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Report:

The fungal flavocytochrome cellobiose dehydrogenase (CDH) participates in lignocellulose degradation with a proposed role in the early events of wood degradation. The 755-residue protein consists of a *b*-type cytochrome linked to a large FAD-binding domain which can be separated proteolytically to yield the individual proteins. CDH oxidizes cellobiose to cellobiono-1,5-lactone with the concomitant reduction of FAD. Reducing equivalents are then transferred to the cytochrome domain, and subsequently to an external electron acceptor. CDHs belong to either of two distinct groups, type-1 or type-2, that differ substantially in terms of association mode of the two domains, and in the mode of binding to the insoluble substrate (lignocellulose).

We have reported the structures of the two domains of the type-1 CDH from *Phanerochaete chrysosporium*. The structure of the CDH cytochrome revealed a for cytochromes unusual fold: a fibronectin-like β -sandwich with the protoheme bound on the surface at one face of the β -core. Moreover, a unique Met-His ligation of the *b*-type heme, *i.e.*, a near-perpendicular arrangement of the Fe ligands, was found. To investigate structural differences between the two CDH groups, the CDH cytochrome of type-2 from *Humicola insolens* has been solved. The structure was determined by MIRAS (one Hg derivative), and is now being refined at 2.0 Å resolution. Although the flavin-domain structure of *H. insolens* is yet to be

determined, the cytochrome structure itself provided important information about the different mode of association between cytochrome and flavin domain in a type-2 CDH.