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AlphaFold 3 screen

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We use this protocol and it's working

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Abstract

This protocol is about the AlphaFold 3 screen.



- 1 Protein sequences were downloaded from the Uniprot server.
- 2 We accessed AlphaFold 3 from its virtual server (<https://alphafoldserver.com>) to run pairwise predictions with 5 models per prediction. 
- 3 Predictions with an ipTM score of > 0.5 were considered putative hits 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. 