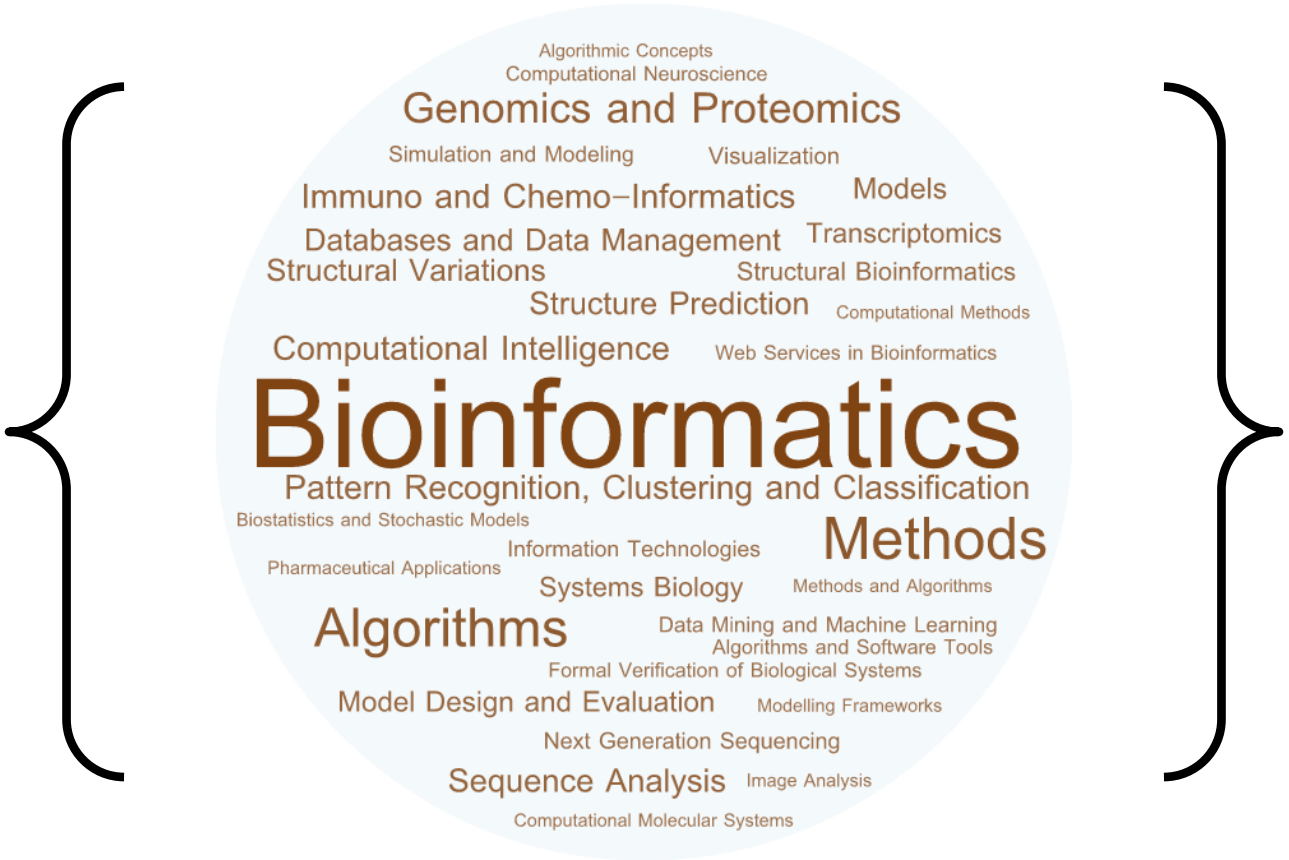
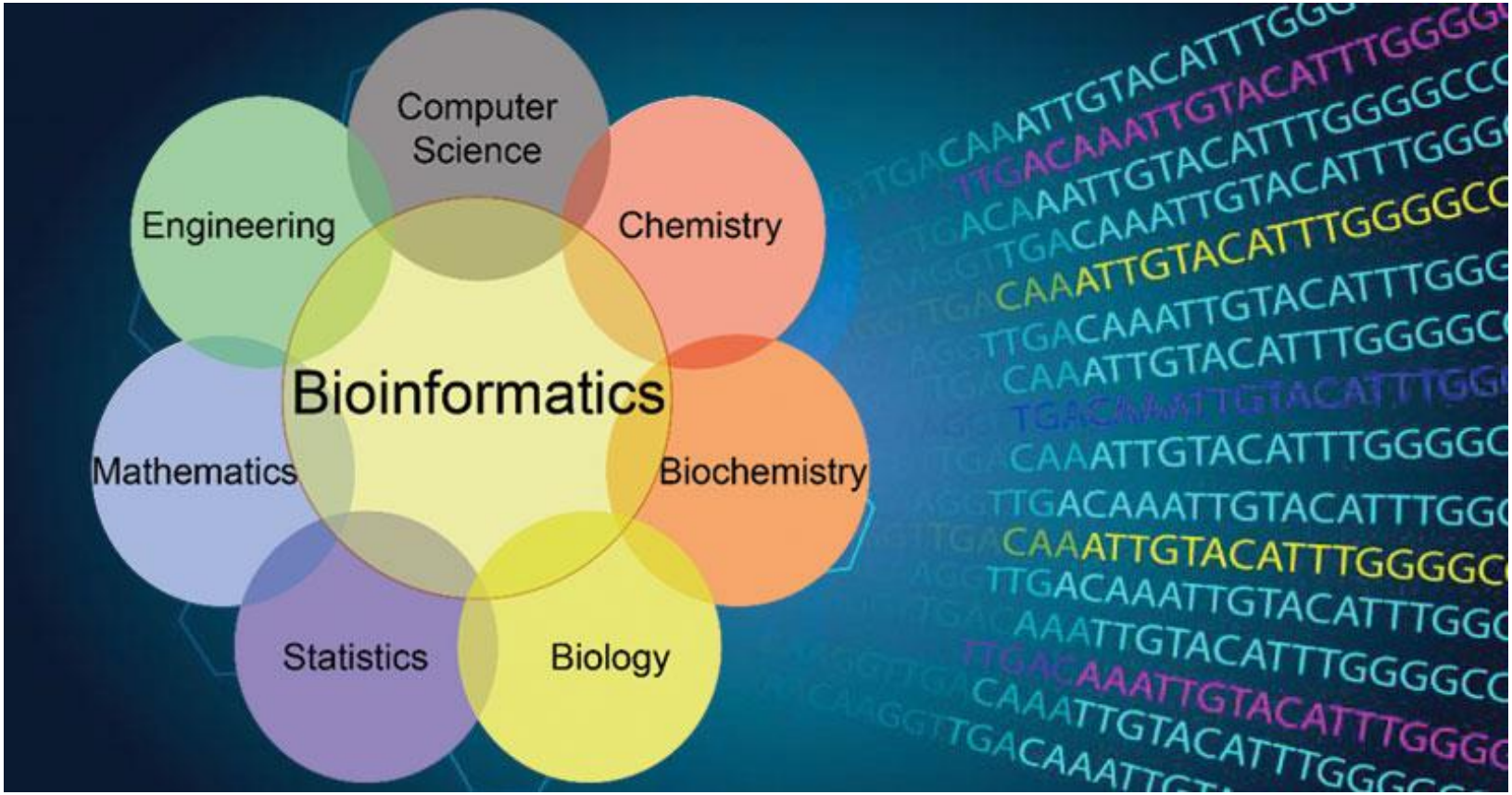
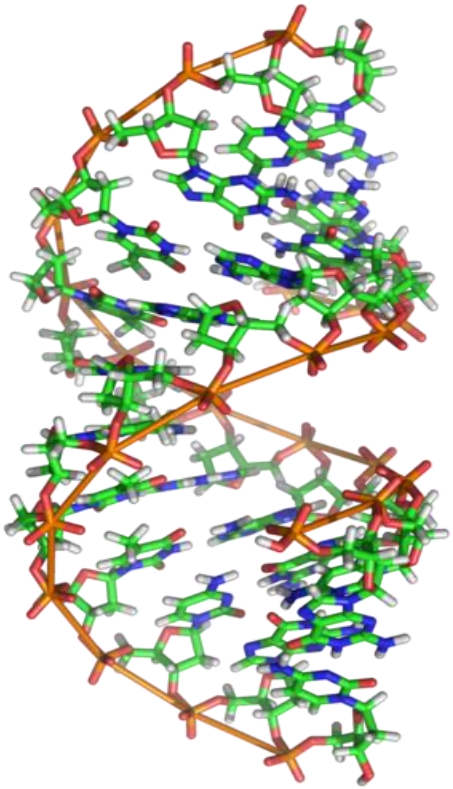
José A. Barbero Aparicio
Antonio Canepa Oneto
Gadea Lucas Pérez

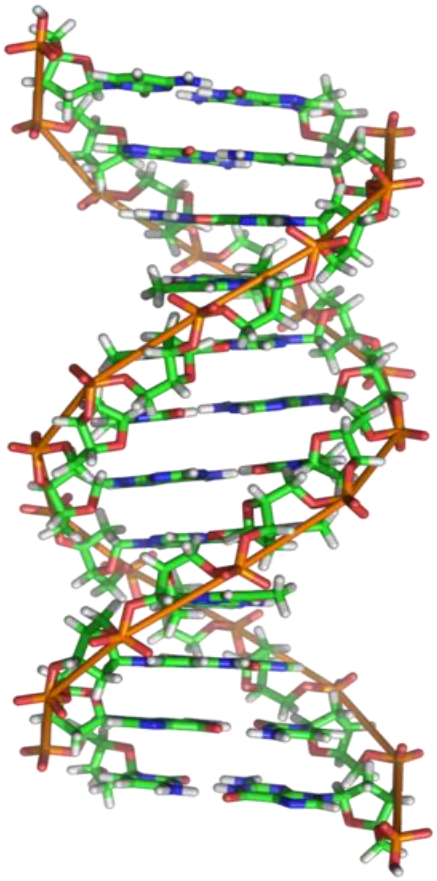


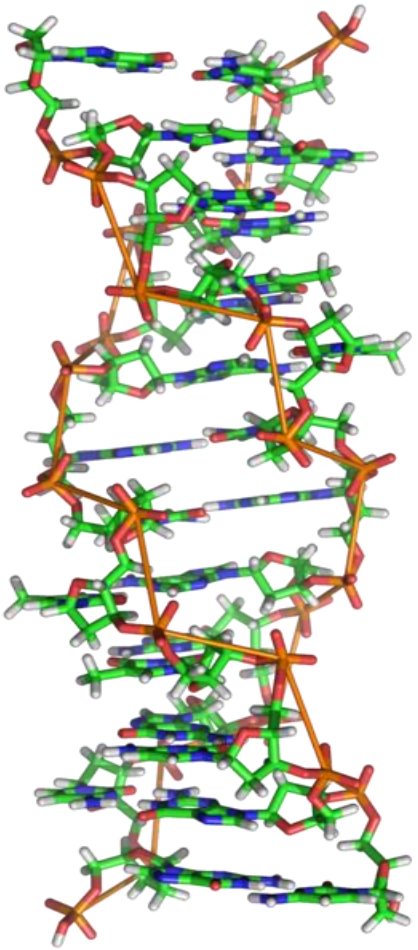

Computer Science
Engineering
Chemistry
Bioinformatics
Mathematics
Biochemistry
Statistics
Biology

La bioinformática permite investigar, desarrollar y aplicar herramientas informáticas y computacionales para permitir y mejorar el manejo de datos biológicos.

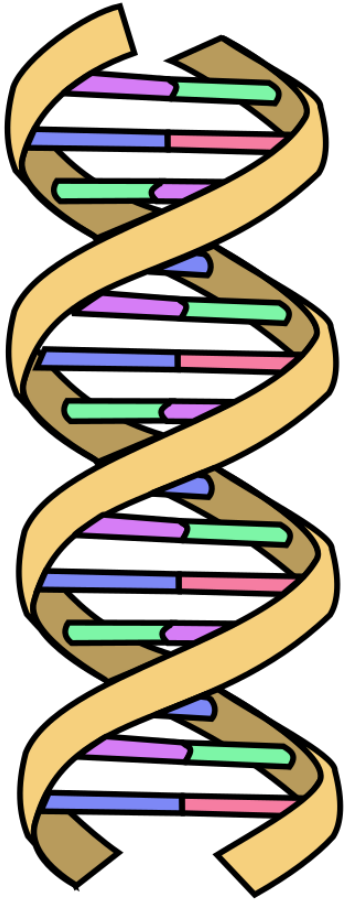
La bioinformática permite investigar, desarrollar y aplicar herramientas informáticas y computacionales para permitir y mejorar el manejo de ***datos biológicos****.*







ADN



=Adenine

= Thymine

= Cytosine

= Guanine

= Phosphate backbone

ADN

- Human Genome Project

ADN

- Human Genome Project

ADN

- Human Genome Project
- 3.000.000.000 bases
- 3.4 GB

ADN

- Human Genome Project
- 3.000.000.000 bases
- 3.4 GB

ADN

- Human Genome Project
- 3.000.000.000 bases
- 3.4 GB

1.000.000 $

ADN

- Human Genome Project
- 3.000.000.000 bases
- 3.4 GB

Coste del Human Genome Project:

1.000.000 $

ADN

- Human Genome Project
- 3.000.000.000 bases
- 3.4 GB

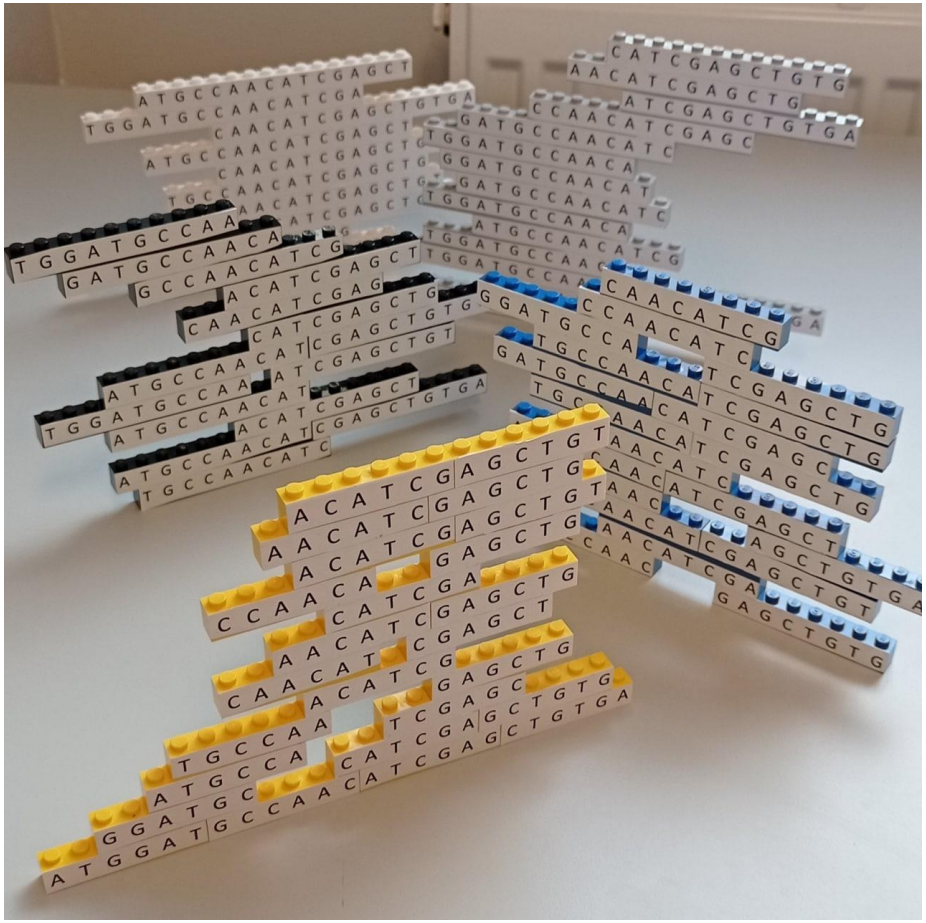
Coste del Human Genome Project:

3.000.000.000 $

1.000.000 $

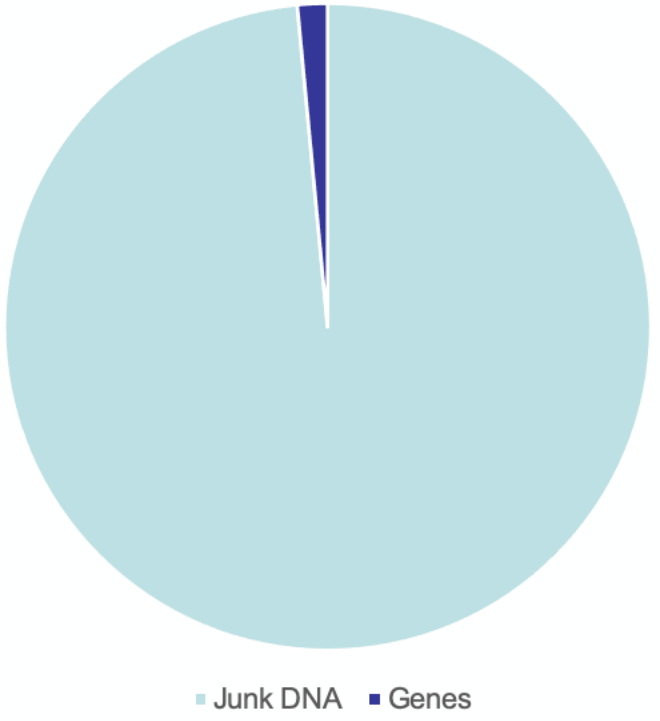
ADN

- Ensamblado:

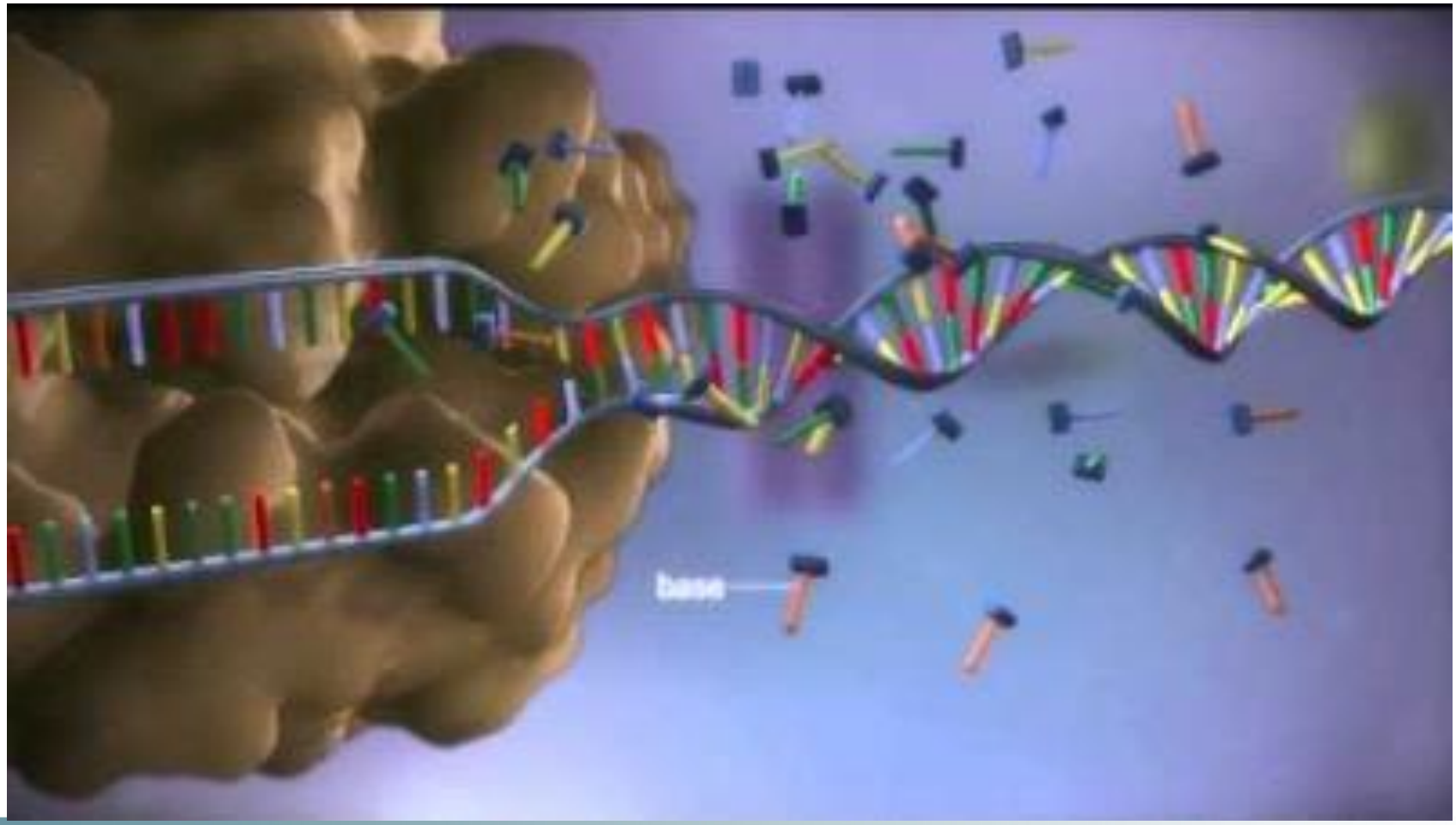


ADN

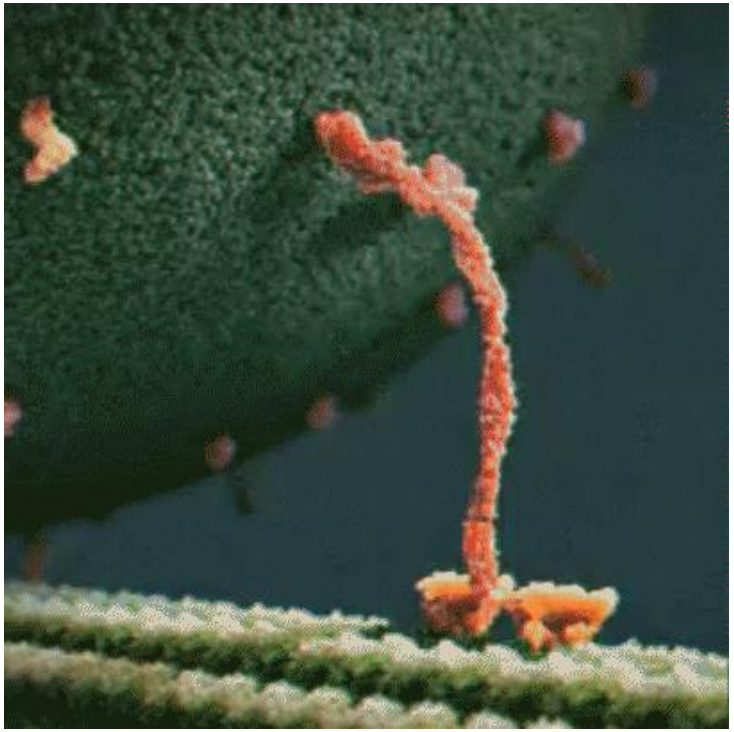
- Human Genome Project
- 3.000.000.000 bases
- 3.4 GB
- 1.5% del genoma: genes



ARN



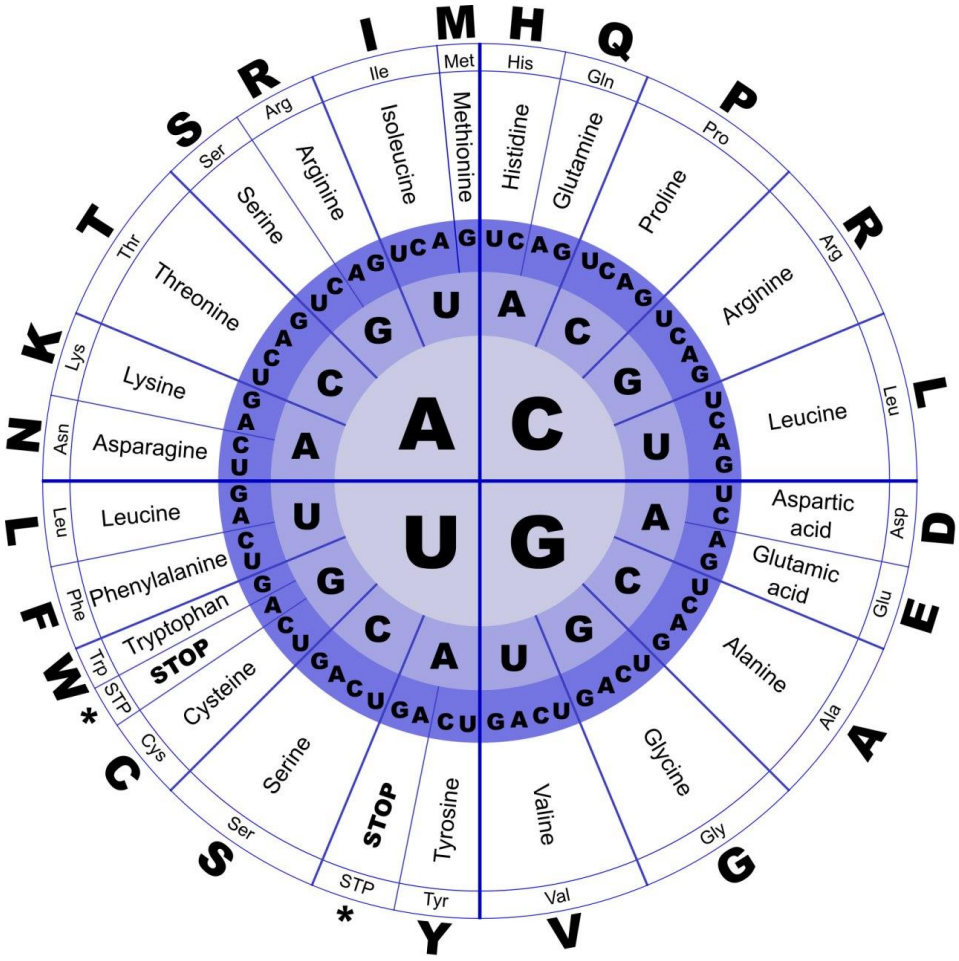
Proteínas



https://bit.ly/3D6ZPH

Proteínas

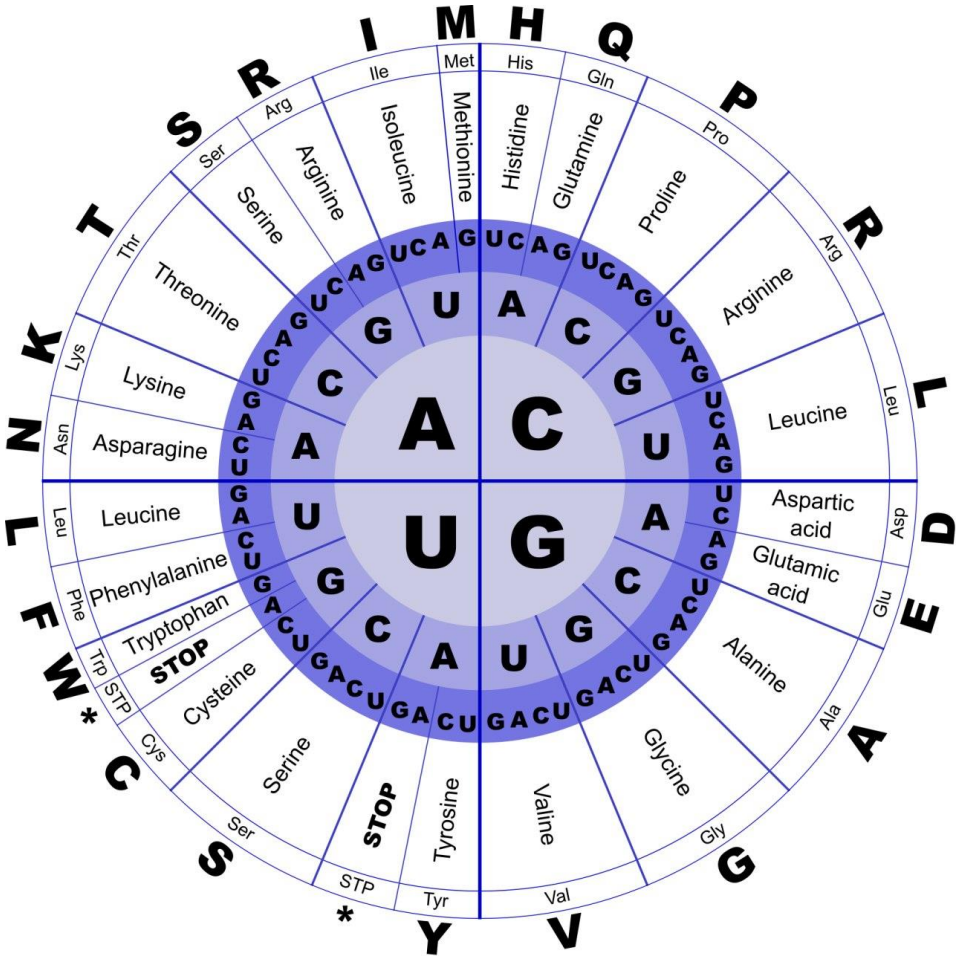
ADN: **ATGTGTCCATAG**



Proteínas

ADN: **ATGTGTCCATAG**

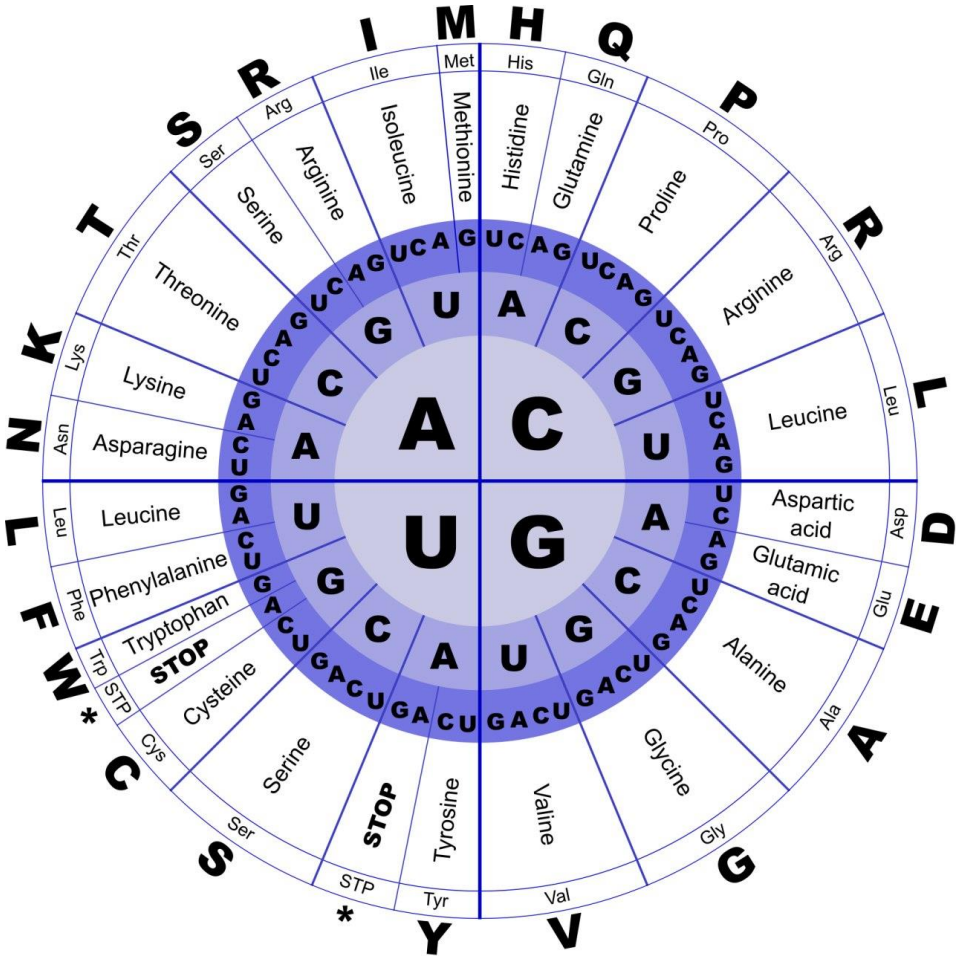
ARN:



Proteínas

ADN: **ATGTGTCCATAG**

ARN: **AUGUGUCCAUAG**

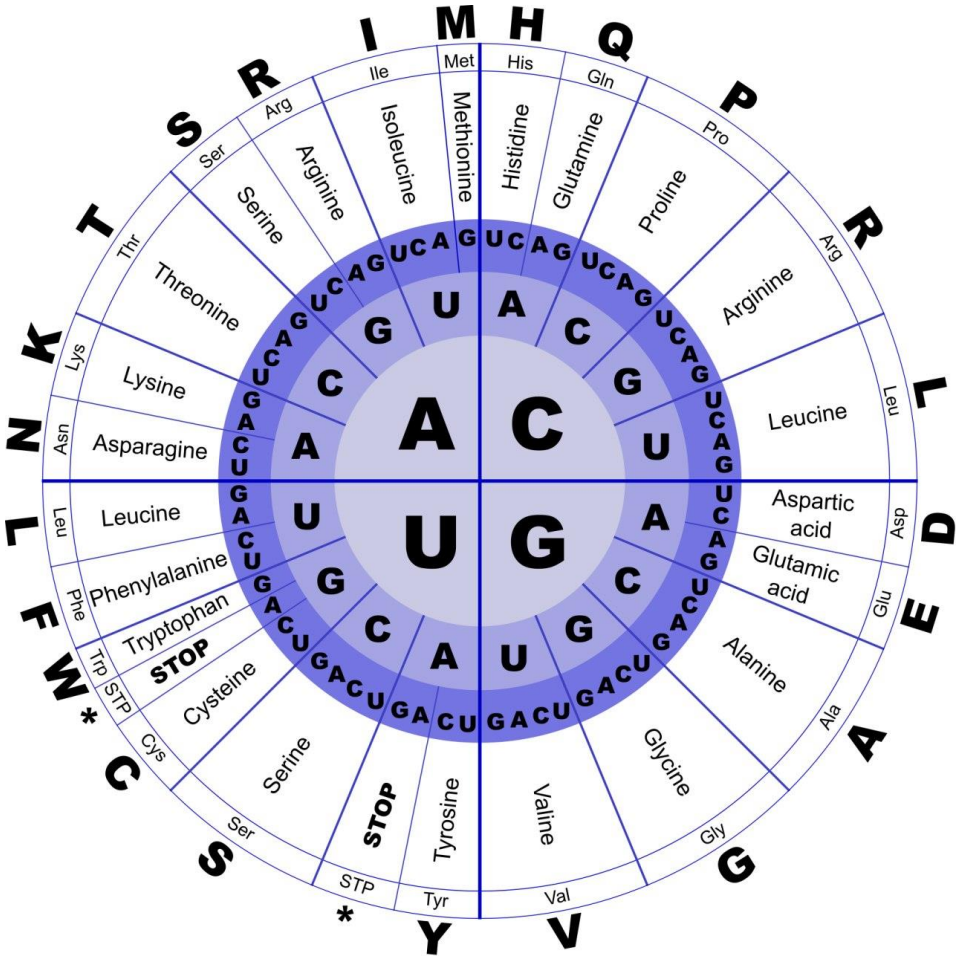


Proteínas

ADN: **ATGTGTCCATAG**

ARN: **AUGUGUCCAUAG**

P:

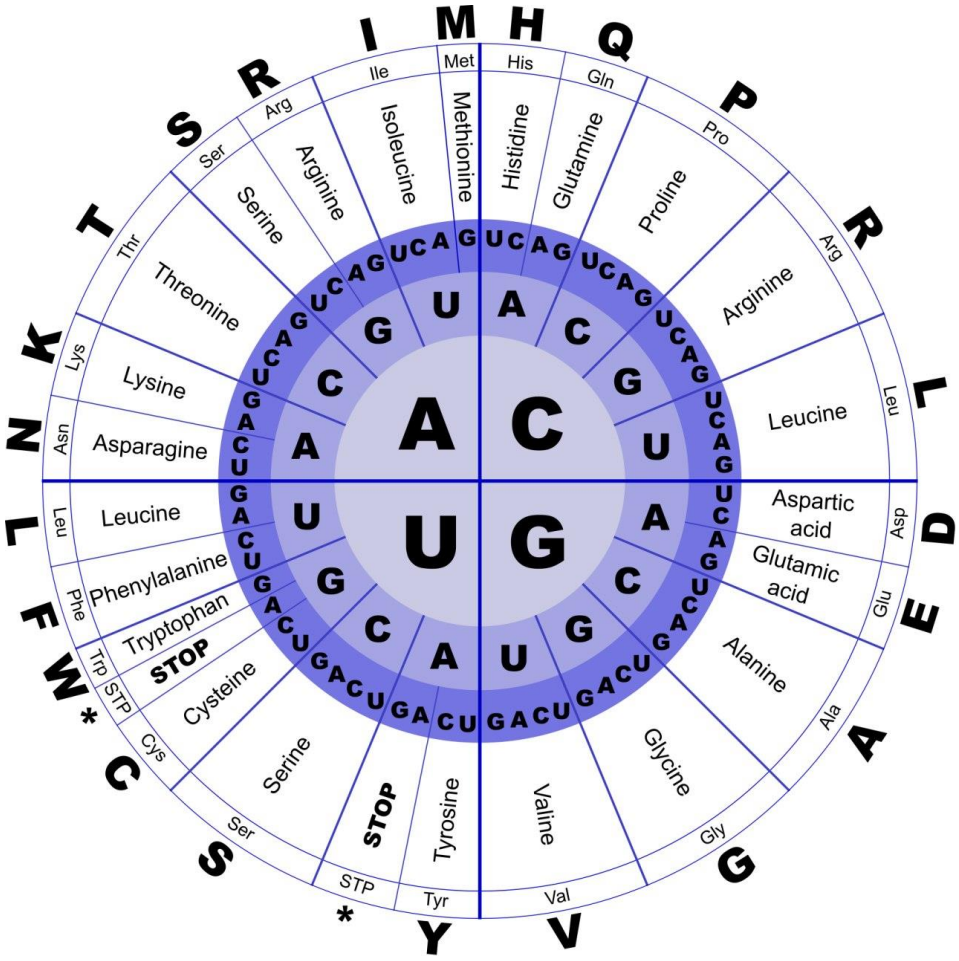


Proteínas

ADN: **ATG TGT CCA TAG**

ARN: **AUG UGU CCA UAG**

P:

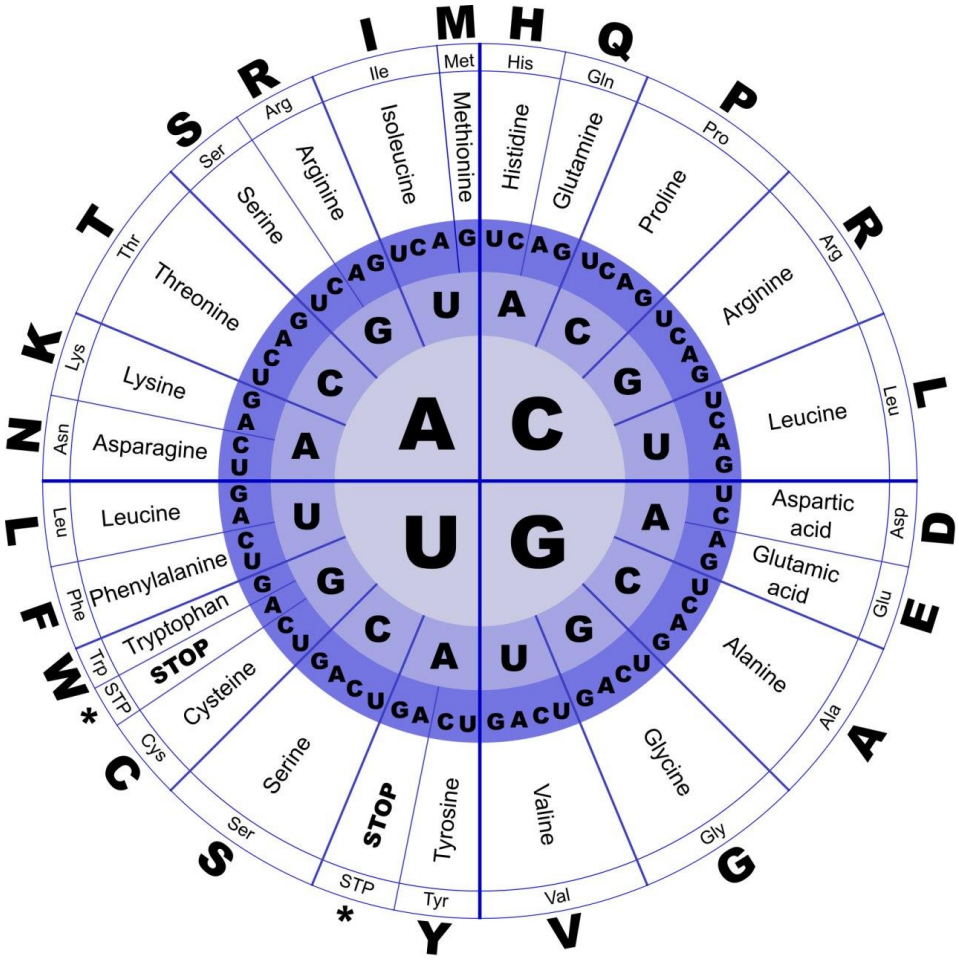


Proteínas

ADN: **ATG TGT CCA TAG**

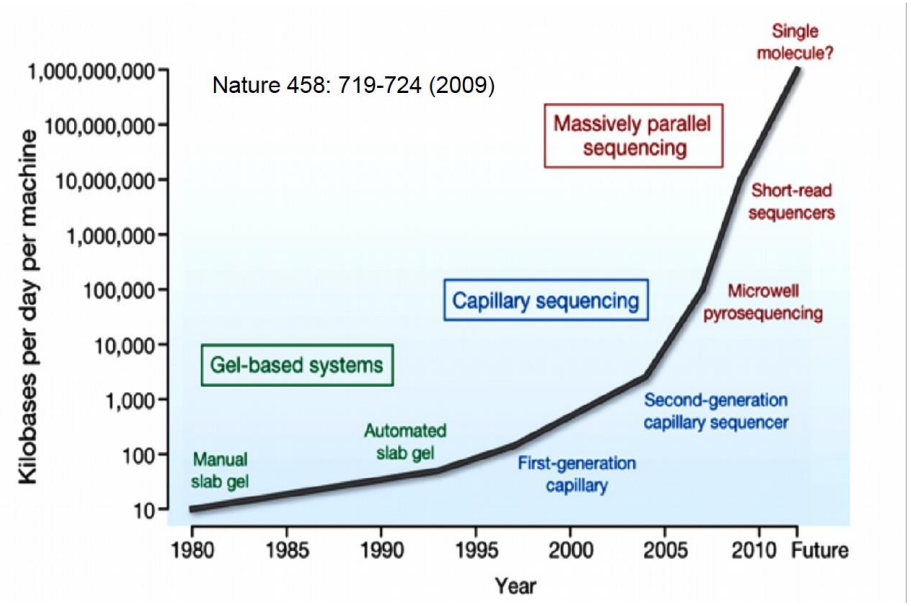
ARN: **AUG UGU CCA UAG**

P: **M C P ***



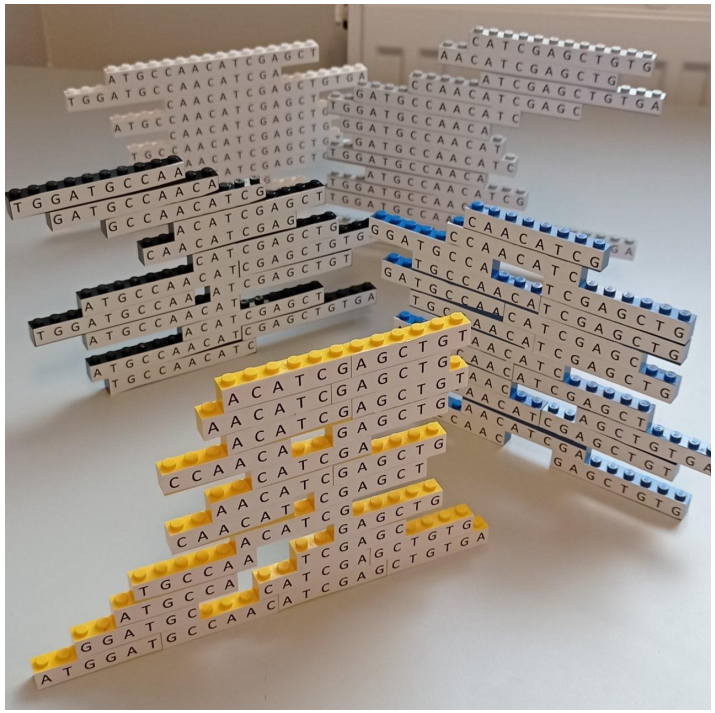
Automatización

- 0 y 1 – A, C, G, T
- Menor coste → Más datos



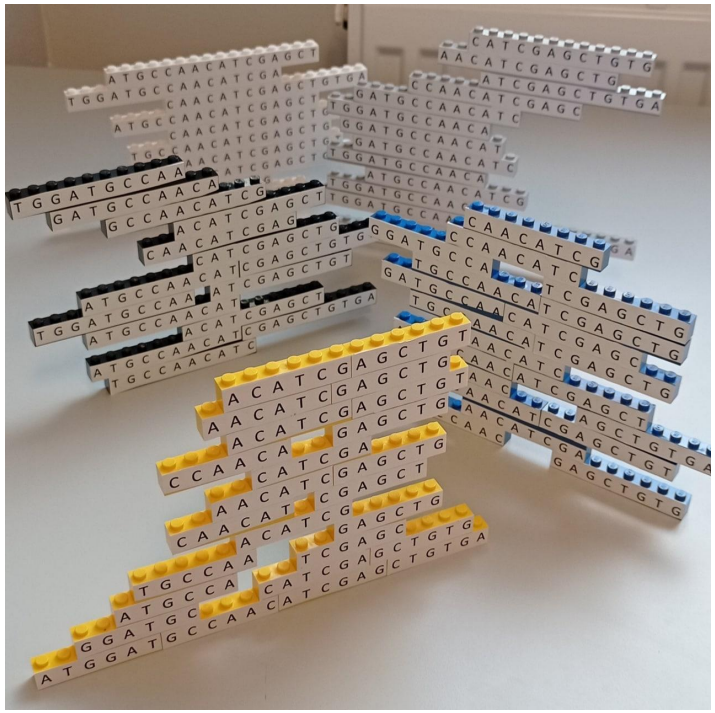
Análisis de Secuencias

ACGATATTACACGTACACTCAAGTCGT
TCGAGATTGCATGTACCCTCAAGCCGTCGG
ACGATATTACACGTACACTCACGTCGT
ACGATATTACACGTACACTCACGTCGTTCGGA
ACGATATTACACGCACACTCAAGTCGTTCGGAACCT
ACGATATTACACGTACACTCACGTCGTTCGGAA
ATTACACGTACACTCACGTCGTTCGGAACCT
TACACGTACACTCAAGTCGTTCGGAACCT
CACGTACACTCAAGTCGTTCTGAACCT
CACGTACACTCACGTCGTTCGGAACCT



Análisis de Secuencias

```
ACGATATTACACGTACACTCAAGTCGT__________
TCGAGATTGCATGTACCCTCAAGCCGTCGG_______
ACGATATTACACGTACACTCACGTCGT__________
ACGATATTACACGTACACTCACGTCGTTCGGA_____
ACGATATTACACGCACACTCAAGTCGTTCGGAACCT
ACGATATTACACGTACACTCACGTCGTTCGGAA____
______ATTACACGTACACTCACGTCGTTCGGAACCT
_________TACACGTACACTCAAGTCGTTCGGAACCT
___________CACGTACACTCAAGTCGTTCTGAACCT
___________CACGTACACTCACGTCGTTCGGAACCT
```

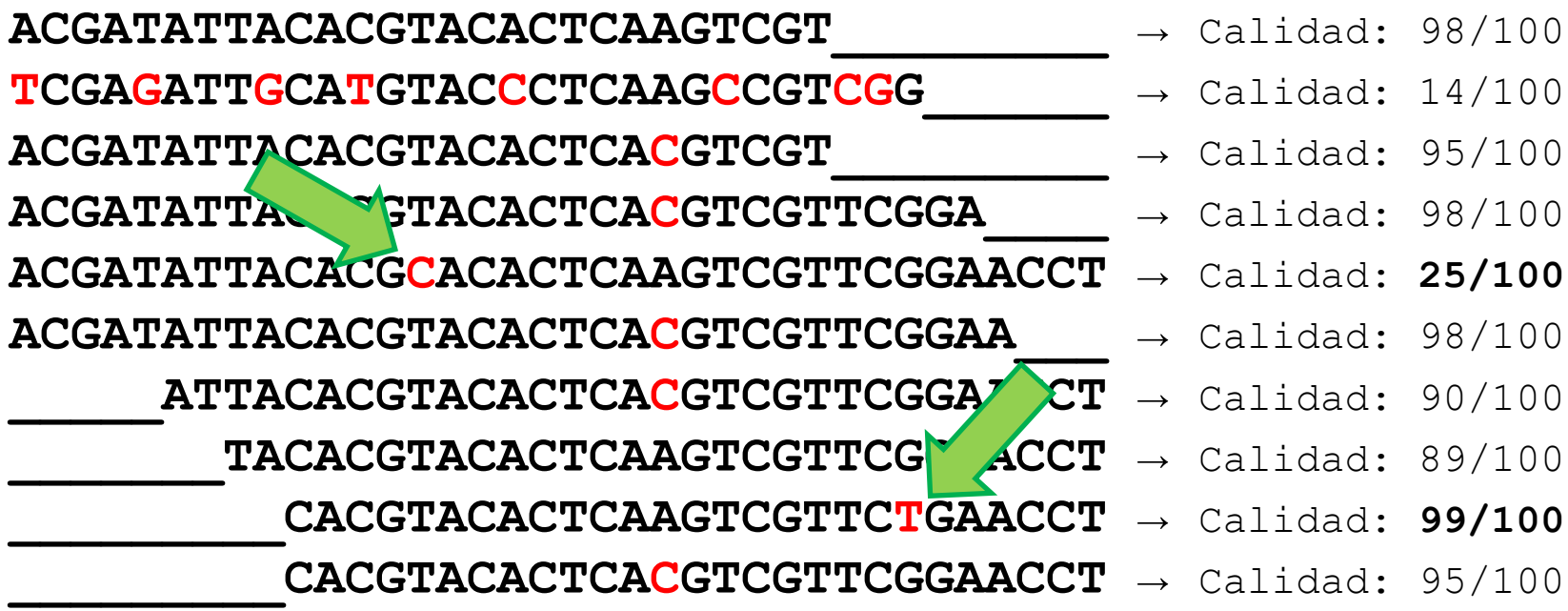


Detección de variantes

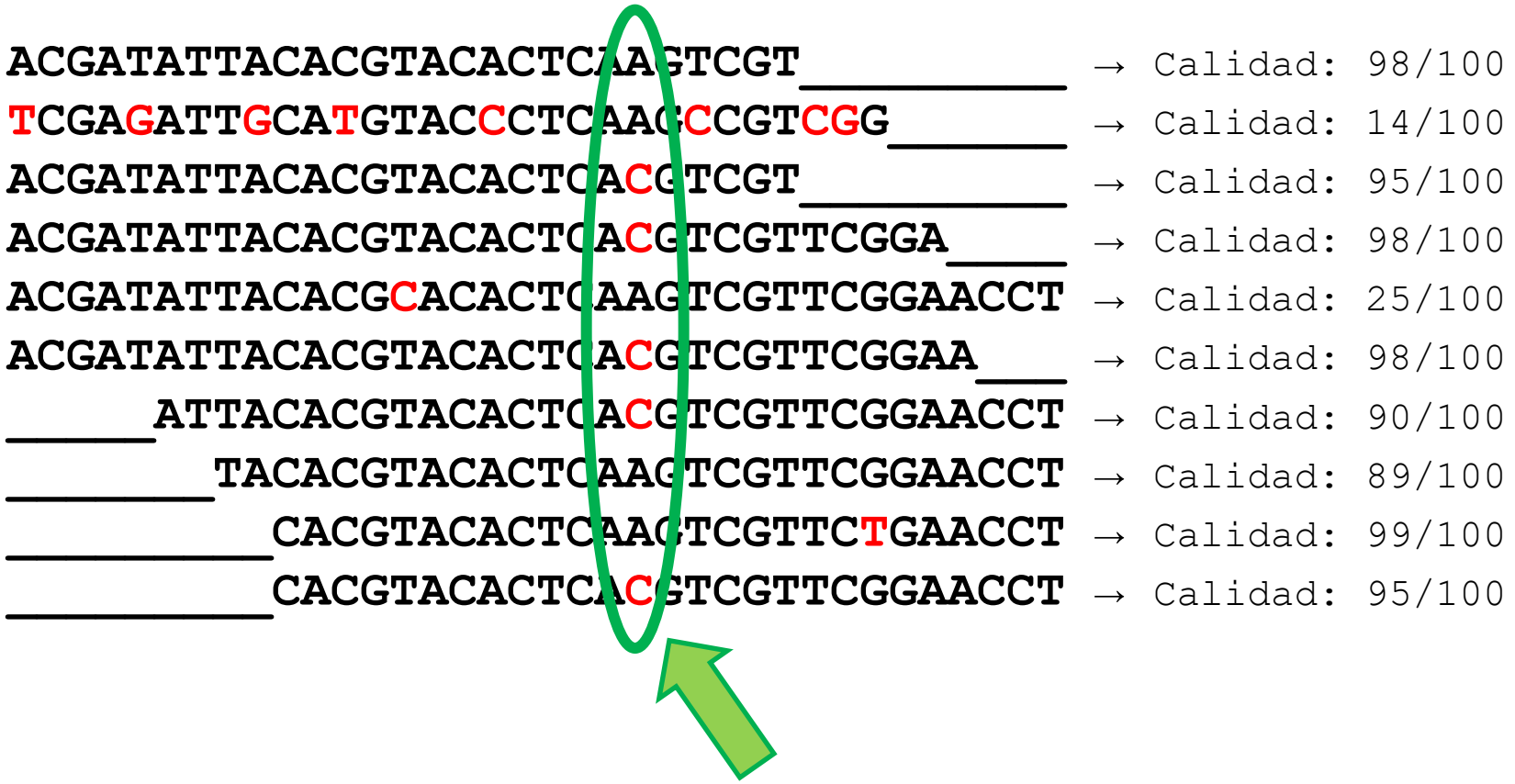
```
ACGATATTACACGTACACTCAAGTCGT__________
TCGAGATTGCATGTACCCTCAAGCCGTCGG_______
ACGATATTACACGTACACTCACGTCGT__________
ACGATATTACACGTACACTCACGTCGTTCGGA_____
ACGATATTACACGCACACTCAAGTCGTTCGGAACCT
ACGATATTACACGTACACTCACGTCGTTCGGAA____
_____ATTACACGTACACTCACGTCGTTCGGAACCT
________TACACGTACACTCAAGTCGTTCGGAACCT
__________CACGTACACTCAAGTCGTTCTGAACCT
__________CACGTACACTCACGTCGTTCGGAACCT
```

Detección de variantes

Detección de variantes



Detección de variantes



Detección de variantes

```
ACGATATTACACGTACACTCAAGTCGATCGGAACCT → Referencia

ACGATATTACACGTACACTCAAGTCGT__________ → Calidad: 98/100
TCGAGATTGCATGTACCCTCAAGCCGTCGG_______ → Calidad: 14/100
ACGATATTACACGTACACTCACGTCGT__________ → Calidad: 95/100
ACGATATTACACGTACACTCACGTCGTTCGGA_____ → Calidad: 98/100
ACGATATTACACGCACACTCAAGTCGTTCGGAACCT → Calidad: 25/100
ACGATATTACACGTACACTCACGTCGTTCGGAA____ → Calidad: 98/100
_____ATTACACGTACACTCACGTCGTTCGGAACCT → Calidad: 90/100
________TACACGTACACTCAAGTCGTTCGGAACCT → Calidad: 89/100
__________CACGTACACTCAAGTCGTTCTGAACCT → Calidad: 99/100
__________CACGTACACTCACGTCGTTCGGAACCT → Calidad: 95/100
```

Detección de variantes

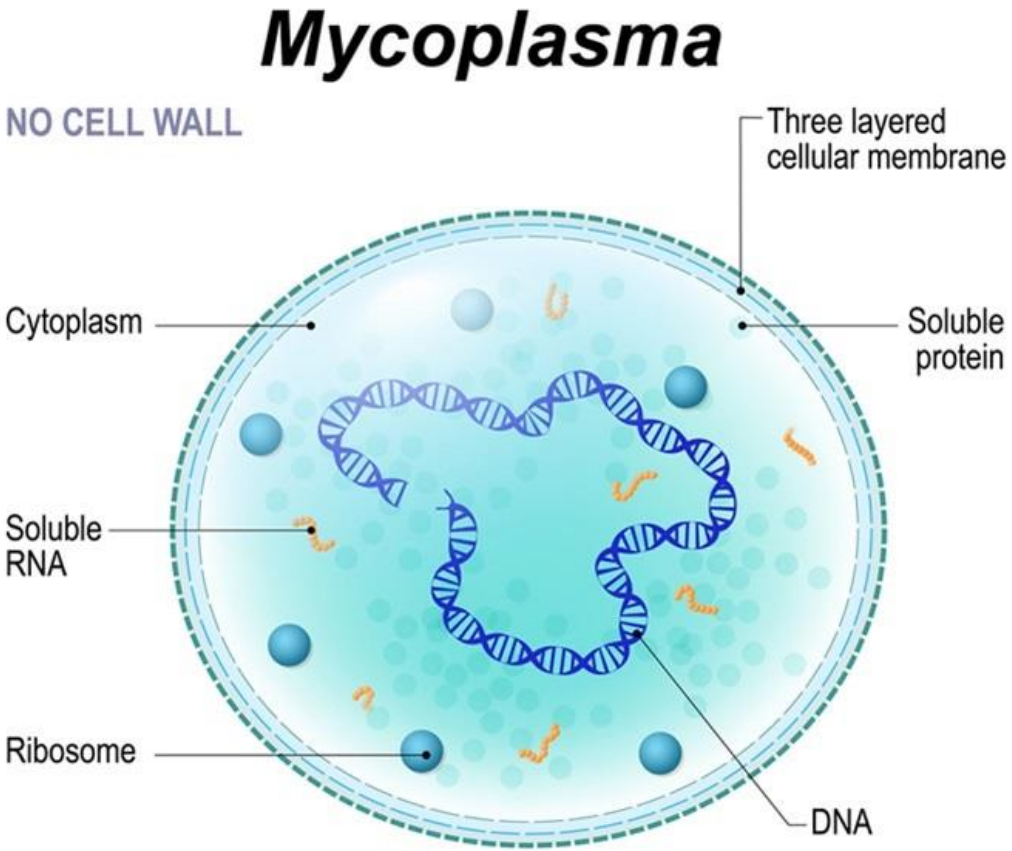
```
ACGATATTACACGTACACTCAAGTCGATCGGAACCT

ACGATATTACACGTACACTCAAGTCGT__________ → Calidad: 98/100
TCGAGATTGCATGTACCCTCAAGCCGTCGG_______ → Calidad: 14/100
ACGATATTACACGTACACTCACGTCGT__________ → Calidad: 95/100
ACGATATTACACGTACACTCACGTCGTTCGGA_____ → Calidad: 98/100
ACGATATTACACGCACACTCAAGTCGTTCGGAACCT → Calidad: 25/100
ACGATATTACACGTACACTCACGTCGTTCGGAA____ → Calidad: 98/100
_____ATTACACGTACACTCACGTCGTTCGGAACCT → Calidad: 90/100
________TACACGTACACTCAAGTCGTTCGGAACCT → Calidad: 89/100
__________CACGTACACTCAAGTCGTTCTGAACCT → Calidad: 99/100
__________CACGTACACTCACGTCGTTCGGAACCT → Calidad: 95/100
```

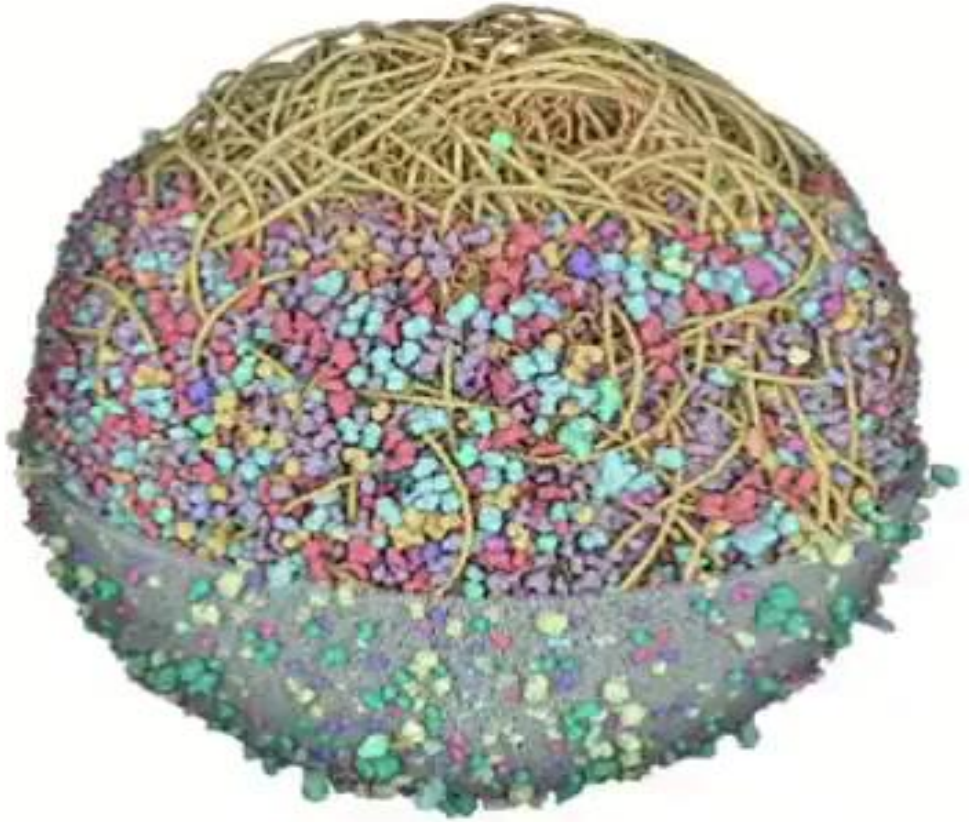
Medicina Personalizada

- www.pandrugs.org

Biología de sistemas

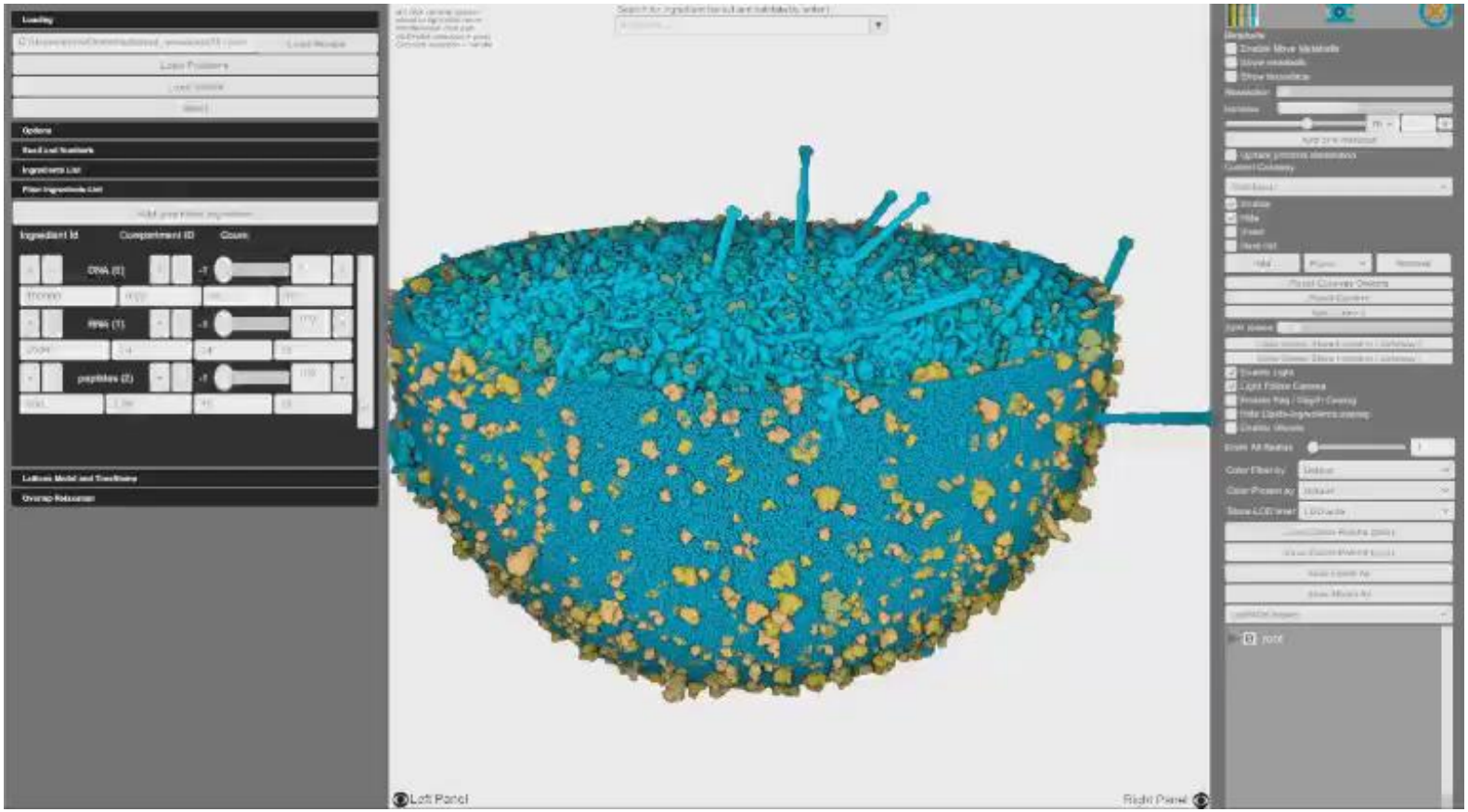


Biología de sistemas



https://doi.org/10.1016/j.jmb.2021.167351

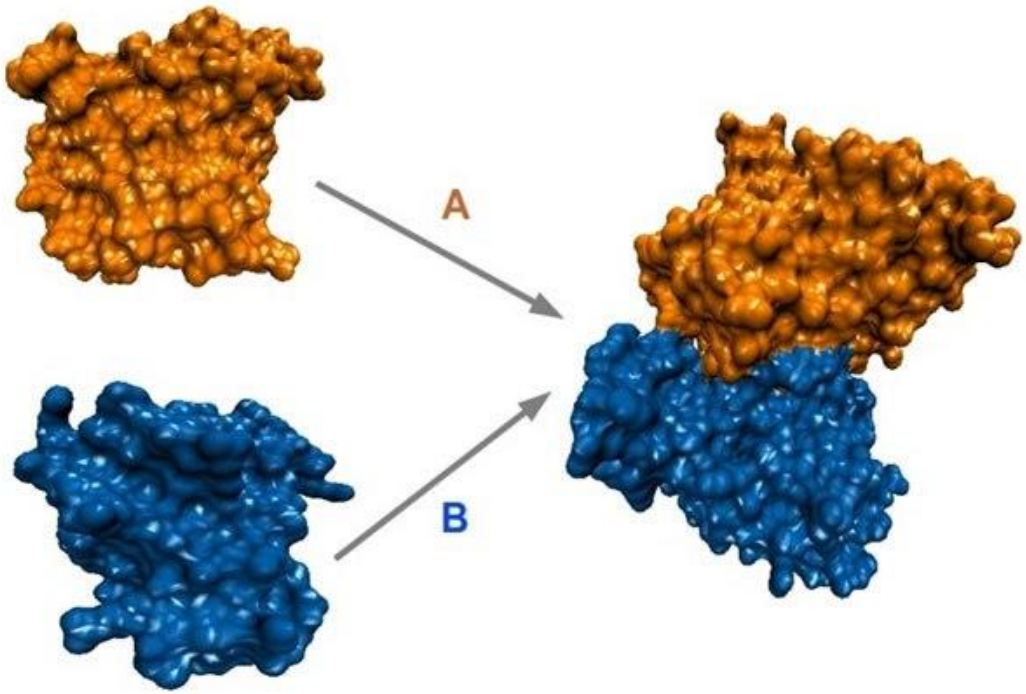
Biología de sistemas



https://doi.org/10.1016/j.jmb.2021.167351

Modelado de proteínas

- Diseño de fármacos

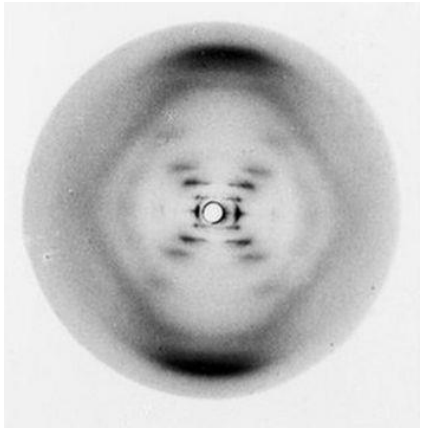


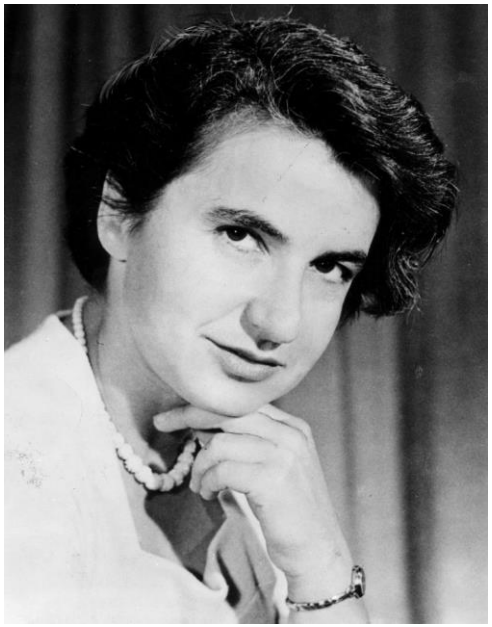
Plegado de proteínas

Plegado de proteínas

Más problemas: Rosalind

ROSALIND





https://bit.ly/BIERosalind