

Taller 1: Bases del Cáncer

ESCUELA DE CÁNCER DE PULMÓN Y OTRAS NEOPLASIAS TORÁNICAS

7 de Abril de 2026

Hospital 12 de Octubre, Madrid

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Grupo de Investigación de Comunicación Intercelular
en Envejecimiento & Cáncer, I+12, Madrid.

¿De qué está formado nuestro cuerpo?



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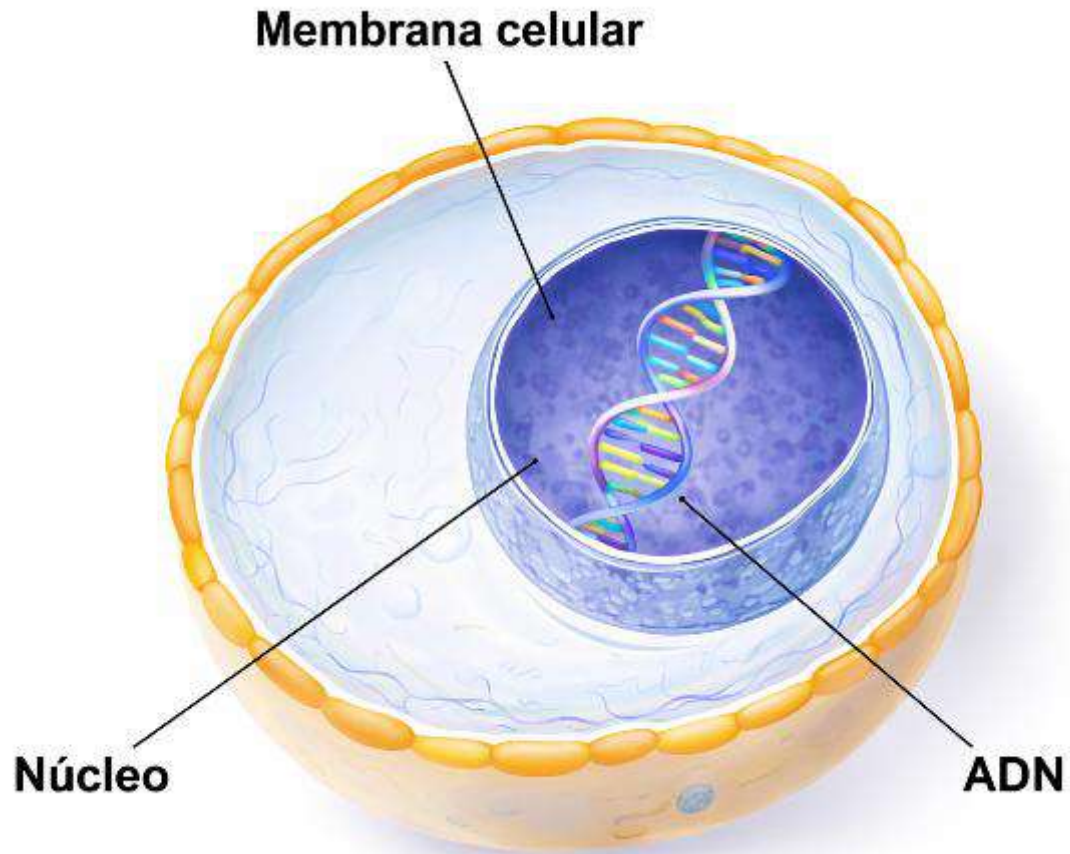


Células

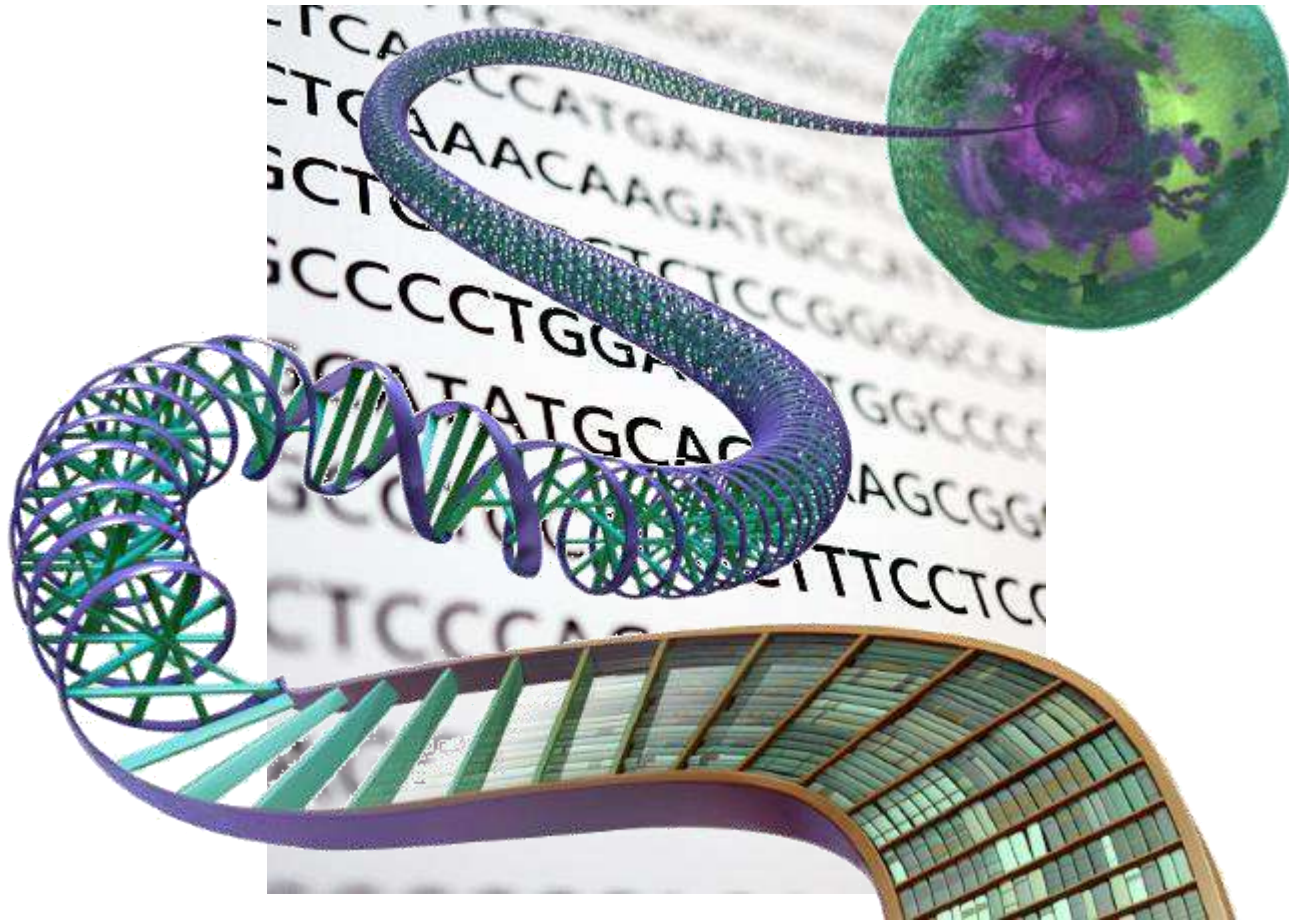
Tejidos

Órganos

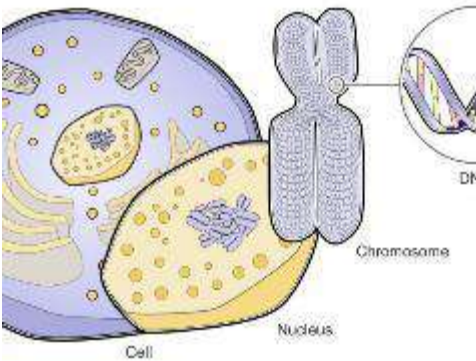
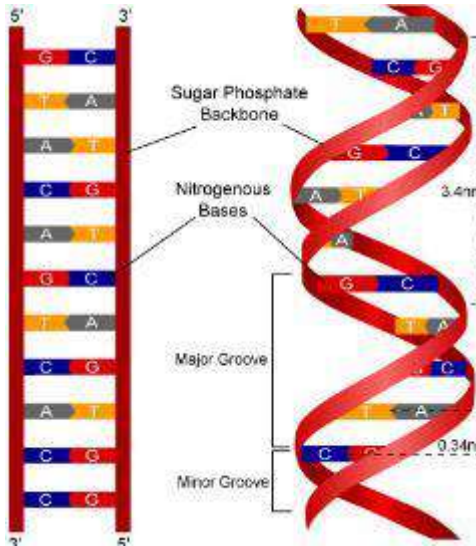
La célula, el núcleo y el ADN



ADN: El manual de instrucciones de las células



ADN: un pequeño gran libro



April 25, 1953 NATURE 737

equipment, and to Dr. H. B. Dole and Dr. ...
 (Liang, K. H., and ...)
 (Liang, K. H., and ...)
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MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribonucleic Acid

WE wish to suggest a structure for the salt of deoxyribonucleic acid (DNA). This structure has several features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Bragg. They kindly made their manuscript available to us in advance of publication. Their model consists of three ribbons twisted about each other, with the phosphate group at the center and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray images in the width of the top edge. Without this side the structure is not what it should be. (2) We believe that the structure is not what it should be. The structure as described is rather ill-defined, and the structure is not what it should be.

Another three-chain structure has also been suggested by Fraser in the press. In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and the structure is not what it should be.



The structure is a very simple one, and it is not what it should be. It is not what it should be. It is not what it should be. It is not what it should be.

is 4 months on each chain, every 2-4 Å, is the distance. We have assumed an angle of 36° between adjacent rungs in the above model, so that the structure repeats after 34 nucleotides on each chain, that is, after 34 Å. The distance of a phosphate group from the ribbons is 1.8 Å. As the phosphate group on the outside, outside have more space to them.

The structure is not what it should be. It is not what it should be. It is not what it should be. It is not what it should be.

The novel feature of the structure is the manner in which the two chains are held together by the protein and phosphate bases. The bases of the bases are perpendicular to the ribbons. They are linked together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two bases lie side by side with identical co-orientation. One of the bases must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: guanine position 1 to pyrimidine position 1; guanine position 6 to pyrimidine position 6.

It is assumed that the bases only occur in the structure in the same relative positions as they do in with the base pairs that the two chains. It is found that only specific pairs of bases can bond together. These pairs are: guanine (paired with thymine (pyrimidine)), and guanine (paired with cytosine (pyrimidine)).

In other words, if an adenine base can combine of a pair, or other bases, then can these combinations the other number must be thymine, cytosine, or guanine and cytosine. The sequence of bases on a single chain must not appear to be specified in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is known, then the sequence on the other chain is automatically determined.

It has been found experimentally that the ratio of the amount of adenine to thymine and the ratio of guanine to cytosine are always very close to unity in deoxyribonucleic acid.

It is probably impossible to build the structure with a ribbon sugar in place of the ribbons, as the cross angles seem would make the structure too rigid. Whole structure.

The previously published X-ray data on deoxyribonucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly correct, but with experimental data, but it must be regarded as a suggested model. It has been checked against more exact results. Some of these are given in the following correspondence. We must not stress of the details of the model presented here unless we derived our structure, which were mainly through our ability in published experimental data and stereochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material. Each strand of the structure, containing the information contained in building it, could work with a set of co-ordinates for the bases, will be published separately.

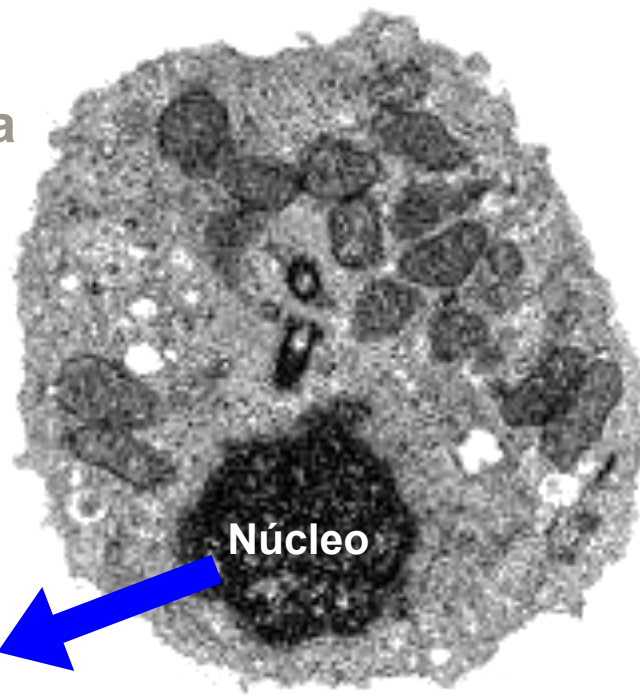
We are much indebted to Dr. Jerry Donnan for several useful and criticisms, especially to Dr. ...
 (Liang, K. H., and ...)
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¡Feliz día del ADN!

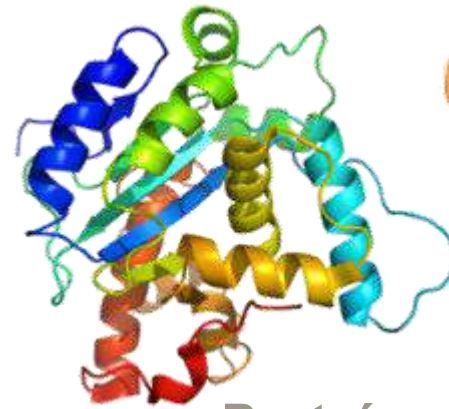


Célula



Núcleo

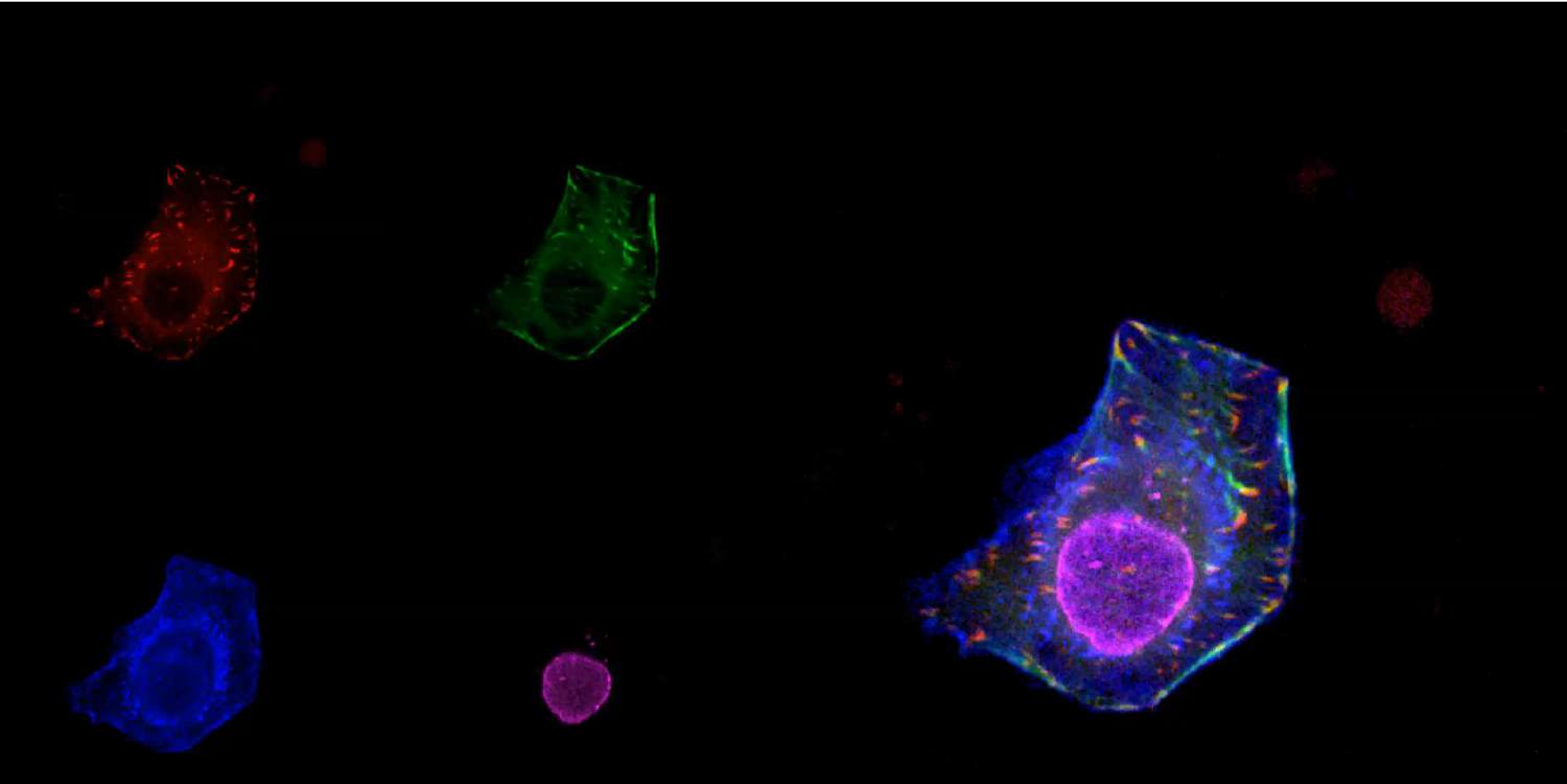
ADN



Proteína



Unidad de Microscopía Confocal del CNIO



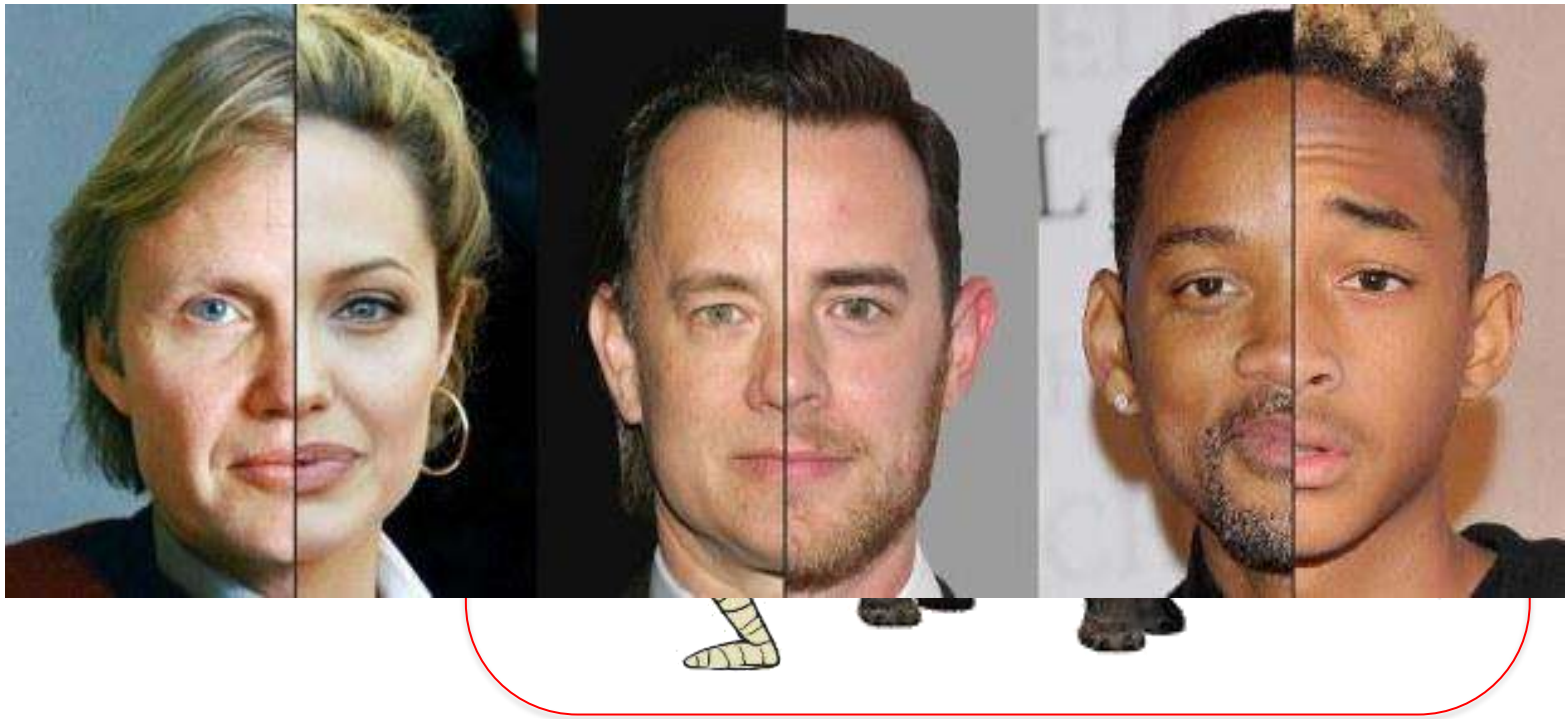
Adhesiones focales

Membrana

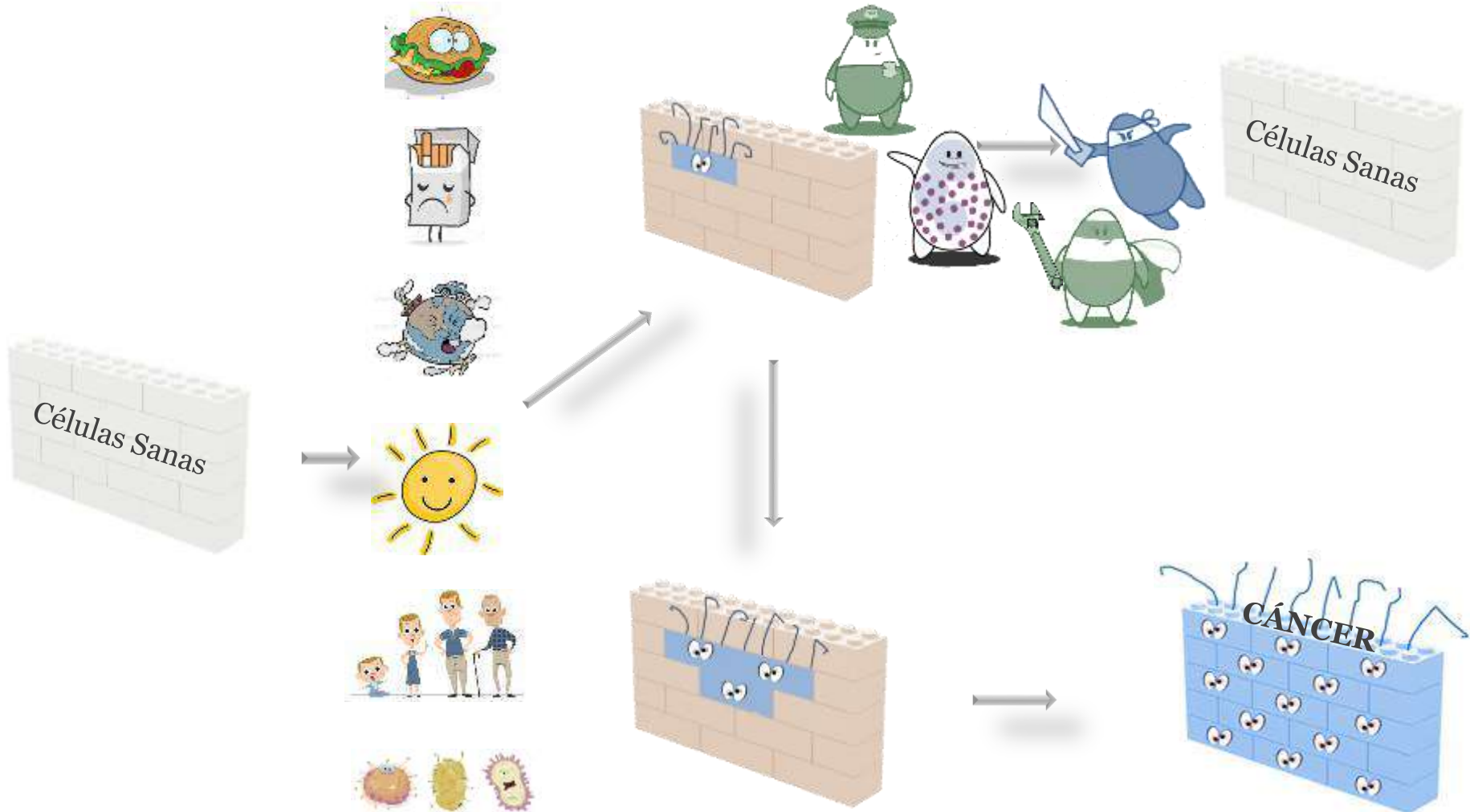
Citoplasma

Núcleo

ADN: el guardián de la información



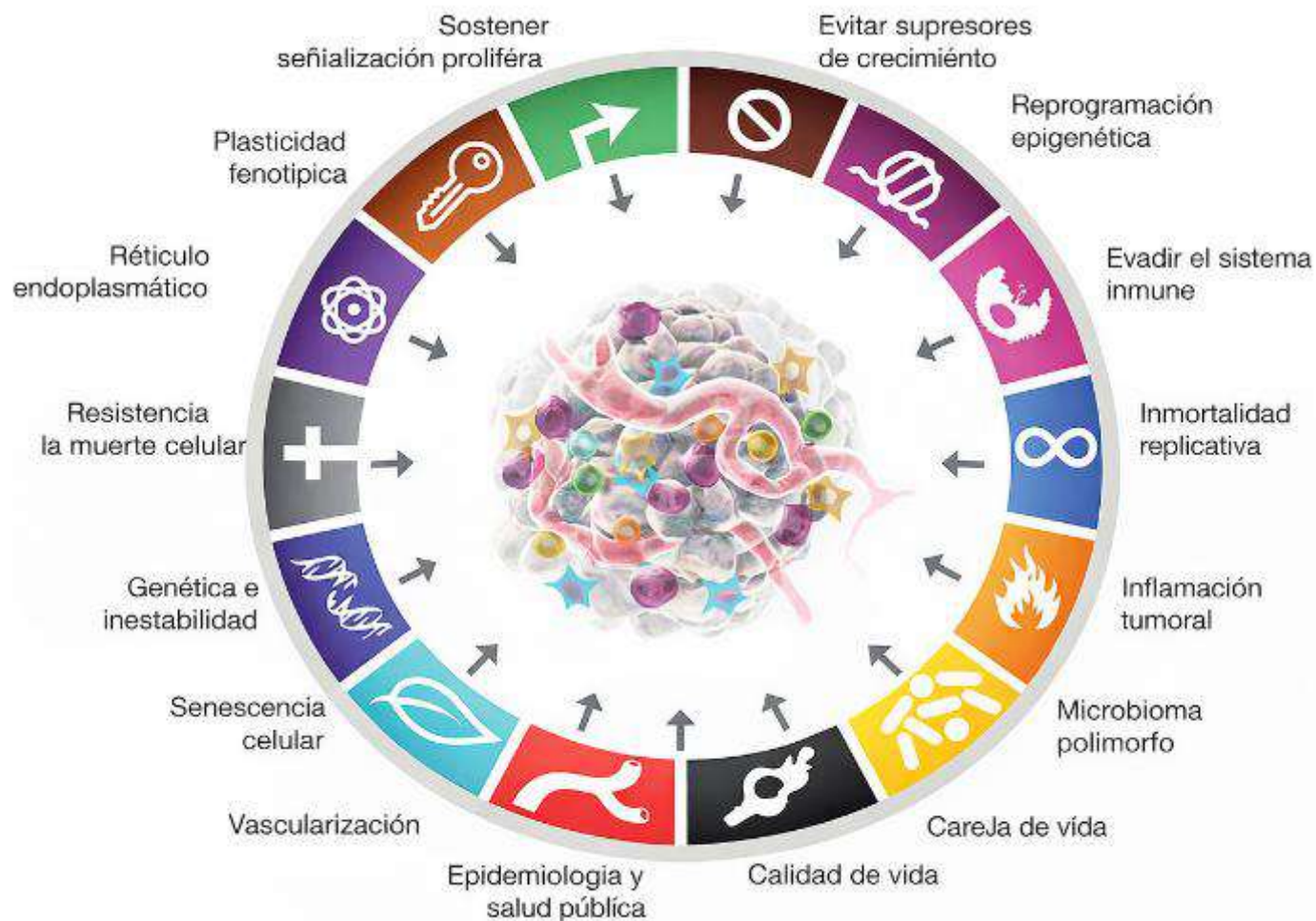
A veces, las células se descontrolan...



Usos del ADN: podemos modificar las instrucciones



Una realidad aún más compleja



Una realidad aún más compleja

Microentorno: el ecosistema del cáncer

Células del sistema inmunitario



Células tumorales



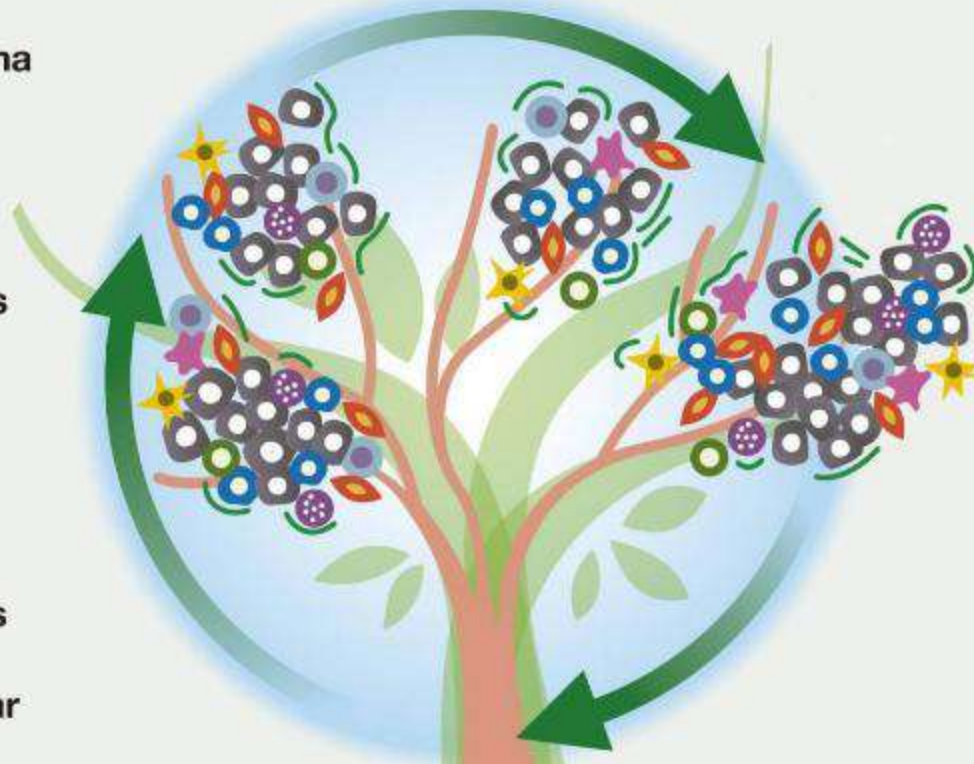
Fibroblasto asociado a tumor



Vasos sanguíneos



Matriz extracelular



SINC / J. A. Peñas

Fuente: Daniele Tauriello, @BattleLab

CLÍNICA

PREVENCIÓN | DIAGNÓSTICO | TRATAMIENTO

PRE-CLÍNICA

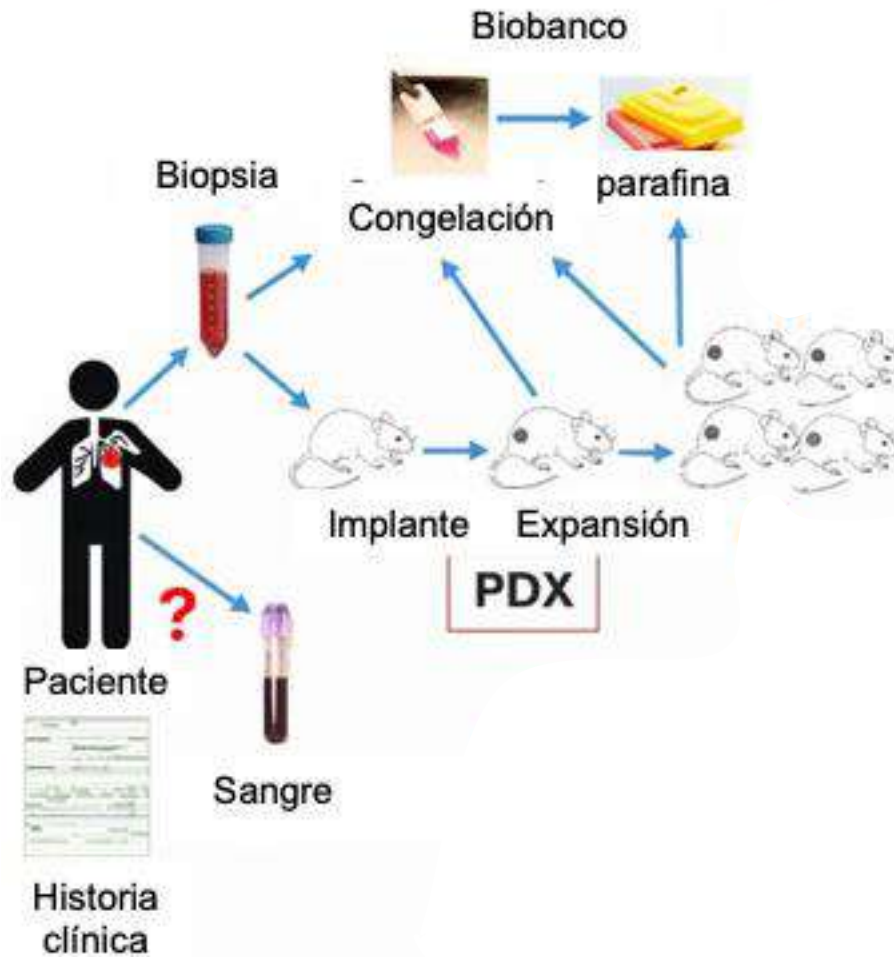
Biología tumoral: Estudiamos las células del tumor y su relación

Inmunología: ¿Cómo reacciona el sistema inmune a un tumor?

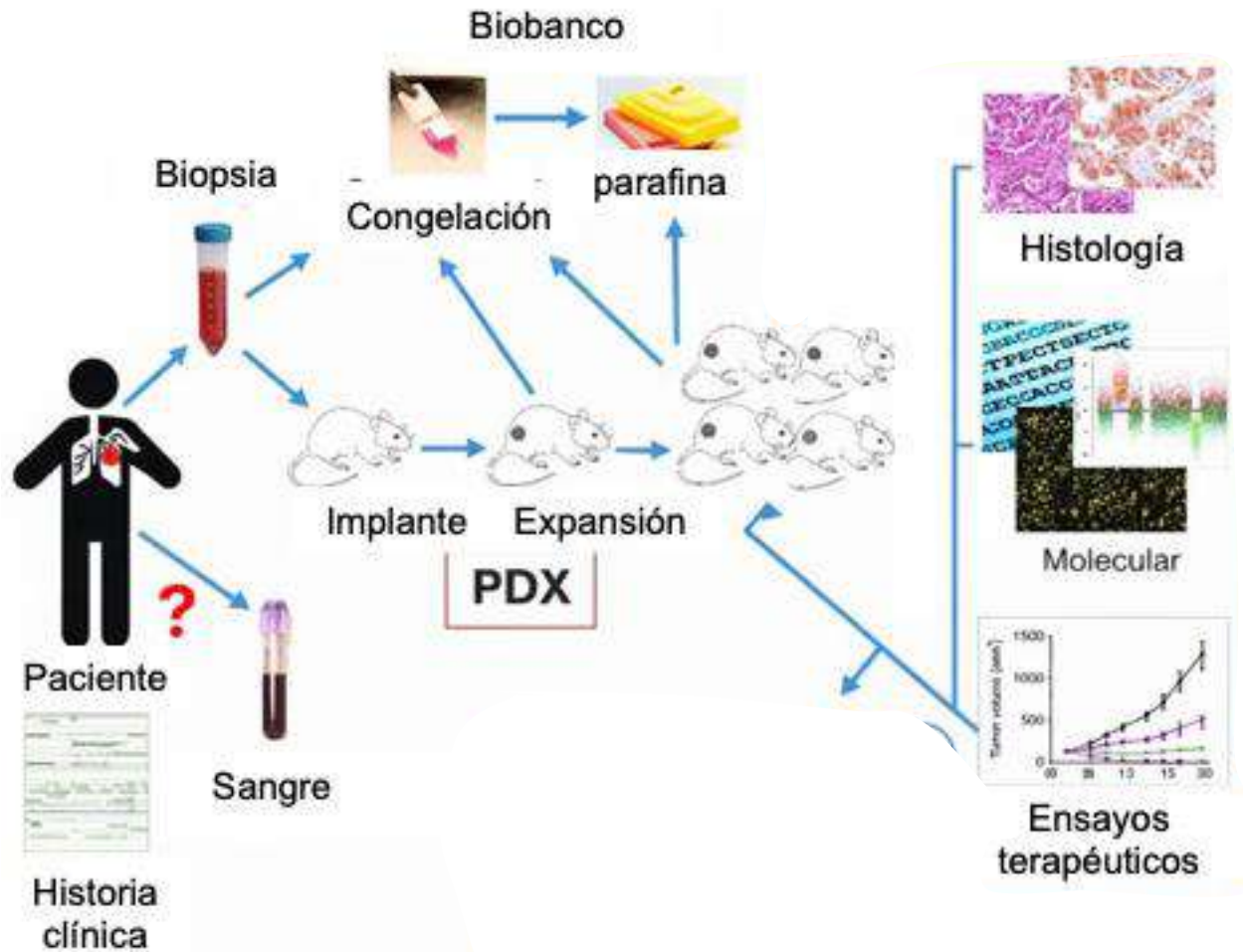
Biomarcadores: No informan de características del tumor

Modelos experimentales: Nos permiten imitar una enfermedad compleja

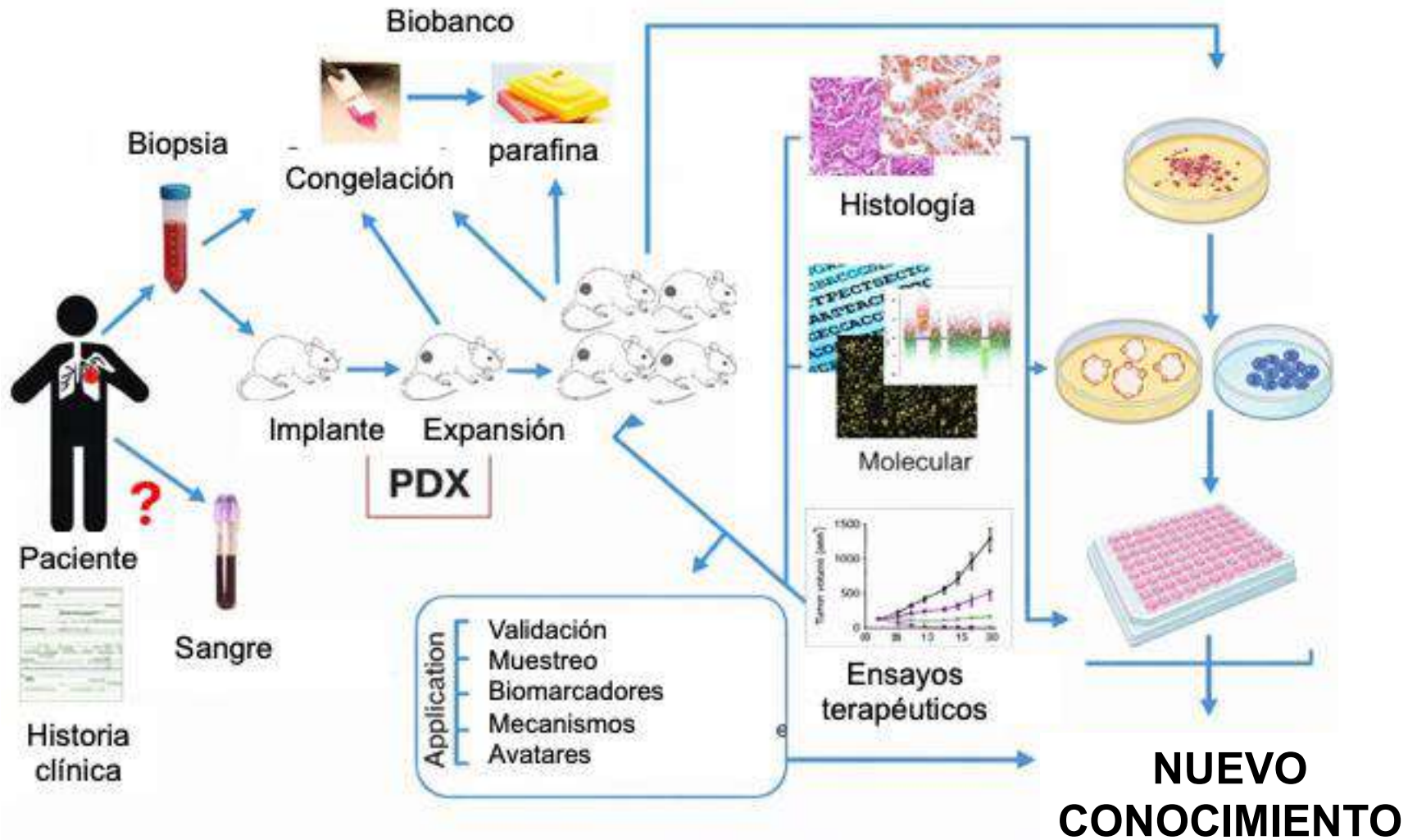
Modelos experimentales: Nos permiten imitar una enfermedad compleja



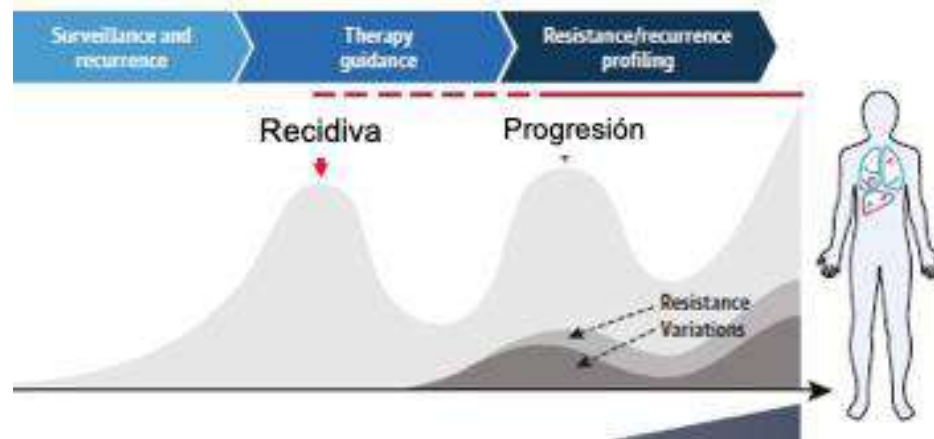
Modelos experimentales: Nos permiten imitar una enfermedad compleja



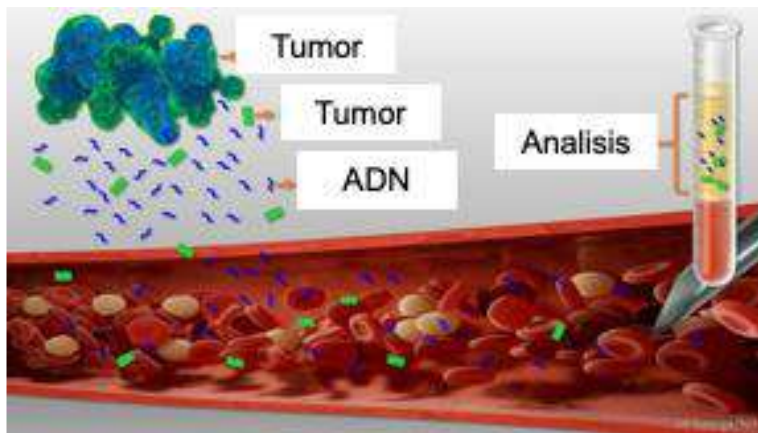
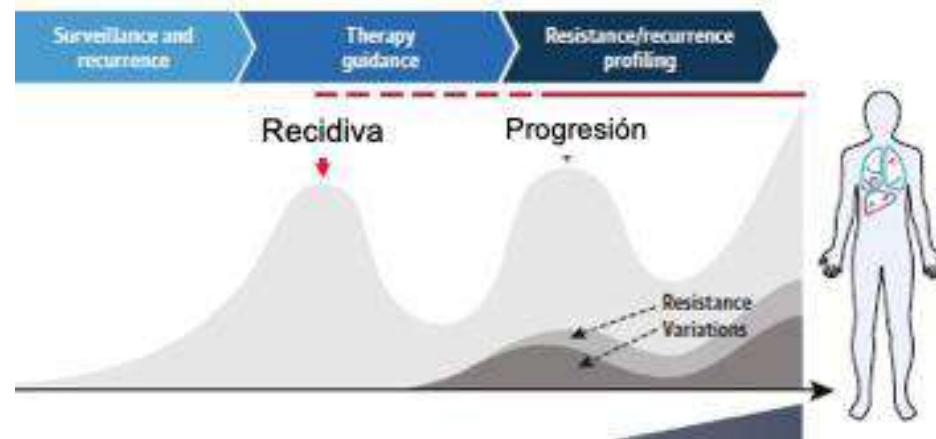
Modelos experimentales: Nos permiten imitar una enfermedad compleja



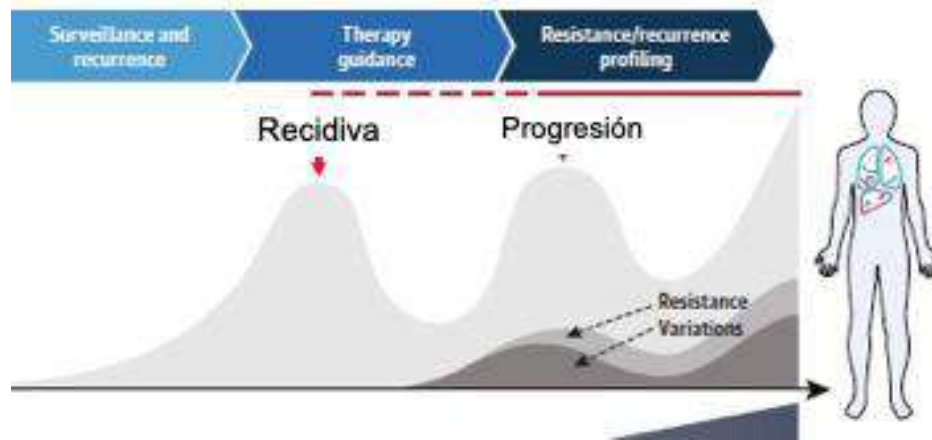
Biomarcadores: No informan de características del tumor



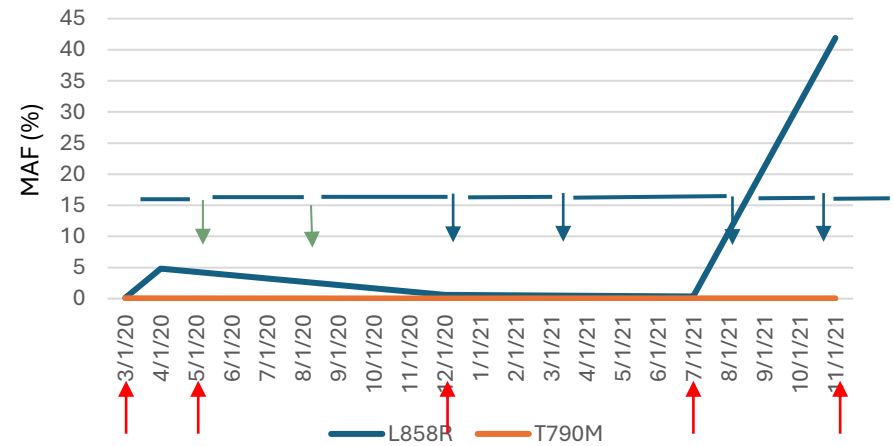
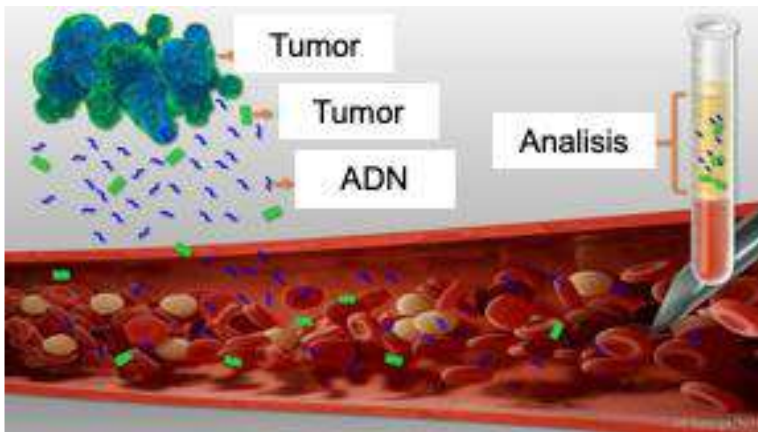
Biomarcadores: No informan de características del tumor



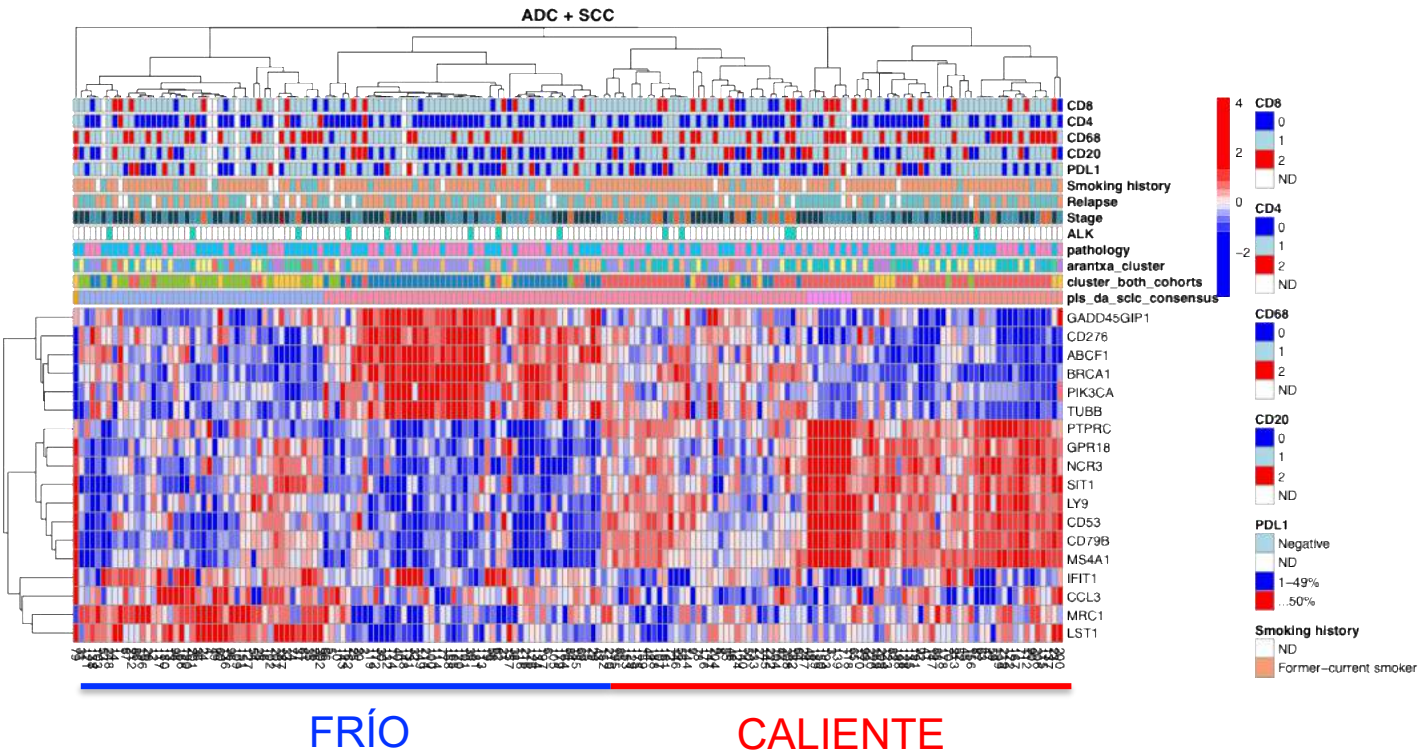
Biomarcadores: No informan de características del tumor



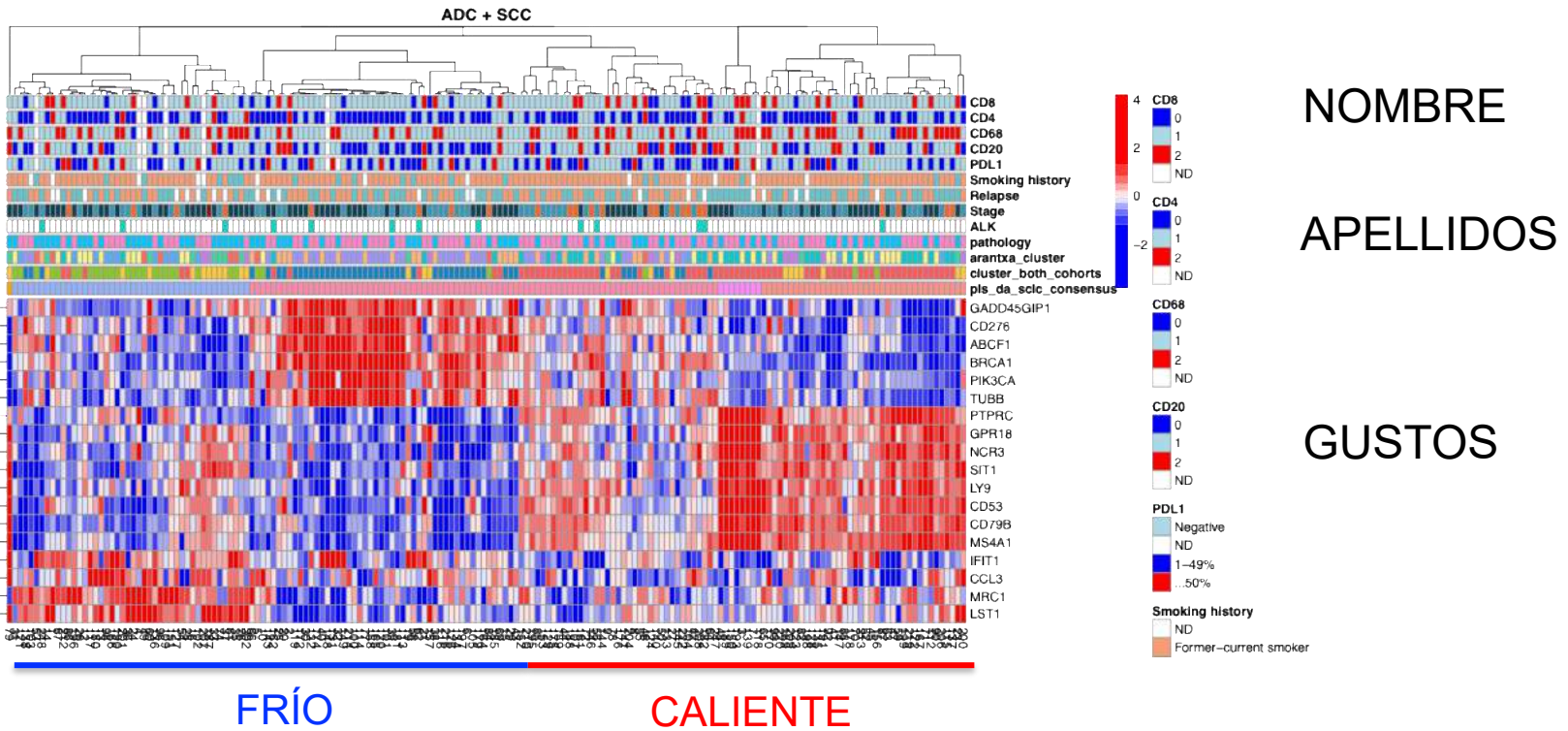
MTB_08



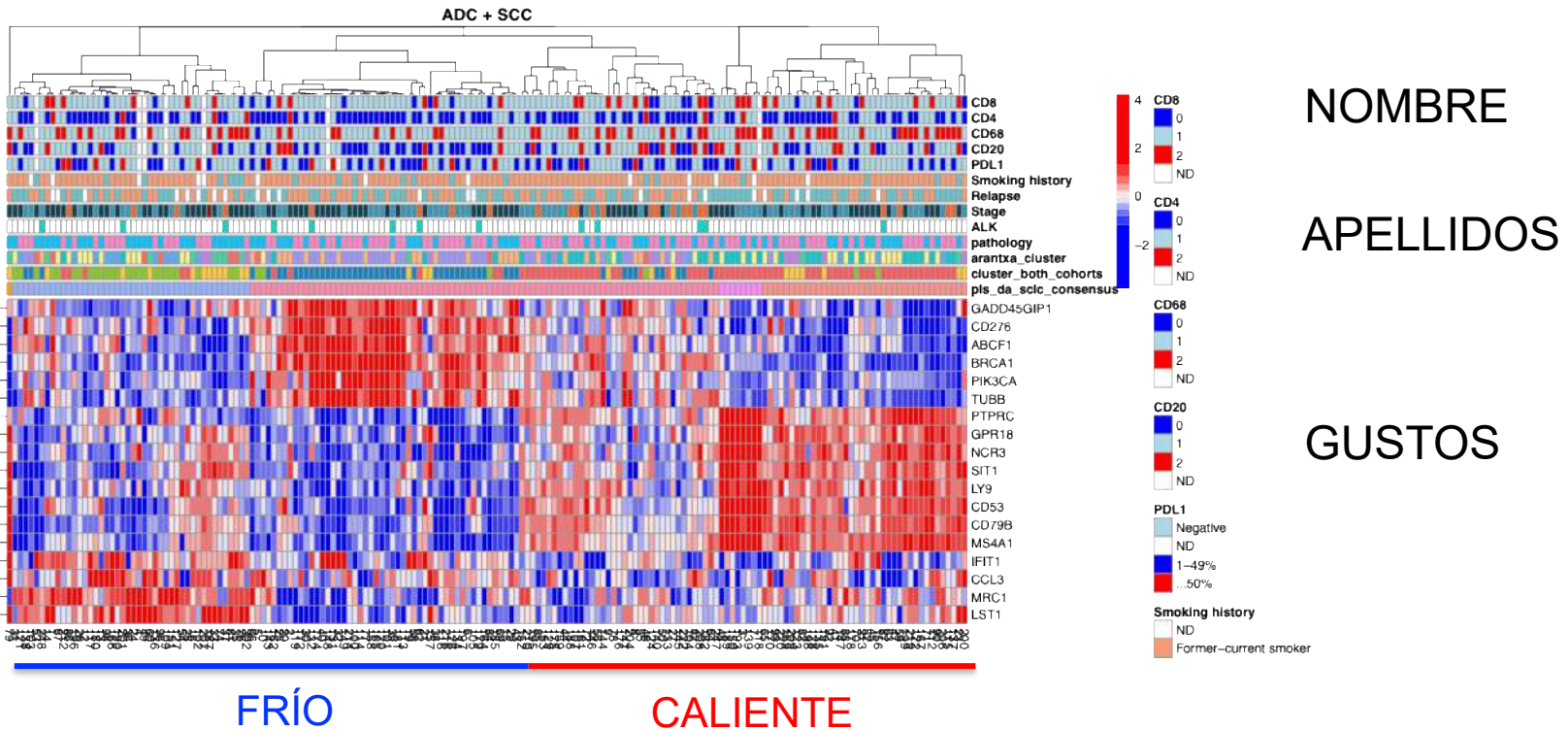
Inmunología: ¿Cómo reacciona el sistema inmune a un tumor?



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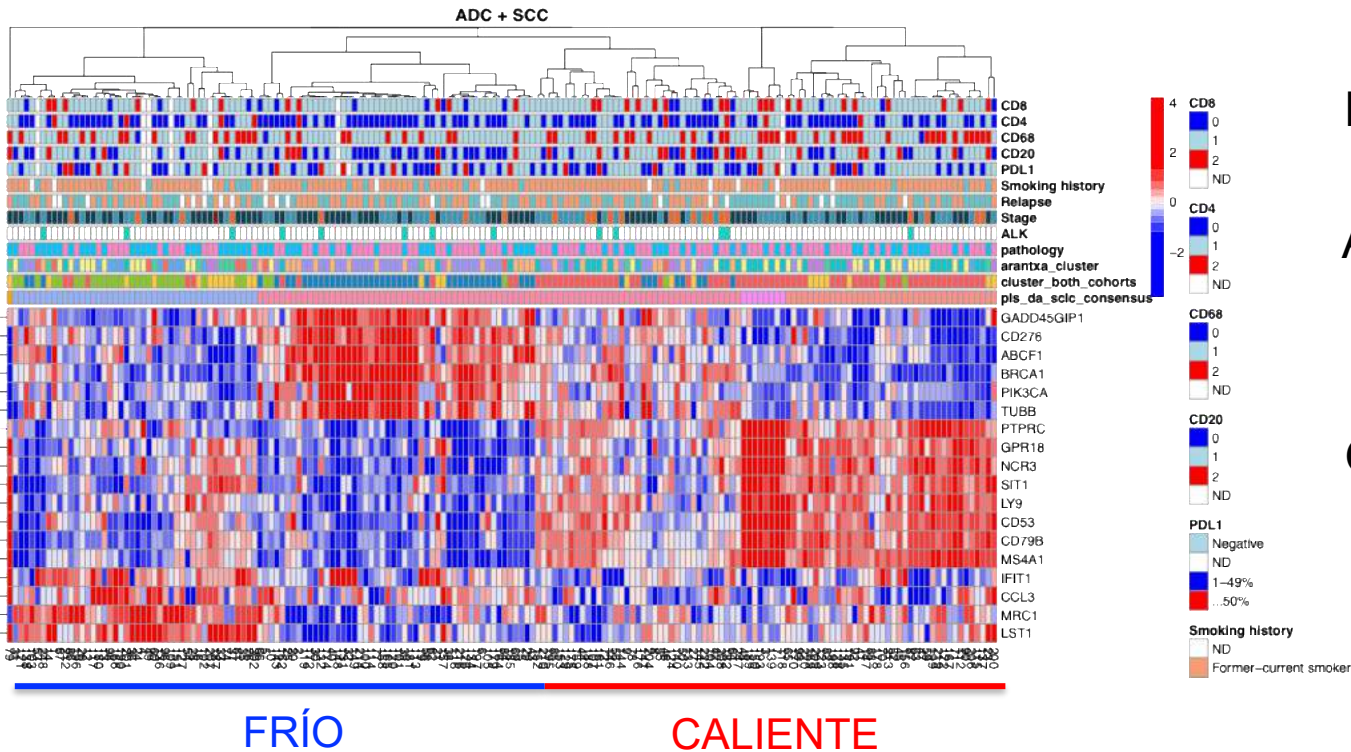


Inmunología: ¿Cómo reacciona el sistema inmune a un tumor?



¿Podemos predecir qué paciente tendrá mejores respuestas a la inmunoterapia?

Inmunología: ¿Cómo reacciona el sistema inmune a un tumor?



NOMBRE

APELLIDOS

GUSTOS

¿Podemos predecir qué paciente tendrá mejores respuestas a la inmunoterapia?

Validaciones en un Ensayo Clínico

GRUPO	RESPUESTA	NO RESPUESTA	TOTAL
CALIENTE	8	1	9
FRÍO	1	4	5
TOTAL	9	5	14

Oncología Traslacional – I+12

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Itziar Otano, PhD

Cristina Cirauqui, PhD

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José Luis Solórzano, MD, PhD

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Elsa Moras

Cristina Ramírez

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Comunicación Intercelular en Envejecimiento & Cáncer

Alvaro C. Ucero, PhD

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Roxana Khoroz

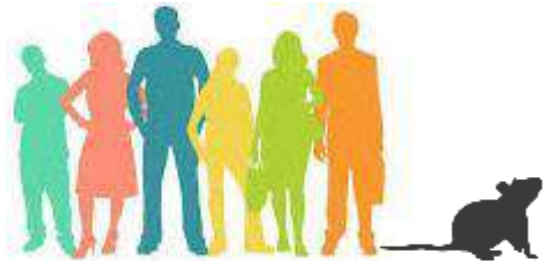
Wajahat Nadeem

Ana Zazo



Medical Oncology Unit – Hospital 12 de Octubre

Cancer Area - Imas12



Patients & animals