



# BIO HACKING CON PYTHON

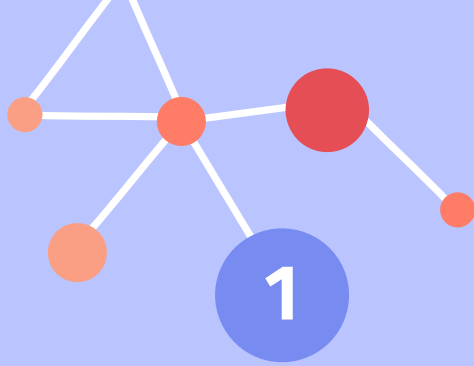
Marina Moro López



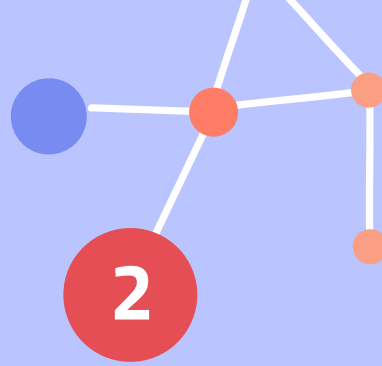
# ¡Hola! :D

- Ingeniera biomédica y máster en biocosas
- Futura doctora en biomedicina
- 'Programadora' a nivel científico

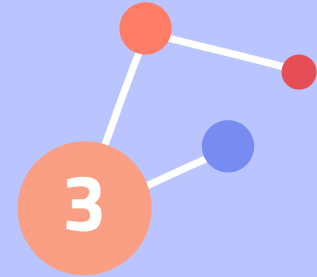




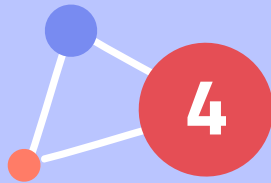
**DEFINICIÓN DE  
BIOHACKING**



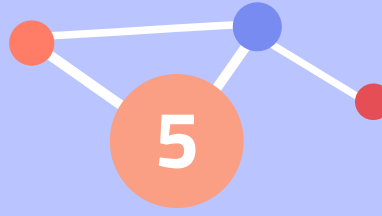
**TIPOS DE  
BIOHACKING**



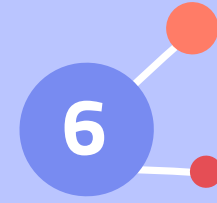
**TEORÍA BÁSICA  
DE GENÉTICA**



**CASO PRÁCTICO**



**CONSIDERACIONES  
IMPORTANTES**

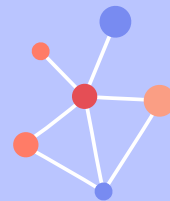
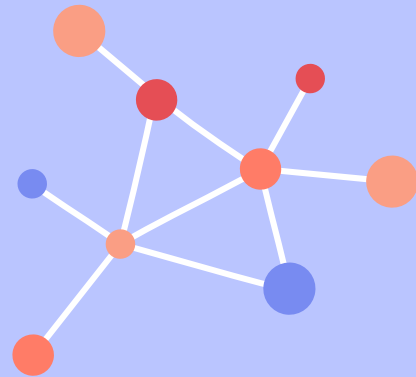
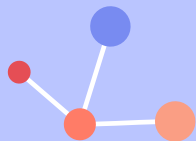


**RONDA DE  
PREGUNTAS**



1

# DEFINICIÓN DE BIOHACKING





# Bio + hacking

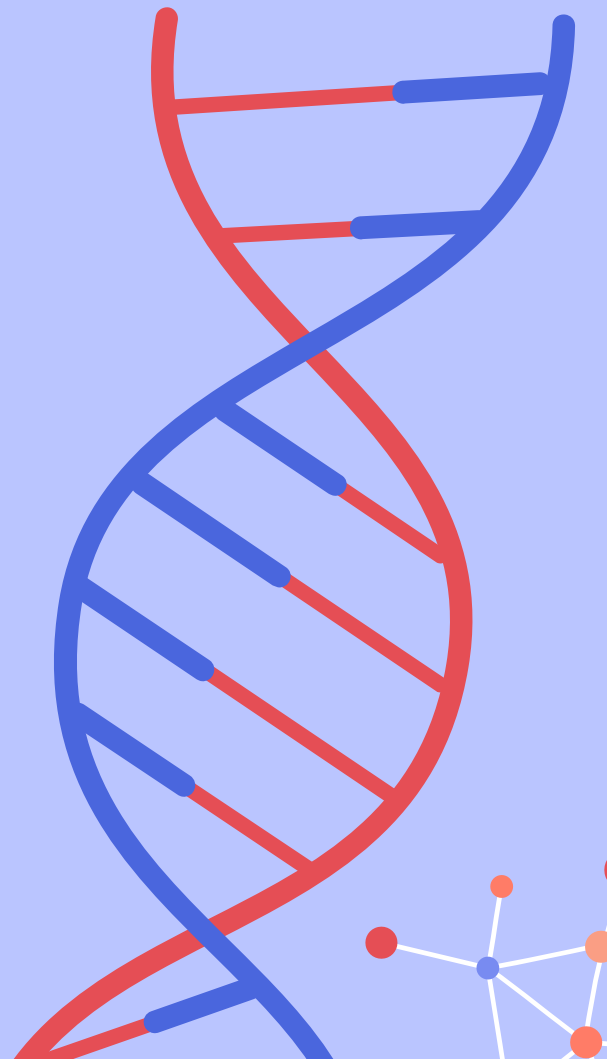
Añadir funcionalidades, resolución de problemas, información al alcance de todos

## Democratización

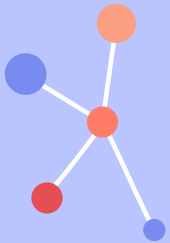
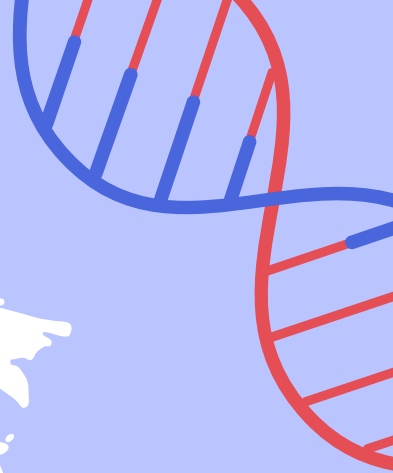
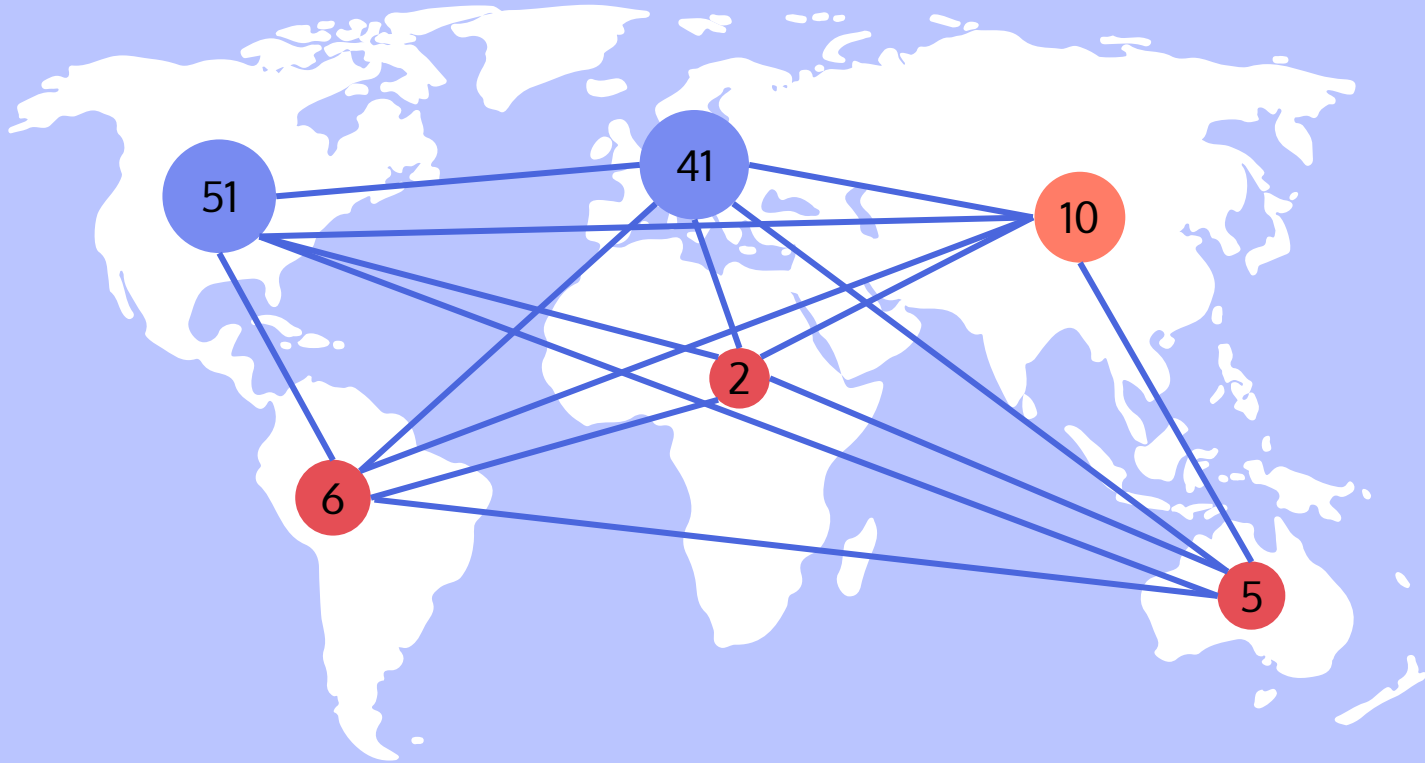
Herramientas biológicas fuera del ámbito institucional

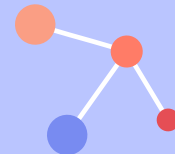
## BioDIY o de garaje

Bajada del coste y simplificación de las técnicas biológicas



# GRUPOS DE BIOHACKING





# ORIGEN DEL BIOHACKING

## DIY

Autosuficiencia y  
comunidad

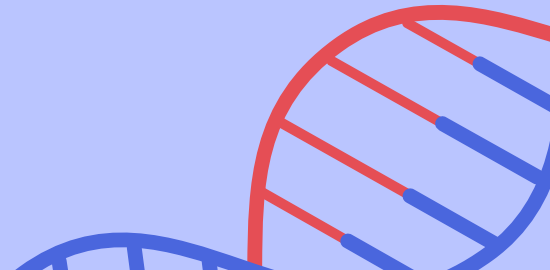
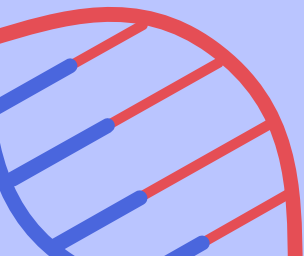
## TRANSHUMANISMO

Superación de límites  
biológicos con tecnología



## HACKING

Democratización y hackeo  
de procedimientos



# ¿QUÉ SE HACE EN EL BIOHACKING?

Proyectos de salud, nutrición, medioambiente y bioarte usando tecnologías de genética, bioquímica, tejidos, biología sintética, electrónica...

- Desarrollo de equipos low-cost
- Producción de medicamentos
- Talleres y conferencias
- Start-ups con los productos desarrollados
- Autoexperimentación y modificaciones corporales





# CÓDIGO ÉTICO DEL BIOHACKING



**TRANSPARENCIA  
Y OPEN ACCESS**



**SEGURIDAD  
Y PAZ**



**EDUCACIÓN**



**MODESTIA  
Y RESPETO**



**COMUNIDAD**

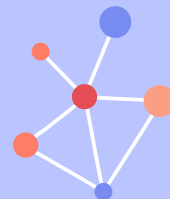
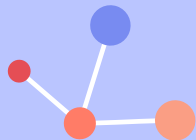
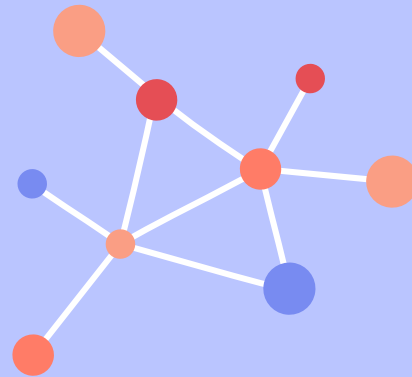


**COMPROMISO Y  
RESPONSABILIDAD**



2

## TIPOS DE BIOHACKING





# BIOHACKING FISIOLÓGICO

Hacking del propio organismo  
con dietas, ingesta de  
suplementos y hábitos de vida

**Ejemplos:** ayuno intermitente,  
exposición a infrarrojos, uso de  
nootrópicos

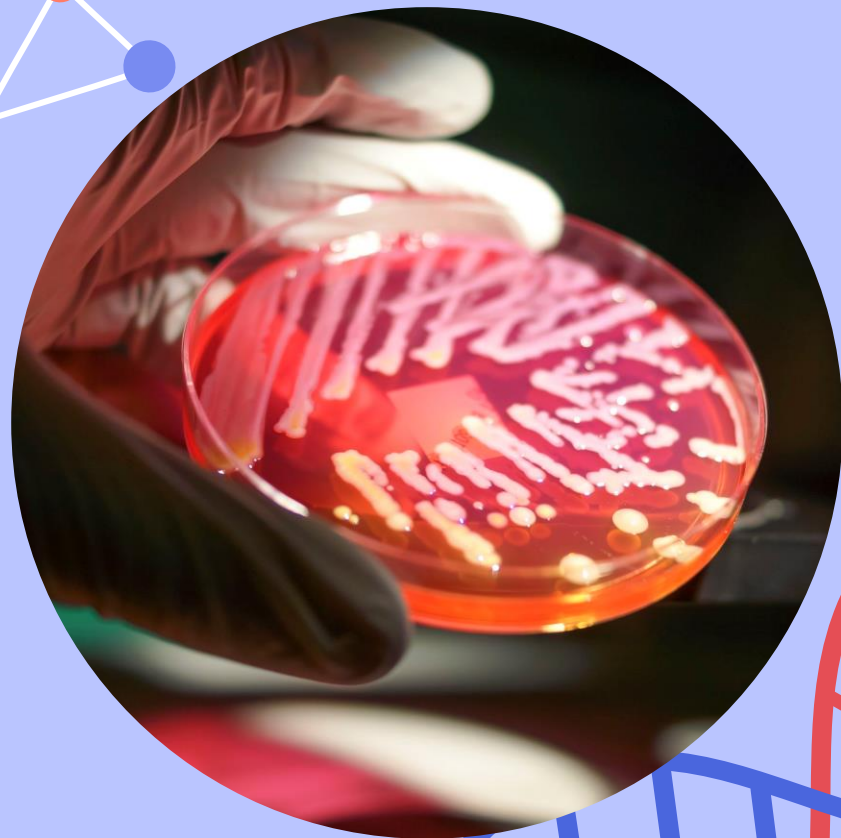




# BIOHACKING/ BIOLOGÍA DIY

Manipulación de la biología a través de técnicas innovadoras por parte de la ciudadanía

**Ejemplos:** biohacking genético, neurohacking, terapia celular, producción de medicamentos y de equipo

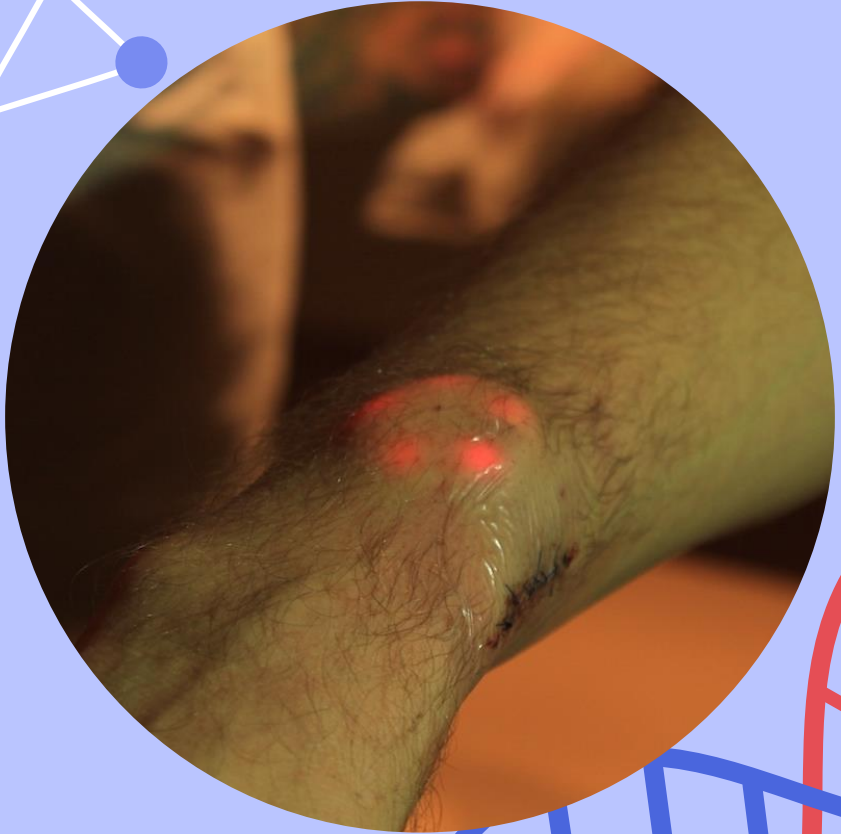


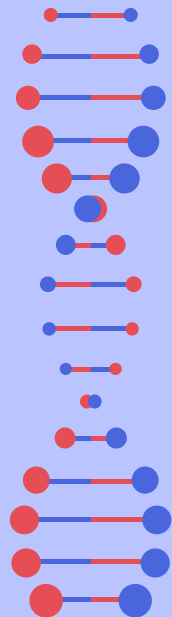


# GRINDER

Manipulación corporal con visión transhumanista (body hacking)

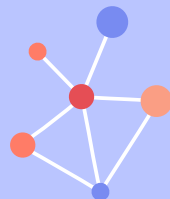
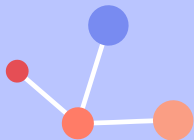
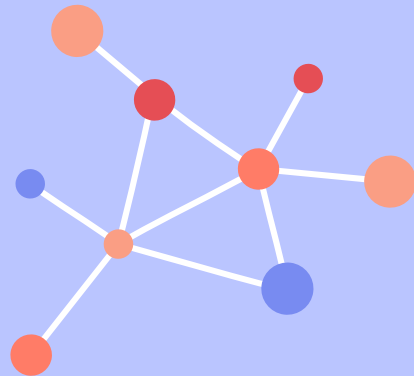
**Ejemplos:** implantación de hardware, modificación de implantes, edición genética y biohacking *in vivo*





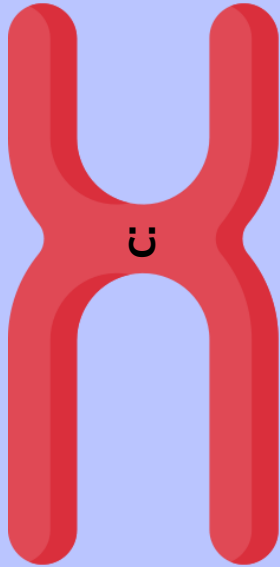
3

# TEORÍA BÁSICA DE GENÉTICA

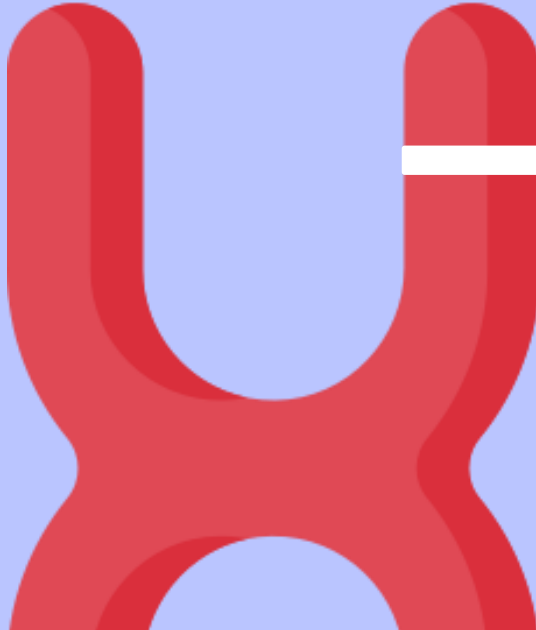


# CROMOSOMA – GEN – ADN

Contiene todos los genes  
de un organismo  
23 cromosomas



Segmento de ADN que  
determina un rasgo  
20-23K genes



Doble hélice formada  
por bases  
50-300M bases/cr

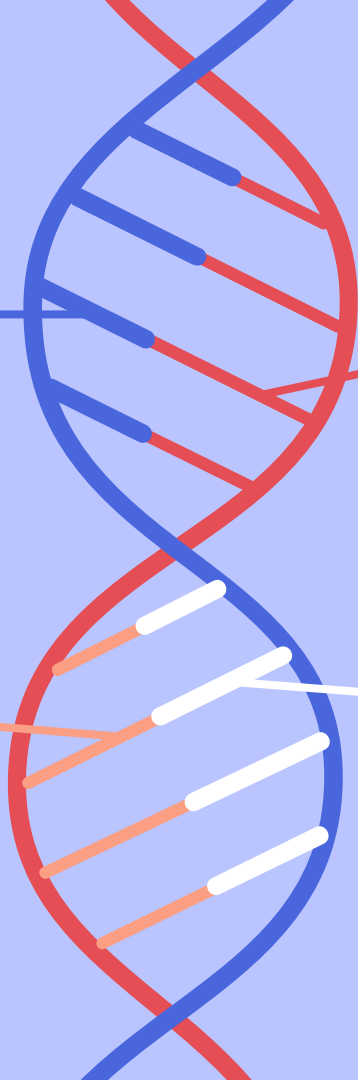


**ADENINA (A)**

**TIMINA (T)**

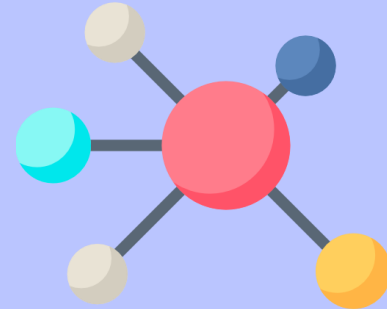
**CITOSINA (C)**

**GUANINA (G)**

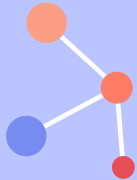
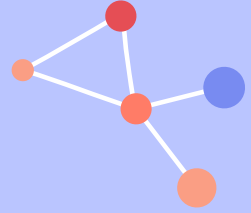




# ADN – ARN – PROTEÍNA

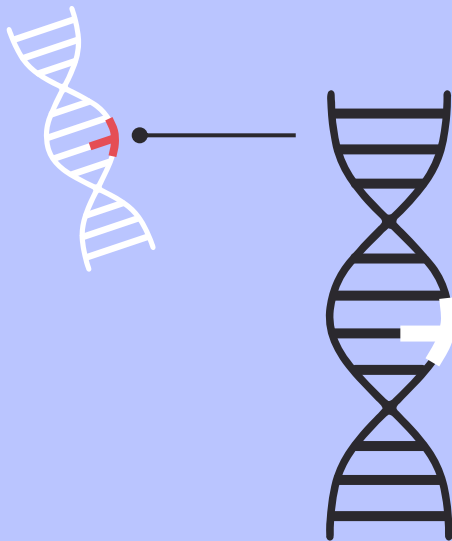


Hélice simple  
 $T > U$



# MUTACIONES DEL ADN

SUSTITUCIÓN



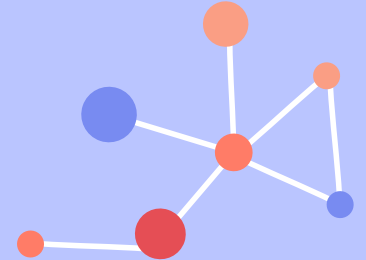
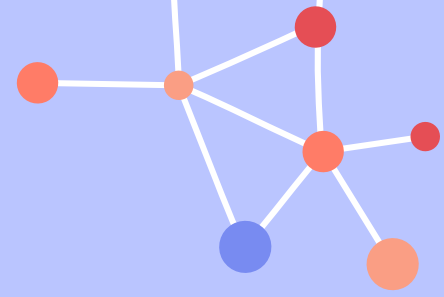
DELECCIÓN



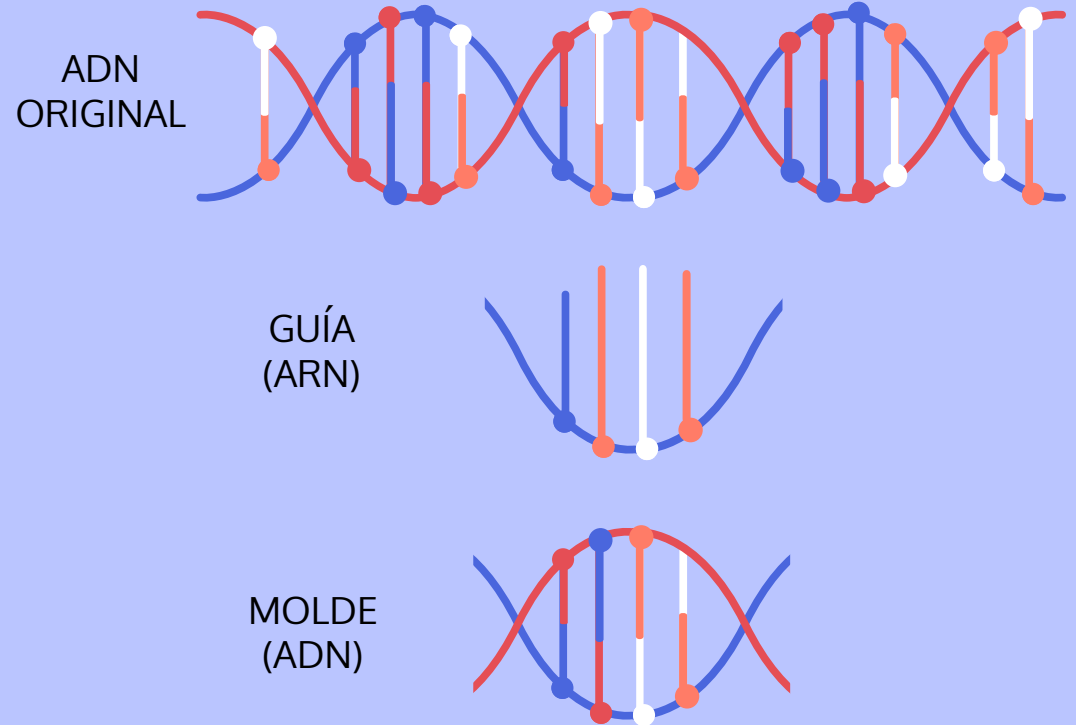
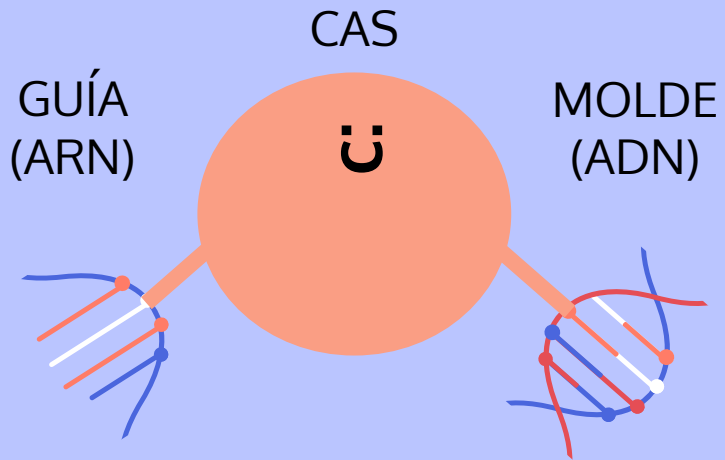


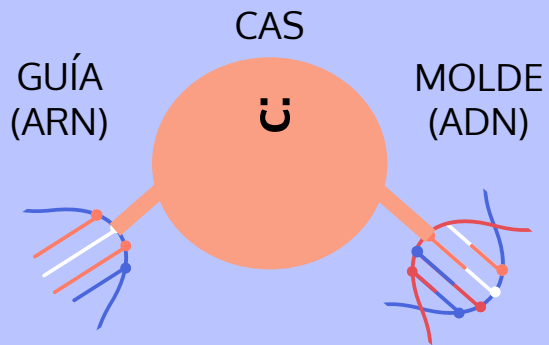
# CRISPR

Sirve para cortar y pegar secuencias de ADN (edición genética)

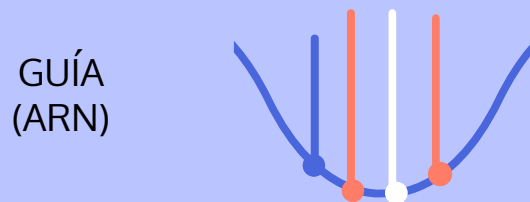
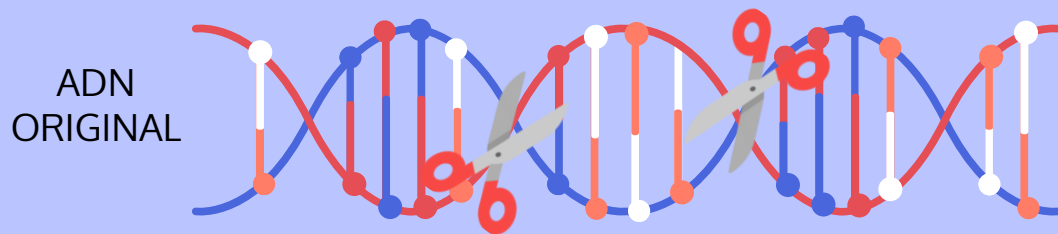


# CRISPR

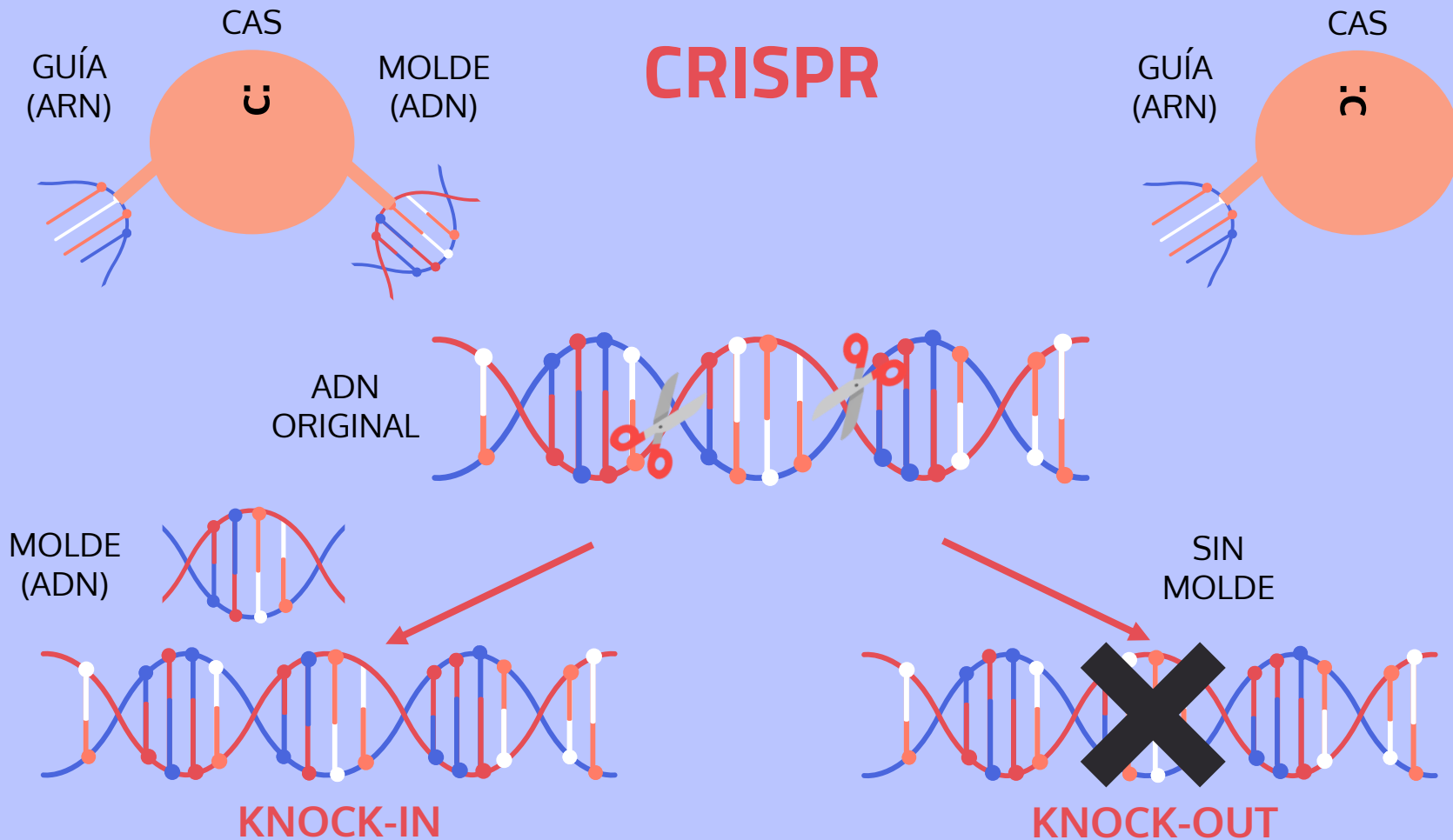


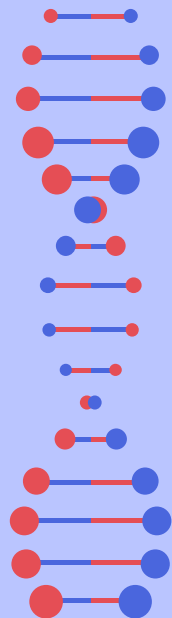


# CRISPR



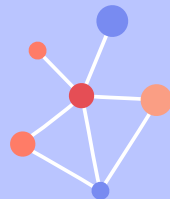
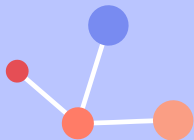
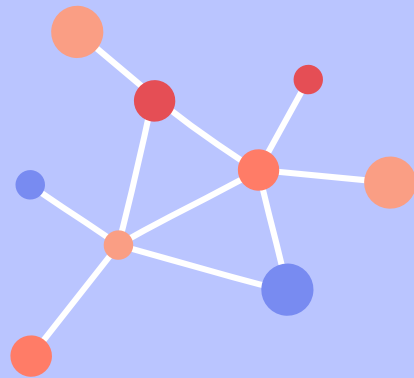
# CRISPR





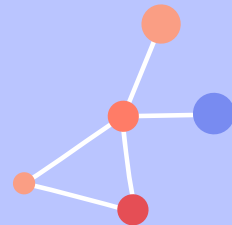
4

# CASO PRÁCTICO





# Cómo convertirnos en el Sr Burns fluorescente





# Cómo convertirnos en el Sr Burns fluorescente



1

Calvicie y pelo canoso



Knock-out del gen IRF4 completo  
Knock-in en mitad del gen AR (363, C>T)

2

Bioluminiscencia



Knock-in de GFP al final del gen TYR

3

Pupilas dilatadas



Sustancias pecaminosas / ciclopentolato

```
def main():
```

```
    gene_file_name = input("Introduce gene file name (e.g. mygene.fasta): ")
    gene_file = open(gene_file_name, 'r')
    gene_seq = gene_file.readlines()[1:]
    gene_seq = ''.join(gene_seq)
    gene_seq = gene_seq.replace('\n', '')
    gene_file.close()
```

```
    mutation_type = input("Introduce mutation type (in/out): ")
    knockin_type = ""
```

```
    if mutation_type == "in":
        knockin_type = input("Introduce the knock-in position in the gene (mid/end): ")
```

```
    if knockin_type == "mid":
        DNA_guide, mutated_gene_seq, mold = knock_in_mid(gene_seq)
    elif knockin_type == "end":
        DNA_guide, mutated_gene_seq, mold = knock_in_end(gene_seq)
    else:
        DNA_guide, mutated_gene_seq, mold = knock_out(gene_seq)
```

```
mutated_gene_file = open('MUTATED_SEQUENCE.txt', 'w')
mutated_gene_file.write(mutated_gene_seq)
mutated_gene_file.close()


guide_file = open('GUIDE.txt', 'w')
guide_file.write(DNA_to_RNA(DNA_guide))
guide_file.close()

mold_file = open('MOLD.txt', 'w')
mold_file.write(mold)
mold_file.close()
```

```
def DNA_to_RNA(DNA_guide):

    RNA_guide = ""
    for base in DNA_guide:
        if base == "T":
            RNA_guide += "A"
        elif base == "A":
            RNA_guide += "U"
        elif base == "C":
            RNA_guide += "G"
        elif base == "G":
            RNA_guide += "C"

    return RNA_guide
```




Gene

TYR

×

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A new NIH initiative to end structural racism and achieve racial equity in the biomedical research enterprise.

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Gene 

Gene 

TYR

×

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GENE 

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👎

[TYR – tyrosinase](#)

[Homo sapiens \(human\)](#)

Also known as: ATN, CMM8, OCA1, OCA1A, OCA1A, SHEP3

Gene ID: 7299

[RefSeq transcripts \(2\)](#) [RefSeq proteins \(2\)](#) [RefSeqGene \(1\)](#) [PubMed \(210\)](#)

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Homo sapiens (459)

Salmo salar (390)

Mus musculus (271)

Camelina sativa (248)

Poecilia mexicana (244)

All other taxa (65927)

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Select

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TYR[All Fields] AND alive[prop]

Search results

Items: 1 to 20 of 67539

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Page 1 of 3377

Next >

Last >>

Nucleotide

Nucleotide

Search

Advanced

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Change selection shown

# Homo sapiens tyrosinase (TYR), RefSeqGene on chromosome 11

NCBI Reference Sequence: NG\_008748.1

[FASTA](#) [Graphics](#)

Go to: [📄](#)

LOCUS

NG\_008748

124888 bp

DNA

linear

PRI 18-FEB-2021

DEFINITION

Homo sapiens tyrosinase (TYR), RefSeqGene on chromosome 11.

ACCESSION

NG\_008748

VERSION

NG\_008748.1

KEYWORDS

RefSeq; RefSeqGene.

SOURCE

Homo sapiens (human)

ORGANISM

[Homo sapiens](#)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 124888)

AUTHORS

Lewis,R.A.

TITLE

Oculocutaneous Albinism Type 1 - RETIRED CHAPTER, FOR HISTORICAL REFERENCE ONLY

JOURNAL

(in) Adam MP, Ardinger HH, Pagon RA, Wallace SE, Bean LJH, Mirzaa G and Amemiya A (Eds.);  
GENEREVIEWS((R));  
(1993)

PUBMED

[20301345](#)

COMMENT

REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The

☒ Complete Record

☐ Coding Sequences

☐ Gene Features

Choose Destination

☒ File

☐ Clipboard

☐ Collections

☐ Analysis Tool

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FASTA

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Create File

Protein

PubMed

Taxonomy

Components (Core)

Full text in PMC

Gene

HomoloGene

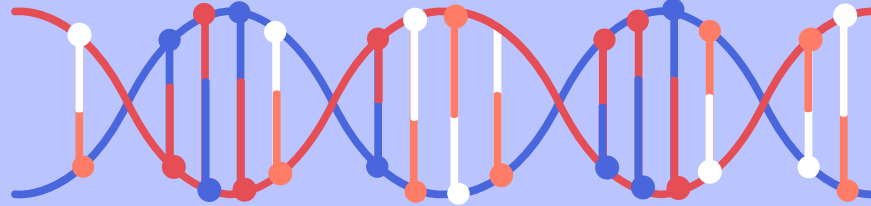
1

Calvicie y pelo canoso



Knock-out del gen IRF4 completo  
Knock-in en mitad del gen AR (363, C>T)

GEN IRF4  
ORIGINAL



GEN IRF4  
MUTADO



1

Calvicie y pelo canoso



Knock-out del gen IRF4 completo  
Knock-in en mitad del gen AR (363, C>T)

```
def knock_out(gene_seq):  
  
    DNA_guide = gene_seq  
    mutated_gene_seq = ""  
    mold = ""  
  
    return DNA_guide, mutated_gene_seq, mold
```



1

Calvicie y pelo canoso



Knock-out del gen IRF4 completo  
Knock-in en mitad del gen AR (363, C>T)

ADN ORIGINAL

```
GTGTCATTCCCCATCCTGGAAACCCTCCAGCAACCCCTGACTCCCCGACCGCCCCACCCCCTGCCGAGCA  
CGTCTACTCAGCCCCATAACTGCTTGTCTTCCCTCCTCTGCCACCCATGCACCTGCCCCGTCTGAGAGCT  
CTCTACCTCACCCCGAGGCCTCCCCGGCCTCCTGGCCATTGTTCTCTCTCGGGCGGTACCCACACTATGG  
CCAGATAATTCTCCTTTACTGTAGTTCTTACCTTATTACGGGGGAATATGAGCCAAAGCCATGTAATC
```

GUÍA (ARN)

```
CACAGUAAGGGGUAGGACCUUUGGGAGGUCGUUGGGGACUGAGGGGCUGGCGGGGUGGGGGACGGCUCGU  
GCAGAUGAGUCGGGGUAUUGACGAACAGGAAGGGAGGAGACGGUGGGUACGUGGACGGGCAGACUCUCGA  
GAGAUGGAGUGGGGCUCCGGAGGGGCCGGAGGACCGGUAACAAGAGAGAGCCCGCCAUGGGUGUGAUACC  
GGUCUAUUAAGGAGGAAAUGACAUCAAGAAUGGAAUAAUGCCCCCUUAUACUCGGUUUCGGUACAUUGAG
```

SIN MOLDE DE ADN

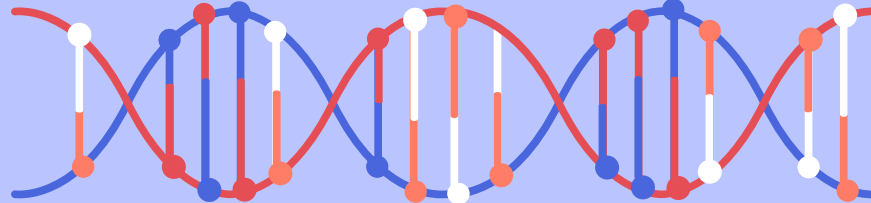
1

Calvicie y pelo canoso

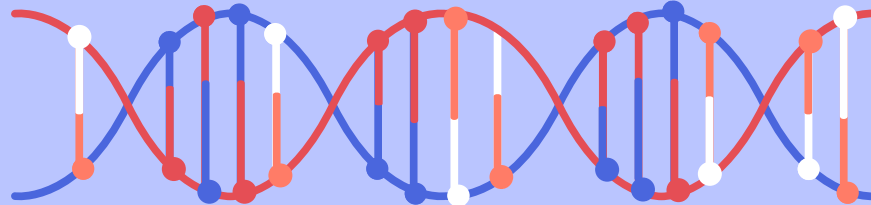


Knock-out del gen IRF4 completo  
Knock-in en mitad del gen AR (363, C>T)

GEN AR  
ORIGINAL



GEN AR  
MUTADO



1

Calvicie y pelo canoso



Knock-out del gen IRF4 completo  
Knock-in en mitad del gen AR (363, C>T)

```
def knock_in_mid(gene_seq):  
  
    mutation_position = int(input("Introduce the numeric position of the mutation base (e.g. 1, 25, 203): "))  
    mutation_base = input("Introduce the new base corresponding to the defined mutation position (A/T/G/C): ")  
  
    DNA_guide = gene_seq[mutation_position-25:mutation_position+25]  
    mutated_gene_seq = gene_seq[:mutation_position-1] + mutation_base + gene_seq[mutation_position:]  
    mold = mutated_gene_seq[mutation_position-25:mutation_position+25]  
  
    return DNA_guide, mutated_gene_seq, mold
```

1

Calvicie y pelo canoso



Knock-out del gen IRF4 completo  
Knock-in en mitad del gen AR (363, C>T)

ADN ORIGINAL

ATGCTAGCTGCCGTTTTGTGTTATCTGTTACAGACTAATACAATTTGCAA

GUÍA (ARN)

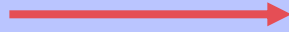
UACGAUCGACGGCAAAACACAAUAGACAAUGUCUGAUUAUGUUAACGUU

MOLDE (ADN)

ATGCTAGCTGCCGTTTTGTGTTATTGTTACAGACTAATACAATTTGCAA

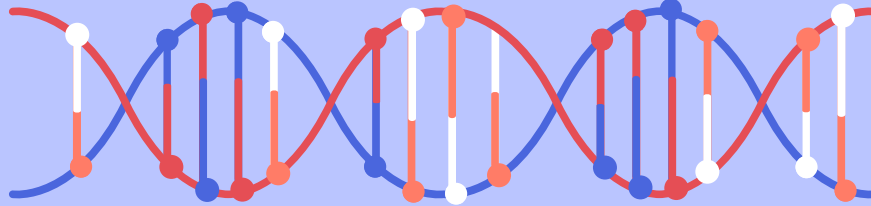
2

Bioluminiscencia

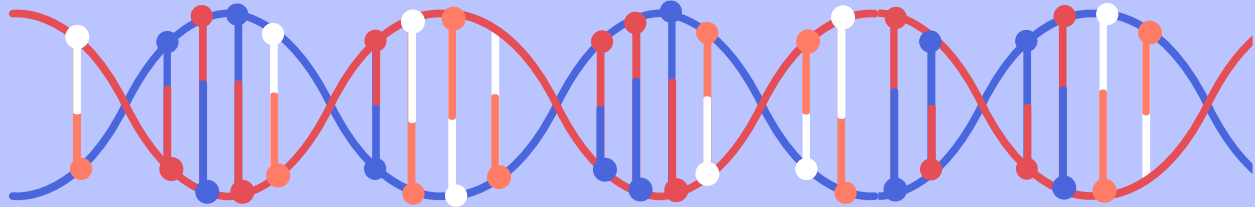


Knock-in de GFP al final del gen TYR

GEN TYR  
ORIGINAL

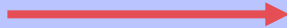


GEN TYR  
MUTADO



2

Bioluminiscencia



Knock-in de GFP al final del gen TYR

```
def knock_in_end(gene_seq):

    plasmid_file_name = input("Introduce plasmid file name (e.g. myplasmid.fasta): ")
    plasmid_file = open(plasmid_file_name, 'r')
    plasmid_seq = plasmid_file.readlines()[1:]
    plasmid_seq = ''.join(plasmid_seq)
    plasmid_seq = plasmid_seq.replace('\n', '')
    plasmid_file.close()

    DNA_guide = gene_seq[len(gene_seq)-50:len(gene_seq)]
    mutated_gene_seq = gene_seq + plasmid_seq
    mold = DNA_guide + plasmid_seq

    return DNA_guide, mutated_gene_seq, mold
```

2

Bioluminiscencia



Knock-in de GFP al final del gen TYR

FINAL DE TYR

TTTGAAGGCAAGATTTTAGTCCAGGGTGGTATGTTTCAATCA|TTTTTGCA

GUÍA (ARN)

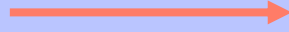
|AAACUCCGUUCUAAAAUCAGGUCCCACCAUACAAAGUUAGUAAAAACGU

MOLDE (ADN)

TTTGAAGGCAAGATTTTAGTCCAGGGTGGTATGTTTCAATCATT|TTTTTGCAATGGTGAGCAAGGGCGAGGAGCTGTTC  
ACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGA  
GGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCACCC  
TCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAG  
TCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGA  
GGTGAAGTTCGAGGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCC  
TGGGGCACAAGCTGGAGTACAACACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAG  
GTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCAT  
CGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGA  
AGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAG

3

Pupilas dilatadas



Sustancias pecaminosas / ciclopentolato







1

Comprar kit CRISPR DIY

2

Preparar las tres jeringas (genes TYR, AR e IRF4) e inyectar



1

Comprar kit CRISPR DIY

2

Preparar las tres jeringas (genes TYR, AR e IRF4) e inyectar

3

Pupilas dilatadas con el medio preferido



1

Comprar kit CRISPR DIY

2

Preparar las tres jeringas (genes TYR, AR e IRF4) e inyectar

3

Pupilas dilatadas con el medio preferido

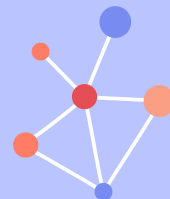
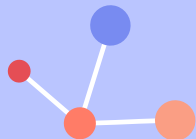
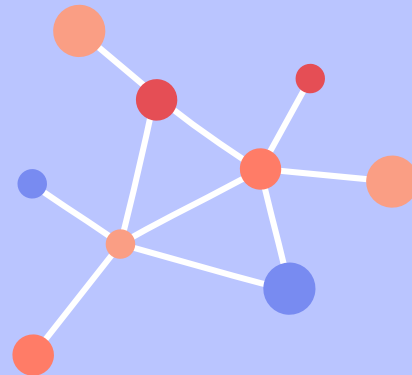


**¡Y listo!**



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# CONSIDERACIONES IMPORTANTES



# RIESGOS Y LEGALIDAD



Condiciones no óptimas y procedimientos peligrosos

Int

Co

In



Código ético y auto-seguridad



Legalidad dudosa

lógicos

er





# ¡Gracias!

## ¿Preguntas?



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