Uniformly Aligned Full-length Membrane Proteins in Lipid Crystalline Bilayers for Structural Characterization

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Sample preparation for Solid-state NMR

Preparation of lipid stocks. 1,2-Dimyristol-sn-Glyero-3-Phosphocholine (DMPC) and 1,2-Dimyristoyl-*sn*-Glycero-3-[Phospho-*rac*-(1-glycerol)] (Sodium Salt) (DMPG) were dissolved in chloroform at a molar ratio of 4:1 in a round-bottom flask and the solvent evaporated in a rotary evaporator followed by vacuum drying overnight. The DMPC/DMPG film was then dissolved in deionized water at a final concentration 20mg/ml, bath sonicated followed by three freeze (liquid-nitrogen)-thaw (37°C) cycle for 3 times.

Reconstitution. The preformed liposomes were added to the purified protein solution in DPC to a final ratio of 10:1 (w:w – lipid to protein dry weight ratio), 20% octyl-glucoside (OG) is then added to the protein liposomes mixtures until the solution clarifies, usually the final OG concentration is about 50 to 100mM. After overnight incubation at 37°C, OG was removed by dialysis.

Aligned sample preparation. Proteoliposomes were pelleted by ultracentrifugation from the dialyzed solution (196000g, 90min) in a 70 Ti rotor. The 50 mg pellet was suspended in 1 mL of HPLC-grade water. Aliquots were spread on 33 glass slides ($12\times5.7\times0.07$ mm) dehydrated in a 78% relative humidity chamber at room temperature for a day. The slides were stacked into a sample cell followed by incubation at 97% relative humidity in a small chamber for one week at 37 °C to achieve a hydration level of approximately 50%. The sample cell was sealed with wax for solid-state NMR experiments.

Oligomeric state of Rv1861

28 mg of Rv1861 per L of minimal media culture are typically achieved in the form of inclusion bodies. Purification via a reconstitution protocol¹ has resulted in high purity samples on SDS PAGE gels. On PFO gels a large oligomeric structure is implicated, potentially an octamer (Figure S1).



Figure S1: PFO- gel of Rv1861 showing that the molecular weight is approximately 80 kDa suggesting an octamer.

PISA wheel as a function of CSA:

Chemical shift tensor anisotropy (CSA) variation will blurr the resonance pattern in the PISEMA spectrum that forms the PISA wheel. Figure S2 shows the PISA wheel at 2 tilt angles with a distribution of 20 ppm for each of the tensor elements. When the tilt angle is small, σ_{11} and σ_{22} have little effect on the shape of the wheel while σ_{33} shifts the position of the wheel. However, when the tilt angle is large, σ_{11} and σ_{22} have a significant influence on the shape of the wheel, while σ_{33} has little effect.



Figure S2: PISA wheel as a function of CSA tensor variation.

Reference:

(1) Page, R. C.; Moore, J. D.; Nguyen, H. B.; Sharma, M.; Chase, R.; Gao, F. P.; Mobley, C. K.; Sanders, C. R.; Ma, L.; Sonnichsen, F. D.; Lee, S.; Howell, S. C.; Opella, S. J.; Cross, T. A. *J Struct Funct Genomics* **2006**, *7*, 51-64.