β-lactamases are enzymes which bacteria have acquired as a defence against β-lactam antibiotics. The crystal structure of a class B β-lactamase from *Staphylococcus aureus* PC1 has been determined at 3.0 Å resolution, and refined at 2.5 Å resolution. The structure determination employed three rather low quality heavy atom derivatives, and solvent flattening of the resulting electron density map. The molecule consists of two closely associated domains with a novel folding topology. One domain is formed by a five stranded antiparallel 8-sheet, and three helices that pack against one face of the sheet. The second domain packs against the second face of the sheet, and is mostly helical. The completely buried nature of the 8-sheet is unusual for an antiparallel structure. The helical domain can be regarded as an insert in the middle of the sheet containing domain, such that the latter domain is formed by the N- and C-termini of the sequence. In the helical domain, a central helix is surrounded by five other helices. The second domain packs against the second face of the sheet. There was one molecule per asymmetric unit. 

Two heavy atom derivatives (K₃PtCl₆ and K₂HgI₄) were prepared by soaking, A 2.9 Å electron density map calculated with double isomorphous replacement was tentatively interpreted. The molecule has an ellipsoidal shape with approximate dimensions of 40x35x30 A. A crevice (10 A in diameter) running through the molecule separates it into two domains. The active site may be in the vicinity of the crevice which is large enough to bind substrate. The detailed structure is in progress.

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