# M13mp18

GenBank Accession #: X02513
Revised sequence file available at www.neb.com.
See page 128 for ordering information.

There are no restriction sites for the following enzymes: AatII, AbsI(x), AcuI, AflII, AgeI, AhdI, AjuI(x), ApaI, ApaLI, AscI, AsiSI, AvrII, BbsI, BcgI, BciVI, BclI, BlpI, BmgBI, BmtI, BpiI(x), BsaI, BsgI, BsiWI, BspEI, BspQI, BssHII, BssSI, BstAPI, BstBI, BstEII, BstXI, BstZ17I, EagI, EcoNI, EcoO109I, EcoRV, FseI, FspAI(x), HpaI, KflI(x), MauBI(x), MfeI, MluI, MreI(x), MteI(x), NcoI, NheI, NmeAIII, NotI, NruI, NsiI, PaeR7I, PaqCI, PasI(x), PflFI, PflMI, PfoI(x), PmeI, PmlI, PpuMI, PshAI, PspOMI, PspXI, PsrI(x), RsrII, SacII, SanDI, SapI, ScaI, SexAI, SfiI, SgrAI, SgrDI(x), SpeI, SrfI(x), StuI, StyI, Tth111I, XcmI, XhoI, ZraI

(x) = enzyme not available from NEB

**We recommend NEBcutter at NEBcutter.com to identify the restriction sites within your DNA sequence. NEBcutter indicates cut frequency and methylation-state sensitivity.**

M13 is a filamentous *E. coli* bacteriophage specific for male (F factor-containing) cells. Its genome is a circular, single-stranded DNA molecule 6407 bases in length, and contains 10 genes. A double-stranded form (RF) arises as an intermediate during DNA replication.

The M13mp phage vectors, derived from M13, contain the *lacZ*α gene and differ from each other by the cloning sites embedded within it. The location of cloning sites inside this gene allows screening for insertions using α-complementation. The map of M13mp18, whose multiple cloning site (MCS) was later employed to construct the plasmid pUC19, is shown below. M13mp19 is identical to M13mp18 except that the MCS region (6231-6288) is inverted.

The complete nucleotide sequences of M13mp18 and M13mp19 have been determined at New England Biolabs (1), resulting in several nucleotide changes relative to the previous sequence data (2,3).

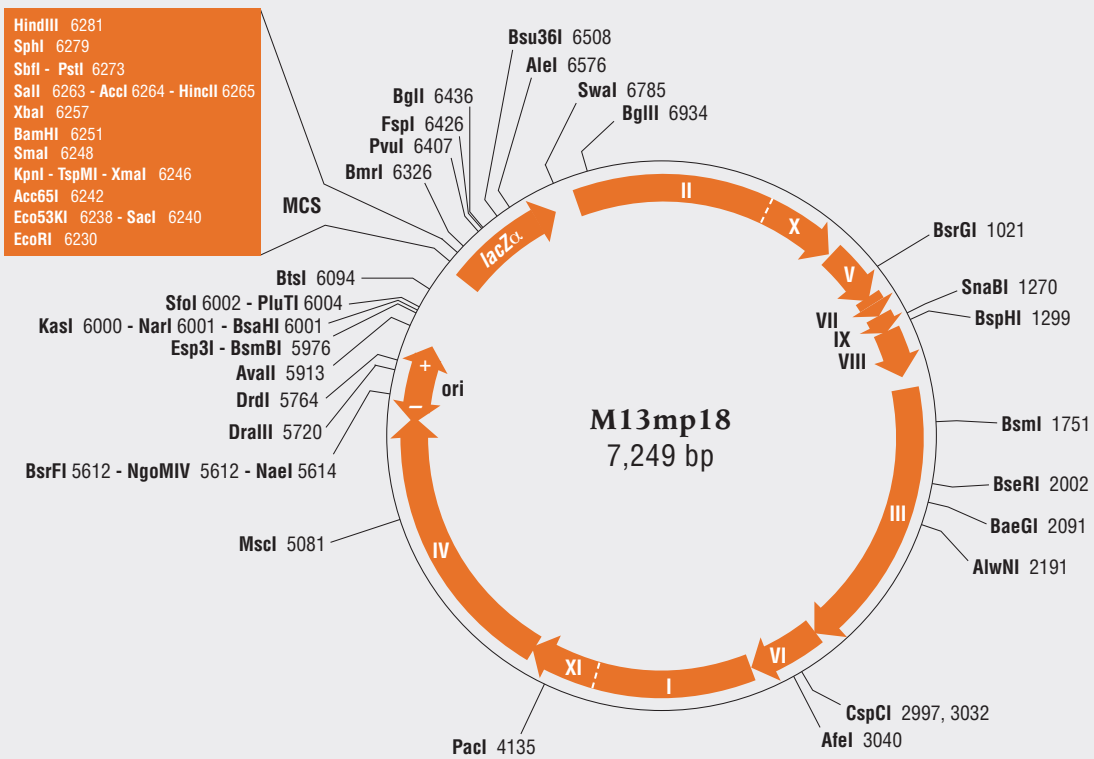
Enzymes with unique restriction sites are shown in **bold** type.
**Coordinates indicate position of cutsite on the top strand. In previous catalogs, coordinates referred to the position of the 5´ most base on the top strand, please make note of new numbering system.**

Open reading frame (ORF) coordinates are in the form "translational start – translational stop"; numbers refer to positions on the top (clockwise) strand, regardless of the direction of transcription and include the start and stop codons.

M13 origin of replication arrows indicate the direction of synthesis of both the (+) and (–) strands.

| Feature | Description | Coordinates |
|---|---|---|
| gene II | replication | 6848-831 (cw) |
| gene X | replication | 496-831 |
| gene V | replication | 843-1106 |
| gene VII | minor coat protein | 1108-1209 |
| gene IX | minor coat protein | 1206-1304 |
| gene VIII | major coat protein | 1301-1522 |
| gene III | minor coat protein | 1578-2852 |
| gene VI | minor coat protein | 2855-3193 |
| gene I | phage assembly | 3195-4241 |
| gene XI (I*) | phage assembly | 3915-4241 |
| gene IV | phage assembly | 4219-5499 |
| ori | M13 origin (+) of replication | 5487-5867 |
| *lacZ*α | for α-complementation | 6216-6722 |
| MCS | multiple cloning site | 6230-6286 |

(cw) = clockwise





**References**
(1) Stewart, F.J. (2002) unpublished observations.
(2) Messing, J. et al. (1977) *Proc. Natl. Acad. Sci.* USA, 74, 3652–3646.
(3) Yanisch-Perron, C., Vieira, J. and Messing, J. (1985) *Gene,* 33, 103–119.