Proteus mirabilis is a Gram-negative bacillus belonging to opportunistic pathogens that cause infections in immunocompromised individuals. *P. mirabilis* accounts for <0.05% of the intestinal microflora of healthy humans. It is mainly associated with urinary tract infections (UTIs), especially catheter-associated urinary tract infections (CAUTIs) in long-term catheterised patients. Urinary tract infections caused by the bacterium in question can lead to renal stone accumulation, complete kidney damage and, in the worst cases, sepsis and bacteraemia. Bloodstream infection caused by *P. mirabilis* is often the result of CAUTI or ZUM and is associated with a high mortality rate among hospital and nursing home patients. *P. mirabilis* is characterised by resistance to polymyxin antibiotics e.g. polymyxin B. A modification in the lipopolysaccharide (LPS) structure involving the attachment of 4-amino-4-deoxy-l-arabinzoy (L-Ara4N) is thought to be responsible for polymyxin B resistance in *P. mirabilis*. As a model organism, I proposed *P. mirabilis* HI4320 strain, whose genome is fully sequenced and described. Two open reading frames encoding the *arnT* gene, which is a potential L-Ara4N transferase, were identified in the genome of the reference strain: 1) PMI1047, located within the *arn* gene operon, and 2) an orphan form of *arnT* (PMI0275). My hypothesis is that the PMI0275 and/or PMI1047 genes present in the *P. mirabilis* HI4320 genome are involved in the attachment of L-Ara4N to the LPS molecule and are responsible for resistance in the strain. Unfortunately, drug resistance among Gram-negative bacteria has increased significantly over the past few years, which is a major public health problem. Available antibiotics are no longer effective and the ability to acquire resistance among bacteria is steadily increasing. For the treatment of infections caused by Gram-negative bacteria, polymyxin B has been proposed as an antibiotic of last resort. Therefore, a thorough understanding of the molecular mechanisms of resistance is important for the treatment of infections caused by *P. mirabilis*. Moreover, *P. mirabilis* is an under-studied organism and the proposed studies will allow to answer questions about further virulence mechanisms of the bacterium. The results obtained may have applications and contribute to the development of new therapeutic approaches.