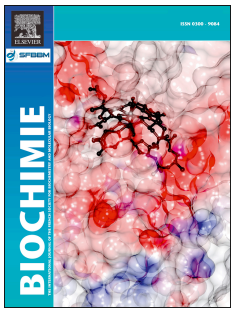
Accepted Manuscript



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PII: S0300-9084(16)30166-3

DOI: 10.1016/j.biochi.2016.08.013

Reference: BIOCHI 5047

To appear in: *Biochimie*

Received Date: 26 December 2015

Accepted Date: 29 August 2016

Please cite this article as: P. Villalobos, F. Soto, M. Baez, J. Babul, Regulatory network of the allosteric ATP inhibition of *E. coli* phosphofructokinase-2 studied by hybrid dimers, *Biochimie* (2016), doi: 10.1016/j.biochi.2016.08.013.

Regulatory network of the allosteric ATP inhibition of *E. coli* phosphofructokinase-2 studied by hybrid dimers

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Abstract

We have proposed an allosteric ATP inhibition mechanism of Pfk-2 determining the structure of different forms of the enzyme together with a kinetic enzyme analysis. Here we complement the mechanism by using hybrid oligomers of the homodimeric enzyme to get insights about the allosteric communication pathways between the same sites or different ones located in different subunits. Kinetic analysis of the hybrid enzymes indicate that homotropic interactions between allosteric sites for ATP or between substrate sites for fructose-6-P have a minor effect on the enzymatic inhibition induced by ATP. In fact, the sigmoid response for fructose-6-P observed at elevated ATP concentrations can be eliminated even though the enzymatic inhibition is still operative. Nevertheless, leverage coupling analysis supports heterotropic interactions between the allosteric ATP and fructose-6-P binding occurring between and within each subunit.