

Nucleotide sequences of the penicillin-binding protein 5 and 6 genes of *Escherichia coli*

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Submitted January 29, 1988

Accession nos. *dacA*=X06479 and *dacC*=X06480

Penicillin-binding proteins (PBPs) 5 and 6 are the major D-alanine carboxypeptidases of *Escherichia coli*. The PBP 5 and PBP 6 genes (*dacA* and *dacC* respectively) have been cloned^{1,2} and the nucleotide sequence of a 1597-bp BamHI-EcoRI fragment containing the *dacA* gene (upper sequence) and of a 1505-bp AhaIII-SalI fragment containing the *dacC* gene (lower sequence) are shown. PBP 5 and PBP 6 are cytoplasmic membrane proteins and are synthesised as pre-proteins³; the amino-termini of the mature proteins are assigned from published data⁴. PBP 5 and PBP 6 show 62% sequence identity.

1
GGATCCAGCTTGGCCATTCGCCAGCAAAAGCGAAGCAGCACTTGCAGCAAGCTTTGCAAAACGGAAGCCAAATACATCATTTTATCTACCGCCGAGAGCGTAAAGCAAGCACTC
121
GATGTGTCAATTTCTGTAAAGTAAAGGACCTTCAAGGACCTCCGCGGAAAGTCAGATGCTCCGCGGATGTCATAGTAGGCGACTTTTTAAATTCATCAGGATGCTGATGATCCGGA
-29
H N T I P S A R I N K R L A L T T A L C T A F I S A A H A A D D L H I K T N H I P
241
CCATGAATACCAATTTTTCCGCTCGATFCAAGGACCGCTTCCAGCCGGCTCTTTGCACAGCCTTATCTCTGCGCAGCATGCCGATGCATGAATACAAATAATGATGATCCGG
20
G V P Q I D A E S Y I L I D Y H S G R V L A E Q H A D V R R D P A S L T K M H T
40
361
GTGTACCGCAGATCGATCGGAGGCTCACTACTCTGTATGATTAACCTCCGCGAAAGTGCTCGCGAAACAGAACCGAGATGTCCGCGCGATCTCTGCCAGCCTGACCAAAATGATGACCA
60
S Y V I G Q A H K A G E K F K E T D L V T I G H D A M A T G T G G C C A C C G G T T A A A G G T T T A A A G G T T C T C C G T A T G T T C C
80
481
GTTACGTTATCGCCAGGCAATGAAGCCGGTAAATTTAAAGAACTGATTTAGTCACTATCGGCAACGACCGCATGGCCCGTAAACCGGTTTAAAGGTTTCCGCTGATGTTCC
100
L K P G M Q V P V A S Q L I R G I N L Q S H D A C V A M D F P A A G S Q D A F V
120
601
TCAAACCGGCGATCAGGTTCCGGTTCTCAGCTGATCCGCGGATTAACCTCGCAATCGGGTAACGATGCTGTGCTGCCATGGCCGATTTGGCCGTGTAGCAGGACGCTTTTGGTTG
140
G L N H S Y V N A L G L K H T H F Q T V H G L D A D G Q V S S A R D M A L I G Q
160
721
GCTGTATGAACAGCTACTGAACCGACTGGGCTGAAATACCCACTTCCAGACGGTACATGCTCGATGCTGATGGTCACTGACGCTCCGCGGAGATAGCGGCTGATCGGCCAGG
180
A L I R D V P H E S I S I T E E K E P T F R G I R L W H G L L W D H S L H V D
200
841
CATTTGCTCCGTGACOTACCGAATGAATACCTGATCTATAAAGAAAAGAAATTTACGTTTAAACGGTATTCCGCGAGCTGAACCGCTGTATGGGATAACAGCTGAAATGTCGCGG
220
G I K T G H T D K A G Y N L V A S A T E G Q H R L I S A V M H G G R T F K G R E A
240
961
GCATCAAACCGGACACACTGCAAGCAGGTTACAACCTGTCTGCGACTGAAGCCAGATGCGCTGTATTTCTGCGGATATGGCGGAGCTACTTTTAAAGCCGTGAAGCGG
260
E S E K K L L T W G F R P F F E T V H P L K V G K E F A S E P V W F G D S D R A S L
280
1081
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300
G V D K D V Y L T I P R G R H K D L K A S Y V L H S S E L H A P L Q K H Q V V G
320
1201
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340
T I N F Q L D G K T I E Q R P L V L Q E I F E G H F F G K I I D Y I A M T F
360
1321
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374
H M P *
1441
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1561
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-27
1
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1
T Q Y S S L R G L A G S A F L F L P A P T A F A E Q T V E A P S W D A R A
1
121
CGCAATATCCTCTCTCGTGLCGTACGGGGTCTGCAATTTTATCTTTTGCACCAAGCGATTCGCGCGGAAACCGTTCGCGCGGAGCAACCGTTCGCGGATGCGCGGTCAT
20
W I L H M T A S G E V L A E G H A D E R L D P A S T E I N T S Y V V G A L K
40
241
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60
A D K I K L T D M V T V G K D A W A T G H F A L R G S S V M F L K P G D Q V S V
80
361
CCGATAAGATTAATCACTCAGGATAGGTGACCTCGGTAAAGATGCTCGGCGACGGGAAATCCGGCACTGCGTGTTCATCGGATATGTCGCAACCGGCGATCAGGTTTCGGTGG
100
A D L N K G V I I Q S G H D A C I A L A D Y V A G S Q E S F I G L N H G Y A K K
120
481
CAGACTTGAACAAAGGTGATTTATCGTCCGGTATGACGCGTGTATGTCGCTGGCTGATTAAGTTCGCGGGAGCAGGAGTCAATTTGGTGTGATGATGGTTATGCCAAAAC
140
L G L T N T T F T V H G L D A P G Q F S T A R D M A L L G K A L I H D V P E
160
601
TGGTCTGACCAACACTACTCTCCAGACGGTGCAGCGGCTGGATGCGCGGGGCACTTCCAGCACCAGCGCGATATGATGCTGCGGTAAGACATTGATCCAGATGTCGCGGAAAGT
180
Y A I H K E K E P T F N K I R Q P N R H R L L M S S W L N E D G M K T G T A G
200
721
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220
A G Y H L V A S A T Q G D N H R L I S V V L G A K T D R I R F N H E S E K L L T W G
240
841
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260
R F R F E T V T P I K P D A T F U T Q R V W F G D K S E G N L E A G S V T
280
961
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300
I P R G Q L K N L K A S Y T L T E P Q L V T A P L K E G V G D S E G V T I D F Q L N K
320
1081
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340
S I E Q R P L I V N E N V E E G G F F G R V W D F V M H K F H Q W F G S W F S
360
1201
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374
1321
CTCTGTAACCGGATCGCGAAACGCTACCGGTTATGCTCATTAACTCAATCAGAACTTAATGCGGCTCGGTACTTCACTACTCATCTCCGCGGCAACATCGCTCACCA
1441
TATCAAAGCGTTTCAGTCCACCTCGCGCGGACGACCTGCGCAAGGATAGTGGTGCAG

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