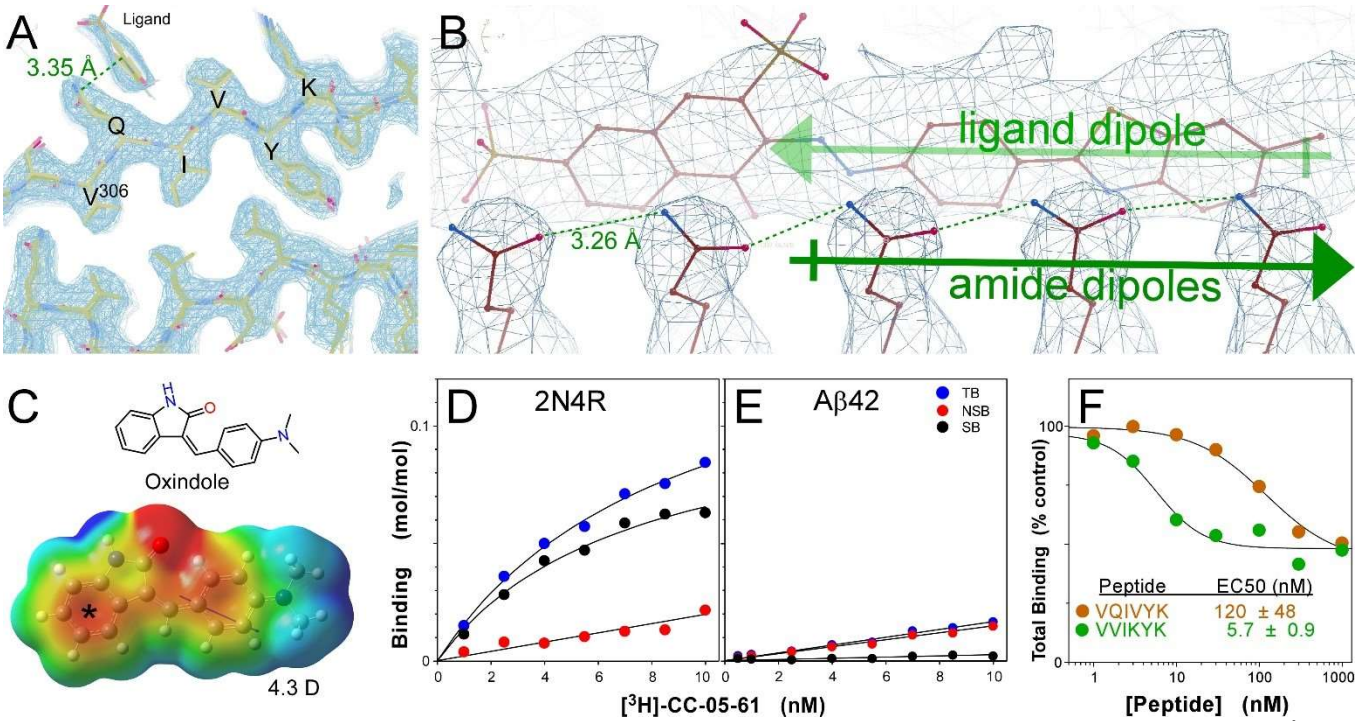

Figure 1: A) Zoomed in view on a cross-β region of geranine G-induced tau filaments (model and map, at 3.2Å resolution), showing a clear extra-protein density next to a Gln307. B) Clear density features allow for fairly accurate real-space refinement of a geranine G molecule into the density, revealing dipole-dipole moments as a potential mediator of binding. C) The most basic unit of our ligand library is shown here, offering a scaffold with which the electronic properties of different ligands can be manipulated. D) A specific member of the library has known affinity for tau filaments and E) no affinity for amyloid-β filaments. F) Example of a biochemical follow-up probing a specific binding site with mutagenesis.

**Note:* Data for Fig. 1 panels A-B is currently being written up for a manuscript.

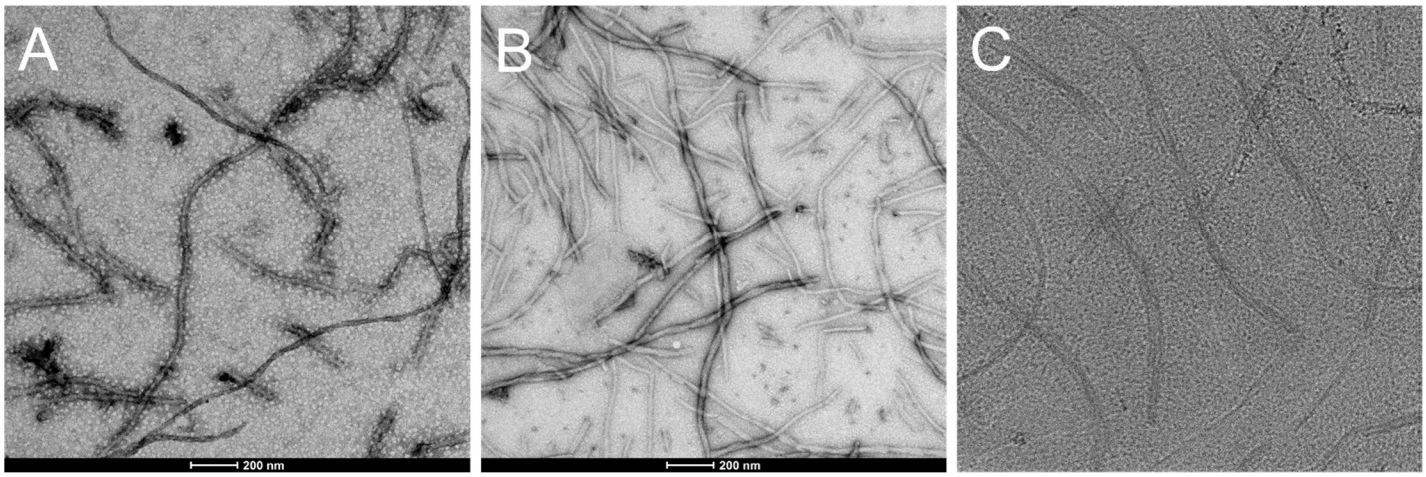

Figure 2: A) ODS-induced tau filaments (15 μM), when applied directly to carbon coated TEM grids followed by 2% uranyl acetate staining and water washing steps, show inconsistently stained filaments with excessive background that consists of ODS micelles and protein oligomers. This background is expected to lead to poor cryoEM datasets. B) Upon sedimentation (x100,000 g) and resuspension in syringe-filtered phosphate buffer (to 15 μM), the TEM grids reveal almost complete elimination of non-filamentous background. Furthermore, filaments show good helicity, a pre-requisite for helical reconstruction with cryoEM. C) Sample of B, when deposited onto Au QuantiFoil 1.2/1.3 300 mesh grids, shows consistently high-quality freezing (including good filament distribution, ice thickness, and contrast) when screened on a Glacios microscope.

**Note 2*: Data for Fig. 2 panels A-B was collected by D. Malyshka on a Tecnai G2-30 TEM (with a 4K CETA camera) at a 4 micron defocus. Data for panel C was collected by D. Malyshka on a Glacios' Falcon 2 camera at a 4 micron defocus during a screening session.