THE STRUCTURAL ELUCIDATION OF THE NOVEL SERINE/LYSINE VIRAL PROTEASE VP4

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In recent yeras, a new class of serine proteases, with a catalytic dyad mechanism have been characterized. Catalytic residues are a serine, which acts as nucleophile, and a lysine, which acts as general base. Members of this group of proteases include VP4 viral proteases, type I signal peptidases, UmuD, and Lon proteases.

The *Birnaviridae* viral family encodes a polyprotein that is processed through the proteolytic activity of its own protease (VP4), to liberate itself from the other viral proteins. Here we present the crystal structure of the viral proteases VP4 from BSNV (blotched snakehead virus).The BSNV VP4 protease (residues 558-773 from the polyprotein) was crystallized and crystals diffracted to 2.2 ? resolution. The structure was solved by SAD. The BSNV VP4 protease structure (figure 1) has a topology for the active site consistent with the Ser692 O? and Lys729 N? directly participating in catalysis. The structure is composed of two domains; domain I is mostly ß-sheet in structure, while domain II is a/ß in structure. The BSNV VP4 protease shows similarities in the active site with many other Ser/Lys proteases. We present a comparison between the BSNV and other proteases with similar mechanism.

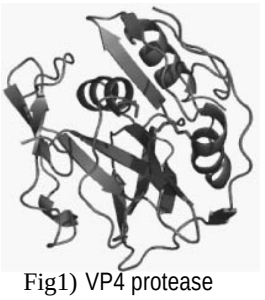

Fig1) VP4 protease from BSNV (Feldman *et al*, 2006).

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