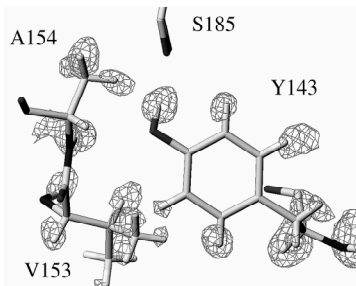


## E0028

**High Resolution Crystal Structure of a Putative Bacterial Lysozyme from *Bacillus stearothermophilus*.** G. Minasov<sup>1</sup>, J.S. Brunzelle<sup>1</sup>, L. Shuvalova<sup>1</sup>, S.F. Moy<sup>2</sup>, F.R. Collart<sup>2</sup>, W.F. Anderson<sup>1</sup>, <sup>1</sup>Northwestern Univ. Feinberg School of Medicine, Dept. MPBC, Chicago, IL USA, <sup>2</sup>Argonne National Laboratory, Biosciences Division, Argonne, IL USA.

The **RBSTP1166** protein consists of 216 amino acids and related sequences appear to occur in a very small range of species. A BLAST search against the sequences of proteins in the PDB did not show significant similarity with any known proteins. The protein was expressed, purified and crystallized. The native crystals belong to  $P2_12_12_1$  space group with unit cell parameters 41.0, 70.6, 74.0, 90.0, 90.0, 90.0 and diffracted to 1.0Å. The N-terminal methionine is the only one in the sequence and Se-Met enzyme crystals did not give detectable signal at the Se edge. The structure was solved by SIRAS using a 2.5Å data set collected on a crystal soaked in platinum nitrate. Three Pt sites were refined in SHARP (FOM 0.31) and phases were modified by SOLOMON (FOM 0.76). ARP/wARP traced 213 residues. The R-factor (R-free) of the SHELX97 refined model is 10.2% (13.5%).



Preliminary structural comparisons suggest the protein may be a lysozyme. Details of the DALI search result as well as possible relationship with known enzymes will be presented.

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