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# Biochemical Characterization and X-ray Crystallography of a Lysozyme Encoded by *Pseudomonas aeruginosa* Bacteriophage SN

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# Biochemical Characterization and X-ray Crystallography of a Lysozyme Encoded by *Pseudomonas aeruginosa* Bacteriophage SN

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Bacteriophage SN is a virulent phage that selectively infects the bacterium *Pseudomonas aeruginosa*. It was isolated from Lake Chernoe in Russia and it is related to the PB1-like species of the Myoviridae family. The DNA genome is composed of 66,391 base pairs, has 89 predicted open reading frames, and encodes more than 20 structural proteins. One of the open reading frames of this newly discovered bacteriophage has high sequence identity to other lysozyme and chitinase genes. It is therefore assumed that this protein encoded by bacteriophage SN is utilized for digestion of the host cell wall prior to injection of the nucleic acid into the host. Determining the high-resolution structure of the protein will aid in later determination of location within the intact phage. The gene of interest has been cloned into *E. coli* by PCR amplification and ligation into the PET30a vector. This protein expressed to high levels and the product has been purified to homogeneity. The protein demonstrated specific enzymatic activity by lysis of *Micrococcus luteus* cells in suspension as purity increased. Crystals of the protein currently diffract to 3.5 Å, the data gathered from optimized crystals will be used to determine the X-ray structure of the lysozyme.