Figure 4. EVFold predictions of novel states of disordered proteins

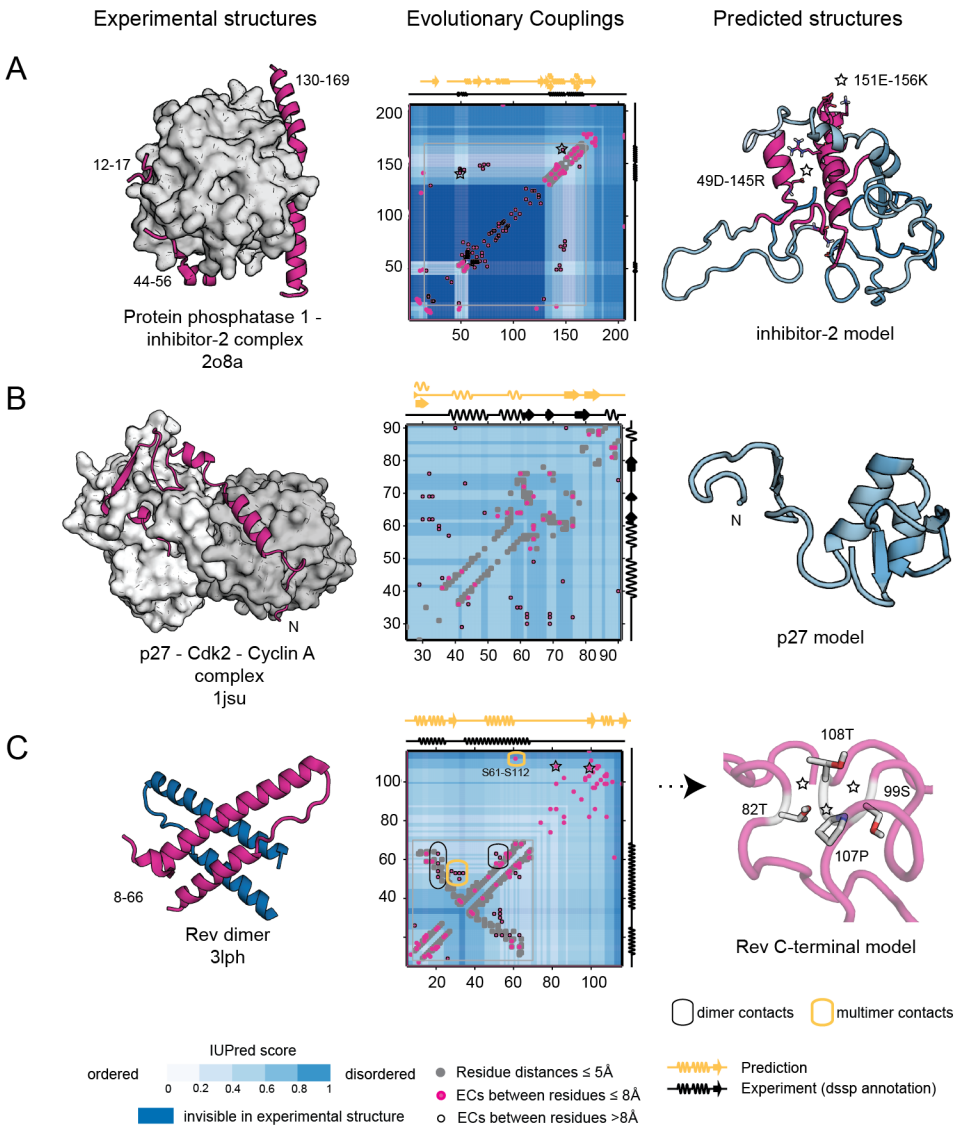

Figure 4. EVFold predictions of novel states of disordered proteins.
(A) Protein phosphatase 1 inhibitor 2 (IPP2_MOUSE), a disordered regulator, binds to its complex partner via three anchoring regions (residues12-17, 44-56, and 148-151), while the rest of the molecule remains invisible in the crystal structure (blue shading). ECs predict the existence of the helical anchors, as well as the long-range interactions between these regions. **(B)** Predicted contact map of p27 (CDN1B_HUMAN) reveals alternative states that are not compatible with the bound structure, and might form when free or bound to another partner. **(C)** Rev protein of HIV (REV_HV1H3) was captured experimentally in a dimeric state that is corroborated by the EC map, which has contacts for the helix-helix packing and the dimer contacts of the experimental structure (3lph). Additionally, possible multimer contacts may explain the higher order oligomerization of Rev. The C-terminal, invisible in experiments thus far, has signal for helical structure and has long-range evolutionary constraints indicative of a folded state (predicted 3D model, C, right).