

# Assembly of $\alpha$ -Helical Nanopores for Ultrasensitive Disease Protein Detection

Varsha Shaji<sup>1</sup>, Rajeev Jain<sup>2</sup>, Neethu Puthumadathil<sup>1</sup>, Krishnananda Chattopadhyay<sup>2</sup>, and  
**Kozhinjampara R Mahendran<sup>1\*</sup>**

<sup>1</sup> *Membrane Biology Laboratory, Transdisciplinary Research Program, Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram 695014, India.*

<sup>2</sup> *Structural Biology and Bioinformatics Division, Indian Institute of Chemical Biology, Kolkata, West Bengal, India.*

Synthetic nanopores are promising candidates for single-molecule protein sensing, with  $\alpha$ -helical nanopores offering a powerful platform for chemical modifications and tunable selectivity. Here, we report a synthetic  $\alpha$ -helical peptide pore, pPorA, which assembles autonomously into octameric pores with both large and small conductance states. Large cyclic sugars bind to small-diameter pores without translocation but traverse through the large-diameter pores, confirming the structural flexibility and size-dependent selectivity of these pores. Furthermore, by utilizing large-diameter pores, we achieved real-time, label-free detection of the conformational states of  $\alpha$ -synuclein and its pathological mutants associated with Parkinson's disease. Multiple pathological  $\alpha$ -synuclein proteins were simultaneously introduced into the bilayer system and were individually resolved and classified based on their distinct current signatures. The small-diameter pores were utilized to distinguish conformational variants of the mitochondrial peptide Humanin and its disease-associated mutants, providing insight into their roles in the regulation of apoptosis. These findings establish the functional versatility of  $\alpha$ -helical peptide pores for complex protein sensing, demonstrating their application in developing next-generation nanopore diagnostics tools.

## References:

1. Krishnan R et al. JACS 2019, 7, 2949.
2. Krishnan R et al. Nature Communications 2022, 13, 5377.
3. Firzan CA et al. Nature Communications 2025, 16, 8666.