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Fig. 25-11. Unrooted phylogenetic tree showing the relationship between inferred amino acid sequences from nine late genes, homologous to phage P2 genes *Q*, *P*, *O*, *N*, *M*, *L*, *S*, *H*, and *T*, from completely sequenced bacteriophage genomes. The tree was constructed with maximum-parsimony criteria and was the shortest tree found using the exhaustive search procedure. Numbers above branches indicate branch length (total 7549, the next shortest tree had a total length of 7732). The total number of characters was 4281 and there were 1913 parsimoniously informative characters. The tree was constructed with the program PAUP, version 4.0b8a (140).

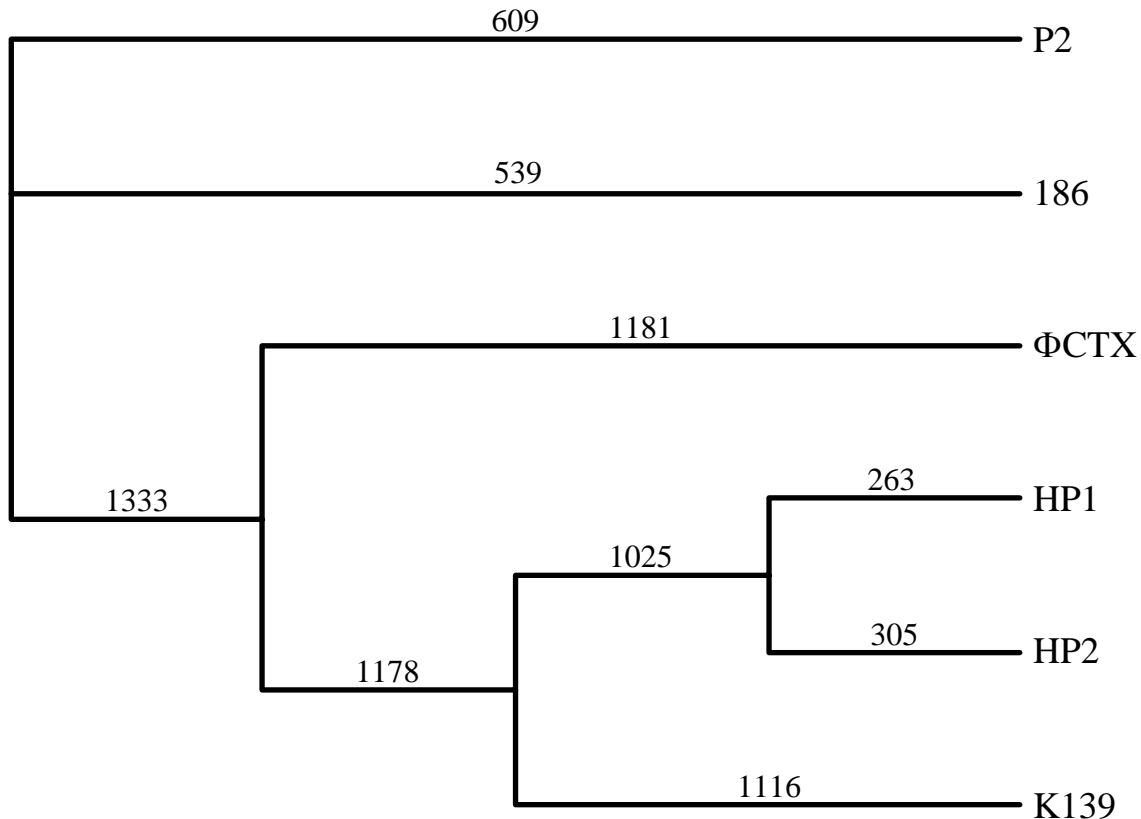


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