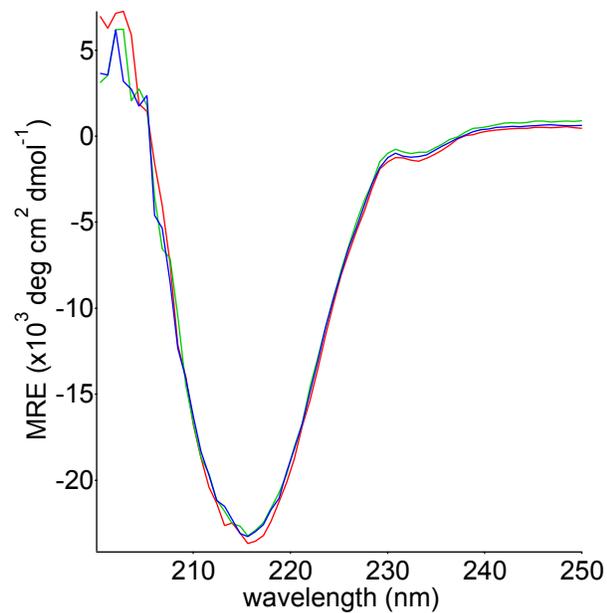
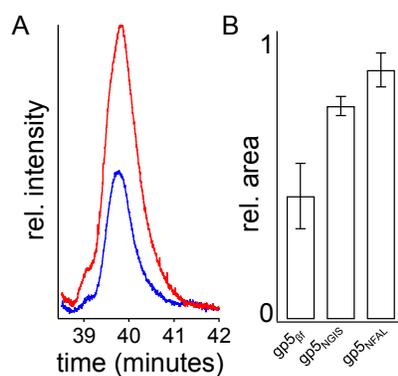


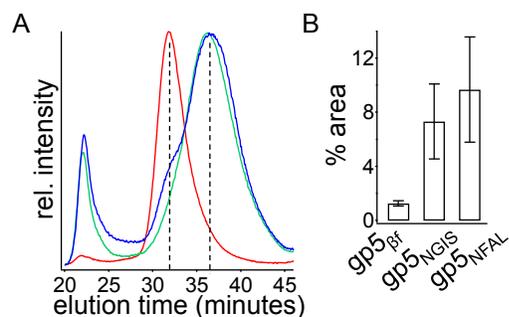
**Supporting Information**

**Figure S1:** Representative assessment of overall fold. Mean residue ellipticities from far-UV circular dichroism are shown for 10  $\mu\text{M}$   $\text{gp5}_{\beta\text{f}}$  (red),  $\text{gp5}_{\text{NGIS}}$  (blue), and  $\text{gp5}_{\text{NFAL}}$  (green), respectively.



**Figure S2:** Soluble fraction of protein after assembly of IAPP<sub>20-29</sub>/gp5 $\beta$ f aggregates.

(A) Reverse phase HPLC chromatograms of 10  $\mu$ M gp5 $\beta$ f before (red) and after (blue) aggregate assembly. (B) Statistics of relative integrated areas from repeated experiments such as shown in (A). Fraction of 10  $\mu$ M of indicated construct remaining in solution after aggregation reactions.



**Figure S3:** Size exclusion assessment of scaffolds after assembly of IAPP $_{20-29}$ /gp5 $\beta$ f aggregates. (A) Representative size exclusion profiles of completed reactions of 750  $\mu$ M IAPP $_{20-29}$  with 10  $\mu$ M of gp5 $\beta$ f (red), gp5 $_{NGIS}$  (blue), or gp5 $_{NFAL}$  (green). Vertical dotted lines represent elution positions assigned (using sizing standards) to trimer (~37 min) and dimer of trimers (~32 min). Profiles were measured at 280 nm (note, IAPP $_{20-29}$  contains no tryptophan or tyrosine). (B) Statistics determined from repeats of such data as (A) in which the relative area of the excluded volume fraction (~22 min) is divided by the area of the entire profile.