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Protein structure prediction with AlphaFold-Multimer

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We use this protocol and it's working

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Abstract

This protocol describes the protein structure prediction with AlphaFold-Multimer.

1 Protein sequences were downloaded from the Uniprot server.

2 A locally installed version of AlphaFold-Multimer was used for structure prediction with 5 models per prediction followed by Amber relaxation.

3 Interaction scores (ipDT) and diagnostic plots (PAE plot and pLDDT plot) as well as the generated structures were manually inspected.

4 Predicted structures were visualized with ChimeraX-1.8.