

Supplementary figures

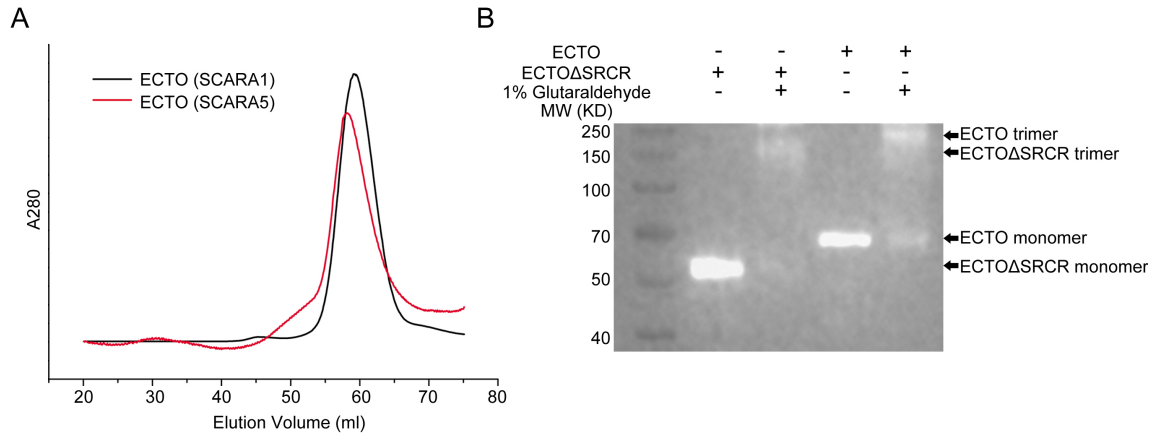


Figure S1. The ectodomain of SCARA5 forms homotrimers.

(A) The SEC profiles of the ectodomains (ECTO) of SCARA5 and SCARA1 had similar elution volumes.

(B) The cross-linked intact ectodomain (ECTO) as well as the ectodomain without the SRCR domain (ECTO Δ SRCR) of SCARA5 run as trimers on SDS-PAGE.

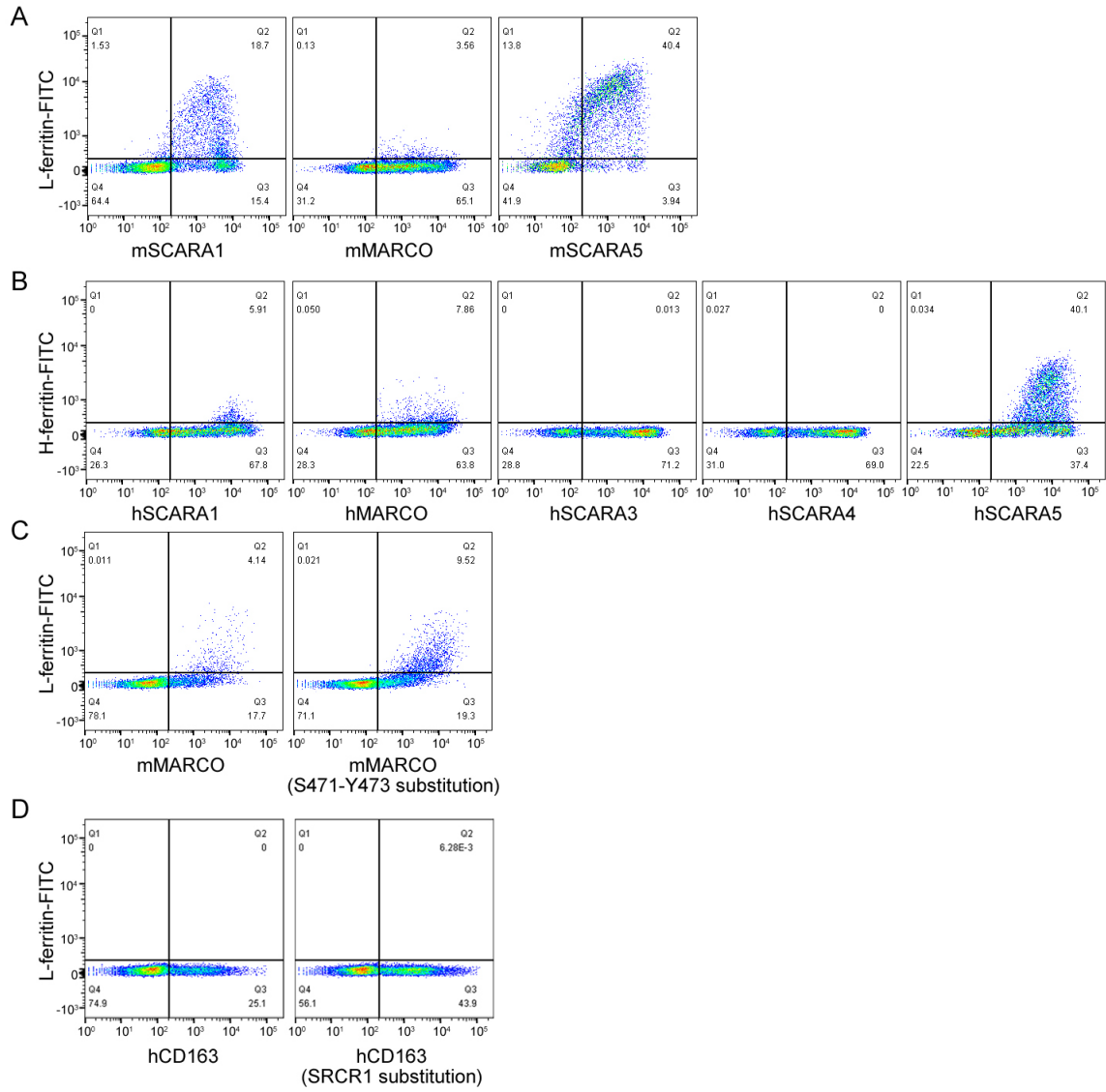


Figure S2. Interactions of the SR-A members with ferritin.

(A) FACS data showed that L-ferritin could bind to the cells transfected with mSCARA5, mSCARA1 or mMARCO, but the binding with mMARCO is much weaker than that of mSCARA5 or mSCARA1.

(B) FACS data showed that H-ferritin could bind to the cells transfected with hSCARA5, hSCARA1 or hMARCO with different affinities, but no binding for the hSCARA3 or hSCARA4 transfected cells.

(C) FACS data showed that when the loop region (S471-Y473) of mMARCO was replaced by the loop (R444-F448) of hSCARA5, it had enhanced interaction with L-ferritin.

(D) FACS data showed that when the N-terminal SRCR domain (SRCR1) of human CD163 was replaced by the SRCR domain of hSCARA5, the chimeric molecule did not show any detectable binding with L-ferritin.

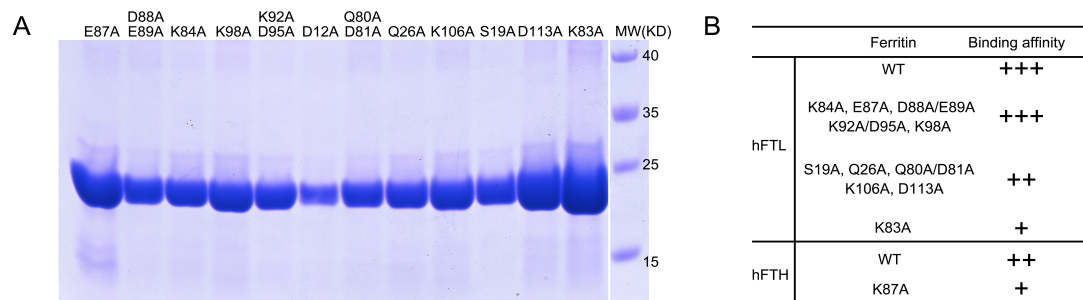


Figure S3. Expression of the ferritin mutants and their binding with SCARA5.

(A) The SDS-PAGE of the L-ferritin mutants after purification.

(B) Binding of the ferritin mutants with SCARA5.

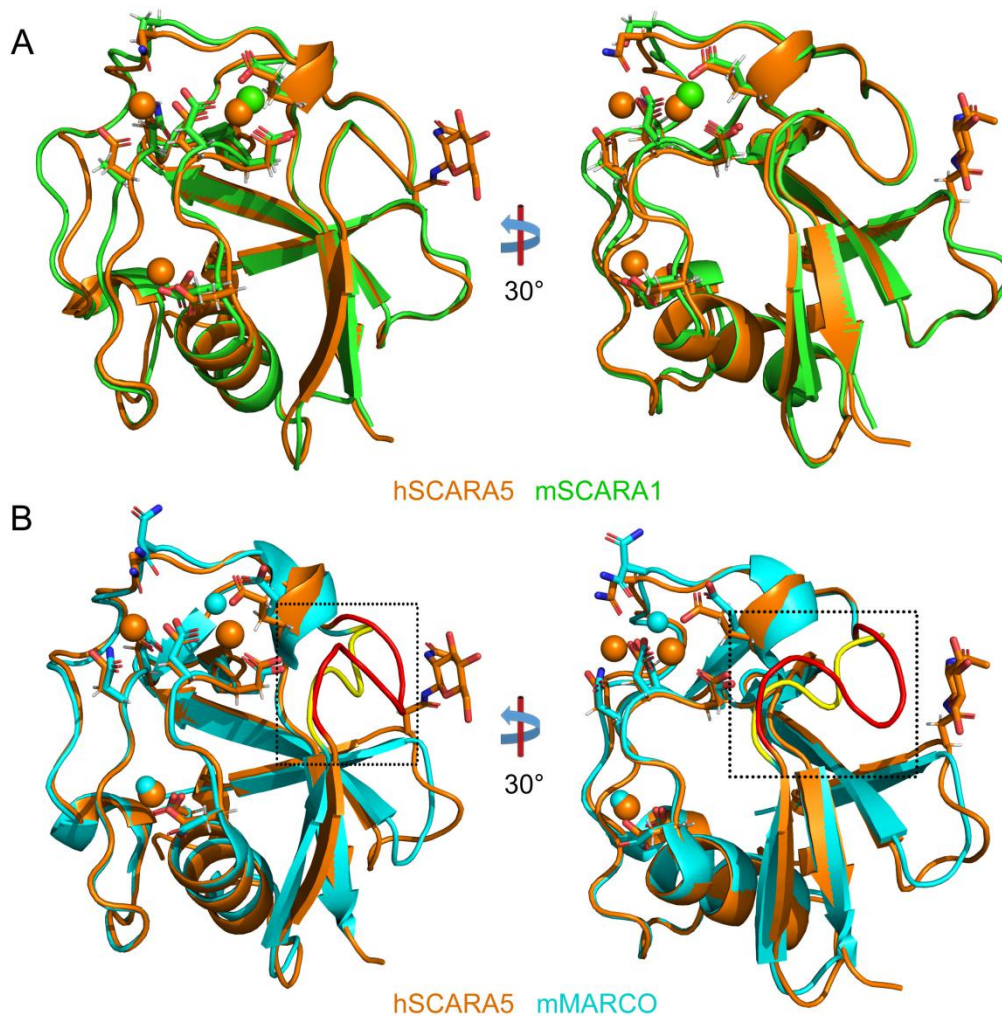


Figure S4. Structural comparison of the SRCR domains of SCARA5, SCARA1 and MARCO.

(A) Superposition of the crystal structures of the SRCR domain of hSCARA5 (orange) and mSCARA1 (green; PDB entry 6J02).

(B) Superposition of the crystal structures of the SRCR domain of hSCARA5 (orange) and mMARCO (cyan; PDB entry 2OY3). The loop regions of SCARA5 (R444-F448, red) and mMARCO (S471-Y473, yellow) are indicated by the dashed black rectangles.

Divalent cations (Ca²⁺ or Mg²⁺) are shown as spheres.

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                                419   420 423 426                444 448 458 459                481   486
human_SCARA5 IRLVNGSGPHEGRVEVYHRRRWGTVCDGWDKKDGDVVCRLMGFRGVAEVYRTARFGQGTGRIWMDVACKGTEETIFRCSFSKWGVTNCGHAEDASVTCT
mouse_SCARA5 IRLVNGSGPHQGRVEVFHRRRWGTVCDGWDKKDGDVVCRLMGFRGVVEVYRTARFGQGTGRIWMDVACKGTESSIFHCQFSKWGVTNCGHAEDAGVTCT
human_MARCO VRLVGS--NRGRAEVYSGTWGTCDDWQNSDALVFCRMLGY-SKGRALYK--GAGTGGIWLNVQCRGTESTLWSCFNKSWGHHDCSHEEDAGVECS
mouse_MARCO VRLMGGT--NRGRAEVYNNWGTICDDWNNDAIVFCRMLGY-SKGRALSS--YGGSSNIWLDNVNCRGTESTLWDCSKNSWGNHNCVINEEDAGVECS
human_SCARA1 VRLVGGSGPHEGRVEILHSGQWGTICDDRWVIRAGQVVCRLSLGYQVLAHVHKAHFQGTGPIWLNVMCFGRESSIEECKIRQWGTACSHSREDAGVTCT
mouse_SCARA1 VRLVGGSGAHEGRVEIFHQQWGTICDDRWDIRAGQVVCRLSLGYQVLAHVHKAHFQGTGPIWLNVMCFGRESSIENCKINQWGLSCSHSREDAGVTCT

Bovine_SCARA5 VRLVNGSGLHQGRVEVYHRRRWGTVCDGWDKKDGDVVCRLMGFRGAEVHRTAQFGQGTGRIWMDVACKGTEESIFRCSFSKWGVTNCGHAEDAGVTCK
Rat_SCARA5 IRLVNGSGPHQGRVEVFHRRRWGTVCDGWDKKDGDVVCRLMGFRGVVEVYRTARFGQGTGRIWMDVACKGTESSIFHCQFSKWGVTNCGHAEDAGVTCT
Bonobo_SCARA5 IRLVNGSGPHEGRVEVYHRRRWGTVCDGWDKKDGDVVCRLMGFRGVVEVYRTARFGQGTGRIWMDVACKGTEETIFRCSFSKWGVTNCGHAEDASVTCT
Sheep_SCARA5 VRLVNGSGPHQGRVEVYHRRRWGTVCDGWDKKDGDVVCRLMGFRGAEVHRTAQFGQGTGRIWMDVACKGTEESIFRCSFSKWGVTNCGHAEDAGVTCK
Cat_SCARA5 IRLVNGSGPHEGRVEVYHRRRWGTVCDGWDKKDGDVVCRLMGFRGVVEVYRTARFGQGTGRIWMDVACKGTEETIFRCSFSKWGVTNCGHAEDAGVTCT
goat_SCARA5 VRLVNGSGPHQGRVEVYHRRRWGTVCDGWDKKDGDVVCRLMGFRGAEVHRTAQFGQGTGRIWMDVACKGTEESIFRCSFSKWGVTNCGHAEDAGVTCK
Horse_SCARA5 IRLVNGSGPHEGRVEVYHRRRWGTVCDGWDKKDGDVVCRLMGFRGAEVSRARFGQGTGRIWMDVACKGTEDTIFRCSFSKWGVTNCGHAEDAGVTCT
elephant_SCARA5 IRLVNGSGPHEGRVEVYHRRRWGTVCDGWDKKDGDVVCRLMGFRSVEVYRTARFGQGTGRIWMDVACKGTEDTIFRCSFSKWGVTNCGHAEDAGVTCT
human_CD163 SRCR2 MRLTRGGNMCGRLEIKFQGRWGTVCDDNFNIDHASVICRQLCCGSAVSFSGSSNFGEGSGPIWFDLINCNGNESALWNCCKHQGWGKHNCDHAEDAGVICS
human_CD163 SRCR3 LRLVDGVTECSGRLEVRFPQGEWGTICDDGWSYDAAVACKQLGCPATAVTAIGRVNASKGFHILWLDVSCQGHPEPAIWQCKHHEWGHKHCNHNEDAGVTCS
human_CD163 SRCR7 LRLVNGGRCAGRVEIYHGGSWGTCDDSWLSDAHVVCRLGCGEALNATGSAHFEGGTGPIWLDKMKCNKESRIWQCHSHGWGQQNCRHKEDAGVICS
human_CD163 SRCR9 IRLQEGFTSCSRVEIWHGGSWGTVCDSDWLDLDAQVVCQQLGCGPALKAFKAEAFQGTGPIWLNVEVKCKGNESLWDCPARRWGHSECGHKEDAAVNCT
human_gp340 SRCR2 LRLVNGGDRCRGRVEVLYRGSWGTVCDDYDTHDANVVCRLGCGWAMSAPGNAQFGQSGPIVLDVVRCSGHESYLWSCPHNGWLTHNCGHSEDAVNTCT

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Figure S5. Sequence alignments of the SRCR domains within the SR-A family among mammals and human CD163. The residues at the Ca²⁺ binding sites and a loop region (444-448 for hSCARA5) are colored in red.