EEN FASCINEREND VACCIN

Het Corona virus ontkroond

top-down

UV lithography

electron-beam lithography

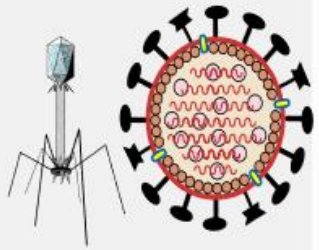
nano-imprint lithography

scanning probe lithography

small molecules

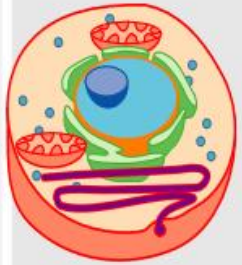
proteins, antibodies

ribosomes

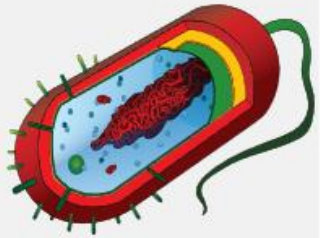


viruses

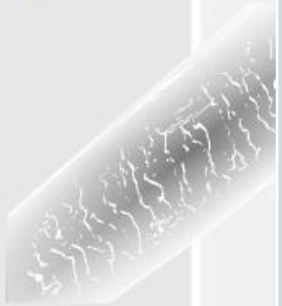
genes



animal cells



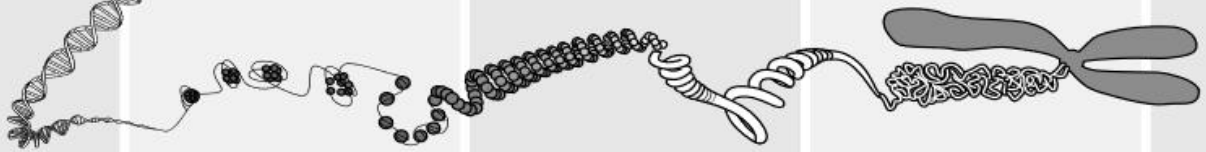
bacteria



human hair

atoms

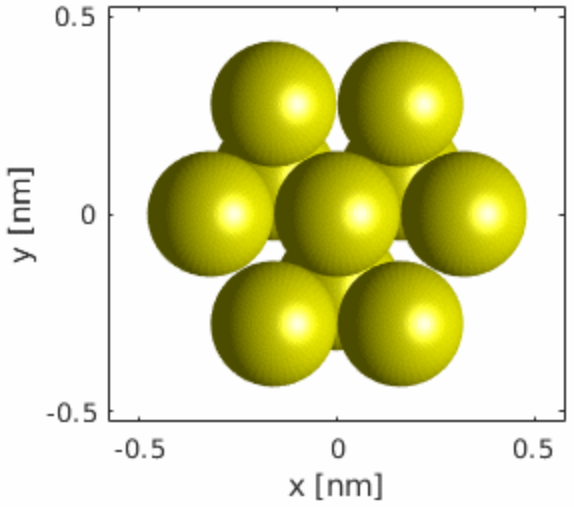
DNA bases

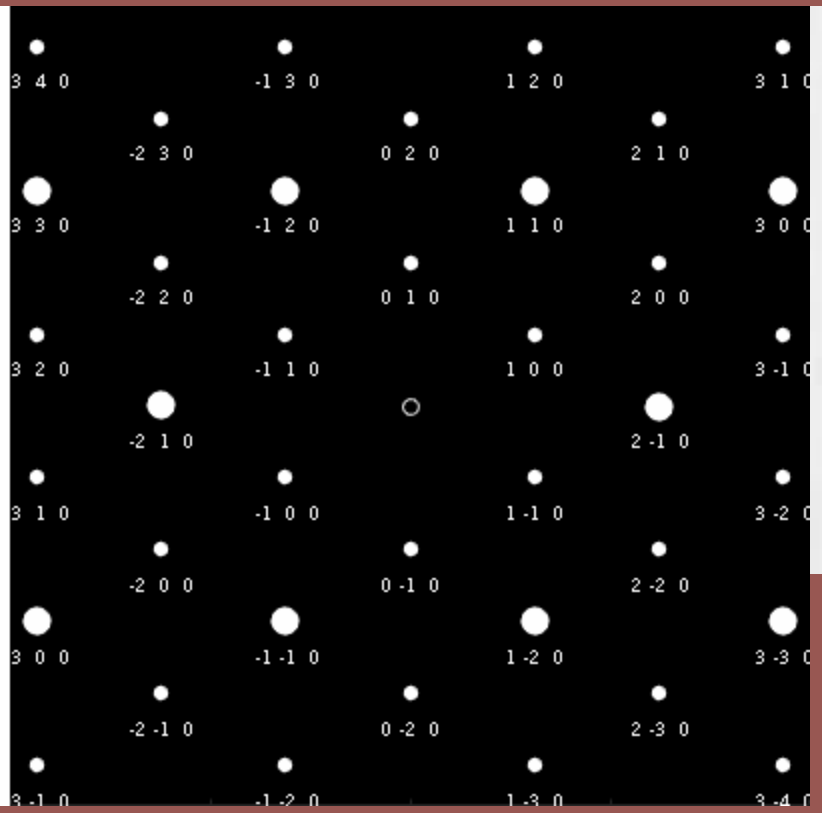


chromosomes

0.1 nm | 1 nm | 10 nm | 100 nm | 1 µm | 10 µm | 100 µm | 1 mm

10 µm	– 1971
6 µm	– 1974
3 µm	– 1977
1.5 µm	– 1981
1 µm	– 1984
800 nm	– 1987
600 nm	– 1990
350 nm	– 1993
250 nm	– 1996
180 nm	– 1999
130 nm	– 2001
90 nm	– 2003
65 nm	– 2005
45 nm	– 2007
32 nm	– 2009
22 nm	– 2012
14 nm	– 2014
10 nm	– 2016
7 nm	– 2018
5 nm	– 2020
3 nm	– 2022
Future	
2 nm	~ 2024


0.5
0
-0.5
y [nm]
-0.5
0
0.5
x [nm]


3 4 0
-1 3 0
1 2 0
-2 3 0
0 2 0
2 1 0
3 3 0
-1 2 0
1 1 0
-2 2 0
0 1 0
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3 2 0
-1 1 0
1 0 0
-2 1 0
2 -1 0
3 1 0
-1 0 0
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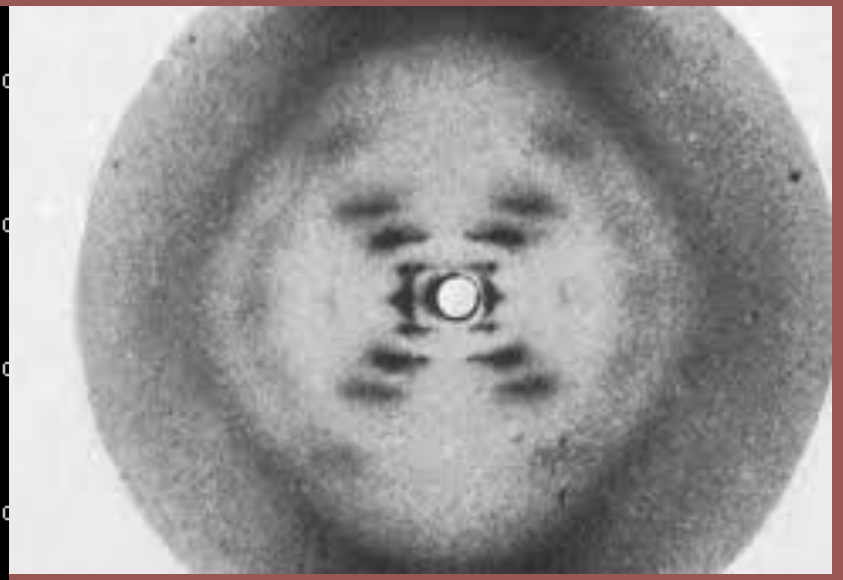
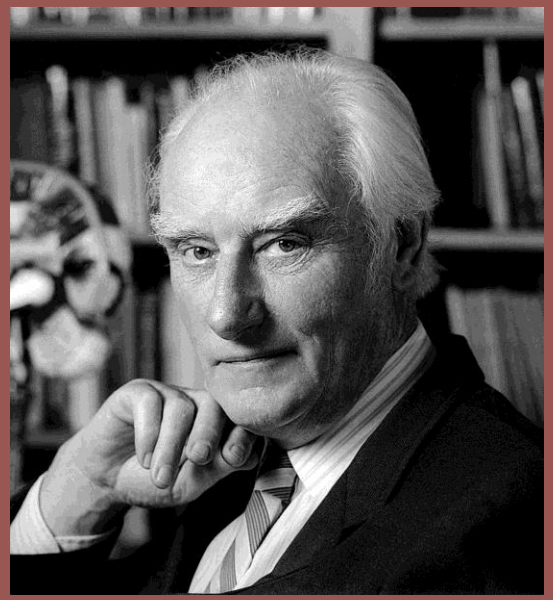
1 -2 0
-2 -1 0
0 -2 0
2 -3 0



DNA

Rosalind Franklin

James Watson



Francis Crick

Maurice Wilkins

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, 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 diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

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 for this reason we shall not comment on it.

This figure is purely diagrammatic. The two ribbons symbolize the two phosphate–sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β-D-deoxyribofuranose residues with 3′,5′ linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There is a residue on each chain every 3·4 A. in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

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

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted 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 given, then the sequence on the other chain is automatically determined.

It has been found experimentally[3,4] that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

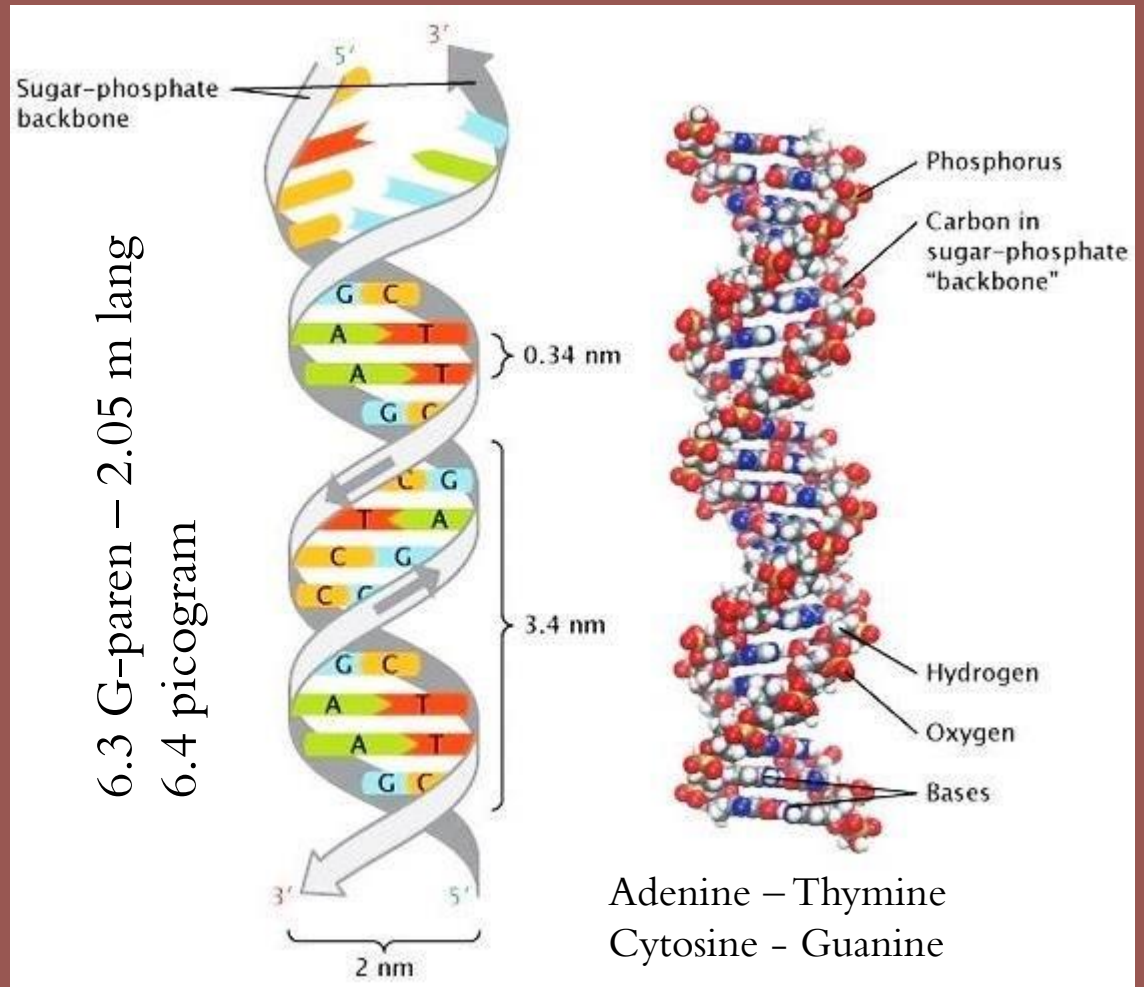
The previously published X-ray data[3,4] on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on 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.

Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

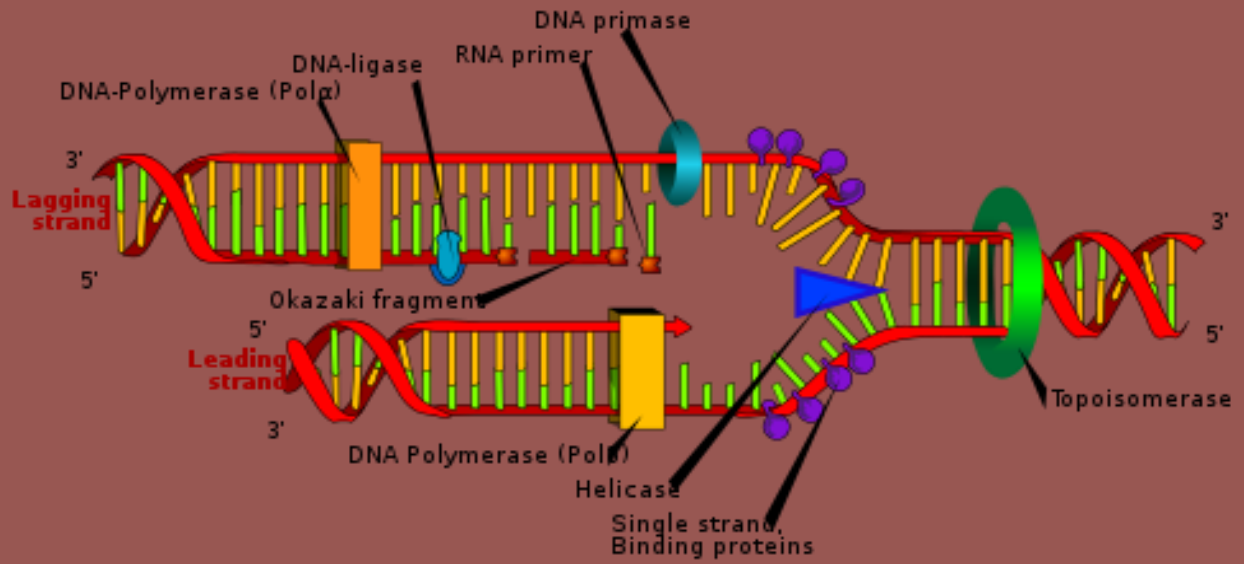
We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on interatomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at

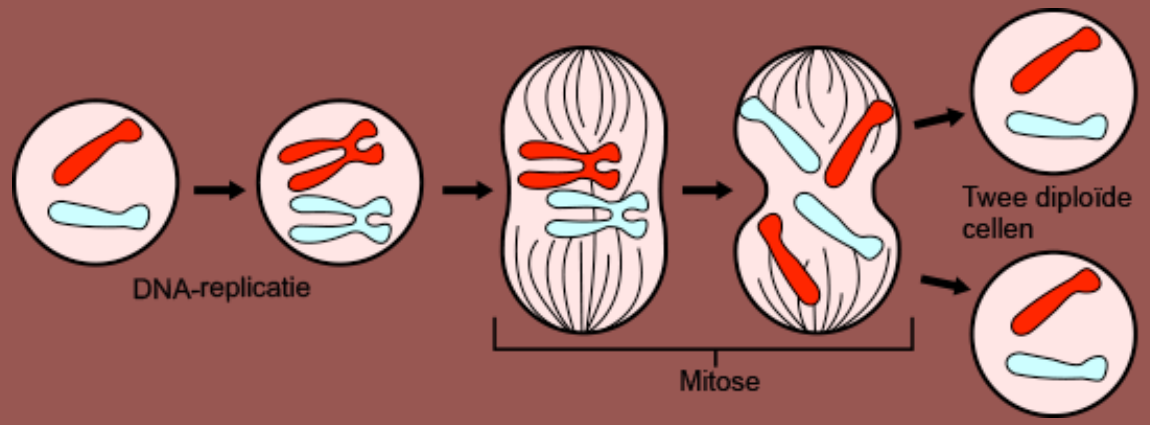
Reprinted from NATURE, Vol. 171, No. 4356, April 25, 1953

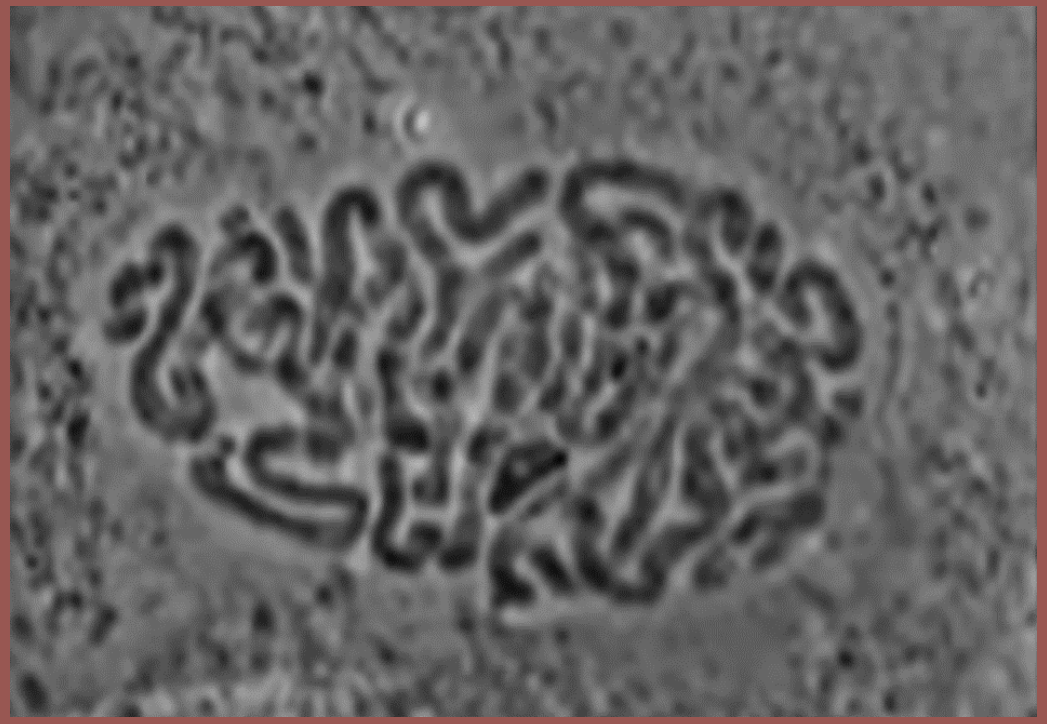


It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

DNA replicatie > celdeling

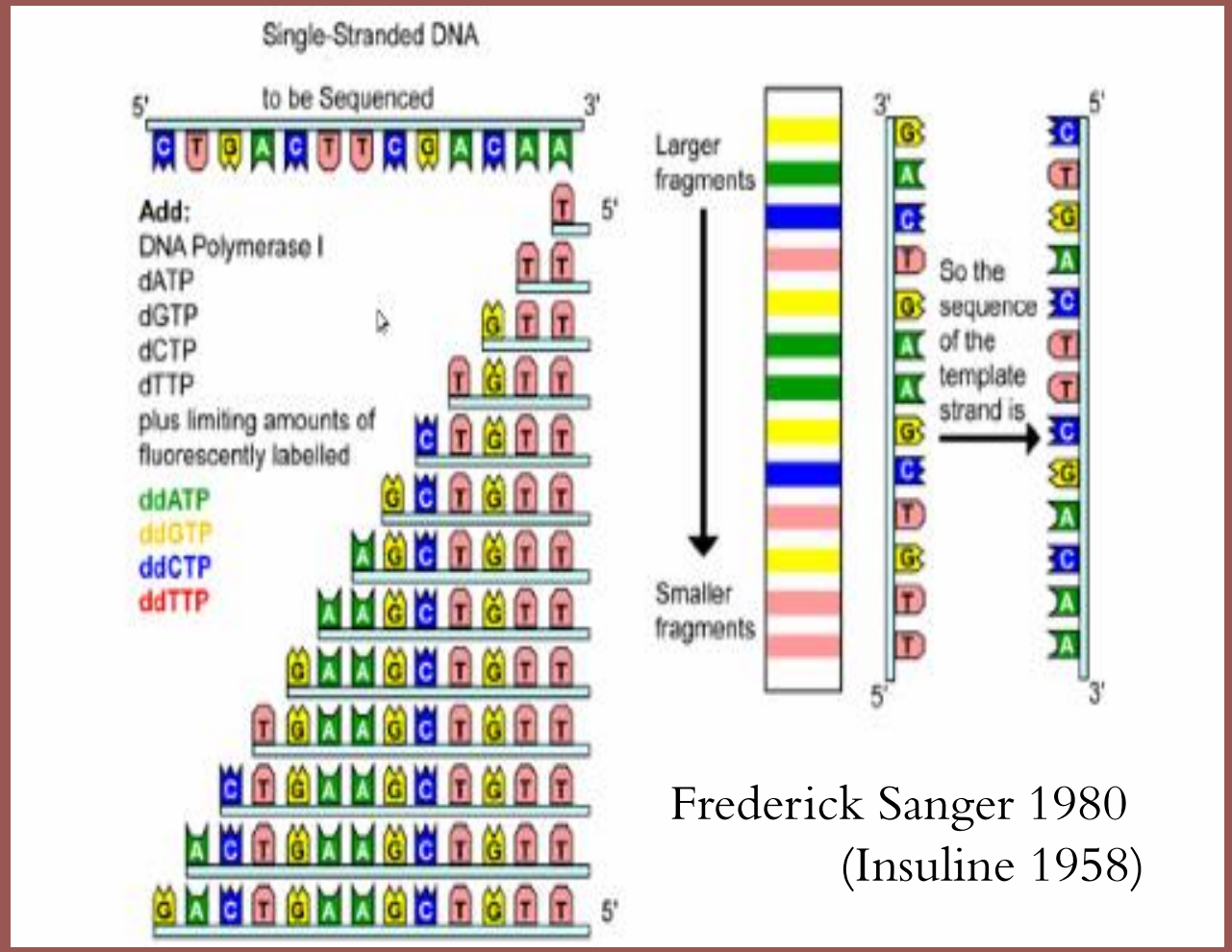




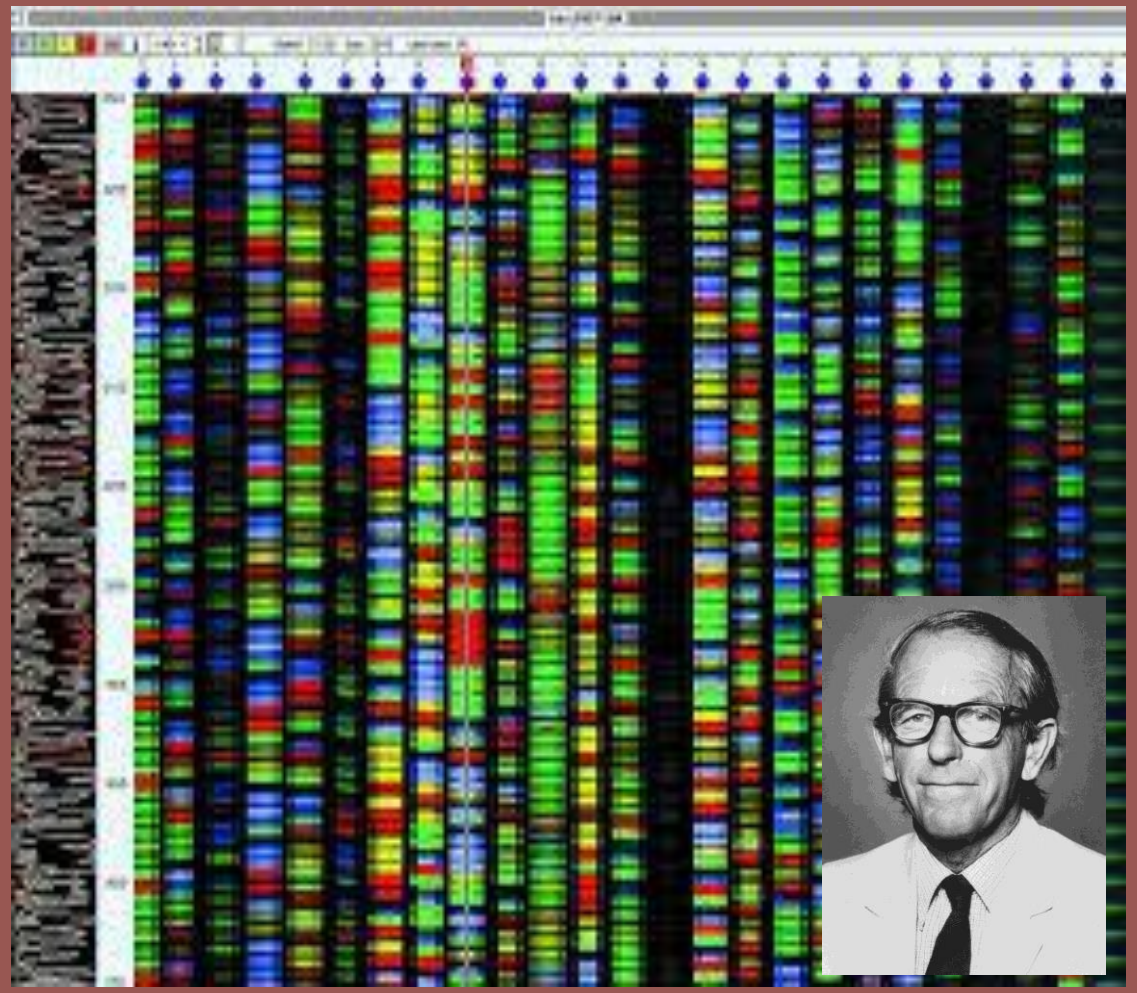


Polymerase Chain Reaction: PCR

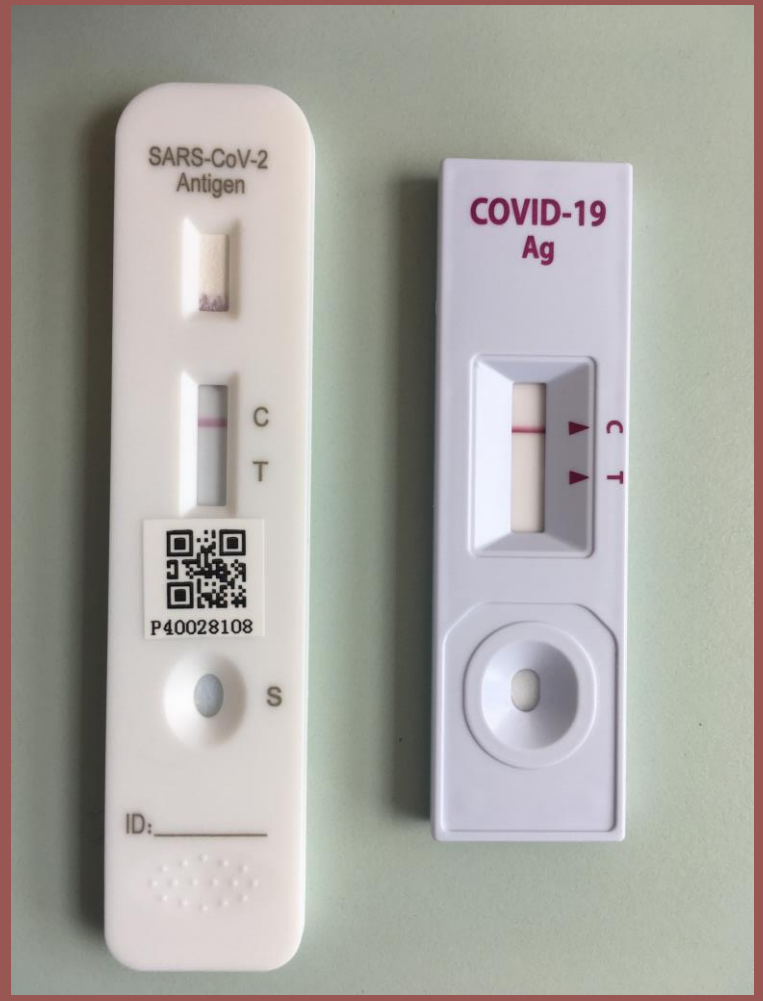
DNA sequencing – chromatografie



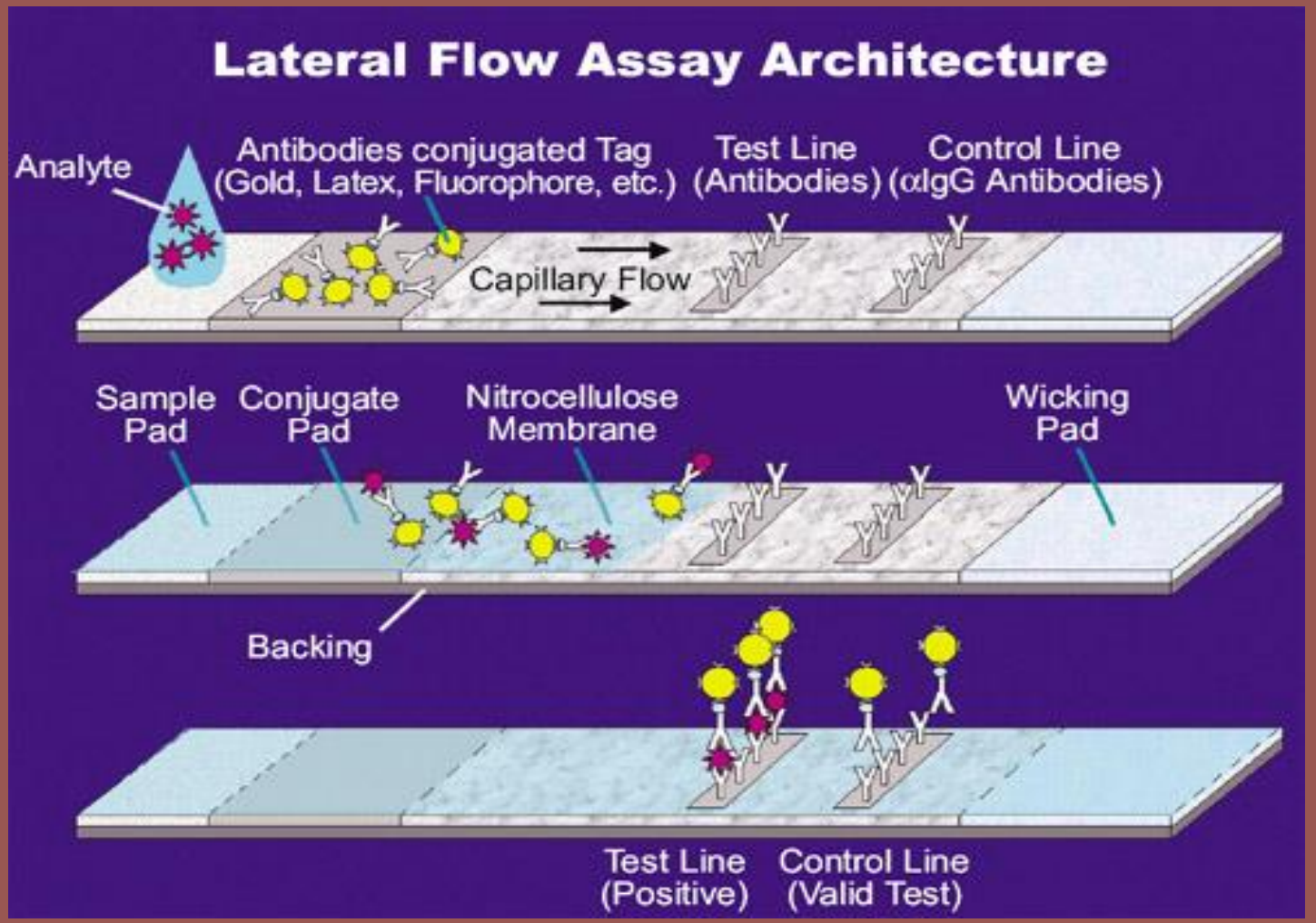
Frederick Sanger 1980
(Insuline 1958)



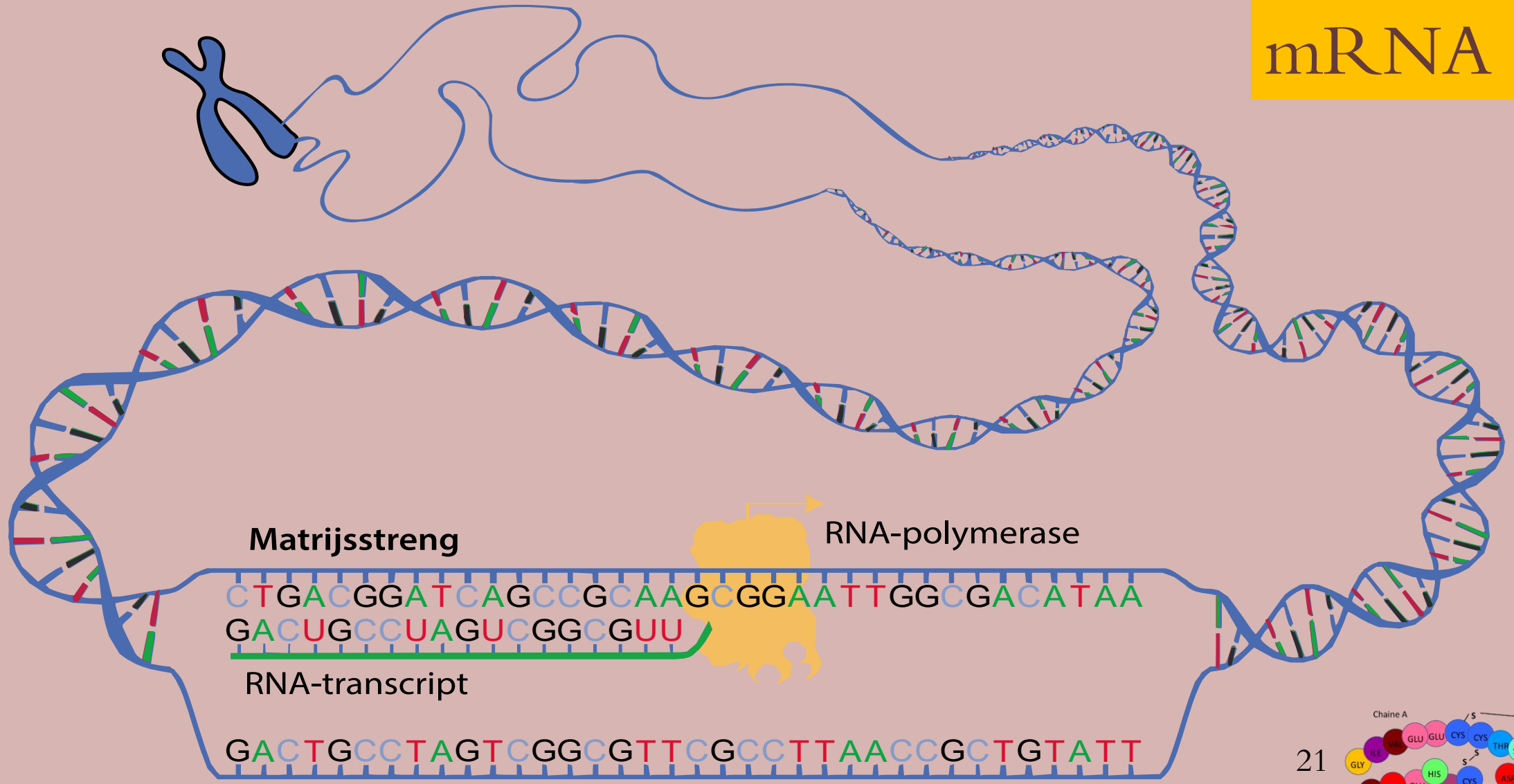
Antigeen test

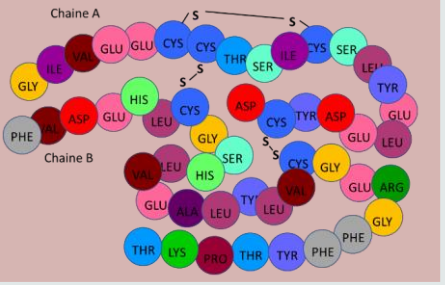


Principe van de test



mRNA

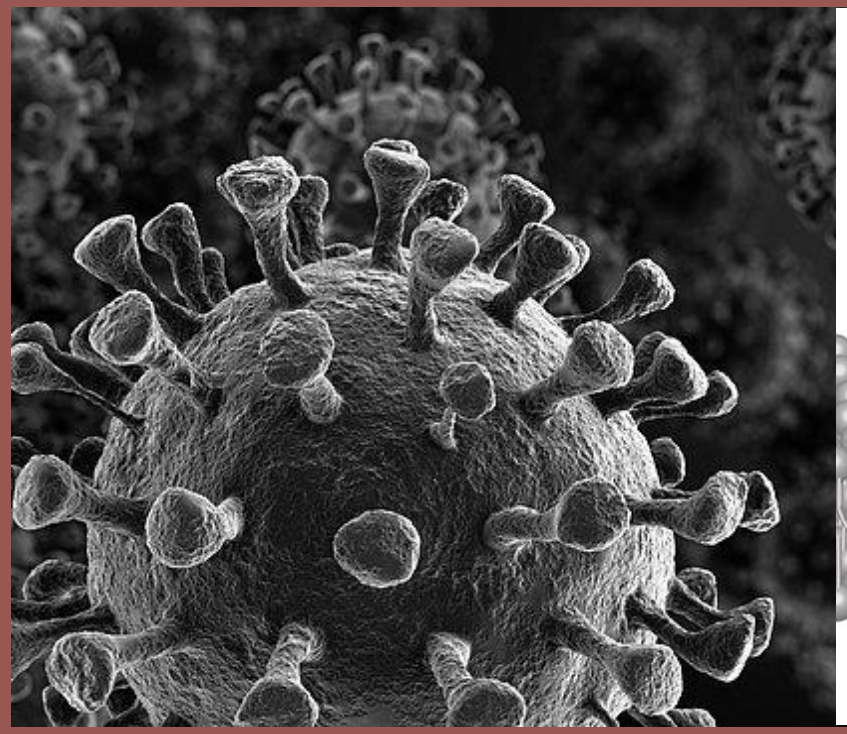


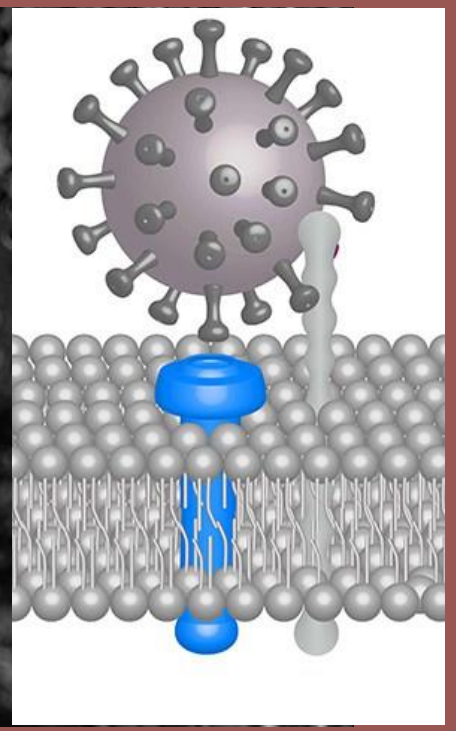


ALA alanine; ARG arginine; ASN asparagine; ASP acide aspartique; CYS cystéine; GLN glutamine; GLP acide glutamique; GLY glycine; HIS histidine; ILE isoleucine; LYS lysine; MET méthionine;

Eigenschappen virus:

- Stukje niet levend DNA
- Nestelt zich in cel
- Herprogrammeert de cel
- Cel gaat meer virus maken





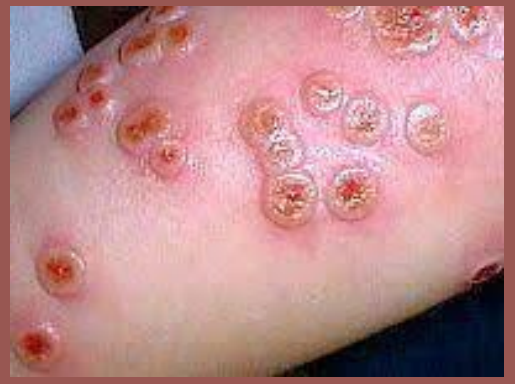
Corona/CoViD-19 virus

- Mantel van Spikes
- Spikes vallen o.a. longblaasjes aan
- ACE2 receptor - Aprovel

Covid-19: 29903 basisparen

Spike: 3831 basisparen

Koepokken



Vacca > Vaccin

Drie methoden – Covid-19 vaccinatie:

1. Verzwakt virus
2. mRNA op ander transport virus
3. mRNA direct

Edward Jenner 1796

Producenten	Bescherming
1. Verzwakt virus	
• Sputnik I	- -
• Sinovac / Sinopharm	50% / 79%
2. mNRA op virus	
• Astra-Zeneca	70 - 82%
• Sputnik V	92%
• Johnson&Johnson (Janssen NL)	67%
3. mNRA direct	
• BioNTech – Pfizer	95%
• Moderna (Spikevax)	95%
• CureVac	47%

Frankrijk: Sanofi
India: Novavax/Nuvaxovid

Ontwikkeling Corona (CoVid-19) vaccin

- 01-12-2019: Eerste patient gerapporteerd in The Lancet journal
- 31-12-2019: China rapporteert WHO mogelijk gevaar pandemie
- 10-01-2020: Type virus wereldwijd bekend gemaakt in GenBank (SARS)
- 27-02-2020: Gehele DNA keten vastgesteld in Brazilië
- 11-03-2020: WHO stelt pandemie vast
- 17-03-2020: Pfizer sluit contract af met BioNTech voor vaccinontwikkeling
- BioNTech verbeterde stabiliteit mRNA met kleine deeltjes lipiden (vetten)
- Uitproberen vaccin-kandidaten in de VS en België · Ugur Sahin/Özlem Türeci
- Direct duidelijk dat lage temperatuur vervoer noodzakelijk zou zijn
- Inschakeling van 15 sub-contractors via video vergaderingen (geen reizen)
- In totaal 280 componenten betrokken in productie
- Nieuwe eigen productiefaciliteiten om aanvoer te verzekeren
- 23-08-2021: Eerste goedkeuring CoVid-19 vaccin, getest op 2 x 22000 pers.