Jan 14, 2026

Generation of conformational ensembles of ULK1C on the membrane

DOI
https://dx.doi.org/10.17504/protocols.io.n2bvjemkngk5/v1

Johannes.Betz[1]

[1]Max Planck Institute of Biophysics

Johannes.Betz

DOI: https://dx.doi.org/10.17504/protocols.io.n2bvjemkngk5/v1

Protocol Citation: Johannes.Betz 2026. Generation of conformational ensembles of ULK1C on the membrane. **protocols.io** https://dx.doi.org/10.17504/protocols.io.n2bvjemkngk5/v1

Protocol status: Working
We use this protocol and it's working

Created: November 11, 2025

Last Modified: January 14, 2026

Protocol Integer ID: 232087

Keywords: ulk1c on the membrane, generation of conformational ensemble, conformational ensemble, ulk1 complex, ulk1c, membrane

Funders Acknowledgements:
Max Planck Society

Abstract

Here, we outline the generation of conformational ensembles of the ULK1 complex as described in the following pre-print: https://doi.org/10.1101/2025.11.07.687251

Generation of IDR Conformational Ensembles

1 Use a local installation of the HCG webserver (https://bio-phys.pages.mpcdf.de/hcg-from-library/) code to generate atomistic ensembles with 100,000 structures each of the ATG13 IDR (res. 230-363), ULK1 IDR (res. 277-840) and the N-terminal section of the ULK1 IDR (res. 277-428).

Generation of AlphaFold Models

2 Run AlphaFold2-Multimer of ULK1C core (ATG13 res. 363-517, 2x FIP200 res. 1-640, ULK1 res. 827-1050), ULK1 KD (res. 1-277) and HORMA dimer with ULK1 bound (ATG101 res. 1-218, ATG13 res. 1-220 ULK1 res. 428-450).

Modeling of Membrane-Tethered ULK1C Core

3 Prepare a snapshot of ATG13-ATG101-WIPI3-WIPI2 complex simulation including the membrane. For every structure in the ATG13 IDR ensemble, align with the snapshot on residue 230 and attach the ULK1C core structure by aligning on ATG13 residue 363. Accept the structure of both alignments have an RMSD below 0.6 Å, no clashes are created and no atom is below the approximate surface of the upper leaflet. Discard overlapping atoms.

4 Perform CCD minimization on the distances of sulfur atoms of ULK1 res. 927 and 1003 and FIP200 res. 413. Iteratively perform small rotations of phi/psi dihedral angles of randomly drawn residues on the ATG13 IDR, accepting moves if they reduce the RMS of the three distances and do not create clashes. Terminate the process if the three atoms are within 5 Å of the approximate surface of the upper leaflet. Repeat for at least three separate ATG13 conformations.

Modeling of ULK1 IDR on the Membrane-Bound Complex

5 Take final structures from the previous step and attach the ULK1 IDR and KD as described in step 3.

6 Take structures from the previous step and remove ULK1 res. 1-449. Add res. 428-450 to the HORMA dimer by superimposing the AF2 model from step 2.

7 Perform CCD on the ULK1 IDR by minimizing the backbone RMSD of overlapping residue 450. Terminate if the RMSD is below 0.6 Å.

8 Take final structures from the previous step and attach the N-terminal part of the ULK1 IDR and the KD as described in step 3.

Analysis

9 Measure the distance between the center of mass of ULK1 KD and the membrane for every structure in ensembles generated by steps 5 (unbound) and 8 (bound).