

# Bioinformatics against COVID-19

Bioinformatics Research Group

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# Overview



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The purpose of Bioinformatics

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## Bioinformatics against COVID-19

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Protein structure prediction

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# Objectives



- ▶ Understand what is Bioinformatics.

# Objectives



- ▶ Understand what is Bioinformatics.
- ▶ Learn areas of research of Bioinformatics related to COVID-19.

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# Presentation



- ▶ MSc. Vicente Enrique Machaca Arceda.

# Presentation



- ▶ MSc. Vicente Enrique Machaca Arceda.
- ▶ Professor at UNSA university.

# Presentation



- ▶ MSc. Vicente Enrique Machaca Arceda.
- ▶ Professor at UNSA university.
- ▶ Full time researcher at La Salle university.

# Presentation



- ▶ MSc. Vicente Enrique Machaca Arceda.
- ▶ Professor at UNSA university.
- ▶ Full time researcher at La Salle university.
- ▶ Leader of research group of Bioinformatics in Arequipa.

# Presentation

## Publications



Year	Country	Title
2018	Brasil	Fast Car Crash Detection in Video
2016	Chile	Fast Face Detection in Violent Video Scenes
2016	Costa Rica	Real Time Violence Detection in Video with ViF and Horn-Schunck
2016	Costa Rica	Optimization model for face detection in video sequences
2015	Chile	Real Time Violence Detection in Video

# Presentation

## Publications



Year	Country	Title
2020		DNA sequence similarity analysis using Chaos Game Representation
2020		Machine Learning and Chaos Game Representation for rapid classification of novel pathogens COVID-19 case study
2020	Canada	An analysis of k-mer frequency features with machine learning models for viral subtyping of Polyomavirus and HIV-1 genomes
2020	Canada	Forecasting time series with Multiplicative Trend Exponential Smoothing and LSTM: COVID-19 case study
2020	USA	Small Ship Detection on Optical Satellite Imagery with YOLO and YOLT

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# The purpose of Bioinformatics

Why a person has cancer?

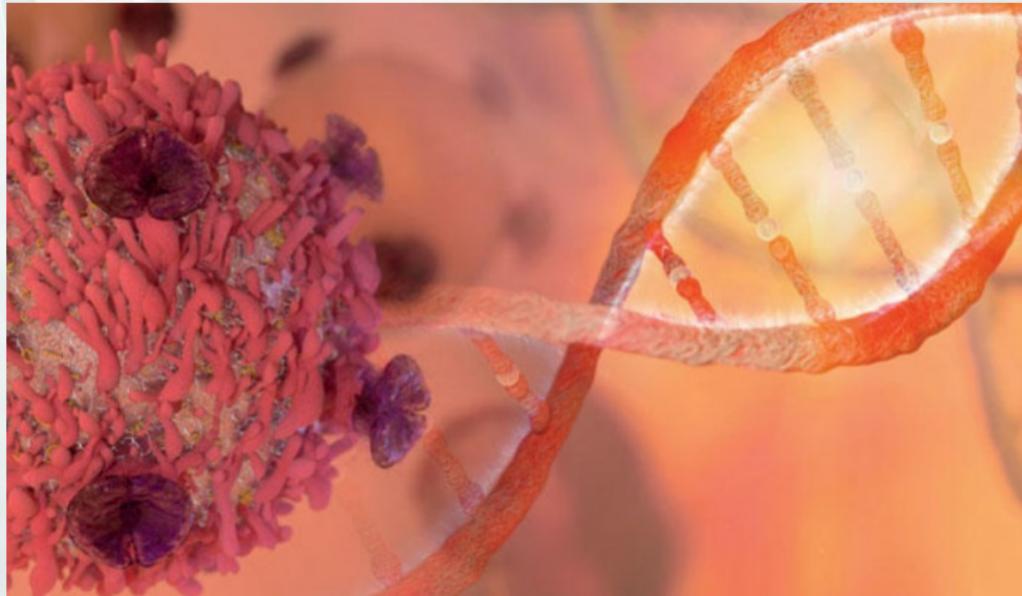


Figure: Why a person has cancer?

# The purpose of Bioinformatics

Why some medicines no work in some persons?



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**Figure:** Why some medicines no work in some persons?

# The purpose of Bioinformatics

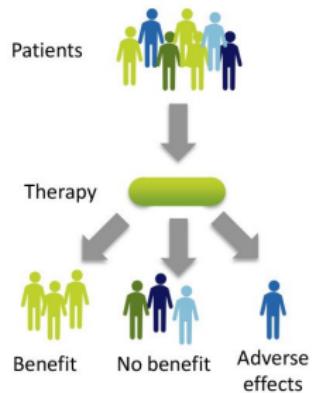
## Treatment Development



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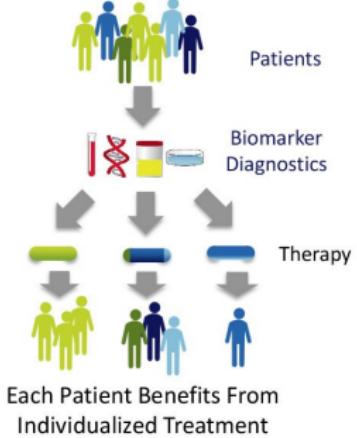
### Without Personalized Medicine:

Some Benefit, Some Do Not



### With Personalized Medicine:

Each Patient Receives the Right Medicine For Them



**Figure:** Personalized Medicine: New Approach to Treatment of Disease

# The purpose of Bioinformatics

Protein structure prediction

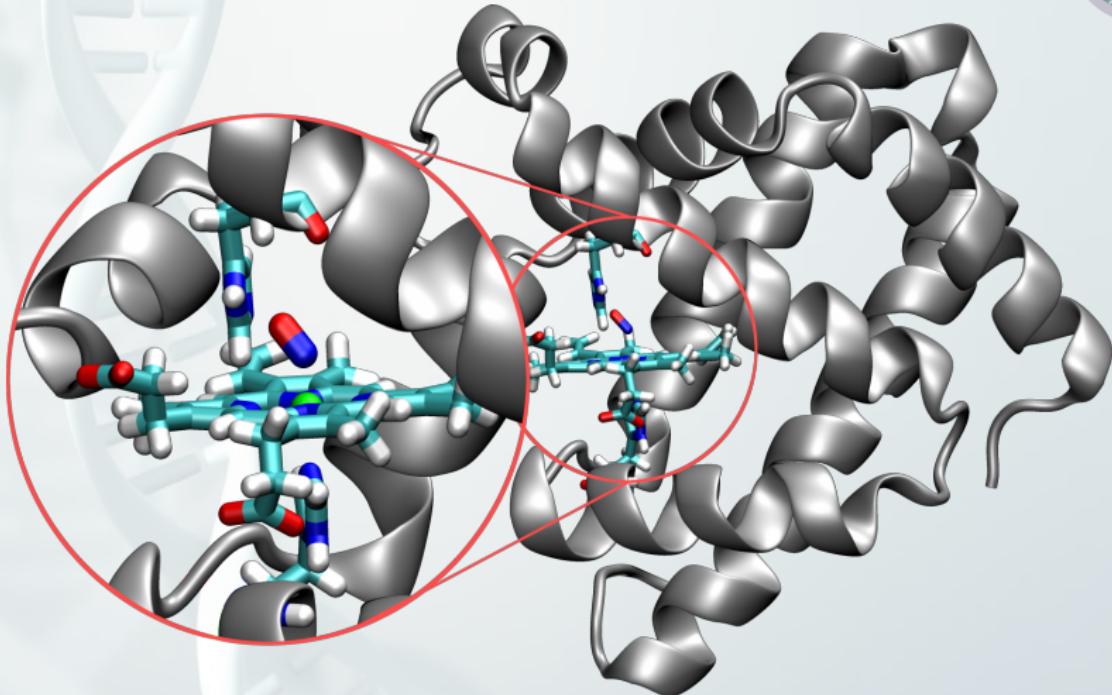


Figure: Computer simulation of protein-ligand.

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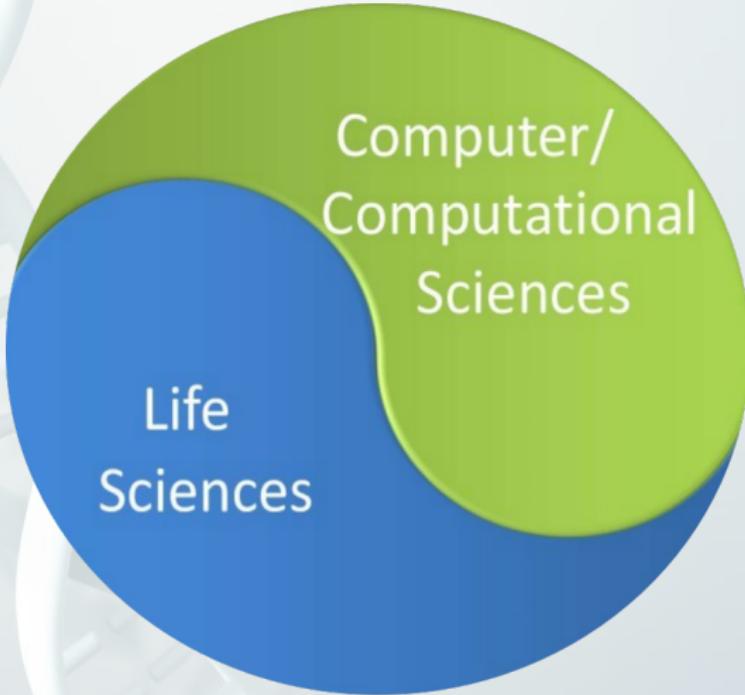
How to learn Bioinformatics?

# Introduction

## What is Bioinformatics?



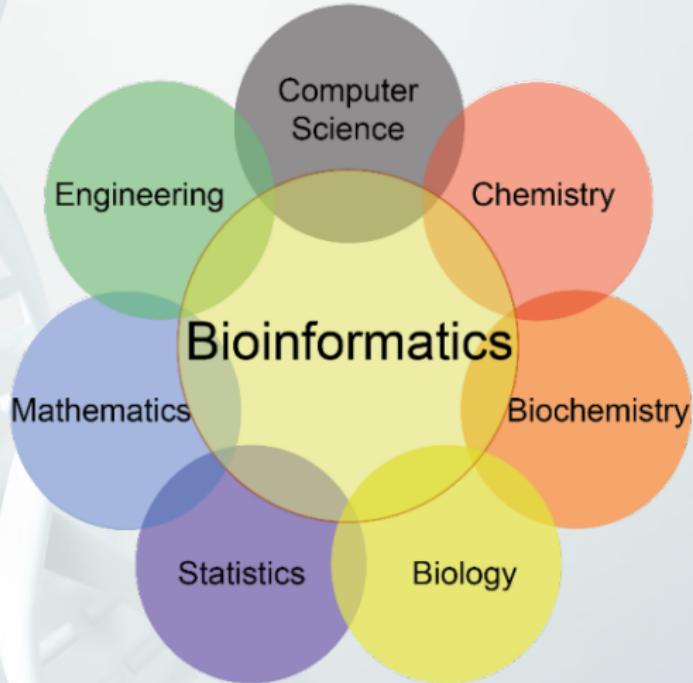
According to Luscombe et al.: **Bioinformatics** involves the technology that uses computers for storage, retrieval, manipulation, and distribution of information related to biological macromolecules such as DNA, RNA, and proteins [1].



# Bioinformatics



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# Bioinformatics

## Concepts



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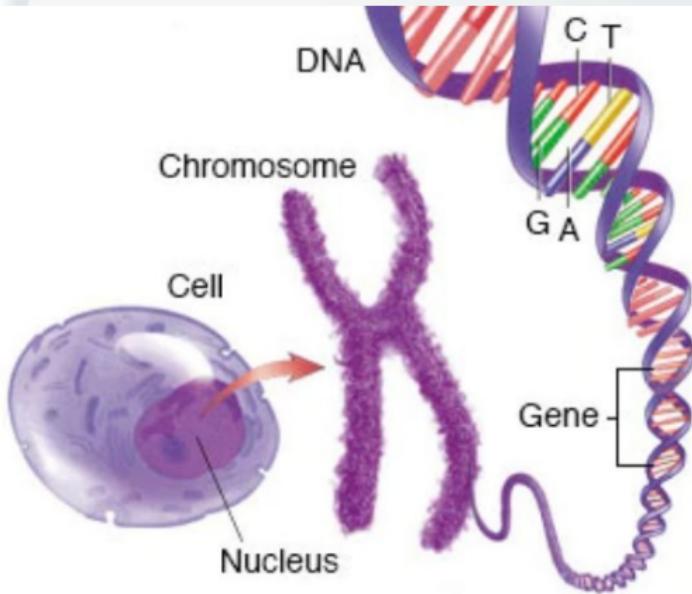


Figure: Where DNA is located [2].

# Bioinformatics

## Concepts

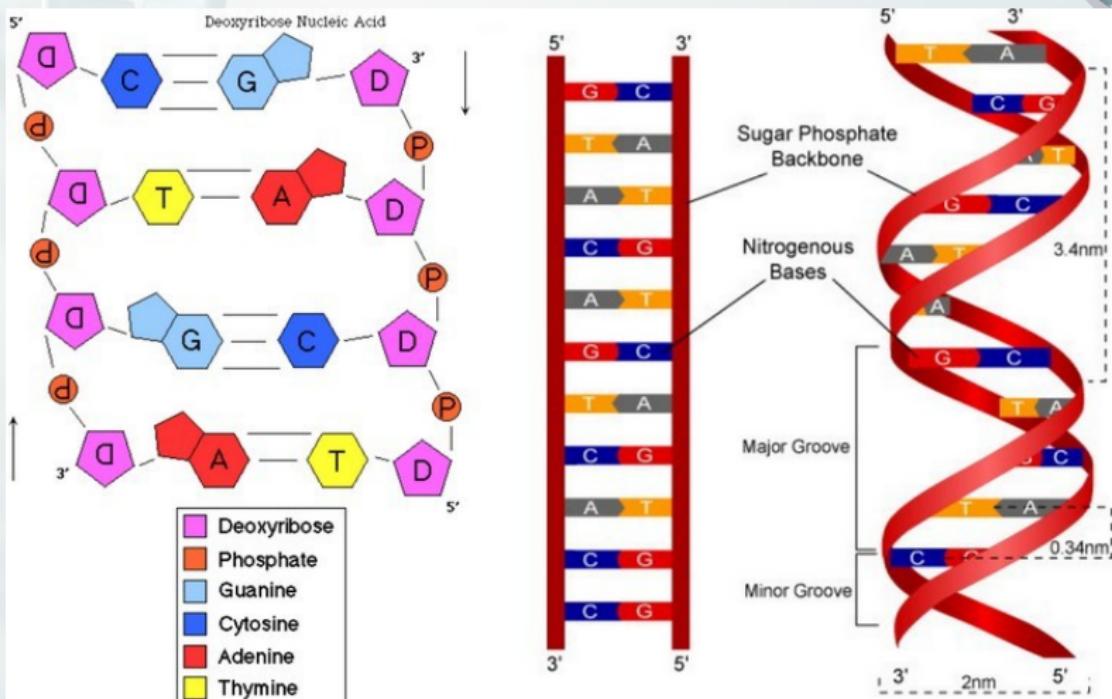


Figure: DNA structure [3].



The human genome is made of **~3.2 billions bp** of DNA.  
~6.4 billions of nucleotides [4].



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The HIV-1 genome is made of **~20k bp** of DNA.  
Meanwhile, the COVID-19 is made of **~32k bp** [5].



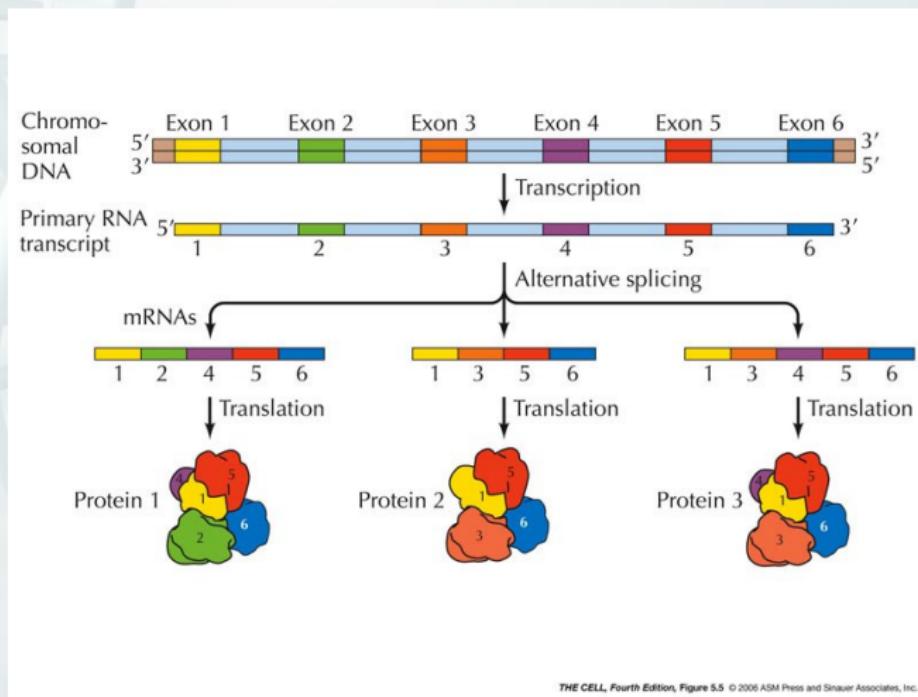
The human genome is made of **~3.2 billions bp** of DNA.  
~6.4 billions of nucleotides [4].

The HIV-1 genome is made of **~20k bp** of DNA.  
Meanwhile, the COVID-19 is made of **~32k bp** [5].

There are approximately **19000 to 25000** genes.  
No one knows for sure [4].

# Bioinformatics

## Concepts



THE CELL, Fourth Edition, Figure 5.5 © 2006 ASM Press and Sinauer Associates, Inc.

Figure: Alternative splicing [6].

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# COVID origin

## Phylogenetic tree and BLAST

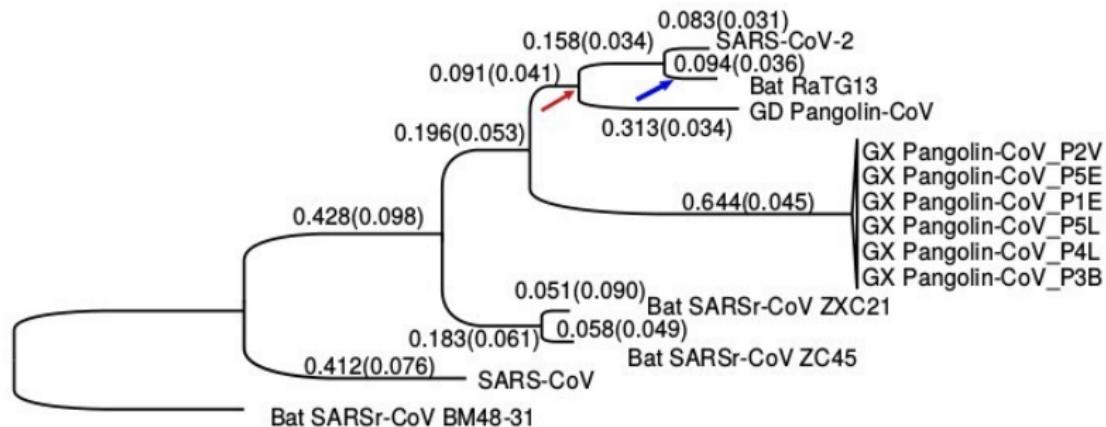


Figure: The phylogenetic tree of SARS-CoV-2 (COVID-19) and the related Coronaviruses [7].

# COVID origin

Novel virus classification using alignment-free methods



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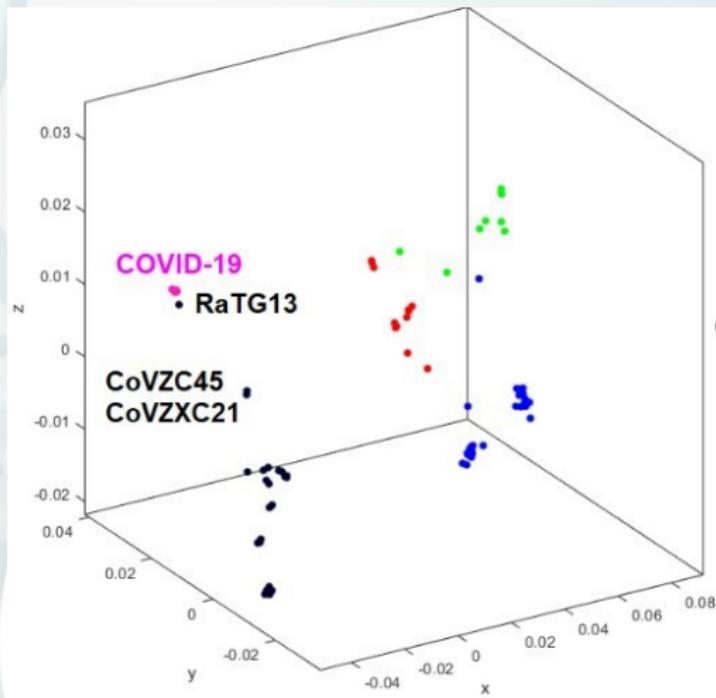


Figure: MoDMap3D of 124 Betacoronavirus sequences and COVID-19 [5].

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# Protein structure prediction

## Definition



### Definition

The prediction of protein three-dimensional structure from amino acid sequence [8].

# Protein structure prediction

## Definition



## Definition

The prediction of protein three-dimensional structure from amino acid sequence [8].

## Methods

- ▶ X-ray crystallography.
- ▶ Nuclear magnetic resonance.
- ▶ Cryo-electron microscopy.

# Protein structure prediction

Using computers



There are two approaches to predicting protein structures:

- ▶ Homology modeling.
- ▶ Physical modeling.

# Protein structure prediction

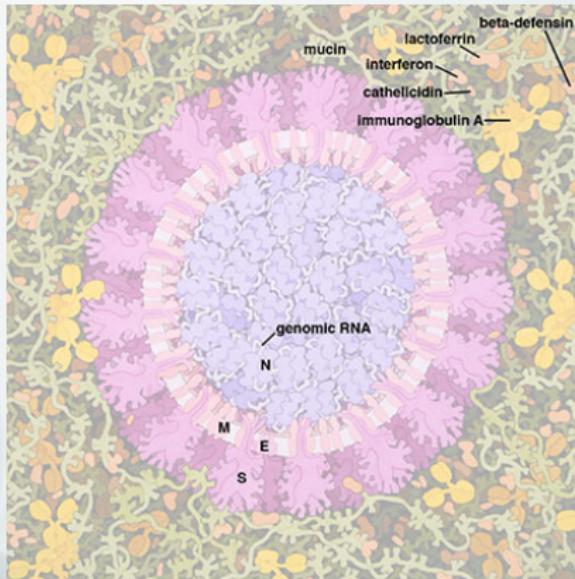
## Proteins in COVID-19



Figure: Graphical view of COVID-19 structure. Source: [9]

# Protein structure prediction

## Proteins in COVID-19



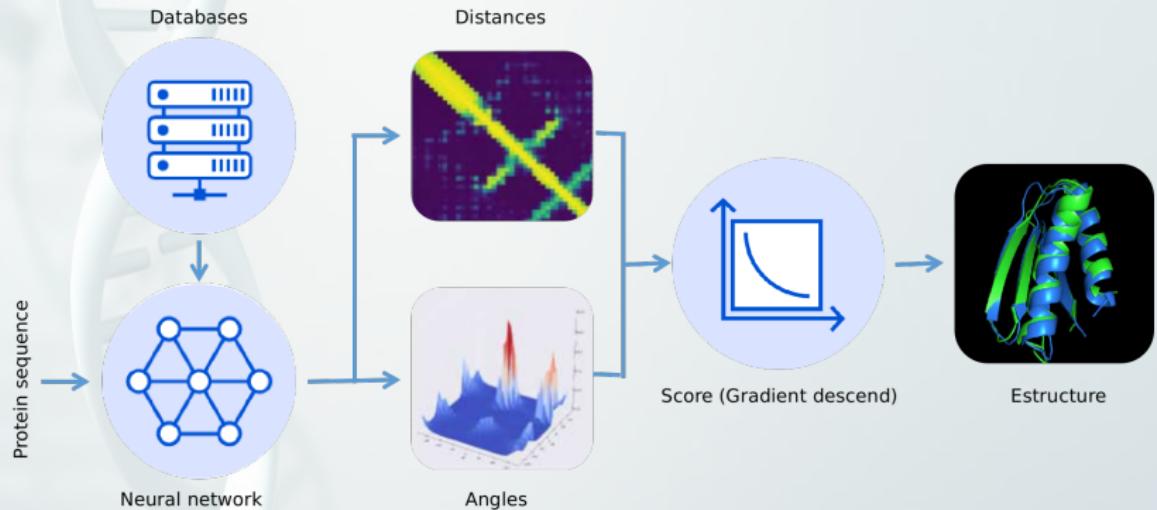
**Figure:** Membrane S (spike) protein, M (membrane) protein, membrane channel E (envelope) protein and the N (nucleocapsid) protein bound to the genomic RNA. Source: [9]

# Protein structure prediction

AlphaFold method



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**Figure:** Protein structure prediction method proposed by AlphaFold. Source: [10]

# Protein structure prediction

## COVID-19 membrane protein

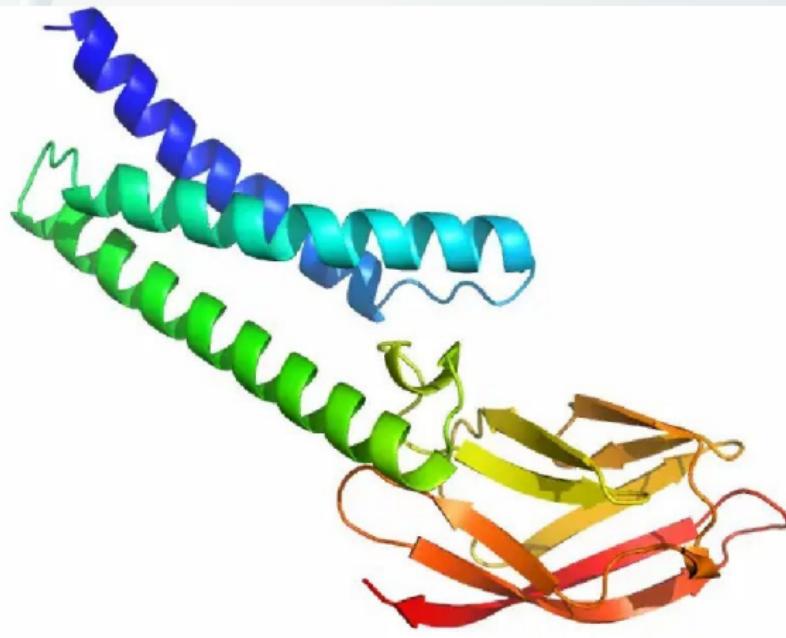
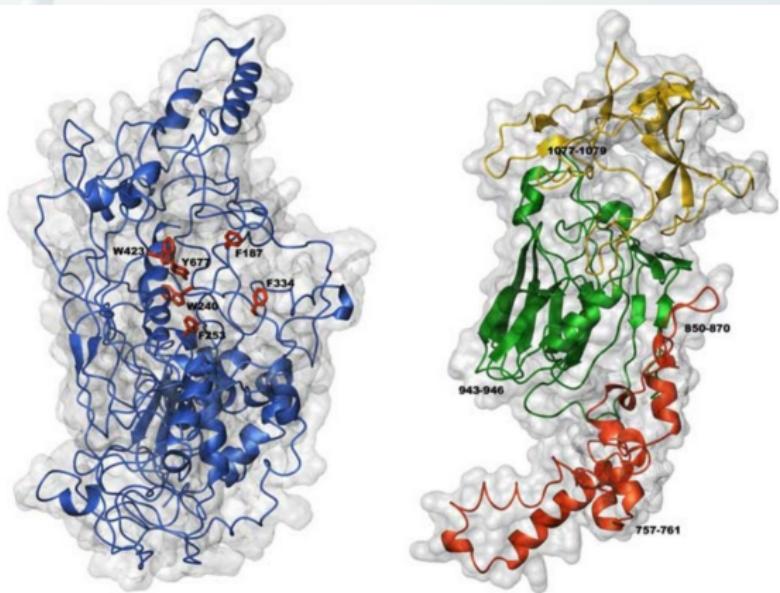


Figure: COVID-19 membrane protein. Source: [10]

# Protein structure prediction

Tertiary representations of the S1 and S2 subunits of the spike protein



**Figure:** Tertiary representations of the S1 and S2 subunits of the spike protein using PsiPred. Source: [11]

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# Drug discovery

## Definition



### Definition

Drug discovery is the process by new candidate medications are discovered [12].

# Drug discovery

From a million to one



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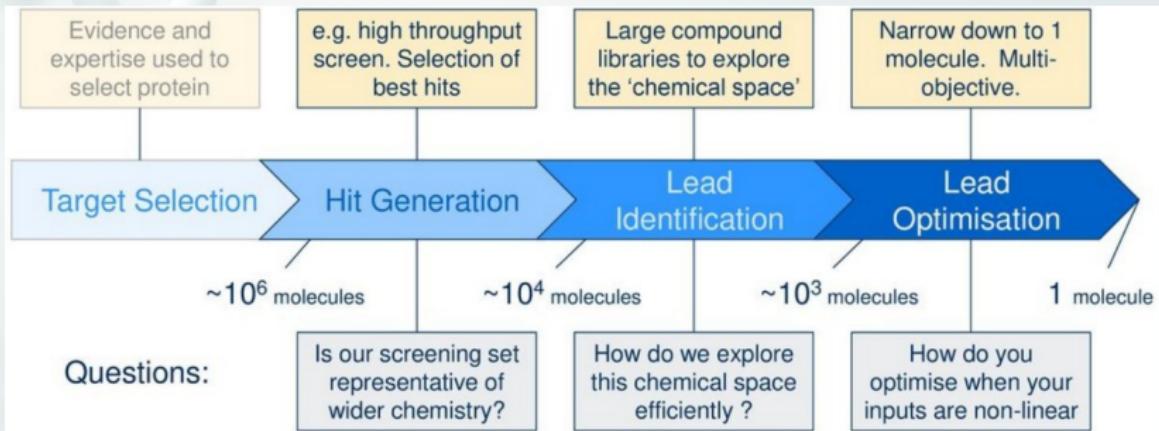


Figure: Process in drug discovery. Source: [13]

# Drug discovery

## COVID-19 main protease

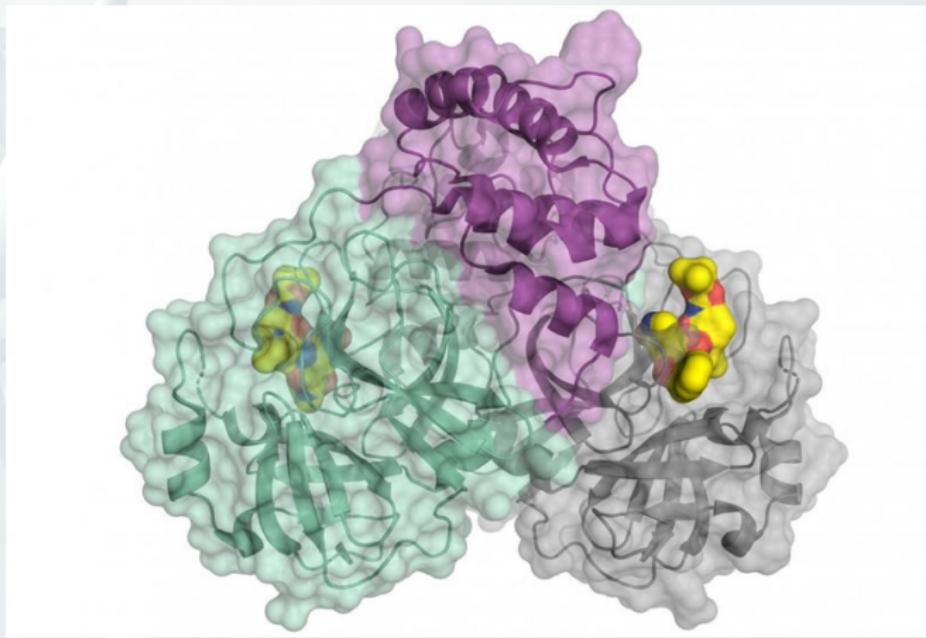
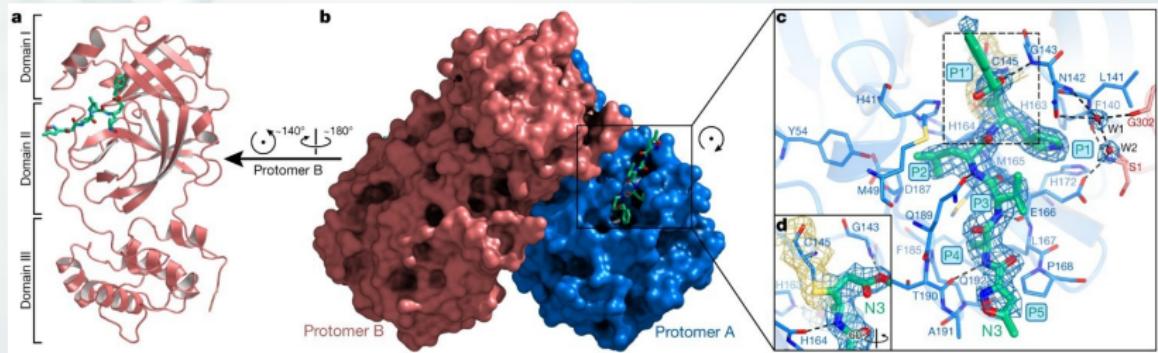


Figure: Schematic representation of the coronavirus protease. Source: [14]

# Drug discovery

## N3 inhibitor of main protease



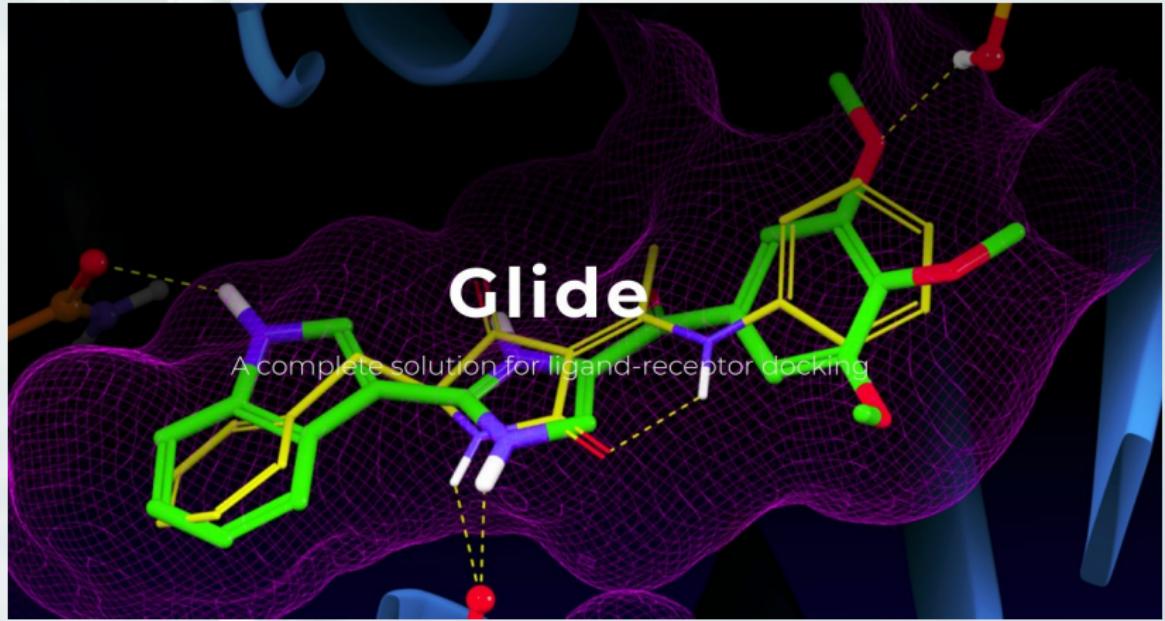
**Figure:** The crystal structure of SARS-CoV-2 main protease N3 inhibitor.  
**Source:** [15]

# Drug discovery

## Molecular docking with Glide



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### Molecular docking

Molecular docking is a computer simulation procedure to predict the conformation of a receptor-ligand complex [16]

Algorithms used:

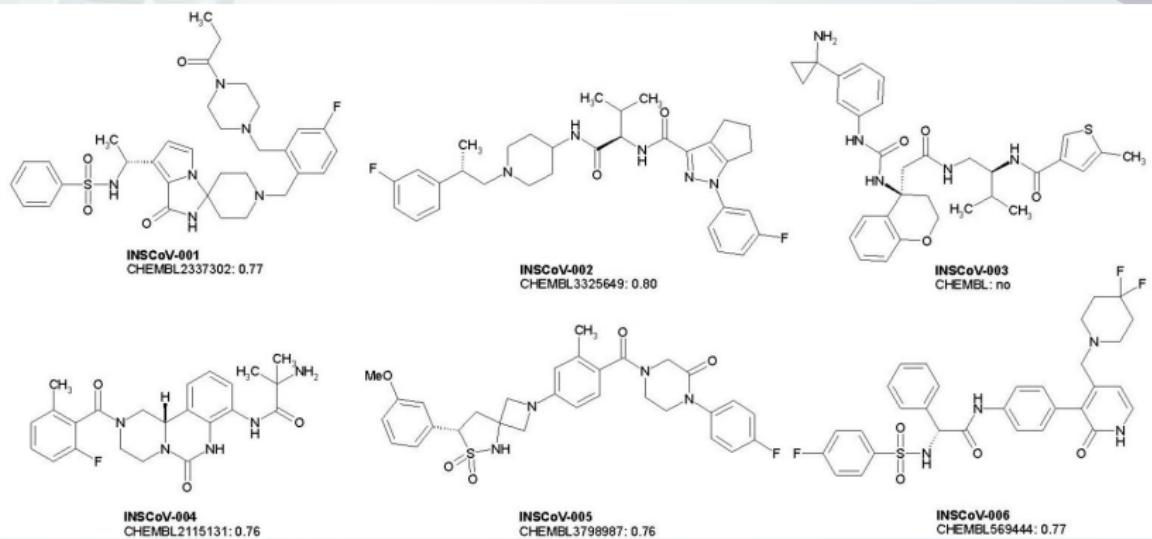
- ▶ Fast shape matching (take into account the geometric).
- ▶ Simulated Annealing.
- ▶ Genetic algorithms.
- ▶ Tabu search.

# Drug discovery

## Protease Inhibitors Designed Using Generative Deep Learning Approaches



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**Figure:** Representative examples of the structures generated to target the main protease of 2019-nCoV. Novelty was assessed using similarity search in ChEMBL Database. Source: [17]

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List of open funding calls and other support for researchers, non-profit organizations and commercial organizations, specifically for COVID-19 and coronavirus-related research ([Link](#)).

# Coronavirus Funding Monitor





MIT is hosting a series of challenges to empower YOU to take action on the COVID-19 crisis ([Link](#)).

# MIT COVID19 CHALLENGE



# FONDECYT

FONDO NACIONAL DE DESARROLLO CIENTÍFICO,  
TECNOLÓGICO Y DE INNOVACIÓN TECNOLÓGICA

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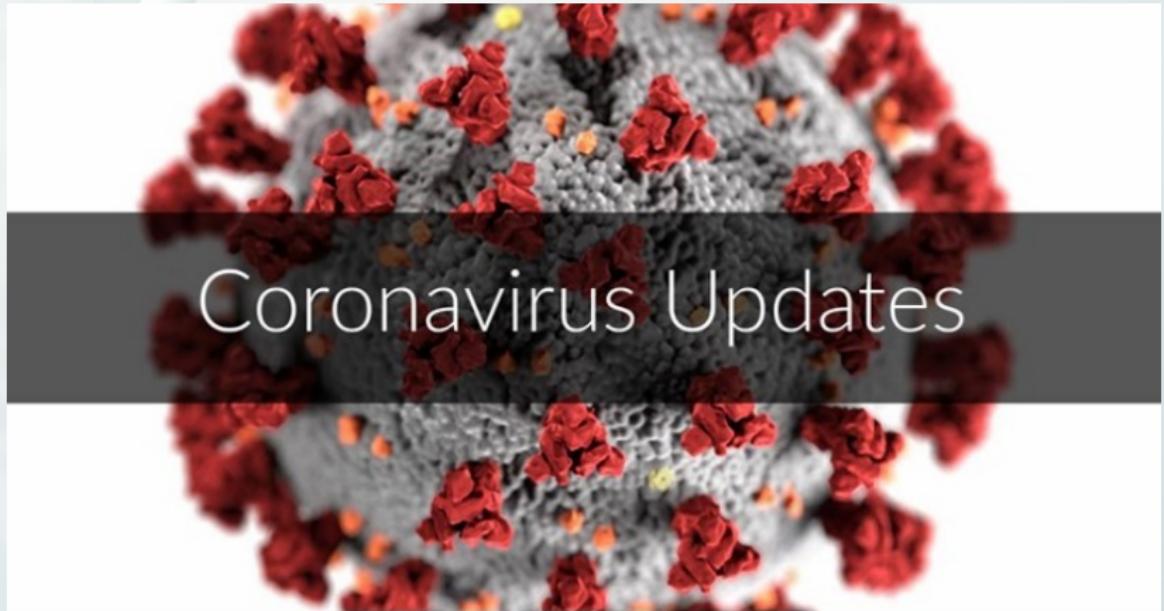
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# Datasets and resources

## Coronavirus updates



Links to bioinformatics resources useful to track the evolution and progression as well as to manage genomics data ([Link](#)).



# Datasets and resources

Institut Français de Bioinformatique (IFB)



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The IFB offers expertise and computing facilities to support the involved teams on COVID-19 ([Link](#)).



# Datasets and resources

The European Bioinformatics Institute (EMBL-EBI)



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EMBL-EBI is gathering and sharing data resources as they become available ([Link](#)).



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# How to learn Bioinformatics?

Biology as a DATA SCIENCE



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T-Bio platform ([Link](#)).



# How to learn Bioinformatics?

Coursera



Coursera ([Link](#)).



# How to learn Bioinformatics?

Bioinformatics Research Group



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Bioinformatics Research Group at la Salle university is a interdisciplinary group open for everybody who have a computer science' background.



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Thank you