Highly heterogeneous in size and shape solutions of the amyloid-β peptide pose a major challenge for proper analysis. To obtain a thorough characterization of species present in differently composed or treated amyloid-β peptide solutions is of tremendous importance for the understanding of the underlying mechanisms and for well-founded assessments of changed aggregation behaviour, e.g. in the course of inhibitor studies. Analytical ultracentrifugation represents a means to determine the hydrodynamic properties of macromolecules in solution requiring no calibration standards. We established a method to analyse the aggregation behaviour of the amyloid-β peptide with sedimentation velocity centrifugation. Important information which becomes accessible by this methodology are the s-value- and shape-distributions of the peptide aggregates present in solution. With the method we characterized the aggregation modifying effect of a small organic molecule, designed as a β-sheet breaker. Co-incubation with the compound resulted in decreased amyloid formation as detected by Thioflavin T measurements. Comparative sedimentation velocity centrifugation experiments with solutions of Aβ(1-42) incubated with and without different amounts of compound demonstrated a pronounced shift of the maximum of the s-value distribution calculated for the formed amyloid-β aggregates to smaller s-values in a concentration dependent manner. Enhanced high-resolution hydrodynamic modelling as implemented in the software package Ultrascan (www.ultrascan.uthscsa.edu) further revealed the presence of differently shaped particles. These results could be confirmed by transmission electron microscopy performed on the identical samples used for sedimentation velocity centrifugation analysis.