M. Tuberculosis Rv0216: Unknown, Now Known?

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Only about half of the *M. tuberculosis* genes identified as being important for *in vivo* growth have any biochemical function assigned to them. The structure of one of the unknown proteins, Rv0216, was recently determined to a resolution of 1.9Å using multiple-wavelength anomalous dispersion from a SeMet-substituted protein.

Rv0216 features two almost identical subunits packed to form a double hotdog fold with a large 10-stranded beta sheet, remotely similar to e.g. the functional dimers of bacterial and eukaryotic hydratases and dehydratase/isomerases.

A deep crevice between the two subunits is lined with residues that are highly conserved in homologous proteins within the Mycobacteriaceae family. This potential active site also shares some structural similarity to the enoyl-CoA hydratases. The counterpart to the catalytic dyad of the hydratases, consisting of a histidine and an aspartate, is in the Rv0216 case a histidine and an asparagine, suggesting a different enzymatic activity. Modelling studies indicate that Rv0216 might have a substrate similar to the crotonyl-CoA of the enoyl hydratases.

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