



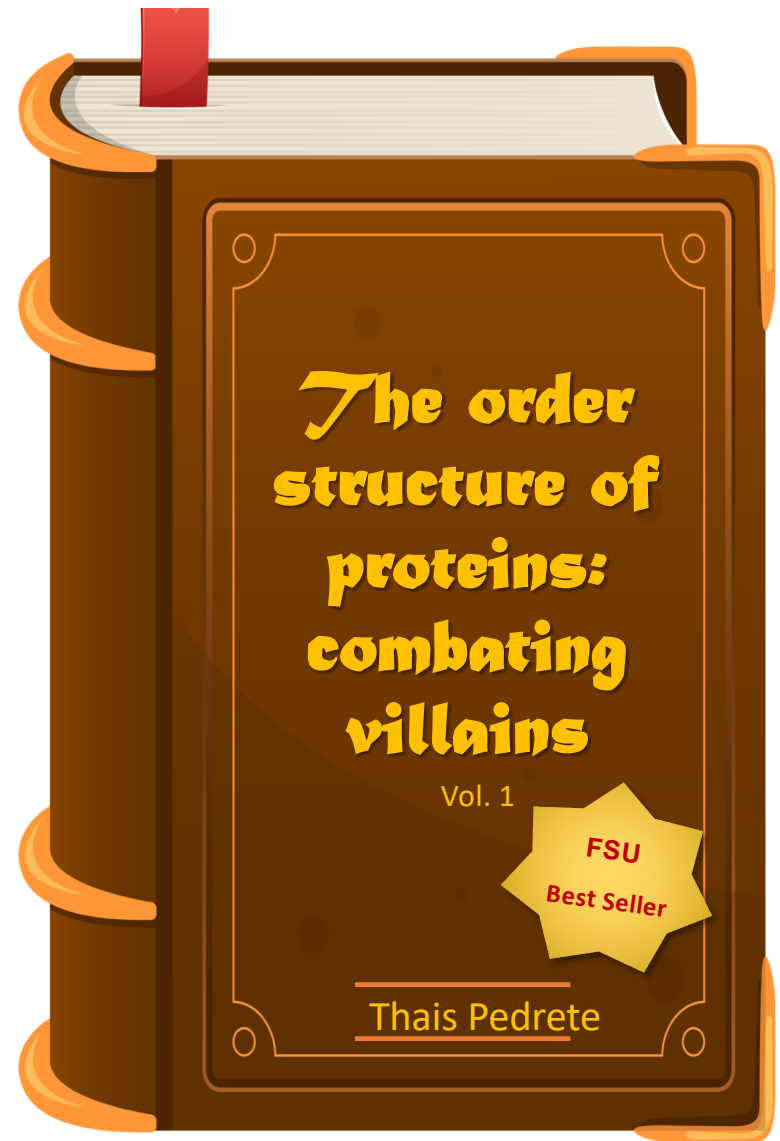
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Chemistry & Biochemistry

The Order Structure of Proteins: Combating Villains

The Office of Postdoctoral Affairs

The Graduate School | Florida State University



Once upon a time...

In a very *FARAWAY* place, there were molecules called *Proteins*, considered essential parts of all living organisms of that kingdom

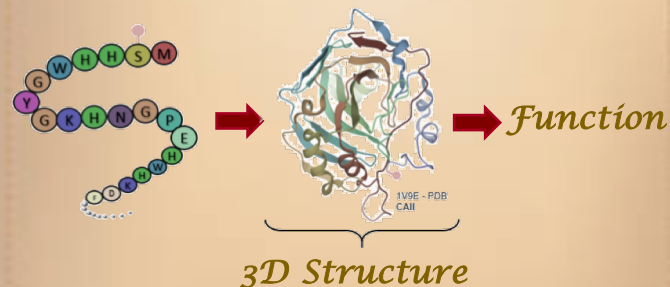
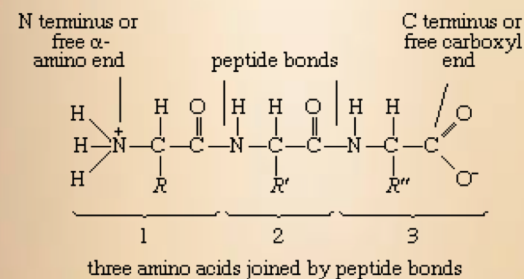


Structure – function relationship of proteins

The proteins consist of a long chain of amino acids, which are connected by peptide bonds.

The order in which the different amino acids are inserted determines structure and function.

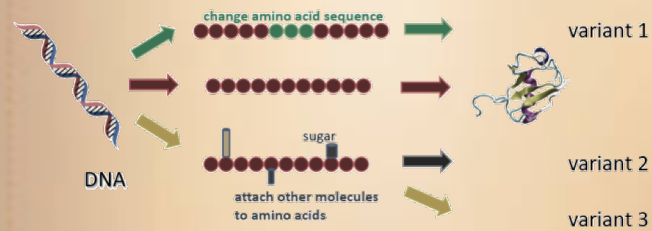
The chain starts folding. Once the protein gets its final three-dimensional structure, it will be able to perform its function.



The complexity of proteins

The structure and function of proteins are coded in the DNA.

1 gene \Rightarrow 1 amino acid sequence \Rightarrow 1 protein structure \Rightarrow function

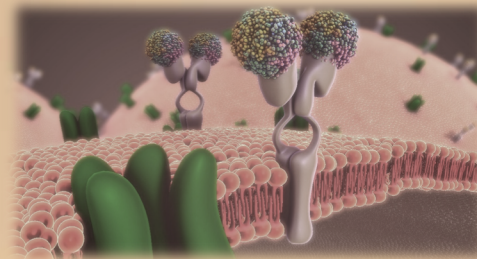
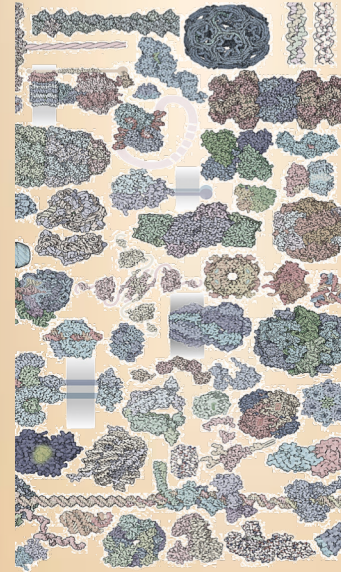


1 gene \Rightarrow many protein variants \Rightarrow different protein structures \Rightarrow different functions

Life in the FARAWAY kingdom

There are proteins with different structures and functions, involved in the chemical processes essential for life.

Everything was so harmonious in the living organisms, until...



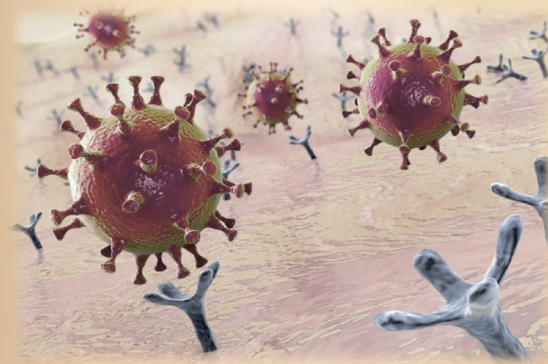
credit: sciencepics/Shutterstock.com

A not so harmonious kingdom

...a threaten showed up:

**severe acute respiratory syndrome
coronavirus 2 (SARS-CoV-2)**

**a strain of coronavirus that causes the
respiratory illness responsible for the
COVID-19 pandemic**



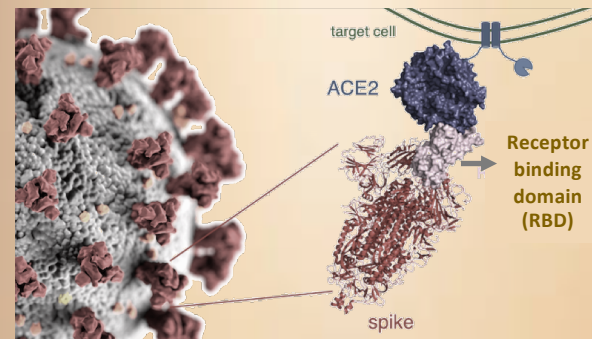
credit: Kateryna Kon / Shutterstock

The villain

The “spike protein” present on the surface of the coronavirus has a receptor binding domain (RBD).

This protein region binds to a protein on human cells called ACE2, a necessary step for infection.

Mutations in the spike protein could change how well SARS-CoV-2 sticks to – and thus infects – human cells.

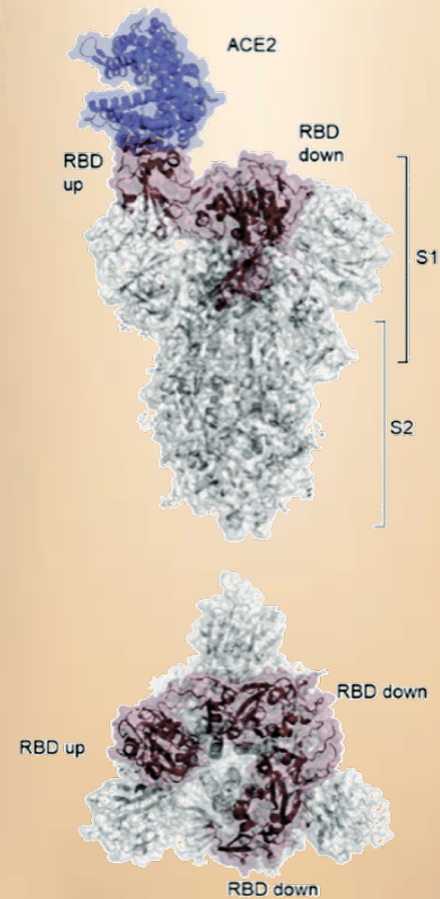


Credit: Tyler Starr/Bloom Lab

The heroes

Some researchers that lived in the kingdom systematically created several versions of the mutated fragments, while others studied possible antibodies that could combat these mutations.

Mutations in the gene lead to different proteins, different structure and consequently, different function.

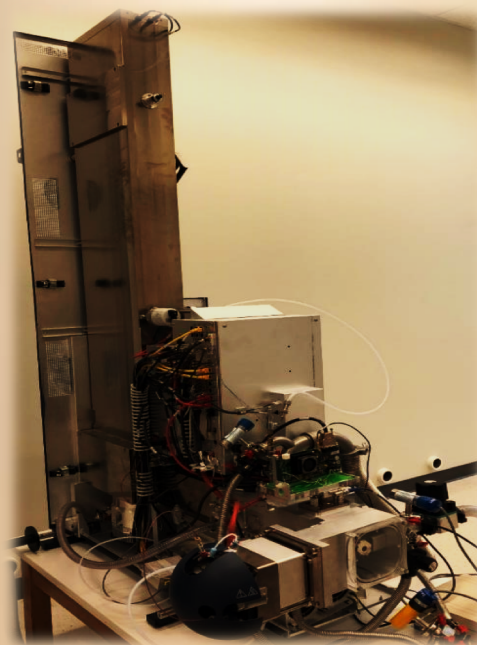


doi: 10.1039/D0MD00083A

The approach

Ion mobility + Mass spectrometer

Characterization of the structure of molecules separating by their shape, according to their mobility and by their mass.

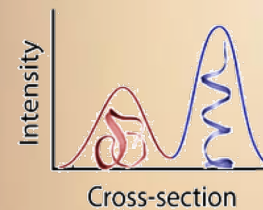


The result

It offers the potential to correlate protein tertiary and quaternary (maximum level of arrangements) structures to variations in their amino acid sequences.

Ion Mobility Spectrum

Same species, different structures



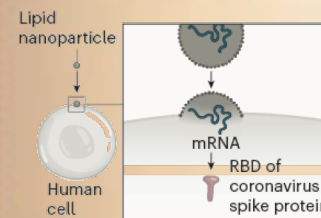
Modeling



The happy ending

The study of the structure of the SARS-CoV-2, as well as others viruses, allows the understanding of the binding to cells of living organisms and the immune response to combat them.

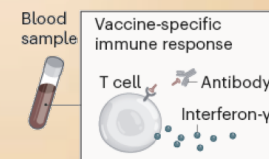
a SARS-CoV-2 vaccine



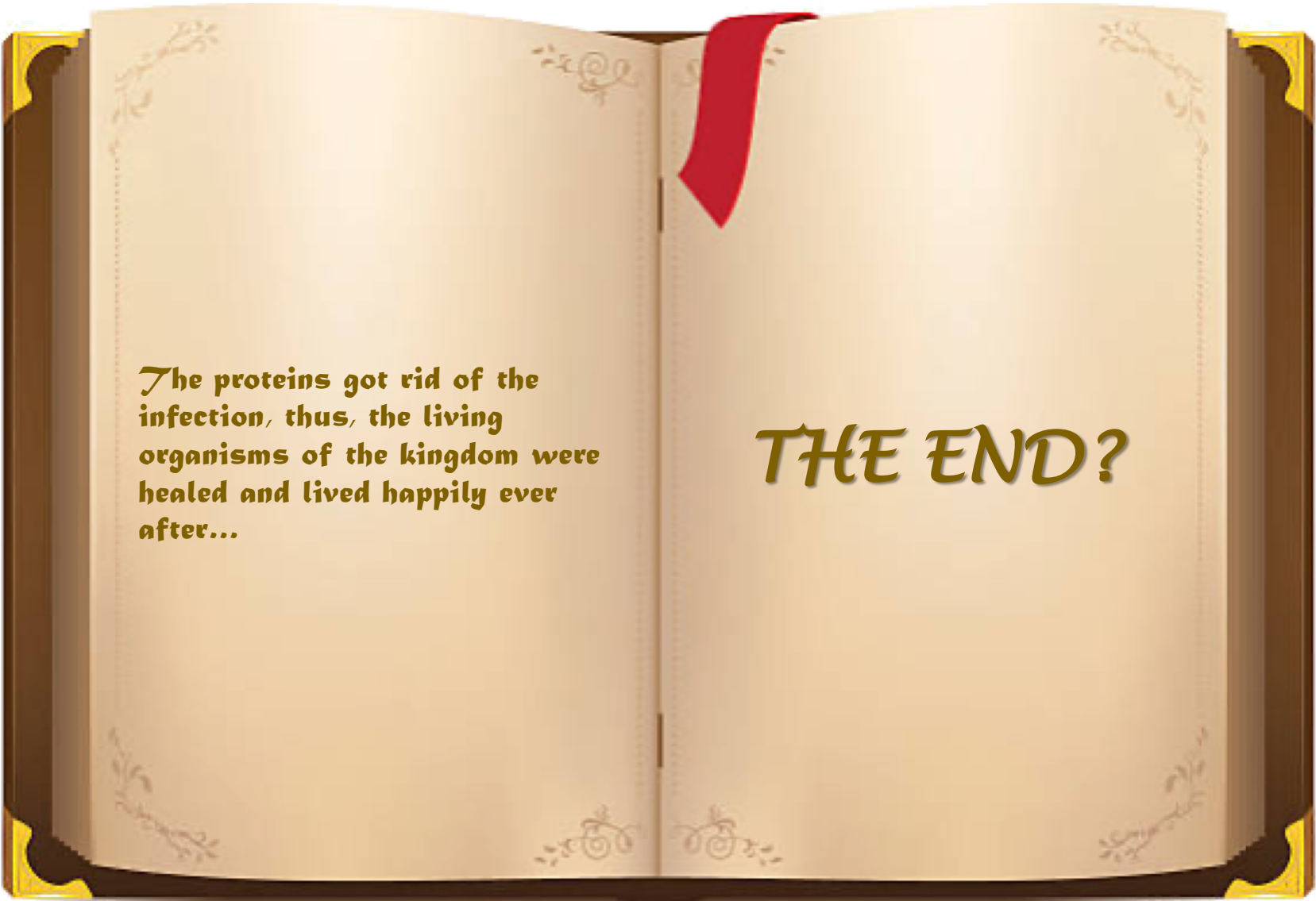
b Assess reactogenicity

Local or systemic symptoms?

Assess immunogenicity



©nature



The proteins got rid of the infection, thus, the living organisms of the kingdom were healed and lived happily ever after...

THE END?



**TO BE
CONTINUED**

...until another pandemic.

