

STORAGE DEVELOPER CONFERENCE



Fremont, CA
September 12-15, 2022

BY Developers FOR Developers

A  SNIA Event

Coding and Decoding, an Experience From a Brazilian Research Center

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Marília Santos Menossi Mortari

Lenovo | ipt

Who are we?

The Institute for Technological Research (IPT) has been contributing actively during 123 years.

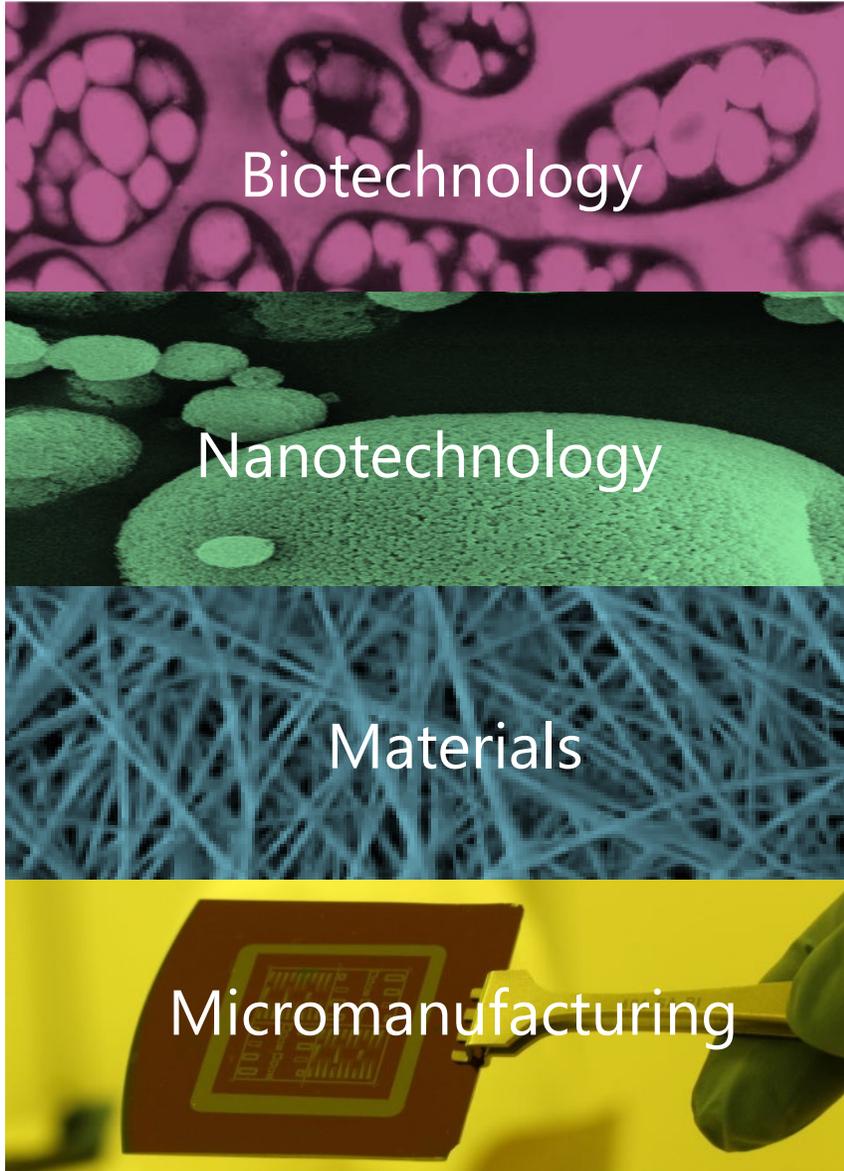
We provide technical solutions for industry, governments and society, enabling them to overcome the challenges of our time.





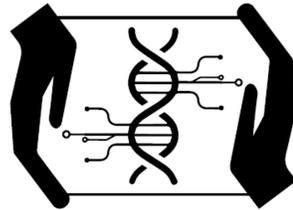
Binanom manufacturing Center

Multidisciplinary team, with doctors, masters,
and specialized technicians



Lenovo

And through this partnership, we are developing a DNA Data Storage project together



PROMETHEUS

Why DNA data storage?

Why DNA Data Storage



- DNA can be stable for thousands of years



- Potential to store Petabytes of data into 1 gram of DNA

Article | [Open Access](#) | [Published: 26 May 2022](#)

Bioarchaeological and palaeogenomic portrait of two Pompeians that died during the eruption of Vesuvius in 79 AD

[Gabriele Scorrano](#) , [Serena Viva](#), [Thomaz Pinotti](#), [Pier Francesco Fabbri](#) , [Olga Rickards](#) & [Fabio Macciardi](#) 

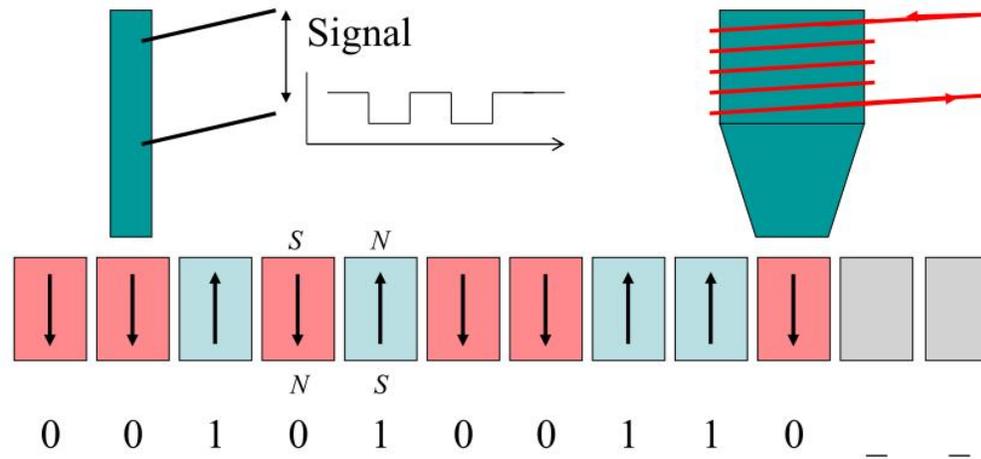
[Scientific Reports](#) **12**, Article number: 6468 (2022) | [Cite this article](#)

- DNA reading will never be outdated and will always be improved

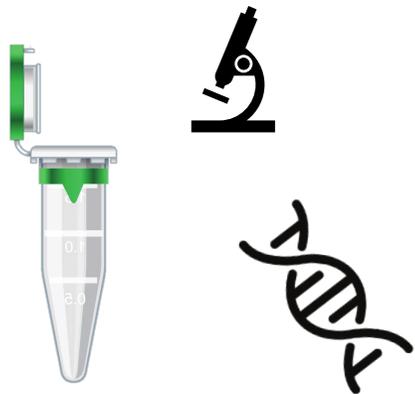
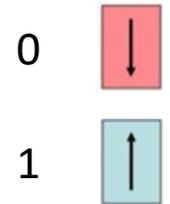
How data is stored in DNA



LTO Tape



Binary code



Quaternary code



DNA data storage pipeline

1.

Converting information to binary code



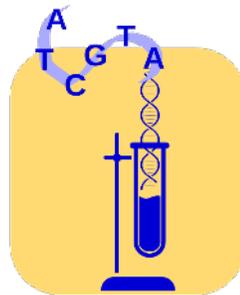
2.

Converting binary code to DNA code



3.

DNA Synthesis



4.

Storage



5.

Recovery



6.

Sequencing

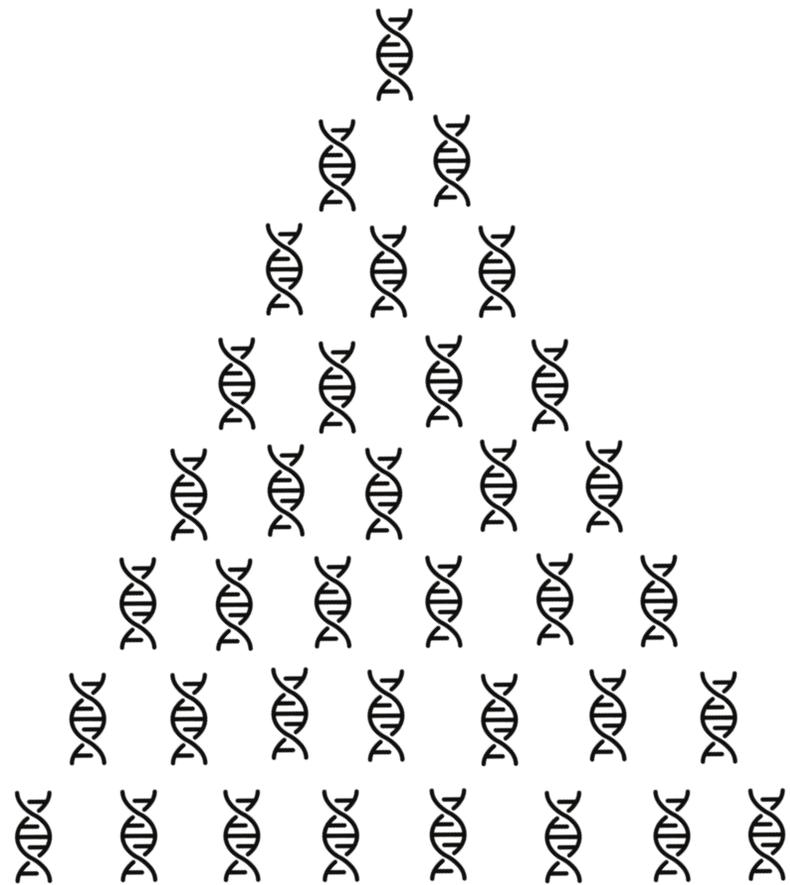
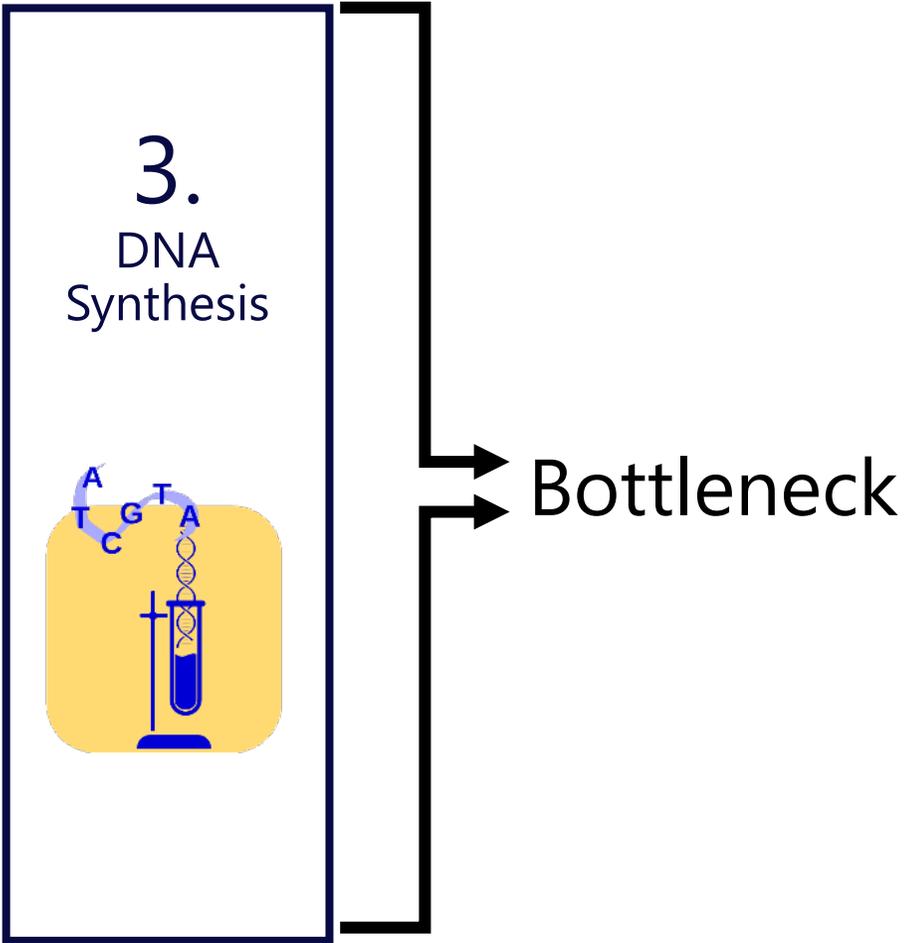


7.

Decoding

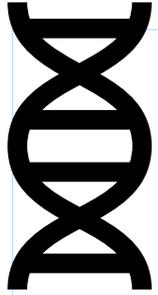


DNA data storage pipeline

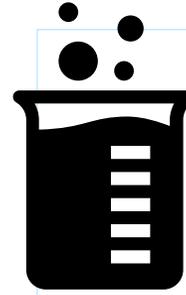


Billions of unique sequences to store Petabytes of data!

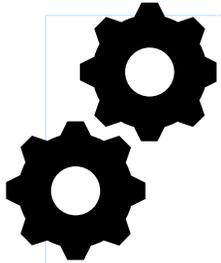
Scope



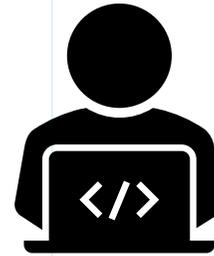
Enzymatic synthesis



Chemical synthesis



Process miniaturization



Coding and decoding



Sequencing methods

Chemical DNA synthesis

Advantages:

- Standardized Technique -> Miniaturize the process;
- Fine synthesis control ;

Disadvantages:

- Hazardous Chemicals;



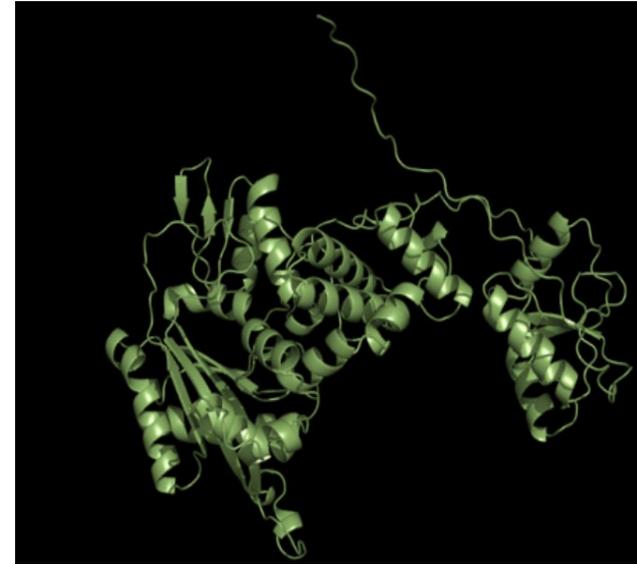
Enzymatic DNA synthesis

Advantages:

- Novel Technique -> Requires ;
- Environmentally friendly process;

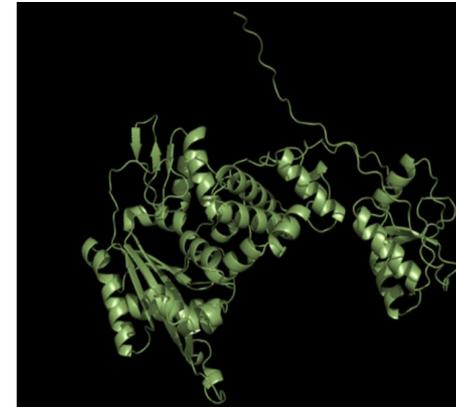
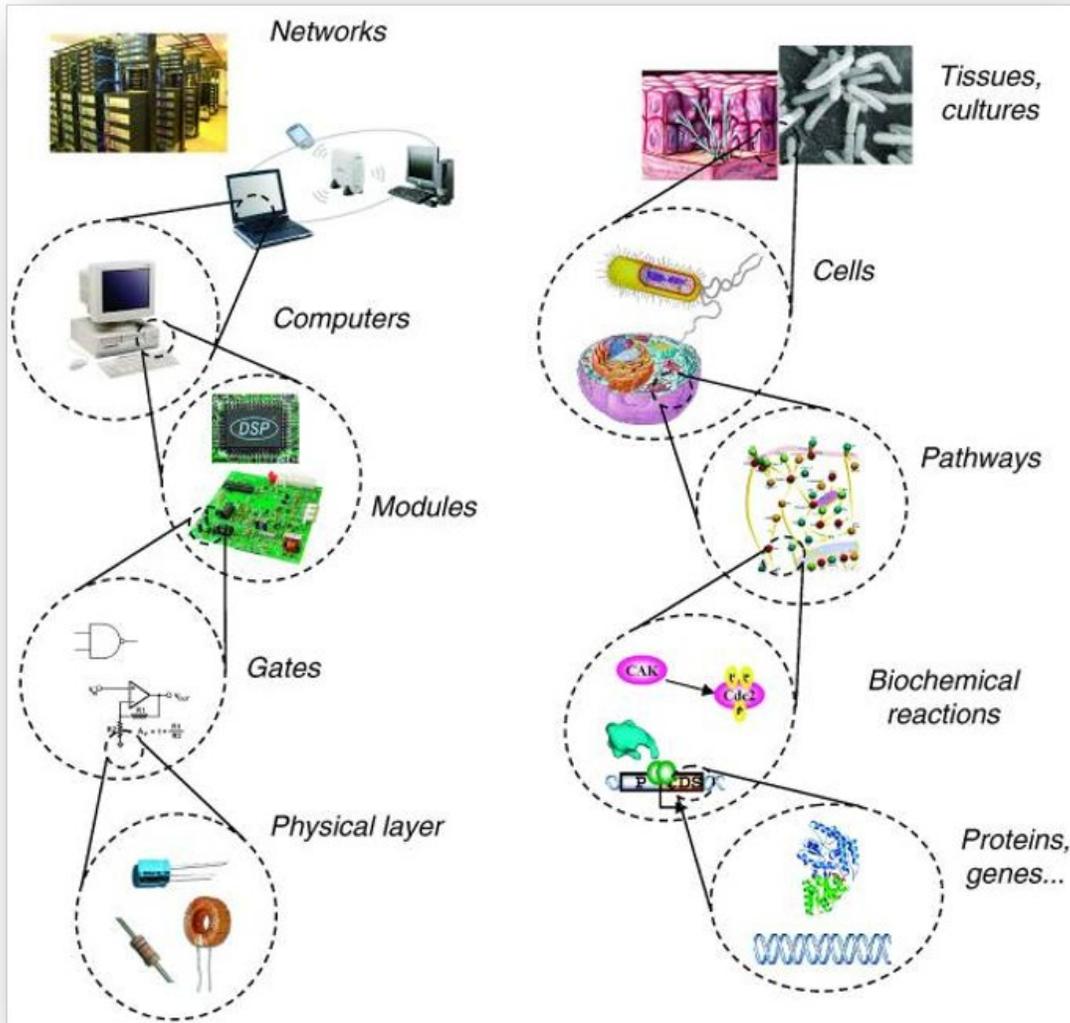
Disadvantages:

- Synthesis control is not simple;



TdT enzyme has been adopted for DNA Data Storage Applications

Biological Systems to manufacture DNA



Enzymes act like the head of a hard disk



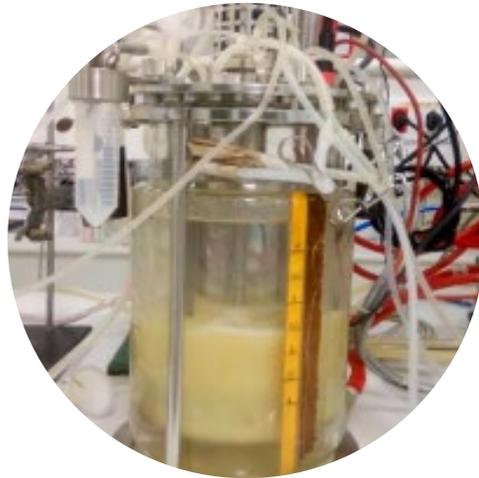
DNA is the physical medium for information being recorded

Development of new Enzymes

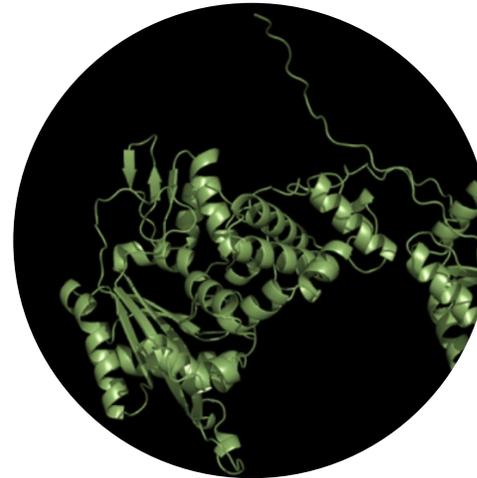
Mass production of TdT enzyme is important to reduce costs of DNA synthesis .



Programmed
Bacteria



Large Scale
Production



Enzyme
Purification

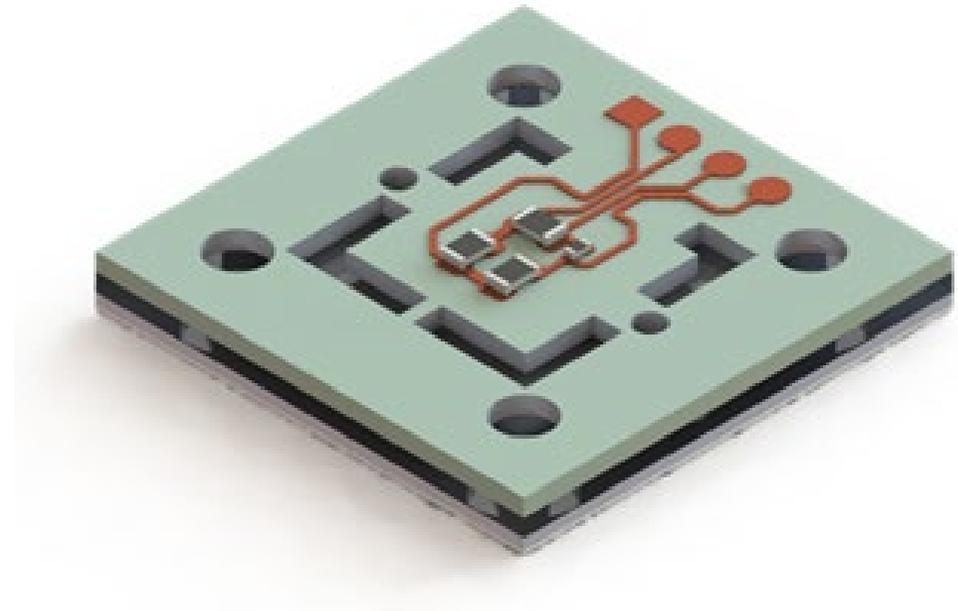
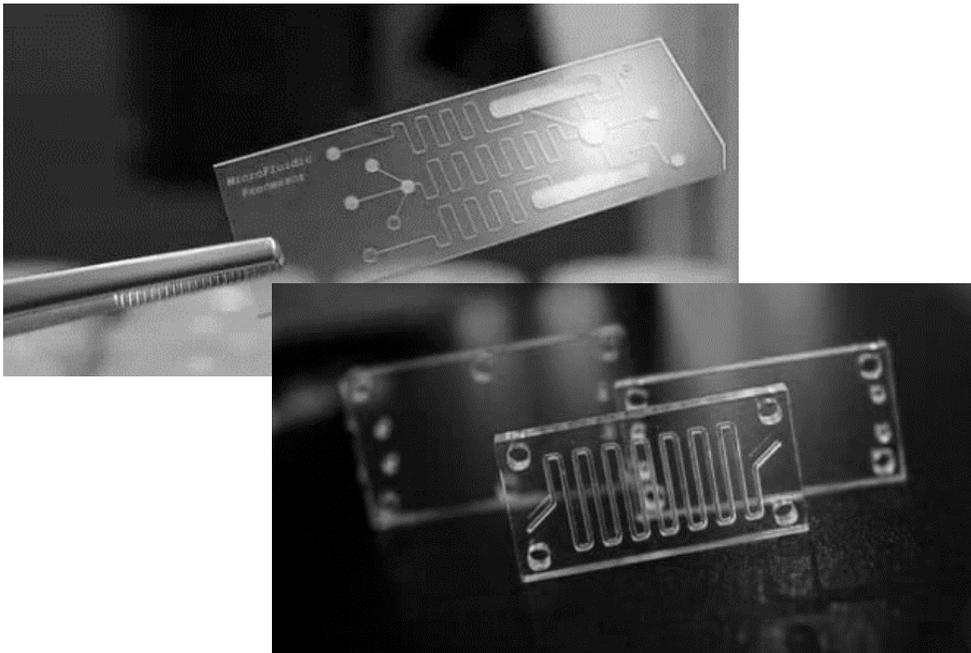


Application in
DNA Synthesis

Developing microdevices

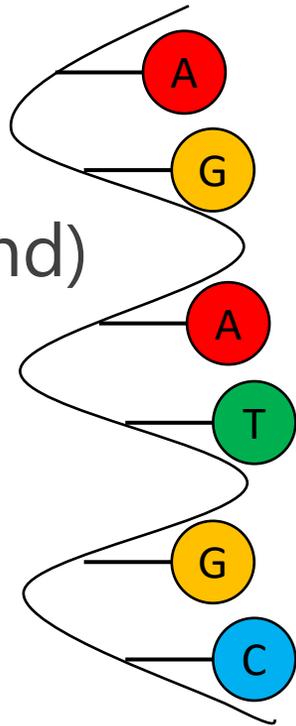
We have been developing a microdevice and working to improve the synthesis process.

- Parallelization of DNA Synthesis
- Working with small volumes



DNA Chemical synthesis

DNA
(single strand)



Phosphoramidite

A Adenine

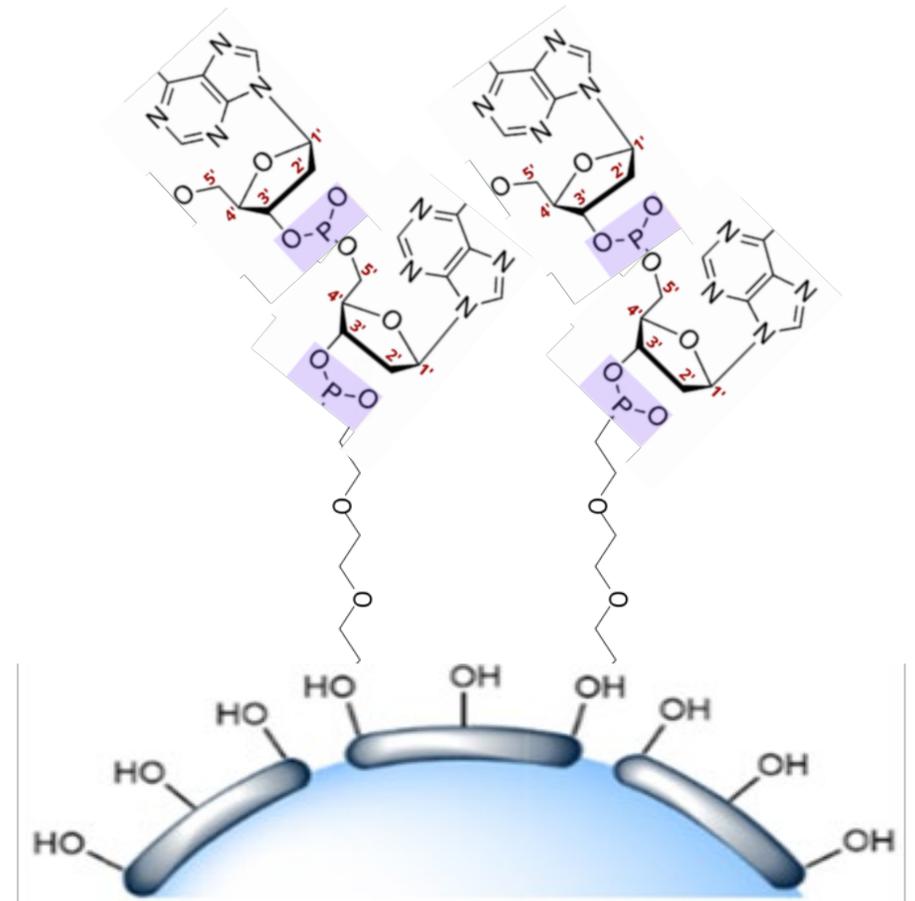
T Thymine

C Cytosine

G Guanine

linker

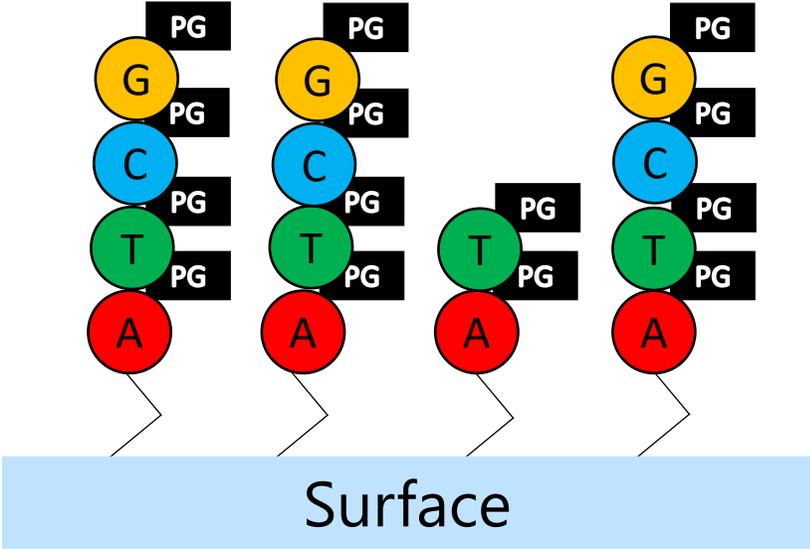
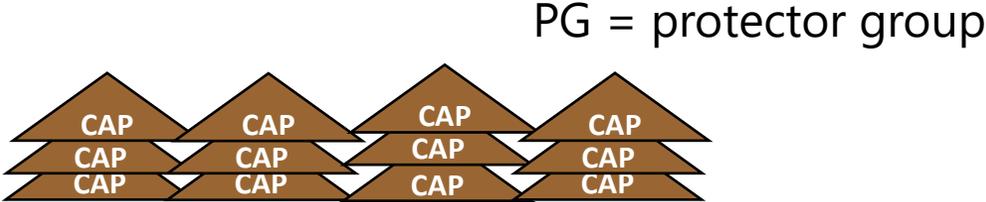
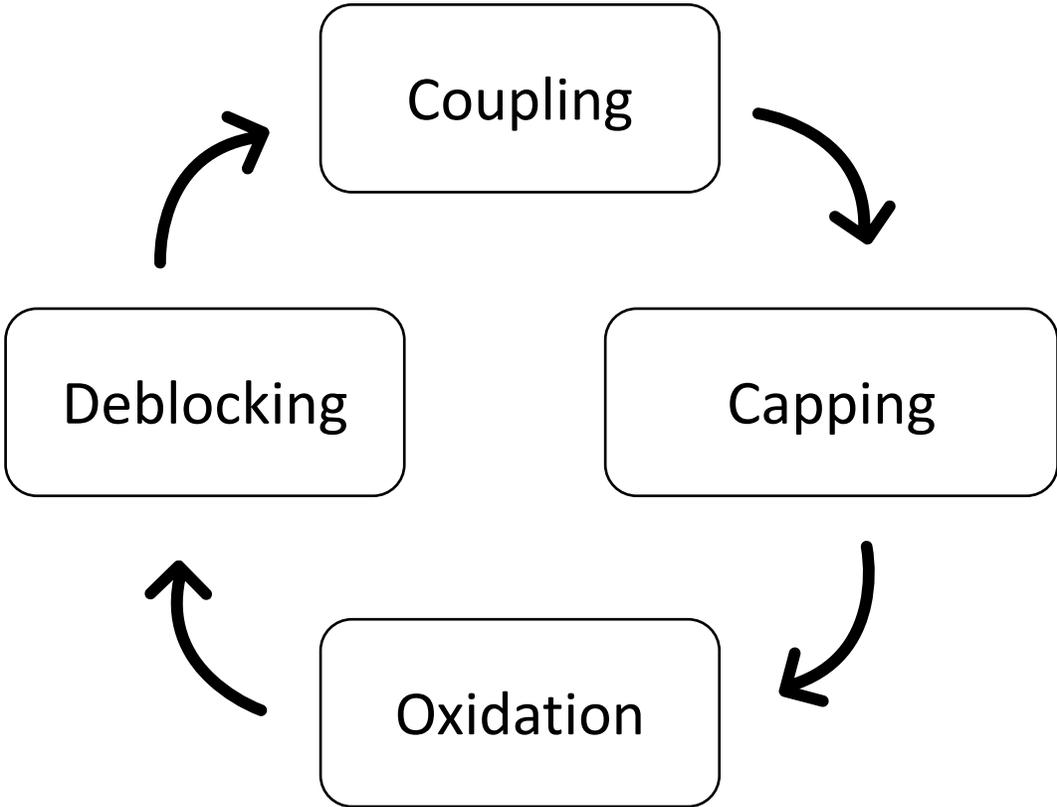
surface



<https://www.twistbioscience.com/blog/science/simple-guide-phosphoramidite-chemistry-and-how-it-fits-twist-biosciences-commercial>

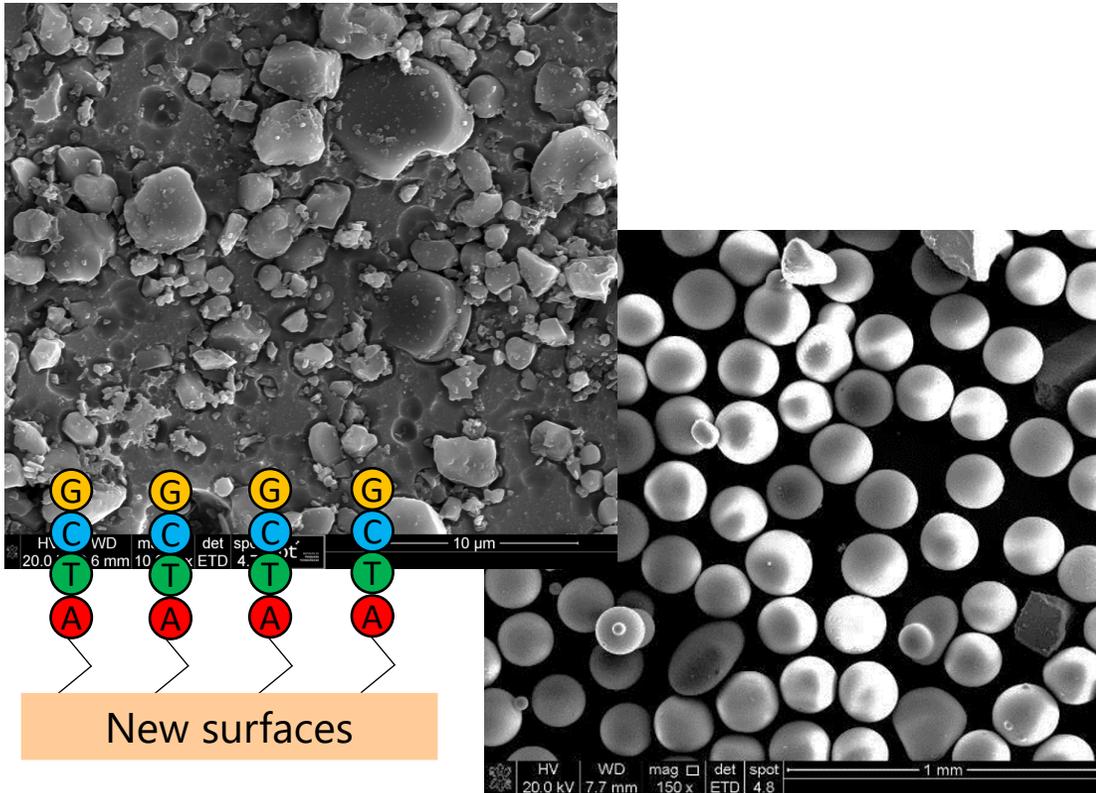
Chemical synthesis

A T C G



DNA synthesis

- On different surfaces



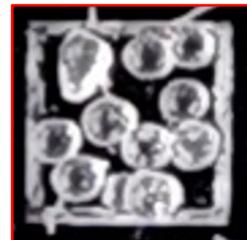
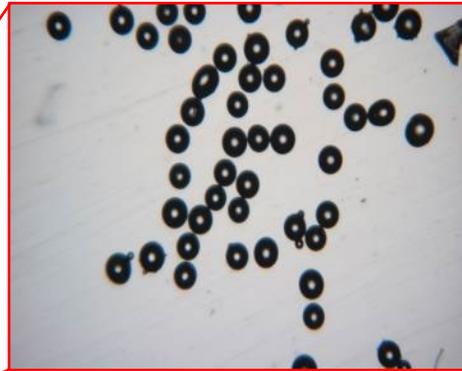
- In microreactors



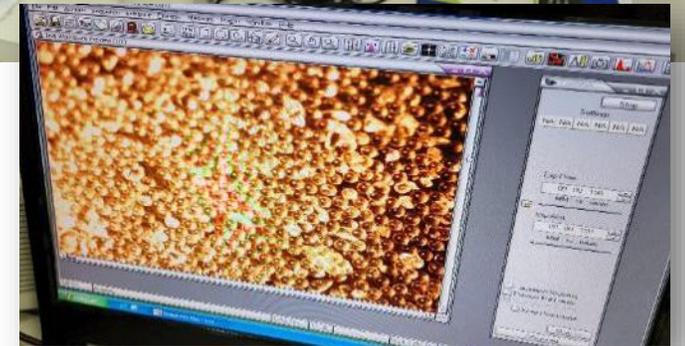
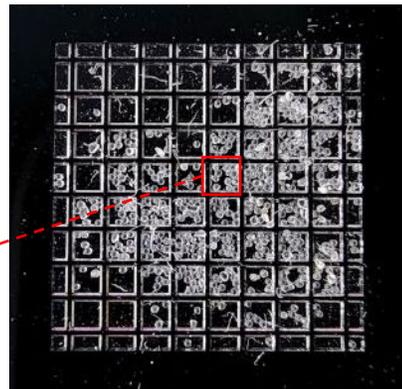
New particles for DNA synthesis



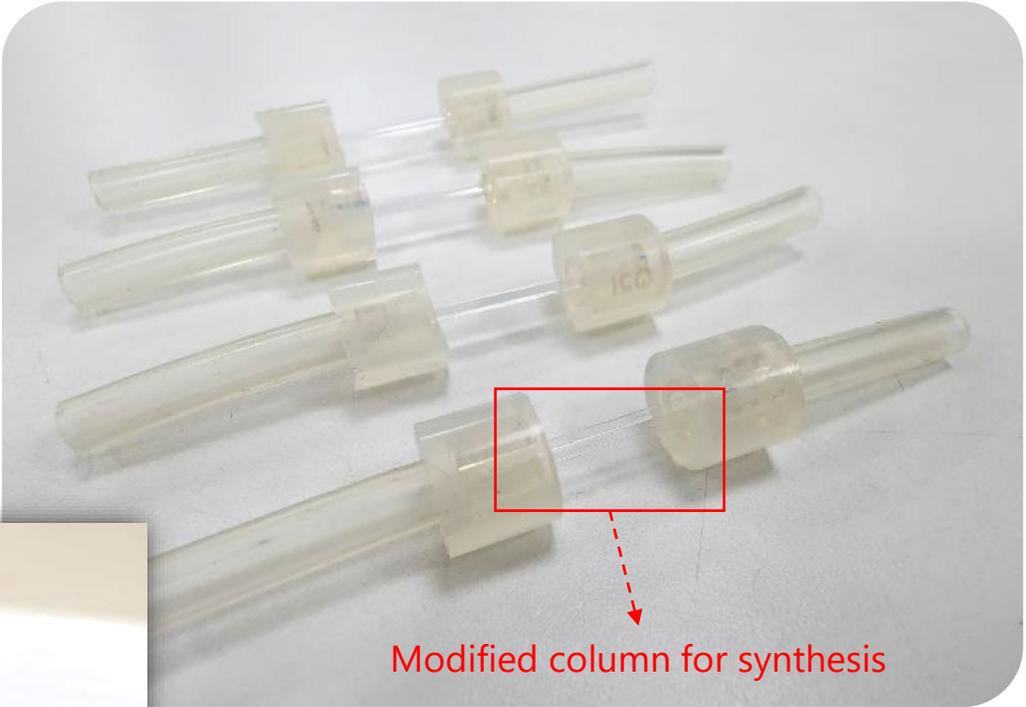
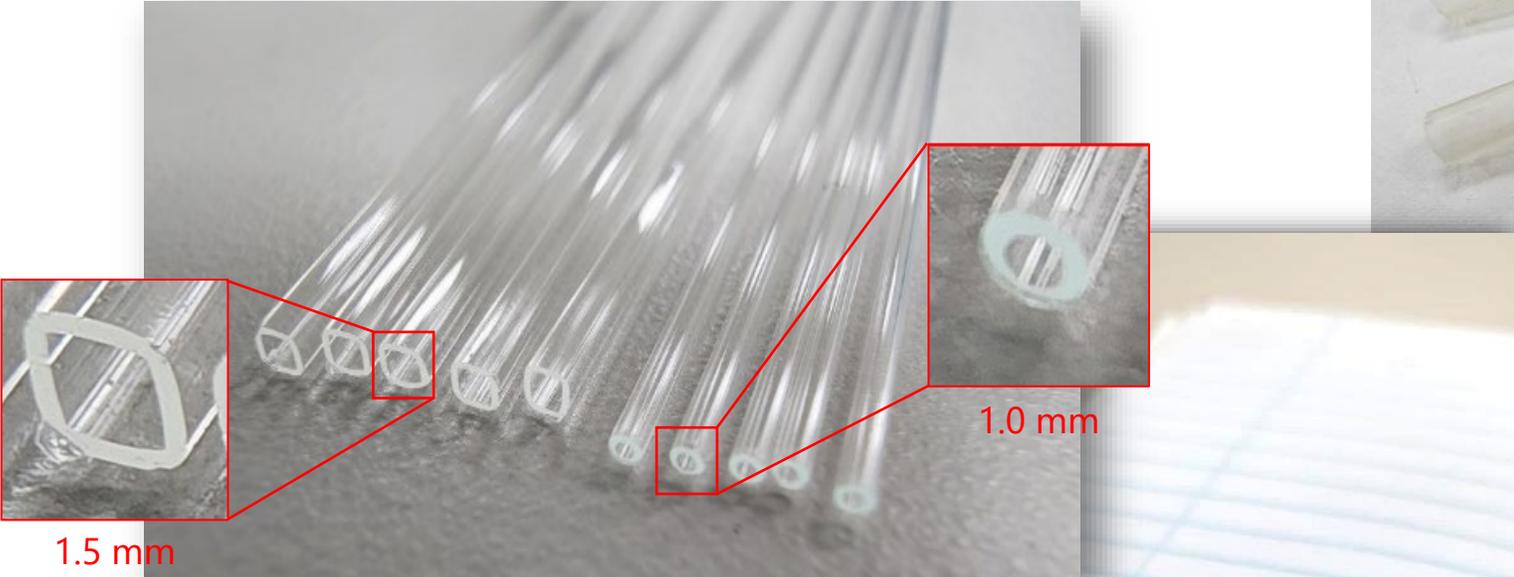
Macro appearance
Reference: SD Card



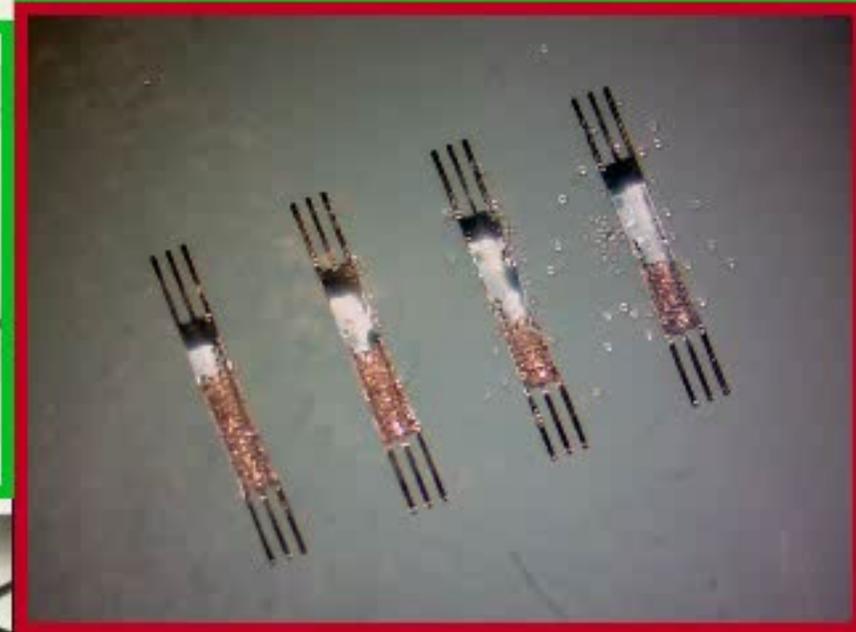
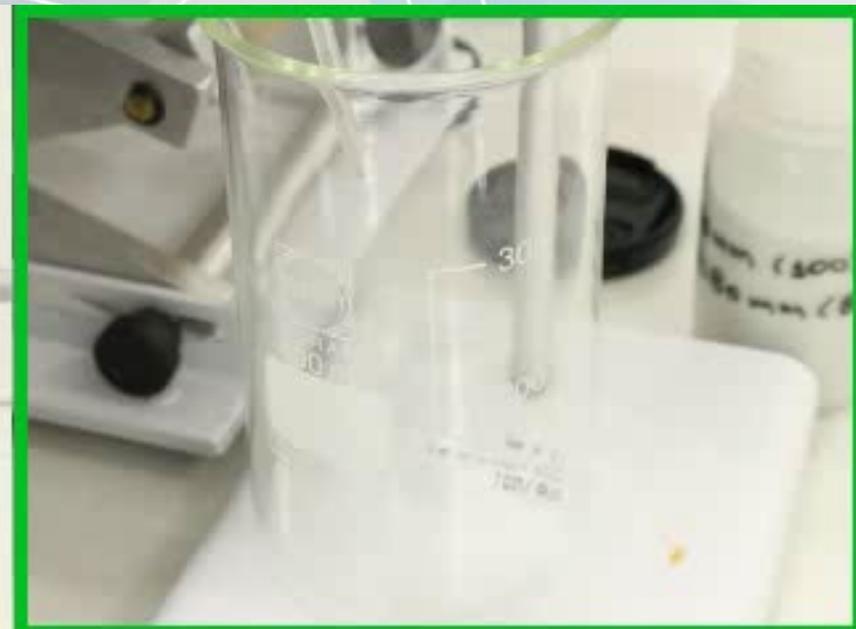
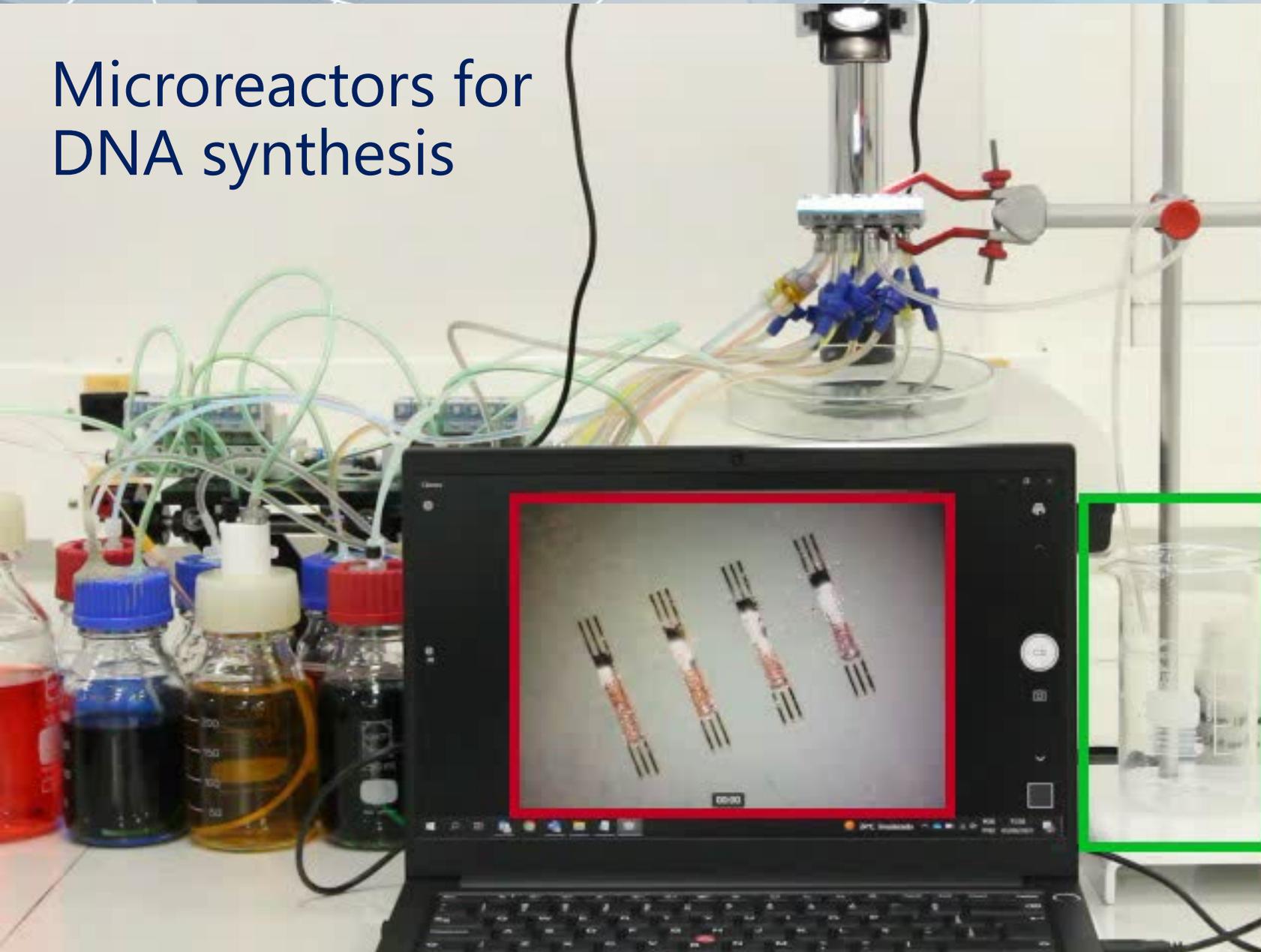
Square size
 ≈ 1 mm



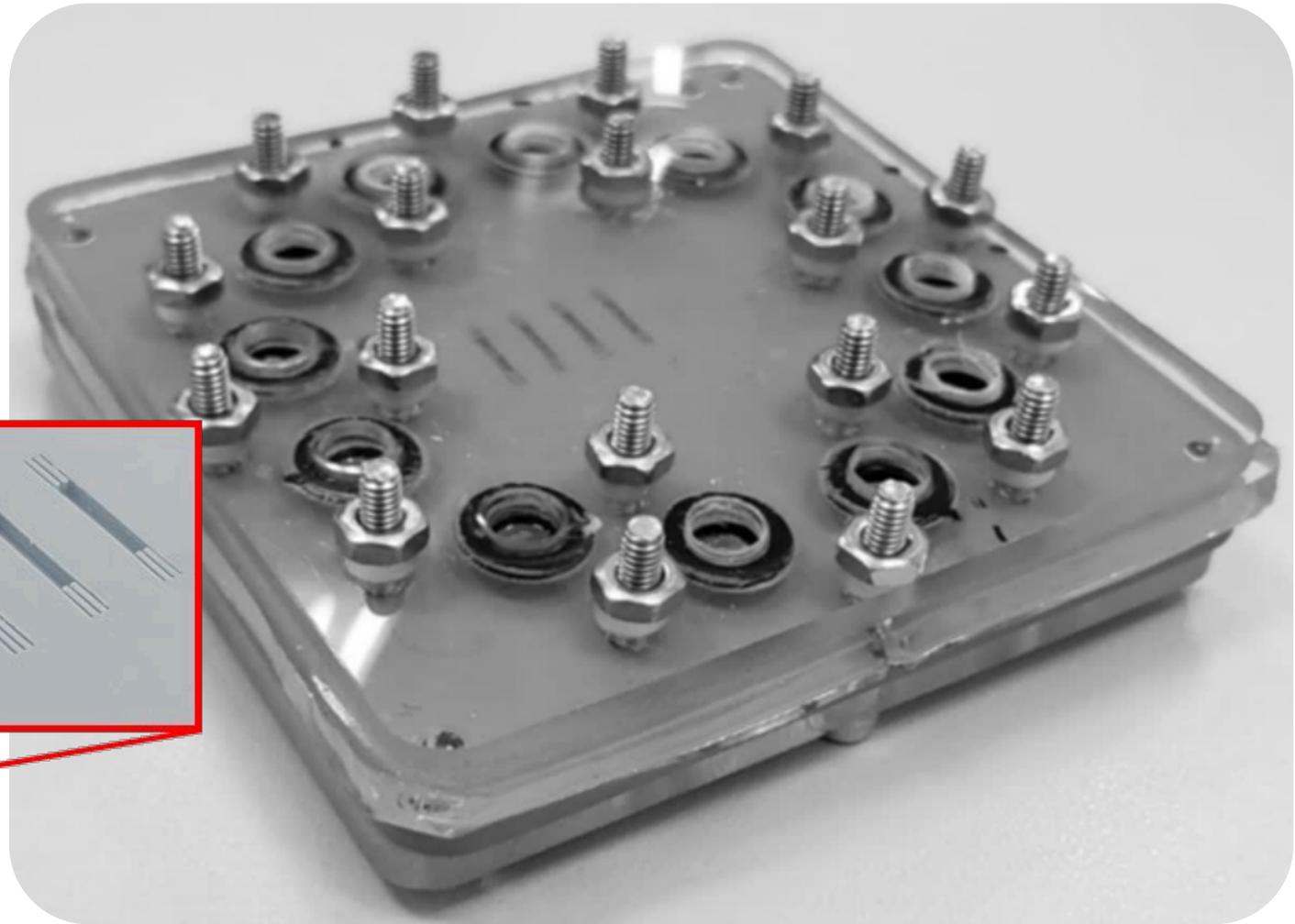
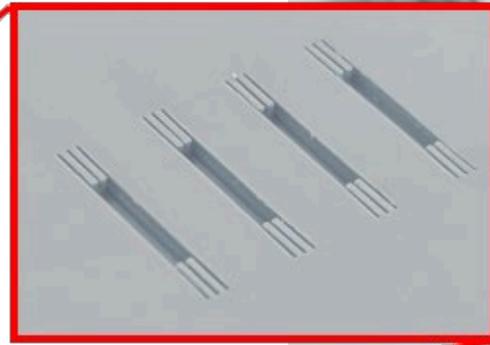
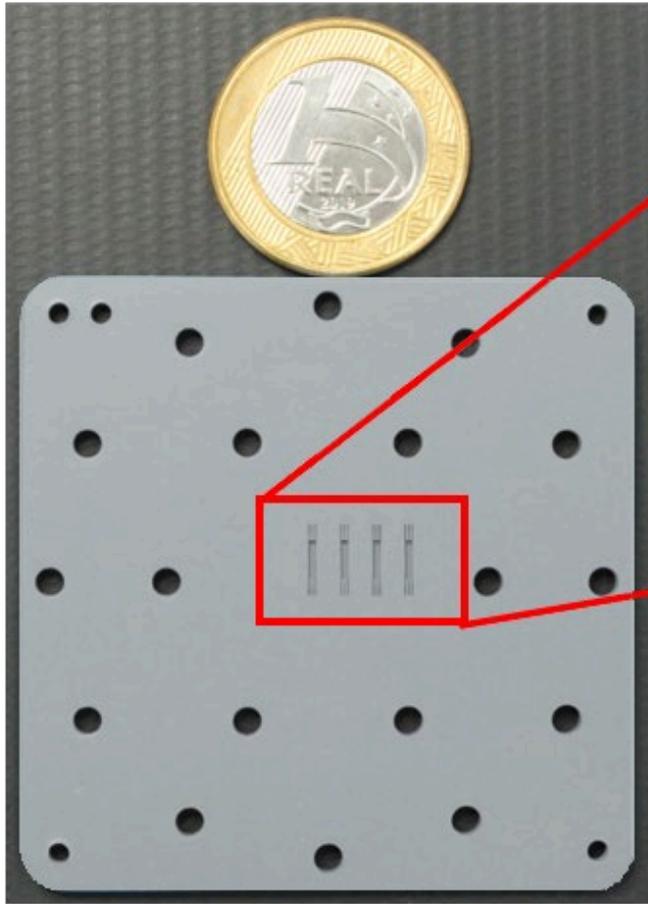
Columns for DNA synthesis

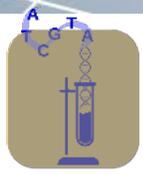


Microreactors for DNA synthesis



Microreactors for DNA synthesis



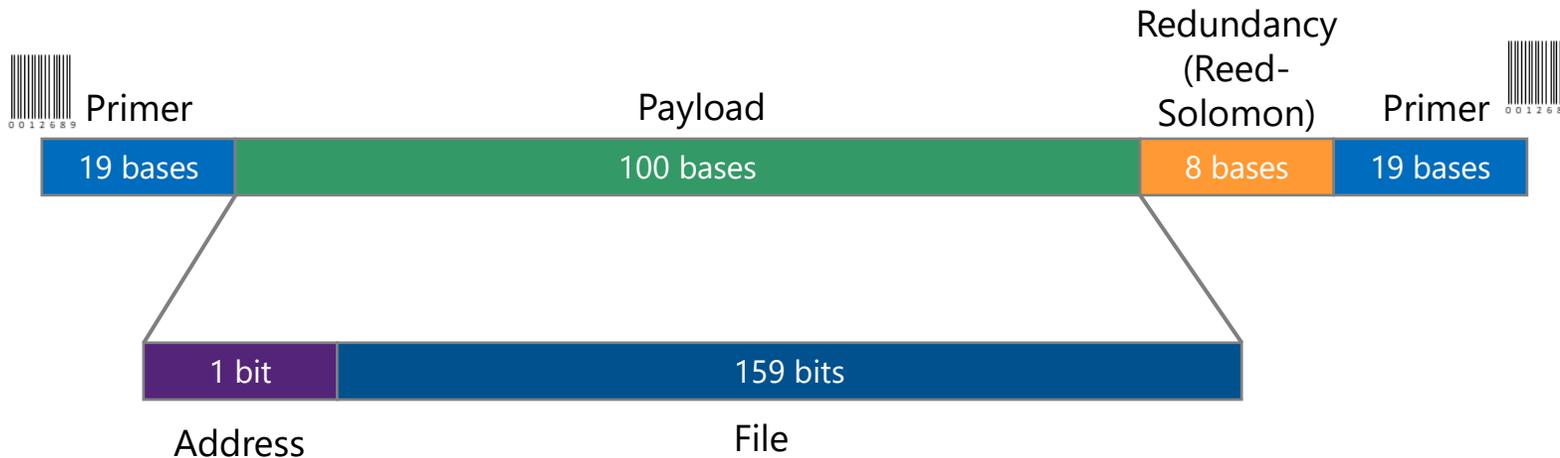


A little part of our results so far

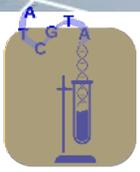
Encoded file: 38byte .txt file containing

IPT and Lenovo, a successful partnership!

2 DNA sequences with 146 bases each



Bases = nitrogeneous bases = A T C G



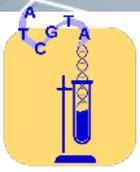
Forward Primer

DNA sequences

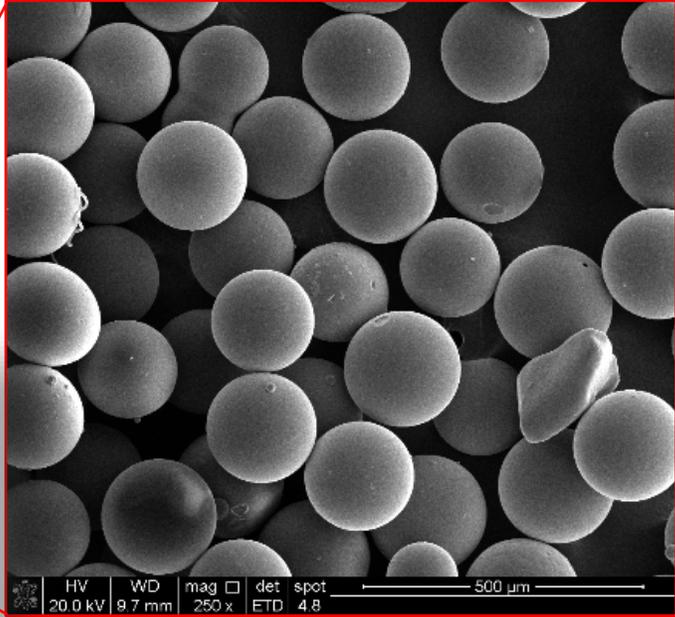
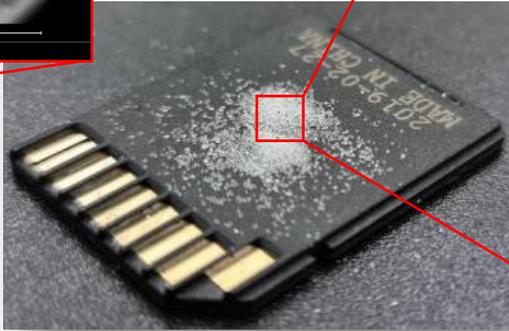
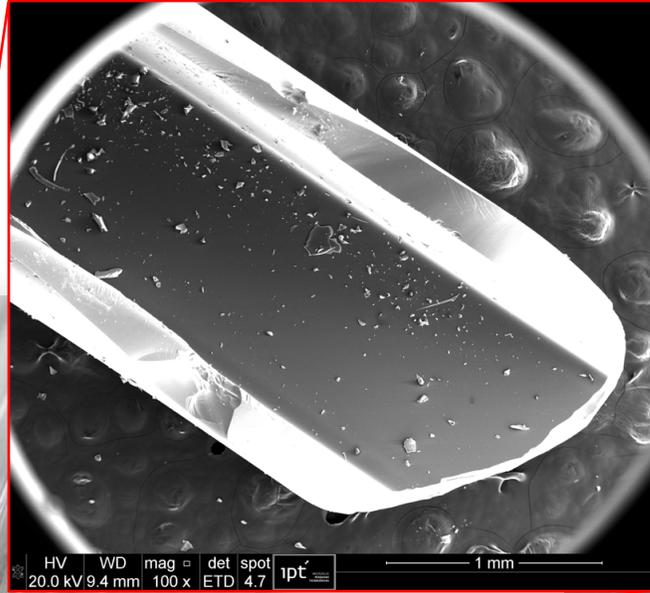
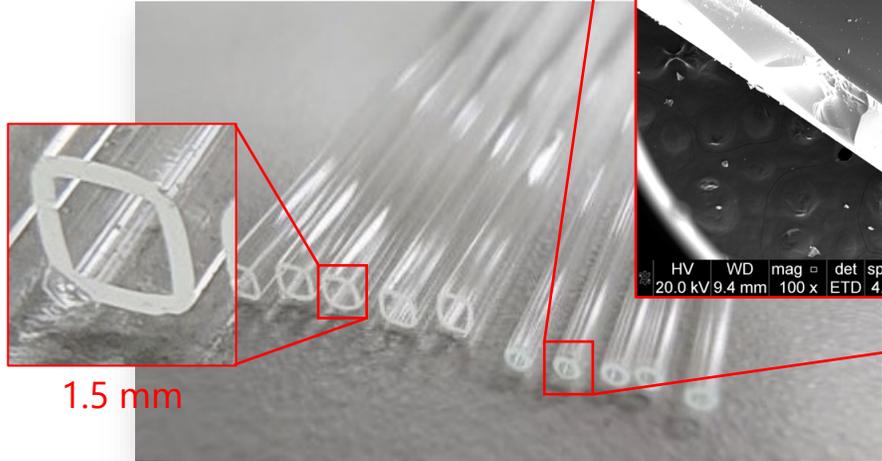
5' **CACGACGTTGTAAAACGAC** **AGACAGGAGAAGCGTACTATATAAGGCCACAGACGATAA**
GGTGCTATCCGGTAGCATGCTGCACGACTATATCGTGTACGGTCACGCTATATCGCATCACG
GGACGCCGGGTCATAGCTGTTTCCTG

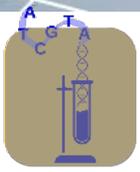
5' **CACGACGTTGTAAAACGACT** **TCGTGGCAGATCAGTCCATAGCCGTCCAGACAAGAACAGT**
ACGGCCAAGAACATATCGTCCCAGATCCGACCATATCCTCTCTGATACGCCATATAACACAG
AGGGATGGGTCATAGCTGTTTCCTG

Reverse Primer

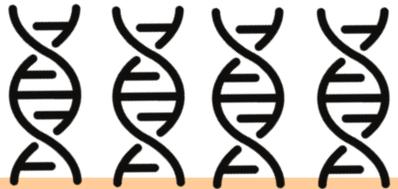


Chemical DNA synthesis on different surfaces





Two options for storage of the synthesized DNA



Surface of the particles or columns

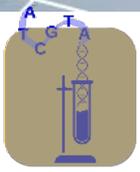


DNA storage



Surface storage with DNA





DNA storage



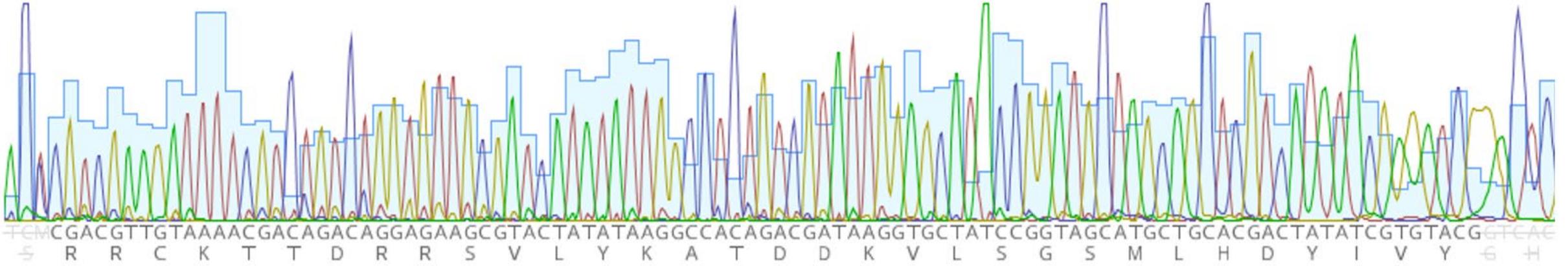
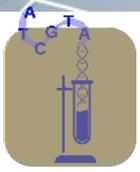
Creating copies by PCR methodology

PCR = Polymerase Chain Reactions

Surface storage
with DNA

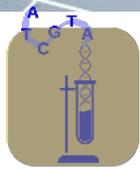


Sequencing



5' CACGACGTTGTAAAACGAC AGACAGGAGAAGCGTACTATATAAGGGCCACAGACGATAAGGGTGCTATCCGGT
AGCATGCTGCACGACTATATCGTGTACGGTCACGCTATATCGCATCACGGGACGCCGGGTCATAGCTGTTTCCTG

5' CACGACGTTGTAAAACGACT TCGTGGCAGATCAGTCCATAGCCGTCCAGACAAGAACAGTACGGCCAAGAAC
ATATCGTCCCAGATCCGACCATATCCTCTCTGATACGCCATATAACACAGAGGGATGGGTCATAGCTGTTTCCTG



ATCTGCA
ATCTGCG
ATCAGCA



Primer

Payload

Redundancy



Primer

ATCTGCA
ATCTGCG
ATCAGCA
ATCTGCA
ATCTGTA
ATATGCA

Alignment and
consensus



Detach of primers



Check of errors via
logical redundancy
(Reed-Solomon)

```

primer |-----|
read1  TC*CGACGTTGTA AAAACGACAGACAGGAGAAGCGTACTATATAAGGCCACAGACGATAAAGGTGCTATCCGGTAGCATGCTGCACGACTATATCGTGTACGGTCACGC*--**C*---*ACG-----|-----|
read2  -----G*A-----*****TAAGGC-*CAGACGATAAAGGTGCTATCCGGTAGCATGCTGCACGACTATATCGTGTACGGTCACSCATATCGCATCACGGGACGCCGGGTCATAGCTGTTTC**GA
consensus C*CGACGTTGTA AAAACGACAGACAGGAGAAGCGTACTATATAAGGCCACAGACGATAAAGGTGCTATCCGGTAGCATGCTGCACGACTATATCGTGTACGGTCACGCTATATCGCATCACGGGACGCCGGGTCATAGCTGTTTC**G
original CACGACGTTGTA AAAACGACAGACAGGAGAAGCGTACTATATAAGGCCACAGACGATAAAGGTGCTATCCGGTAGCATGCTGCACGACTATATCGTGTACGGTCACGCATATCGCATCACGGGACGCCGGGTCATAGCTGTTTCCTG
errors      X                                                                                                                                           XX
  
```

```

primer |-----|
read1  TC*CGACGTTGTA AAAACGACTCGTGGCAGATCAGTCCATAGCCGTCCAGACAAGAACAGTACGGCCAAGAACATATCGTCCCAGATCCGACCAT*-CCTCTC-*A**--GC*****A-----|-----|
read2  -----****G---T---CGT-CAGAC-AGAACAGTACGGCCAAGAACATATCGTCCCAGATCCGACCATATCCTCTCTGATACGCCATATAACACA*AGGGATGGGTCATAG*TGTTTC**GA
consensus C*CGACGTTGTA AAAACGACTCGTGGCAGATCAGTCCATAGCCGTCCAGACAAGAACAGTACGGCCAAGAACATATCGTCCCAGATCCGACCATATCCTCTCTGATACGCCATATAACACA*AGGGATGGGTCATAG*TGTTTC**G
original CACGACGTTGTA AAAACGACTCGTGGCAGATCAGTCCATAGCCGTCCAGACAAGAACAGTACGGCCAAGAACATATCGTCCCAGATCCGACCATATCCTCTCTGATACGCCATATAACACAGAGGGATGGGTCATAGCTGTTTCCTG
errors      X                                                                                                                                           X           XX
  
```

Inverse mapping
back to bit
sequence

File reassembling
according to
segment addresses

0101
1001
0110

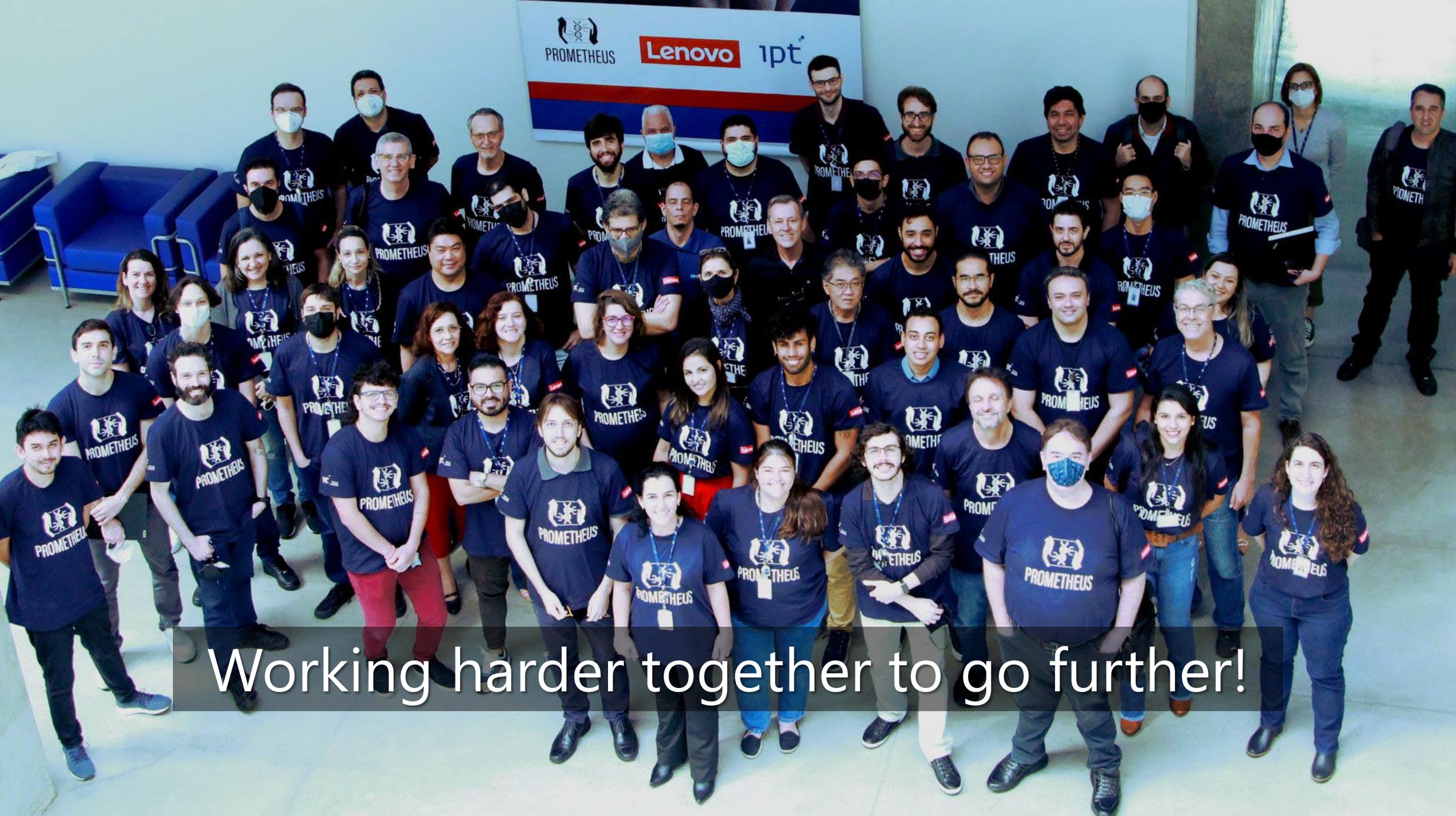
010 0101001
010 1111101
101 0101010
0100100101001
1110101111101
0100100101001



Ongoing work

- Select the best surface for:
 - DNA synthesis
 - Recover of the synthesized DNA
- Develop a DNA storage protocol
- DNA synthesis inside the microfluidic device





Working harder together to go further!

Thank you!

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Marília Santos Menossi Mortari (mariliam@ipt.br)