

### **Exploring ligand-transport pathways in proteins** Structure, dynamics, function & dysfunction

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# Journey to the protein core and back

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UNIVERSITY

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# Outline

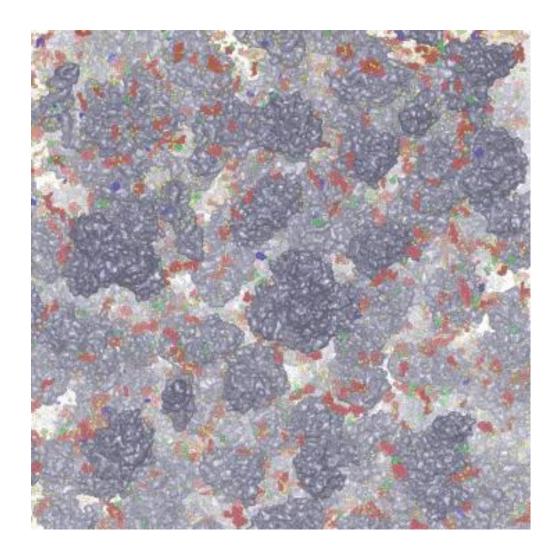
- Transport pathways in soluble/globular proteins
- Bioinformatics methods for pathway analysis
- Effect of mutations in transport pathways
- **Roles of transport pathways in pathology and drug discovery**

# **Cellular environment**

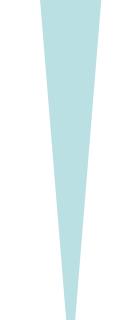
- Proteins
- Nucleic acids
- Membranes
- Metabolites
  - lipids, peptides & sugars
- Water & ions

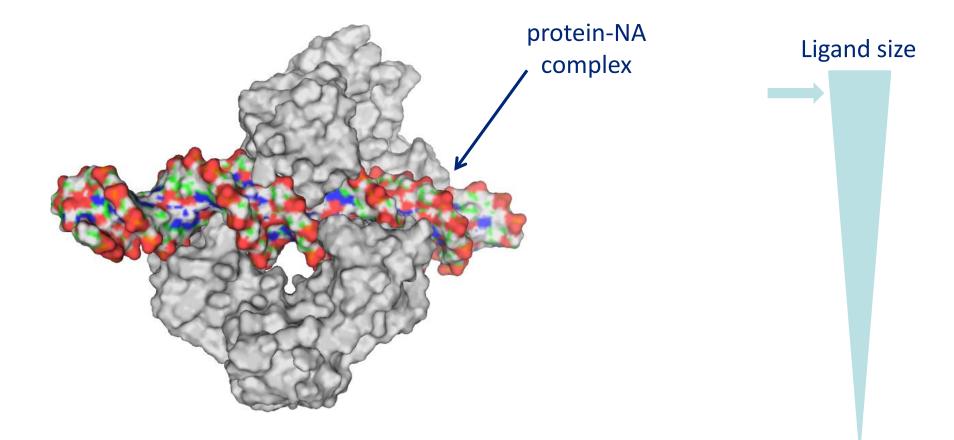
# **Cellular environment**

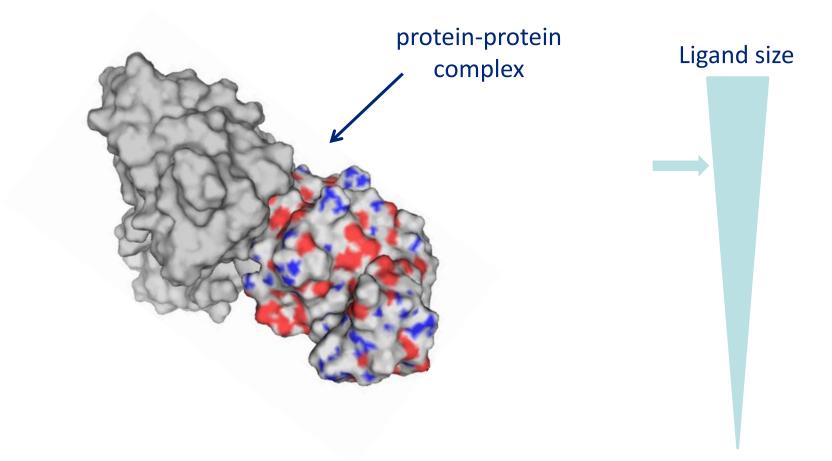
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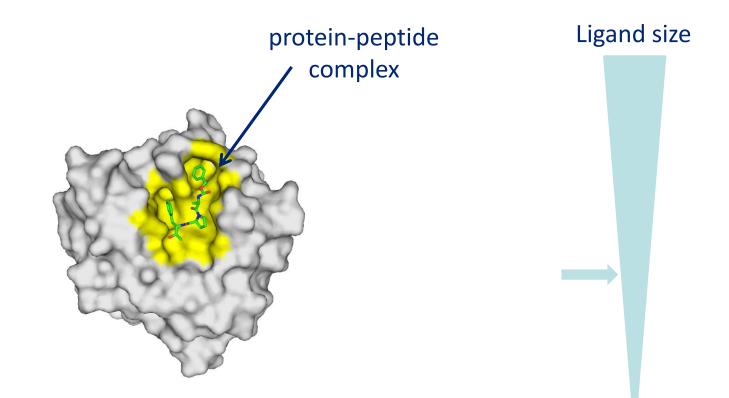


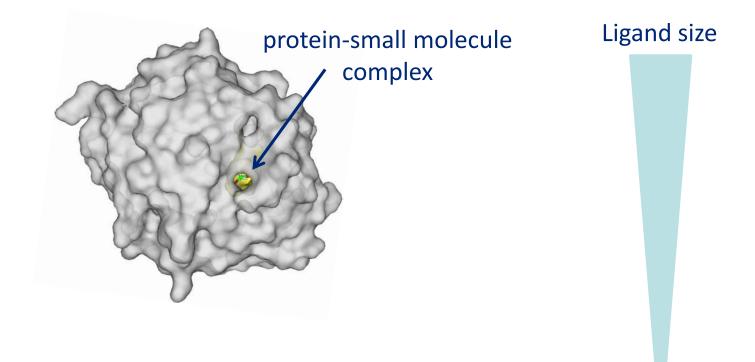


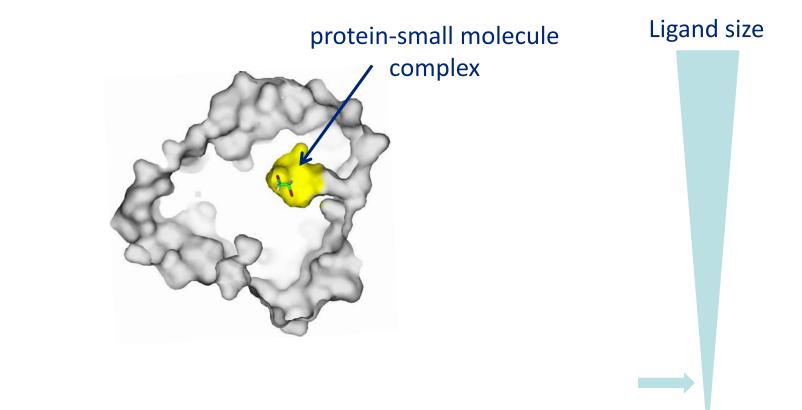


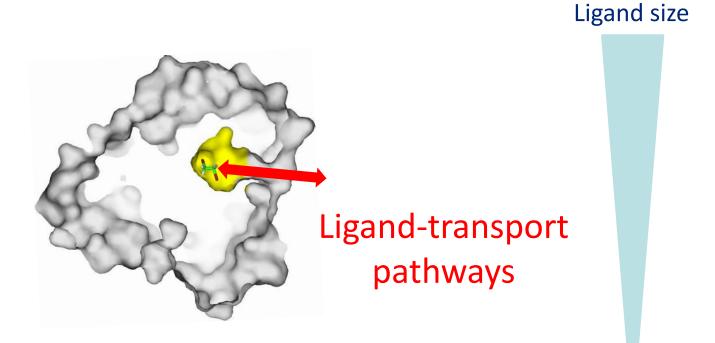




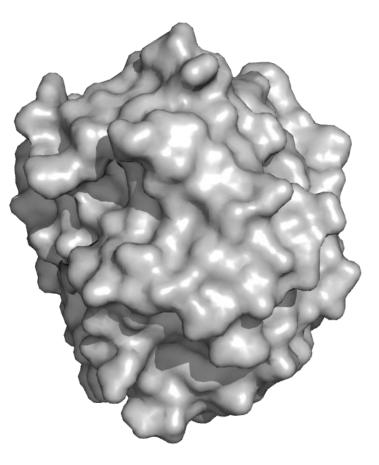




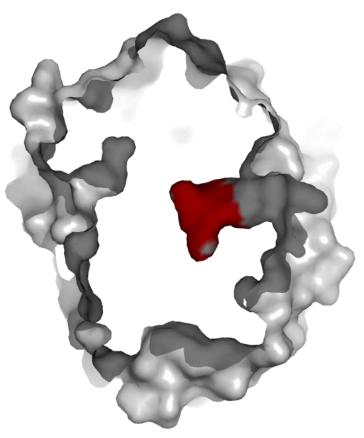




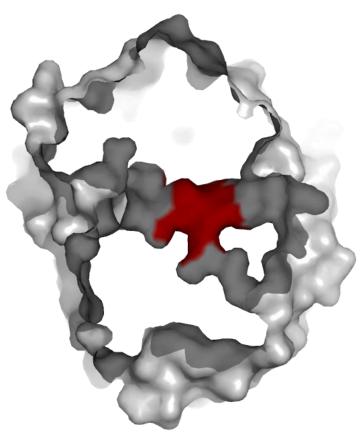
#### **Proteins with functional sites located in occluded cavities**



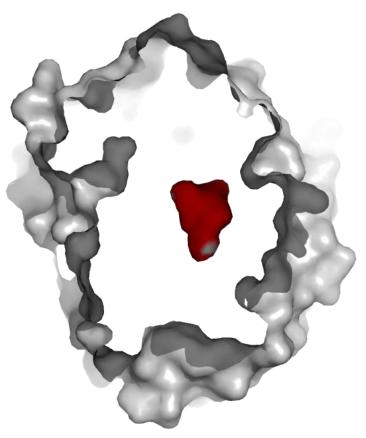
- Proteins with functional sites located in occluded cavities
- **Cognate ligands enter such sites via transport pathways tunnels**



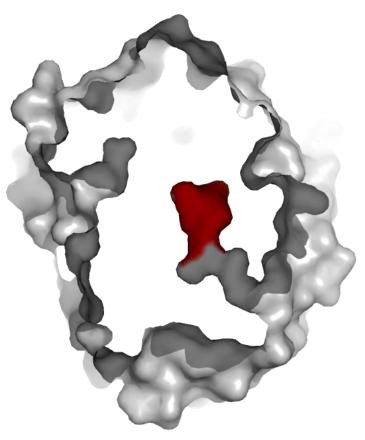
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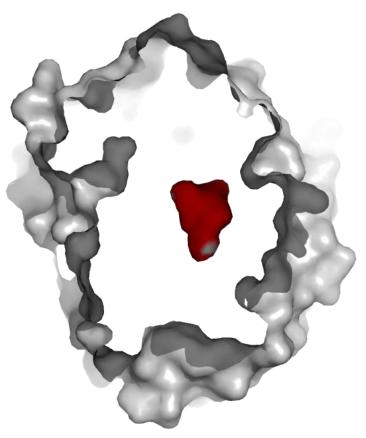
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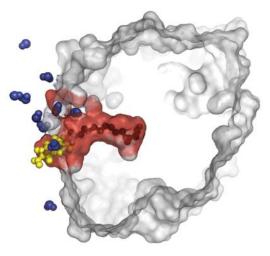


- Proteins with functional sites located in occluded cavities
- **Cognate ligands enter such sites via transport pathways tunnels**



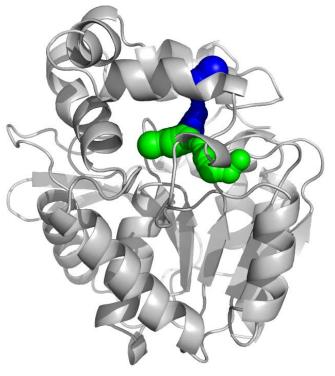
- Proteins with functional sites located in occluded cavities
- **Cognate ligands enter such sites via transport pathways tunnels**
- **Game basic questions** 
  - How widespread are the tunnels?
  - What types of tunnels do exist?
  - What are functional roles of the tunnels?

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- Some basic questions
  - How widespread are the tunnels?
  - What types of tunnels do exist?
  - What are functional roles of the tunnels?
- Hard to study
  - inaccessible to direct experiments
    => simulations needed



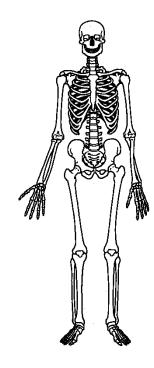
- Proteins with functional sites located in occluded cavities
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- Some basic questions
  - How widespread are the tunnels?
  - What types of tunnels do exist?
  - What are functional roles of the tunnels?
- Hard to study
  - inaccessible to direct experiments
    => simulations needed
- □ Need tools/methods to detect, evaluate and design the tunnels

- Software tool that accounts for protein dynamics while analyzing tunnels
  - to identify transient tunnels
  - to estimate importance of tunnels



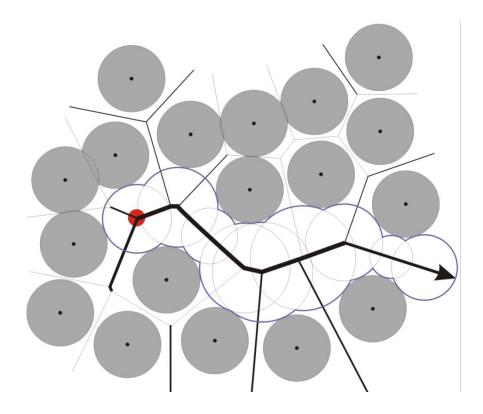
- **G** Software for analysis of tunnel dynamics
  - analysis of pathways in Voronoi diagrams





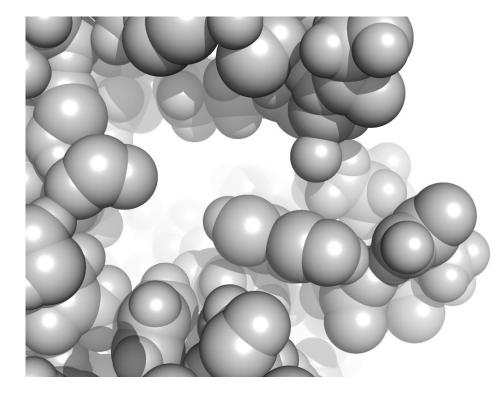
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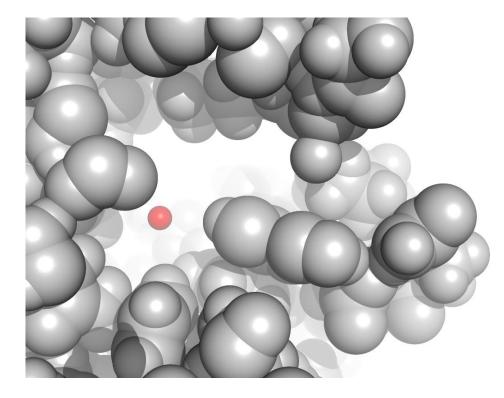
- **G** Software for analysis of tunnel dynamics
  - pathway from a cavity to the bulk solvent





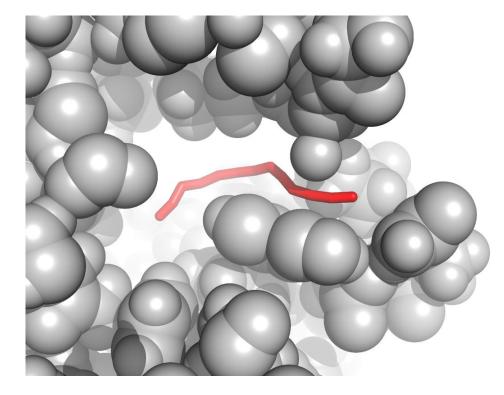
- **G** Software for analysis of tunnel dynamics
  - starting from a point in the cavity





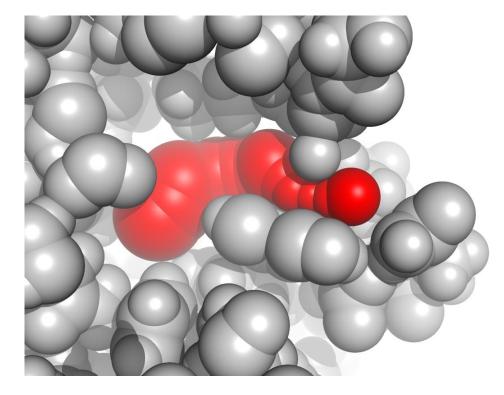
- **G** Software for analysis of tunnel dynamics
  - the shortest and widest pathway identified

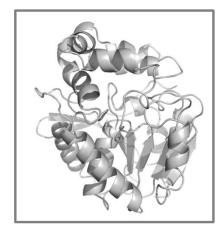




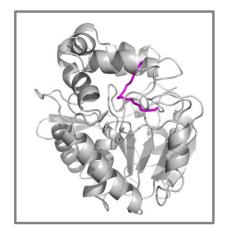
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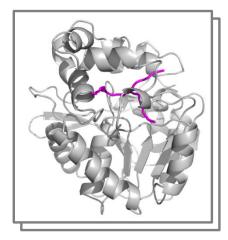




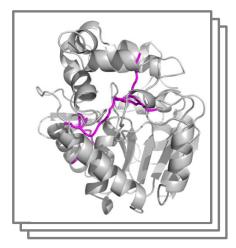




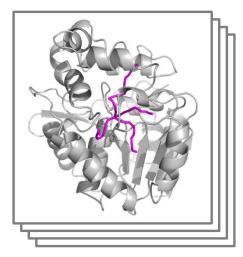




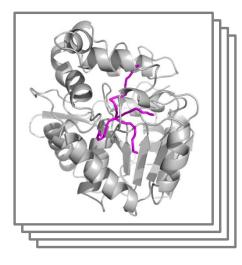


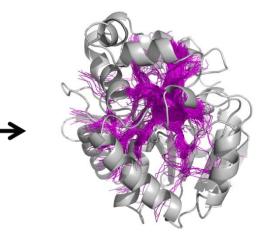






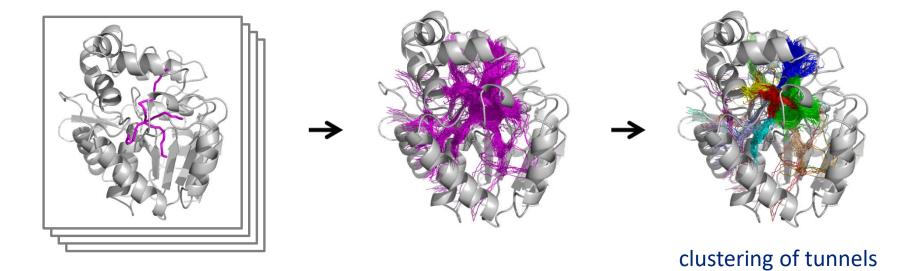




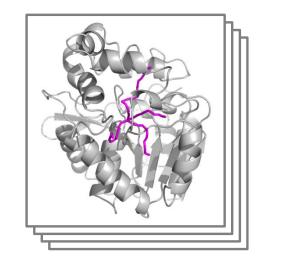


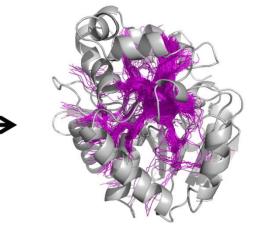
merging all identified tunnels

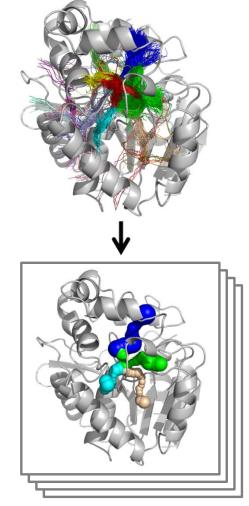








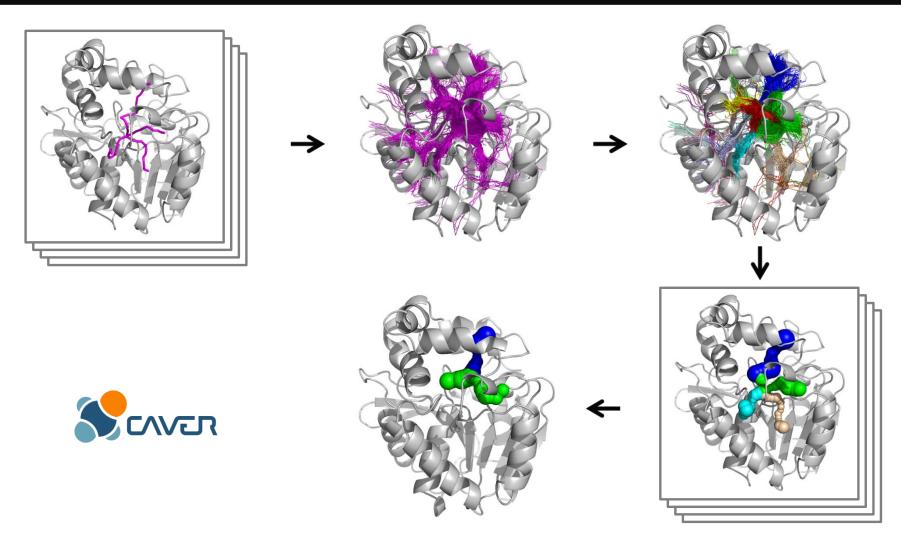






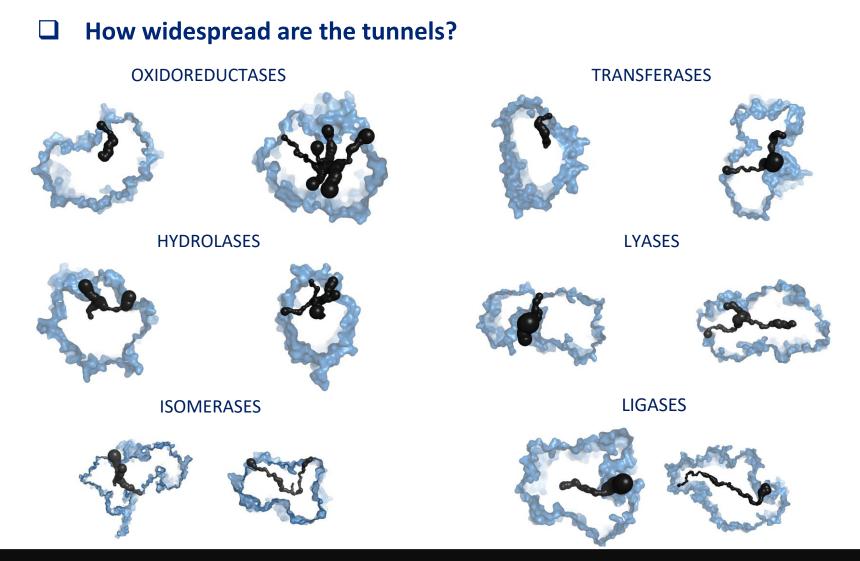


## **Ligand-transport pathways – software tools**



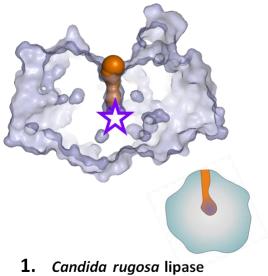
analysis of tunnel dynamics

# Ligand-transport pathways – spread



### Ligand-transport pathways – types

- What types of tunnels exist?
  - single tunnel connecting the active site cavity with the bulk solvent

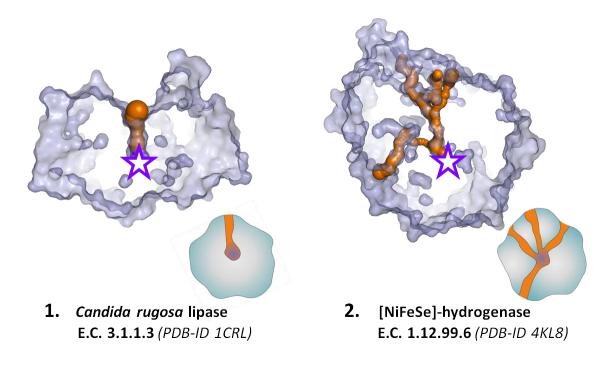


E.C. 3.1.1.3 (PDB-ID 1CRL)

Marques et al. 2016, Understanding Enzymes - Function, Design, Engineering and Analysis, PanStanford, pp. 421-464.

## Ligand-transport pathways – types

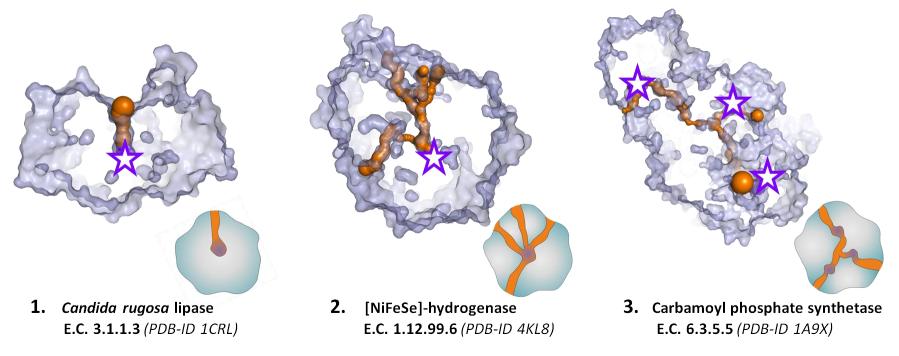
- What types of tunnels exist?
  - single tunnel connecting the active site cavity with the bulk solvent
  - multiple tunnels connecting the active site cavity with the bulk solvent



Marques et al. 2016, Understanding Enzymes - Function, Design, Engineering and Analysis, PanStanford, pp. 421-464.

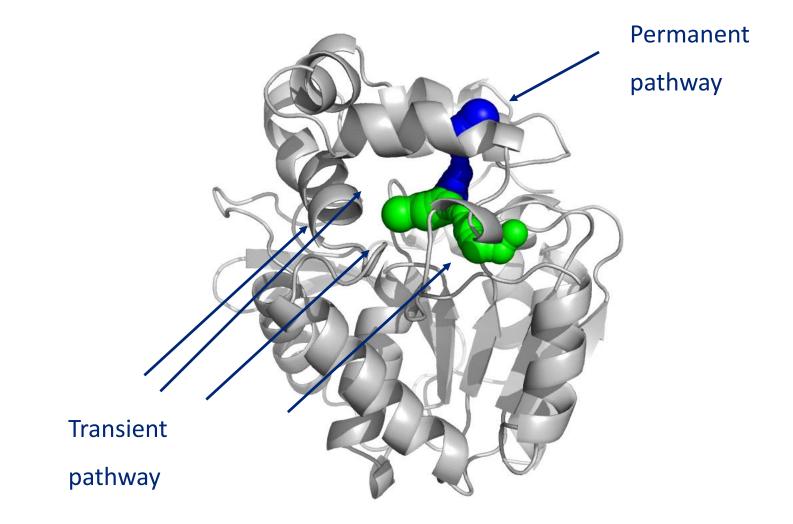
# Ligand-transport pathways – types

- What types of tunnels exist?
  - single tunnel connecting the active site cavity with the bulk solvent
  - multiple tunnels connecting the active site cavity with the bulk solvent
  - multiple tunnels connecting several active sites

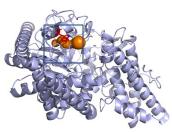


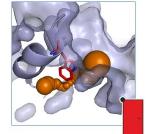
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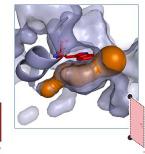
## **Ligand-transport pathways – dynamics**



# Ligand-transport pathways – gates





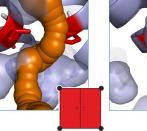


1.  $\alpha$ -amylase E.C. 2.4.1.18; PDB-ID 3N98

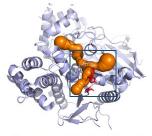




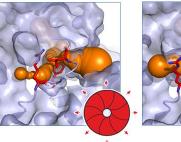
2. Methane monooxygenase hydroxylase E.C. 1.14.13.25; PDB-ID 1MHY, 1XVG

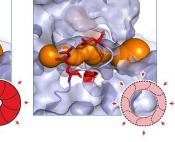




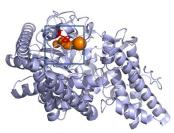


3. Acetylcholinesterase E.C. 3.1.1.7; PDB-ID 2XI4

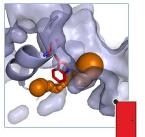


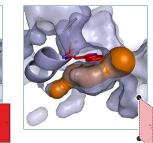


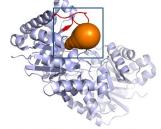
## Ligand-transport pathways – gates



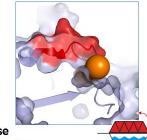
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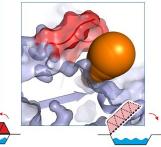


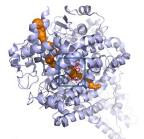




4. Triosephosphate isomerase E.C. 5.3.1.1; PDB-ID 1TIM, 1TPH

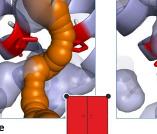


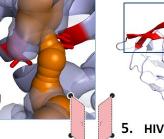


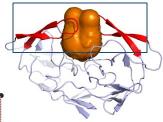




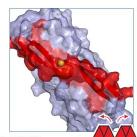
2. Methane monooxygenase hydroxylase E.C. 1.14.13.25; PDB-ID 1MHY, 1XVG

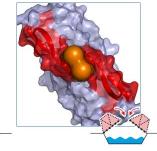


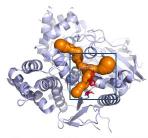




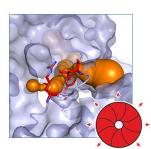
**HIV Protease** E.C. 3.4.23.16; PDB-ID 1HVR, 2PC0

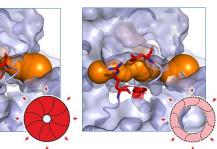


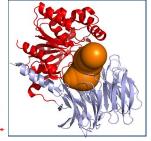




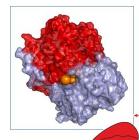
3. Acetylcholinesterase E.C. 3.1.1.7; PDB-ID 2XI4

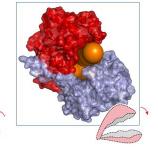




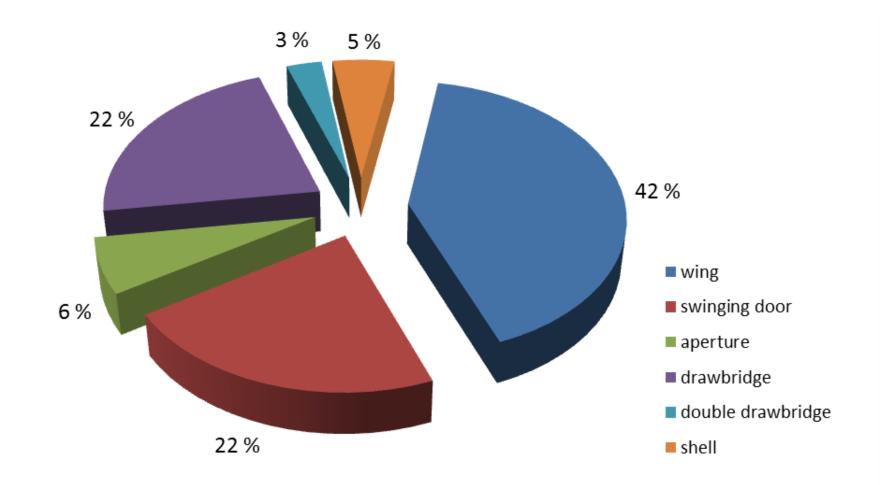


6. Acylaminoacyl peptidase E.C. 3.4.19.1; PDB-ID 304G



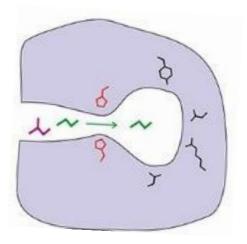


### Ligand-transport pathways – gates

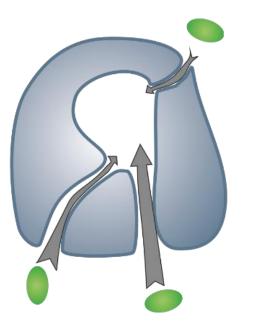


Gora et al. 2013, Chem. Rev. 113: 5871–5923.

- What are functional roles of the tunnels?
  - control the ligands entry and release to/from the active site

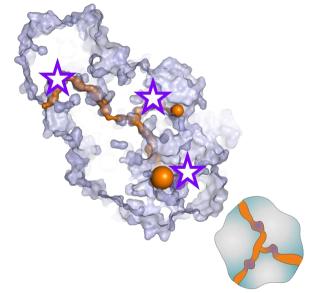


- What are functional roles of the tunnels?
  - control the ligands entry and release to/from the active site
  - synchronize reactions requiring contact of multiple substrates or cofactors



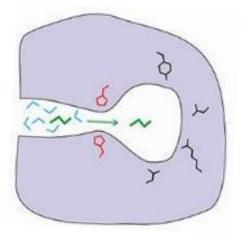
#### What are functional roles of the tunnels?

- control the ligands entry and release to/from the active site
- synchronize reactions requiring contact of multiple substrates or cofactors
- prevent potentially toxic intermediates to be released into the medium
- avoid labile intermediates to be released into the medium and undergo side reactions



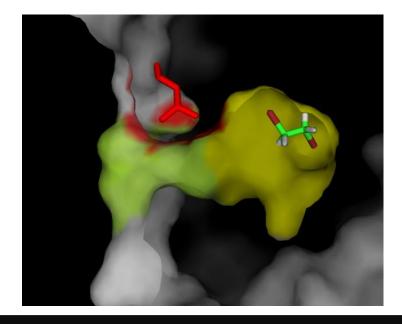
#### What are functional roles of the tunnels?

- control the ligands entry and release to/from the active site
- synchronize reactions requiring contact of multiple substrates or cofactors
- prevent potentially toxic intermediates to be released into the medium
- avoid labile intermediates to be released into the medium and undergo side reactions
- control access of various solvents to the active sites
- prevents dissipation of electrons by solvent



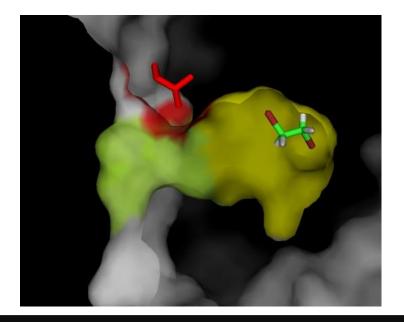
Mutations in existing pathways

Mutations in existing pathways



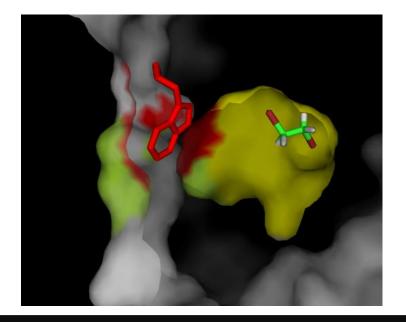
### Mutations in existing pathways

alter properties permanent pathways



#### Mutations in existing pathways

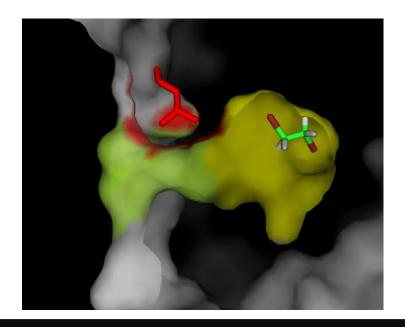
- alter properties permanent pathways
- introduce gate (permanent -> transient)



Koudelakova et al. 2013, Angew. Chem. Int. Ed Engl. 52: 1959–1963. Marques et al. 2017, J. Chem. Inf. Model. 50: 1970–1989.

#### Mutations in existing pathways

- alter properties permanent pathways
- introduce gate (permanent -> transient)
- remove gate (transient -> permanent)
- modulate gating frequency or amplitude



Liskova et al. 2015, ChemCatChem 7: 648–659.

#### Mutations in existing pathways

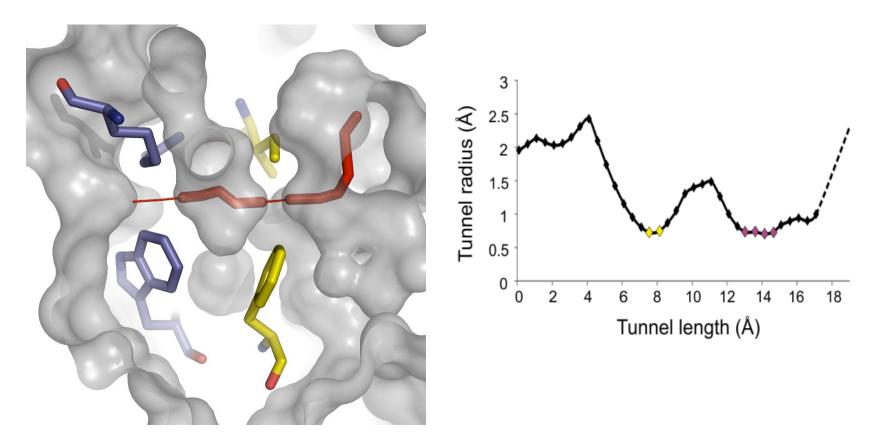
- alter properties permanent pathways
- introduce gate (permanent -> transient)
- remove gate (transient -> permanent)
- modulate gating frequency or amplitude

### **Gain-of-function mutations in potential pathways**

activate new functional pathways

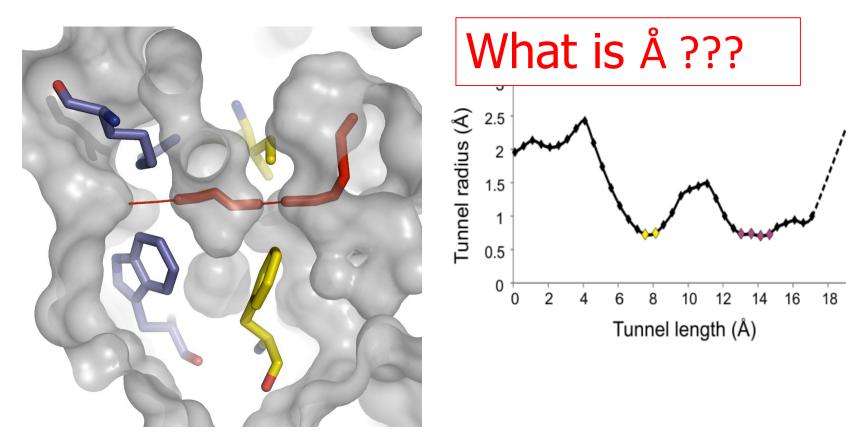
#### **D** Potential pathways – globular proteins

leading through voids of proteins with only sub-Å dimension



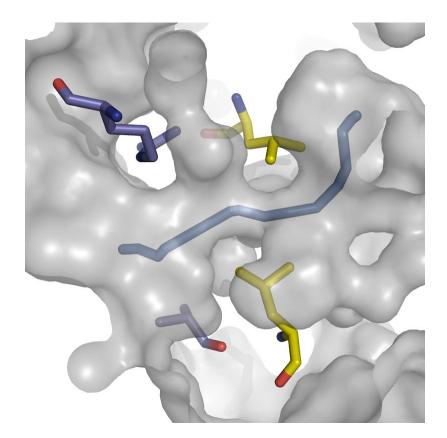
#### Potential pathways – globular proteins

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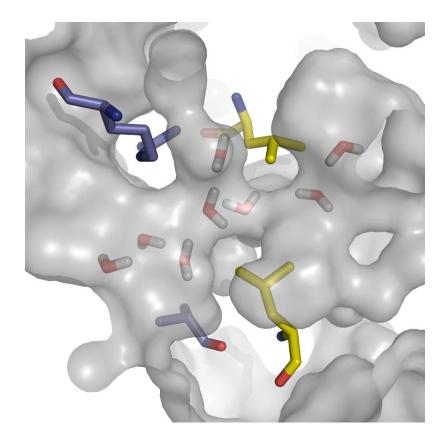
#### **D** Potential pathways – globular proteins

upon gain-of-function mutations, leading to well-defined tunnel



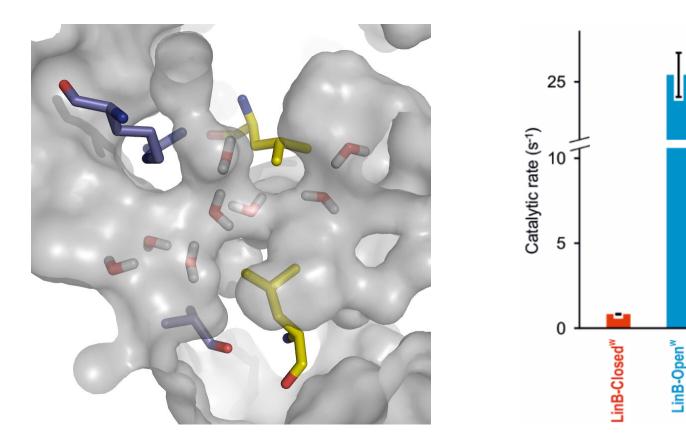
#### **D** Potential pathways – globular proteins

• the open tunnel enables efficient transport of waters to the active site

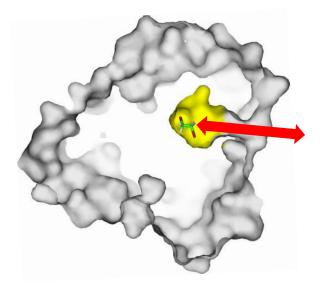


#### **D** Potential pathways – globular proteins

the opening of the tunnel have profound functional consequences

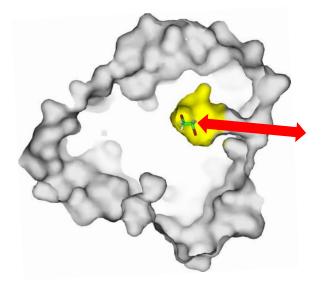


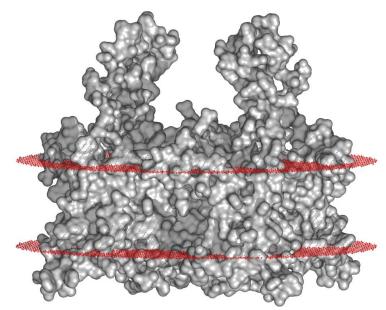
### Soluble/globular proteins



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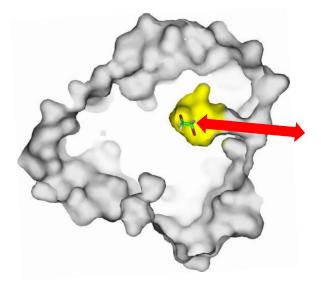
### Transmembrane proteins

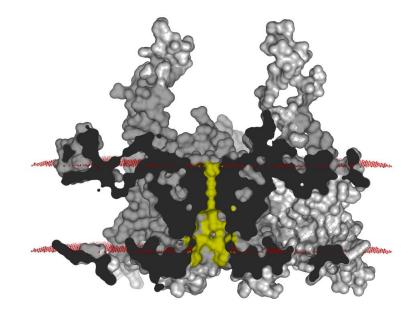




### Soluble/globular proteins

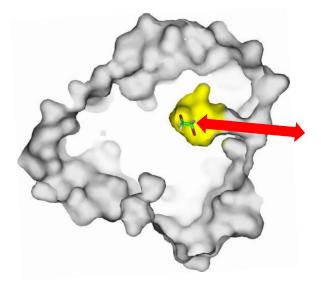
### Transmembrane proteins

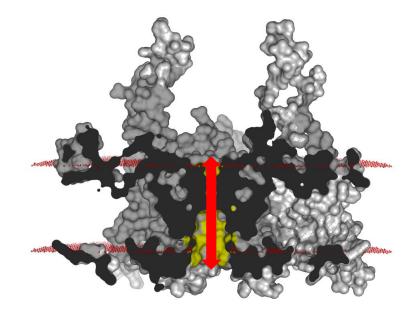




### Soluble/globular proteins

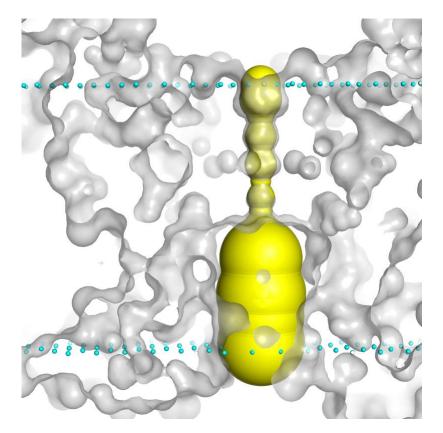
### Transmembrane proteins





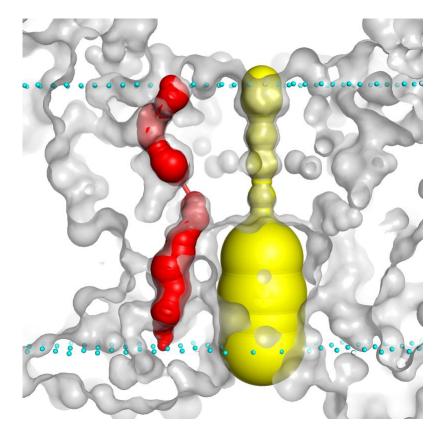
### **D** Potential pathways – transmembrane channels

leading through voids of proteins with only sub-Å dimension



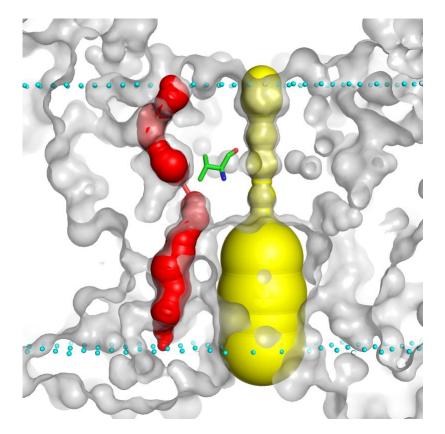
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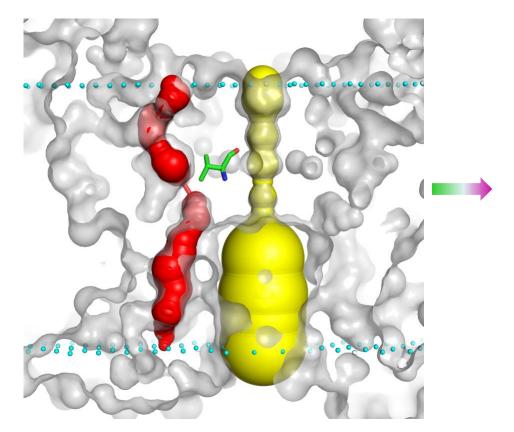
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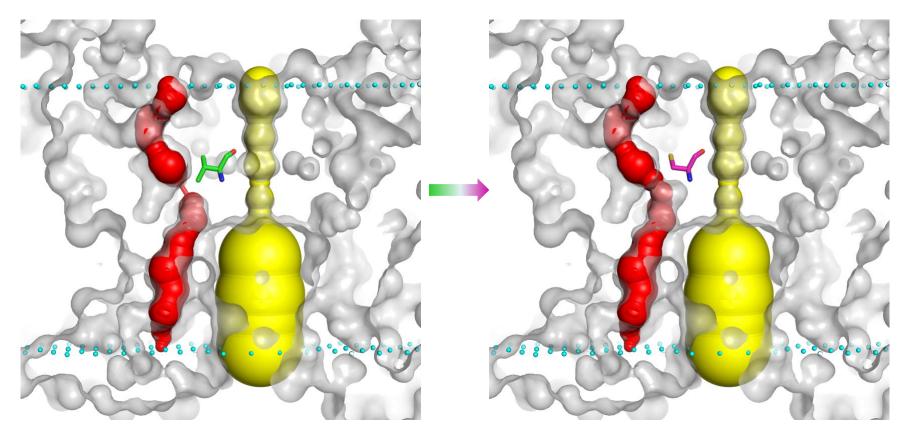
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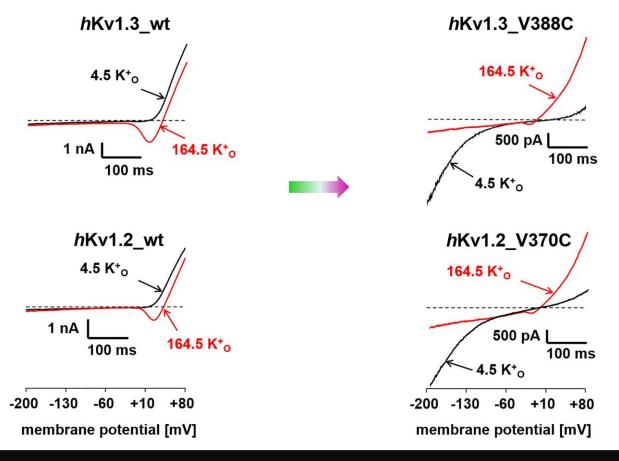
### **D** Potential pathways – transmembrane channels

viable upon gain-of-function mutations



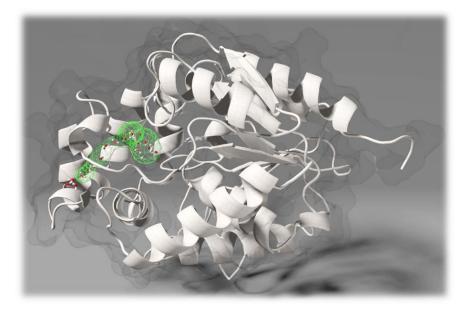
### **D** Potential pathways – transmembrane channels

notable functional consequences



# **Gain-of-function mutations in water pathways**

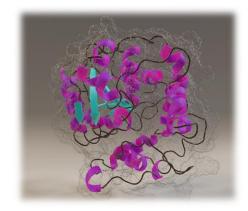
- hydrolytic enzymes require water for their catalytic action
- water migrate via internal tunnel network
- despite its vital role, water transport has been largely neglected due to difficulties in tracking those rare phenomena



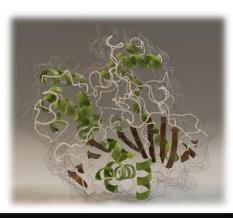
# Gain-of-function mutations in water pathways

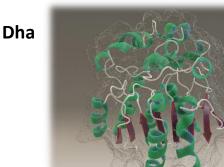
 extensive MD simulations (5 μs) of three members of the hydrolase superfamily

- haloalkane dehalogenase from *Rhodococcus rhodochrous* (Dha)
- potato epoxide hydrolase 1 (Epx)
- lipase from Candida rugose (Lip)



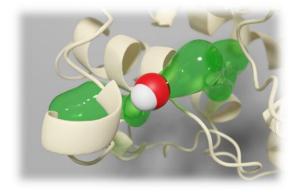
Ерх

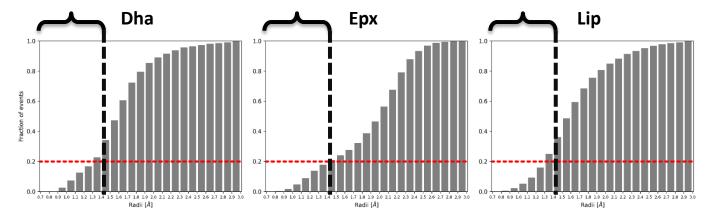




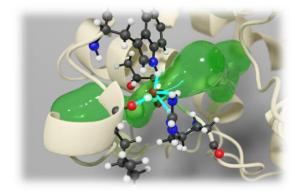
Lip

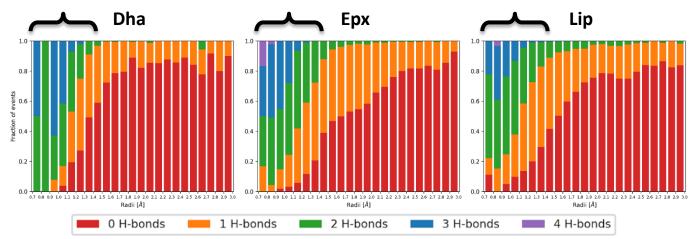
~20% of water travels through unexpectedly narrow tunnels (bottleneck radius <1.4 Å)</p>





multiple H-bonds stabilize water transport via such narrow tunnels

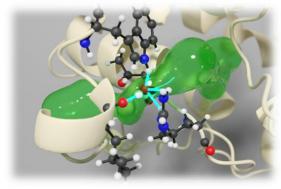


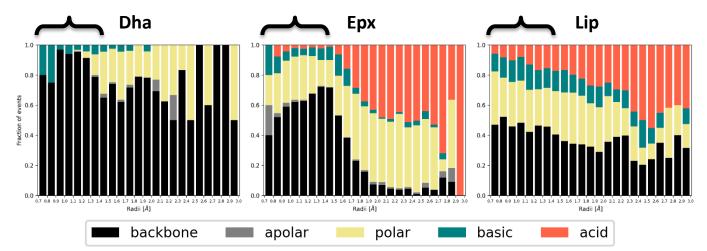


#### => New functionally relevant sites

Sequeiros-Borja et al., in preparation

□ these H-bond are mainly formed with backbone atoms

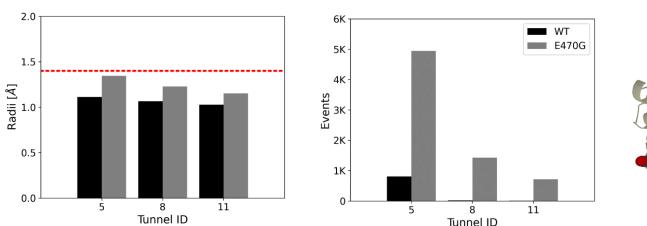


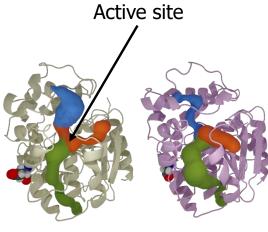


=> Conservation of paths within a protein fold

Sequeiros-Borja et al., in preparation

- human epoxide hydrolase pathology: mutation E470G remote from active site => increased catalytic activity; associated with higher stroke incidence
- simulations showed visible differences in the three narrow tunnels
- facilitates water transport => significantly increasing availability of water cosubstrates for catalytic action of the enzyme





### => Novel indicator of mutation hot-spots

Sequeiros-Borja et al., in preparation

# Ligand-transport pathways – pathology

#### **Only rarely considered when interpreting molecular bases of diseases**

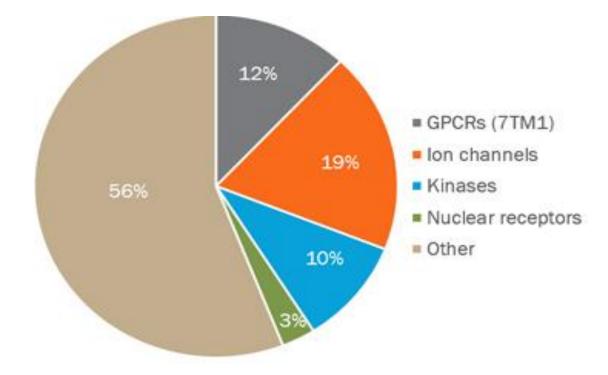
- tunnels in soluble proteins have been accepted as functionally important just recently
- hindered by the lack of information on the presence of transient tunnels and potential ones with high propensity for opening

# Pathologies linked to ligand-transport pathways

| Protein   | Disease/pathology   |
|---|---|
| Dihydroorotate dehydrogenase                        | autoimmune and parasitic diseases,<br>immunosuppression, cancer, inflammation   |
| Nitric oxide synthase                               | neurological diseases, inflammation, rheumatoid<br>arthritis, immune-type diabetes, stroke, cancer,<br>thrombosis, infection susceptibilities |
| Glycogen phosphorylase                              | diabetes  |
| Leukotriene-A4 hydrolase                            | inflammatory diseases   |
| Neurolysin  | nervous and endocrine systems disorders   |
| Plasma cholesteryl ester<br>transfer protein CETP   | atherosclerosis   |
| β-hydroxyacyl-acyl carrier protein dehydratase FabZ | gastric diseases  |
| voltage-gated Na, K, Ca<br>channels                 | periodic paralyses, mixed arrhythmias, dilated cardiomyopathy, neuronal hyperexcitability,  |

#### **U** Tunnels promising targets in drug discovery

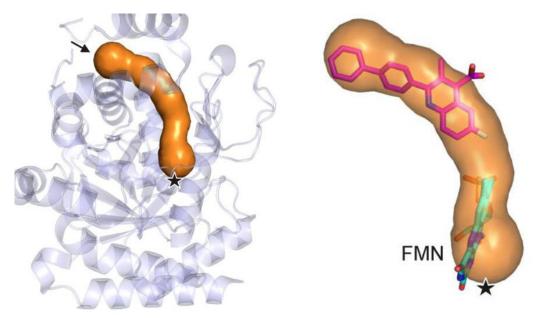
- new functional locations to target
- selective drugs due to relatively lower evolutionary conservation



Marques et al. 2016, Med. Res. Rev. 37: 1095-1139 Santos et al. 2017, Nat. Rev. Drug Discov. 16: 19-34

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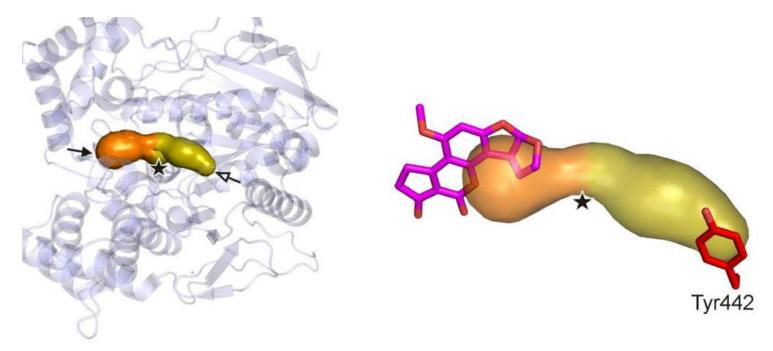


Dihydroorotate dehydrogenase inhibited by *brequinar* analog. While the active sites of the these enzymes in human and pathogenic species (e.g. *Plasmodium falciparum* or *Helicobacter pylori*) closely resemble one another, their access tunnels differ markedly.

Marques et al. 2016, Med. Res. Rev. 37: 1095-1139

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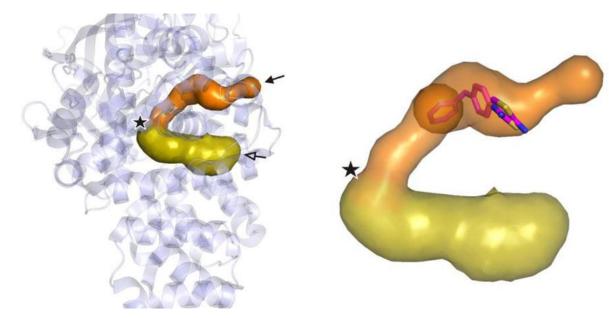


*Aflatoxin* blocking the main tunnel of Acetylcholinesterase, the secondary transient tunnel gated by Tyr442 still enables residual activity.

Marques et al. 2016, Med. Res. Rev. 37: 1095-1139

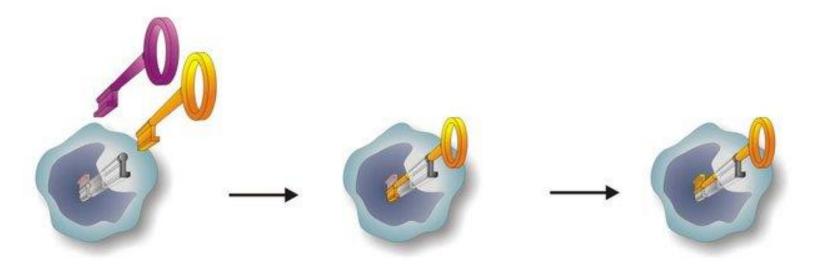
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*ARM1* inhibitor blocking the tunnel used for the access of LTA4 substrate to Leukotriene A4 hydrolase/aminopeptidase, while leaving the transport path for PGP unaffected.

□ Ligand-transport pathways are of functional importance not only in transmembrane proteins but also in a wide range of soluble proteins



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- handful of conservative mutations
- pronounced functional impact
- in regions otherwise functionally irrelevant

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  - engineer enzymes with improved properties for various biotechnologies
  - discover novel mutations linked to the development of various diseases

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#### Pathways represents interesting targets for drug discovery