The crystal structure of photolyase (DNA photoactivating enzyme) from the cyanobacterium, *Anacystis nidulans*, has been solved by the multiple isomorphous replacement. The refinement of the structure is still in progress and the present R value is 0.24 at 2.5 Å resolution.

Photolyase has activities of DNA damage recognition and binding, photon absorption, energy transfer from chromophore to DNA, resulting in photoreactivation of UV-induced pyrimidine dimer monomer. Photolyases are single chain proteins of 50 to 70 kDa molecular weight, containing two different chromophores in equimolar amount. Deduced FAD was found to be an essential chromophore for the lights-dependent repair process and the second cofactor besides FAD (1,5,10-pentaphenyl porphyrin) from the cyanobacterium.*Anacystis nidulans* photolyase with absorption maxima around 420 nm. On the other hand, 3,10-methylenetetrahydroladilic acid (MTTH) is the second cofactor with absorption maxima around 380 nm in *E. coli* photolyase whose structure was recently determined (Park et al., Science, 268, 186, 1995).

Photolyase from *A. nidulans* crystallized in the both tetragonal and trinodal systems (Miki et al., J. Mol. Biol., 233, 167, 1993; Tamada et al., J. Struct. Biol., 115, 57, 1995). The present structure analysis by the use of the tetragonal crystals showed that the whole folding pattern is essentially similar to that of *E. coli* photolyase but that the binding mode of the second chromophore is different.

The three-dimensional structure of macrophage migration inhibitory factor (MIF) from human lymphocytes was recently determined by the multiple isomorphous replacement. MIF was strongly activated in the electron cascade reactions and is likely to be a critical in cell-mediated immune host defenses. The present structure analysis by crystallographic analysis showed the whole folding pattern is essentially similar to that of *E. coli* photolyase but that the binding mode of the second chromophore is different. The electron density at the domains which are connected to each other by a double strand comes from a next monomer. This crystal contains additional two β-strands, those make β-sheets structure with two neighboring MIF monomer. Thus, the structure of human MIF has seven-stranded β-sheets, which consist from three monomers. The crystallographic R-factor of the current structure is 24% (Rfree=29%) at 2.1 Å, and refinement is in progress.

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