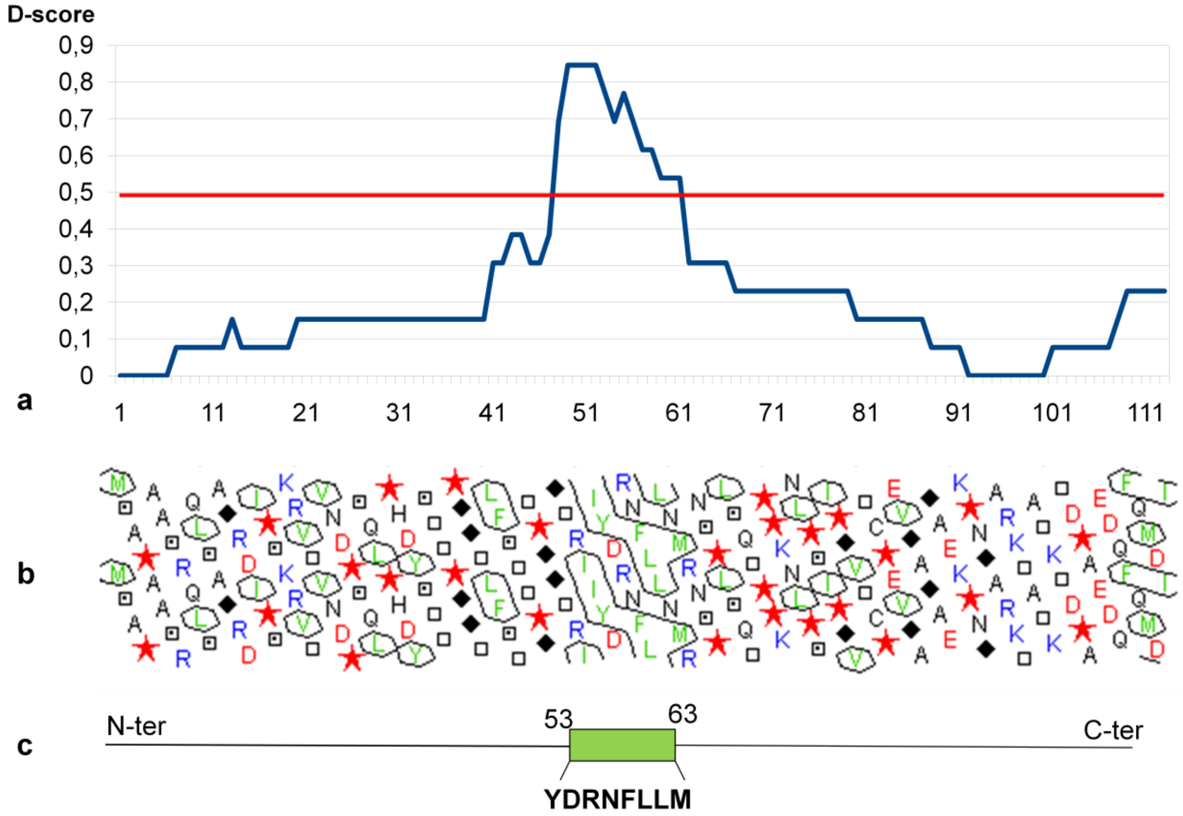

Supplementary Fig.3: Disorder predicted from the primary sequence of 4E-BP

a. Score for disorder (D-score) as a function of residue number. Consensus disordered regions are defined as regions with a D-score <0,50 (below the red line). The score has been calculated on the *Strongylocentrotus purpuratus* 4E-BP sequence as described in the supplementary methods.

b. Hydrophobic Cluster Analysis (http://www.vazymolo.org/MeDor/index.html) of Sp 4E-BP sequence. The amino acid sequences are represented (in duplicate) along diagonals from upper left to lower right with the one-letter amino acid code except that black diamonds indicate glycine, squares indicate threonine, squares with central dots indicate serine, and stars indicate proline residues. Sets of adjacent hydrophobic residues in green are encompassed by contour lines.

c. Location of the disordered regions (black line) and the structured domain (green box) containing the eIF4E-binding motif YDRNFLLM in Sp 4E-BP sequence. Numbers above the boxe indicate the boundaries of the consensus disordered regions.