CATALOG NUMBER

821222 M13MP 18 RF — 10 µg
M13mp18 and mp 19 RF DNA's are circular molecules of 7250 base pairs and contain polylinker regions of 54 base pairs. The parental bacteriophage, M13, is a filamentous, male-specific, *E.coli* phage in which the DNA molecule is single stranded and circular. Infected *E.coli* contain the double stranded, or replicative form (RF), DNA while the virions containing the (+) strand are secreted into the medium.
The polylinker regions contain recognition sites for 14 commonly used restriction enzymes, enabling cloning of a wide variety of restriction fragments. The 54 base pair polylinker region in M13mp 19 is in the reverse orientation to that in M13mp 18.
Both M13mp18 and 19 RF DNA's are supplied as an aqueous solution in 10 mM tris HCl, pH 8.0, 1 mM EDTA at a concentration of 0.5 µg/ul.
Also see M13mp19 RF

821223 M13MP19 RF — 10 µg
See description under M13mp18 RF

821224 pAT153 — 25 µg
pAT153 is a 3658 bp insertion vector isolated from *E.coli*. It contains ampicillin and tetracycline resistance genes. pAT153 is supplied as an aqueous solution in 10 mM tris HCl, pH 7.5, 1 mM EDTA at a concentration of 0.5 µg/µl.

821225 pBR322 — 25 µg
pBR322 is a 4363 bp vector purified from *E.coli*. It contains single restriction sites for Pst 1 and Pvu 1 within the ampicillin-resistance gene and single restriction sites for BamH I, Sal I, Sph I, EcoR V, Nru 1 and Xma III within the tetracycline-resistance gene. Supplied in 10 mM tris HCl, pH 7.5, 1 mM EDTA at a concentration of 0.5 µg/µl.

821226 pUC18 — 25 µg
pUC 18 and 19 are small vectors of approximately 2.7 Kb, and contain the Pvu II/EcoR I fragment of pBR322 and the lacZ gene multiple cloning site from M13mp18 (in pUC18) or mp19 (in pUC 19).
Both supplied in 10 mM tris HCl, pH 7.5, 1 mM EDTA at a concentration of 0.5 µg/µl.

821227 pUC19 — 25 µg
A small cloning vector of approx. 2.7 Kb. See pUC18 for more description.

OLIGONUCLEOTIDES

DNA Linkers (non-phosphorylated)

Linkers are end duplexes of oligodeoxyribonucleotides with terminal 5' and 3' -OH groups. Linkers can be used in molecular cloning protocols requiring the insertion of restriction sites into DNA. Each product is tested for purity and performance.

153383 0-5°C Aat II LINKER — 1 U
5′-d(GGACGTCC)-3′
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153384 0-5°C Apa I LINKER — 1 U
d(GGGGCCCC)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

CATALOG NUMBER

153385 0-5°C ApaL I LINKER — 1 U
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153386 0-5°C Avr II LINKER — 1 U
d(GCCTAGGC)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker

153387 0-5°C BamH I LINKER — 1 U
d(CGGATCCG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker

153388 0-5°C BamH I LINKER — 1 U
d(CGGGATCCCG)
1u = 1 A_{260} unit . One A_{260} unit is approx. 40 µg of linker.

153389 0-5°C BamH I LINKER — 1 U
d(CGCGGATCCGCG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153390 0-5°C Bcl I LINKER — 1 U
d(CTGATCAG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153391 0-5°C Bgl II LINKER — 1 U
d(CAGATCTG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153392 0-5°C Bgl II LINKER — 1 U
d(GGAAGATCTTCC)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153393 0-5°C Bgl II (*Mbo* II - *Mbo* II) LINKER — 1 U
d(GAAGATCTTC)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker

153394 0-5°C BspM II LINKER — 1 U
d(CTCCGGAG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153395 0-5°C BssH II LINKER — 1 U
d(CGCGCGCG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153396 0-5°C Cla I LINKER — 1 U
d(CATCGATG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153397 0-5°C Cla I LINKER — 1 U
d(CCATCGATGG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153398 0-5°C Cla I LINKER — 1 U
d(CCCATCGATGGG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

CATALOG NUMBER		
153399 0-5°C	**Cla I LINKER** (substrate for *dam* methylase) d(GATCGATC) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153400 0-5°C	**Cla I - Mbo II** (requires complement) d(ATCGATCTTC) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153401 0-5°C	**Cla I - Mbo II** (requires complement) d(GAAGATCGAT) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153402 0-5°C	**Dde I/Dra III** d(CACT A/T AGTG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153403 0-5°C	**EcoR I LINKER** d(GGATTCC) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153404 0-5°C	**EcoR I LINKER** d(CGGAATTCCG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker	1 U
153405 0-5°C	**EcoR I LINKER** d(CCGGAATTCCGG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153406 0-5°C	**EcoR I LINKER** (tailing) d(AATTCCGGAATT) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153407 0-5°C	**HinD III LINKER** d(CAAGCTTG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker	1 U
153408 0-5°C	**HinD III LINKER** d(CCAAGCTTGG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker	1 U
153409 0-5°C	**HinD III LINKER** d(CCCAAGCTTGGG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker	1 U
153410 0-5°C	**Kpn I LINKER** d(GGGTACCC) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker	1 U
153411 0-5°C	**Mlu I LINKER** d(GACGCGTC) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker	1 U
153412 0-5°C	**Mlu I LINKER** d(CGACGCGTCG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker	1 U
153413 0-5°C	**Nco I LINKER** d(CCCATGGG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153414 0-5°C	**Nco I LINKER** (methionine codon) d(CATGCCATGGCATG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153415 0-5°C	**Nde I LINKER** d(CCATATGG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153416 0-5°C	**Nhe I LINKER** d(GGCTAGCC) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153417 0-5°C	**Nhe I LINKER** d(CGGCTAGCCG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153418 0-5°C	**Nhe I LINKER** (nonsense codon) d(CTAGCTAGCTAG) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153419 0-5°C	**Not I LINKER** d(GCGGCCGC) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153420 0-5°C	**Not I LINKER** d(AGCGGCCGCT) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153421 0-5°C	**Not I LINKER** d(TTGCGGCCGCAA) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153422 0-5°C	**Nsi I LINKER** (cysteine codon) d(TGCATGCATGCA) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153423 0-5°C	**Pst I LINKER** d(GCTGCAGC) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U
153424 0-5°C	**Pst I LINKER** (cysteine codon) d(TGCACTGCAGTGCA) 1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.	1 U

Oligonucleotides

CATALOG NUMBER

153425 0-5°C **Pvu I LINKER** 1 U
d(CCGATCGG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153426 0-5°C **Pvu I (*Cla* I - *Cla* I)** 1 U
d(ATCGATCGAT)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153427 0-5°C **Pvu I (*Nru* I - *Nru* I)** 1 U
d(TCGCGATCGCGA)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153428 0-5°C **Pvu II LINKER** 1 U
d(CCAGCTGG)
1u = 1 A_{260}unit. One A_{260} unit is aprrox. 40 µg of linker.

153429 0-5°C **Sac I (*Sst* I) LINKER** 1 U
d(CGAGCTCG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153430 0-5°C **Sac II LINKER** 1 U
d(GCCGCGGC)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153431 0-5°C **Sac II LINKER** 1 U
(beta-turn proline codon)
d(TCCCCGCGGGGA)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153432 0-5°C **Sal I LINKER** 1 U
d(GGTCGACC)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153433 0-5°C **Sal I LINKER** 1 U
d(CGGTCGACCG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153434 0-5°C **Sal I LINKER** 1 U
d(CCGGTCGACCGG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153435 0-5°C **Sca I LINKER** 1 U
(cationic lysine codon)
d(AAAAGTACTTTT)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153436 0-5°C **Sfi I LINKER** 1 U
d(GGCCGC A/T GCGGCC)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153437 0-5°C **Sma I LINKER** 1 U
d(CCCCGGGG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

CATALOG NUMBER

153438 0-5°C **Sma I LINKER** 1 U
d(CCCCCGGGGG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153439 0-5°C **Sma I LINKER** 1 U
(beta-turn proline codon)
d(TCCCCCGGGGGA)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153440 0-5°C **Spe I LINKER** 1 U
d(GACTAGTC)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153441 0-5°C **Spe I LINKER** 1 U
d(GGACTAGTCC)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153442 0-5°C **Spe I LINKER** 1 U
d(CGGACTAGTCCG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153443 0-5°C **Spe I LINKER** 1 U
(nonsense codon)
d(CTAGACTAGTCTAG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153444 0-5°C **Sph I LINKER** 1 U
d(GGCATGCC)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153445 0-5°C **Sph I LINKER** 1 U
(methionine codon)
d(CATGCATGCATG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153446 0-5°C **Sph I LINKER** 1 U
(methionine or cysteine codon)
d(ACATGCATGCATGT)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153447 0-5°C **Xba I LINKER** 1 U
d(CTCTAGAG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153448 0-5°C **Xba I LINKER** 1 U
d(GCTCTAGAGC)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153449 0-5°C **Xba I LINKER** 1 U
d(TGCTCTAGAGCA)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153450 0-5°C **Xba I LINKER** 1 U
(nonsense codon)
d(CTAGTCTAGACTAG)
1u = 1 A_{260} unit. One A_{260}unit is approx. 40 µg of linker.

CATALOG NUMBER

153451 0-5°C **Xho I LINKER** 1 U
d(CCTCGAGG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153452 0-5°C **Xho I LINKER** 1 U
d(CCCTCGAGGG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153453 0-5°C **Xho I LINKER** 1 U
d(CCGCTCGAGCGG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

153454 0-5°C **Xma III LINKER** 1 U
d(CCGGCCGG)
1u = 1 A_{260} unit. One A_{260} unit is approx. 40 µg of linker.

DNA Primers

Primers are synthetic, single-stranded oligodeoxyribonucleotides used to prime (promote) DNA synthesis via DNA Polymerase and/or Reverse Transcriptase. Primers are also used in the generation of a hybridization probe for cloned sequences. Each product is tested for purity and performance.

153455 0-5°C **pBR322 *Bam*H I SITE, 20MER** 3 µg
(Clockwise)
5F128é...CACTATCGACTAC-GCGATCA...3′

153456 0-5°C **pBR322 *Eco*R I SITE, 16MER** 3 µg
(Clockwise)
5′...GTATCACGAGGCCCTT...3′

153457 0-5°C **pBR322 *Bam*H I SITE, 16MER** 3 µg
(Counter-clockwise)
5′...ATGCGTCCGGCGTAGA...3′

153458 0-5°C **pBR322 *Eco*R I SITE, 15MER** 3 µg
(Counter-clockwise)
5′...GATAAGCTGTCAAAC...3′

153459 0-5°C **pBR322 *Hind* III SITE, 15MER** 3 µg
(Clockwise)
5′...GACAGCTTATCATCG...3′

153460 0-5°C **pBR322 *Hind* III SITE, 16MER** 3 µg
(Counter-clockwise)
5′...GCAATTTAACTGTGAT...3′

153461 0-5°C **pBR322 *Pst* I SITE, 16MER** 3 µg
(Clockwise)
5′...GCTAGAGTAAGTAGTT...3′

153462 0-5°C **pBR322 *Pst* I SITE, 15MER** 3 µg
(Counter-clockwise)
5′...AACGACGAGCGTGAC...3′

153463 0-5°C **pBR322 *Sal* I, 15MER** 3 µg
(Clockwise)
5′...ATGCAGGAGTCGCAT...3′

153464 0-5°C **pBR322 *Sal* I, 15MER** 3 µg
(Counter-clockwise)
5′...AGTCATGCCCCGCGC...3′

CATALOG NUMBER

821335 **gt 11 FORWARD** 2 µg
5′-GACTCCTGGAGCCCG-3′
These primers are complementary to parts of the lacZ gene of gt 11 at either side of the Eco RI cloning site. Their use enables direct dideoxy sequencing of each end of the inserted DNA without further subcloning.

821336 **gt 11 REVERSE** 2 µg
gt 11 reverse
5′-GGTAGCGACCGGCGC-3′
These primers are complementary to parts of the lacZ gene of gt 11 at either side of the Eco RI cloning site. Their use enables direct dideoxy sequencing of each end of the inserted DNA without further subcloning.

HIV Primers
See: HIV Products Section

821228 **M13 15-MER** 2 µg
5′-TCCCAGTCACGACGT-3′.
This was the first M13 sequencing primer developed and it anneals to the (+) strand 37 bases upstream of the first restriction site in the multiple cloning site.

821229 **M13 SEQUENCING PRIMER (-20) 17-MER** 4 µg
5′-GTAAAACGACGGCCAGT-3′.
A universal primer with little complimentarity to other regions of the M13 DNA. It anneals close to the multiple cloning site. Since pUC vectors contain the same β-galactosidase gene as M13mp18/19, the same primer can be used to determine DNA sequences cloned into pUC vectors.

153465 0-5°C **M13 SEQUENCING PRIMER (-40) 17-MER** 4 µg
5′...GTTTTCCCAGTCACGAC...3′

153466 0-5°C **M13 HYBRIDIZATION PROBE PRIMER, 16-MER** 3 µg
5′...CACAATTCCACACAAC...3′

821230 **M13 PROBE PRIMER** 2 µg
5′-GAAATTGTTATCC-3′.
This primer is used
to generate hybridization probes from (+) strand M13 DNA carrying inserts.
The primer hybridizes downstream of the cloning site and during second strand synthesis in the presence of radioactive precursors, a partially double stranded molecule is generated which is single stranded in the region of the inserted DNA. This region of the inserted DNA can base pair with complementary sequences during hybridization reactions.

821231 **M13 REVERSE SEQUENCE PRIMER** 2 µg
5′-AACAGCTATGACCATG-3′
This reverse sequencing primer can be used to obtain sequence from the opposite end of the
insert in M13/pUC vectors to that obtained using the universal M13 primer.
It is not complementary to the (+) strand of M13 phage and therefore either double stranded sequencing must be performed or a partial second strand is generated using Klenow enzyme.