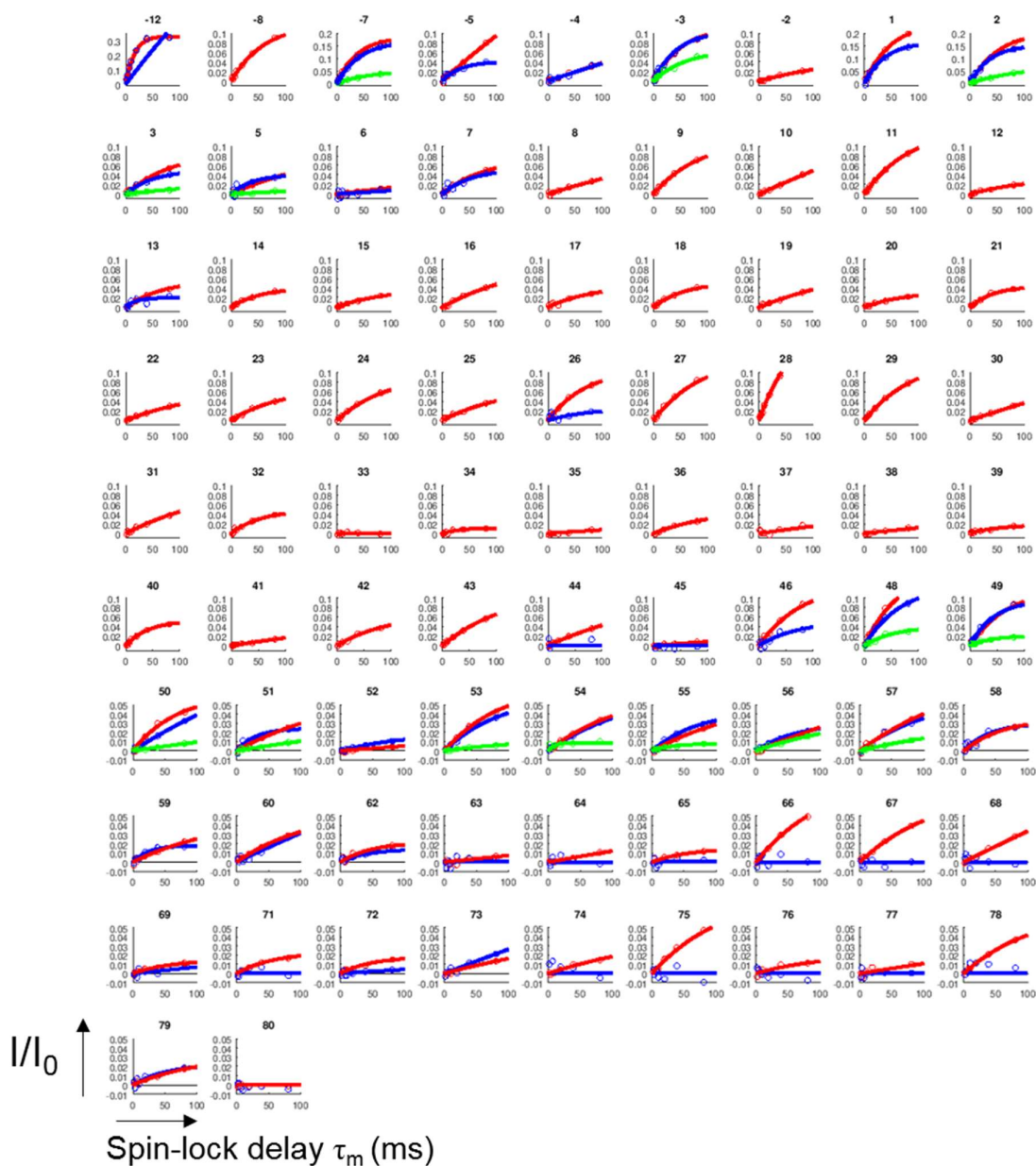Figure S1. The signal intensity as a function of the spin-lock delay in the CLEANEX-PM experiments for CP12red at pH 7 (red), CP12ox at pH 7 (blue), CP12ox at pH 6 (green) for all CP12 residues. The fits are performed as indicated in the Material and Methods section. The number on each plot from 1 to 80 corresponds to the start (S) and to the end (D) of the amino acid sequence of the mature protein. For CP12ox, all rates at pH 6 are significantly lower than those at pH 7, indicating that the exchange falls in the EX2 regime. This allows the determination of ΔG of folding.
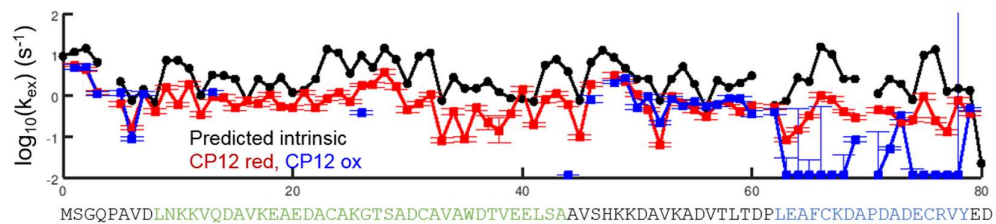
Figure S2. Solvent-amine intrinsic proton exchange rates calculated using Sphere (black) and solvent-amide proton exchange rates measured using CLEANEX-PM experiment on CP12red (red) and on CP12ox (blue).
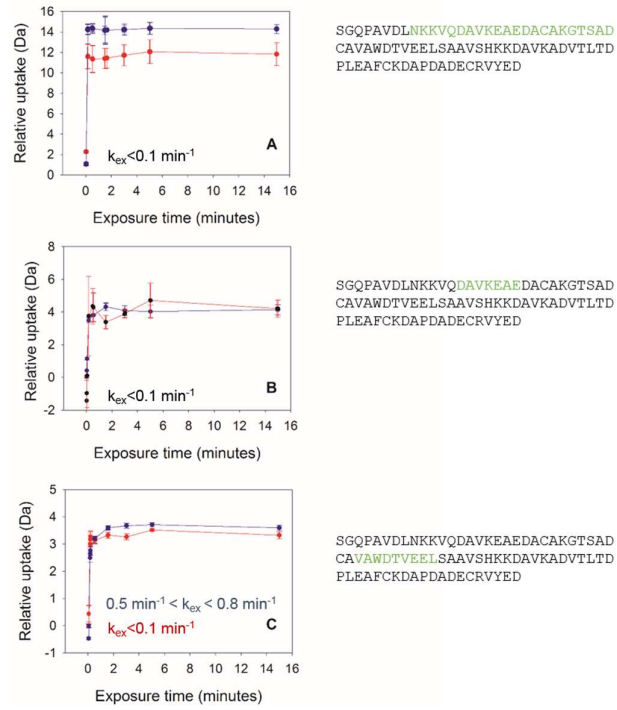
Figure S3. Relative uptake in mass of three peptides corresponding to the N-terminal region upon mixing with Deuterium of CP12$_{red}$ (red) and CP12$_{ox}$ (blue). The very rapid increase in mass confirms the dynamic nature of this region. The peptides are highlighted in green next to the corresponding graph.
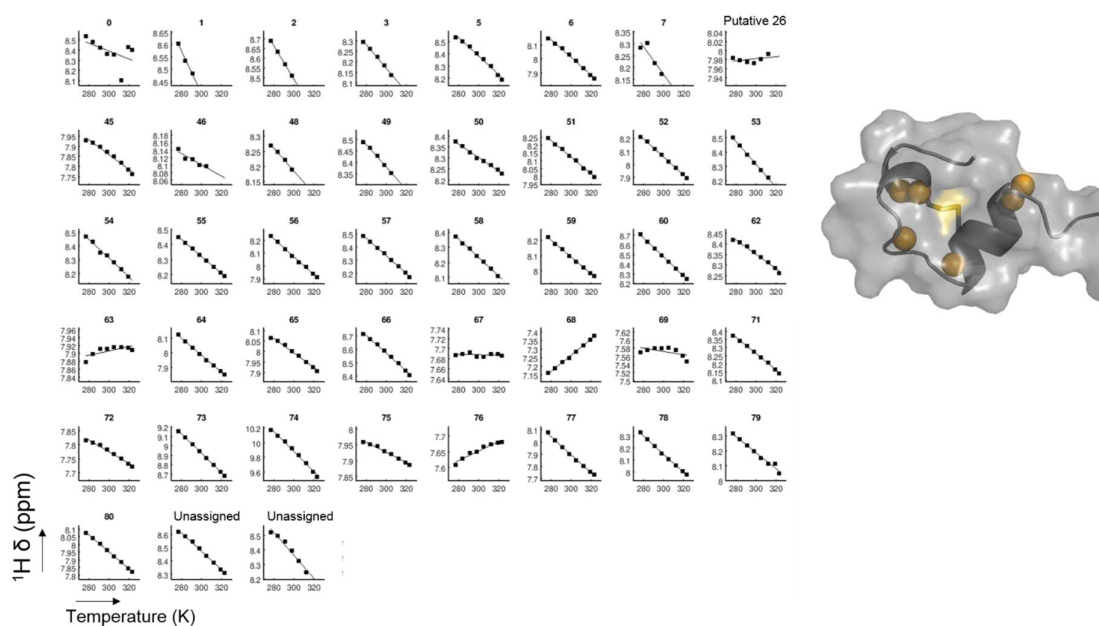
Figure S4. Temperature dependence of the proton chemical shift for the amine proton of all CP12$_{ox}$ residues. The fits are performed as indicated in the Material and Methods section. The structure on the right is that of the CP12$_{ox}$ C-terminal helical turn, with the amide protons that have a non-linear temperature dependence of their chemical shift highlighted in orange. This indicates that the N-terminal interconversion influences the C-terminal residues chemical shifts. The number on each plot corresponds to the amino acid position on the sequence of the protein.
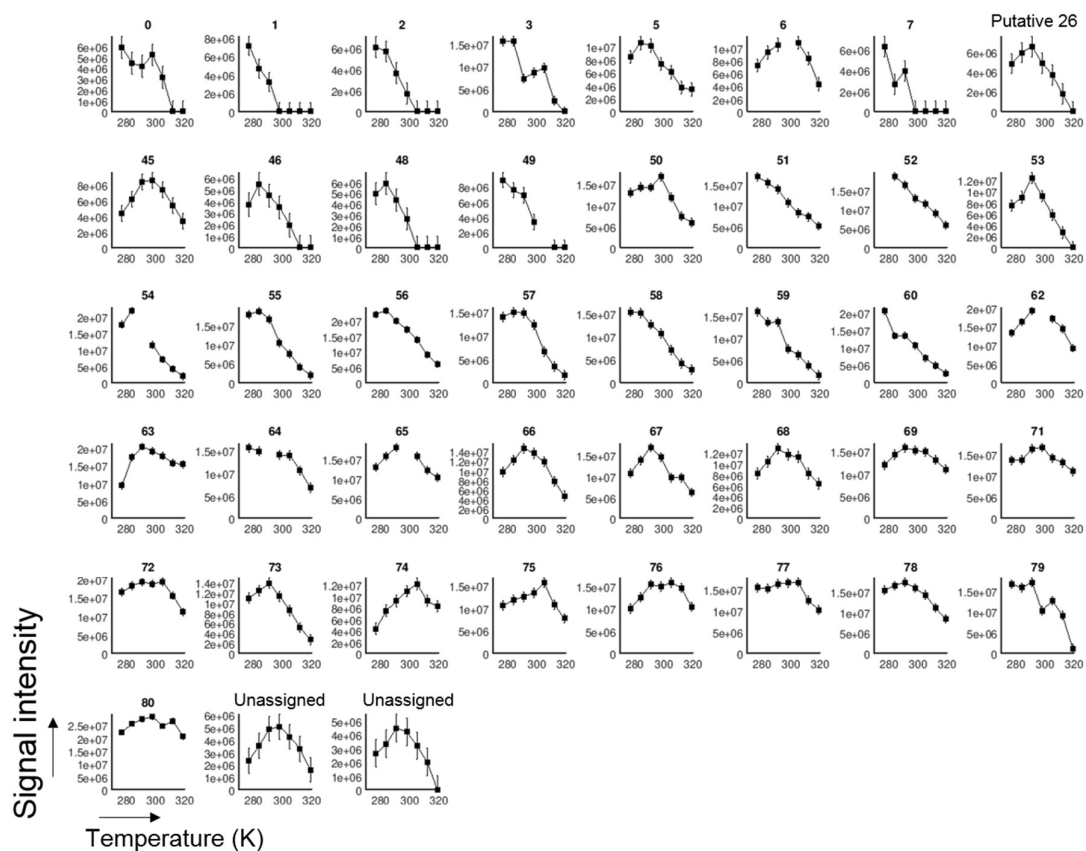
Figure S5. The temperature dependence of the ^{1}H-^{15}N signal intensity for the resonances of all CP12${}_{ox}$ residues. The number on each plot corresponds to the amino acid position on the sequence of the protein.
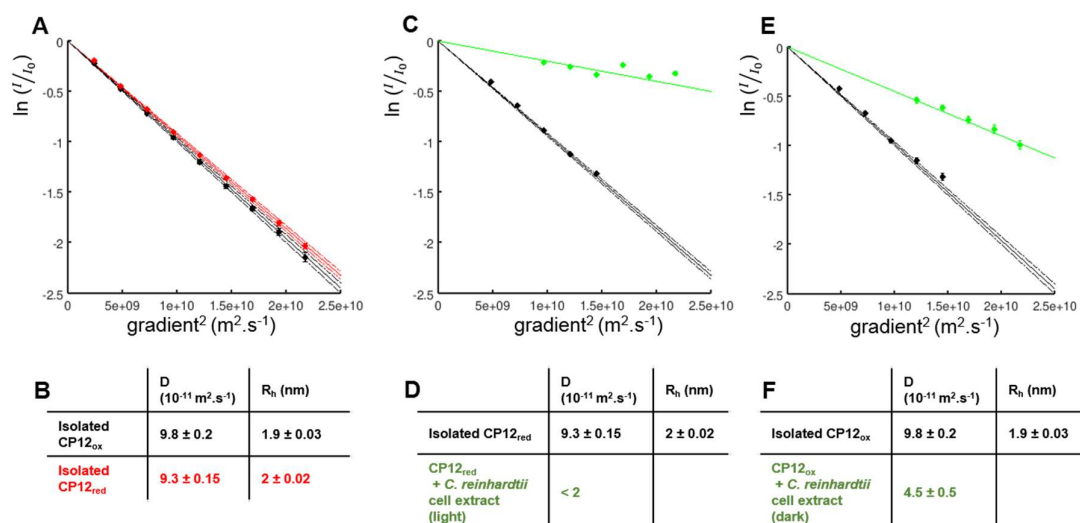
B	D (10^-11 m²·s⁻¹)	R_h (nm)
Isolated CP12ox	9.8 ± 0.2	1.9 ± 0.03
Isolated CP12red	9.3 ± 0.15	2 ± 0.02

D	D (10^-11 m²·s⁻¹)	R_h (nm)
Isolated CP12red	9.3 ± 0.15	2 ± 0.02
CP12red + C. reinhardtii cell extract (light)	< 2	

F	D (10^-11 m²·s⁻¹)	R_h (nm)
Isolated CP12ox	9.8 ± 0.2	1.9 ± 0.03
CP12ox + C. reinhardtii cell extract (dark)	4.5 ± 0.5	

Figure S6. Hydrodynamics of CP12ox and CP12red measured by DOSY-NMR. A: STE on isolated CP12ox (black) and CP12red (red). **C:** XSTE on CP12red isolated (black) and in the presence of cell extract (green). **E:** XSTE on CP12ox isolated (black) and in the presence of cell extract (green).On the graphs A, C and E: the x-axis is the square of the gradient strength and on the y axis is the normalized intensity on a ln scale (refer to Material and Methods section). A linear dependency indicates a homogenous monomeric state of the protein. The tables of B, D and F show the measured diffusion coefficient from the data shown in A, C and E respectively, as well as the hydrodynamic radius for isolated CP12.
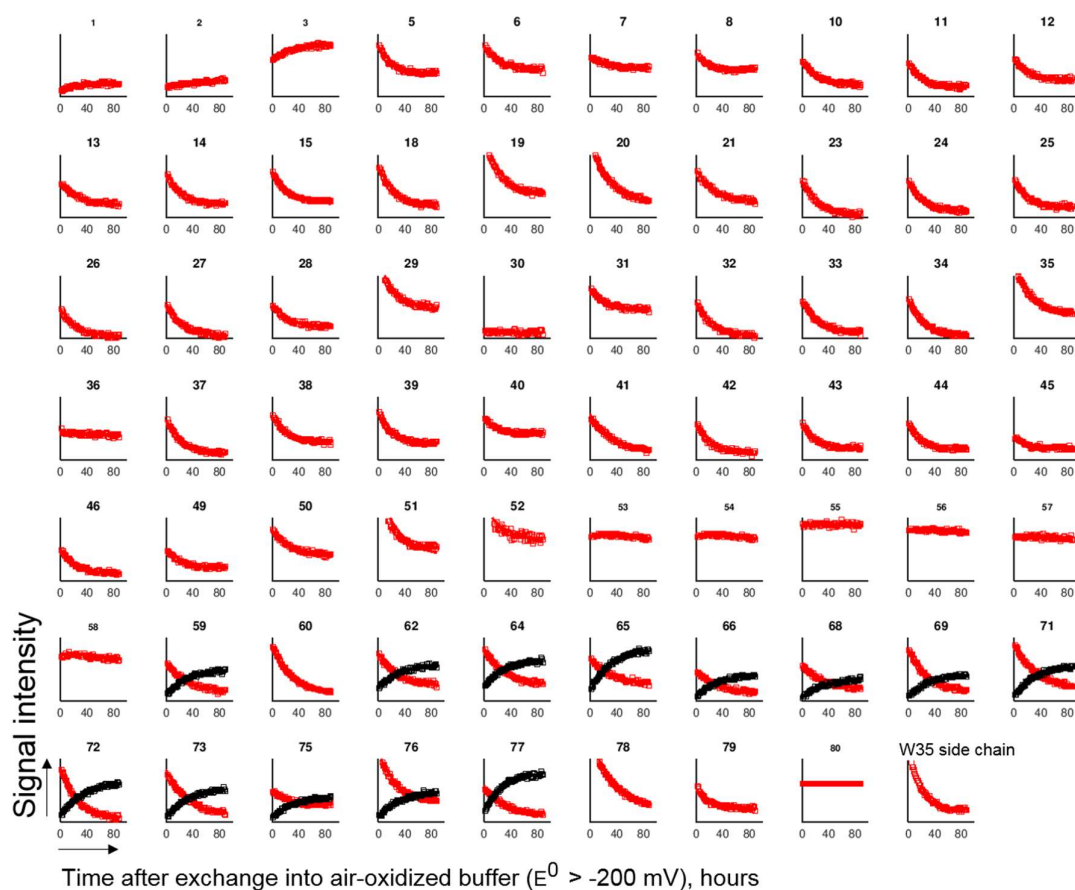

Figure S7. Real time monitoring of the oxidation for all CP12 residues. Red: Intensities of resonances of CP12red. Black: Intensities of resonances of CP12ox.
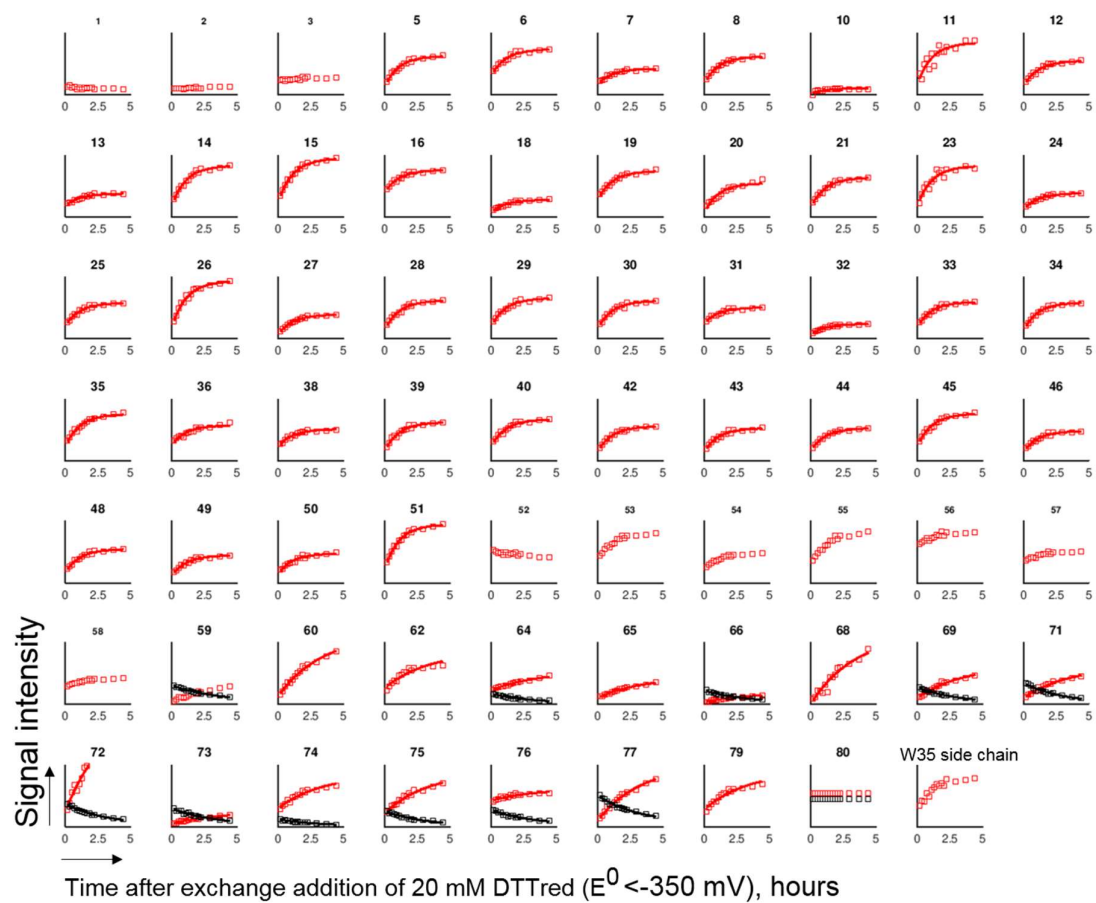
Figure S8. Real-time monitoring of the reduction for all CP12 residues. Red: Intensities of resonances of CP12$_{red}$. Black: Intensities of resonances of CP12$_{ox}$.