



**Figure S1. Implications of the conformation of  $\beta 2$  for the folding of full-length A3G.** (A) View of the extended  $\beta$ -sheet that connects the N- and C-CDA in a homology model of full-length A3G as a dimer [12]. Monomer subunits are shown in magenta and green. The inner N-CDA domains mediate dimerisation of A3G and the catalytically active C-CDA domains are on the outer part of the model. In the left-hand monomer subunit of the full-length A3G homology model (shown in magenta), the structure of the XRAY1 C-CDA is superimposed (shown in blue) (B) Close up of the proposed  $\beta 2$ - $\beta 2$  interaction in the model of full-length A3G showing the  $\beta 1$ - $\beta 2$  sheets from the N- and C-CDA in magenta. (C) The distorted  $\beta 2$  strand observed in NMR-2K3A is shown in blue and impedes interaction with  $\beta 2$  of N-CDA model. (D) The ordered conformation of  $\beta 2$  observed in XRAY1 is shown in blue and would be consistent with connecting the N- and C-CDA domains through  $\beta 2$ - $\beta 2$  interactions.