NEBcutter® V3.0

Open Existing Project

Name 1 ×

Name 2 ×

Name 3 ×

Log in to have unlimited access to your projects.

☑ Disable cookies Explain

Enter a DNA sequence, or select from other options, to identify cut sites.
Once you submit a sequence, you may choose to customize your digest.

1. Input or choose sequence. Explain

Paste Sequence

Plain or FASTA/
Max: 300 KBases

OR **Upload File (xx MB max.)** Upload File No file selected.

OR **Enter Gen Bank** Browse Gen Bank

OR **Select Sequence** Select Plasmid Vectors Select Viral and Phage

2. Update preferences. Explain

☑ Circular Additional Preferences

3. Name project (optional). Explain

Save

Submit

Open Existing Project

Name 1 ×

Name 2 ×

Name 3 ×

Log in to have unlimited access to your projects.

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Additional Preferences

Enzymes to include:

- ■ NEB enzymes (Type II & Type III)
- ☐ Time-Saver™ qualified enzymes
- ☐ All commercially available specificities
- ☐ All specificities
- ☐ All & defined oligonucleotide sequences
- ☐ Only defined oligonucleotide sequences
  Define Oligos

In addition to Type II & commercially-available Type III enzymes, also include:

- ☑ Type I & III enzymes
- ☑ Homing endonucleases
- ☑ Nicking enzymes

Methylation sensitivities to include:

- ☑ CpG methylation
- ☑ Dam methylation
- ☑ Dcm methylation
- ☑ EcoBI methylation
- ☑ EcoKI methylation

Minimum ORF length:

aa

Genetic code for ORFs:

Select Genetic Code

Process this region only: – bp

Save Cancel

Plain or FASTA/
Max: 300 KBases

nk

and Phage

3. Name project (optional). Explain

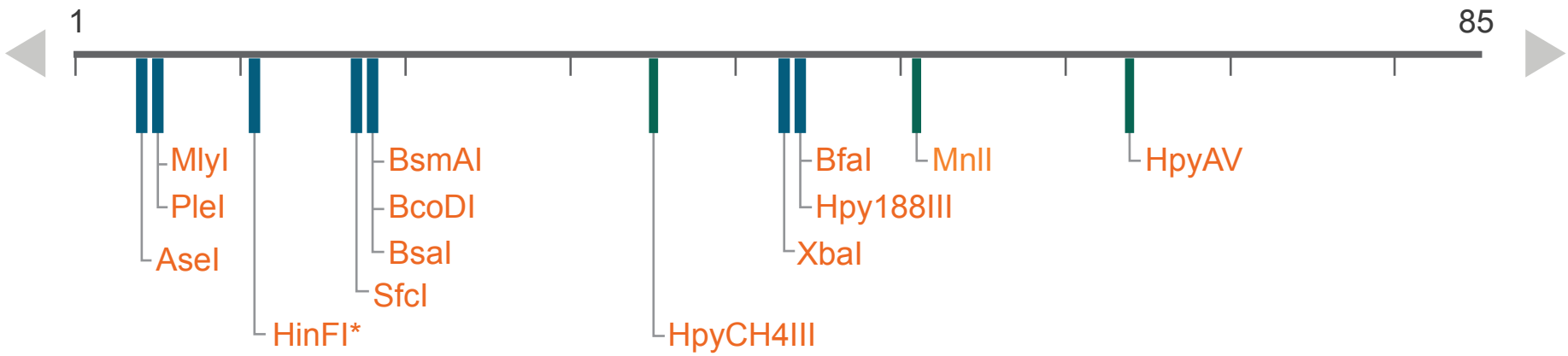
Save

Submit

Standard Digest for PURExpr prmr

Make PDF | Print

Use the menu to explore this digest, or to create a custom digest.



- Graphical View
- Enzyme List
- Sequence
- ORF Summary
- Customize Digest

Results For:

- Linear
- NEB single cutter restriction enzymes
- Main non-overlapping, min. 100 aa ORFs

Sequence Information:

2817 bp
GC = 34% AT = 66%

Update Preferences

Start Over

Display

- ☑ 1 cutters
- ☑ 2 cutters
- ☑ 3 cutters

Cleavage Code

- Blunt-End Cut
- Cuts 1 strand
- 5´ Extension
- 3´ Extension

Enzyme Code

- NEB
- Other supplier
- Not commercially available

Update Colors

Methylation

- * CpG methylation
- # dam/dcm methylation
- ( ) Ambigous site

Standard Digest for PURExpr prmr

Make PDF | Print

Graphical View

Enzyme List

Sequence

ORF Summary

Customize Digest

Results For:

- Linear
- NEB single cutter restriction enzymes
- Main non-overlapping, min. 100 aa ORFs

Sequence Information:

2817 bp

GC = 34% AT = 66%

Update Preferences

Start Over

Cut Position ▼	Enzyme ▲	Recognition Sequence	Me Sens.
2	MluCI	^AATT_	
5	AseI	AT^TA_AT	
5	MseI	T^TA_A	
6	FspEI	CC(N)12^NNNN_	
6	PleI	GAGTCNNNN^N_	
6	MlyI	GAGTC(N)5|	
7	FspEI	CC(N)12^NNNN_	
7	MspJI	CNNR(N)9^NNNN_	
12	HinfI	G^ANT_C	CpG
18	SfcI	C^TRYA_G	
19	FspEI	CC(N)12^NNNN_	CpG
19	BsmAI	GTCTCN^NNNN_	
19	BsaI	GGTCTCN^NNNN_	
19	BcoDI	GTCTCN^NNNN_	
26	MspJI	CNNR(N)9^NNNN_	
36	HpyCH4III	AC_N^GT	
42	FspEI	CC(N)12^NNNN_	
42	MspJI	CNNR(N)9^NNNN_	
42	MspJI	CNNR(N)9^NNNN_	
44	XbaI	T^CTAG_A	

Display

- ✓ 0 cutters
- ✓ 2 cutters
- ✓ All sites
- ✓ Flanking enzymes

NEB Restriction Enzyme Activity/Performance Chart

Standard Digest for LITMUS39

Make PDF | Print

Graphical View

Enzyme List

Sequence

ORF Summary

Customize Digest

Results For:

- Circular
- NEB single cutter restriction enzymes
- Main non-overlapping, min. 100 aa ORFs

Sequence Information:

2817 bp

GC = 34% AT = 66%

Update Preferences

Start Over

```
   1  GTTAACTACG TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT
  61  TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGAT AAATGCTTCA
 121   ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTC CGTGTCGCCC TTATTCCCTT
 181  TTTTGCGGCA TTTTGCCTTC CTGTTTTTGC TCACCCAGAA ACGCTGGTGA AAGTAAAAGA
 241  TGCTGAAGAT CAGTTGGGTG CACGAGTGGG TTACATCGAA CTGGATCTCA ACAGCGGTAA
 301  GATCCTTGAG AGTTTTCGCC CCGAAGAACG TTCTCCAATG ATGAGCACTT TTAAAGTTCT
 361  GCTATGTGGC GCGGTATTAT CCCGTGTTGA CGCCGGGCAA GAGCAACTCG GTCGCCGCAT
 421  ACACTATTCT CAGAATGACT TGGTTGAGTA CTCACCAGTC ACAGAAAAGC ATCTTACGGA
 481  TGGCATGACA GTAAGAGAAT TATGCAGTGC TGCCATAACC ATGAGTGATA ACACTGCGGC
 541  CAACTTACTT CTGACAACGA TCGGAGGACC GAAGGAGCTA ACCGCTTTTT TGCACAACAT
 601  GGGGGATCAT GTAACTCGCC TTGATCGTTG GGAACCGGAG CTGAATGAAG CCATACCAAA
 661  CGACGAGCGT GACACCACGA TGCCTGTAGC AATGGCAACA ACGTTGCGCA AACTATTAAC
 721  TGGCGAACTA CTTACTCTAG CTTCCCGGCA ACAATTAATA GACTGGATGG AGGCGGATAA
 781  AGTTGCAGGA CCACTTCTGC GCTCGGCCCT TCCGGCTGGC TGGTTTATTG CTGATAAATC
 841  TGGAGCCGGT GAGCGTGGGT CTCGCGGTAT CATTGCAGCA CTGGGGCCAG ATGGTAAGCC
 901  CTCCCGTATC GTAGTTATCT ACACGACGGG GAGTCAGGCA ACTATGGATG AACGAAATAG
 961  ACAGATCGCT GAGATAGGTG CCTCACTGAT TAAGCATTGG TAACTGTCAG ACCAAGTTTA
1021  CTCATATATA CTTTAGATTG ATTTACCCCG GTTGATAATC AGAAAAGCCC CAAAAACAGG
1081  AAGATTGTAT AAGCAAATAT TTAAATTGTA AACGTTAATA TTTTGTTAAA ATTCGCGTTA
1141  AATTTTTGTT AAATCAGCTC ATTTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT
1201  AAATCAAAAG AATAGCCCGA GATAGGGTTG AGTGTTGTTC CAGTTTGGAA CAAGAGTCCA
1261  CTATTAAAGA ACGTGGACTC CAACGTCAAA GGGCGAAAAA CCGTCTATCA GGGCGATGGC
1321  CCACTACGTG AACCATCACC CAAATCAAGT TTTTTGGGGT CGAGGTGCCG TAAAGCACTA
1381  AATCGGAACC CTAAAGGGAG CCCCCGATTT AGAGCTTGAC GGGGAAAGCG AACGTGGCGA
1441  GAAAGGAAGG GAAGAAAGCG AAAGGAGCGG GCGCTAGGGC GCTGGCAAGT GTAGCGGTCA
1501  CGCTGCGCGT AACCACCACA CCCGCCGCGC TTAATGCGCC GCTACAGGGC GCGTAAAAGG
1561  ATCTAGGTGA AGATCCTTTT TGATAATCTC ATGACCAAAA TCCCTTAACG TGAGTTTTCG
1621  TTCCACTGAG CGTCAGACCC CGTAGAAAAG ATCAAAGGAT CTTCTTGAGA TCCTTTTTTT
1681  CTGCGCGTAA TCTGCTGCTT GCAAACAAAA AAACCACCGC TACCAGCGGT GGTTTGTTTG
1741  CCGGATCAAG AGCTACCAAC TCTTTTTCCG AAGGTAACTG GCTTCAGCAG AGCGCAGATA
```

Standard Digest for LITMUS39

Make PDF | Print

Graphical View

Enzyme List

Sequence

ORF Summary

Customize Digest

Gene	Product	a.a. Seq.	Coordinates	Protein ID	Closest Enzyme 5´ End	Closest Enzyme 3´ End	Flanking Enzymes
bla	beta-lactamase	286 aa	143..1003	–	EarI	BsaJI	Show
lacZalpha	beta-galactosidase alpha fragment	121 aa	2424..2789	–	*BsrBI	HpaI	Show

Results For:

- Circular
- NEB single cutter restriction enzymes
- Main non-overlapping, min. 100 aa ORFs

Sequence Information:

2817 bp

GC = 34% AT = 66%

Update Preferences

Start Over

Custom Digest for pUC19

Make PDF | Print

Graphical View

Enzyme List

Fragments

Gel

Digested With:
- EcoRI
- HindIII

Sequence Information:

2686 bp
GC = 51% AT = 49%

Update Preferences

Start Over

EcoRI

NEB #R0101

Features:
- 5 minute Time-Saver
- Buffer: NEBuffer EcoRI
- Salt: 50 mM NaCl
- Main: 100 mM Tris-HCl
- pH: 7.5
- Mg: 10 mM MgCl2
- Triton: 0.025%
- Rxn temp.: 37 °C
- Neoschizomers: None
- Isoschizomers: None
- Sites in sequence: 1
- End produced at 396: 5´ overhang: AATT

REBASE page

NEB Restriction Enzyme Activity/Performance Chart

Methylation:

! This site overlaps a CpG site: GAATTCg , overlapping sites may impair cleavage if methylated.

Enzymes producing compatible ends:

Enzymes with no sites in pUC19:

Create Custom Digest for pUC19

Only enzymes that cut the sequence and match your selection of availability are shown. Non-NEB neoschizomers are not listed, but you can enter it in the search field and its prototype will be selected.

Jump to enzyme(s) or oligo sequence(s)

Select All	Enzyme ▼	Recognition Sequence	Cuts
☐	AatII	GACGTC	1
☐	Acc65I	GGTACC	1
☐	AccI	GTMKAC	1
☐	AciI	CCGC	34
☐	AclI	AACGTT	2
☐	AcuI	CTGAAG(N)14NN	2
☐	AflIII	ACRYGT	1
☐	AhdI	GACNNNNNGTC 1	1
☐	AluI	AGCT	16
☐	AlwI	GGATCNNNNN	10
☐	AlwNI	CAGNNNCTG	1
☐	ApaLI	GTGCAC	3
☑	ApeKI	GCWGC	12
☐	ApoI	RAATTY	1
☐	AseI	ATTAAT	3
☐	AvaI	CYCGRG	1
☐	AvaII	GGWCC	2
☑	BaeGI	GKGCMC	3
☐	BamHI	GGATCC	1
☐	BanI	GGYRCC	4

Digest Reset

Filter

- ☑ Enzymes with compatible buffers
- ☑ Enzymes producing blunt ends
- ☑ Enzymes producing 5' overhangs
- ☑ Enzymes producing 3' overhangs
- ☑ Enzymes with a particular site length
- ☑ Enzymes cutting N times
- ☑ Non-palindromic enzymes

Selections:

- ApeKI
- BaeGI
- EcoRI

Custom Digest for pUC19

Make PDF | Print

- **Graphical View**
- Enzyme List
- Fragments
- Gel

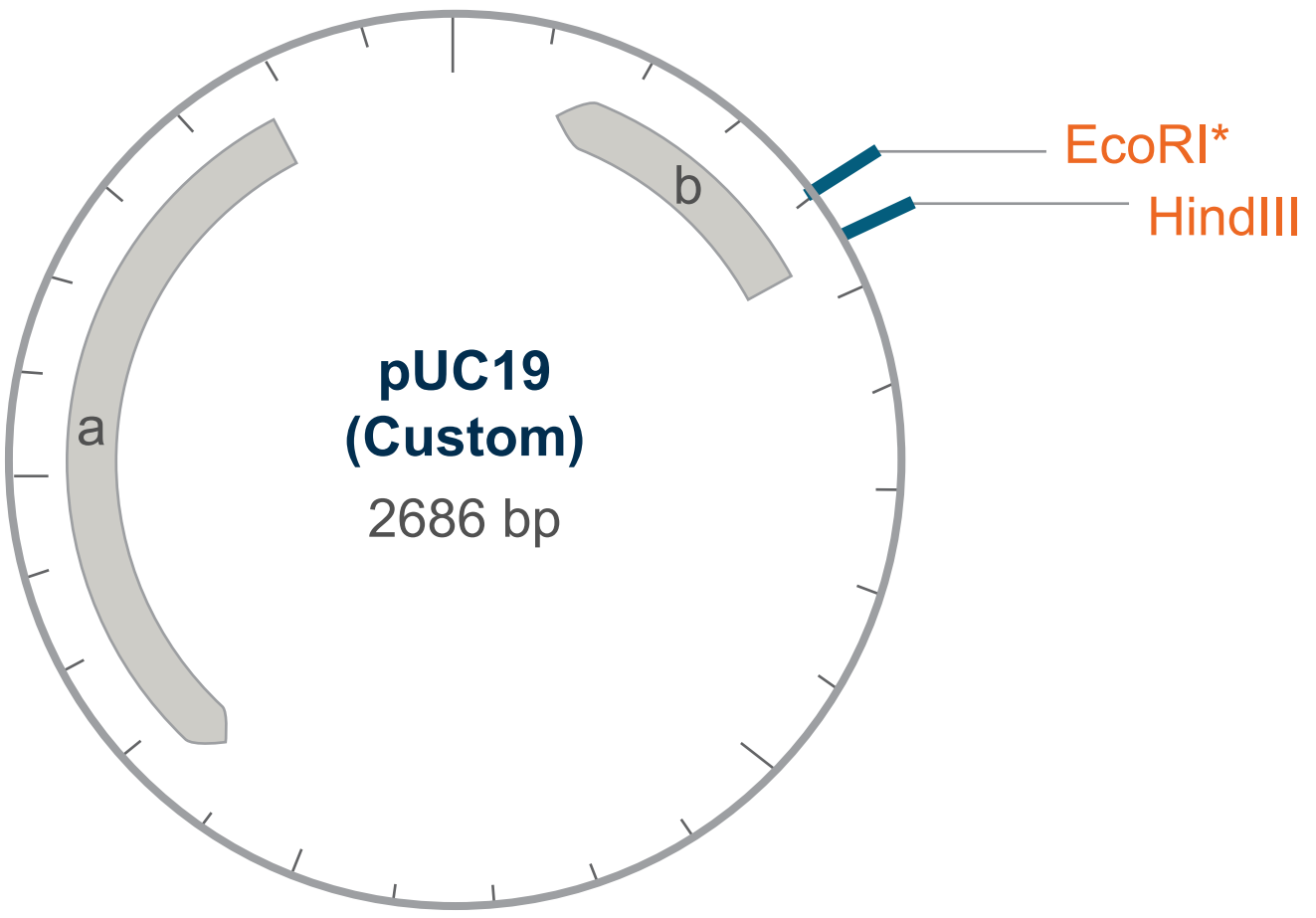
Digested With:
- EcoRI
- HindIII

Sequence Information:

2686 bp
GC = 51% AT = 49%

Update Preferences

Start Over



Display
- Circular
- Linear

To zoom into cut sites, use linear display.

Cleavage Code
- Blunt-End Cut
- Cuts 1 strand
- 5´ Extension
- 3´ Extension

Enzyme Code
- NEB
- Other supplier
- Not commercially available

Update Colors

Methylation
- * CpG methylation
- # dam/dcm methylation
- ( ) Ambigous site

ORFs
a: bla
b: lacZalpha

Custom Digest for pUC19

Make PDF | Print

- **Graphical View**
- Enzyme List
- Fragments
- Gel

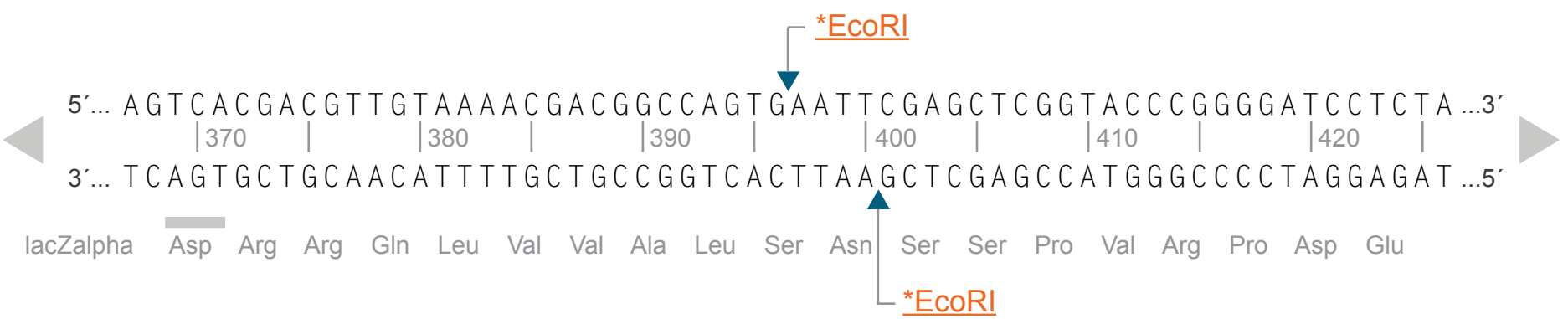
Digested With:
- EcoRI
- HindIII

Sequence Information:

2686 bp
GC = 51% AT = 49%

Update Preferences

Start Over



Display
- ☐ Circular
- ■ Linear

To zoom into cut sites, use linear display.

Cleavage Code
- Blunt-End Cut
- Cuts 1 strand
- 5′ Extension
- 3′ Extension

Enzyme Code
- NEB
- Other supplier
- Not commercially available

Update Colors

Methylation
- * CpG methylation
- # dam/dcm methylation
- ( ) Ambigous site

ORFs
a: bla
b: lacZalpha

Custom Digest for pUC19

Make PDF | Print

Graphical View

Enzyme List

Fragments

Gel

Sort By

#	Enzyme ▼	Recognition Sequence	Cuts	Sites & Flanks	Cut Positions	Blunt/ Overhang
1	EcoRI	G^AATT^C	1	Show	*396/400	5´
2	HindIII	A^AGCT^T	1	Show	447/451	5´

Save as Text

Digested With:
- EcoRI
- HindIII

Sequence Information:

2686 bp
GC = 51% AT = 49%

Update Preferences

Start Over

Display

- ✓ 0 cutters
- ✓ 2 cutters
- ✓ All sites
- ✓ Flanking enzymes

NEB Restriction Enzyme Activity/Performance Chart

Custom Digest for pUC19

Make PDF | Print

Graphical View

Enzyme List

Fragments

Gel

Sort by

#	Ends	Coordinates	Length (bp)
1	HindIII-EcoRI	448-396	26351
2	EcoRI-HindIII	397-447	51

#	Ends	Coordinates	Length (bp)
1	EcoRI-HindIII	397-447	51
2	HindIII-EcoRI	448-396	2635

Save as Text

Digested With:

- EcoRI
- HindIII

Sequence Information:

2686 bp

GC = 51% AT = 49%

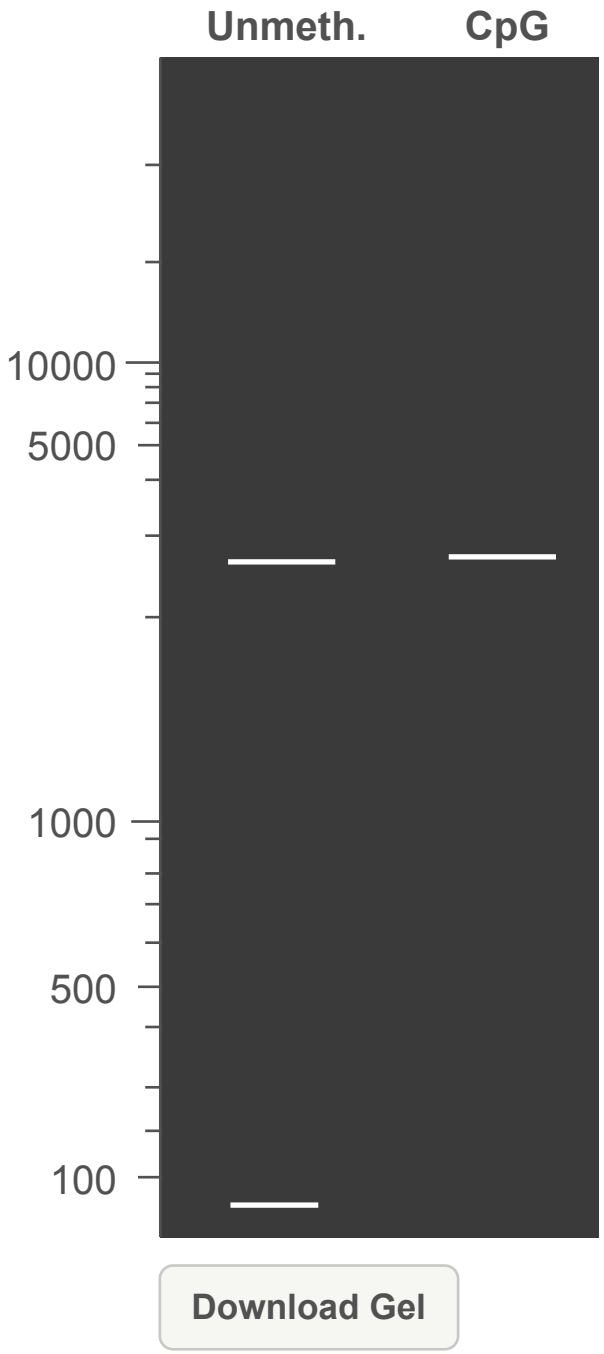
Update Preferences

Start Over

Custom Digest for pUC19

Make PDF | Print

This virtual gel was generated by interpolating experimental data. See details.



Download Gel

#	Ends	Coordinates	Length (bp)
1	HindIII-EcoRI	448-396	26351
2	EcoRI-HindIII	397-447	51

Graphical View

Enzyme List

Fragments

Gel

Digested With:
- EcoRI
- HindIII

Sequence Information:

2686 bp
GC = 51% AT = 49%

Update Preferences

Start Over

Gel Length

– mm Update

Color

White on black

Black on white

Gel Type

Marker

DNA Type