
BIOLOGICAL
CRYSTALLOGRAPHY

**Volume 71 (2015)**

**Supporting information for article:**

# Structural evidence for asymmetric ligand binding to transthyretin

**Michele Cianci, Claudia Folli, Francesco Zonta, Paola Florio, Rodolfo Berni and Giuseppe Zanotti**

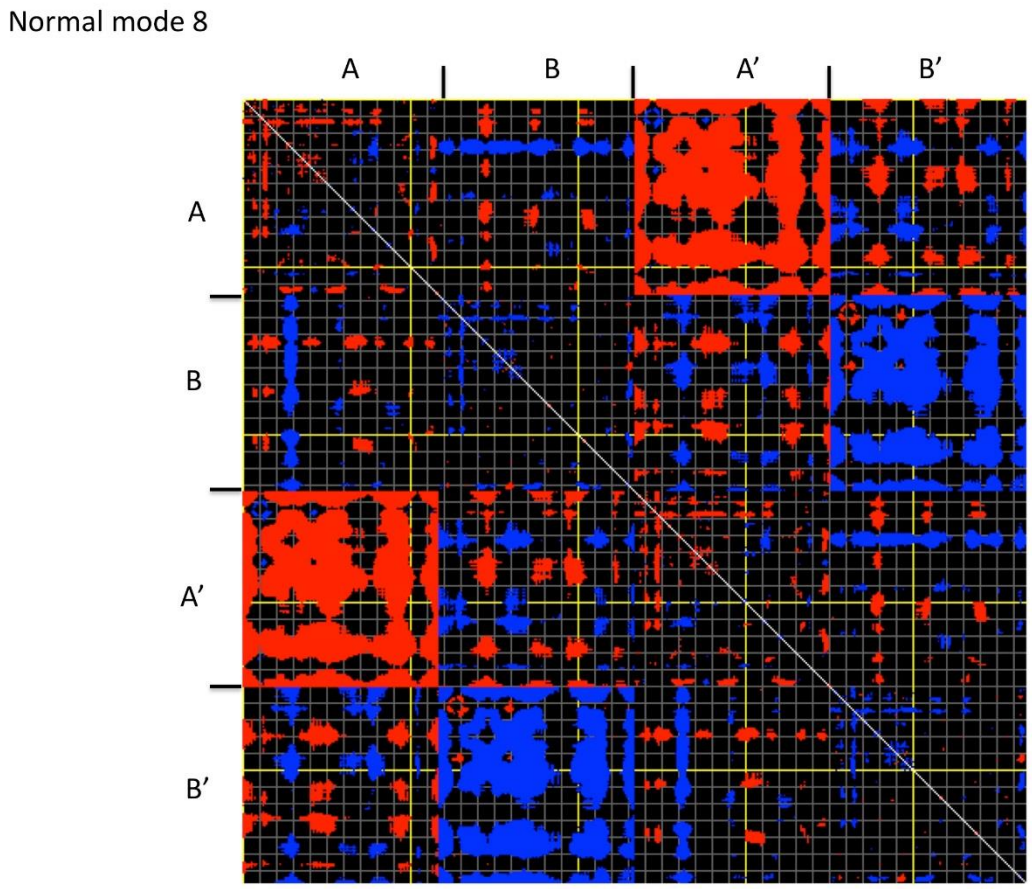


**Figure S1** Normal mode 2. Red color indicates that distance between two residues increases, blue that decreases. In this mode monomers A and A' are going away, whilst monomers B and B' become closer.

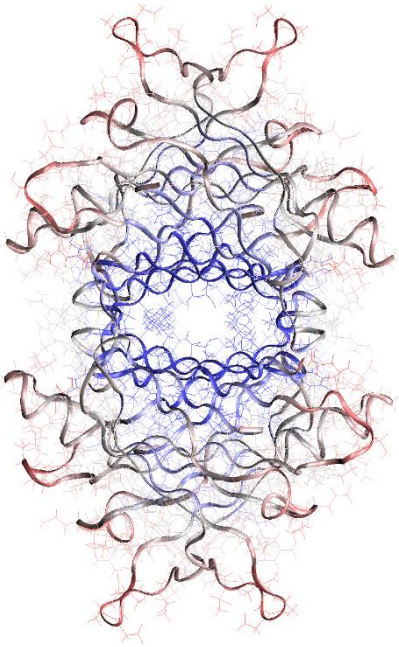

**Figure S2** Root mean square fluctuations of alpha carbons during the dynamics. The color code goes from blue (low fluctuations) through gray to red (high fluctuations). The inner cavity is the stiffer part of the protein complex.

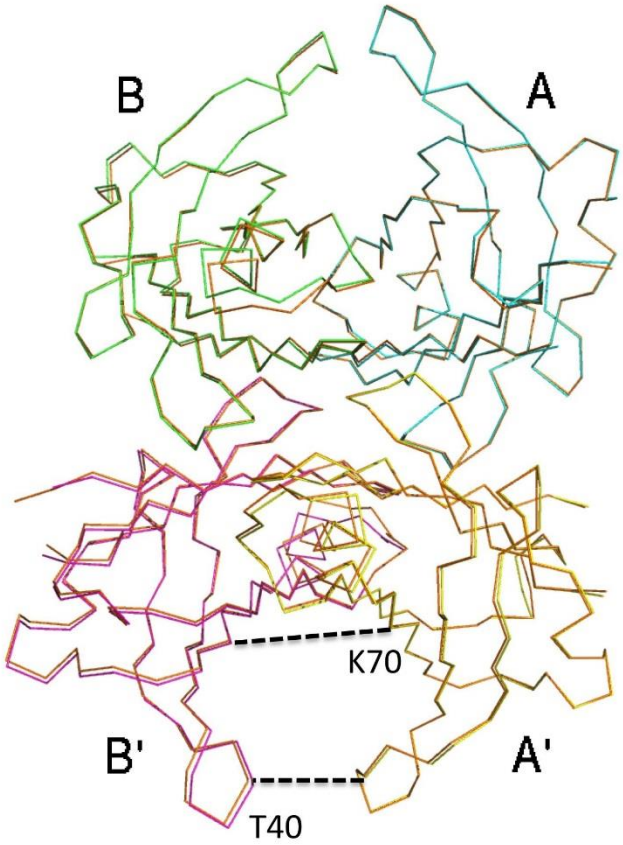


**Figure S3** Superposition of the Cα chain trace of the TTR-apigenin complex (the four chains of the tetramer are in different colors) to that of the unliganded TTR structure (PDB 2QGB), shown in orange. It is possible to appreciate the small shift of the other subunits after superposition of monomers A. Distances reported in Table 2 were measured between Cα atoms of Thr40 and Lys70 of monomers A and B.