Report Beamtime use Gilda, Nov. 2012

In the November 2012 shift assigned to us on the ESRF beamline Gilda, we collected a total of 7 spectra on the following human α-synuclein (AS) samples:

a) whole construct
b) α-synuclein truncated form (residues 1-99)
c) α synuclein N-terminal peptide 1-15
d) α synuclein peptide 113-130

XAS data at the Ag K-edge were collected on Ag(I) loaded samples a-d with Ag(I) final concentration of about 0.8 mM and Ag.protein(peptide) stoichimetric ratio ~0.8:1.

XAS data at the Cu K-edge were collected on samples a and c (two samples)

The data of taken at the Ag K-edge, although a bit noisy, are of sufficiently good quality, while the one collected at the Cu K-edge are affected by numerous glitches that prevent any confident analysis.

A preliminary analysis of the available Ag data allow us to observe that spectra from sample A (AS truncated) and B (whole construct) are very similar and suggest the involvement of both sulfur from Met residues and N from the only His present (His50) in Ag coordination (camelback features), all ligand residues coming from the 1-99 region of AS. See figure 1.

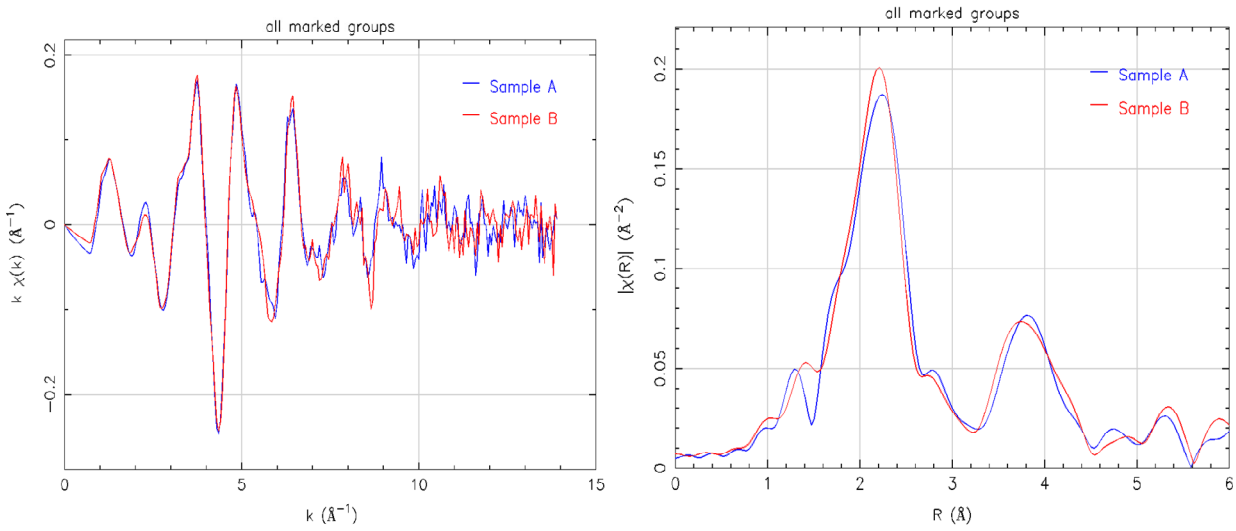

Figure 1. Superimposition of the EXAFS data (a) and of their FT (b) of samples A and B.

On the contrary spectra from samples C and D differ from each other and also differ from the spectra of samples A and B and show only S/N/O ligation (figure 2).

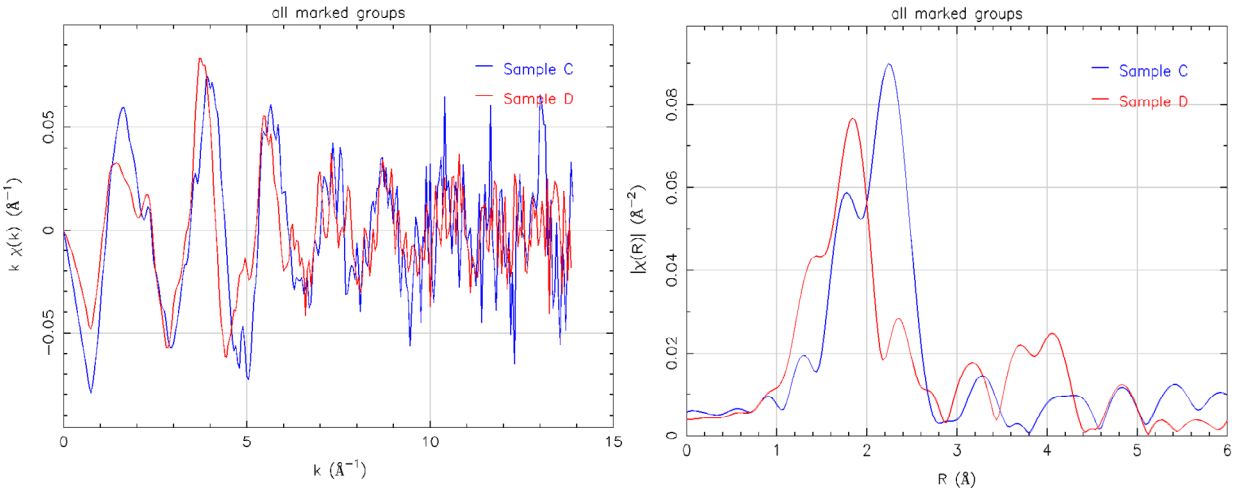

Figure 2. Superimposition of the EXAFS data (a) and of their FT (b) of samples C and D.