Discovery and in vitro characterization of a human anti-CD36 scFv

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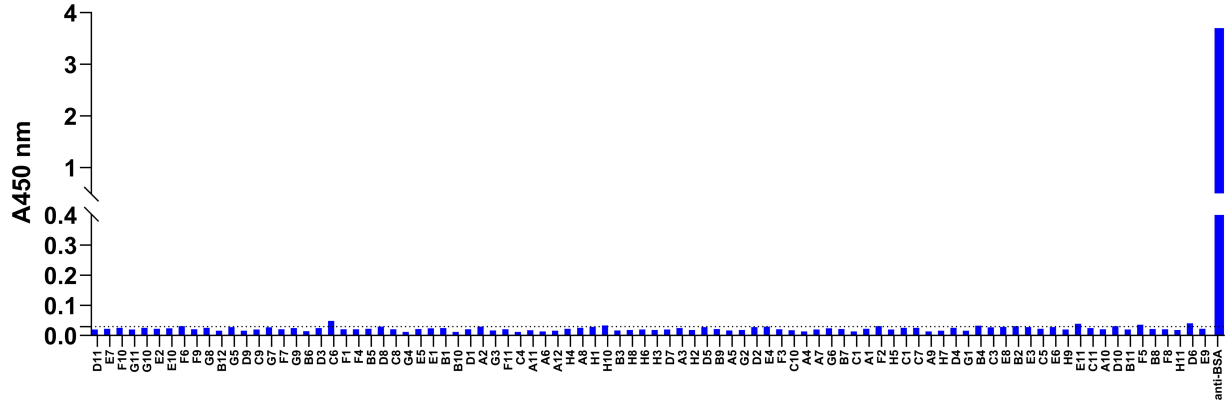
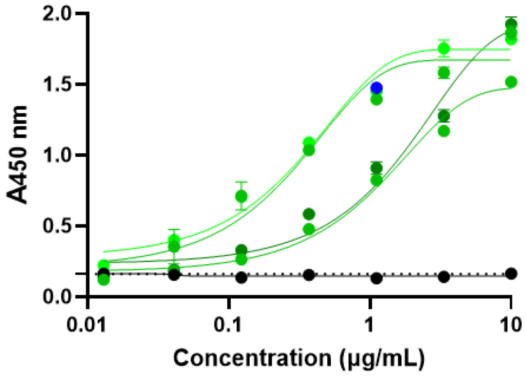
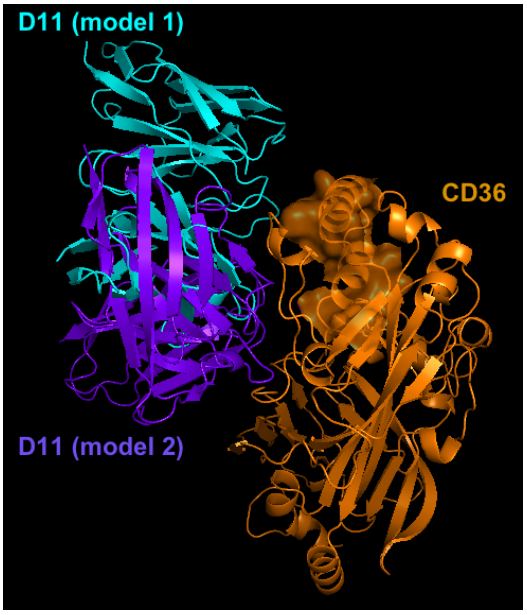
Supplementary Information



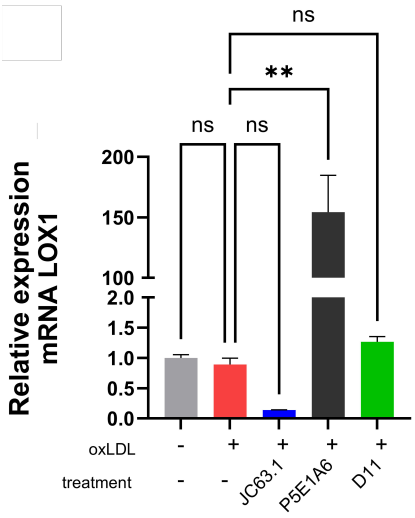
Suppl. Figure 1 Phage ELISA for 90 clones from the third round of panning analyzing the binding to BSA



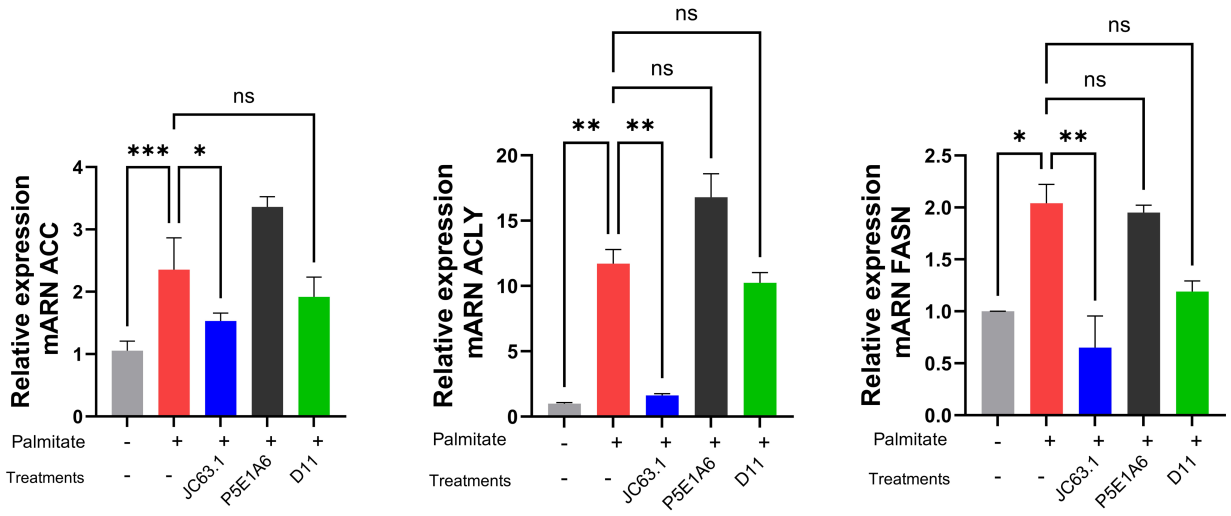
Suppl. Figure 2 Batch-to-batch comparison of the binding of purified scFv D11 to hrCD36 by ELISA



Suppl. Figure 3: Predicted binding modes for D11 on CD36. The D11 antibody was modeled using the SAbPred server (73) and then docked onto CD36 (PDB ID: 5LGD) using the ClusPro software (74) in antibody mode. Two distinct binding models for D11 (cyan and purple) on CD36 (orange) were identified. Analysis of the interacting residues using the Prodigy server (75) revealed that both D11 models interact with a common region of CD36 comprising residues Arg183-Thy202. The oxLDL binding site on CD36 is depicted as a translucent surface



Suppl. Figure 4 RT-qPCR for the quantification of LOX-1 mRNA expression in THP-1 differentiated to foam cells



Suppl. Figure 5 RT-qPCR for the quantification of the indicated mRNAs in HepG2 cells exposed to palmitate

Supplementary Table 1 Primers employed for qPCR.

Primer	*Sequence*	*Reference*
CD36-Forward	GGACATACTTGGATATTGAACC	[52]
CD36-Reverse	ACACCAACACTGAGTAAGAT	
SR-A1-Forward	CCTTTACCTCCTCGTGTTT	
SR-A1-Reverse	TGTTGCTCATGTGTTCCA	
LOX-1-Forward	TCTGACCTCCTAACACAAGA	
LOX-1-Reverse	AGATTCTGGTGGTGAAGTTC	
ACAT1-Forward	CGCTGCTGTAGAACCTATT	
ACAT1-Reverse	CCGTATTCTCCTTGCTTCA	

Supplementary references

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