CRYSTAL STRUCTURE OF THE RECOMBINANT PEPTIDE AMIDASE FROM STENOTROPHOMONAS MALTOPHILIA

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In vitro the peptide amidase from Stenotrophomonas maltophilia selectively hydrolyses C-terminal amides of peptides, but not amides in the side chains of glutamine or asparagine. The cellular function of the peptide amidase is not known. Sequence analysis showed, that the peptide amidase belongs to an amidase signature family. Here we present the first native and complexed X-ray structures from this family. The crystal data were collected at beam line ID14-1 of the ESRF (Grenoble, France) tuned to a wavelength of 0.931 Å using a MAR-CCD detector . The crystals belong to the monoclinic space group $P2_1$, with unit-cell parameters around a = 74.18 Å, b = 62.60 Å, c = 101.91 Å and $\beta = 90°$. The amidase consists of 507 amino acids and the molecular weight is 53.9 kDa. The native structure was solved by multiple isomorphous replacement with anomalous scattering. The 1.4 Å native structure was used as a starting model in the refinement of the complex chymostatin-amidase at a resolution of 1.8 Å.