Supplementary Information for

Structural Heterogeneity in
Familial Alzheimer's Disease Mutants of Amyloid-Beta Peptide

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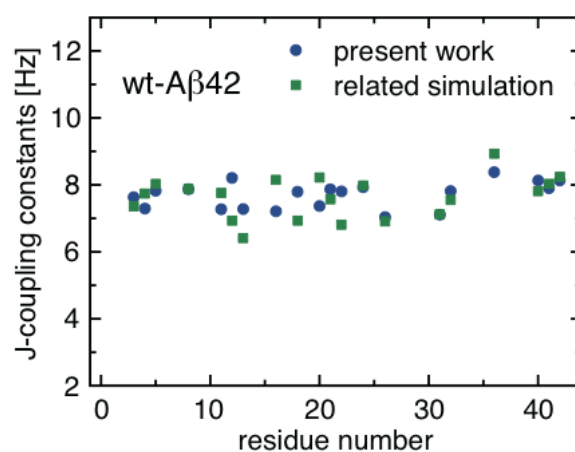*Cheongpa-ro 47-gil 100, Yongsan-Ku, Seoul 140-742, Korea*

Figure S1. *J*-coupling constants versus amino acid residue for the wt-Aβ42 from the present work (blue circles) are compared with those from the related simulation study (K. A. Ball *et al*., *Biochemistry*, 2011, **50**, 7612–7628, green squares).
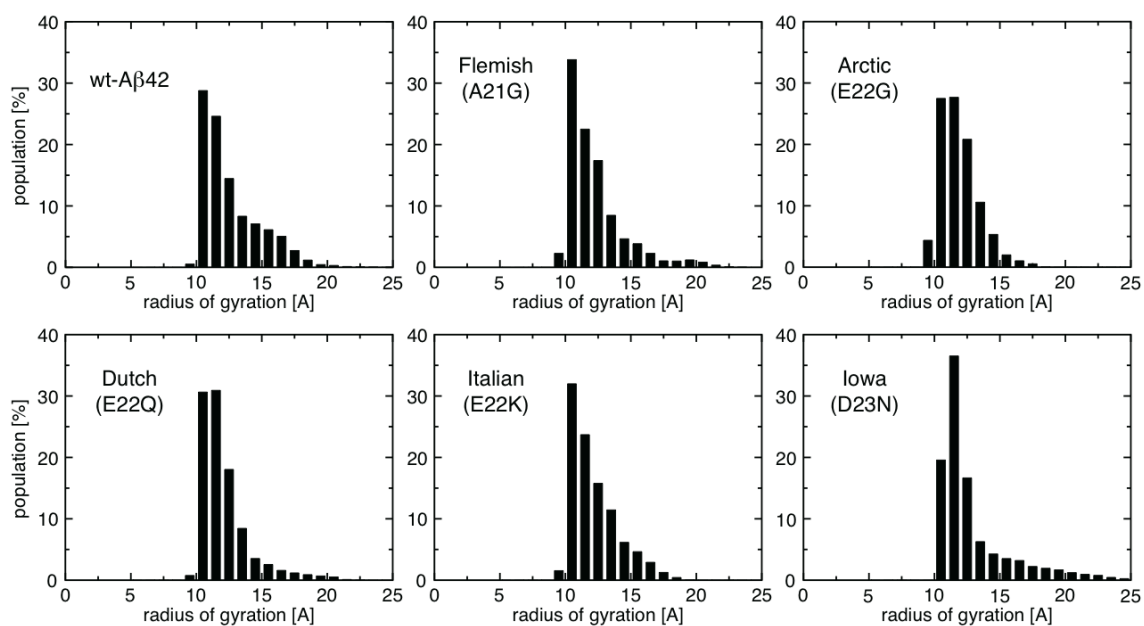
Figure S2. Distribution of the radius of gyration for wt-Aβ42 and its familial AD mutants indicated in each panel.
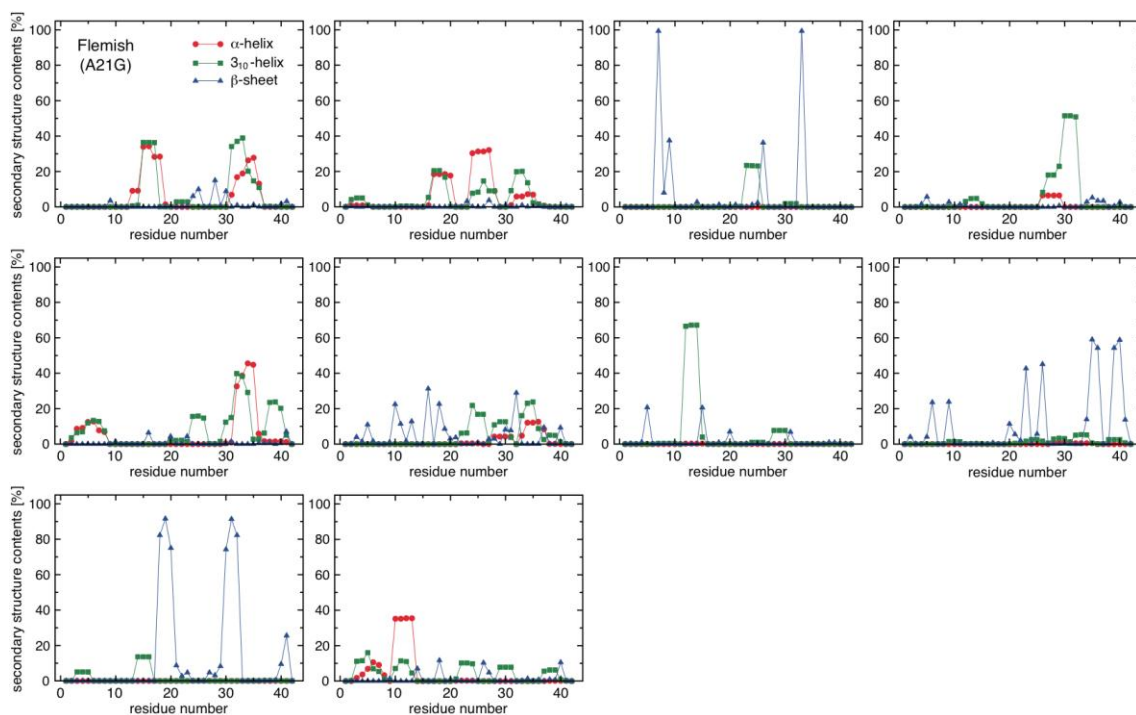
Figure S3. Average secondary-structure contents versus amino acid residue in each of 10 independent trajectories of the Flemish (A21G) mutant of Aβ42 (red circles: α-helix, green squares: 3_{10}-helix, blue triangles: β-sheet).
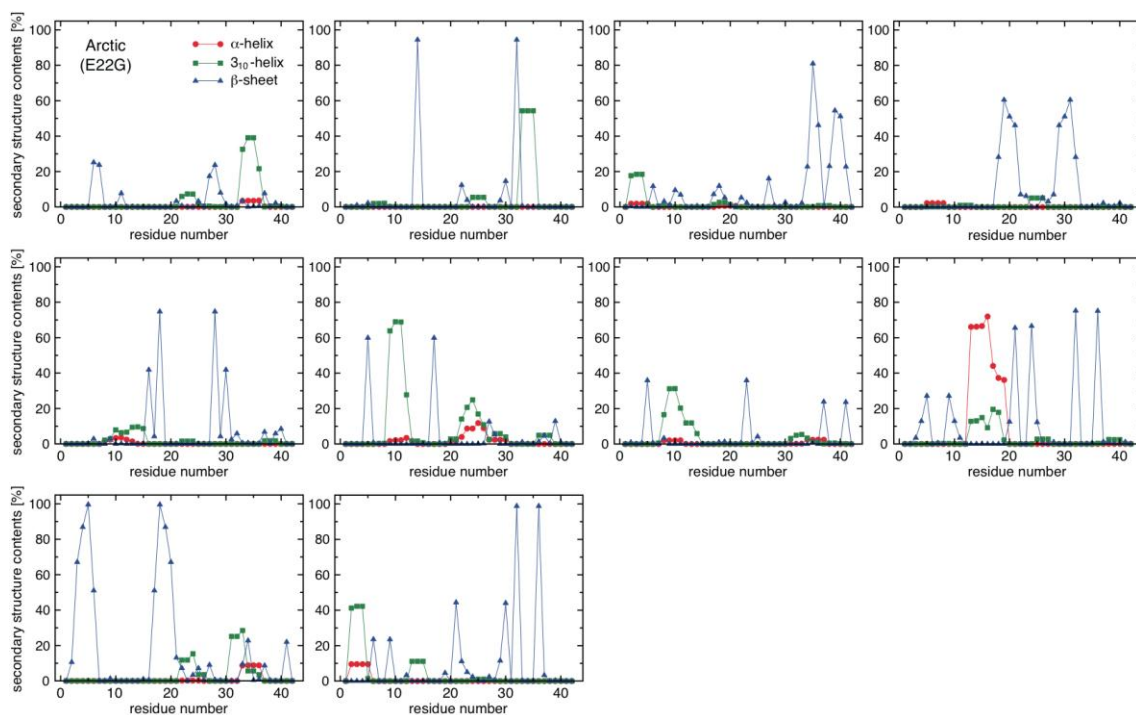
Figure S4. Average secondary-structure contents versus amino acid residue in each of 10 independent trajectories of the Arctic (E22G) mutant of Aβ42 (red circles: α-helix, green squares: 3_{10}-helix, blue triangles: β-sheet).
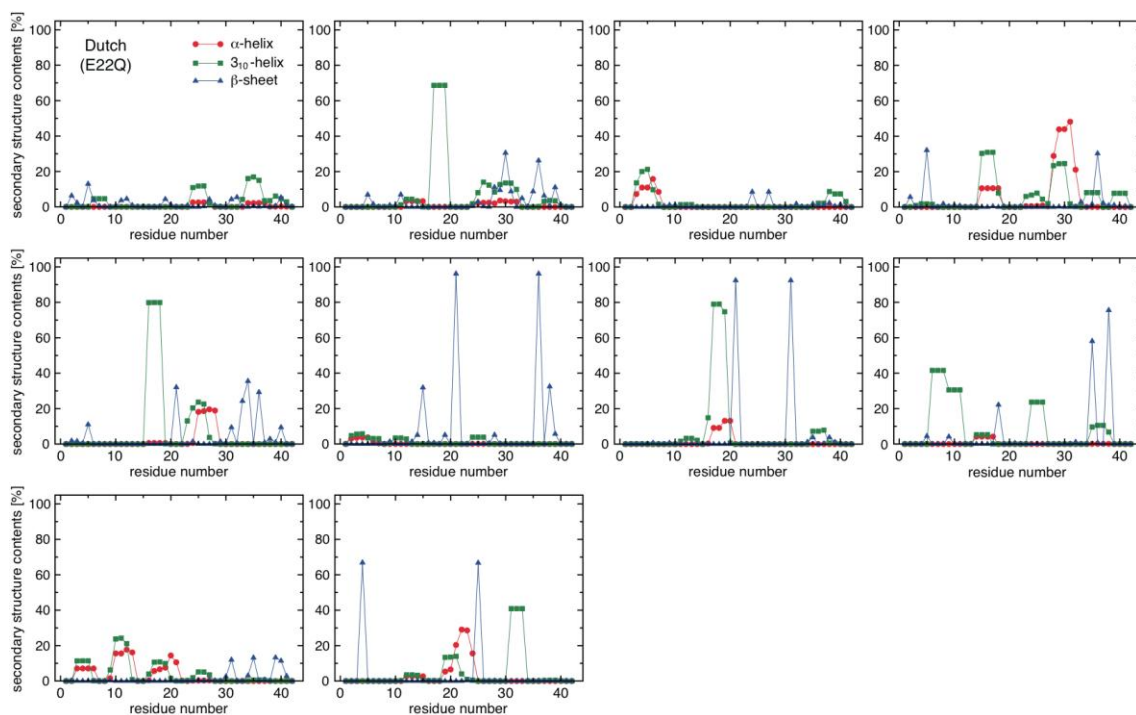
Figure S5. Average secondary-structure contents versus amino acid residue in each of 10 independent trajectories of the Dutch (E22Q) mutant of Aβ42 (red circles: α-helix, green squares: 3_{10}-helix, blue triangles: β-sheet).
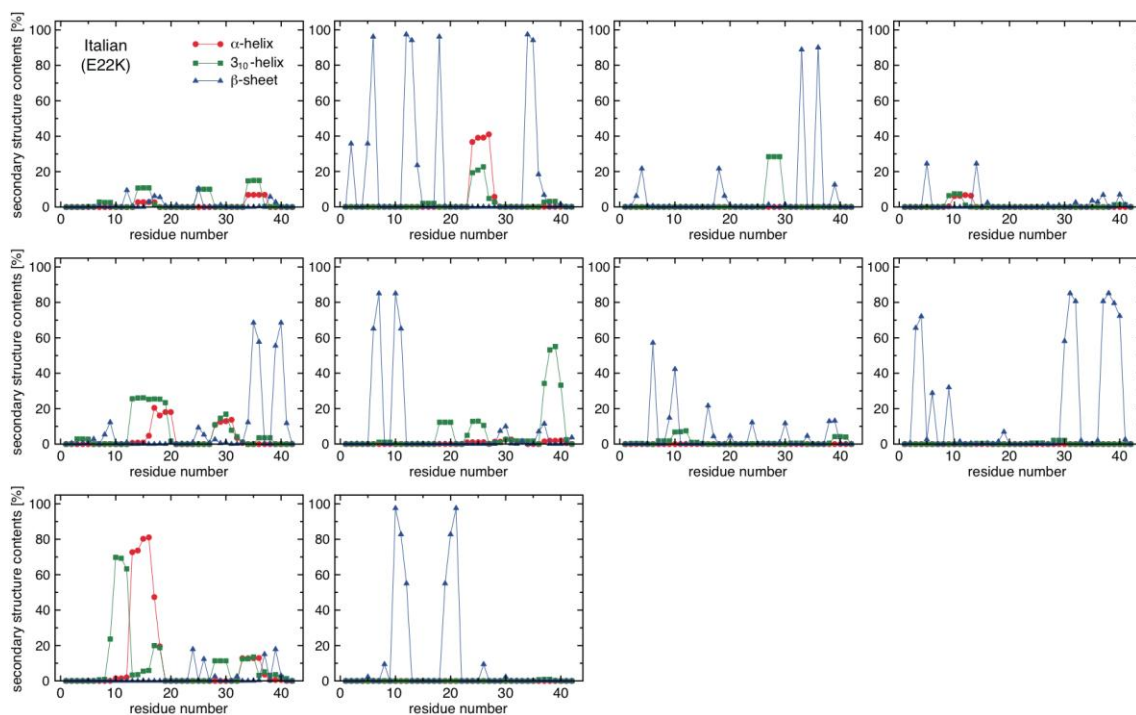
Figure S6. Average secondary-structure contents versus amino acid residue in each of 10 independent trajectories of the Italian (E22K) mutant of Aβ42 (red circles: α-helix, green squares: 3_{10}-helix, blue triangles: β-sheet).

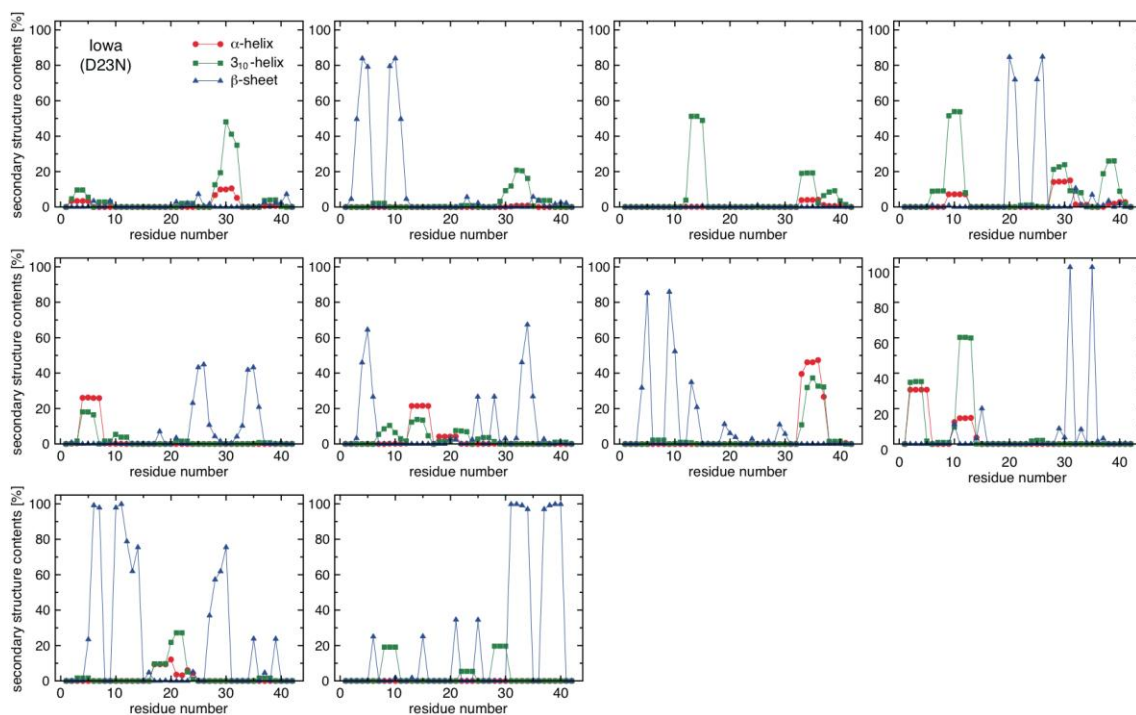**Figure S7.** Average secondary-structure contents versus amino acid residue in each of 10 independent trajectories of the Iowa (D23N) mutant of Aβ42 (red circles: α-helix, green squares: 3_{10}-helix, blue triangles: β-sheet).