

## Supplemental figures

**Supplementary Figure 1 A**, Comparison of all known synuclein sequences. **B**, Comparison of human, mouse and  $\alpha$ -,  $\beta$ - and  $\gamma$ -synuclein sequences. Program used: ClustalW2 (<http://www.ebi.ac.uk/Tools/clustalw2/index.html>).

**Supplemental Figure 2:** Mapping the CK1 phosphorylation sites: WT, S129A and S129E were phosphorylated for 24 h with CK1 and the different phosphorylated species (I,II,III) were separated by semi-preparative RP-HPLC and analyzed by MALDI-MS. **A**, The Coomassie blue stained SDS gels of the mono-, di-, and unphosphorylated species of each protein. The S129A  $\alpha$ -syn was subjected to further trypsin digestion and tandem mass spectrometry. **B**, 4280-4380 m/z inset covering the pseudomolecular region of C-terminal peptide [103-140] of S129A analyzed by MALDI-MS in positive ion mode. The peak corresponding to the monophosphorylated peptide at m/z 4363.4 could not be detected. **C**, MALDI-MS spectra in negative ion mode showing the m/z region 1450–1850 of the tryptic digest of unphosphorylated (blue), monophosphorylated (red), and diphosphorylated (green) peaks obtained from an in vitro phosphorylation of S129A with CK1. The peak at m/z 1478.0 corresponds to the sequence TVEGAGSIAAATGFVKK ([81-96]), which contains three potential phosphorylation sites. The difference in mass of 80 or 160 Da is consistent with the addition of one and two phosphate groups, respectively. **D**, CID spectrum of the doubly modified peptide [81-96]. Fragmentation pattern of the  $[M + 2H]^{2+}$  81-96 peptide bearing two phosphates on S87 and T92 residues. (Top right) Sequence coverage based on detected y and b fragment ions. Ions carrying the phosphate group are shown with one or two stars (\* and \*\*) on the sequence.

**Supplemental Figure 3.** CK1-mediated phosphorylation inhibits the fibrillization of S129A and S129E  $\alpha$ -syn. **A**, ThT fluorescence measurements of CK1-phosphorylated S129A and **B**, S129E  $\alpha$ -syn (100  $\mu$ M) (white) and their unphosphorylated control (black). S129A and S129E  $\alpha$ -syn were phosphorylated for 24 h with CK1 and then aggregated for the indicated length of time. Negatively stained TEM images of phosphorylated S129A and S129E and their unphosphorylated control after 12 h of incubation at 37°C under agitating conditions (scales bar 0.2  $\mu$ m). **C**, ThT fluorescence measurements of CK1-phosphorylated S129E  $\alpha$ -syn (20  $\mu$ M). S129E was phosphorylated for 24 h with CK1 and then the different phosphorylated species were separated by RP-HPLC. S129E and S129E/S87-P samples were aggregated for the indicated length of time. Negatively stained TEM images of S129E and S129E/S87-P after 24 h of incubation at 37°C under agitating conditions (scales bar 0.2  $\mu$ m).

**Supplemental Figure 4. A**, Comparison of two-dimensional  $^1H$  - $^{15}N$  HSQC spectra of unphosphorylated WT (blue) and phosphorylated WT (red)  $\alpha$ -syn. A dashed rectangle marks glutamine and asparagine side chain resonances. **B**, Comparison of 3J(HN,H $\alpha$ ) scalar couplings observed in nonphosphorylated WT (black), nonphosphorylated S129D (blue) and phosphorylated S129D (grey)  $\alpha$ -syn at 15 °C. **C**, Comparison of  $^{15}N$  R1 $\rho$  spin relaxation rates

in nonphosphorylated WT (black) and phosphorylated S129D (grey). The domain organization of  $\alpha$ -syn is shown on the top: basic N-terminal domain (red), hydrophobic NAC region (yellow), acidic C-terminal domain (blue) and the six repeats (green).

**Supplemental Figure 5.** *In vitro* phosphorylation of  $\alpha$ -syn monomers and fibrils as a function of time by CK1. Samples were separated on a 12% SDS gel and probed with anti- $\alpha$ -syn (211, 1:500), anti-S129-P (1:5000) or anti-S87-P (1:100)  $\alpha$ -syn antibodies.

A

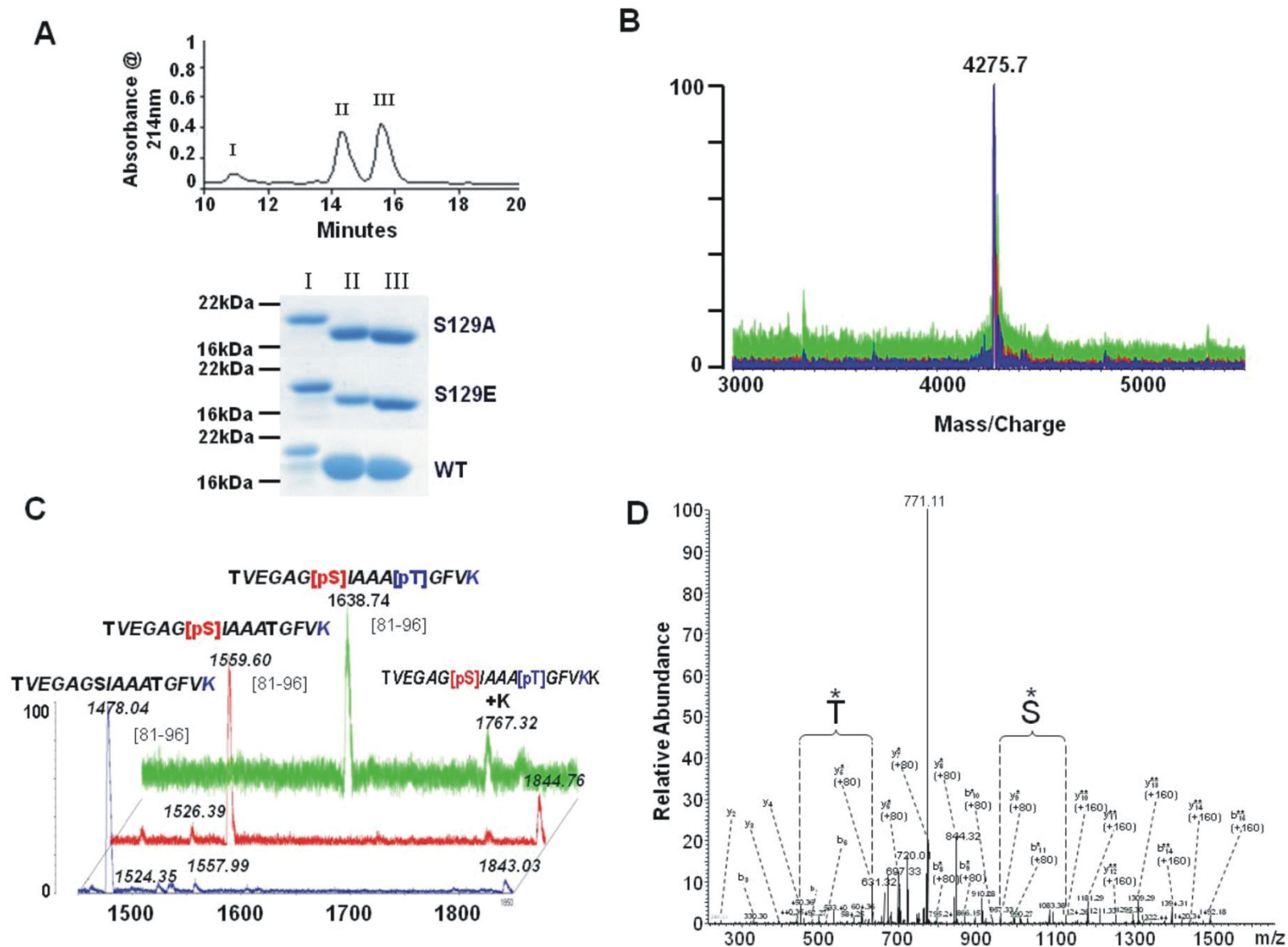
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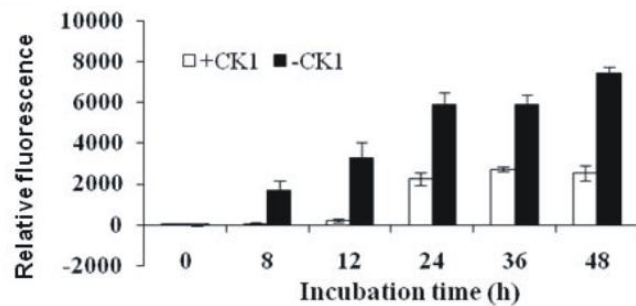
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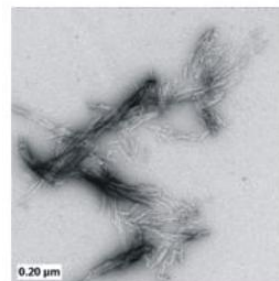
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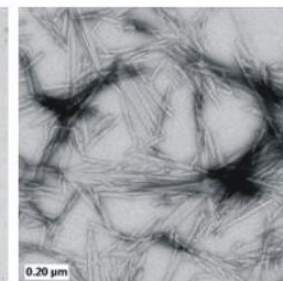
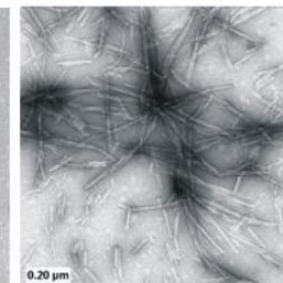
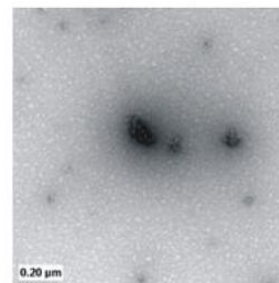
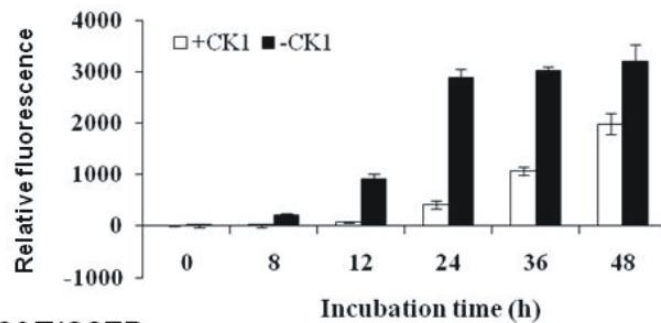
**A S129A**

CK1

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**B S129E****C S129E/S87P**