

# The Nanoscience Behind the Art of *in-meso* Crystallization of Membrane Proteins

## Supporting Information

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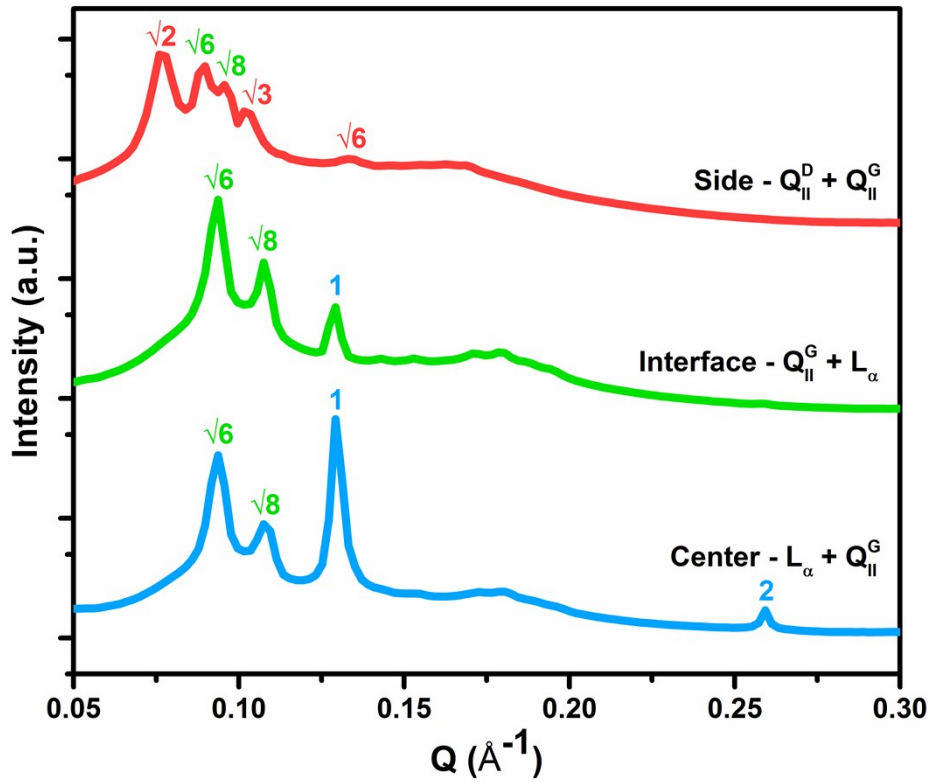
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### *Intimin expression and purification*

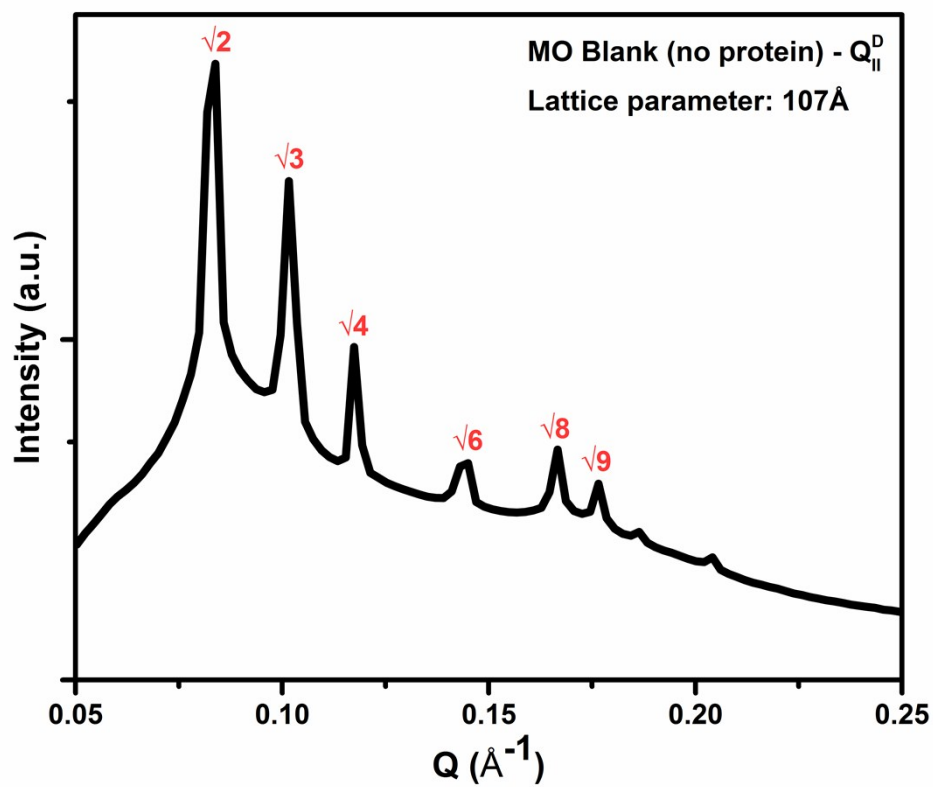
The plasmid containing the *E. coli* O157:H7 gene was transformed into BL21 (DE3) cells and plated onto LB plates containing kanamycin. Single colonies were pre-screened by means of Western Blotting to identify overexpression of the target protein. Overexpressing colonies were pre-cultured into 40mL of TB containing 50 $\mu$ g/mL kanamycin until an OD value of 1. 5mL of pre-culture was then transferred into 500mL of TB-kanamycin media and allowed to grow at 20°C for 2-3 days while shaking at 220rpm until they reached a terminal OD of 15-20. Cells were harvested by means of centrifugation (5000rpm, 10 min, 4°C) using a Beckman JA14 rotor and then stored at -80°C.

Cells were thawed on ice and resuspended in lysis buffer (50mM TRIS pH 8.0, 200mM NaCl, 5 mg/ml Lysozyme, 1 tablet of protease inhibitor cocktail – EDTA free - Roche) and then lysed using a probe sonicator (Misonix S4000), in 30 seconds interval at 60% amplitude. Cell debris and unlysed *E. coli* were collected by centrifugation at 12000xg for 30 minutes at 4°C. Membranes containing the desired protein were harvested from the supernatant by ultra-centrifugation (160,000xg, 60 min, 4°C). Membrane proteins were solubilized by resuspension in solubilization buffer (50mM TRIS pH 8.0, 200mM NaCl, 20mM Imidazole, 5% Eluent (Calbiochem)) and left stirring O/N at 4°C. The next morning, the sample underwent ultra-centrifugation (250,000xg, 60 min, 4°C) to remove insoluble material. Supernatant was loaded onto a Ni-NTA affinity column that was pre-equilibrated with 50mM TRIS pH 8.0, 200mM NaCl, 10% glycerol, and 0.1% DDM (n-dodecyl- $\beta$ -D-maltopyranoside)(Anatrace). The protein was eluted with 50mM TRIS pH 8.0, 200mM NaCl, 10% glycerol, 0.1% DDM, and 250mM imidazole. Fractions containing protein were desalted into 50mM TRIS pH 8.0 using a High Performance Desalting column (GE Healthcare) that was pre-equilibrated with Buffer A (50mM TRIS pH 8.0, 0.1 % DDM). Fractions containing protein were concentrated in a YM30 Amicon Ultra concentrator (Millipore) to prepare for crystallization experiments.

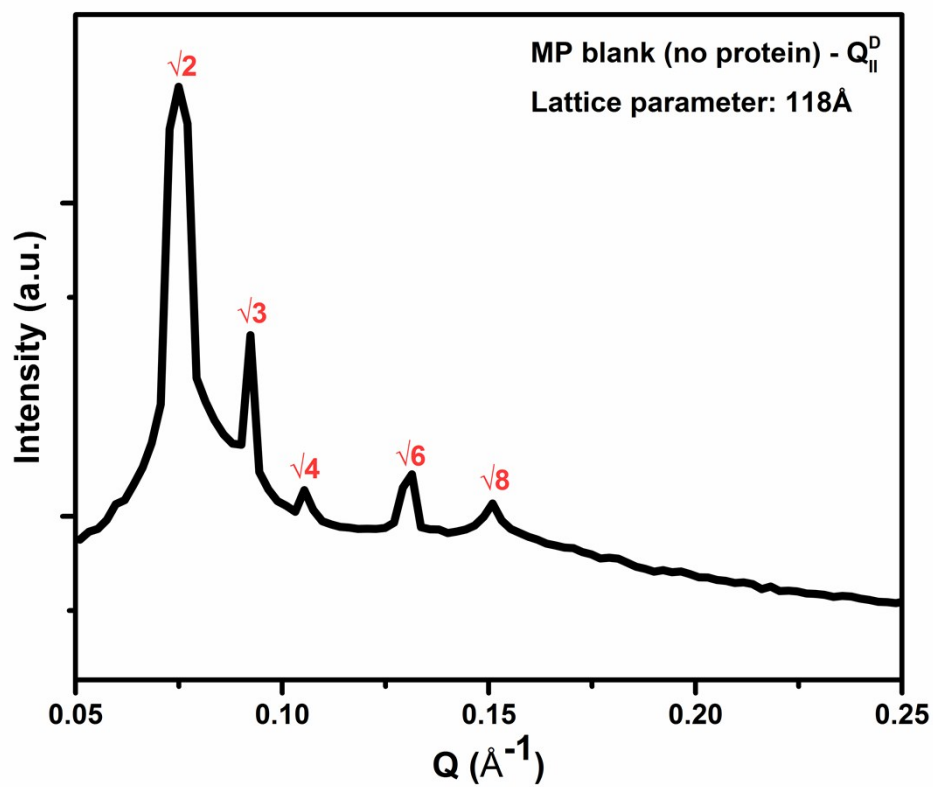
**Table S1.** 96 conditions randomized screen based for intimin crystallization. The screen was designed around previously found conditions (1) 20% MPD; 0.1M NaCitrate/citric acid pH 4.5-5.5 (private communication, Dr. Susan K Buchanan) (2) 0.2-2% w/v PEG 6000; 0.1M NaCitrate/citric acid pH 4.5-5.5 (private communication, Dr. Susan K Buchanan) (3) 0.1M NaCitrate/citric acid pH 4.5-5.5, 0.05-0.1M NaCl, 0.1-0.15M MgCl<sub>2</sub>, 30-34 % v/v PEG 400 (39), in order to optimize growth and ensure reproducibility.



**Figure S1.** 1D spectra of scattered intensities versus scattering vector,  $q$ , showing the distinct symmetries adopted by the lipidic mesophase in three different regions of a LCP drop: (1) The crystal growth region in the center of the LCP bolus where crystal growth invariably occurs; (2) The interface region found towards the edge of the protein concentrated region of the LCP bolus; (3) The LCP region found towards the edge of the well where the LCP is depleted in protein and crystal growth does not occur.



**Figure S2.** 1D SAXS spectra showing a control crystallization experiment for the MO system comprising of an identical LCP drop and crystallization buffer but without added protein.



**Figure S3.** 1D SAXS spectra showing a control crystallization experiment for the MP system comprising of an identical LCP drop and crystallization buffer but without added protein.

<b>PDB</b>	<b>5G26</b>
<b>Space group</b>	<b>C222<sub>1</sub></b>
<b>Cell dimensions</b>	
<i>a, b, c</i> (Å)	<b>115.6, 119.7, 39.0</b>
<i>a, b, c</i> (°)	<b>90, 90, 90</b>
<b>Resolution (Å)</b>	<b>41.6-2.42 (2.51-2.42)</b>
<i>R</i> <sub>merge</sub>	<b>0.143 (0.822)</b>
<i>R</i> <sub>pim</sub>	<b>0.046 (0.266)</b>
<i>CC1/2</i>	<b>0.998 (0.888)</b>
<i>I</i> / <i>sI</i>	<b>12.3 (2.9)</b>
<b>Completeness (%)</b>	<b>99.1 (91.8)</b>
<b>Redundancy</b>	<b>10.2 (10.1)</b>
<b>Refinement</b>	
<b>Resolution (Å)</b>	<b>41.5 - 2.42</b>
<b>Unique reflections</b>	<b>10,728</b>
<i>R</i> <sub>work</sub> / <i>R</i> <sub>free</sub> (%)	<b>22.2 / 27.8</b>
<b>No. atoms</b>	<b>2,089</b>
<b>Protein</b>	<b>1,964</b>
<b>Lipid</b>	<b>92</b>
<b>Water</b>	<b>33</b>
<b><i>B</i>-factors (Å<sup>2</sup>)</b>	<b>40.7</b>
<b>Protein</b>	<b>40.5</b>
<b>Lipid</b>	<b>55.0</b>
<b>Water</b>	<b>36.0</b>
<b>R.m.s. deviations</b>	
<b>Bond lengths (Å)</b>	<b>0.012</b>
<b>Bond angles (°)</b>	<b>1.527</b>

**Table S2.** Data collection and refinement statistic for the native intimin protein crystallized from an MP-based cubic phase.