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| Title:       | Energy migration captures membrane-induced oligomerization of the prion protein  |
| Authors:     | Agarwal, Aishwarya (/jspui/browse?type=author&value=Agarwal%2C+Aishwarya)<br>Das, Debapriya (/jspui/browse?type=author&value=Das%2C+Debapriya)<br>Banerjee, Tisya (/jspui/browse?type=author&value=Banerjee%2C+Tisya)<br>Mukhopadhyay, S. (/jspui/browse?type=author&value=Mukhopadhyay%2C+S.)   |
| Keywords:    | Depolarization kinetics<br>Förster resonance energy transfer<br>Fluorescence anisotropy<br>Intrinsically disordered regions  |
| Issue Date:  | 2020   |
| Publisher:   | Elsevier   |
| Citation:    | Biochimica et Biophysica Acta - Proteins and Proteomics 1868(2),   |
| Abstract:    | Excitation energy migration via homo-Förster resonance energy transfer (homo-FRET) can serve as an intermolecular proximity ruler within complex biomolecular assemblies. Here we present a unique case to demonstrate that energy migration can be a novel and sensitive readout to capture the membrane-mediated misfolding and oligomerization of the human prion protein (PrP), which is known to undergo an aberrant conformational conversion from an $\alpha$ -helical form into a self-propagating aggregated $\beta$ -rich state causing deadly transmissible neurodegenerative diseases. Using site-specific energy migration studies by monitoring steady-state and time-resolved fluorescence anisotropy of fluorescently-tagged PrP, we elucidate the molecular details of lipid membrane-induced oligomers. We show that the intrinsically disordered N-terminal segment is critical for lipid-induced conformational sequestration of PrP into higher-order, $\beta$ -rich oligomeric species that exhibit membrane permeabilization. Our results revealed that the N-terminal regions constitute the central core of the oligomeric architecture, whereas the distal C-terminal ends participate in peripheral association with the lipid membrane. Our study will find applications in the sensitive detection and in the structural characterization of membrane-induced protein misfolding and aggregation in a variety of deadly amyloid diseases. |
| URI:         | <a href="https://www.sciencedirect.com/science/article/pii/S1570963919302092?via%3Dihub">https://www.sciencedirect.com/science/article/pii/S1570963919302092?via%3Dihub</a><br>( <a href="https://www.sciencedirect.com/science/article/pii/S1570963919302092?via%3Dihub">https://www.sciencedirect.com/science/article/pii/S1570963919302092?via%3Dihub</a> )<br><a href="http://hdl.handle.net/123456789/3408">http://hdl.handle.net/123456789/3408</a> ( <a href="http://hdl.handle.net/123456789/3408">http://hdl.handle.net/123456789/3408</a> )  |
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