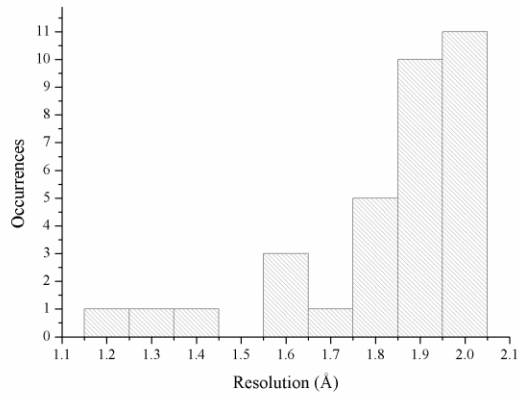


Supplementary Material

Interplay between peptide bond geometrical parameters in non-globular structural contexts

Luciana Esposito, Nicole Balasco, Alfonso De Simone, Rita Berisio, Luigi Vitagliano.

A



B

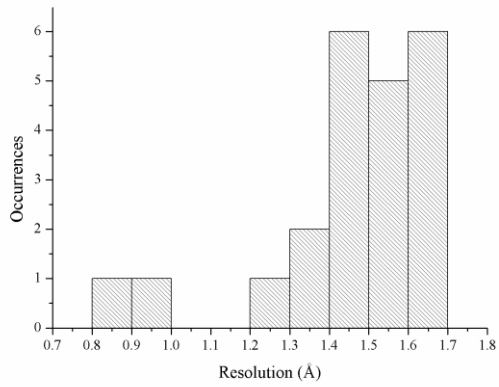


Figure S1: Distribution of the resolution of membrane protein (A) and amyloid-like peptide (B) crystal structures considered in the present study.

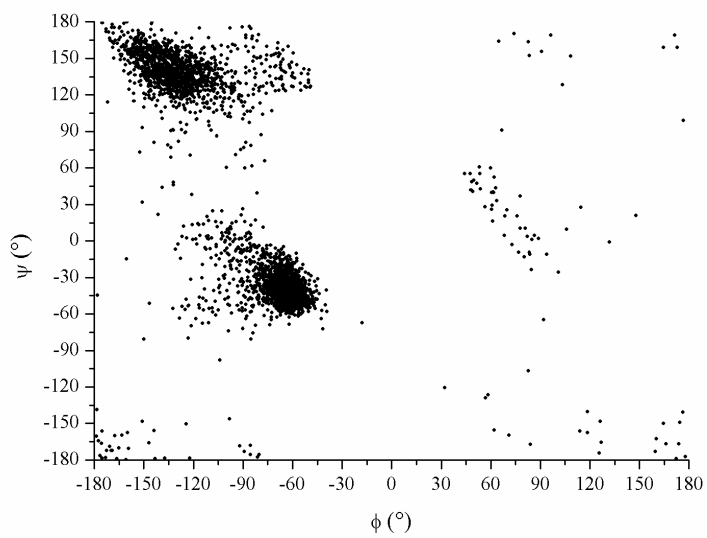
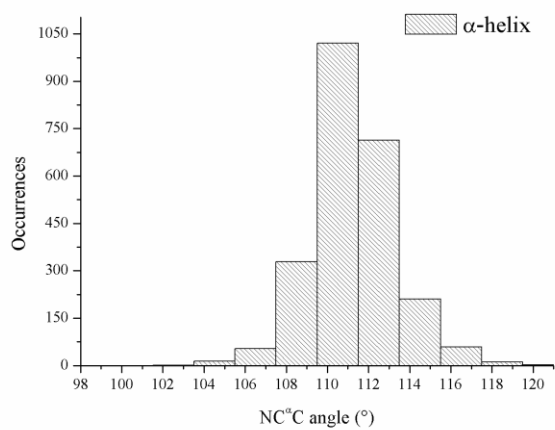
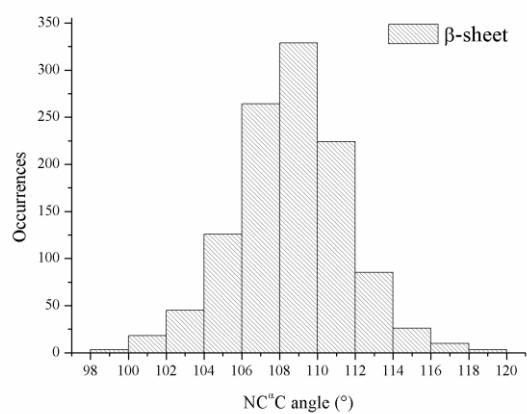


Figure S2: Overall Ramachandran plot for residues of membrane protein structures.

A



B



C

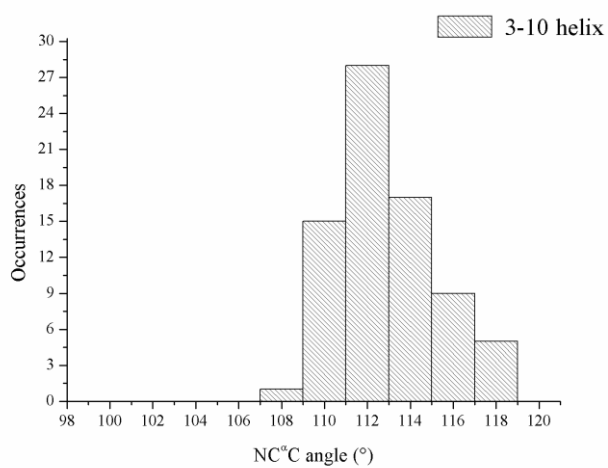
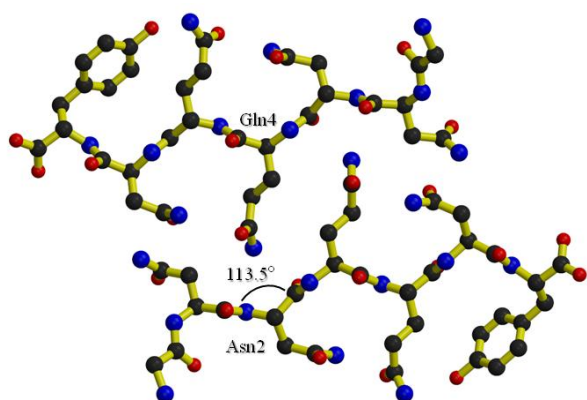
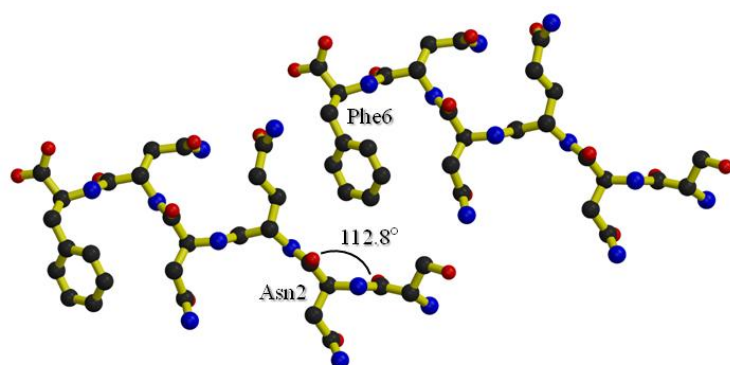


Figure S3. Distribution of N-C^α-C values for residues in α -helices (A), β -sheets (B) and 3-10 helices (C) of membrane proteins.

A



B



C

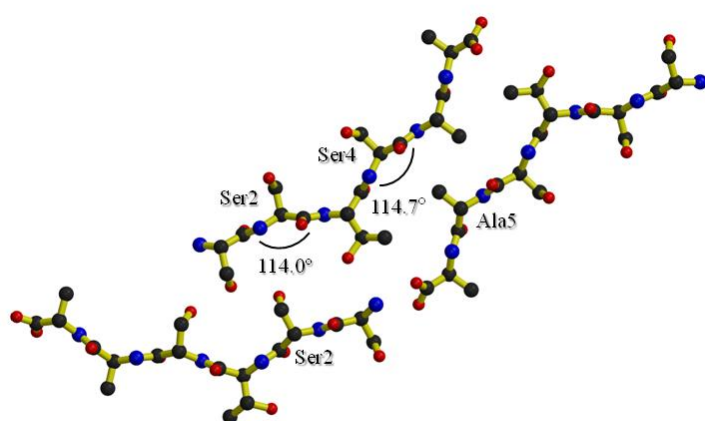


Figure S4. Examples of steric zipper assemblies: GNNQQNY (A), SNQQNF (B), SSTSSA (C). The deformation of some angles induced by interdigitation is shown.

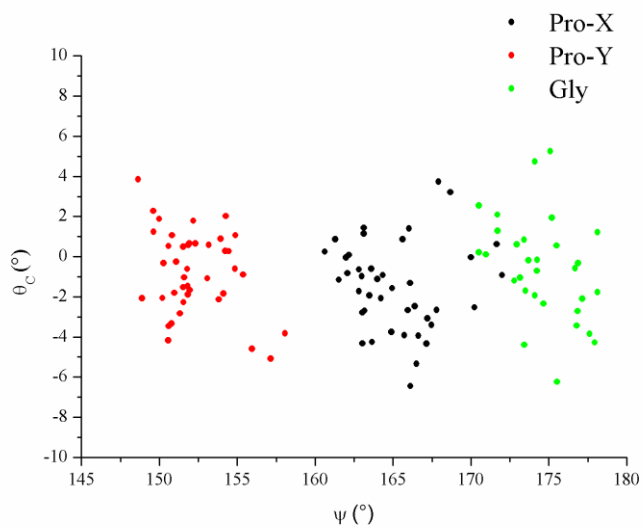


Figure S5: θ_C versus ψ for residues of the collagen-like peptide (Pro-Pro-Gly)₉.