Lincomycin is a naturally occurring member of a lincosamide group of antibiotics. The cluster of lincomycin biosynthetic gene was already decribed and the function of many of genes has been clarified.

This work, “Characterization of N-demethyllincomycin-methyltransferase”, is focused on the study of the final step of lincomycin biosynthetic pathway - the methylation of nitrogen atom from the pyrollo ring of the propylproline unit of the N-demethyllicomycin (NDL). The aim of this work was the characterization of the protein LmbJ, catalysing this final biosynthetic step. All the experiments were provided for the enzyme LmbJ with N-terminal histidine tag, which had been prepared by the heterologous expression in E.coli cells. The pH and temperature optimum was determined as well as the Michaelis constants for both substrates of the reaction - N-demethyllincomycin and S-adenosyl methionine (SAM – a methyl group donor). With the exception of the pH optimum, all specified parameters have markedly differed from the data published for the enzyme isolated from the natural source. Based on the comparison of electron microscopy, blue native gel electrophoresis and gel filtration results, the hypothetical model of the LmbJ quarternary structure was created. Majority of methyltranserases, so far described occure in monomeric, dimeric or tetrameric form. By contrast in our case the most probable model of quarternary structure is a hexamer.