The Structure of λ O Protein Fragment Provides Insights About Replisome Assembly

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Bacteriophage λ replication initiator, known as λ O protein, is one of the two replication proteins encoded by the bacteriophage's own genome. Its role in initiating bacteriophage DNA replication has been firmly established. Crystals of λ O protein N-terminal fragment, belonging to space group p2₁2₁2 and diffracting to 2.5 Å, were obtained and solved by using anomalous dispersion of selenium atoms. There are two λ O dimers in the asymmetric unit, related to each other by a two-fold non-crystallographic symmetry operator. Genetic data and molecular surface area considerations seem to indicate that the interface(s) between these dimers could be physiologically important and not just a crystallization artifact.

Despite very low homology at the amino-acid sequence level (11% for the structurally aligned regions), the DNA-binding region of λ O displays great similarity to the CAP DNA-binding domain. This structural homology, in combination with genetic data, indicates that DNA-binding mode for λ O protein is similar to the one present in CAP.

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