M13mp18

GenBank Accession #: X02513
Revised sequence file available at www.neb.com.
See page 118 for ordering information.

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

(x) = enzyme not available from NEB

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; sequences of the MCS region from other M13mp vectors are shown on the previous page. M13mp19 is identical to M13mp18 except that the MCS region (6231-6288) is inverted.

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

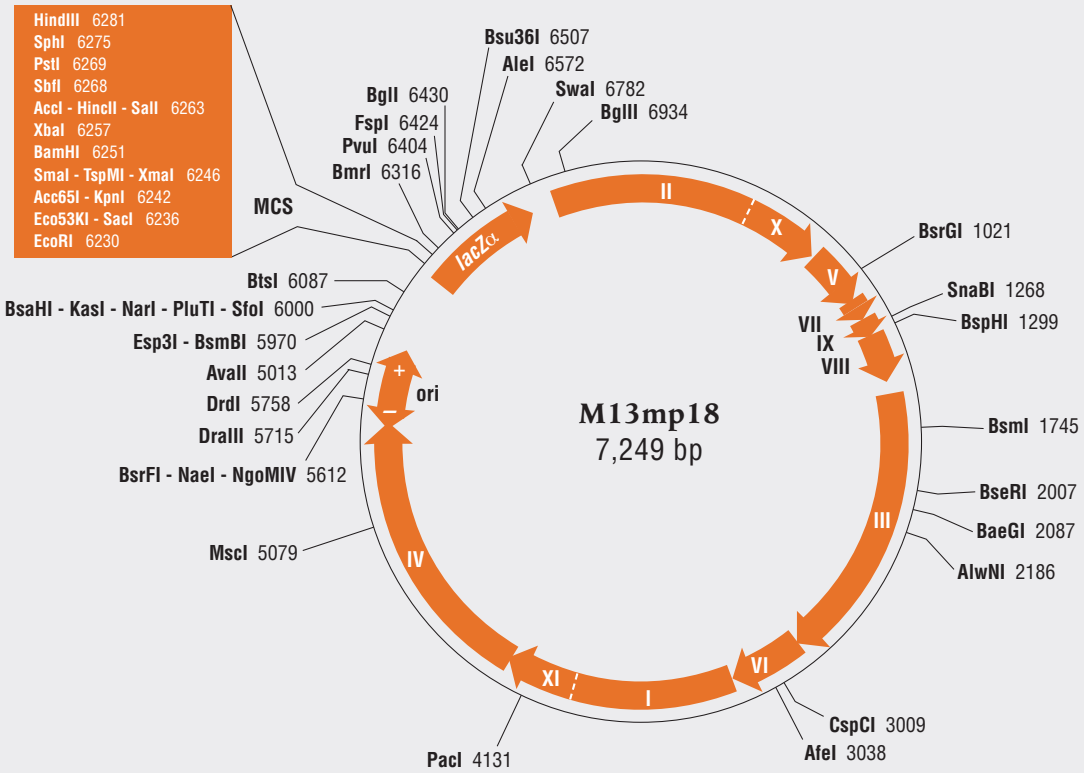
Enzymes with unique restriction sites are shown in **bold** type. Location of sites of all NEB restriction enzymes for select plasmids can be found on the NEB website (choose Tools & Resources > DNA Sequences and Maps tool). Restriction site coordinates refer to the position of the 5´-most base on the top strand in each recognition sequence.

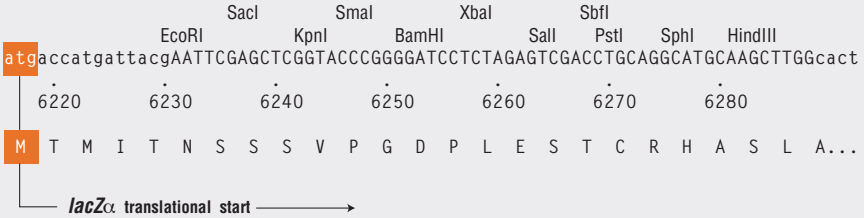
Open reading frame (ORF) coordinates are in the form "translational start – translational stop"; numbers refer to positions on the top (clockwise) strand, regardless of the direction of transcription and include the start and stop codons.

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.