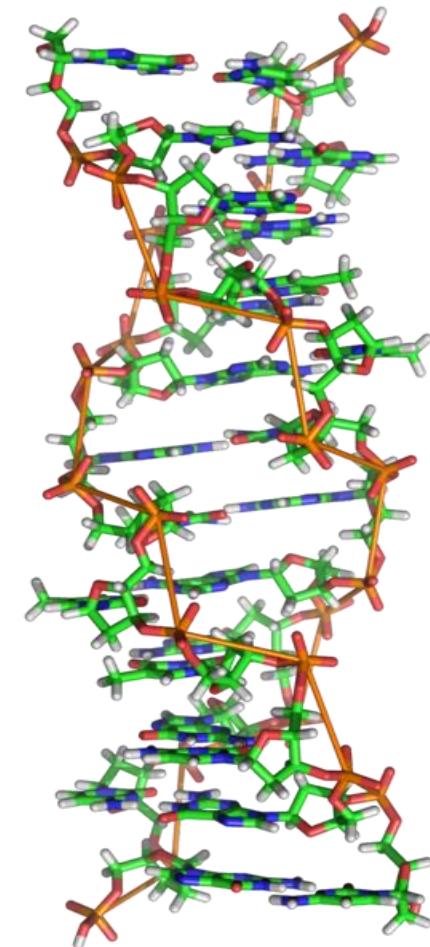
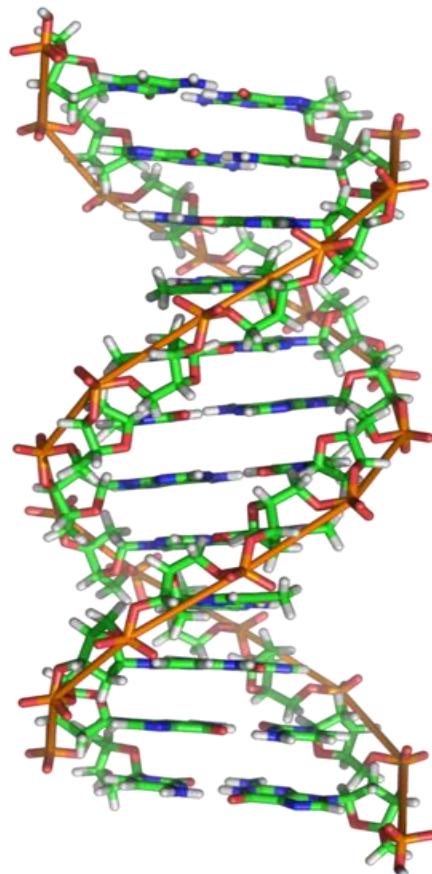
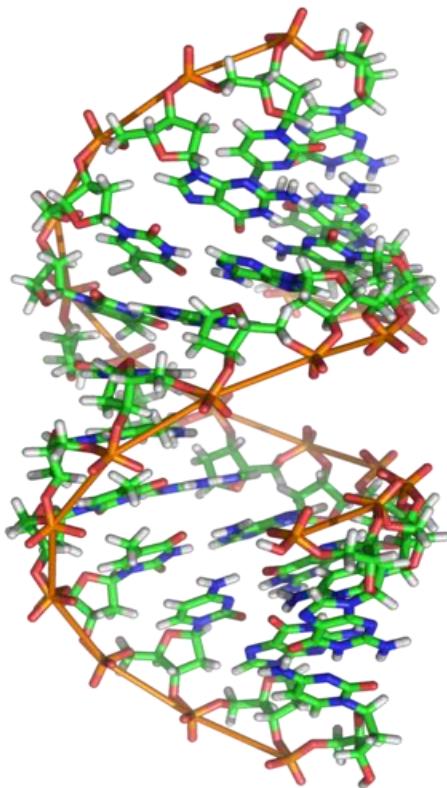




La bioinformática permite investigar, desarrollar y aplicar herramientas informáticas y computacionales para permitir y mejorar el manejo de datos biológicos.

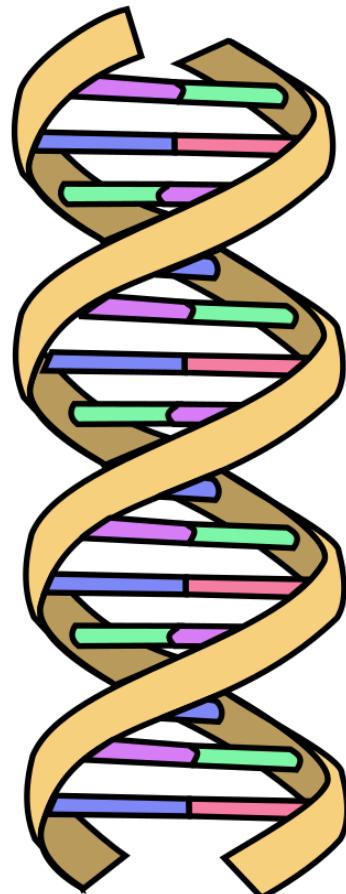


*La bioinformática permite investigar, desarrollar y aplicar herramientas informáticas y computacionales para permitir y mejorar el manejo de **datos biológicos**.*





ADN



- = Adenine
- = Thymine
- = Cytosine
- = Guanine

- = Phosphate backbone



ADN

- Human Genome Project





ADN

- Human Genome Project



<https://www.youtube.com/watch?v=s6rJLXq1Re0>





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 \$

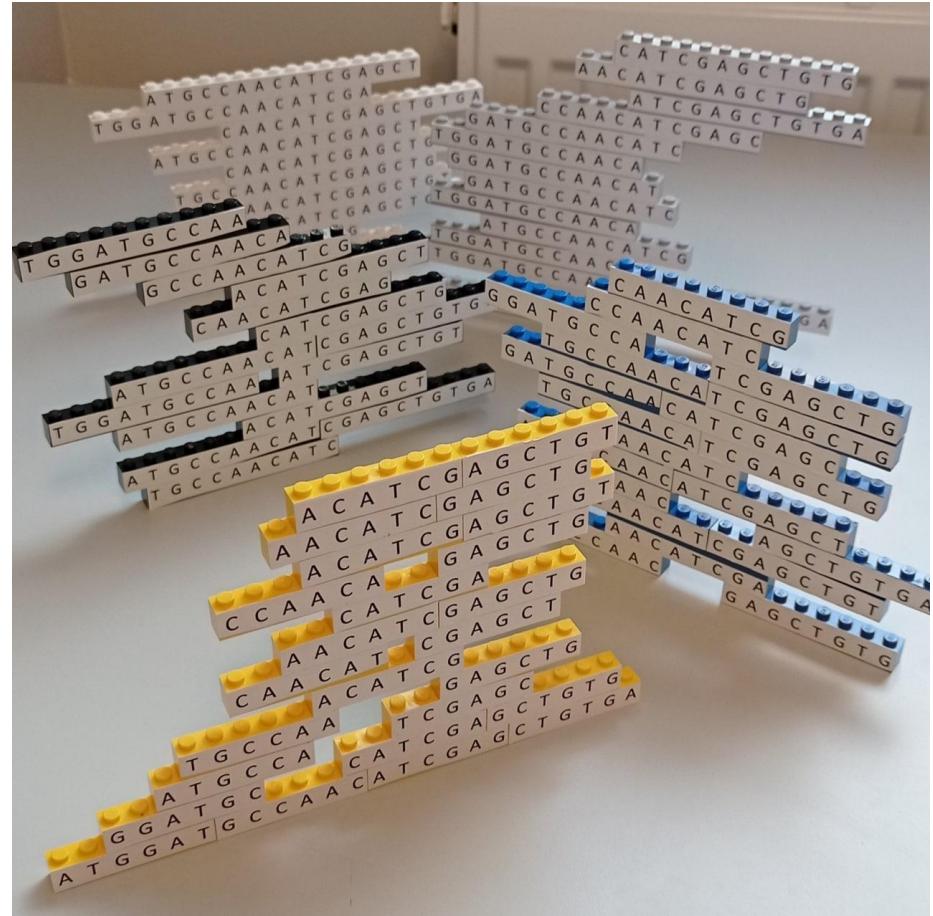


1.000.000 \$



ADN

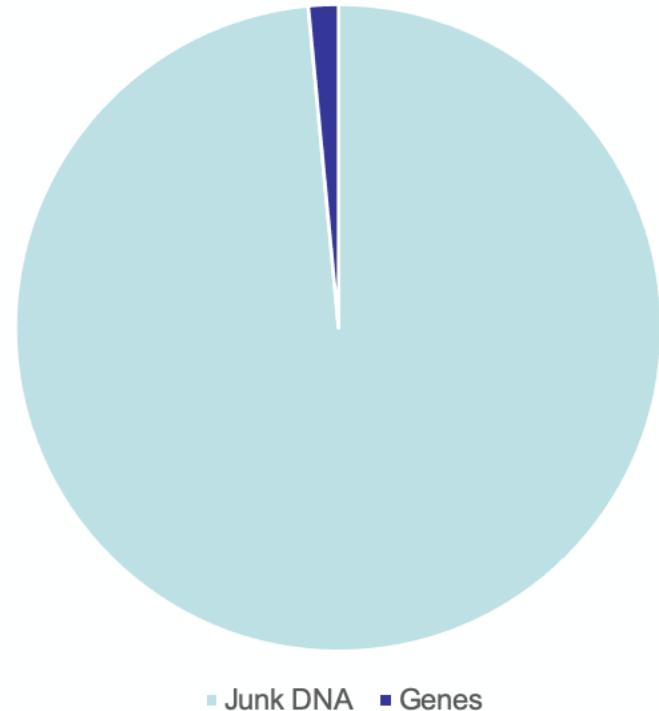
- Ensamblado:





ADN

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





¡A programar!

Tecnología

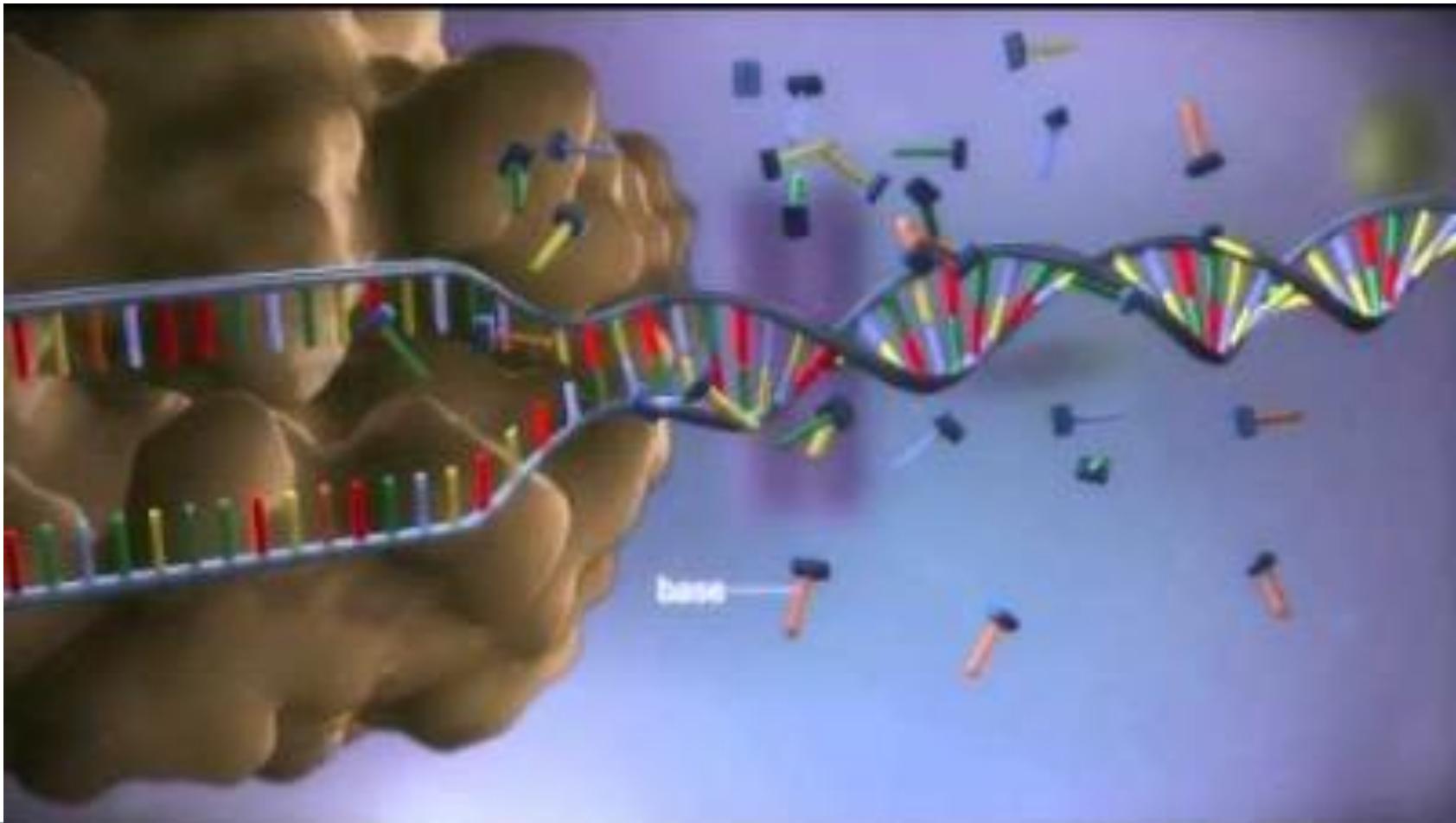
Python
Notebooks



bit.ly/BIEBio



ARN



<https://www.youtube.com/watch?v=gG7uCskUOrA>



¡A programar!

Tecnología

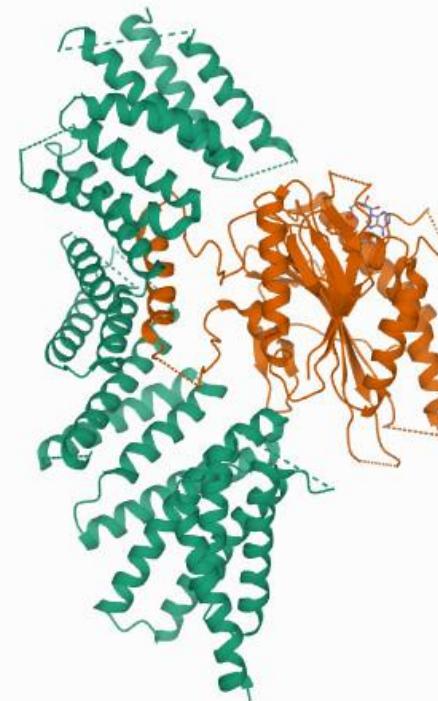
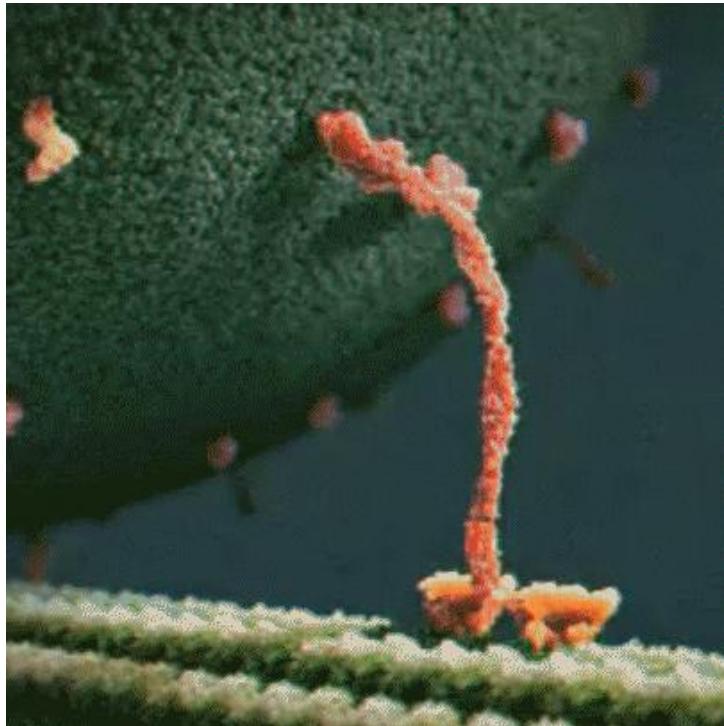
Python
Notebooks



bit.ly/BIEBio



Proteínas

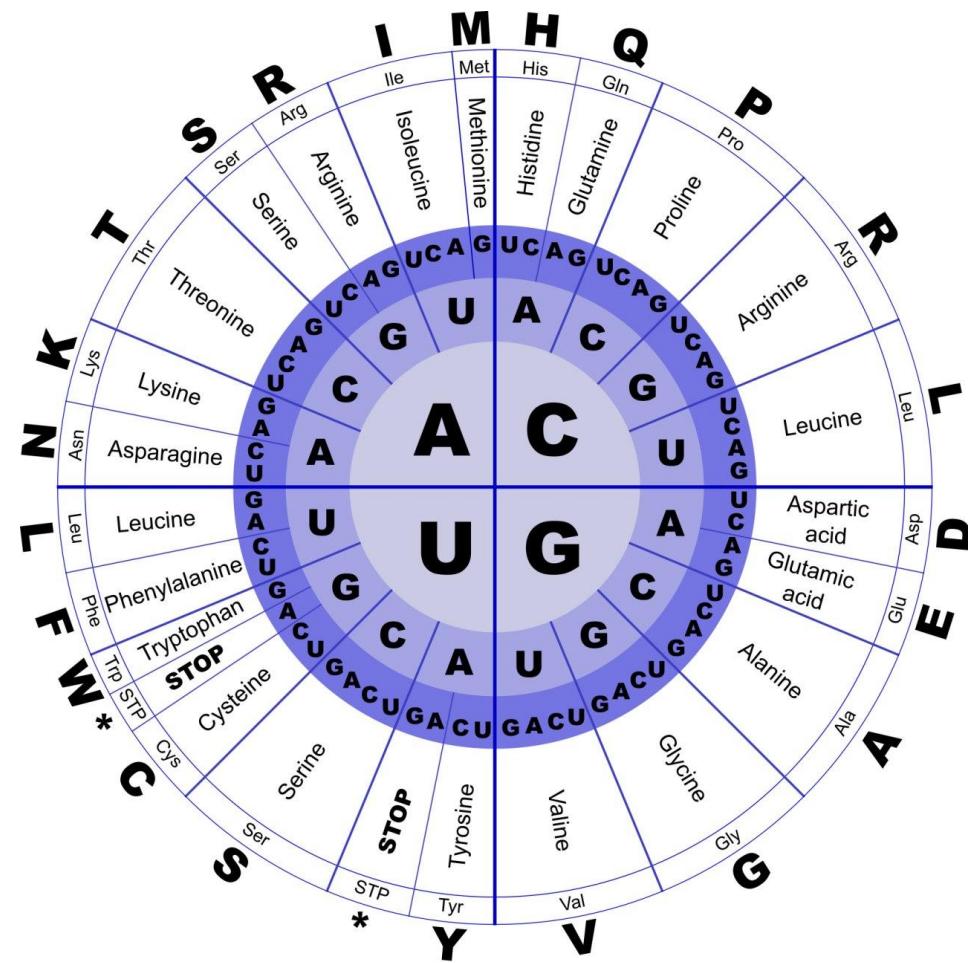


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Proteínas

ADN: ATGTGTCCATAG

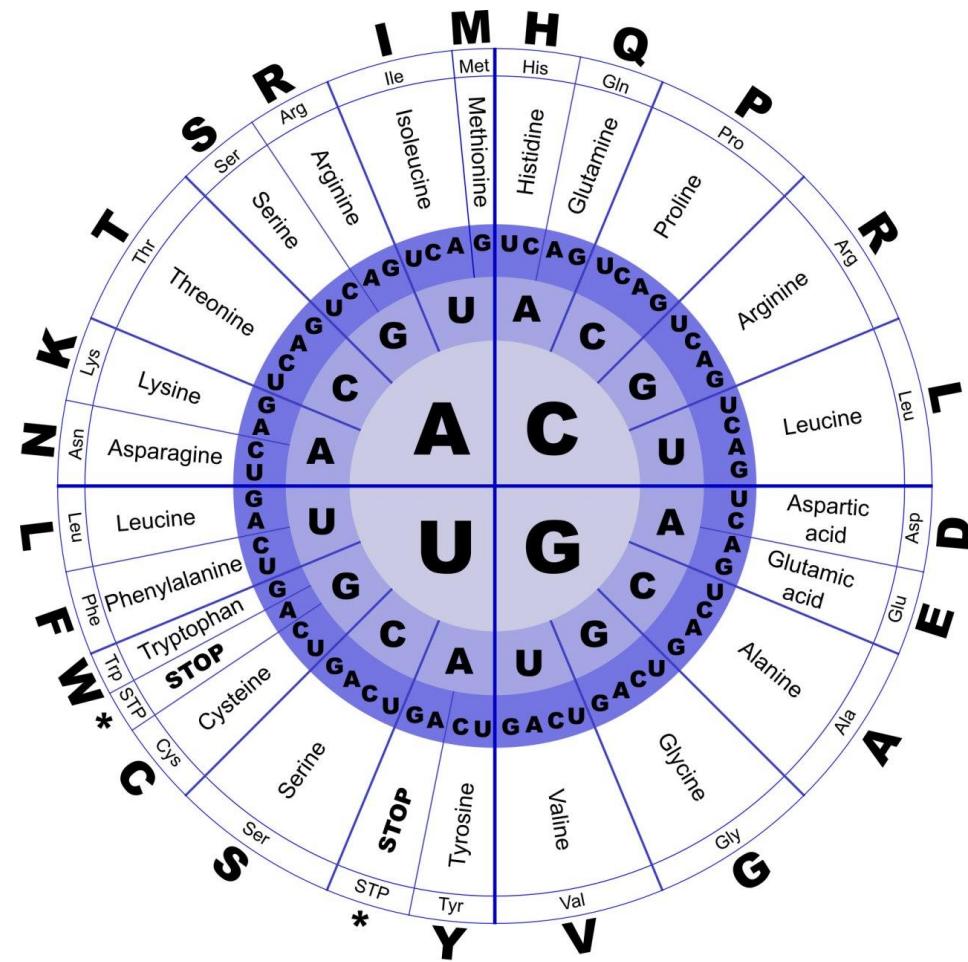




Proteínas

ADN: ATGTGTCCATAG

ARN:

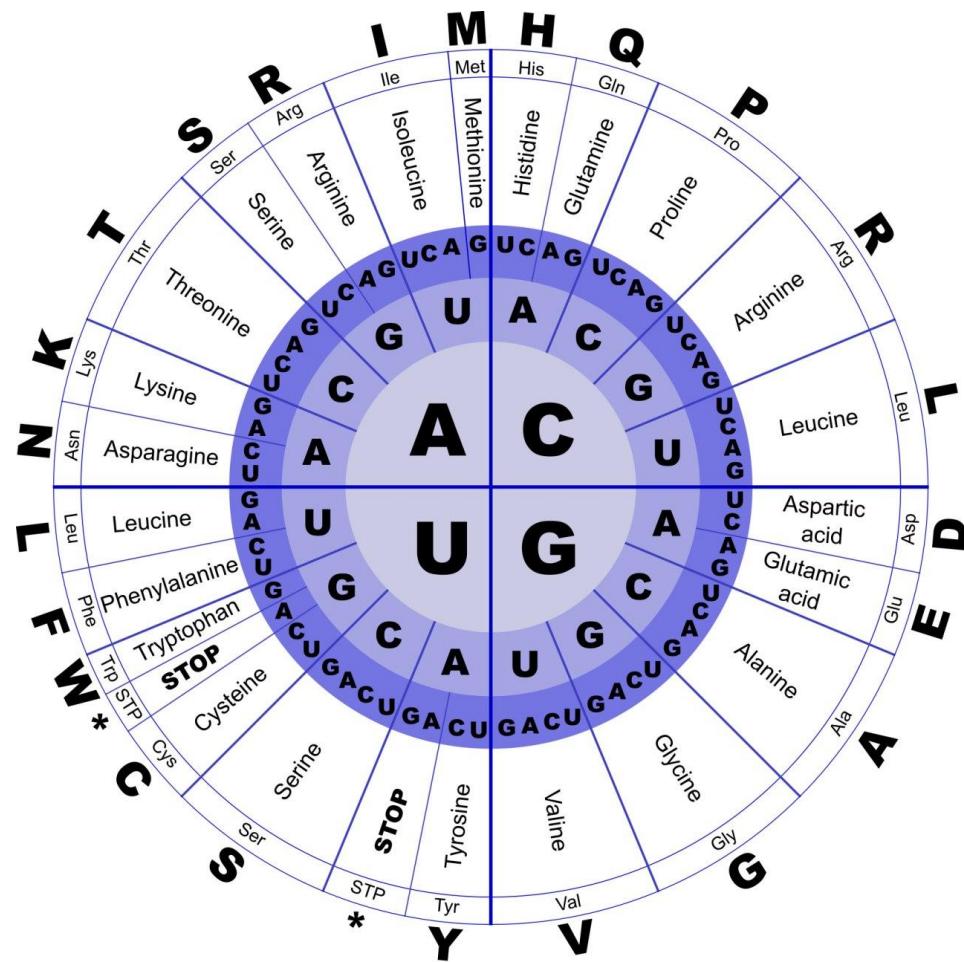




Proteínas

ADN: ATGTGTCCATAG

ARN: AUGUGUCCAUAG



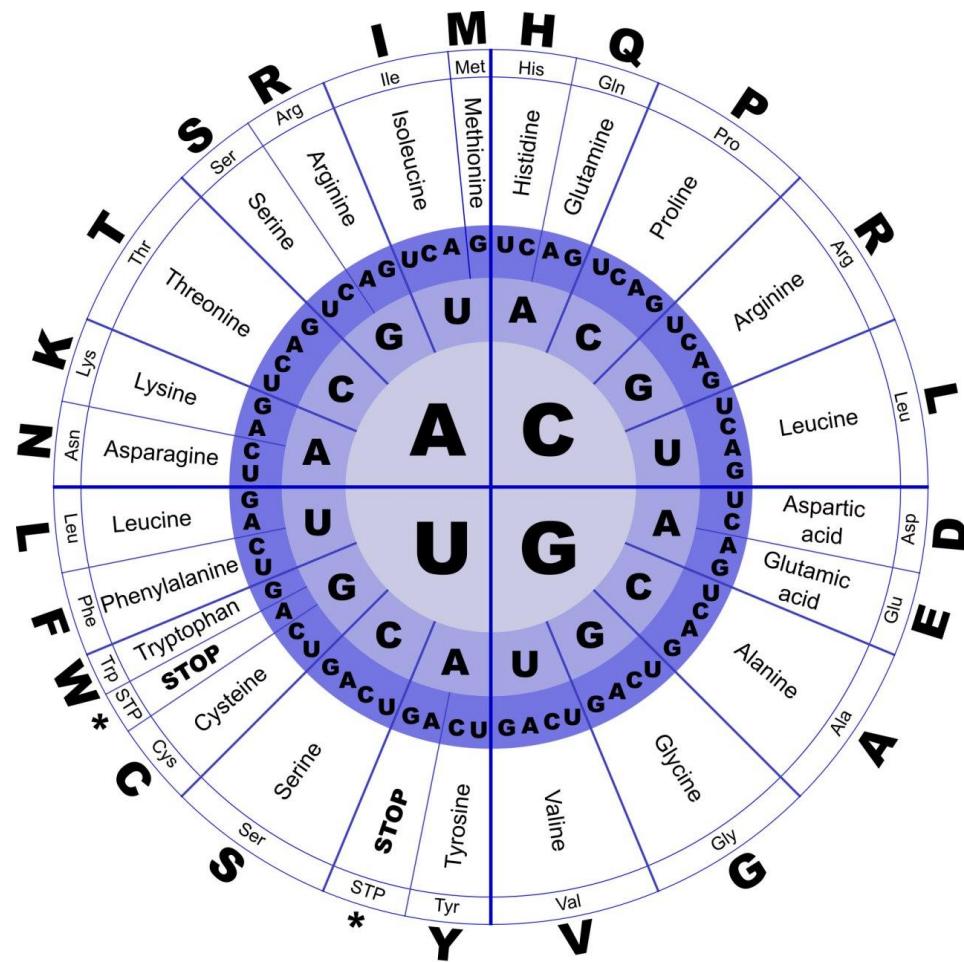


Proteínas

ADN: ATGTGTCCATAG

ARN: AUGUGUCCAUAG

P.



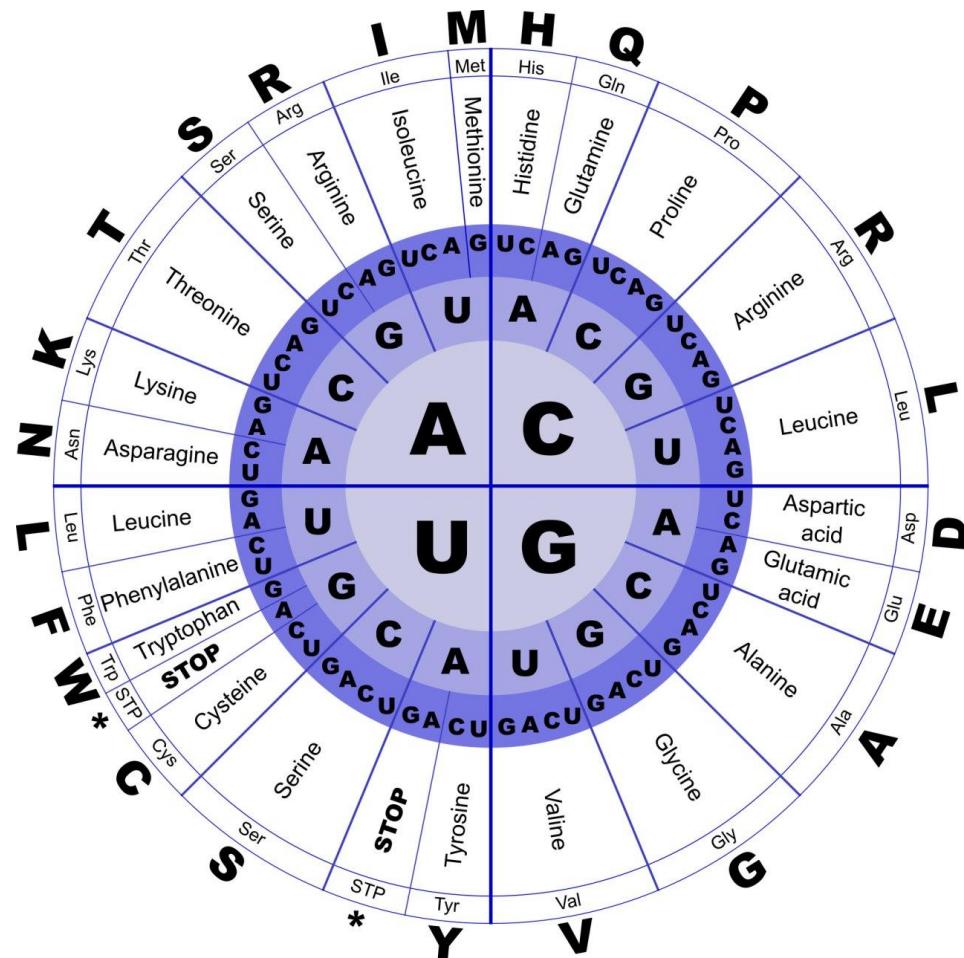


Proteínas

ADN: ATG TGT CCA TAG

ARN: AUG UGU CCA UAG

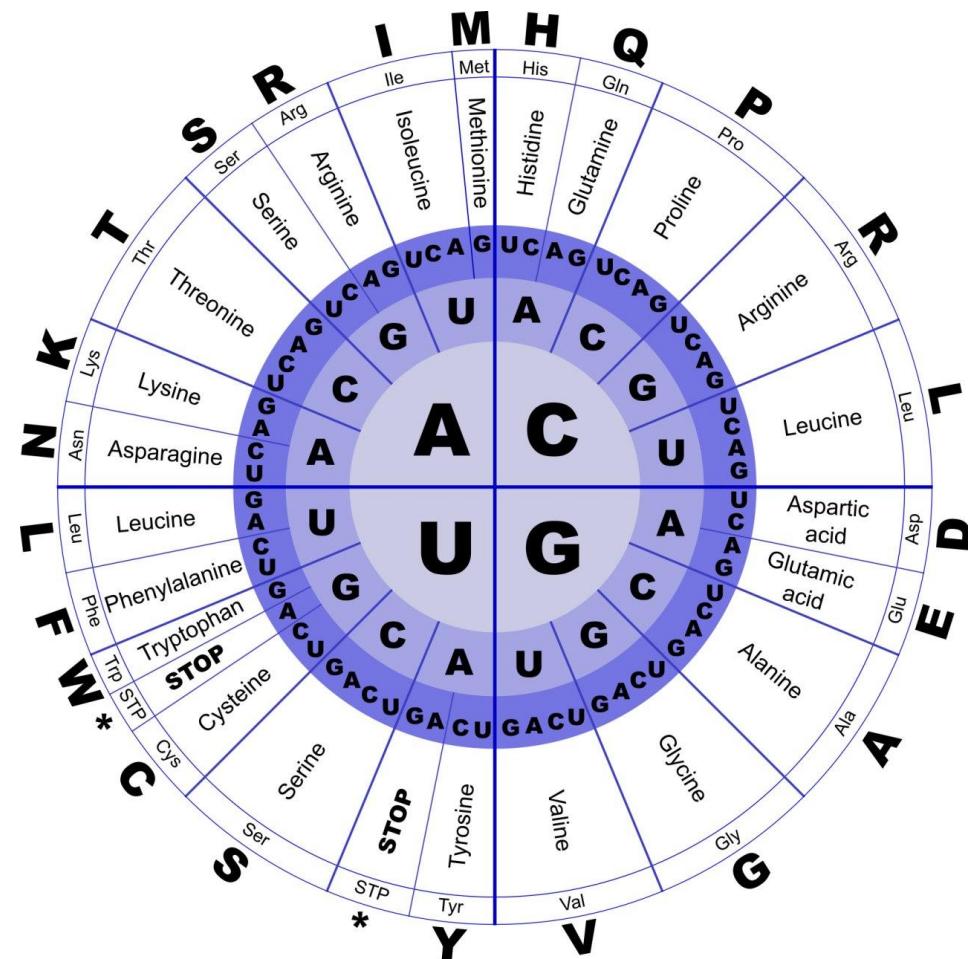
P.





Proteínas

ADN:	ATG	TGT	CCA	TAG
	↓	↓	↓	↓
ARN:	AUG	UGU	CCA	UAG
	↓	↓	↓	↓
P:	M	C	P	*





¡A programar!

Tecnología

Python
Notebooks

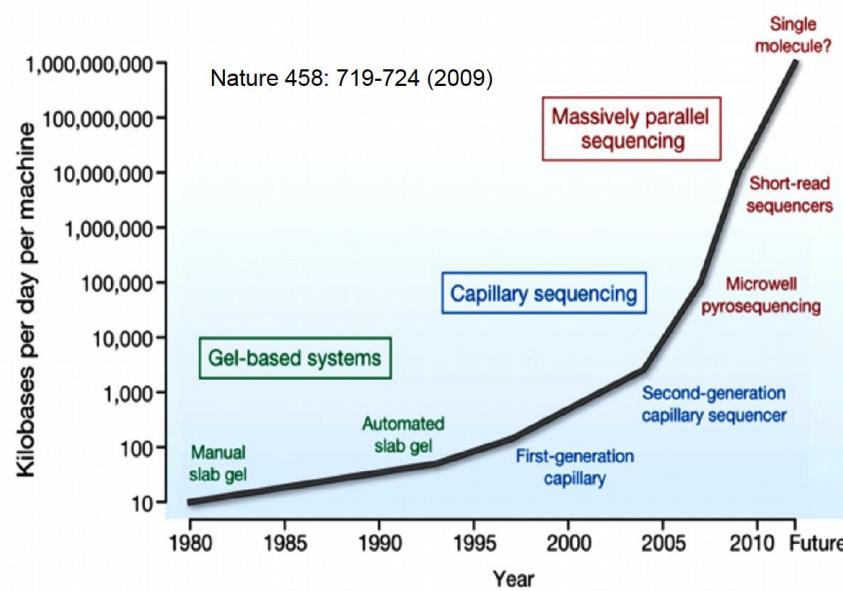


bit.ly/BIEBio



Automatización

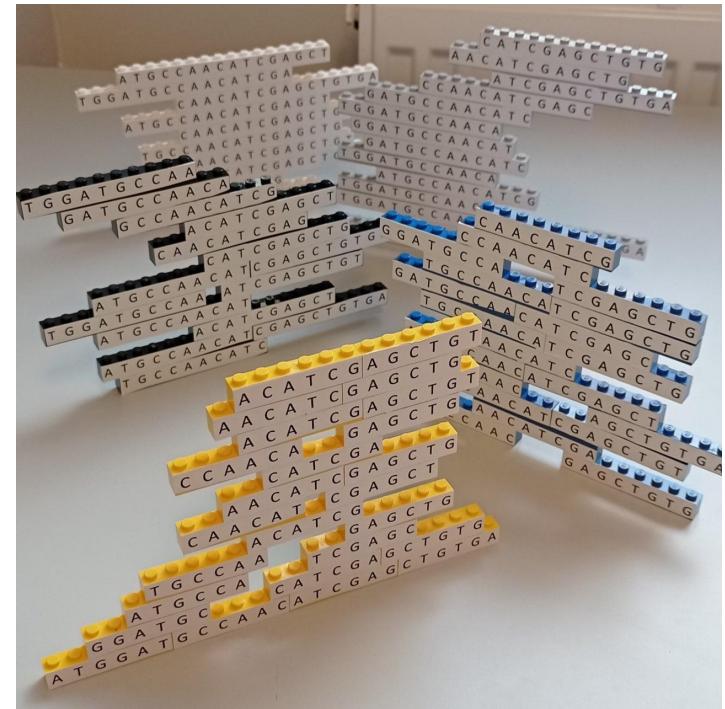
- 0 y 1 – A, C, G, T
- Menor coste → Más datos





Análisis de Secuencias

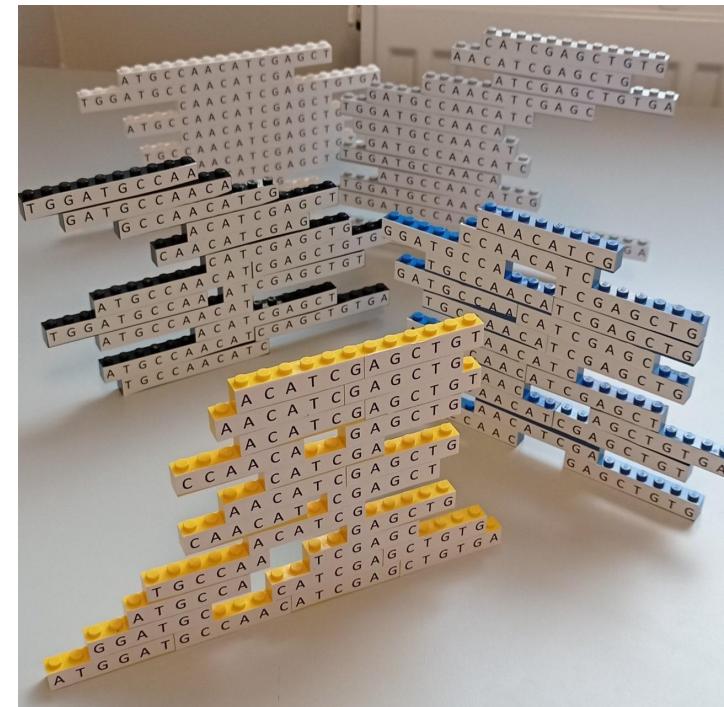
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ACGATATTACACGTACACTCACGTCTCGGA
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ACGATATTACACGTACACTCACGTCTCGGAA
ATTACACGTACACTCACGTCTCGAACCT
TACACGTACACTCAAGTCGTTCTGAACCT
CACGTACACTCAAGTCGTTCTGAACCT
CACGTACACTCACGTCTCGAACCT





Análisis de Secuencias

ACGATATTACACGTACACTCAAGTCGT _____
TCGAGATTGCATGTACCCTCAAGCCGTCGG _____
ACGATATTACACGTACACTCACGTCTCGGA _____
ACGATATTACACGCACACTCAAGTCGTTCGGAACCT
ACGATATTACACGTACACTCACGTCTCGGAA _____
ATTACACGTACACTCACGTCTCGGAACCT
TACACGTACACTCAAGTCGTTCGGAACCT
CACGTACACTCAAGTCGTTCTGAACCT
CACGTACACTCACGTCTCGGAACCT





Detección de variantes

ACGATATTACACGTACACTCAAGTCGT _____
TCGAGATTGCATGTACCCCTCAAGCCGTCGG _____
ACGATATTACACGTACACTCAC**GTCGT** _____
ACGATATTACACGTACACTCAC**GTCGTTCGGA** _____
ACGATATTACACG**CACACTCAAGTCGTTCGGAACCT**
ACGATATTACACGTACACTCAC**GTCGTTCGGAA** _____
_____ **ATTACACGTACACTCACGTCGTTCGGAACCT**
_____ **TACACGTACACTCAAGTCGTTCGGAACCT**
_____ **CACGTACACTCAAGTCGTT**T**GAACCT**
_____ **CACGTACACTCACGTCGTTCGGAACCT**



Detección de variantes

ACGATATTACACGTACACTCAAGTCGT _____
TCGAGATTGCATGTACCCCTCAAGCCGT CGG _____
ACGATATTACACGTACACTCACCGTCGT _____
ACGATATTACACGTACACTCACCGTCGTTGGAA
ACGATATTACACG CACACTCAAGTCGTTGGAACCT
ACGATATTACACGTACACTCACCGTCGTTGGAA
_____ ATTACACGTACACTCACCGTCGTTGGAACT
_____ TACACGTACACTCAAGTCGTTCG AACCT
_____ CACGTACACTCAAGTCGTTCTGAACCT
_____ CACGTACACTCACCGTCGTTGGAACCT



The image shows two green arrows pointing to specific sequence variations. One arrow points to the 'C' in 'ACG' at the top of the first column, indicating a change from 'ACG' to 'TCG'. Another arrow points to the 'T' in 'CTGAACCT' at the bottom of the last column, indicating a change from 'CTGAACCT' to 'CTGAACCT'.



Detección de variantes

ACGATATTACACGTACACTCAAGTCGT _____	→ Calidad: 98/100
TCGAGATTGCATGTACCCTCAAGCCGTCGG _____	→ Calidad: 14/100
ACGATATTACACGTACACTCAC GTCGT _____	→ Calidad: 95/100
ACGATATTACACGTACACTCAC GTCGTTCGGA _____	→ Calidad: 98/100
ACGATATTACAC G CACACTCAAGTCGTTCGGAACCT	→ Calidad: 25/100
ACGATATTACACGTACACTCAC GTCGTTCGGAA _____	→ Calidad: 98/100
_____ ATTACACGTACACTCAC GTCGTTCGGA ACCT	→ Calidad: 90/100
_____ TACACGTACACTCAAGTCGTTCG A ACCT	→ Calidad: 89/100
_____ CACGTACACTCAAGTCGTT T GAACCT	→ Calidad: 99/100
_____ CACGTACACTCAC GTCGTTCGGA ACCT	→ Calidad: 95/100

The sequence ACGATATTACACGTACACTCAAGTCGT is shown in black. The sequence TCGAGATTGCATGTACCCTCAAGCCGTCGG is shown in red, with a green arrow pointing to the first 'G'. The sequence ACGATATTACACGTACACTCACGTCGT is shown in black. The sequence ACGATATTACACGTACACTCACGTCGTTCGGA is shown in black. The sequence ACGATATTACACGCAACACTCAAGTCGTTCGGAACCT is shown in black, with a green arrow pointing to the second 'G'. The sequence ACGATATTACACGTACACTCACGTCGTTCGGAA is shown in black. The sequence ATTACACGTACACTCACGTCGTTCGGAACCT is shown in black, with a green arrow pointing to the first 'A'. The sequence TACACGTACACTCAAGTCGTTCGAACCT is shown in black, with a green arrow pointing to the second 'A'. The sequence CACGTACACTCAAGTCGTTCTGAACCT is shown in black, with a green arrow pointing to the third 'T'. The sequence CACGTACACTCACGTCGTTCGGAACCT is shown in black.



Detección de variantes

ACGATATTACACGTACACTCAAGTCGT _____ → Calidad: 98/100
TCGAGATTGCATGTACCCTCAAGCCGTCGG _____ → Calidad: 14/100
ACGATATTACACGTACACTCAACGTTCGTTCGGA → Calidad: 95/100
ACGATATTACACGTACACTCAACGTTCGTTCGGA → Calidad: 98/100
ACGATATTACACGCAACACTCAAGTCGTTCGGAACCT → Calidad: 25/100
ACGATATTACACGTACACTCAACGTTCGTTCGGAA → Calidad: 98/100
ATTACACGTACACTCAACGTTCGTTCGGAACCT → Calidad: 90/100
TACACGTACACTCAAGTCGTTCGGAACCT → Calidad: 89/100
CACGTACACTCAAGTCGTTCTGAACCT → Calidad: 99/100
CACGTACACTCAACGTTCGTTCGGAACCT → Calidad: 95/100



50%



Detección de variantes

ACGATATTACACGTACACTCAAGTCGATCGGAACCT → Referencia

ACGATATTACACGTACACTCAAGTCGT _____ → Calidad: 98/100
TCGAGATTGCATGTACCCTCAAGCCGT~~CGG~~ _____ → Calidad: 14/100
ACGATATTACACGTACACTCAC~~GTCGT~~ _____ → Calidad: 95/100
ACGATATTACACGTACACTCAC~~GTCGT~~CGTTCGGA _____ → Calidad: 98/100
ACGATATTACACG~~C~~ACACTCAAGTCGTTCGGAACCT → Calidad: 25/100
ACGATATTACACGTACACTCAC~~GTCGT~~CGGAA _____ → Calidad: 98/100
_____ ATTACACGTACACTCAC~~GTCGT~~CGTTCGGAACCT → Calidad: 90/100
_____ TACACGTACACTCAAGTCGTTCGGAACCT → Calidad: 89/100
_____ CACGTACACTCAAGTCGTTC~~T~~GAACCT → Calidad: 99/100
_____ CACGTACACTCAC~~GTCGT~~CGTTCGGAACCT → Calidad: 95/100



Detección de variantes

ACGATATTACACGTACACTCAAGTCGATCGGAACCT

ACGATATTACACGTACACTCAAGTCG T	→ Calidad: 98/100
TCGAGATTGCATGTACCCTCAAGCCGTCGG	→ Calidad: 14/100
ACGATATTACACGTACACTCA CGTCG T	→ Calidad: 95/100
ACGATATTACACGTACACTCA CGTCG TTCGGA	→ Calidad: 98/100
ACGATATTACACG CAC ACTCAAGTCG TTCGG AACCT	→ Calidad: 25/100
ACGATATTACACGTACACTCA CGTCG TTCGGAA	→ Calidad: 98/100
ATTACACGTACACTCA CGTCG TTCGGAACCT	→ Calidad: 90/100
TACACGTACACTCA AGTCG TTCGGAACCT	→ Calidad: 89/100
CACGTACACTCA AGTCG TTCTGAACCT	→ Calidad: 99/100
CACGTACACTCA CGTCG TTCGGAACCT	→ Calidad: 95/100



Medicina Personalizada

- www.pandrugs.org

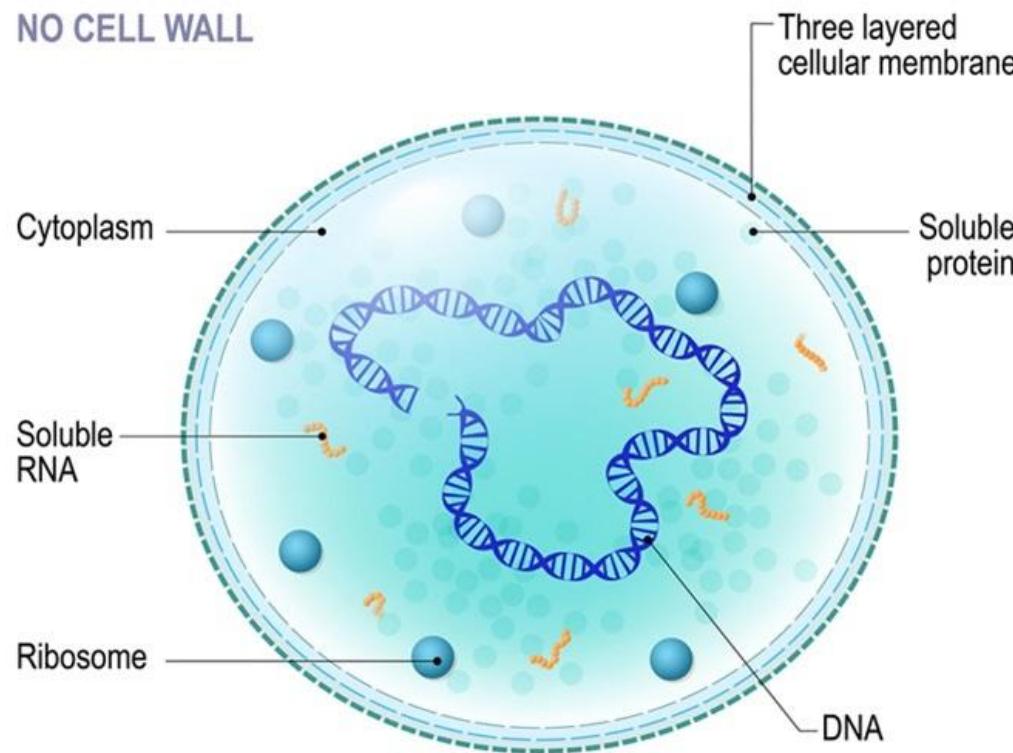
Welcome to
PANDRUGS
A novel method for
prioritizing therapies using
individual genomic data

Query! ✓



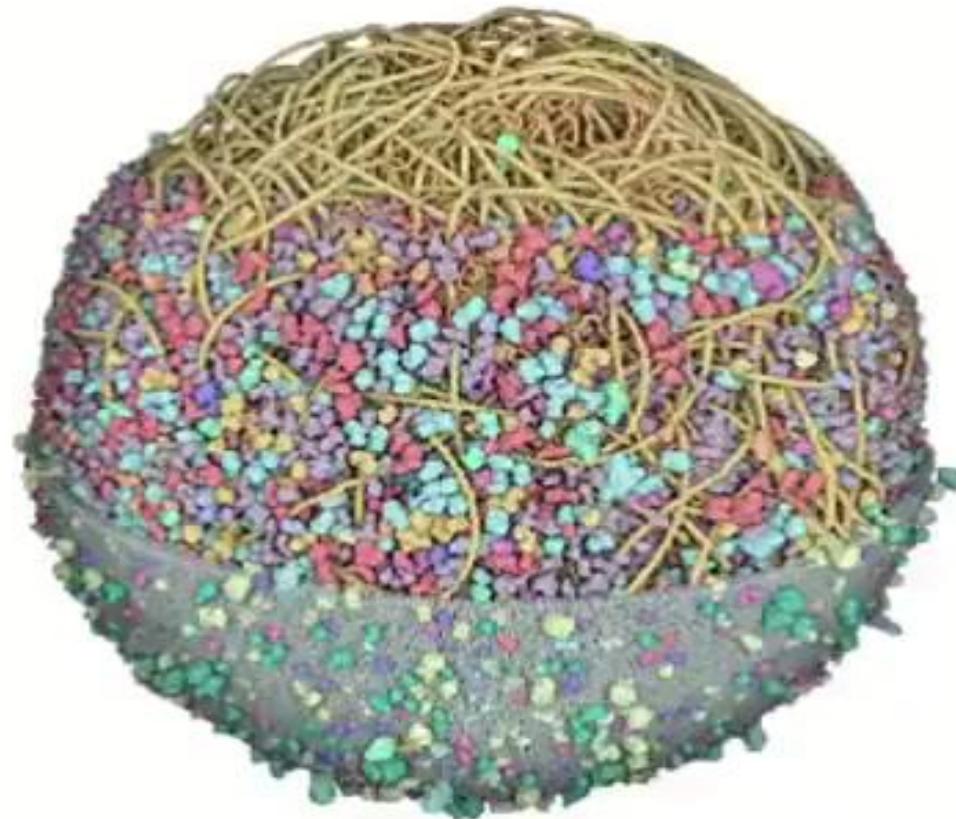
Biología de sistemas

Mycoplasma



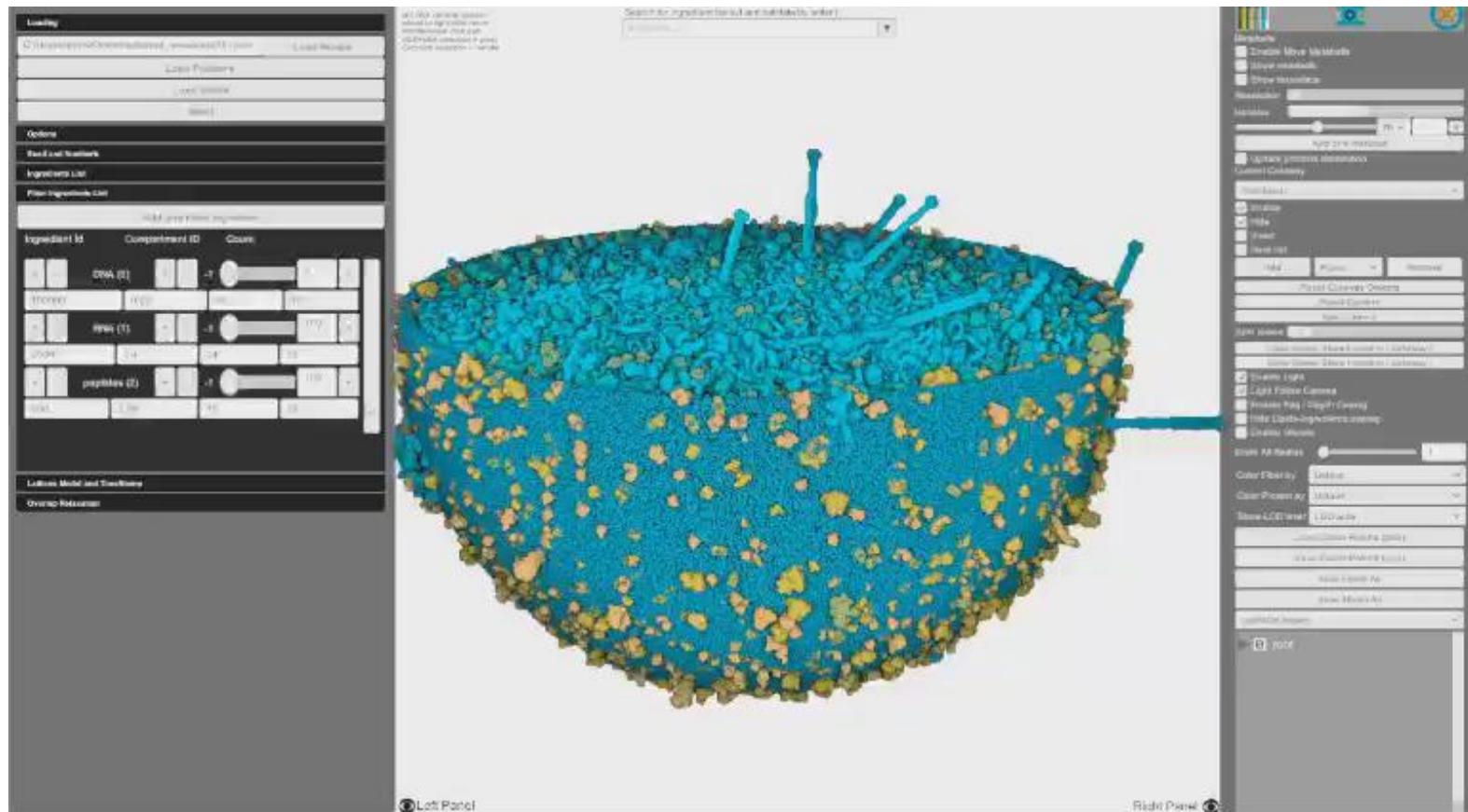


Biología de sistemas





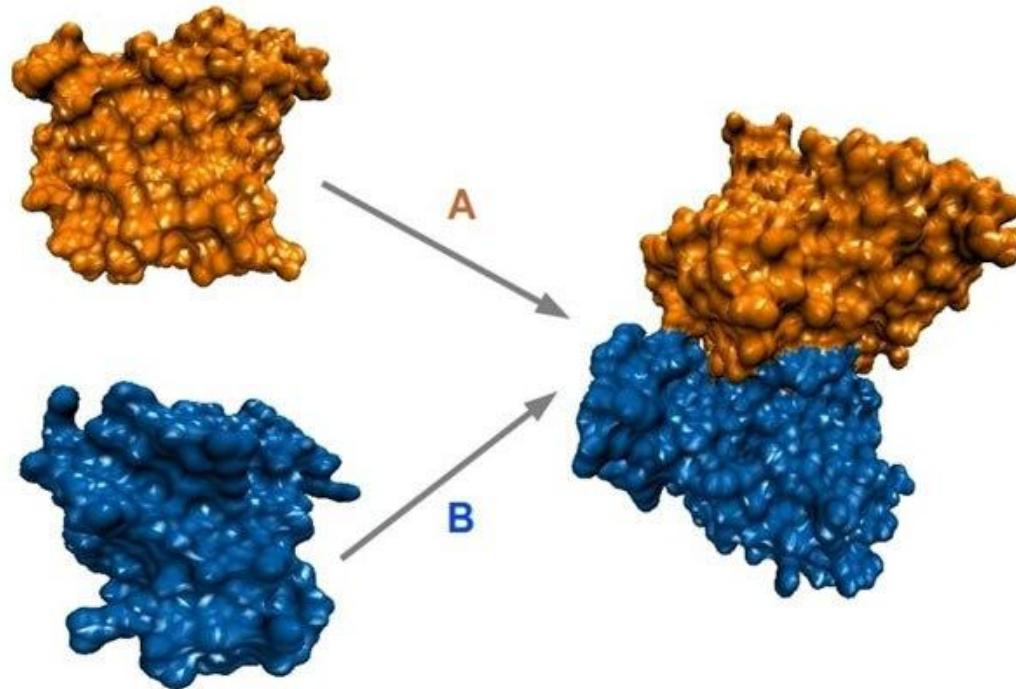
Biología de sistemas





Modelado de proteínas

- Diseño de fármacos





Plegado de proteínas





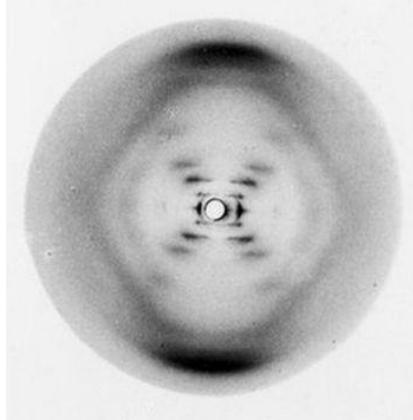
Plegado de proteínas





Más problemas: Rosalind

ROSALIND



<https://bit.ly/BIERosalind>