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**Crystal Structure of trp Aporepressor Point Mutant Leu-->Phe 75**
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**Beamline: X12C**

**Introduction:** The L75F trp repressor (TrpR) point mutation confers a temperature-sensitive repression phenotype, and displays global biophysical changes not expected for a simple hydrophobic residue substitution (1). The crystal structure of the mutant was determined in order to investigate the structural basis for these changes.

**Methods and Materials:** Thin plate like crystals of L75F Trp-apo repressor were grown by vapor diffusion over a reservoir of 30% PEG4000, 100mM Tris pH 8.5, and 200mM MgCl2. Crystals trays were transported to the NSLS and transferred to a single solution of cryoprotectant containing the above components plus 20% glycerol for about 30 seconds, then flash cooled to 100K on a nitrogen cryostream. The wavelength of incident radiation was set to 1.0 Angstrom.

**Results:** The crystals were determined to have space group symmetry P2(1) and unit cell dimensions of a=36, b=54 c=56 Angstrom, beta=100°, with one biological dimer per asymmetric unit. Native diffraction data were collected from a single crystal to 2.4 Angstrom at X12C. The structure was solved by molecular replacement and has been refined to R-free = 27.9% and R = 22.3%.

**Conclusions:** One subunit of the two fold-symmetric structure strongly resembles wild type trp aporepressor. The other subunit has a large deformation of the E-helix, located about ten residues away from the L75F mutation. The N-terminal half of the E-helix is displaced by a registration shift of three residues. This structure demonstrates that point mutations can have significant, global effects on protein conformation.

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