

Name

Student ID number

Assignment 3

1. (6 points) Demonstrate the effect of sequence topology on restriction digests.

a) Answer question a here. *The data in the boxes is dummy data. Replace it with your actual results.*

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                        BACHREST   Version 09/30/2012
pBS_SK-GUS           Topology: CIRCULAR   Length:      5978 bp
-----
Search parameters:
  Recognition sequences between      6 and    21 bp
  Ends: 5' protruding, Blunt, 3' protruding
  Type: Symmetric, Asymmetric
  Minimum fragments:      0      Maximum fragments: 6000
  Maximum fragments to print:    30
-----

```

Enzyme	Recognition Sequence	# of Sites	Sites	Frag	Begin	End
AarI	CACCTGC(4/8)	4	6448	7225	13981	6447
			7178	3609	7178	10786
			10787	3194	10787	13980
			13981	730	6448	7177
OliI	CACNN^NNGTG	3	6392	10798	10352	6391
			6410	3942	6410	10351
			10352	18	6392	6409

```

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                        BACHREST   Version 09/30/2012
pBS_SK-GUS.fsn      Topology: LINEAR   Length:      5978 bp
-----
Search parameters:
  Recognition sequences between      6 and    21 bp
  Ends: 5' protruding, Blunt, 3' protruding
  Type: Symmetric, Asymmetric
  Minimum fragments:      0      Maximum fragments: 6000
  Maximum fragments to print:    30
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```

Enzyme	Recognition Sequence	# of Sites	Sites	Frag	Begin	End
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			6410	3942	6410	10351
			10352	18	6392	6409

b) Answer question b here.

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Search parameters:
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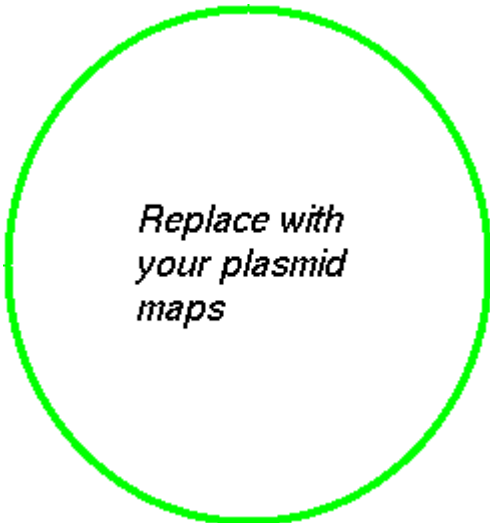
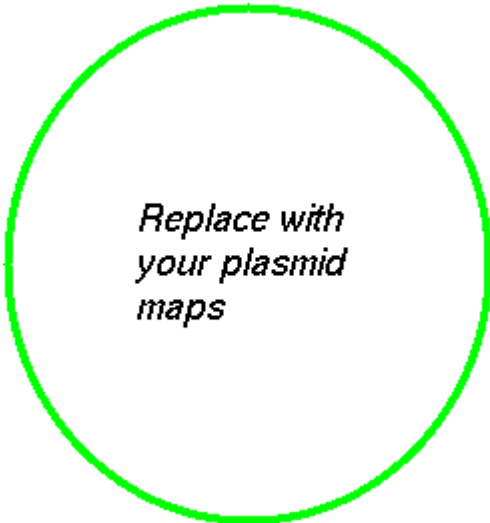
```

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pBS_SK-GUS.fsn  Topology: LINEAR  Length:    5978 bp
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			6410	3942	6410	10351
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2. (6 points) Create a construct using pBluescript SK(+), for comparison with the construct made using pBluescript SK(-). KEEP BOTH MAPS ON THIS PAGE. You may need to resize.



3. (6 points) Use BACHREST to find restriction digests that would allow us to determine which of the two Bluescript vectors was used in the real construct. *The data in the boxes is dummy data. Replace it with your actual results.*

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                        BACHREST  Version 09/30/2012
pBS_SK+GUS           Topology: CIRCULAR  Length:    5978 bp
-----
Search parameters:
  Recognition sequences between    6 and   21 bp
  Ends: 5' protruding, Blunt, 3' protruding
  Type: Symmetric, Asymmetric
  Minimum fragments:    0    Maximum fragments:  6000
  Maximum fragments to print:   30
-----

```

Enzyme	Recognition Sequence	# of Sites	Sites	Frag	Begin	End
PstI	CTGCA^G	3	3020	7888	4967	12854
			4967	4923	12855	3019
			12855	1947	3020	4966
PvuI	CGAT^CG	3	4025	10677	8106	4024
			7730	3705	4025	7729
			8106	376	7730	8105
PvuII	CAG^CTG	5	3073	5081	12750	3072
			4772	4218	8532	12749
			8075	3303	4772	8074
			8532	1699	3073	4771
			12750	457	8075	8531

```

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-----
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  Ends: 5' protruding, Blunt, 3' protruding
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  Minimum fragments:    0    Maximum fragments:  6000
  Maximum fragments to print:   30
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PvuII	CAG^CTG	5	3073	5081	12750	3072
			4772	4218	8532	12749
			8075	3303	4772	8074
			8532	1699	3073	4771
			12750	457	8075	8531

Discussion of data for question 3 here.

KEEP BOTH MAPS ON THIS PAGE. You may need to resize.

