

Nucleotide sequence of the *aroP* gene encoding the general aromatic amino acid transport protein of *Escherichia coli* K-12: homology with yeast transport proteins

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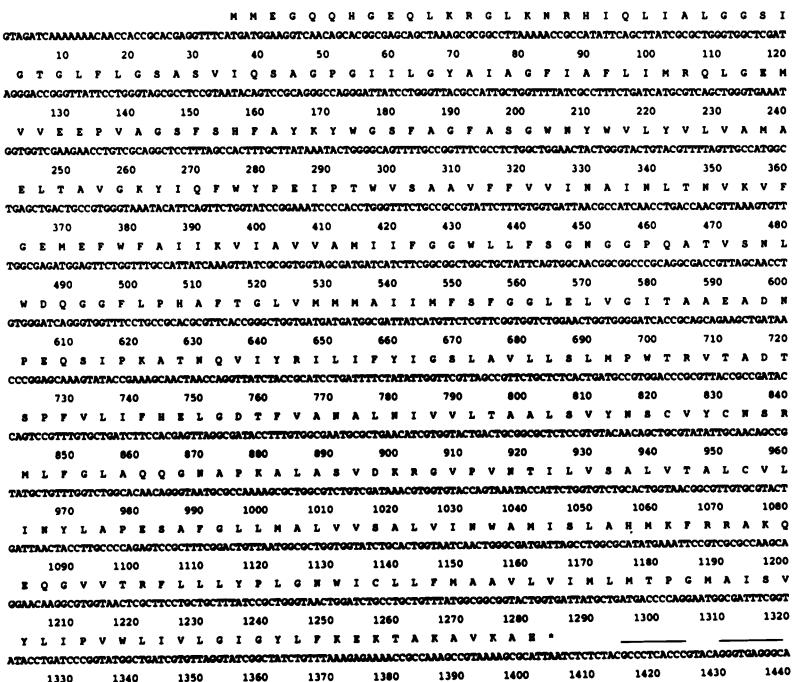
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The *aroP* gene is situated between the *ampDE* operon (1) and the *gA-aceEF* gene cluster at 2.6 min. on the *E. coli* linkage map (2). Its complete nucleotide sequence has been determined and used to deduce the primary structure of AroP, a transport protein that takes up tryptophan, phenylalanine and tyrosine. Consistent with its membrane location (3) AroP is highly hydrophobic and apparently comprises two equivalent domains, each composed of six alpha-helical segments with membrane-spanning potential. In common with many transport proteins the observed molecular weight of AroP, 37 kD (3), is significantly lower than that predicted from the sequence, 49.6 kD. Although the hydropathy profile and general organisation of AroP resemble those of other bacterial transporters (4) there is no homology at the primary structure level. In contrast, AroP is highly homologous to two transport proteins from *Saccharomyces cerevisiae* involved in

arginine and histidine uptake (5, 6). AroP and the yeast histidine permease HIP1 show 30% identity over 405 amino acid residues, suggesting a common evolutionary origin.

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