CORRECTION

Correction to: A suite of ^{19}F based relaxation dispersion experiments to assess biomolecular motions

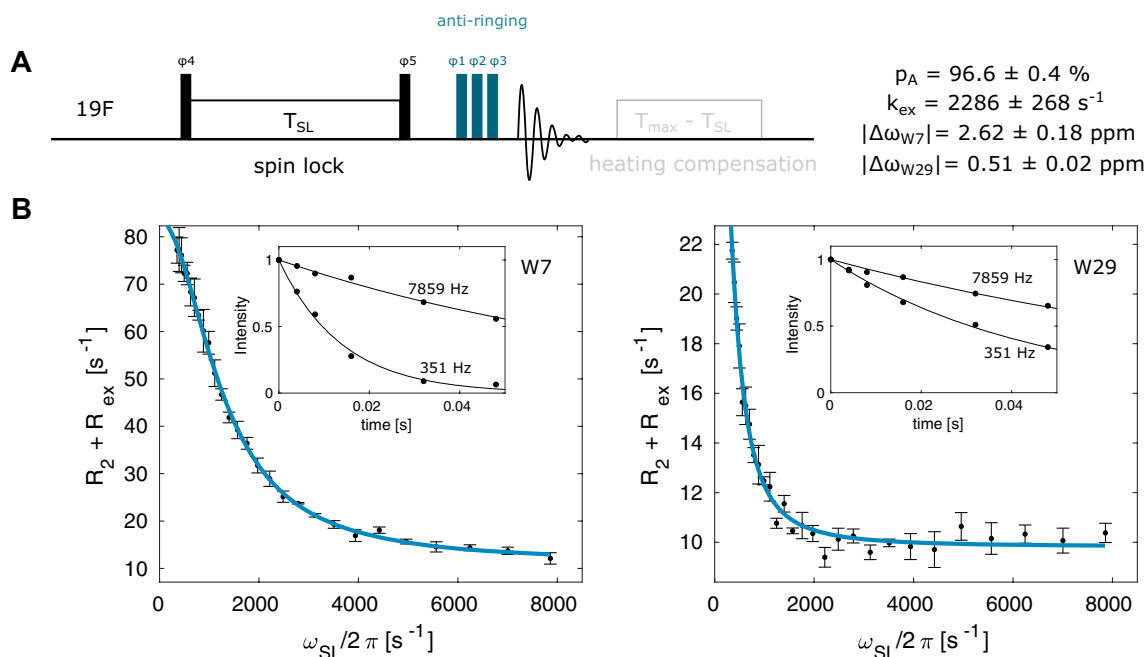Jan H. Overbeck[1] · Werner Kremer[1] · Remco Sprangers[1]

Correction to: Journal of Biomolecular NMR
https://doi.org/10.1007/s10858-020-00348-4

In the original publication, Figures 3 and 6 were displayed incorrectly due to a mistake made by the publisher. The correct version of Figs. 3 and 6 are given below.

The original article has been corrected.

Fig. 3 ^{19}F on-resonance $R_{1\rho}$ experiment. **a** Pulse sequence for the ^{19}F on-resonance $R_{1\rho}$ experiment. Narrow (wide) rectangles indicate 90° (180°) pulses, which are applied along the x-axis unless indicated otherwise. The phase cycle is φ1 = x, φ2 = [− x, x], φ3 = [x, x, − x, − x, y, y, − y, − y], φ4 = [y], φ5 = [− y], φ$_{rec}$ = [x, − x, − x, x, y, − y, − y, y]. **b** On-resonance $R_{1\rho}$ relaxation dispersion profiles for W7 and W29. The size of the error-bars correspond to 1 standard deviation

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✉ Remco Sprangers
remco.sprangers@ur.de

1 Department of Biophysics I, Regensburg Center for Biochemistry, University of Regensburg, 93053 Regensburg, Germany
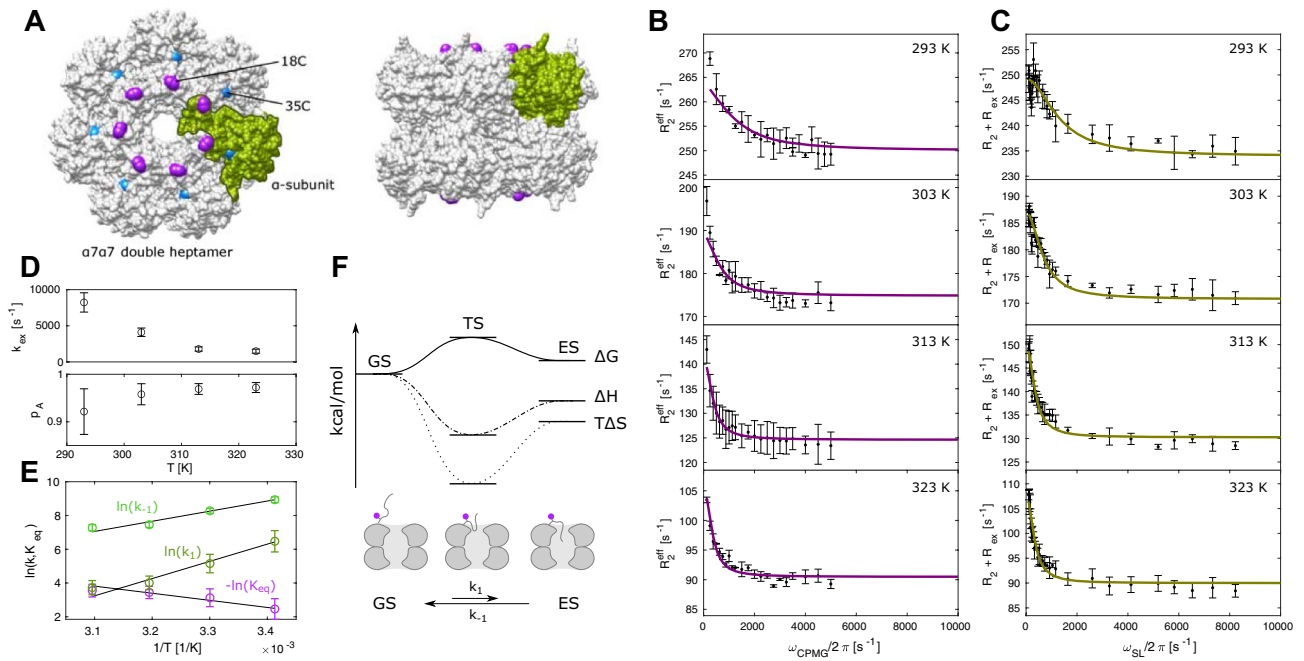
Fig. 6 ^{19}F Relaxation dispersion experiments of the 360 kDa $\alpha_7\alpha_7$ double heptamer. **a** Model of the double heptameric $\alpha_7\alpha_7$ complexes with 14 BTFA labeling sites at position 18C (purple) of each subunit. Position 35 that does not show exchange (Fig. S8) is indicated in cyan. The model of the complex is based on the structure of the 20S proteasome from *T. acidophilum* (PDB ID 1PMA). **b** CPMG experiments from 293 to 323 K. **c** On-resonance $R_{1\rho}$ experiments from 293 to 323 K. **d** Plot of exchange rates against temperatures as derived from the global fit of all RD data. **e** Logarithmic plot of kinetic rates against inverse temperature. **f** Schematic presentation of ΔG, ΔH and $T\Delta S$ changes from the ground state GS to the excited state ES via a transition state TS