Curriculum Vitae

Name

Jung-Hsin Lin

Current Position

Research Fellow, Biomedical Translation Research Center & Research Center for Applied Sciences, Academia Sinica
Jointly-Appointed Professor, College of Medicine, School of Pharmacy, National Taiwan University & College of Engineering Sciences, Chang Gung University

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Education

Ph.D. in Biophysics, 1996.10-2000.1, Institut für Festkörperforchung (Institute of Solid State Research), Forschungszentrum Jülich (Research Center Jülich) & Institute of Physics, Duisburg University, Germany
M.S., 1990.9-1992.6, Graduate Institute of Physics, National Taiwan University
B.S. 1986.10-1990.6, Department of Physics, National Taiwan University

Professional Experiences

Deputy Director, Biomedical Translation Research Center, Academia Sinica (2020.11-2025.10)
Chief Executive Officer of the Thematic Center for Intelligence Medicine, Biomedical Translation Research Center, Academia Sinica (2021.4-2024.8)
Deputy Director, Research Center for Applied Sciences, Academia Sinica (2019.2-2020.10)
Chief Executive Officer of the Thematic Center for Biomedical Applications, Research Center for Applied Sciences, Academia Sinica (2015.1-2020.10)
Bioinformatics Specialist (2000.9-2002.8): Howard Hughes Medical Institute, University of California at San Diego, U.S.A.
Postdoctoral researcher (2000.1-2000.9): John von Neuman Institute for Computing, Forschungszentrum Jülich, Germany

Research Interests

Computational biophysics, bioinformatics, structural biology, molecular dynamics simulations, membrane biophysics, drug discovery and drug design

Selected Publications (※3-5 major papers)

Shu-Yu Huang, Orion Shih, U-Ser Jeng, Chi-Fon Chang, **Jung-Hsin Lin***, and Thérèse E Malliavin*. **pH sensitivity of the SERF1a conformational ensemble**. *ACS Omega* **11:** 2614-2627 (2026).

Ting-Wei Chang, Sheng-Hann Wang, Iuan-Sheau Chin, Pei-Zhen Li, Shu-Cheng Lo, Shu-Yi Hsieh, Jung-Hsin Lin*, Pei-Kun Wei*
Biomimetic affinity sensor for ultrasensitive detection of nicotinoids.
Biosensors and Bioelectronics. **239:** 115630 (2023)

Dhananjay C. Joshi, Charlie Gosse, Shu-Yu Huang and **Jung-Hsin Lin***
A curvilinear-path umbrella sampling approach to characterizing the interactions between rapamycin and three FKBP12 variants
Front. Mol. Biosci. **9:** 879000 (2022)

Dhananjay Joshi and **Jung-Hsin Lin***
Delineating protein-protein curvilinear dissociation pathways and energetics with multiple-walker umbrella sampling simulations.
J. Comput. Chem. **40:** 1652-1663 (2019)

Lecture Title

Biophysical and structural characterization of an intrinsically disordered protein catalyzing amyloidogenesis in neurodegenerative diseases

Abstract (500 words maximum)

We recently proposed a novel scheme for determining the structures of intrinsically disordered proteins (IDPs) with a systematic structure enumeration method, named Threading-Augmented Interval Branch-and Pruned (TAiBP), which is based on a distance geometry algorithm and can be used to harness the information from nuclear magnetic resonance (NMR) and small angle X-ray scattering (SAXS) experiments, to achieve very comprehensive generation of protein structures. All-atom explicit solvent molecular dynamics simulations were also conducted to generate more expanded conformation ensembles. For the first time, the structure determination of the human SERF1a protein has been carried out with this new approach. SERF1a belongs to the MOAG-4/SERF class of proteins, which is a positive regulator of the aggregate formation of amyloid proteins and has been suggested to play important roles in numerous aging-related neurodegenerative diseases. Previous studies indicated that SERF1a is a very flexible protein, containing at least one α-helical region. Here we had provided the first description of the conformational ensembles of SERF1a at two pH values (6 and 6.8). We also compared the conformation generations for the case of SERF1a using CYANA-FLYA procedure and the TAiBP procedure. In our integrated scheme the generated conformations were filtered using the Pepsi-SAXS program by fitting the intensive curves from the SAXS experiments combining with size exclusion chromatography (i.e., SEC-SAXS). At pH 6.8, a good fit of the SEC-SAXS curves can be obtained with the CYANA and TAiBP conformations, while at pH 6, the NMR conformations from the CYANA procedure cannot match the SEC-SAXS curves with both Pepsi-SAXS and WAXSiS, implying a problem of limited conformation generation due to the additional long-range nuclear Overhauser effects (NOEs) between residues Lys^{13} and Thr^{32} in this pH condition. The conformations generated by the TAiBP scheme indicated that the shortening of the C-terminal α-helix, as well as the destabilization of the N-terminal α-helix at acidic pH, may be related to the physiological function of SERF1a in the nucleoli. Interestingly, the conformations generated by TAiBP demonstrated that the N-terminal region of SERF1a displays numerous possible binding pockets, particularly in the region interacting with α-synuclein, as assessed by chemical shift perturbations. Our recent NMR-based screening using F^{19} compounds also discovered several compounds that can bind significantly with SERF1a, supporting the existences of these binding pockets. The conformations of SERF1a generated by TAiBP can also be used to derive a description of the internal dynamics in agreement with NMR relaxation. In general, the TAiBP procedure allows for a more comprehensive exploration conformational space which enables consistent interpretation of multifaceted biophysical characterization.