

**Design of New Chemical Tools
(Artificial Enzymes)
for Future Biotechnology**

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What Are Artificial Enzymes?

Artificial materials which show remarkable catalysis (activity & selectivity) like naturally occurring enzymes.

They catalyze

- (1) various reactions which are never catalyzed by naturally occurring enzymes
(any model in the nature is unnecessary),**
- (2) (in some case) even with higher specificity than naturally occurring enzymes.**
- (3) under non-physiological conditions**

Two Kinds of “Artificial Enzymes”

1. Completely man-made enzymes
= Chemically synthesized catalysts
(usually involve no proteins)

2. Semi-artificial enzymes
= Mutant proteins obtained by protein engineering

In this lecture, we focus to the first ones
which can be freely designed according to our need.

Why We Need Artificial Enzymes?

**All the livings in the Nature do
what is necessary for their existence (not for us).**

- 1. Physiological conditions (pH 7, r.t., 1 atm) are really the best for our practical purposes?**
- 2. All the reactions we need are covered by naturally occurring enzymes?**

Necessity of Artificial Enzymes for Future Biotechnology

**In order to achieved desired reactions
under desired reaction conditions ,
we have to prepare “tools” for ourselves**



Artificial Enzymes

**Catalysis proceeds via ES complex and
shows both high rates and high specificity.**

How to Prepare Artificial Enzymes

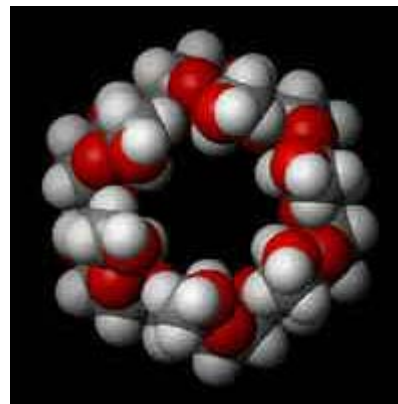
**(i) Molecules which bind the substrate
(and place the reaction center near the catalyst)**

+

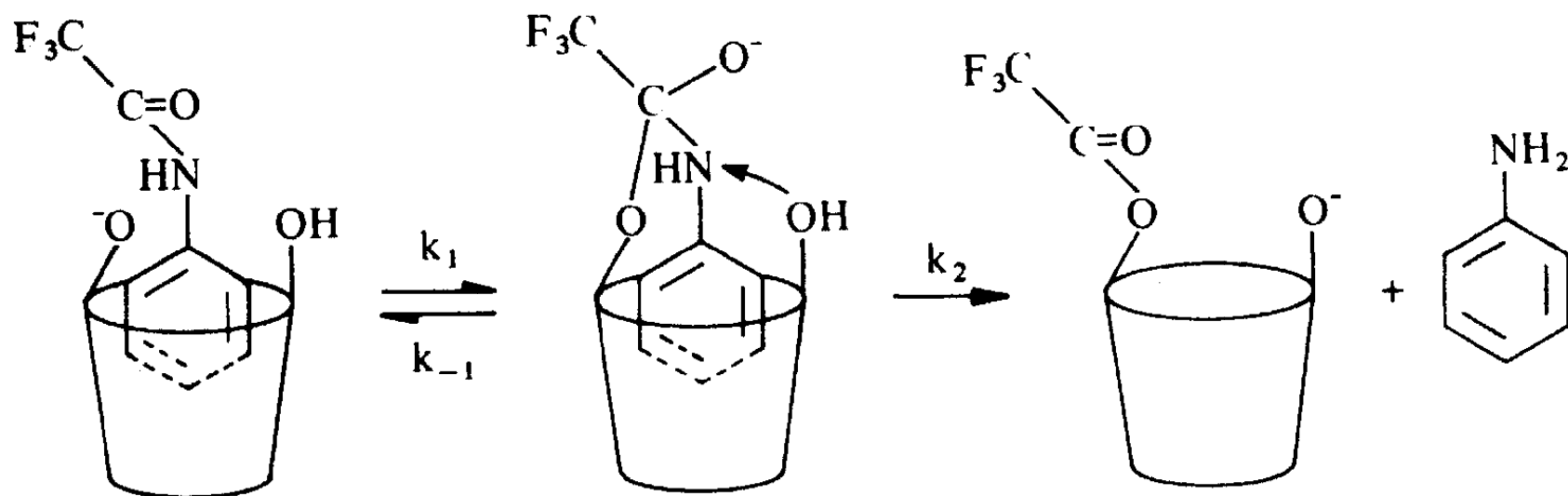
(ii) Catalyst for desired reaction

***Typical examples of the molecules used for (i)**

- Cyclodextrin
- Crown ether
- Cyclophane
- Calixarene
-



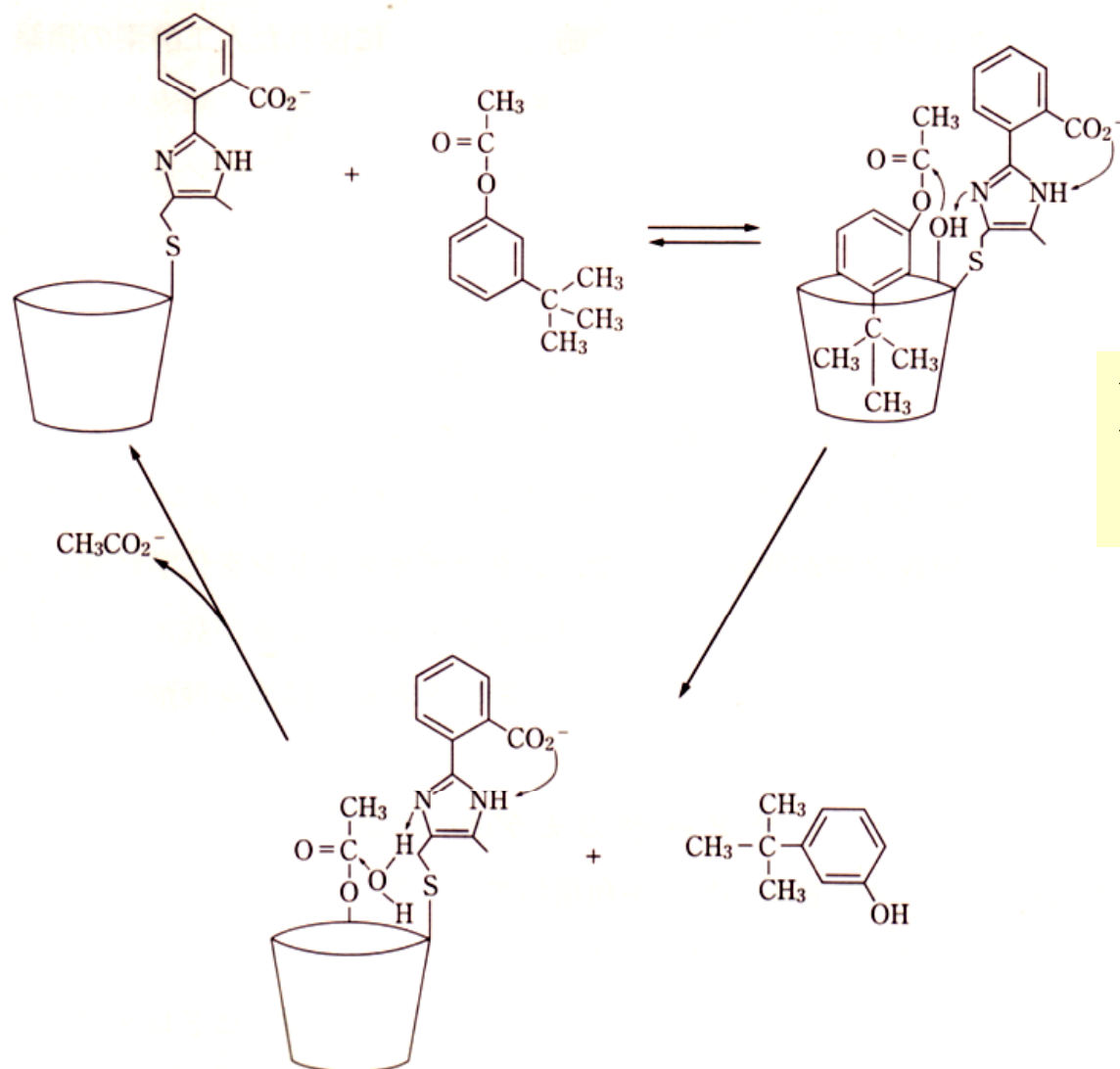
Example 1: Cyclodextrin for amide hydrolysis



**Enzyme-
Substrate
complex**

- Large reaction rate
- Substrate-specificity

Example 2: Chemically modified cyclodextrin as a model of charge-relay system in serine protease



Proton transfer
Ser→His→Asp

Artificial Restriction DNA Cutter (ARCUT) as Tools for Molecular Biology

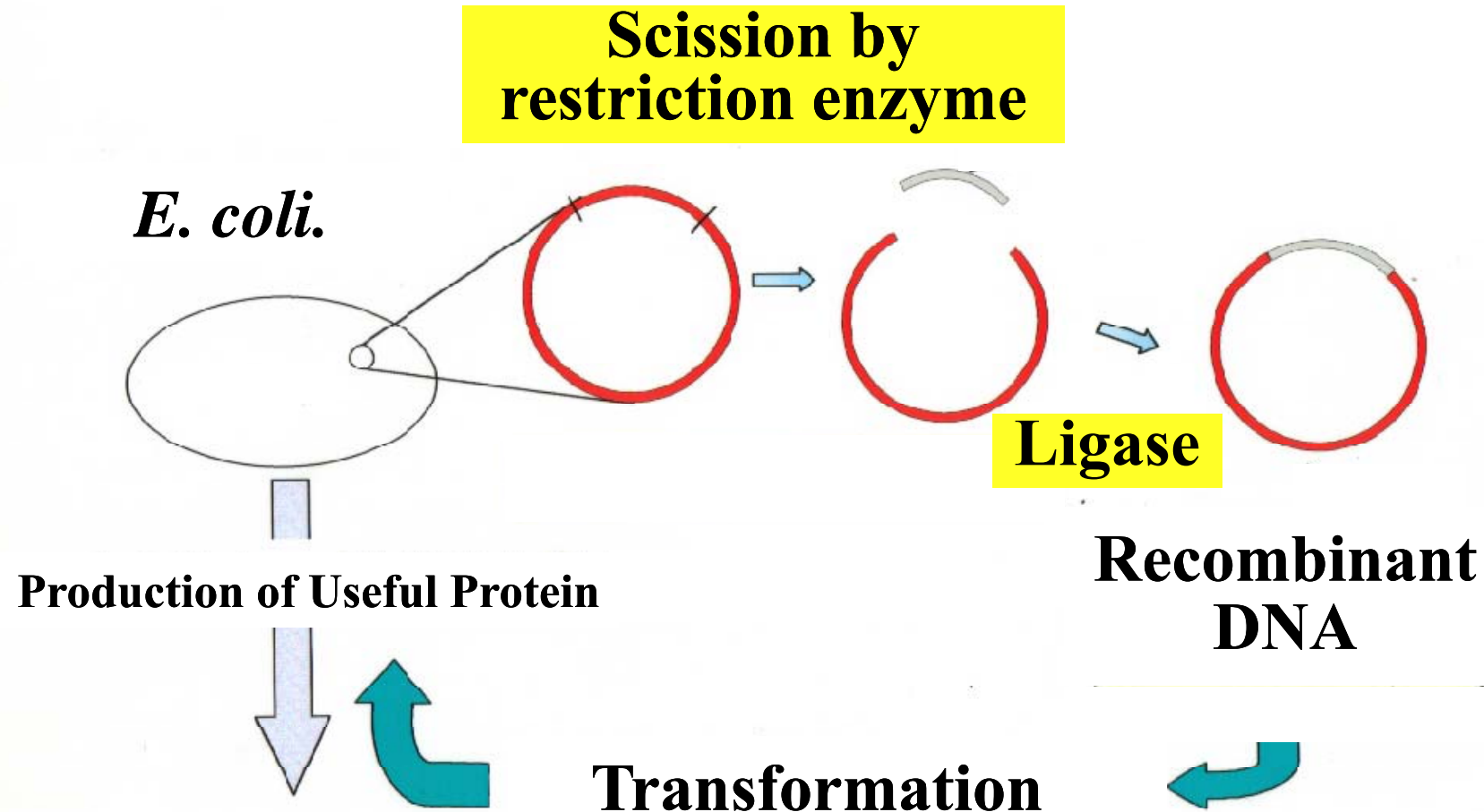
Features of our ARCUT

- 1. The cutters are completely chemistry-based
and contain no proteins.**
- 2. Scission occurs by hydrolysis of
phosphodiester linkages as in enzymatic scission.**
- 3. Scission-site is determined by Watson-Crick rule
and thus the cutter is straightforwardly designed.**

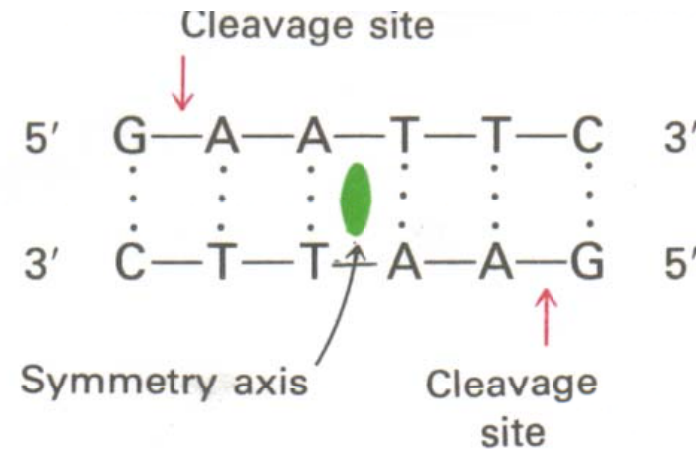
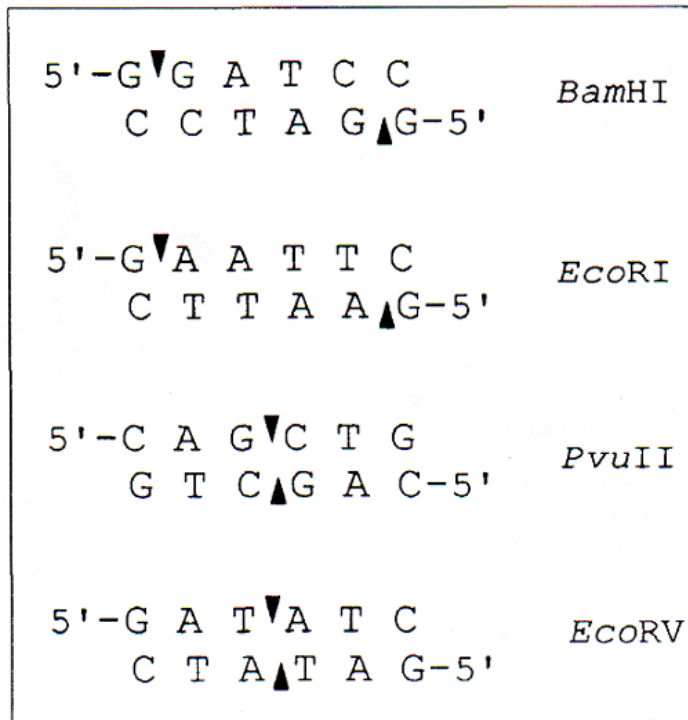
Even huge DNA can be cut at desire site.

<Background>

Typical Procedure of Gene Manipulation



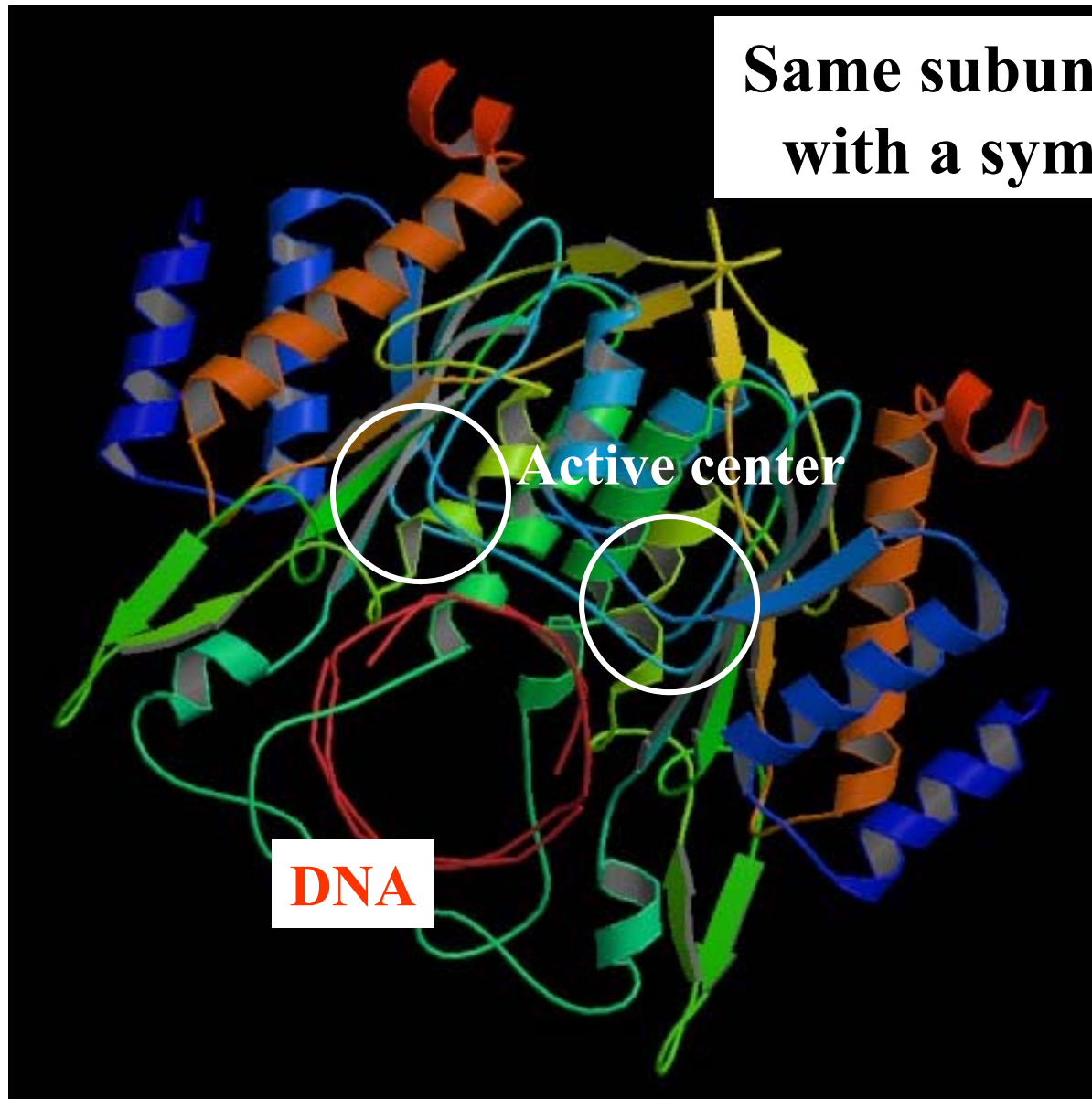
Scission Site of Restriction Enzymes



*Eco*RI

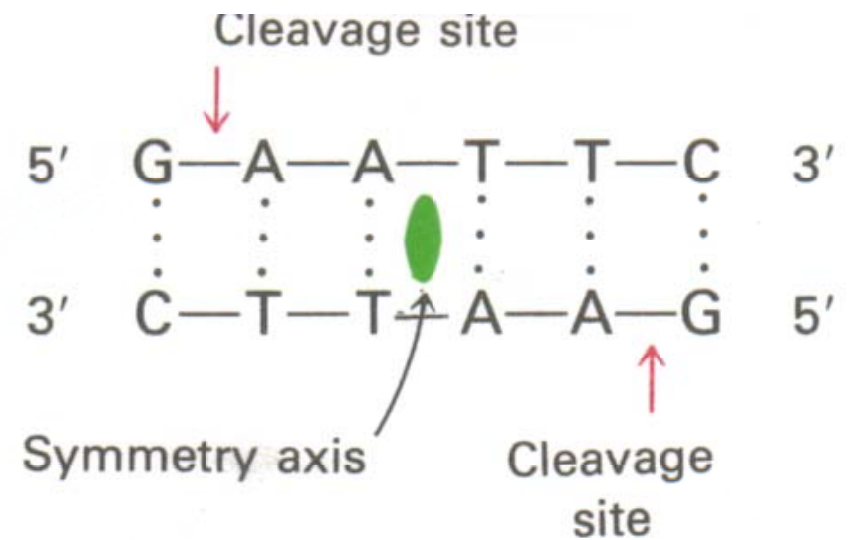
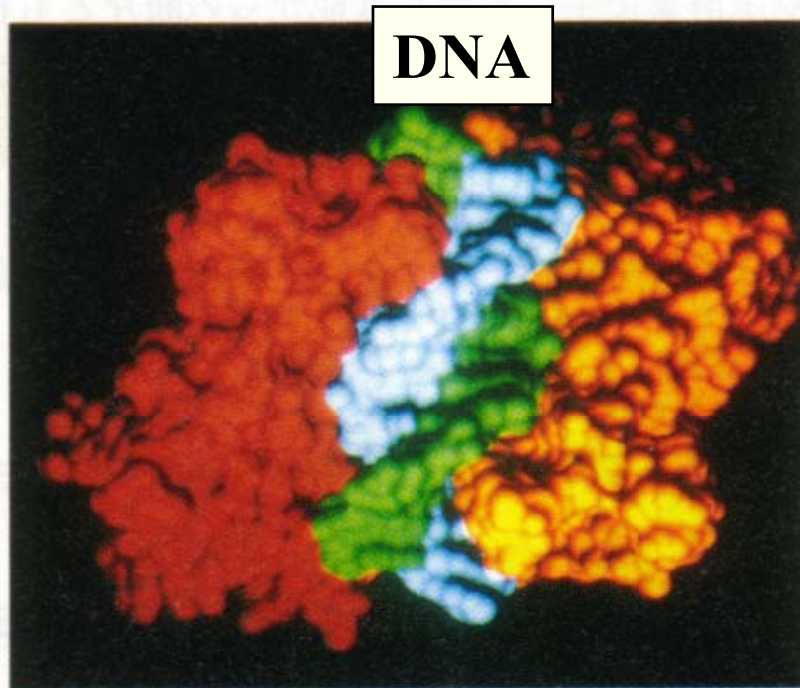
Palindrome site is recognized and cut

Typical Restriction Enzyme *EcoRI*



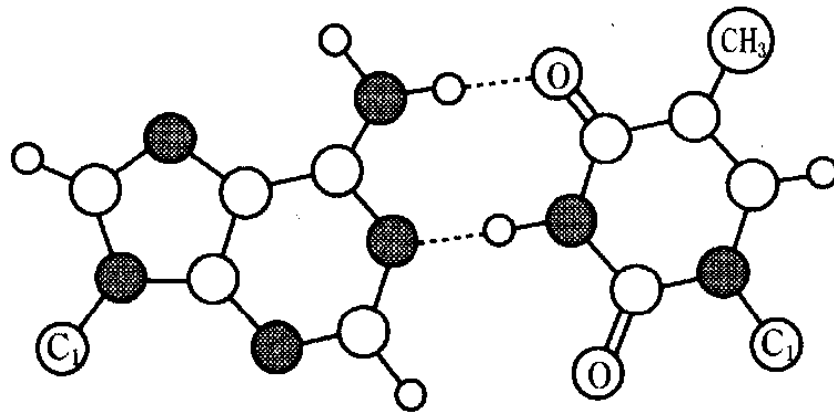
Same subunits are combined
with a symmetrical center

Complex of *EcoRI* with DNA



Major Groove & Minor Groove

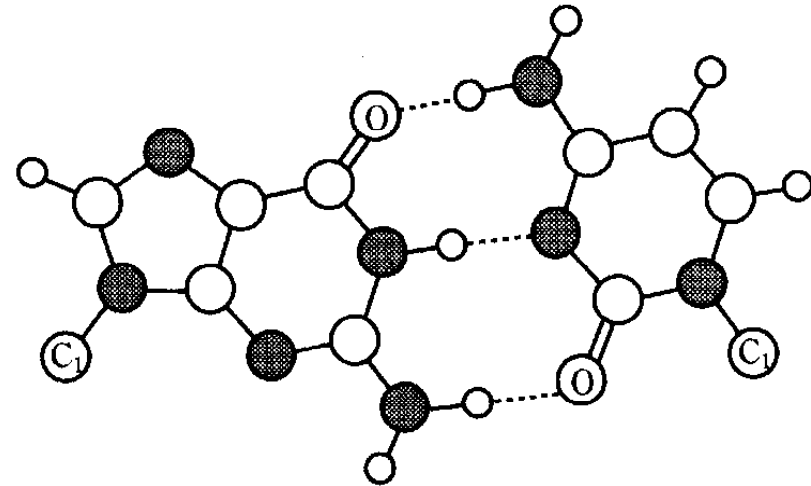
Major Groove



A-T対

Minor Groove

Major Groove

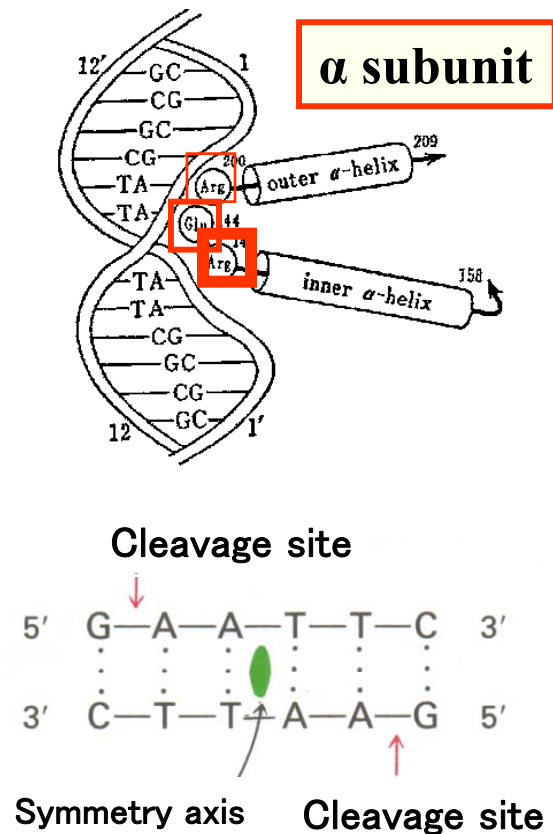


G-C対

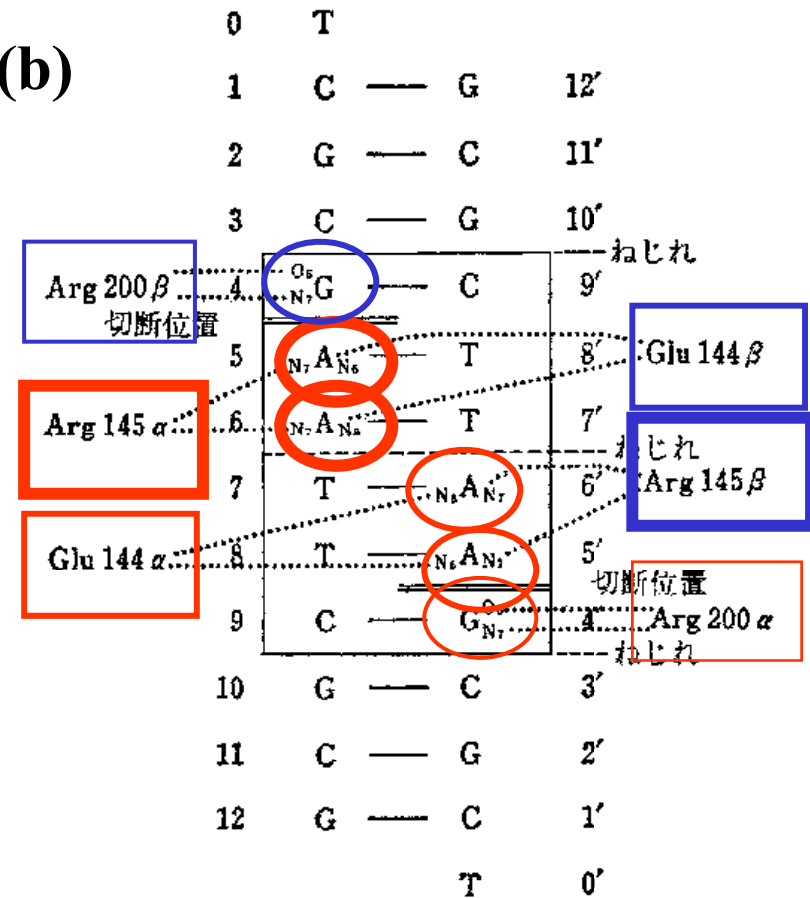
Minor Groove

Mechanism of Sequence-recognition by *EcoRI*

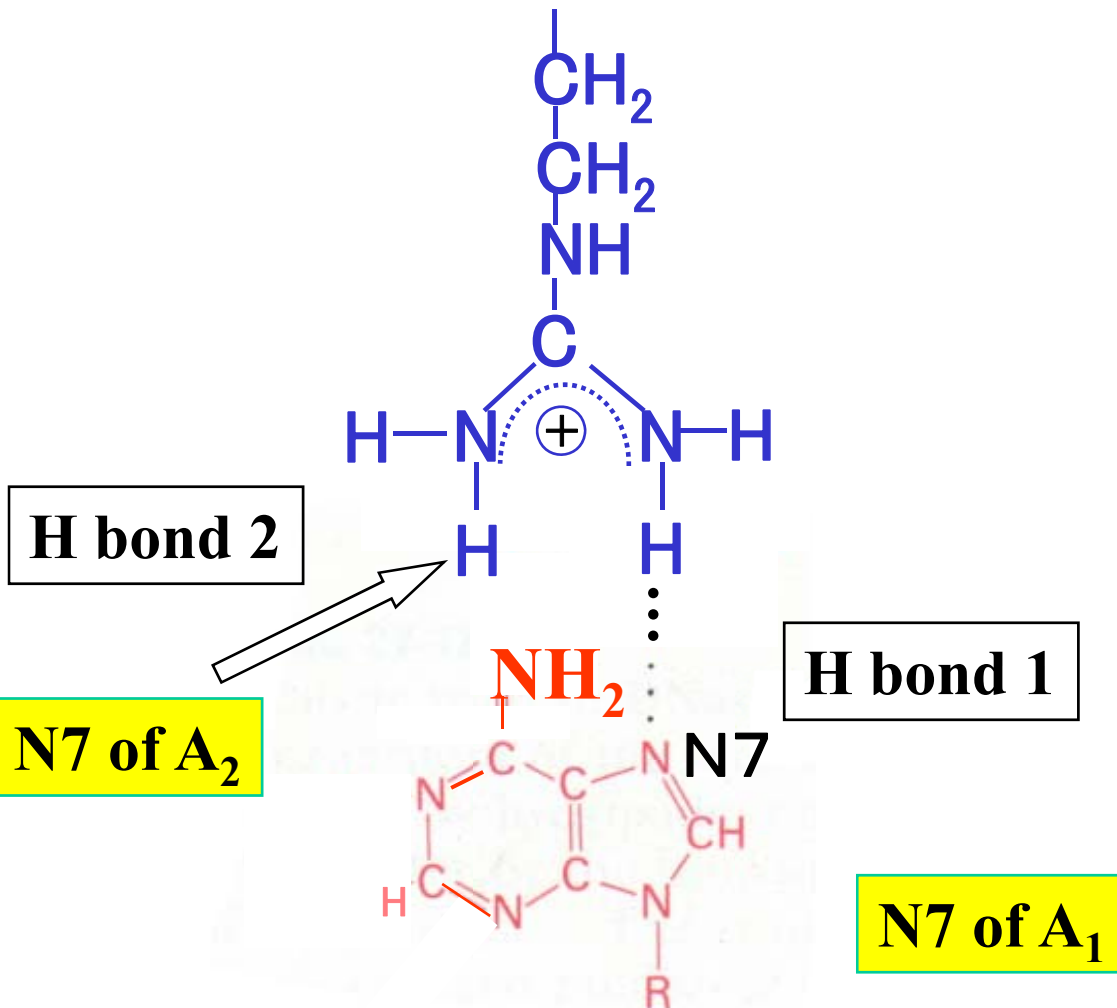
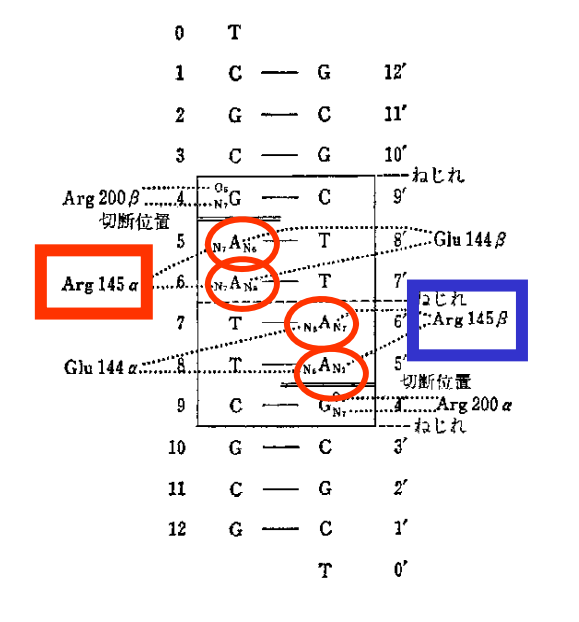
(a)



(b)

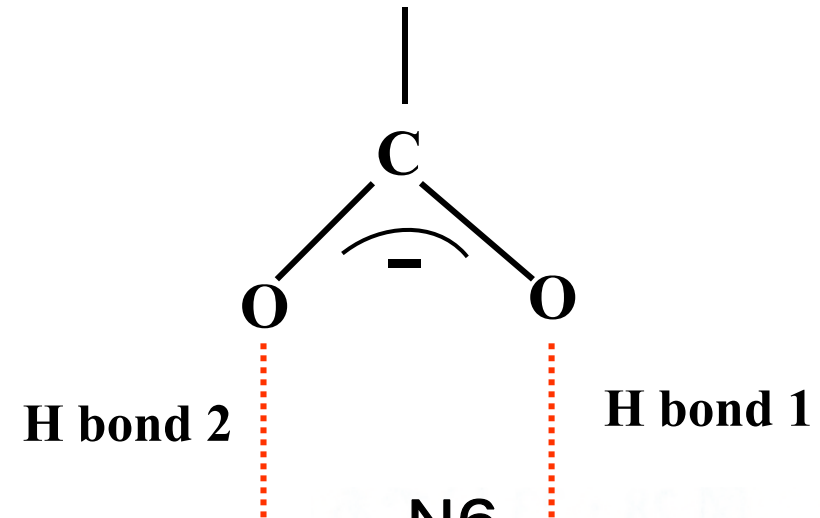


Binding of Arg to Two Adenines

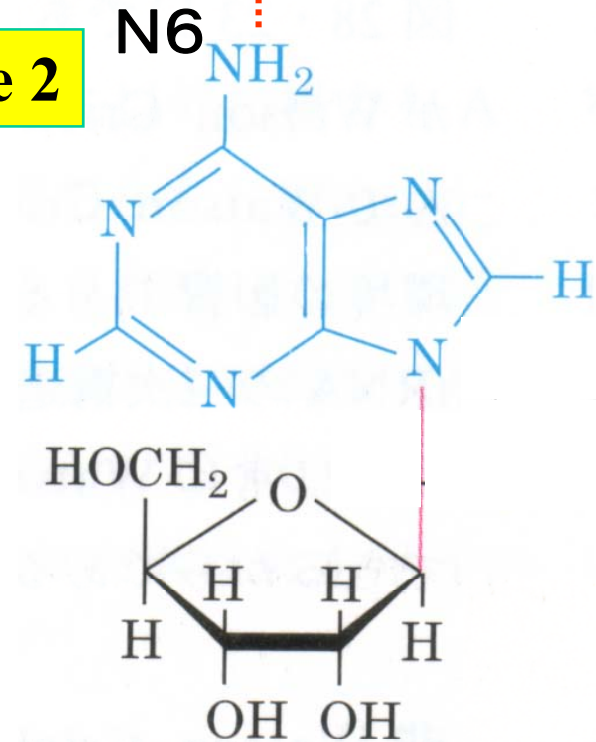


Binding of Glu to Two Adenines

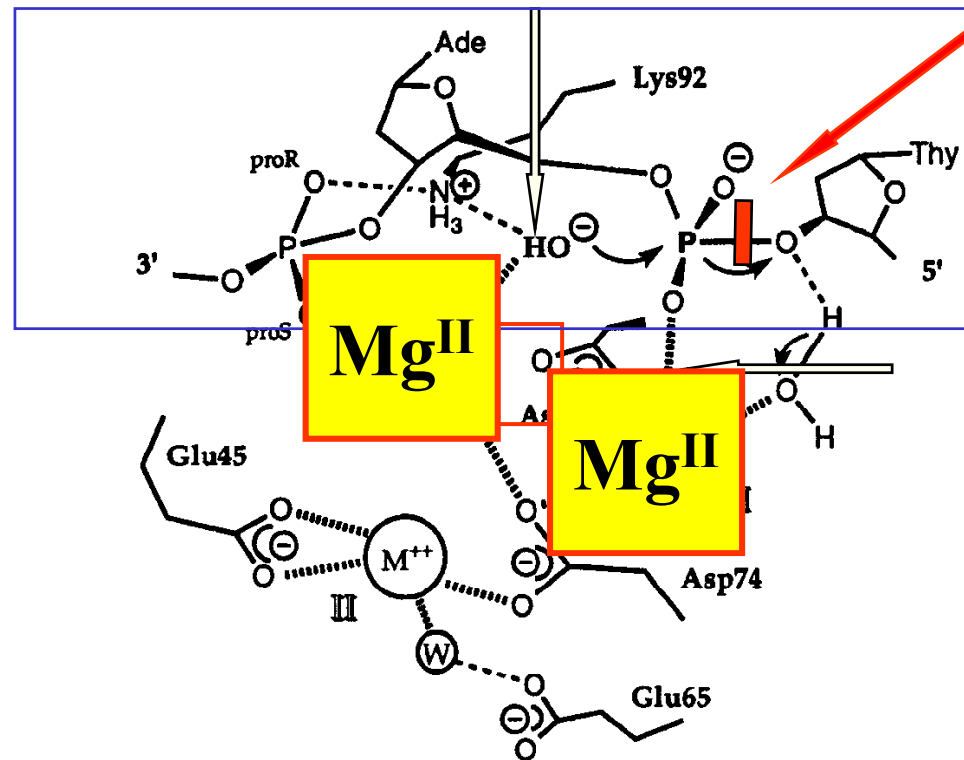
0	T		
1	C	— G	12'
2	G	— C	11'
3	C	— G	10'
Arg 200 β	4	$O_6 N_1 G$ — C	9'
切断位置	5	$N_1 A N_6$ — T	8'
Arg 145 α	6	$N_1 A N_6$ — T	7'
	7	T — $N_1 A N_6$	6'
Glu 144 α	8	T — $N_1 A N_6$	5'
	9	C — $O_6 N_1$	4'
	10	G — C	3'
	11	C — G	2'
	12	G — C	1'
		T	0'



N6 of adenine 2



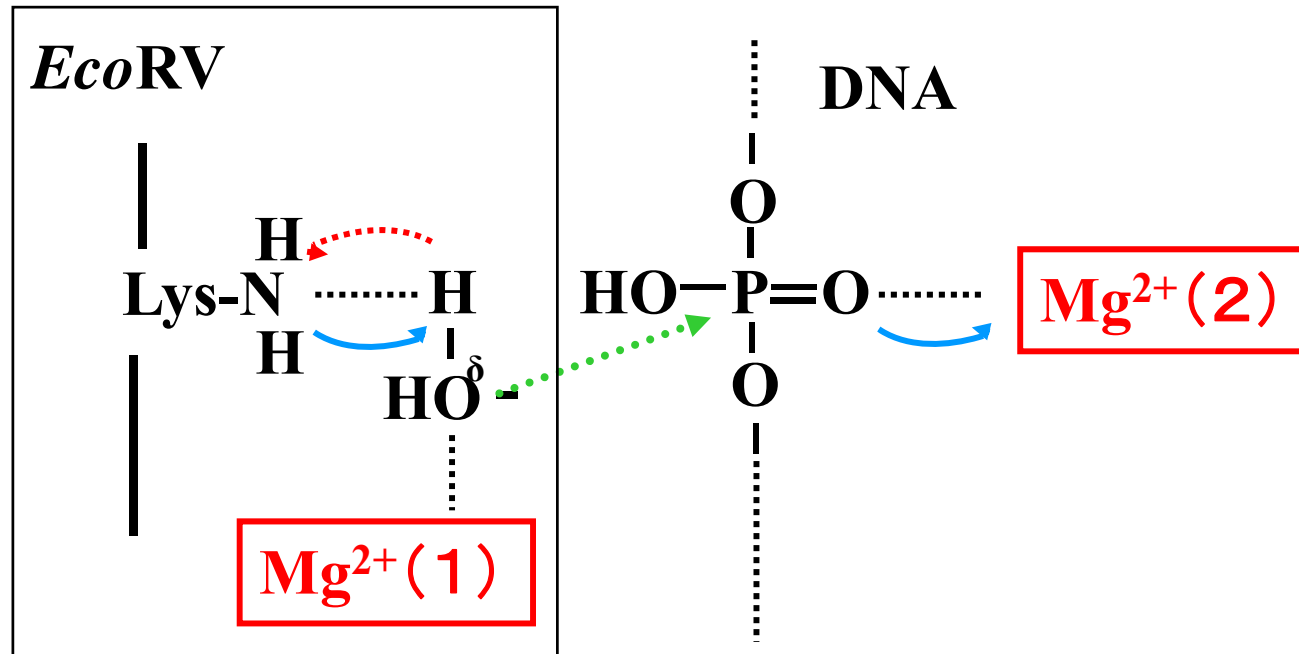
DNA Scission by Restriction Enzyme (EcoRV)



Scissile
Phosphodiester
Linkage

- 1) **One Mg(II) ion** provides OH⁻ as the nucleophile.
- 2) **Another Mg(II) ion** activates the phosphodiester linkage.

Mechanism of DNA Hydrolysis by Restriction Enzyme



$\text{Mg}^{2+}(1)$: Activate water by electron withdrawal

Lys : Proton removal from the water
(General base catalysis)

$\text{Mg}^{2+}(2)$: Electron removal from the phosphodiester

Genomes of higher livings are far larger than plasmid DNA

Plasmid DNA	4-5 kb
Phage	50
Genome of <i>E. coli</i>	4,600
Genome of yeast	13,500
Human beings	3,000,000

In order to pin down one site in human genome, we must recognize 16 or 17 base-sequence!

($4^{16} > 30 \times 10^8$ = the number of base-pairs in human genome)

Most of Naturally Occurring Restriction Enzymes

Recognize Mostly 4 or 6 DNA-Base Sequence

5'-G[▼]G A T C C
C C T A G[▲]G-5' *Bam*HI

5'-G[▼]A A T T C
C T T A A[▲]G-5' *Eco*RI

5'-C A G[▼]C T G
G T C[▲]G A C-5' *Pvu*II

5'-G A T[▼]A T C
C T A[▲]T A G-5' *Eco*RV

Frequency of appearance
of scission site
 $= 1/4^6 (= 1/4096)$

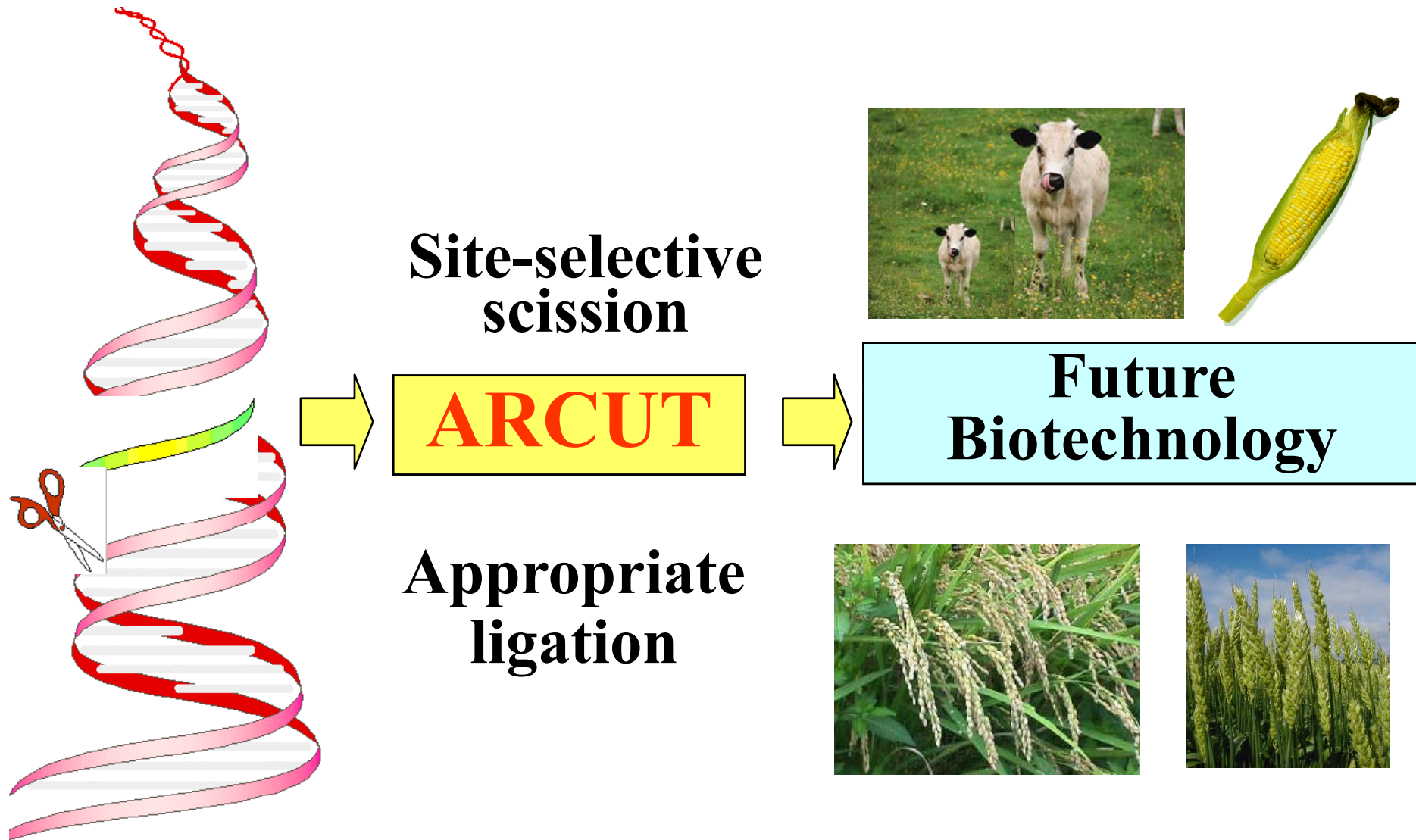
Note that this number is
comparable with
the size of plasmid.

Limitations of Naturally Occurring Restriction Enzymes As Tools

- (1) Huge DNA cannot be manipulated.**
- (2) Scissile sequence is strictly limited.**
- (3)**
- (4)**

Necessity of new tools

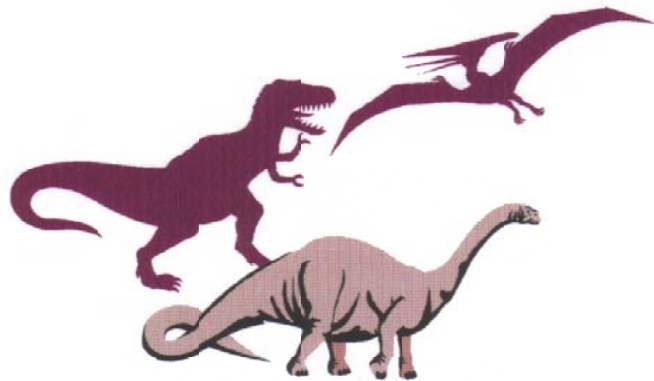
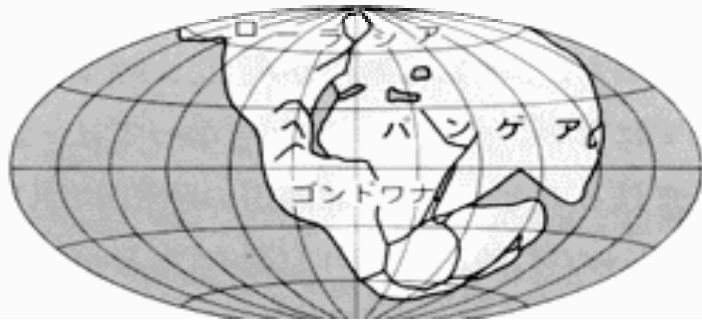
One of the Next Goals of Biotechnology



1. Preparation of Catalyst as the First Step Towards Artificial Restriction Enzyme

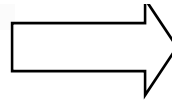
DNA is unbelievably stable!

(it takes more than 10^8 years to hydrolyze it without enzyme)



The earth of 10^8 years ago

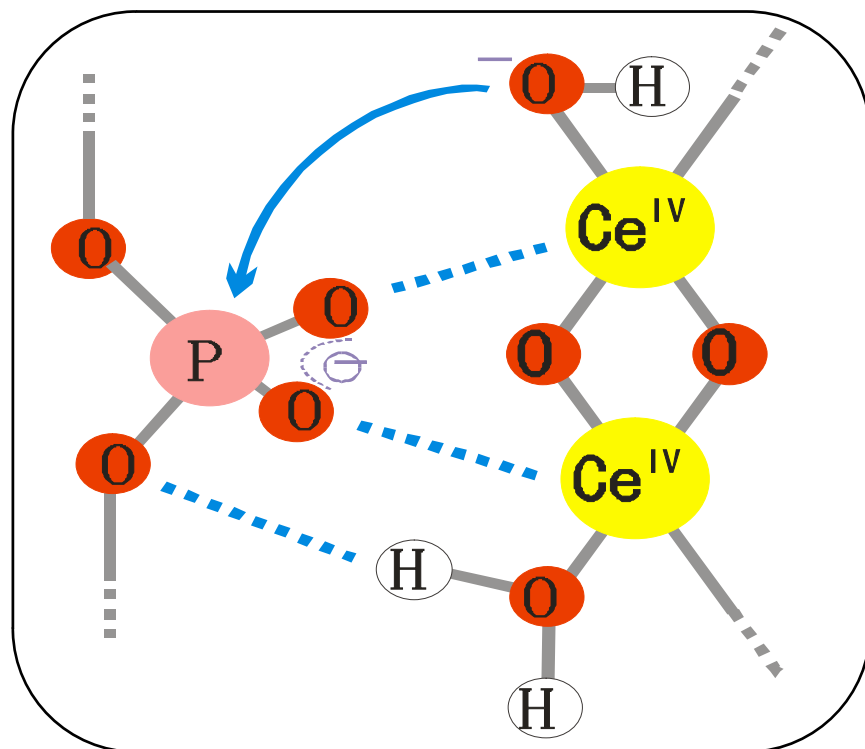
Ce(IV)



**Hydrolysis
within a few hours
under
physiological conditions**

<div><div><div>● Alkali Metals</div><div>● Alkaline Earth Metals</div><div>● Transition Metals</div><div>● Other Metals</div><div>● Metalloids</div><div>● Nonmetals</div></div><div><div>● Halogens</div><div>● Noble Gases</div><div>● Lanthanides</div><div>● Actinides</div></div></div>																		18
1																	2	
1 H																	2 He	
3	4															10		
Li	Be															Ne		
11	12															18		
Na	Mg															Ar		
		3											13	14	15	16	17	
19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	
K	Ca	Sc	Ti	V	Cr	Mn	Fe	Co	Ni	Cu	Zn	Ga	Ge	As	Se	Br	Kr	
37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	
Rb	Sr	Y	Zr	Nb	Mo	Tc	Ru	Rh	Pd	Ag	Cd	In	Sn	Sb	Te	I	Xe	
55	56	57	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	
Cs	Ba	La	Hf	Ta	W	Re	Os	Ir	Pt	Au	Hg	Tl	Pb	Bi	Po	At	Rn	
87	88	89	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	
Fr	Ra	Ac	Rf	Db	Sg	Bh	Hs	Mt	Ds	Rg	Uub	Uut	Uuq	Uup	Uuh	Uus	Uuo	

Mechanism of Ce(IV)-Induced DNA Hydrolysis



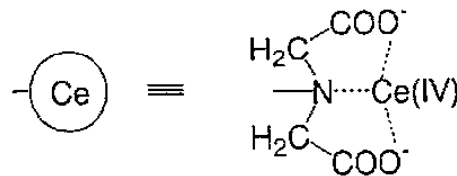
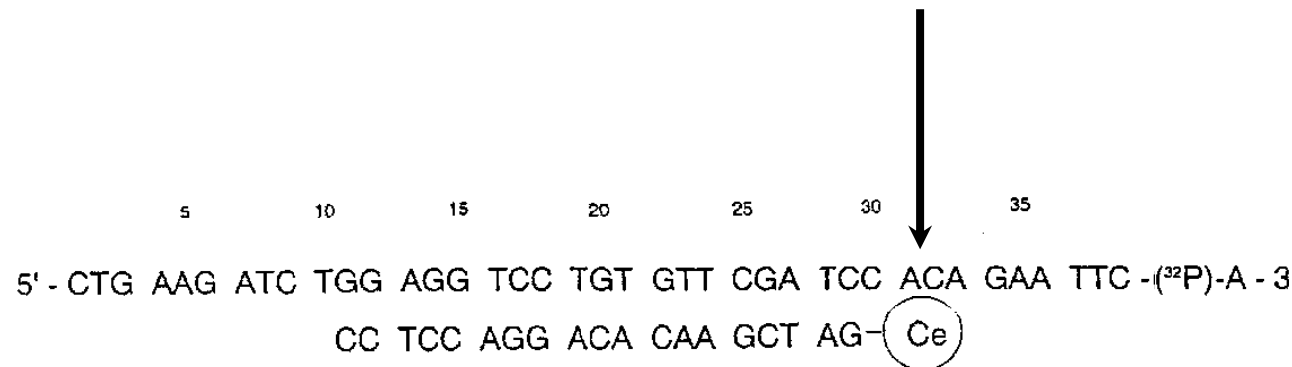
**Remarkable
electron-withdrawal
from the P atom**

↕

the major driving force

Cerium is the sole lanthanide ion whose +4 state is sufficiently stable ($\text{Ce(IV)} \rightleftharpoons \text{Ce(III)}$).

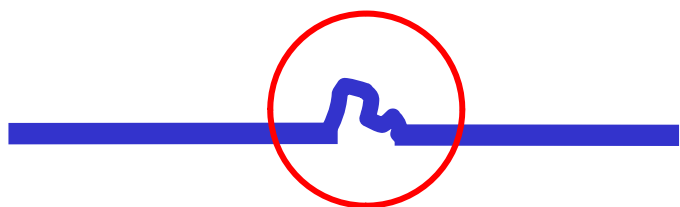
The First-generation Artificial Restriction Enzymes for Sequence-Selective DNA Scission



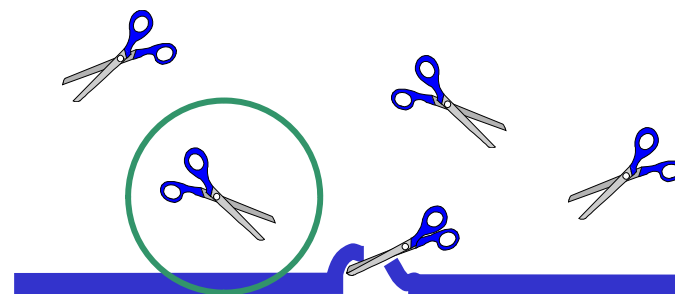
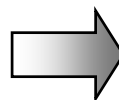
(1994)

Useful new tools were obtained, but double-stranded DNA could not be cleaved.

New Strategy Developed by Our Group for Site-Selective DNA Scission



**Differentiation of target
site in terms of reactivity**

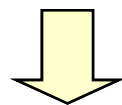


**Site-selective scission
by catalysts showing
high substrate-specificity**

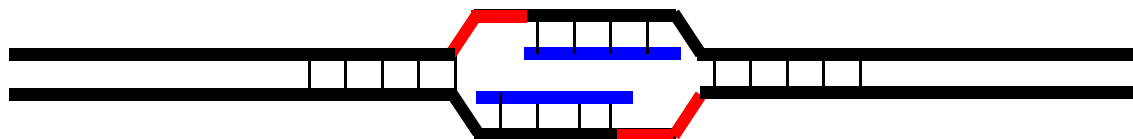
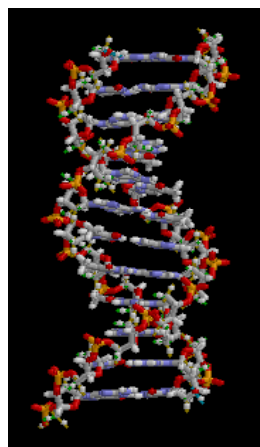
**From simple “proximity effect” in the first generation
to “site-selective activation of target-site”**

2. Molecular Design of Site-Selective Scission of Double-stranded DNA

Activation of **target site** in double-stranded DNA



Scission of **this site** by Ce(IV) complex



Two Components of ARCUT

(1) Ce(IV) /EDTA complex

hydrolyzes the hot spot (single-stranded portion)

formed in double-stranded DNA

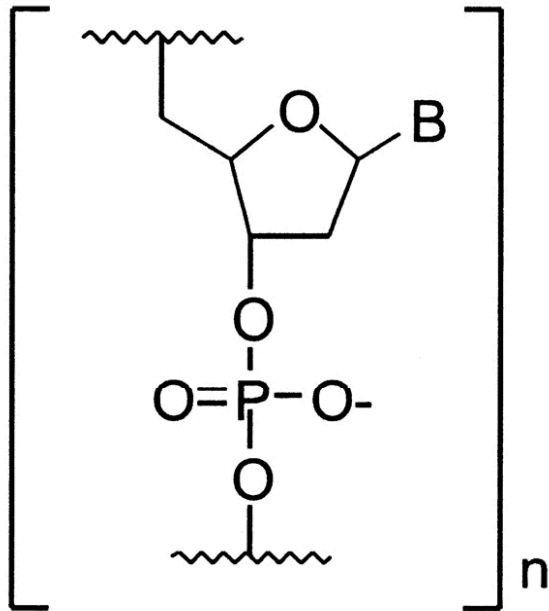
(intrinsic scission activity: ssDNA >> dsDNA)

(2) PNA

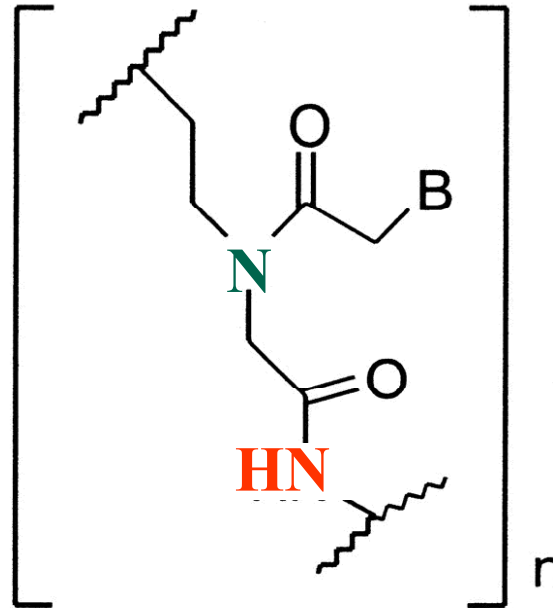
forms hot spot (single-stranded portion)

at the target site in dsDNA

PNA (Peptide Nucleic Acid) for the Formation of Hot Spot in dsDNA

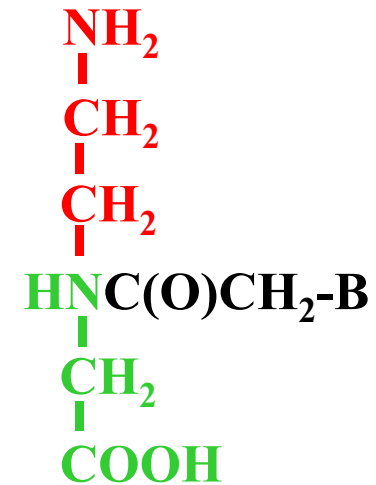


DNA



PNA

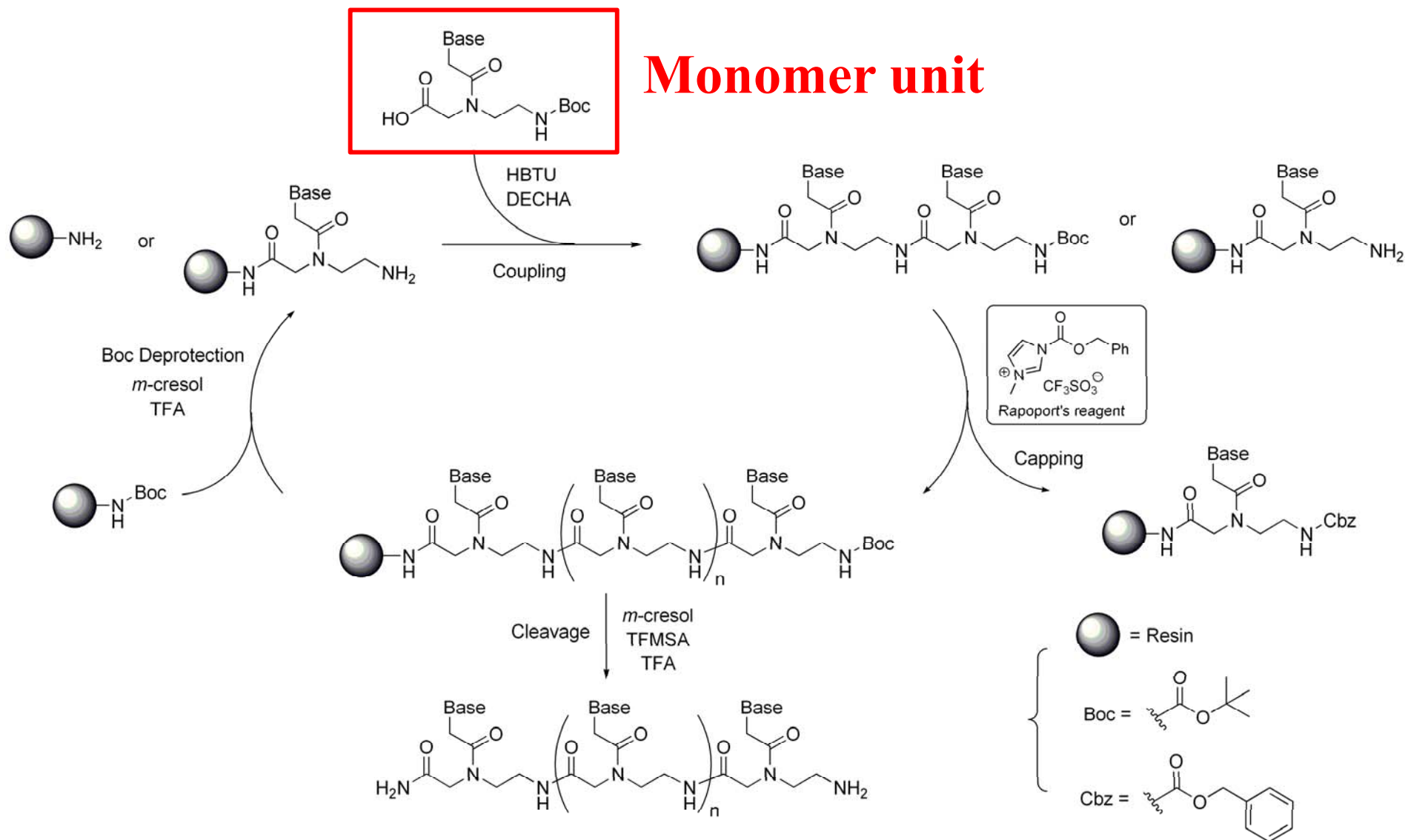
(**P**eptide **N**ucleic **A**cid)



**Condensation polymer
of N-aminoethylglycine**

Solid Phase Synthesis of PNA

Monomer unit

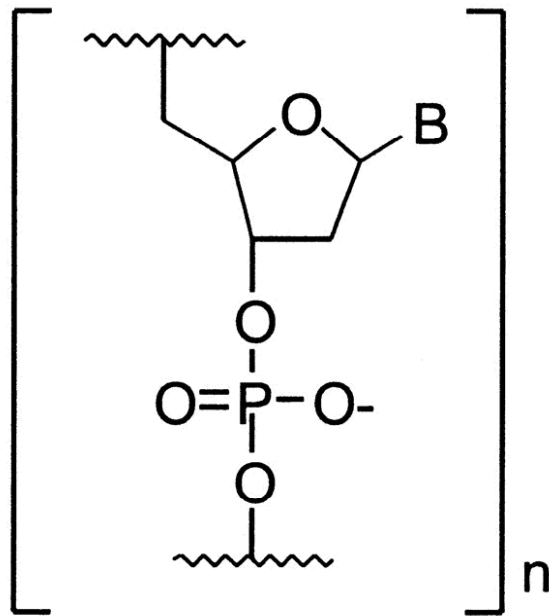


DNA Synthesizer

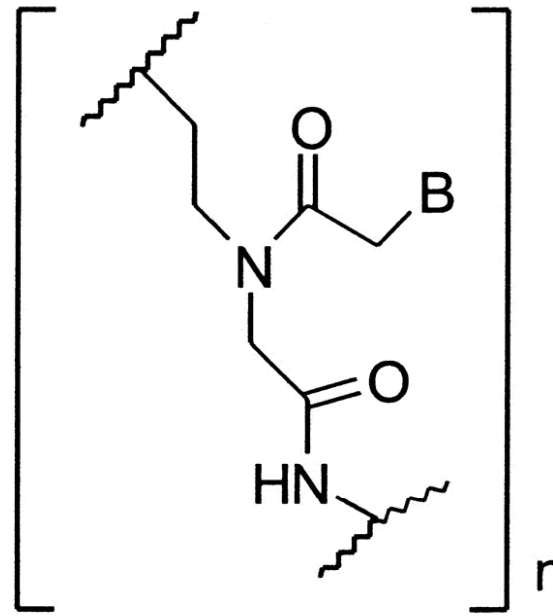


1 unit ~ 10 min → 60-70 base nucleotide in 10 h

Backbone of **PNA** Is Neutral In Contrast to Negative Charges of DNA



DNA

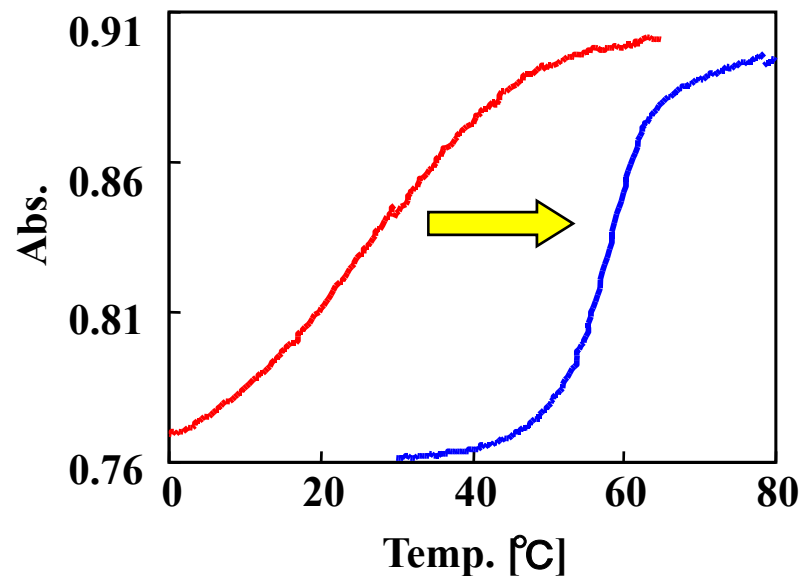


PNA

In DNA/DNA duplexes, electrostatic repulsion is operative between two strands

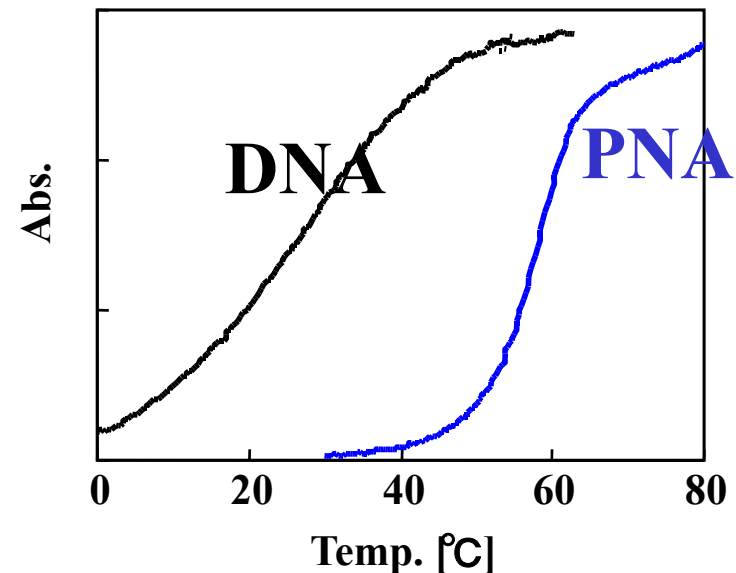
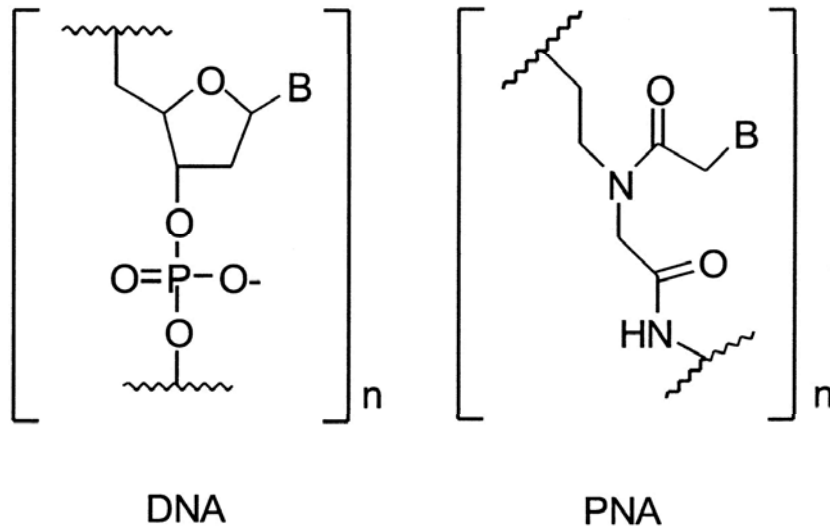
\therefore Stability of DNA duplexes (T_m) are strongly dependent on ionic strength.

- 1. If you add salt (e.g., KCl) to the solution, electrostatic repulsion between negative charges decreases.**
- 2. This factor increases the stability of DNA/DNA duplex, and increases of its T_m .**



Features of Peptide Nucleic Acid (PNA)

1. Formation of duplexes with complementary DNA
2. Stability: $\text{DNA} \cdot \text{PNA} > \text{DNA} \cdot \text{DNA}$
(absence of electrostatic repulsion)
3. Resistance against nucleases



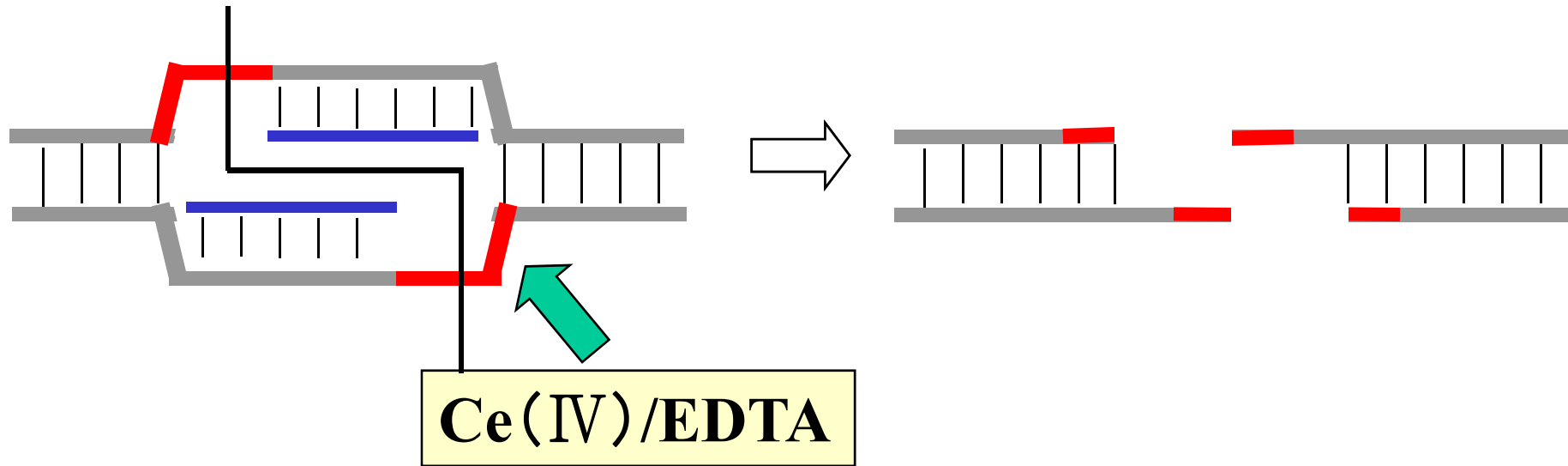
Typical melting curve

36

**DNA/PNA duplexes are more stable
than DNA/DNA duplexes**

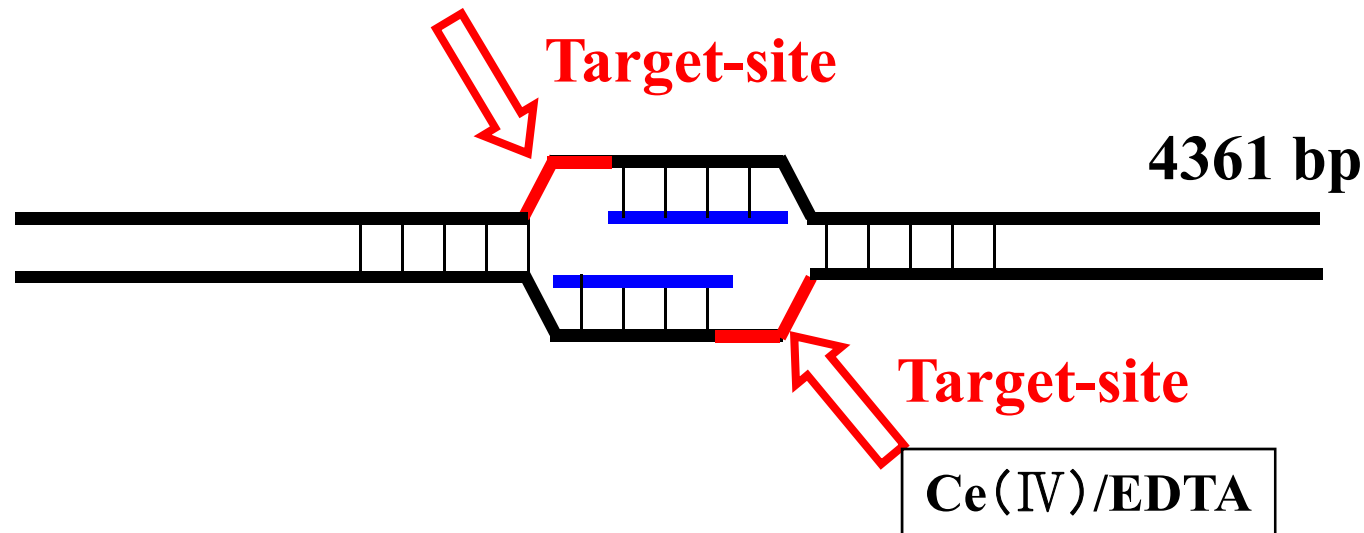
Duplexes		T _m	
DNA/DNA	5'-TGTACGTCACAACTA-3' 3'-ACATGCAGTGTTGAT-5'	53 °C	17 °C
PNA/DNA	<i>TGTACGTCACAACTA</i> 3'-ACATGCAGTGTTGAT-5'	70 °C	
DNA/DNA	5'-ACATCATGGTCG-3' 3'-TGTAGTACCAGC-5'	48 °C	11 °C
PNA/DNA	<i>ACATCATGGTCG</i> 3'-TGTAGTACCAGC-5'	59 °C	

Invasion of Two PNA Strands to dsDNA for Differentiation of Target Site in **ARCUT**



Both strands are hydrolyzed at desired site.

Invasion of PNA to Double-stranded DNA



5'-...CGTTCCAGTAACCGGGCATG **TTCAT**CATCAGTAACCCGTA TCGTGAGCATCCTCTCTCGT...-3'

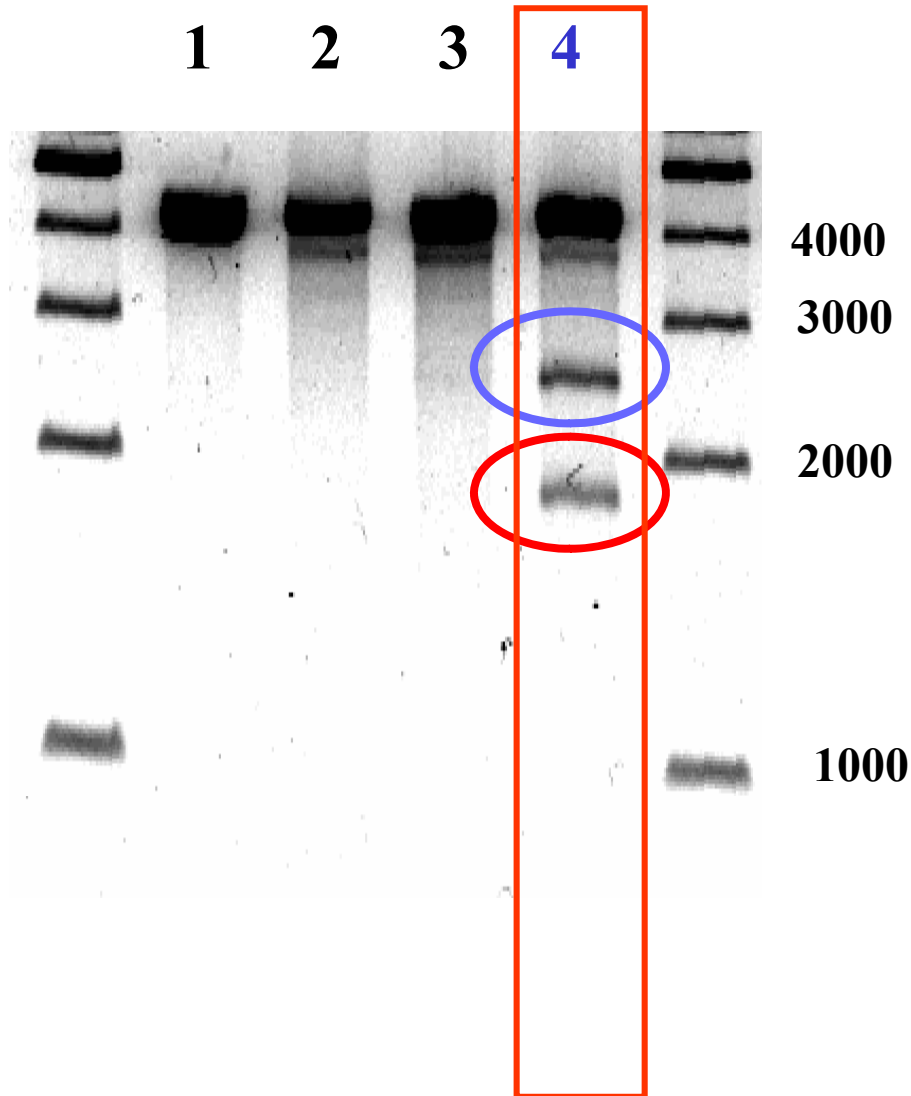
pcPNA1 H₂NCO-(Lys)**GUDGUCDUUGGGCDU**(Lys)-NH₂

pcPNA2 H₂N-(Lys)**UUCDUCDUCDGUDDC**(Lys)-CONH₂

3'-...GCAAGGTCATTGGCCCGTAC **AAGTAGTAGTCATTG****GGCAT**AGCACTCGTAGGAGAGAGCA...-5'

(U ≡ T, D ≡ A)

ARCUT for Site-selective Scission of Linearized Plasmid DNA

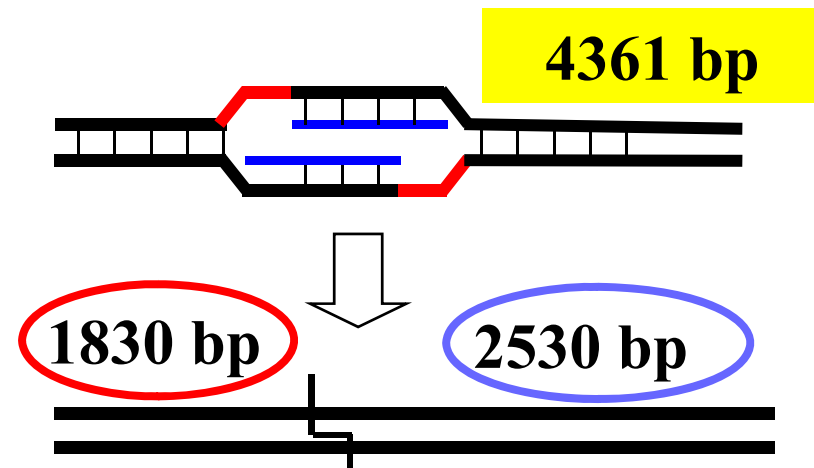


lane 1 control

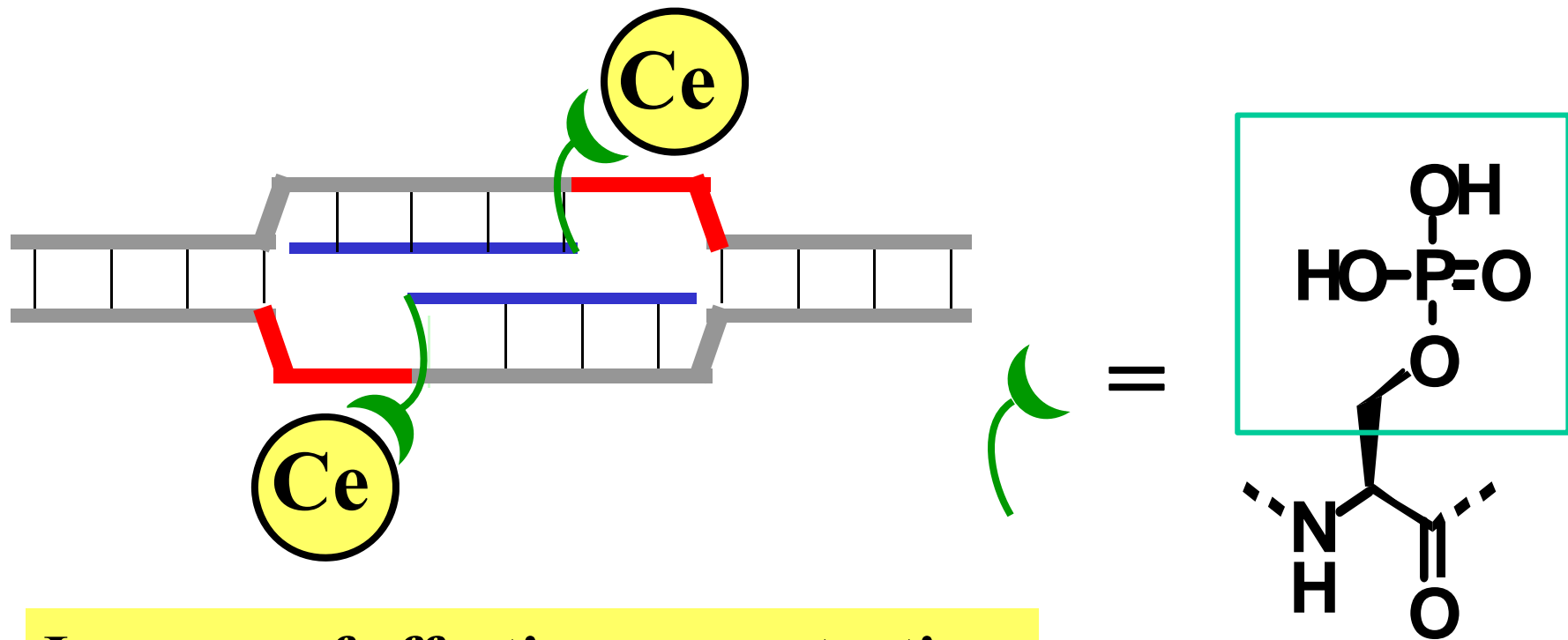
lane 2 Ce(IV)/EDTA only

lane 3 Ce(IV)/EDTA + pcPNA 3&4

lane 4 Ce(IV)/EDTA + pcPNA 1&2



Introduction of Monophosphate to **ARCUT** for Promotion of Scission Efficiency



**Increase of effective concentration
of Ce(IV) near the target site**

Site-selective DNA Scission by **PNA** Bearing **Monophosphate** at the N-Termini

Lane 1 control (DNA only)

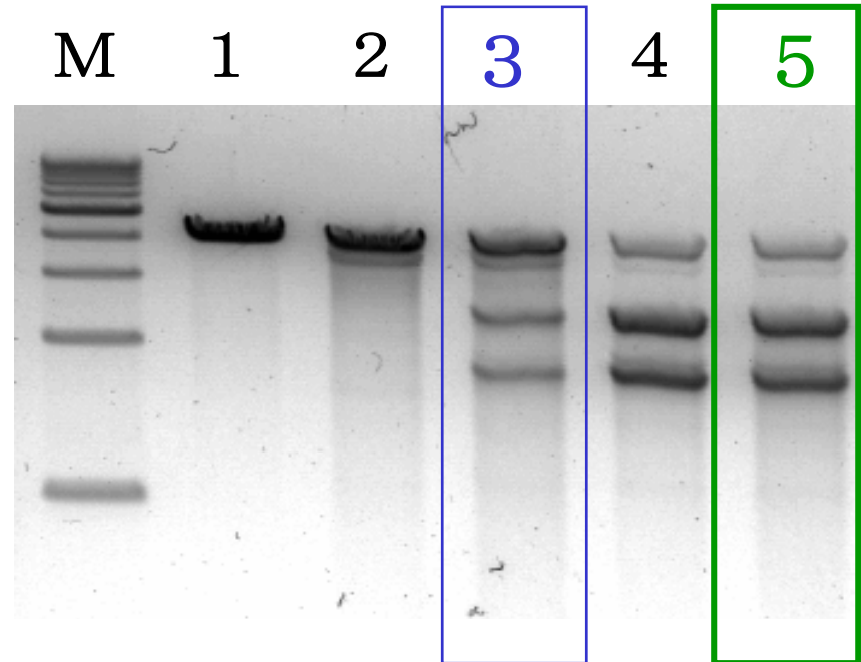
Lane 2 without pcPNA

Lane 3 with PNA 5&6

Lane 4 with PNA 5II&6II

Lane 5 with PNA 5P&6P

Lane M 1kbp ladder marker



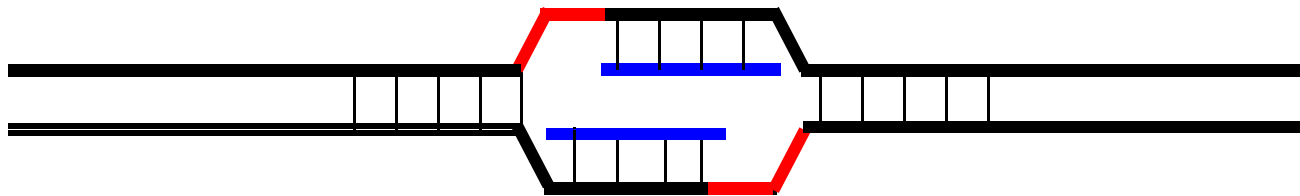
**Yields of Desired Fragments
= 50-60% in 20 h**

Reaction conditions: pBR322 DNA 8 nM, pcPNA 200 nM, HEPES buffer (pH 7) 5 mM, NaCl 100 mM, Ce(IV)/EDTA 200 μ M, 50 $^{\circ}$ C, 20 h

3. Applications of **ARCUT** to molecular biology

Advantages of **ARCUT**

1. High site-specificity
(\gg naturally occurring restriction enzyme)
2. Choice of scission site is free.



Length & sequence of PNA: Free!

(1) Site-selective Scission of λ phage DNA (49 kbp)

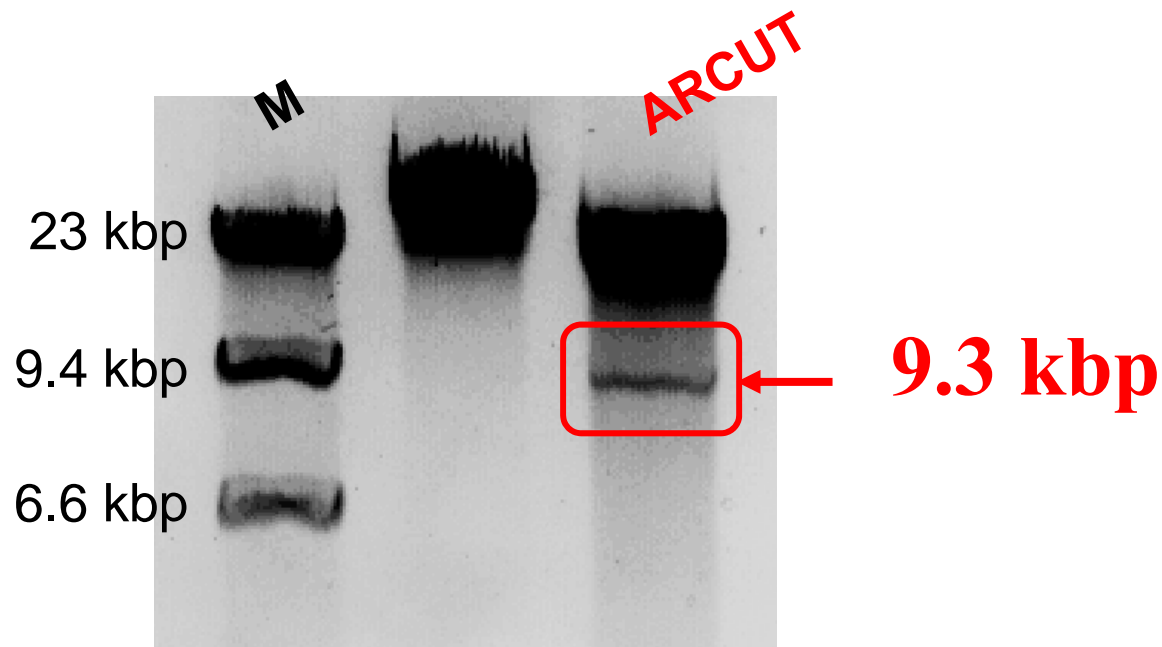


5' - ...AAAGAT **TATTCGTCAG** AGAATTCTGGCGAATCCTCTGACCA... - 3'

pcPNA⁽⁵⁾ H₂N(Lys)₂UCUDDGDCCGCUUDGGDGD(Lys)-H

pcPNA⁽⁶⁾ H(Lys)UDUUCGUCDGDGDDUUCUGG(Lys)₂NH₂

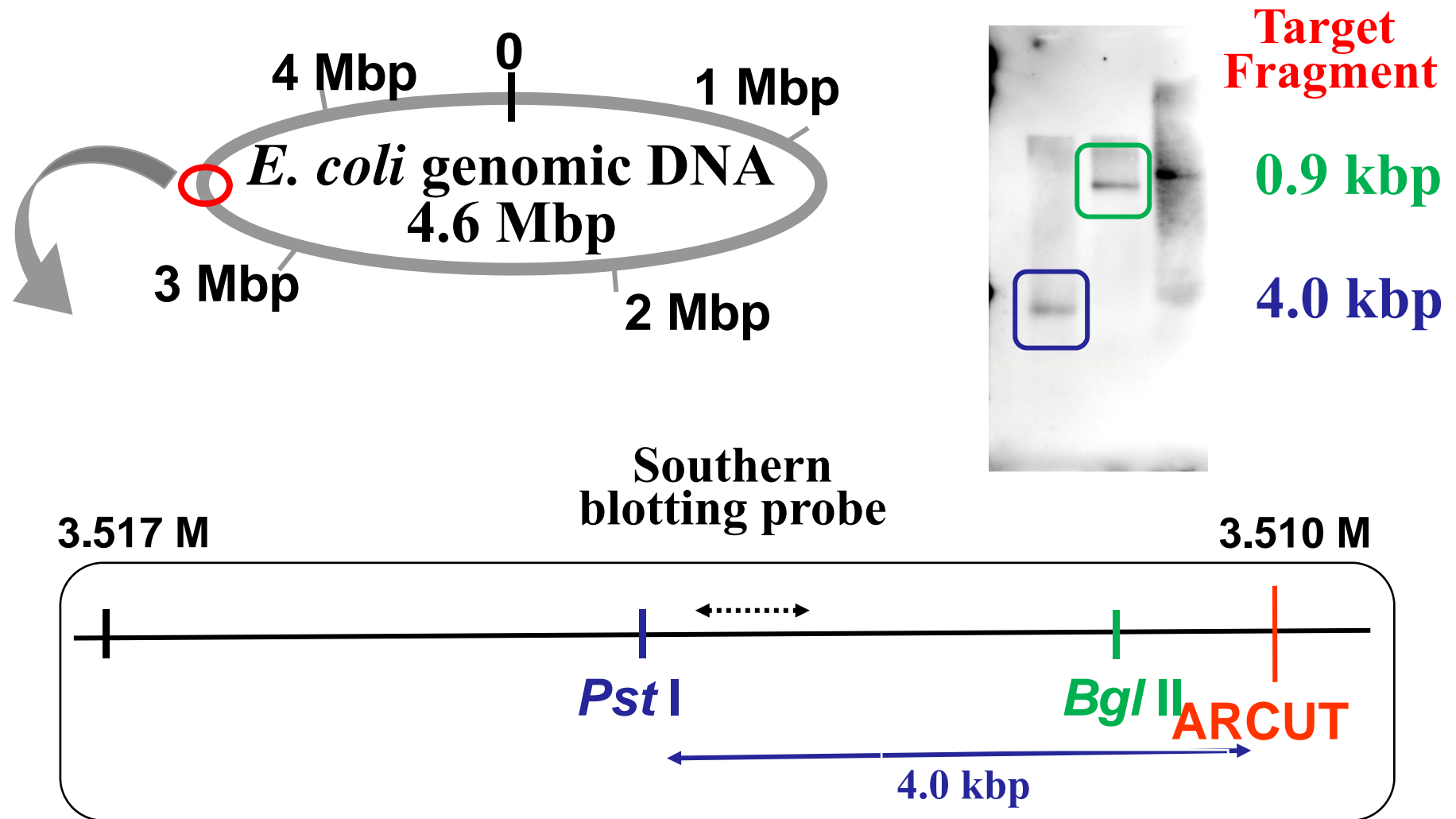
3' - ...TTTCTAATAAGCAGTCTCTTAAGACC **GCTTAGGAGA** CTGGT... - 5'



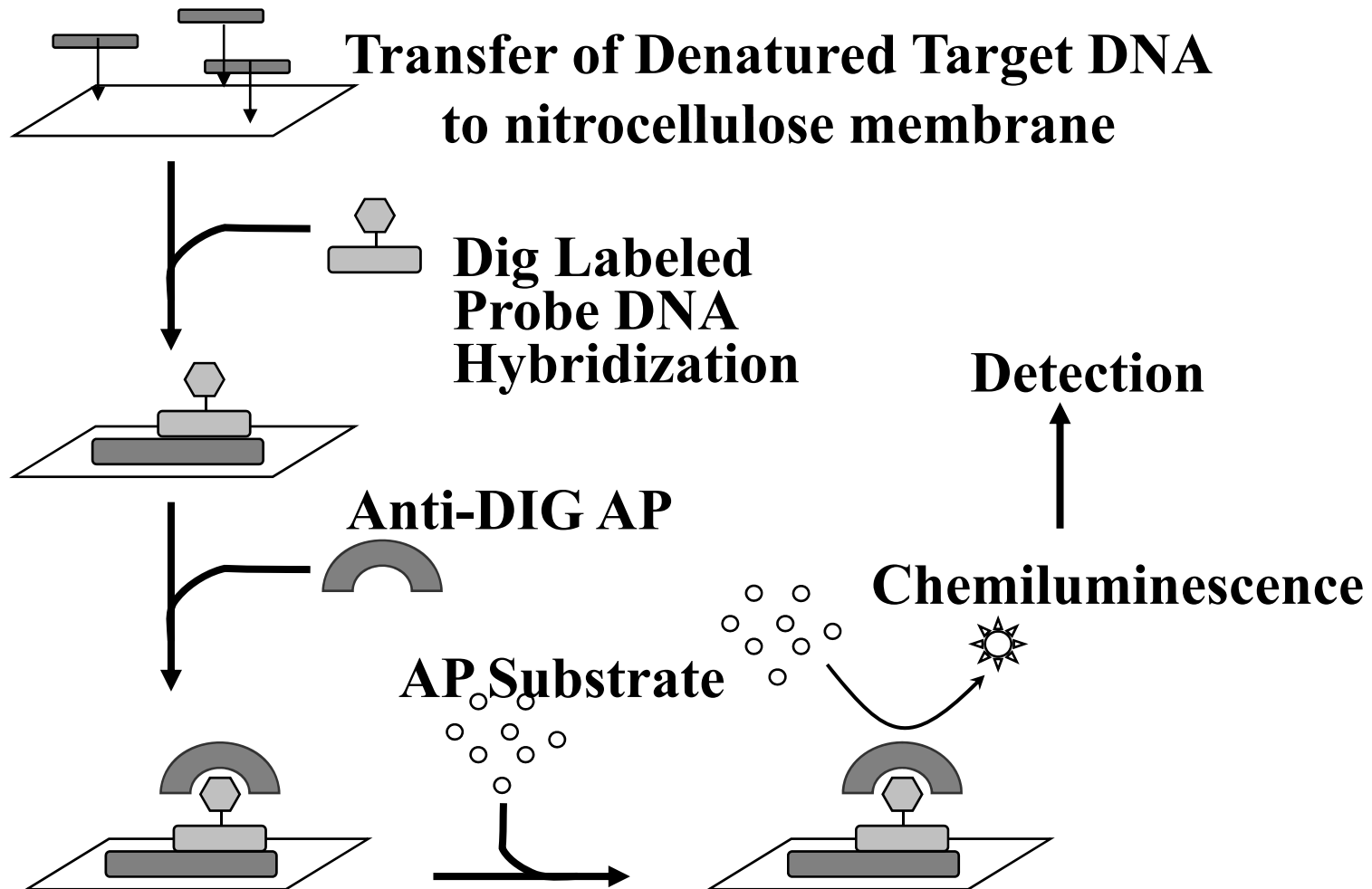
(2) Site-selective Scission of Genome DNA of *E. coli* (4.6 Mbp)

**If this huge DNA is treated with
conventional restriction enzyme**

number of scission sites
 $= 4,600,000/4^6 = 1100$

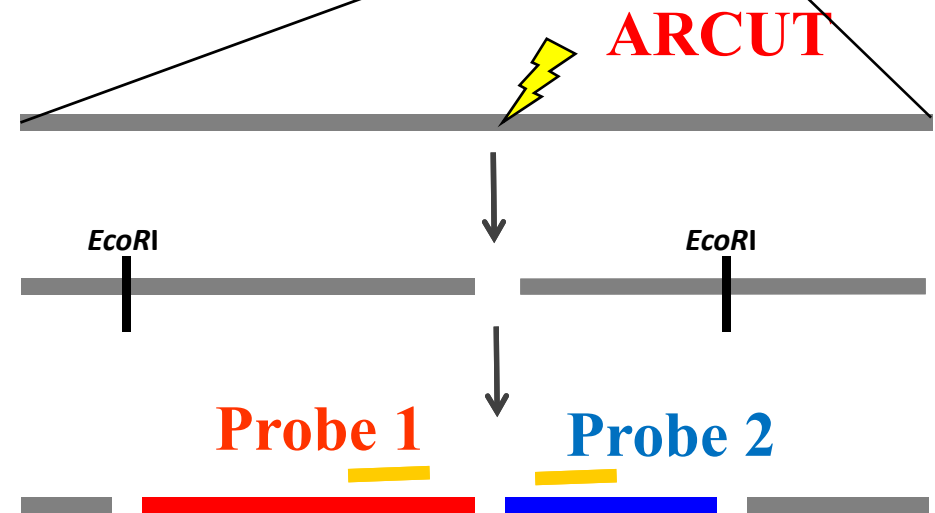
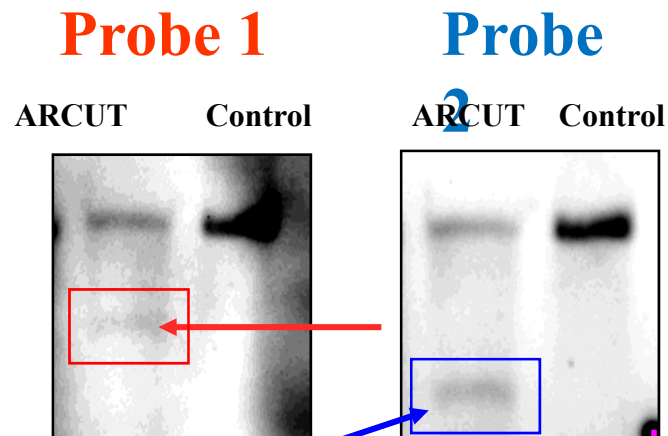
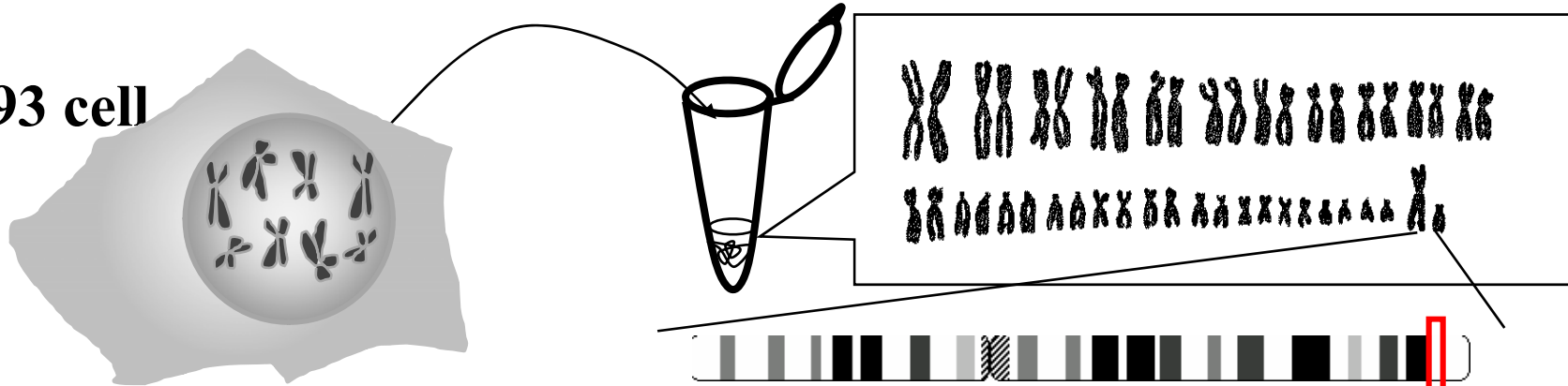


Southern Blotting



(3) Site-selective scission of human genome (3×10^9 bp) at one target site

293 cell



Southern Blotting

Mismatch-recognition by ARCUT in site-selective scission of human genome

Target site (in FMR1 in X chromosome)

5'-**AAT**GGGCGCTTTCTACAAG**GT**-3'
3'-**TTA**CCCGCGGAAAGATGTTCA**CA**-5'

is efficiently hydrolyzed

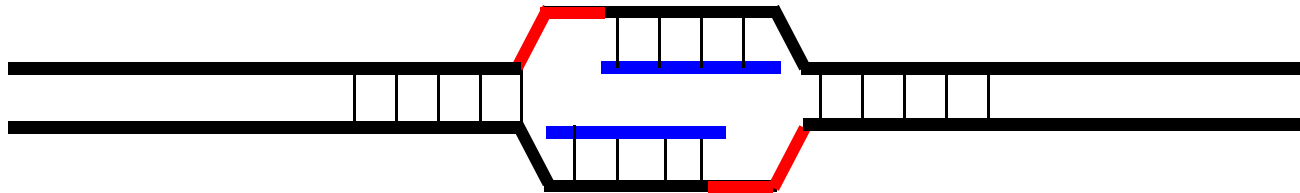
A homologous site (in chromosome 7)

5'-**CAG**GGGCGCTTTCTACAAG**AT**-3'
3'-**GTC**CCCGCGGAAAGATGTTCTA**TA**-5'

is never hydrolyzed

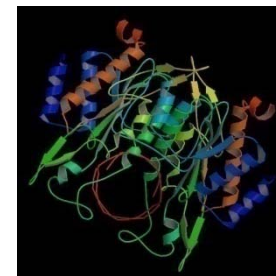
Advantages of **ARCUT**

2. Choice of scission site is free.

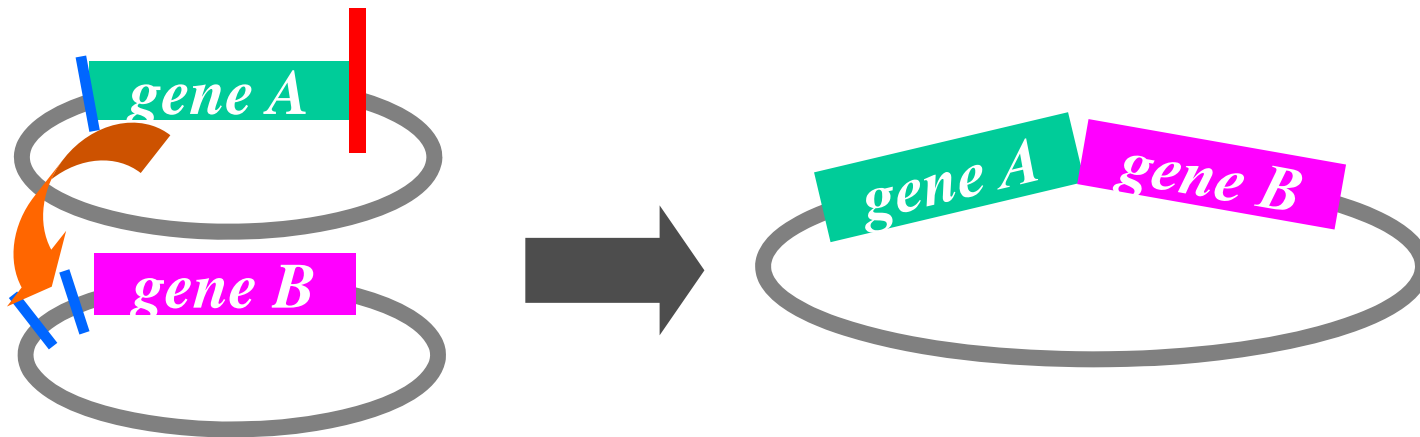


Sequence of PNA: Free!

Cf. *EcoRI* -GAATTC-



Formation of Fusion Protein by **ARCUT**



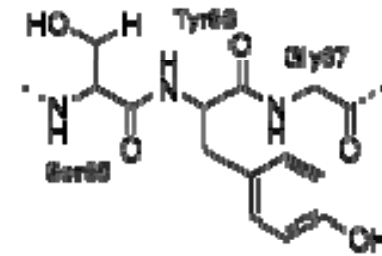
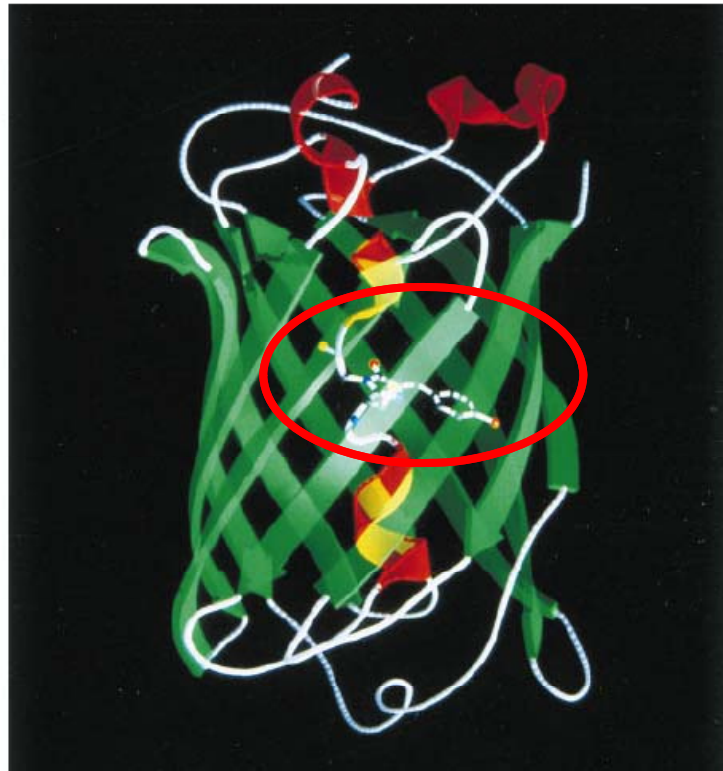
Key points:

(1) How to cut the DNA just before the **stop codon** for **gene A**?

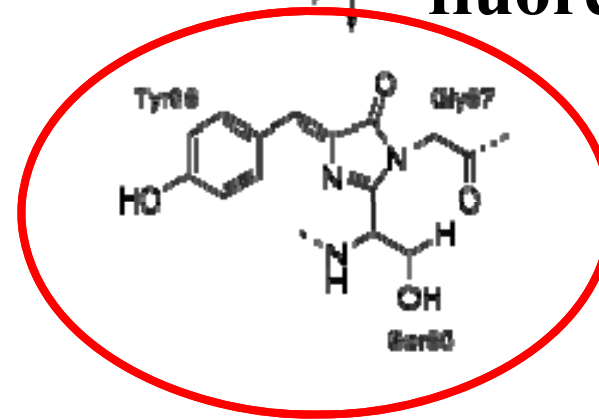
(Mostly, no restriction enzyme is directly available)

(2) The reading frame must be precisely adjusted.

GFP (Green Fluorescent Protein)

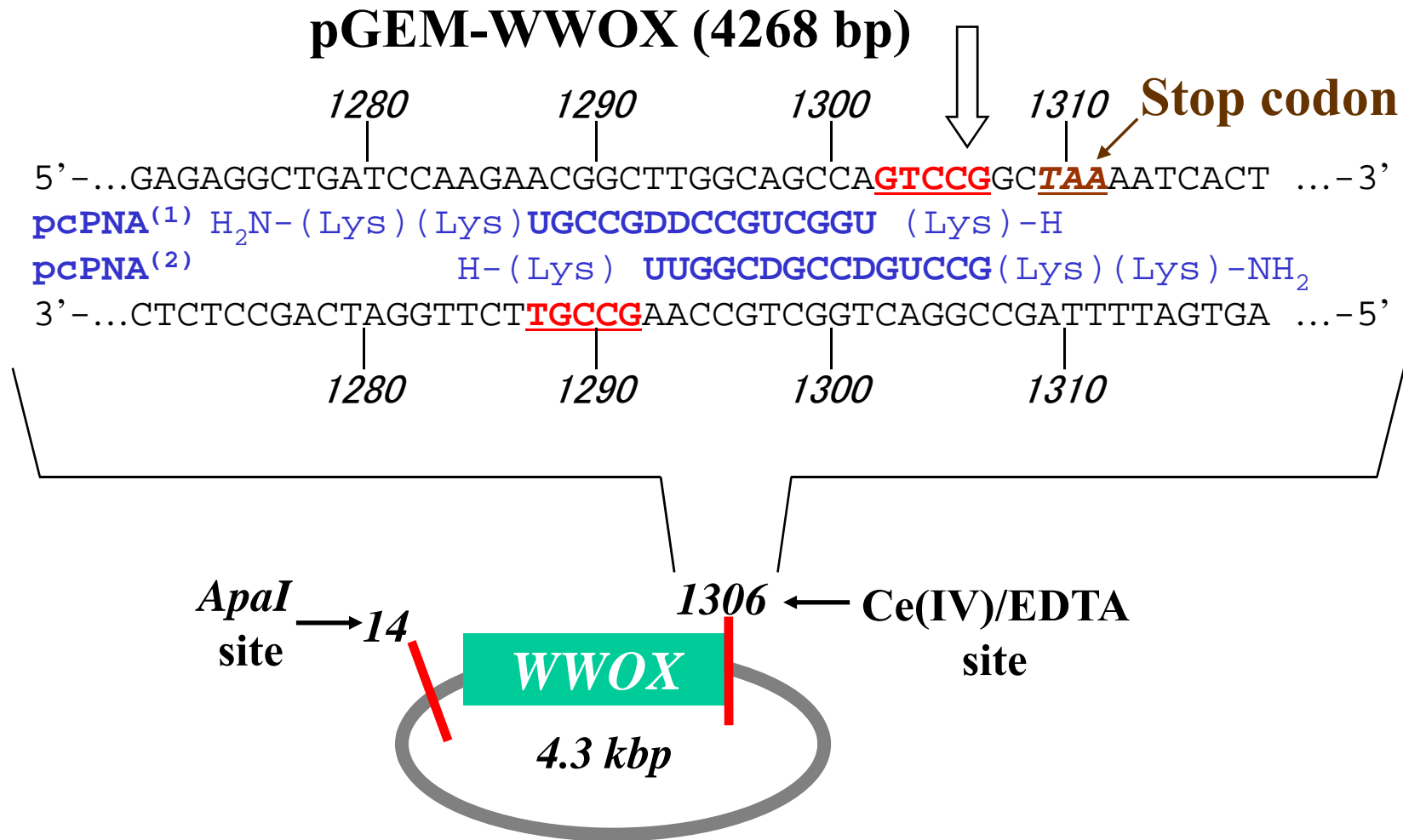


**Formation of
fluorescent center**



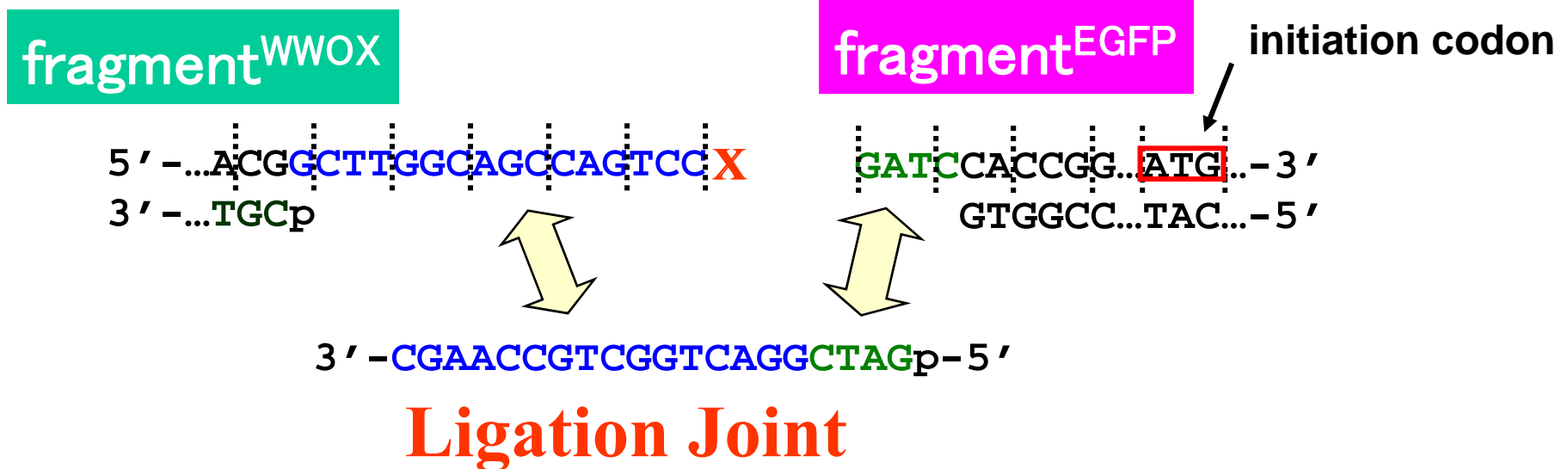
Proc. Natl. Acad. Sci. USA, 94, 2306-2311 (1997)

Selective Scission Just Before the Stop Codon



WWOX = WW domain-containing oxidoreductase

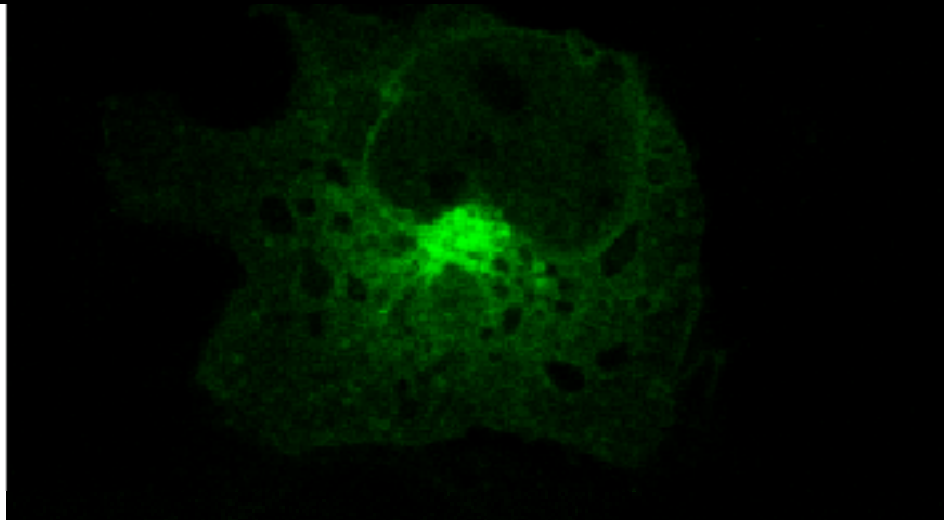
Selection of Desired Scission Fragment by Using Appropriate **Ligation Joint**



f is picked up from the reaction mixture
and selectively ligated with **f**

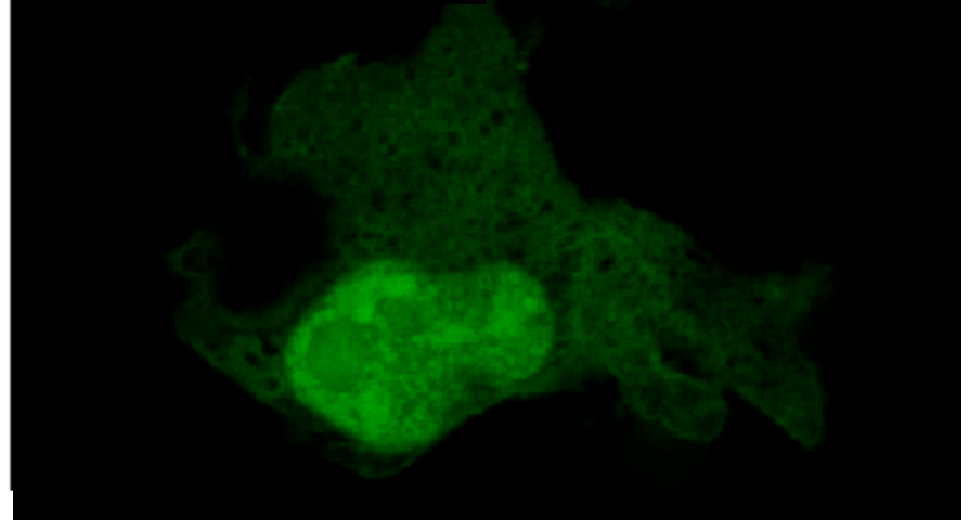
Fluorescence From Fusion Protein

(A) WWOX-EGFP



Localized in golgi

(B) EGFP

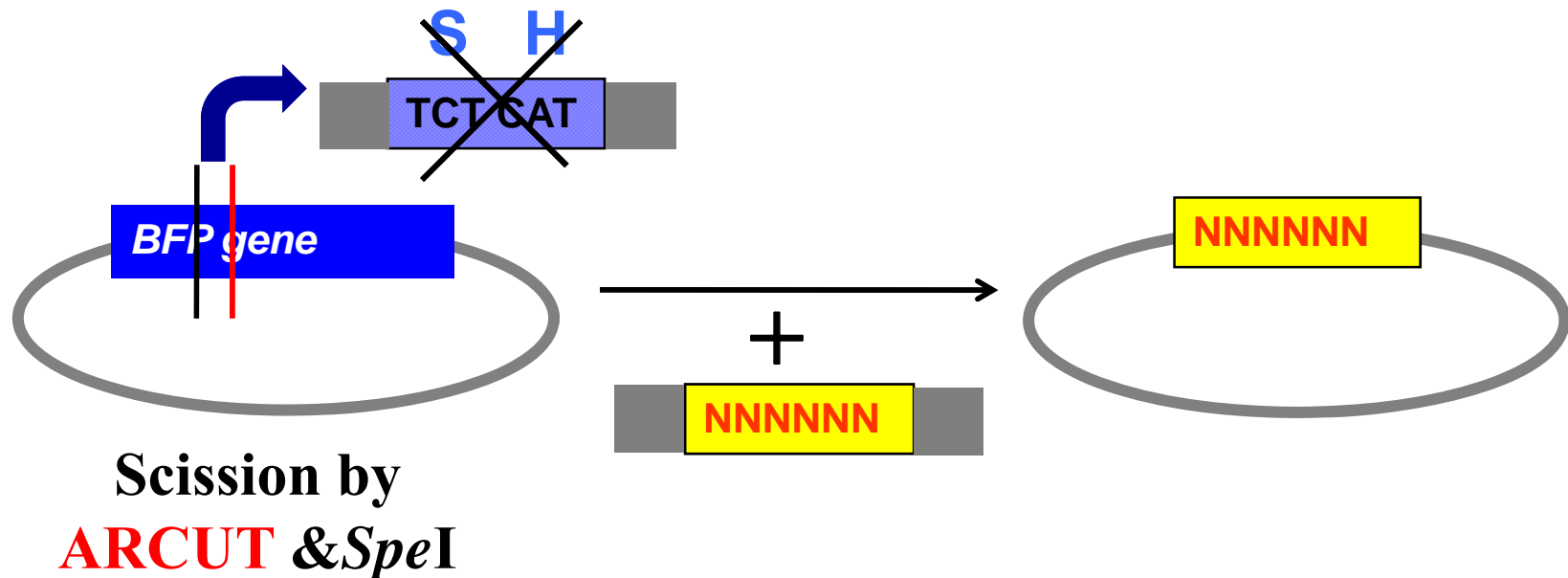


Localized in nuclei

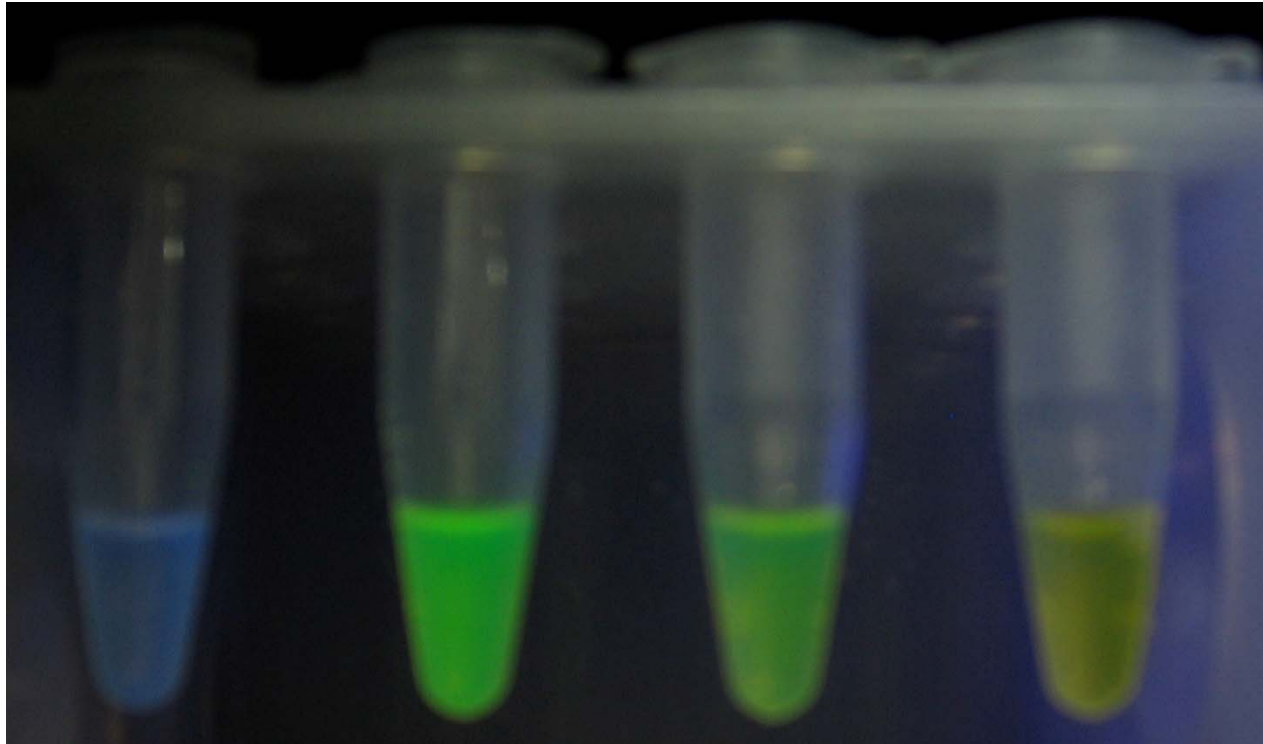
**DNA is completely kept intact
throughout the manipulation**

Engineering of Fluorescent Protein Using **ARCUT**

Randomization at 65-66 of **BFP**
through site-selective scission by **ARCUT**



Recombinant Proteins Obtained



Ser⁶⁵-His⁶⁶
(BFP)

Cys-Tyr
(EGFP)

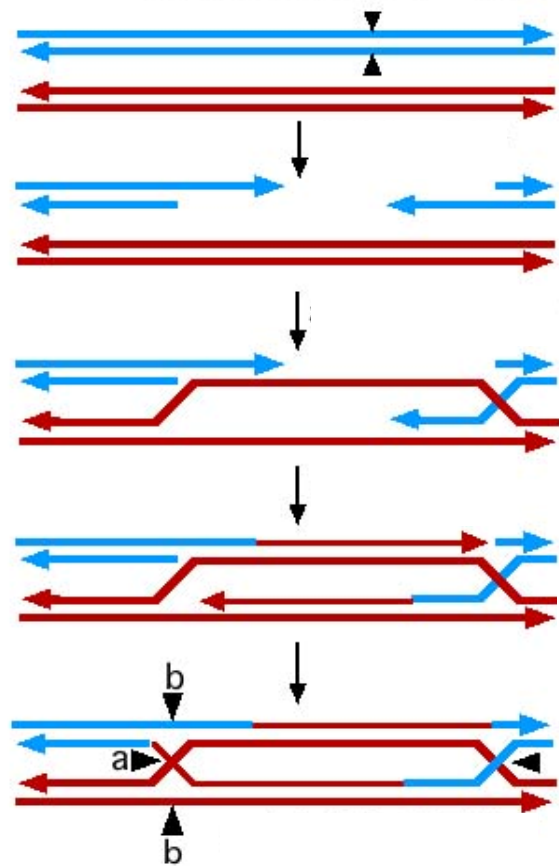
Glu-Tyr

Gly-Tyr

ARCUT is useful to manipulate
even small DNA like plasmid

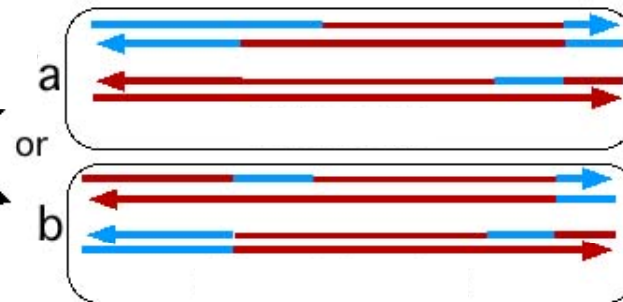
Application to Homologous Recombination for Genetic Manipulation in Human Cells

Double-strand break for promotion of HR

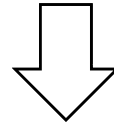


Szostak, J. W., *et al.* (1983) *Cell* 33, 25-35

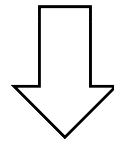
- Gene manipulation
- Gene disruption
- Gene therapy
- Research tool
-



Frequency of homologous recombination is too low to use as tools for gene manipulation

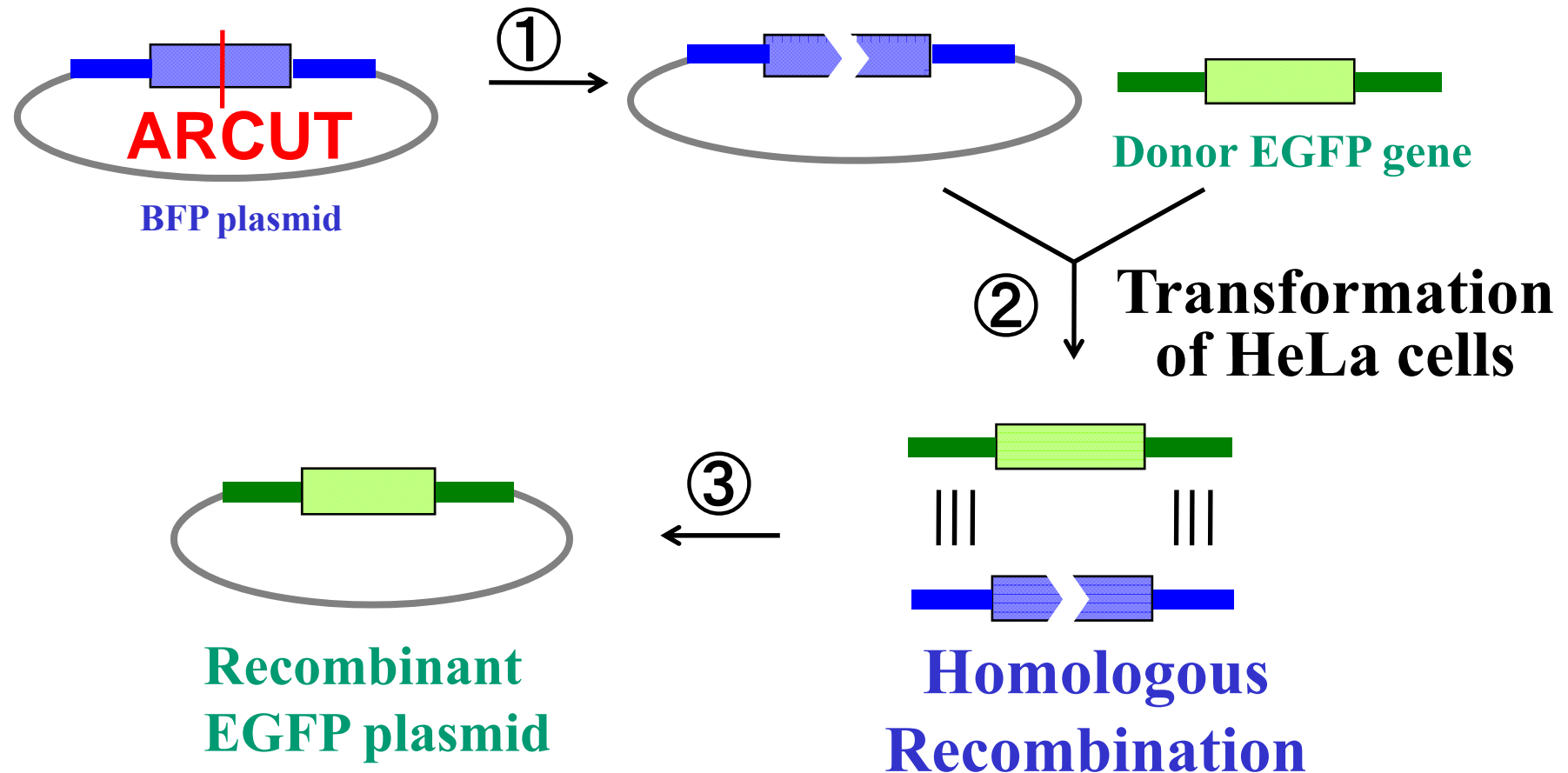


It is greatly promoted when DNA is damaged at the target site (repair system is activated)



Is **ARCUT useful for this purpose?**

Double-strand break by **ARCUT** promotes homologous recombination in human cells!



ARCUT used for BFP → EGFP conversion

BFP ...TCGTGACTACTCTT**AGT**CATGGTGTACAGTGCTT...

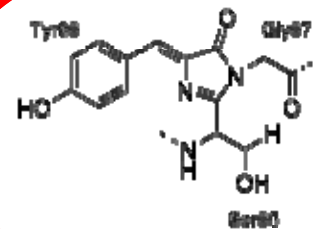
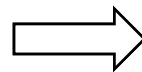
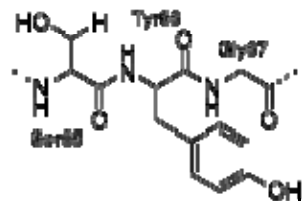
EGFP ...TCGTGACCACCCTGACCTACGGCGTGCAGTGCTT...

5' - ...TGGCCCACCCTCGTGACTACTCTT**AGT**CATGGTGTACAGT...-3'

pcPNA¹ H₂N- (Lys)₂ UGDUGDGDUCDUD (Lys) P-H

pcPNA² H-P (Lys) UCGUGDCUDCUCUUD (Lys)₂ -NH₂

3' - ...ACCGGGTGGGAGCACTGATGAGAATCAGTACCACATGTCA...-5'



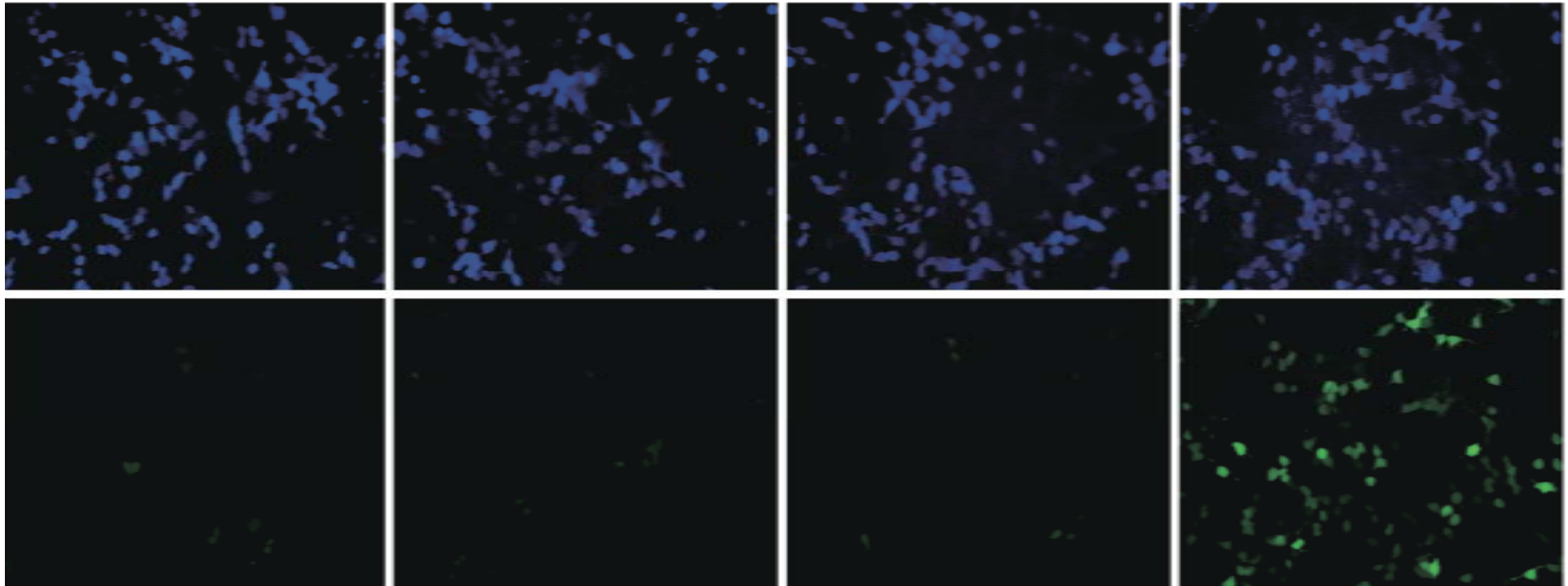
Promotion of homologous recombination in human cells by **ARCUT**

No cut

StuI

PNA only

ARCUT



Upper: BFP

Lower: GFP (product of recombination)

**Substrate gene
(BFP)**

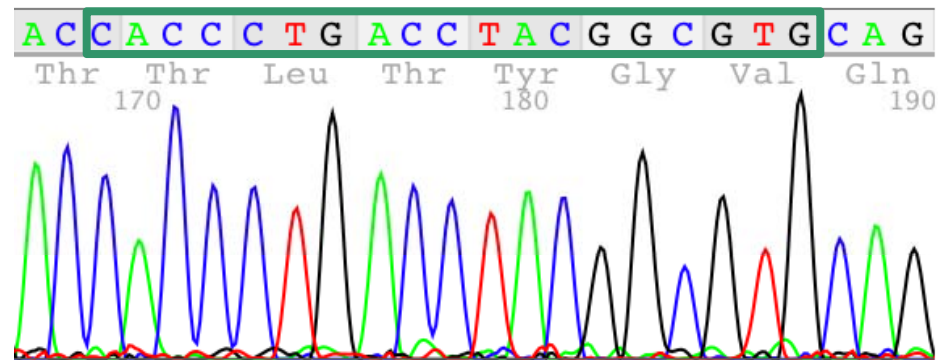
...TCGTGAC**TACTCTAGTCA**TGG**TGTAC**AGTGCTTCA...

Homologous
recombination

**Recombinant
gene**

...TCGTGAC**CACCCTGACCTACGGCGTGCAGTG**CTTCA...

(from EGFP)

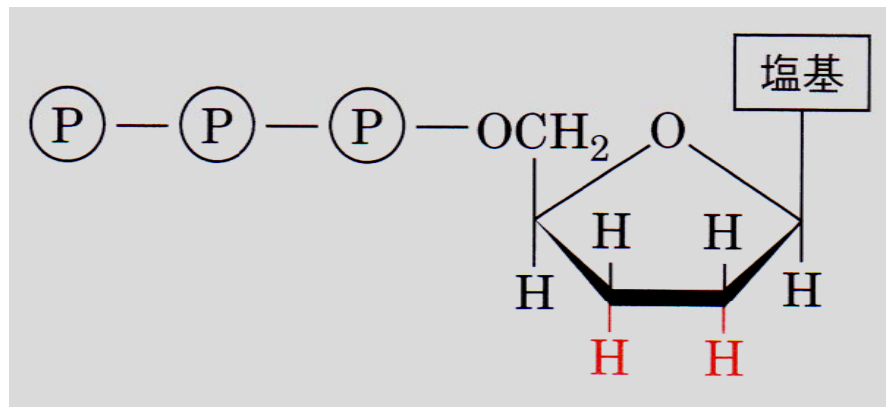


**Homologous recombination at desired site
is indicated.**

Determination of DNA Sequence (dideoxy chain termination method)

In DNA polymerase reaction using the sample DNA as template, a small amount of **dideoxy-compound** is added

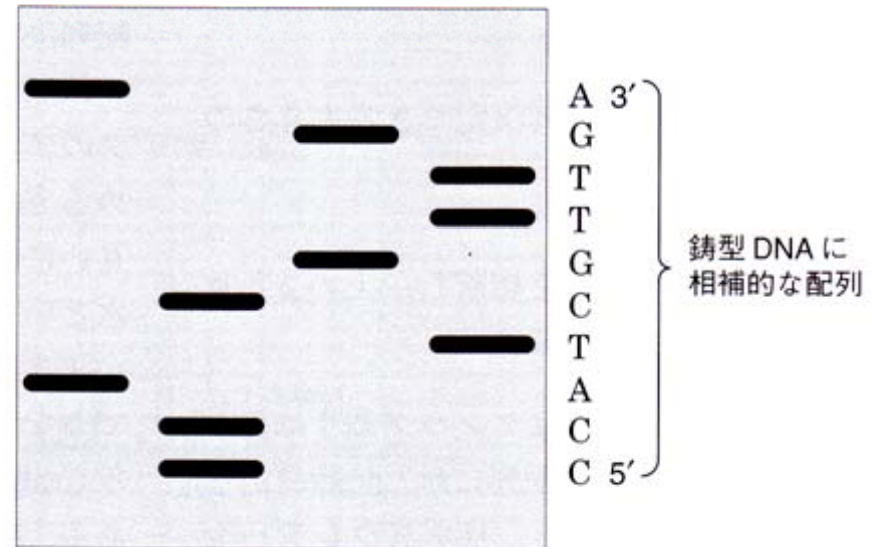
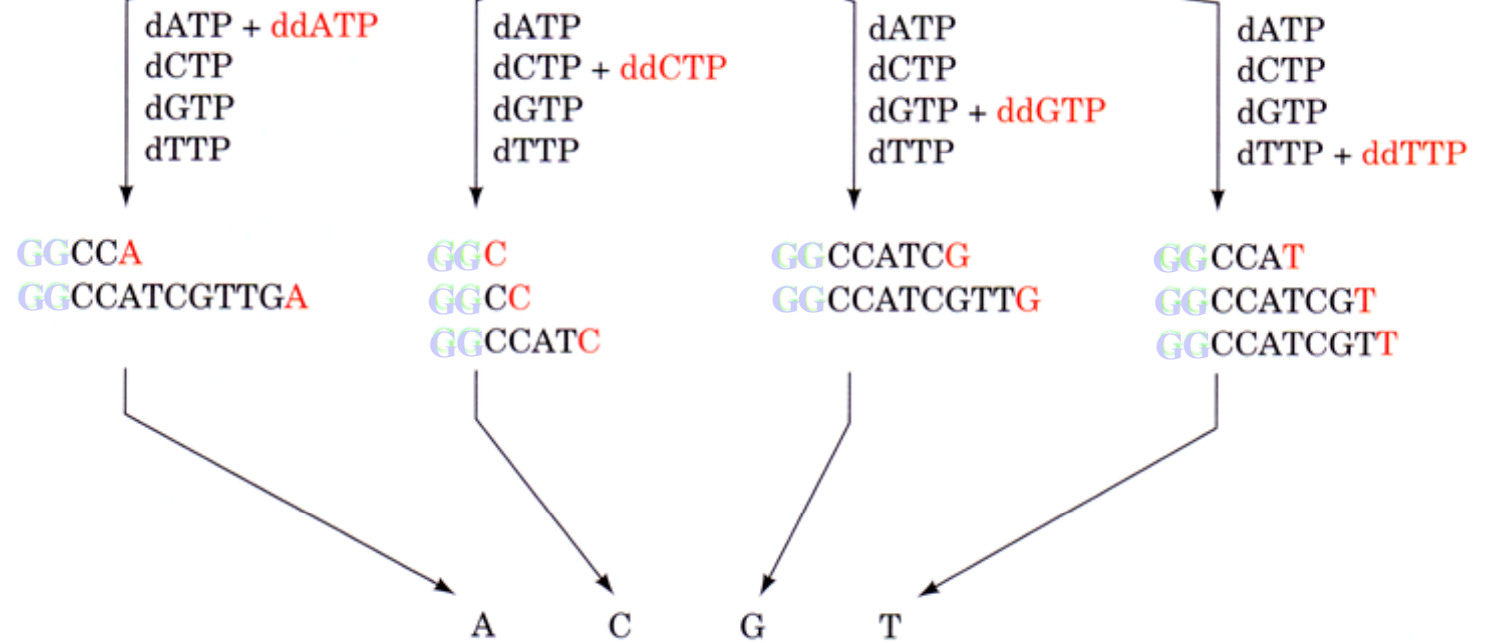
- the polymerization stops there because of the lack of 3'-OH
- formation of shorter fragment depending on the sequence
- sequence is determined from the lengths of the fragments



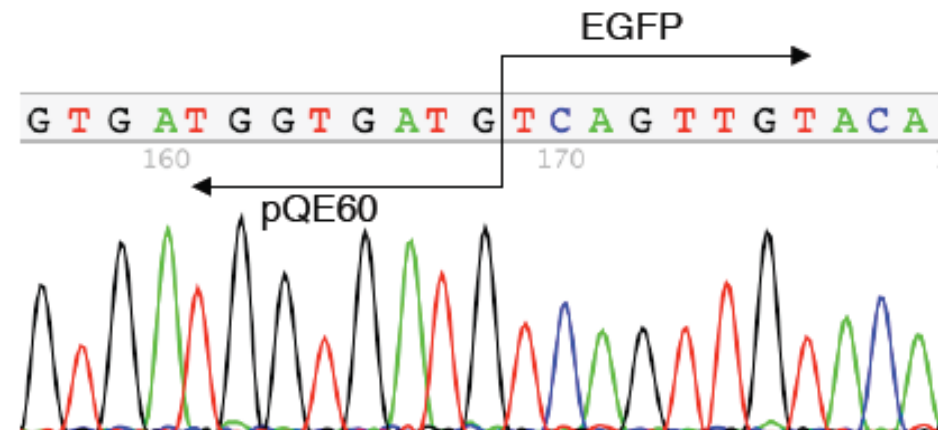
2',3'-dideoxynucleotide triphosphate

template
primer

3' — CCGGTAGCAACT — 5'
5' — GG — 3'



DNA Sequencer

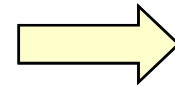


Naturally occurring restriction enzyme vs. **ARCUT**

Enzyme

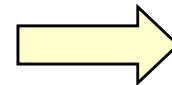
ARCUT

(1) DNA recognition
Protein



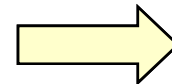
PNA

(2) Catalyst
Mg(II)



Ce(IV) complex

(3) Scission site & specificity
Limited



Freely designable

Conclusion

- 1. New tools for site-selective hydrolysis of (huge) double-stranded DNA at any site have been developed.**
- 2. The resultant fragments are enzymatically ligated with various foreign DNAs, and recombinant DNA is expressed in cells.**
- 3. These tools should pave the way to new molecular biology and biotechnology.**