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Supporting information for article:

**Putting *AlphaFold* models to work with
phenix.process_predicted_model and *ISOLDE***

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S1. AlphaFold prediction of PDB ID: 7LW7

In section 8 we remark on some of the low confidence areas of the *AlphaFold* prediction of the UniProt id: Q9H790 corresponding to the PDB ID:7LW7. The *AlphaFold* Protein Structure Database contains structural predictions of the human proteome. In anticipation of future improvements to *AlphaFold* the structures in that database may not remain static over time. The *AlphaFold* prediction of the UniProt id: Q9H790 corresponding to PDB ID:7LW7 and the associated PAE matrix at the time of writing is therefore made available as supplementary material.

S2. AlphaFold prediction of PDB ID: 6L5L and 6j09

The *PHENIX* Colab notebook *AlphaFold* predictions of the amino acid sequence corresponding to the structures with PDB ID: 6L5L and 6j09 discussed in section 7 produces coordinate files (.pdb) and associated PAE matrix files (.jsn). All files are available as supplementary material.

S3. Additional video

The *ChimeraX ISOLDE* video mentioned in section 7.4 is available as supplementary material.