Supporting Information

Familial Alzheimer's Disease Osaka Mutant (ΔE22) β-Barrels Suggest an Explanation for the Different $Aβ_{1-40/42}$ Preferred Conformational States Observed by Experiment

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Title Running Head: Structure of FAD-linked Osaka mutant ΔE22 barrel

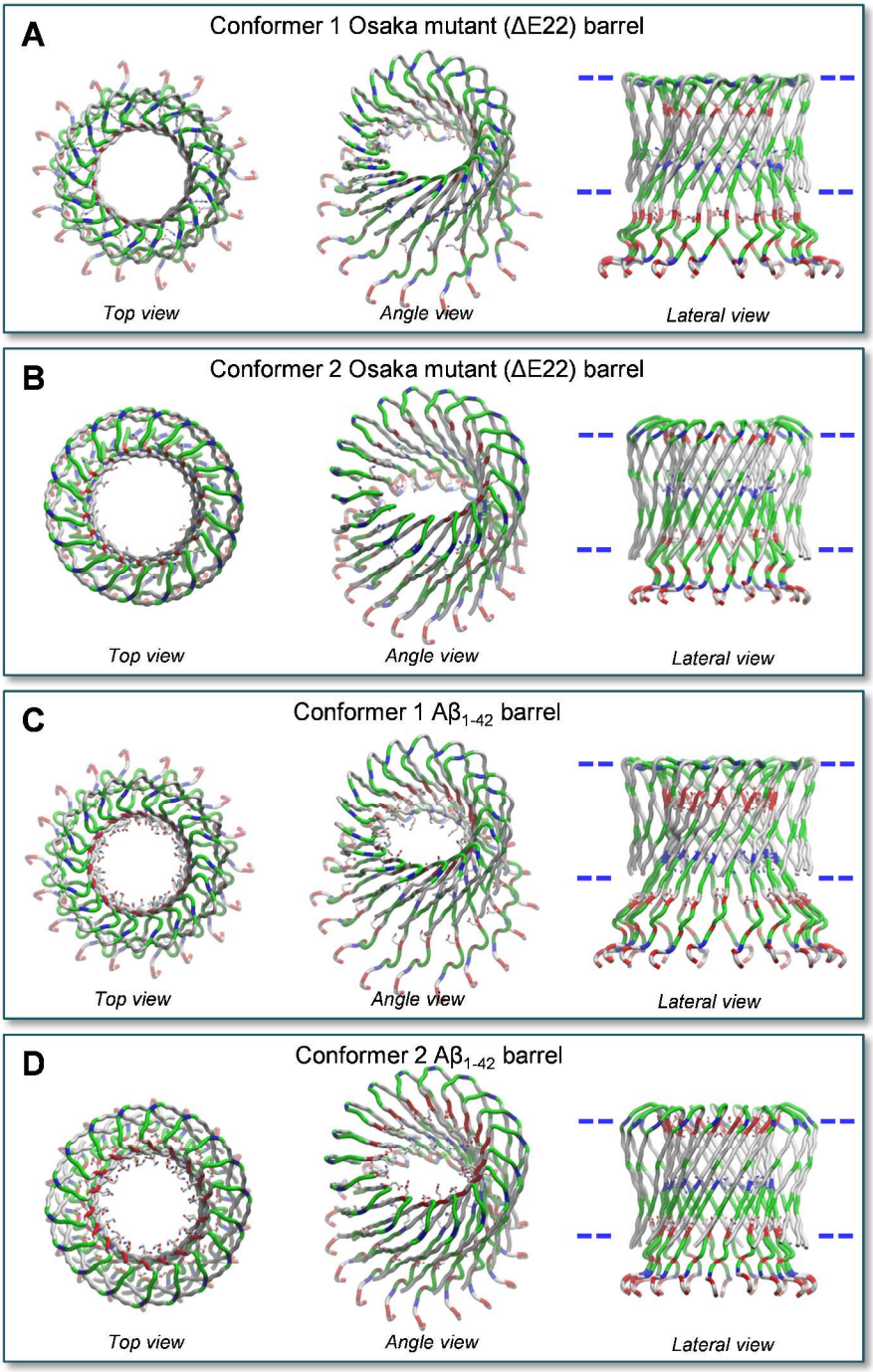
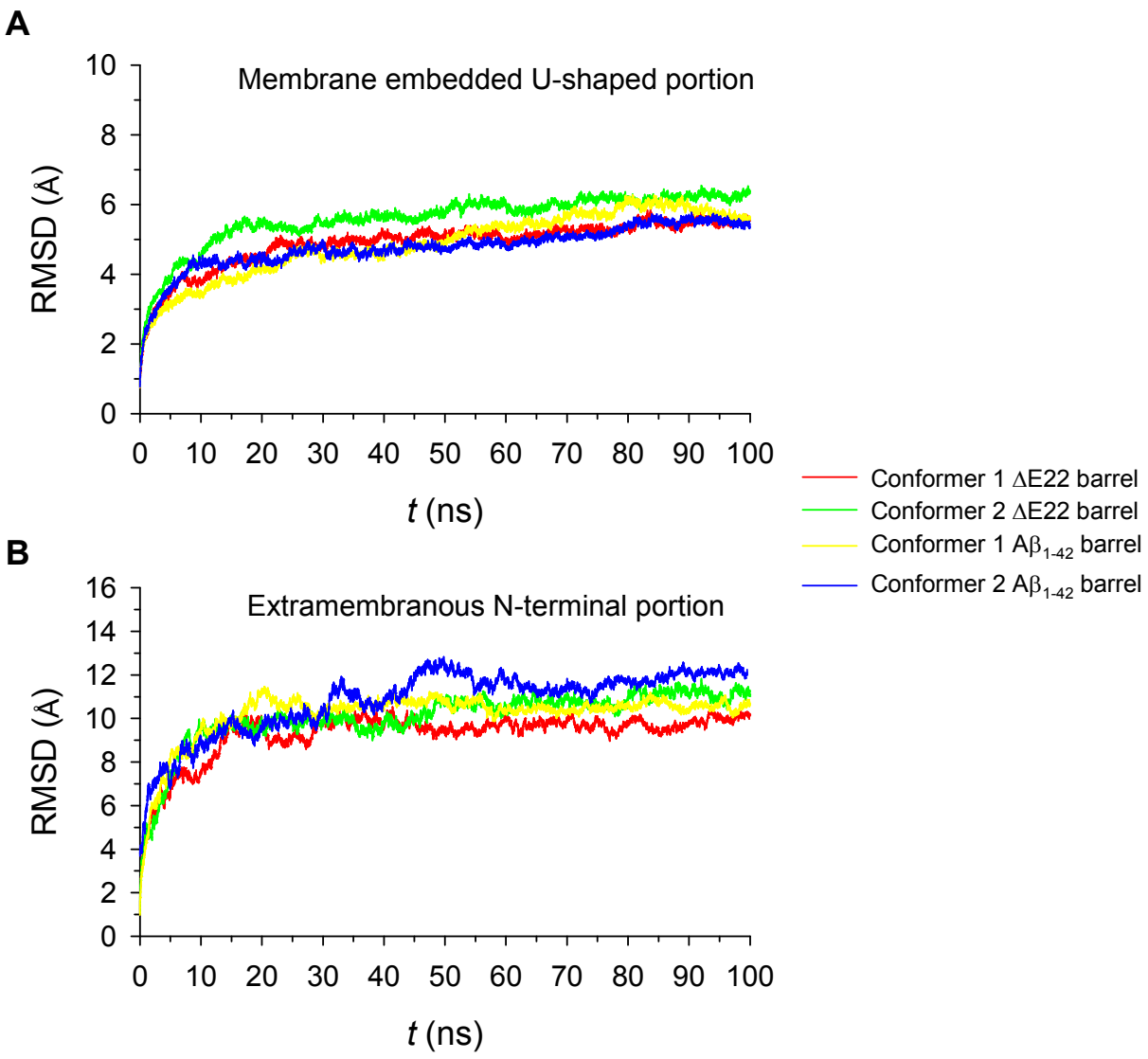


Figure S1. The initial barrel structures of MD simulations in ribbon representation for the (A) conformer 1 and (B) conformer 2 Osaka mutant (ΔE22) barrels, and the (C) conformer 1 and (D) conformer 2 $A\beta_{1\text{-}42}$ barrels. In the peptide ribbon, hydrophobic, polar/Gly, positively charged, and negatively charged residues are colored white, green, blue, and red, respectively. Charged side-chains of three selected residues, Glu11 and Lys16 for both mutant and wild type barrels, and Glu22 for the wild type barrels only, are shown as threads.


A
Membrane embedded U-shaped portion
RMSD (Å)
t (ns)
B
Extramembranous N-terminal portion
RMSD (Å)
t (ns)
Conformer 1 ΔE22 barrel
Conformer 2 ΔE22 barrel
Conformer 1 Aβ1-42 barrel
Conformer 2 Aβ1-42 barrel

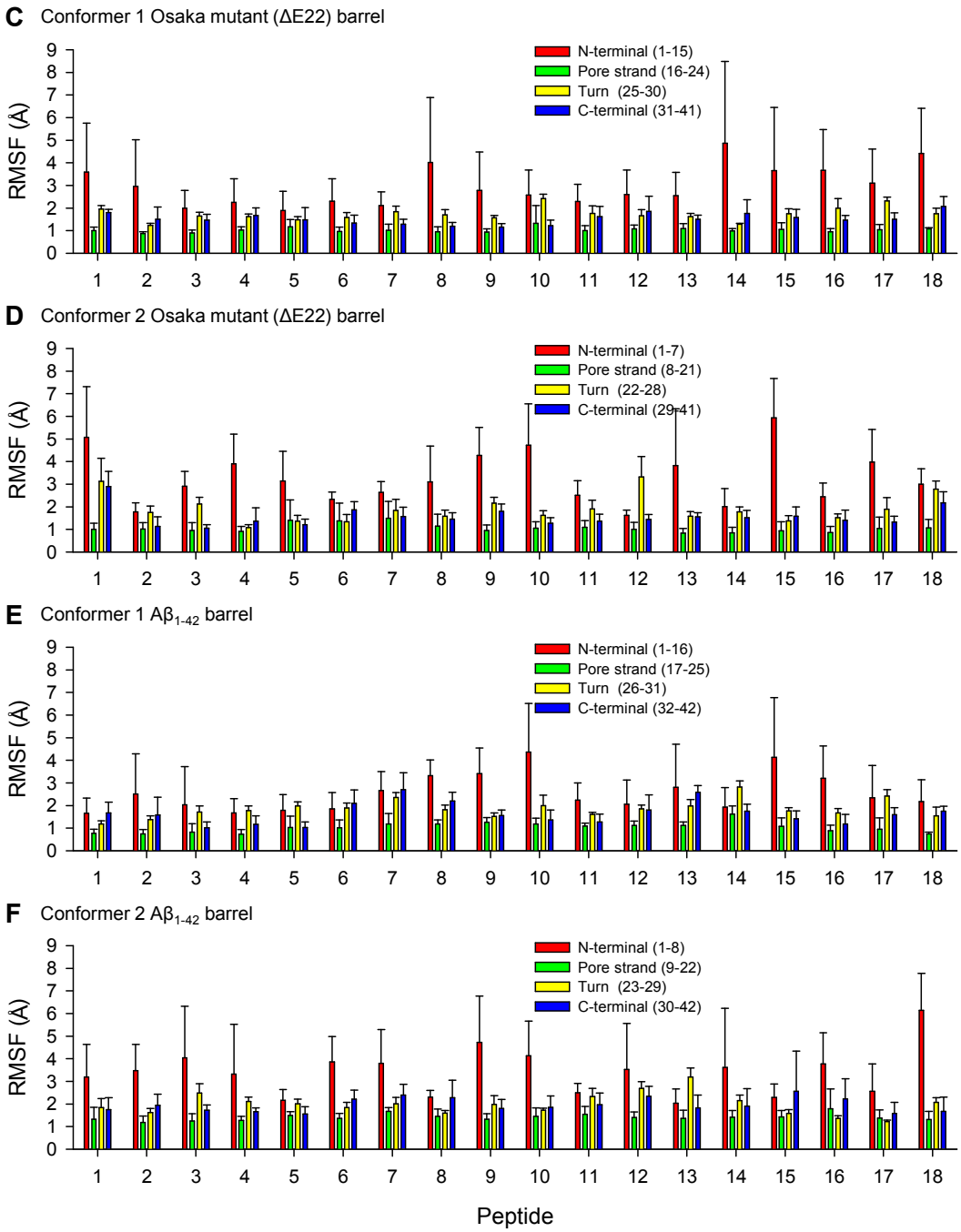


Figure S2. The root-mean-squared deviation (RMSD) from the starting point for backbone heavy atoms of (A) the membrane embedded U-shaped portion and (B) extramembranous N-terminal portion of Aβ barrels: the conformer 1 (red lines) and conformer 2 (green line) Osaka mutant (ΔE22) barrels, and the conformer 1 (yellow line) and conformer 2 (blue line) $A\beta_{1-42}$ barrels. The average root-mean-squared-fluctuation (RMSF) from the starting point for backbone atoms of each monomer for the (C) conformer 1 and (D) conformer 2 Osaka mutant (ΔE22) barrels, and the (E) conformer 1 and (F) conformer 2 $A\beta_{1-42}$ barrels.

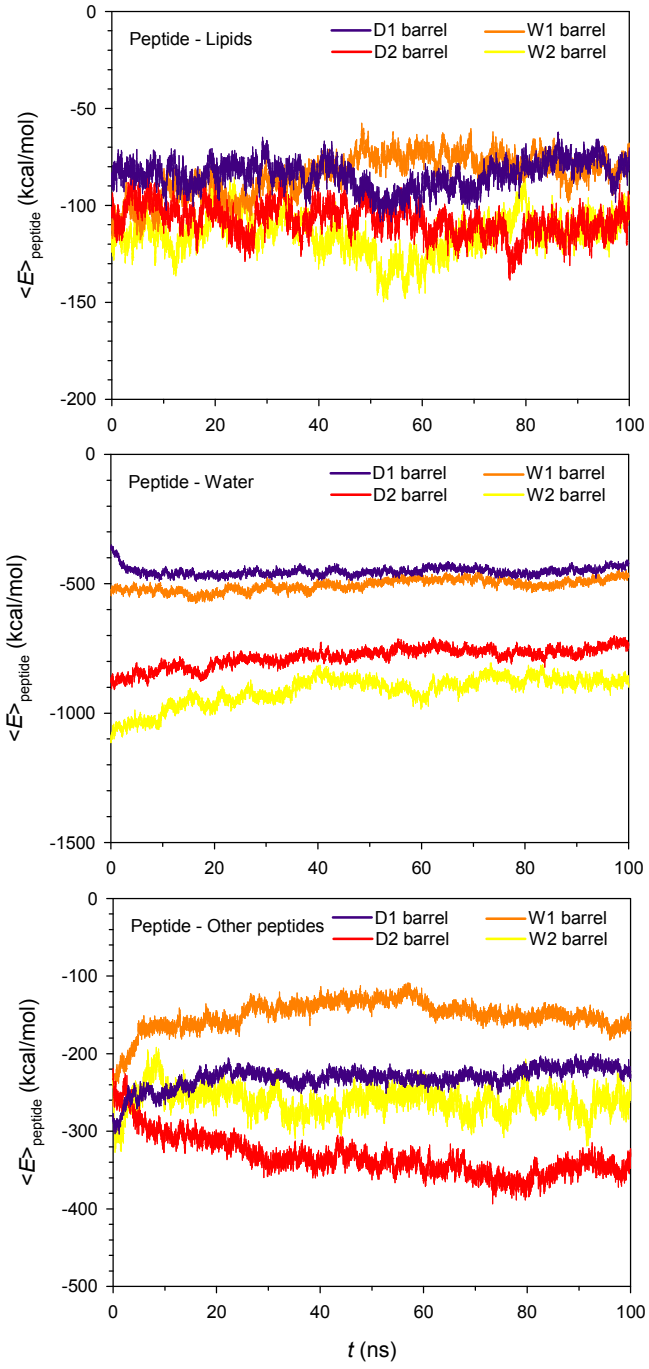


Figure S3. Time series of averaged interaction energy of the membrane embedded U-shaped portion of the peptide with lipids (upper panel), water (middle panel), and other peptides (bottom panel) for the conformer 1 and 2 Osaka mutant (ΔE22) barrels (denoted as D1 and D2, respectively), and the conformer 1 and 2 wild type $A\beta_{1\text{-}42}$ barrels (denoted as W1 and W2, respectively).

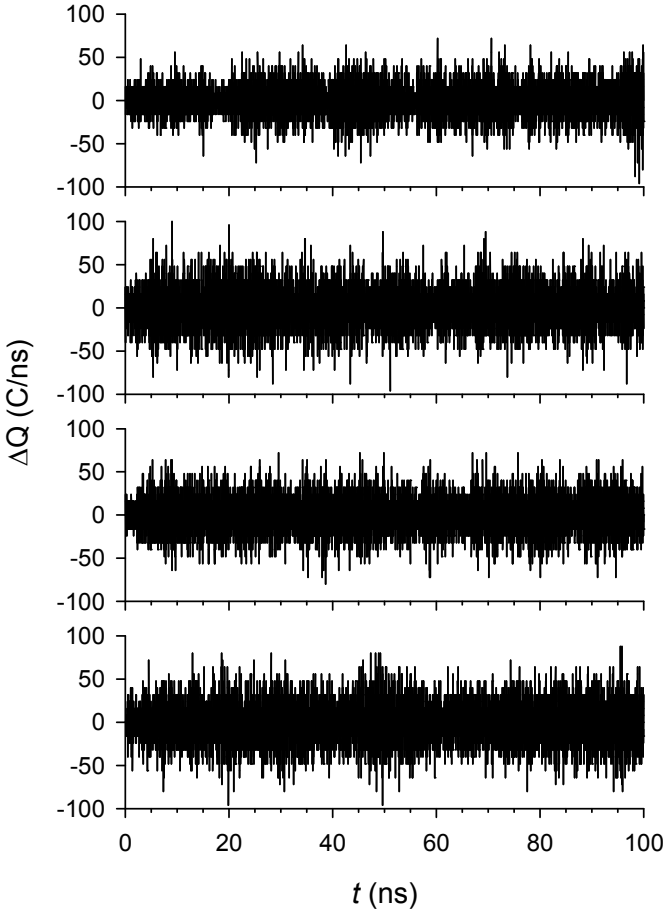


Figure S4. Change in total charge in the pore as a function of the simulation time for the conformer 1 and 2 Osaka mutant (ΔE22) barrels (1st and 2nd rows), and the conformer 1 and 2 $A\beta_{1\text{-}42}$ barrels (3rd and 4th rows). The pore height with cutoff along the pore axis, $-1.8 < z < 1.8$ nm was used.