

## Nucleotide sequence of the *fadA* and *fadB* genes from *Escherichia coli*

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A portion of the 9-kb *Bam*HI fragment (in clone # 550 of Kohara's library) upstream from the *rrnA* operon at about 86-min. was sequenced, and the *fadA* and the *fadB* genes were found. The *fadA* gene showed 40.9% homology with the gene for thiolase from *Zoogloea ramigera* (1). The *fadB* showed 35.0% and 31.1% homology with 3-hydroxyacyl-CoA dehydrogenase from pig mitochondria (2) and enoyl-CoA:hydratase-3-hydroxyacyl-CoA dehydrogenase from rat peroxisomes (3), respectively. The genes formed an operon in the order of B to A, which is the opposite direction to that reported by Spratt *et al.* (4), and transcribed in a counterclockwise direction with respect to the genetic map of *E. coli*.

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