

# The nucleotide sequence of *ptsH* gene from *Klebsiella pneumoniae*

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We have determined the nucleotide sequence of the *ptsH* gene of *Klebsiella pneumoniae* 1033-5P14 strain KAY2026 (1). Its gene product HPr is involved in carbohydrate uptake (2) and chemotaxis (3) through the phosphoenolpyruvate-dependent carbohydrate:phosphotransferase system (PTS). A 278 bp fragment comprising the whole coding region of the *ptsH* gene was cloned from genomic DNA into pUC18. The function was tested by the ability to complement *E. coli* K12 *ptsH* mutants in sugar fermentation and chemotactical response. The *Klebsiella ptsH* gene has a high homology to the corresponding genes from *E. coli* K12 (4) and *S. typhimurium* (5, 6). The deduced amino acid sequence shows only an Ile 63 → Leu exchange (underlined), indicating that the HPr is a highly conserved protein in closely related enterobacteria.

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## REFERENCES

1. Sprenger, G.A. and Lengeler, J.W. (1984) *J. Bacteriol.* **157**, 39–45.
2. Postma, P.W. and Lengeler, J.W. (1985) *Microbiol. Rev.* **49**, 232–269.
3. Lengeler, J.W. and Vogler, A.P. (1989) *FEMS Microbiol. Rev.* **63**, 81–92.
4. De Reuse, H., Roy, A. and Danchin, A. (1985) *Gene* **35**, 199–207.
5. Byrne, C.R., Monroe, R.S., Ward, K.A. and Kredich, N.M. (1988) *J. Bacteriol.* **170**, 3150–3157.
6. Schnierow, B.J., Yamada, M. and Saier, M.H., Jr. (1989) *Mol. Microbiol.* **3**, 113–118.

	SD	
<i>K. pneumoniae</i>	<u>GTTGGGGAAATATA</u>	-1
<i>E. coli</i>	.....C.	
<i>S. typhimurium</i>	.....C.	

METPheGlnGlnGluValThrIleThrAlaProAsnGlyLeuHisThrArgProAlaAlaGlnPhe  
 ATGTTCCAGCAAGAAGTTACCATTACCGCTCCGAACGGTCTGCACACCCGCCCTGCTAGTTTG 66  
 .....C.....  
 .....

VallLysGluAlaLysGlyPheThrSerGluIleThrValThrSerAsnGlyLysSerAlaSerAla  
 CTTAAAGAAGCTAAAGGCTTCACTTCTGAGATCACTGTAACCTCCAACGGCAAAGCGCCAGCGCCA 132  
 ..A.....G.....A..T....G..T.....G  
 .....A.....T....G..T.....G

LysSerLeuPheLysLeuGlnThrLeuGlyLeuThrGlnGlyThrValValThrLeuSerAlaGlu  
 AAAAGCCTGTTCAAAGTGCAGACTCTGGGCCTGACCCAGGGCACCCTATGACCCCTCCGCTGAAG 198  
 .....T.....T..A..T....T....TA.....A...  
 .....T.....T..A.....C..C...A.....A...

GlyGluAspGluGlnLysAlaValGluHisLeuValLysLeuMETAlaGluLeuGlu\*\*\*  
 GGCGAAGATGAGCAGAAAGCTGTTGAGCATCTGGTTAAACTGATGGCTGAACTCGAGTAAGTTCAC 264  
 .....C.....G.....A.....G.....T...C.  
 ..T.....G.....A.....G.....TTT