

Complete Genome Sequence of an Aerobic Hyper-thermophilic Crenarchaeon, *Aeropyrum pernix* K1 (Supplement)

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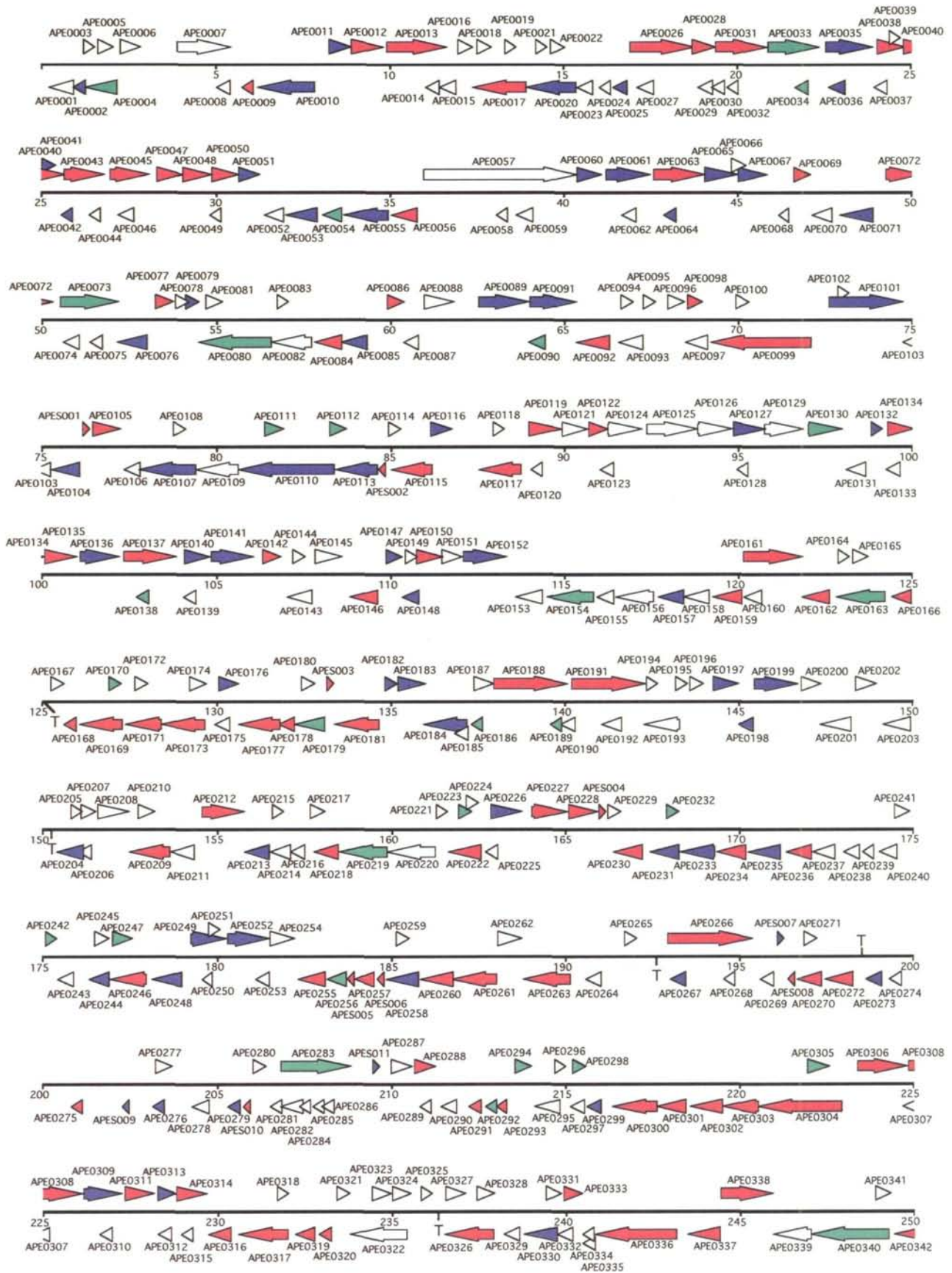
(Received 9 March 1999)

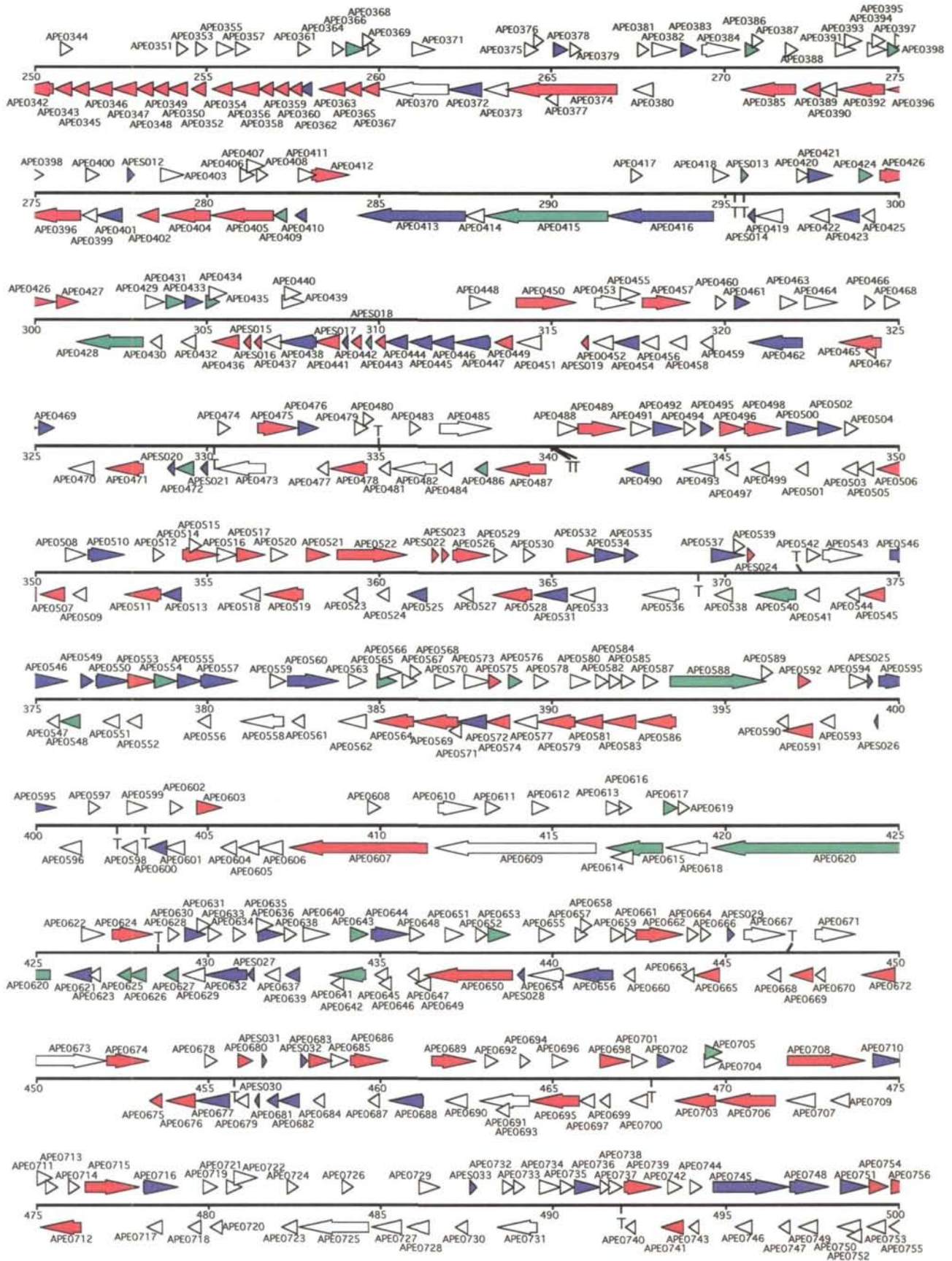
The circular genome of *Aeropyrum pernix* K1, (1669695 bp long) was opened at the junction of *Swa* I-A and *Swa* I-D fragments, and is represented by a linear map starting from this site. The nucleotide positions are indicated on the linear map in kilobases. Above and below the physical maps, the potential protein-coding regions (ORFs) assigned are indicated by boxes with arrowheads, showing the direction of transcription. The detailed assignment procedures are described in the main article in this issue (pp. 83–101). The results of ORF similarity and motif search are shown using the following color codes: red, similarities to reported genes with known functions; blue, similarities to hypothetical genes;

green, some motifs but without significant similarity to the registered sequences; and no color, no apparent similarity to any reported genes and no significant protein motifs. The ORF name defined in the main article are given to each ORF, and the positions of rRNA and tRNA genes are indicated by closed boxes and vertical bars with "T", respectively. The sequence data reported here have been deposited in the DDBJ/Genbank/EMBL databases under accession numbers AP000058 (nucleotide positions 1–202,000), AP000059 (202,001–369,000), AP000060 (369,001–716,800), AP000061 (716,801–985,000), AP000062 (985,001–1,236,700), AP000063 (1,236,701–1,422,000) and AP000064 (1,422,001–1,669,695).

Communicated by Mituru Takanami

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