Protein Construct Sequences

The following amino acid sequence of ApoA-I protein was used in the cell-free experiments:

MSGSHHHHHHSSGIEGRGRLIKHMLNLLENWDTLGSTVSQLQERLGPLTRDFWDNLEKETDWVRQEMNKDLEEVKQ
KVQPYLDEFQKKWKEDVELYRQKVAPLGAELQESARQKLQELQGRLSPVAEEFRDRMRTHVDSLRTQLAPHSEQMRE
SLAQRLAELKSNPTLNEYHTRAKTHLKTLGEKARPALEDLRHSLMPMLETLKTKAQSVIDKASETLTAQGSG

The following amino acid sequence of ApoA-I protein was used in *in vitro* assembly experiments:

MHHHHHHGENLYFQGMLNLLENWDTLGSTVSQLQERLGPLTRDFWDNLEKETDWVRQEMNKDLEEVKQKVQPYL
DEFQKKWKEDVELYRQKVAPLGAELQESARQKLQELQGRLSPVAEEFRDRMRTHVDSLRTQLAPHSEQMRESLAQRL
AELKSNPTLNEYHTRAKTHLKTLGEKARPALEDLRHSLMPMLETLKTKAQSVIDKASETLTAQ

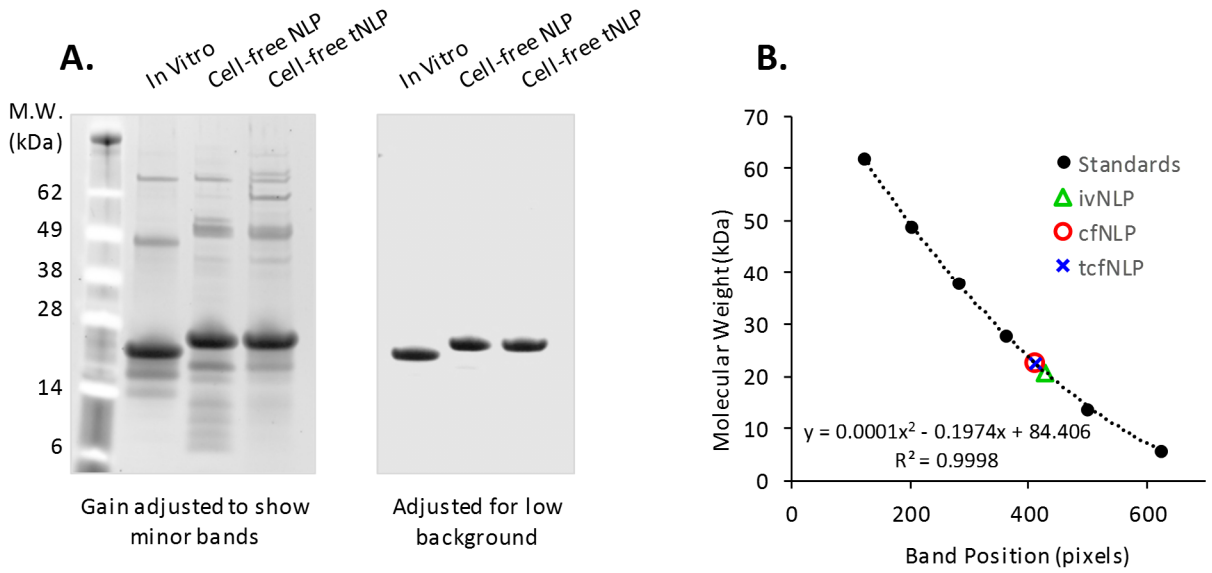

Figure S1. After initial IMAC purification, NLP preps were analyzed by SDS-PAGE using 4 µg of ApoA-I per lane. **(A)** Gels were SYPRO* stained, and imaged for 2 minutes at 600 nm using a LI-COR system. NLPs were >95% pure. **(B)** NLP band positions were compared to standards to verify their molecular weights. ApoA-I proteins used in cell-free and *in vitro* assembly experiments had apparent molecular weights of 22.4 kDa and 20.7 kDa, respectively. Calculated molecular weights based on primary sequence were 26.1 kDa and 25.1 kDa, respectively. The difference is within the level of variation typically seen in SDS-PAGE measurements.

* Certain trade names and company products are identified in order to specify adequately the experimental procedure. In no case does such identification imply recommendation or endorsement by the National Institute of Standards and Technology, nor does it imply that the products are necessarily the best for the purpose.

Model Calculations

The following equations relate molecular quantities and layer dimensions (which were the direct fitting parameters) to the layer SLDs (which are used internally in the scattering calculations for the "Core-Shell Bicelle Model" that is built in to SasView). Direct fitting parameters are shown in red. Parameters that vary as a function of fitting parameters are shown in blue. Constants are **black** and are fixed throughout fitting, but different values may be used for the different datasets, e.g. using scattering lengths appropriate to neutrons for SANS datasets or x-rays for SAXS datasets.

Equations

$$\rho_c = \frac{N_l b_t}{\pi r_c^2 h_c}$$

$$f_{H_2O} = 1 - f_{D_2O}$$

$$b_w = f_{D_2O} b_{D_2O} + f_{H_2O} b_{H_2O}$$

$$\rho_s = \frac{b_w}{V_w}$$

$$\rho_f = \frac{N_l \left(b_{hg} + N_w^{hg} b_w\right)}{2\pi r_c^2 h_f}$$

$$r = r_c + t_R$$

$$\rho_R = \frac{N_{msp}\left(f_{D_2O} b_{msp}^D + f_{H_2O} b_{msp}^H + N_w^{msp} b_w\right)}{\pi\left(h_c + 2h_f\right)\left(r^2 - r_c^2\right)}$$

Definitions

ρ_c	SLD of the core
N_l	Number of DMPC lipids
b_t	DMPC tail scattering length
r_c	Radius of hydrophobic core
h_c	Height of hydrophobic core
b_w	Average scattering length of a water molecule at the specified fraction of D_2O.
f_{D_2O}	Fraction (v/v) of D_2O in the buffer
f_{H_2O}	Fraction (v/v) of ^1H_2O in the buffer
b_{D_2O}	Scattering length of a D_2O molecule
b_{H_2O}	Scattering length of a ^1H_2O molecule
ρ_s	SLD of the solvent/buffer
V_w	Volume of a water molecule
ρ_f	SLD of the face
b_{hg}	DMPC headgroup scattering length
N_w^{hg}	Number of waters per headgroup
h_f	Height of the face
r	Outer radius of the disc
t_R	Thickness of the rim
ρ_R	SLD of the rim
N_{msp}	Number of MSP molecules in the rim
b_{msp}^D	Scattering length of an MSP molecule with all exchangeable hydrogens fully occupied with D
b_{msp}^H	Scattering length of an MSP molecule with all exchangeable hydrogens fully occupied with ^1H
N_w^{msp}	Number of waters per MSP

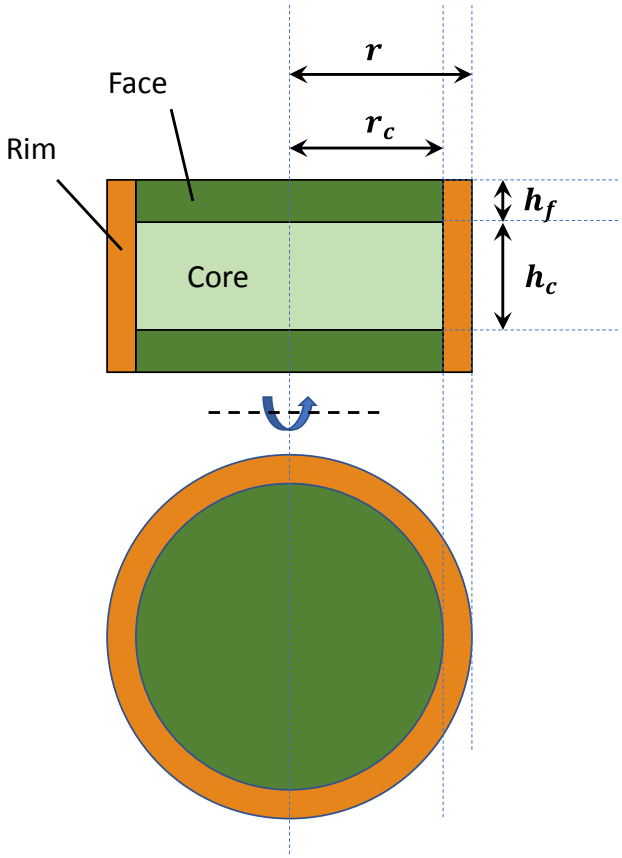

Figure S2. Model Schematic

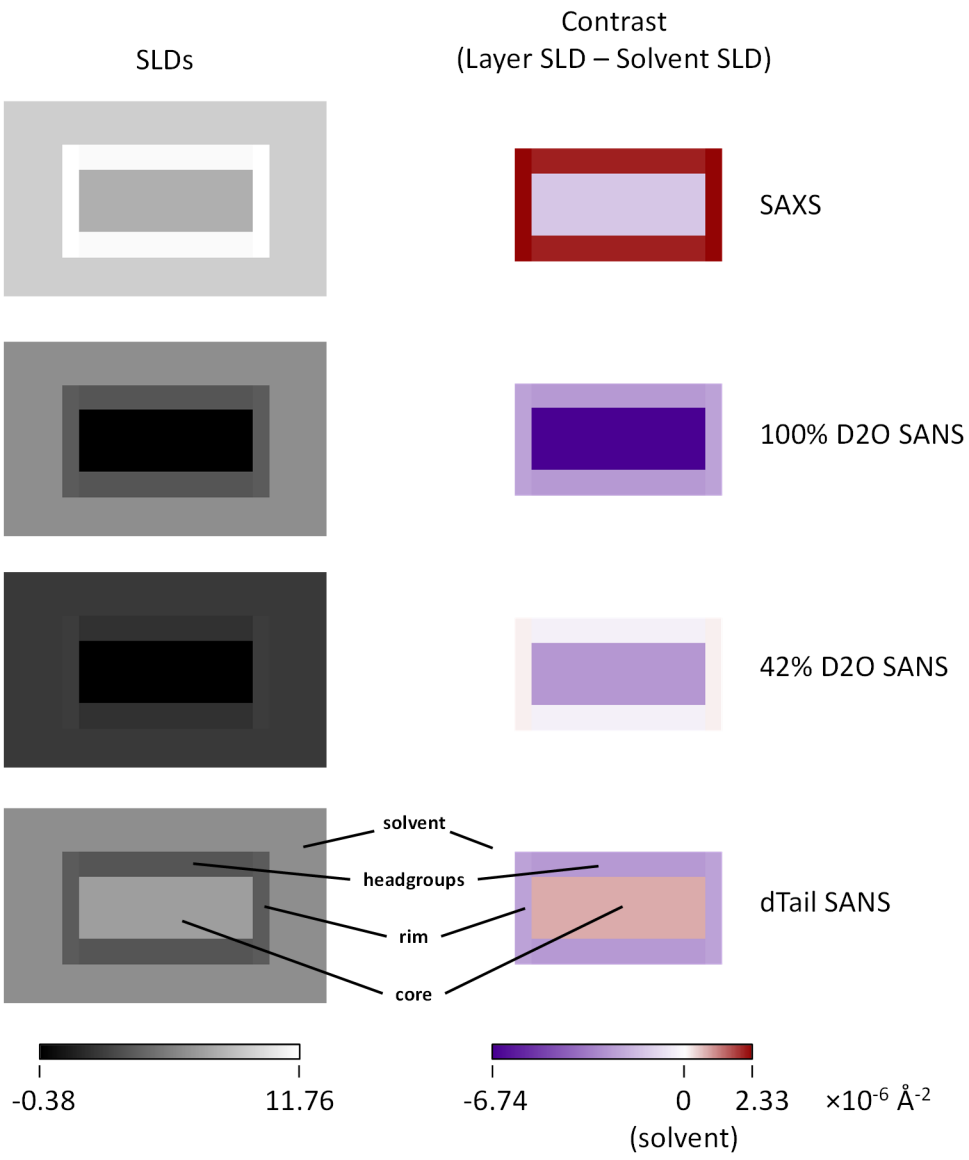

Figure S3. Accurately-scaled diagram of the final model geometry showing layer scattering length densities (SLDs) under the four data collection conditions: SAXS, SANS with 100% and 42% D_2O buffer, and SANS in 100% D_2O buffer on NLPs containing tail-deuterated DMPC lipids.