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Bioinformatic analyses presented in Figure 1 are described in detail in the Methods section and additional data required for the analysis are supplied in Table 1, Supplementary Table 2, and Supplementary Table 2.

For Mass Spectrometry analysis of OM proteome samples, the method is described in detail in the Methods section and the data are presented in Supplementary Table 2.

For the NMR structural analysis, the methods are described in detail in the Methods section, the validation report for PDB 7A2D is provided, the structure is also uploaded to BMRB (19760), and structural statistics are reported in Table 2.

For the lipid interaction analysis, the Methods are described in detail in the Methods section and the top 200 models were ranked according to their experimental energies and statistics derived from the 20 lowest energy conformers reported in Table 5. The lipid titration data is represented in the figures and the source data is supplied in files “Figure-3-and-4-source-data” and “Figure-3-source-data”.

We have supplied original images for Figure 1-figure supplement 1, Figure 1-figure supplement 5, Figure 2, Figure 3-figure supplement 1A,B, Figure 3-figure supplement 2, Figure 4B and Figure 5A,B,C. We have also supplied raw data for Figure 1-figure supplement 4B, Figure 2B, Figure 3-figure supplement 2B,C and D, and Figure 3.

For all other analyses, information is reported in the Figure Legends, or Methods section.