



Aug 29, 2024

AlphaFold 3 screen

 [Nature Cell Biology](#)

DOI

<https://dx.doi.org/10.17504/protocols.io.6qpvr8rm2lmk/v1>

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DOI: <https://dx.doi.org/10.17504/protocols.io.6qpvr8rm2lmk/v1>

External link: <https://doi.org/10.1038/s41556-025-01712-y>

Protocol Citation: Elias Adriaenssens 2024. AlphaFold 3 screen. **protocols.io**

<https://dx.doi.org/10.17504/protocols.io.6qpvr8rm2lmk/v1>

Manuscript citation:

Adriaenssens, E., Schaar, S., Cook, A.S.I. *et al.* Reconstitution of BNIP3/NIX-mitophagy initiation reveals hierarchical flexibility of the autophagy machinery. *Nat Cell Biol* **27**, 1272–1287 (2025). <https://doi.org/10.1038/s41556-025-01712-y>

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Protocol status: Working

We use this protocol and it's working

Created: July 22, 2024

Last Modified: August 29, 2024

Protocol Integer ID: 103958

Keywords: ASAPCRN, alphafold, screen, protocol

Funders Acknowledgements:

Aligning Science Across Parkinson's (ASAP)

Grant ID: ASAP-000350

Marie Skłodowska-Curie MSCA Postdoctoral fellowship

Grant ID: 101062916

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.

