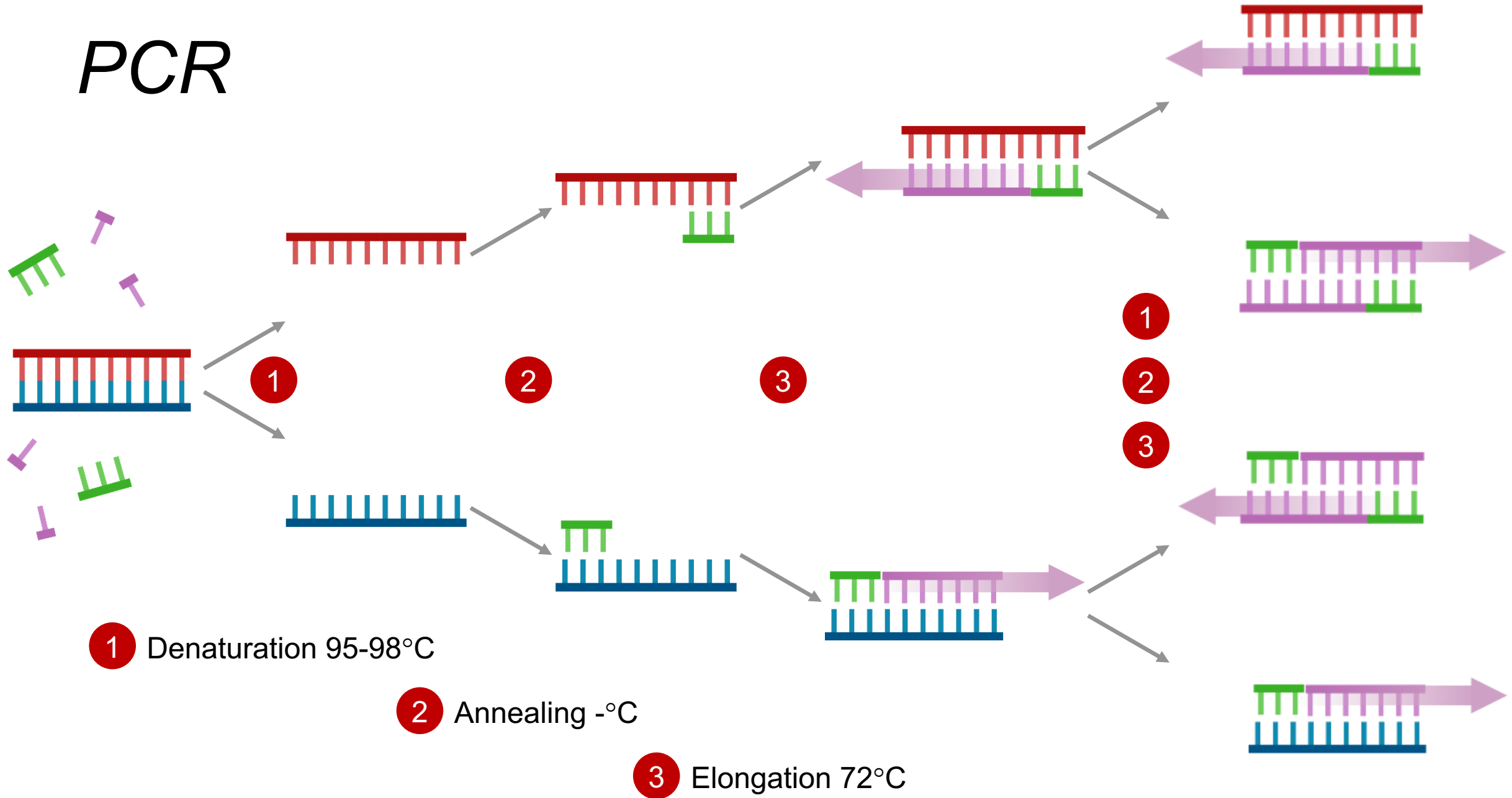


PCR



Choosing the polymerase

1. Thermal stability
2. Extension rate
3. Fidelity
4. Processivity

Choosing the polymerase

- Standard thermostable DNA polymerases
- Hot-start (HS) polymerases
- High-fidelity polymerases (Hi-Fi)
- Polymerases for amplification of long amplicons

Commercial polymerases

Taq DNA Polymerases

EpiMark® Hot Start *Taq* DNA Polymerase

Pf Q5® High-Fidelity DNA Polymerases

NEBNext® High-Fidelity 2X PCR Master Mix

Phu NEBNext® Q5® Hot Start HiFi PCR Master Mix

Phu NEBNext® Ultra™ II Q5® Master Mix

Phu NEBNext® Q5U® Master Mix

Q5® High-Fidelity 2X Master Mix

Phu Q5® High-Fidelity DNA Polymerase

Phu Q5® High-Fidelity PCR Kit

Phu Q5® Hot Start High-Fidelity 2X Master Mix

Phu Q5® Hot Start High-Fidelity DNA Polymerase

Q5® Reaction Buffer Pack

Phu Q5U® Hot Start High-Fidelity DNA Polymerase

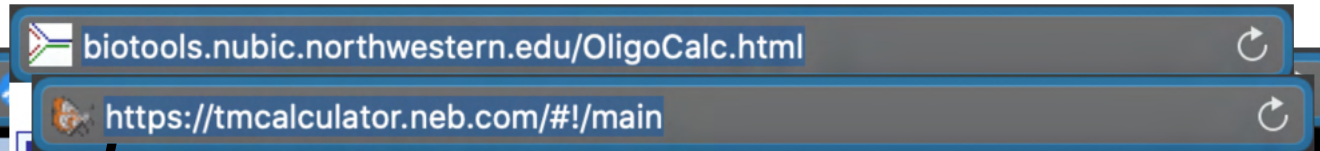
Taq PCR Kit

ThermoPol® Reaction Buffer Pack

ThermoPol® II (Mg-free) Reaction Buffer Pack

Primer design

Tm Calculator



version 1.13.0

- Primers should always be designed towards 5' → 3'.

Use the NEB Tm Calculator to estimate an appropriate annealing temperature when using NEB PCR products.

- 40–60% GC content is ideal.

- 3' end should contain G or C to promote binding.

Instructions

- Select the product group of the polymerase or kit you plan to use.
- Select the polymerase or kit from the list of products.
- If needed, modify the recommended primer concentration.
- Enter primer sequences (with up to 3 ambiguities/bases). Spaces allowed.

Note that an annealing temperature will only be displayed if both primer sequences are entered.

Product Group

Q5

Polymerase/Kit

Q5 High-Fidelity DNA Polymerase

Primer Concentration (nM)

500 Reset concentration

Primer 1

PRIMER 1 SEQUENCE

Primer 2

PRIMER 2 SEQUENCE

Switch to batch mode

Clear

Use example input

Anneal at

--- °C

Primer 1

--- nt

---% GC

Tm: ---°C

Primer 2

--- nt

---% GC

Tm: ---°C

Primer3Plus

pick primers from a DNA sequence

[Primer3Manager](#)

[Help](#)

[About](#)

[Source Code](#)

[Primer3](#) [Source Code](#)

Select the [Task](#) for primer selection

[Template masking](#) [Gene description](#)
[Select species](#) Example: Mus musculus
[Primer failure rate cutoff](#) < 0.1

Primer3 & Primer3Plus

Select primer pairs to detect the given template sequence. Optionally targets and included/excluded regions can be specified.

Paste source sequence below (5'->3', string)

Pick left primer, or use left primer below

- [Sequence Id](#)
- [Targets](#)
- [Overlap Junction List](#)
- [Excluded Regions](#)
- [Pair OK Region List](#)
- [Included Region](#)
- [Start Codon Position](#)
- [Internal Oligo Excluded Region](#)

[Force Left Primer Start](#) -1000 [Force Right Primer Start](#) 1000
[Force Left Primer End](#) -1000 [Force Right Primer End](#) 1000

[Sequence Quality](#)

[Min Sequence Quality](#) 0 [Min End Sequence Quality](#)

General Primer Picking Conditions

Upload the settings from a file

[Primer Size](#) Min 18 Opt 20 Max
[Primer Tm](#) Min 57.0 Opt 59.0 Max
[Product Tm](#) Min -100.0 Opt 0.0 Max
[Primer GC%](#) Min 30.0 Opt 50.0 Max

- Main**
- General Settings**
- Advanced Settings**
- Internal Oligo**
- Penalty Weights**
- Sequence Quality**

[Sequence Id:](#)

[Paste source sequence below](#)

Or upload sequence file: no file selected

Mark selected region:

[Excluded Regions:](#) < >

[Targets:](#) []

[Included Region:](#) { }

Pick left primer or use left primer below.

Pick hybridization probe (internal oligo) or use oligo below.

Pick right primer or use right primer below (5'->3' on opposite strand).

Align Sequences Nucleotide BLAST

blastn blast blastx tblastn tblastx

BLASTN programs search nucleotide subjects using a nucleotide query. [more...](#)

Reset page Bookmark

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

Or, upload file no file selected [?](#)

Job Title


Enter a descriptive title for your BLAST search [?](#)

Align two or more sequences [?](#)

Query subrange [?](#)

From

To

New columns added to the Description Table
Click 'Select Columns' or 'Manage Columns'. 

Enter Subject Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

Or, upload file no file selected [?](#)

Subject subrange [?](#)

From

To

Program Selection

- Optimize for
- Highly similar sequences (megablast)
 - More dissimilar sequences (discontiguous megablast)
 - Somewhat similar sequences (blastn)
- Choose a BLAST algorithm [?](#)

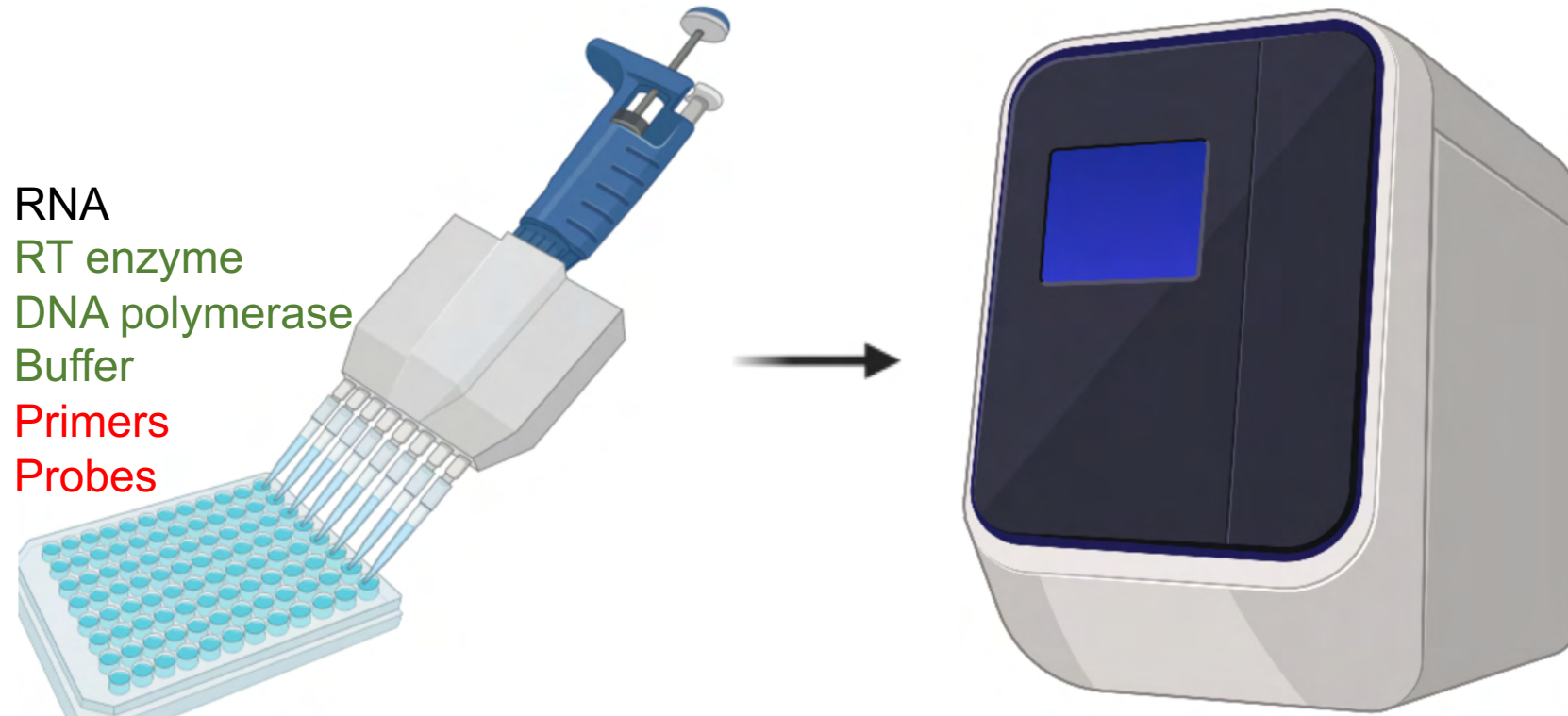
BLAST

Search nucleotide sequence using Megablast (Optimize for highly similar sequences)

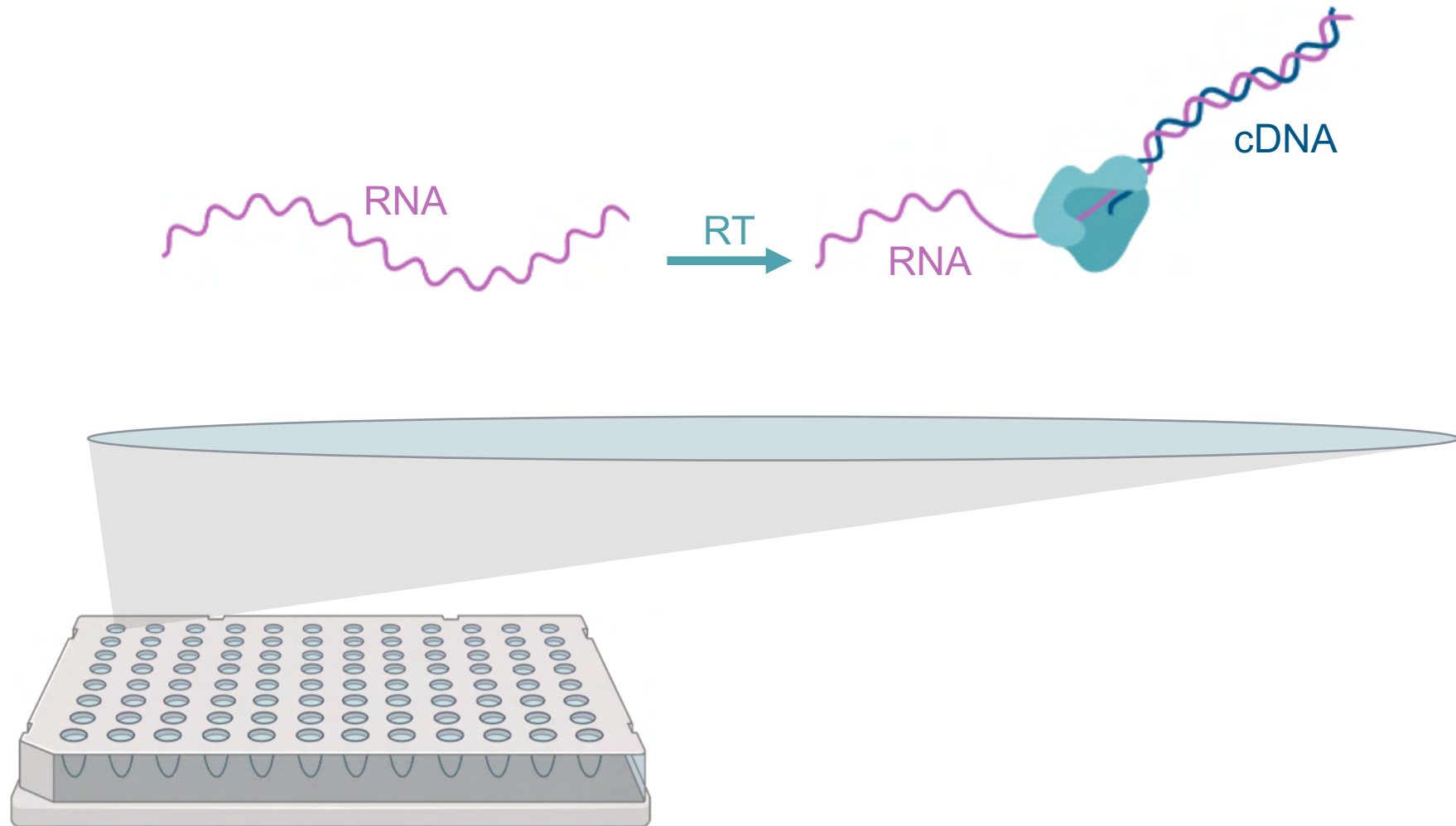
Show results in a new window

+ Algorithm parameters

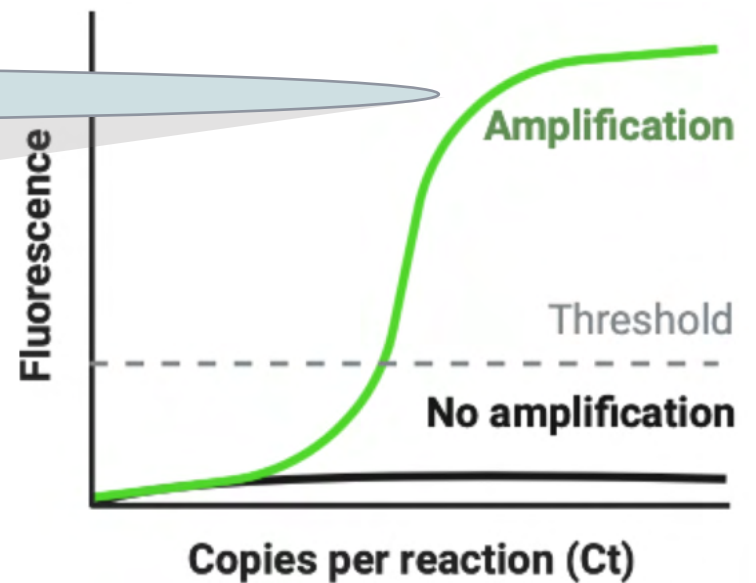
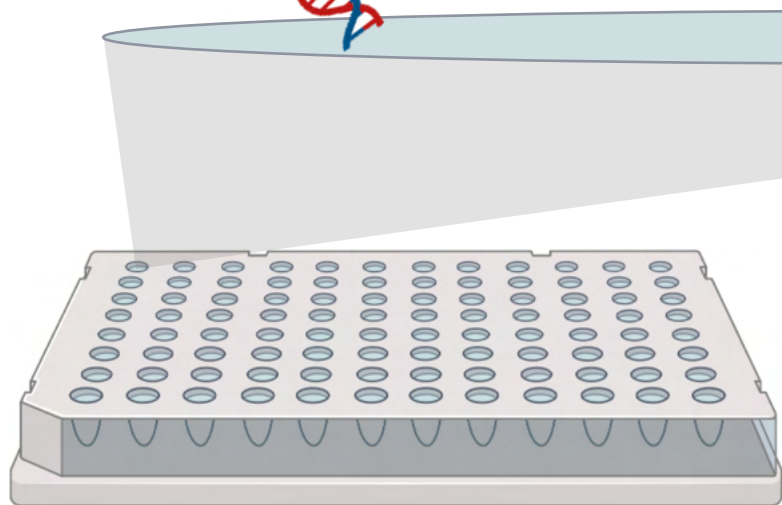
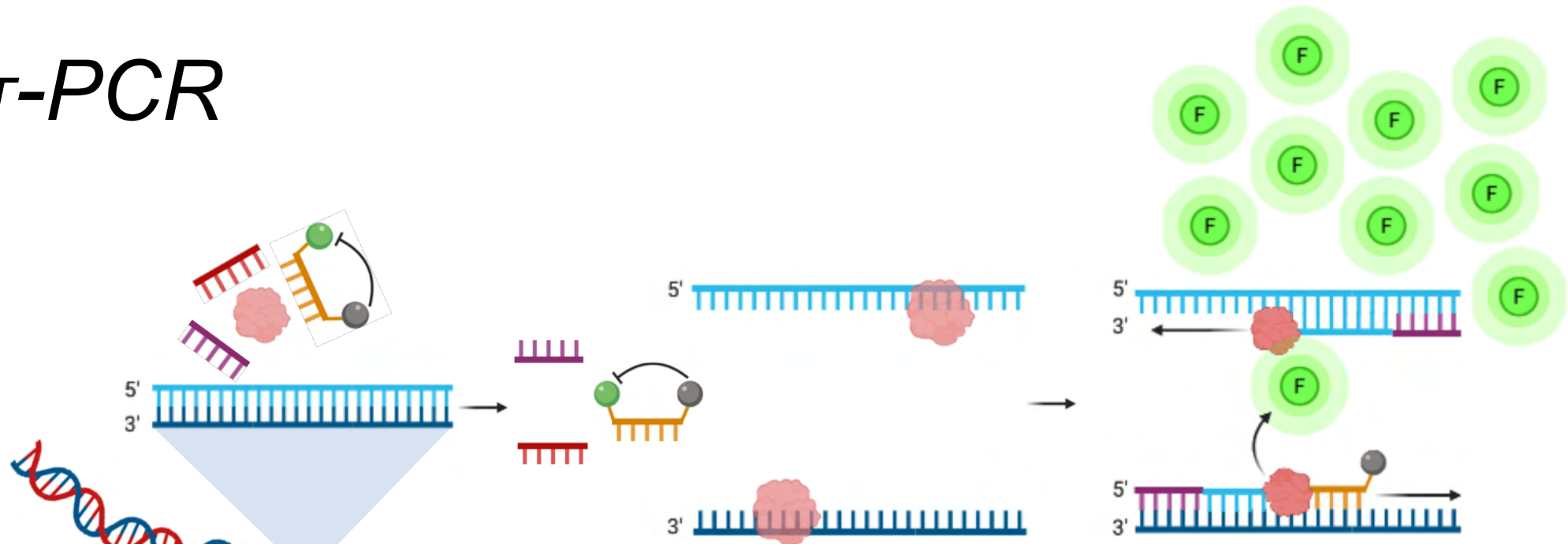
RT-PCR



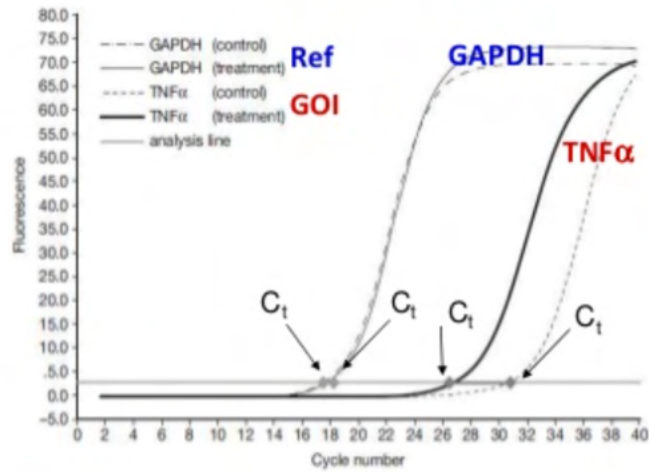
RT-PCR



RT-PCR



RT-qPCR



$$\Delta\Delta Ct = \Delta Ct (TNF\alpha_{treat} - GAPDH_{treat}) - \Delta Ct (TNF\alpha_{control} - GAPDH_{control})$$

The fold change = $2^{(-\Delta\Delta Ct)}$

single data ($n = 1$) e.g. array results:

$$\text{relative expression} = \frac{E_{\text{target}}^{\Delta CP_{\text{target}} (\text{control} - \text{sample})}}{E_{\text{ref}}^{\Delta CP_{\text{ref}} (\text{control} - \text{sample})}}$$

Pfaffl, Nucleic Acids Research 2001

multiple data ($1 < n < 16$) e.g. experimental groups:

$$\text{relative expression} = \frac{E_{\text{target}}^{\Delta CP_{\text{target}} (\text{MEAN control} - \text{MEAN sample})}}{E_{\text{ref}}^{\Delta CP_{\text{ref}} (\text{MEAN control} - \text{MEAN sample})}}$$

Pfaffl et al., Nucleic Acids Research 2002

MIQE guidelines for RT-qPCR

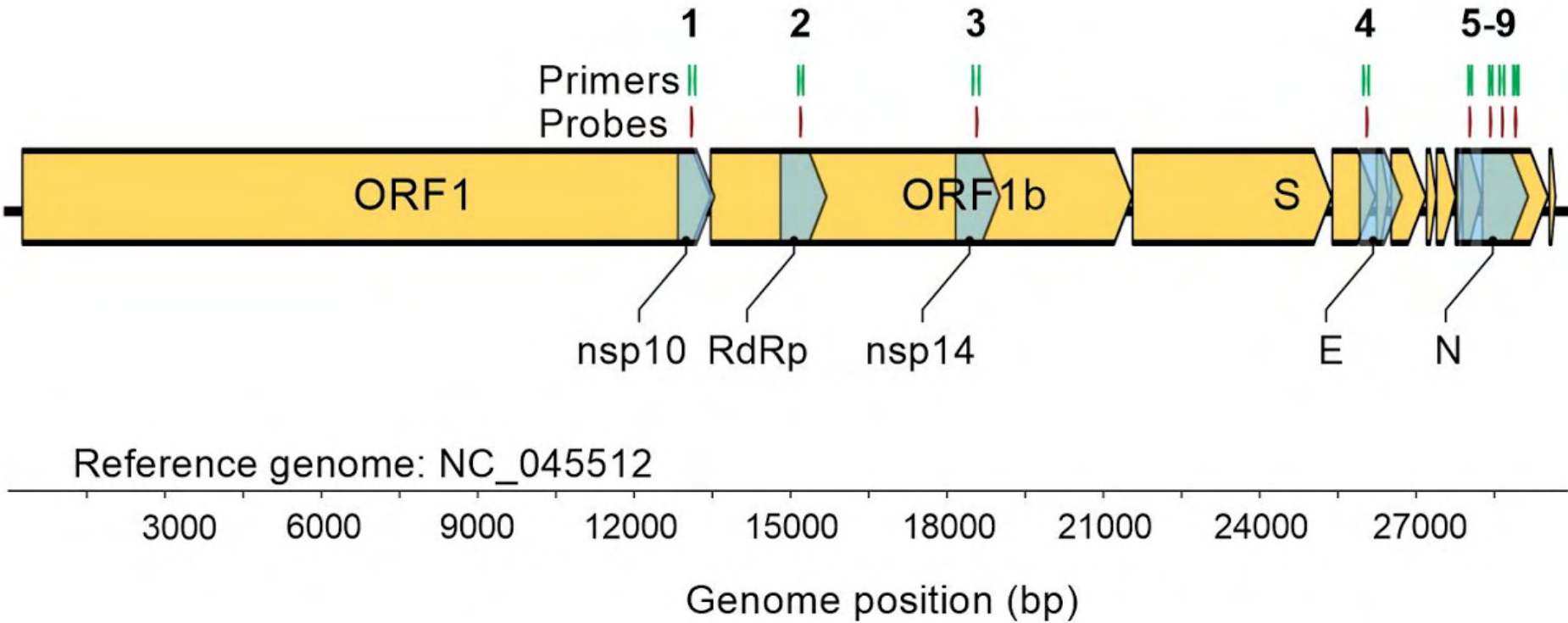
Clinical Chemistry 55:4
611–622 (2009)

Special Report

The MIQE Guidelines: Minimum Information for Publication of Quantitative Real-Time PCR Experiments

Stephen A. Bustin,^{1*} Vladimir Benes,² Jeremy A. Garson,^{3,4} Jan Hellemans,⁵ Jim Huggett,⁶
Mikael Kubista,^{7,8} Reinhold Mueller,⁹ Tania Nolan,¹⁰ Michael W. Pfaffl,¹¹ Gregory L. Shipley,¹²
Jo Vandesompele,⁵ and Carl T. Wittwer^{13,14}

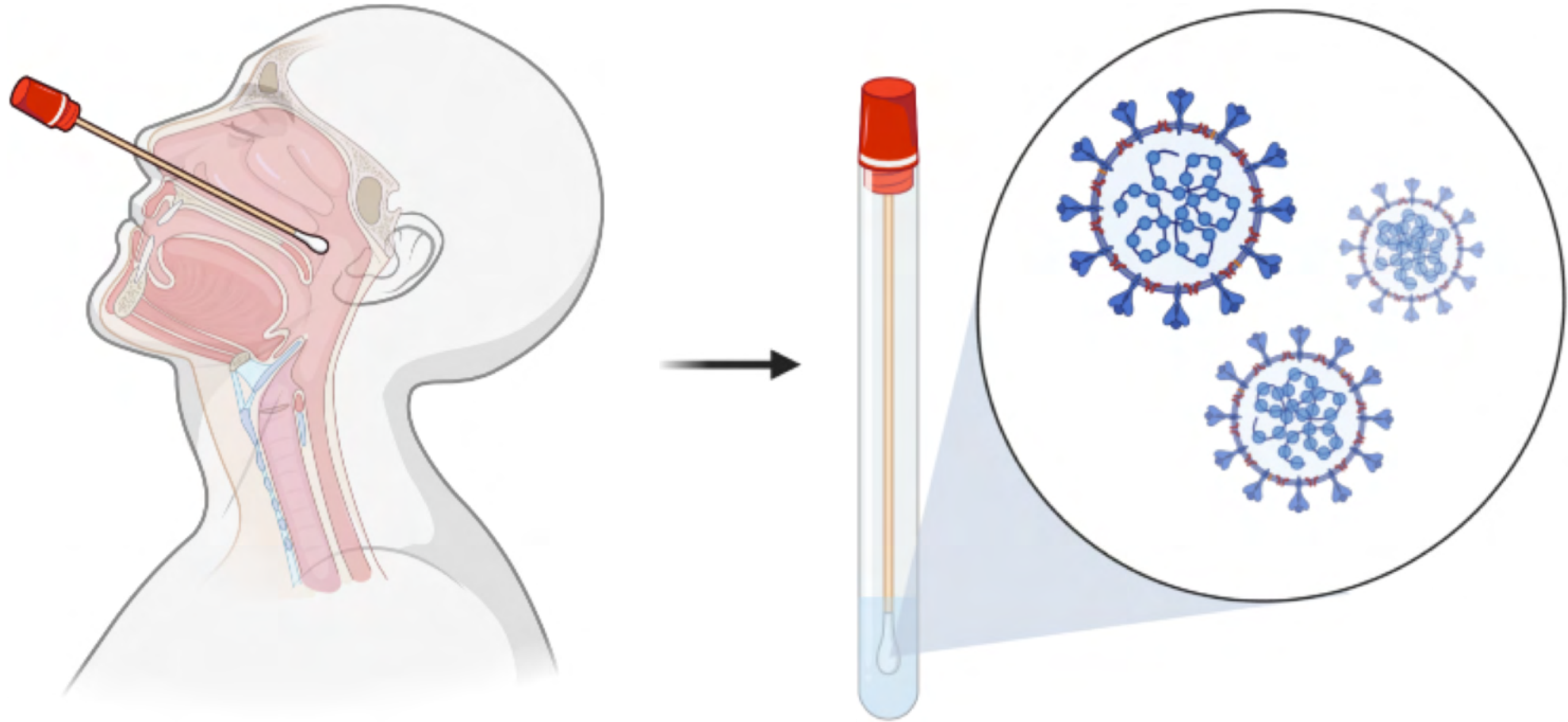
Applications: famous COVID19 tests



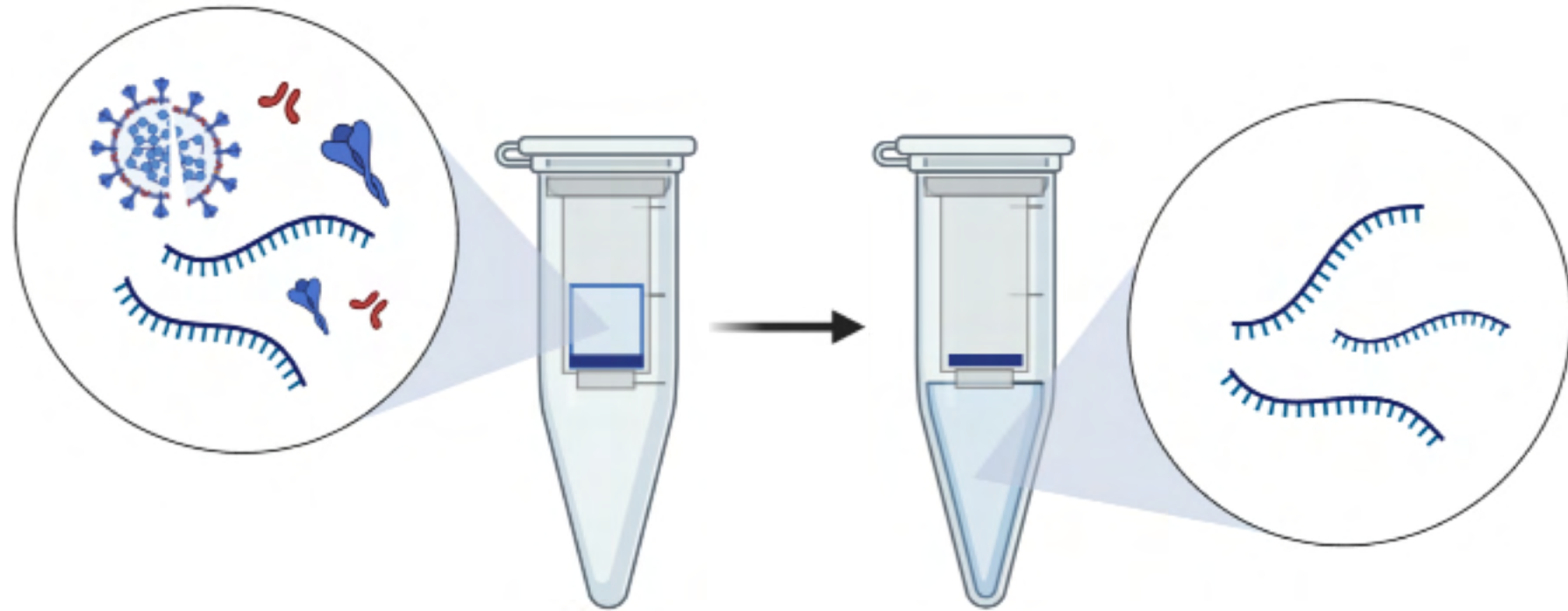
Design of Primers

- Internal control primers:
 - GAPDH, RNaseP, ACTB, eEF-1 etc.
- Viral DNA primers: N region
 - N gene (CDC Panel, Hong Kong Panel, Japan National Institute of Infectious Diseases Panel)
 - E gene (Berlin-Charité Panel, Institut Pasteur Panel)
 - ORFab primers (Berlin-Charité Panel, China CDC panel)
 - RdRp (Berlin-Charité Panel, Institut Pasteur Panel)
 - S gene

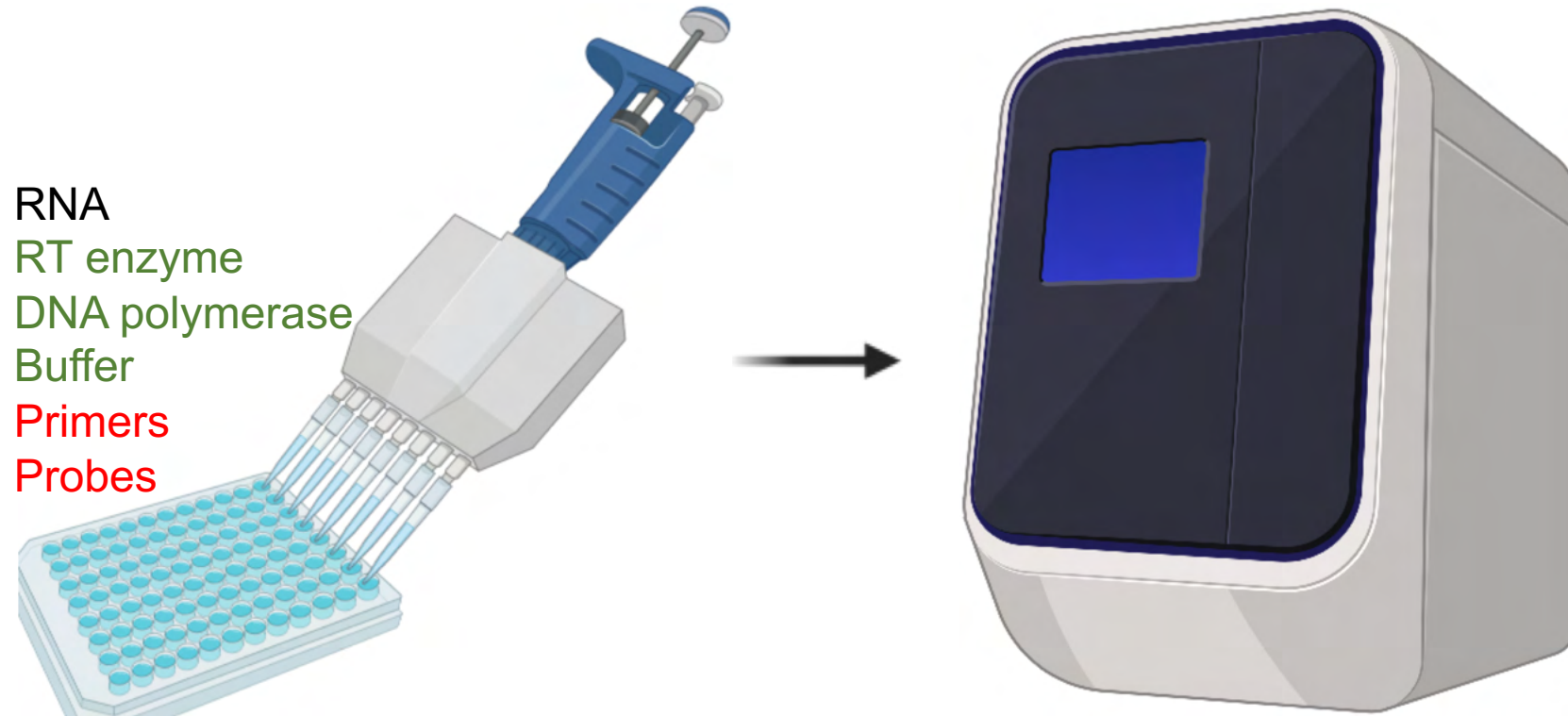
Nasopharyngeal & Oropharyngeal swabs



RNA isolation



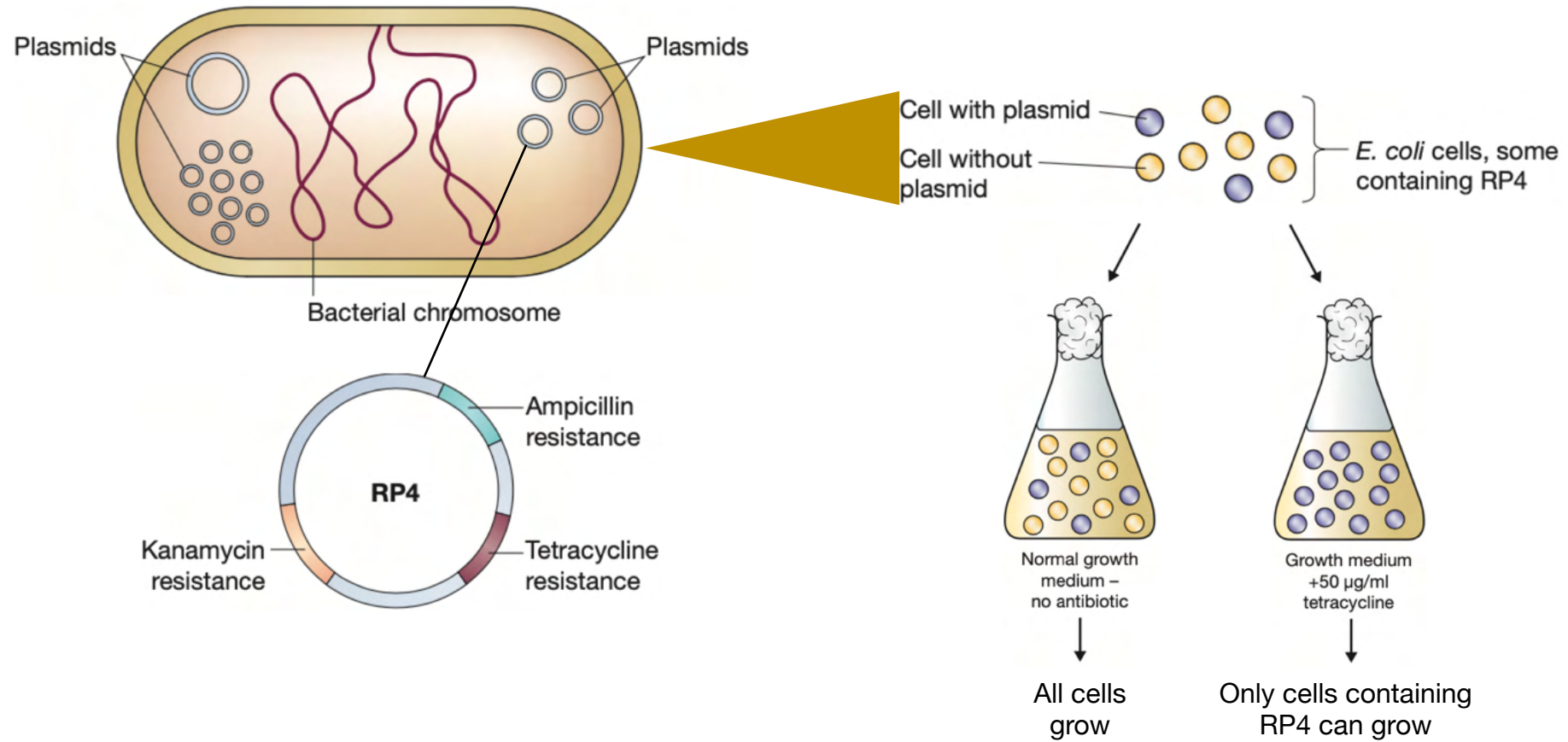
RT-PCR

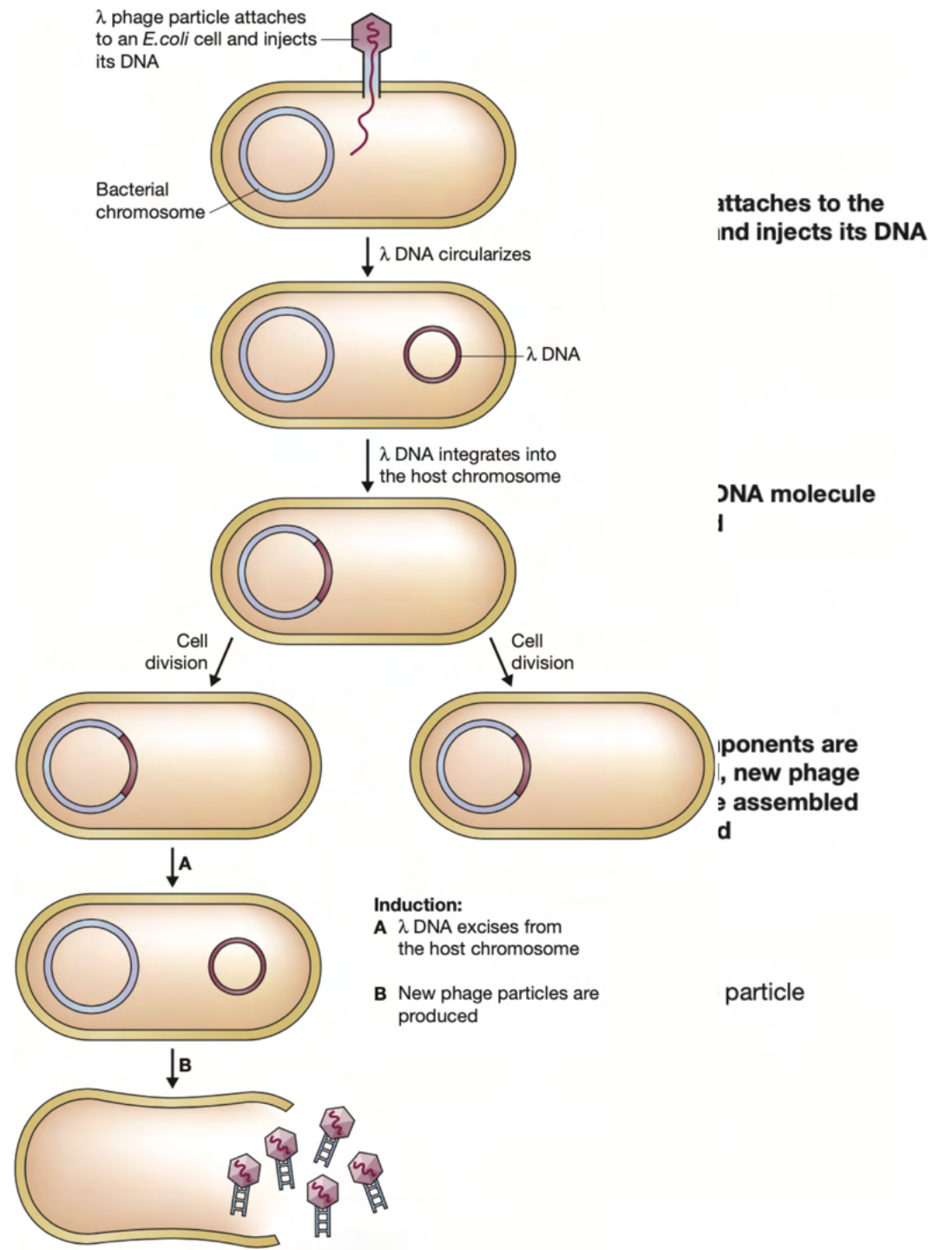
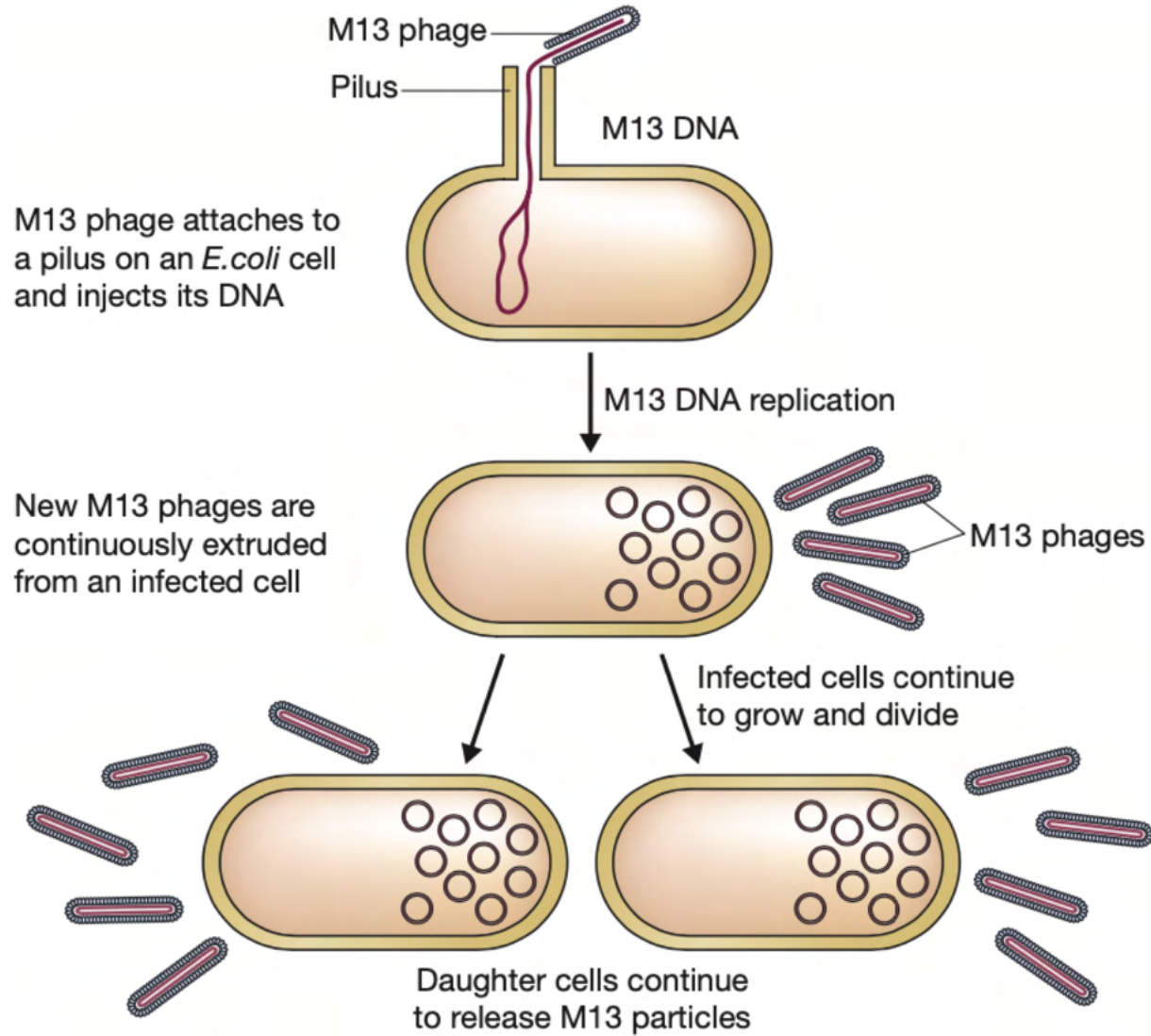


GENE CLONING

Part I: Vectors for Gene Cloning

Plasmids

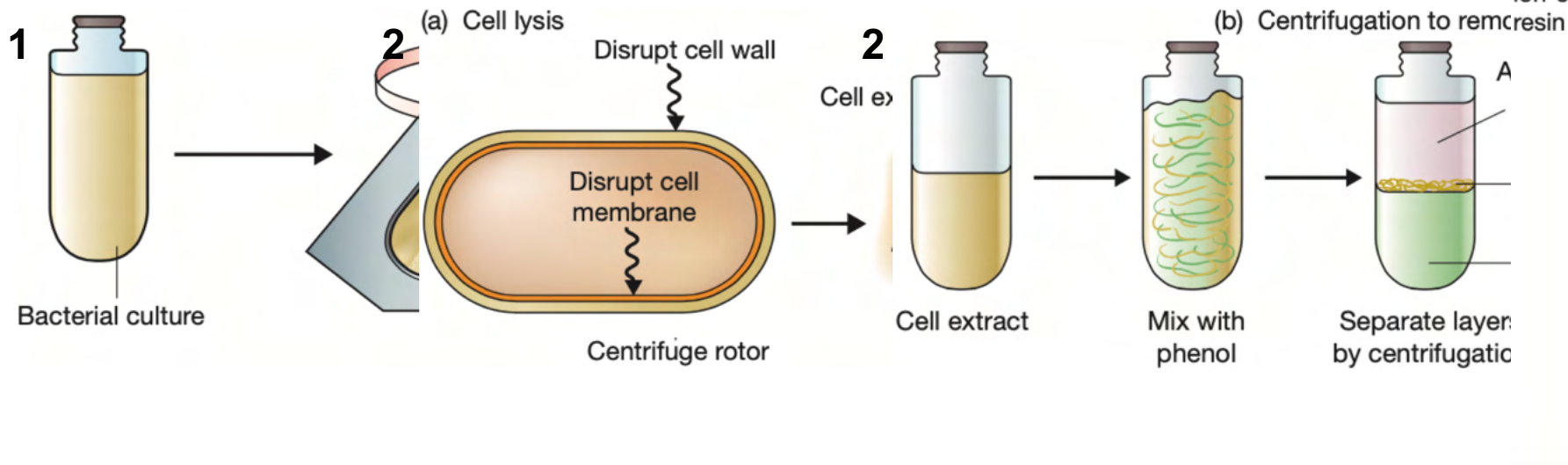
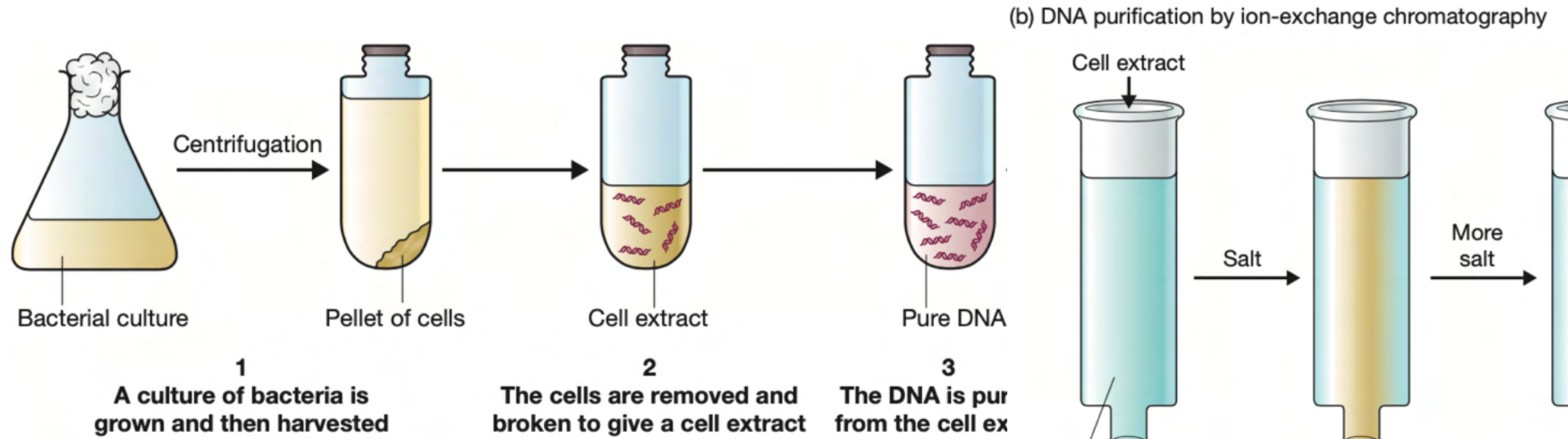




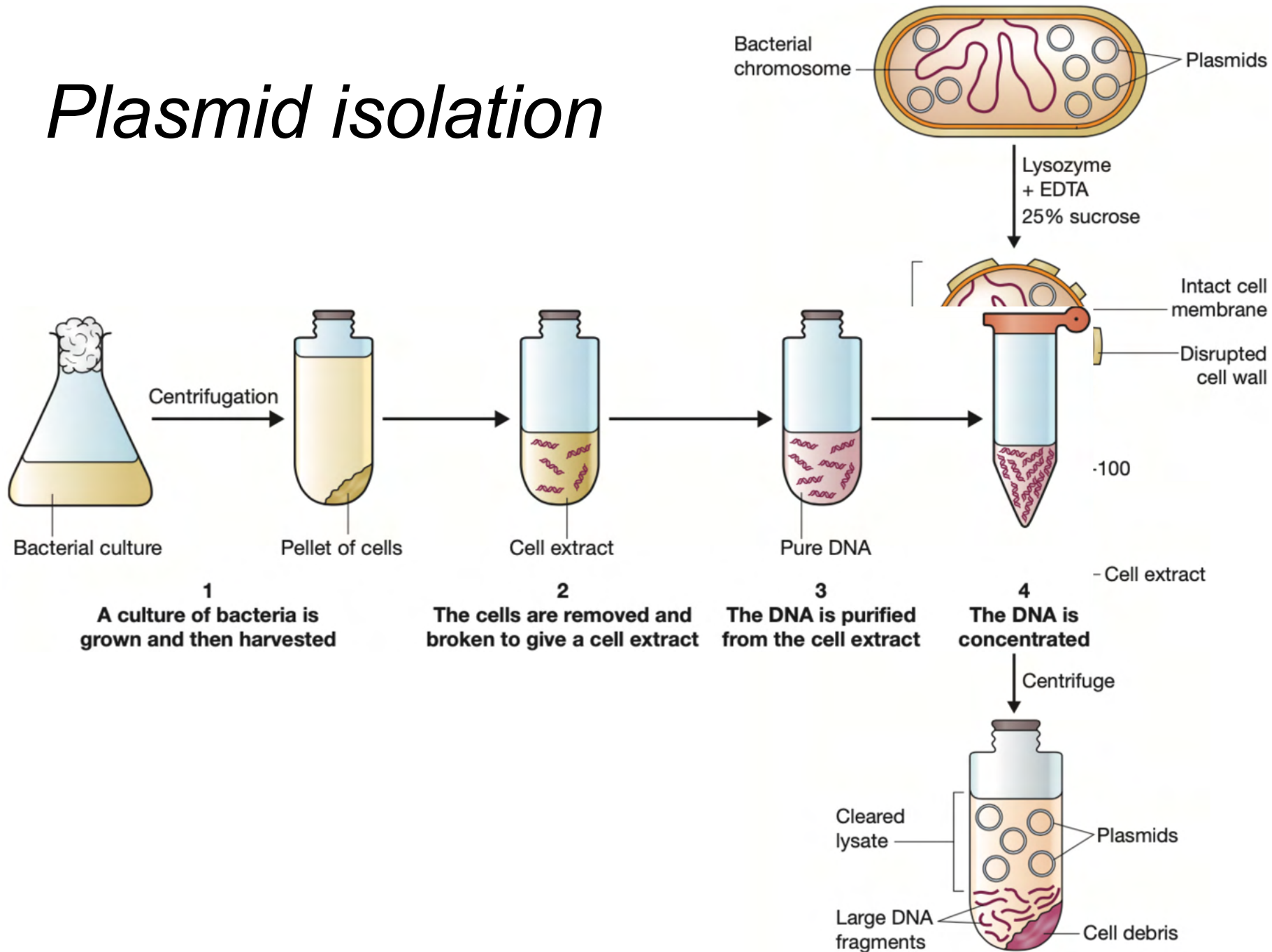
Viruses are cloning vectors for other organisms

- **adenoviruses** are used in **gene therapy**.
- **baculoviruses** are used to synthesize important pharmaceutical proteins in insect cells.
- **caulimoviruses** and **geminiviruses** have been used for cloning in plants.

Purification of DNA from Living Cells



Plasmid isolation



GENE CLONING

Part II: Manipulating the DNA

Manipulation of the DNA

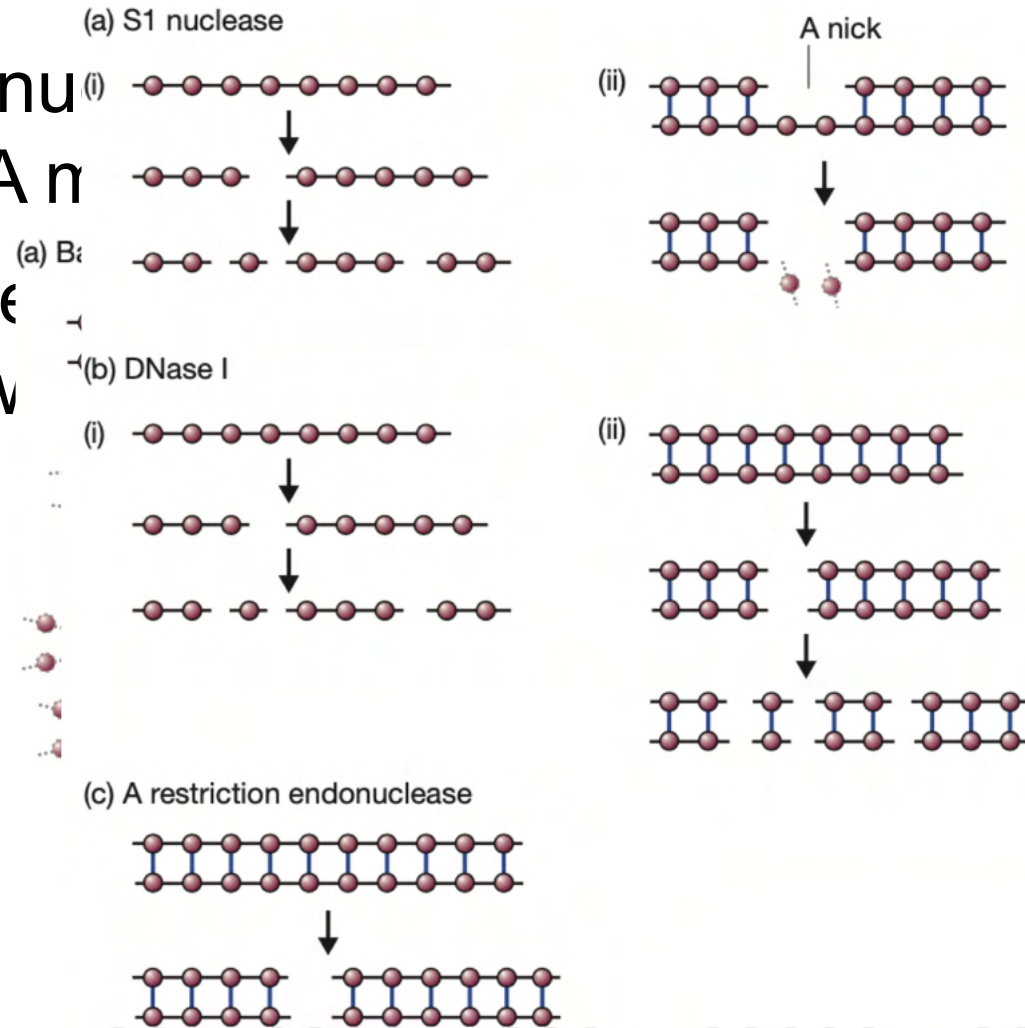
1. The range of DNA manipulative enzymes.
2. Enzymes for cutting DNA—restriction endonucleases.
3. Ligation—joining DNA molecules together.

DNA manipulative enzymes

- Nucleases, are enzymes that cut, shorten, or degrade NA molecules.
- Ligases, join NA molecules together.
- Polymerases, makes copies of NA molecules.
- Modifying enzymes, remove/add chemical groups.

Nucleases

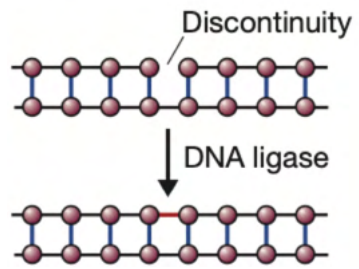
- Exonucleases, remove nucleotides from the end of a DNA molecule
- Endonucleases, are able to cut DNA at specific bonds within the molecule



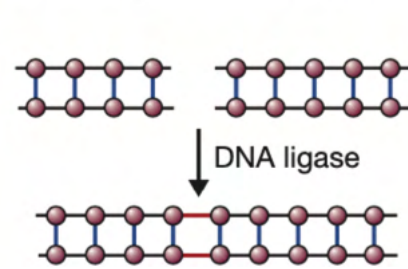
the end
ter

Ligases

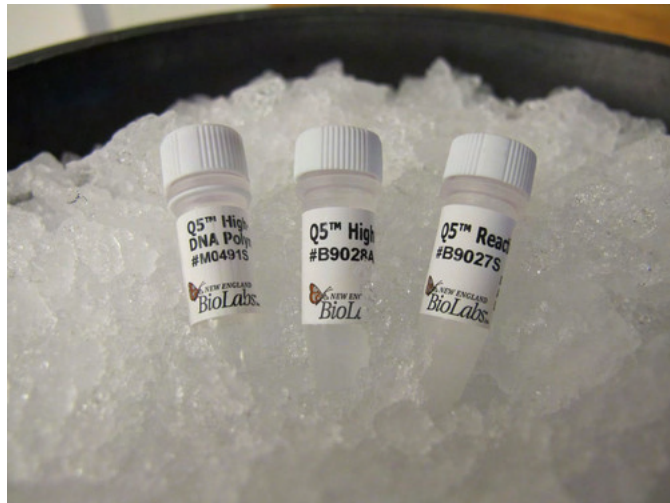
(a) Discontinuity repair



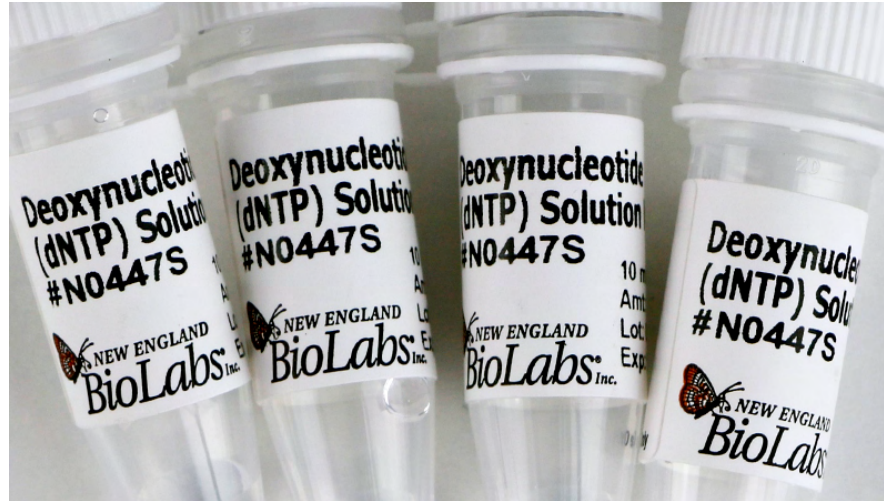
(b) Joining two molecules



DNA polymerase



DNA polymerase



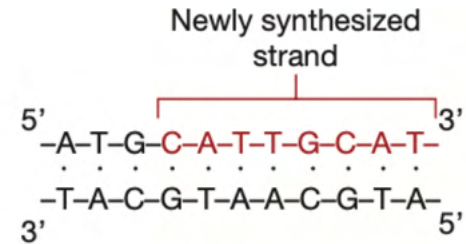
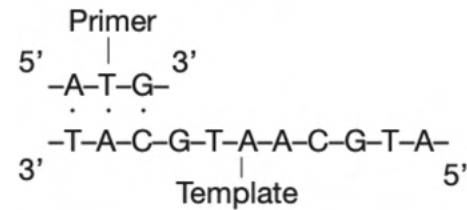
dNTPs



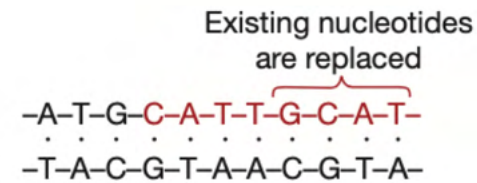
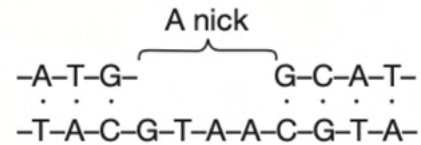
Primers

catalyzed by DNA polymerase

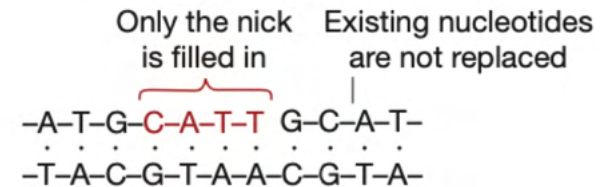
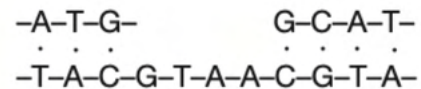
(a) The basic reaction



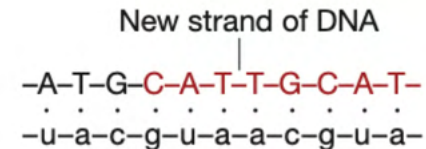
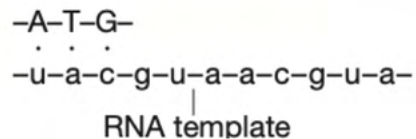
(b) DNA polymerase I



(c) The Klenow fragment



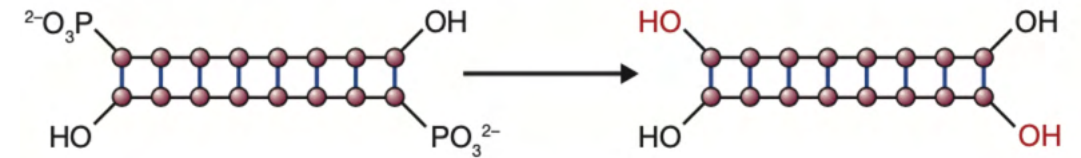
(d) Reverse transcriptase



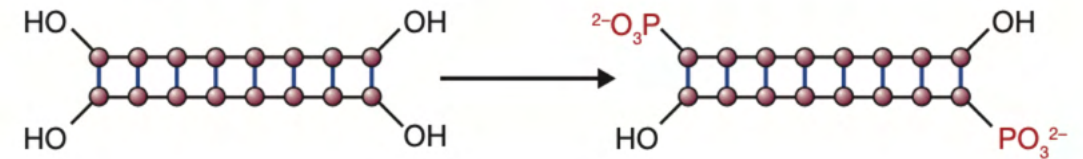
DNA modifying enzymes

- Alkaline phosphatase, removes the phosphate group present at the 5' terminus of a DNA molecule.
- Polynucleotide kinase adds phosphate groups onto free 5' termini
- Terminal deoxynucleotidyl transferase adds one or more deoxyribonucleotides onto the 3' terminus of a DNA molecule.

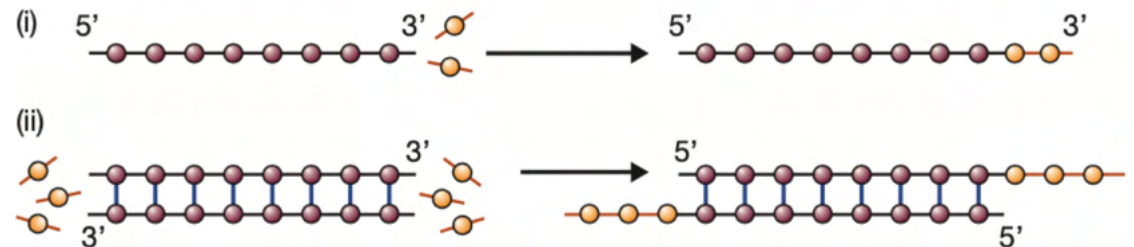
(a) Alkaline phosphatase



(b) Polynucleotide kinase

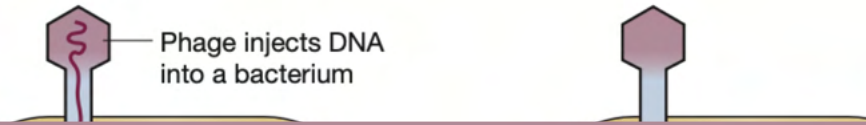


(c) Terminal deoxynucleotidyl transferase



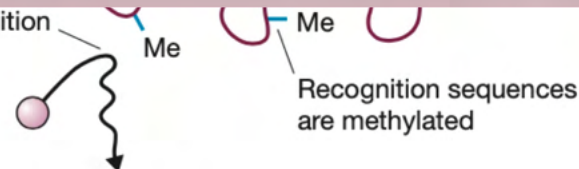
Restriction endonucleases

(a) Restriction of phage DNA



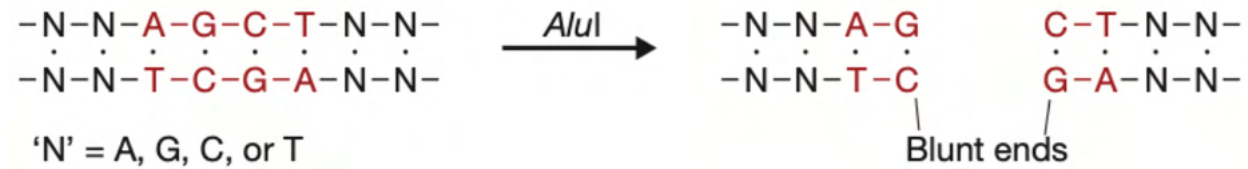
ENZYME	ORGANISM	RECOGNITION SEQUENCE*	BLUNT OR STICKY END
<i>EcoRI</i>	<i>Escherichia coli</i>	GAATTC	Sticky
<i>BamHI</i>	<i>Bacillus amyloliquefaciens</i>	GGATCC	
<i>BglII</i>	<i>Bacillus globigii</i>	AGATCT	
<i>PvuI</i>	<i>Proteus vulgaris</i>	CGATCG	
<i>PvuII</i>	<i>Proteus vulgaris</i>	CAGCTG	
<i>HindIII</i>	<i>Haemophilus influenzae</i> R _d	AAGCTT	
<i>HinI</i>	<i>Haemophilus influenzae</i> R _f	GANTC	Sticky
<i>Sau3A</i>	<i>Staphylococcus aureus</i>	GATC	
<i>AluI</i>	<i>Arthrobacter luteus</i>	AGCT	
<i>TaqI</i>	<i>Thermus aquaticus</i>	TCGA	
<i>HaeIII</i>	<i>Haemophilus aegyptius</i>	GGCC	
<i>NotI</i>	<i>Nocardia oitidis-caviarum</i>	GCGGCCGC	
<i>SfiI</i>	<i>Streptomyces fimbriatus</i>	GGCCNNNNNGGCC	Sticky

cannot bind to the recognition sequence



blunt vs sticky ends

(a) Production of blunt ends



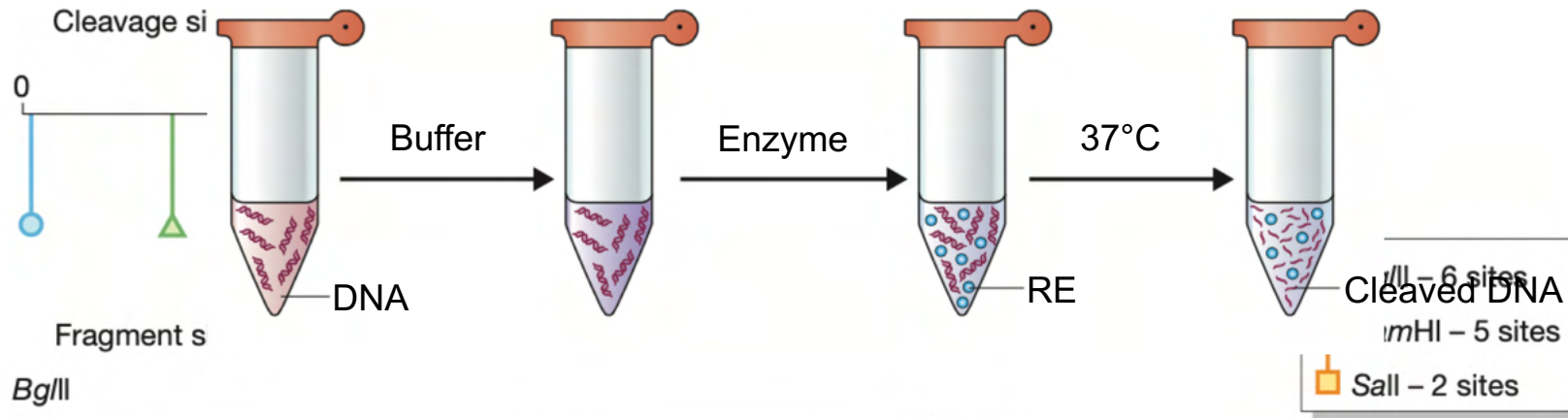
(b) Production of sticky ends



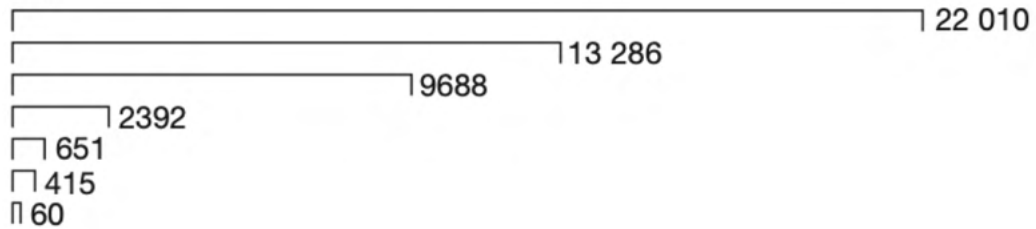
(c) The same sticky ends produced by different restriction endonucleases



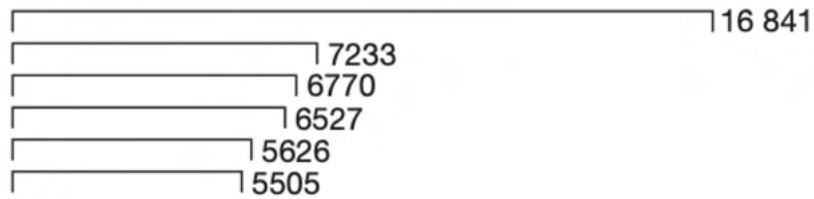
Restriction digestion @lab



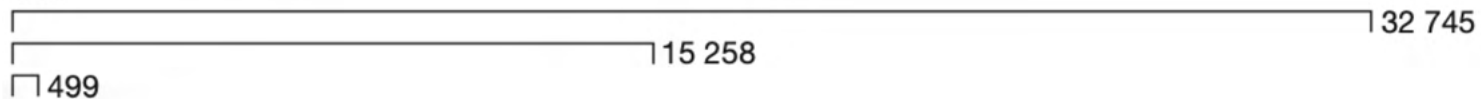
*Bgl*II



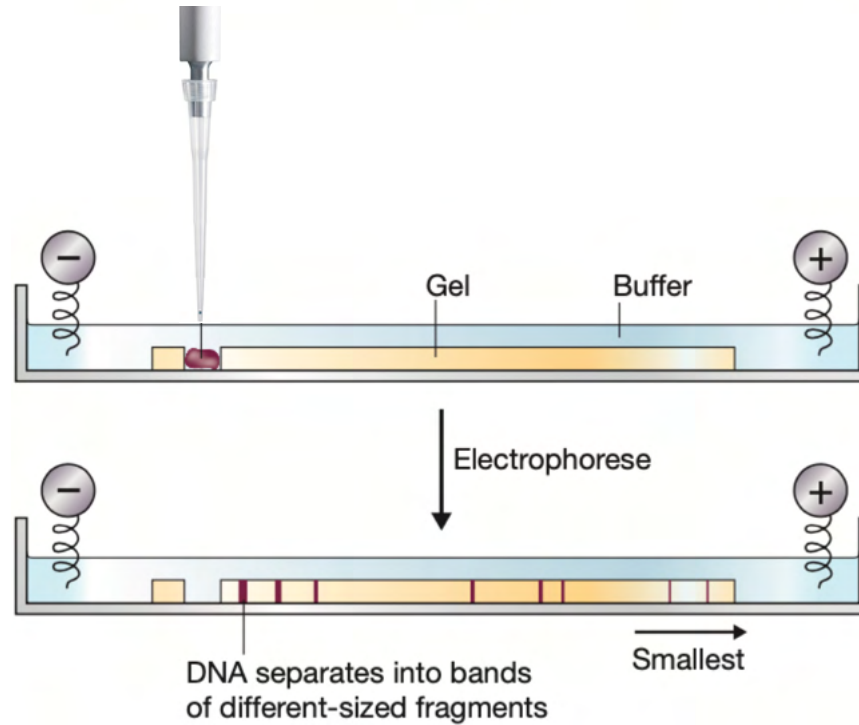
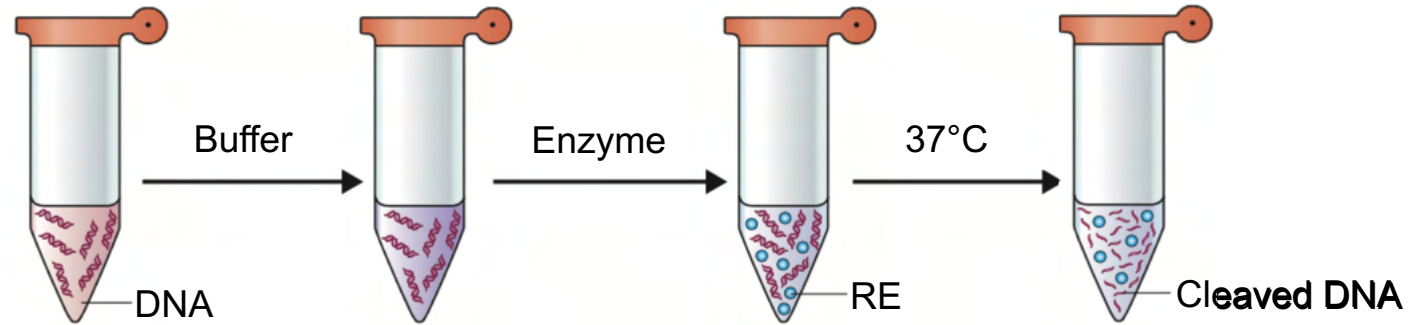
*Bam*HI



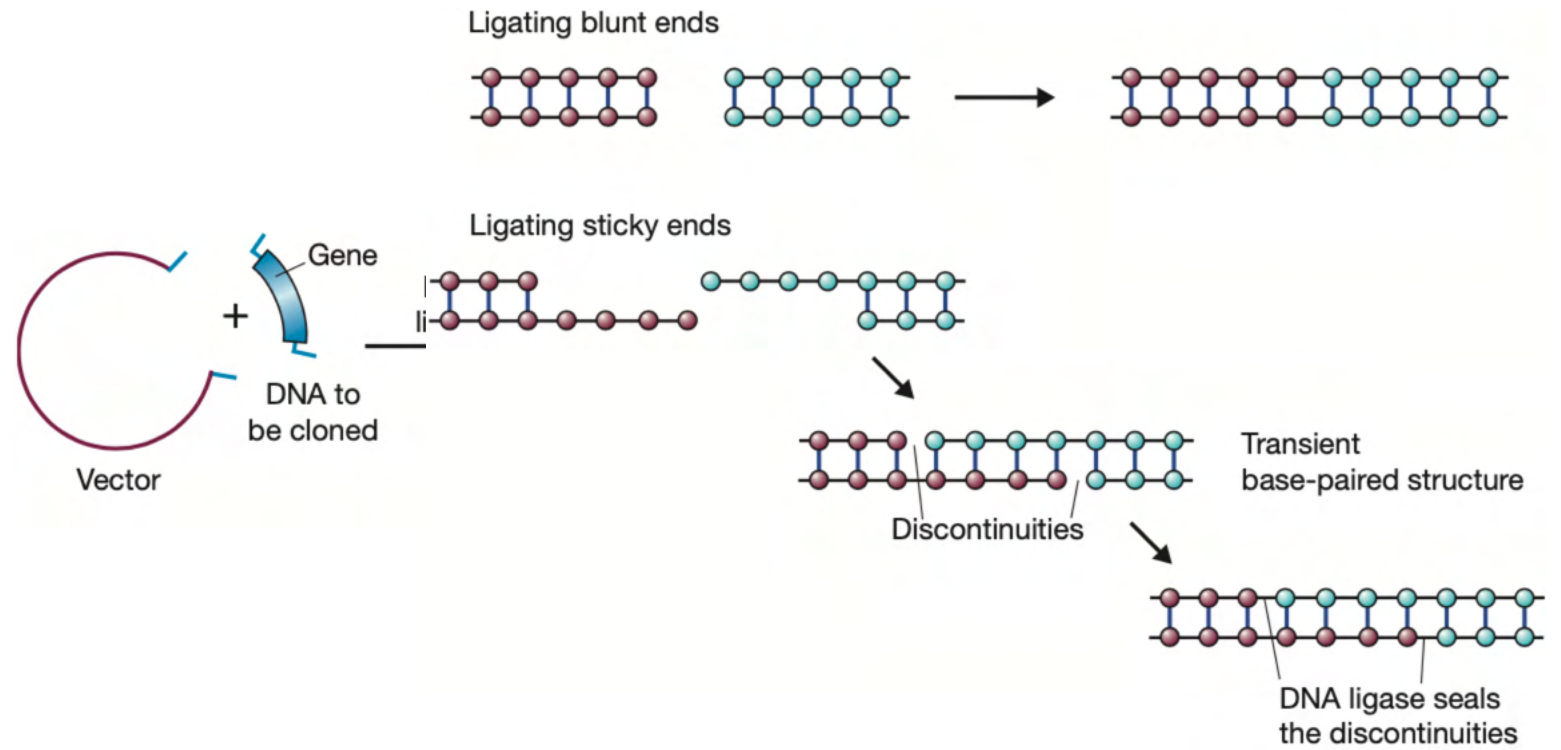
*Sal*I




Restriction digestion @lab



ligating the DNA



calculating the DNA to insert ratio

 www.insilico.uni-duesseldorf.de/Lig_Input.html 

LIGATION CALCULATOR

Please provide the following information:

.....vector size (in bp):

vector amount (in ng):

.....insert size (in bp):

Please enter the molar vector : insert ratio:

(normally a vector to insert ratio of 1 to 3 is used of cohesive end ligations. higher molar ratios can be used for blunt end ligations)

When pressing the "do calculation" button the tool calculates the required amount of insert DNA (in ng) resulting in the given molar ratio

INTRODUCTION OF DNA INTO LIVING CELLS

pcDNA3.1

