3D modeling of BmpA, BmpB, BmpC and BmpD from *Borrelia burgdorferi*

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*B. burgdorferi* is one of the main Borrelia species causing Lyme disease in humans. The pathogens are transmitted by the *Ixodes* ticks and there are 60,000-200,000 Lyme disease infections in Europe annually. The BmpA, BmpB, BmpC and BmpD proteins are expressed by *B. burgdorferi* in infected patients, but the exact role of the proteins is still unknown. The Bmp proteins are reported to be homologous to *T. pallidum* PnrA (Purine nucleoside receptor A), which has been characterized as a substrate binding lipoprotein of the ATP binding cassette (ABC) transporter family, preferentially binding purine nucleosides. Based on our 3D homology models, the Bmp proteins share the typical fold of the substrate-binding protein family. Moreover, the residues involved in binding the ribose moiety of the nucleoside are highly conserved in the Bmp models, whereas the residues in the purine binding site are less conserved. In particular, the BmpC model has differences in the residues binding the base moiety of the nucleoside. In conclusion, the revealed differences indicate that the Bmp proteins could prefer different nucleosides and thus, might have distinct biological functions.

**Figure 1:** A typical structure of an ABC-type substrate-binding lipoprotein. The protein is attached to the membrane by a lipid anchor. The ligand-binding site is found between the two domains (shown as gray surface).

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Biography
Mia Åstrand completed her Master’s degree in Biology and a Bachelor’s degree in Pharmaceutical Sciences and is currently doing a PhD in Structural Biology at the Structural Bioinformatics Laboratory at Åbo Akademi University. She is working on determining the structure and function of proteins involved in the infection processes of highly pathogenic bacteria. Protein structure determination is done by both experimental and computational methods and docking studies and phylogenetic analyses are used for further analyzing protein functions.

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