

# Sequenze

# The Nobel Prize in Chemistry 1980



Paul Berg

Prize share: 1/2



Walter Gilbert

Prize share: 1/4



Frederick Sanger

Prize share: 1/4

The Nobel Prize in Chemistry 1980 was divided, one half awarded to Paul Berg *"for his fundamental studies of the biochemistry of nucleic acids, with particular regard to recombinant-DNA"*, the other half jointly to Walter Gilbert and Frederick Sanger *"for their contributions concerning the determination of base sequences in nucleic acids"*.

Per **sequenziare** il DNA, si utilizzano 2 metodi:

### Metodo chimico o di Maxam-Gilbert

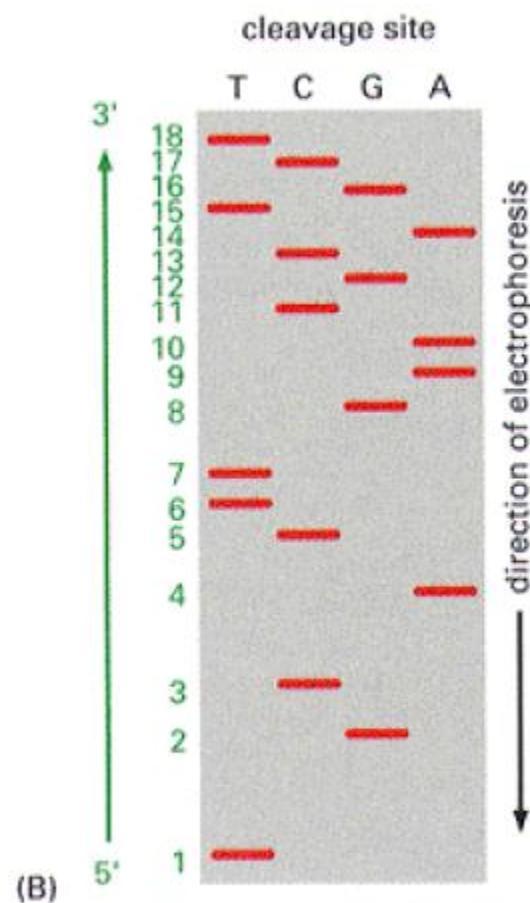
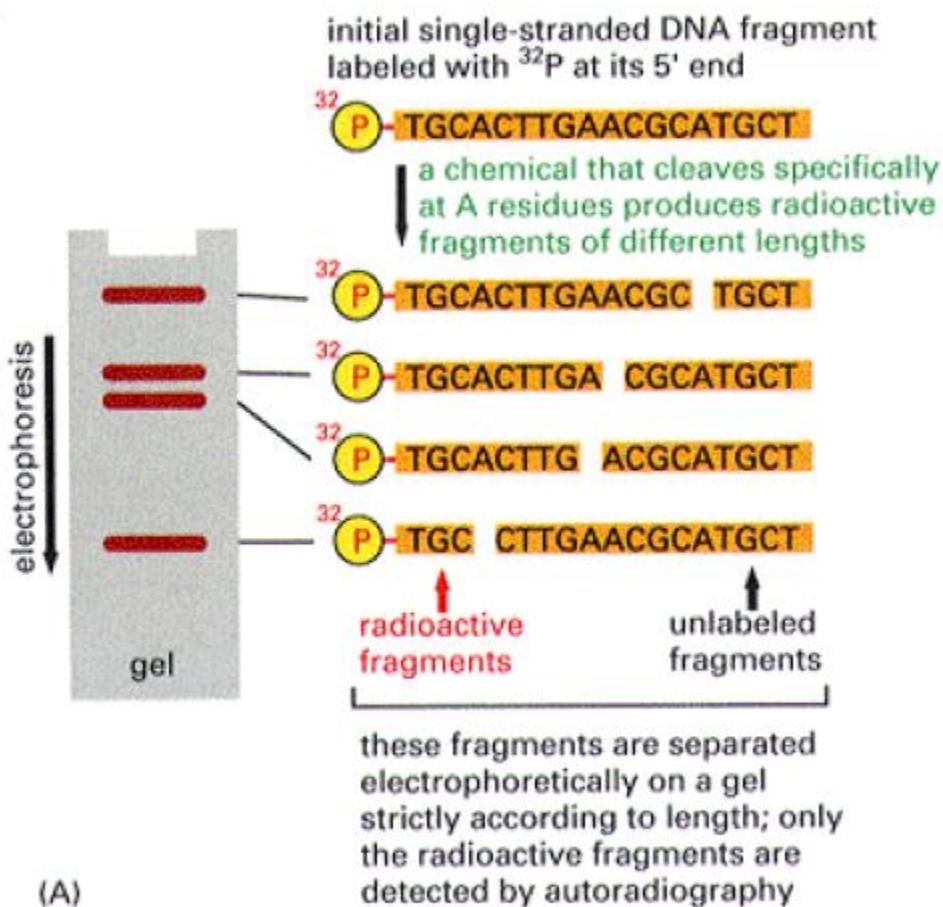
In questo caso, una molecola di DNA viene marcata con  $^{32}\text{P}$  ad una estremità. Sulla molecola marcata, si eseguono poi **quattro reazioni separate**, che portano alla rottura del DNA in corrispondenza di una base specifica. Le reazioni vengono condotte **in difetto del reagente**, in modo che ogni molecola di DNA venga tagliata in media una volta sola. I frammenti prodotti dalle 4 reazioni vengono poi separati con elettroforesi ad alta risoluzione su gel di poliacrilamide, capace di separare (risolvere) due molecole di DNA che differiscono per lunghezza anche di un solo nucleotide.

### Metodo enzimatico di Sanger

Questo metodo si basa sulla sintesi di nuove molecole di DNA, sullo stampo da sequenziare, troncate a livello di basi specifiche, e fa uso di speciali nucleotidi, preparati chimicamente, che mancano dell'ossidrile in posizione 3': i *2',3' dideoxinucleotidi trifosfati*.

# Maxam-Gilbert DNA chemical sequencing

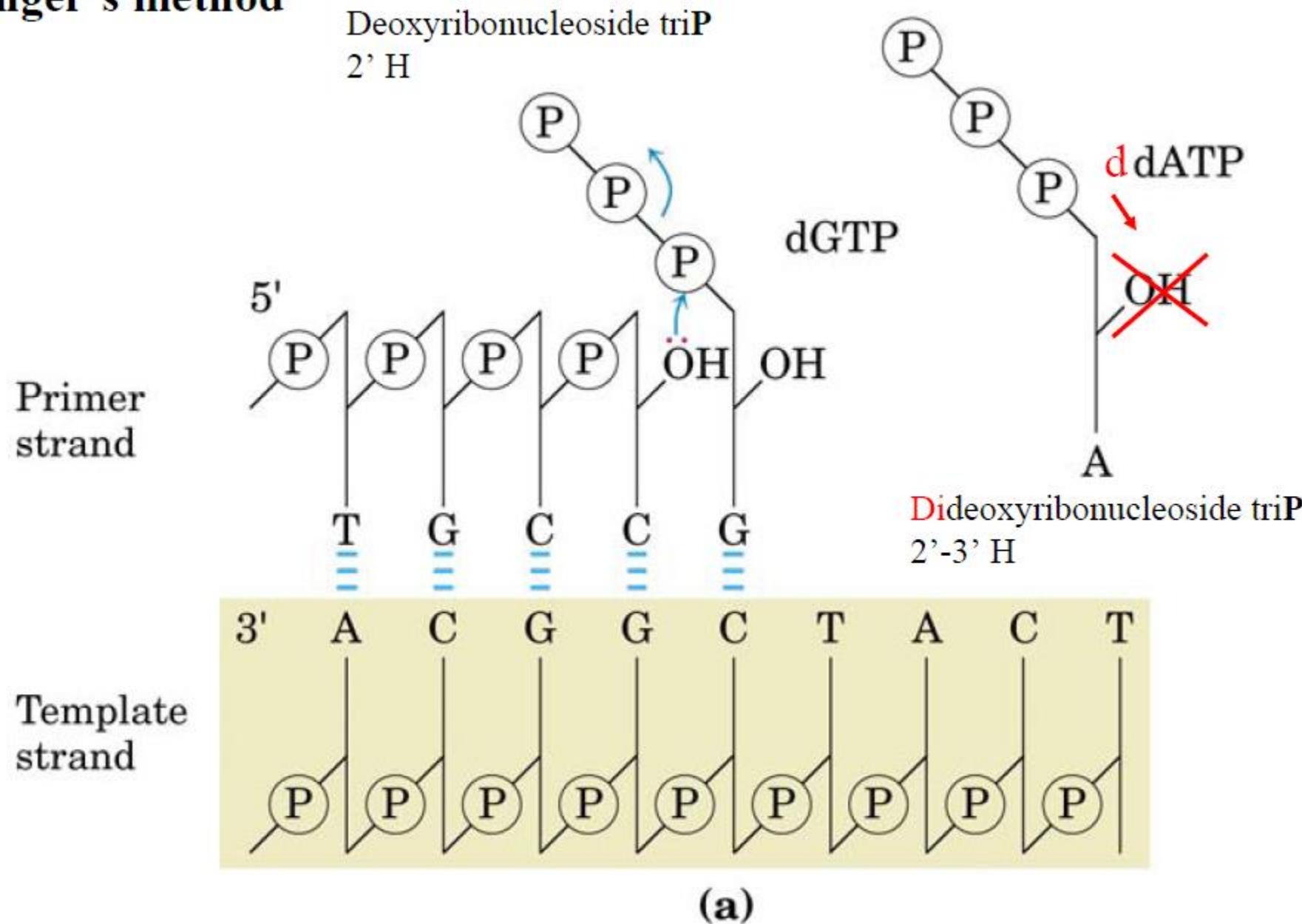
## Example for A



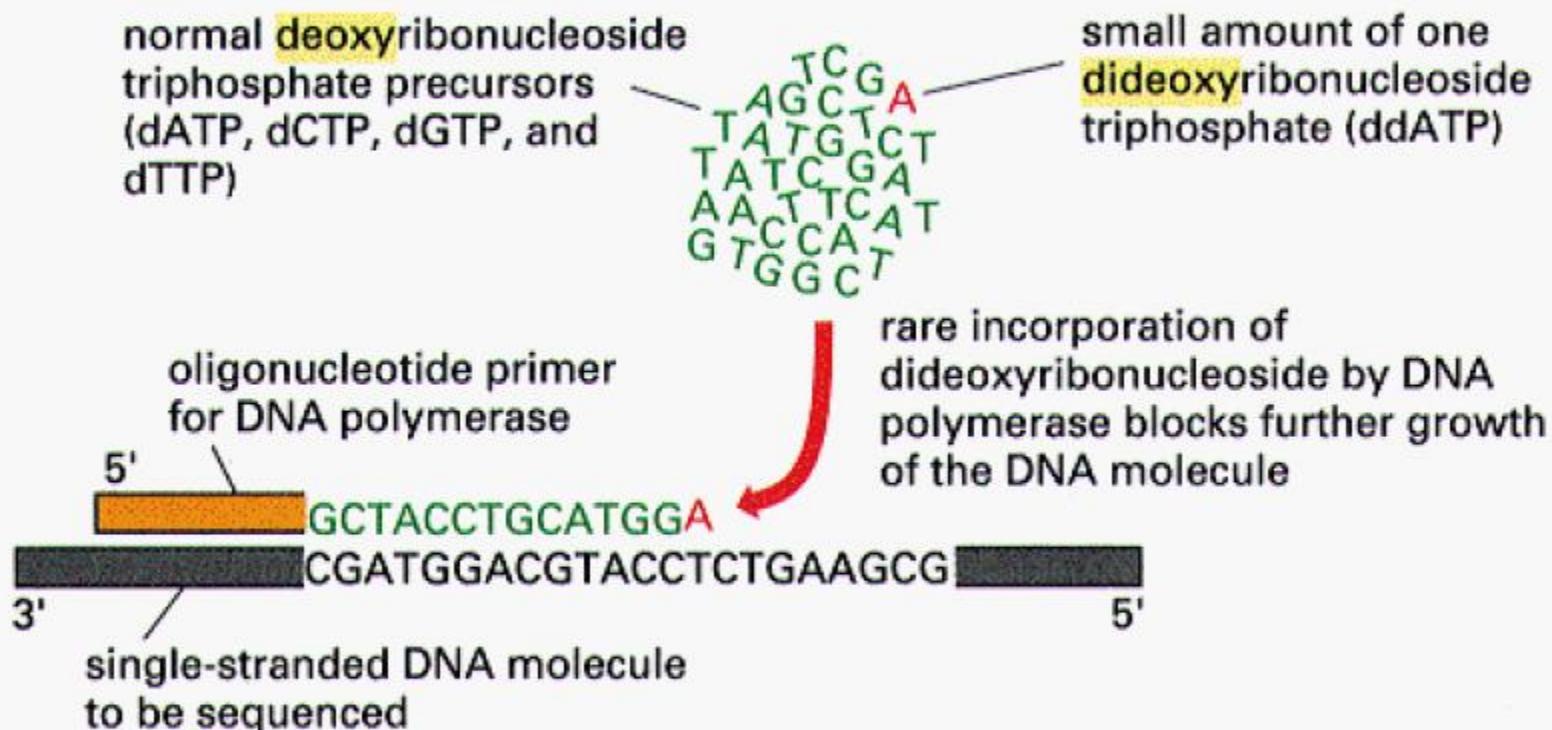
DNA sequence, reading directly from the bottom of the gel upward, is

TGCAC TTGAAC GCGATGCT  
1 18

## Sanger's method



(A)



(B)

5' GCATATGTCAGTCCAG 3'  
 3' CGTATAACAGTCAGGGTC 5'

double-stranded DNA

3' CGTATAACAGTCAGGGTC 5'

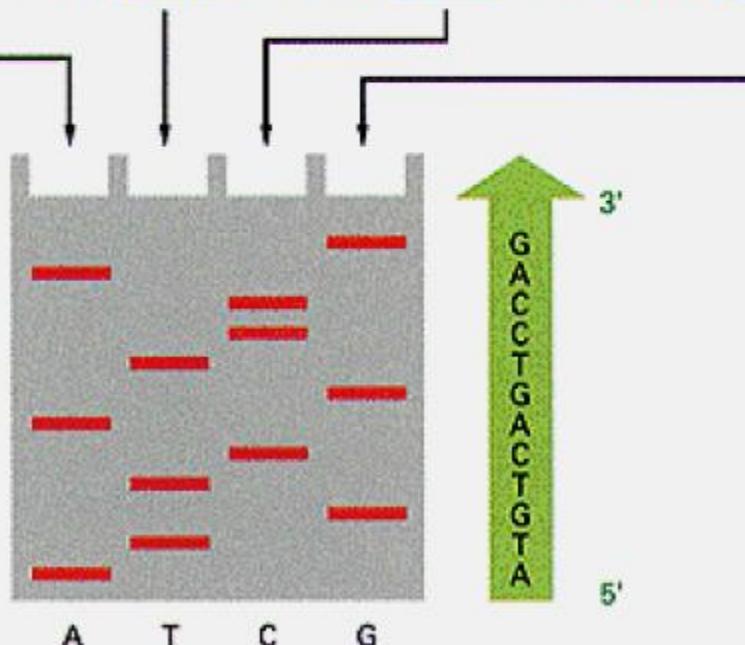
single-stranded DNA



5' GCAT 3'  
 labeled primer

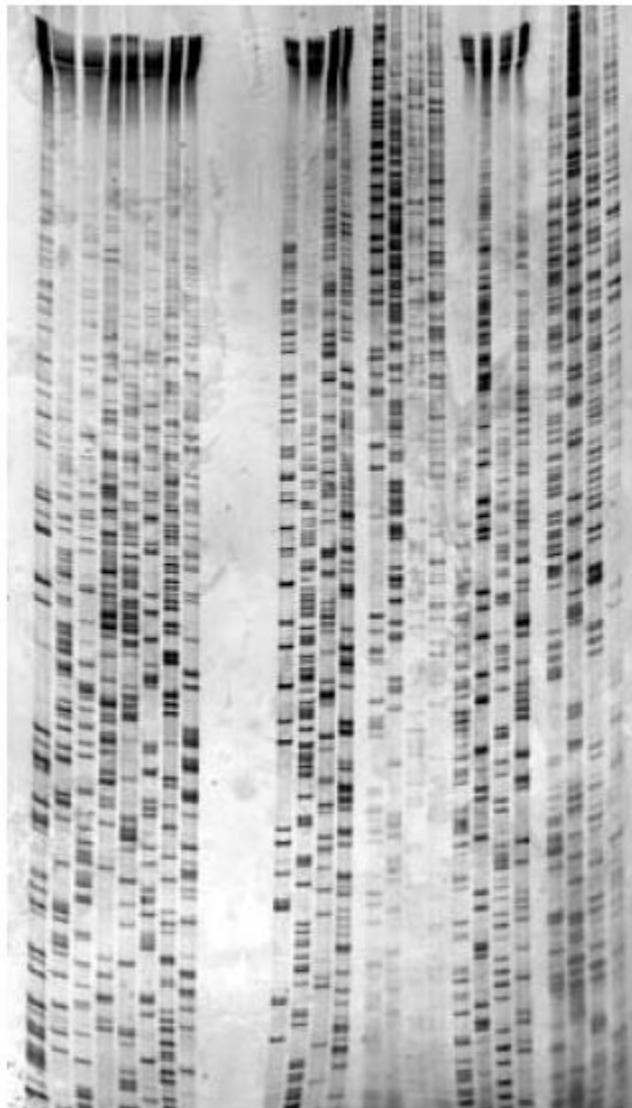
+ DNA polymerase  
 + excess dATP  
 dTTP  
 dCTP  
 dGTP

+ ddATP	+ ddTTP	+ ddCTP	+ ddGTP
GCAT A	GCAT AT	GCAT ATGT C	GCAT ATG G
GCAT ATGTCA	GCAT ATGT	GCAT ATGTCAGTC	GCAT ATGTCAG G
GCAT ATGTCAGTCCA A	GCAT ATGTCAGT T	GCAT ATGTCAGTCC C	GCAT ATGTCAGTCCA G



The label is usually  $^{32}\text{P}$ ,  
 so that detection  
 requires  
 autoradiography

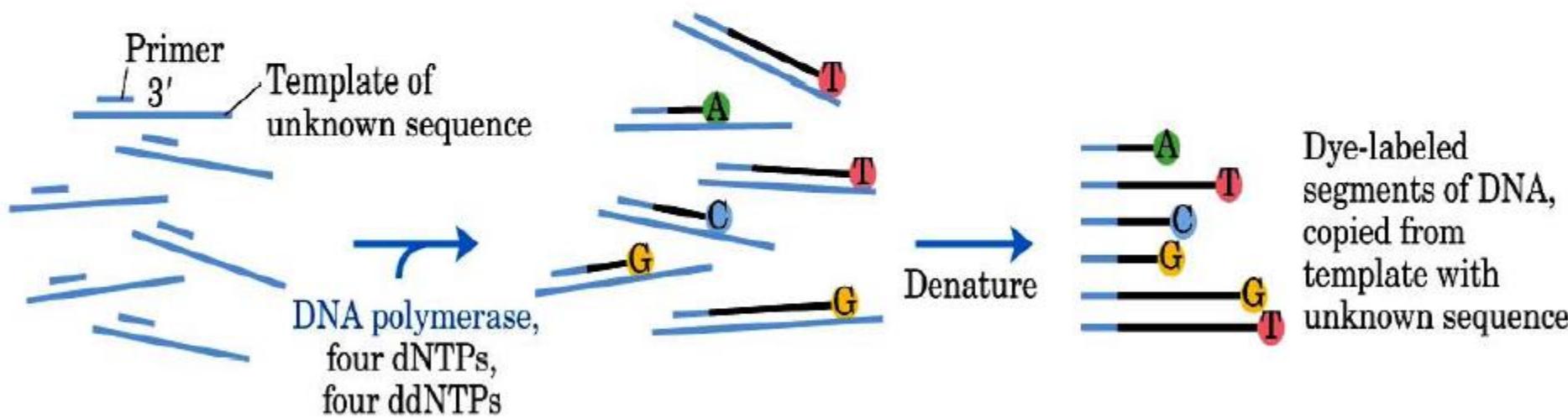
# SEQUENZIAMENTO DEL DNA

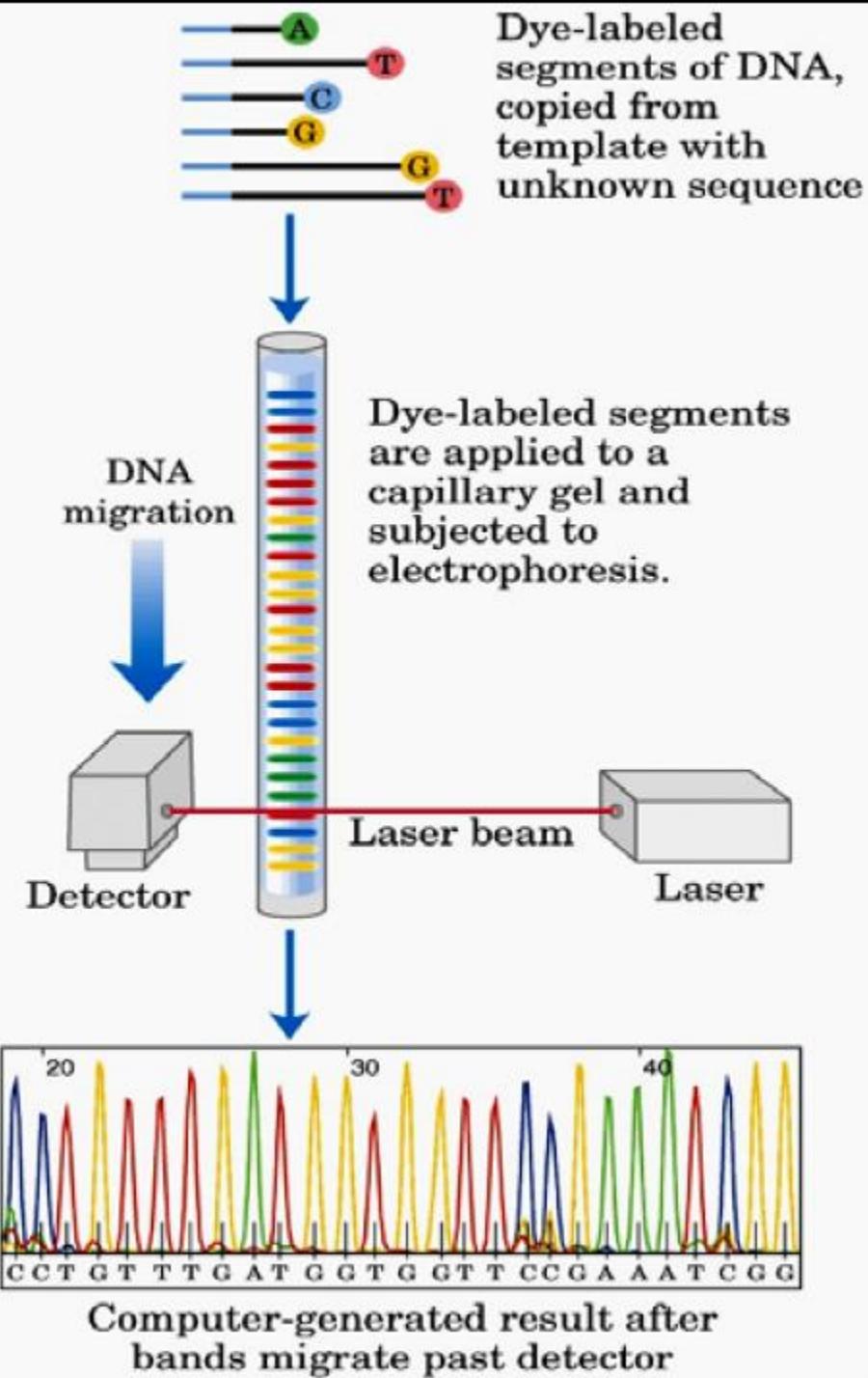


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121 gtctttatc caggggctgg tctcgaggcc cttggaggag gagcgcgtgg gcctggagggc  
181 aaacctctta agccaggatcc cggaggggctt gcccgggtctg gccttggggc agggctcgcc  
241 gcctcccccg cagttaccc tccgggggctt ctggtgccctg gtggagtggc tgacgctgt  
301 gcagccata aagctgctaa ggctggcgct gggcttgggtg gtgtcccaagg agttgggtggc  
361 ttaggagtgt ctgcaggatgc ggtggttcct cagcctggag ccggagtgaa gcctggggaaa  
421 gtgcgggtg tggggctgccc aggtgtatcc ccaggtggcg tgctccagg agctcggttc  
481 cccggtgtgg ggggtctccc tggagttccc actggagcag gagttaaagcc caaggctcca  
541 ggttaggtg gagctttgc tggaaatccca ggagttggac ccttgggg accgcaaccc  
601 ggaggcccac tggggtatcc catcaaggcc cccaagctgc ctggtggtca tggactgccc  
661 tacaccacag gaaaaactgcc ctatggctat gggcccgag gagttggctgg tgcagcgggc  
721 aaggctgggtt acccaacacagg gacaggggtt ggcccccaagg cagcagcagc agcggcagct  
781 aaagcagcag caaagttcg tggatggagca gccggagtcc tccctgggtt tggaggggt  
841 ggtttcctg gcgtgctgg ggcaattcct ggaattggag gcatcgagg cggtggact  
901 ccagctgcag ctgcagctgc agcagcagcc gctaaggcag ccaagtatgg agctgctgca  
961 ggcttagtgc ctgggtggcc aggcttggc ccggagtag ttgggttccc aggagctggc  
1021 gttccagggtg ttgggttccc aggagctggg attccagttg tccctgggtc tggatccca  
1081 ggtgtcgcc ttccagggtt tggatggacca gaagcagctg ctaaggcagc tgcaaaggca  
1141 gccaaatacg gggccaggcc cggagtcggc gttggaggca ttctactta cgggggttgg  
1201 gctgggggtt ttcccggtt tggatggcga gtcggaggta tccctggagt cgcagggtgc  
1261 cctagtgtcg gaggtgttcc cggagtcggc ggtgtcccg gatggcat tccccccgaa  
1321 gctcaggccag cagctggccgc caaggctgcc aagtacggag tggggacccc agcagctgca  
1381 gctgtaaaag cagccggccaa agccggccag tttgggttag tccctgggtt cggcgtggct  
1441 cctggagttg gcgtggctcc tggatggcgtt gtggctctg gagttggctt ggtctctgg  
1501 gttggcgtgg ctccctggagt tggatgggtt cctggcgttg gcgtggctcc cggcattggc  
1561 cctgggtggag ttgcagctgc agcaaaatcc gtcggccaaagg tggctgccaa agcccaagctc  
1621 cgagctgcag ctgggttgg tggatggcattc cctggacttg gagttgggtt cggcgtccct  
1681 ggacttggag ttggatggcgtt tggatggcgtt cttggagttt gtgtgggtt tccctggctt  
1741 gggccagggtg cagatggagg agttggccgg agcctgtccc ctgagctcag ggaaggagat  
1801 ccctccctt ctcagcaccc cccagccacc ccctcatcac ccagggtacc tggagccctg  
1861 gctggccgtt aaggccaa atatggagca gcaatgcgtt gggcccttgg agggctcgcc  
1921 gctctcggtg gagtaggcattt cccaggccgtt gtggatggag ccggacccgc cggccggccgt  
1981 gcccggccaa aagctgtgc cttggccccc cagttggcc tagtggagc ctgtgggtt  
2041 ggaggactcg gagtcggagg gctggagtt ccagggtttt gggcccttgg aggtataacct  
2101 ccagctgcag cccctaaaggc agctaaatcc ggtgtgtcc gcttggagg tggatgggtt  
2161 ggtggccggcc agttccact tggaggatgtt gcaatgcgtt ccggcccttggc attgtctccc  
2221 atttcccaag gtggggctt cctggggaaa gcttgggtt ggaagagaaaa atga

## SEQUENZIATORE AUTOMATICO

Una successiva evoluzione del metodo ha permesso l'automazione del sequenziamento del DNA. In questo caso, i nucleotidi dideoxisterminatori sono marcati mediante l'addizione di un gruppo chimico fluorogeno, diverso per ogni base.





## Tip\_1g\_27\_09\_04\_G10.ab1 - Chromas

File Edit Options Help

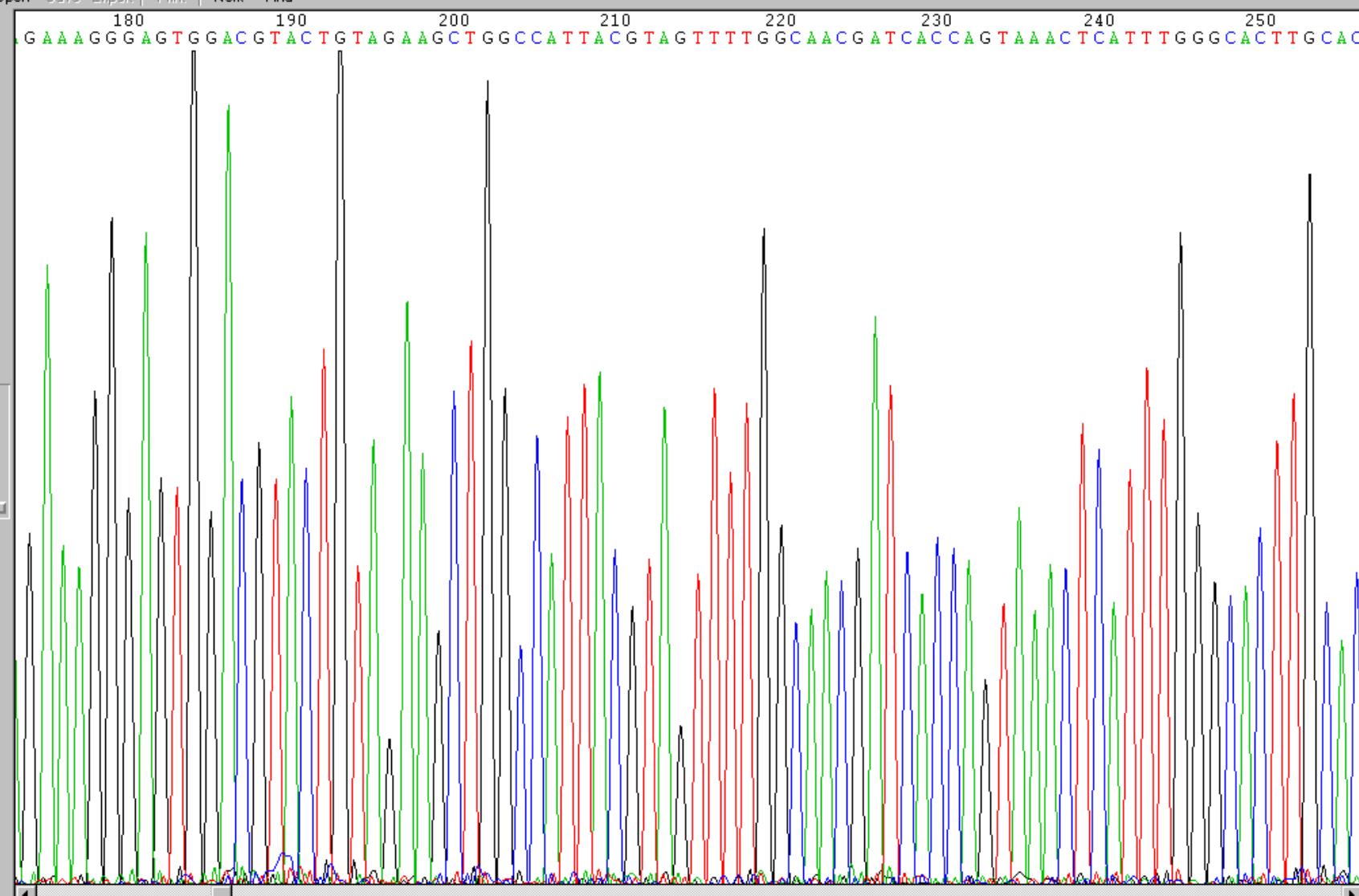
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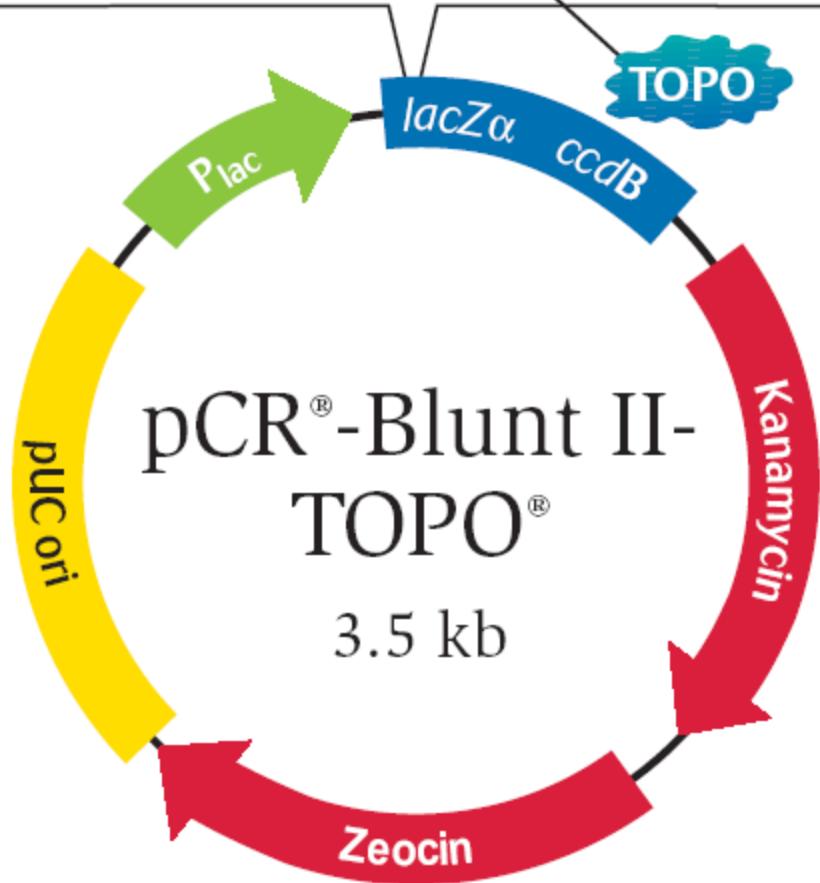
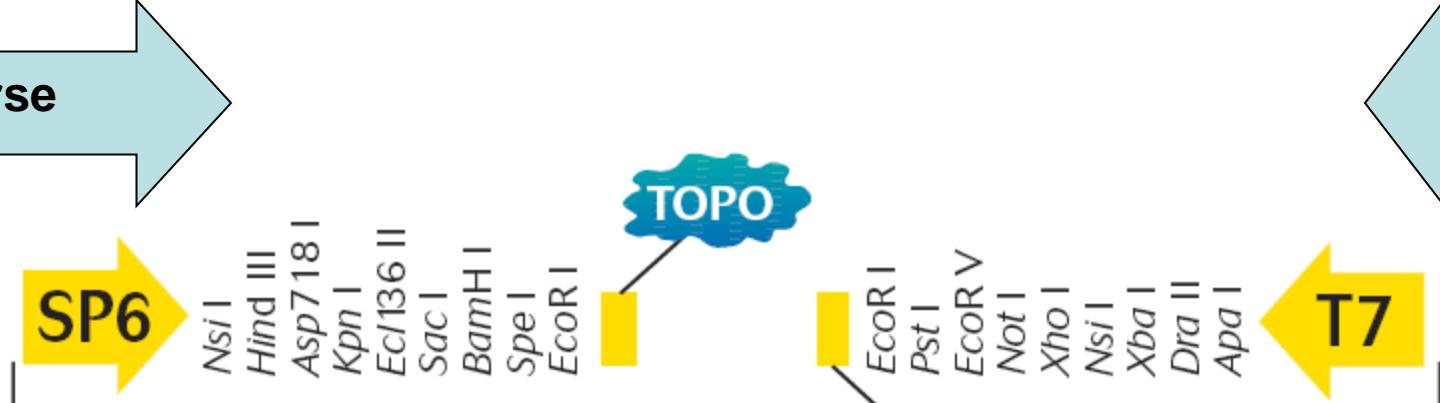
Next Find



Sample: Tip\_1g

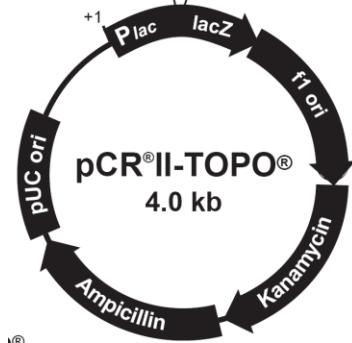






**reverse primer** → SP6 promoter/priming site ↓  
 201 CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTAT TTAGGTGACA CTATAGAATA  
 GTGTGTCCTT TGTCGATACT GGTACTAATG CGGTTCGATA AATCCACTGT GATATC TTAT  
*Nsi I Hind III Asp718 I Kpn I Ech136 II Sac I BamH I Spe I*  
 CTCAAGCTAT GCATCAAGCT TGGTACCGAG CTCGGATCCA CTAGTAACGG CCGCCAGTGT  
 GAGTTCGATA CGTAGTTCGA ACCATGGCTC GAGCCTAGGT GATCATTGCC GGCGGTACACA  
*EcoR I*  
 GCTGGAATTG GCCCTT | **Blunt PCR Product** | AAGGGCGAATTCT GCAGATA  
 CGACCTTAAG CGGGAA | *Pst I EcoRV*  
 TTCCATCACAC TGGCGGCCGC | *Not I Xba I Nsi I Xba I Dra II Apa I T7 promoter/priming site*  
 AGGTAGTGTG ACCGCCGGCG | TCGAGCATGC ATCTAGAGGG CCCAATTCGC CCTATAGTGA  
 TAGATCTCCC GGGTTAACCGG GGATATCACT  
 ← universal primer →  
 GTCGTATTAC AATTCACTGG CCGTCGTTT ACAACGTCGT GACTGGAAA ACCCTGGCGT 476  
 CAGCATAATG TTAAGTGACC GGCAGCAAAA TGTTGCAGCA CTGACCCATT TGGGACCGCA

**reverse primer:**  
5'-CAGGAAACAGCTATGAC-3'



**universal primer:**  
5' -GTAAAACGACGGCCAG-3'

reverse

GCTTATTG

## SEQUENZE

5'-GCTATTGGCCATTGACCAATTGGCCAATTGAAATTGCCATTGGTAA-3'

3'-CGATAAACCGGTAACGGTTAACCGGTTAACCTTAACCGGTAAACCATT-5'

AAACCATT

universal

reverse

GCTTATTG

CGATAAACCGGTAACGGTTAACCGGTTAACCTTAACCGGTAAACCATT

Sequenza con reverse:

5' - CCATTGACCAATTGGCCAATTGAAATTGCCATTGGTAA - 3'

GCTATTGGCCATTGACCAATTGGCCAATTGAAATTGCCATTGGTAA

AAACCATT

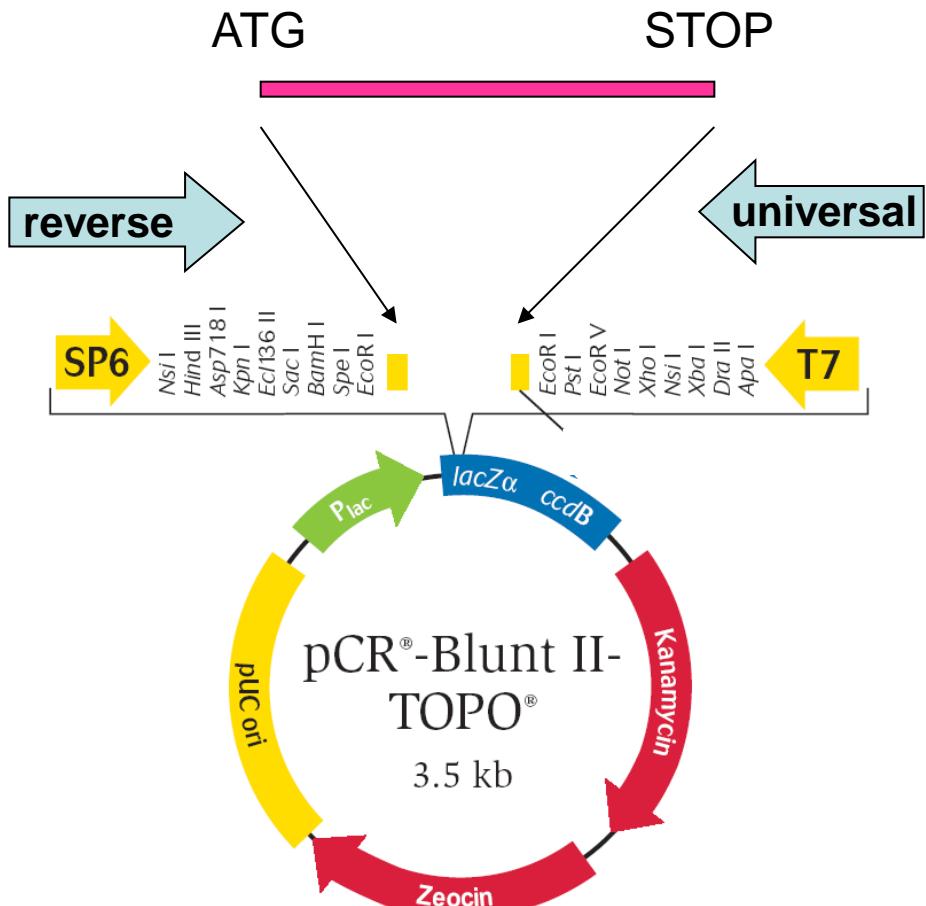
universal

Sequenza con universal:

5' - TGGCCAATTCAATTGGCCAATTGGTCAATGCCAAATAGC - 3'

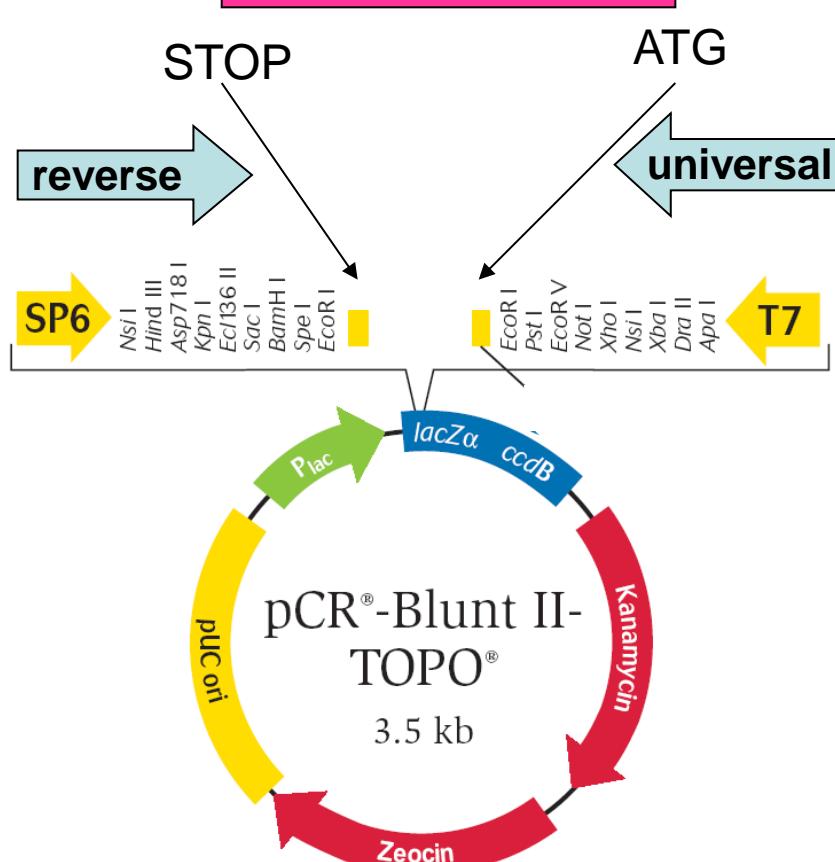
# SENSO

5' -**ATGCGTACCTTTAACTCGTAG**-3'  
 3' -TACGCATGGAAATTGAGGCATC-5'

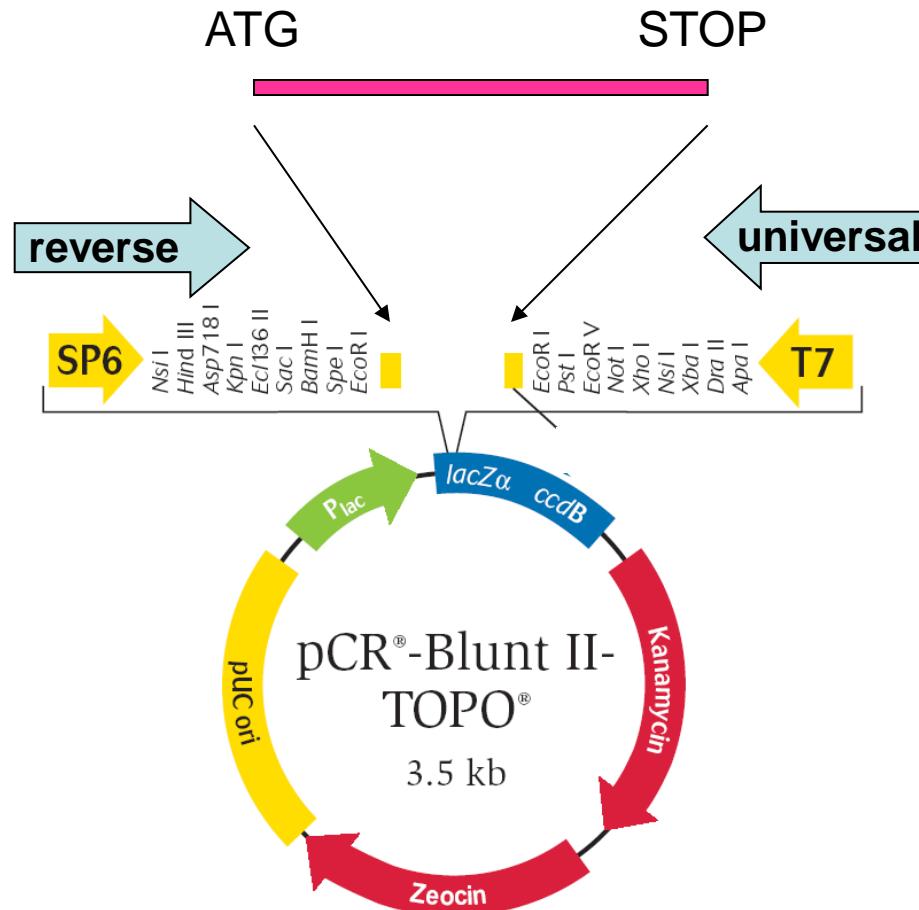


# ANTISENSO

5' -CTACGAGTTAAAGGTACGCAT-3'  
 3' -**GATGCTGAATTCCATGC GTA**-5'



**reverse** → 5' -ATGCGTACCTTAACTCG**TAG**-3'  
 3' -TACGCATGGAAATTGAGCATC-5' ← **universal**

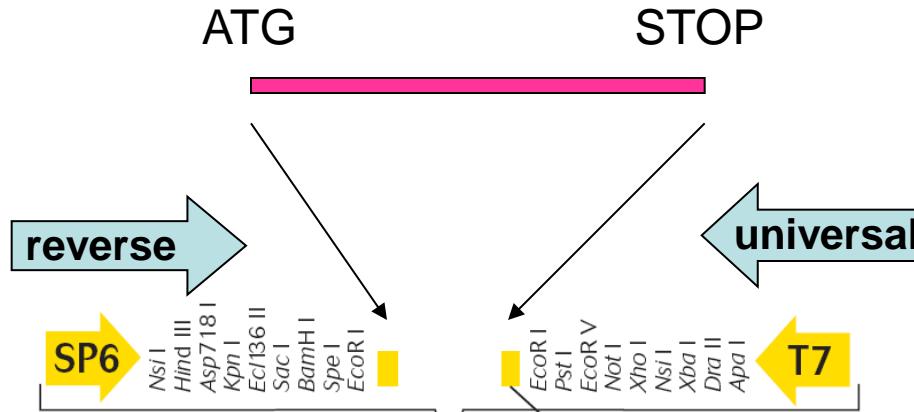


**reverse**

5' - **ATG**CGTACCTTAAC $\tau$ CG**TAG**-3'  
3' - TACGCATGGAAATTGAGC $\tau$ TC-5'

**universal**

REVERSE : NNNNNNN**ATG**CGTACCTTAAC $\tau$ CG**TAG**NNNNNNN



reverse

5' -ATGCGTACCTTAACTCG**TAG**-3'  
 3' -TACGCATGGAAATTGAGCATC-5'

universal

REVERSE :

NNNNNN**ATG**CGTACCTTAACTCG**TAG**NNNNNNN

UNIVERSAL :

NNNNNNCTACGAGTTAAAGGTACGCATNNNNNNN

ATG STOP

reverse

SP6

- Nsi*I
- Hind*III
- Asp718*I
- Kpn*I
- Ecl136*II
- Sac*I
- Bam*H I
- Spe*I
- Eco*R I

universal

T7

- ECOR*I
- Pst*I
- ECOR*V
- Not*I
- Xba*I
- Nsi*I
- Xba*I
- Dra*II
- Apa*I

200bp

100bp

**reverse**

5' -**ATG**CGTACCTTTAACTCG**TAG**-3'  
3' -TACGCATGGAAATTGAGCATC-5'

universal

REVERSE: NNNNNN**ATGCGTACCTTAACTCGTAG**NNNNNN

UNIVERSAL: NNNNNCTACGAGTTAAAGGTACGCATNNNNNN

## BLAST:

**Query:** 1 ATGCGTACCTTTAACTCG**TAG** 21  
||||| ||||| ||||| ||||| |||||

**Subject Reverse:** 201 ATGCGTACCTTTAACTCG**TAG** 221

**Query:** 1 ATGCGTACCTTTAACTCGTAG 21  
| | | | | | | | | | | | | | | | | | | |

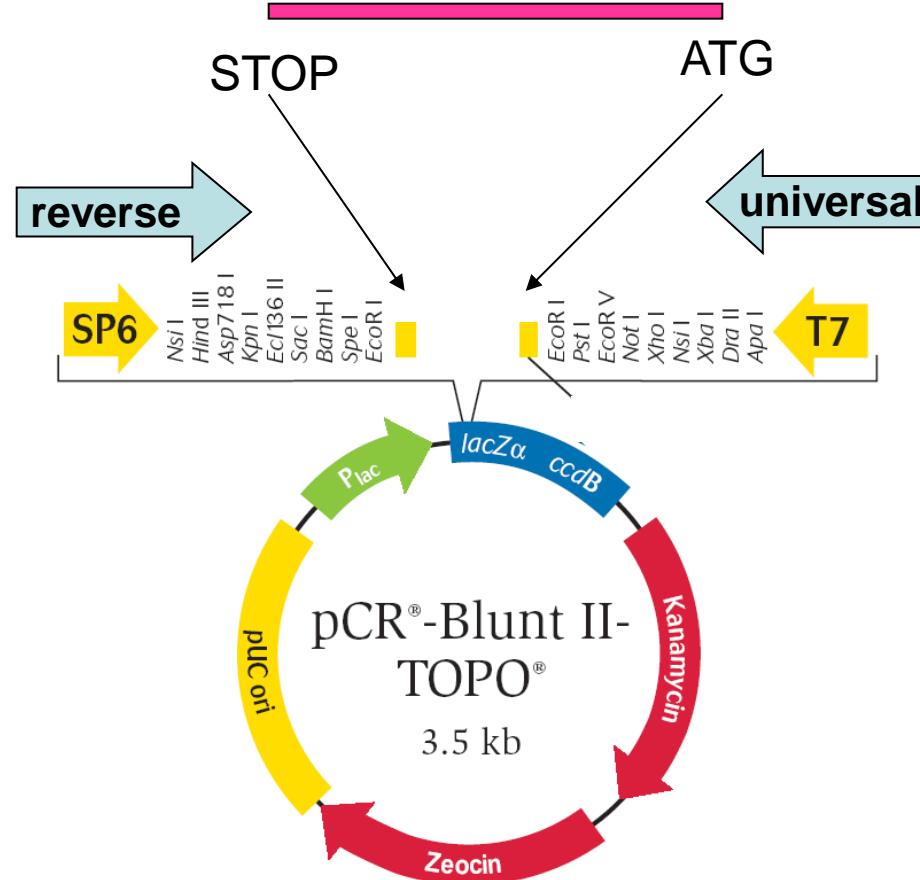
**Subject Universal:** 121 ATGCGTACCTTTAACTCGTAG 101

## ATG STOP

**reverse**

universal

**reverse** → 5' -CTACGAGTTAAAGGTACGCAT-3'  
 3' -**GAT**GCTGAATTCCATGC**GTA**-5' ← **universal**



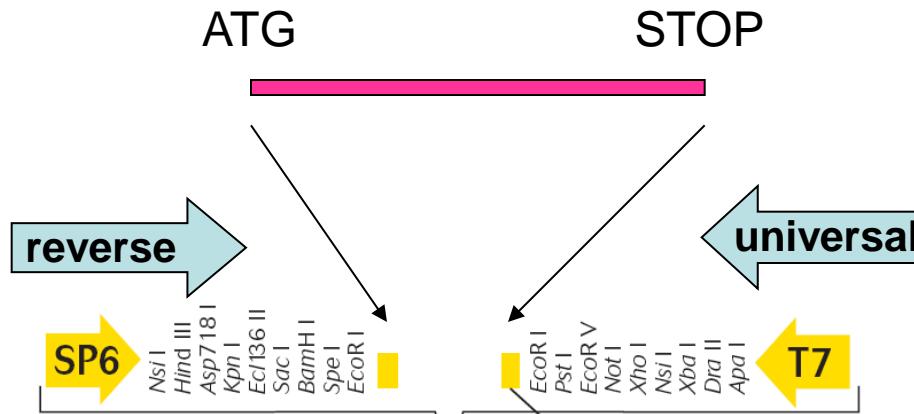
**reverse**

5' -CTACGAGTTAAAGGTACGCAT-3'  
3' -**GAT**GCTGAATTCCATGC**GTA**-5'

**universal**

REVERSE :

NNNNNNNCTACGAGTTAAAGGTACGCATNNNNNN



reverse

5' -CTACGAGTTAAAGGTACGCAT-3'  
 3' -**GAT**GCTGAATTCCATGC**GTA**-5'

universal

REVERSE :

NNNNNNNNCTACGAGTTAAAGGTACGCATNNNNNNN

UNIVERSAL :

NNNNNNNN**ATG**CGTACTTAACTCG**TAG**NNNNNNN

ATG STOP

reverse

SP6

- Nsi*I
- Hind*III
- Asp718*I
- Kpn*I
- Ecl136*II
- Sac*I
- Bam*H I
- Spe*I
- Eco*R I

universal

T7

- ECO*R I
- Pst*I
- ECO*R V
- Not*I
- Xba*I
- Nsi*I
- Xba*I
- Dra*II
- Apa*I

200bp

100bp

reverse

5' -CTACGAGTTAAAGGTACGCAT-3'  
 3' -**GAT**GCTGAATTCCATGC**GTA**-5'

universal

REVERSE : NNNNNNNCTACGAGTTAAAGGTACGCATNNNNNNN

UNIVERSAL : NNNNNNN**ATG**CGTACCTTAACTCG**TAG**NNNNNNN

BLAST :

Query : 1 **ATG**CGTACCTTAACTCG**TAG** 21

```
||||| ||||| ||||| ||||| ||||| |||||
```

Subject Reverse : 221 **ATG**CGTACCTTAACTCG**TAG** 201Query : 1 **ATG**CGTACCTTAACTCG**TAG** 21

```
||||| ||||| ||||| ||||| ||||| |||||
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Subject Universal : 101 **ATG**CGTACCTTAACTCG**TAG** 121

ATG

STOP

reverse

universal

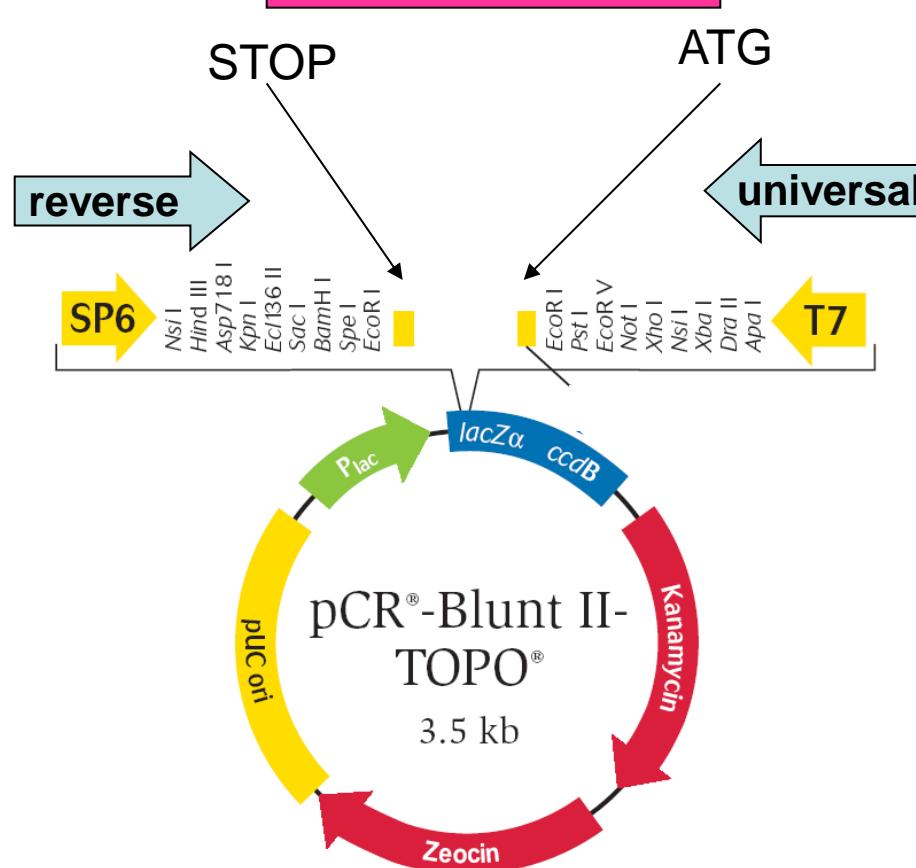
C → T

ANTISENO  
MUTATO

reverse

5' -CTACGAGTTAAA**A**GTACGCAT-3'  
3' -**GAT**GCTGAATTTCATGC**GTA**-5'

universal



C → T

ANTISENO  
MUTATO

reverse

5' -CTACGAGTTAAA**A**GTACGCAT-3'  
3' -**G**ATGCTGAATTTCATGC**GTA**-5'

universal

REVERSE :

NNNNNNNCTACGAGTTAAA**A**GTACGCATNNNNNN

ATG STOP

reverse

Nsi I  
Hind III  
Asp718 I  
Kpn I  
Ecl136 II  
Sac I  
BamHI  
SpeI  
EcoRI

universal

ECOR I  
Pst I  
ECOR V  
Not I  
Xba I  
Nsi I  
Xba I  
Dra I  
Apa I

T7

SP6

C → T

ANTISENO  
MUTATO

reverse

5' -CTACGAGTTAAA**A**GTACGCAT-3'  
3' -**G**ATGCTGAATTTCATGC**GTA**-5'

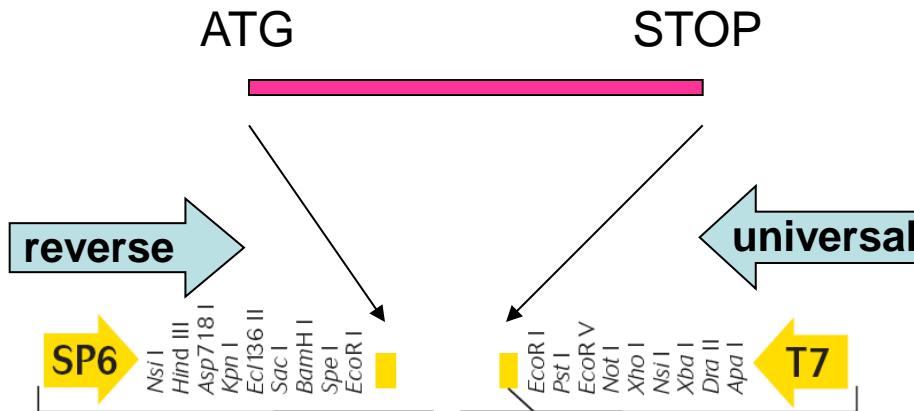
universal

REVERSE :

NNNNNNNCTACGAGTTAAA**A**GTACGCATNNNNNN

UNIVERSAL :

NNNNNNN**ATG**CGTACTTTAACTCG**TAG**NNNNNN



ANTISEN  
MUTATO

200bp

C → T

100bp

reverse

5' -CTACGAGTTAAA**A**GTACGCAT-3'  
3' -**G**ATGCTGAATTTCATGC**GTA**-5'

universal

REVERSE : NNNNNNNCTACGAGTTAAA**A**GTACGCATNNNNNN

UNIVERSAL : NNNNNNN**ATG**CGTACT**T**TTAACTCG**TAG**NNNNNN

BLAST:

**Query :** 1 **ATG**CGTAC**CTTAA**CTCG**TAG** 21

||||| |||| | ||| ||| ||| |||

**Subject Reverse :** 221 **ATG**CGTACT**TTAAC**TCG**TAG** 201

**Query :** 1 **ATG**CGTAC**CTTAA**CTCG**TAG** 21

||||| |||| | ||| ||| ||| |||

**Subject Universal :** 101 **ATG**CGTACT**TTAAC**TCG**TAG** 121

ATG

STOP

reverse

universal

**ANTISEN  
O  
MUTATO**

200bp

C → T

100bp

**reverse**

5' -CTACGAGTTAAA**A**GTACGCAT-3'  
3' -**G**ATGCTGAATTTCATGC**GTA**-5'

**universal**

REVERSE : NNNNNNNCTACGAGTTAAA**A**GTACGCATNNNNNN

UNIVERSAL : NNNNNNN**ATG**CGTACTTTAACTCG**TAG**NNNNNN

BLAST:

**Query :**

1 **ATGCGTACCTTAACTCGTAG** 21

||||| |||| | ||||| ||| |||

**Subject Reverse :** 221 **ATGCGTACTTTAACTCGTAG** 201

**Query :**

1 **ATGCGTACCTTAACTCGTAG** 21

||||| |||| | ||||| ||| |||

**Subject Universal :** 101 **ATGCGTACTTTAACTCGTAG** 121

Identifico la posizione della mutazione sulle sequenze Query, Reverse ed Universal:

<b>Query</b>	<b>Reverse</b>	<b>Universal</b>
9	213	109



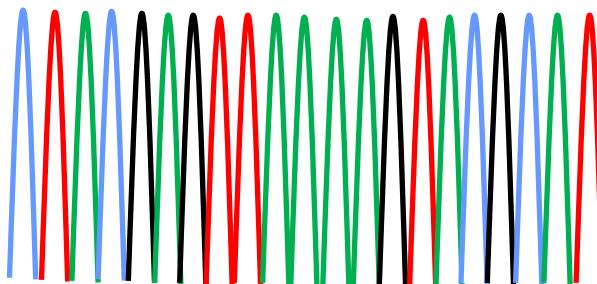
ANTISEN  
MUTATO

213

|

REVERSE :

NNNNNNNC**TACGAGTTAAAAGTACGCA**TNNNNNNN



109

|

UNIVERSAL :

NNNNNNNA**TGCGTACTTTAACTCGTAGNNNNNNN**

