Supplementary figures

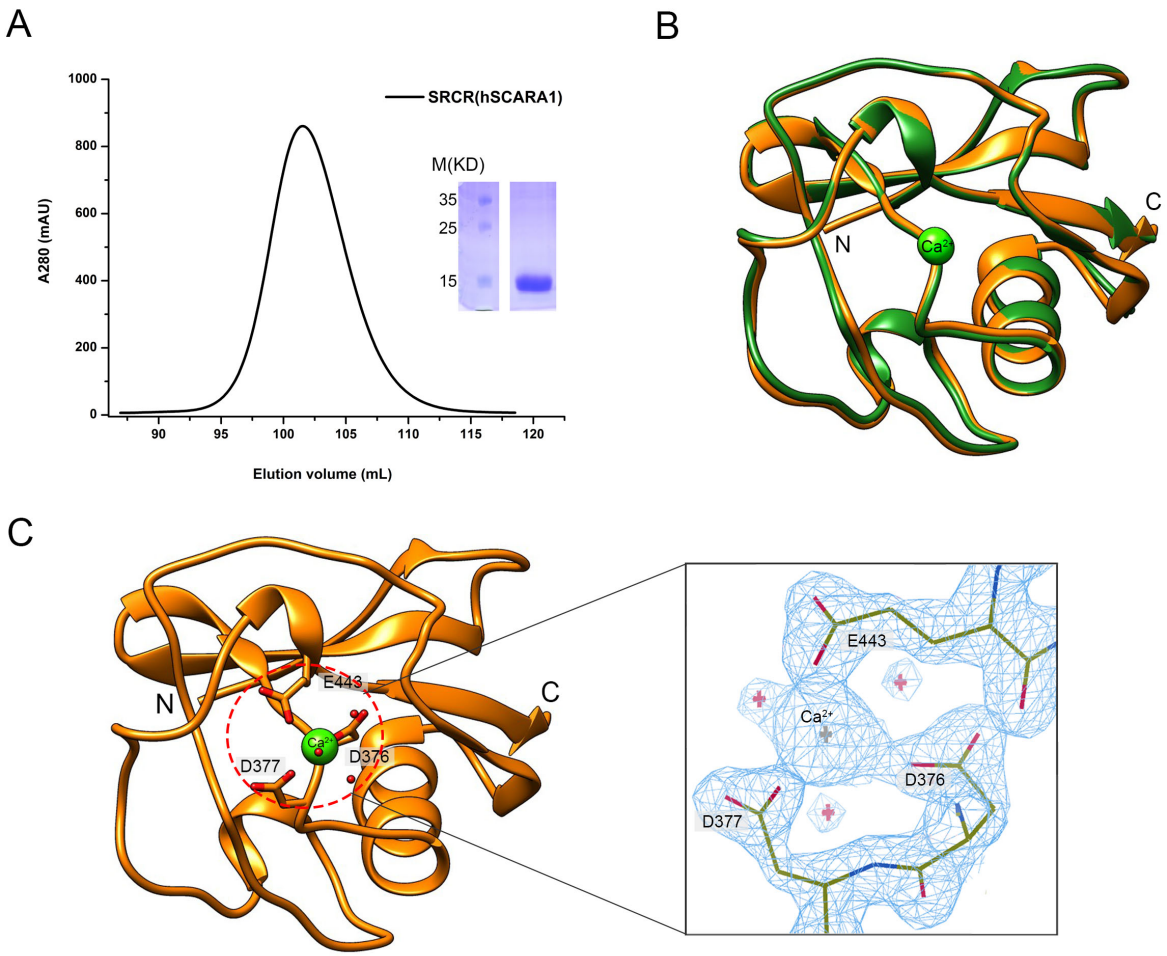

Figure S1. Crystal structure of the SRCR domain of hSCARA1.

(A) The SEC profile and SDS-PAGE of the SRCR domain of hSCARA1.

(B) Superposition of the crystal structures of the SRCR domains of hSCARA1 (orange) and mSCARA1 (green; PDB entry: 6J02). Ca^{2+} is shown as a green sphere.

(C) *Left,* the crystal structure of the SRCR domain of hSCARA1 (orange). Water molecules are shown as small red spheres. *Right,* the electron density of the Ca^{2+} (gray cross) binding site. Water molecules are indicated by red crosses.

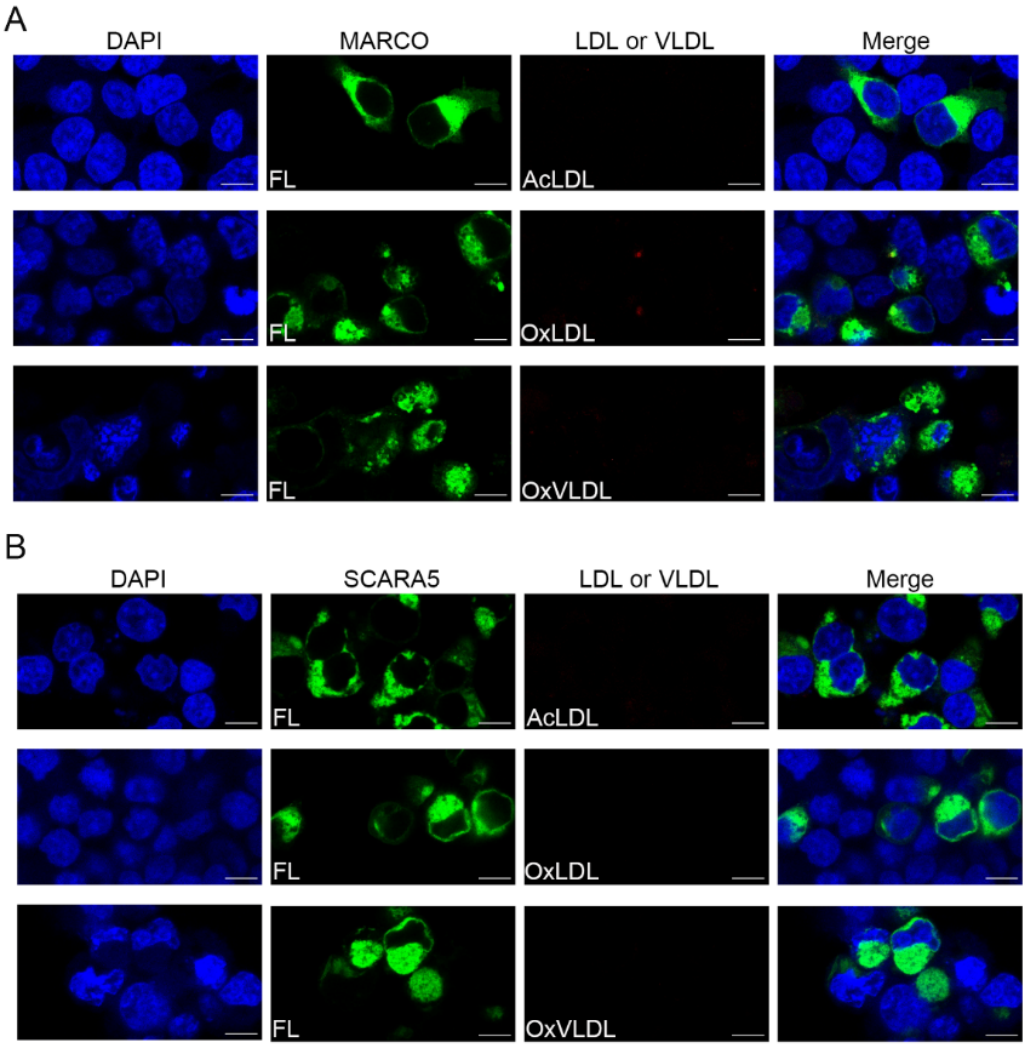

Figure S2. MARCO or SCARA5 does not internalize the modified LDL or VLDL in the presence of EDTA.

(A) Confocal fluorescent images of the hMARCO (with GFP tag) transfected cells incubated with the modified LDL or VLDL in the presence of EDTA (bar, 25 μm).

(B) Confocal fluorescent images of the hSCARA5 (with GFP tag) transfected cells incubated with the modified LDL or VLDL in the presence of EDTA (bar, 25 μm).

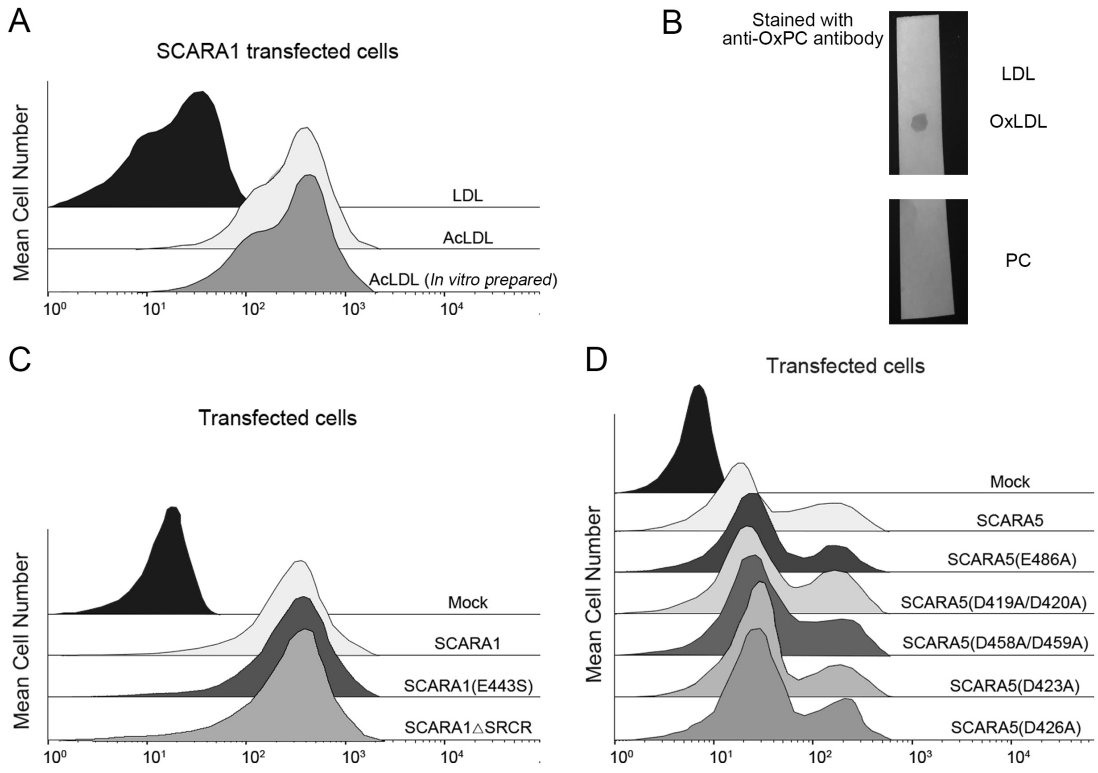

Figure S3.

(A) FACS data of the hSCARA1 transfected cells incubated with the AcLDL prepared *in vitro* as well as the AcLDL isolated from human plasma.

(B) Dot-blot assay showed that OxPC was found on the OxLDL produced *in vitro*, but not on LDL, and could be recognized by anti-OxPC antibody. Unmodified PC was applied as a negative control.

(C) FACS data showed the interactions of anti-SCARA1 antibody with the cells transfected with the wild-type SCARA1, SCARA1(E443S) or SCARA1△SRCR. Mock represents non-transfected cells.

(D) FACS data showed the interactions of anti-SCARA5 antibody with the cells transfected with the wild-type SCARA5, SCARA5(E486A), SCARA5(D419A/D420A), SCARA5(D458A/D459A), SCARA5(D423A) or SCARA5(D426A).

Supplementary Table S1

Table 1. Crystallographic Statistics of the Structure of the SRCR domain of human SCARA1	
Data Collection and Scaling	
Beamline	SSRF BL18U
Wavelength (Å)	0.98
Space group	P 21 21 21
Cell parameters	
a, b, c (Å)	37.03, 57.09, 62.22
a, b, g (°)	90.00, 90.00, 90.00
Resolution (Å)	27.80 – 2.00 (2.07 – 2.00)
R_{merge}	0.091(0.571)
Unique reflections	29312 (9388)
I/ σ (I)	18.3 (4.3)
Completeness (%)	96.8 (95.5)
Multiplicity	4.3 (4.1)
Solvent content (%)	49
Refinement	
R_{work}	0.208(0.223)
R_{free}	0.252(0.158)
Protein atoms	905
Solvent atoms	113 H2O, 1 Ca^{2+}
Validation	
RMSD bonds (Å)	0.006
RMSD angles (°)	0.78
Ramachandran favored (%)	98.0
Ramachandran outliers (%)	0%

Note: Values in parentheses are for the highest-resolution shell.