

# Structural studies of hGBP1 helical domain ( $\alpha 7$ - $\alpha 13$ )

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The INF- $\gamma$  inducible guanylate binding proteins (GBP) belongs to the family of large GTP - binding proteins including Mx and dynamin. GBP1 plays an important role in the host defense against intracellular pathogens<sup>(1)</sup>. The common property of hGBP's is the ability to undergo oligomerization as a function of GTP binding and hydrolysis. Structurally the human GBP1 full length is composed of a LG (Large G) domain and an elongated  $\alpha$ -helical domain<sup>(2)</sup>. Binding of GTP induces the formation of dimers interacting at the LG-domains, whereas in the presence of GDP.AIF\*, this protein is able to form tetramers<sup>(3)</sup>. The interaction of the LG-Domains within this complex is well characterized by various biochemical experiments and the X-ray structure shows it as a dimer<sup>(4)</sup>.

The aim of this study is to elucidate the complex formation using the helical part of this protein as the second interaction domain. Therefore, we have determined the three-dimensional structure of hGBP1 helical domain ( $\alpha 7$ - $\alpha 13$ ) by solving the X-ray structure at 2.5Å resolution. We found out that the isolated helical domain ( $\alpha 7$ - $\alpha 13$ ) is able to form dimers in the crystal structure, as well. Furthermore, as the full length structure shows back folding of helix  $\alpha 13$  our new data of the  $\alpha 7$ - $\alpha 13$  helical domain indicates structural changing by an elongation of helices  $\alpha 12$  and  $\alpha 13$ .

## References:

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