Movie S1. Structural simulation of non-succinylated Acs. Molecular dynamics simulation of Acs that is not succinylated on lysine 193 or lysine 366.The lysine residues (K193, K366) are shown in sticks model structures.The circular section marks the CoA-binding region that is relatively stable.

Movie S2. Structural simulation of Acs-K193R. Molecular dynamics simulation of Acs that is mutated to R on lysine 193.The K (K366) and R (K193R) residues are shown in sticks model structures. The circular section marks the CoA-binding region that is relatively stable.

Movie S3. Structural simulation of Acs-K366R. Molecular dynamics simulation of Acs that is mutated to R on lysine 366.The K (K193) and R (K366R) residues are shown in sticks model structures. The circular section marks the CoA-binding region that is relatively stable.

Movie S4. Structural simulation of Acs-K193R/K366R. Molecular dynamics simulation of Acs that is mutated to R on lysine 193 and lysine 366. The R residues (K193R, K366R) are shown in sticks model structures. The circular section marks the CoA-binding region that is relatively stable.

Movie S5. Structural simulation of Acs-K193su. Molecular dynamics simulation of Acs that is succinylated on K193.The succinylated K (K193su) and non-succinylated K (K366) residues are shown in sticks model structures. The circular section marks the CoA-binding region that is highly unstable.

Movie S6. Structural simulation of Acs-K366su. Molecular dynamics simulation of Acs that is succinylated on K366. The non-succinylated K193 and succinylated K366su residues are shown in sticks model structures. The circular section marks the CoA-binding region that is highly unstable.

Movie S7. Structural simulation of Acs-K193su/K366su. Molecular dynamics simulation of Acs that is succinylated on K193 and K366. The succinylated K residues (K193su, K366su) are shown in sticks model structures. The circular section marks the CoA-binding region that is highly unstable.