Supplementary Information

Amyloid precipitation in biofluids using a structure-specific chemical antibody

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Supplementary Methods

Atomic Force Microscopy (AFM)

AFM was performed on freshly cleaved mica substrates. Aliquots (10 μL) of each diluted sample were deposited on the substrate at room temperature, incubated for 10 min, rinsed with 1 mL Milli Q water, and then dried under a gentle nitrogen flow. AFM maps were generated by means of a JPK nanowizard2 system (JPK Instruments, Germany) operating in tapping mode and equipped with a silicon tip (PPP-NCHR, 5 Nm^{-1}) with a nominal radius of <10 nm.

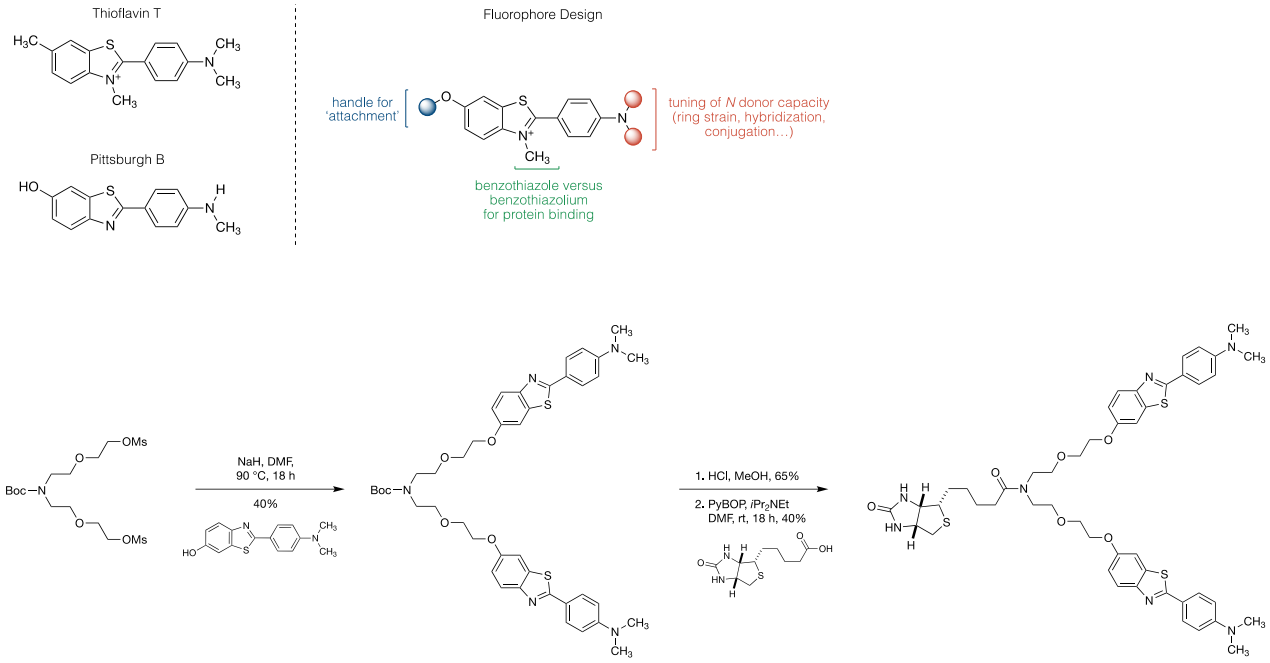
Imaging of amyloid-β_{1-42} and tau fibrils

1 μM amyloid-β_{1-42} ($a\beta_{42}$) and 100 nM tau fibrils were imaged in similar way to α-synuclein. Prior to imagining protein aggregates were diluted in PBS and incubated with either 5 μM of ThT or CAP-1, or 50 nM of pFTAA (tau). $A\beta_{42}$ fibrils were obtained by incubating 4 μM of monomeric $a\beta_{42}$ (Stratech, Catalogue Number: A-1167-2-RPE) in PBS for 4h at 37°C with constant agitation. Tau aggregation reactions were performed using 50 μM 0N4R htau (InVivo BioTech Services GmbH, Germany) in buffer containing 100 mM Tris, 150 mM NaCl and 0.1 mM EDTA. The aggregation was initiated by the addition of 0.05 mg/ml heparin (1:4 heparin:tau ratio). The aggregation reaction was incubated at 37°C under quiescent conditions for 120 h before imaging.

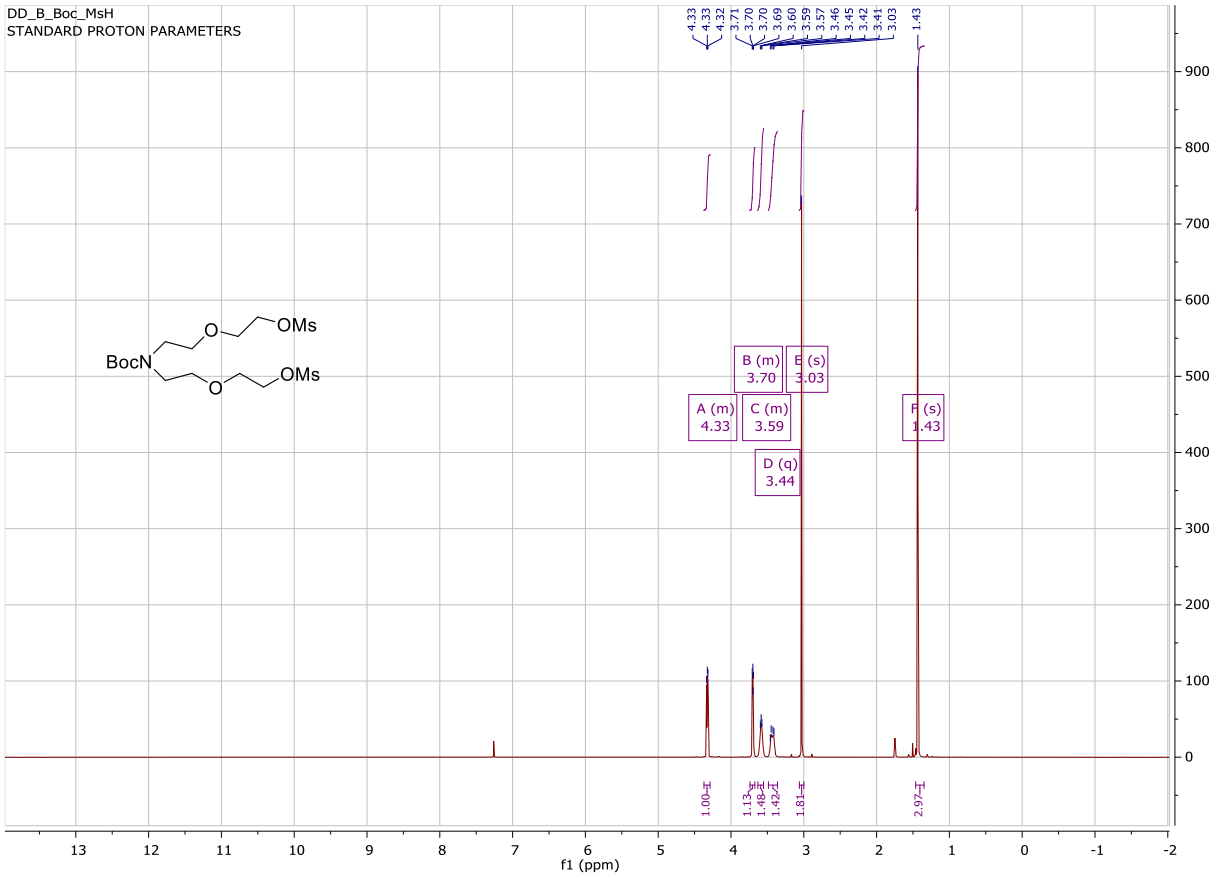
Electron microscopy

Electron microscopy images were acquired on a scanning electron microscopy with a retractable STEM detector (TESCAN MIRA3 FEG-SEM) using 30kv. Holey carbon grids (EM Resolutions, 300 mesh Copper) were glow-discharged for hydrophilization using Quorum Technologies GloQube Dual Chamber Glow Discharge System (25 mA, 60 sec, negative) and then 10 μL of α–synuclein samples (fibrils or sonicated fibrils) was added and let dry for 15 min (excess carefully removed with filter paper). Prior to imaging grids were plasma cleaned (Fischione Model 1070 Nanoclean Plasma Cleaner) using a 25% oxygen and 75% argon gas mixture to remove carbonaceous debris, for 15 sec.

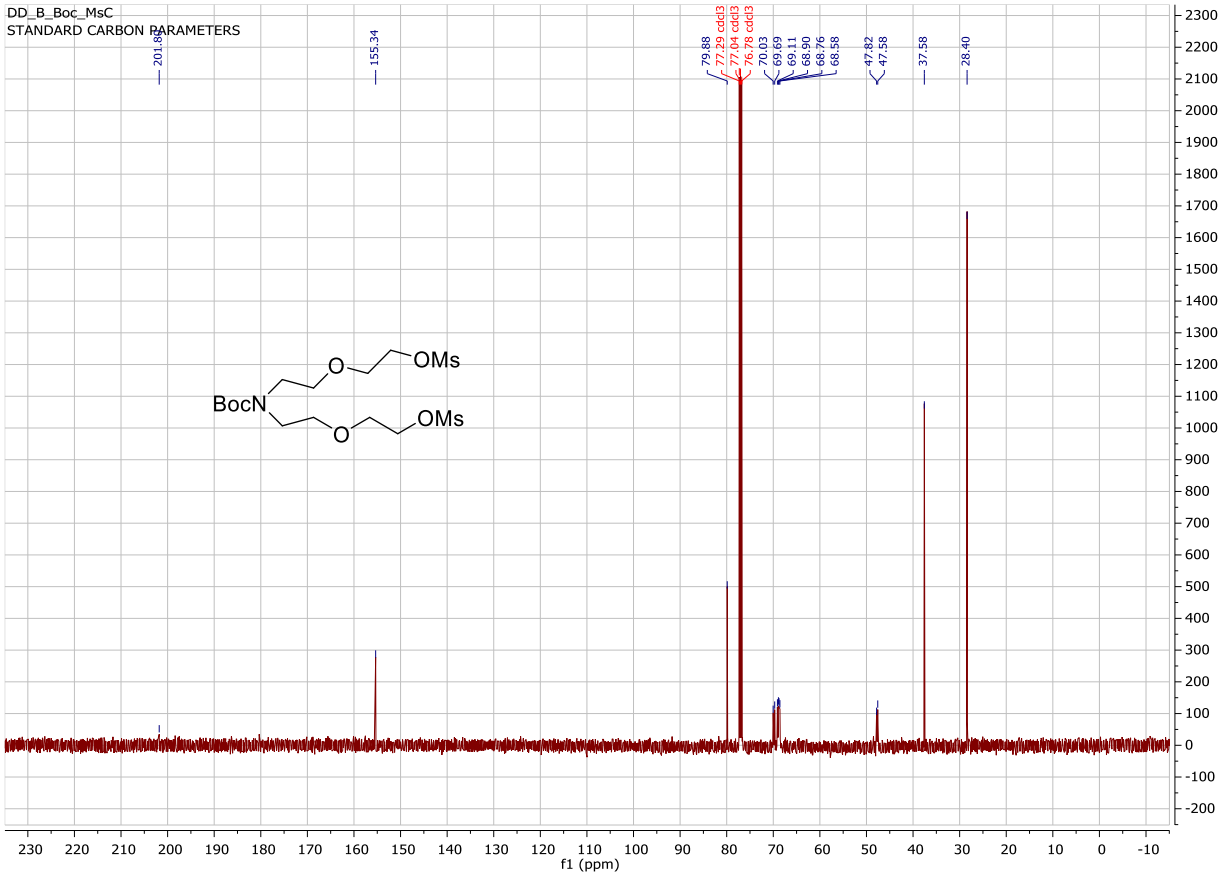
Supplementary Figures



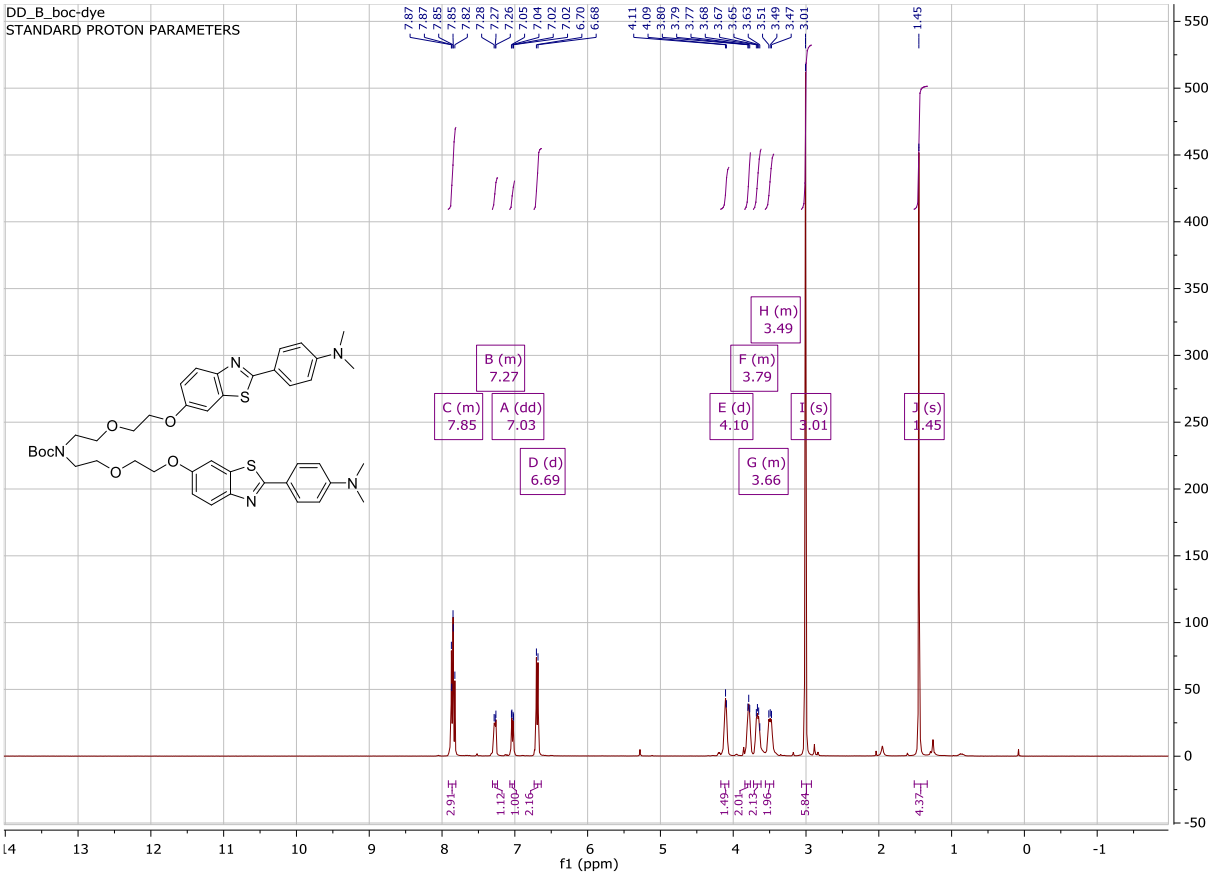
SI.1 - Rational design and characterization of CAP-1. (**a**) Outline of CAP-1design and synthesis.



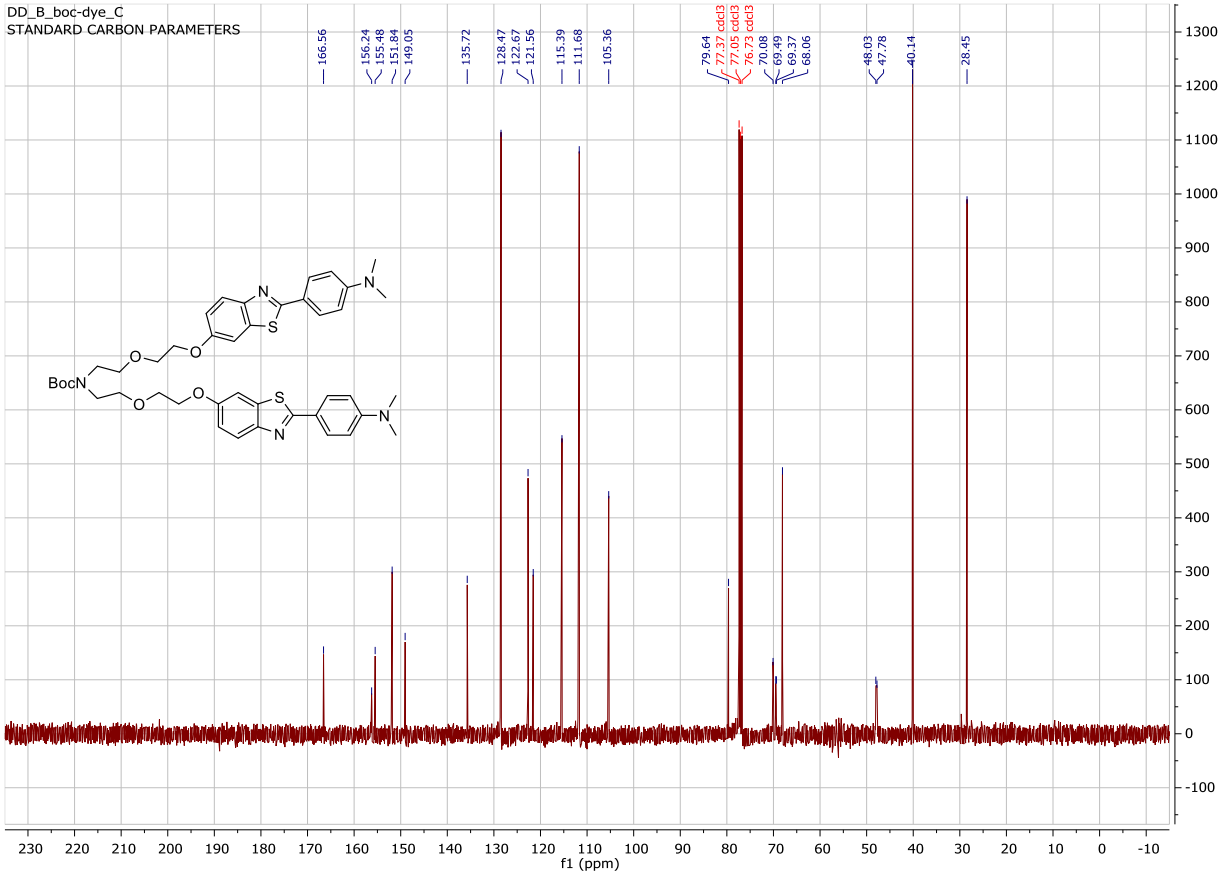
SI.2 - ^{1}H NMR spectra of (**A**) bis-Mesylate.



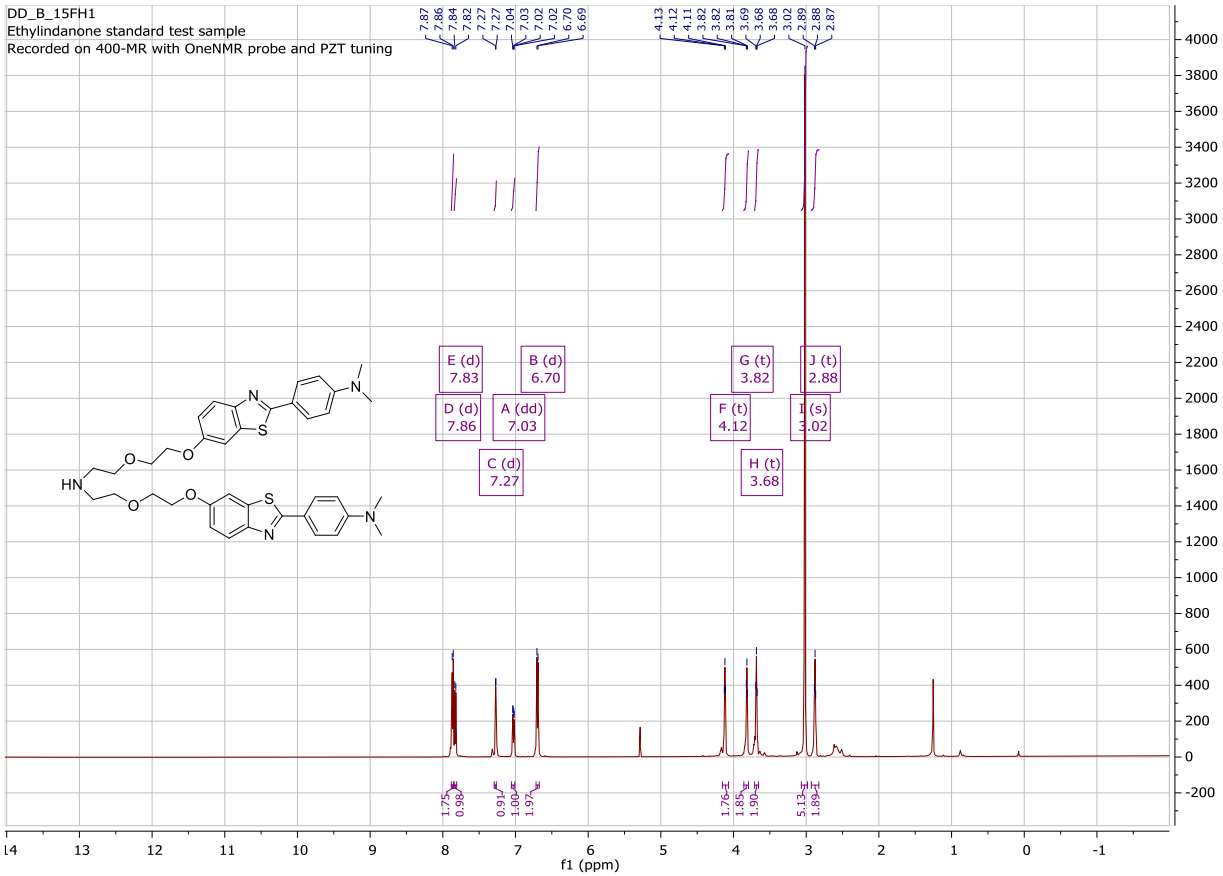
SI.3 - ^{13}C NMR spectra of (**A**) bis-Mesylate.



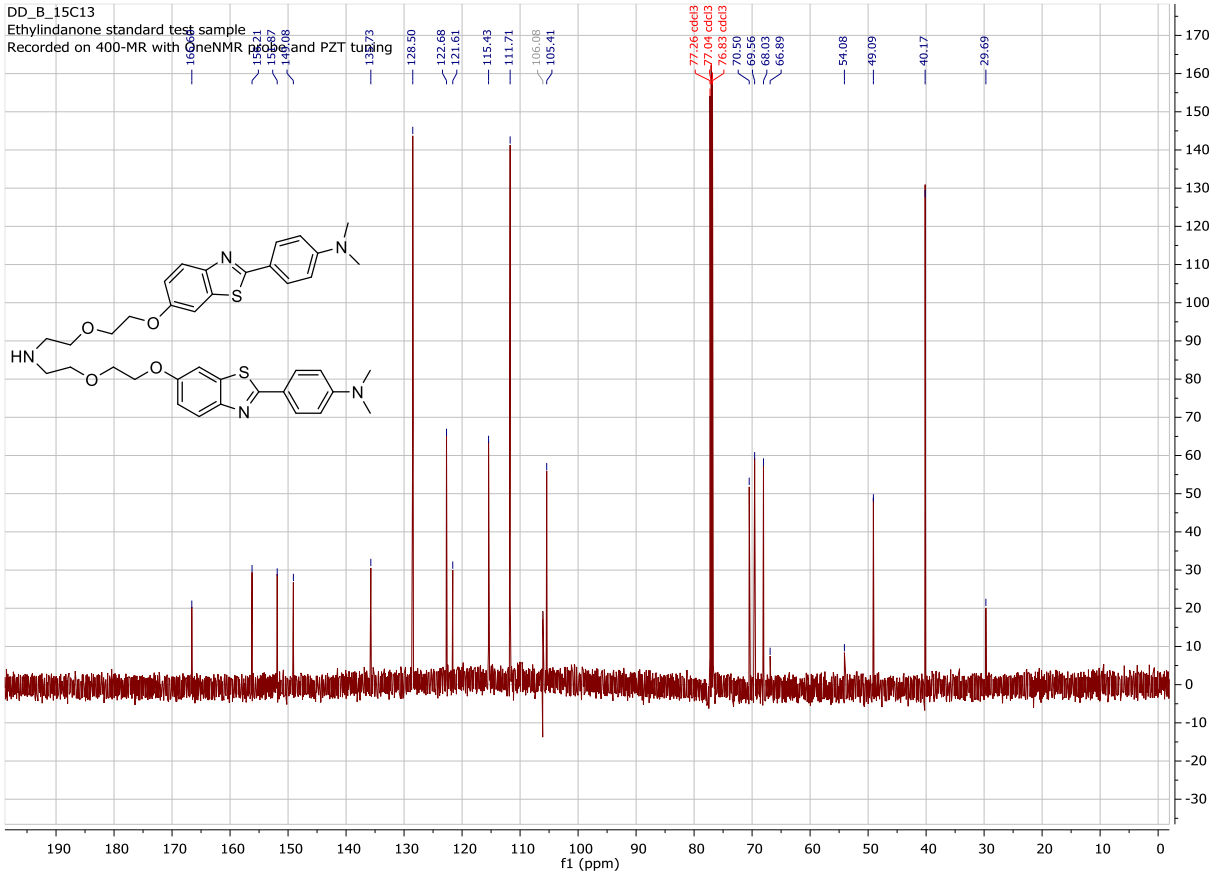
SI.4 - ^{1}H NMR spectra (B) Boc-protected bis-benzothiazole.



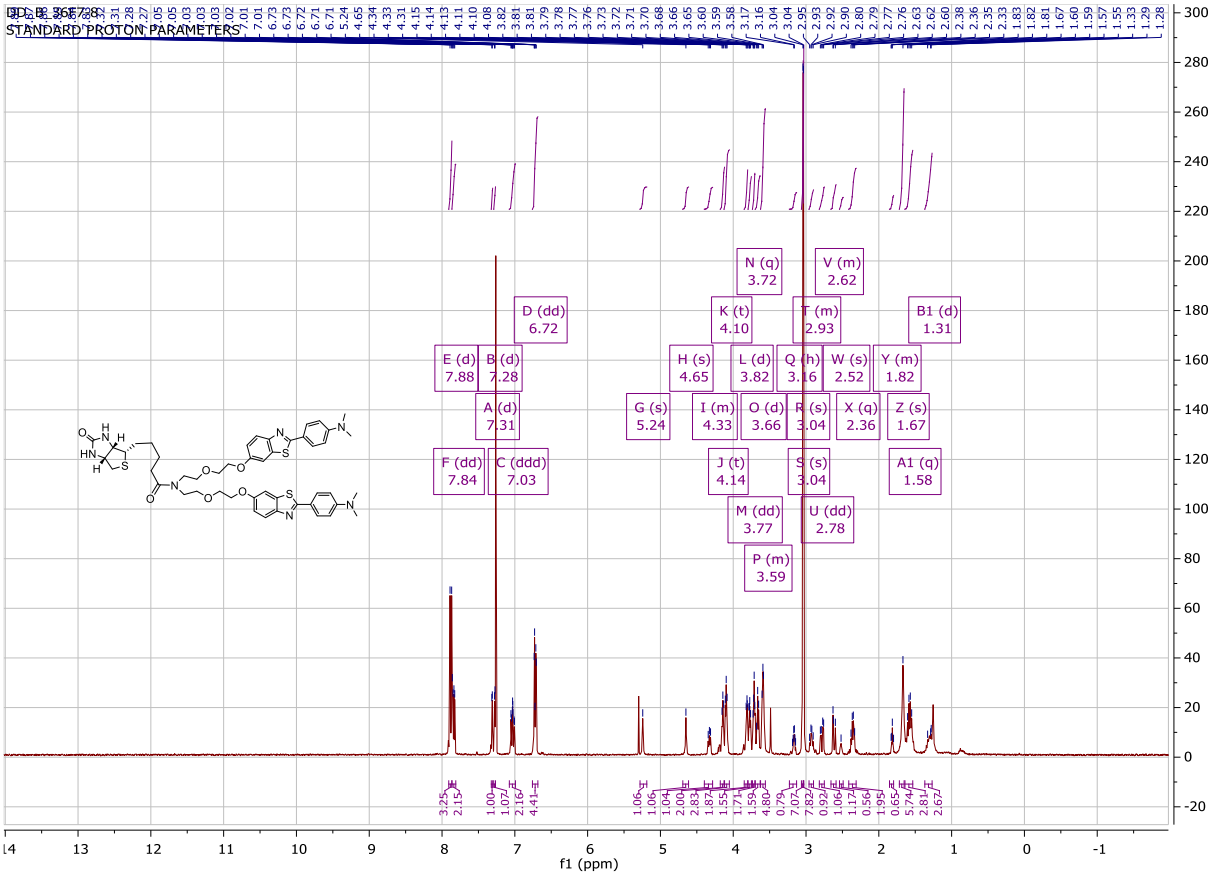
SI.5 – ^{13}C NMR spectra (B) Boc-protected *bis*-benzothiazole.



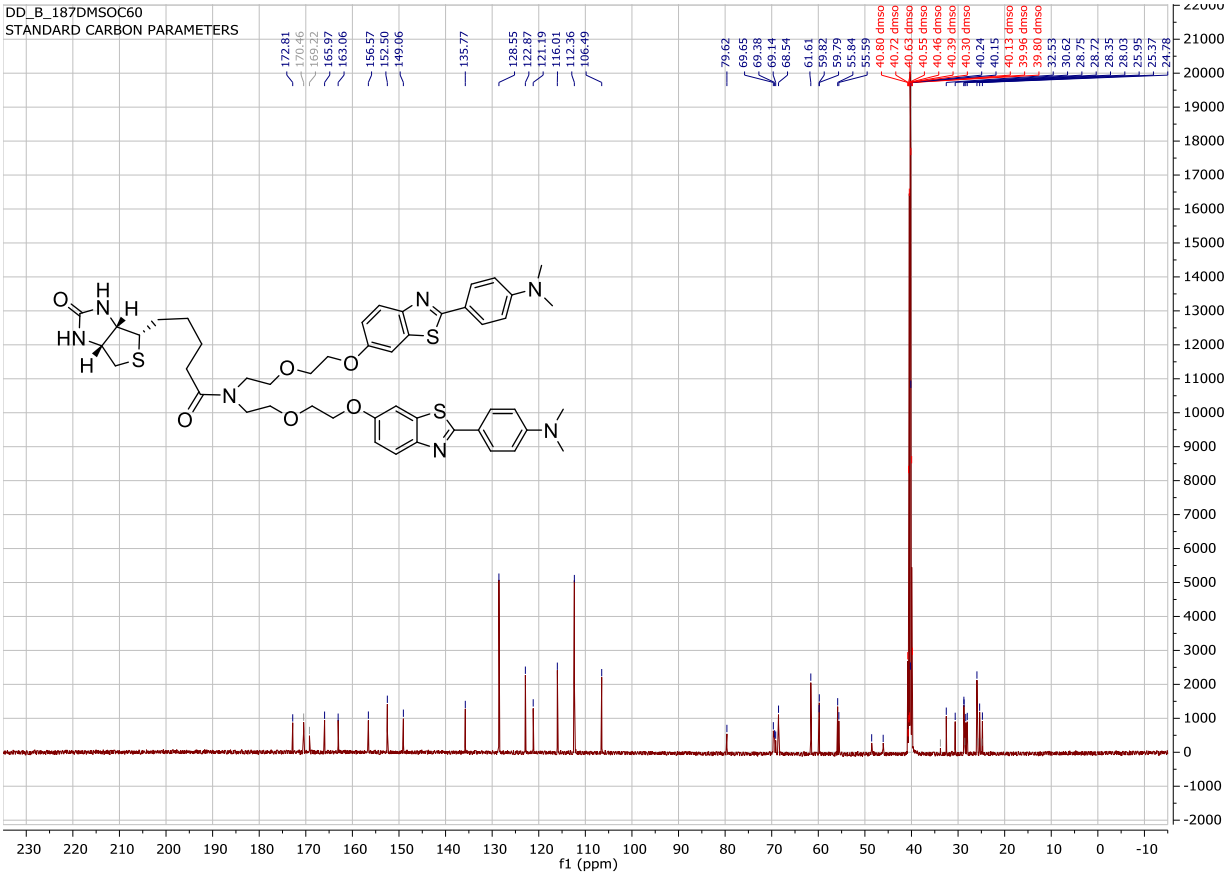
SI.6 - ^{1}H NMR spectra (C) NH *bis*-benzothiazole.



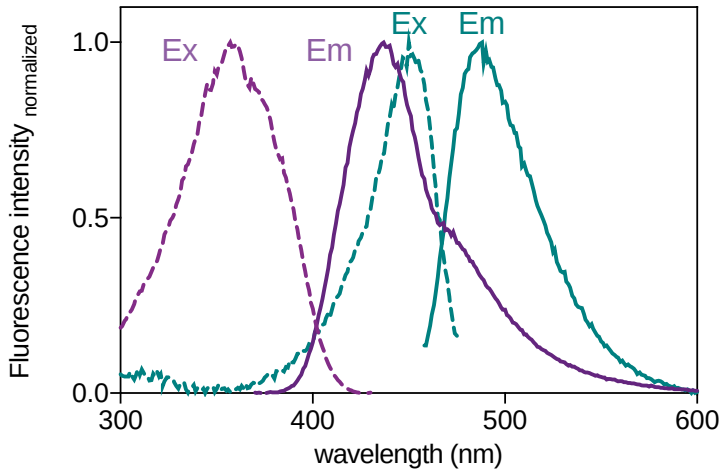
SI.7 – ^{13}C NMR spectra (C) NH *bis*-benzothiazole.



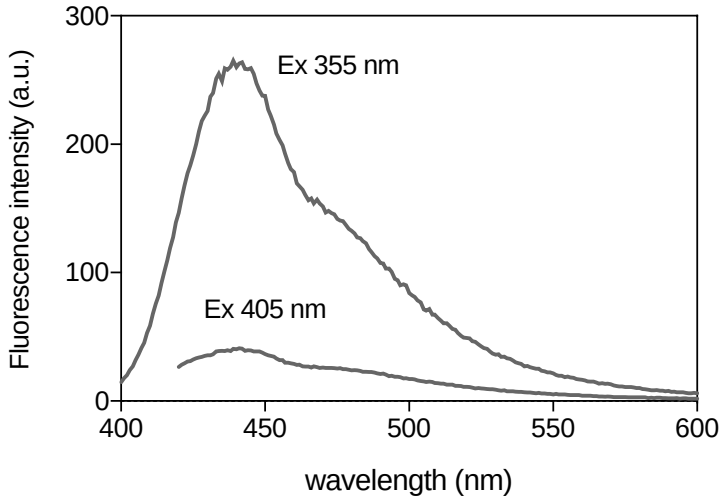
SI.8 - ^{1}H NMR spectra (D) N-Biotinylated *bis*-benzothiazole.



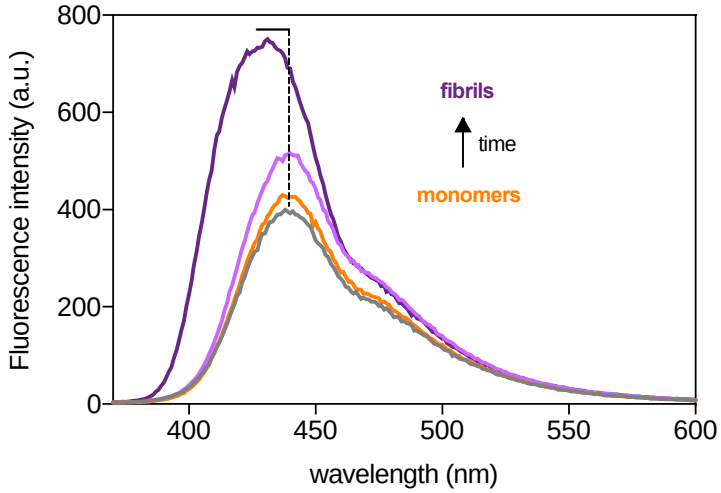
SI.9 - ^{13}C NMR spectra (D) N-Biotinylated *bis*-benzothiazole.



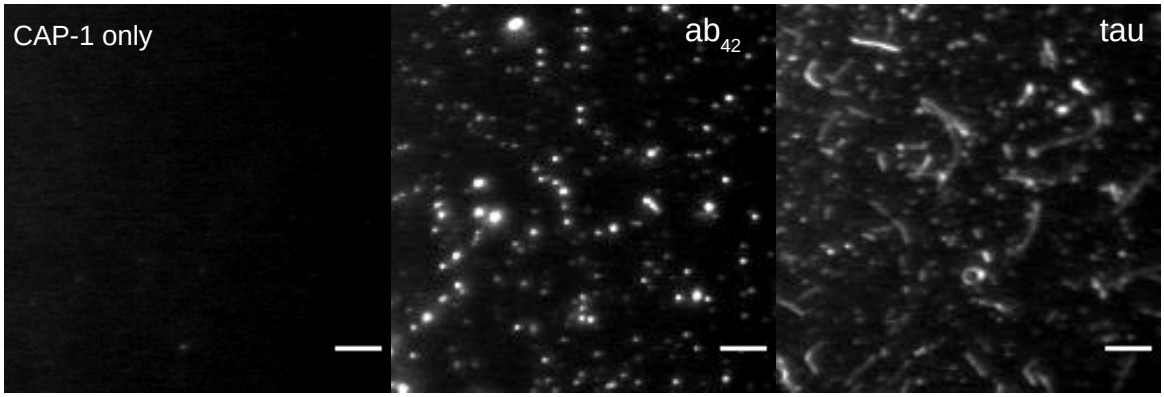
SI.10 - Excitation and emission spectrum of 20 μM CAP-1(-) and 20 μM ThT (-) in the presence of 10 μM α-synuclein fibrils.



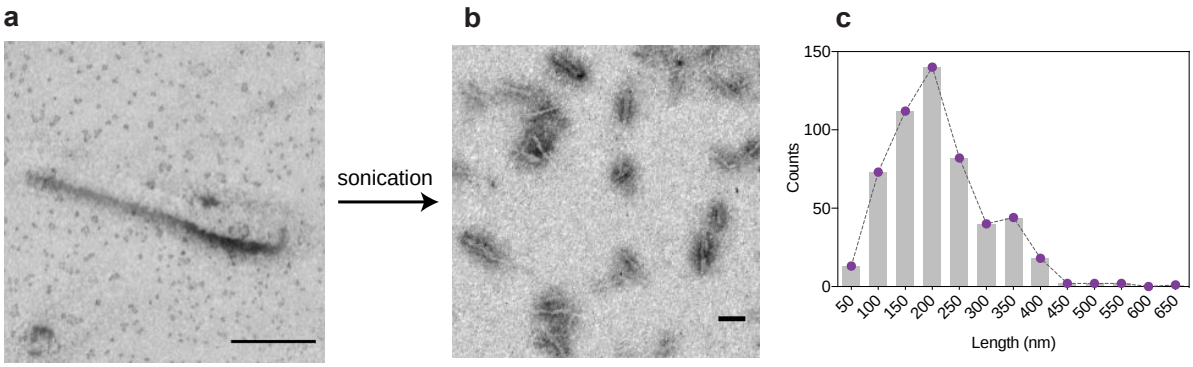
SI.11 - Decrease in the fluoresce intensity of α-synuclein fibrils emission spectrum from using using λ_{ex}=355 nm to λ_{ex}=405 nm.



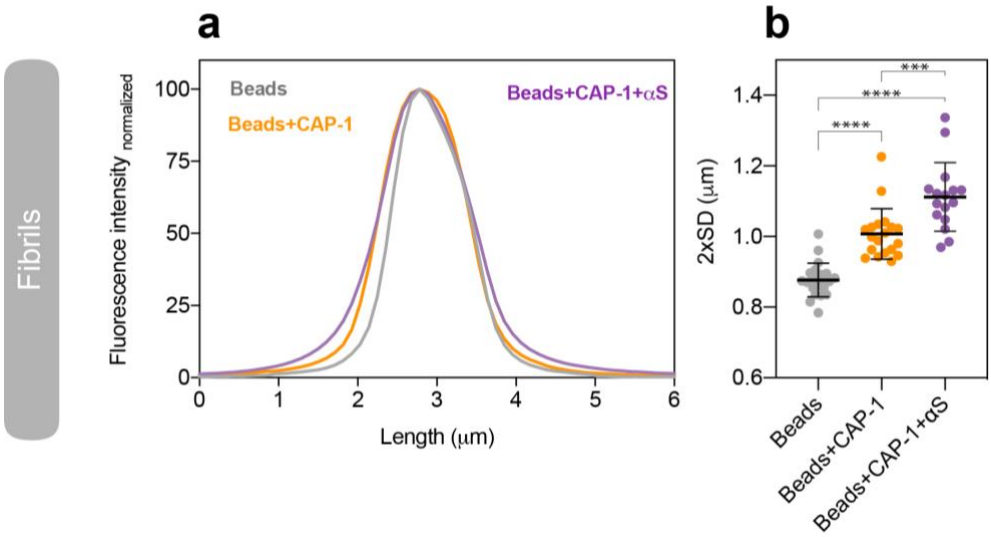
SI.12 - Emission spectra of 20 μM CAP-1 alone and in the presence of different time points of 10 μM α-synuclein aggregation reaction: CAP-1 only (–), t=0h (– monomers), t=8h (– oligomers) and t=24h (– fibrils).



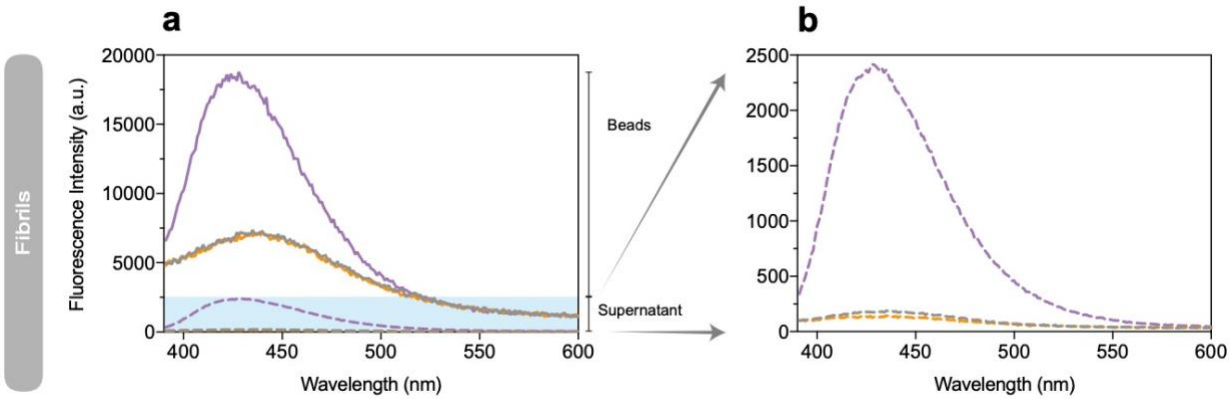
SI.13 - TIRFM images of 5 μM CAP-1 only (left panel), with 1 μM $a\beta_{42}$ (middle) and with 100 nM tau (right). Scale bar = 5 μm.



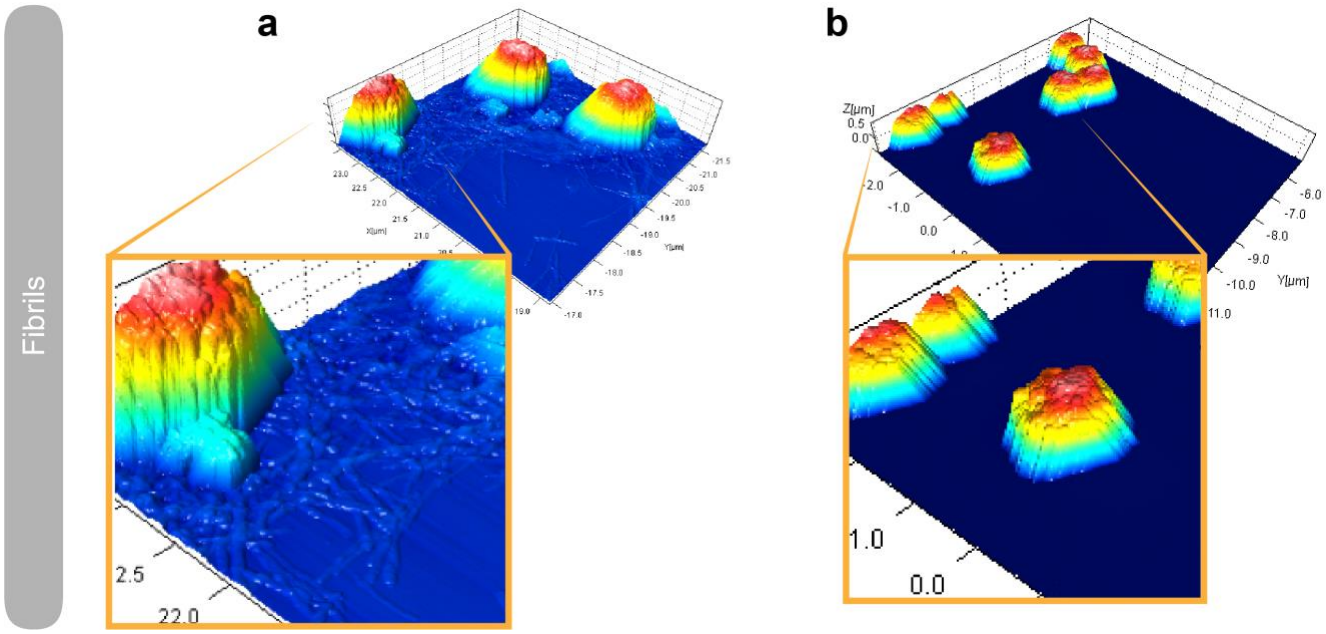
SI.14 - STEM images of α-synuclein fibril before and after sonication. (**a**) fibril length ~3 μm. Scale bar = 1 μm. (**b**) α-synuclein fibrils sonicated, scale bar = 200 nm and (**c**) histogram of fibril length distribution from 549 individual aggregates.



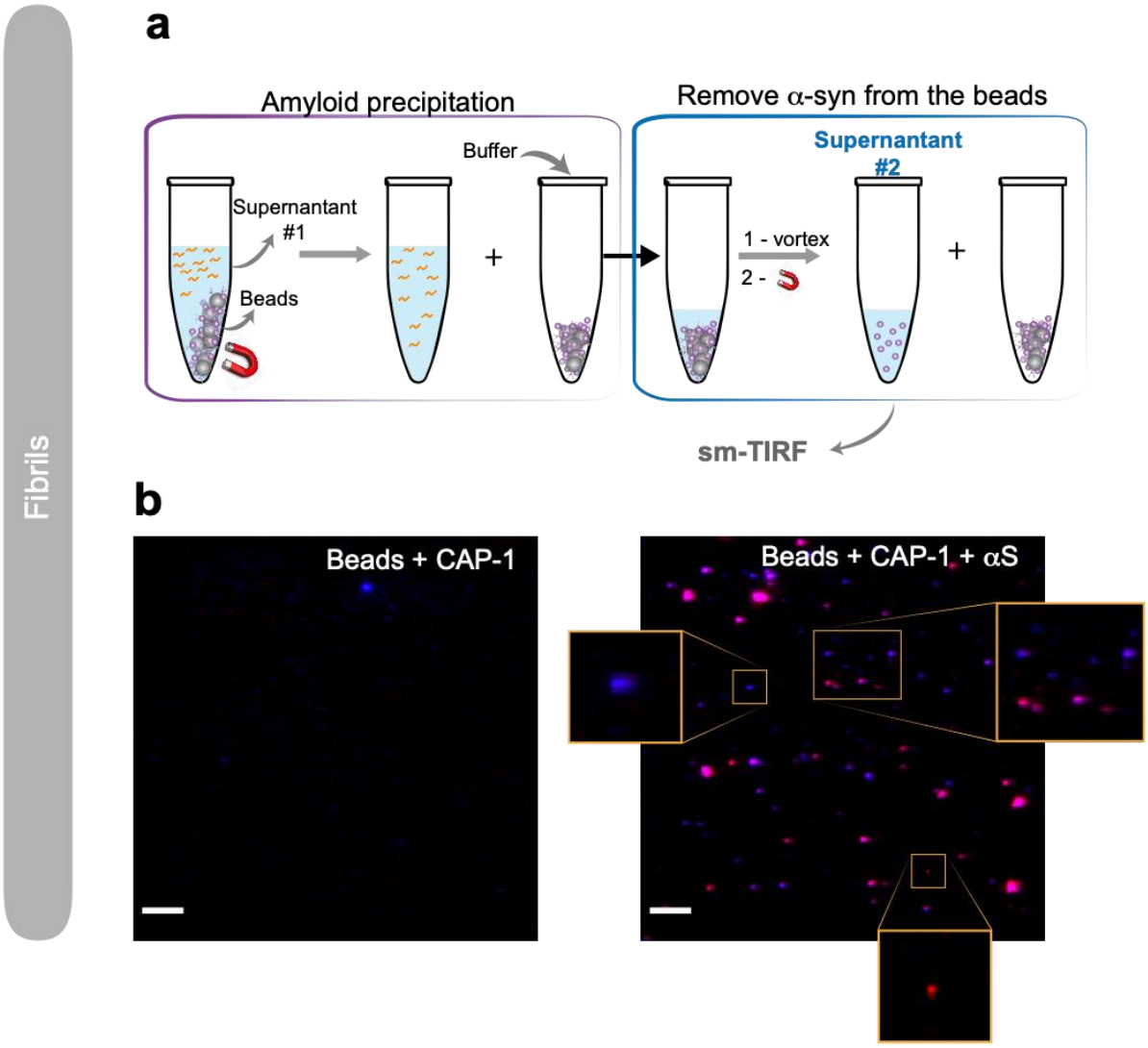
SI.15 - Normalized fluorescence intensity profile of beads. **(a)** Average of intensity profiles for beads alone (—), in the presence of CAP-1 (—) and in the presence of CAP-1 and α-synuclein (—). **(b)** Width of the fluorescence intensity profile measured as the double of the standard deviation (SD) of the Gaussian fitting of the average of all beads' profiles per sample, error bar corresponds to the SEM of the fitting. **(c)** Width of the fluorescence intensity profile measured as the double of the standard deviation (SD) of the Gaussian fitting for each bead profile separately (two independent experiment per sample at least 30 beads measured). Error bar corresponds to the SD of the bead-to-bead variation and the p-value corresponds to the result of a one-way ANOVA, and Tukey's post hoc comparison. **** $p<0.0001$, *** $p=0.0002$.



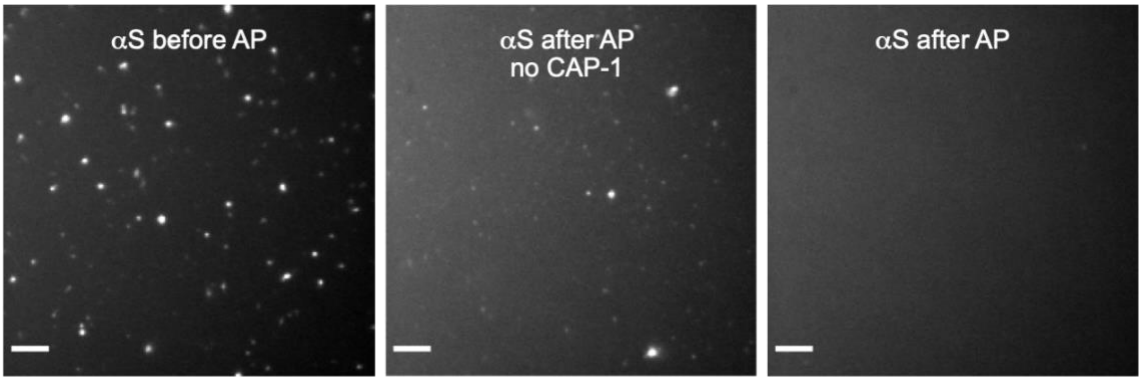
SI.16 - Read-out of protein capture mediated by CAP-1. Emission spectrum of beads and supernatant after AP using 10 μM α-synuclein sonicated fibrils, (**a**) beads and supernatant and (**b**) supernatant.



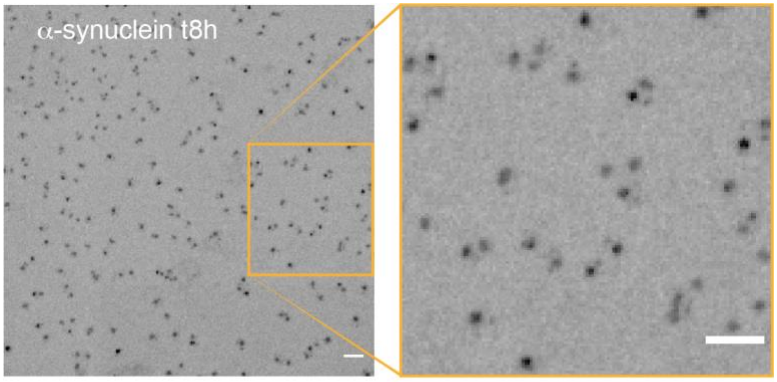
SI.17 - AFM height images after AP in the presence a) and absence b) of α-synuclein fibrils. Fibrils preferentially localize around the beads a).



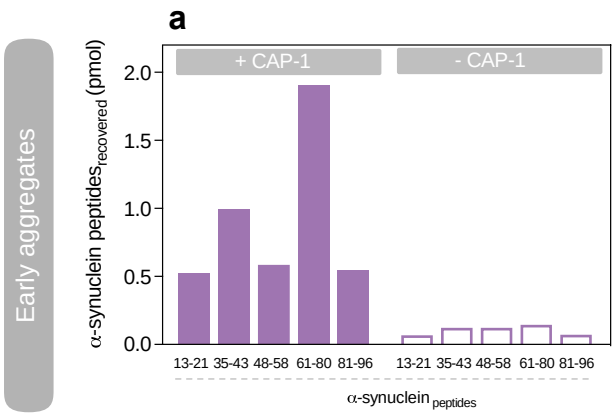
SI.18 - Removal of α-synuclein aggregates from beads. **(a)** Outline of the AP protocol followed by a second dilution and incubation of beads with a small volume of buffer and 5 cycles of 30 sec vortex. **(b)** TIRFM of the new supernatant fraction (#2) after addition of 5 μM ThT. Left, beads+CAP-1 (control) and right beads+CAP-1+ α-synuclein. Images are the result of co-localizing CAP-1 (434/17-25 emission filter - red) and ThT (480/40-25 nm emission filter - blue) channels. The presence of aggregates labelled in blue, red or pink is consistent with the successful removal of aggregates from the beads. Given the reduced overlap between the two channels it is possible to conclude that: aggregates labelled in blue were only labelled by ThT (added prior to imaging) and are therefore free of CAP-1; aggregates labelled in red are aggregates that only have CAP-1 from the beads attached to them; and finally the pink aggregates are larger aggregates where despite the presence of CAP-1 from the beads also ThT found available binding sites.



SI.19 - Amyloid-precipitation (AP) of early aggregates using CAP-1. TIRFM 7 μM α-synuclein before (left) and after AP in the presence (right) and absence (middle) of 5 μM CAP-1 using the supernatant fraction. In the middle and right panel, we used 3x times the volume used in the left (before AP) *i.e.* the equivalent to 21 μM to increase the fluorescent puncta signal needed for quantitative analysis. Scale bar = 5 μm.



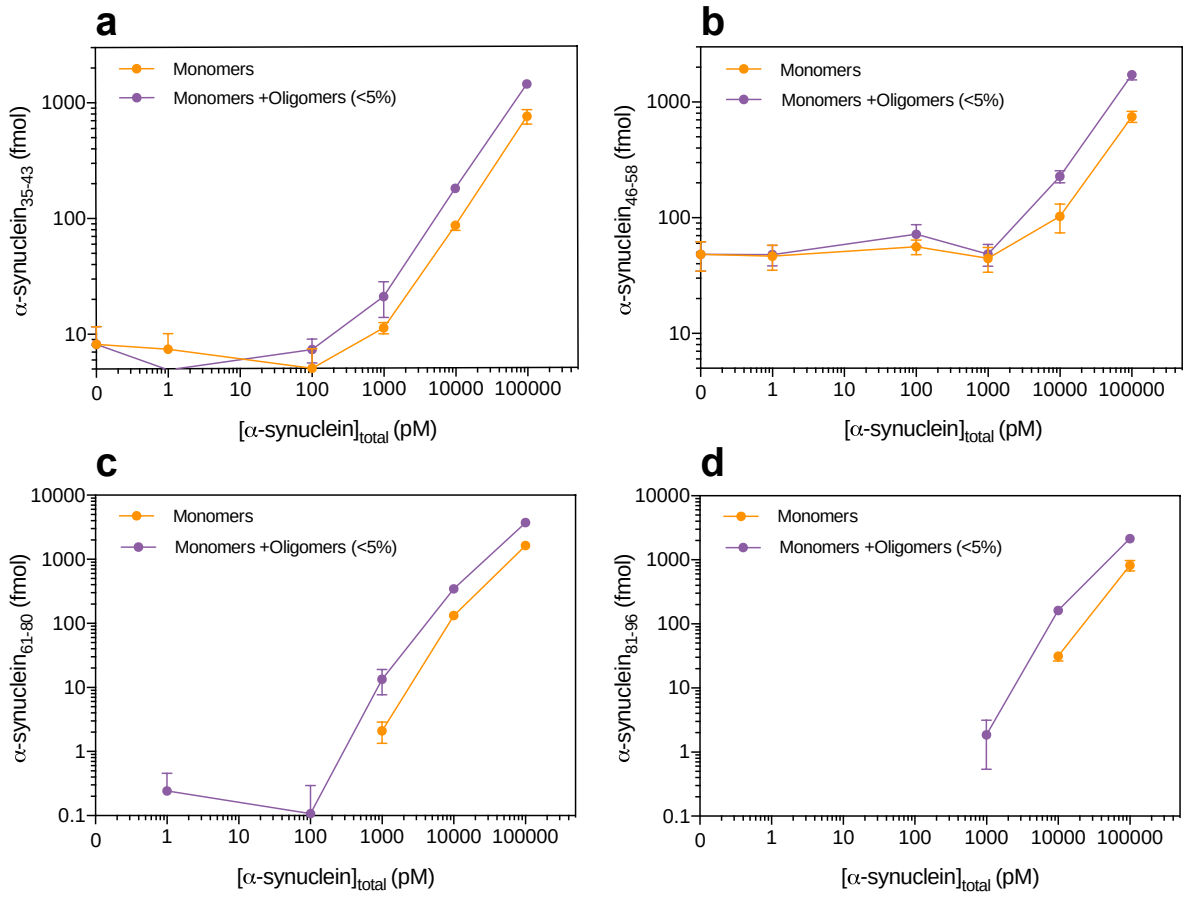
SI.20 - STEM image of α-synuclein oligomers from t=8h in the aggregation reaction (left). Scale bar = 200 nm.



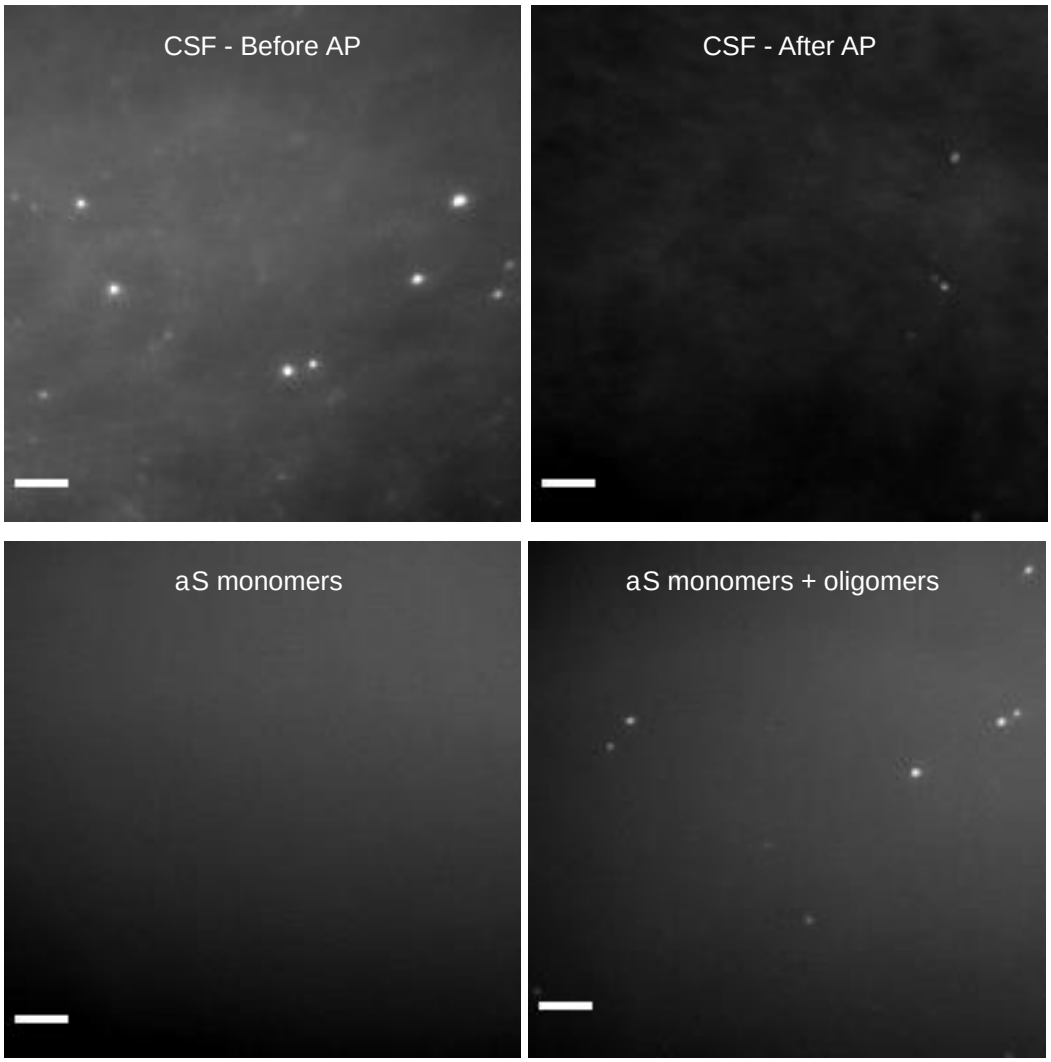
b

Peptide ID	Peptide sequence
α-syn13_21	EGVVAAAEK
α-syn35_43	EGVLYVGSK
α-syn46_58	EGVVHGVATVAEK
α-syn61_80	EQVTNVGGAVVTGVTAVAQK
α-syn81_96	TVEGAGSIAAATGFVK

SI.21 - (a) PRM-MS quantification of α-synuclein peptides recovered after amyloid-precipitation (AP) in presence and absence of CAP-1 using recombinant α-synuclein. **(b)** Table with the amino acid sequence of α-synuclein triptic petides used in the experiment.



SI.22 - PRM-MS quantification of α-synuclein peptides recovered after amyloid-precipitation (AP) from the background of CSF (complement to Figure 3 of the main text). Prior to AP recombinant α-synuclein (1 pM to 100 nM) monomers or monomers+oligomers were added to control CSF. After AP and on bead digestion the recovered peptides were quantified using PRM-MS **(a)** α-synuclein$_{35-43}$, **(b)** α-synuclein$_{46-58}$, **(c)** α-synuclein$_{61-80}$, **(d)** α-synuclein$_{81-96}$.



SI.23 - TIRFM images of control CSF and α-synuclein used in Figure 3 of the main text. CSF before and after amyloid - precipitation (top panels, left to right), and α-synuclein monomers and monomers+oligomers (bottom panels, left to right).

Table 1 - Comparison between **control CSF** proteins pulldown in the presence (+) and absence (-) of CAP-1. Total number of unique proteins present in all replicates and both conditions (presence and absence of CAP-1), exclusive proteins in the presence of CAP-1 and exclusive proteins in the absence of CAP-1 (see Methods for filtering conditions). % of α-helix and % of β-strand determined by protein sequence analysis using PASTA 2.0[1]. Results are from one CSF sample tested in triplicate in each condition (presence and absence of CAP-1). Mean and standard deviation (SD) for the % of α-helix or β-strand predicted for each protein in the different lists (see Table 3-5).

Control CSF	**Nr. of proteins**	**% α-helix**	**% β-strand**
		Mean ± SD	Mean ± SD
Common proteins	44	30 ± 22	20 ± 12
Exclusive (+) CAP-1	21	21 ± 18	25 ± 11
Exclusive (-) CAP-1	4	35 ± 17	19 ± 9

Table 2 - Comparison between **PD CSF** proteins pulldown in the presence (+) and absence (-) of CAP-1. Total number of unique proteins present in all replicates and both conditions (presence and absence of CAP-1), exclusive proteins in the presence of CAP-1 and exclusive proteins in the absence of CAP-1 (see Methods for filtering conditions). % of α-helix and % of β-strand determined by protein sequence analysis using PASTA 2.0[1]. Results are from three different CSF samples tested in triplicate in each condition (presence and absence of CAP-1). Mean and standard deviation (SD) for the % of α-helix or β-strand predicted for each protein in the different lists (see Table 6-8).

PD CSF	**Nr. of proteins**	**% α-helix**	**% β-strand**
		Mean ± SD	Mean ± SD
Common proteins	31	33 ± 24	19 ± 11
Exclusive (+) CAP-1	35	14 ± 14	26 ± 12
Exclusive (-) CAP-1	12	35 ± 31	19 ± 16

Table 3 - List of common proteins pulldown from **control CSF** in the presence and absence of CAP-1 and protein sequence analysis using PASTA 2.0[1]. Results are from one CSF sample tested in triplicate in each condition (presence and absence of CAP-1).

Protein name	length	# amyloids	best energy	% disorder	% α-helix	% β-strand	% coil	UniProtKB accession numbers
Adipocyte enhancer-binding protein 1	1158	20	-6.837548	33.59	22.54	13.47	63.99	Q8IUX7
Amyloid-beta precursor protein	770	20	-20.171292	14.67	46.36	10.78	42.86	P05067
Apolipoprotein D	189	20	-11.361203	4.761	20.63	33.86	45.5	P05090
ıt membrane-specific heparan sulfate proteoglycan core protein	4391	20	-11.599164	1.753	4.12	38.21	57.66	P98160
Collagen alpha-2(I) chain	1366	20	-6.783046	82.86	4.03	8.35	87.63	P08123
Complement C3	1663	20	-15.550313	0.901	24.05	31.03	44.92	P01024
C-X-C motif chemokine 10	98	20	-10.055459	28.57	50	10.2	39.8	P02778
Extracellular matrix protein 2	699	20	-13.318841	27.32	30.19	14.02	55.79	O94769
Fibrinogen alpha chain	866	20	-10.907301	35.33	16.17	24.02	59.82	P02671
Fibronectin	2477	20	-8.093383	4.602	1.7	43.4	54.91	P02751
Fibulin-1	703	20	-14.691325	1.28	12.94	32.29	54.77	P23142
Fibulin-2	1184	20	-7.635911	22.38	11.99	26.52	61.49	P98095
Gelsolin	782	20	-8.072905	12.4	21.74	27.24	51.02	P06396
Growth arrest-specific protein 6	678	20	-7.025432	5.014	22.42	28.76	48.82	Q14393
Hemoglobin subunit beta	147	20	-7.976094	13.6	73.47	0	26.53	P68871
Immunoglobulin kappa constant	107	13	-6.871533	57	1.87	43.93	54.21	P01834
Pleiotrophin	168	20	-8.628732	35.71	45.24	12.5	42.26	P21246
Proteoglycan 4	1404	20	-12.394352	67.8	4.77	15.95	79.27	Q92954
Secretogranin-1	677	3	-5.28399	69.27	39.44	1.92	58.64	P05060
Albumin	609	20	-9.230629	1.97	78	0	22	P02768
Signal peptide, CUB and EGF-like domain-containing protein 1	988	20	-8.710191	5.263	10.02	31.07	58.91	Q8IWY4
SPARC-like protein 1	664	0	-4.875821	64.9	30.57	9.64	59.79	Q14515
Spondin-1	807	20	-7.521185	8.55	26.89	16.6	56.51	Q9HCB6
Transthyretin	147	20	-8.269028	12.92	21.09	29.93	48.98	P02766
Vitamin K-dependent protein S	676	20	-7.754854	3.106	21.45	29.14	49.41	P07225
Actin, cytoplasmic 1	375	5	-6.030025	1.866	34.13	18.4	47.47	P60709
Alpha-2-HS-glycoprotein	367	18	-6.731075	14.16	24.52	23.43	52.04	P02765
Angiotensinogen	485	20	-7.332547	7.422	40	12.99	47.01	P01019
Apolipoprotein A-I	267	20	-7.585395	6.367	91.39	0	8.61	P02647
Apolipoprotein E	317	20	-7.905302	6.94	90.54	0	9.46	P02649
Carboxypeptidase E	476	20	-8.888563	10.5	34.87	17.44	47.69	P16870
Clusterin	449	20	-7.161453	6.458	64.14	5.35	30.51	P10909
EGF-containing fibulin-like extracellular matrix protein 1	493	20	-9.719066	4.665	5.68	36.11	58.21	Q12805
Extracellular superoxide dismutase [Cu-Zn]	240	20	-6.904548	24.16	26.67	22.92	50.42	P08294
Fibrinogen beta chain	491	20	-10.265117	9.979	31.57	21.38	47.05	P02675
Fibrinogen gamma chain	453	20	-10.663145	9.05	29.58	25.17	45.25	P02679
Glyceraldehyde-3-phosphate dehydrogenase	335	20	-6.530456	2.686	26.27	27.16	46.57	P04406
Immunoglobulin heavy constant gamma 1	330	20	-8.945009	13.63	6.36	33.33	60.3	P01857
Monocyte differentiation antigen CD14	375	4	-5.199154	5.866	36	12.27	51.73	P08571
Osteopontin	314	20	-10.253145	95.54	14.33	8.92	76.75	P10451
Phospholipid transfer protein	493	20	-8.704384	5.07	30.43	23.94	45.64	P55058
Prothrombin	622	9	-6.070176	1.929	30.39	14.47	55.14	P00734
Secreted frizzled-related protein 3	325	2	-5.784988	15.69	29.54	13.54	56.92	Q92765
Vitronectin	478	20	-7.916569	29.07	16.53	20.29	63.18	P04004
Mean (%)					**29.7**	**19.8**		
SD					22.0	11.8		

Table 4 - List of exclusive proteins pulldown from **control CSF** in the presence of CAP-1 and protein sequence analysis using PASTA 2.0[1]. Results are from one CSF sample tested in triplicate in each condition (presence and absence of CAP-1).

Protein name	length	# amyloids	best energy	% disorder	% α-helix	% β-strand	% coil	UniProtKB accession numbers
Calsyntenin-1	981	20	-23.180393	11.82	14.58	34.86	50.56	O94985
Ceruloplasmin	1065	20	-9.458505	1.314	7.61	40	52.39	P00450
Coagulation factor V	2224	20	-10.169181	16.18	13.98	24.82	61.2	P12259
Collagen alpha-1(XIV) chain	1796	20	-11.613298	22.77	17.48	27.23	55.29	Q05707
Collagen alpha-1(XVIII) chain	1754	20	-9.187466	62.59	12.31	12.26	75.43	P39060
Complement C1r subcomponent	705	20	-7.21306	2.836	9.79	34.04	56.17	P00736
Complement C1s subcomponent	688	20	-10.45933	1.453	4.36	34.01	61.63	P09871
Complement factor H	1231	20	-10.155511	0.974	2.44	38.51	59.06	P08603
Cystatin-C	146	20	-8.518981	31.5	33.56	15.75	50.68	P01034
Hemoglobin subunit alpha	142	8	-6.722631	9.859	69.01	0	30.99	P69905
Pre-B-cell leukemia transcription factor-interacting protein 1	731	20	-8.736379	63.06	43.37	6.84	49.79	Q96AQ6
Prostaglandin-H2 D-isomerase	190	5	-5.703427	5.789	31.58	23.68	44.74	P41222
Beta-Ala-His dipeptidase	506	20	-8.626567	1.976	42.69	14.82	42.49	Q96KN2
Complement C1q subcomponent subunit B	253	20	-8.602751	37.15	7.91	30.04	62.06	P02746
Complement C1q subcomponent subunit C	245	20	-10.420788	35.91	5.71	30.2	64.08	P02747
Complement component C9	559	20	-8.159938	6.082	23.43	23.97	52.59	P02748
EGF-containing fibulin-like extracellular matrix protein 2	443	20	-7.246752	11.28	9.71	29.57	60.72	O95967
Fibulin-5	448	20	-11.868578	1.339	0	40.18	59.82	Q9UBX5
Heparin cofactor 2	499	20	-9.391957	9.819	40.88	17.23	41.88	P05546
Lactadherin	387	20	-8.356042	1.291	20.67	29.72	49.61	Q08431
Major prion protein	253	20	-16.038002	35.96	32.02	11.46	56.52	P04156
Mean (%)					**21.1**	**24.7**		
SD					17.5	11.3		

Table 5 - List of exclusive proteins pulldown from **control CSF** in the absence of CAP-1 and protein sequence analysis using PASTA 2.0[1]. Results are from one CSF sample tested in triplicate in each condition (presence and absence of CAP-1).

Protein name	length	# amyloids	best energy	% disorder	% α-helix	% β-strand	% coil	UniProtKB accession numbers
Band 3 anion transport protein	911	20	-27.518775	12.29	60.26	6.48	33.26	P02730
Complement C4-A	1744	20	-8.773181	1.777	26.26	27.24	46.5	P0C0L4
Vitamin K-dependent protein C	461	20	-7.204106	7.375	32.1	18.66	49.24	P04070
Coagulation factor X	488	20	-7.08814	9.221	21.72	23.98	54.3	P00742
Mean (%)					**35.1**	**19.1**		
SD					17.3	9.1		

Table 6 - List of common proteins pulldown from **PD CSF** in the presence and absence of CAP-1 and protein sequence analysis using PASTA 2.0[1]. Results are from three different CSF samples tested in triplicate in each condition (presence and absence of CAP-1).

Protein name	length	# amyloids	best energy	% disorder	% α-helix	% β-strand	% coil	UniProtKB accession numbers
Adipocyte enhancer-binding protein 1	1158	20	-6.837548	33.59	22.54	13.47	63.99	Q8IUX7
Angiogenin	147	20	-10.376892	7.482	22.45	25.85	51.7	P03950
Apolipoprotein D	189	20	-11.361203	4.761	20.63	33.86	45.5	P05090
Calsyntenin-1	981	20	-23.180393	11.82	14.58	34.86	50.56	O94985
Fibrinogen alpha chain	866	20	-10.907301	35.33	16.17	24.02	59.82	P02671
Fibronectin	2477	20	-8.093383	4.602	1.7	43.4	54.91	P02751
Inactive carboxypeptidase-like protein X2	756	20	-8.010832	19.84	21.3	22.62	56.08	Q8N436
Latent-transforming growth factor beta-binding protein 2	1821	18	-5.602549	23.66	6.04	24.05	69.91	Q14767
Matrix Gla protein	103	20	-11.076716	10.67	84.47	0	15.53	P08493
Pleiotrophin	168	20	-8.628732	35.71	45.24	12.5	42.26	P21246
Prostaglandin-H2 D-isomerase	190	5	-5.703427	5.789	31.58	23.68	44.74	P41222
Proteoglycan 4	1404	20	-12.394352	67.8	4.77	15.95	79.27	Q92954
Ribonuclease pancreatic	156	20	-15.116791	30.12	25.64	28.85	45.51	P07998
Albumin	609	20	-9.230629	1.97	78	0	22	P02768
Signal peptide, CUB and EGF-like domain-containing protein 1	988	20	-8.710191	5.263	10.02	31.07	58.91	Q8IWY4
Spondin-1	807	20	-7.521185	8.55	26.89	16.6	56.51	Q9HCB6
Transthyretin	147	20	-8.269028	12.92	21.09	29.93	48.98	P02766
Apolipoprotein A-I	267	20	-7.585395	6.367	91.39	0	8.61	P02647
Apolipoprotein E	317	20	-7.905302	6.94	90.54	0	9.46	P02649
Clusterin	449	20	-7.161453	6.458	64.14	5.35	30.51	P10909
Fibrinogen beta chain	491	20	-10.265117	9.979	31.57	21.38	47.05	P02675
Fibrinogen gamma chain	453	20	-10.663145	9.05	29.58	25.17	45.25	P02679
Glia-derived nexin	398	20	-9.936162	1.758	28.14	27.89	43.97	P07093
Glyceraldehyde-3-phosphate dehydrogenase	335	20	-6.530456	2.686	26.27	27.16	46.57	P04406
Major prion protein	253	20	-16.038002	35.96	32.02	11.46	56.52	P04156
Mimecan	298	20	-6.921483	1.677	27.85	18.12	54.03	P20774
Olfactomedin-like protein 3	406	20	-9.374003	2.955	30.05	20.69	49.26	Q9NRN5
Phospholipid transfer protein	493	20	-8.704384	5.07	30.43	23.94	45.64	P55058
Secreted frizzled-related protein 3	325	2	-5.784988	15.69	29.54	13.54	56.92	Q92765
Secreted frizzled-related protein 4	346	20	-10.232728	23.41	44.22	5.2	50.58	Q6FHJ7
SPARC-related modular calcium-binding protein 1	434	20	-7.035247	15.66	24.42	16.36	59.22	Q9H4F8
Mean (%)					**33.3**	**19.3**		
SD					24.0	11.2		

Table 7 - List of exclusive proteins pulldown from **PD CSF** in the presence of CAP-1 and protein sequence analysis using PASTA 2.0[1]. Results are from three different CSF samples tested in triplicate in each condition (presence and absence of CAP-1).

Protein name	length	# amyloids	best energy	% disorder	% α-helix	% β-strand	% coil	UniProtKB accession numbers
nt membrane-specific heparan sulfate proteoglycan core protein	377	20	-8.945009	18.56	5.84	30.77	63.4	P98160
Coagulation factor V	2224	20	-10.169181	16.18	13.98	24.82	61.2	P12259
Collagen alpha-1(I) chain	1464	7	-5.272464	79.37	2.12	8.33	89.55	P02452
Collagen alpha-1(XVIII) chain	1754	20	-9.187466	62.59	12.31	12.26	75.43	P39060
Collagen alpha-2(I) chain	1366	20	-6.783046	82.86	4.03	8.35	87.63	P08123
Complement C4-A	1744	20	-8.773181	1.777	26.26	27.24	46.5	P0C0L4
Complement factor H	1231	20	-10.155511	0.974	2.44	38.51	59.06	P08603
Elastin	786	14	-7.851138	11.83	21.88	1.15	76.97	P15502
Fibrillin-1	2871	20	-7.913752	3.065	4.25	31.8	63.95	P35555
Fibulin-1	703	20	-14.691325	1.28	12.94	32.29	54.77	P23142
Fibulin-2	1184	20	-7.635911	22.38	11.99	26.52	61.49	P98095
Gelsolin	782	20	-8.072905	12.4	21.74	27.24	51.02	P06396
Immunoglobulin kappa light chain	214	13	-6.871533	32.71	4.67	42.52	52.8	P0DOX7
Latent-transforming growth factor beta-binding protein 1	1721	20	-7.848722	14.93	6.16	26.84	67	Q14766
Macrophage receptor MARCO	520	20	-19.116756	59.23	18.46	12.31	69.23	Q9UEW3
Matrilin-2	956	20	-8.212839	9.623	29.18	29.39	41.42	O00339
Papilin	1278	20	-6.706005	32.39	2.97	28.79	68.23	O95428
Probable carboxypeptidase X1	734	11	-5.605048	10.62	19.48	25.07	55.45	Q96SM3
venger receptor cysteine-rich domain-containing protein SSC5D	1573	9	-6.311401	57.21	8.52	14.94	76.54	A1L4H1
Target of Nesh-SH3	1075	20	-11.356688	42.88	4.47	27.07	68.47	Q7Z7G0
Tenascin-X	4244	20	-8.156655	13.03	1.84	38.81	59.35	P22105
C4b-binding protein alpha chain	597	20	-7.953199	5.192	10.72	36.18	53.1	P04003
Chondroadherin	359	20	-7.114148	12.25	57.1	1.95	40.95	O15335
Complement C1q subcomponent subunit C	245	20	-10.420788	35.91	5.71	30.2	64.08	P02747
EGF-containing fibulin-like extracellular matrix protein 1	493	20	-9.719066	4.665	5.68	36.11	58.21	Q12805
EGF-containing fibulin-like extracellular matrix protein 2	443	20	-7.246752	11.28	9.71	29.57	60.72	O95967
Fibulin-5	448	20	-11.868578	1.339	0	40.18	59.82	Q9UBX5
Glutaminyl-peptide cyclotransferase	361	20	-8.459151	2.216	45.43	9.7	44.88	Q16769
Immunoglobulin heavy constant alpha 1	353	20	-8.311744	20.39	12.18	31.73	56.09	P01876
Immunoglobulin heavy constant gamma 3	4390	20	-11.599164	1.753	3.96	38.45	57.59	P01860
Immunoglobulin mu heavy chain	576	20	-13.628103	2.604	1.74	48.26	50	P0DOX6
16270|IBP7_HUMAN Insulin-like growth factor-binding protein 7	282	12	-6.416259	10.63	8.16	28.37	63.48	Q16270
Lysyl oxidase homolog 1	574	20	-8.110721	45.64	10.63	21.6	67.77	Q08397
Prothrombin	622	9	-6.070176	1.929	30.39	14.47	55.14	P00734
Secreted frizzled-related protein 2	295	3	-6.152469	3.728	44.75	12.2	43.05	Q96HF1
Mean (%)					**13.8**	**25.5**		
SD					13.7	11.8		

Table 8 – List of exclusive proteins pulldown from **PD CSF** in the absence of CAP-1 and protein sequence analysis using PASTA 2.0[1]. Results are from three different CSF samples tested in triplicate in each condition (presence and absence of CAP-1).

Protein name	length	# amyloids	best energy	% disorder	% α-helix	% β-strand	% coil	UniProtKB accession numbers
Apolipoprotein A-II	100	20	-7.08197	10	86	0	14	P02652
Apolipoprotein C-III	99	20	-9.551744	21.21	84.85	0	15.15	P02656
Cadherin-1	882	20	-15.327144	15.64	10.09	36.73	53.17	P12830
C-reactive protein	143	16	-6.941046	27.97	20.98	26.57	52.45	P02741
Cystatin-C	146	20	-8.518981	31.5	33.56	15.75	50.68	P01034
Hornerin	2850	20	-9.874367	97.47	2.63	7.44	89.93	Q86YZ3
Midkine	224	20	-6.492262	3.571	3.13	50	46.88	P21741
Protocadherin alpha-9	950	20	-24.095895	26.73	9.05	34.74	56.21	Q9Y5H5
Sodium/iodide cotransporter	643	20	-29.572005	9.02	59.41	4.51	36.08	Q92911
Stromal cell-derived factor 1	93	20	-15.459366	6.451	63.44	11.83	24.73	P48061
Shadow of prion protein	151	0	-4.344823	51.65	27.81	15.89	56.29	Q5BIV9
Sushi repeat-containing protein SRPX	464	20	-7.759716	10.34	20.26	29.96	49.78	P78539
Mean (%)					**35.1**	**19.5**		
SD					30.6	16.1		

Table 9 – Comparison between the total number of proteins and amyloid proteins for both samples, control and PD CSF, in the presence (+) and absence (-) of CAP-1 determined by the web server RFAmyloid[2].

	Total nr. proteins		**Amyloid proteins**	
	(+) CAP-1	(-) CAP-1	(+) CAP-1	(-) CAP-1
Control CSF	65	48	37	27
PD CSF	66	43	38	27

References

1. Walsh, I., Seno, F., Tosatto, S. C. E. & Trovato, A. PASTA 2.0: An improved server for protein aggregation prediction. *Nucleic Acids Res.* **42**, 301–307 (2014).
2. Niu, M., Li, Y., Wang, C. & Han, K. RFAmyloid: A web server for predicting amyloid proteins. *Int. J. Mol. Sci.* **19**, (2018).