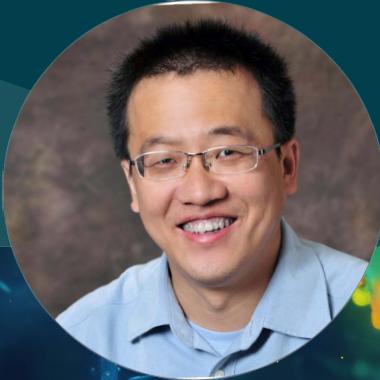


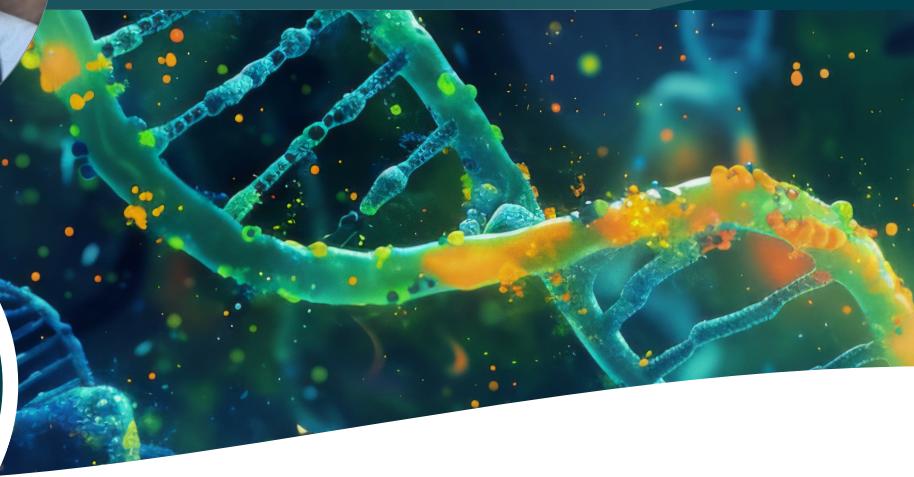
STRECH



Seminars in Translational Research



January 23, 2026
9:00AM-10:00AM
Virtual Seminar



SCAN ME



Molecular Understanding and Evidence of Amyloid Cross-seeding **Presented by Jie Zheng, PhD**

Distinguished Research Professor
Department of Biomedical Engineering and Chemical Engineering
The University of Texas at San Antonio

Accumulating evidence indicates that misfolded proteins from distinct amyloid diseases can cross-interact to accelerate each other's aggregation—a process known as amyloid cross-seeding. This phenomenon is increasingly recognized as a key mechanism underlying the propagation of shared pathological features across different tissues and diseases, including Alzheimer's disease (AD), Parkinson's disease (PD), and type 2 diabetes (T2D). To elucidate the molecular basis of amyloid cross-seeding, we systematically investigated several representative systems—A β /hIAPP (AD/T2D), prion/A β /hIAPP (PD/AD/T2D), antimicrobial peptides/A β /hIAPP, SEVI/A β —through complementary experimental and computational approaches. Specifically, we:

- (i) demonstrated cross-seeding phenomena via aggregation kinetics, structural characterization, and cytotoxicity assays;
- (ii) uncovered both promotion and inhibition effects arising from heterologous interactions;
- (iii) revealed that cross-seeding extends beyond amyloid–amyloid interactions to include amyloid–non-amyloid disease-related proteins, suggesting a broader molecular interface between neurodegenerative and systemic disorders;
- (iv) identified the molecular binding modes between distinct amyloid species through atomistic simulations.

Together, these findings establish a structure-based framework for understanding amyloid cross-seeding mechanisms and provide molecular-level insights into the interconnected pathology of diverse amyloid-related and protein-misfolding diseases.

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