

Functional and structural study of the glucose metabolism protein Fructose biphosphate aldolase in anaerobic bacteria *Desulfovibrio gigas*.

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Abstract

Glycolysis is the first process of sugar metabolism, with sequence of ten enzyme-catalyzed reactions, glucose ($C_6H_{12}O_6$) is converted to pyruvate ($CH_3COCOO^- + H^+$), the free energy which is released in the process can form the high energy molecule ATP (adenosine triphosphate) and NADH (reduced nicotinamide adenine dinucleotide).

The fourth step of glycolysis, Fructose biphosphate aldolase can cleavage the carbon-bond of Fructose-1,6 biphosphate to G3P(glyceraldehyde 3-phosphate) and DHAP (Dihydroxyacetone phosphate).

Fructose biphosphate aldolase (FBPA, FBA or Aldolase) could be divided to three types: FBPA I, FBPA IA and FBPA II. FBPA I and FBPA IA will produce side product Schiff Base in glycolysis, and FBPA I exists in Eukaryote, the protein structure usually be homotetramer, FBPA IA exists in bacteria and archeal, the structure usually be homodecamer (two identical pentamer). FBPA II will coordinate with metal ion, such as iron and Zinc, exist in bacterial and fungi. These three groups have the structure of $(\beta\alpha)_8$ barrel fold (TIM barrel).

FBPA exist in organism widely, and could be the evolutionary tool. In our lab, we can express and purify anaerobic bacteria. While studied the membrane protein in electron transfer pathway, also got the high purity FBPA protein, and we interest the structure and functional residue of FBPA.

Desulfovibrio gigas belongs to Sulfate-Reducing Bacteria also be anaerobic bacteria, depends on fermentation of anaerobic respiration, reducing sulfate to H_2S and S^{2-} and got nutrient to survive. Because of the special survive condition and metabolism pathway, we interest the structure and functional residue of FBPA, and we have the initial structure from the crystallography, and it shows pentamer shape under electron microscopy.

Function residues Lysine-177(K), Tyrosin-146(Y) and Aspartate-24(D) conserved in *Desulfovibrio gigas*, but the hydrophobic hole and continuous stacking residue still unknown, the future work is to determine the other function residues, and find their function in the metabolism pathway.

Keywords: Fructose biphosphate aldolase, anaerobic bacteria, Glycolysis, Fructose-1,6 biphosphate, G3P(glyceraldehyde 3-phosphate), DHAP (Dihydroxyacetone phosphate).