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Nucleotide sequence of the diaminopimelate-decarboxylase gene from *Bacillus subtilis*

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The Bacillus subtilis lys gene, encoding the diaminopimelate (DAP)-decarboxylase (EC4.1.1.20), was cloned in a temperate B. subtilis phage ρ11 from the B. subtilis chromosomal DNA [1], and the gene was then recloned into the B. subtilis plasmid pUB110. The figure shows the complete necleotide sequence (981 bp) of the lys gene and the prediction of an amino acid sequence (327 amino acid residues). The B. subtilis lys gene was 93 amino acid residues shorter than that of the Escherichia coli lysA gene encoding DAP-decarboxylase at its COOH-terminal region. The B. subtilis lys gene shared 45% and 25% homology at the nucleotide and deduced amino acid level to those of the E. coli lysA gene [2].

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        HindIII
        AAGCTTGGCAACAAATGAGCCGTCTTGTCCTCATGATACTCGTTGCTTTATTTCATATAAAAGGGCTCGTCATCGGATTTACAGTGCTAATTATGCCATGGCAAGCATCAAATCC
                                                                                  200
CTTCAGACACCGTACTTATGGCCGCTGATTCCCTTTAACGGAAAGGCGCTGTGGCAGGTGCTTGTCCCGACAGCGAAACCTGGCGCAAAAGTAAGACCCAGCATCGTTCACCCCAAAAATCGC

TTAAGGCAGCCTACCAATTCATAATCGCATTGAAACTGACTGAAGAGTATGATAATGTATGTCTTAATTATGAAGGGACAGTCCATAAAACTGTCCTTTCATCCATAAGCGGAGAAAGAGGGA
                                                400
ATG ACA TTG TTC TTA CAC GGC ACA AGC AGA CAA AAT CAA CAT GGT CAT TTA GAA ATC GGA GGT GTG GAT GCT CTC TAT TTA GCG GAG AAA TAT
Met Thr Leu Phe Leu His Gly Thr Ser Arg Gln Asn Gln His Gly His Leu Glu Ile Gly Gly Val Asp Ala Leu Tyr Leu Ala Glu Lys Tyr 31
                                                                  HindIII                      PstI
GGT ACA CCT CTT TAC GTA TAT GAT GTG GCT TTA ATA CGT GAG CGT GCT AAA AGC TTT AAG CAG GCG TTT ATT TCT GCA GGG CTG AAA GCA CAG
Gly Thr Pro Leu Tyr Val Tyr Asp Val Ala Leu Ile Arg Glu Arg Ala Lys Ser Phe Lys Gln Ala Phe Ile Ser Ala Gly Leu Lys Ala Gln 62
                                                                   600
GTG GCA TAT GCG AGC AAA GCA TTC TCA TCA GTC GCA ATG ATT CAG CTC GCT GAG GAA GAG GGA CTT TCT TTA GAT GTC GTA TCC GGA GAG AGC
Val Ala Tyr Ala Ser Lys Ala Phe Ser Ser Val Ala Met Ile Gln Leu Ala Glu Glu Glu Gly Leu Ser Leu Asp Val Val Ser Gly Glu Ser 93

TAT ATA CGG CTG TTG CAG CAG GCT TTC CGG CAG AAC GCA TCC ACT TTC ATG GAA ACA ATA AGA GCA GGG AAG AAC TGC GGA TGG CGC TTG AGC
Tyr Ile Arg Leu Leu Gln Gln Ala Phe Arg Gln Asn Ala Ser Thr Phe Met Glu Thr Ile Arg Ala Gly Lys Asn Cys Gly Trp Arg Leu Ser 124
                                                                                      800                 ClaI
ACC GCA TCG GCT GCA TTG TGG TGG ATA ATT TCT ATG AAA TCG TCG CTT CTT GAA GAC CTA TGT AAA GAA ACG GGT CAC TCC ATC GAT GTT CTT
Thr Ala Ser Ala Ala Leu Trp Trp Ile Ile Ser Met Lys Ser Ser Leu Leu Glu Asp Leu Cys Lys Glu Thr Gly His Ser Ile Asp Val Leu 155

CTT CGG ATC ACG CCC GGA GTA GAA GCG CAT ACG CAT GAC TAC ATT ACA ACG GGC CAG GAA GAT TCA AAG TTT GGT TTC GAT CTT CAT AAC GGA
Leu Arg Ile Thr Pro Gly Val Glu Ala His Thr His Asp Tyr Ile Thr Thr Gly Gln Glu Asp Ser Lys Phe Gly Phe Asp Leu His Asn Gly 186
                                                            PvuII                                      1000
CAA ACT GAA CGG GCC ATT GAA CAA GTA TTA CAA TCG GAA CAC ATT CAG CTG CTG GGT GTC CAT TGC CAT ATC GGC TCG CAA ATC TTT GAT ACG
Gln Thr Glu Arg Ala Ile Glu Gln Val Leu Gln Ser Glu His Ile Gln Leu Leu Gly Val His Cys His Ile Gly Ser Gln Ile Phe Asp Thr 217

GCC GGT TTT GTG TTA GCA GCG GAA AAA ATC TTC AAA AAA CTA GAC GAA TGG AGA GAT TCA TAT TCA TTT GTA TCC AAG GTG CTG AAT CTT GGA
Ala Gly Phe Val Leu Ala Ala Glu Lys Ile Phe Lys Lys Leu Asp Glu Trp Arg Asp Ser Tyr Ser Phe Val Ser Lys Val Leu Asn Leu Gly 248
                                                                                                                         1200
GGA GGT TTC GGC ATT CGT TAT ACG GAA GAT GAT GAA CCG CTT CAT GCC ACT GAA TAC GTT GAA AAA ATT ATC GAA GCT GTG AAA GAA AAT GCT
Gly Gly Phe Gly Ile Arg Tyr Thr Glu Asp Asp Glu Pro Leu His Ala Thr Glu Tyr Val Glu Lys Ile Ile Glu Ala Val Lys Glu Asn Ala 279

TCC CGT TAC GGT TTT GAC ATT CCG GAA ATT TGG ATC GAA CCG GGC CGT TCT CTC GTG GGA GAC GCA GGC ACA ACT CTT TAT ACG GTT GGC TCT
Ser Arg Tyr Gly Phe Asp Ile Pro Glu Ile Trp Ile Glu Pro Gly Arg Ser Leu Val Gly Asp Ala Gly Thr Thr Leu Tyr Tyr Val Gly Ser 310
                                                                                              HindIII
CAA AAA GAA GTG GAT AAG CTG TAC AAT CGT TTC ATC ATT CGG CGT GCG AAT TAA GAAAGGTCTCATTGCGCCTGTAAAGCTTACGCGTATTTCTGCTCCTTCAAG
Gln Lys Glu Val Asp Lys Leu Tyr Asn Arg Phe Ile Ile Arg Arg Ala Asn                                                         327
1400
CACCTTTAGTGCATCCAGCATATATTTGGACTAAAAGAGATATTTAATTCCTCACCTTCAATTTGATCCGCAACAATTGCTTCCACAACTTTACCGATTTCTGGCGAATTGGAAGAAATTTC
                                                                             1600      EcoRI
AATGGATTCAGCCGGTTTTGCGGACAGTTTTACAACGTTGTTGCGTCCCTCTCTAGCTAAAAGAGATGCACGATCAATGGCCTGAAGGAATTC
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