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Crystal Structure of a New Type of NADPH-Dependent Quinone Oxidoreductase YtfG from *Escherichia coli*

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Escherichia coli YtfG, catalyzing reduction of *p*-benzoquinone, is a new type of soluble NAD(P)H-dependent quinone oxidoreductase with distinct primary sequence and oligomeric conformation from previously known quinone oxidoreductases. The crystal structures of both native YtfG and YtfG-NADPH complex reveal that YtfG belongs to the short-chain dehydrogenase/reductase (SDR) family and consists of two domains: N-domain and C-domain. The N-domain adopting the Rossmann fold provides platform for the binding of NADPH, and the C-domain, containing a hydrophobic pocket connected to the NADPH-binding site, appears to play important roles in the substrate binding. Tyr140 and Asn143 near the NADPH-binding site have been identified as putative catalytic residues from the structural and mutational analyses. Moreover, the disappearance of several enzymes implicated in the carbon metabolism in the *ytfG*-overexpressed strain and the growth retardation of the strain suggest that YtfG could play some physiological roles beyond the quinone reducing activity.