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Hydrophobins are small proteins, about 100 amino acid residues in size, secreted by filamentous fungi. They are characterized by eight conserved cysteine residues in the sequence and their ability to change the character of a surface by spontaneous self-assembly on a hydrophobic-hydrophilic interface. Hydrophobins are also among the most surface-active biomolecules known. The biological properties of hydrophobins have been studied widely but the molecular bases of their function has remained largely unknown in lack of a three-dimensional structural model.

We have determined the crystal structure of *Trichoderma reesei* hydrophobin HFBII to an atomic resolution of 1.0 Å [1], [2]. The structure is novel, containing four antiparallel β-stands and an α-helix. The β-stands form a small barrel, inside which two of the four disulfide bridges are located. The remaining bridges connect the N-terminal loop and the α-helix to the β-barrel. A flat, hydrophobic patch is found on the surface of the protein giving rise to the amphiphilic nature of the molecule. In the crystal structure, two hydrophobin molecules pack together, partly concealing the hydrophobic patches in between them. This makes HFBII, in spite of its name, quite water-soluble.

Solving the structure of hydrophobin HFBII has changed conceptions about these proteins dramatically. Hydrophobins were stated to be largely unstructured in solution and thought to function through large conformational changes, which seems unlikely in the light of the determined structure, which is quite compact. Also the assumption of the cysteines forming disulfide bridges consecutively was found incorrect. These findings underline the importance of experimental structure determination.

[1] Hakanpää J., Paananen A., Askolin S., Nakari-Setälä T., Parkkinen T., Penttilä M., Linder M.B., Rouvinen J. (2004) *J. Biol. Chem.***279** 534-539

[2] Hakanpää J., Parkkinen T., Hakulinen N., Linder M. B., Rouvinen J. (2004) *Acta Cryst.* D**60** 163-165