Supporting Information for "Incorporation of the Dopamine D2L receptor and bacteriorhodopsin within bicontinuous cubic lipid phases. 2. Relevance to *in meso* crystallization of integral membrane proteins in novel lipid systems"

(1) Representative 1-D diffraction plots

In all images the {hkl} reflections corresponding to the particular lipid mesophase adopted are highlighted. Peaks corresponding to a Q_{II}^{D} cubic phase are indicated in normal type, peaks corresponding to a Q_{II}^{G} cubic phase in bold type and peaks corresponding to a H_{II} phase in italic type. For some plots the intensity has been plotted on a logarithmic scale to visualize less intense peaks.

Incorporation of dopamine D2L receptor within FE

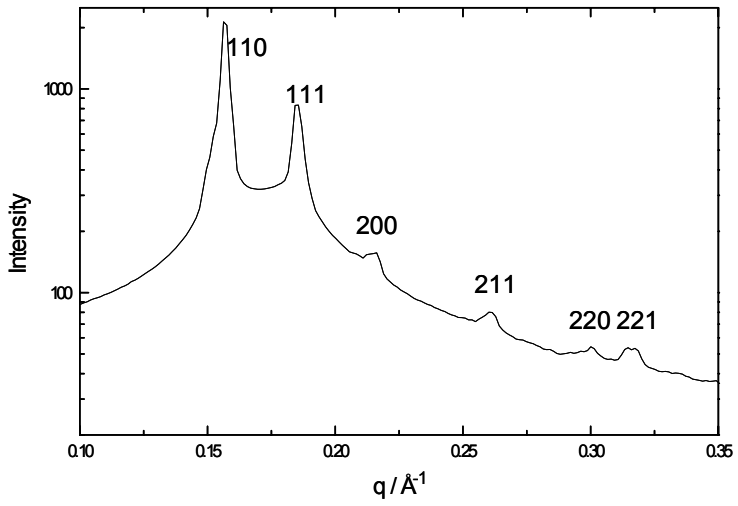

Figure S1. 1D diffraction pattern for FE 40wt% D2L receptor buffer. T=20°C. Peaks corresponding to a Q_{II}^{D} phase are observed.

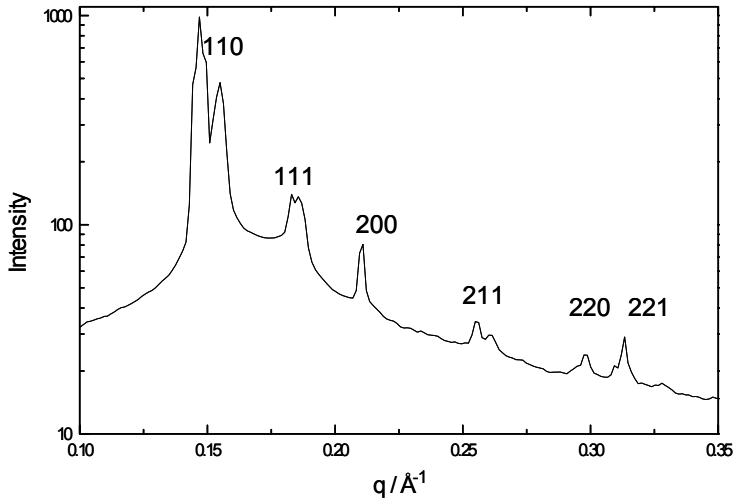

Figure S2. 1D diffraction pattern for FE 40wt% D2L receptor at 0.55 mgs/ml. T=20°C. Peaks corresponding to a Q_{II}^{D} phase are observed. The 2-D diffraction pattern is spotty resulting in split peaks.

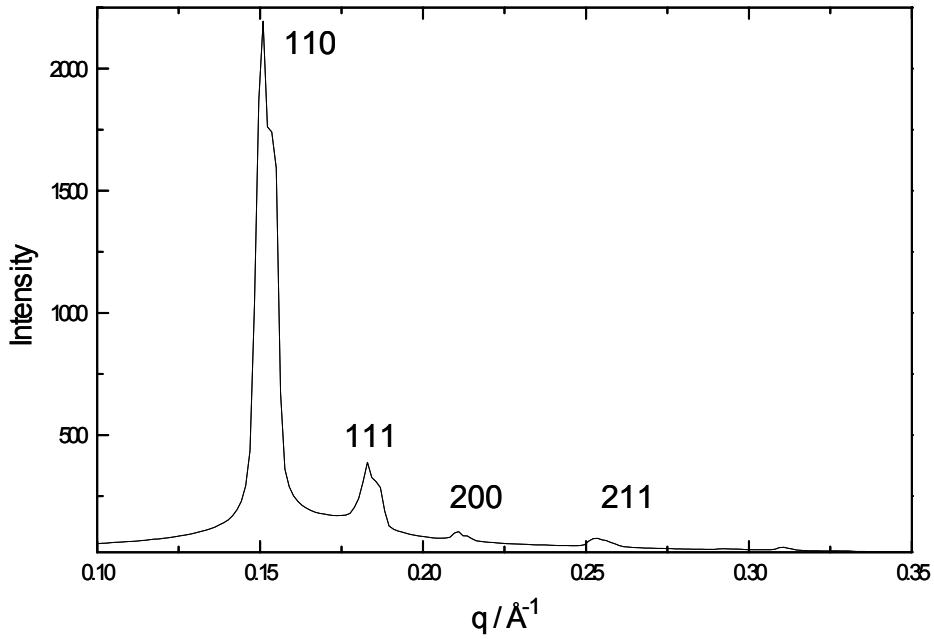

Figure S3. 1D diffraction pattern for FE 40wt% D2L receptor at 1.1 mgs/ml. T=20°C. Peaks corresponding to a Q_{II}^{D} phase are observed. This corresponds to Fig. 4(A) but with intensity plotted on a linear axis.

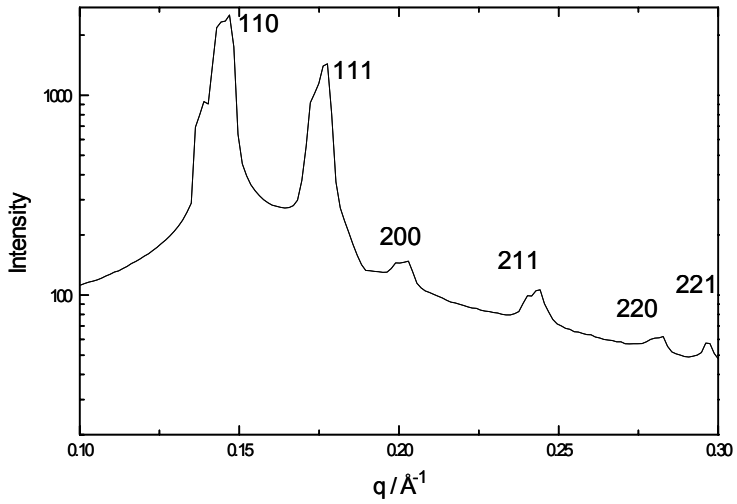

Figure S4. 1D diffraction pattern for AE 50wt% D2L receptor buffer. T=15°C. Peaks corresponding to a Q_{II}^{D} phase are observed.

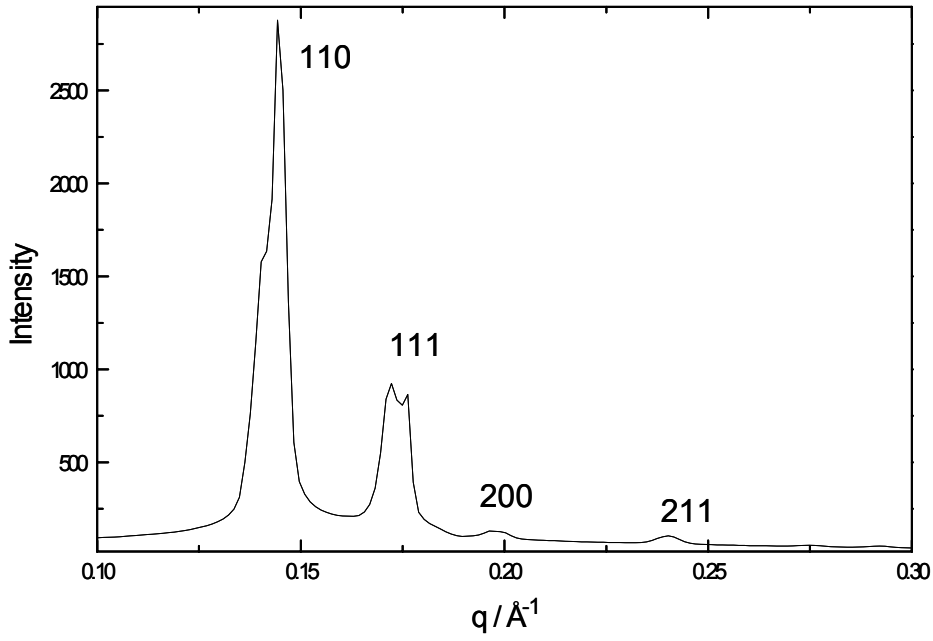

Figure S5. 1D diffraction pattern for AE 50wt% D2L receptor at 0.55 mgs/ml. T=15°C. Peaks corresponding to a Q_{II}^{D} phase are observed. This corresponds to Fig. 4(B) but with intensity plotted on a linear axis.

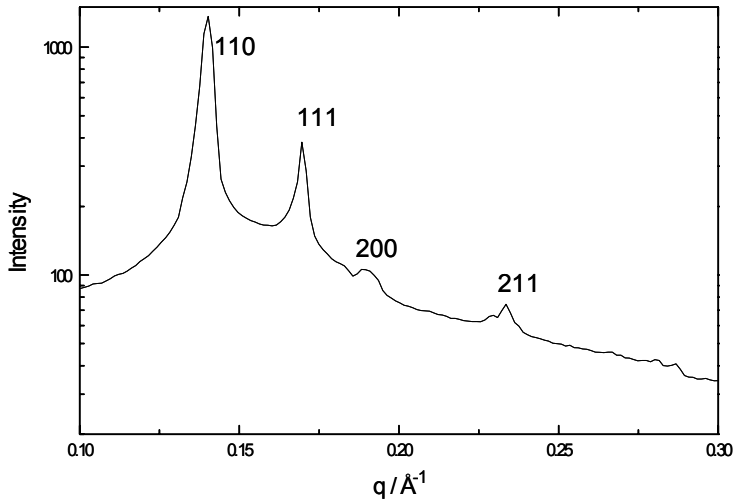

Figure S6. 1D diffraction pattern for AE 50wt% D2L receptor at 1.1 mgs/ml. T=15°C. Peaks corresponding to a Q_{II}^{D} phase are observed.

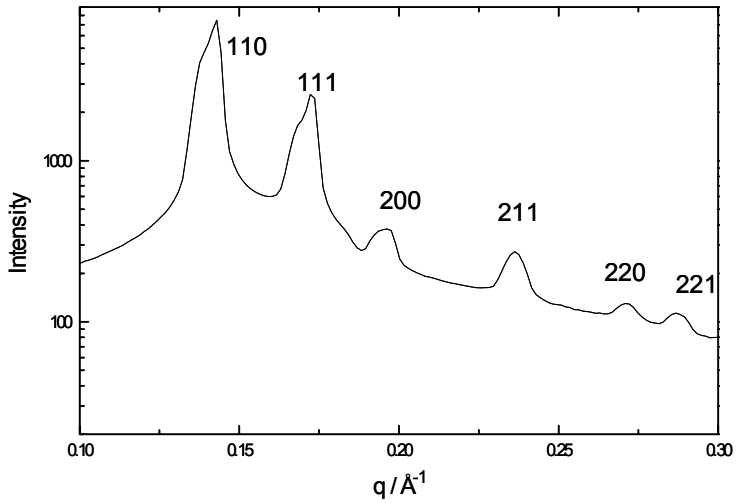

Figure S7. 1D diffraction pattern for AE 50wt% D2L receptor at 2.2 mgs/ml. T=15°C. Peaks corresponding to a Q_{II}^{D} phase are observed.

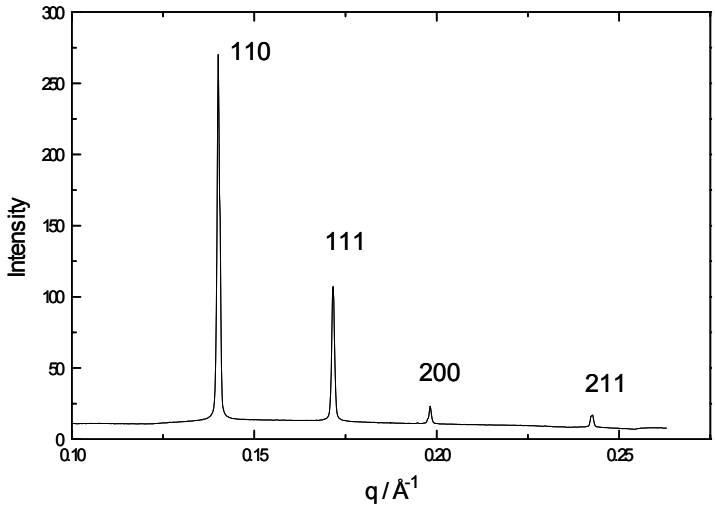

Figure S8. 1D diffraction pattern for FE 40wt% Na K phosphate buffer. T=20°C. Peaks corresponding to a Q_{II}^{D} phase are observed

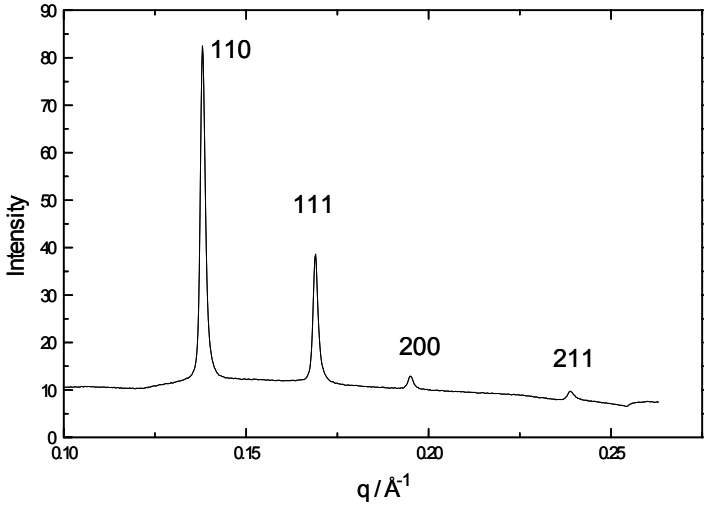

Figure S9. 1D diffraction pattern for FE 40wt% bR at 12 mgs/ml. T=20°C. Peaks corresponding to a Q_{II}^{D} phase are observed.

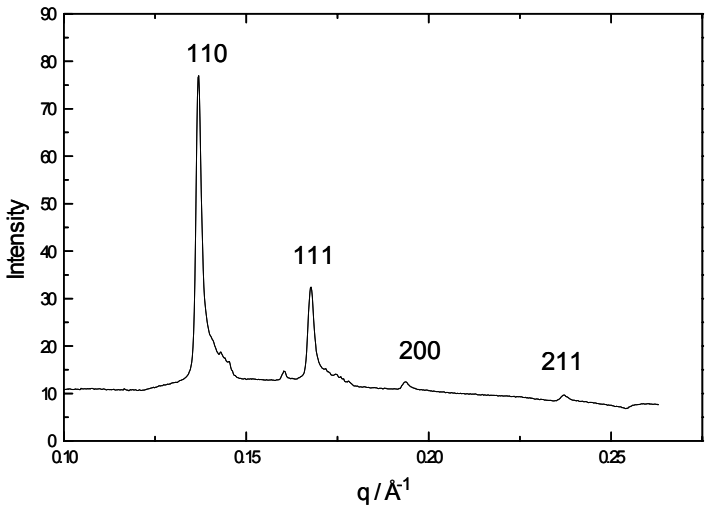

Figure S10. 1D diffraction pattern for FE 40wt% bR at 18 mgs/ml. T=20°C. Peaks corresponding to a Q_{II}^{D} phase are observed. Some additional peaks indicate an element of disorder within the sample at this protein concentration.

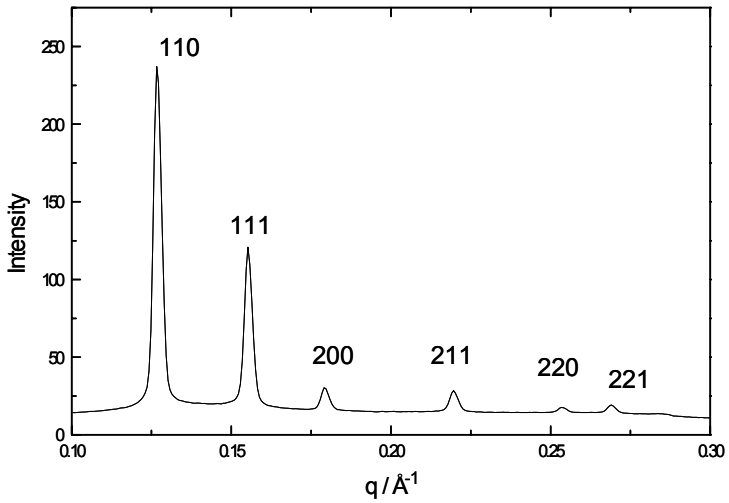

Figure S11. 1D diffraction pattern for AE 50wt% bR at 9 mgs/ml. T=9°C. Peaks corresponding to a Q_{II}^{D} phase are observed.

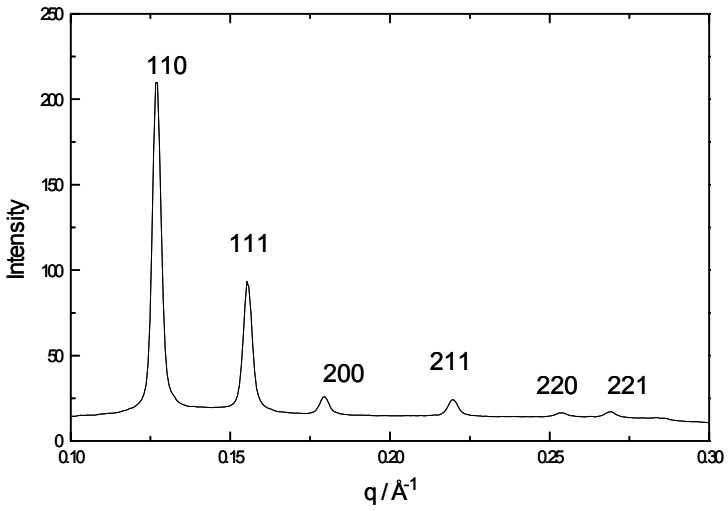

Figure S12. 1D diffraction pattern for AE 50wt% bR at 18 mgs/ml. T=9°C. Peaks corresponding to a Q_{II}^{D} phase are observed.

(2) Analysis of bilayer thickness and water channel radius

For a sample of known sample composition, lipid length, l, was calculated from the lattice parameter, a, by using Eq. 1[18]

$$\Phi_l = 2A_0\left(\frac{l}{a}\right) + \frac{4\pi\chi}{3}\left(\frac{l}{a}\right)^3 \qquad (1)$$

Where Φ_l is the percentage of lipid by volume within the sample, and A_0 and χ are the dimensionless surface area and the Euler characteristic of the specific cubic phase [A_0 = 3.091 (Q_{II}^{G}); 1.919 (Q_{II}^{D}) and χ = -8 (Q_{II}^{G}) and -2 (Q_{II}^{D})].

Φ_l, the percentage of lipid by volume within the sample, is calculated from the known sample composition, c, using Eq. 2[19] where $\Phi_l = 1 - \Phi_w$, the water density ρ_w = 1g/cm^3 and the density of the lipid sample ρ_L. ρ_{AE} = 0.92g/cm^3. ρ_{FE} is not known but is assumed to be the same as phytantriol (Phy) which has a similar branched structure ρ(Phy) = 0.94g/cm^3.

$$\Phi_w = \frac{c}{c + (1-c)\frac{\rho_w}{\rho_L}} \qquad (2)$$

The water channel radius, r_w, may then be calculated using Eq. 3.[18]

$$r_w = \sqrt{\frac{-A_0 a^2}{2\pi\chi}} - l \qquad (3)$$