The *Escherichia coli* rpoN (*glnF*) gene encodes the novel RNA polymerase sigma factor σ^70 (4, 5, 9). During the isolation of the homologous gene from *Klebsiella pneumoniae*, we purified R-prime DNA carrying *K. pneumoniae* rpoN from an *E. coli* K-12 strain and cloned the gene by complementation (10). Two classes of plasmid were obtained, one (pMM17) with a 1.8-kb *ClaI* insert carrying *K. pneumoniae* rpoN and one (pMM18) with a 4.6-kb *ClaI* insert carrying *E. coli* rpoN. Both plasmids have since been used in a number of laboratories to characterize rpoN homologs in other bacterial species (6, 12).

In *E. coli* and other enteric species rpoN has been genetically mapped at around 70 min (2, 3, 11), and in order to map the gene precisely on the *E. coli* physical map, we have determined the restriction map of pMM18 and compared it with the Kohara restriction map (7) and the nucleotide sequence of *E. coli* rpoN (6a, 13). These comparisons (Fig. 1) unambiguously locate rpoN at 3411 to 3413 kb on the *E. coli* physical map, in that every restriction site predicted by Kohara et al. (7) to occur within pMM18 is present and no unpredicted sites were found. The only minor differences are the presence of two adjacent *EcoRV* sites between 3412 and 3413 kb and the reversal of the order of the *EcoRV* and *PstI* sites between 3410 and 3411 kb, both of which were determined by sequencing. These data also confirm that the gene is transcribed clockwise as proposed by Castano and Bastarrachea (1).

Sequence analysis of the region downstream of rpoN (6a unpublished) has identified three additional open reading frames, all of which are transcribed in the same direction as rpoN (Fig. 1). The predicted translation products of these three genes are homologous to open reading frames 95, 162, and 193, which lie immediately downstream of rpoN in *K. pneumoniae* (8).

**REFERENCES**


