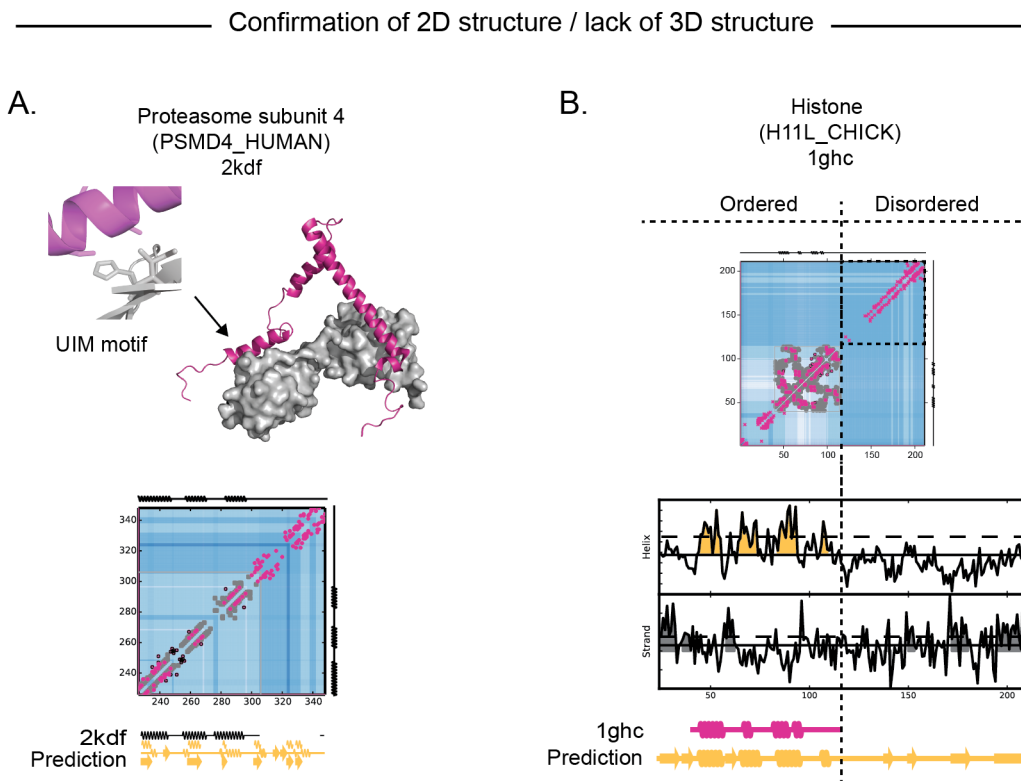


Figure 5. Accurate prediction of structure without long-range contacts.



**Figure 5. Accurate prediction of structure without long-range contacts.**

(A) The experimental 3D structure of PSMD4 in complex with di-ubiquitin (2kdf) has no long range contacts between the helices ensuring the separation of the two ubiquitin interacting motifs (UIMs) (top). Consistent with this, there are no ECs between residues distance in chain but nevertheless local ECs identify the helices formed when bound to ubiquitin as well as a weaker signal for possible  $\beta$ -strands. (B) ECs (pink circles) match the known contacts (grey circles) in the structure of the N terminal end of the histone H1.1 (1ghc) but do not predict long-in-chain contacts in the C terminal tail, consistent with observations that the histone tail is flexible in vivo. Secondary structure prediction of C terminal region suggest  $\beta$ -strands.