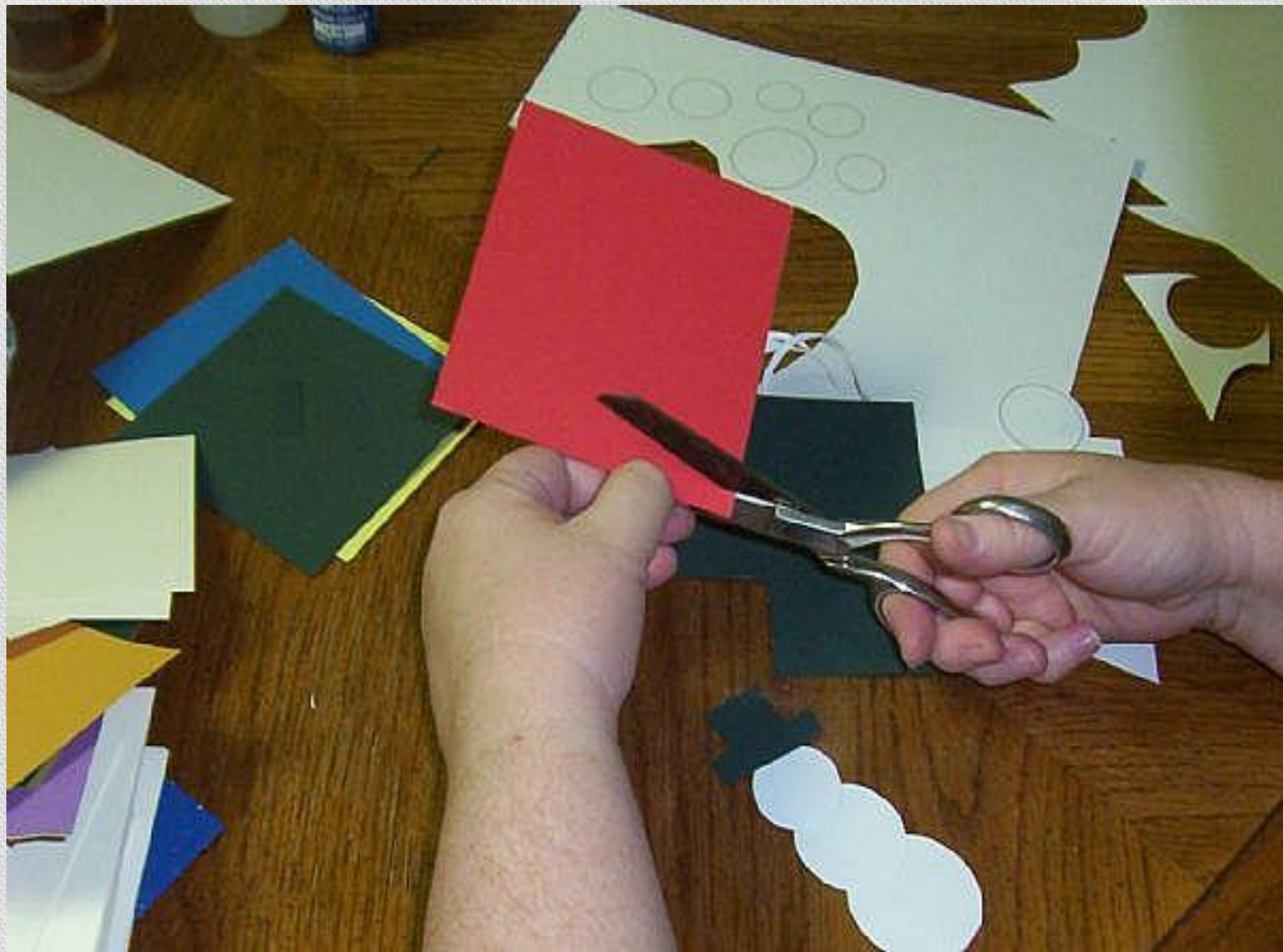


End is not the end, in fact E.N.D is
"Effort Never Dies" and if you get NO in an
answer, then remember NO is
"Next Opportunity". Always be positive.



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RESTRICTION ENDONUCLEASES, (CUTTING DNA)

(LIGATION)

LIGASES & PHOSPHATASES

Restriction enzyme = Restriction Endonuclease

Is an enzyme that cuts DNA at or near specific recognition nucleotides sequences known as **Restriction site**.

These enzymes are found in bacteria and provide a defense mechanism against invading viruses.

To cut DNA, all restriction enzymes make two incisions, once through each sugar-phosphate backbone (i.e. each strand) of the DNA double helix.

Restriction enzyme = Restriction Endonuclease

The phenomenon was first identified in work done in the laboratories of Salvador Luria and Giuseppe Bertani in early 1950s. It was found that *a bacteriophage λ* that can grow well in one strain of *Escherichia coli*, for example *E. coli C*, when grown in another strain, for example *E. coli K*, its yields can drop significantly, by as much as 3-5 orders of magnitude. *The E. coli K* host cell, known as the restricting host, appears to have the ability to reduce the biological activity of the phage λ. If a phage becomes established in one strain, the ability of that phage to grow also become restricted in other strains. In the 1960s, it was shown in work done in the laboratories of Werner Arber and Matthew Meselson that *the restriction is caused by an enzymatic cleavage of the phage DNA, and the enzyme involved was therefore termed a restriction enzyme.*

Restriction enzyme = Restriction Endonuclease

Over 3000 restriction enzymes have been studied in detail, and more than 600 of these are available commercially.

Restriction site:

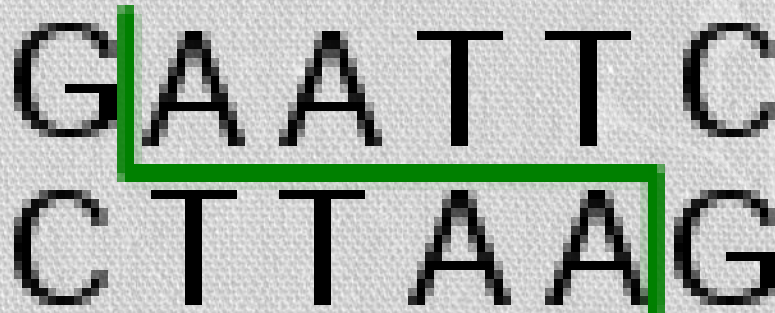
Restriction enzymes recognize a specific sequence of nucleotides and produce a double-stranded cut in the DNA.

The recognition sequences usually vary between 4 and 8 nucleotides, and many of them are **palindromic**, meaning the base sequence reads the same backwards and forwards

Restriction site:

In theory, there are two types of palindromic sequences that can be possible in DNA.

The *mirror-like palindrome* is similar to those found in ordinary text, in which a sequence reads the same forward and backwards on a single strand of DNA strand.



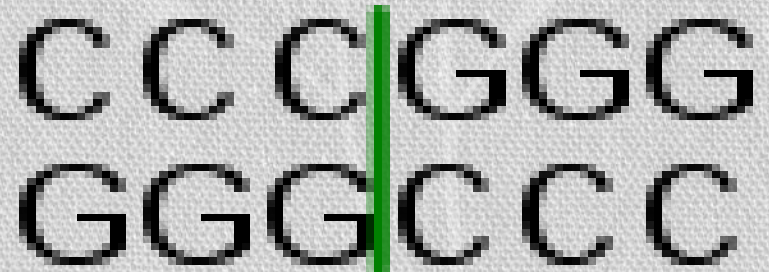
The diagram illustrates a mirror-like DNA palindrome. It consists of two horizontal sequences of nucleotides. The top sequence is G A A T T C and the bottom sequence is C T T A A G. A green line is drawn vertically between the first 'A' of the top sequence and the first 'T' of the bottom sequence, and another green line is drawn vertically between the second 'T' of the top sequence and the second 'A' of the bottom sequence. These two vertical lines are connected by a horizontal green line, forming a rectangular frame that highlights the palindromic core 'AATT'.

```
G A A T T C  
C T T A A G
```


Restriction site:

The inverted repeat palindrome is also a sequence that reads the same forward and backwards, but the forward and backward sequences are found in complementary DNA strands.

Inverted repeat palindromes are more common and have greater biological importance than mirror-like palindromes.

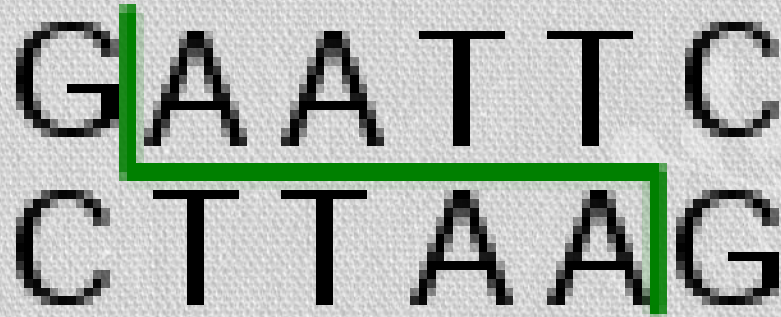


The diagram shows two complementary DNA strands. The top strand is 5'-CCCCGGGG-3' and the bottom strand is 3'-GGGGCCCC-5'. A vertical green line is positioned between the third and fourth nucleotides of each strand, indicating the site of cleavage for a restriction enzyme. This represents an inverted repeat palindrome where the sequence on one strand is the reverse complement of the sequence on the other strand.

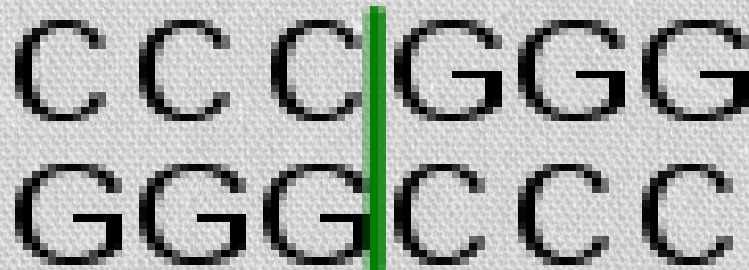
```
CCCCGGGG  
GGGGCCCC
```


Restriction site:

- **EcoRI** digestion produces "sticky" ends:



- whereas **SmaI** restriction enzyme cleavage produces "blunt" ends:



Restriction endonucleases (restriction enzymes)

sticky ends

blunt ends

Nomenclature

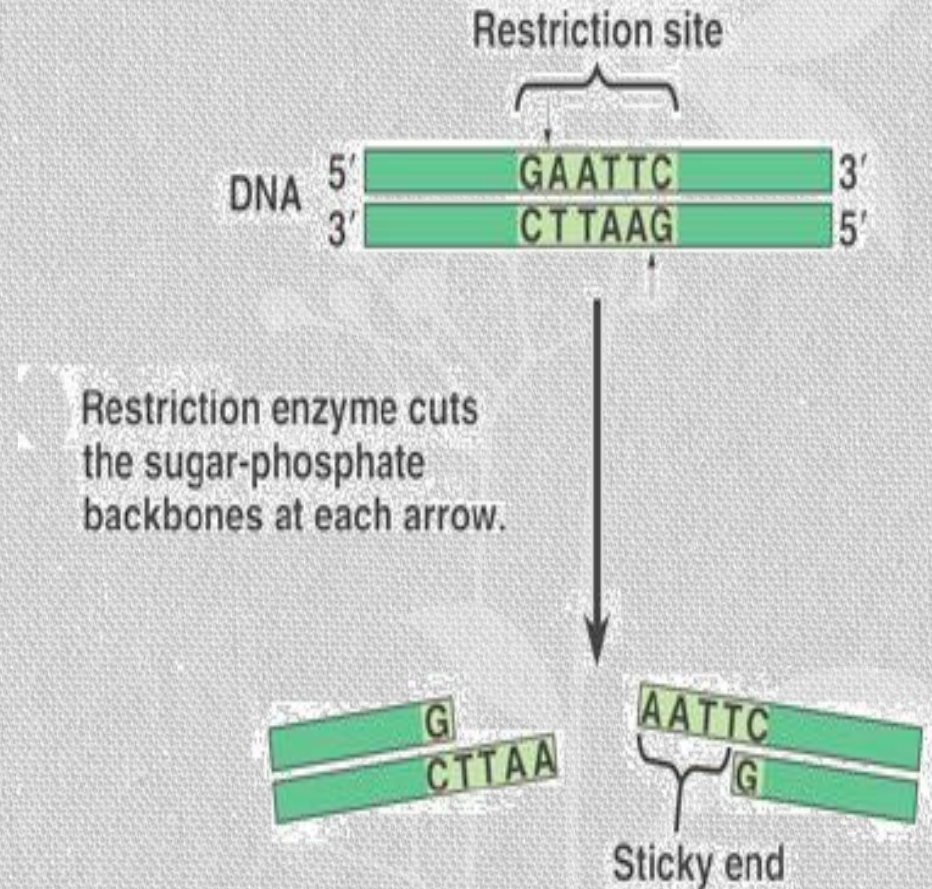
EcoRI

E = genus (*Escherichia*)

co = species (*coli*)

R = strain

I = # of enzyme



Restriction Endonucleases:

Enzyme	Source	Recognition Sequence	Cut
<u>EcoRI</u>	<u>Escherichia coli</u>	5'GAATTC 3'CTTAAG	5'---G AATTC---3' 3'---CTTAA G---5'
<u>EcoRII</u>	<u>Escherichia coli</u>	5'CCWGG 3'GGWCC	5'--- CCWGG---3' 3'---GGWCC ---5'
<u>BamHI</u>	<u>Bacillus amyloliquefaciens</u>	5'GGATCC 3'CCTAGG	5'---G GATCC---3' 3'---CCTAG G---5'
<u>HindIII</u>	<u>Haemophilus influenzae</u>	5'AAGCTT 3'TTCGAA	5'---A AGCTT---3' 3'---TTCGA A---5'
<u>TaqI</u>	<u>Thermus aquaticus</u>	5'TCGA 3'AGCT	5'---T CGA---3' 3'---AGC T---5'
<u>SmaI*</u>	<u>Serratia marcescens</u>	5'CCCGGG 3'GGGCCC	5'---CCC GGG---3' 3'---GGG CCC---5'

Which enzymes I should use

PubMed

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

```
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CDS       1..642
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          /db_xref="InterPro:IPR011250"
          /db_xref="UniProtKB/TrEMBL:BSU6Y0"
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AGAGLEAKLTDNILGRVEYRYTQYGNKNYDLAGTNVRNKLDTQDIRVGIGYKF"

ORIGIN
    1 atgcgcactc ttaagtctct cgtaatcgtc tcggctgcgc tgctgccgtt ctctgcgacc
   61 gcttttgctg ccgacgccat ccaggaacag cctccggttc cggctccggt tgaagtagct
  121 cccaggtata gctgggctgg tggctatacc ggtctttacc tcggctacgg ctggaacaag
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  241 ggctggaact tccagcagga ccagatcgta tatggtgttg aaggatgatc aggttattcc
  301 tgggccaaga agtccaagga cggcctggaa gtcaagcagg gctttgaagg ctcgctgcgt
  361 gcccgcgctg gctacgacct gaaccgggtt atgccgtacc tcacggctgg tattgccggt
  421 tcgcagatca agcttaacaa cggcttggac gacgaaagca agttccgctg gggttggacg
  481 gctggtgccc gtctcgaagc caagctgacg gacaacatcc tcggccgctg tgagtaccgt
  541 tacaccaggt acggcaacaa gaactacgat ctggccggta 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 II 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: <input type="text"/>		<input type="button" value="Browse..."/>	Standard sequences:
GenBank number: <input type="text"/>		[Browse GenBank]	# Plasmid vectors ▾
or paste in your DNA sequence: <i>(plain or FASTA format)</i>			# Viral + phage ▾
<div style="border: 1px solid black; height: 150px; width: 100%;"></div>		<input type="button" value="Submit"/>	
		<input type="button" value="More options"/>	
The sequence is:	<input checked="" type="radio"/> Linear	Enzymes to use:	<input checked="" type="radio"/> NEB enzymes
	<input type="radio"/> Circular		<input type="radio"/> All commercially available specificities
			<input type="radio"/> All specificities
			<input type="radio"/> All + defined oligonucleotide sequences
			<input type="radio"/> Only defined oligonucleotide sequences
			[define oligos]
Minimum ORF length to display: <input type="text" value="100"/>		a.a.	
		<input type="button" value="Set colors"/>	

Copy and paste sequence

copy

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AGAGLEAKLTDNILGRVEYRYTQYGNKNYDLAGTNVRNKLDTQDIRVGIGYKF"  
  
ORIGIN  
1 atgcgcactc ttaagtctct cgtaatcgtc tcggctgcgc tgctgccggt ctctgcgacc  
61 gctttttgctg ccgacgccat ccaggaacag cctccggttc cggctccggt tgaagtagct  
121 cccaggtata gctgggctgg tggctatacc ggtctttacc tcggctacgg ctggaacaag  
181 gccaaagacca gcaccggttg cagcatcaag cctgacgatt ggaaggctgg cgcttttgct  
241 ggctggaact tccagcagga ccagatcgta tatggtgttg aagggtgatgc aggttattcc  
301 tgggccaaaga agtccaagga cggcctggaa gtcaagcagg gctttgaagg ctgcgtcgct  
361 gcccgcgtcg gctacgacct gaaccocggt atgcgcgtac tcacggctgg tattgccggt  
421 tcgcagatca agcttaacaa cggcttggac gacgaaagca agttccgcgt ggggtggacg  
481 gctggtgccc gtctcgaagc caagctgacg gacaacatcc tcggccgcgt tgagtaccgt  
541 tacaccaggt acggcaacaa gaactacgat ctggccggtg cgaatgtccg caacaagctg  
601 gacacgcagg atatccgctg cggcatcggc tacaagttct aa  
  
//
```

paste



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 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)

tattgccggt
421 tcgcagatca agcttaacaa cggcttggac gacgaaagca agttccgcgt
gggttggagc
481 gctggtgccc gtctcgaagc caagctgacg gacaacatcc tcggccgcgt
tgagtaccgt
541 tacaccaggt acggcaacaa gaactacgat ctggccggtg cgaatgtccg
caacaagctg
601 gacacgcagg atatccgctg cggcatcggc tacaagttct aa

Standard sequences:
Plasmid vectors
Viral + phage

Submit

More options

Set colors

The sequence is: ☒ Linear ☐ Circular

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

Minimum ORF length to display: 100 a.a.

Restriction Map

Noncutters: AarI, AatII, AbsI, AccI, AclI, AflIII, AjuI, AlfI, 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, PstI, 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

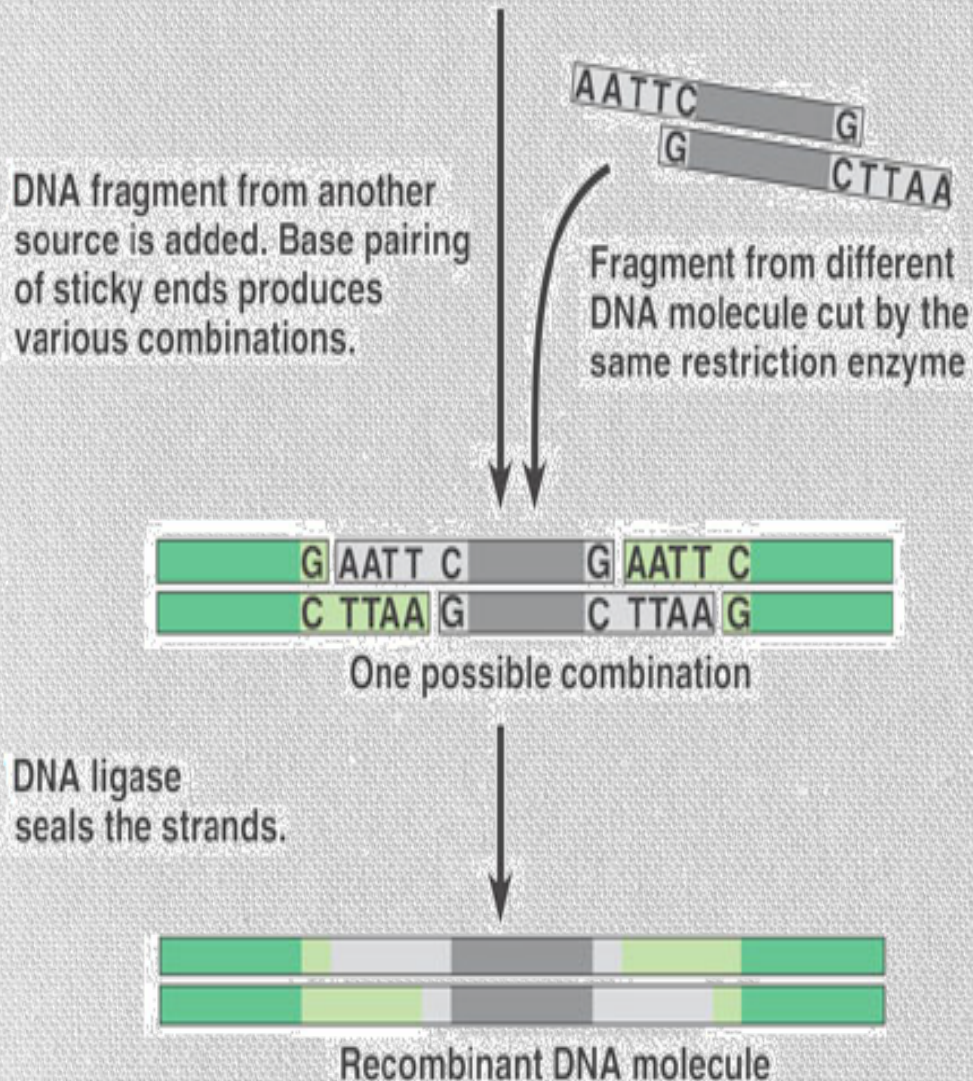
Ligation (Ligases & Phosphatases)

Ligation in molecular biology is the joining of two nucleic acid fragments through the action of an enzyme.

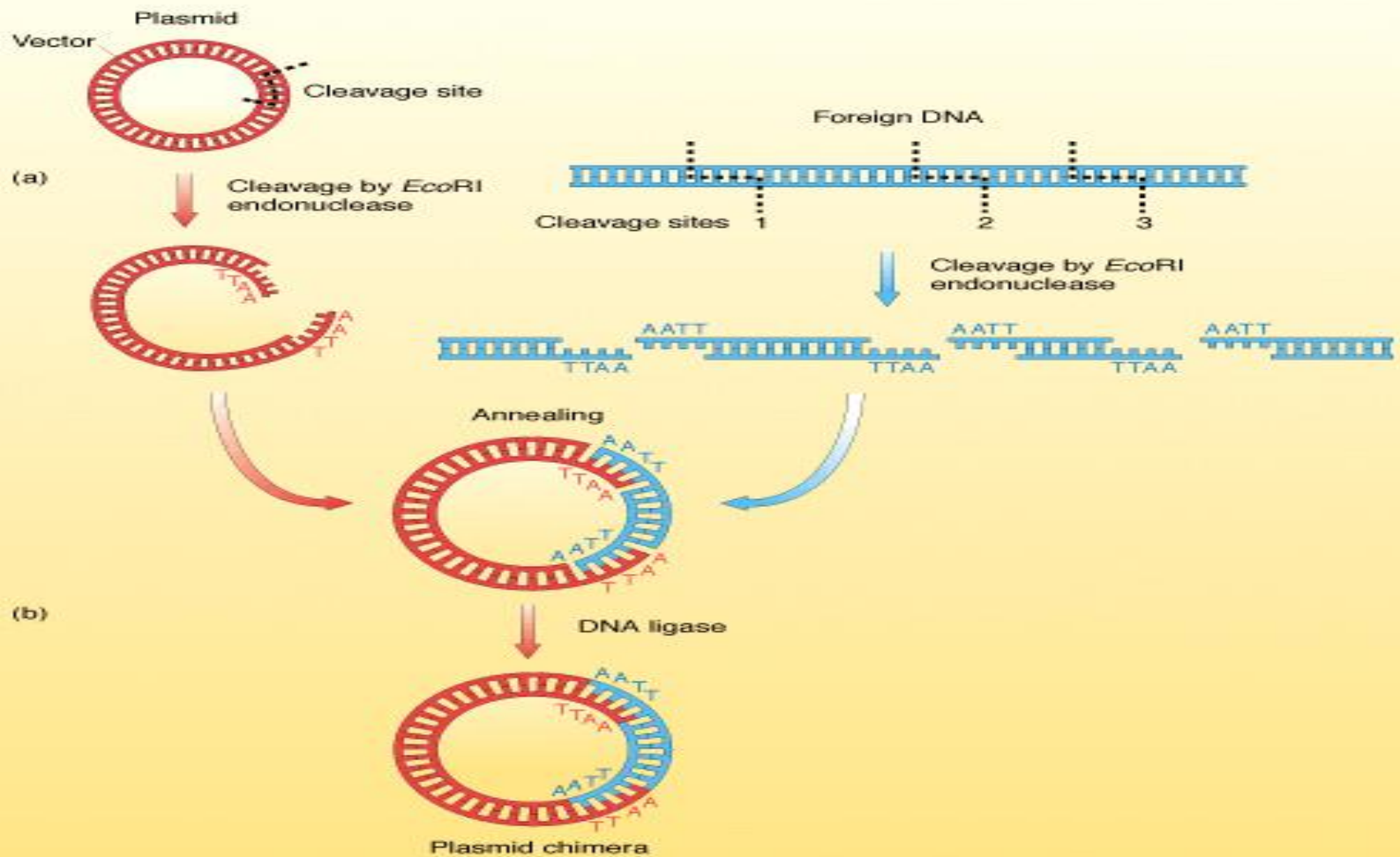
It is an essential laboratory procedure in the **molecular cloning** by which DNA fragments are joined together to create recombinant DNA molecules, such as when a foreign DNA fragment is inserted into a plasmid.

The ends of DNA fragments are joined together by the formation of phosphodiester bonds between the 3'-hydroxyl of one DNA termini with the 5'-phosphoryl of another.

Pasting DNA



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



Sticky-end ligation

In cloning experiments most commonly-used restriction enzymes generate a 4-base single-stranded overhang called **the sticky or cohesive end**.

These sticky ends can anneal to other compatible ends and become ligated in a sticky-end (or cohesive end) ligation.

EcoRI for example generates an AATT end, and since A and T have lower melting temperature than C and G, its melting temperature T_m is low at around 6°C. For most restriction enzymes, the overhangs generated have a T_m that is around 15°C. For practical purposes, sticky end ligations are performed at 12-16°C, or at room temperature, or alternatively at 4°C for a longer period.

Blunt-end ligation

Blunt end may be ligated to another blunt end, Blunt ends may be generated by restriction enzymes such as SmaI and EcoRV.

However a major advantage of blunt-end cloning is that the desired insert does not require any restriction sites in its sequence as blunt-ends are usually generated in a PCR, and the PCR generated blunt-ended DNA fragment may then be ligated into a blunt-ended vector generated from restriction digest.

Disadvantages of blunt-end ligation:

- 1- ligation is much less efficient than sticky end ligation, typically the reaction is 100X slower than sticky-end ligation.
- 2- The concentration of ligase used is higher than sticky end ligation (10x or more).
- 3- The concentration of DNA used in blunt-end ligation is also higher to increase the likelihood of collisions between ends.
- 4- Longer incubation time may also be used for blunt-end ligations.

Method of Ligation

Add 1 μl of the PDrive vector of the ligation in 0.2 μl or 0.5 μl PCR tubes,

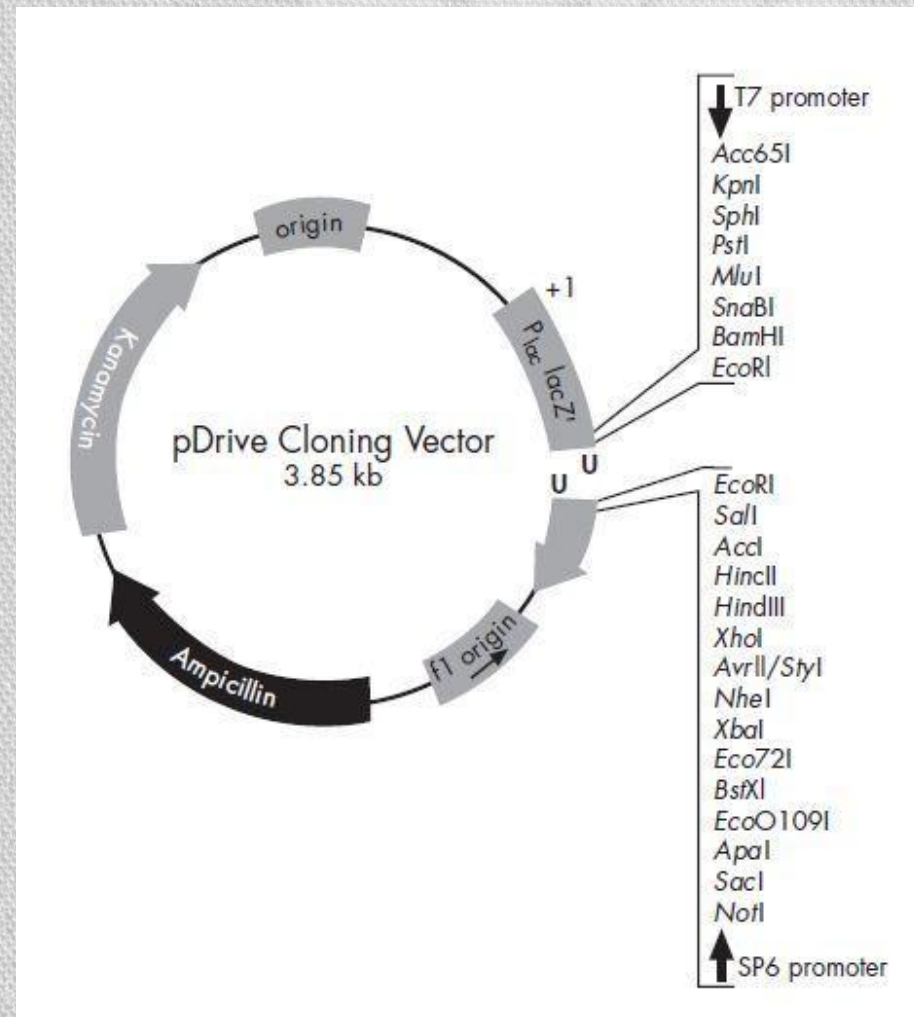
Add 1:4 μl of the purified PCR product,

Add 5 μl of ligation master mix &

Variable μl of water then put in the thermo cycler for four hours at 16°C.

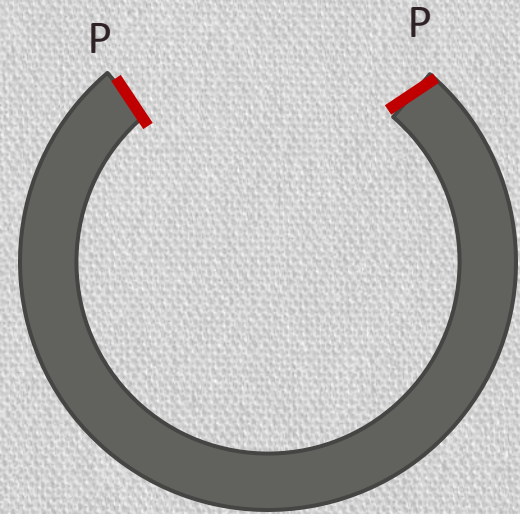
pDrive Cloning Vector

- Ampicillin and kanamycin selection
- Blue/white screening
- Unique restriction endonuclease recognition sites around the cloning site
- T7 and SP6 promoter on either side of the cloning site allowing *in vitro* transcription of cloned PCR products as well as sequence analysis using standard sequencing primers.
- Phage f1 origin to allow preparation of single-stranded DNA



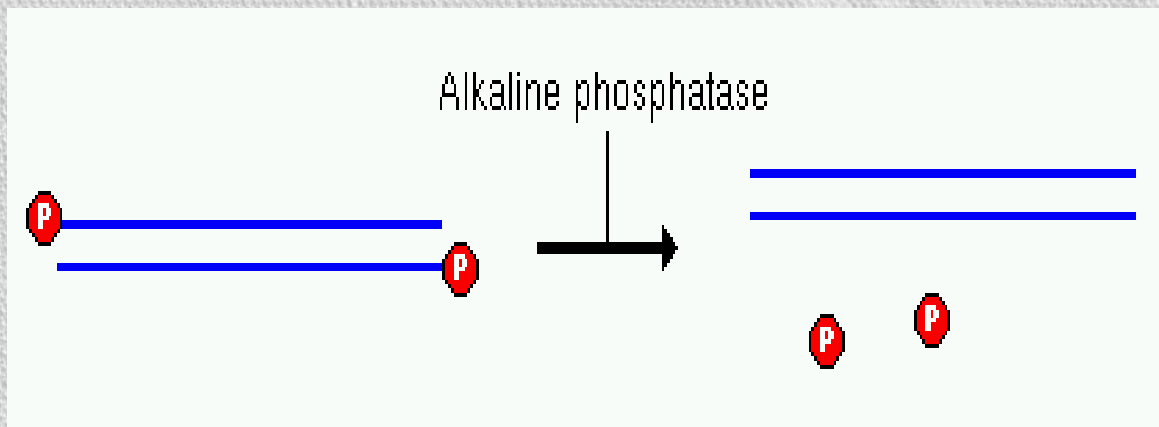
Alkaline phosphatase dephosphorylation

Removing phosphate
group to prevent self
ligation of the vector



Alkaline phosphatase:

Removes 5' phosphate groups from DNA and RNA. It will also remove phosphates from nucleotides and proteins. These enzymes are most active at alkaline pH - hence the name.



There are several sources of alkaline phosphatase that differ in how easily they can be inactivated:

Bacterial alkaline phosphatase (BAP) is the most active one, but also the most difficult to destroy at the end of the dephosphorylation reaction.

Calf intestinal alkaline phosphatase (CIP) is purified from bovine intestine. This is phosphatase most widely used in molecular biology labs because, although less active than BAP, it can be effectively destroyed by protease digestion or heat (75C for 10 minutes in the presence of 5 mM EDTA).

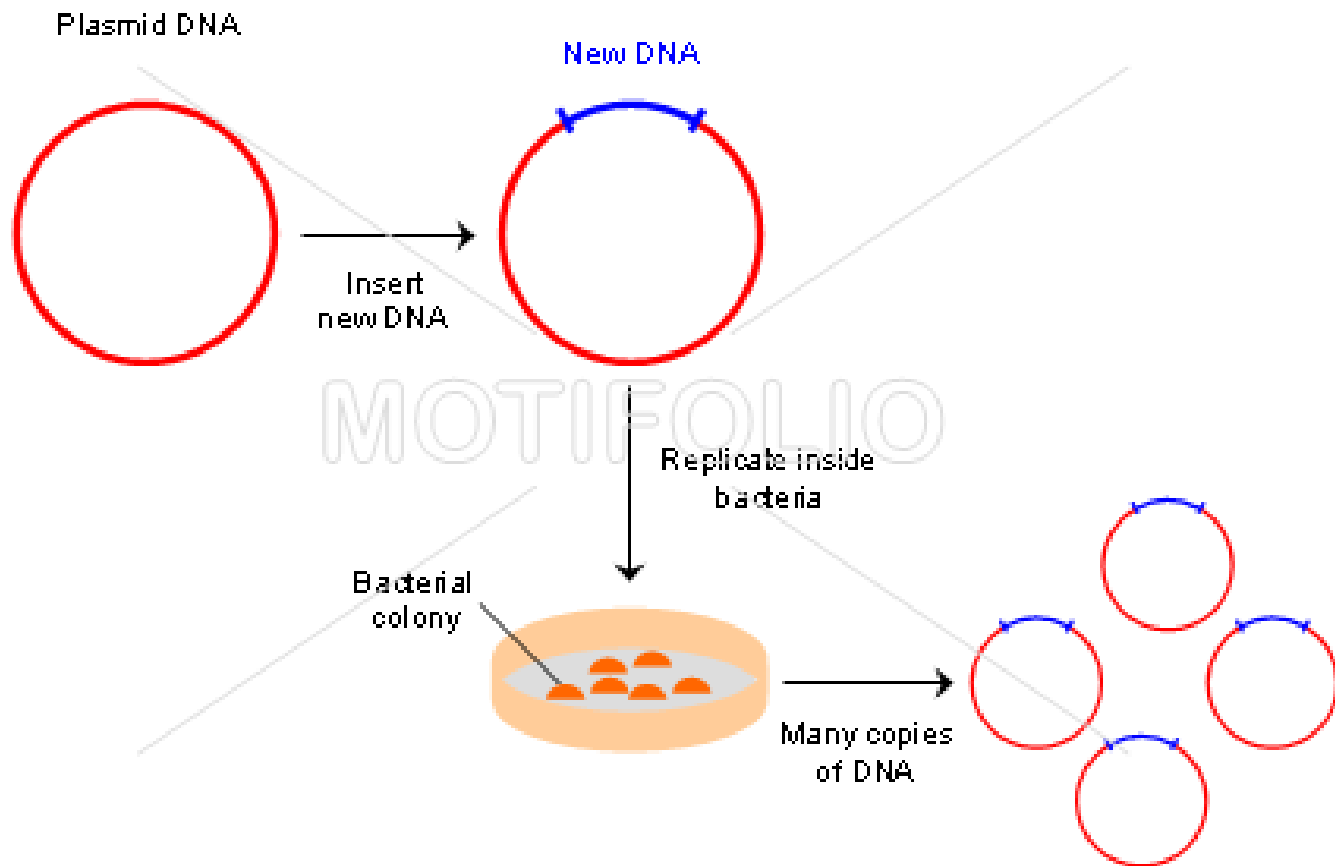
Shrimp alkaline phosphatase is derived from a cold-water shrimp and is promoted for being readily destroyed by heat (65C for 15 minutes).


Trouble-shooting

Sometimes ligation fail to produce the desired ligated products, and some of the possible reasons may be:

- 1- Damaged DNA - over-exposure to UV radiation during preparation of DNA for ligation can damage the DNA.
- 2- Excessive amount of DNA used.
- 3- Incomplete DNA digest, The vector DNA that is incompletely digested will give rise to a high background. Insert that is not completely digested will also not ligate properly and circularize.
- 4- Incomplete ligation. Blunt-ends DNA and some sticky-ends DNA that have low-melting temperature require more ligase and longer incubation time.

Molecular cloning





Always laugh when you
can. It is cheaper than
medicine.

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Thanks a lot

with my Best Regards and My Best wishes

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Mob. (002) 01004477501