The nucleotide sequence of the *nifJ* gene of *Klebsiella pneumoniae*

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The nucleotide sequence of the 3,567 bp Sal1 fragment upstream of *nif H* of *Klebsiella pneumoniae* (*K.p.*) is presented here together with the preceding 239 bp EcoR1 to Sal1 fragment taken from Shen et al. (1.), which occurs just upstream of the *nif H* promoter. This brings to completion the sequencing of all the known *nif* genes of *K.p.* which occur in a contiguous cluster of 23,701 bp between *hisG* and *shiA*.

This sequence contains a 3,516 bp open-reading-frame and allows for the coding of a 128,143 dalton polypeptide (1,171 amino acids). This size polypeptide and its location with respect to *nifH* and the pattern of cysteinyl residues in this sequence are all consistant with this being the *nif J* sequence whose gene product has been described as a pyruvate: flavodoxin-oxidoreductase which transfers electrons via *nifF* to the Fe protein of nitrogenase (2,3and 4).

Klebsiella pneumoniae nifJ

GAATTCGCGCTAACTCTTCTGTCATCCGCGAGCTGGCACAGGCTGTGCTTGAGGCAACAACTGGGTTTGCCGCTTATTTGAGGCGGCGAAGATGCCTCTCA
CCTTCGAGGATTGAACAATGTCCGGAAAAATGAAAACAATGGATGGCAACGCCGCGGCGGCCTGGATCTCTTATGCCTTTACCGAG
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CGGCGACCGGCCGATCAATTCGCCCTACCTGATCCATCGGGCCGATTTTATCTCCTGTTCGCAGCAGTCCTACGTTGAGCGCTAC
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TTCATCCGCGATATTCTGCAGCCGATGAACCGCCAGTGCGGCGACCAGCTGCCGGTGAGCGCGTTCGTCGGTATGGAGGACGGG
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GCGGTCTCGATCACGTGCTGGCGAGCGGGGAAGACGTCAATATTCTGGTGTTTGACACCGAGGTTTACTCCAATACCGGCGGCC
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AGGCCGAAGCCTGGCCGGGACCGTCGCTGGTGATTGCCTACGCCGCCTGCTATAACCACGGGCTGAAAGCCGGTATGCGCTGCA
GCCAGCGCGAGGCGAAACGGGCGGTTGAGGCGGGATACTGGCACCTGTGGCGCTATCATCCGCAGCGGGAAGCGGAAGGTAAG
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AAAACGACGCCGCATCTGGCGGATGCGCTCTTTAGCCGAACCGAGGAGGACGCGCGGGCCCGCTTTGCCCAGTATCGGCGGCT
GGCCGGCGAGGAGTAGCGGGCCTTTAGTTCTCCTGCTGCATGACCTTAAGCAGCGTATCCAGCAGGCCGGGAAAGCGCGCGTCTAAATCTTCCCGGC
GCAGCGAAATCAAGTTCTCCCGCCCCTGTGGGCGCTGCCAGATCACACCGCTGTCGCGCAGGACGCGCCAGTGGTGGGTCATGGTCGA

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