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Supporting information for article:

**Insights into the mechanism of high lipid-detergent (HiLiDe)
crystallization of membrane proteins**

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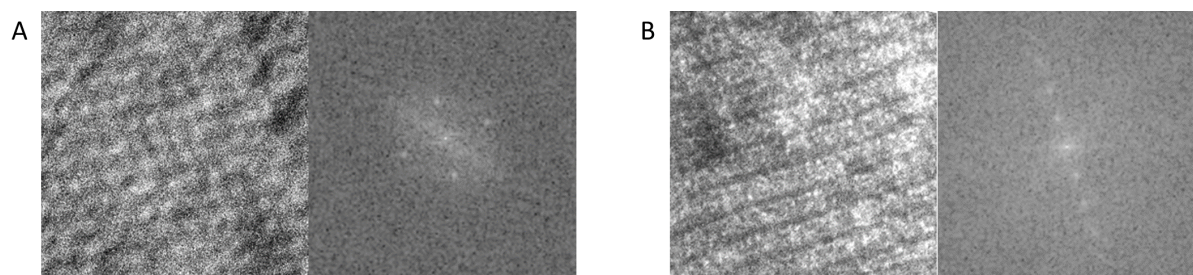


Figure S1 Fourier transforms of NS-TEM images. **A.** MhsT crystal (same as in figure 4A). Real space image and its FFT, with the latter showing a 2D pattern of spots. **B.** Lamellar structure (same as in figure 4C). Real space image and its FFT, with the latter showing a 1D pattern of spots.

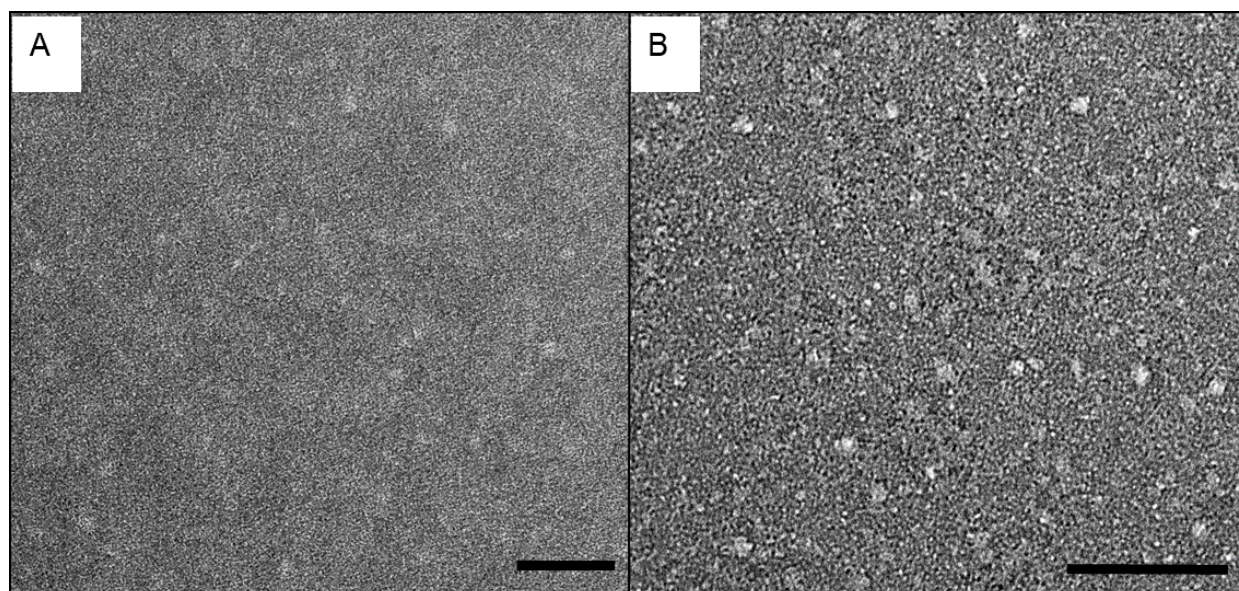


Figure S2 NS-TEM images of crystallization trays drops of control proteins. **A.** Sugar transporter protein 6 (STP6). **B.** lysozyme. The scale bar is 100 nm.

Table S1 Protein/Lipid/detergent conditions screened for MhsT. Key to symbols: * = crystals obtained, X = no crystals, – = condition not tested. Colours indicate: 13% (black), 14% (red), 16% (blue) and 19% (green) PEG 400, respectively.

Detergent	Lipid	0.2	0.4	0.5	0.6	0.8	1.0	1.2	1.4	1.6	1.8	2.0	2.25
0.24		-	-	-	-	X	X***	***	X**	*--	-	-	-
0.18		-	-	-	X	X	**X	X**	***	-	-	-	-
0.12		-	-	X	*	***	***	***	***	*--	*--	-	-
0.06		-	X	X	X	***	***	***	***	*--	-	-	*--
0		-	***	*	***	***	***	***	***	-	*--	*--	-

Table S2 Data statistics for synchrotron X-ray diffraction studies of MhsT:Trp crystals. Letters in parentheses refer to labelled samples in Figure 1A. * The presence or absence of a screw axis was assessed based on systematic absences, and the cell dimensions compared to previously determined MhsT structures that are known to represent space groups P2 (PDB: 6YU3, 6YU4, 6YU7) and P2₁ (PDB: 6YU5, 6YU6). These data sets are not intended for structure determination, but for assessment of diffraction quality.

Sample	MhsT:Trp (C)	MhsT:Trp (H)	MhsT:Trp (I)
p/l/d ratio	3/0.8/0.12	3/1.6/0.12	3/2.25/0.06
Beamline	DESY P14	DESY P14	DLS I24
No. of data sets	1	11	1
Space group*	P2 ₁	P2 ₁	P2
Cell dimensions			
<i>a, b, c</i> (Å)	44.1, 215.0, 50.9	44.3, 215.1, 50.1	44.2, 50.0, 109.9
<i>α, β, γ</i> (°)	90, 90.17, 90	90, 90.00, 90	90, 96.49, 90
Resolution (Å)	4.2 (4.3–4.2)	2.8 (2.9–2.8)	2.4 (2.5–2.4)
I/σI	1.8 (1.1)	3.0 (1.1)	6.4 (1.6)
CC(1/2) (%)	89.4 (42.2)	79.1 (25.8)	98.8 (47.0)
Completeness (%)	80.2 (79.2)	21.8 (22.3)	99.8 (99.8)
Multiplicity	1.2 (1.2)	1.8 (1.7)	6.7 (6.8)