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depressione è una malattia
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genome and build a human

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From DNA to protein - 3D

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L'ingegneria Genetica

Cambierà Tutto Per Sempre -

CRISPR *What Makes Us Human?*

- *with Adam Rutherford* **La**

fortuna degli Etruschi:

l'eredità degli Etruschi

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dalla genetica ai fumetti

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they affect the sizes or

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numbers of restriction
fragments Point mutations
are more difficult to detect
The ultimate map is to
determine the sequence of
the DNA From the sequence,
we can identify genes and
the distances

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genome can be recognized because they affect the sizes or numbers of restriction fragments. Point mutations are more difficult to detect. The ultimate map

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is to determine the sequence of the DNA. From the sequence, we can identify genes and the distances between them. By analyzing the pro-te-in-coding potential of a sequence of the DNA, we can

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From genes to genomes

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Advances in genome
sequencing and annotation
have eased the difficulty of
identifying new gene

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sequences. Predicting the functions of these newly identified genes remains challenging. Genes descended from a common ancestral sequence are likely to have common functions. As a result, homology is widely

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used for gene function
prediction.

Non-homology-based
prediction of gene functions
in maize ...

Genome synthesis potentially
allows the researchers to

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gain a much greater degree of control of an organism, and it also leads to a completely new way to understand the biology of genomes. In 2008, the first mega-size bacteria genome was built from

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oligonucleotides . Next, the 4-Mb genome of E. coli was redesigned and engineered [2, 3].

Sc3.0: revamping and
minimizing the yeast genome
| Genome ...

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By systematically examining the oncological applications of gene editing tools and critical factors challenging their medical translation, genome editing has substantial contributions to cancer driver gene

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discovery, tumor cell
epigenome normalization,
targeted delivery, cancer
animal model establishment,
and cancer immunotherapy and
prevention in clinics.

Innovative Precision

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To make the pan-genome represent the full range of genetic diversity of soybean, we sequenced a total of 2,898 soybean

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accessions (871 from our previous studies [Fang et al., 2017, Zhou et al., 2015] and 2,027 from this study) by Illumina technology with an average coverage depth of more than 13x for each accession

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(Figure 1A; Table S1). These accessions included 103 wild soybeans, 1,048 ...

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