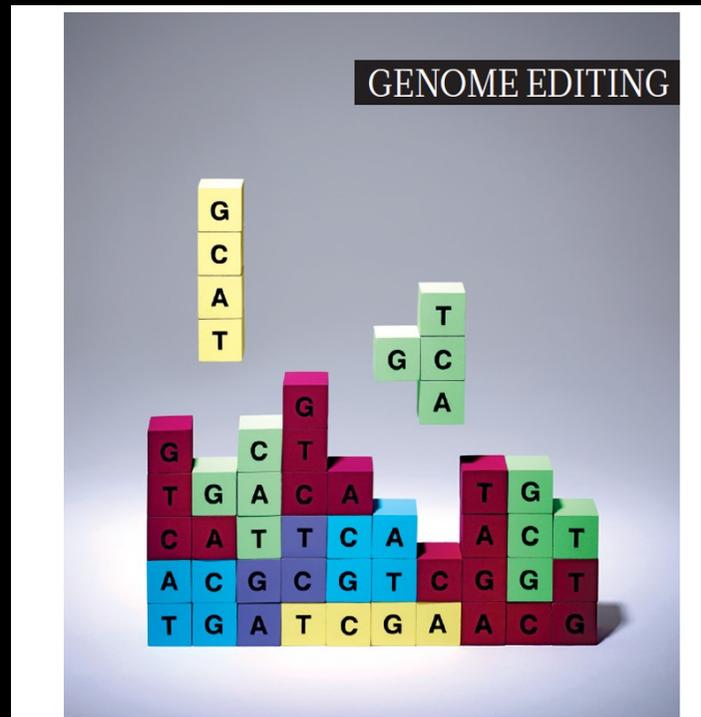


GENOME ENGINEERING: CRISPR/CAS9



- Laurea Magistrale Scienze Biomolecolari dell'Evoluzione
- Corso di Macromolecole Biologiche

A new tool for DNA cutting

Beyond Restriction Enzymes
A very specific way to cut DNA



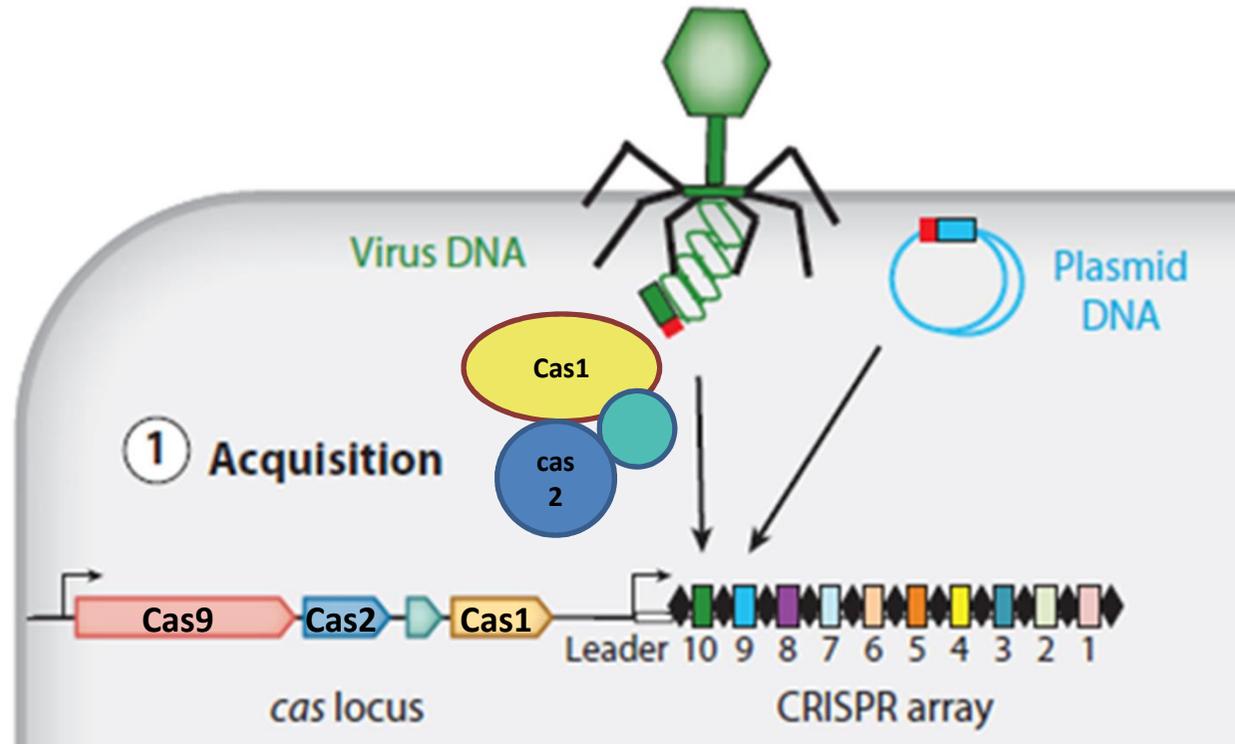
**CRISPR (clustered regularly interspaced short
palindromic repeats).**

40% Bacteria Genome and 90% Archea genomes



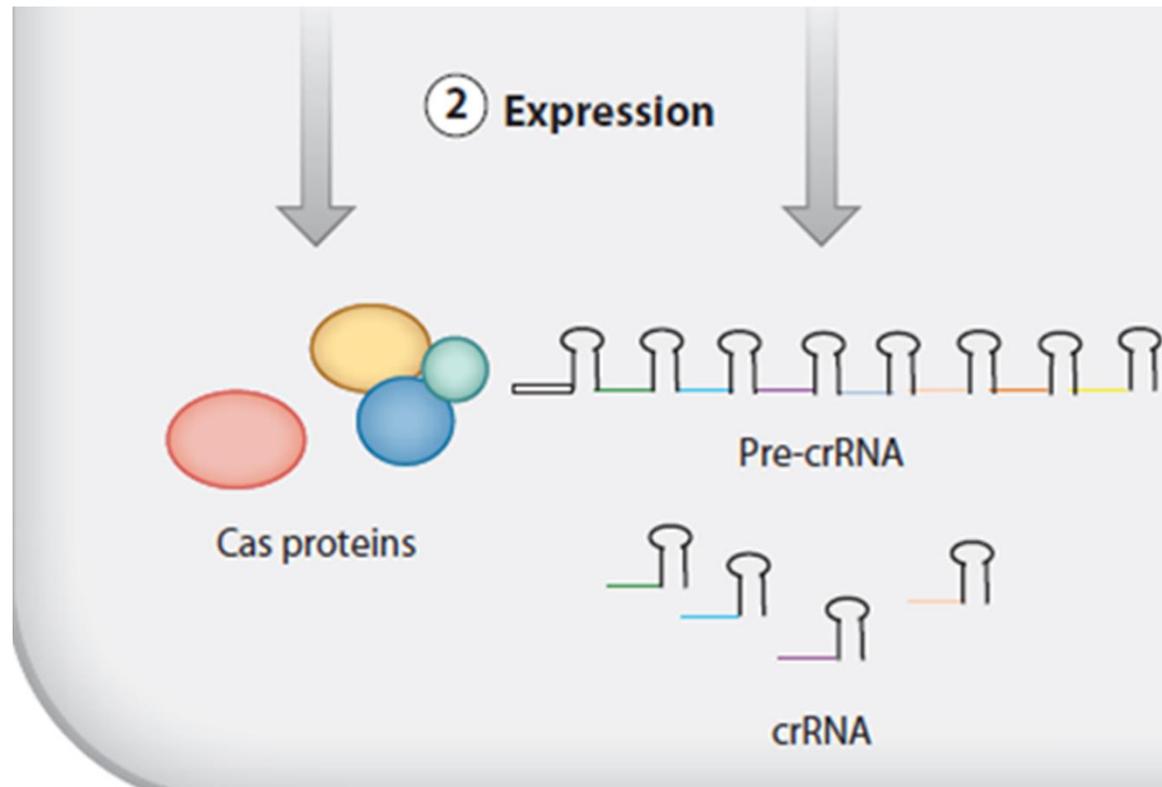
Immune Adaptative System

Immune Adaptative System



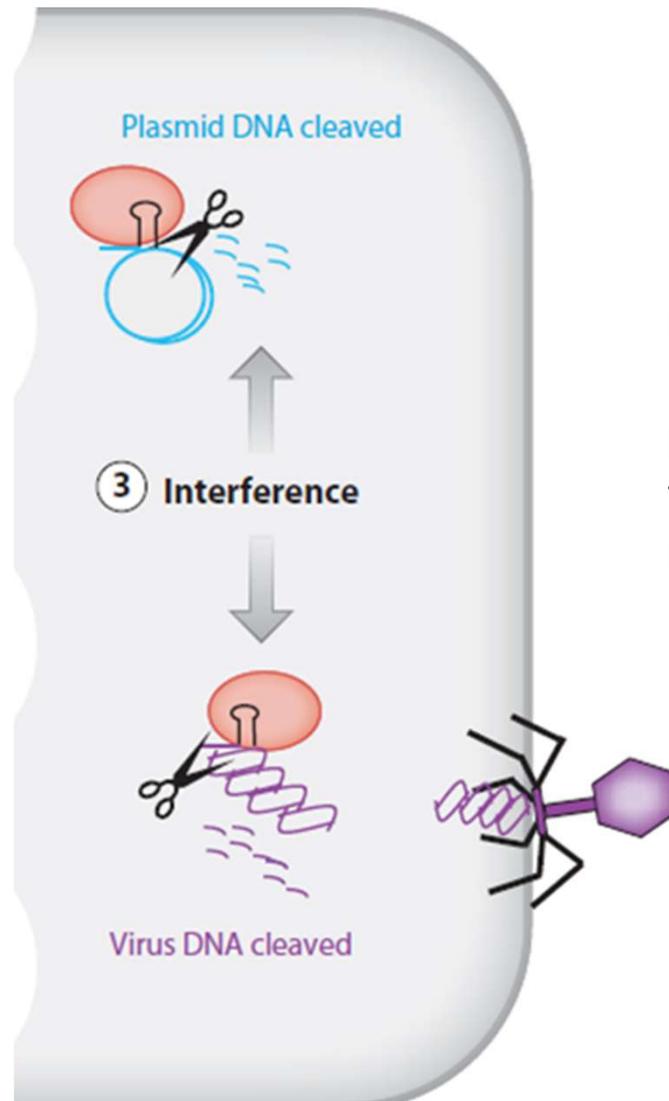
- 1. Acquisition:** Invasive **Virus** or **Plasmid** DNA is cleaved by Cas proteins and it is inserted in the CRISPR array between crisper **repeats**. This cut is made before a sequence named **PAM** that is naturally present Viral or Plasmid DNA.

Immune Adaptative System



- 2. Expression:** CRISPR array is transcribed and the single molecule of RNA (Pre-crRNA) matured in different crRNA that are specific for target sequences present in Virus or Plasmidic DNA from the first contact.

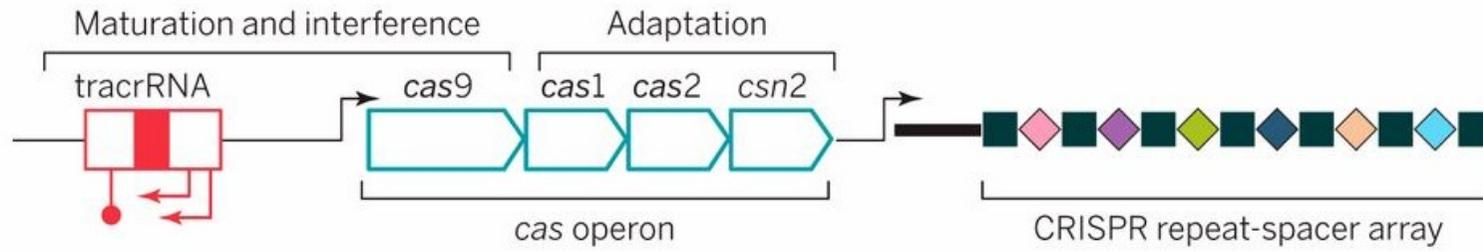
Immune Adaptative System



3) Interference: The crRNA recognizes the target of a second infection of the pathogen and Cas9 degrades the Viral or Plasmidic DNA after recognition

Inside the mechanism:

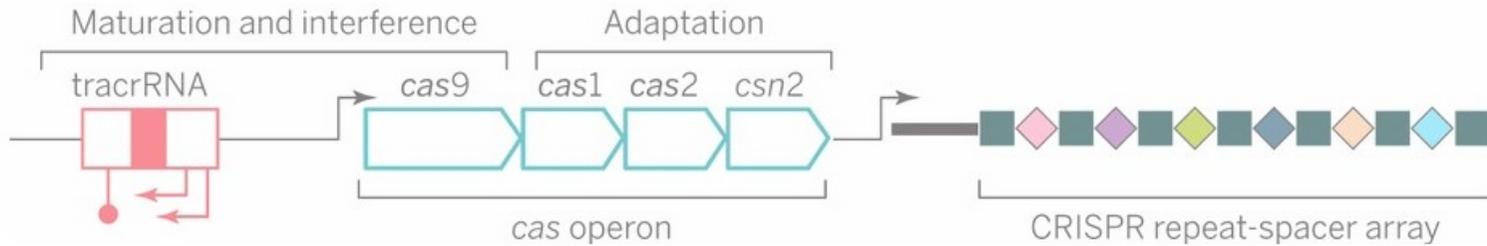
Genomic CRISPR locus



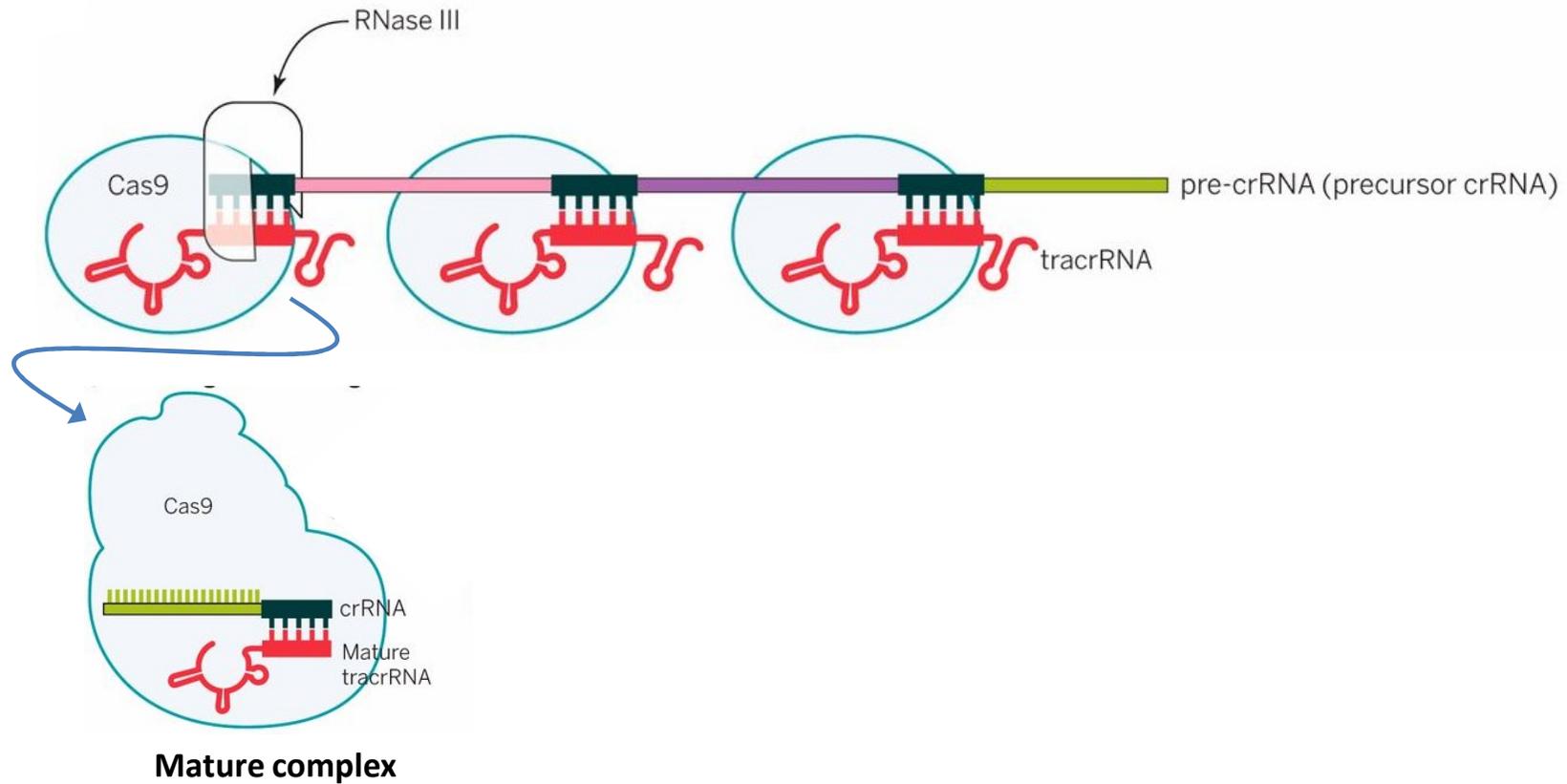
Viral DNA from previous infections

Inside the mechanism:

Genomic CRISPR locus

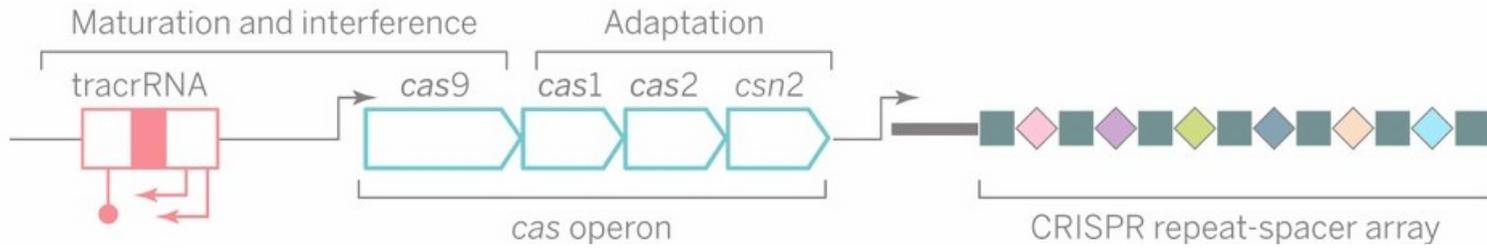


tracrRNA:crRNA co-maturation and Cas9 co-complex formation

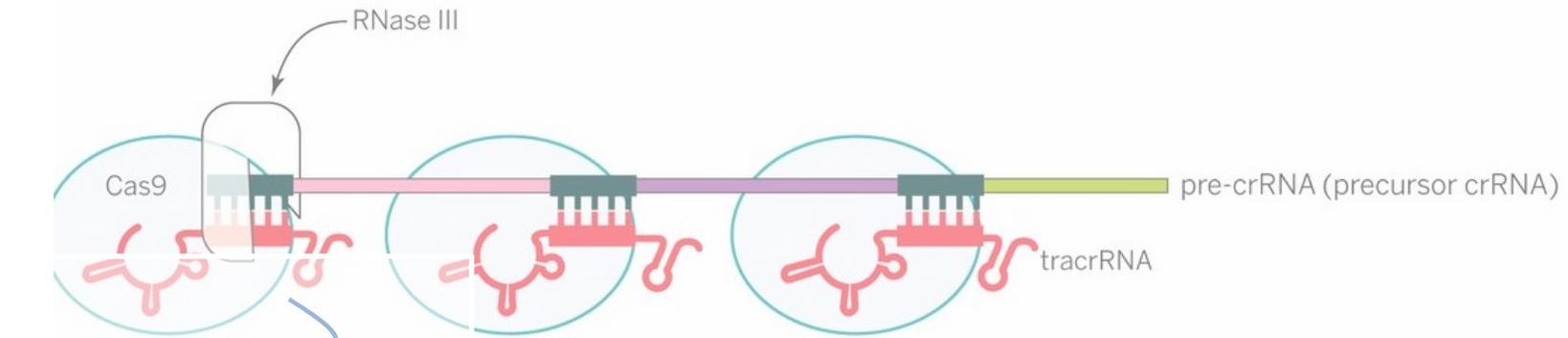


Inside the mechanism:

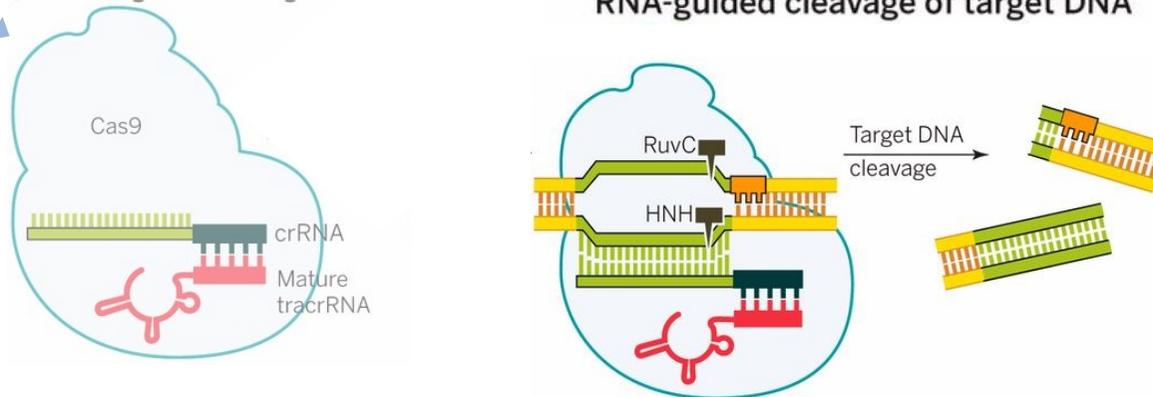
Genomic CRISPR locus



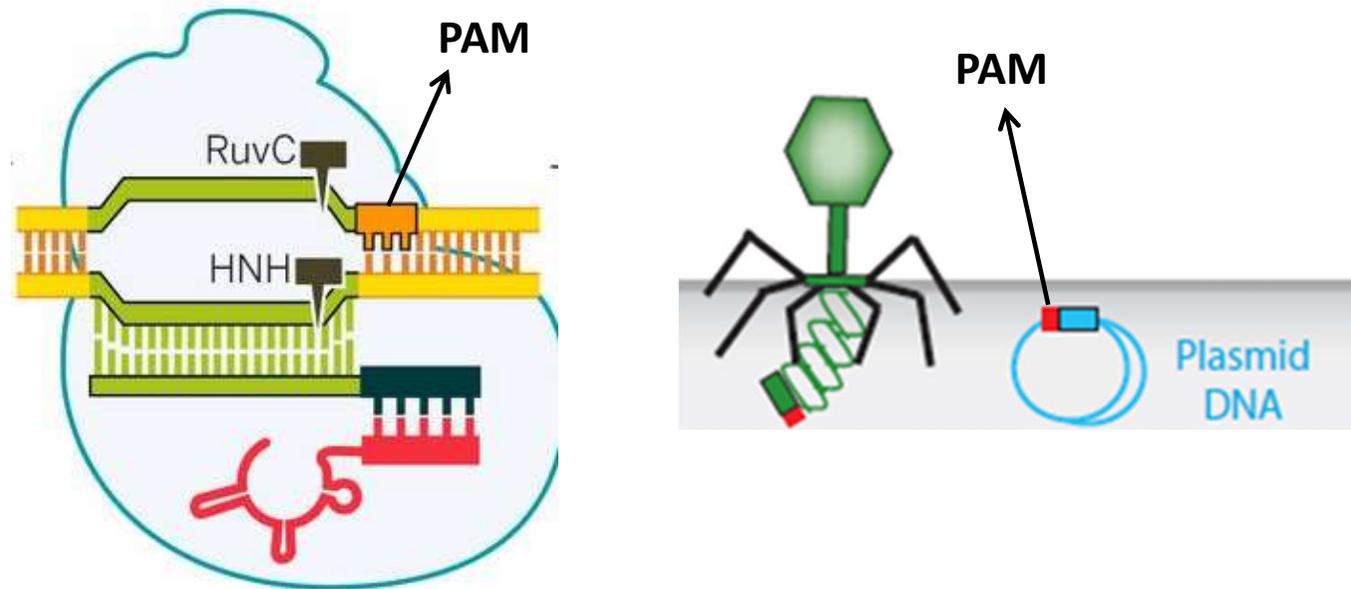
tracrRNA:crRNA co-maturation and Cas9 co-complex formation



RNA-guided cleavage of target DNA



Protospacer Adjacent Motif



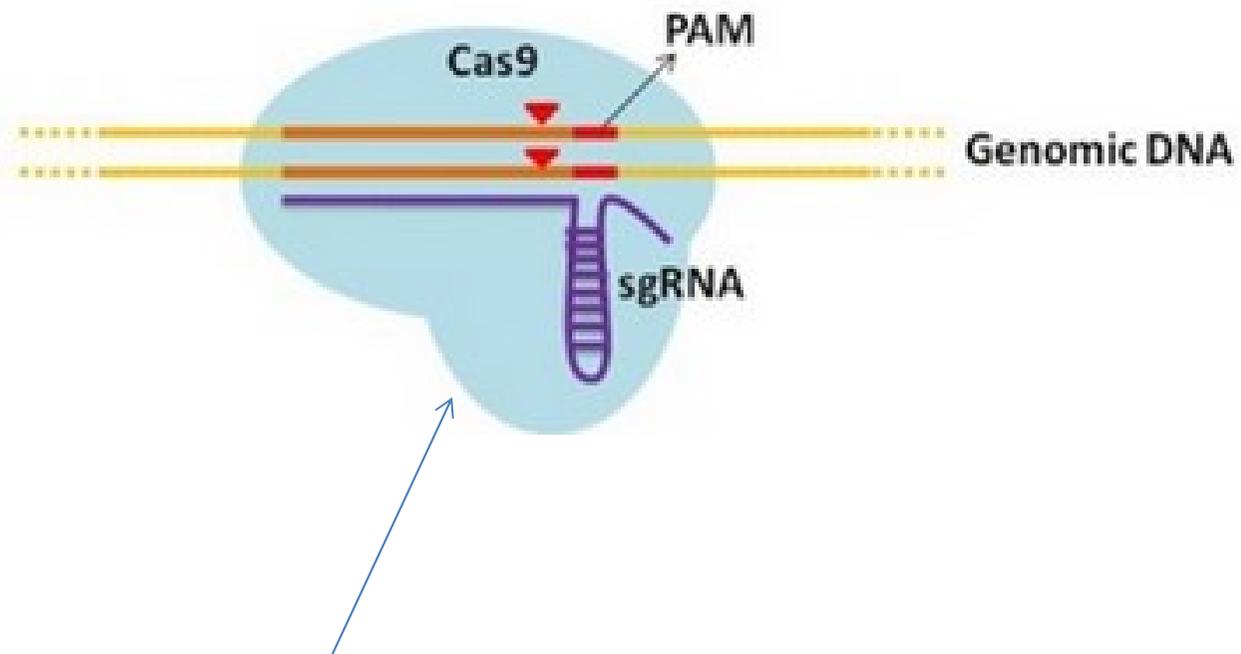
Protospacer adjacent motif (PAM)

PAM is a component of the invading virus or plasmid, but is not a component of the bacterial CRISPR locus.

Is an essential targeting component which distinguishes bacterial *self* from *non-self DNA*, thereby preventing the CRISPR locus from being targeted and destroyed by nuclease.

The canonical PAM of *S. Pyogenes* is the sequence **5'-NGG-3'**.

Engineered system



All in one RNA crRNA+tracrRNA

Genome Knockout using CRISPR/Cas9: TERRA example

Locus 20q

WT allele: gRNA
Start2 gRNA
End1
CAGGCTGGCGCGACGTGCGG CCCACCACCTTAGCGGATCA
 CACCCCACGCCGCGCGGGGCACAGAGAGGCCCAACCGCGCCGGCGCAGGGCGCGCACAGGCTGGCGCGACGTGCGC // 8.1KB // CCCACCACCTTAGCGGATCAAGGCACAGTAG

CRISPR allele:

Clone C4

CACCCCACGCCGCGCGGGGCACAGAGAGGCCCAACCGCGCCGGCGCAGGGCGCGCACAGGCTGGCGCGACGTG-----8.1KB-----TCAAGGCACAGTAG

Clone A2 allele 1

CACCCCACGCCGCGCGGGGCACAGAGAG----ACCCGCGCG-----8.1KB-----CAAGGCACAGTAG

Clone A2 allele 2

CAC-----8.2KB-----AGTAG

Clone B4 allele 1

CACCCCACGCCGCGCGGGGCACAGAGAGGCCCAACCGCGCCGGCGCAGGGCGCGCACAGGCTGGCGCGACGTGCGGGGA---8.1KB-----AGGCACAGTAG

Clone B4 allele 2

CAC-----8.2KB-----AGTAG

Locus XP

WT allele: gRNA
Start2 gRNA
End2
TCCGAGTATGATATGGTGGC GGATGAAGCCGGTGTAGACC
 TGGCCATGATTGTCCCTCCGAGTATGATATGGTGGC // 9.5KB // TGATCCAGGATGAAGCTGTTGTAGACC GCC

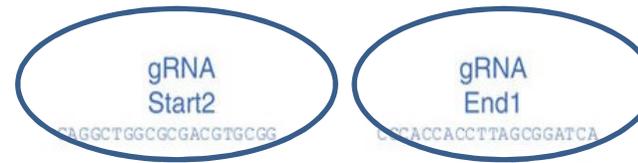
CRISPR allele:

Clone D8

TGGCCATGATTGTCCCTCCG-----9.5KB-----TGAAGCTGTTGTAGACC GCC

Genome Knockout using CRISPR/Cas9: TERRA example

Locus 20q



WT allele:

CACCCCACGCCCGCCGCGGGCACAGAGAGGCCCAACCGCGCCGGCGCAGGGCGCGCACAGGCTGGCGCGACGTGCGC//8.1KB//CCCACCACCTTAGCGGATCAAGGCACAGTAG

CRISPR allele:

8,1 KB

Clone C4

CACCCCACGCCCGCCGCGGGCACAGAGAGGCCCAACCGCGCCGGCGCAGGGCGCGCACAGGCTGGCGCGACGTG-----8.1KB-----TCAAGGCACAGTAG

Clone A2 allele 1

CACCCCACGCCCGCCGCGGGCACAGAGAG---ACCCGCGCG-----8.1KB-----CAAGGCACAGTAG

Clone A2 allele 2

CAC-----8.2KB-----AGTAG

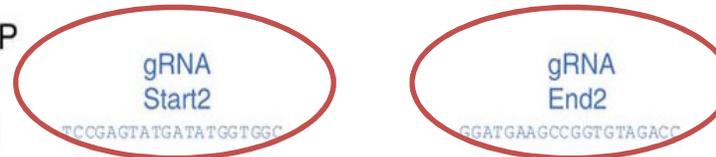
Clone B4 allele 1

CACCCCACGCCCGCCGCGGGCACAGAGAGGCCCAACCGCGCCGGCGCAGGGCGCGCACAGGCTGGCGCGACGTGCGGGGA---8.1KB-----AGGCACAGTAG

Clone B4 allele 2

CAC-----8.2KB-----AGTAG

Locus XP



WT allele:

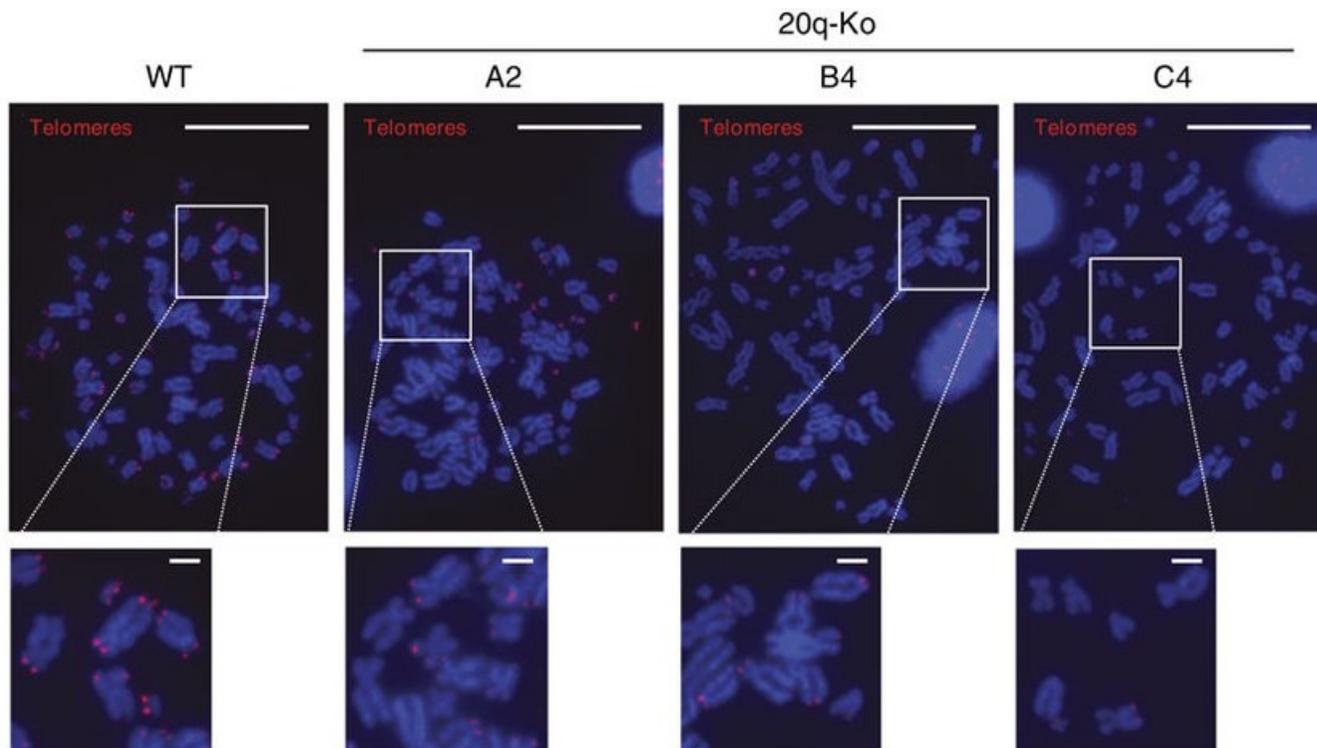
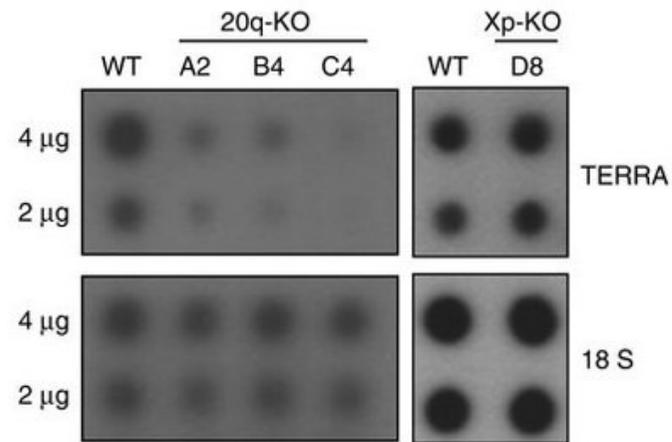
TCCGAGTATGATATGGTGGC//9.5KB//TGATCCAGGATGAAGCTGTTGTAGACCGCC

CRISPR allele:

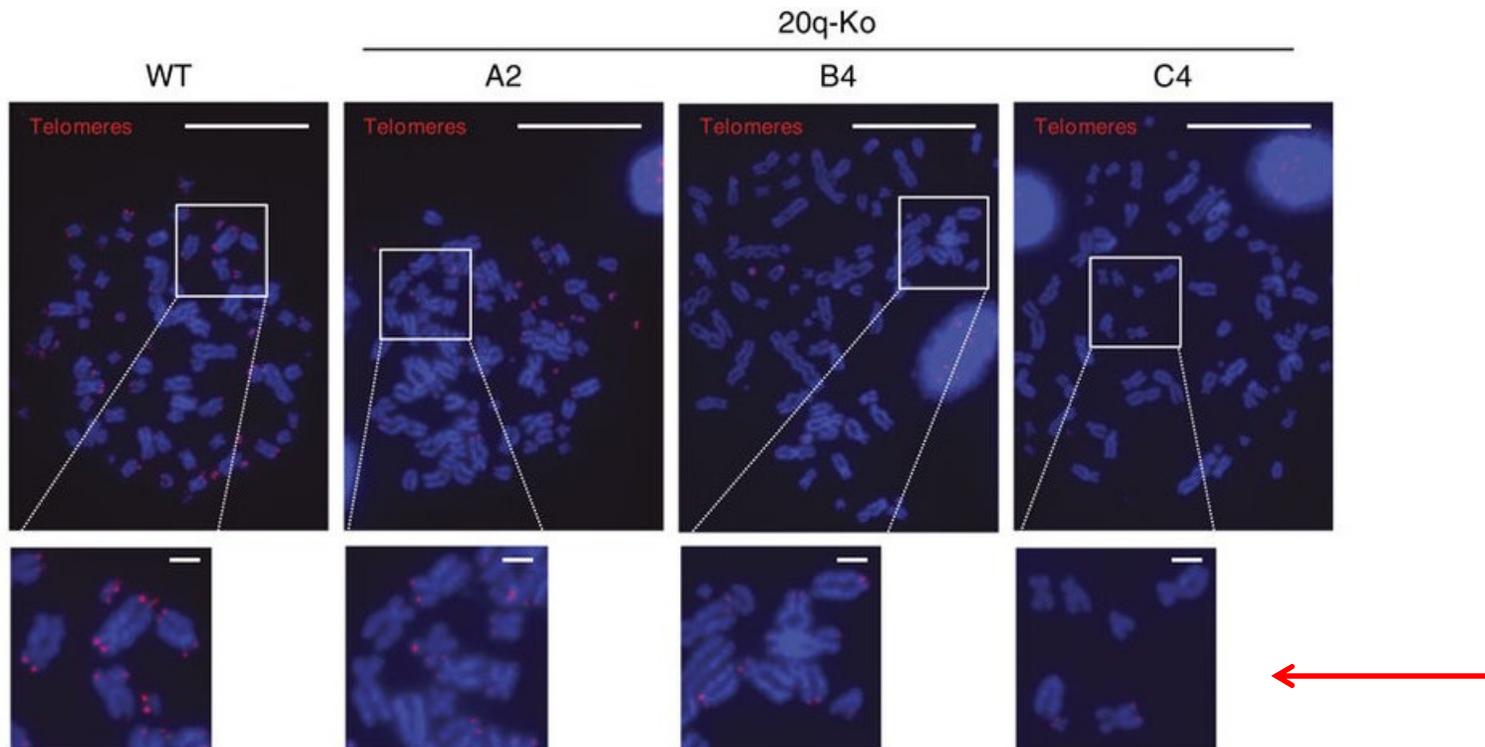
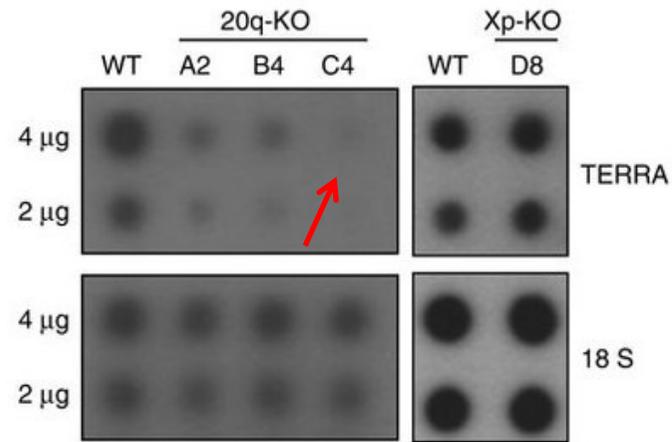
Clone D8

TGGCCATGATTGTCCCTCCG-----9.5KB-----TGAAGCTGTTGTAGACCGCC

TERRA Knockout using CRISPR/Cas9: Effects



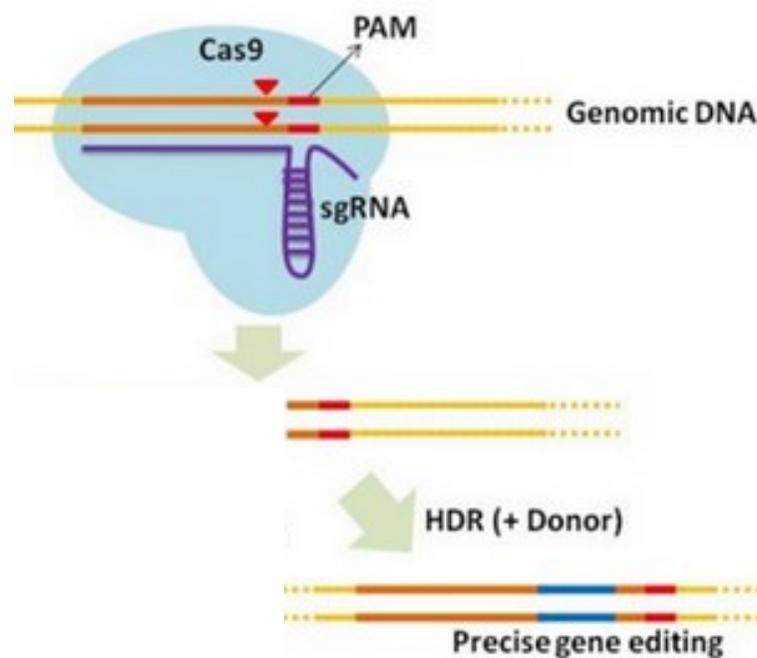
TERRA Knockout using CRISPR/Cas9: Effects



But...The big trend is to insert specific sequences

Taking advantage of the double strand break resulting from the CRISPR/Cas9 Cutting there is the possibility to **insert** specifically a mutation or a bigger portion of DNA.

This mechanism is permitted by the Homologous Direct Repair pathway, giving a «Donor» sequence.

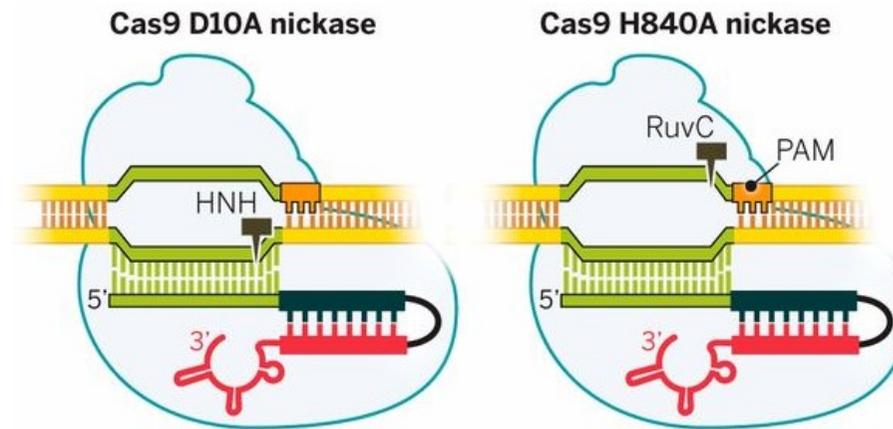


Genome Engineering and Disease

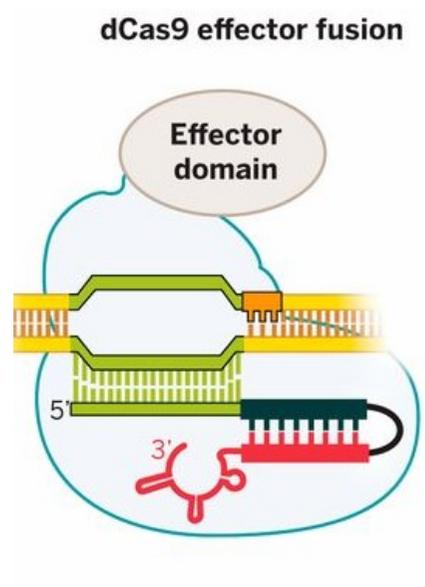
| Disease type | Nuclease platform | Therapeutic strategy |
|--|--------------------------|---|
| Hemophilia B | ZFN | HDR-mediated insertion of correct gene sequence |
| HIV | ZFN and CRISPR | NHEJ-mediated inactivation of CCR5 |
| Duchenne muscular dystrophy (DMD) | CRISPR and TALEN | NHEJ-mediated removal of stop codon, and HDR-mediated gene correction |
| Hepatitis B virus (HBV) | TALEN and CRISPR | NHEJ-mediated depletion of viral DNA |
| SCID | ZFN | HDR-mediated insertion of correct gene sequence |
| Cataracts | CRISPR | HDR-mediated correction of mutation in mouse zygote |
| Cystic fibrosis | CRISPR | HDR-mediated correction of CFTR in intestinal stem cell organoid |
| Hereditary tyrosinemia | CRISPR | HDR-mediated correction of mutation in liver |

Cas9 can also be engineered:

To be able to create nicks in a single strand



Can be fused to a Transcriptional Activator Domain





CRISPRpapers
@CRISPR_papers
Automatic Twitterbot for papers on CRISPR/Cas genome engineering.
crisprflydesign.org

TWEET 438 FOLLOWER 751

Tweet Tweet e risposte

CRISPRpapers @CRISPR_papers · 21 nov
From Hacking the Human Genome to Editing Organs. dlvr.it/CpCmQM

CRISPRpapers @CRISPR_papers · 20 nov
Engineering Enhanced Vaccine Cell Lines to Eradicate Preventable Diseases: The Polio Endgame. dlvr.it/CpCmQM



REVIEW SUMMARY

GENOME EDITING

The new frontier of genome engineering with CRISPR-Cas9

Jennifer A. Doudna* and Emmanuelle Charpentier*



10/20/2015

THE PROMISING AND PERILOUS SCIENCE OF GENE EDITING

Dan Kedzney

REVIEW



**nature
biotechnology**

CRISPR-Cas systems for editing, regulating and targeting genomes

Jeffrey D Sander^{1,2} & J Keith Joung^{1,2}

Targeted genome editing using engineered nucleases has rapidly gone from being a niche technology to a mainstream method used by many biological researchers. This widespread adoption has been largely fueled by the emergence of the clustered, regularly interspaced, short palindromic repeat (CRISPR) technology, an important new approach for generating RNA-guided nucleases, such as Cas9, with customizable specificities. Genome editing mediated by these nucleases has been used to rapidly, easily and efficiently modify endogenous genes in a wide variety of biomedically important cell types and in organisms that have traditionally been challenging to manipulate genetically. Furthermore, a modified version of the CRISPR-Cas9 system has been developed to recruit heterologous domains that can regulate endogenous gene expression or label specific genomic loci in living cells. Although the genome-wide specificities of CRISPR-Cas9 systems remain to be fully defined, the power of these systems to perform targeted, highly efficient alterations of genome sequence and gene expression will undoubtedly transform biological research and spur the development of novel molecular therapeutics for human disease.

A fun explanation

<https://videopress.com/v/2gVkUyqq>