Supporting Information for:

Structural Features of α-Synuclein Amyloid Fibrils Revealed by Raman Spectroscopy

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Table S1. MS analysis taken after incubating recombinant WT (**A**), A30P (**B**), E46K (**C**), G51D (**D**), or A53T (**E**) α-syn fibrils (30 µM) with either 150, 300, 450 or 600 nM CtsL for 24 h at pH 5 and 37 ºC.

A

CtsL (150–600 nM) + WT α-syn$_f$ (30 µM)

Observed Mass (Da)	Theoretical Mass (Da)	Position of α-syn sequence
14459.22	14460.10	1–140
13836.00	13836.37	6–140
13450.40	13450.91	10–140
12832.55	12833.49	1–126
12667.13	12667.97	18–140
12340.35	12341.00	1–122
11717.43	11717.22	6–122
11456.61	11457.07	1–114
10547.98	10548.82	18–122
10447.18	10447.83	10–114
9664.44	9664.89	18–114
8679.97	8680.77	28–114

B

CtsL (150–600 nM) + A30P α-syn$_f$ (30 µM)

Observed Mass (Da)	Theoretical Mass (Da)	Position of α-syn sequence
14485.21	14486.19	1–140
13861.37	13862.41	6–140
13476.13	13476.95	10–140
12692.04	12694.01	18–140
12366.44	12367.04	1–122
11742.44	11743.26	6–122
10574.10	10574.86	18–122
9690.55	9690.93	18–114

C

CtsL (150–600 nM) + E46K α-syn$_f$ (30 µM)

Observed Mass (Da)	Theoretical Mass (Da)	Position of α-syn sequence
14458.34	14459.21	1–140
13834.72	13835.43	6–140
12339.30	12340.06	1–122
13449.16	13449.97	10–140
12666.34	12667.03	18–140
11716.04	11716.28	6–122
11455.67	11456.13	1–114
10574.10	10574.88	18–122
9663.29	9663.95	18–114
8678.99	8679.83	28–114

D

CtsL (150–600 nM) + G51D α-syn$_f$ (30 µM)

Observed Mass (Da)	Theoretical Mass (Da)	Position of α-syn sequence
14517.28	14518.19	1–140
13893.28	13894.41	6–140
13508.08	13508.95	10–140
12725.48	12726.01	18–140
12398.06	12399.04	1–122
11514.06	11515.11	1–114
10605.84	10606.85	18–122
9722.55	9722.93	18–114
8738.14	8738.81	28–114

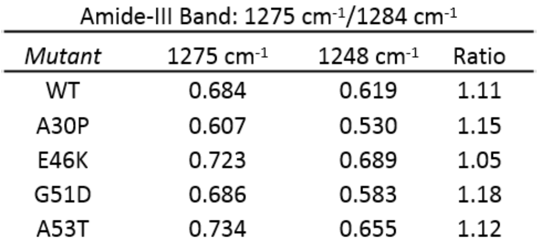
E

CtsL (150–600 nM) + A53T α-syn$_f$ (30 µM)

Observed Mass (Da)	Theoretical Mass (Da)	Position of α-syn sequence
14489.26	14490.18	1–140
11485.84	11487.10	1–114
12369.34	12371.03	1–122
10578.06	10578.84	18–122
9694.32	9694.92	18–114
8709.92	8710.79	28–114

Table S2. Raman peak ratio comparison for (**A**) amide-III and (**B**) C-H deformation stretches for WT and mutant α-syn.

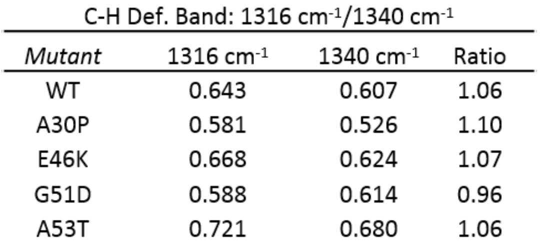
A



Amide-III Band: 1275 cm^{-1}/1284 cm^{-1}

Mutant	1275 cm^{-1}	1248 cm^{-1}	Ratio
WT	0.684	0.619	1.11
A30P	0.607	0.530	1.15
E46K	0.723	0.689	1.05
G51D	0.686	0.583	1.18
A53T	0.734	0.655	1.12

B



C-H Def. Band: 1316 cm^{-1}/1340 cm^{-1}

Mutant	1316 cm^{-1}	1340 cm^{-1}	Ratio
WT	0.643	0.607	1.06
A30P	0.581	0.526	1.10
E46K	0.668	0.624	1.07
G51D	0.588	0.614	0.96
A53T	0.721	0.680	1.06

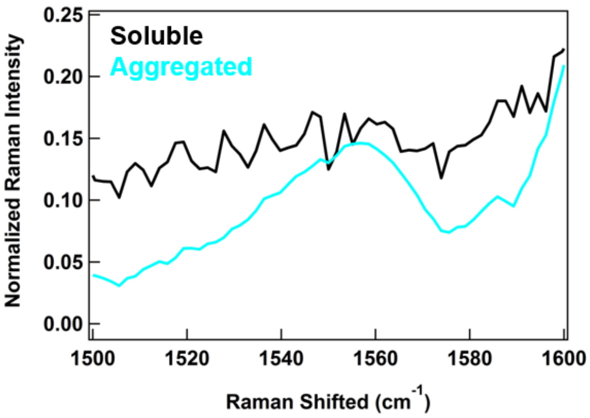


Figure S1. Expanded view of amide-II band for soluble (black trace) and aggregated (cyan trace) WT-α-syn.

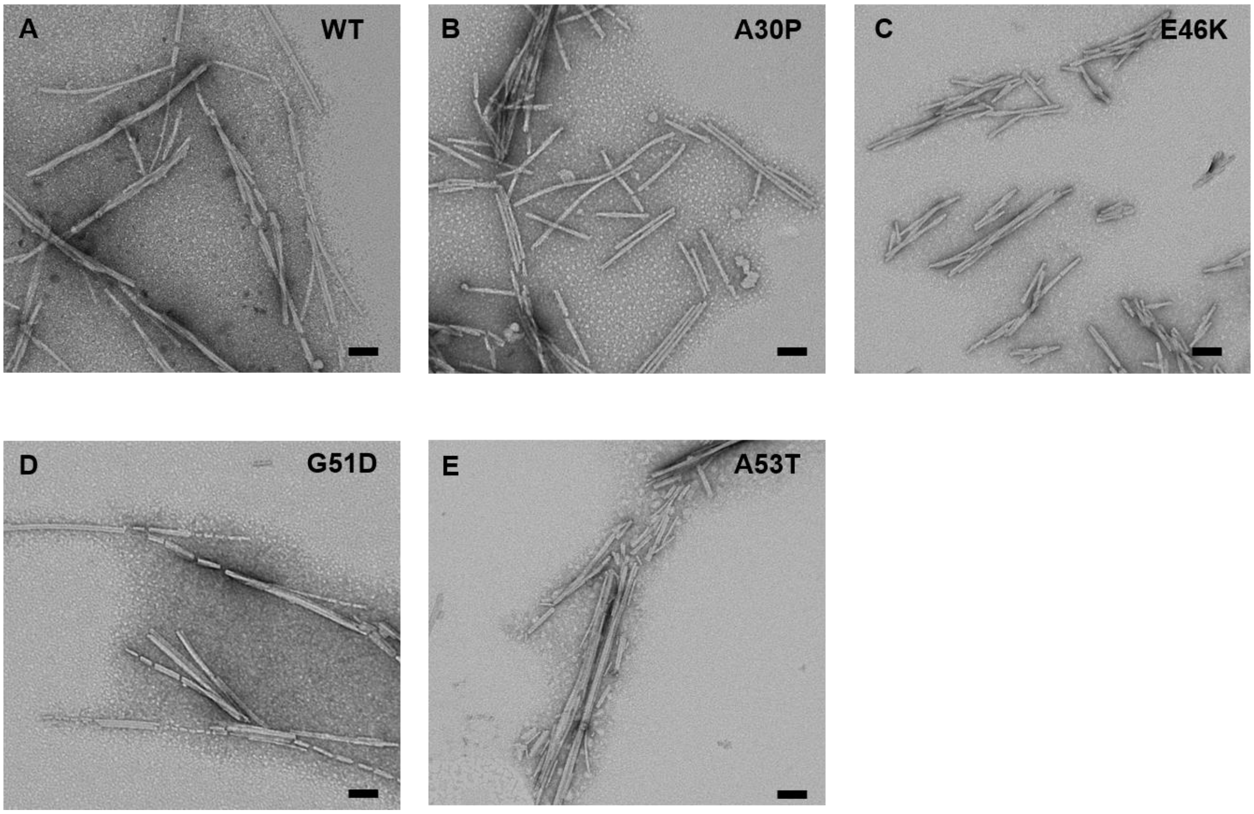


Figure S2. Representative negatively-stained transmission electron microscopy images of WT (A), A30P (B), E46K (C), G51D (D), and A53T (E) α-syn fibrils formed at 40 μM, 10 mM NaOAC, 100 mM NaCl, pH 5, 37 °C. Scale bars: 100 nm.

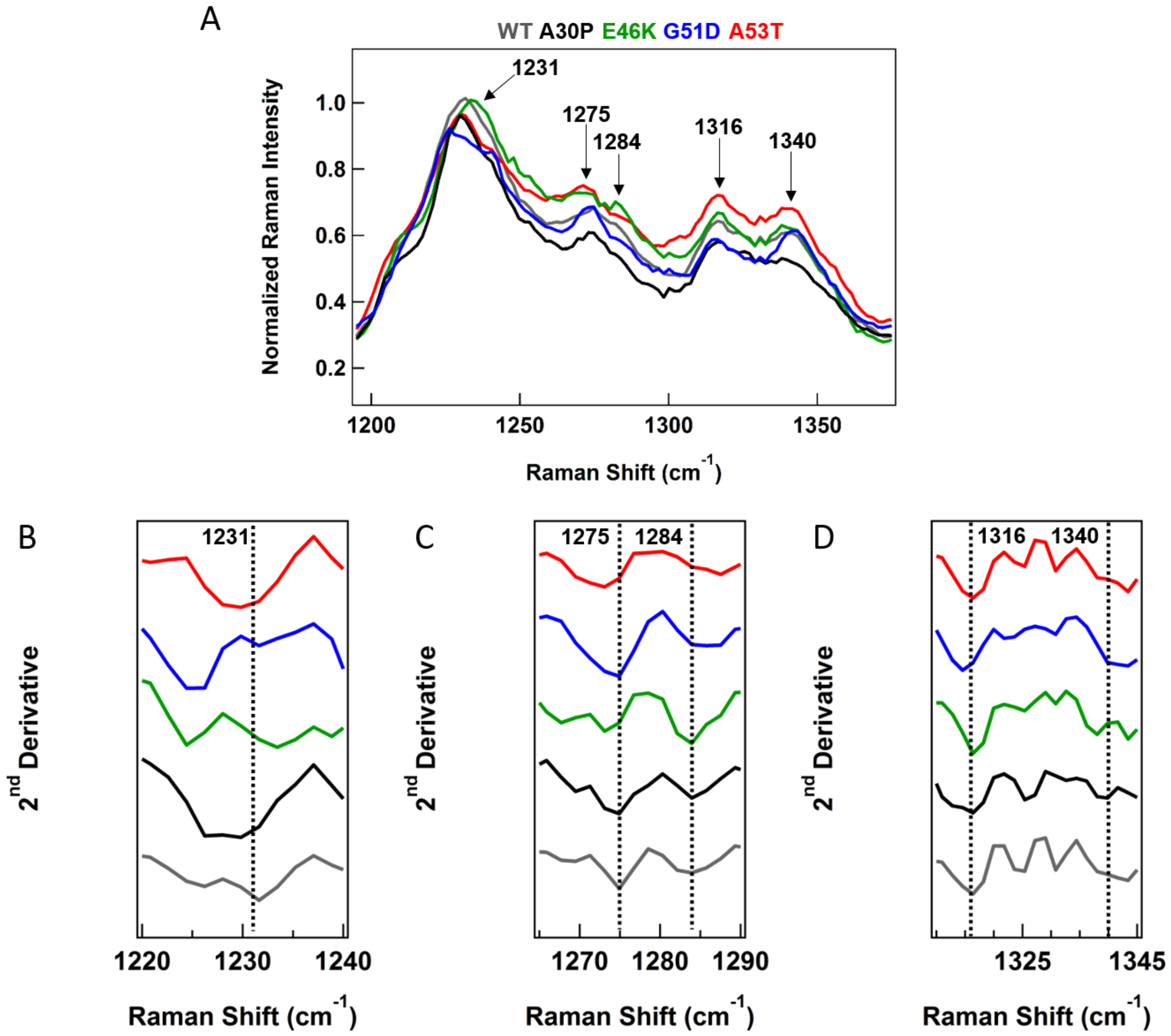


Figure S3. (A) Expanded view of fingerprint region for WT and mutant α-syn. Second derivative analysis for amide-III region (**B**, **C**) and C-H deformation stretches (**D**).