

# Shu-Fang Cheng

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10193424/publications.pdf>

Version: 2024-02-01

32  
papers

553  
citations

687363

13  
h-index

642732

23  
g-index

32  
all docs

32  
docs citations

32  
times ranked

601  
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of single-chain variable fragments (scFv) against influenza virus targeting hemagglutinin subunit 2 (HA2). Archives of Virology, 2016, 161, 19-31.	2.1	17
2	Kinetics Study on the HIV-1 Ectodomain Protein Quaternary Structure Formation Reveals Coupling of Chain Folding and Self-Assembly in the Refolding Cascade. Journal of Physical Chemistry B, 2014, 118, 12827-12836.	2.6	0
3	Stability of gp41 hairpin and helix bundle assembly probed by combined stacking and circular dichroic approaches. Journal of Structural Biology, 2011, 175, 406-414.	2.8	1
4	An efficient production and characterization of HIV-1 gp41 ectodomain with fusion peptide in Escherichia coli system. Journal of Biotechnology, 2011, 153, 48-55.	3.8	4
5	The fusion peptide domain is the primary membrane-inserted region and enhances membrane interaction of the ectodomain of HIV-1 gp41. Molecular Membrane Biology, 2010, 27, 31-44.	2.0	8
6	Membrane interaction and structure of the transmembrane domain of influenza hemagglutinin and its fusion peptide complex. BMC Biology, 2008, 6, 2.	3.8	54
7	The application of perfluorooctanoate to investigate trimerization of the human immunodeficiency virus gp41 ectodomain by electrophoresis. Electrophoresis, 2008, 29, 3175-3182.	2.4	8
8	Direct solid-phase synthesis and fluorescence labeling of large, monodisperse mannosylated dendrons in a peptide synthesizer. Organic and Biomolecular Chemistry, 2008, 6, 1377.	2.8	27
9	pH-dependence of intermediate steps of membrane fusion induced by the influenza fusion peptide. Biochemical Journal, 2006, 396, 557-563.	3.7	9
10	Self-association of glutamic acid-rich fusion peptide analogs of influenza hemagglutinin in the membrane-mimic environments: Effects of positional difference of glutamic acids on side chain ionization constant and intra- and inter-peptide interactions deduced from NMR and gel electrophoresis measurements. Biochimica Et Biophysica Acta - Biomembranes, 2005, 1712, 37-51.	2.6	14
11	Structure and membrane interaction of the internal fusion peptide of avian sarcoma leukosis virus. FEBS Journal, 2004, 271, 4725-4736.	0.2	15
12	Secondary structure, phospholipid membrane interactions, and fusion activity of two glutamate-rich analogs of influenza hemagglutinin fusion peptide. Archives of Biochemistry and Biophysics, 2004, 425, 173-183.	3.0	10
13	Effects of alterations of the amino-terminal glycine of influenza hemagglutinin fusion peptide on its structure, organization and membrane interactions. Biochimica Et Biophysica Acta - Biomembranes, 2003, 1612, 41-51.	2.6	20
14	Fluorescence evidence for a loose self-assembly of the fusion peptide of influenza virus HA2 in the lipid bilayer. Molecular Membrane Biology, 2003, 20, 345-351.	2.0	15
15	The LLSGIV stretch of the N-terminal region of HIV-1 gp41 is critical for binding to a model peptide, T20. Protein Engineering, Design and Selection, 2003, 16, 311-317.	2.1	42
16	Conformation and Interaction with the Membrane Models of the Amino-Terminal Peptide of Influenza Virus Hemagglutinin HA2 at Fusion pH. Archives of Biochemistry and Biophysics, 2001, 396, 89-98.	3.0	5
17	The leucine zipper motif of the envelope glycoprotein ectodomain of human immunodeficiency virus type 1 contains conformationally flexible regions as revealed by NMR and circular dichroism studies in different media. Chemical Biology and Drug Design, 2001, 57, 234-239.	1.1	2
18	A helix initiation motif, XLLRA, is stabilized by hydrogen bond, hydrophobic and van der Waals interactions. BBA - Proteins and Proteomics, 2000, 1478, 39-50.	2.1	5

#	ARTICLE	IF	CITATIONS
19	The Amino-terminal Region of the Fusion Peptide of Influenza Virus Hemagglutinin HA2 Inserts into Sodium Dodecyl Sulfate Micelle with Residues 16-18 at the Aqueous Boundary at Acidic pH. <i>Journal of Biological Chemistry</i> , 2000, 275, 19150-19158.	3.4	43
20	Biophysical Characterization of the Structure of the Amino-terminal Region of gp41 of HIV-1. <i>Journal of Biological Chemistry</i> , 1999, 274, 5299-5309.	3.4	39
21	Proline-induced kink in a helix arises primarily from dihedral angle energy: a molecular dynamics simulation on alamethicin. <i>Chemical Physics Letters</i> , 1999, 301, 453-457.	2.6	5
22	Proline Affects Oligomerization of a Coiled Coil by Inducing a Kink in a Long Helix. <i>Journal of Structural Biology</i> , 1999, 128, 270-279.	2.8	54
23	Determination of the equilibrium micelle-inserting position of the fusion peptide of gp41 of human immunodeficiency virus type 1 at amino acid resolution by exchange broadening of amide proton resonances. , 1998, 12, 549-552.		12
24	Determination of the Binding Constant of a Protein Kinase C Substrate, NG(28-43), to Sodium Dodecyl Sulfate via the Diffusion Coefficient Measured by Pulsed Field Gradient Nuclear Magnetic Resonance. <i>Analytical Biochemistry</i> , 1998, 264, 211-215.	2.4	14
25	The FLG Motif in the N-Terminal Region of Glucoprotein 41 of Human Immunodeficiency Virus Type 1 Adopts a Type-I beta Turn in Aqueous Solution and Serves as the Initiation Site for Helix Formation. <i>FEBS Journal</i> , 1997, 247, 896-905.	0.2	18
26	NMR and circular dichroism studies on the conformation of a 44-mer peptide from a CD4-binding domain of human immunodeficiency virus envelope glycoprotein. <i>Chemical Biology and Drug Design</i> , 1997, 49, 432-443.	1.1	3
27	The amino-terminal fusion domain peptide of human immunodeficiency virus type 1 gp41 inserts into the sodium dodecyl sulfate micelle primarily as a helix with a conserved glycine at the micelle-water interface. <i>Journal of Virology</i> , 1997, 71, 6593-6602.	3.4	85
28	Solution Structure Studies of the Cobalt Complex of a Bleomycin Functional Model Bound to d(CGCAATTGCG) <sub>2</sub> by Two-Dimensional Nuclear Magnetic Resonance Methods and Restrained Molecular Dynamics Simulation. <i>Bioconjugate Chemistry</i> , 1996, 7, 670-679.	3.6	6
29	On the importance of van der Waals interaction in the groove binding of DNA with ligands: restrained molecular dynamics study. <i>International Journal of Biological Macromolecules</i> , 1996, 19, 279-285.	7.5	13
30	Circular dichroism study on the secondary structural change induced by complex formation of a peptide derived from a CD4 binding site of HIV-1 envelope glycoprotein gp120 and a peptide from the N-terminal domain of CD4. <i>International Journal of Peptide Research and Therapeutics</i> , 1996, 3, 293-300.	0.1	1
31	Characterization of Conformation and Dynamics of CD4 Fragment (81-92) TYICEVEDQKEE and Its Benzylated Derivative by <sup>1</sup> H NMR Spectroscopy and Molecular Modeling: Relevance of Conformation to Biological Function. <i>Journal of Acquired Immune Deficiency Syndromes</i> , 1996, 11, 222-232.	0.3	2
32	Molecular mechanics calculations on the complexes between analogues of Hoechst 33258 and d(CGCGAAT-TCGCG) <sub>2</sub> : influence of bulky group substitution on base pair preference of DNA minor groove binders. <i>Canadian Journal of Chemistry</i> , 1995, 73, 878-884.	1.1	2