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Crystal Structure of Penicillin Binding Protein 4 (dacB) from *Escherichia coli*, Both in the Native Form and Covalently Linked to Various Antibiotics. Hiroyuki Kishida, Satoru Unzai, Jeremy R.H. Tame and Sam-Yong Park, Protein Design Laboratory, Yokohama City Univ., Suehiro 1-7-29, Tsurumi-ku, Yokohama 230-0045, Japan.

The crystal structure is presented of penicillin binding protein 4 (PBP4) from *Escherichia coli*, a bifunctional enzyme with both DD-endopeptidase and DD-carboxypeptidase activity. PBP4 is one of 12 penicillin binding proteins in *E.coli* involved in the synthesis and maintenance of the cell wall. The model contains a penicillin binding domain similar to known structures, but includes a large insertion which folds into domains with unique folds. The structures of the protein covalently attached to five different antibiotics presented here show the active site residues are unmoved compared to the apo protein, but nearby surface loops and helices are displaced in some cases. Movement of conserved residues suggests a possible cause for the slow deacylation rate of PBP4.