

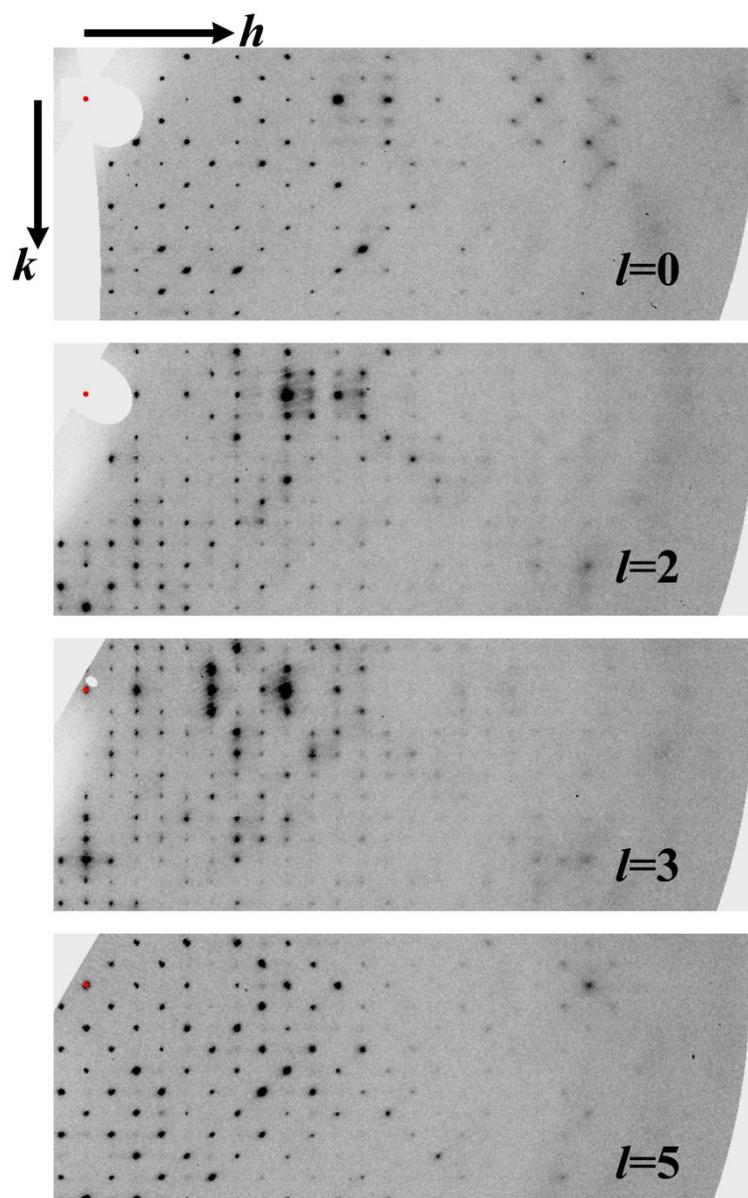
# Acta Crystallographica Section D

Volume 70 (2014)

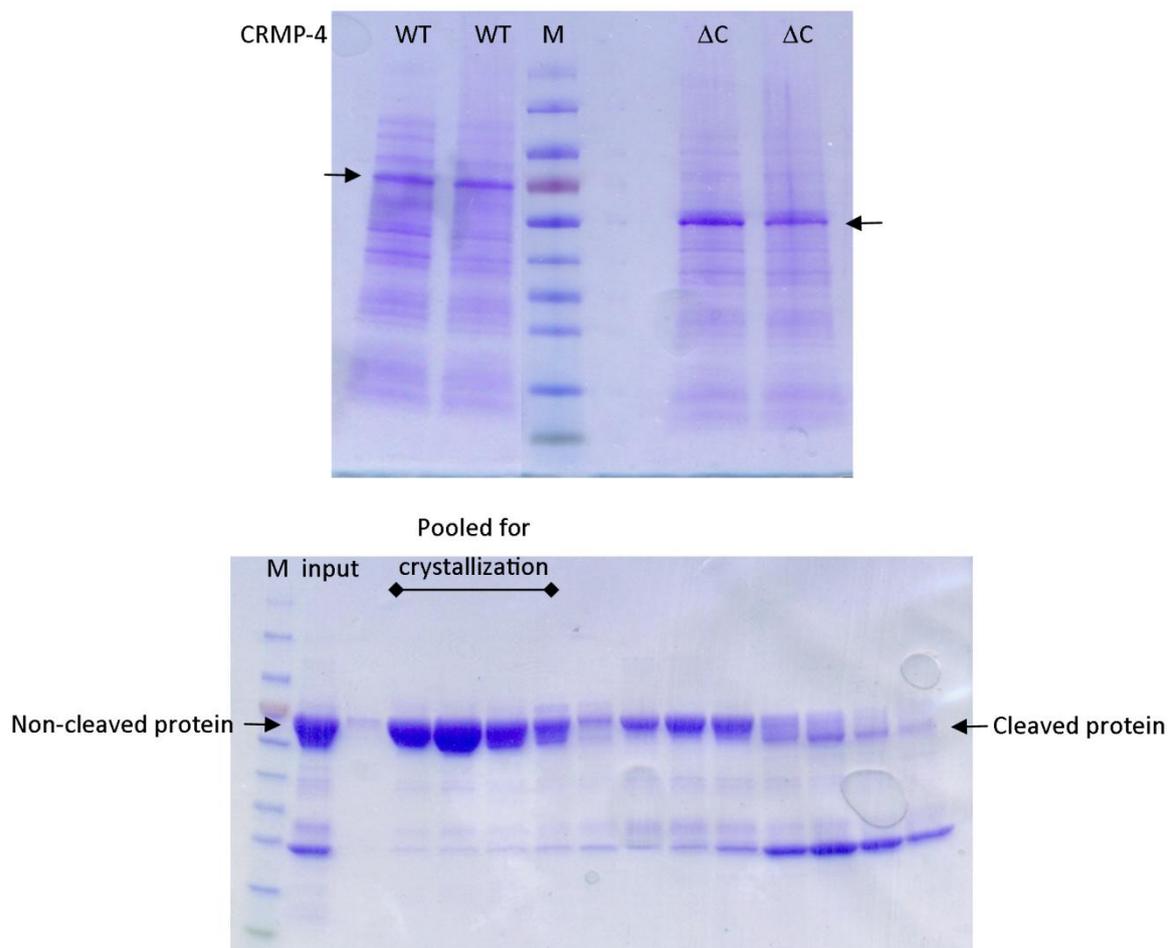
Supporting information for article:

**Crystal structure of human CRMP-4: correction of intensities for  
lattice-translocation disorder**

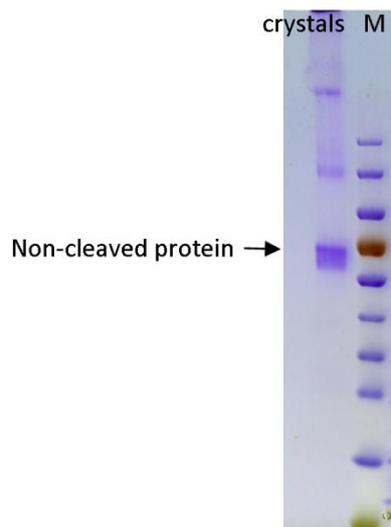
**Rajesh Ponnusamy, Andrey A. Lebedev, Steffen Pahlow and Bernhard  
Lohkamp**



**Figure S1** Pseudo-precession diffraction patterns from WT CRMP-4 crystals (form B) indicate 2-dimensional disorder. Shown are  $hkl$  planes for  $l=0, 2, 3,$  and  $5$ . Layers for  $l=5n$  show sharp reflections. From the perpendicular directions the halos are seen as streaks, as in **Error! Reference source not found.**(a). The other reflections are diffuse in 2 dimensions with halos around the reflections. *LABELIT* (Sauter *et al.*, 2004) was used to calculate the diffraction image from experimental data and to produce the figure.

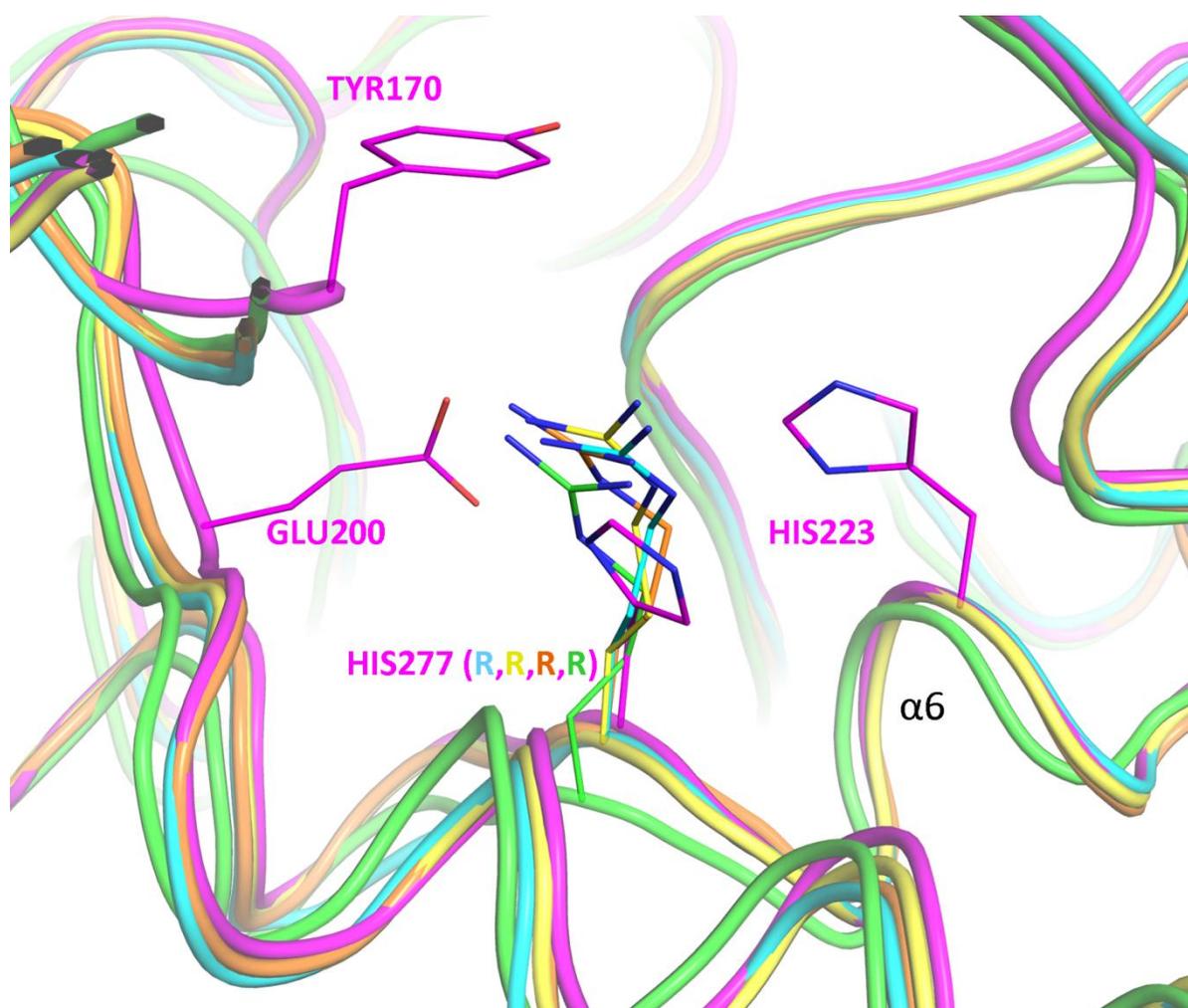


**Figure S2** SDS-PAGE of CRMP-4 WT and  $\Delta C$ . The top gel shows the expression levels of the two versions in the bacterial cell lysate. The bottom gel shows the protein content of fractions from size-exclusion chromatography to purify CRMP-4 WT for crystallisation.



**Figure S3** SDS-PAGE of CRMP-4 WT crystals. Approx. 15-20 crystals were washed extensively and dissolved in SDS running buffer before loading it onto the gel.





**Figure S5** Putative active site in CRMP-3. CRMP-1 (cyan), CRMP-2 (yellow), CRMP-4 (orange) and CRMP-5 (green) are superimposed onto the model of CRMP-3 (magenta). Residues potentially involved in zinc ion binding and histone deacetylase activity are labelled and shown in stick.