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Addition/Correction

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Correction to "Molecular Simulations Indicate Marked Differences in the Structure of Amylin Mutants, Correlated with Known Aggregation Propensity"

Cayla Miller, Gül H. Zerze, and Jeetain Mittal*

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The horizontal axes in Figures 3 and 9 were incorrectly numbered in reverse order, from the C-terminal to the N-terminal end, while our interpretation followed the standard N- to C-terminal numbering. The corrected Figures 3 and 9 are shown herein. The major conclusions remain unaltered, as results in the original paper from free energies on RMSD from known NMR and X-ray crystal structures supported the importance of both regions 8−17 and 22−28, and long-range effects of mutations remain. Upon the basis of the renumbered Figure 3, we now find that the major difference in α-helical propensity between sequences, correlated with aggregation propensity, appears over residues 22−31.

The helical region identified over residues 22−31 coincides, in part, with the experimentally known amyloidogenic region 20−29, as well as with the region 22−28. In the original paper, over the latter region, we already performed RMSD from near-membrane amylin structures and found our hIAPP and hIAPP S20G trajectories to sample structures similar to those from membrane-mimicking environments, whereas neither rIAPP nor hIAPP I26P sampled similar structures. Furthermore, the renumbered Figure 9 shows that reduction of the disulfide bond in both human and rat amylin is associated with reduced α-helix propensity of the N-terminal residues, in agreement with experimental work cited in our paper, while β-sheet propensity of the N-terminal residues is increased. Long-range contacts appear to affect the secondary structure of C-terminal residues as well.

Additionally, the first and second columns in Figure 8 should be labeled "R_g" and "E2E," respectively, and in-text references to said figure interchanged likewise. The conclusions remain the same, as qualitative trends in these lengths are unaffected.

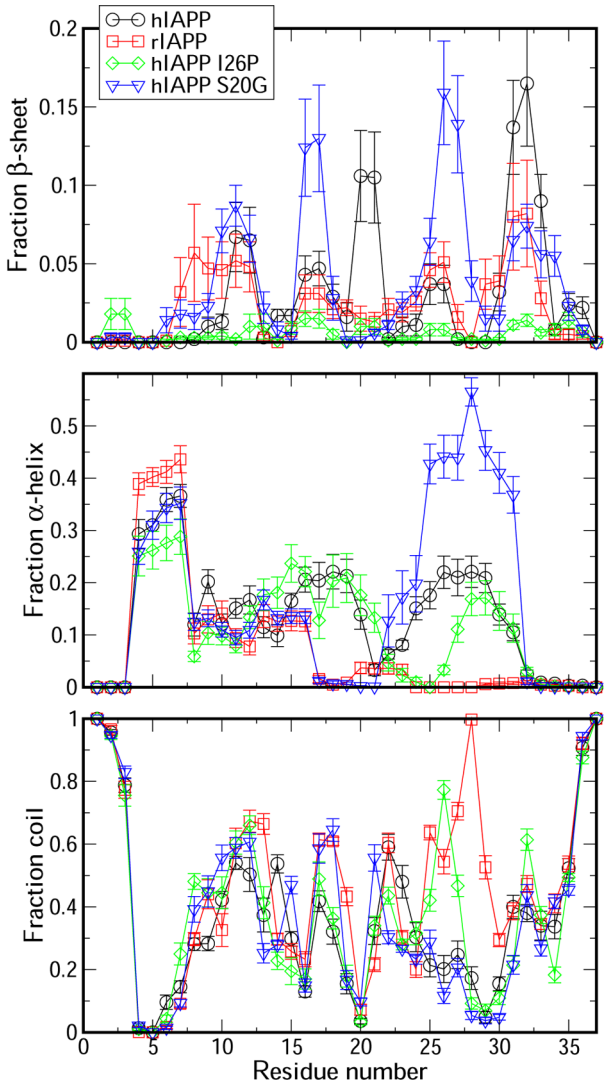

Figure 3. Per-residue fraction of time spent in secondary structure over the last 150 ns for wild-type hIAPP, rIAPP, hIAPP S20G, and hIAPP I26P.

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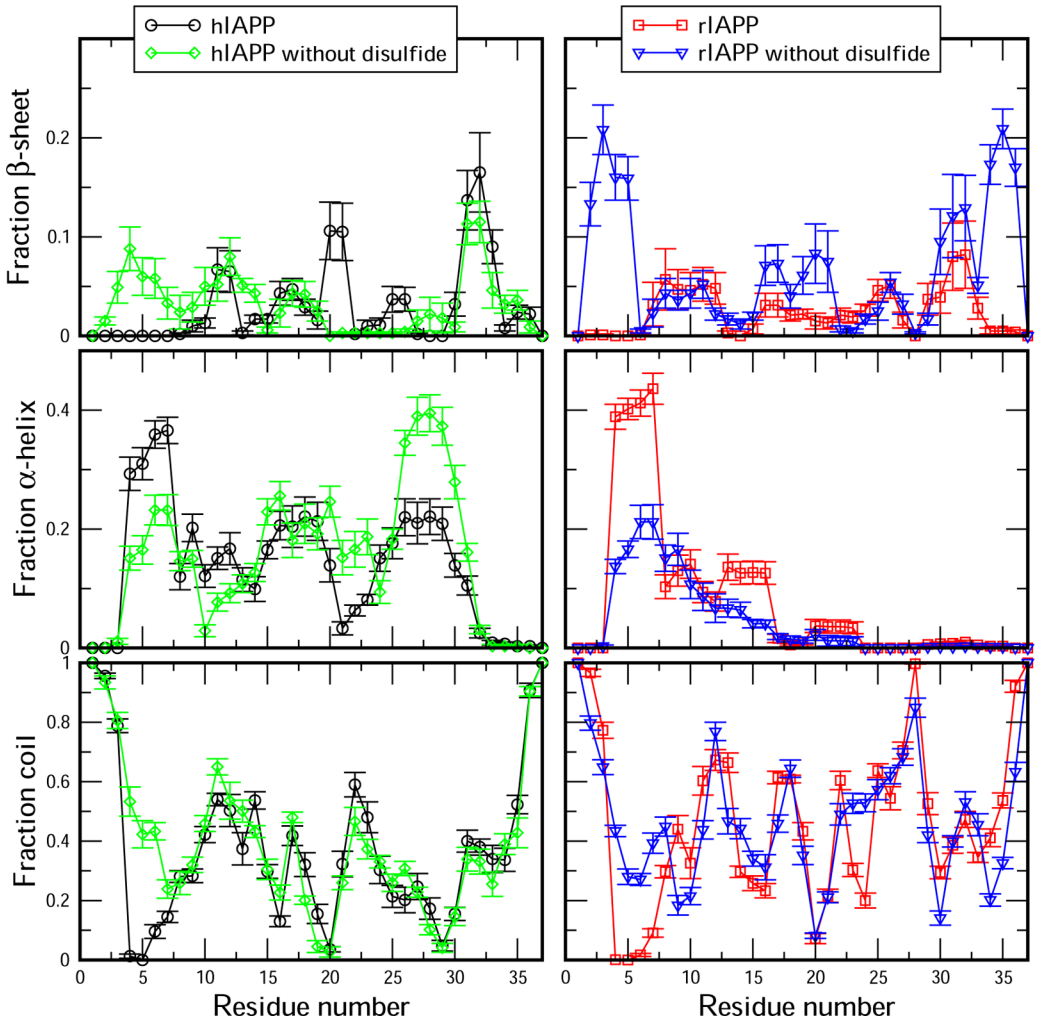

Figure 9. Per-residue fraction of time spent in secondary structure over the last 150 ns for wild-type hIAPP and rIAPP, as well as both hIAPP and rIAPP without the disulfide bond.

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