignments of the dimeric ribosome binding domain of trigger factor from <i>Escherichia coli</i> . <i>Biomolecular NMR Assignments</i> , 2009, 3, 17-20.	0.4	12
76	<sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C assignments of domain 5 of Dictyostelium discoideum gelation factor (ABP-120) in its native and 8M urea-denatured states. <i>Biomolecular NMR Assignments</i> , 2009, 3, 29-31.	0.4	18
77	<sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C assignments of yellow fluorescent protein (YFP) Venus. <i>Biomolecular NMR Assignments</i> , 2009, 3, 67-72.	0.4	15
78	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N assignments of a camelid nanobody directed against human $\alpha$ -synuclein. <i>Biomolecular NMR Assignments</i> , 2009, 3, 231-233.	0.4	29
79	Chaperone proteostasis in Parkinson's disease: stabilization of the Hsp70/ $\alpha$ -synuclein complex by Hip. <i>EMBO Journal</i> , 2009, 28, 3758-3770.	3.5	110
80	A G-Rich Sequence within the <i>c-kit</i> Oncogene Promoter Forms a Parallel G-Quadruplex Having Asymmetric G-Tetrad Dynamics. <i>Journal of the American Chemical Society</i> , 2009, 131, 13399-13409.	6.6	195
81	Accurate Random Coil Chemical Shifts from an Analysis of Loop Regions in Native States of Proteins. <i>Journal of the American Chemical Society</i> , 2009, 131, 16332-16333.	6.6	85
82	Probing Side-Chain Dynamics of a Ribosome-Bound Nascent Chain Using Methyl NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2009, 131, 8366-8367.	6.6	37
83	Use of Protonless NMR Spectroscopy To Alleviate the Loss of Information Resulting from Exchange-Broadening. <i>Journal of the American Chemical Society</i> , 2009, 131, 7222-7223.	6.6	69
84	Structure, Dynamics and Folding of an Immunoglobulin Domain of the Gelation Factor (ABP-120) from Dictyostelium discoideum. <i>Journal of Molecular Biology</i> , 2009, 388, 865-879.	2.0	32
85	The folding, stability and conformational dynamics of $\beta$ -barrel fluorescent proteins. <i>Chemical Society Reviews</i> , 2009, 38, 2951.	18.7	72
86	A Small Molecule That Disrupts G-Quadruplex DNA Structure and Enhances Gene Expression. <i>Journal of the American Chemical Society</i> , 2009, 131, 12628-12633.	6.6	123
87	A Nonpeptidic Reverse Turn that Promotes Parallel Sheet Structure Stabilized by C-H...O Hydrogen Bonds in a Cyclopropane $\beta$ -Peptide. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 7099-7102.	7.2	45
88	Diarylethynyl Amides That Recognize the Parallel Conformation of Genomic Promoter DNA G-Quadruplexes. <i>Journal of the American Chemical Society</i> , 2008, 130, 15950-15956.	6.6	151
89	Evolution Rescues Folding of Human Immunodeficiency Virus-1 Envelope Glycoprotein GP120 Lacking a Conserved Disulfide Bond. <i>Molecular Biology of the Cell</i> , 2008, 19, 4707-4716.	0.9	12
90	The extremely slow exchanging core and acid denatured state of green fluorescent protein. <i>HFSP Journal</i> , 2008, 2, 378-387.	2.5	17

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91	Structure and dynamics of a ribosome-bound nascent chain by NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16516-16521.	3.3	116
92	Structural Motifs of Lipid II-Binding Lantibiotics as a Blueprint for Novel Antibiotics. Anti-Infective Agents in Medicinal Chemistry, 2006, 5, 245-254.	0.6	5
93	The Solution Structure of the AppA BLUF Domain: Insight into the Mechanism of Light-Induced Signaling. ChemBioChem, 2006, 7, 187-193.	1.3	111
94	Characterization and Structural Analyses of Nonspecific Lipid Transfer Protein 1 from Mung Bean. Biochemistry, 2005, 44, 11646-11646.	1.2	0
95	Isolation and structural characterization of epilancin 15X, a novel lantibiotic from a clinical strain of Staphylococcus epidermidis. FEBS Letters, 2005, 579, 1917-1922.	1.3	71
96	Entropy Calculation of HIV-1 Env gp120, its Receptor CD4, and their Complex: An Analysis of Configurational Entropy Changes upon Complexation. Biophysical Journal, 2005, 88, 15-24.	0.2	60
97	Characterization and Structural Analyses of Nonspecific Lipid Transfer Protein 1 from Mung Bean. Biochemistry, 2005, 44, 5703-5712.	1.2	56
98	Atomic insight into the CD4 binding-induced conformational changes in HIV-1 gp120. Proteins: Structure, Function and Bioinformatics, 2004, 55, 582-593.	1.5	39
99	The nisin-lipid II complex reveals a pyrophosphate cage that provides a blueprint for novel antibiotics. Nature Structural and Molecular Biology, 2004, 11, 963-967.	3.6	505
100	NMR Study of Mersacidin and Lipid II Interaction in Dodecylphosphocholine Micelles. Journal of Biological Chemistry, 2003, 278, 13110-13117.	1.6	113
101	Mapping the Targeted Membrane Pore Formation Mechanism by Solution NMR: The Nisin Z and Lipid II Interaction in SDS Micelles. Biochemistry, 2002, 41, 7670-7676.	1.2	68
102	The solution structure of [d(CGC)r(amamam)d(TTTGCG)] <sub>2</sub> . Journal of Biomolecular NMR, 2001, 21, 209-220.	1.6	3
103	The solution structure of [d(CGC)r(aaa)d(TTTGCG)] <sub>2</sub> : hybrid junctions flanked by DNA duplexes. Nucleic Acids Research, 2000, 28, 1322-1331.	6.5	9
104	Hydration of [d(CGC)r(aaa)d(TTTGCG)] <sub>2</sub> . Journal of Molecular Biology, 2000, 295, 1129-1137.	2.0	6