A porin from Klebsiella pneumoniae : sequence homology, three-dimensional model, and complement binding

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A recombinant plasmid containing ompK36, the gene coding for the Klebsiella pneumoniae outer membrane protein OmpK36, was constructed by transposon mutagenesis and subcloning. Clones were identified in a cosmid library in Escherichia coli on the basis of their reaction with antiserum against the OmpK36 protein and by the presence in gel electrophoretic analysis of a band in E. coli outer membranes migrating with a mobility corresponding to 36 kDa. The ompK36-encoded protein exhibited characteristic properties of porins, such as heat modifiability and resistance to trypsin. The sequence of the gene revealed that OmpK36 is a close relative of the enterobacterial porin family, with a high degree of homology with E. coli OmpC, PhoE, and OmpF. On the basis of the structures of OmpF and PhoE porins, determined previously by X-ray analysis, it appears likely that the three-dimensional structure of OmpK36 also contains the motif of a 16-stranded beta-barrel, with long loops on one end and short turns on the other. Like the OmpC porin from E. coli, OmpK36 contains a long insertion in loop 4. The results of a binding study of complement component C1q to OmpK36 and the analysis of the OmpK36 model suggest that C1q binding sites are covered by the lipopolysaccharide core in the native porin.
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