Lambda (λ) is a large, temperate E. coli bacteriophage with a linear, largely double-stranded DNA genome (1-5). At each end, the 5´ strand overhangs the 3´ strand by 12 bases. These single-stranded overhangs are complementary and anneal to form a cos site following entry into a host cell. Once annealed, the genome is a circular, completely double-stranded molecule which serves as a template for rolling-circle replication.

Many laboratory strains of lambda are derivatives of the strain λ cI857 in d1 Sam7, which contains four point mutations relative to the wild type strain. The in d1 mutation in the cI gene creates a new HindIII site at 37584 not present in the wild type. All lambda products sold by NEB are λ cI857 in d1 Sam7.

Numbering of the genome sequence begins at the first (5´-most) base of the left end (bottom of diagram below) and continues rightward from late genes nu1 and A towards the early genes. The map below shows the positions of all known ORFs larger than 200 codons. Enzymes with unique restriction sites are shown in bold type and enzymes with two restriction sites are shown in regular type. Location of sites of all NEB restriction enzymes can be found on the NEB web site (choose Technical Reference > DNA Sequences and Maps). Restriction site coordinates refer to the position of the 5´-most base on the top strand in each recognition sequence.

References