

**LOSCHMIDT  
LABORATORIES**



# Computational Tools to Aid Modelling, Analysis, and Virtual Screening

**Gaspar Pinto @ EJIBCE 2018**



ST. ANNE'S UNIVERSITY HOSPITAL BRNO  
INTERNATIONAL CLINICAL RESEARCH CENTER

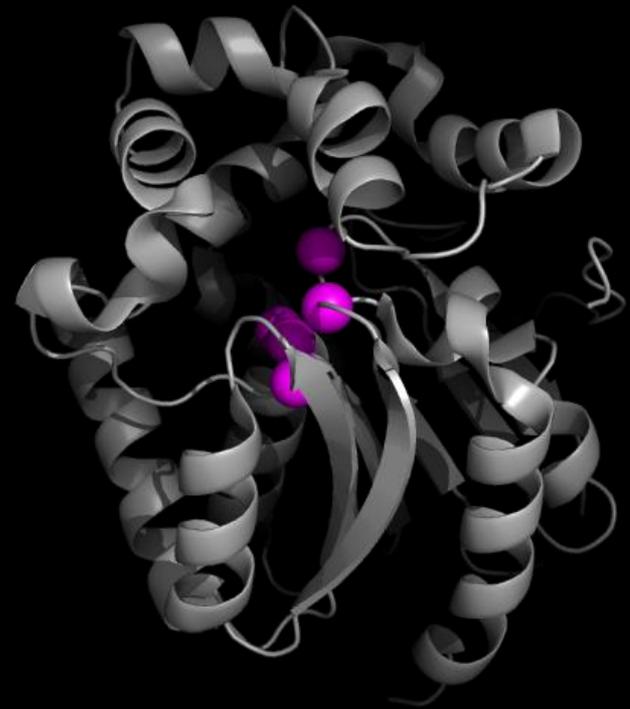
# Introduction

- Who we are



# Introduction

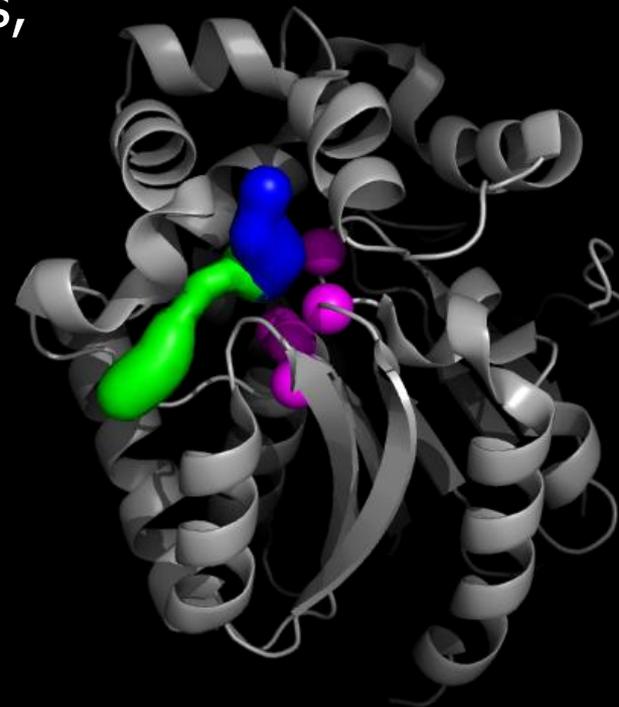
- Enzymes with buried active site



Haloalkane dehalogenase DhaA

# Introduction

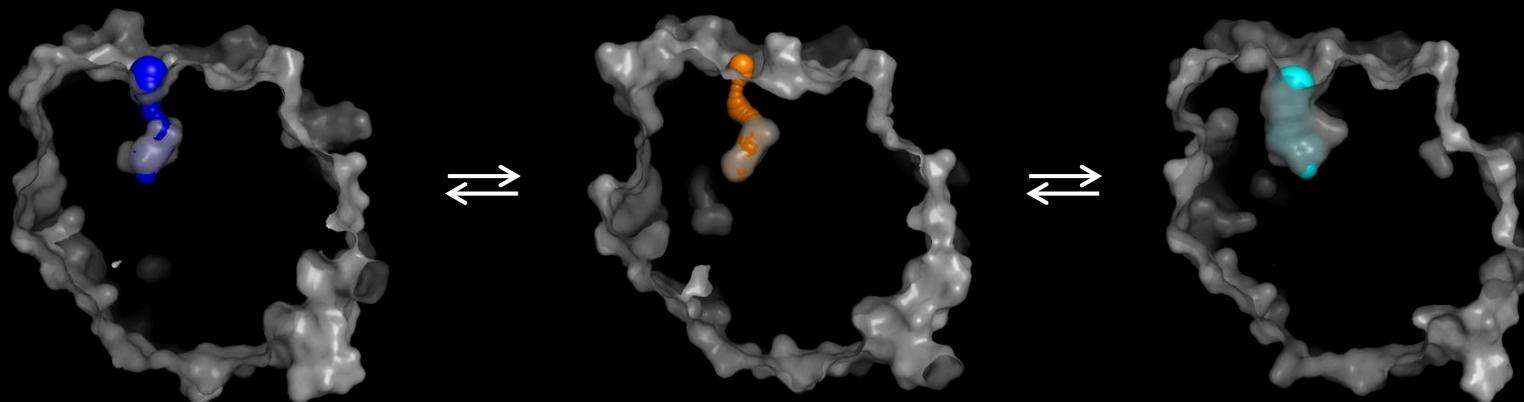
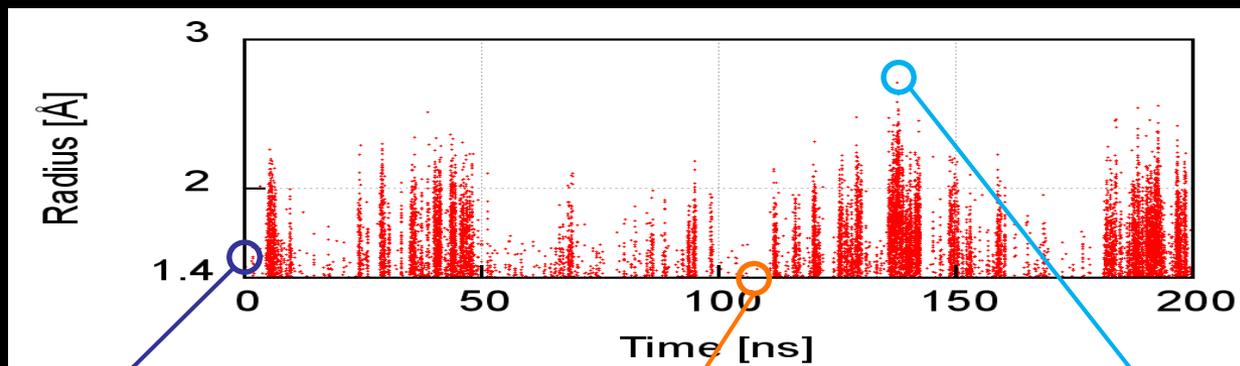
- Enzymes with buried active site... need tunnels
  - Transport of substrates, products, solvent, cofactors
  - Wide-spread features
    - 64% of known enzymes
    - All 6 enzyme classes



Haloalkane dehalogenase DhaA

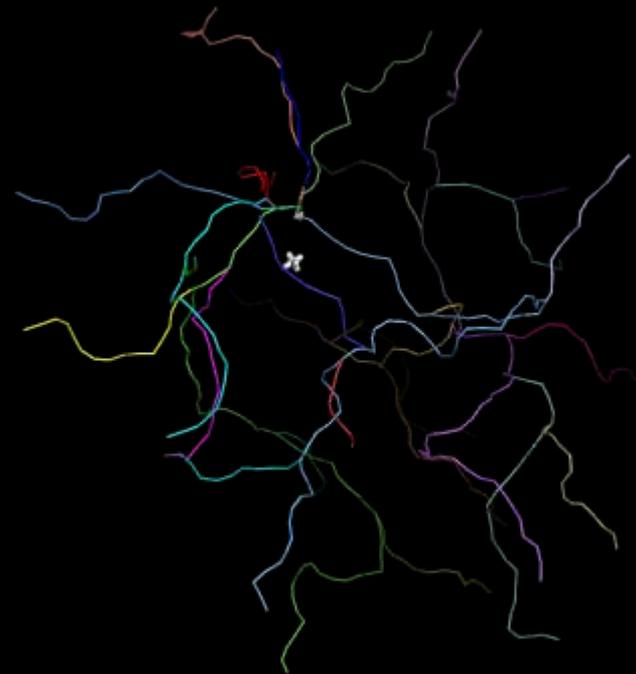
# Introduction

- Protein tunnels: dynamic features



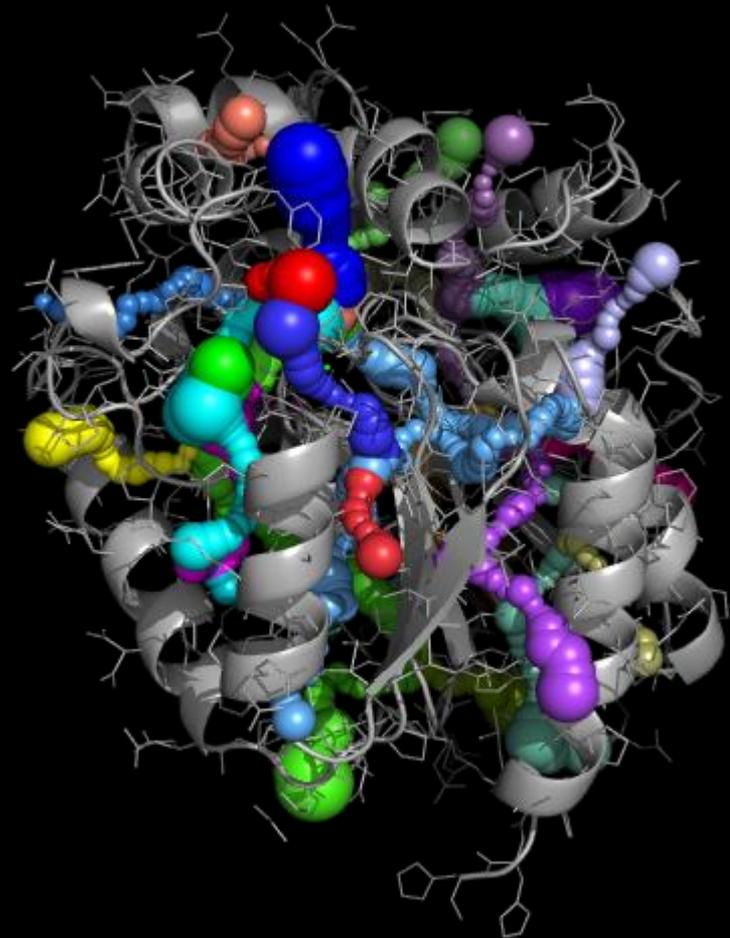
# CAVER

- Tool for tunnel computation
  - Space characterization
  - Voronoi diagrams
  - Search for pathways
    - Origin, probe radius, shell radius, clustering threshold



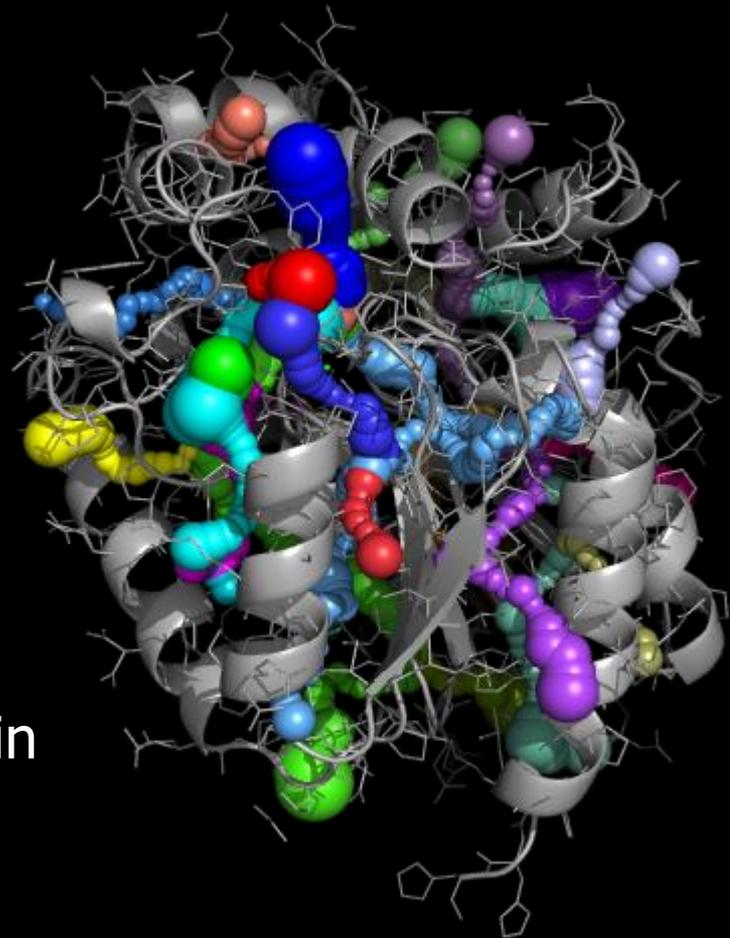
# CAVER

- Tool for tunnel computation
  - Space characterization
  - Voronoi diagrams
  - Search for pathways
    - Origin, probe radius, shell radius, clustering threshold



# CAVER

- Tool for tunnel computation
  - Space characterization
  - Voronoi diagrams
  - Search for pathways
  - Ranking of tunnels
    - Based on bottleneck radius, length, curvature
  - Command-line, PyMOL plugin



# CAVER

- Dynamic tunnels
  - Structure ensemble



identification of tunnels  
in each snapshot

# CAVER

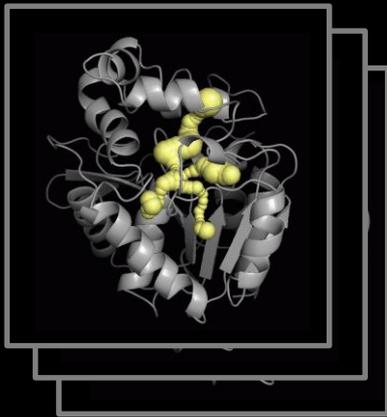
- Dynamic tunnels
  - Structure ensemble



identification of tunnels  
in each snapshot

# CAVER

- Dynamic tunnels
  - Structure ensemble



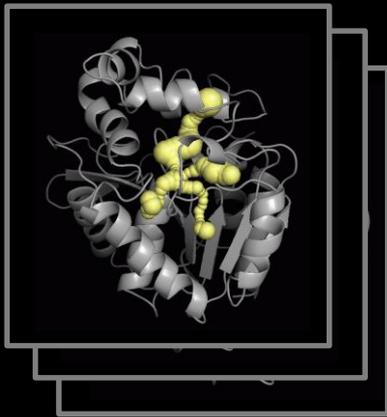
identification of tunnels  
in each snapshot



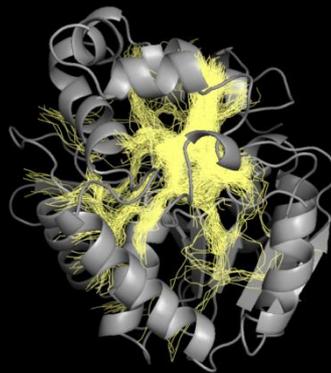
merging all identified  
tunnels

# CAVER

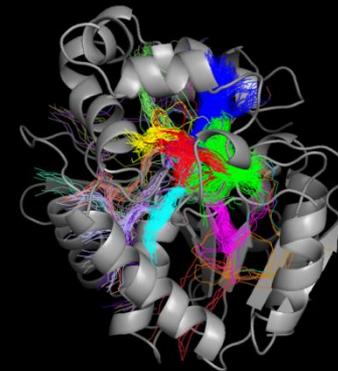
- Dynamic tunnels
  - Structure ensemble
  - Clustering of tunnels



identification of tunnels  
in each snapshot



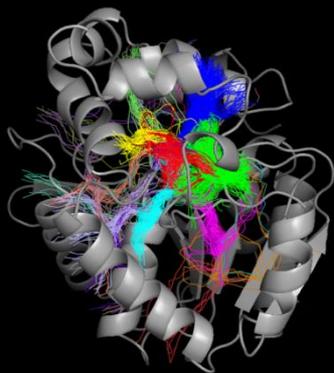
merging all identified  
tunnels



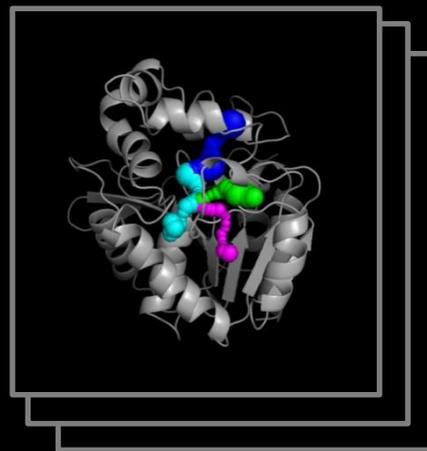
clustering of tunnels

# CAVER

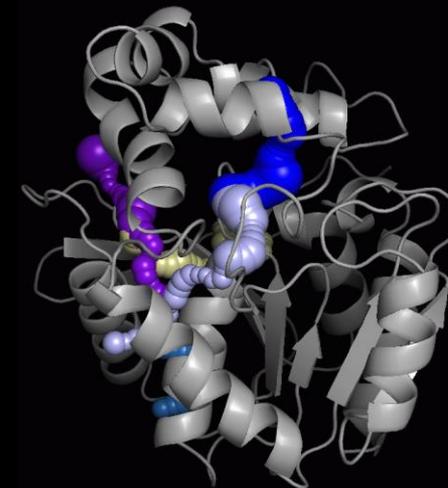
- Dynamic tunnels
  - Analysis of tunnel dynamics
  - Statistics, analysis and visualization output



clustering of tunnels

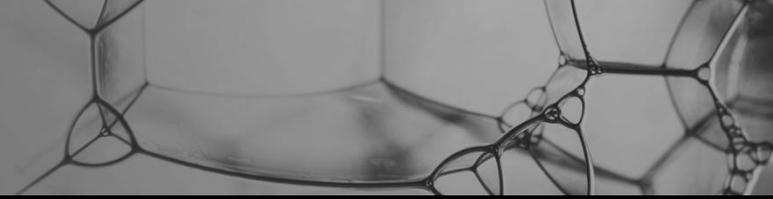


analysis of tunnels



tunnel dynamics

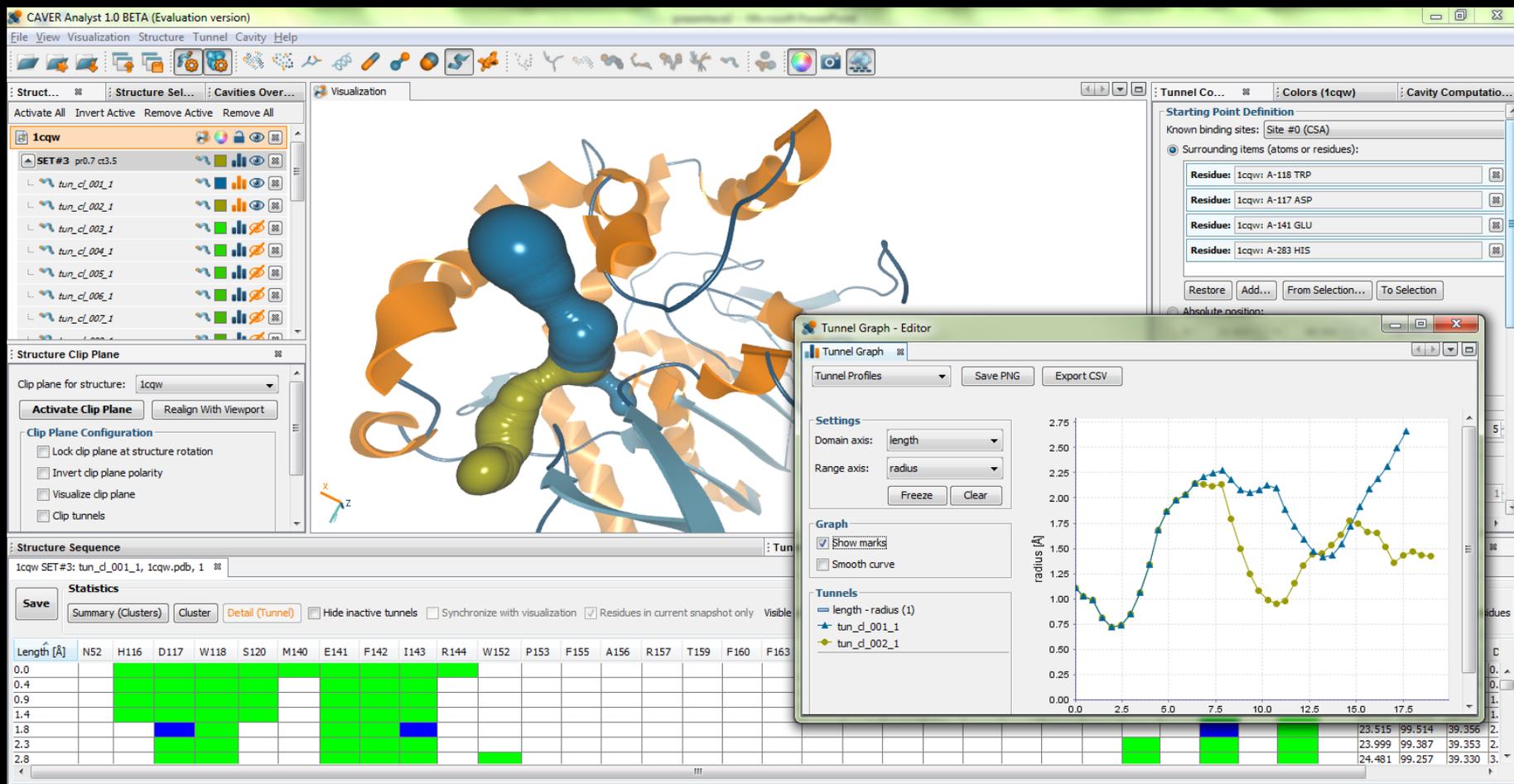
# Caver Analyst



- Graphical interface to CAVER
  - User-friendly
  - Static and dynamic structures
  - Versatile representations

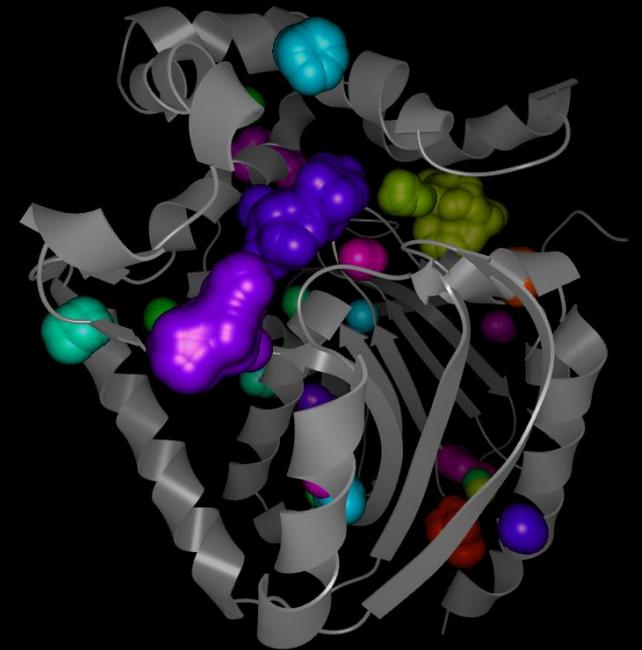
# Caver Analyst

## ■ Graphical interface to CAVER



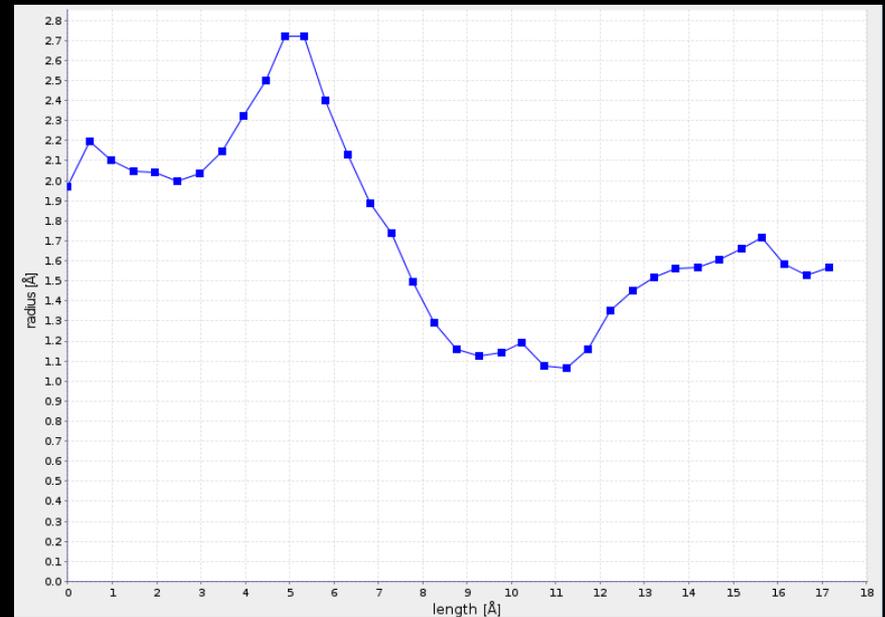
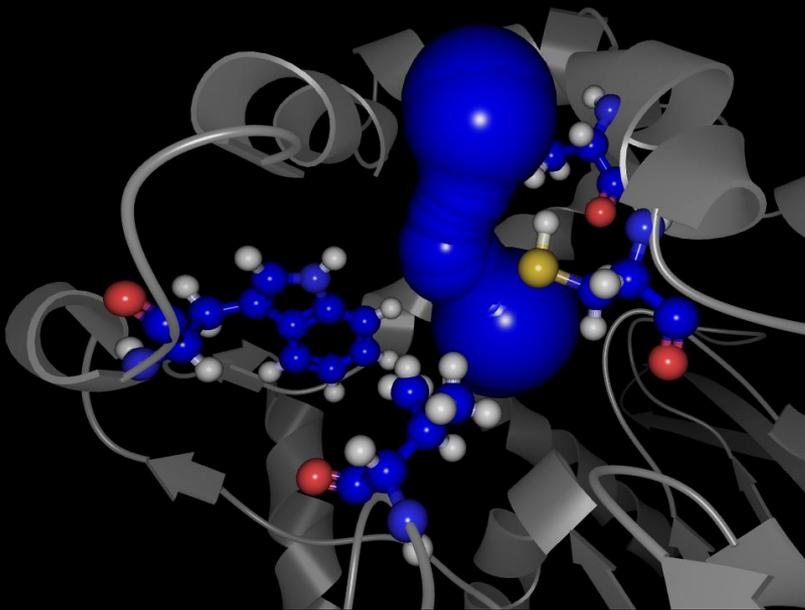
# Caver Analyst

- Graphical interface to CAVER
  - User-friendly
  - Static and dynamic structures
  - Versatile representations
  - Compute protein cavities



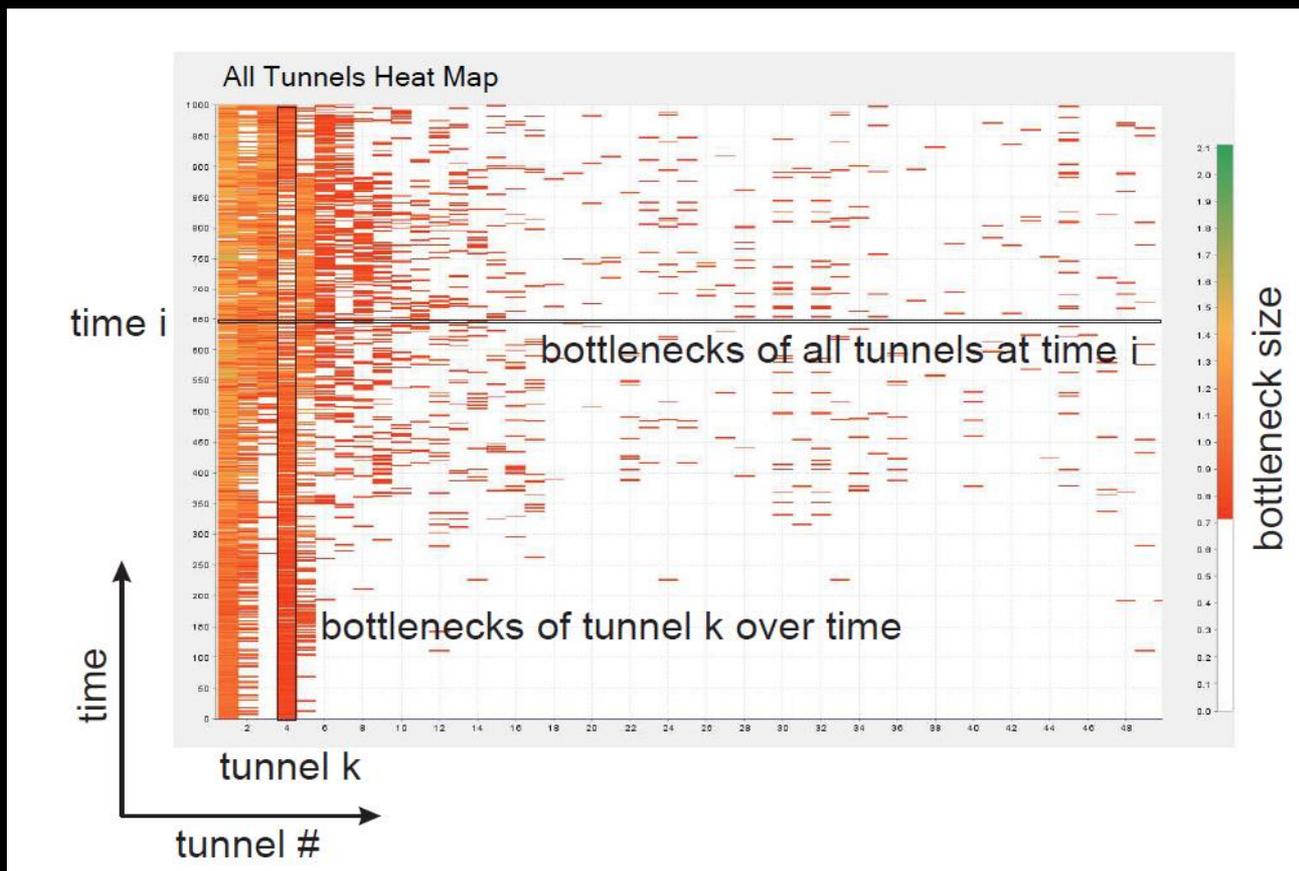
# Caver Analyst

- Graphical interface to CAVER



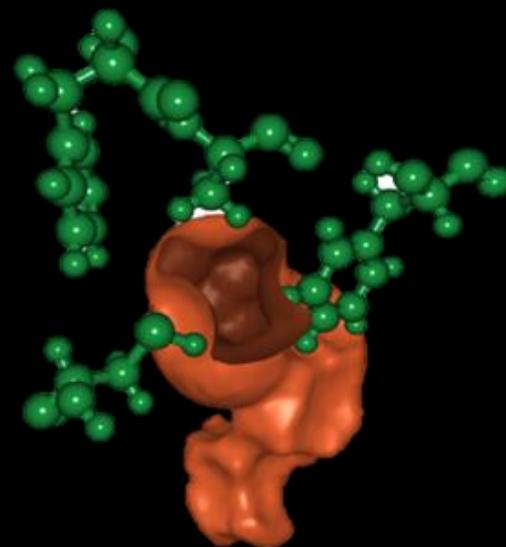
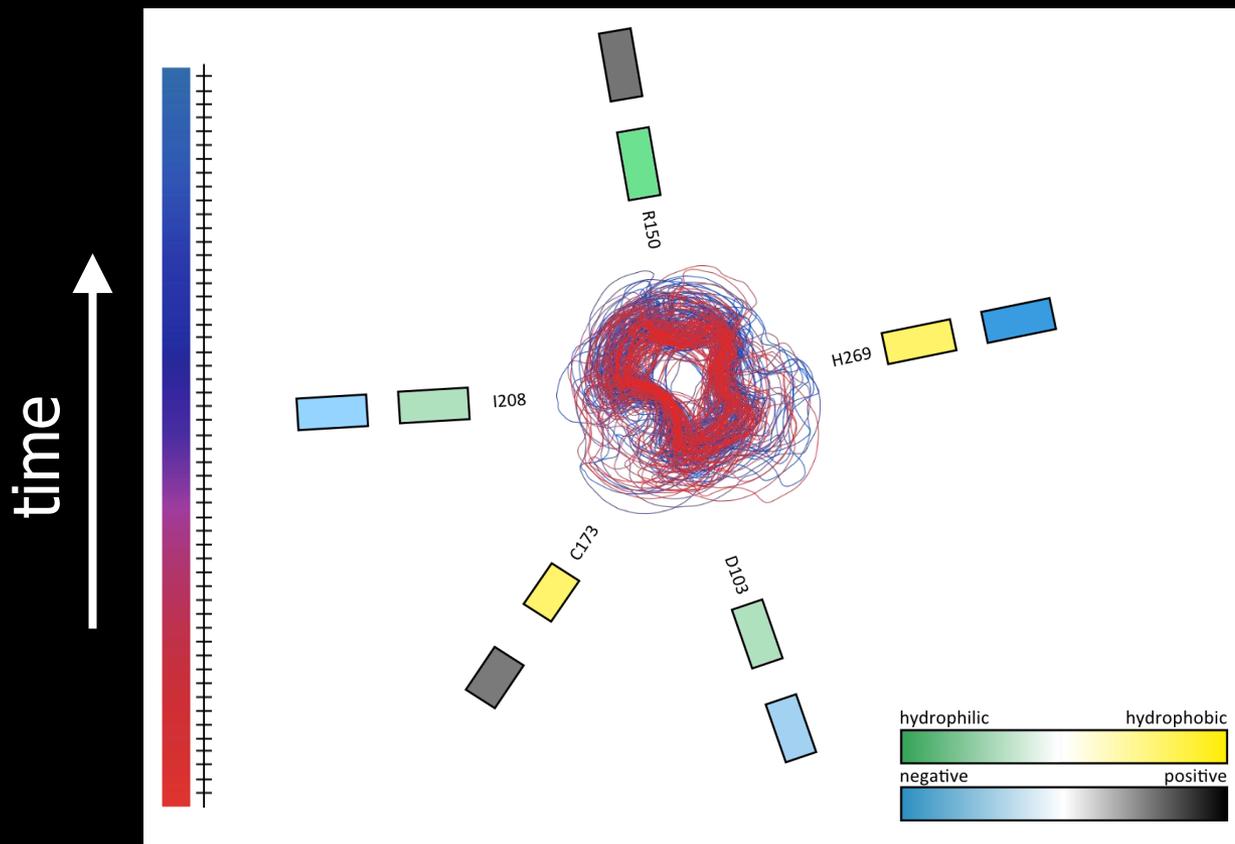
# Caver Analyst

- Graphical interface to CAVER



# Caver Analyst

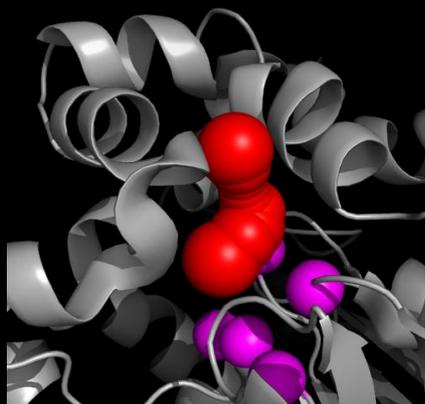
- Graphical interface to CAVER



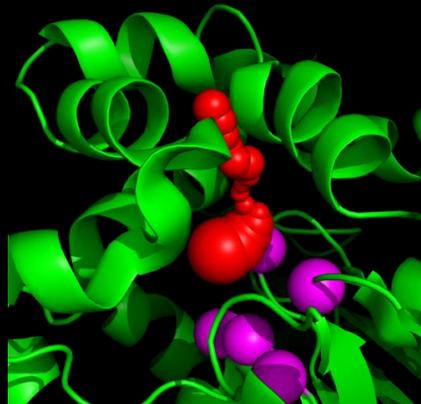
# Caver Analyst – case study



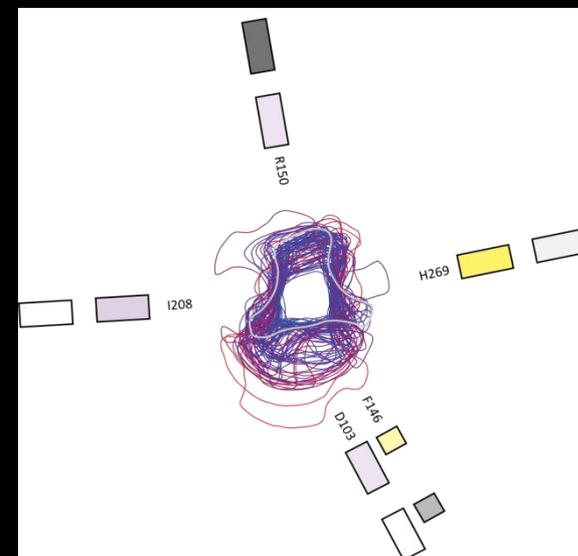
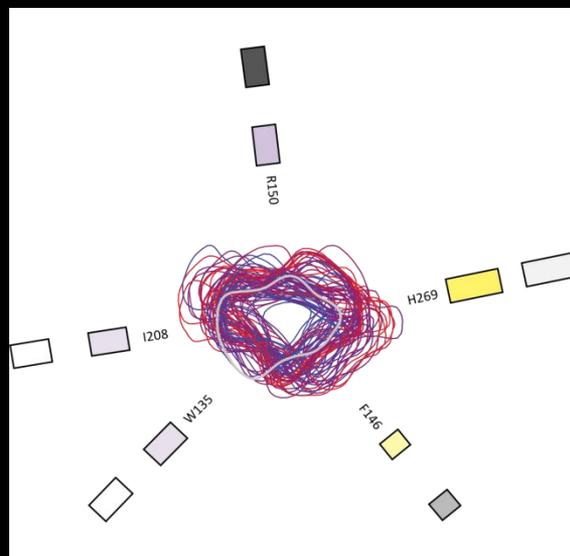
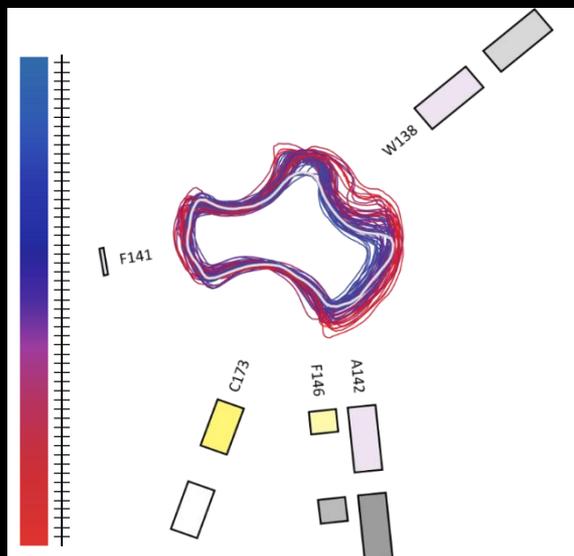
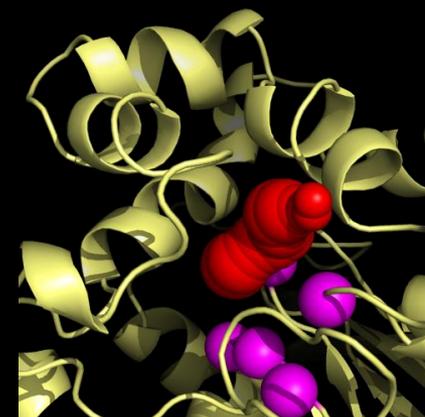
DhaA



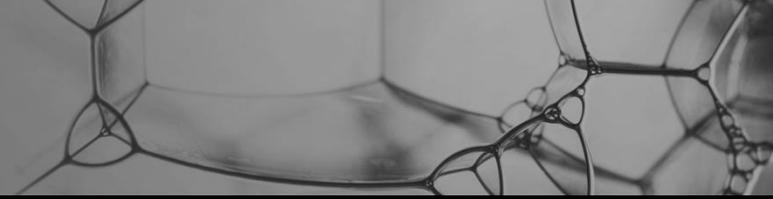
DhaA80



DhaA106



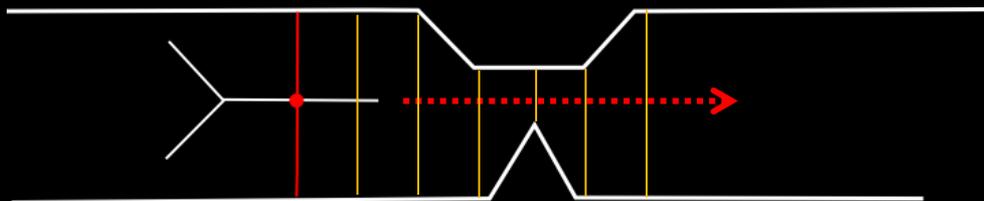
# Caver Analyst



- Caver Analyst 2.0
  - Improved tunnel analysis
  - Mutagenesis
  - Enhanced visualization
  - Video recording
  - Saving images with no background
  - [www.caver.cz](http://www.caver.cz)

# CaverDock

- Tool to study ligand transport through tunnels
  - Substrate, products, inhibitors
  - Based on CAVER and AutoDock Vina
  - Trajectory computation



# CaverDock

- Tool to study ligand transport through tunnels
  - Substrate, products, inhibitors
  - Based on CAVER and AutoDock Vina
  - Lower-bound trajectory



# CaverDock

- Tool to study ligand transport through tunnels
  - Substrate, products, inhibitors
  - Based on CAVER and AutoDock Vina
  - Continuous movement



# CaverDock

- Tool to study ligand transport through tunnels
  - Substrate, products, inhibitors
  - Based on CAVER and AutoDock Vina
  - Optimized trajectory



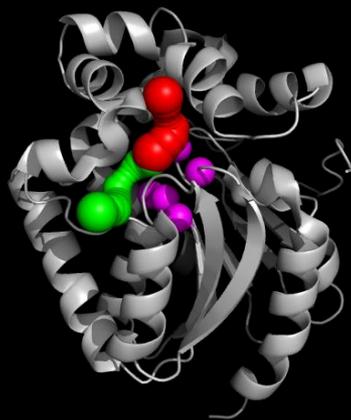
# CaverDock



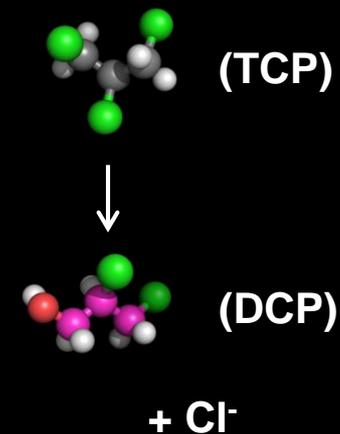
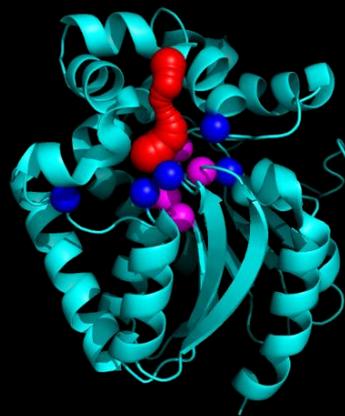
- Tool to study ligand transport through tunnels
  - Substrate, products, inhibitors
  - Based on CAVER and AutoDock Vina
  - Flexibility can be added
  - Trajectory and binding energy along tunnel

# CaverDock – case study

DhaA

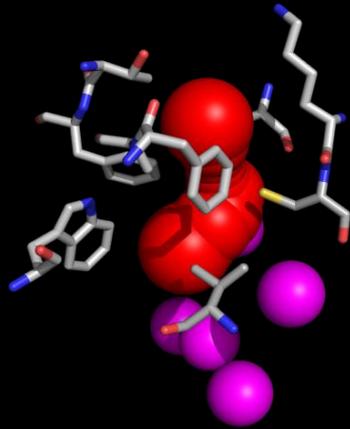


DhaA31

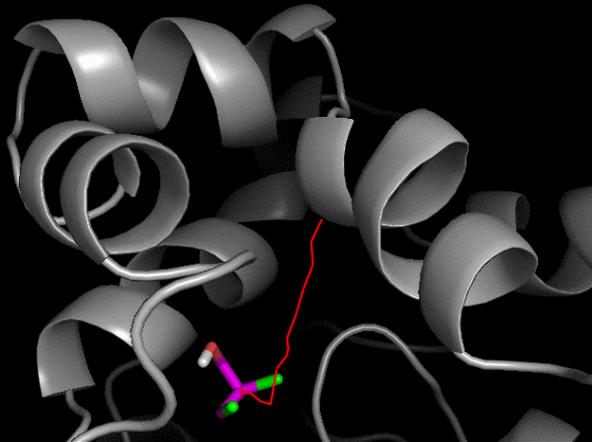
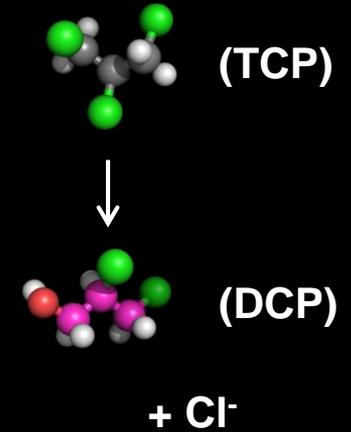
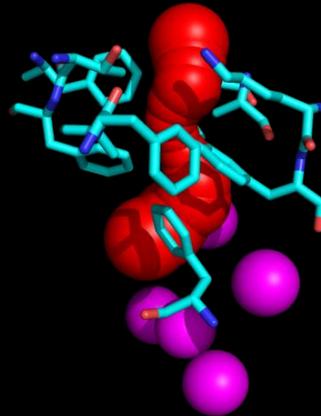


# CaverDock – case study

DhaA

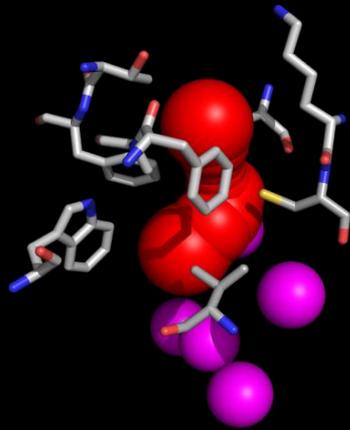


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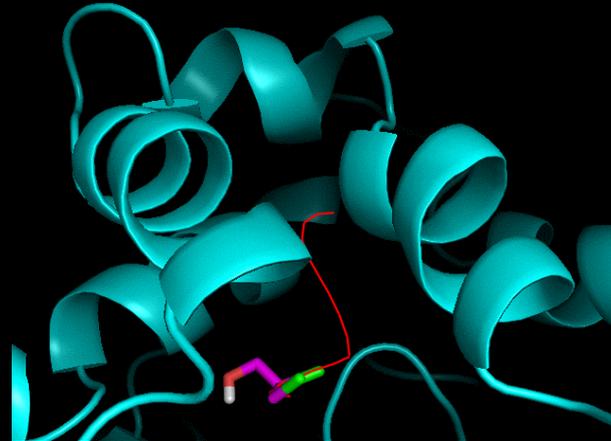
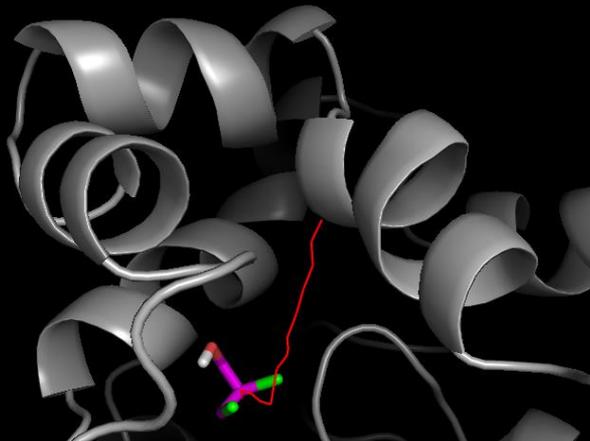
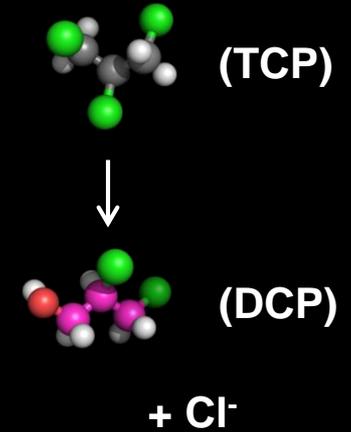
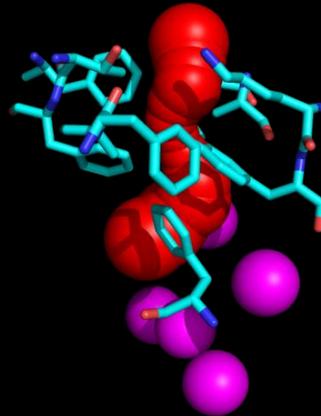


# CaverDock – case study

DhaA

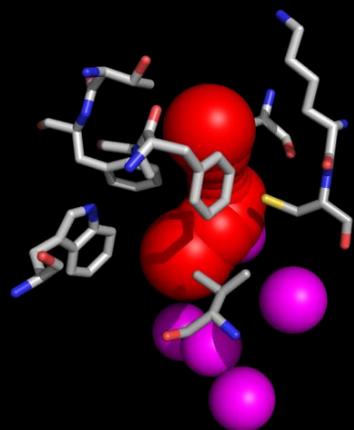


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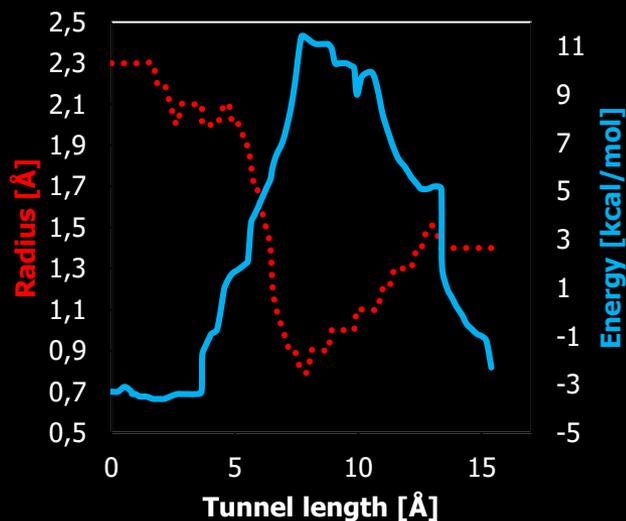
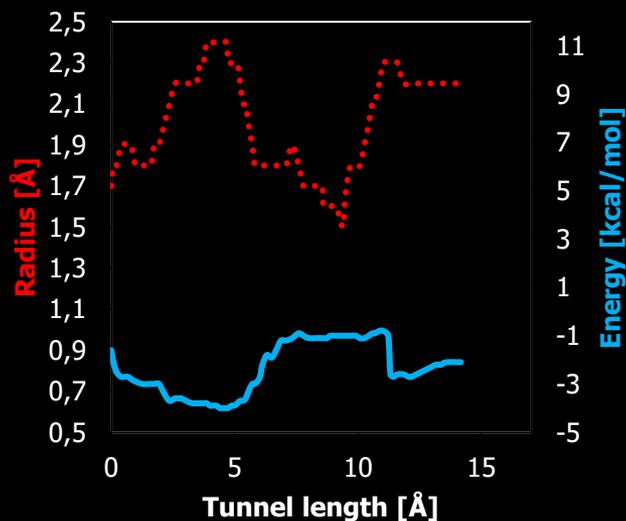
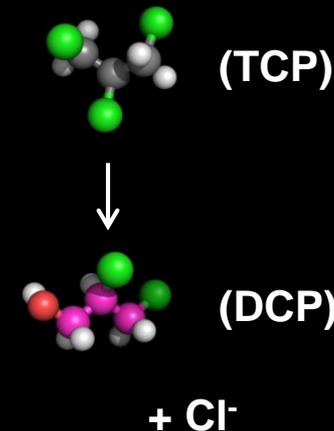
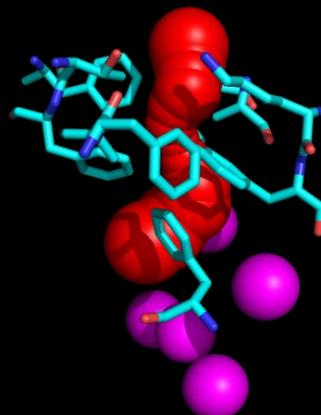


# CaverDock – case study

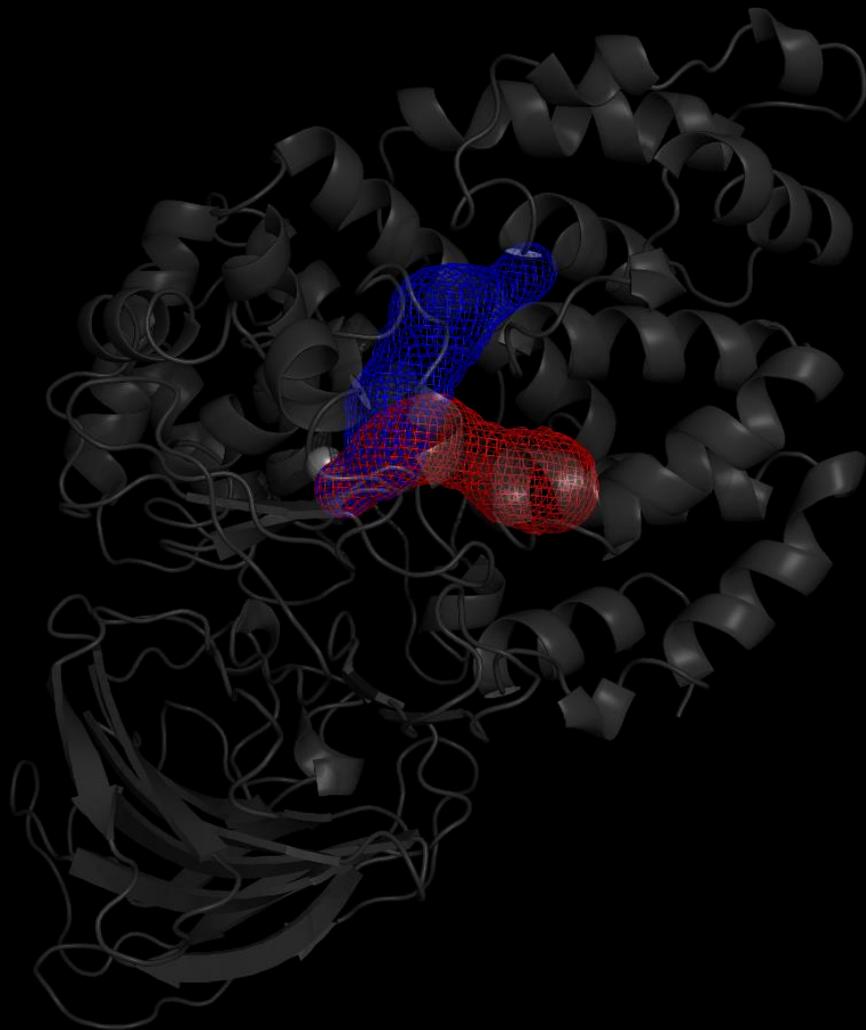
DhaA



DhaA31



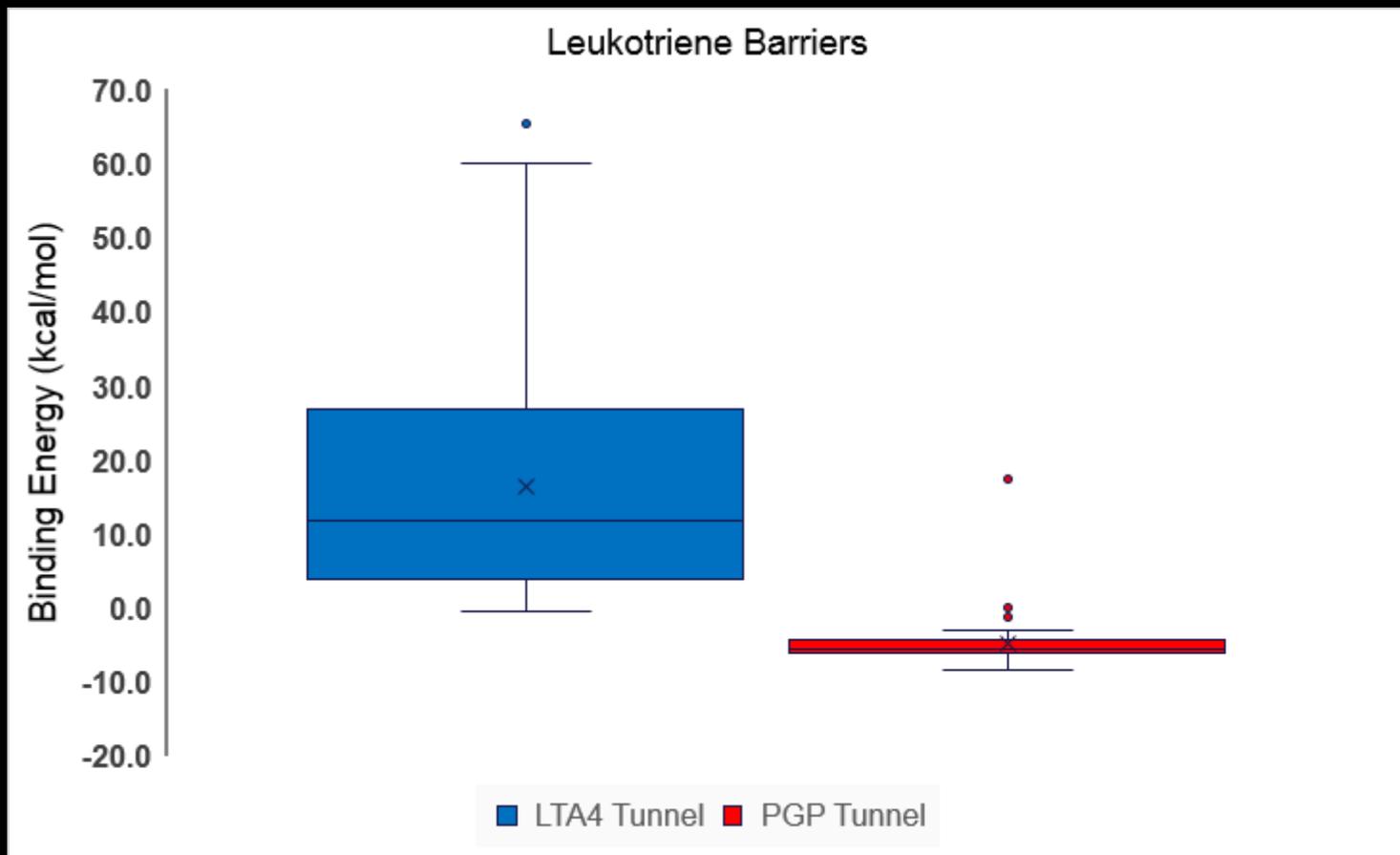
# Virtual screening – Caver Analysis



## Leukotriene A4

- Biosynthesis of a pro-inflammatory mediator
- Screening library:
  - Anti-inflammatory agents
  - 56 molecules
  - 2 ligands discarded from the set

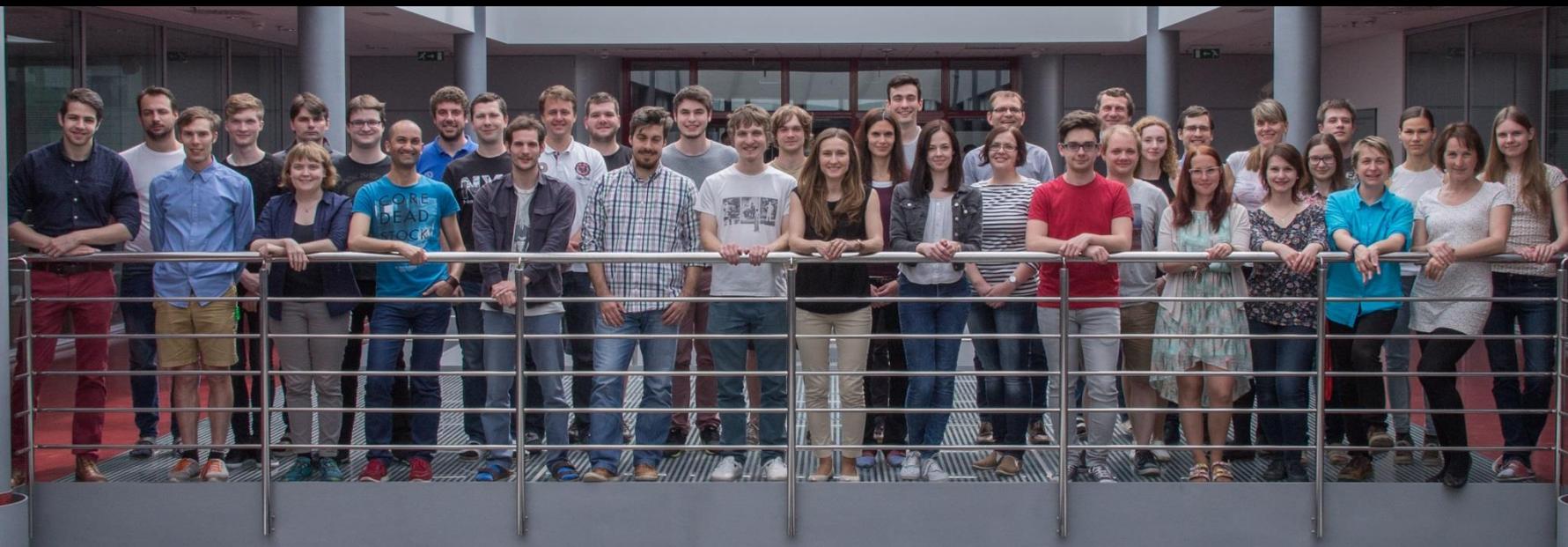
# Virtual screening – Data Analysis



# Acknowledgements



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Computational Tools to Aid Modelling, Analysis and Virtual Screening

# Software tools by LL & Co.



CAVER, Caver Analyst

<http://www.caver.cz>



FireProt

<http://loschmidt.chemi.muni.cz/fireprot>



Hotspot Wizard

<http://loschmidt.chemi.muni.cz/hotspotwizard>



Predict SNP

<http://loschmidt.chemi.muni.cz/predictsnp>



CalFitter

<http://https://loschmidt.chemi.muni.cz/calfitter>