FBrf0082873

DEPARTMENT OF MOLECULAR AND CELLULAR BIOLOGY
HARVARD UNIVERSITY

16 Divinity Avenue
Cambridge, Massachusetts 02138

11 October 1995

Dr. Ethan Bier
Department of Biology 0322
University of California
La Jolla, CA 92093-0322

FAX: [redacted]

Dear Dr. Bier,

FlyBase is trying to compile a description of all the major cloning vectors, enhancer traps, etc., commonly used by Drosophilists. We would like to provide a compiled sequence, when possible. We have presented partial sequences in many cases, especially when only small regions are unknown. I am the curator responsible for compiling this type of information and would appreciate your assistance in describing P{lacW}.

If you would like to see the type of reports we are presenting, a sample can be viewed if you have access to FlyBase via the WWWeb, using the SymbolSearch tool. (Suggestions and comments are welcome!)

The only information I have describing P{lacW} is the 1989 Genes Dev. paper. Would you be able to provide a more complete description of the construction or composition of both the transposon and the plasmid?

Thank you in advance for your assistance.

Sincerely,

Lynn Crosby

Lynn Crosby (for FlyBase)

[redacted]
FAX:
e-mail: [redacted]

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DEPARTMENT OF BIOLOGY, 0322
FAX NUMBER: [redacted]

9500 GILMAN DRIVE
LA JOLLA, CALIFORNIA 92093-0322

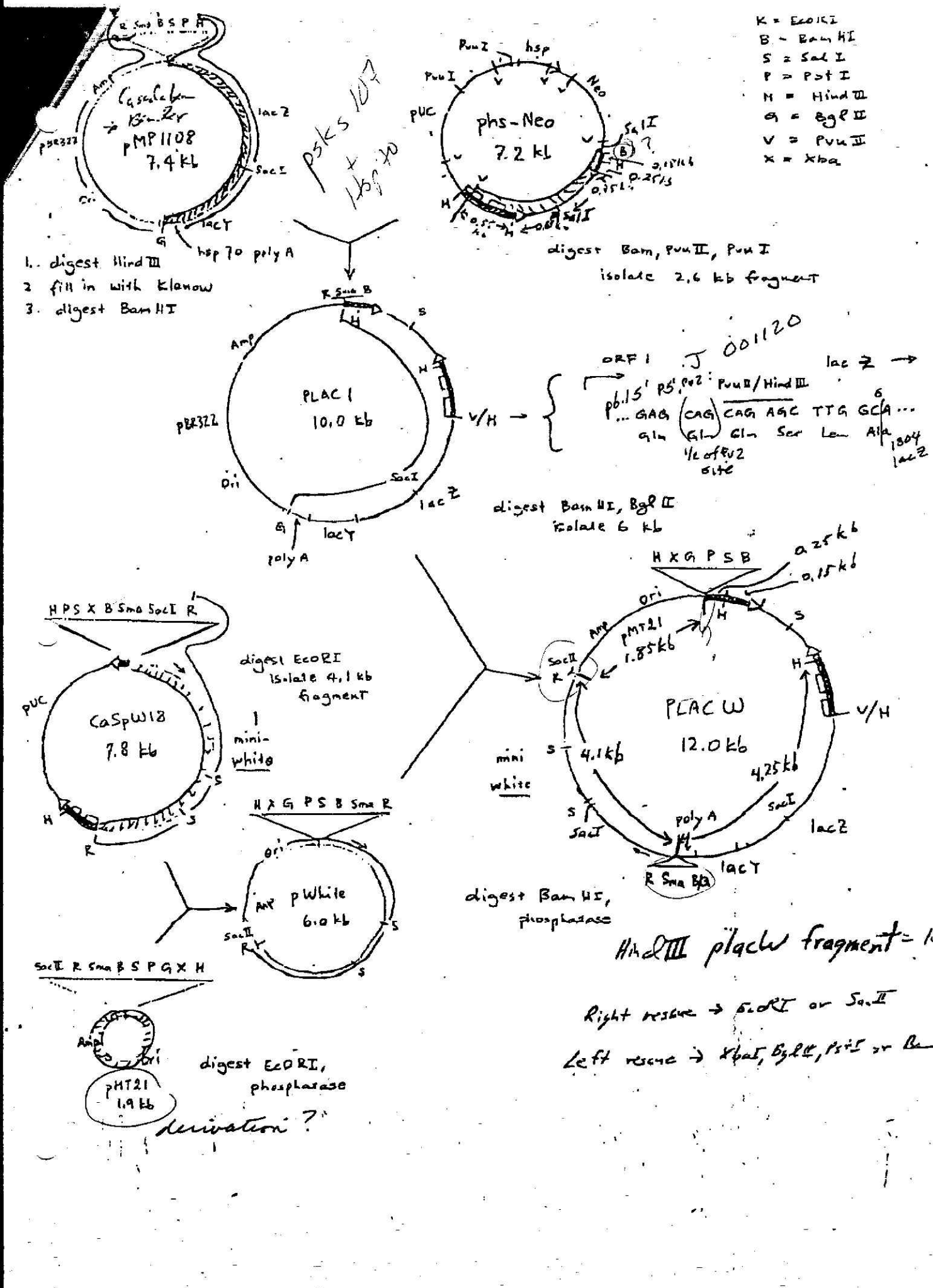
10/13/95

Dear Lynn,

Here is a PLACW map.

Best Wishes,

Ethan Bier


K = EcoRI
B = Bam HI
S = Sal I
P = Pst I
H = Hind III
G = Bgl II
V = Pvu II
X = Xba
pMP1108
7.4 kb
phs-Neo
7.2 kb
pKS 102
+
pKS 120
1. digest Hind III
2 fill in with Klenow
3. digest Bam HI
hsp 70 poly A
digest Bam, Pvu II, Pvu I
isolate 2.6 kb fragment
PLAC I
10.0 kb
ORF 1
lac Z
Pvu II / Hind III
digest Bam HI, Bgl II
isolate 6 kb
CaSpW18
7.8 kb
digest EcoRI
isolate 4.1 kb
fragment
1
mini-
white
pWhite
6.0 kb
digest EcoRI,
phosphatase
pHT21
1.9 kb
derivation ?
PLAC W
12.0 kb
mini
white
4.1 kb
4.25 kb
0.25 kb
0.15 kb
poly A
lac Z
lac Y
digest Bam HI,
phosphatase
Hind III placW fragment = 10.2 kb
Right rescue → EcoRI or Sac II
Left rescue → Xba I, Bgl II, Pst I or Bam HI

FAX COVER PAGE

~~10/9/95~~
10/19/95

Department of Biology
University of California, San Diego
Fax Number: [redacted]

Number of Pages_____
(Including Cover Sheet)

Mailed to:
LYNN CROSBY
_____
[redacted]

Mailed from:
_____
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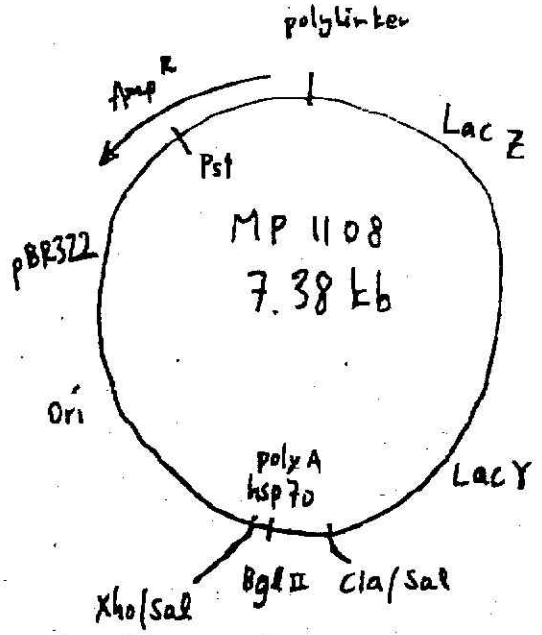
MESSAGE:

pMP1108 - DNA prep, reducing polylinker

1-26-87 Welcome Bender has sent us a LacZ containing vector (with poly A tail from hsp70) called pMP1108. This construction should be a starting point for a p-element vector I'll make. My vector will have the LacZ gene from MP1108 fused to the transposase promoter, which will function in Drosophila as a means of probing the genome for tissue specific enhancers. The vector can be also used for mutagenesis.

I'll need first of all to make more pMP1108 DNA. I transformed bacteria, picked a colony, grew up a O/N culture, did a DNA prep as per usual.

I estimated my DNA concentration at ~0.05 μg/μl.



polylinker:

G AAT TCC CGG GGA TCC GTC GAC

EcoRI SmaI BamHI SalI

6 7 8

CTG CAG CCA AGC TTG GCA CTG GCC

Pst HindIII Lac Z →

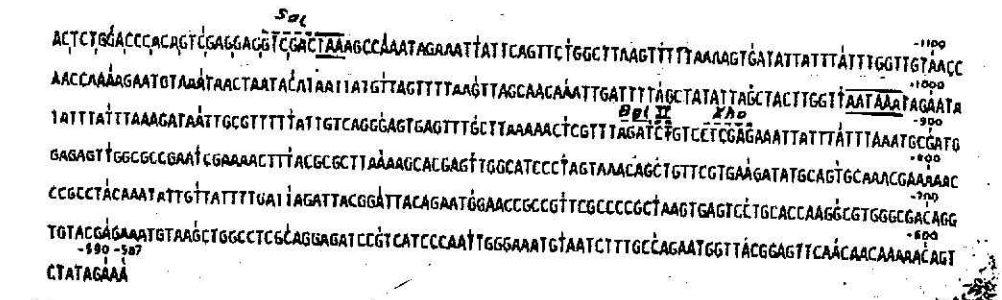


FIG. 4. Nucleotide sequence of the 132E3 spacer. The nucleotide sequence starts 29 nucleotides upstream from the termination triplet of the first 132E3 gene. The continuation of the base sequence, corresponding to the duplicated region of 132E3 is shown in Fig. 3 starting from position −586, upper line. Thus the numbering corresponds to that of Fig. 3. The termination triplet and the A-A-T-A-A-A motif are shown by thick lines. The restriction sites of some relevant enzymes are indicated. The hyphens have been omitted for clarity.

(d) *A very A+T-rich sequence conserved in front of two hsp70 genes*

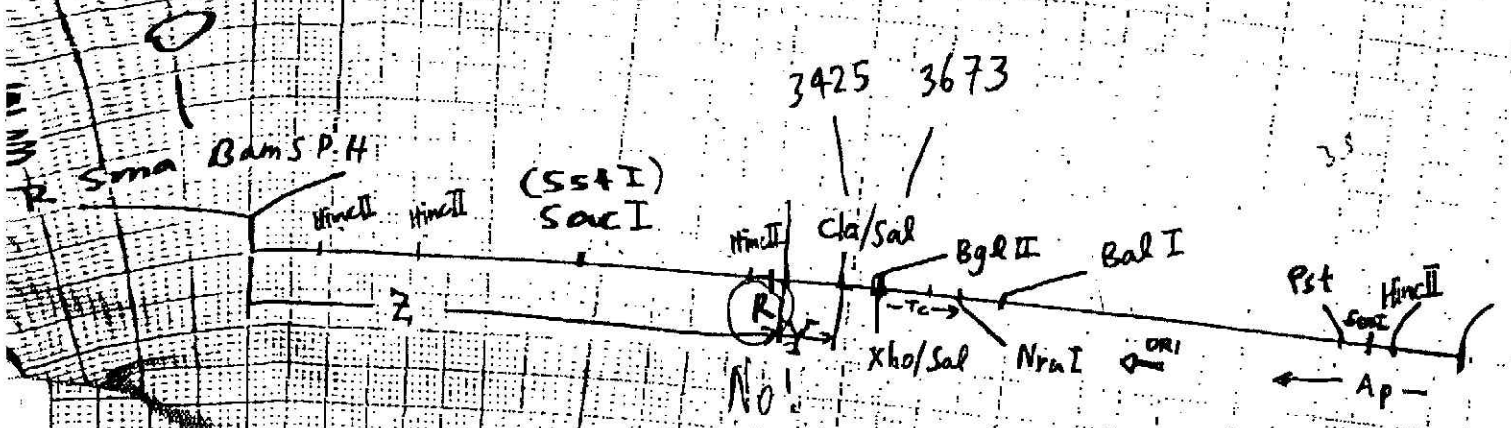
In front of the first 132E3 gene, in the region corresponding to X, we find an A+T-rich stretch of 150 bases, from position −753 to −603, of which 140 are homologous to an A+T-rich segment at the same position in 56H8 (*Fig.* 3). This observation confirms the suspicion that this A+T-rich region is characteristic of the X element (Török & Karch, 1980). Interestingly, the X sequence appears to be directly duplicated in front of the first 132E3 gene, since it is also found from position −922 to −772. In front of the second gene, however, we find no sequence corresponding to X, confirming the data of Goldschmidt-Clermont (1980). Moreover, we assume that this sequence homology corresponds to X_b described by Goldschmidt-Clermont (1980).

4. Discussion

(a) *Sequences of hsp70 genes*

The genes for the major heat shock protein of 70,000 M_r are present as two variants, each originating from one of two sites on the chromosomes, 87A7 and 87C1 (Ish-Horowicz *et al.*, 1979). The *D. melanogaster* DNA insert in plasmid 132E3 contains two hsp70 genes from site 87C1 arranged in tandem. We have sequenced a region upstream from the first gene which contains the elements X and Z_{ne} homologous to similar elements in front of other hsp70 genes (Moran *et al.*, 1979; Artavanis-Tsakonas *et al.*, 1979); the beginning and the end of the first hsp70 coding sequence Z_c, the spacer between the two repeated genes, the element Z_{ne} and the beginning of Z_c in the second repeat (see Introduction for a definition of the sequence elements X, Y, Z_{ne} and Z_c). Similar analysis of the other hsp70 gene variant in 56H8, originating from site 87A7, have been reported (Török & Karch, 1980) and recently, Ingolia *et al.* (1980) have published the complete primary sequence of one hsp70 gene contained in the hybrid plasmid G3.

MP1108



Bam - Bgl fragment ~ 3673

other fragment 3710

cuts in pBR but not in lacZ or hsp70 (once) : BalI, EagI, NruI, ScaI

cuts pBR twice XmnI

BglI - 1444, 3565
RssHII - 2796
ClaI - 2121

pMT21

...sequence has 7% base strand pMT21
from the 'standard restriction' file.

Sequence too long or too many sites for condensed map.

1 GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGC
CGCAACGACCGCAAAAAGGTATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTTAGCTGCG

23 NlaIV, 42 SrfMI, 54 TaqI, 56 HgaI,

61 TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGA
AGTTCAGTCTCCACCGCTTTGGGCTGTCCTGATATTTCTATGGTCCGCAAAGGGGGACCT

69 MnlI, 102 EcorII ScrFI, 115 EcorII ScrFI,

121 AGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTT
TCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAA

121 AluI, 126 MnlI, 132 HhaI, 153 Fnu4HI, 161 HpaII,

181 CTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTG
GAGGGAAGCCCTTCGCACCGCGAAAGAGTTACGAGTGCGACATCCATAGAGTCAAGCCAC

198 HaeII, 199 HhaI, 229 DdeI,

241 TAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGC
ATCCAGCAAGCGAGGTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGGCTGGCGACG

257 AluI, 268 Bsp1286 HaiAI, 294 NspBII, 296 BbvI Fnu4HI, 29
9 HhaI,

301 GCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTG
CGGAATAGGCCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGAC

308 HpaII, 311 NaeIII, 325 HinfI, 333 NciI ScrFI, 334 HpaII,

361 GCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTC
CGTCGTCGGTGACCATTGTCCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAG

361 BbvI Fnu4HI, 364 BbvI Fnu4HI, 374 HaeIII, 393 MnlI,

421 TTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTG
AACTTCACCACCGGATTGATGCCGATGTGATCTTCCTGTCATAAACCATAGACGCGAGAC

430 HaeI, 431 HaeIII, 449 MaeI, 473 HhaI,

481 CTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACC
GACTTCGGTCAATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTTTGGTGG

490 HaeIII, 514 AluI, 521 BinI MboI, 524 HpaII, 528 TthIII2,
535 HsiEII, 539 NspBII,

541 GCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCT
CGACCATCGCCACCAAAAAAACAAACGTTCGTCGTCTAATGCGCGTCTTTTTTTCCTAGA

561 TthIII2, 567 TthIII2, 570 BbvI Fnu4HI, 581 ThaI, 582 Hha
I, 595 BinI XhoII, 596 MboI,

601 CAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGT
GTTCTTCTAGGAAACTAGAAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGCA

604 MboII, 606 XhoII, 607 BinI MboI, 615 MboI, 634 HgaI, 638
DdeI, 657 MaeII,

DdeI, 657 MaeII,

661 TAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAA
ATTCCCTAAAACCAGTACTCTAATAGTTTTTCCTAGAAGTGGATCTAGGAAAATTTAATT

673 NlaIII, 692 BinI XhoII, 693 MboI, 693 MboII, 698 HpaI, 7
02 MaeI, 704 XhoII, 705 BinI MboI, 711 AhaIII,

721 AAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAA
TTTACTTCAAAATTTAGTTAGATTTCATATATACTCATTTGAACCAGACTGTCAATGGTT

730 AhaIII, 773 MaeIII,

781 TGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCC
ACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGG

793 MnlI, 795 EsnI NlaIV, 804 DdeI, 810 MboI, 827 FokI,

841 TGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCT
ACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGGTCACGA

842 HinfI, 874 MnlI, 889 HaeXII NlaIV Sau96I, 898 BbvI Fnu4H
I,

901 GCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA
CGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTCGGT

911 ThaI, 925 HphI, 928 HpaII, 930 NlaIV,

961 GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATT
CGGCCTTCCCGGCTCGCGTCTTCACCAGGACGTTGAAATAGGCGGAGGTAGGTCAGATAA

961 BalI, 962 HpaII, 968 Sau96I, 969 HaeIII, 973 HhaI, 985 A
vaII Sau96I, 1004 MnlI, 1008 FokI,

1021 AATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTT
TTAACAACGGCCCTTCGATCTCATTCATCAAGCGGTCAAGTTATCAAACGCGTTGCAACAA

1029 HpaII NciI ScrFI, 1035 AluI, 1037 MaeI, 1067 FspI, 1068
HhaI, 1073 MaeII,

1081 GCCATTGCTGCAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCC
CGGTAACGACGTCCGTAGCACCACAGTGCGAGCAGCAAACCATACCGAAGTAAGTCGAGG

1087 BbvI Fnu4HI, 1088 EvaI, 1094 SfaNI, 1104 MaeIII, 1135 A
luI, 1139 HpaII,

1141 GGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGC
CCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTCGCCAATCG

1141 NlaIV, 1151 MboI, 1162 MaeIII, 1166 NlaIII, 1169 BinI M
boI, 1176 NlaIII, 1198 AluI,

1201 TCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTT
AGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACCGGCCTCACAATAGTGAGTACCAA

1207 AvaII Sau96I, 1210 MnlI, 1214 PvuI, 1215 MboI, 1235 Cfr
I, 1236 HaeIII, 1237 Fnu4HI, 1254 NlaIII,

1261 ATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACT
TACCGTCGTGACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACTGA

1264 BbvI Fnu4HI, 1290 NlaIII, 1293 FokI, 1304 SfaNI, 1315 M
aeIII,

CCACTCATGAGTTGGTTCAGTAAGACTCTTATCACATACGCCGCTGGCTCAACGAGAACG

1321 HphI, 1325 ScaI, 1326 KasI, 1344 DdeI, 1359 Fnu4HI, 1380 NciI SerFI,

1381 CCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATT
GGCCGCAGTTGTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTCACGAGTAGTAA

1381 HpaII, 1383 AhaII, 1384 HgaI, 1386 HincII, 1404 ThaI, 1405 HhaI, 1422 AheIII, 1429 Bsp1286 HgiAI,

1441 GGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCG
CCTTTTGCAAGAAGCCCCGCTTTTGAGAGTTCCTAGAATGGCGACAACTCTAGGTCAAGC

1442 XmnI, 1446 NaeII, 1450 NlaII, 1472 BinI XhoII, 1473 NboI, 1480 NspBII, 1489 XhoII, 1490 BinI NboI, 1498 TaqI,

1501 ATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCT
TACATTGGGTGAGCACGTGGGTTGACTAGAAGTCGTAGAAAATGAAAGTGGTCGCAAAGA

1503 MaeIII, 1514 Bsp1286 HgiAI, 1526 MboI, 1528 MboII, 1534 SfaNI, 1547 HphI,

1561 GGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAA
CCCACTCGTTTTTGTCCTTCCGTTTTACGGCGTTTTTTCCCTTATTCCCGCTGTGCCTTT

1562 HphI, 1588 Fnu4HI,

1621 TGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGT
ACAACTTATGAGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACA

1637 MboII, 1649 SspI,

1681 CTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGC
GAGTACTCGCCTATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCCAAGGCGCG

1683 NlaIII, 1731 NlaIV, 1736 ThaI, 1737 HhaI,

1741 ACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACC
TGTAAAGGGGCTTTTCACGGTGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGG

1765 AsuII AhaII, 1766 MaeII, 1770 DdeI, 1788 NlaIII,

1801 TATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAAGAATTAATTCCGCGGAATTCC
ATATTTTTATCCGCATAGTGCTCCGGGAAAGCAGAAGTTCTTAATTAAGGCGCCTTAAGG

1821 MnlI, 1823 HaeIII Sau96I, 1833 NboII, 1840 XmnI, 1849 NspBII SacII, 1850 ThaI, 1854 EcoRI, 1859 AvaI NciI SerFI, SmaI, 1860 HpaII NciI SerFI,

1861 CGGGGATCCGTCGACCTGCAGATCTCTAGAAGCTT
GCCCCTAGGCAGCTGGACGTCTAGAGATCTTCGAA

1864 BamHI BinI NlaIV XhoII, 1865 BinI NboI, 1870 AccI HincII SalI, 1871 TaqI, 1876 PstI, 1880 BglII XhoII, 1881 NboI, 1885 XbaI, 1886 NaeI, 1890 HindIII, 1891 AluI,

1921

4361 = 1842

Arguments in DNA rmt21
relative to the 'standard restriction' file.

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AccI-4	GTCGAC	1:	1870					
AhaII-2	GGCGTC	1:	1383					
AhaII-3	GACGTC	1:	1765					
AhaII		2:	1383	1765				
AhaIII	TTTAAA	3:	711	730	1422			
AluI	AGCT	7:	121	257	514	1035	1135	
			1198	1891				
AvaI-4	CCCGGG	1:	1859					
AvaII-2	GGTCC	2:	980	1207				
BamHI	GGATCC	1:	1864					
BanI-3	GGCACC	1:	795					
BbvI-1	GCTGC	3:	296	898	1087			
BbvI-2	GCAGC	4:	361	364	570	1264		
BbvI		7:	296	361	364	570	898	1087
			1264					
BglII	AGATCT	1:	1980					
BglI	GCC-----GGC	1:	961					
BinI-1	GGATC	4:	595	692	1472	1864		
BinI-2	GATCC	6:	521	607	705	1169	1490	
			1865					
BinI		10:	521	595	607	692	705	1169
			1472	1490	1864	1865		
Bsp1286-6	GTGCTC	1:	1429					
Bsp1286-9	GTGCAC	2:	268	1514				
Bsp1286		3:	268	1429	1514			
CfrI-2	TGGCCG	1:	1235					
DdeI	CT-AG	5:	229	638	804	1344	1770	
EcoRI	GAATTC	1:	1864					
EcoRII-1	CCAGG	1:	102					
EcoRII-2	CCTGG	1:	115					
EcoRII		2:	102	115				
Fnu4HI	GC-GC	11:	153	296	361	364	570	
			898	1087	1237	1264	1359	1388
FokI-2	GATGC	3:	827	1008	1295			
FspI	TGCGCA	1:	1067					
HaeI-2	TGGCCT	1:	430					
HaeII-3	GGCGCT	1:	198					
HaeIII	GGCC	5:	431	889	969	1236	1823	
HgaI-1	GACGC	2:	56	634				
HgaI-2	GCGTC	1:	1384					
HgaI		3:	56	634	1384			
HgiAI-2	GTGCTC	1:	1429					
HgiAI-3	GTGCAC	2:	268	1514				
HgiAI		3:	268	1429	1514			
HgiEII	ACC------GGT	1:	535					
HhaI	GCGC	9:	132	189	299	473	582	
			975	1068	1405	1737		
HincII-2	GTCAAC	1:	1386					
HincII-4	GTCGAC	1:	1870					
HincII		2:	1386	1870				
HindIII	AAGCTT	1:	1890					
HinfI	GA-TC	2:	325	842				
HpaII	CCGG	10:	161	308	334	524	928	
			962	1029	1139	1381	1860	
HphI-1	GGTGA	2:	1321	1562				
HphI-2	TCACC	3:	698	925	1547			
HphI		5:	698	925	1321	1547	1562	
HpaI	GTTAA	4:	449	702	1037	1886		

MaeII	ACGT	4:	657	1073	1446	1766		
MaeIII	GT-AC	8:	311	374	490	773	1104	
			1162	1313	1503			
MboI	GATC	15:	521	596	607	615	693	
			705	810	1151	1169	1215	1473
			1490	1526	1665	1881		
MboII-1	GAAGA	1:	604					
MboII-2	TCTTC	5:	695	1450	1528	1637	1833	
MboII		6:	604	695	1450	1528	1637	1833
MnlI-1	CCTC	3:	126	1004	1210			
MnlI-2	GAGG	5:	69	393	793	874	1821	
MnlI		8:	69	126	393	793	874	1004
			1210	1821				
NciI-1	CCCGG	3:	333	1380	1859			
NciI-2	CCGGG	2:	1029	1860				
NciI		3:	333	1029	1380	1859	1860	
NlaIII	CATG	7:	675	1166	1176	1254	1290	
			1683	1788				
NlaIV	GG--CC	7:	23	795	889	930	1141	
			1731	1864				
NspBII-2	CCGCTG	3:	294	539	1480			
NspBII-4	CCGCGG	1:	1849					
NspBII		4:	294	539	1480	1849		
•PstI	CTGCAG	2:	~~1081~~	1876				
PvuI	CGATCG	1:	1214					
RsaI	GTAC	1:	1326					
SacII	CCGCGG	1:	1849					
•SalI	GTCGAC	1:	1870					
ScaI	AGTACT	1:	1325					
Sau96I	GG-CC	5:	889	968	985	1207	1823	
ScrFI	CC-GG	7:	102	115	333	1029	1380	
			1859	1860				
SfaNI-1	GCATC	3:	42	1091	1534			
SfaNI-2	GATGC	1:	1304					
SfaNI		4:	42	1094	1304	1534		
SmaI	CCCGGG	1:	1859					
SspI	AATATT	1:	1649					
TaiI	CGCG	5:	581	911	1404	1736	1850	
TaqI	TCGA	3:	54	1498	1871			
TthIII2-1	CAAACA	1:	528					
TthIII2-2	CAAGCA	1:	567					
TthIII2-3	TGTTTG	1:	561					
TthIII2		3:	528	561	567			
•XbaI	TCTAGA	1:	1885					
XhoII-1	AGATCC	3:	606	704	1489			
XhoII-2	GGATCT	3:	595	692	1472			
XhoII-3	GGATCC	1:	1864					
XhoII-4	AGATCT	1:	1880					
XhoII		8:	595	606	692	704	1472	1489
			1864	1880				
XmnI	GAA----TTC	2:	1442	1840				

The following enzymes were not found:

NAME	SEQUENCE	NAME	SEQUENCE	NAME	SEQUENCE
AccI-1	GTAGAC	AccI-2	GTCTAC	AccI-3	GTATAC
AflII	CTTAAG	AflIII-1	ACATGT	AflIII-2	ACGTGT
AflIII-3	ACACGT	AflIII-4	ACGCGT	AhaII-1	GACGCC
AhaII-4	GGCGCC	ApaI	GGGCCC	AsuII	TTCGAA
AvaI-1	CTCGAG	AvaI-2	CCCGAG	AvaI-3	CTCGGG
AvaII-1	GGACC	AvaII	[illegible]	[illegible]	[illegible]

ThIII2-3	TGTTTG	1:	581				
TthIII2		3:	528	581	587		
XbaI	TCTAGA	1:	1885				
XhoII-1	AGATCC	3:	606	704	1489		
XhoII-2	GGATCT	3:	595	692	1472		
XhoII-3	GGATCC	1:	1864				
XhoII-4	AGATCT	1:	1880				
XhoII		8:	595	606	692	704	1472	1489
			1864	1880				
XmnI	GAA----TTC	2:	1442	1840				

The following enzymes were not found:

NAME	SEQUENCE	NAME	SEQUENCE	NAME	SEQUENCE
AccI-1	GTAGAC	AccI-2	GTCTAC	AccI-3	GTATAC
AflII	CTTAAG	AflIII-1	ACATGT	AflIII-2	ACGTGT
AflIII-3	ACACGT	AflIII-4	ACGCGT	AhaII-1	GAGGCC
AhaII-4	GGCGCC	ApaI	GGGCCC	AsuII	TTCGAA
AvaI-1	CTCGAG	AvaI-2	CCCGAG	AvaI-3	CTCGGG
AvaII-1	GGACC	AvrII	CCTAGG	BalI	TGGCCA
BanI-1	GGTACC	BanI-2	GGTGCC	BanI-4	GGCGCC
BanII-1	GAGCTC	BanII-2	GAGCCC	BanII-3	GGGCTC
BanII-4	GGGCCC	BclI	TGATCA	BsmI	GAATGC
Bsp1286-1	GGGCCC	Bsp1286-2	GAGCCC	Bsp1286-3	GTGCCC
Bsp1286-4	GGGCTC	Bsp1286-5	GAGCTC	Bsp1286-7	GGGCAC
Bsp1286-8	GAGCAC	BssHII	GCGCGC	BstEII	GGT-ACC
BstXI	CCA------TGG	Cfr1-1	TGGCCA	Cfr1-3	CGGCCA
Cfr1-4	CGGCCG	ClaI	ATCGAT	DraII-1	GGGNCCC
DraII-2	GGGNCCT	DraII-3	AGGNCCC	DraII-4	AGGNCCT
DraIII	CACNNNGTG	EcoRV	GATATC	FokI-1	GGATG
HaeI-1	AGGCCA	HaeI-3	AGGCCT	HaeI-4	TGGCCA
HaeII-1	AGCGCT	HaeII-2	AGCGCC	HaeII-4	GGCGCC
HgiAI-1	GAGCAC	HgiAI-4	GAGCTC	HincII-1	GTTAAC
HincII-3	GTTGAC	HpaI	GTTAAC	KpnI	GGTACC
MluI	ACGCGT	NaeI	GCCGGC	NarI	GGCGCC
NcoI	CCATGG	NdeI	CATATG	NheI	GCTAGC
NruI	TCGCGA	NsiI	ATGCAT	NspBII-1	CAGCTG
NspBII-3	CAGCGG	Nsp7524I-1	ACATGT	Nsp7524I-2	ACATGC
Nsp7524I-3	GCATGT	Nsp7524I-4	GCATGC	PvuII	CAGCTG
SacI	GAGCTC	SfiI	GGCC-----GGCC	SnaI	GTATAC
SnaBI	TACGTA	SpeI	ACTAGT	SphI	GCATGC
StuI	AGGCCT	StyI-1	CCAAGG	StyI-2	CCATGG
StyI-3	CCTTGG	StyI-4	CCTAGG	TthIII1	GAC---GTC
TthIII2-4	TGCTTG	XhoI	CTCGAG	XmaIII	CGGCCG