enzyme activity, oligomerisation state, interaction with other proteins, sub-cellular localization or half-life. Signal transduction through reversible protein phosphorylation is a key regulatory mechanism of both prokaryotes and eukaryotes. Phosphorylation frequently occurs in response to environmental signals and is mediated by specific protein kinases.

Recent studies reported that the eukaryotic-type serine/threonine kinase PrkC from *Bacillus subtilis* is also involved in bacterial exit from dormancy [1]. Under conditions of nutritional limitation, *B. subtilis* produces dormant spores, which are resistant to harsh environmental conditions and can survive in a dormant state for years [1].

Generally, growing bacteria release muropeptides in the surrounding environment, due to cell wall peptidoglycan remodelling associated to cell growth and division [1-7]. Therefore, the presence of muropeptides in the close environment of dormant bacteria is a clear signal that conditions are optimal for growth. The process of bacterial cell growth and resuscitation regulation in pathogenic bacteria will be discussed.

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Keywords: bacterial, pathogen, protein structure.

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Crystallization and preliminary X-ray diffraction analysis of a thioredoxin from *Streptococcus pneumoniae*

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Thioredoxins (TRX) are ubiquitous proteins involved on a wide number of critical celular functions comprising protein folding and repair, DNA synthesis and oxidative stress response [1]. These proteins share a conserved active sequence site [Cys-X-X-Cys] and a common 3D architecture known as thioredoxin motif composed of four α-helices and five β-sheets. TRX are responsible of keeping the cellular reducing environment accepting electrons from a donor by NADPH reduction and transferring them to other acceptors. Recently, a pneumoccocal thioredoxine-like protein have been crystalize using the hanging-drop vapour-diffusion method at 291K. Diffraction quality of tetragonal crystals belongs to space group $P4_32_12$ with unit-cell parameters a = 62.85, b = 62.85 *and* c = 89.60Å. X-ray data sets were obtained up to 1.3Å. structural characterization and functional properties are currently undergoing.

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Keywords: thioredoxin, macromolecules, redox protein

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Crystal structure of the class D β-lactamase OXA-40

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. β−Lactam antibiotics have been widely used since World War II. These antibiotics efficiently inhibit bacterial peptidoglycan transpeptidases, which leads to cell lysis and death of the growing bacteria. β-Lactamases hydrolyze the β-lactam ring of β-lactam antibiotics following an acylation and deacylation steps. β-Lactamases are divided into four classes, A, B, C and D, according to their sequence similarities. Class B enzymes are metalloproteins that require a zinc ion for their enzymatic activity, whereas classes A, C and D β-lactamases contain serine residue in their active site.

OXA-40 is a class D β-lactamase isolated from *Acinetobacter baumannii.* OXA-40 hydrolyzes carbapenems which are one of the antibiotics of last resort for many bacterial infections. In this study we expressed OXA-40 in *E. coli* and purified. Crystals suitable for X-ray structure determination were obtained by hanging drop vapor diffusion method at pH 8.5. The crystals belong to space group $P4_12_12$ with cell dimensions a=b=102.6 Å, c=84.9Å. The three dimensional structure of OXA-40 has been solved by the molecular replacement method using OXA-24 as a search model and refined to 1.53 Å resolution.

OXA-40 is a monomeric enzyme which consists of two domains, one containing five α-helices and the other one containing a six-stranded antiparallel β-sheet flanked by N- and C-terminal helices on one side, and a helix on the other side. The active site lies at the junction of the two domains. The general base Lys84 in the active site is carbamylated. Crystallization conditions of complexes with β-lactam antibiotics are being searched.

Keywords: β-lactamase, carbapenem resistance, X-ray analysis

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Crystallization of MID962-1200: A trimeric autotransporter from *M. catarrhalis*

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Moraxella catarrhalis is a newly emerging pathogenic bacterium that is involved in otitis media and sinusitis in children as well as lower respiratory tract infections in adults with chronic obstructive pulmonary disease (COPD). Over the last 20 to 30 years, the bacterium has emerged as a genuine pathogen. In immuno compromised hosts, the bacterium can cause a variety of severe infections including pneumonia, endocarditis, septicemia, and meningitis [1]. Today more than 90% of all clinical isolates are β-lactam resistant [2]. One of the most important virulence factors for *M. catarrhalis* is a 200 kDa outer membrane protein, which is responsible for the IgD binding, namely the Moraxella IgD-binding (MID) protein [3]. MID belongs to the trimeric autotransporter protein family and has N-terminal signal peptide, internal passenger domain and C-terminal translocator domain.

Having an elongated shape the trimeric MID962-1200 shows misleading results in size exclusion chromatography and behaves