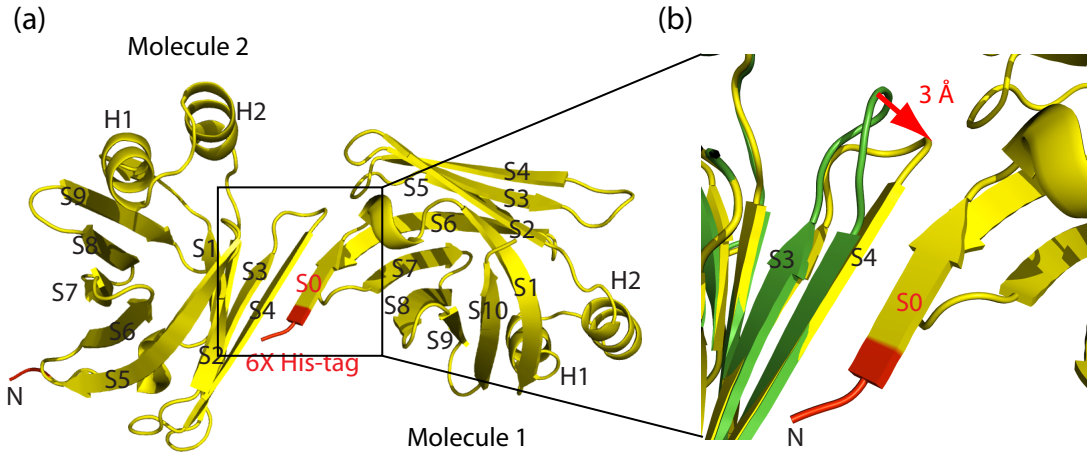
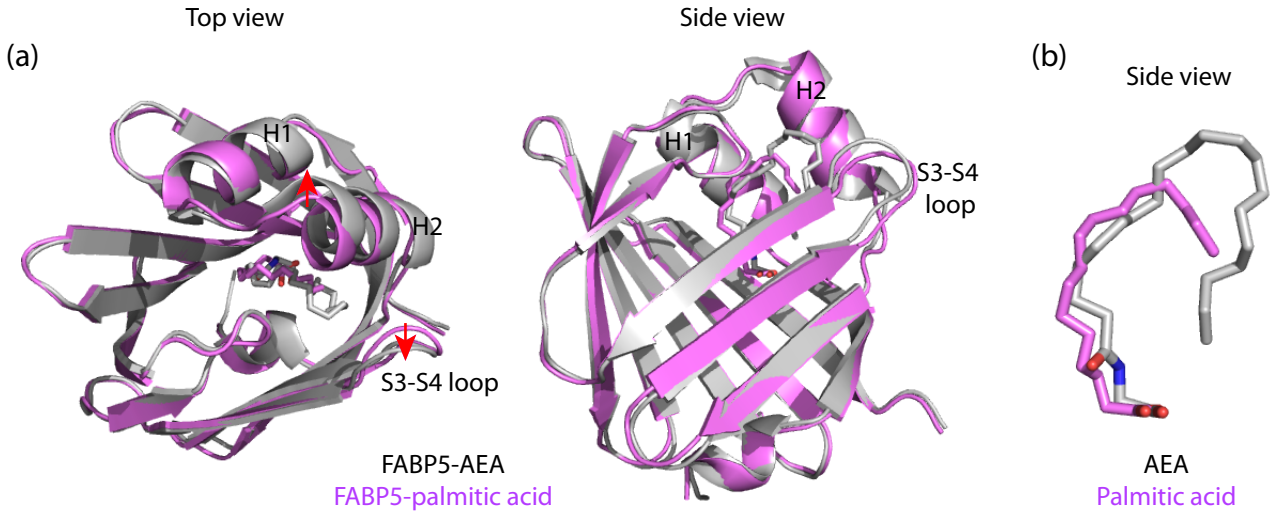
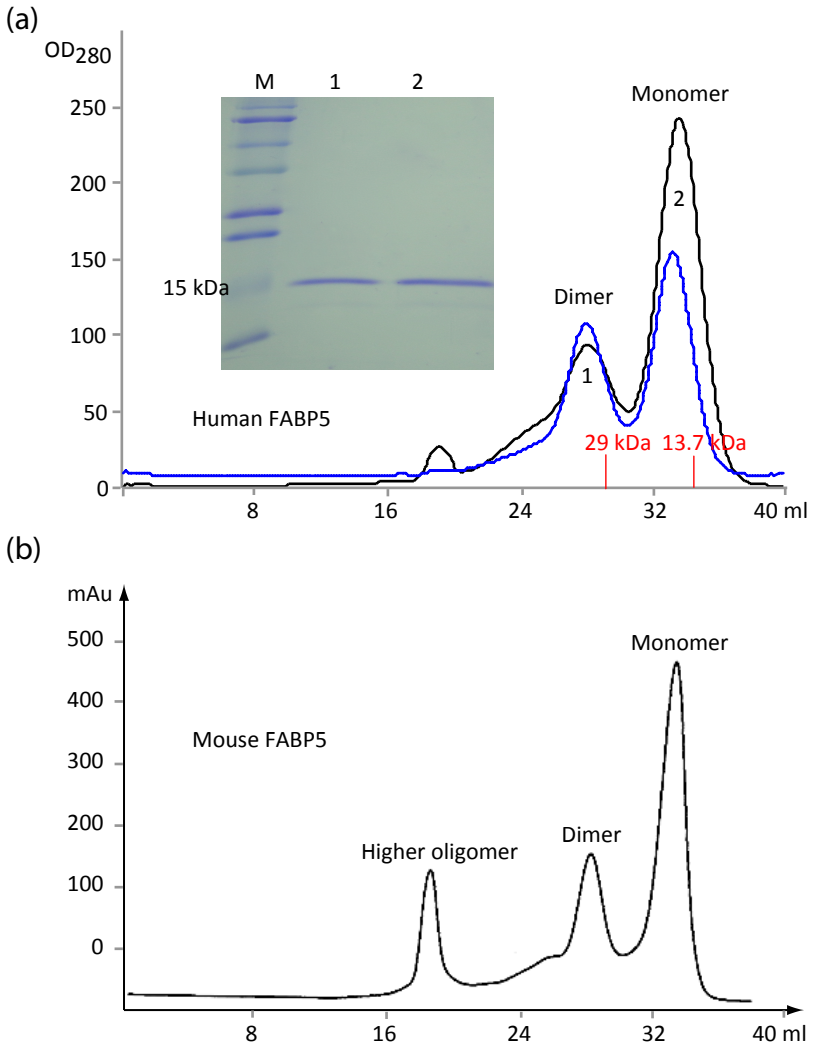


Supplementary fig. 1 (a) The N-terminal 6XHis-tag of the mouse FABP5, together with several N-terminal residues, inserts into the space between S4 and S5, forming a new β-strand (S0) complementing the S4 β-strand of its partner molecule. (b) Close-up view of the boxed region in (a). Insertion of the S0 β-strand of the FABP molecule 1 causes the loop linking S3 and S4 of the FABP molecule 2 to open up, moving outwards by ~3 Å as compared to the monomeric mouse FABP5 shown as a green cartoon. This observation suggests that the β-strands S3 and S4 may be mobile.



Supplementary fig. 2 (a) Superposition of the FABP5-AEA structure (PDB ID 4AZP, grey)) and the FABP5-palmitic acid structure (PDB ID 1B56, violet). The red arrows indicate outward movement of H1-H2 motif and the S3-S4 loop by ~ 1.5 Å - 2.0 Å. (b) The substrates AEA and palmitic acid are shown in an enlarged side view.



Supplementary fig. 3 FABP5 is in a dynamic equilibrium between monomeric and dimeric states. (a) The black curve is the gel filtration profile of the bacterially expressed 6XHis-tag-cleaved human FABP5. This profile shows the coexistence of monomers, dimers, and a smaller amount of higher oligomers. The elution volumes for the protein standards, the bovine ribonuclease A (13.7 kDa) and bovine carbonic anhydrase (29.0 kDa) are indicated by red vertical lines. SDS-PAGE of fractions from peaks 1 and 2 shows that both peaks are FABP5 (Inset). The gel filtration associated to the blue curve was run from the monomeric species (collected from the fractions corresponding to peak 2 in the black curve). Note that the OD280 values (mAU) of the blue curve were multiplied by a factor of 10. (b) The gel filtration profile of the recombinant and 6XHistag-cleaved mouse FABP5 shows the coexistence of monomers, dimers, and higher oligomers in solution.