

TABLE S1. HDX Data Summary and list of experimental parameters

Data Set	Fixed lipoprotein size. 1:10 particles SAA-POPC (~10 nm in size)		Lipoprotein size comparison
States analyzed	State 1: SAA alone State 2: SAA-POPC (5 °C)	State 3: SAA alone (15 °C) State 4: SAA-POPC (15 °C) State 5: SAA alone (25 °C) State 6: SAA-POPC (25 °C)	State 7: 1:10 SAA-POPC (5 °C) (~10nm in size) State 8: 1:30 SAA-POPC (5 °C) (~30nm in size) State 9: 1:80 SAA POPC (5 °C) (~80nm in size)
HDX reaction details ^a	Final D ₂ O concentration = 94.6%, pH _{read} = 7.1		
HDX time course	0.083, 0.167, 3, 10, 30, 60, 240 minutes	0.167, 1, 10, 60, 240 minutes	0.25, 2, 10, 60 minutes
HDX controls	12 undeuterated controls, 6 for each state	12 undeuterated controls, 3 for each state	6 undeuterated controls, 2 for each state
Back-exchange	30-35%		
Number of peptides	33 followed; 42 identified	33 followed; 35 identified	12 followed; 17 identified
Filtering parameters	0.2 products per a.a., 2 consecutive products, 10ppm error, file threshold of 7	0.2 products per a.a., 2 consecutive products, 10ppm error, file threshold of 6	0.2 products per a.a., 2 consecutive products, 10ppm error, file threshold of 6
Sequence coverage	95.1%	100.0%	95.1%
Average peptide length	14.8	15.4	20.3
Redundancy	5.00	4.93	2.48
Replicates	4 total per state: 2 biological; 2 technical	1 technical for each state	1 technical for each state
Repeatability	+/- 0.30 relative Da		
Significant differences	> 0.8 Da		

^a 18-fold dilution with labeling buffer [10 mM sodium phosphate, pD 7.5, 99.9% D₂O].
1:1 (v/v) dilution with quench buffer [150 mM sodium phosphate, pH 2.3, H₂O].