MS07-P10 | Interdomain Conformational Flexibility Of The Peptidoglycan N-Acetylglucosaminidases Of Staphylococcus Aureus

Pintar, Sara (Jozef Stefan Institute, Ljubljana, SVN); Borišek, Jure (National Institute of Chemistry, Ljubljana, SVN); Usenik, Aleksandra (Jožef Stefan Institute, Ljubljana, SVN); Perdih, Andrej (National Institute of Chemistry, Ljubljana, SVN); Turk, Dušan (Jožef Stefan Institute, Ljubljana, SVN)

Bacterial cell wall enables the cell to withstand the osmotic pressure and thus enables its survival in a large set of different habitats. Yet for cells to grow and divide it has to be remodeled in a controlled manner. Cell wall is composed of glycan strands comprising alternating N-acetylglucosamine (NAG) and N-acetylmuramic acid (NAM) and cross-linked by peptides. Peptidoglycan hydrolases have been shown to be important for peptidoglycan maturation, turnover and recycling as well as antibiotic resistance.

Bacterial peptidoglycan N-acetylglucosaminidases have a typical lysozyme-like fold with active site glutamate in centre of the highly conserved core that consists of five or six helices. Crystal structures of two N-acetylglucosaminidases, SagB and AtlA-gl, revealed very similar fold to another *S. aureus* N-acetylglucosaminidase, AtlE, however with unexpectedly different L- and R-domain packing. Consequentially, the substrate binding clefts of SagB and AtlA-gl are significantly wider than in that of AtlE.

Structural analysis and mutational studies confirmed that substrate interacts with active site residues on the left and right side of the active site cleft. This suggests that a substantial conformational change has to take place to enable productive binding of the substrate and subsequential reaction to transpire.