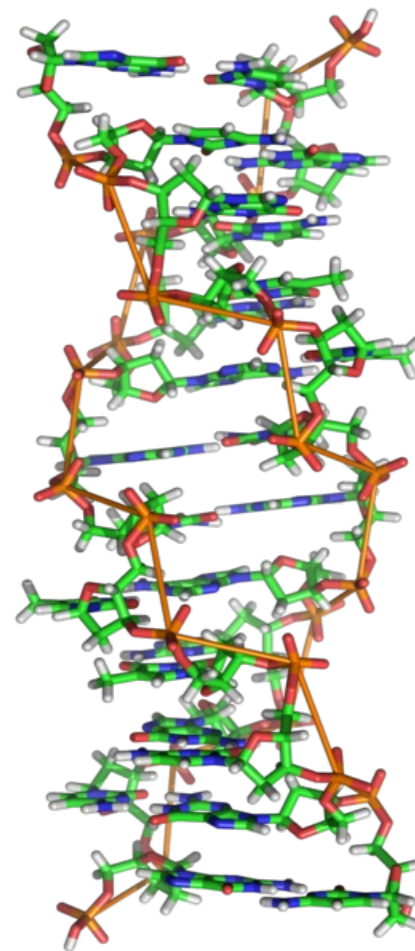
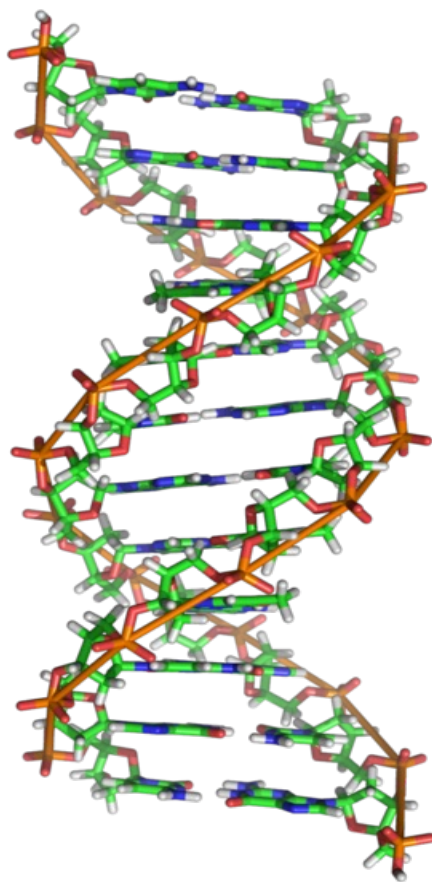
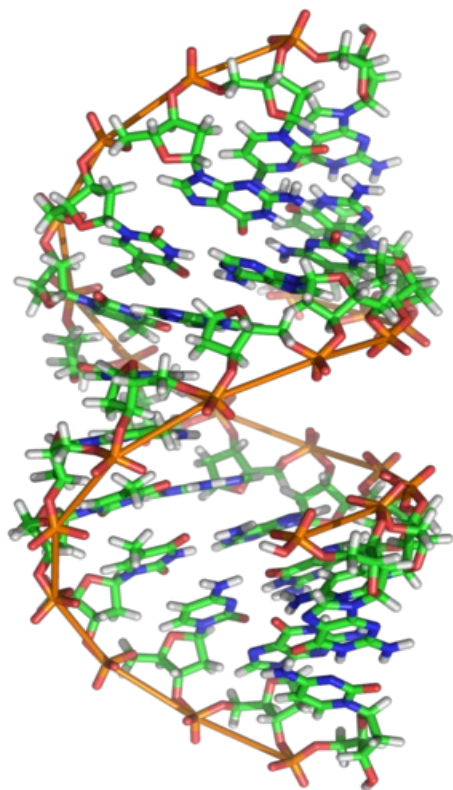




La bioinformática permite investigar, desarrollar y aplicar herramientas informáticas y computacionales para permitir y mejorar el manejo de datos biológicos.

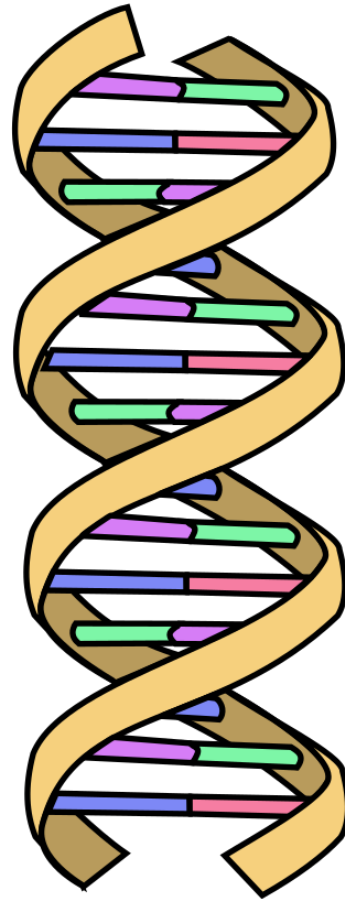



*La bioinformática permite investigar, desarrollar y aplicar herramientas informáticas y computacionales para permitir y mejorar el manejo de **datos biológicos**.*






ADN




 = Adenine

 = Thymine

 = Cytosine

 = Guanine

 = Phosphate
backbone



ADN

- Human Genome Project





ADN

- Human Genome Project





ADN

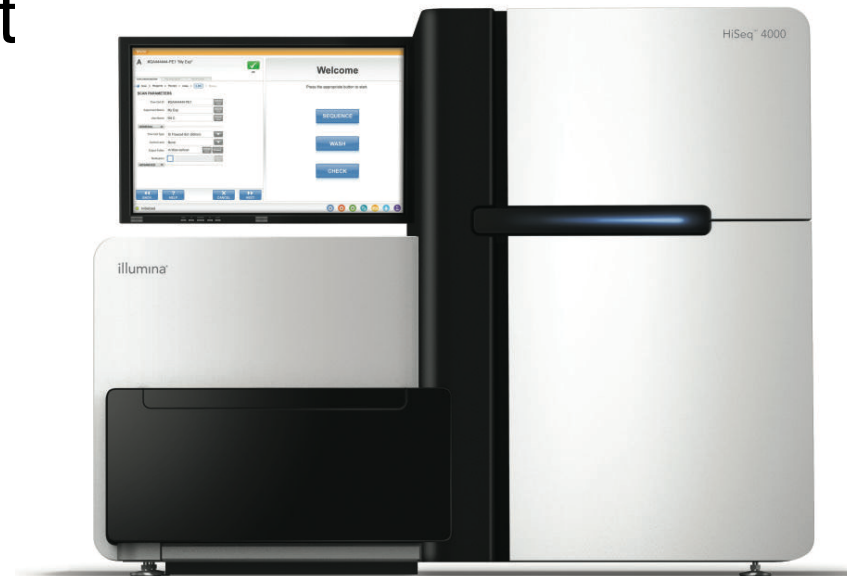
- Human Genome Project
- 3.000.000.000 bases
- 3.4 GB





ADN

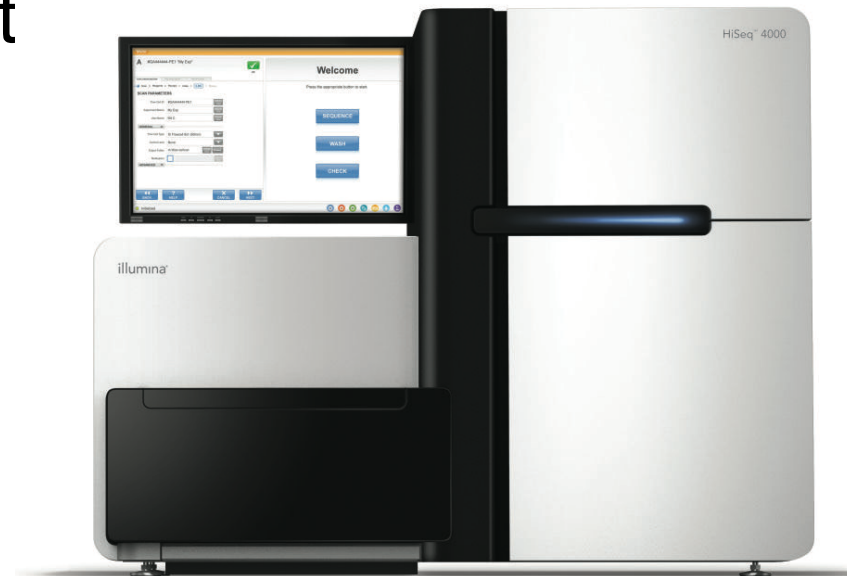
- Human Genome Project
- 3.000.000.000 bases
- 3.4 GB





ADN

- Human Genome Project
- 3.000.000.000 bases
- 3.4 GB



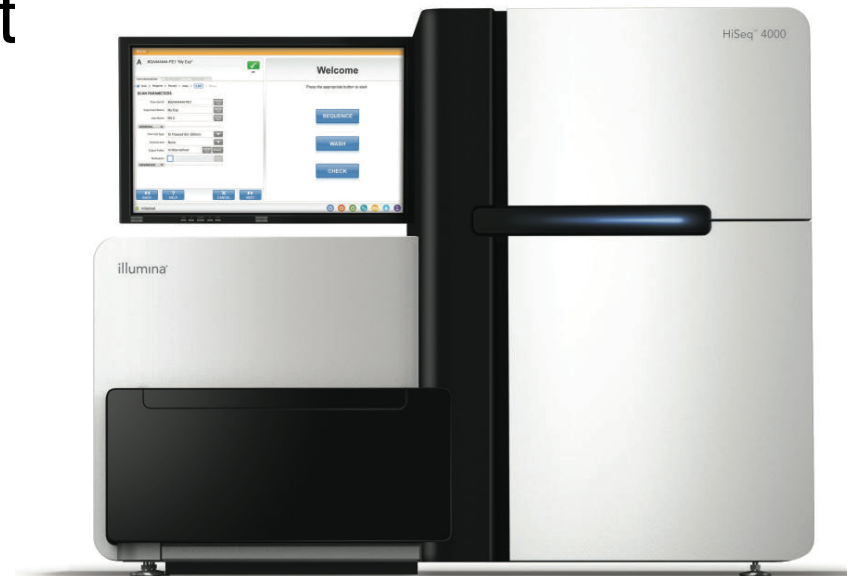
1.000.000 \$



ADN

- Human Genome Project
- 3.000.000.000 bases
- 3.4 GB

Coste del Human Genome Project:



1.000.000 \$

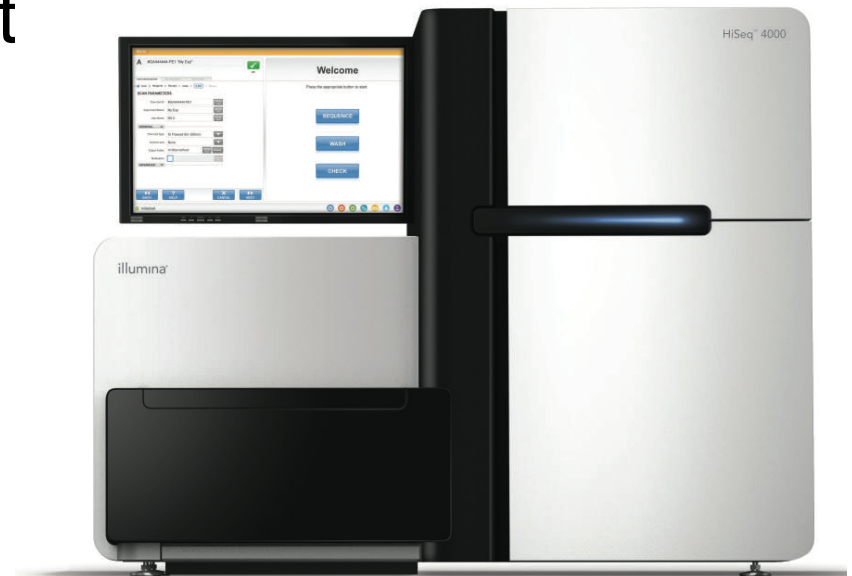


ADN

- Human Genome Project
- 3.000.000.000 bases
- 3.4 GB

Coste del Human Genome Project:

3.000.000.000 \$

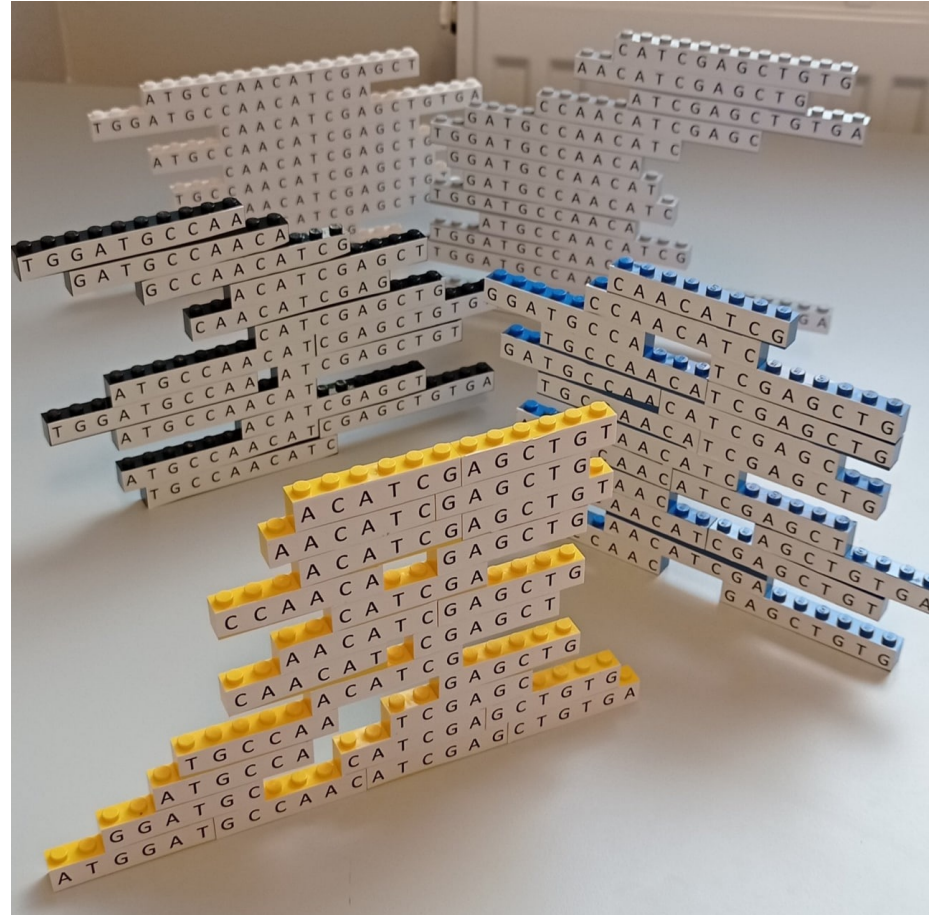


1.000.000 \$



ADN

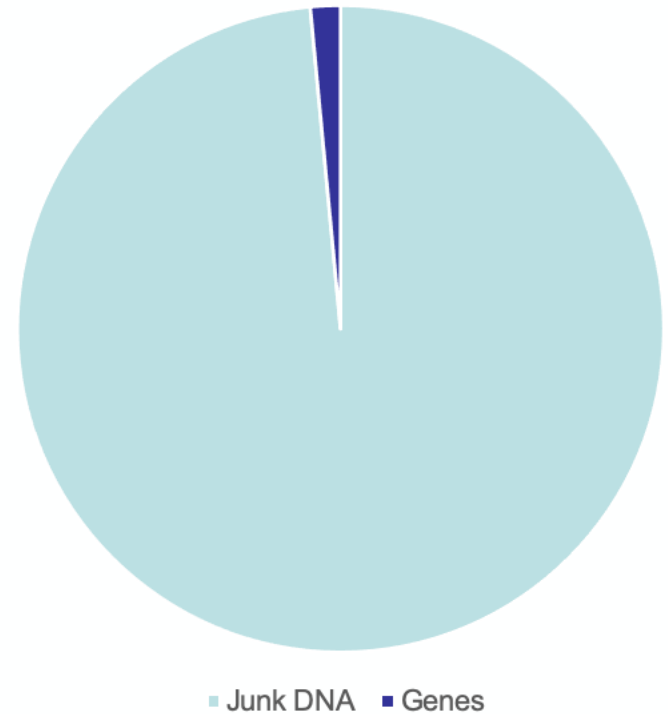
- Ensamblado:





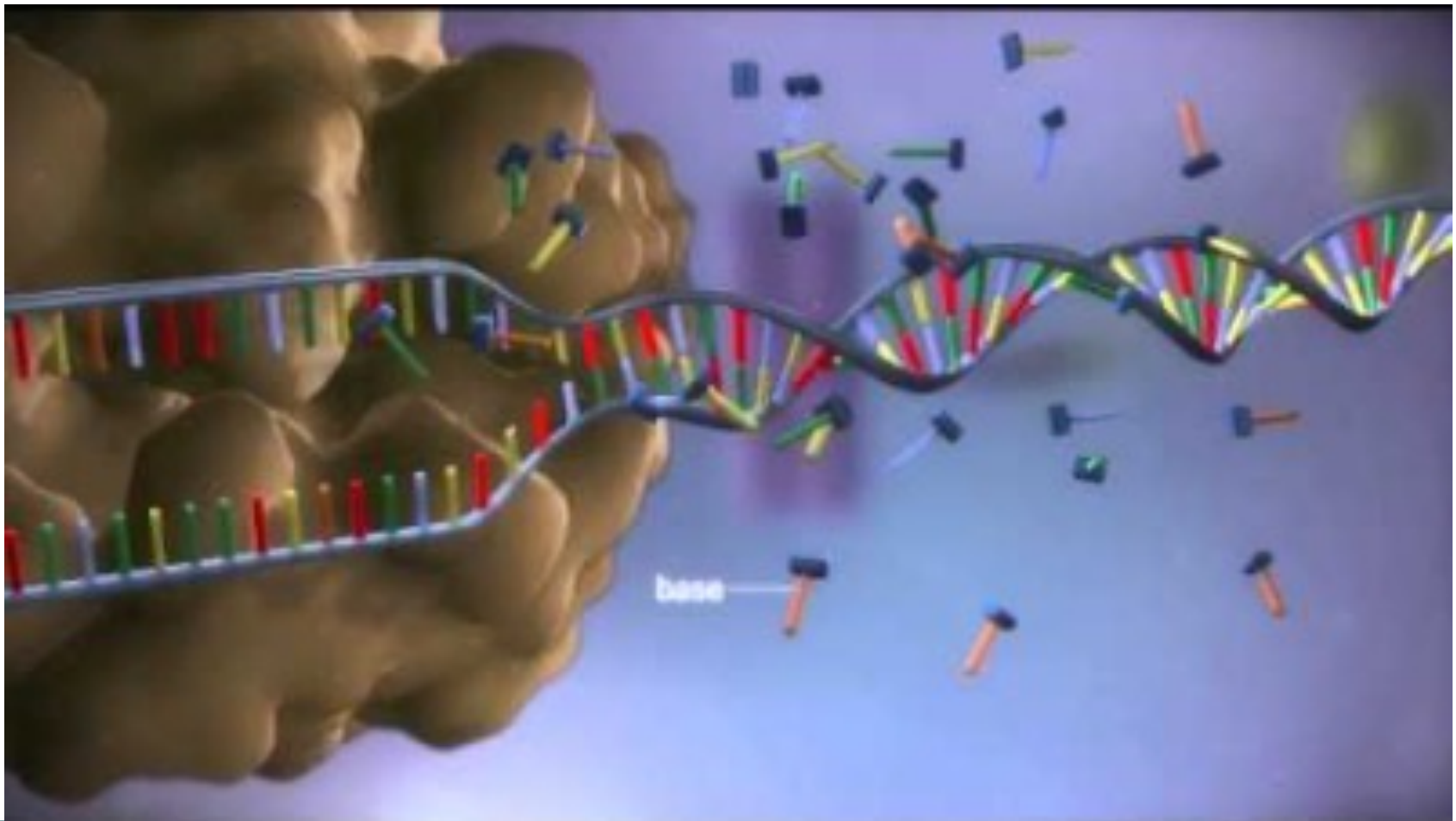
ADN

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





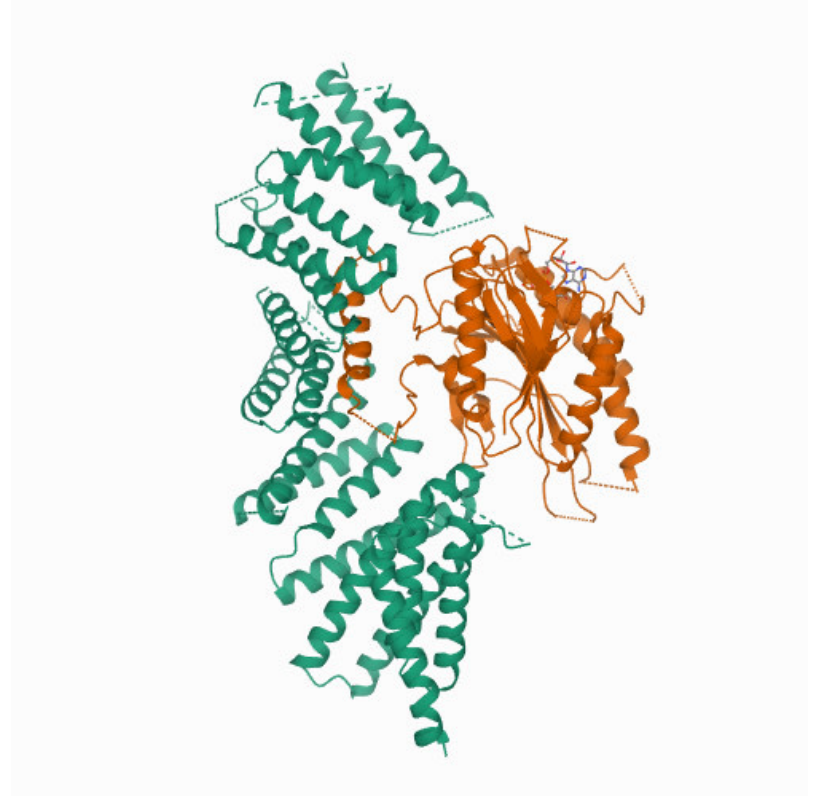
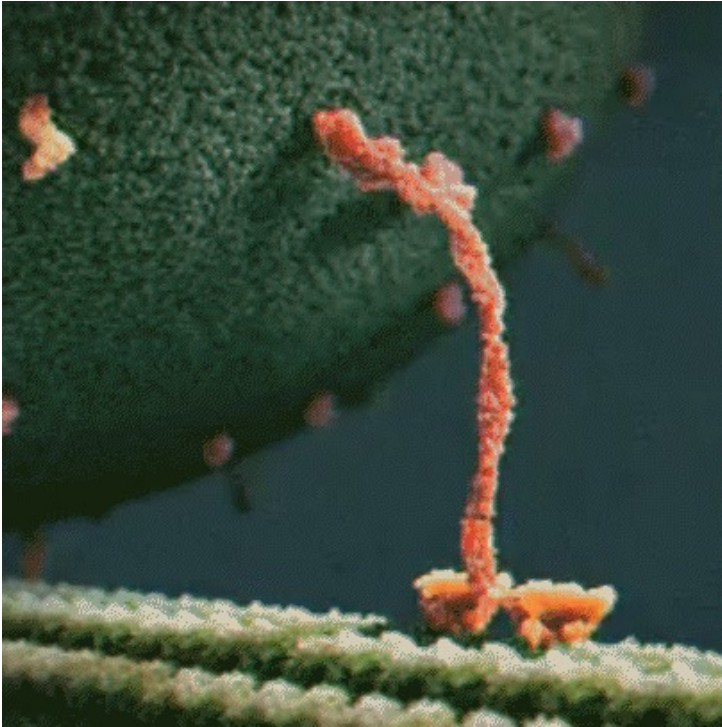
ARN





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Proteínas

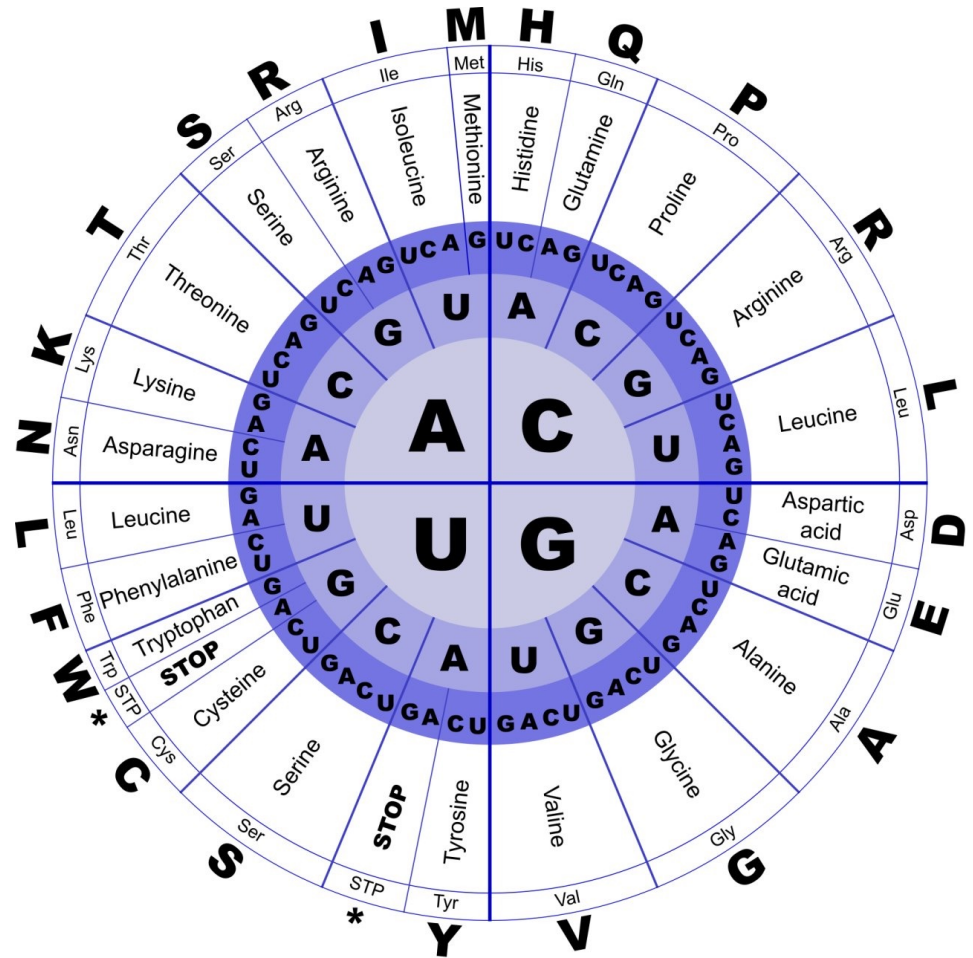


<https://bit.ly/3D6ZPH>



Proteínas

ADN: ATGTGTCCATAG





ADN: **ATGTGTCCATAG**

The circular genetic code chart (codon wheel) displays the mapping from mRNA codons to amino acids. The center contains the four bases A, C, U, G. The first ring shows the second base, and the second ring shows the third base. The outer edge lists the amino acids in three-letter codes. Stop codons are marked with an asterisk.

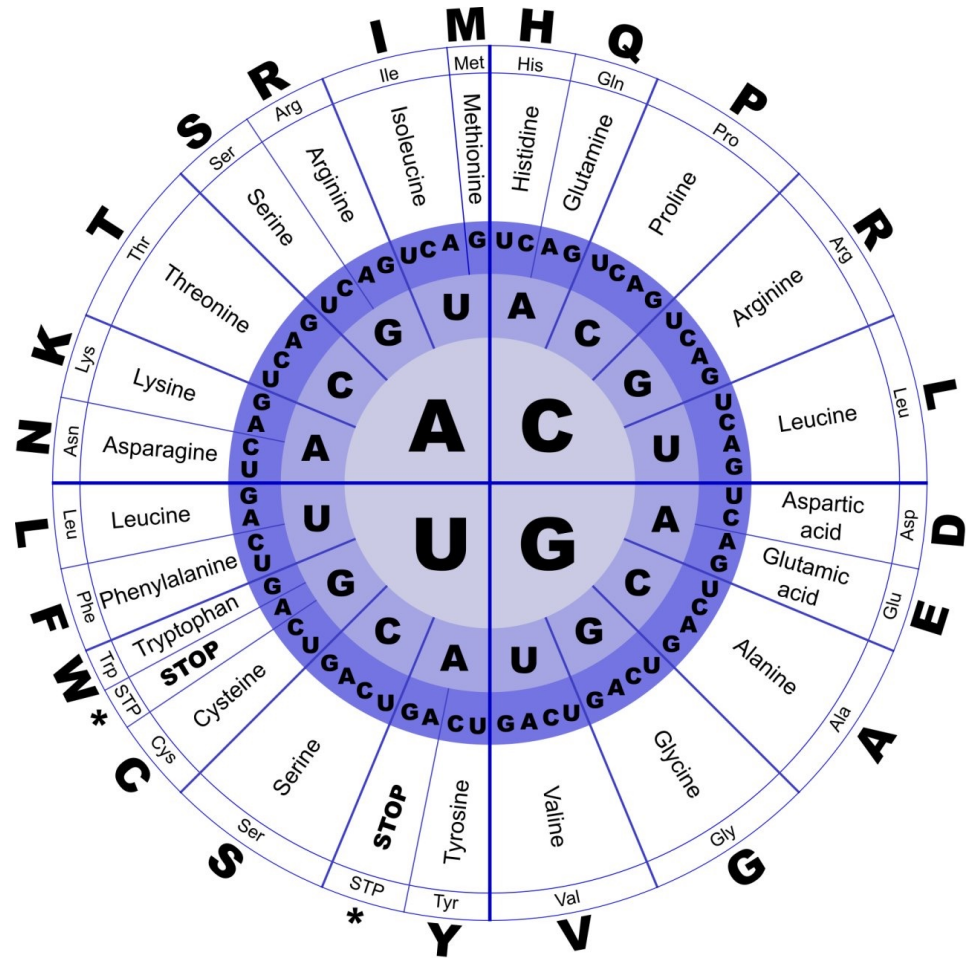
First Base	Second Base	Third Base	Amino Acid
A	U	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
A	C	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
A	G	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
A	U	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
C	U	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
C	C	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
C	G	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
C	U	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
U	U	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
U	C	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
U	G	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
U	U	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
G	U	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
G	C	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
G	G	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine
G	U	A	Asparagine
		C	Asparagine
		G	Asparagine
		U	Asparagine



Proteínas

ADN: ATGTGTCCATAG

ARN: AUGUGUCCAUAG



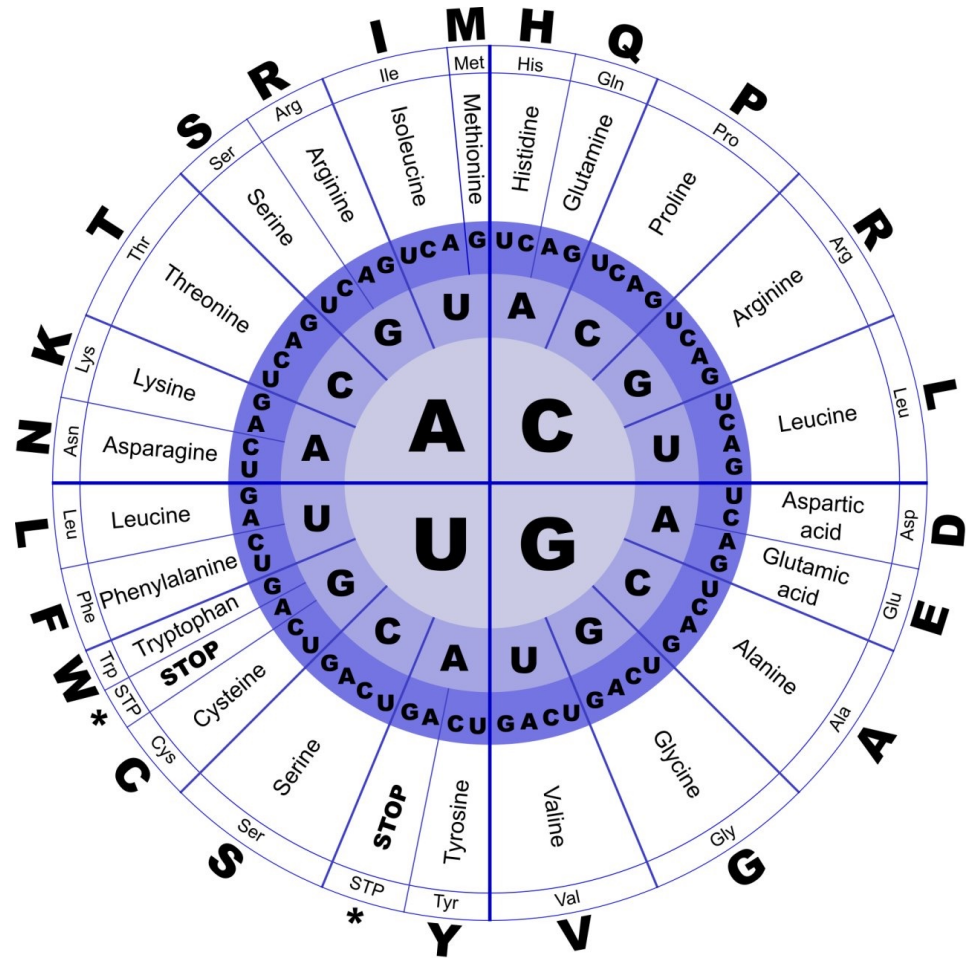


Proteínas

ADN: ATGTGTCCATAG

ARN: AUGUGUCCAUAG

P:



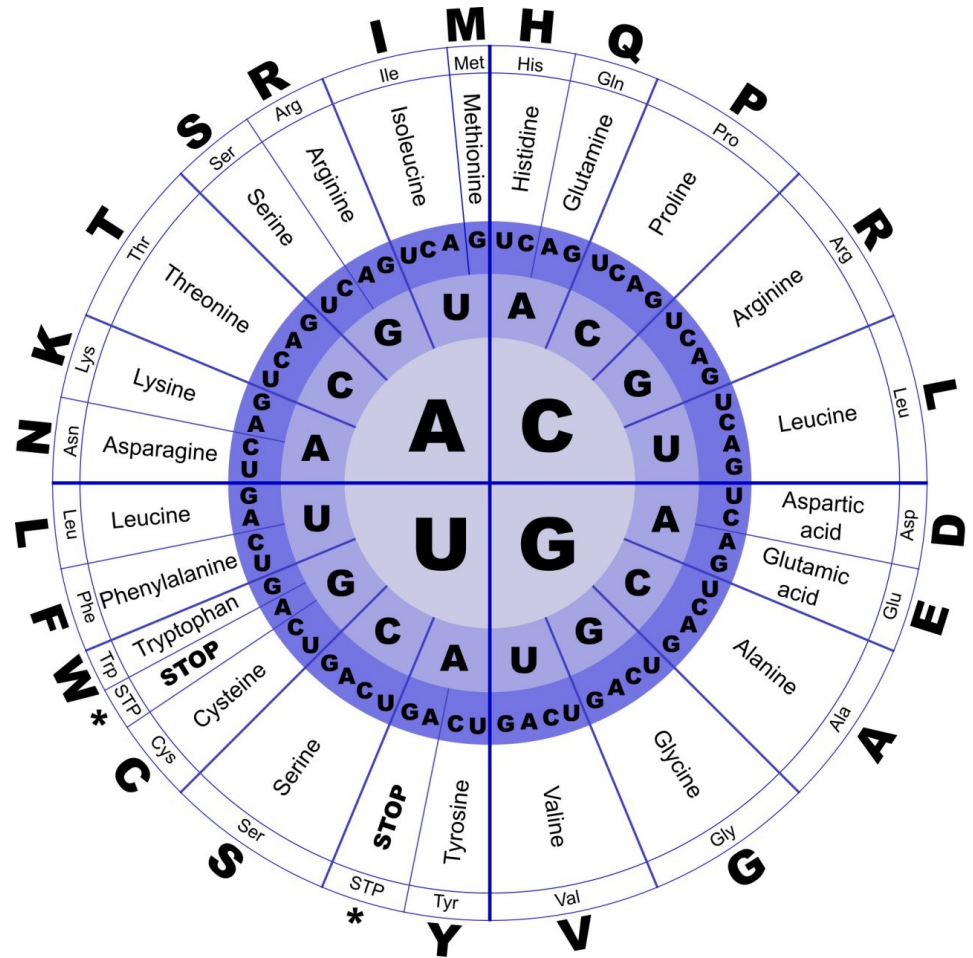


Proteínas

ADN: ATG TGT CCA TAG

ARN: AUG UGU CCA UAG

P:



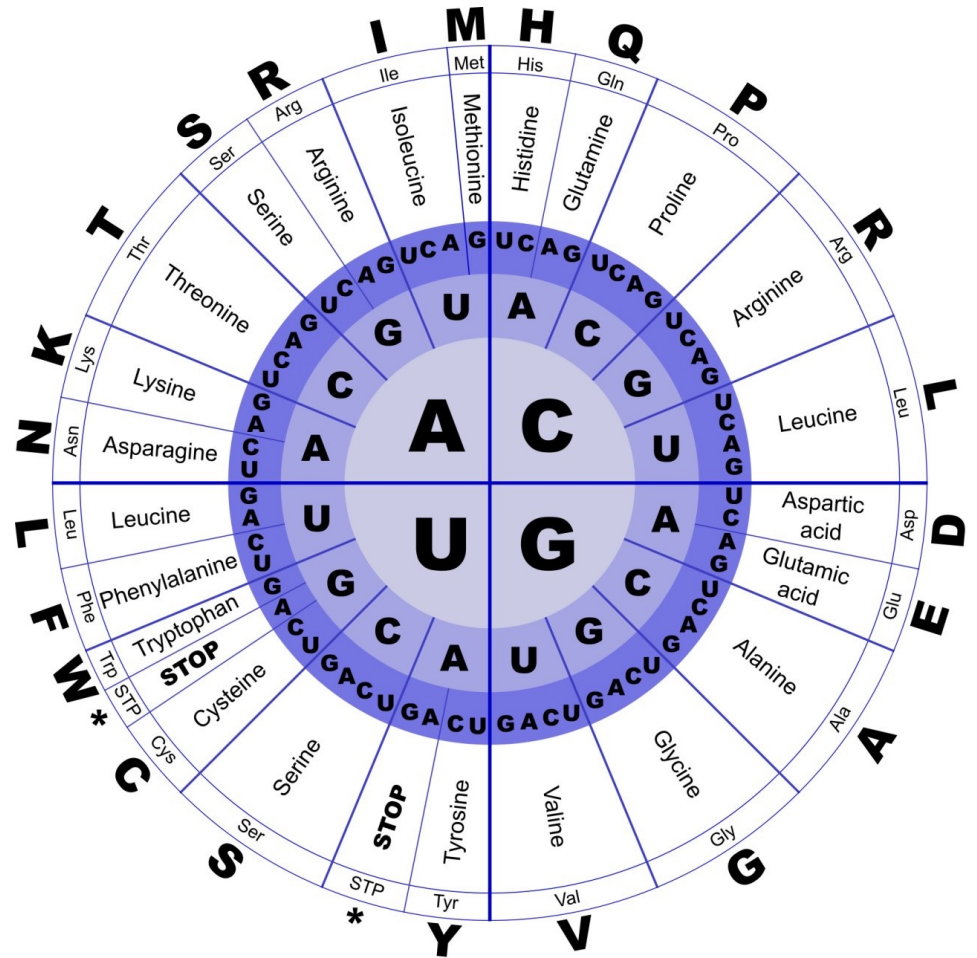


Proteínas

ADN: ATG TGT CCA TAG

ARN: AUG UGU CCA UAG

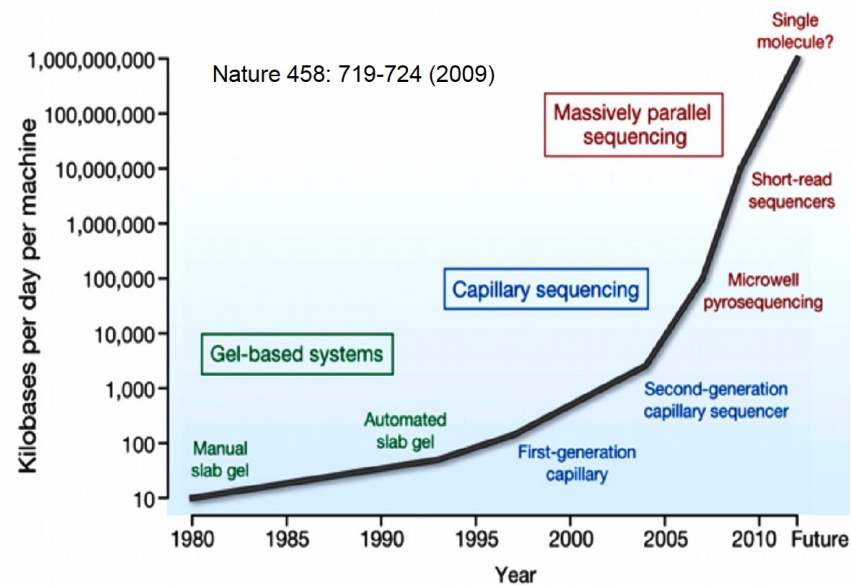
P: M C P *





Automatización

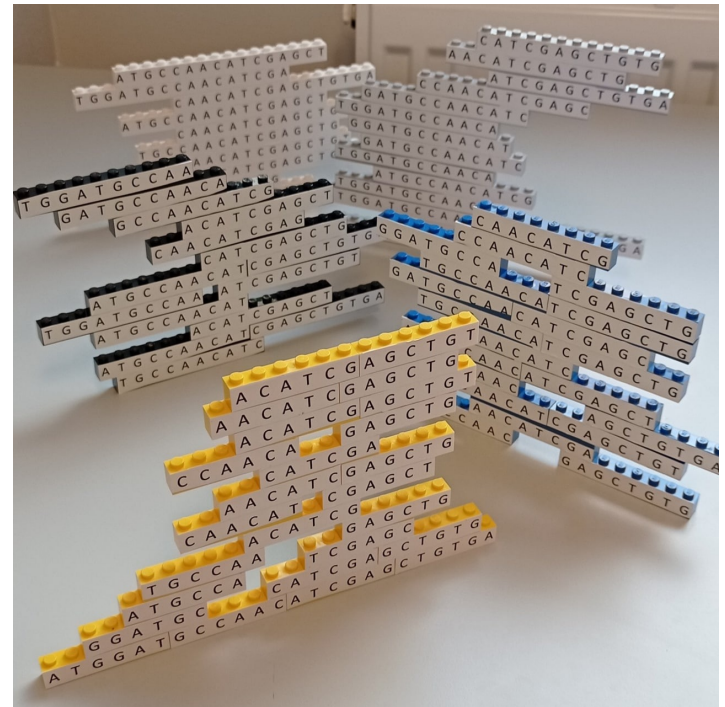
- 0 y 1 – A, C, G, T
- Menor coste → Más datos





Análisis de Secuencias

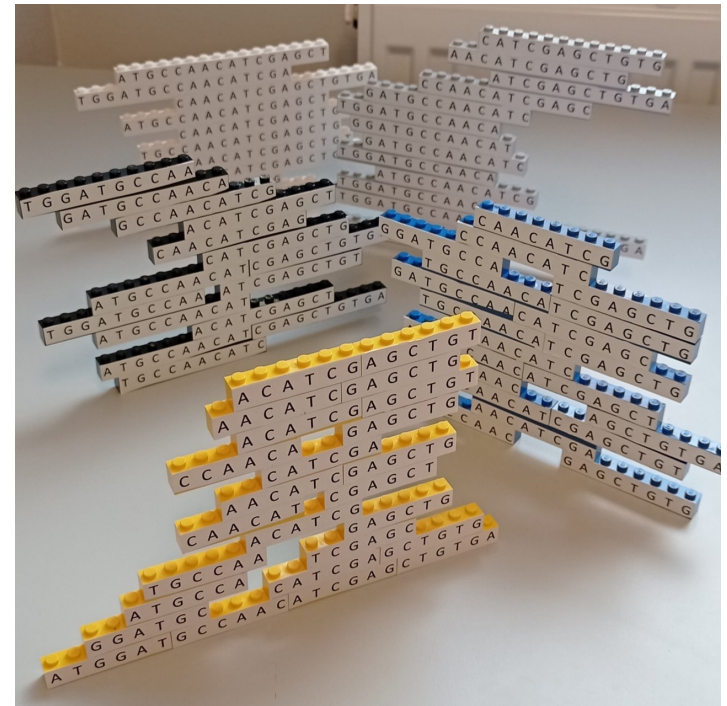
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TCGAGATTGCATGTACCCTCAAGCCGTCGG
ACGATATTACACGTACACTCACGTCGT
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ACGATATTACACGTACACTCACGTCGTTTCGGAA
ATTACACGTACACTCACGTCGTTTCGGAACCT
TACACGTACACTCAAGTCGTTTCGGAACCT
CACGTACACTCAAGTCGTTCTGAACCT
CACGTACACTCACGTCGTTTCGGAACCT





Análisis de Secuencias

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





Detección de variantes

ACGATATTACACGTACACTCAAGTCGT _____
TCGAGATTGCATGTACCCTCAAGCCGT**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 _____
TCGAGATTGCATGTACCCTCAAGCCGT**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
TCGAGATTGCATGTACCCTCAAGCCGTCGG _____	→ Calidad: 14/100
ACGATATTACACGTACACTCA C GTCGT _____	→ Calidad: 95/100
ACGATATTAC C GTACACTCA C GTCGTT CGGA _____	→ Calidad: 98/100
ACGATATTACAC G CACACTCAAGTCGTT CGGAACCT	→ Calidad: 25/100
ACGATATTACACGTACACTCA C GTCGTT CGGAA _____	→ 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 CGGAAACCT	→ Calidad: 95/100



Detección de variantes

ACGATATTACACGTACACTCAAGTCGT _____	→ Calidad: 98/100
TCGAGATTGCATGTACCTCAAGCCGTCCG _____	→ 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

50%



Detección de variantes

ACGATATTACACGTACACTCAAGTCGATCGGAACCT → Referencia

ACGATATTACACGTACACTCAAGTCGT_____ → Calidad: 98/100

TCGAGATTGCATGTACCTCAAGCCGTCGG****_____ → Calidad: 14/100

ACGATATTACACGTACACTCA**C**GTCGT_____ → Calidad: 95/100

ACGATATTACACGTACACTCA**C**GTCGTT**CGGA**_____ → Calidad: 98/100

ACGATATTACACG**C**ACACTCAAGTCGTT**CGGAACCT** → Calidad: 25/100

ACGATATTACACGTACACTCA**C**GTCGTT**CGGAA**_____ → Calidad: 98/100

_____ATTACACGTACACTCA**C**GTCGTT**CGGAACCT** → Calidad: 90/100

_____TACACGTACACTCAAGTCGTT**CGGAACCT** → Calidad: 89/100

_____CACGTACACTCAAGTCGTT**C****TGAACCT** → Calidad: 99/100

_____CACGTACACTCA**C**GTCGTT**CGGAACCT** → 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
PANDRUGS

A novel method for
prioritizing therapies using
individual genomic data

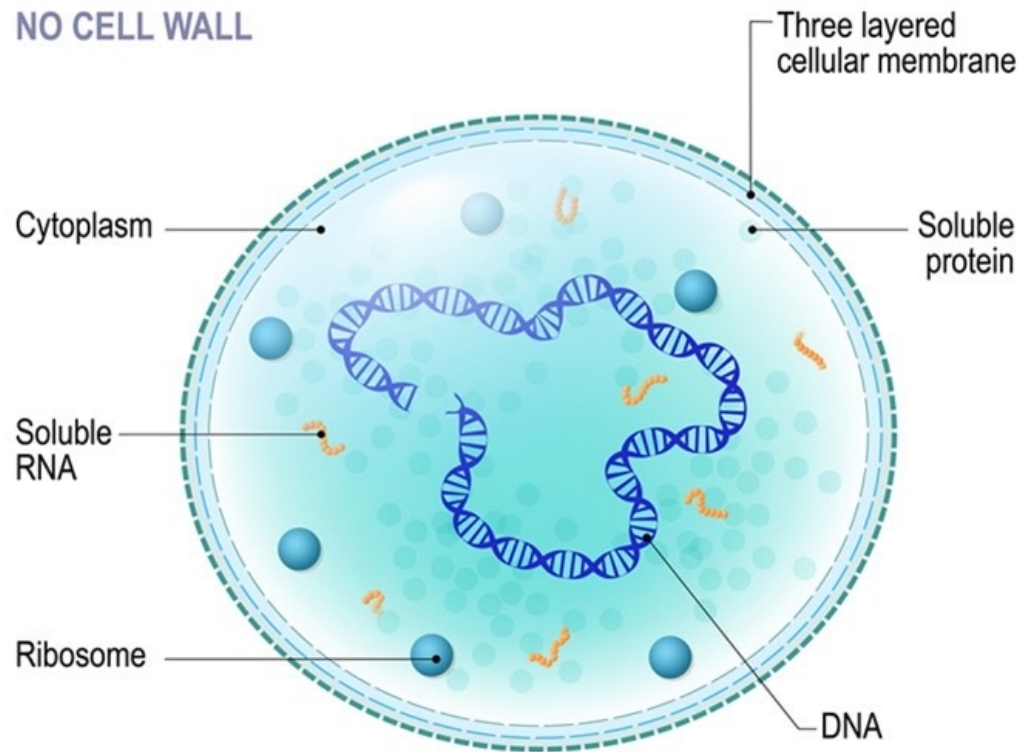
Query! ✓



Biología de sistemas

Mycoplasma

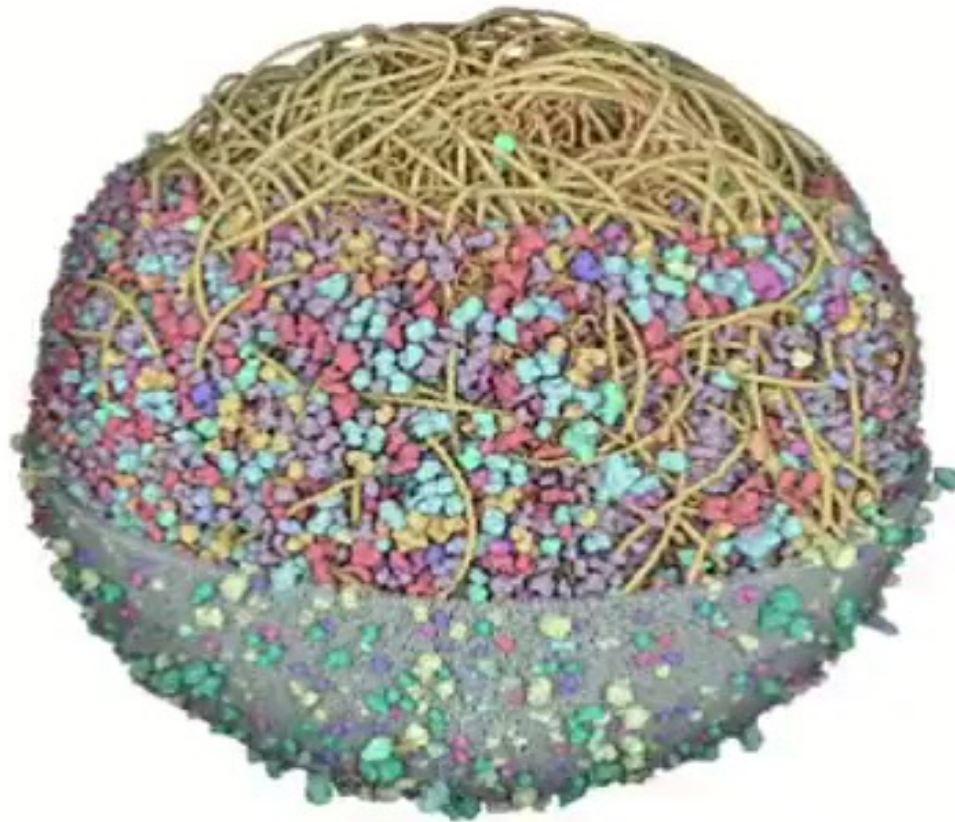
NO CELL WALL





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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

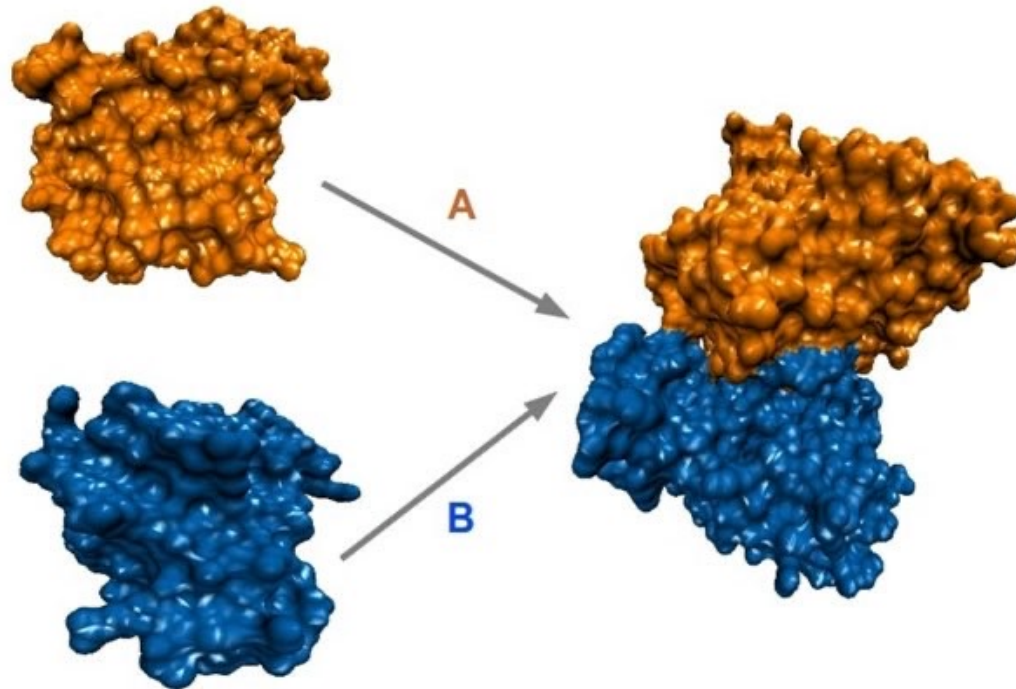
Browse files

<https://bit.ly/XRAYBIE>



Modelado de proteínas

- Diseño de fármacos





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Plegado de proteínas





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Plegado de proteínas

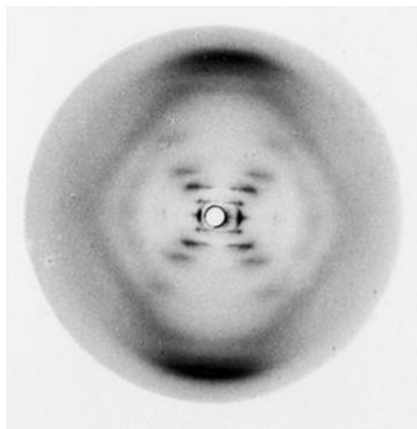




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Más problemas: Rosalind

R  SALIND



<https://bit.ly/BIERosalind>