nucleotide base that is specifically cleaved during catalytic activity. The unit cell dimensions of these crystals are; a = 48.4 b = 44.5 c = 137.4A and beta = 94.5 deg., showing a significant change in the beta angle. Diffraction data collected on a RAXIS IIC system has a Rm value of 6.4% to 2.2A for the space group $P2_1$. We have solved the structure of the complex using MR, and the current R-factor is 21%. Difference electron density for the nucleotide is seen in the active site region. The refined structure of the complex, and a comparison with the native structure will be reported.

PS04.01.99 X-RAY STRUCTURE OF GELONIN AND GELONIN-AMP COMPLEX. M. V. Hosur, Bindu Nair, P. Satyamurthy, S. Misquith*, A. Surolia*, K. K. Kannan, Solid State Physics Division, B. A. R. C., Bombay-400085, *Molecular Biophysics Unit, I. I. Sc., Bangalore-560012 India

Ribosome Inactivating Proteins (RIPs) are applications in the treatment of cancer and AIDS. Detailed structure at the atomic level of RIP's and their substrate complexes are needed to understand the molecular mechanism of their immunotoxicity and N-glycosidase activity. Gelonin, is a type I RIP isolated from seeds of the plant Gelonium multiflorum. Single crystals of gelonin, grown using PEG4000, belong to the space group $P2_1$, with a=49.4 Å, b=44.9 Å, c=137.4 Å and beta=98.4 deg. There are two molecules of gelonin in the asymmetric unit, and these are related by a non-crystallographic two fold symmetry axis. X-ray diffraction data collected to 1.8A resolution limit has a Rm value of 7.3%. We have recently solved and refined this structure of Gelonin (J. Mol. Biol. (1995) 250, 368-380). We have soaked for 72 hours crystals of native gelonin into a solution containing 0.1M Tris buffer of pH 8.5, 23% PEG4000 and saturated amounts of AMP, which is the