Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.


# Supporting Information: Proline isomerization effects in the amyloidogenic protein $\beta_2$-microglobulin

M.C. Maschio *et al.**

E-mail: stefano.corni@unipd.it

## Supplementary Figures

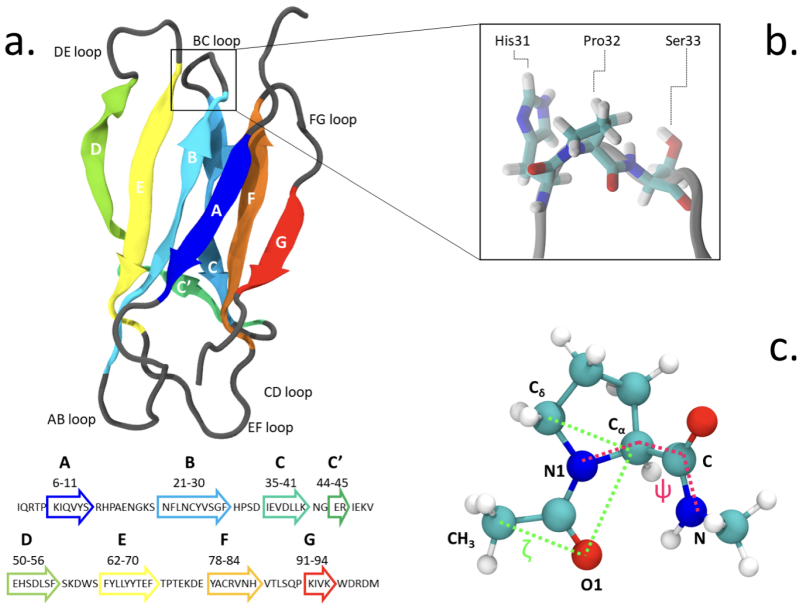


Figure S1: **Simulated system**— This is also Fig. 1 in the main text and is reported here for convenience. In Fig. S1, the $\zeta$ coordinate is defined as in Panel **c)**. In Figs S2 and S3, the color scheme of the residues which aids reading the hydrogen bond network is retained from panel **a)**

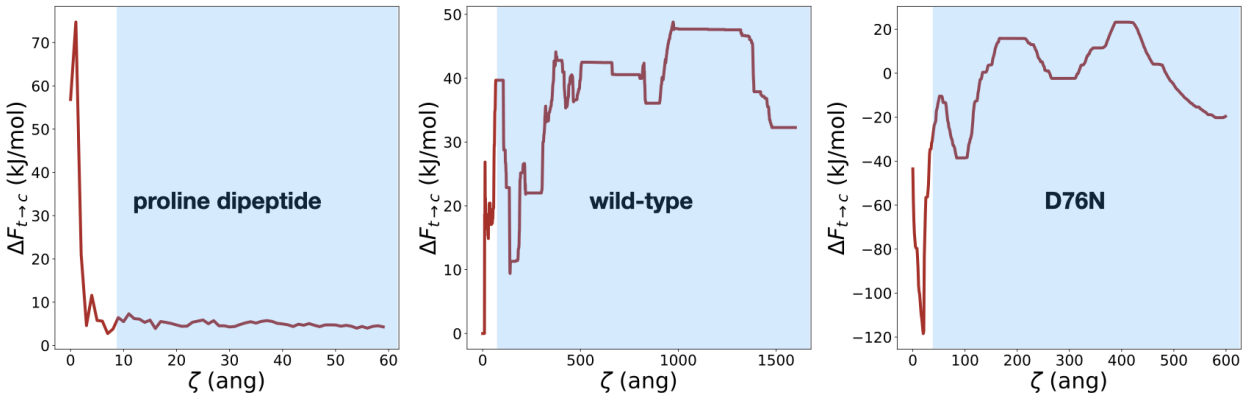


Figure S2: **Relative stability between the *trans-* and cis-Pro32**— Relative stability (in kJ/mol) of the isomers during the metadynamics simulations. The white window accounts for the equilibration time, so it is discarded for the integration. The free energy profiles in Fig. 2 of the main text are obtained by integrating the free energy for each $\zeta$ point of the curve. The time window for the integration is reported in light blue. The integration procedure is described in Ref. 52 of the main text.

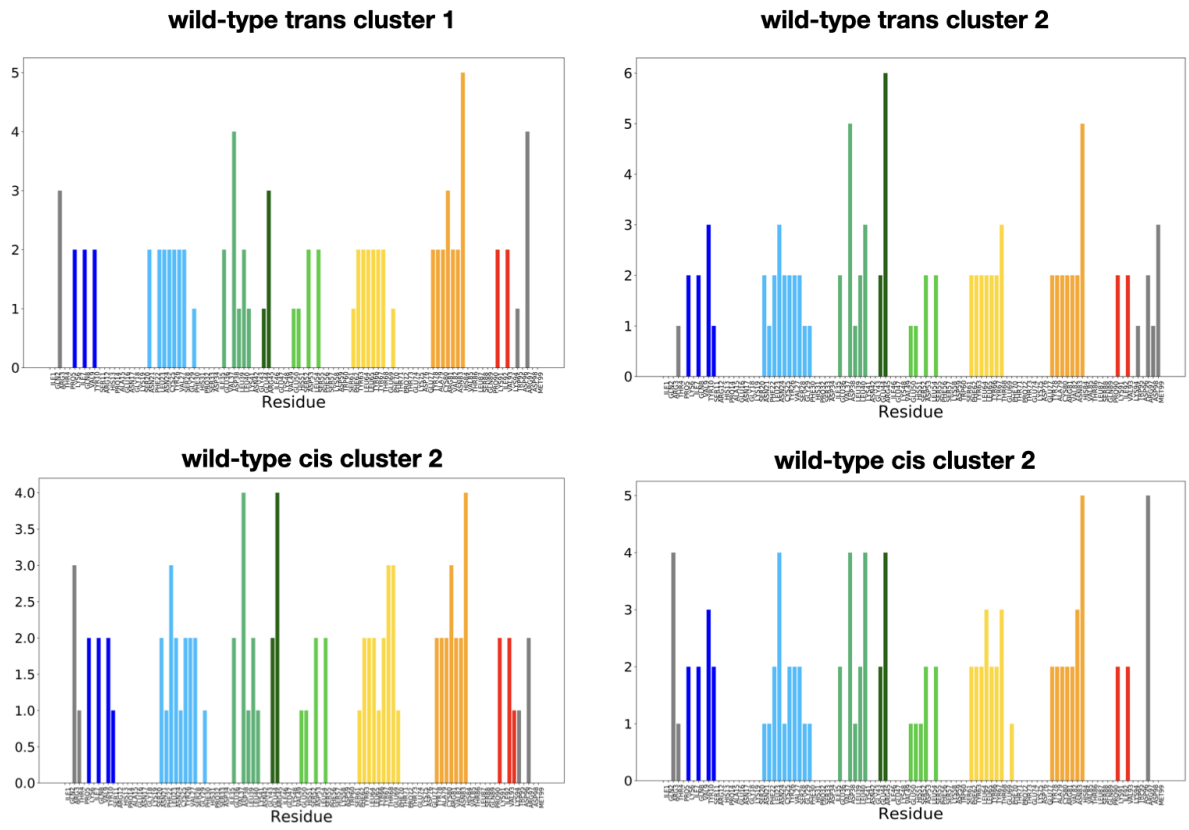


Figure S3: **Normalized hydrogen bond occurrence for each residue and each conformation during the metadynamics for the wild-type**— The configurations of the proteins are clustered from the snapshots of the metadynamics by selecting the $\psi$ and $\zeta$ coordinates. The selection window surrounds the minima of the maps reported in Fig. 2. The structures sampled correspond to the most probable structures of the protein when Pro32 is in *trans* or *cis*. The color scheme refers to Fig. S1

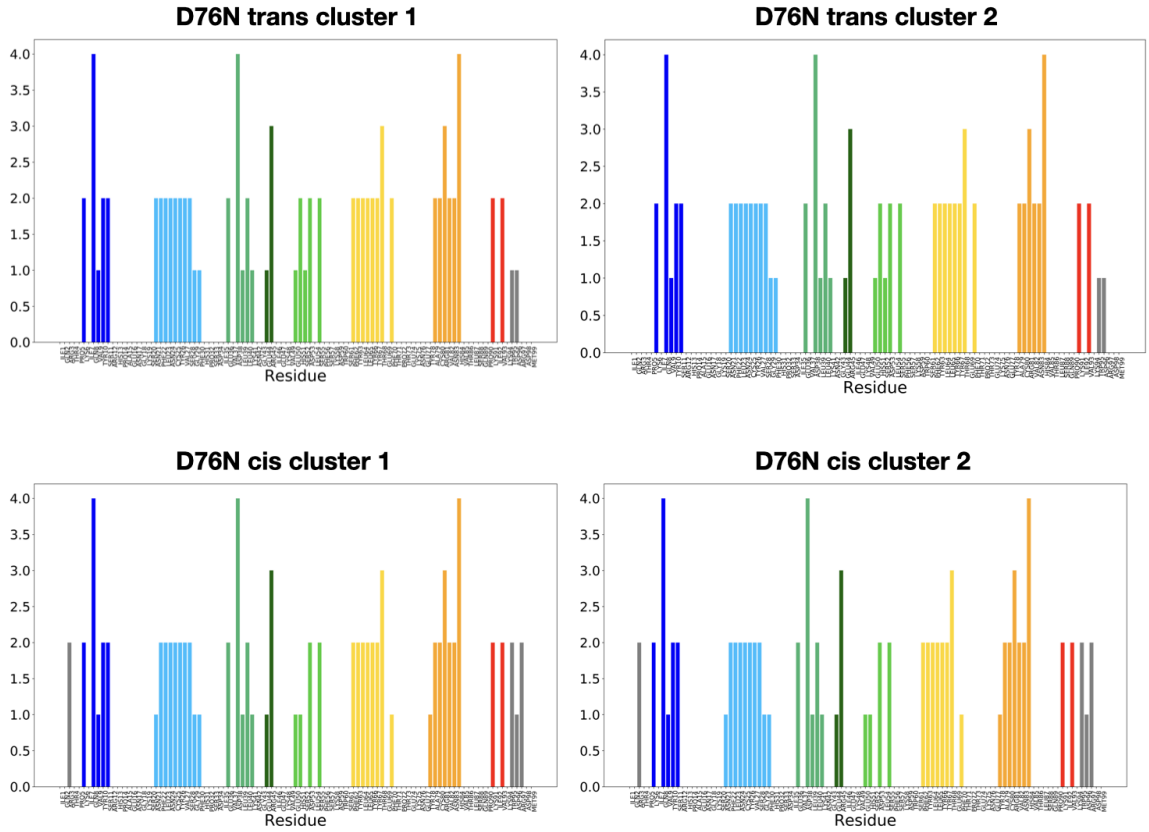


Figure S4: **Normalized hydrogen bond occurrence for each residue and each conformation during the metadynamics for D76N**— The color scheme refers to Figure S1

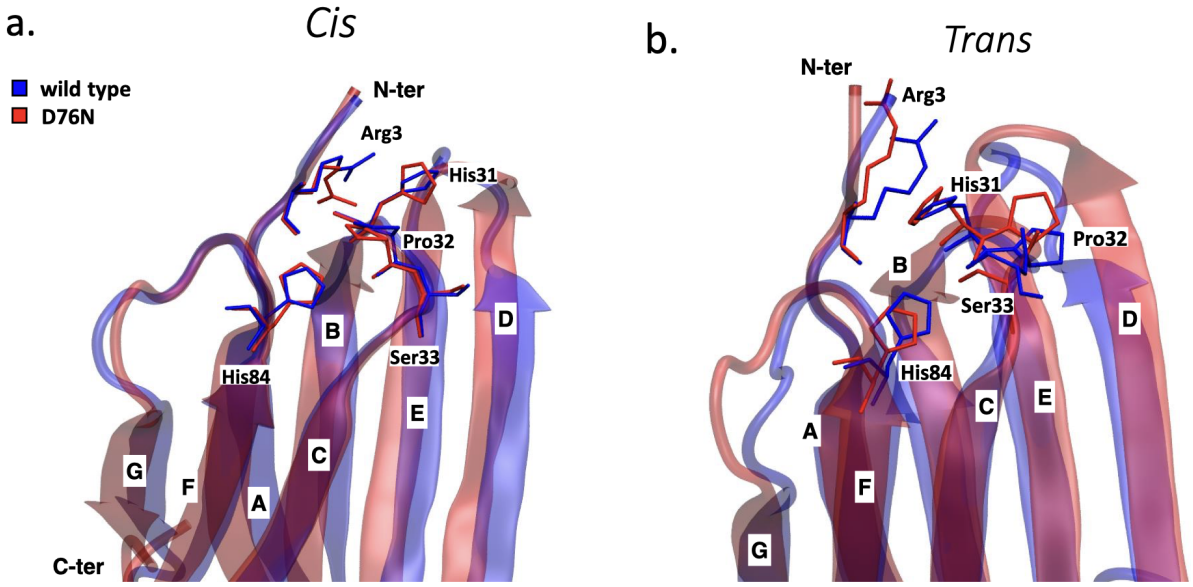


Figure S5: **Structure alignment of the residues surrounding cis and trans Pro32**—. Starting from the most populated clusters of the free energy minima, we show the arrangement of the relevant residues to the h-bond network presented in Table 2 and Figure 3 of the main text, focussing on the surroundings of the Pro32.