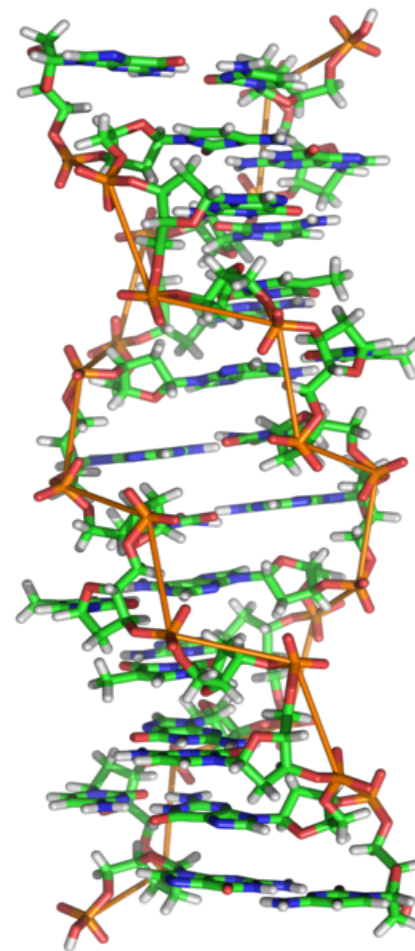
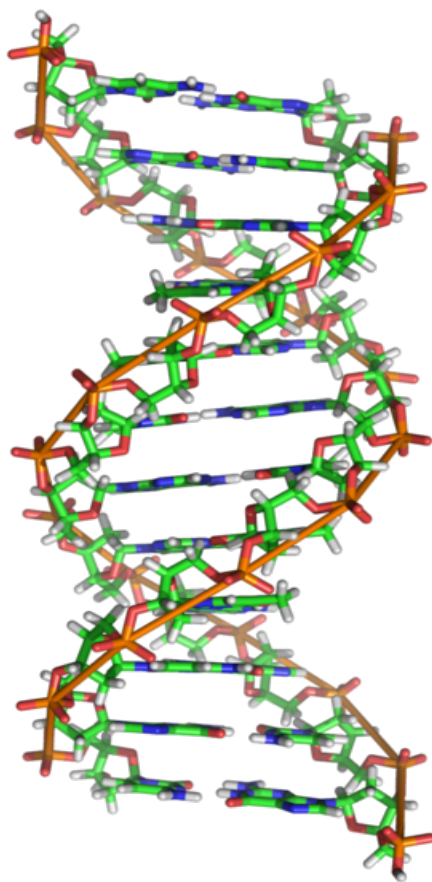
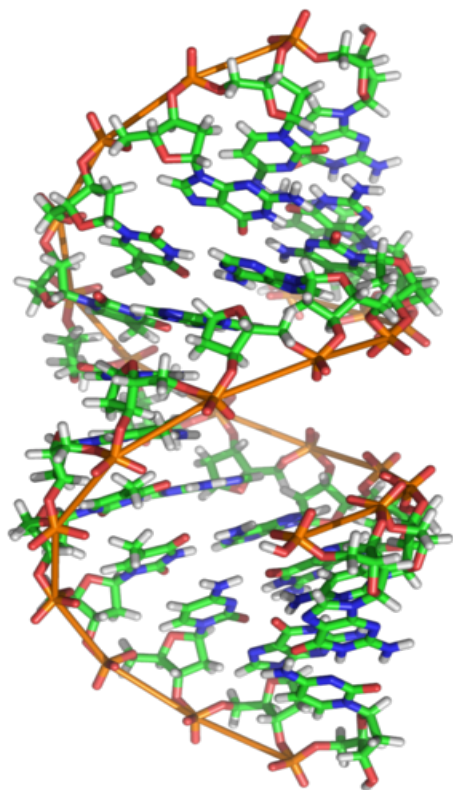




La bioinformática permite investigar, desarrollar y aplicar herramientas informáticas y computacionales para permitir y mejorar el manejo de datos biológicos.

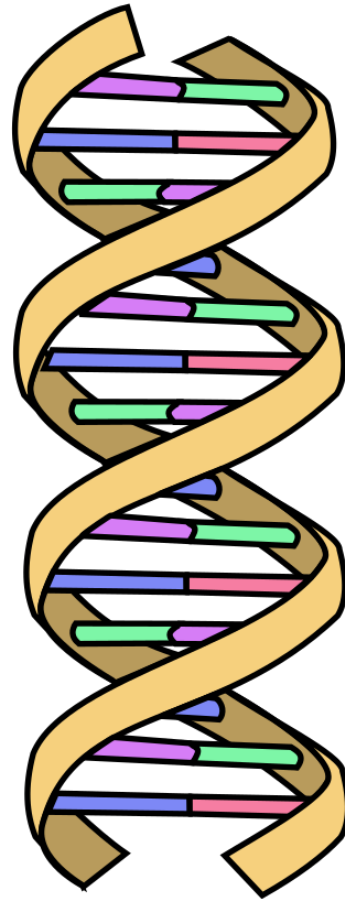



*La bioinformática permite investigar, desarrollar y aplicar herramientas informáticas y computacionales para permitir y mejorar el manejo de **datos biológicos**.*






ADN




 = Adenine

 = Thymine

 = Cytosine

 = Guanine

 = Phosphate
backbone



ADN

- Human Genome Project





ADN

- Human Genome Project
- 3.100.000.000 bases





ADN

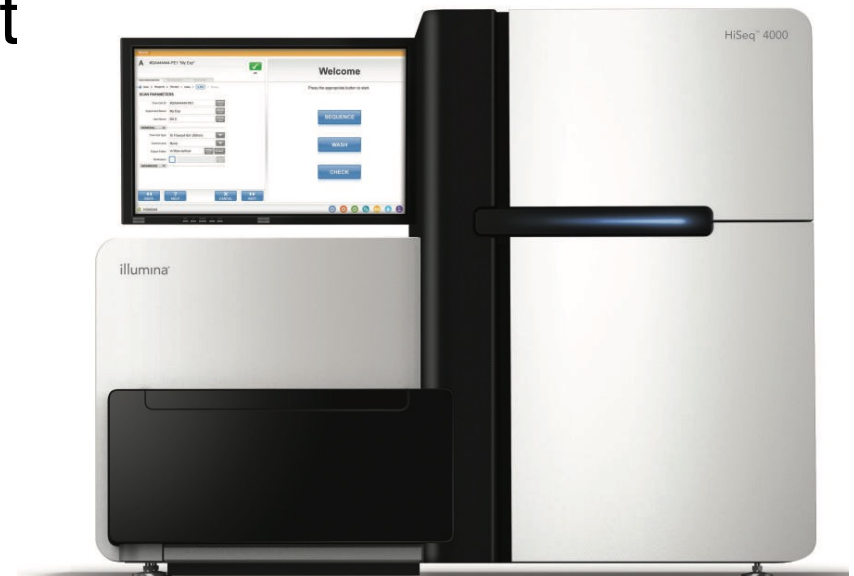
- Human Genome Project
- 3.100.000.000 bases
- 3.4 GB





ADN

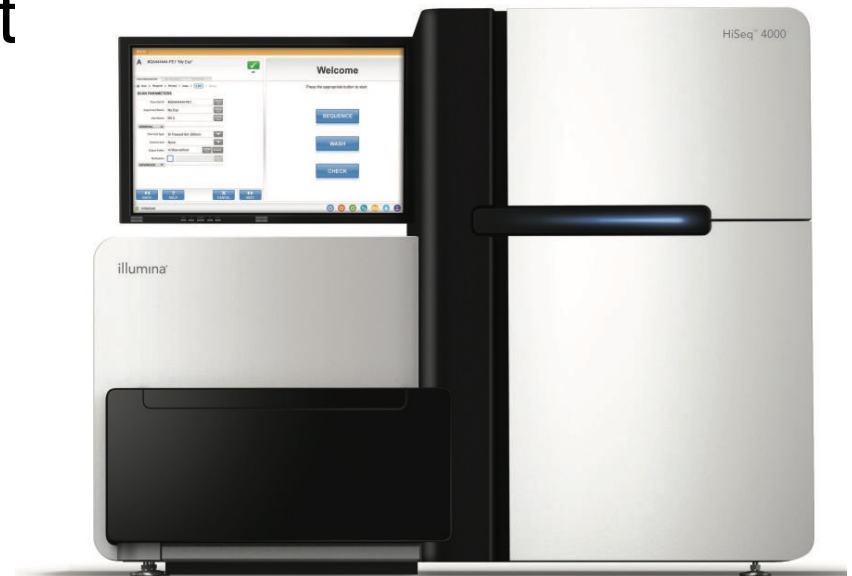
- Human Genome Project
- 3.100.000.000 bases
- 3.4 GB





ADN

- Human Genome Project
- 3.100.000.000 bases
- 3.4 GB



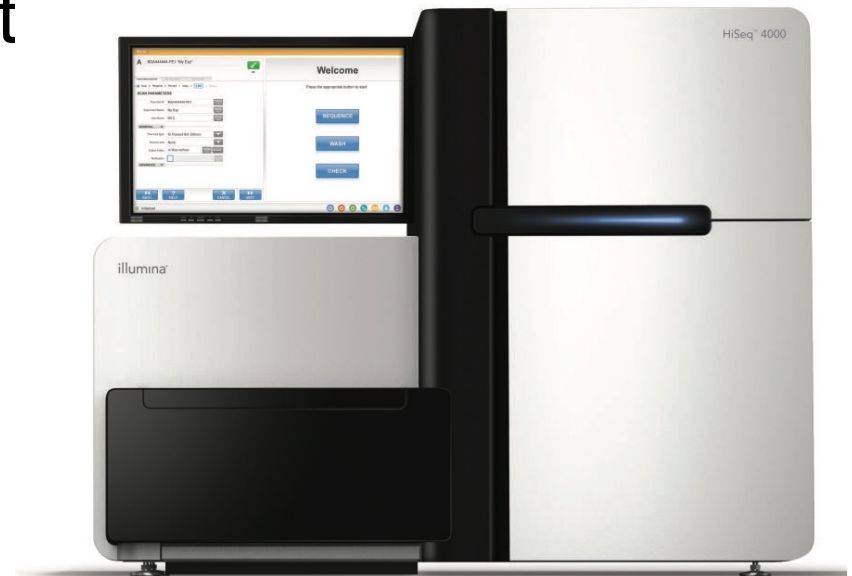
1.000.000 \$



ADN

- Human Genome Project
- 3.100.000.000 bases
- 3.4 GB

Coste del Human Genome Project:



1.000.000 \$

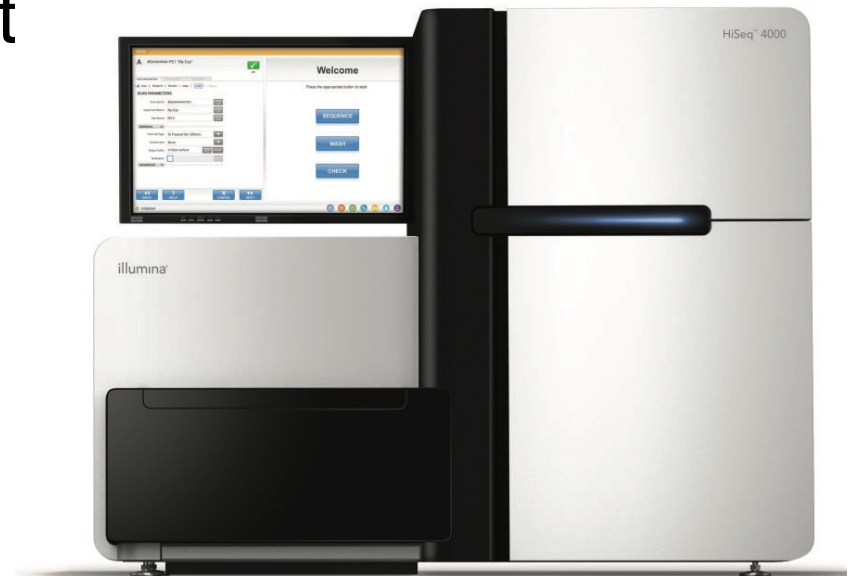


ADN

- Human Genome Project
- 3.100.000.000 bases
- 3.4 GB

Coste del Human Genome Project:

3.000.000.000 \$

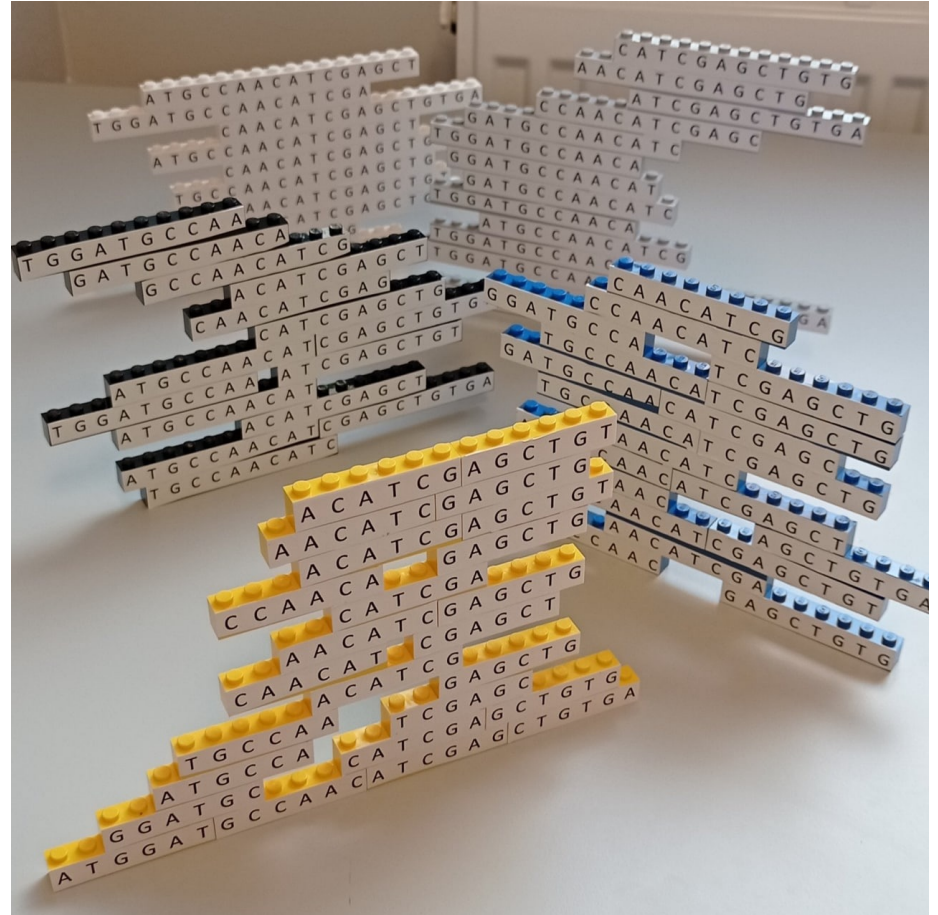


1.000.000 \$



ADN

- Ensamblado:



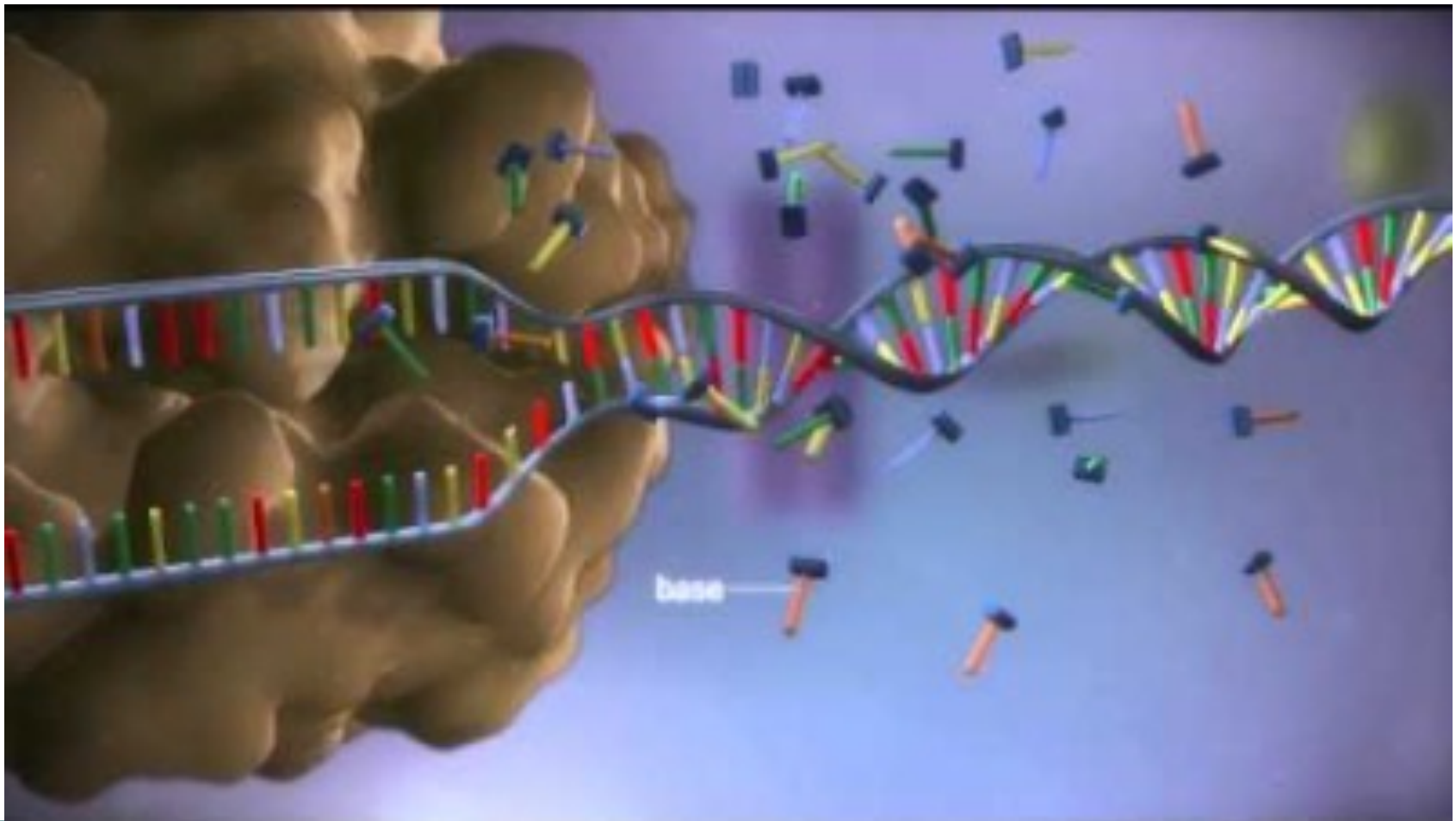


ADN

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



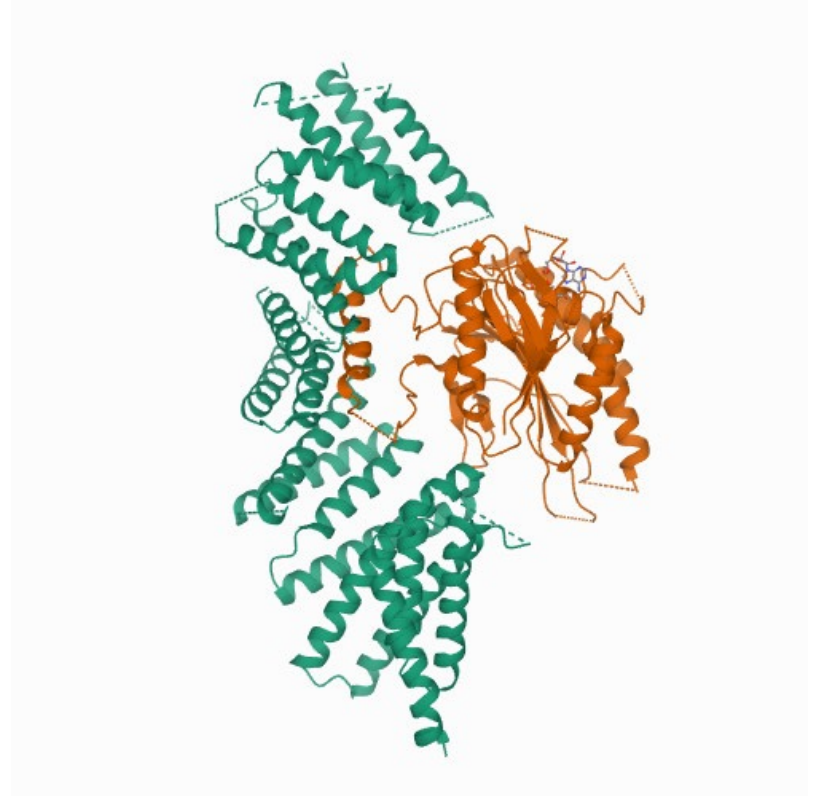
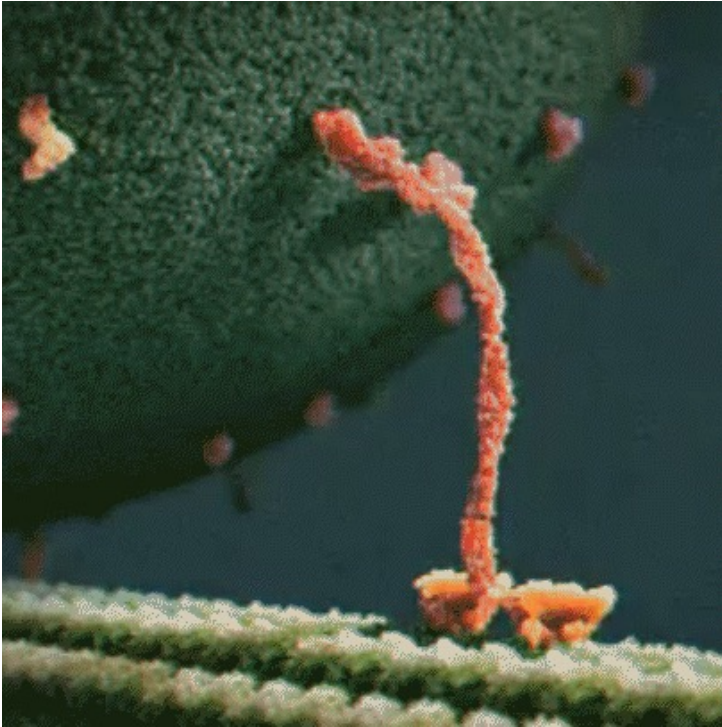
ARN





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Proteínas

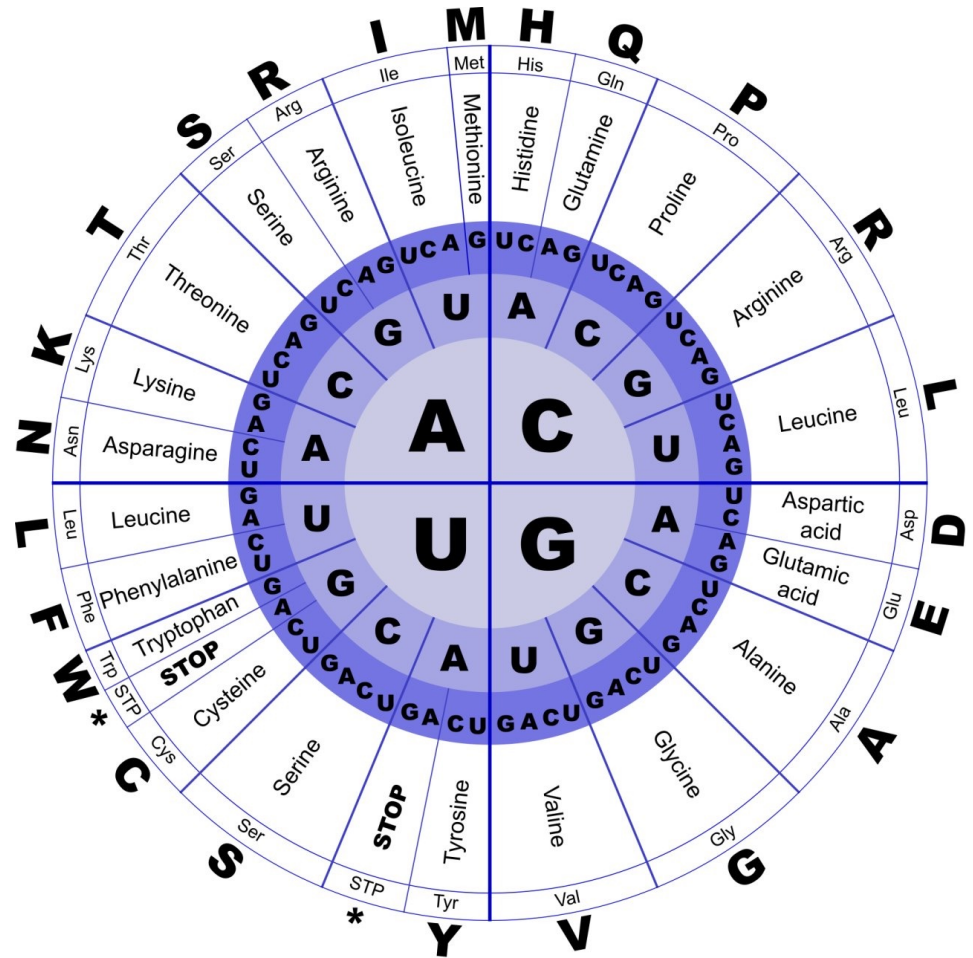


<https://cutt.ly/LluFZJg>



Proteínas

ADN: ATGTGTCCATAG





The circular genetic code chart (codon wheel) displays the mapping from mRNA codons to amino acids. The chart is organized into concentric rings:

- Center:** The four RNA bases: A, C, U, G.
- First Ring:** The second base of the codon.
- Second Ring:** The third base of the codon.
- Outer Edge:** The amino acids, listed in three-letter codes.

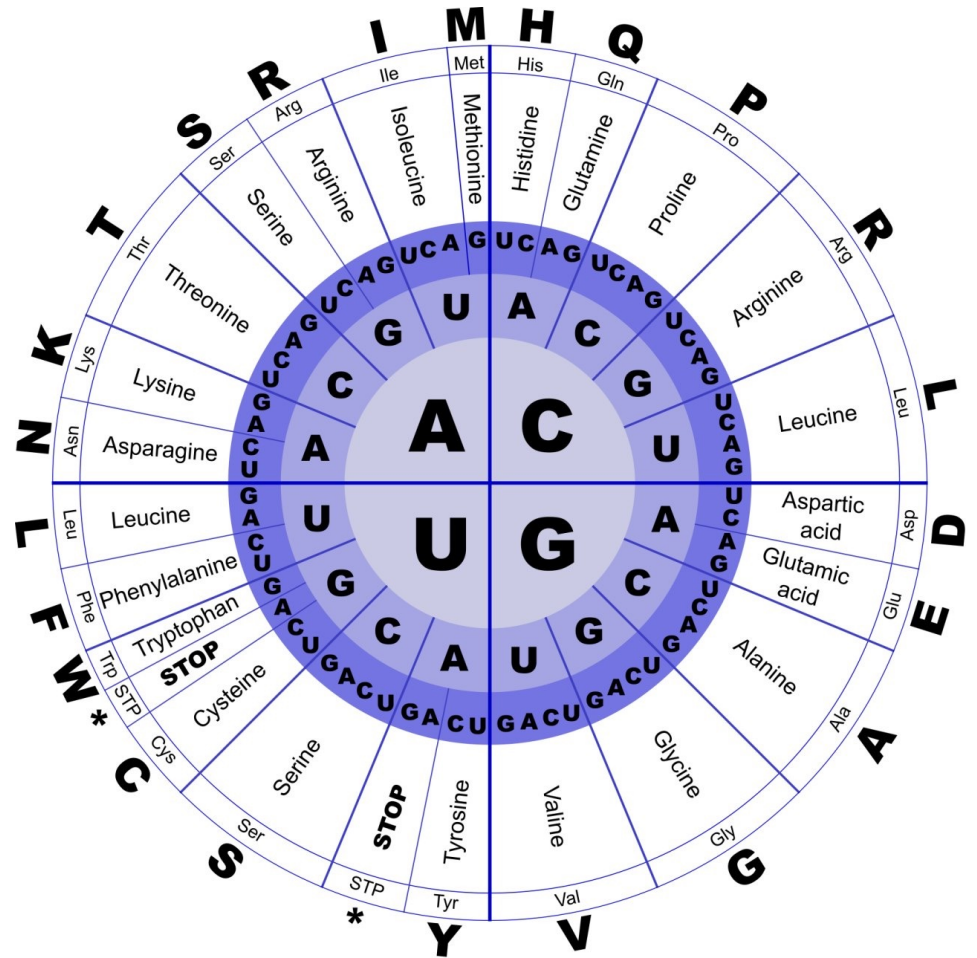
Key features of the chart include:

- Start Codon:** AUG, which codes for Methionine (Met).
- Stop Codons:** UAA, UAG, and UGA, marked with an asterisk (*) and labeled "STOP".
- Redundancy:** Multiple codons code for the same amino acid (e.g., Leucine is coded by UUA, UUG, CUU, CUC, CUA, and CUG).

ARN:



ARN: AUGUGUCCAUG



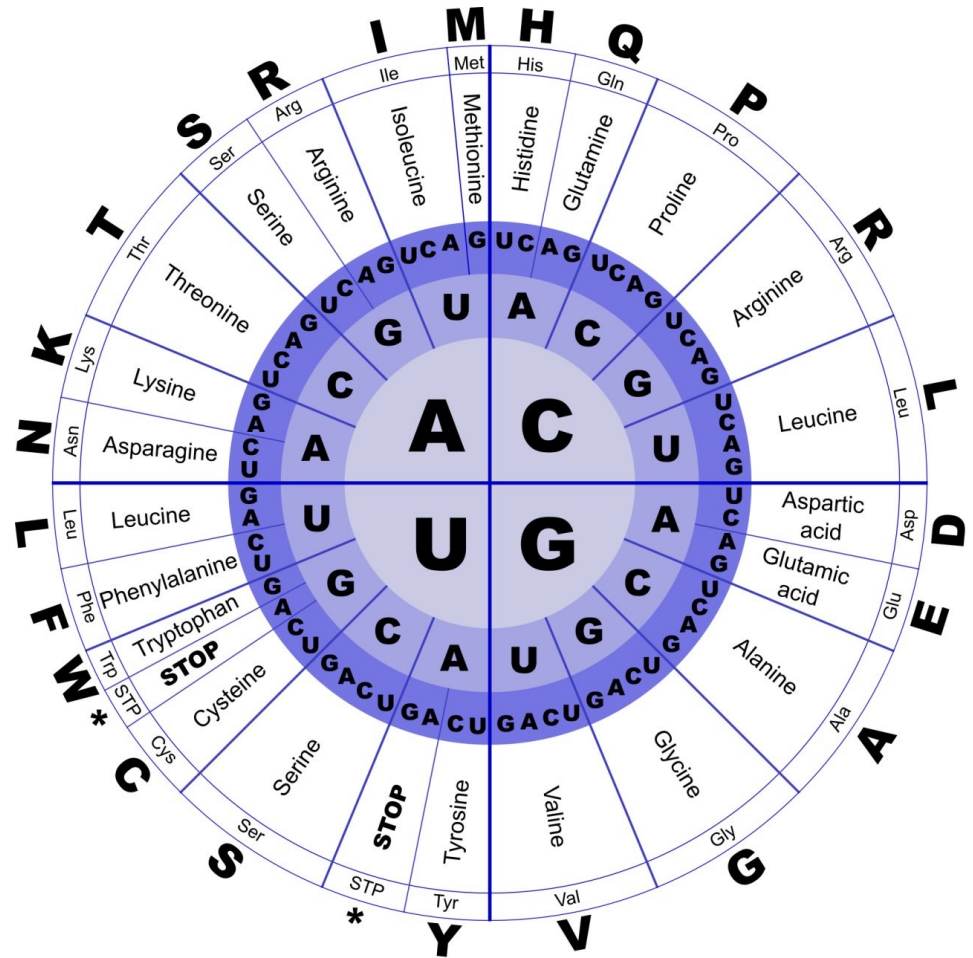


Proteínas

ADN: ATGTGTCCATAG

ARN: AUGUGUCCAUAG

P:



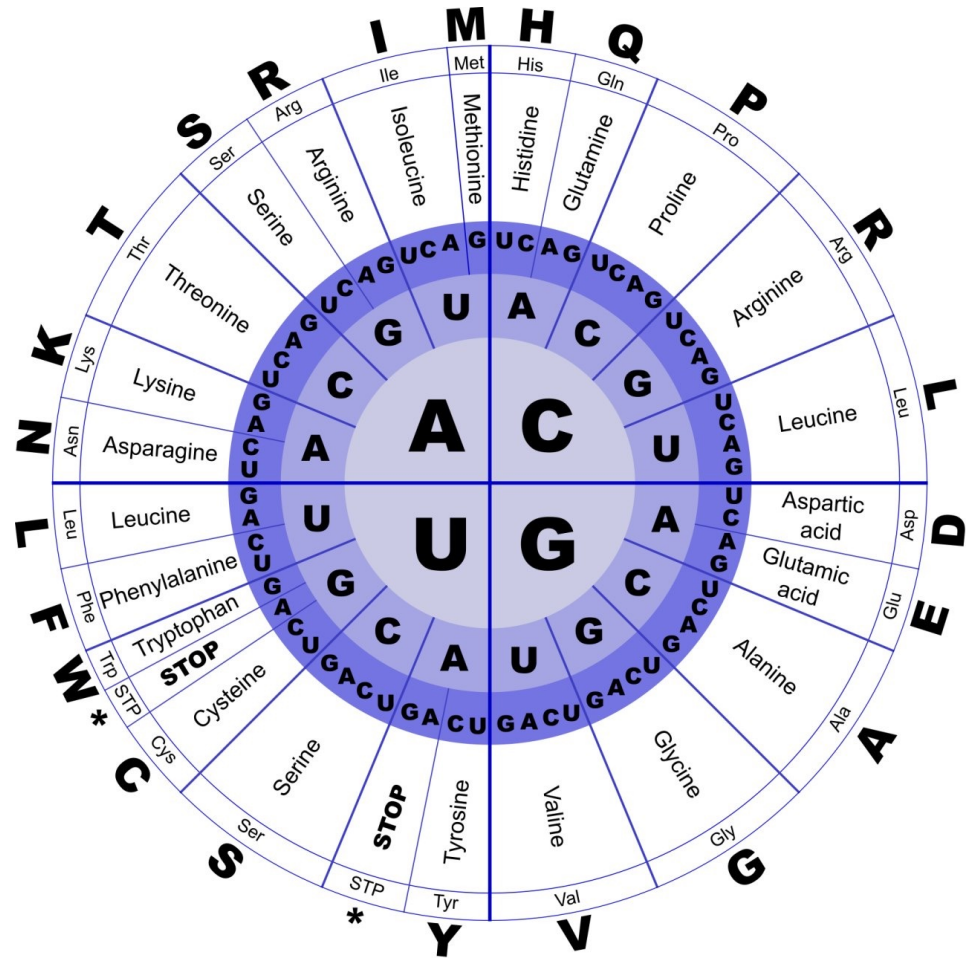


Proteínas

ADN: ATG TGT CCA TAG

ARN: AUG UGU CCA UAG

P:



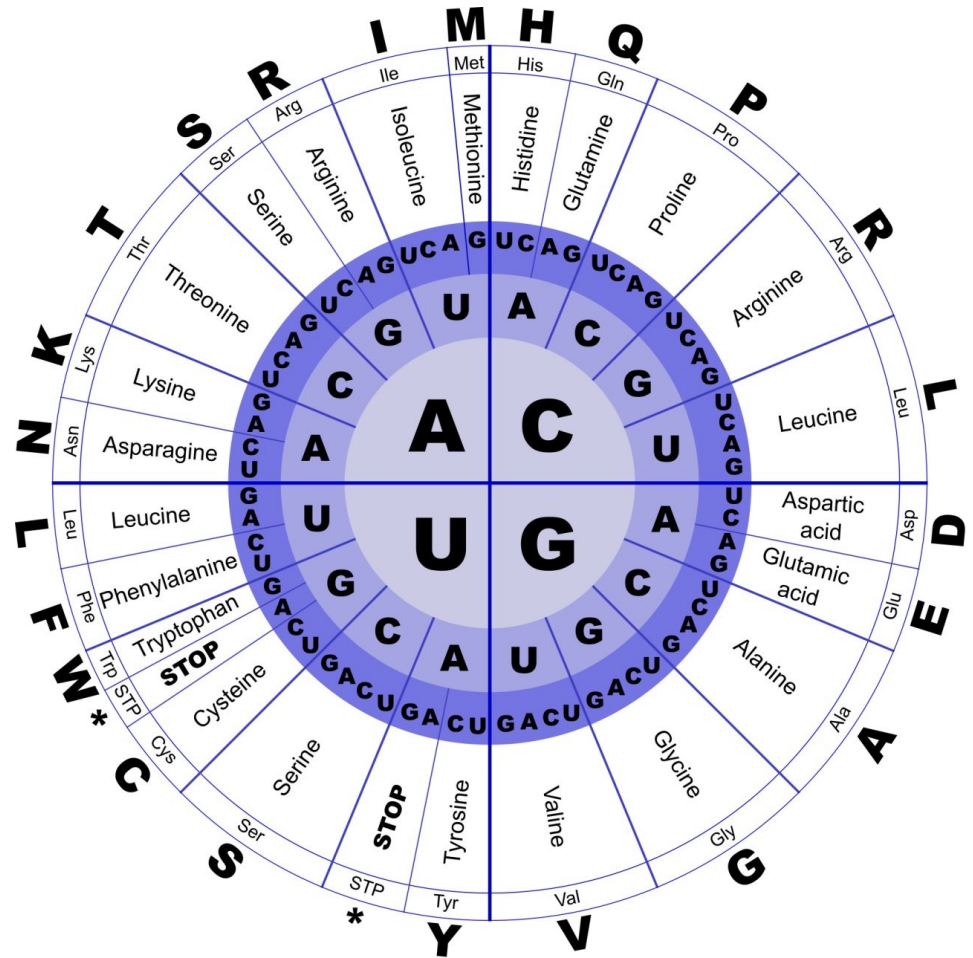


Proteínas

ADN: ATG TGT CCA TAG

ARN: AUG UGU CCA UAG

P: M C P *





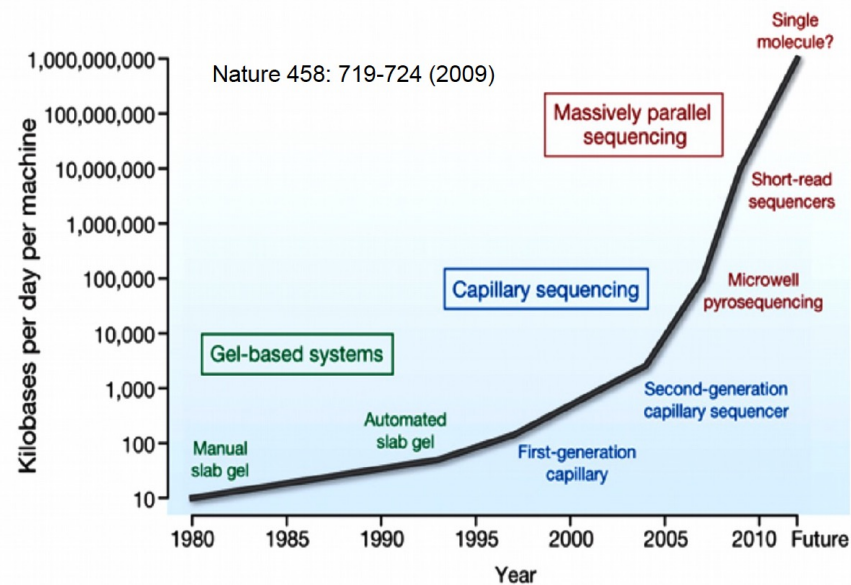
ADN

- Human Genome Project
- 3.100.000.000 bases
- 3.4 GB
- 1.5% del genoma: genes
- ¿Y el resto?



Automatización

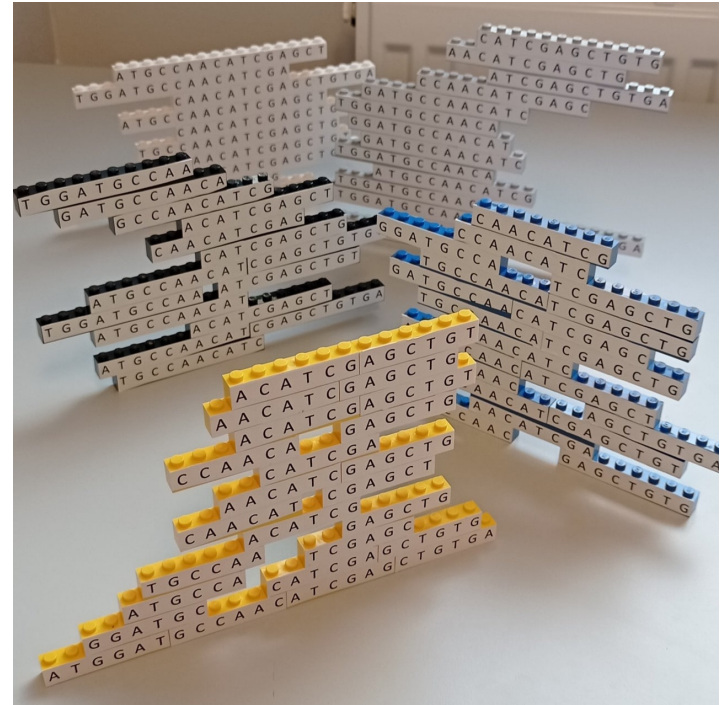
- 0 y 1 – A, C, G, T
- Menor coste → Más datos





Análisis de Secuencias

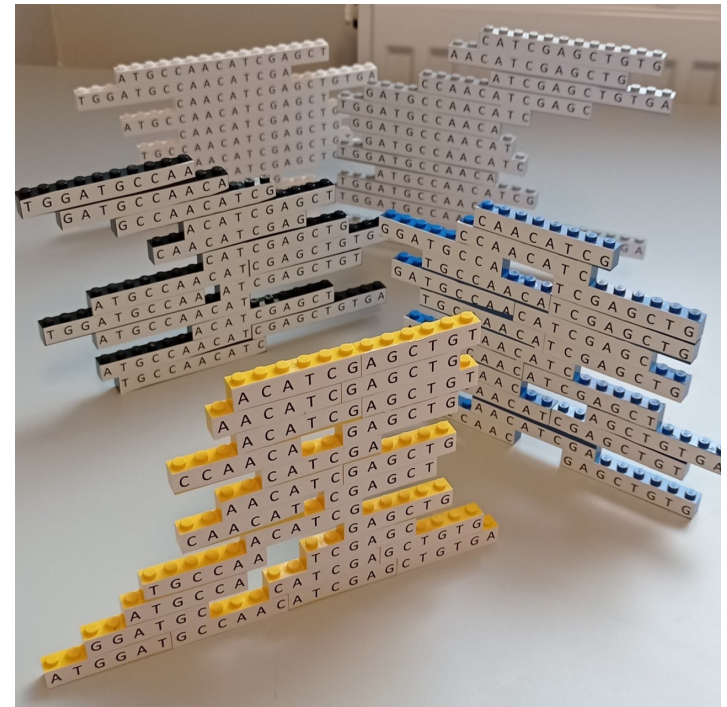
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ACGATATTACACGTACACTCACGTCGTTTCGGAA
ATTACACGTACACTCACGTCGTTTCGGAACCT
TACACGTACACTCAAGTCGTTTCGGAACCT
CACGTACACTCAAGTCGTTCTGAACCT
CACGTACACTCACGTCGTTTCGGAACCT





Análisis de Secuencias

ACGATATTACACGTACACTCAAGTCGT _____
TCGAGATTGCATGTACCCTCAAGCCGTCGG _____
ACGATATTACACGTACACTCACGTCGT _____
ACGATATTACACGTACACTCACGTCGTTTCGGA _____
ACGATATTACACGCACACTCAAGTCGTTTCGGAACCT _____
ACGATATTACACGTACACTCACGTCGTTTCGGAA _____
_____ ATTACACGTACACTCACGTCGTTTCGGAACCT
_____ TACACGTACACTCAAGTCGTTTCGGAACCT
_____ CACGTACACTCAAGTCGTTCTGAACCT
_____ CACGTACACTCACGTCGTTTCGGAACCT





Detección de variantes

ACGATATTACACGTACACTCAAGTCGT _____
TCGAGATTGCATGTACCTCAAGCCGT**CGG** _____
ACGATATTACACGTACACTCA**C**GTCGT _____
ACGATATTACACGTACACTCA**C**GTCGTT**CGGA** _____
ACGATATTACACG**C**ACACTCAAGTCGTT**CGGAACCT**
ACGATATTACACGTACACTCA**C**GTCGTT**CGGAA** _____
_____ ATTACACGTACACTCA**C**GTCGTT**CGGAACCT**
_____ TACACGTACACTCAAGTCGTT**CGGAACCT**
_____ CACGTACACTCAAGTCGTT**C**TGAACCT
_____ CACGTACACTCA**C**GTCGTT**CGGAACCT**



Detección de variantes

ACGATATTACACGTACACTCAAGTCGT _____
TCGAGATTGCATGTACCTCAAGCCGT**CGG** _____
ACGATATTACACGTACACTCA**C**GTCGT _____
ACGATATTACGTACACTCA**C**GTCGTTTCGGA _____
ACGATATTACACG**C**ACACTCAAGTCGTTTCGGAACCT
ACGATATTACACGTACACTCA**C**GTCGTTTCGGAA _____
_____ ATTACACGTACACTCA**C**GTCGTTTCGGAACT
_____ TACACGTACACTCAAGTCGTTTCGACCT
_____ CACGTACACTCAAGTCGTTCT**T**GAACCT
_____ CACGTACACTCA**C**GTCGTTTCGGAACCT



Detección de variantes

ACGATATTACACGTACACTCAAGTCGT _____	→ Calidad: 98/100
TCGAGATTGCATGTACCTCAAGCCGTCGG _____	→ Calidad: 14/100
ACGATATTACACGTACACTCA C GTCGT _____	→ Calidad: 95/100
ACGATATTAC CG GTACACTCA C GTCGTT CGGA _____	→ Calidad: 98/100
ACGATATTACAC G CACACTCAAGTCGTT CGGA ACCT	→ Calidad: 25/100
ACGATATTACACGTACACTCA C GTCGTT CGGA A _____	→ Calidad: 98/100
_____ATTACACGTACACTCA C GTCGTT CGGA CT	→ Calidad: 90/100
_____TACACGTACACTCAAGTCGTT CG ACCT	→ Calidad: 89/100
_____CACGTACACTCAAGTCGTT C TGAACCT	→ Calidad: 99/100
_____CACGTACACTCA C GTCGTT CGGA ACCT	→ Calidad: 95/100



Detección de variantes

ACGATATTACACGTACACTCAAGTCGT _____	→ Calidad: 98/100
TCGAGATTGCATGTACCCTCAAGCCGTGG _____	→ Calidad: 14/100
ACGATATTACACGTACACTCAAGTCGT _____	→ Calidad: 95/100
ACGATATTACACGTACACTCAAGTCGTTTCGGA _____	→ Calidad: 98/100
ACGATATTACACGCACACTCAAGTCGTTTCGGAACCT _____	→ Calidad: 25/100
ACGATATTACACGTACACTCAAGTCGTTTCGGAA _____	→ Calidad: 98/100
_____ ATTACACGTACACTCAAGTCGTTTCGGAACCT _____	→ Calidad: 90/100
_____ TACACGTACACTCAAGTCGTTTCGGAACCT _____	→ Calidad: 89/100
_____ CACGTACACTCAAGTCGTTCTGAACCT _____	→ Calidad: 99/100
_____ CACGTACACTCAAGTCGTTTCGGAACCT _____	→ Calidad: 95/100



Detección de variantes

ACGATATTACACGTACACTCAAGTCGATCGGAACCT	→ Referencia
ACGATATTACACGTACACTCAAGTCGT_____	→ Calidad: 98/100
TCGAGATTGCATGTACCCTCAAGCCGTCTGG_____	→ Calidad: 14/100
ACGATATTACACGTACACTCACGTCGT_____	→ Calidad: 95/100
ACGATATTACACGTACACTCACGTCGTTCTGGA_____	→ Calidad: 98/100
ACGATATTACACGCACACTCAAGTCGTTCTGGAACCT	→ Calidad: 25/100
ACGATATTACACGTACACTCACGTCGTTCTGGAA_____	→ Calidad: 98/100
_____ATTACACGTACACTCACGTCGTTCTGGAACCT	→ Calidad: 90/100
_____TACACGTACACTCAAGTCGTTCTGGAACCT	→ Calidad: 89/100
_____CACGTACACTCAAGTCGTTCTGAACCT	→ Calidad: 99/100
_____CACGTACACTCACGTCGTTCTGGAACCT	→ Calidad: 95/100



Detección de variantes

ACGATATTACACGTACACTCAAGTCGATCGGAACCT

ACGATATTACACGTACACTCAAGTCG T _____	→ Calidad: 98/100
T CGAGATT G CA T GTAC C CTCAAG C CG T CGG_____	→ Calidad: 14/100
ACGATATTACACGTACACTCA C GTCG T _____	→ Calidad: 95/100
ACGATATTACACGTACACTCA C GTCG T TCGGA_____	→ Calidad: 98/100
ACGATATTACACG C ACACTCAAGTCG T TCGGAACCT	→ Calidad: 25/100
ACGATATTACACGTACACTCA C GTCG T TCGGAA_____	→ Calidad: 98/100
_____ATTACACGTACACTCA C GTCG T TCGGAACCT	→ Calidad: 90/100
_____TACACGTACACTCAAGTCG T TCGGAACCT	→ Calidad: 89/100
_____CACGTACACTCAAGTCG T TC T GAACCT	→ Calidad: 99/100
_____CACGTACACTCA C GTCG T TCGGAACCT	→ Calidad: 95/100



Medicina Personalizada

- www.pandrugs.org

Welcome to
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A novel method for
prioritizing therapies using
individual genomic data

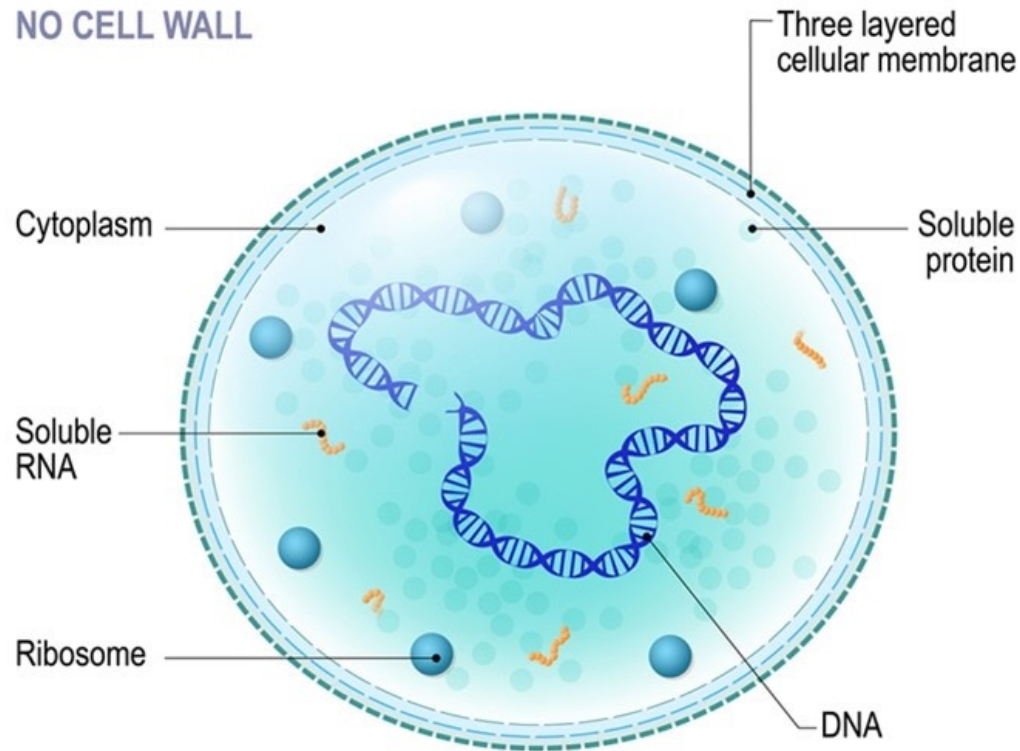
Query! ✓



Biología de sistemas

Mycoplasma

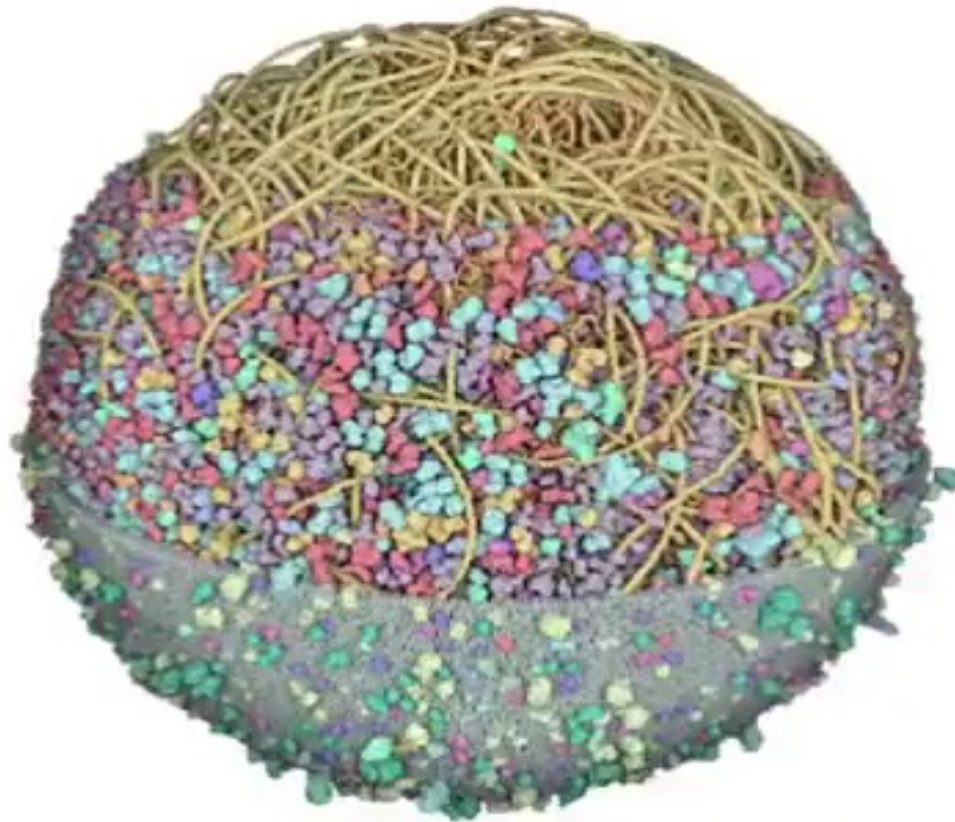
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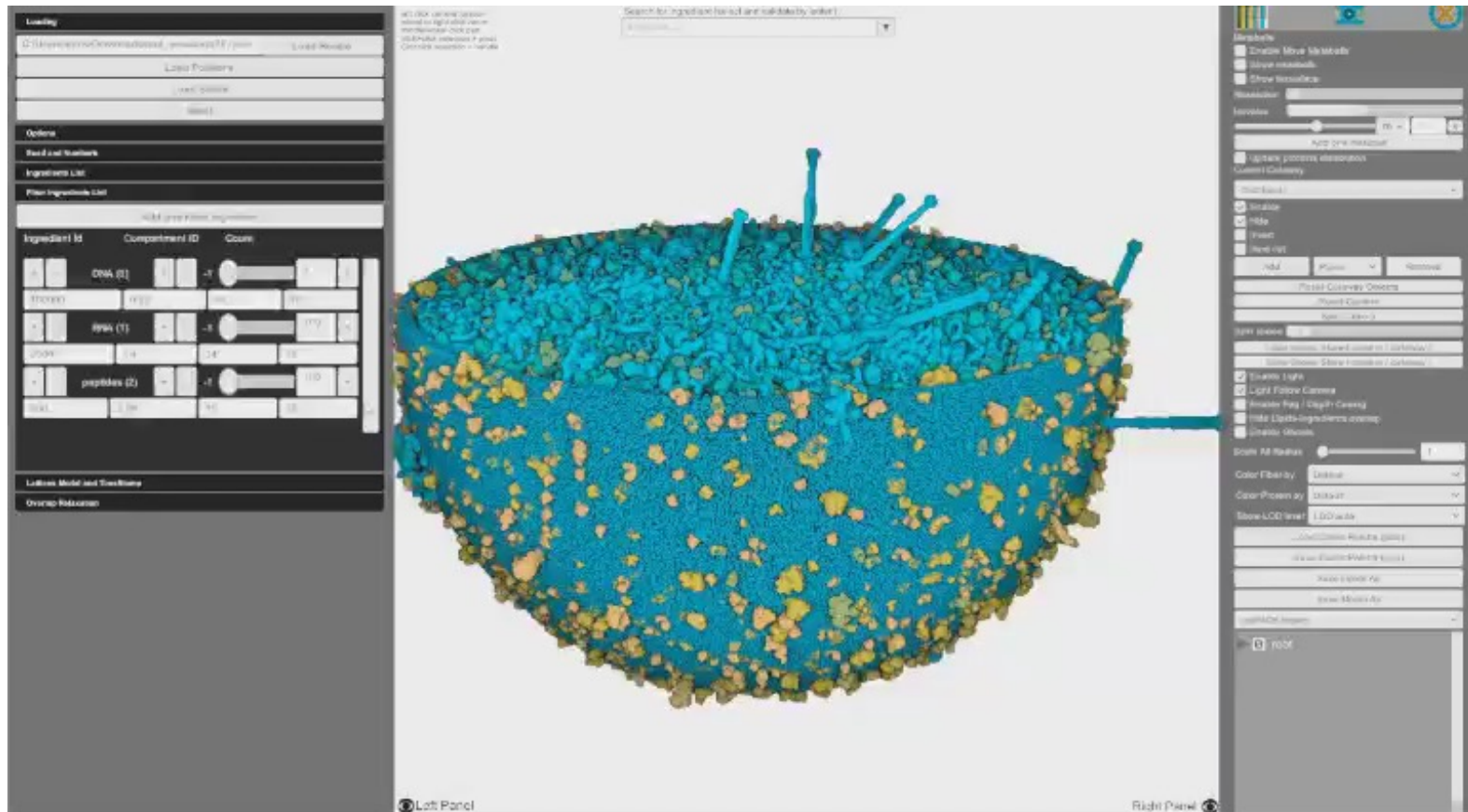
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Biología de sistemas





Biología de sistemas





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Análisis de imágenes clínicas

X-Ray Classification [Pneumonia/Normal]

by Hardik :)

Upload X-Ray Image



Drag and drop file here

Limit 200MB per file

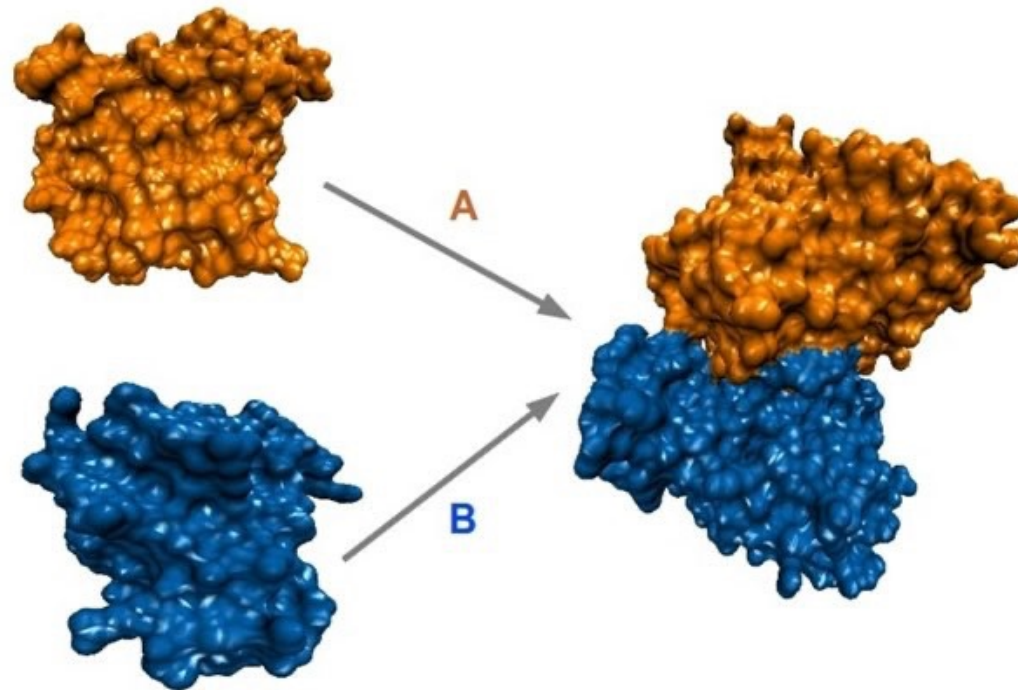
Browse files

<https://cutt.ly/jlf5HM7>



Modelado de proteínas

- Diseño de fármacos





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Plegado de proteínas





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Plegado de proteínas





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Más problemas: Rosalind

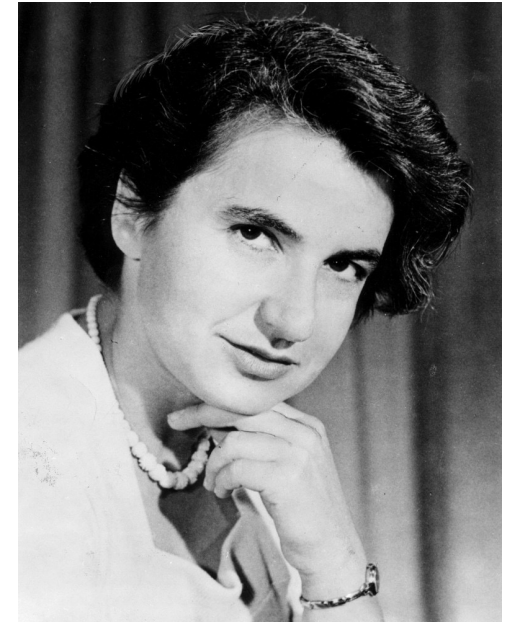


<https://rosalind.info/problems/list-view/>



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Más problemas: Rosalind



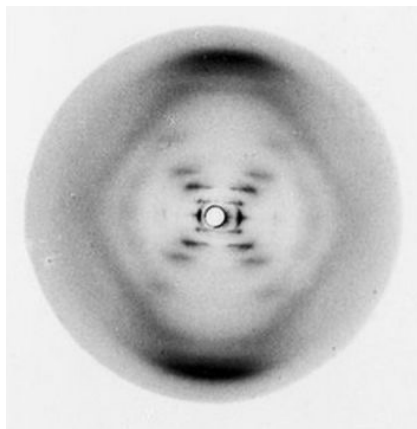
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Más problemas: Rosalind

R  SALIND



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