## Crystal Structure of a Glycyl Radical Enzyme from *Archaeoglobus fulgidus*

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We have solved the crystal structure of a PFL2 from Archaeglobus fulgidus at 2.9 Å resolution. Of the two previously solved enzyme structures of PFL-family, pyruvate formate lyase and glycerol dehydratase, the latter is clearly more similar to our model. In our structure we have a glycerol molecule bound to the active site, which, however, is bound in a different orientation than in glycerol dehydratase, due to the changes in the residues forming the binding site. However,the active site of PFL2 is so similar to that of glycerol dehydratase, that it is likely to catalyze, not the same, but perhaps a very similar reaction.

Crystal packing, small angle scattering and ultaracentrifugation experiments show that PFL2 is a tetrameric protein in contrast to our earlier result indicating trimeric arrangement [1]. This higher oligomeric state is one of the explanations for the thermostability of the enzyme.

[1] Lehtio L., Goldman A., *Protein Eng Des Sel*, 2004, **17**, 545. Keywords: pyruvate formate lyase, glycerol dehydratase, glycyl radical