ESRF	**Experiment title:** Amyloid fibrillation mechanism elucidated by structural investigation of initial stages, stabilized oligomers and mature fibrils.	**Experiment number**: MX-1326
Beamline: ID 14-3	**Date of experiment**: from: 22 Sept 2011 16:00 (09:30) to: 23 Sept 2011 08:00	**Date of report**:
Shifts: 2 (of 3)	**Local contact(s)**: Adam Round	*Received at ESRF:*

Names and affiliations of applicants (* indicates experimentalists):

Bente Vestergaard, University of Copenhagen (main applicant)

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Report:

The aim of the experiments performed is structural elucidation of species relevant to the protein fibrillation process. This includes characterization of pre-fibrillar states, stabilized oligomeric structures, mature fibrils and models for cytotoxicity and membrane interactions.

Despite the great expertise at this beamline, we lost the first (of three) allocated shifts as a consequence of problems with the sample cell at the beamline and subsequent challenges in fixing this issue. The two remaining shift were used fully to collect a range of data on different samples, all relevant towards a greater understanding of the protein fibrillation process.

We succesfully collected data on two chemically modified variants of GLP2, which has a modified pre-fibrillar solution behaviour and fibrillation kinetics, as well as comparable data on the native form of the peptide. The data collected are currently being analysed, but are expected to be publishable without further data collections.

Data were also collected on stabilized protofibrils of a different modified amyloidogenic peptide. These data may be included as complementary data in a publication, but are however preliminary and mainly used to plan more extensive experiments towards a description of the structural changes during the fibrillation.

Originally, experiments were planned to study an apparently different fibrillation pathway of equine lysozyme, but due to a long term sick-leave of the student focusing on this work, this project has been postponed.

In addition, we collected preliminary data towards characterizing the interaction of fibrillation relevant species with liposomes. These data show surprising and somewhat unexpected results, that merits a thorough analysis and extensive further data collection using complementary biophysical methods but publication is definitely expected. Further SAXS data will also be needed.

Also, a few preliminary data were collected on monoclonal antibodies (hIgG1, hIgG2 and hIgG4). These data confirmed an excellent sample quality and have later been complemented with additional data from DESY/EMBL for a study on the correlations between structure and stability.