



S2 Fig. A. 2D diagram of the 3-domain architecture of RMCAH, generated using Pro-origami (Stivala et al., 2011). Each domain consists a 4-stranded β -sheet. Domain 1 and 2 have three α -helices, whereas in domain 3, the helix 2 in domain 1 is changed to a small 2-pleated β -sheet. **B.** Per residue C α distances between the open and closed conformation for domain 3. The segment with biggest r.m.s.d. connects the active site and the Ca²⁺ binding site.

Stivala, A., Wybrow, M., Wirth, A., Whisstock, J. C., and Stuckey, P. J. (2011) Automatic generation of protein structure cartoons with Pro-origami. *Bioinformatics (Oxford, England)* **27**, 3315-3316