Electronic Supplementary Material (ESI) for Chemical Science.
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Supplementary Information

Table S1 Sequences of Laf1-AK-Laf1, Dbp1N-AK-Dbp1N, AK, Laf1, Ddx4 and Aβ42 peptide. Red, grey and yellow backgrounds indicate the His-tag, the low complexity domains (LCDs) and the globular domain, respectively.

Name	Sequence
Laf1_AK_Laf1	MGSSHHHHHHSSGLVPRGSHMESNQSNNGGSGNAALNRGGRYVPPHLRGGDGGAAAAASAGGDDRRGGAG GGGYRRGGGNSGGGGGGGYDRGYNDNRDDRDNRGGSGGYGRDRNYEDRGYNGGGGGGGNRGYNNNRGGGG GGYNRQDRGDGGSSNFSRGGYNNRDEGSDNRGSGRSYNNDRRDNGGDGMRIILLGAPGAGKGTQAQFIME KYGIPQISTGDMLRAAVKSGSELGKQAKDIMDAGKLVTDELVIALVKERIAQEDCRNGFLLDGFPRTIPQ ADAMKEAGINVDYVLEFDVPDELIVDRIVGRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTTRKDDQEE TVRKRLVEYHQMTAPLIGYYSKEAEAGNTKYAKVDGTKPVAEVRADLEKILGMESNQSNNGGSGNAALNR GGRYVPPHLRGGDGGAAAAASAGGDDRRGGAGGGGYRRGGGNSGGGGGGGYDRGYNDNRDDRDNRGGSGG YGRDRNYEDRGYNGGGGGGGNRGYNNNRGGGGGGYNRQDRGDGGSSNFSRGGYNNRDEGSDNRGSGRSYN NDRRDNGGDG
Dbp1N_AK_Dbp1N	MGSSHHHHHHSSGLVPRGSHMADLPQKVSNLSINNKENGGGGGKSSYVPPHLRSRGKPSFERRSPKQKDK VTGGDFFRRAGRQTGNNGGFFGFSKERNGGTSANYNRRGSSNYKSSGNRWVNGKHIPGPKNAKLQKAELF GVHDDPDYHSSGIKFDNYDNIPVDASGKDVPEPILMRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDML RAAVKSGSELGKQAKDIMDAGKLVTDELVIALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDY VLEFDVPDELIVDRIVGRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMT APLIGYYSKEAEAGNTKYAKVDGTKPVAEVRADLEKILGMADLPQKVSNLSINNKENGGGGGKSSYVPPH LRSRGKPSFERRSPKQKDKVTGGDFFRRAGRQTGNNGGFFGFSKERNGGTSANYNRRGSSNYKSSGNRWV NGKHIPGPKNAKLQKAELFGVHDDPDYHSSGIKFDNYDNIPVDASGKDVPEPIL
AK	MGSSHHHHHHSSGLVPRGSHMRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDMLRAAVKSGSELGKQAK DIMDAGKLVTDELVIALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDYVLEFDVPDELIVDRI VGRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMTAPLIGYYSKEAEAGN TKYAKVDGTKPVAEVRADLEKILG
Laf1	MGSSHHHHHHSSGLVPRGSHMESNQSNNGGSGNAALNRGGRYVPPHLRGGDGGAAAAASAGGDDRRGGAG GGGYRRGGGNSGGGGGGGYDRGYNDNRDDRDNRGGSGGYGRDRNYEDRGYNGGGGGGGNRGYNNNRGGGG GGYNRQDRGDGGSSNFSRGGYNNRDEGSDNRGSGRSYNNDRRDNGGDG
DDX4	MGSSHHHHHHSSGLVPRGSHMGDEDWEAEINPHMSSYVPIFEKDRYSGENGDNFNRTPASSSEMDDGPSR RDHFMKSGFASGRNFGNRDAGECNKRDNTSTMGGFGVGKSFGNRGFSNSRFEDGDSSGFWRESSNDCEDN PTRNRGFSKRGGYRDGNNSEASGPYRRGGRGSFRGCRGGFGLGSPNNDLDPDECMQRTGGLFGSRRPVLS GTGNGDTSQSRSGSGSERGGYKGLNEEVITGSGKNSWKSEAEGGES
Aβ42	MDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA

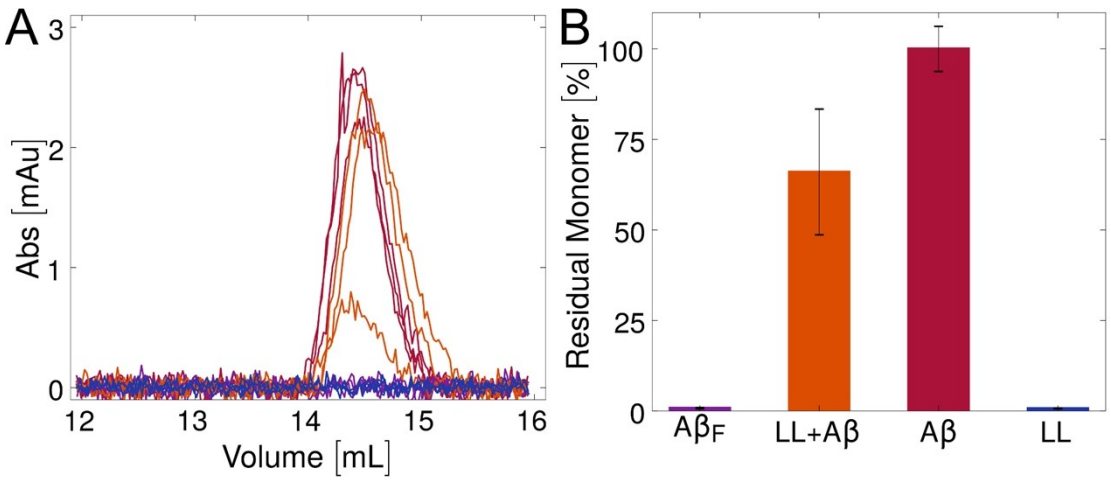

Figure S1 Evaluation of residual monomer by SEC analysis. (A) The amount of residual Aβ42 monomer at the end of the aggregation experiments was measured by size exclusion chromatography on a Superdex 75 10/30 column. All samples apart from the intial fresh Aβ42 monomeric solution ($A\beta$, red) were incubated for 20 hours in a 96 half area well plate with polystyrene bottom at 27.5 °C in 20 mM phosphate buffer and pH 8.0: amyloid Aβ42 fibrils in a homogeneous solution ($A\beta_F$, violet), mixture of 20 μM Laf1-AK-Laf1 and Aβ42 ($LL + A\beta$, orange) and control with chimeric proteins alone (LL, blue). Relative areas corresponding to the Aβ42 monomer peaks in the chromatograms shown in (C). Error bars indicate standard errors of three replicates.

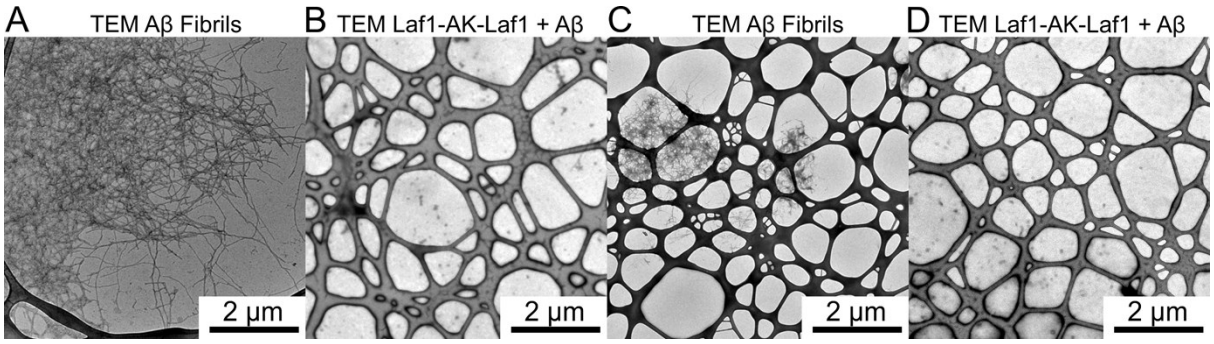

Figure S2 TEM images of final samples of Aβ42 solutions with and without Laf1-AK-Laf1. TEM images of solutions of 4 μM Aβ42 without (A-C) and with (B-D) 10 μM Laf1-AK-Laf1 after 3 days incubation (A-B) and after 6 days incubation (C-D) in glass bottom 384 well plates in 20 mM phosphate at pH 8.0 and 27.5°C. Amyloid fibrils are observed only in the absence of condensates.

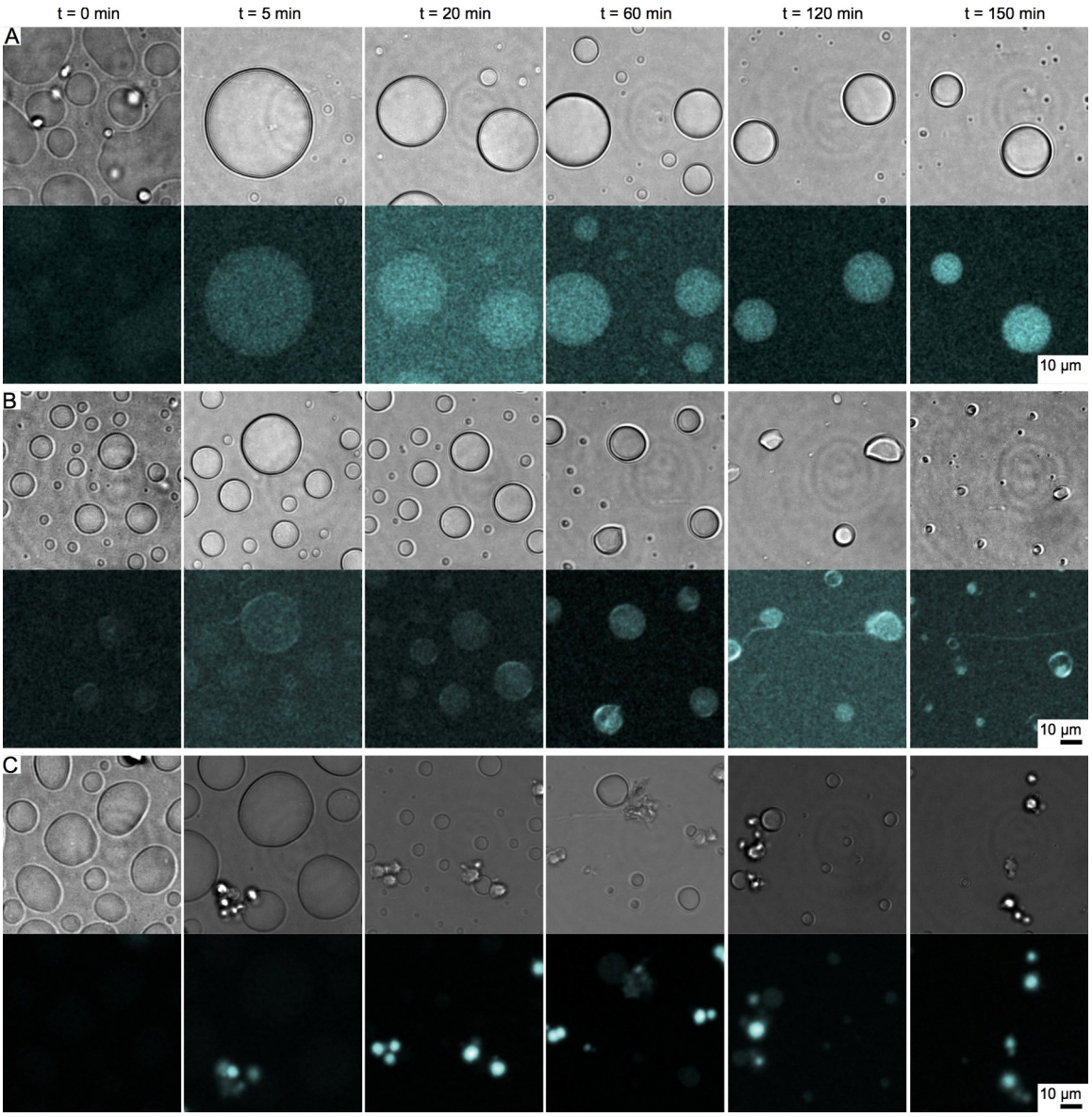

Figure S3 Brightfield (top panels) and fluorescence (bottom panels) confocal images of (A) 10 µM Laf1-AK-Laf1; (B) 10 µM Laf1-AK-Laf1 and 2 µM Aβ42; (C) 10 µM Laf1-AK-Laf1 and 2 µM Aβ42 with 400 nM (monomer equivalent) of Aβ42 pre-formed fibrils. All samples were incubated with 20 µM ThT over 2.5 hours in a plastic bottom 384 well plate. The addition of pre-formed fibrils accelerates the disruption of the condensate structure.

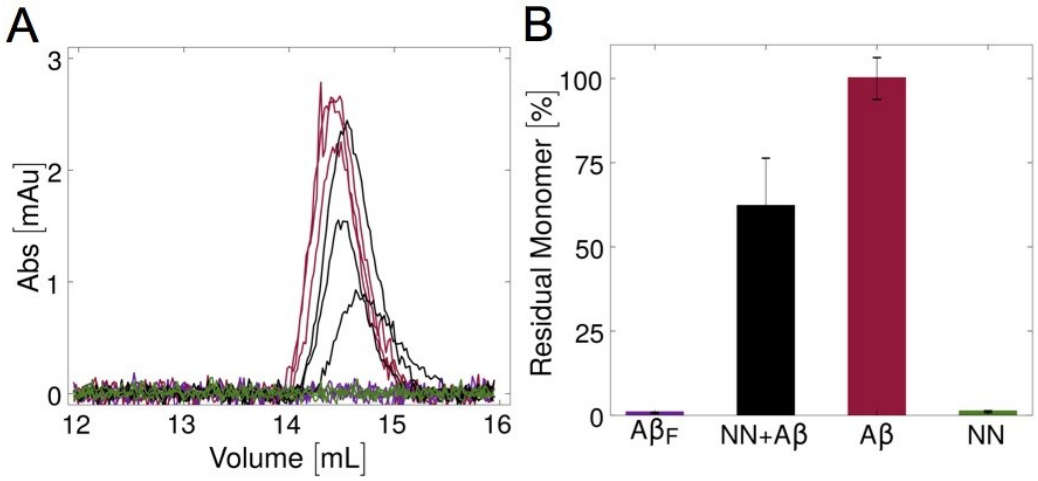

Figure S4 Evaluation of residual monomer by SEC analysis. (A) The amount of residual Aβ42 monomer at the end of the aggregation experiment was measured by size exclusion chromatography on a Superdex 75 10/30 column. All samples apart from the intial fresh Aβ42 monomeric solution ($A\beta$, red) were incubated for 20 hours in a 96 half area well plate with polystyrene bottom at 27.5 °C in 20 mM phosphate buffer and pH 8.0: amyloid Aβ42 fibrils in a homogeneous solution ($A\beta_F$, violet), mixture of 20 μM Dbp1N-AK-Dbp1N and Aβ42 ($NN + A\beta$, orange) and control with chimeric proteins alone (NN, blue). (B) Relative areas corresponding to the Aβ42 monomer peaks in the chromatograms shown in (A). In all panels error bars indicate standard errors of three replicates.

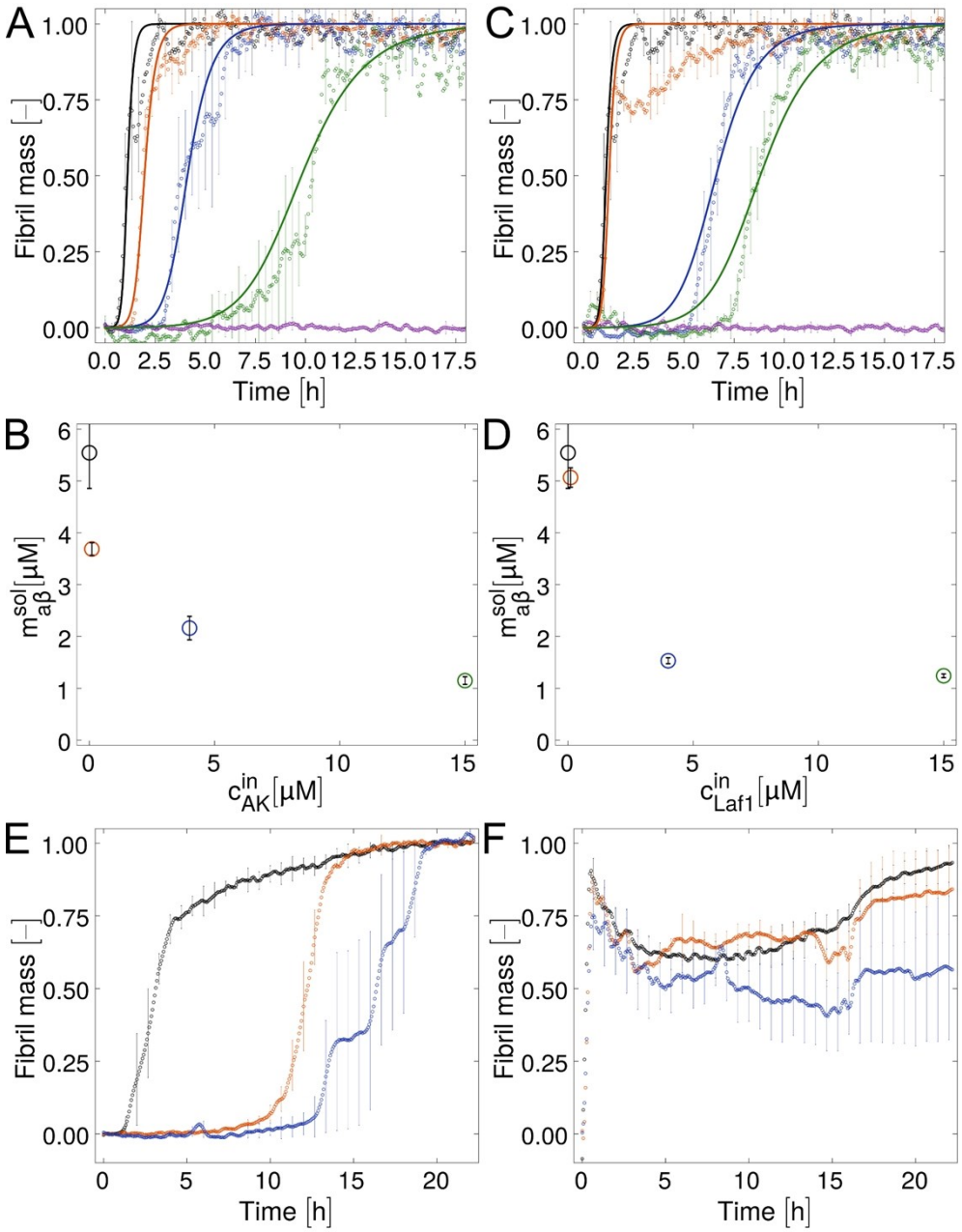

Figure S5 ThT kinetic assays of Aβ42 with AK and Laf1. (A) Aggregation profiles of 6 μM Aβ42 in the absence (black) and presence of 0.1 μM (orange), 4 μM (blue) and 15 μM (green) of AK in the standard assay buffer (20 mM phosphate, 0.2 mM EDTA, pH 8.0). Violet color indicates 15 μM of AK without Aβ42. Solid lines represent model simulations and error bars indicate standard errors of three replicates. (B) Concentration of unbound Aβ42 monomers estimated from the model simulations versus the concentration of AK. Error bars indicate the standard error of three replicates. (C) Aggregation profiles under the same conditions described in (A) but in the presence of Laf1. Error bars indicate the standard error of three replicates. (D) Concentration of unbound Aβ42 monomers estimated from the model simulations versus the concentration of Laf1. Error bars indicate the standard error of three replicates. (E) Aggregation profiles of 2 μM Aβ42 in the absence (black line) and presence of 8 μM (orange line) and 15 μM (blue line) AK in the standard assay buffer. (F) Aggregation profiles of 2 μM Aβ42 in the absence (black line) and presence of 8 (orange line) and 15 (blue line) μM AK in the standard assay buffer supplemented with 150 mM NaCl.