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**Phasing and Modeling of Large Structures with Se-SAD - Crystal Structure of Deblocking Aminopeptidase.**

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Structure of deblocking aminopeptidase (DAP) from *B. cereus* was solved as part of Midwest Center for Structural Genomics project. DAP from *B. cereus* is a 349 amino acids protein that assembles into large multi-subunit structure. The Se-Met labeled crystals were obtained that belong to R3 rhombohedral space group (a=240.9 Å, b=240.9 Å, c=294.8 Å). An asymmetric unit contained sixteen molecules corresponding to 5,584 residues (632 kDa) with 112 potential Se sites. The SAD (0.9794 Å) data set to 2.65 Å was collected at 19-ID beamline and phased with HKL2000-PH. Auto-chain tracing failed using conventional programs. The initial model was built manually and refined to R=19.4 % (R<sub>free</sub>=26.4 %). Final structure has one dodecamer and 1/3 of another dodecamer/A.U. The biological unit resembles tetrahedral aminopeptidase. This is the largest protein structure/A.U. solved by Se-SAD among PDB-deposited coordinates. Details assembly and function will be presented.

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