

**CONSERVATION of APOLIPOPROTEIN A-I's CENTRAL DOMAIN STRUCTURAL  
ELEMENTS UPON LIPID ASSOCIATION ON DIFFERENT HDL SUBCLASSES**

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**SUPPLEMENTAL FIGURE LEGENDS**

**Fig. S1.** Human wild-type apoA-I sequence. Helix distribution derived by sequence analysis (1, 2). The 21 residues under investigation in this study are highlighted in yellow, Pro are marked in red.

**Fig. S2.** Representative fluorescence emission spectra of a single-Trp apoA-I variant (L144W) in the lipid-free and lipid-associated (7.8 and 9.6 nm rHDL) states.

**Fig. S3.** Schiffer-Edmunson helical wheel projections of  $\alpha$ 18/5 (top) and  $\alpha$ 11/3 (bottom) pitch (3) of regions 111-128, 133-150, and 157-174. Residues were color coded according to side chain polarities: dark grey for hydrophobic, white for polar and uncharged, and pink for charged residues. The orientation of the amphipathic wheels was solely based on clustering of hydrophobic residue on a sector of the wheel. The apolar and polar solvation space were color-coded yellow and blue, respectively.

## SUPPLEMENTAL REFERENCES

1. Andrews, A. L., Atkinson, D., Barratt, M. D., Finer, E. G., Hauser, H., Henry, R., Leslie, R. B., Owens, N. L., Phillips, M. C., and Robertson, R. N. (1976) Interaction of apoprotein from porcine high-density lipoprotein with dimyristoyl lecithin. 2. Nature of lipid-protein interaction, *Eur J Biochem* 64, 549-563.
2. Segrest, J. P., Jones, M. K., De Loof, H., Brouillette, C. G., Venkatachalapathi, Y. V., and Anantharamaiah, G. M. (1992) The amphipathic helix in the exchangeable apolipoproteins: a review of secondary structure and function, *J Lipid Res* 33, 141-166.
3. Segrest, J. P., Jones, M. K., Mishra, V. K., and Anantharamaiah, G. M. (2002) Experimental and computational studies of the interactions of amphipathic peptides with lipid surfaces, in *Peptide-Lipid Interactions*, pp 397-435, Academic Press.

Figure S1

	1	DDPPQSP	7
	8	WDRVKDLATVYVDVLKDSGRDYVSQF	33
	34	EGSALGKQLN	43
Helix 1	44	LKLLDNWDSVTSTFSKLREQLG	65
Helix 2	66	PVTQEFWDNLEKETEGLRQEMS	87
Helix 3	88	KDLEEVKAKVQ	98
Helix 4	99	PYLDDFQKKWQEEMELYRQK <b>VE</b>	120
Helix 5	121	<b>PLRA</b> ELQEGARQ <b>KL</b> HELQ <b>EKLS</b>	142
Helix 6	143	<b>PLGE</b> EMRDRARAHVDALR <b>THLA</b>	164
Helix 7	165	<b>PYSDEL</b> RQRLAARLEALKENGG	186
Helix 8	187	ARLAEYHAKATEHLSTLSEKAK	208
Helix 9	209	PALEDLRQGLL	219
Helix 10	220	PVLESFKVSFLSALEEYTKKLN	241
	242	TQ	243

Figure S2

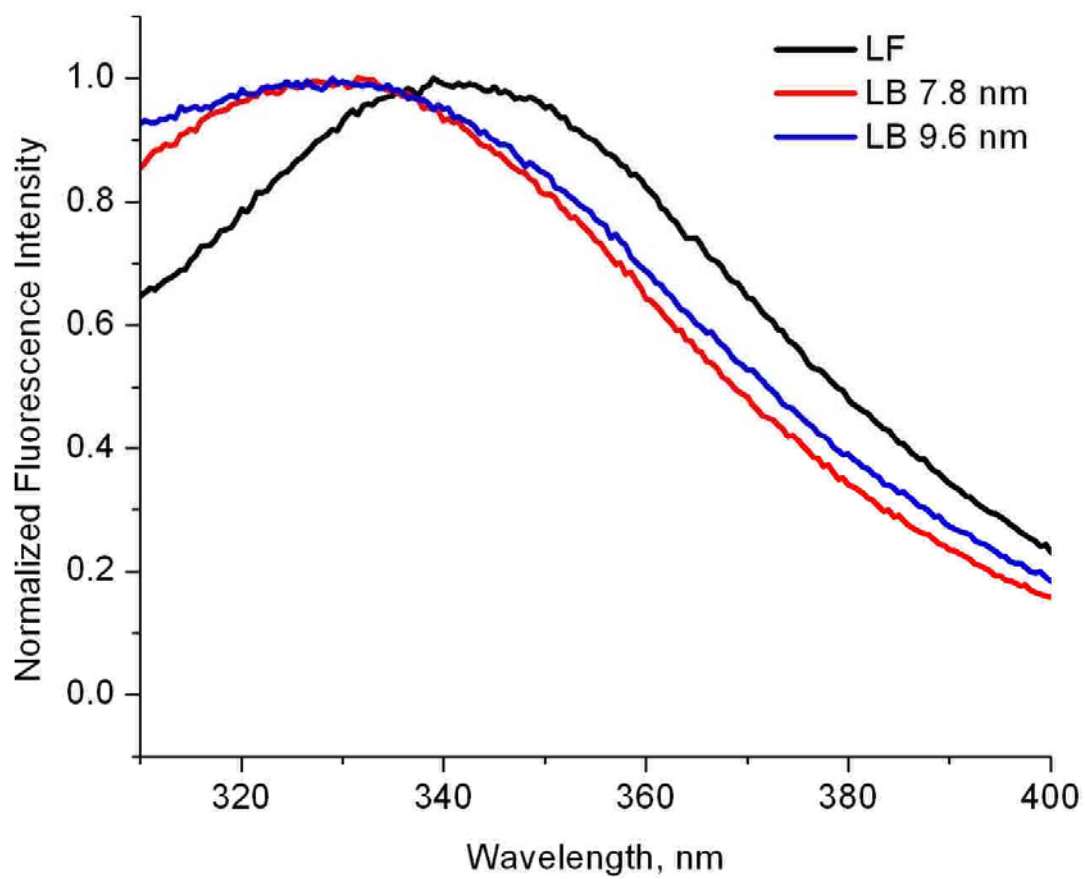


Figure S3

