

**Plant Gene Register**

# Nucleotide Sequence of the *Rhodobacter capsulatus* *hemE* Gene<sup>1</sup>

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*Rhodobacter capsulatus*, a purple, nonsulfur photosynthetic bacterium, produces four tetrapyrrole end products: heme, bacteriochlorophyll, vitamin B<sub>12</sub>, and siroheme. These end products are synthesized via a common pathway from aminolevulinate to uroporphyrinogen III. At this point, uroporphyrinogen III is either methylated, leading to siroheme and vitamin B<sub>12</sub>, or decarboxylated to form coproporphyrinogen III, the precursor of bacteriochlorophyll and heme. The decarboxylation is catalyzed by the product of the *hemE* gene, uroporphyrinogen decarboxylase.

The *R. capsulatus hemE* gene was cloned by complementing an *Escherichia coli hemE* mutant, AJB555 (E. Kanazireva and A. J. Biel, unpublished data), using an *R. capsulatus* chromosomal library in the expression vector pKK223-3 (Brosius and Holy, 1984). The putative amino acid sequence shares an overall identity of 34% with uroporphyrinogen decarboxylase from yeast (Garey et al., 1992) and *Bacillus subtilis* (Hansson and Hederstedt, 1992) and is 36% identical with the rat enzyme (Romana et al., 1987). The *R. capsulatus* enzyme has the conserved sequence PxWxM-RQAGR found in the N-terminal sequence of all other uroporphyrinogen decarboxylases (Garey et al., 1992). To our knowledge, this is the first report of a *hemE* gene sequence from a photosynthetic bacterium (Table I).

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The GenBank accession number for the sequence reported in this article is U16796.

### LITERATURE CITED

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**Table I.** Characteristics of the *R. capsulatus hemE* gene

Organism:	<i>Rhodobacter capsulatus</i> , PAS100 (Taylor et al., 1983).
Location on Chromosome:	<i>Xba</i> I fragment 7 (Fonstein and Haselkorn, 1993).
Function:	Encodes uroporphyrinogen decarboxylase (EC 4.1.1.31).
Techniques:	Nested deletions made in plasmid clones and dideoxy sequencing of both strands using CircumVent Thermal Cycle Sequencing kit (New England Biolabs).
Method of Identification:	Complementation of an <i>E. coli hemE</i> mutant.
Structural Features:	Open reading frame of 344 amino acids; calculated <i>M<sub>r</sub></i> , 43,611.
Codon Usage:	(G+C) content 64%; exhibits typical <i>R. capsulatus</i> codon preference (Young et al., 1989).

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