Rationally designed peptoids modulate aggregation of amyloidbeta 40

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Matrix-assisted laser desorption/ionization mass spectrometry

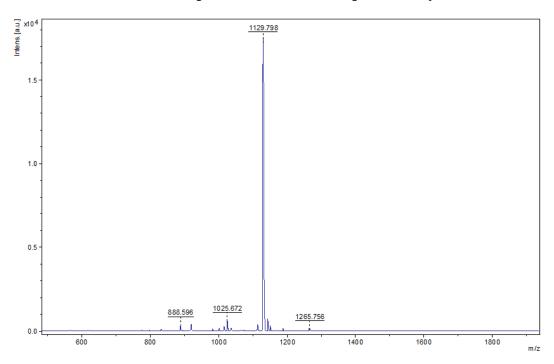


Figure S1. MALDI-TOF mass spectrometry was used to confirm that the purified peptoid mass matched the theoretical mass. Peptoid JPT1 theoretical mass was 1130.48 Da.

Analytical reverse-phase high pressure liquid chromatography

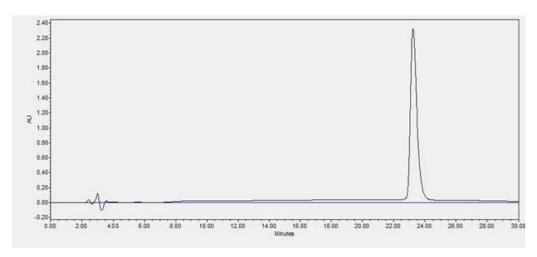


Figure S2. Peptoids were confirmed to be >98% pure via analytical HPLC (Waters 2695 Separations Module) equipped with a Duragel G C18 150 x 2.1 mm column (Peeke Scientific) using a linear gradient of 5 to 95% solvent D in C (solvent D: acetonitrile, 0.1% TFA; solvent C: water, 0.1% TFA) over 30 min.

Aggregation Studies via ThT Fluorescence

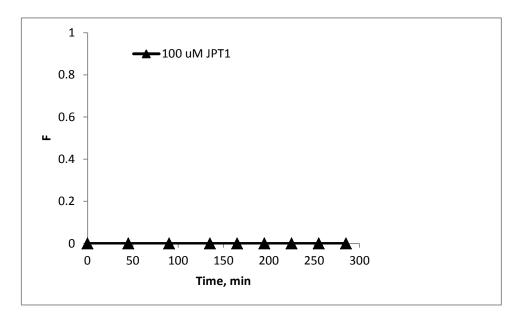


Figure S3. ThT analysis shows that peptoid JPT1 does not aggregate in the absence of A β 40. The presence of β -sheet aggregates was detected by ThT fluorescence. Aggregation assays were in 40 mM Tris-HCl (pH 8.0) and 150 mM NaCl. Peptoid JPT1 was dissolved in DMSO and added at 100 μ M such that the final DMSO concentration was 1.25% (v/v). Assays were performed at 25 °C under agitation on an orbital shaker at 800 RPM.

Dot Blot Analysis

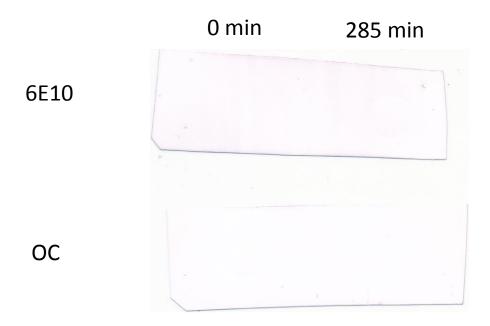


Figure S4. Dot blot analysis shows that peptoid JPT1 does not bind to sequence-specific antibody 6E10 or conformation-specific antibody OC in the absence of A β 40. Samples were spotted at 0 min and 285 min, respectively.