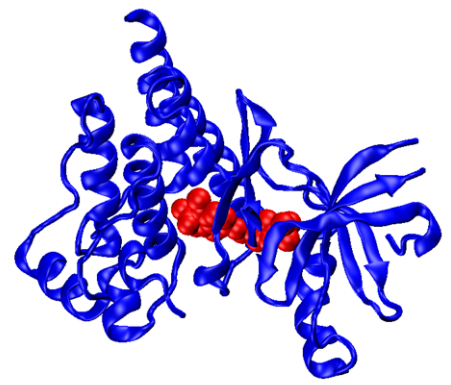




# HYPERION



## Allosteric site finder solution

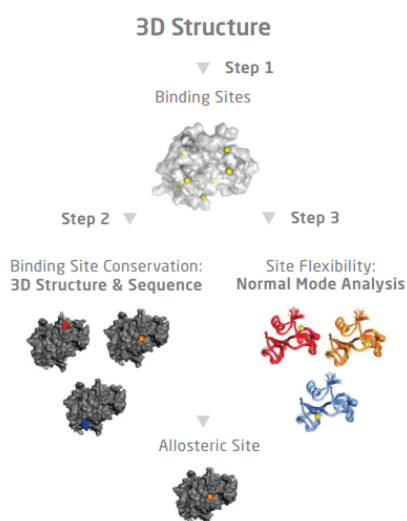
**HYPERION** is a computational tool which identifies allosteric sites in proteins that could affect to the protein activity and function, manipulating the protein's conformation.

## Working with **HYPERION**

- ◆ In order to analyze and predict allosteric sites, the only thing we need is the structure of the protein to be analyzed.

## How does **HYPERION** works?

- ◆ **HYPERION** calculates the allosteric pockets of a given protein.
- ◆ Information considered is obtained in three different levels:
  - Sequence conservation
  - Protein flexibility
  - Electristatic poteintial
- ◆ **HYPERION** uses Normal Mode Analysis to study local flexibility in the protein,



## **HYPERION's** applications

- ◆ Identification of new allosteric sites
- ◆ Clustering of binding pockets
- ◆ Determination of allosteric binders
- ◆ Study of Mechanisms of Action based on allosteric modulators
- ◆ Exploitation of specific binding drugs

## Competitive Advanges

- ◆ **HYPERION** uses a multicriteria approximation to identify new allosteric pockets.
- ◆ **HYPERION** localize allosteric binding sites considering sequence information, flexibility as well as structural information.
- ◆ **HYPERION** is run by Intelligent Pharma's experts so you do not need to be trained and we provide the supercomputational resources.

# Visit us!

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