

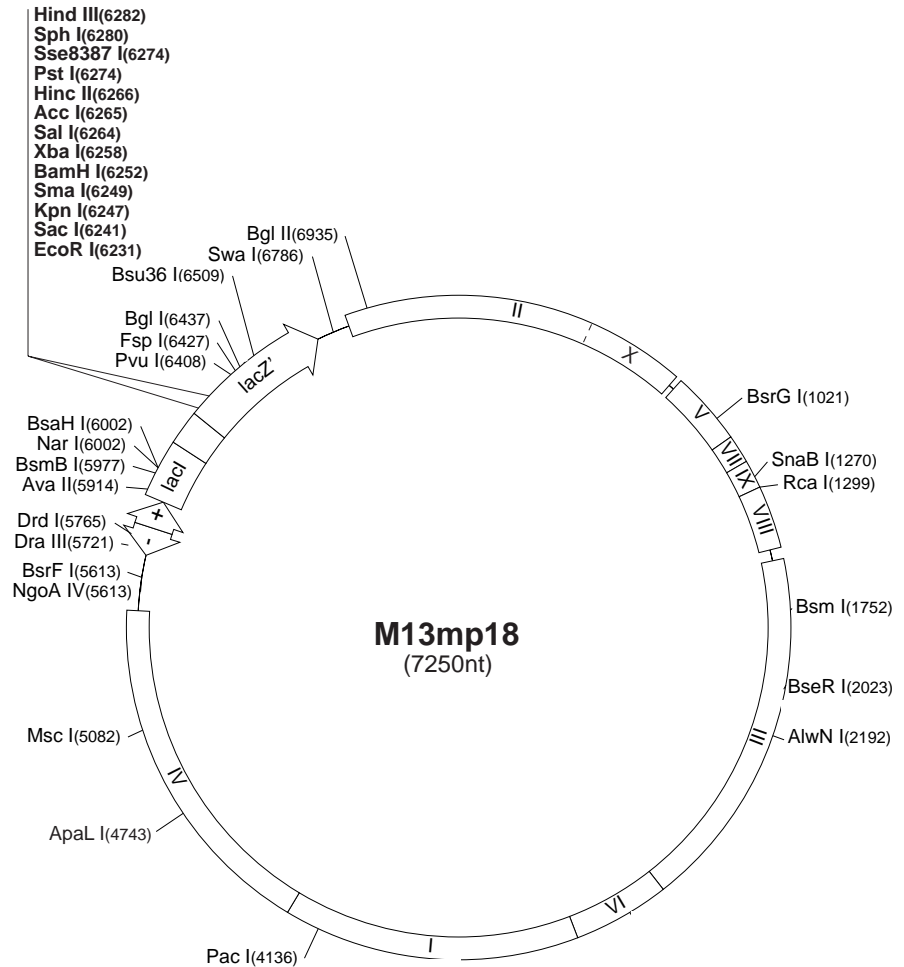
M13mp18 Vector

M13mp18 is a single-stranded filamentous phage vector derived from M13 (1). Double-stranded molecules (RF I) accumulate within cells during replication and can be isolated for cloning purposes. The sequence used to generate this map was the same as Genbank accession #X02513, except that a single T residue was added at position 898 to restore the reading frame of gene V as in wild-type M13 (F. Pfeiffer, MPI, Martinsreid). The vector is 7,250 bases in length and is numbered beginning at the first A of a *Hinc* II site that was modified during vector construction. All coding sequences are transcribed clockwise. Only the + strand product (shown below) of single-stranded replication is packaged into virions; therefore, sequencing of single-stranded DNA should be performed with the U-19mer primer (Cat. No. 69819-3).

1. Yanisch-Perron, C., Vieira, J. and Messing, J. (1985) *Gene* **33**, 103-119

M13mp18 sequence landmarks

<i>lacZ</i> start codon	6217
<i>lacZ'</i> α -peptide	6217-6720
multiple cloning region (<i>EcoR</i> I - <i>Hind</i> III)	6231-6282
M13 gene coding sequences	
II	6849-831
X	496-831
V	843-1106
VII	1108-1209
IX	1206-1304
VIII	1301-1522
III	1579-2853
VI	2856-3194
I	3196-4242
IV	4220-5500
IG region (interrupted by <i>lac</i> insertion, 5869-6711)	5501-6848



R-20mer primer #69835-3

CAGCTATGACCATGATTACG

6212

CAGCTATGACCATGATTACGAAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAAC

MetThrMetIleThr...

lacZ start

Blunt cloning site

Sma I

Acc I

Hinc II

Sse8387 I

EcoR I *Sac* I *Kpn* I *BamH* I *Xba* I *Sal* I *Pst* I *Sph* I *Hind* III

TGCAGCACTGACCCTTTTG

U-19mer primer #69819-3

M13mp18 cloning region

M13mp18 Restriction Sites

Enzyme	# Sites	Locations	Enzyme	# Sites	Locations	Enzyme	# Sites	Locations
AccI	1	6265	DrdI	1	5765	SphI	1	6280
AccIII	2	50 6717	DrdII	7	322 2303 2393 4473 4950	Sse8387I	1	6274
AcII	42				5713 5870	SspI	6	501 2662 5025 5215 6769
AfiIII	3	195 3618 3717	DsaI	2	2763 6617			6790
AluI	27		EaeI	3	5080 6036 6293	Swal	1	6786
AlwI	4	1376 2215 6247 6260	EarI	2	4080 6386	TaqI	12	
Alw21I	3	4747 5469 6241	EcII	2	1964 6605	TaqII	4	1439 2461 3269 5694
Alw44I	1	4743	Eco47III	2	2712 3041	TfiI	19	
AlwNI	1	2192	EcoRI	1	6231	ThaI	18	
ApoI	11		EcoRII	7	1013 1965 5940 5997 6136	TseI	10	933 1368 2522 3133 4872
AvaI	2	5825 6247			6327 6454			5537 5924 6053 6356 6429
Avall	1	5914	FauI	10	1393 1992 3332 5438 5510	Tsp45I	8	1376 1774 2542 2620 2743
BaeI	3	1800 2141 6522			5579 6035 6077 6406 7139			5110 5540 6313
BamHI	1	6252	FokI	4	7 225 3560 6347	Tsp509I	64	
BanI	7	1249 5677 6001 6131 6243	FspI	1	6427	Tth111II	7	3385 3436 4247 4522 4661
		6465 6477	GdIII	2	6036 6293			5894 6883
BanII	2	5647 6241	HaeI	4	2246 5082 5346 6683	UbaII	7	1395 2286 2289 2313 2358
BbvI	10	944 1354 2508 3119 4858	HaeII	6	2714 3043 5563 5571 6005			5501 5515
		5548 5910 6064 6367 6440			6450	VspI	7	4132 4136 4239 4629 6047
BccI	14		HaeIII	15				6106 6967
Bce83I	5	853 2026 2084 2597 5355	HgaI	7	535 2173 2488 3246 4072	XbaI	1	6258
BceII	7	1320 1968 3456 4735 5691			5147 6696	XmnI	2	361 2650
		6281 6592	HgiEII	1	6473			
Bfal	5	3827 5565 6259 6861 6979	HhaI	26				
BglI	1	6437	Hin4I	5	256 446 1077 2849 5156			
BglII	1	6935	HincII	1	6266			
BmgI	1	2090	HindIII	1	6282			
BpmI	2	6514 6884	HinfI	27				
Bpu10I	4	1371 1417 4013 4281	HphI	18				
BsaAI	5	1270 4448 5039 5464 5718	KpnI	1	6247			
BsaBI	2	1153 3978	MaeII	22				
BsaHI	1	6002	MaeIII	24				
BsaJI	9	2763 2894 5997 6136 6247	MbolI	11				
		6248 6327 6617 6838	MmeI	4	281 5466 5743 6652			
BsaWI	6	313 965 2377 2395 3369	MnlI	61				
		3841	MscI	1	5082			
BsaXI	4	1895 2671 5770 6021	MseI	63				
Bsbl	2	640 5811	MslI	2	2800 7000			
BscGI	8	1280 2088 2114 3087 3483	MspI	18				
		5624 5970 6633	MspA1I	4	1633 5962 6055 6377			
BseRI	1	2023	MwoI	20				
BsiEI	4	1425 3882 6408 6524	NarI	1	6002			
BsII	17		NciI	4	1925 6248 6249 6839			
BsmI	1	1752	NdeI	3	2724 3804 6847			
BsmAI	5	2018 2183 4041 5977 7022	NgoAIV	1	5613			
BsmBI	1	5977	NlaIII	15				
BsmFI	2	5075 6514	NlaIV	18				
BsoFI	17		NspI	6	199 3535 3622 3721 6280			
Bsp24I	2	2155 2187			6860			
Bsp1286I	5	2092 4747 5469 5647 6241	Pacl	1	4136			
BspGI	1	3642	Pfi1108I	2	1258 3425			
BspLU11I	3	195 3618 3717	PleI	8	2019 2853 4066 5323 5774			
BspMI	3	1104 2267 6277			5782 6270 6898			
BsrI	18		Psp1406I	2	4635 6774			
BsrBI	4	4571 5433 5574 6187	PstI	1	6274			
BsrDI	3	5205 6920 7066	PvuI	1	6408			
BsrFI	1	5613	PvuII	3	5962 6055 6377			
BsrGI	1	1021	RcaI	1	1299			
BstYI	3	2220 6252 6935	RleAI	1	3007			
Bsu36I	1	6509	RsaI	19				
Cac8I	28		SacI	1	6241			
CjeI	16		Sall	1	6264			
CjePI	6	2149 2182 6603 6636 6646	Sau96I	4	5724 5914 5938 6396			
		6679	Sau3AI	7	1381 1713 2220 6252 6405			
Clal	2	2528 6883			6501 6935			
CviJI	102		ScrFI	11				
CviRI	18		SfaNI	7	15 378 1344 3988 4840			
Ddel	29				6536 6549			
DpnI	7	1383 1715 2222 6254 6407	Sfcl	7	205 1329 1751 2470 5495			
		6503 6937			6270 6673			
DraI	5	191 474 4624 6786 7076	SmaI	1	6249			
DrallI	1	5721	SnaBI	1	1270			

Enzymes that do not cut M13mp18:

AatII	AfiII	AgeI	ApaI	ApaBI
AscI	AvrII	BbsI	BcgI	BcgII
BclI	Bpu1102I	BsaI	BsgI	BsII
BspEI	BssHII	Bst1107I	BstEII	BstXI
EagI	Eam1105I	Eco57I	EcoNI	EcoO109I
EcoRV	FseI	HpaI	MluI	MunI
NcoI	NheI	NotI	NruI	NsiI
NspV	PfiMI	PmeI	PmlI	PshAI
Psp5II	RsrII	SacII	SapI	Scal
SexAI	SfiI	SgfI	SgrAI	SpeI
SrfI	StuI	StyI	SunI	Tth111I
XcmI	XhoI			