

Restriction endonucleases and ligases



Mohamed N. Seleem

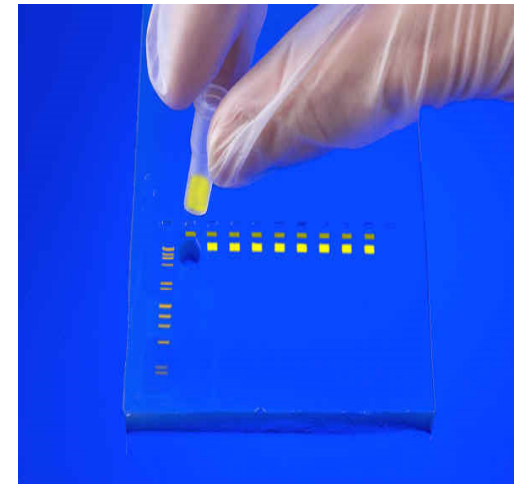
Big picture: Gene cloning

- From Gene to Protein
- Generally use bacteria as the “factory”



What we have done so far?

- Decide which gene to clone
- Designing primers
- PCR amplification (xx billions copies)
- Gel electrophoresis
- Cutting our gene from gel



What is next



- Move my gene to the bacteria to purify protein as a final product.

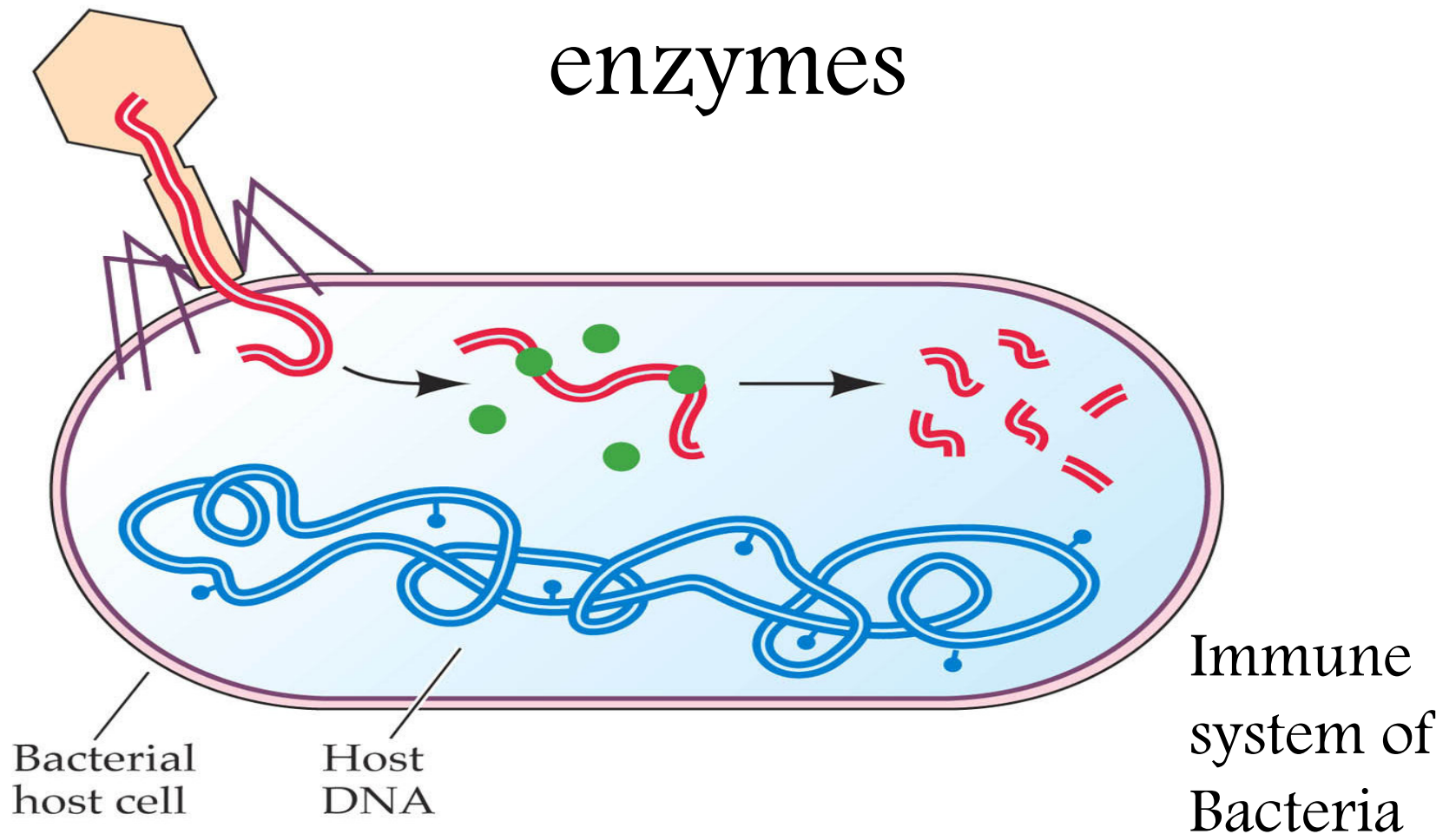
Problem: Gene by itself does not go inside bacteria, it needs a carrier (vector or plasmid)

Cloning Tools

- Restriction endonucleases
- Ligase
- Vectors
- Host
- Methods for introducing DNA into a host cell



Restriction endonucleases enzymes



Haemophilus influenzae

To date well over 3000
diff REs to choose from,
which were found
from screening > 10000
bacteria



Hamilton Smith
1973 Nobel Prize

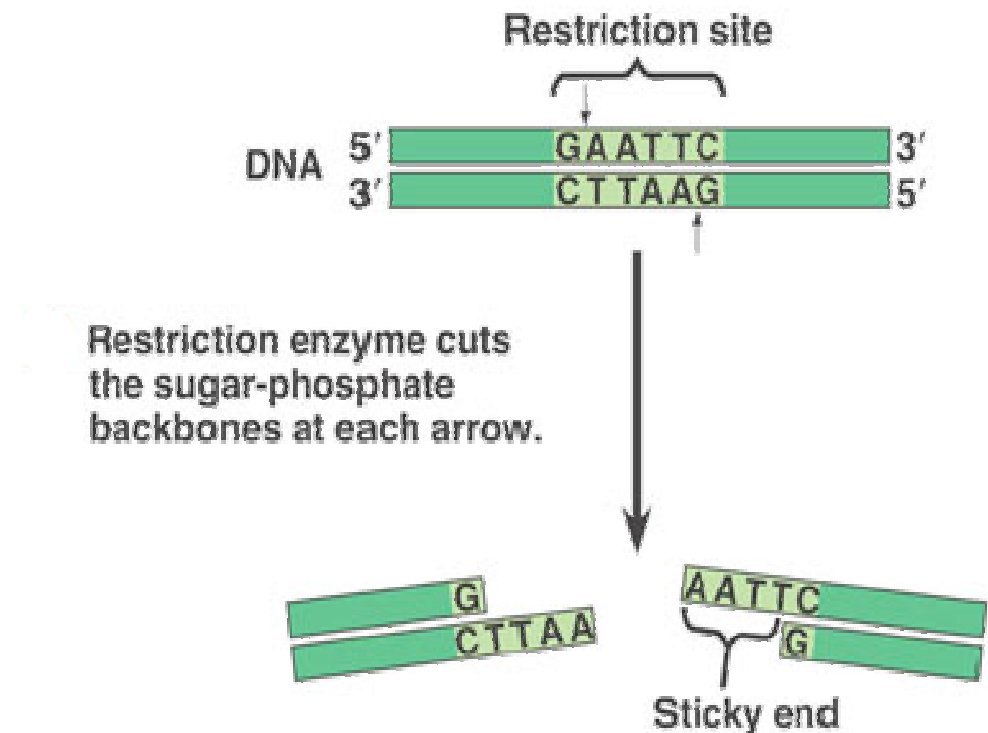
Cutting DNA

- Restriction endonucleases (restriction enzymes)

- sticky ends
- blunt ends

- Nomenclature

- *EcoRI*
- *E* = genus (*Escherichia*)
- *co* = species (*coli*)
- *R* = strain
- *I* = # of enzyme



Some restriction enzymes

Table 8.1 Properties of Some Restriction Enzymes

Enzyme	Bacterial Source	Restriction Site*
<i>Bam</i> HI	<i>Bacillus amyloliquefaciens</i> H	G [↓] GATCC CCTAG _↑ G
<i>Eco</i> RI	<i>Escherichia coli</i> RY13	G [↓] AATTC CTTAA _↑ G
<i>Eco</i> RII	<i>E. coli</i> R245	CC [↓] GG GG _↑ CC
<i>Hind</i> II	<i>Haemophilus influenzae</i> Rd	GTPy [↓] PuAC CAPu _↑ PyTG
<i>Hind</i> III	<i>H. influenzae</i> Rd	A [↓] AGCTT TTCGA _↑ A
<i>Hin</i> FI	<i>H. influenzae</i> Rf	G [↓] ANTC CTNA _↑ G
<i>Hpa</i> I	<i>H. parainfluenzae</i>	GTT [↓] AAC CAA _↑ TTG
<i>Msp</i> I	<i>Moraxella</i> sp.	CC [↓] GG GG _↑ CC
<i>Sma</i> I	<i>Serratia marcescens</i>	CCC [↓] GGG GGG _↑ CCC

*Arrows indicate sites of cleavage; Py = pyrimidine (either T or C); Pu = purine (either A or G); N = any nucleotide (A, T, G, or C).

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- 100's of restriction enzymes (RE's) are commercially available
- Artificial RE sites can be inserted at ends of any gene
- RE's and ligase allow precise cutting and pasting of any DNA sequences

Which enzymes I should use

Pubmed

<http://www.ncbi.nlm.nih.gov>

Omp25 *Brucella*

```

gene      1..642
          /gene="omp25"
CDS       1..642
          /gene="omp25"
          /codon_start=1
          /product="outer membrane protein 25"
          /protein_id="CAQ68393.1"
          /db_xref="GI:206596726"
          /db_xref="GOA:B5U6Y0"
          /db_xref="InterPro:IPR011250"
          /db_xref="UniProtKB/TrEMBL:B5U6Y0"
          /translation="MRTLKSLVIVSAALLPFSATAFAADAIQEQQPPVPAPVEVAPQYS
WAGGYTGLYLGYGWNKAKTSTVGSIKPDDWKAGAFAGWNFQQDQIVYGVEGDAGYSWA
KKSKDGLLEVKGQGFEGSLRARVGYDLNPFVMPYLTAGIAGSQIKLNGLDDESKFRVGWT
AGAGLEAKLTDNILGRVEYRYTQYGNKNYDLAGTNVRNKLDLTQDIRVGIGYKF"

ORIGIN
    1 atgcgcactc ttaagtctct cgtaatcgtc tcggctgcgc tgctgcggtt ctctgcgacc
   61 gcttttgctg ccgacgccat ccaggaacag cctccgggtc cggctccggt tgaagtagct
  121 cccaggtata gctgggctgg tggctatacc ggtctttacc tcggctacgg ctggaacaag
  181 gccaagacca gcaccgttgg cagcatcaag cctgacgatt ggaaggctgg cgcttttgct
  241 ggctggaact tccagcagga ccagatcgta tatggtgttg aaggatgatc aggttattcc
  301 tgggccaaga agtccaagga cggcctggaa gtcaagcagg gctttgaagg ctcgctgcgt
  361 gcccgcgctc gctacgacct gaaccgggtt atgccgtacc tcacggctgg tattgccggt
  421 tcgcagatca agcttaacaa cggcttggac gacgaaagca agttccgctg gggttggacg
  481 gctggtgccg gtctcgaagc caagctgacg gacaacatcc tcggccgctg tgagtaccgt
  541 tacaccagc acggcaacaa gaactacgat ctggccggtg cgaatgtccg caacaagctg
  601 gacacgcagg atatccgctg cggcatcggc tacaagttct aa
//

```

NEBcutter V2.0

This tool will take a DNA sequence and find the large, non-overlapping open reading frames using the E.coli genetic code and the sites for all Type II and commercially available Type I restriction enzymes that cut the sequence just once. By default, only enzymes available from NEB are used, but other sets may be chosen. Just enter your sequence and "submit". Further options will appear with the output. **The maximum size of the input file is 1 MByte, and the maximum sequence length is 300 KBases.**

[What's new in V2.0](#) [Citing NEBcutter](#)

Local sequence file:

GenBank number: [\[Browse GenBank\]](#)

or paste in your DNA sequence: *(plain or FASTA format)*

☒ Linear
☐ Circular

The sequence is:

☒ NEB enzymes
☐ All commercially available specificities
☐ All specificities
☐ All + defined oligonucleotide sequences
☐ Only defined oligonucleotide sequences
[\[define oligos\]](#)

Enzymes to use:

Minimum ORF length to display: a.a.

Standard sequences:
Plasmid vectors ▾
Viral + phage ▾

Copy and paste sequence

copy


```

/db_xref="GOA:B5U6Y0"
/db_xref="InterPro:IPR011250"
/db_xref="UniProtKB/TrEMBL:B5U6Y0"
/translation="MRTLKSLVIVSAALLPFSATAFAADAIQEQQPVPAPVEVAPQYS
WAGGYTGlyLGYGWNKAKTSTVGSIKPDDWKAGAFAGWNFQQDQIVYGVEGDAGYSWA
KKS KDGLEVKQGFEGLSLRARVGYDLNPFVMPYLTAGIAGSQIKLNNGLDDESKFRVGT
AGAGLEAKLTDNILGRVEYRYTQYGNKNYDLAGTNVRNKLDTQDIRVGIGYKF"

ORIGIN
1  atgcgcactc ttaagtctct cgtaaatcgtc tcggctgcgc tgctgcccgtt ctctgcgacc
61  gctttttgctg cccgacgccat ccaggaacag cctccgggttc cggctccgggt tgaagtagct
121  ccccagttata gctgggcttg tggctatacc ggtctttacc tcggctacgg ctggaacaag
181  gccaaagacca gcaccggttg cagcatcaag cctgacgatt ggaaggctgg cgcttttctg
241  ggctgggaact tccagcagga ccagatcgta tatggtgttg aagggtgatgc aggttatttc
301  tgggccaaga agtccaagga cggcctggaa gtcaagcagg gctttgaagg ctgctgcgt
361  gcccgcgctcg gctacgacct gaaccgggtt atgcccgtacc tcacggctgg tattgcccgt
421  tcgcagatca agcttaacaa cggcttggac gacgaaagca agttccgcgt ggggttgacg
481  gctggtgccc gtctcgaagc caagctgacg gacaacatcc tcggccgcgt tgagtagcgt
541  tacacccagt acggcaacaa gaactacgat ctggccggta cgaatgtccg caacaagctg
601  gacacgcagg atatccgcgt cggcatcggc tacaagttct aa
//

```

paste



NEBcutter V2.0

[Program Guide](#)
[Help](#)
[Comments](#)

This tool will take a DNA sequence and find the large, non-overlapping open reading frames using the E.coli genetic code and the sites for all Type II and commercially available Type III restriction enzymes that cut the sequence just once. By default, only enzymes available from NEB are used, but other sets may be chosen. Just enter your sequence and "submit". Further options will appear with the output. **The maximum size of the input file is 1 MByte, and the maximum sequence length is 300 KBases.**

[What's new in V2.0](#)
[Citing NEBcutter](#)

Local sequence file: [Browse...](#)
GenBank number: [Browse GenBank](#)
or paste in your DNA sequence: *(plain or FASTA format)*

Standard sequences:
Plasmid vectors ▾
Viral + phage ▾

tattgcccgt
421 tcgcagatca agcttaacaa cggcttggac gacgaaagca agttccgcgt
gggttggaag
481 gctggtgccc gtctcgaagc caagctgacg gacaacatcc tcggccgcgt
tgagtagcgt
541 tacacccagt acggcaacaa gaactacgat ctggccggta cgaatgtccg
caacaagctg
601 gacacgcagg atatccgcgt cggcatcggc tacaagttct aa

☒ NEB enzymes
☐ All commercially available specificities
☐ All specificities
☐ All + defined oligonucleotide sequences
☐ Only defined oligonucleotide sequences
[define oligos](#)

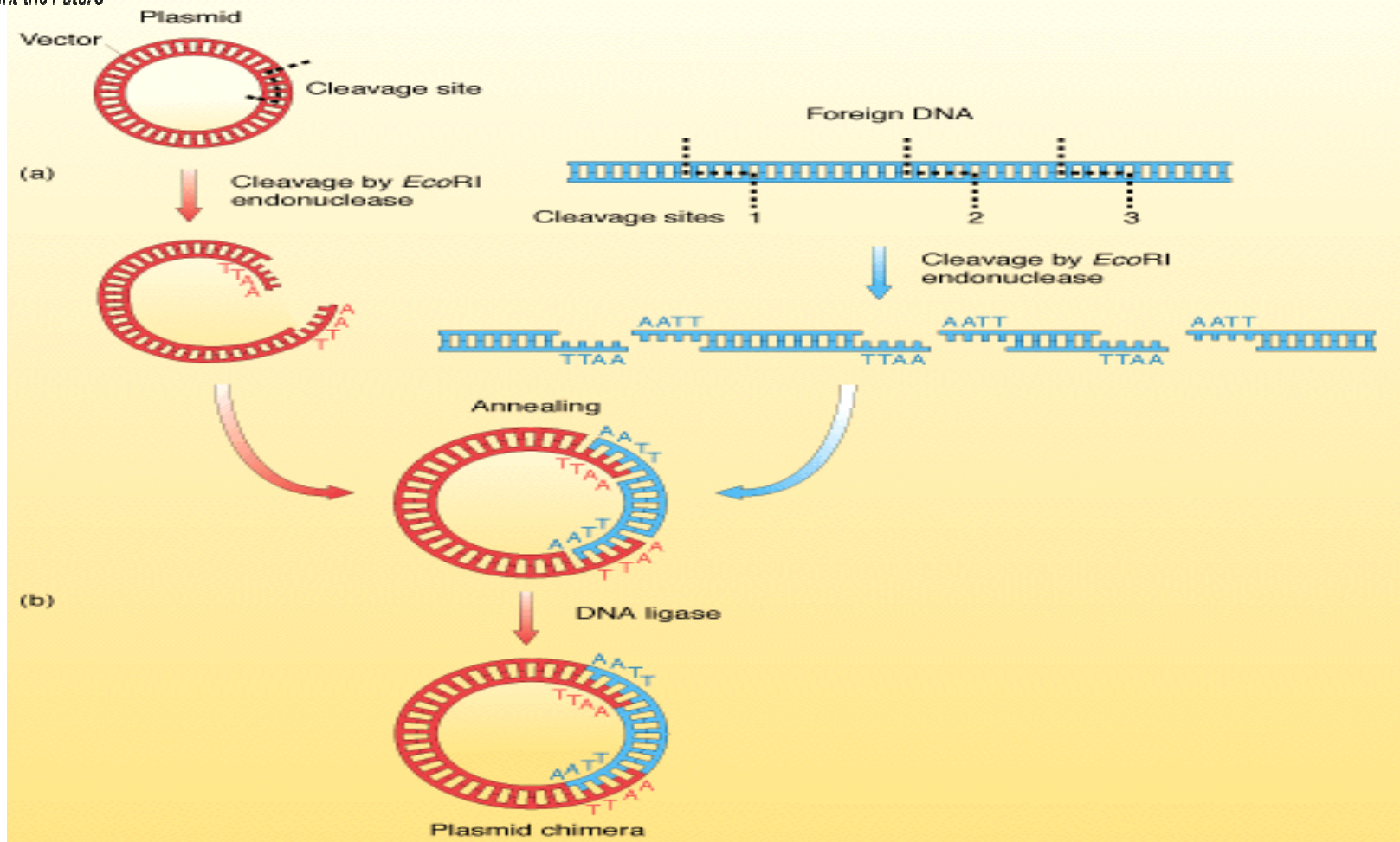
The sequence is: ☒ Linear ☐ Circular
Enzymes to use:

Minimum ORF length to display: 100 a.a.

Restriction Map

Noncutters: AarI, AatII, AbsI, AccI, AclI, AflIII, AjuI, AklI, AloI, AlwNI, ApaI, ApaLI, ApoI, ArsI, AscI, AsuII, Aval, AvrII, BalI, BamHI, BarI, BbvCI, BcgI, BciVI, BclI, BdaI, BglI, BglII, BplI, Bpu10I, BsaAI, BsaBI, BsaXI, BseMII, BsePI, BseRI, BsgI, BsmI, Bsp1407I, BspHI, BsrBI, BsrDI, BstEII, BstXI, BtgZI, BtrI, BtsI, ClaI, CspCI, DraII, DraIII, DrdI, Eam1105I, EciI, Eco47III, Eco57I, Eco57MI, EcoNI, EcoRI, FseI, GsuI, HaeIV, Hin4I, HindII, HpaI, KpnI, MauBI, MboII, MfeI, MluI, MslI, NaeI, NarI, NcoI, NdeI, NheI, NotI, NruI, NspI, OsiI, PacI, PaeI, PflMI, PleI, PmaCI, PmeI, PpiI, PpuMI, PshAI, PsiI, PI-PspI, PstI, PvuI, PvuII, RsrII, SacI, SacII, SalI, SanDI, SapI, Scal, PI-SceI, SexAI, SfiI, SgfI, SgrAI, SgrDI, SmaI, SnaBI, SpeI, SphI, SrfI, Sse8387I, SspI, StuI, SwaI, TaqII, TatI, TfiI, Tsp45I, TspDTI, TspRI, Tth111I, VspI, XbaI, XhoI, XhoII, XmnI

Name	Sequence	Site Length	Overhang	Frequency	Cut Positions
EcoRV	GATATC	6	blunt	1	612
FspAI	RTGCGCAY	8	blunt	1	4
AcyI	GRCGYC	6	five_prime	1	74
AflII	CTTAAG	6	five_prime	1	10
AgeI	ACCGGT	6	five_prime	1	148
AvaII	GGWCC	5	five_prime	1	258
BccI	CCATC	5	five_prime	1	85
BseYI	CCCAGC	6	five_prime	1	131
BspMI	ACCTGC	6	five_prime	1	280
Eco31I	GGTCTC	6	five_prime	1	496
Esp3I	CGTCTC	6	five_prime	1	33
FauI	CCCGC	5	five_prime	1	370



GGATCC ATGCGCACTCTTAAGTCTCTCGTAATCGTCTCGGCTGCGCTGCTGCCGTCCAGCACCGTTACAAGTTCTAAGGATCC
TACGCGTGAGAATTCAGAGAGCATTAGCAGAGCCGACGCGACGACGGCAGGTCGTGGCAATGTTCAAGATTCTAGG

Put sequence of Non
cutting enzymes at both
ends of the gene

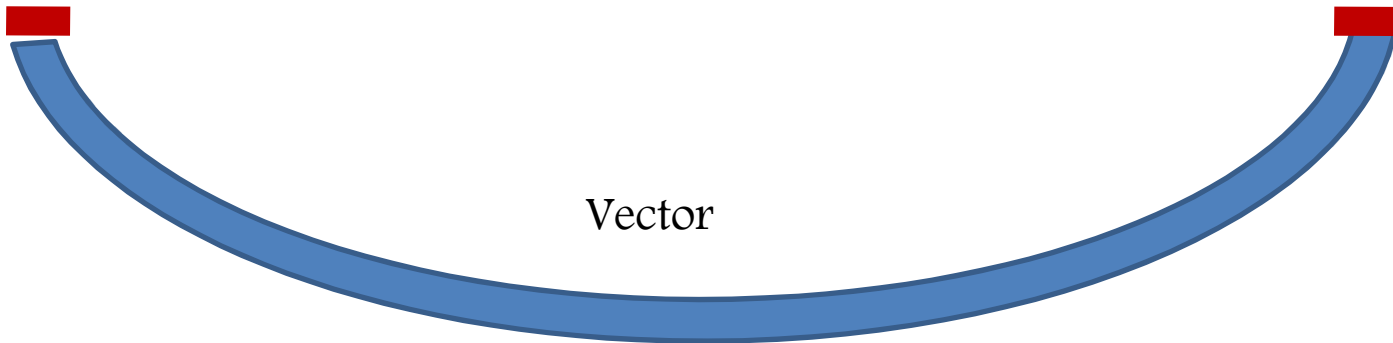
How? PCR and Primers

Gene



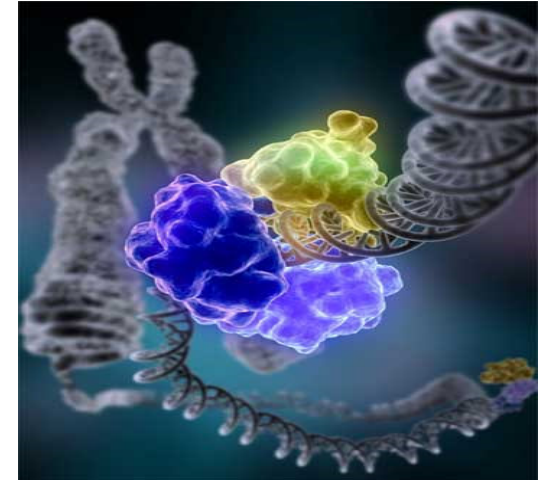
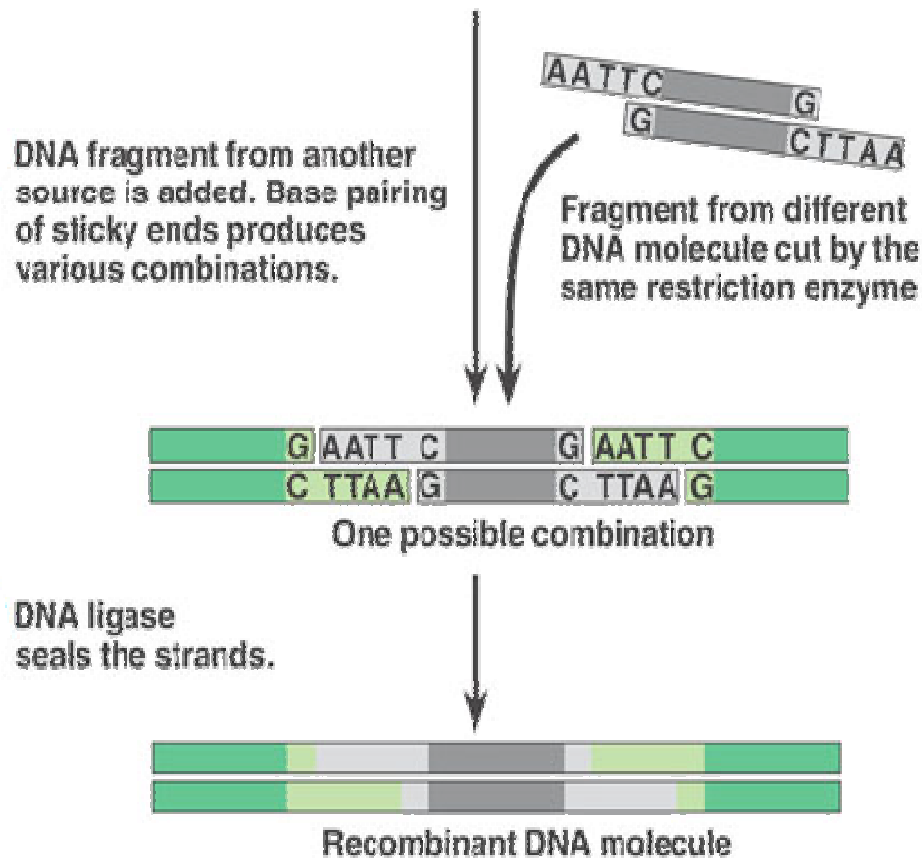
Adding sequence to the ends by PCR

linkers



Vector

Pasting DNA



- Complementary ends (sticky ends) H-bond
- Ligase forms phosphodiester bond to seal strands together.

How to chose your enzymes

- Non cutting enzymes
- Enzymes on Vector
- Enzymes that work together (Double digest)
- Price
- Company (I highly recommend Promega)

Don't waste clean thinking on dirty enzymes

Efraim Racker, Cornell University

How use your enzymes

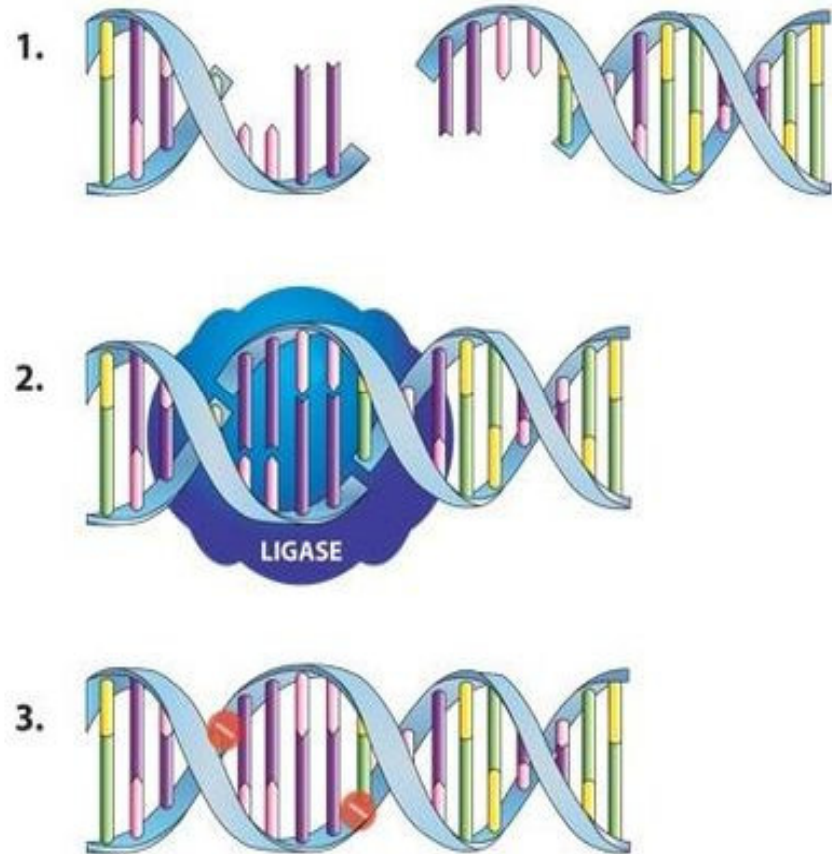
- Ice
- No Vortex
- Set up reaction of 10 μ l at least
- 1 μ l (10 units) enzyme 1 μ l 10xbuffer and 8 μ l DNA(you need 1 unit to cut 1 μ g of DNA)
- Incubate (usually 37 °C for at least 1 hour)
- Clean your DNA after cutting

Enzyme
and
buffer

Joining DNA

Ligase enzyme
anneal two pieces of
compatible ends of
DNA together

Repair Mechanism
in biological system



How to join DNA

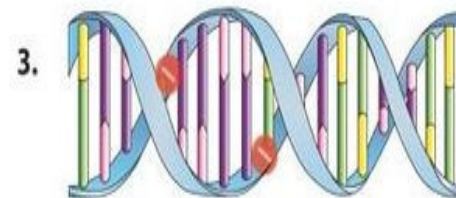
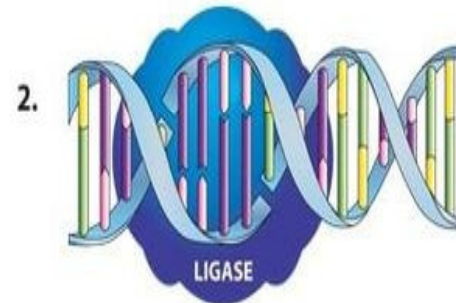
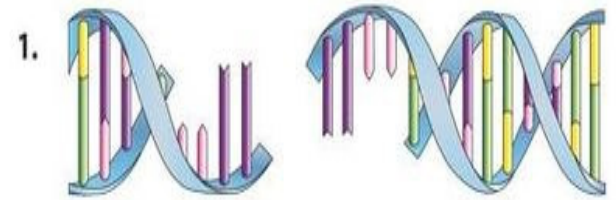
Get rid of restriction enzymes

1 μ l (3 units) enzyme

1 μ l 10xbuffer

4 μ l gene

4 μ l vector (plasmid)



Incubation ligation reaction

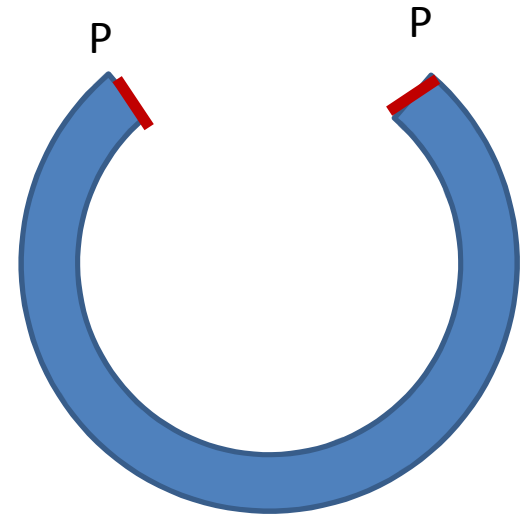
- 4 °C over night or 16 °C over night
- 25 °C 3 hours
- TCL (temperature cycle ligations) Lund et al., 1996
99 cycles (1 min 30 ° C 1 min 10 ° C) 4 fold increase ligation
- 5 minutes ligation buffer (Polyethylene glycol PEG 6000)

How to check for successful ligation reaction

- Transformation and count number of good colonies

Alkaline phosphatase dephosphorylation

Removing phosphate
group to prevent self
ligation of the vector



Add it only to the vector

Questions!!!!



Suddenly, Bobby felt very alone in the world.