

Nucleotide sequence of the murF gene encoding the UDP-MurNAC-pentapeptide synthetase of Escherichia coli

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The nucleotide sequence of the murF gene encoding the UDP-MurNAC-pentapeptide synthetase of Escherichia coli was determined within a 1.9 kilobase-pair PvuI-PvuII fragment from plasmid pLC26-6 of the Clarke and Carbon library. The sequence contains only one open reading frame in the clockwise direction. The coding region contains 1356 nucleotides which are translated into 452 amino acids corresponding to a protein with a molecular weight of 47492. This latter value is in agreement with that of the purified synthetase (1)(2) or that of the protein expressed by the maxicell technique (3)(4). The N-terminal amino acid sequence determined from the DNA sequence is in agreement with that of the purified protein (2). The synthetase activity requires ATP hydrolysis. Two domains characteristic of ATP binding proteins were found extending from amino acid 107 to 119 (domain A) and from amino acid 352 to 360 (domain B). A 8 bp hairpin structure follows the TAG stop codon.

-39 CGATCGCGTCACGGTGGCGGCTGCTGCTGGGGGTGATTGCCATGATTAGCGTAACCCCTTAGCCAACCTTACCGACATCTTCAACGGTGAACGTCAAGGT
58 GCAGATATCACCCCTTGATGCTGTAAACCACTGATACCCGAAAACAGCGCCGGCTGCTGTTTGTTCCTGAAAGCGAACGTTTGTATGCCAC
154 GATTTGCGGACAGCGAAAAGCTGGCGGGCAGCGGCACTACTGGTTAGCCGTCGGCTGGACATCGACCTCCGCAGTTAATCGTCAAGATACG
250 CGCTGGCGTTTGGTGAACCTGGCTGCATGGTTCGCGCAGCAAGTTCGGCGCGGCTGGTTGCTCGACGGGCTCCTCCGGCAAAAACCTCCGTATAA
346 GAGATGACGGCGCGGATTTAAGCCAGTGGCGCAACACGCTTTATACGGCAGGCAATCTCAACACGACATCGGTGTACCGTACGCTGTTGGC
442 TTAACGGCGGAAATACGATTACGCAGTTATTGAACATGGCGGCAACCATCAGGCGCAAAATAGCCTGGACTGTGAGTCTGACTCGCCGGAACGTTGGC
538 CTGGTCAACAACCTGGCAGCGGCGCATCGGAAGTTTGGCTCGCTTGGCGGATGTCGCGAAAGCGAAAGGTTAAATCTTACGGCGCTCCCGGAA
634 AACGGTATCGCCATTATGAACGGCGACAAACAAGCTGGCTGAACCTGGCAGAGCGTAATGGCTACAGCAAAAGTGGCGTTTCTCACCCAATGCC
730 GCCAACAGCGATTACCGCGCCACCAATATCCATGTGACCTCGCACGGTACGGAAATTTACCTACAAAACCCCAACGGTACGGTCGATGTTCTGCTG
826 CCGTTGCGGGGGCTCACAATATTGGCAATGCGCTGGCAGCGCTCGCTCCATGTCCGTTGGGCGCAACGCTTGATGCTATCAAAGCGGGGCTG
922 GCAAACTGAAAAGCTGTTCCAGGCGCTGTTCCCCATCCAACCTGGCAGAAAACAGTTGCTGCTCGACGACTCCTACACGCCAATGTCCGTTCA
1018 ATGACTGCAGCAGTCCAGGTAAGTGGCTGAAAAGCGCGGCTACCCGCTGCTGGTGGTGGGGATATGGCGGAACCTGGGCGCTGAAAACGAAAGCTGC
1114 CATGTACAGGTGGCGAGCGGCGAAAAGCTGCTGGTATTGACCCGCTGTTAAGCGTGGGTAACAAAGCCTGCTATCAGCACCGCCAGCGCGTT
1210 GCGCAACATTTTGGTATAAACTCGTTAATACCGCGCTTAAATTAATCTGATGCTGAGCAACAGGTAATTAATGTTAGTTAAGGTTACAGCT
1306 AGTCCGCGCATGGAAGAGGTAGTACGCGCTTACAGGAGAATGGACATGTTAGTTGGCTGGCCGAACATTTGGTCAAATATATCGCGCTTAAAC
1402 GTCCTTTCTATCTACGCTTTCGCGCCACTGTCAGCCTGCTGCACCGGCTG

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