

Nucleotide sequence of the F41 fimbriae subunit gene in *Escherichia coli* B41

David A.Fidock, Paul A.McNicholas and Philip R.Lehrbach\*

Biotechnology Australia Pty, Ltd, PO Box 20, Roseville, NSW 2069, Australia  
Submitted March 13, 1989

EMBL accession no. X14354

A clone encoding the F41 fimbrial sub-unit gene from *E. coli* B41, was isolated from an EMBL3 library using an oligonucleotide based on the published N-terminal amino acid sequence (1). The DNA sequence of an 1166bp fragment revealed an open reading frame encoding a protein of 277 amino acids including a 22 amino acid leader sequence (dash underlined). This corresponds to a mature protein of 29004 daltons which correlates with the molecular weight estimation of 29500 daltons by SDS-PAGE (1). Extensive homology with the K88 fimbrial sub-unit gene (2,3) was found in the 5' untranslated and leader sequence regions (underlined). A dyad repeat (arrowed) in the 3' untranslated region represents a putative transcription terminator. A similar sequence of the F41 fimbrial gene from a porcine *E. coli* VAC1676 has recently been reported (4).

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1      ctgcagggtgaagactgaggattcatttcccttataaaatgcagtagcatccatgattccggagcgggcatattggtaaagggattaccgctctttaaaa
101    cggsaataacgtaaaaactattctgagttaaactctgtgttaatgaaatcgcggtattttaaatgaaatccgcaggggatgggttttgcggtaatccggaaa
201    aataagattgcccaggtcagtttatttattgaaatgcaaggtgattatTTATGAAAAGACTCTGATTGCACTGGCTGTGGCTGCATCAGCGGCAG
                                     MetLysLysThrLeuIleAlaLeuAlaValAlaAlaSerAlaAlaV
301    TATCTGGTTCAGTGATGGCTGCTGATTGGACGGAAGGTCAACCAGGTGACATTATTGTTGGTGGTGAATAATACATCACCATCTGTTAAATGGCTATGGAA
alSerGlySerValMetAlaAlaAspTrpThrGluGlyGlnProGlyAspIleIleIleGlyGlyGluIleThrSerProSerValLysTrpLeuTrpLy
401    GACTGGAGAGGGACTTTCATCTTTAGCAATACTACAATGAAATGTTAAACGGAAGTGAATATTCTGTTCCAACGGATGAATATTTTTAGCAGCG
sThrGlyGluGlyLeuSerSerPheSerAsnThrThrAsnGluIleValLysArgLysLeuAsnIleSerValProThrAspGluLeuPheLeuAlaAla
501    AAGATGAGTGATGGGATTAAGGTGTTTTCCTAGGGAATACACTCATTCTTAAGATTGAAATGGCATCTTATGATGGTAGTGTATTACACCTAGTTTCA
LysMetSerAspGlyIleLysGlyValPheValGlyAsnThrLeuIleProLysIleGluMetAlaSerTyrAspGlySerValIleThrProSerPheT
601    CTTCAAATACAGCAATGGATATTGCTGTAAAAGTAAAAACTCAGGTGATAAATACTGAGCTAGGACTCTTTCTGTCTCTTGTTCATTGGTGGCGCAT
hrSerAsnThrAlaMetAspIleAlaValLysValLysAsnSerGlyAspAsnThrGluLeuGlyThrLeuSerValProLeuSerPheGlyAlaAlaVa
701    TGCAACTATTTTTGATGGCGATACTACTGATAGCGCTGAGCGCATATTATCGGTGGTCTGCTGTTACAGTATTTGAAGGGCTGTTAATCCAGGTCCA
lAlaThrIlePheAspGlyAspThrThrAspSerAlaValAlaHisIleIleGlyGlySerAlaGlyThrValPheGluGlyLeuValAsnProGlyArg
801    TTTACTGATCAGAATATAGCCTATAAATGGAATGGACTCTCAAAGCTGAAATGGCTGGTATGTAGAAAAGTAAATGCCAGGGCAAAGTGCTTCAACST
PheThrAspGlnAsnIleAlaTyrLysTrpAsnGlyLeuSerLysAlaGluMetAlaGlyTyrValGluLysLeuMetProGlyGlnSerAlaSerThrS
901    CTTATAGTGGTTCCACAATGGGATGACCTCAGTCACAGCAACTATACTTCTGCAATAAAGGCATCTTATCTCTTATGGATCTGGTGTCTTCTGCAGG
erTyrSerGlyPheHisAsnTrpAspAspLeuSerHisSerAsnTyrThrSerAlaAsnLysAlaSerTyrLeuSerTyrGlySerGlyValSerAlaGl
1001  TAGTACTTATGTTATGAATTTAAATAAGGATGTGGCGGTGCAGCTTGAATGGTGGCTCCAGTGACTATCACCGTTATTTATAGTTAAatcatcttctgc
ySerThrLeuValMetAsnLeuAsnLysAspValAlaGlyArgLeuGluTrpValAlaProValThrIleThrValIleTyrSer***
1101  ccttccccctgtttatcttccgggggaagggcggtagttggggcgagtgagtgcttctgcacatgc

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\*Present address: Arthur Webster Pty, Ltd, PO Box 234, Baulkham Hills, NSW 2153, Australia

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