Helix-formation Due to the Binding of *α*- with *β*$_2$-subunit of Tryptophan Synthase

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When the tryptophan synthase α- and β_2-subunits combine to form the $\alpha_2\beta_2$ complex, the enzymatic activity of each subunit is stimulated by one to two orders of magnitude. In order to elucidate the structural basis of this mutual activation, it is necessary to determine the structures of the α- and β-subunits alone and together with the $\alpha_2\beta_2$ complex. The crystal structures of the tryptophan synthase $\alpha_2\beta_2$ complex from *S. typhimurium* (*St*$\alpha_2\beta_2$) has been reported. Therefore, we determined the crystal structure of the tryptophan synthase α-subunit alone from *E. coli* (*Ec*α) at 2.3Å resolution. The biggest difference between the structures of the *Ec*α and the α-subunit in the *St*$\alpha_2\beta_2$ (*St*α) was as follows. The helix-2' in the *St*α including an active site residue (Asp60) changed to a flexible loop in the *Ec*α. The conversion of the helix to a loop resulted in collapse of the correct active site conformation. This region is also an important part for the mutual activation in the *St*$\alpha_2\beta_2$ and interaction with the β-subunit. These results suggest that the formation of helix-2' essential for the stimulation of the enzymatic activity of the α-subunit is constructed by the induced-fit mode involved in conformational changes upon interaction between the α- and β-subunits.

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