

Crystallization in the Lipidic Cubic Phase (LCP) has evolved into an important method for crystallization of membrane proteins, with the lipid Monoolein being the first choice to create a stable LCP. In the past few years however, the short lipids 7.7 MAG^[4,7], 7.8 MAG^[6-8], 7.9 MAG^[5,7] have become increasingly popular and the recent progress in applying the highly viscous lipidic cubic phase for serial femtosecond crystallography (LCP-SFX)^[1-3] further accelerates the success of the LCP method by

- › delivering the crystal-loaded viscous LCP directly into the XFEL beam (thereby reducing sample consumption in comparison to liquid injectors),
- › taking advantage of the inherently small crystals grown in LCP,
- › avoiding tricky crystal mounting from LCP.

Online catalog
LCP Lipids at [↗](#)



LCP Lipid	Lipid structure	Cat.-No.	Amount
Monoolein 9.9 MAG		X-LCP-101	1 g
7.7 MAG		X-LCP-105	100 mg
7.8 MAG		X-LCP-106	100 mg
7.9 MAG Stable at low temperatures ^[9]		X-LCP-107	100 mg
Monopalmitolein 9.7 MAG		X-LCP-102	1 g
Monovaccenin 11.7 MAG		X-LCP-103	100 mg
Monoeicosenoïn 11.9 MAG		X-LCP-104	1 g

JBScreen LCP is designed for efficient screening of crystallization conditions in LCP. Each of the LCP Lipids from the table above is capable to create a stable Lipid Cubic Phase which can be set up for crystallization with JBScreen LCP. Its 96 conditions result from data mining of 192 integral membrane proteins, that were successfully crystallized by the *in meso* method and have yielded structures^[7]. The screen is ordered by concentration and type of the precipitant and is free of cacodylate.

Product	Cat.-No.	Amount
JBScreen LCP	CS-340	4×24 solutions (10 ml each)
JBScreen LCP HTS	CS-213L	96 solutions (1,7 ml each)

Online catalog
LCP Screens at [↗](#)



[1] Nogly *et al.* (2016) Lipidic cubic phase injector is a viable crystal delivery system for time-resolved serial crystallography. *Nat. Commun.* **7**:12314.
 [2] Zhu *et al.* (2016) Serial Femtosecond Crystallography of Membrane Proteins. *Adv. Exp. Med. Biol.* **922**:151.
 [3] Balyuk *et al.* (2016) Native phasing of x-ray free-electron laser data for a G protein-coupled receptor. *Sci. Adv.* **2**:e1600292.
 [4] Coincon *et al.* (2016) Crystal structures reveal the molecular basis of ion translocation in sodium/proton antiporters. *Nat. Struct. Mol. Biol.* **23**:248.
 [5] Li *et al.* (2015) Ternary structure reveals mechanism of a membrane diacylglycerol kinase. *Nat. Commun.* **6**:10140.
 [6] Fowler *et al.* (2015) Gating Topology of the Proton-Coupled Oligopeptide Symporters. *Structure* **23**:290.
 [7] Caffrey (2015) A comprehensive review of the lipid cubic phase or in meso method for crystallizing membrane and soluble proteins and complexes. *Acta Cryst F* **71**:3.
 [8] Li *et al.* (2013) Crystal structure of the integral membrane diacylglycerol kinase. *Nature* **497**:521.
 [9] Misquitta *et al.* (2004) Rational design of lipid for membrane protein crystallization. *Journal of Structural Biology* **148**:169.

