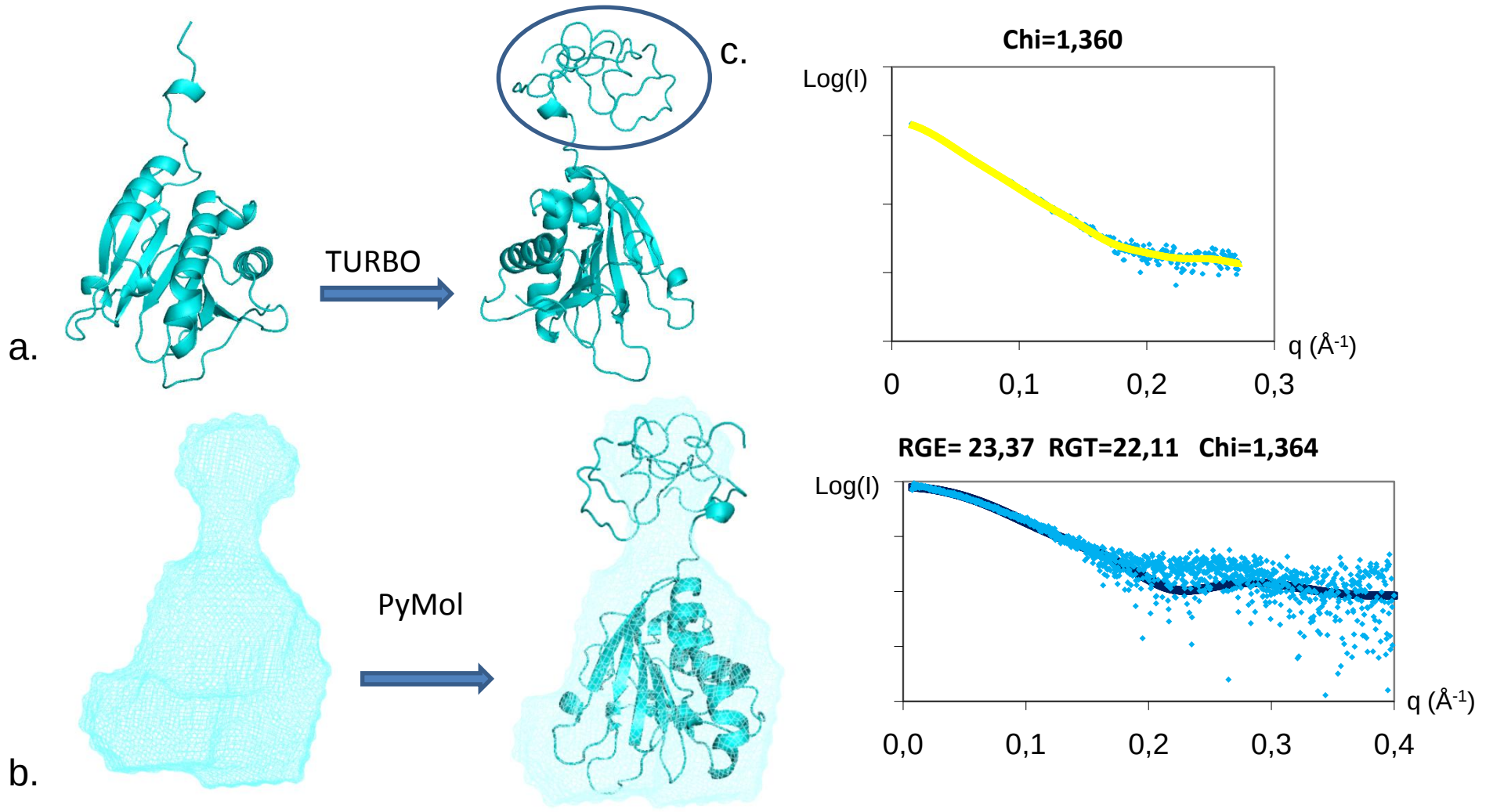

Supplementary Fig.2: Solution structure of eIF4E.

a. Cristallographic structure of eIF4E1 (PDB number: 1L8B) where the 30 aminoacids on the N-ter are missing due to the fact that this disordered region is a problem for crystallization. The 30 amino acids of the Nter extremities have been added using the program TURBO. To simulate the flexibility of this region , we created 4 different orientations (blue circle).

b. Low resolution model of eIF4E display in cyan blue obtained by SAXS, superimposed with the TURBO model created from eIF4E cristallographic structure.

c. Experimental SAXS profile of eIF4E (cyan blue) fitted by the scattering curves calculated with the program DAMMIF (yellow) and the program CRYSOL (dark blue). RGE: Radius of gyration estimated from the experimental curve. RGT: Radius of gyration estimated from theoretical curve. Chi: Discrepancy between theoretical and experimental curves.