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The Structures of Two Homologs from *Agrobacterium tumefaciens* Show a Ferrodoxin-Like Split βαβ Fold. H. Axelrod, M.Miller, C. Rife, [1]The Joint Center for Structural Genomics, [2]SSRL, Stanford Univ., Menlo Park, CA.

The x-ray crystal structures of two homologous proteins, NP_356512 and NP_396154, from the soil bacterium *Agrobacterium tumefaciens* have been determined at resolutions of 1.5 Å (R_{value}=15.1%, R_{free}=17.7%) and 2.4 Å (R_{value}=18.6%, R_{free}=24.4%) respectively. Both homologs show amino acid sequence similarity to the nipsnap1 protein from the human and mouse genomes. The two structures reported here provide additional examples of a ferrodoxin-like split βαβ fold, a topology similar to that recently reported for quinol monoxygenase from *E. coli* (PDB ID 1R6Y) and ActVa-Orf6 polyketide from *Streptomyces coelicor* (PDB ID 1LQ9). In the structures from *E. coli* and *S. coelicor*, two α-helices arch over a β-sheet to form a cavity for substrate binding. A comparison of the *A. tumefaciens* structures with those from the other species show that the active site residues are not strictly conserved. This suggests a different function and/or substrate specificities for the *A. tumefaciens* homologs.

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