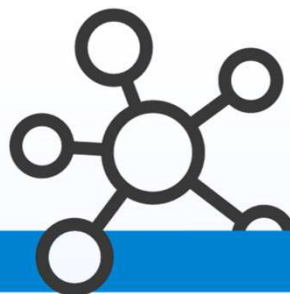


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# EJIBCE

2018

Encontro de Jovens Investigadores de Biologia Computacional Estrutural  
Faculdade de Medicina da Universidade do Porto

## Changing the Paradigm in Petroleum Industry: Enhancing the catalytic rate of DszD by QM/MM calculations

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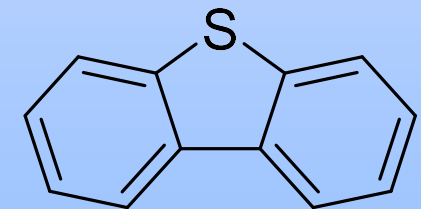
# 1. Background

# 1. Background

3

## The problem:

- ▶ Sulfur compounds are present in crude oil in concentrations between 0.1 and 8% (w/w).
- ▶ Legal restrictions in increasingly more nations regarding the sulfur content in fossil fuels.
- ▶ The main method to desulfurize crude oil is the energetically expensive chemical hydrodesulfurization (HDS).
  - ▶ High temperature and high pressure



**Fig 1.** Chemical structure of dibenzothiophene (DBT)

# 1. Background

4

## The alternative:

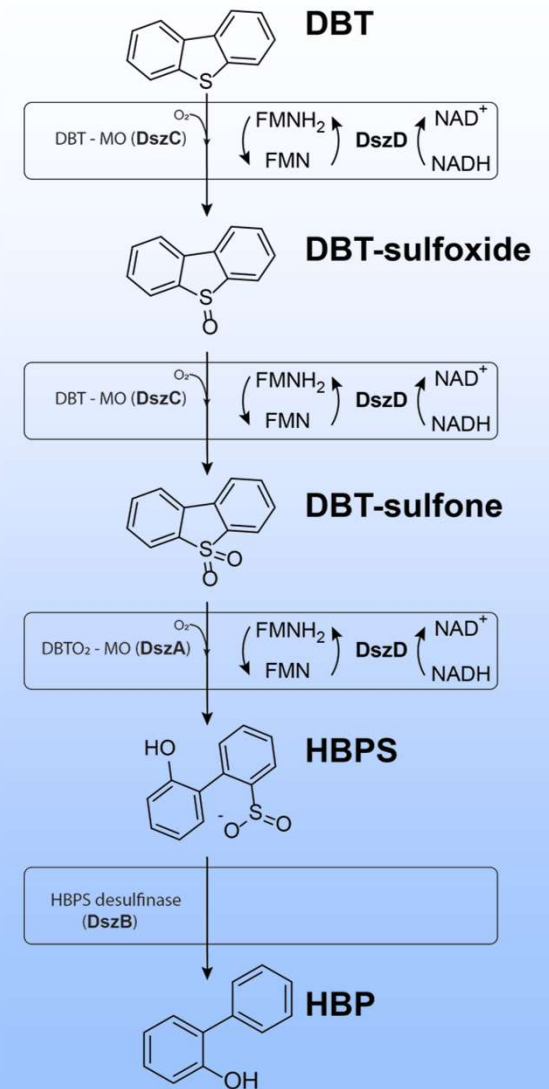
- ▶ Biocatalytic desulfurization (BDS)
  - ▶ Explores the process “4S pathway” of *Rhodococcus erythropolis*
    - ▶ Uses DBT as a source of sulfur
  - ▶ Maintains the energetic value of the oil
  - ▶ Much cheaper than HDS
  - ▶ Does not produce undesirable by products
  - ▶ **PROBLEM:**
    - ▶ Catalytic rate not attractive for industrial application

# 1. Background

5

## 4S pathway

- Desulfurization of DBT to 2'-hydroxybiphenyl
- Carried out by four enzymes of *Rhodococcus erythropolis*:
  - DszA
  - DszB
  - DszC
  - DszD



# 1. Background

6

## DszD

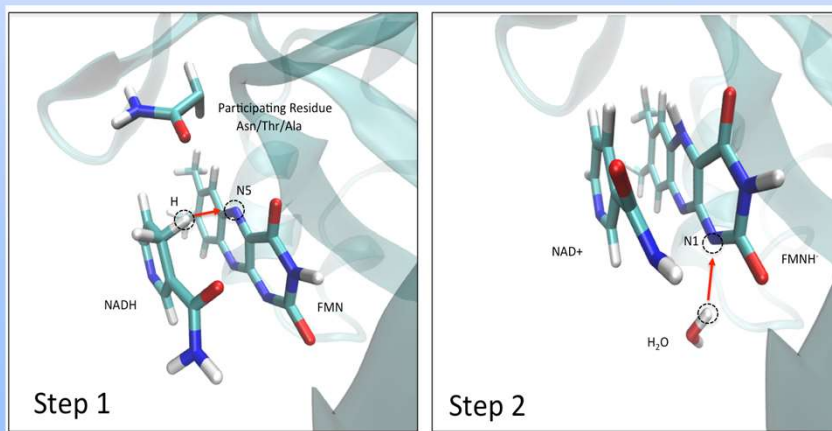
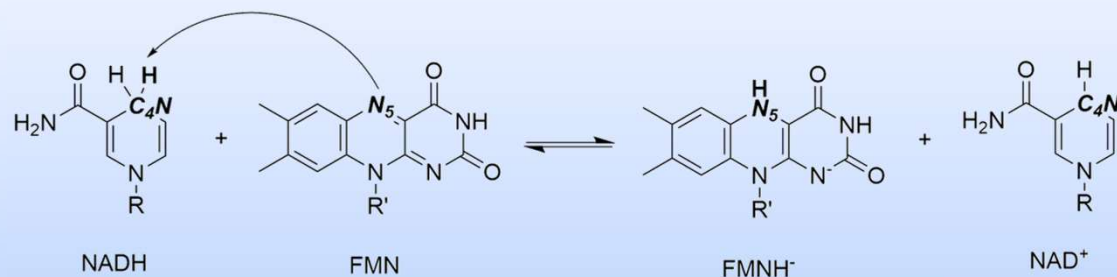


- Responsible for supplying FMNH<sub>2</sub> in the 4S pathway
- Overexpression of DszD improves the catalytic rate of the whole pathway
- Experimental studies revealed the importance of Thr<sup>62</sup>
- Mutation of Thr<sup>62</sup> by Asn and Thr improved the catalytic rate

# 1. Background

7

DszD



Sérgio F. Sousa et al. *The Journal of Physical Chemistry A* **2016** 120 (27), 5300-5306

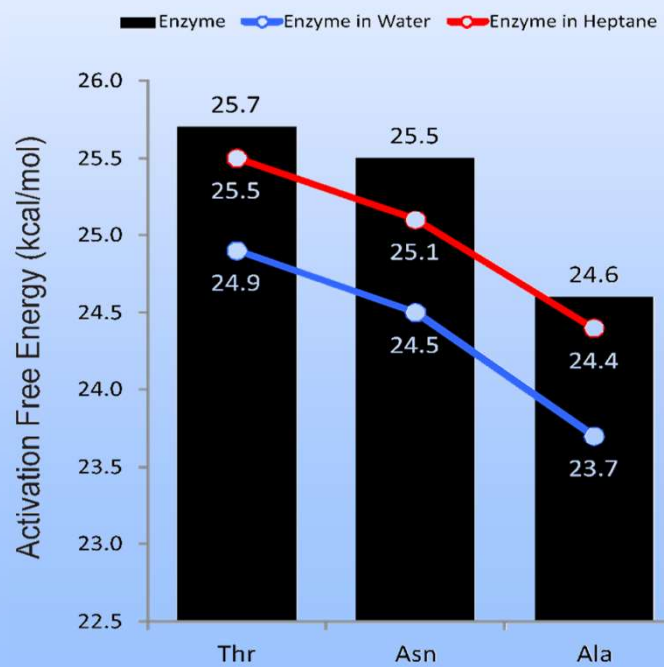
# 1. Background

8

DszD



Step 1 - Activation Free Energy



Sérgio F. Sousa et al. *The Journal of Physical Chemistry A* **2016** 120 (27), 5300-5306



# 1. Background

9

## Goal

- ▶ Attempt to find ways to accelerate the limiting step of the DszD reaction using hybrid quantum mechanics/molecular mechanics (QM/MM) methods, by systematic mutation of Thr62 for 18 different amino acid residues.

## 2. Methods

## 2. Methods

11

### Mutations

- Mutation of the participating residue by all amino acids
- Using pymol mutation feature
- *Dunbrack rotamer library* of rotamers

### Minimization

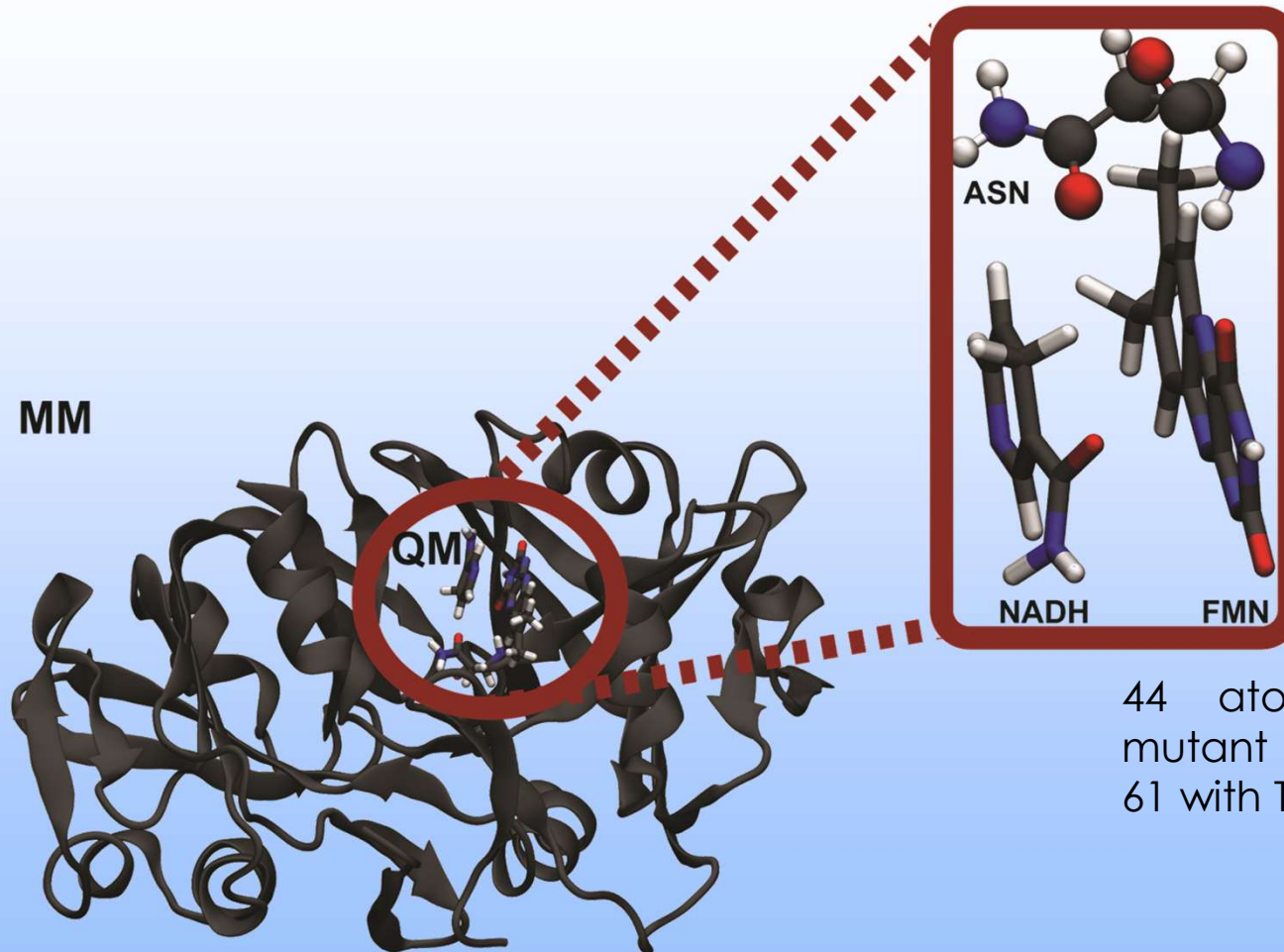
- Minimization of the mutated residue

### ONIOM

- Optimization of the reactants
- Linear transit scan of the rate limiting step
- Characterization of the transition state
- Intrinsic reaction coordinate (IRC) calculations to find the minima
- Final energies at B3LYP-D3/6-31 1++G(2d,2p):FF99SB//B3LYP/6-31G(d):FF99SB

## 2. Methods

12

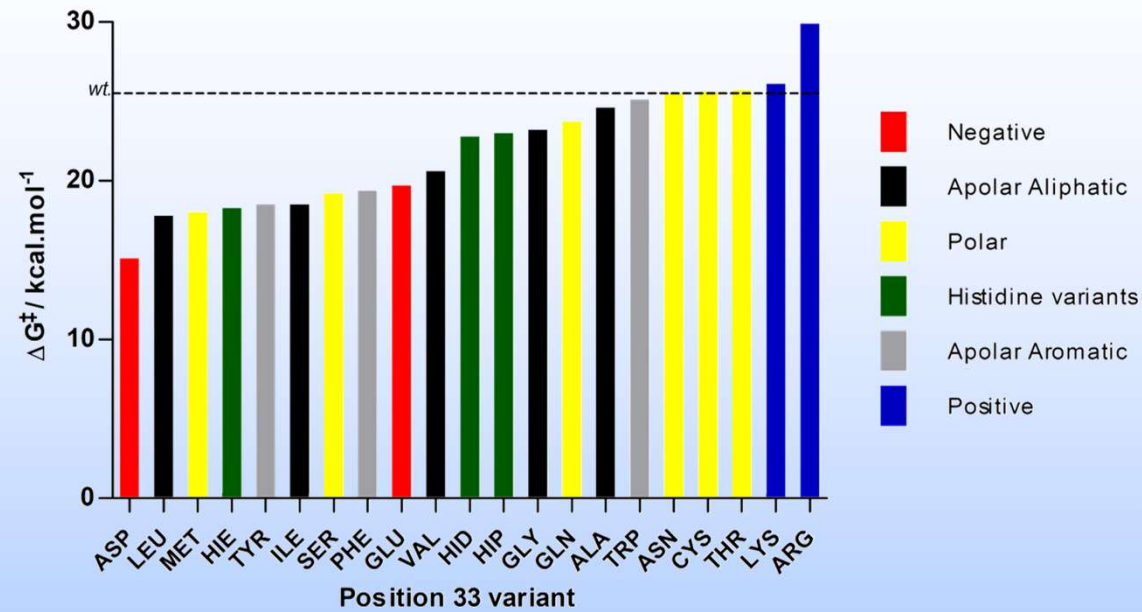


44 atoms in the mutant with Gly to 61 with Trp

# 3. Results

# 3. Results

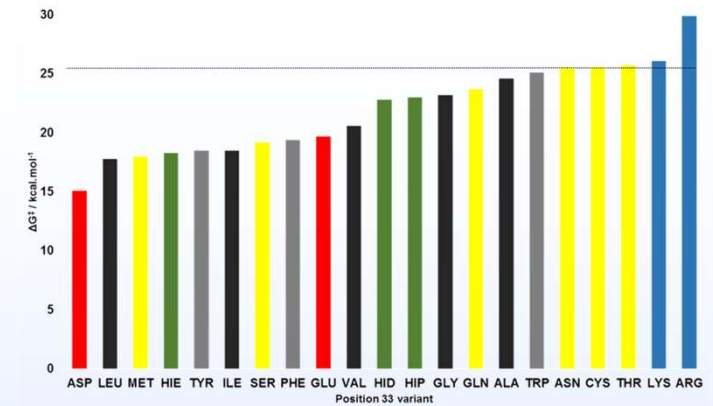
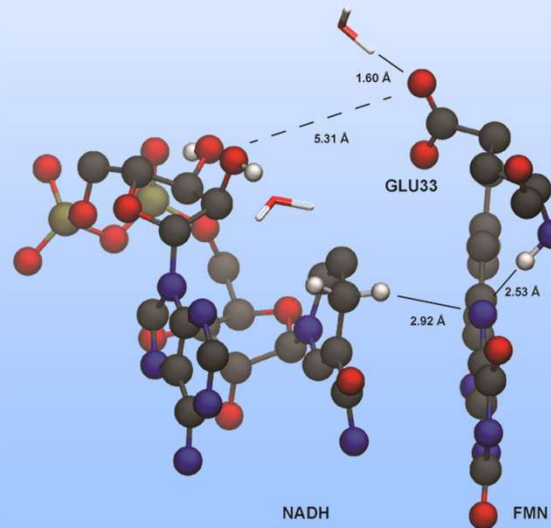
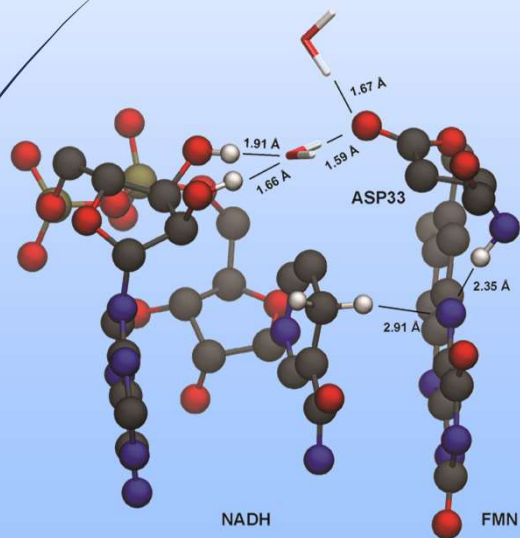
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- ▶ The results confirm the potential that the reaction rate of DszD has to be enhanced through
- ▶ A direct correlation between the “type” of the residue and the activation free energy of the reaction cannot be drawn

### 3. Results

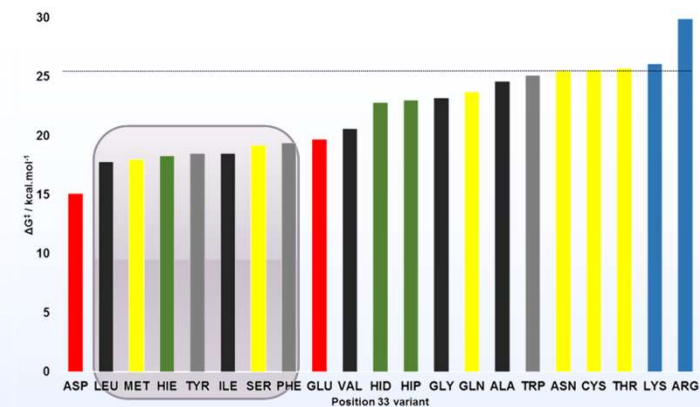
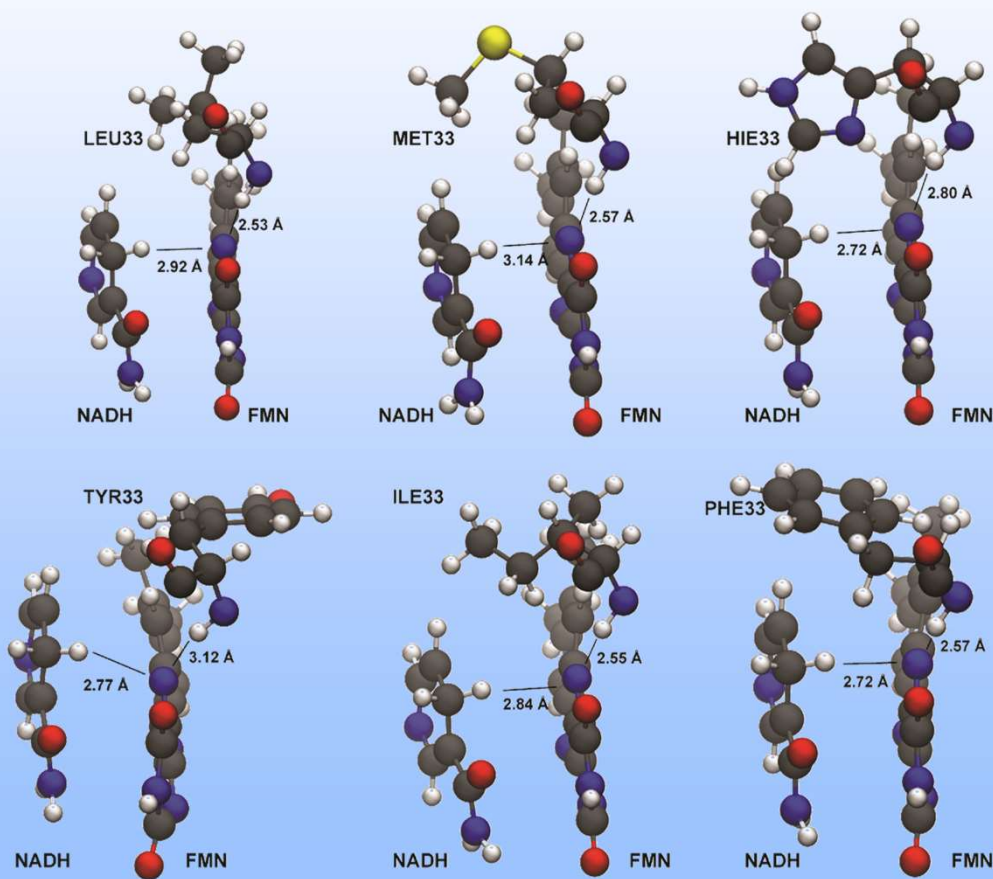
#### Structural analysis



- Negative charge may stabilize NAD<sup>+</sup>
- Hydrogen bonding system between water, ASP and NAD<sup>+</sup> is unique
- GLU is farther from NADH than ASP which may explain the higher activation barrier

# 3. Results

## Structural analysis

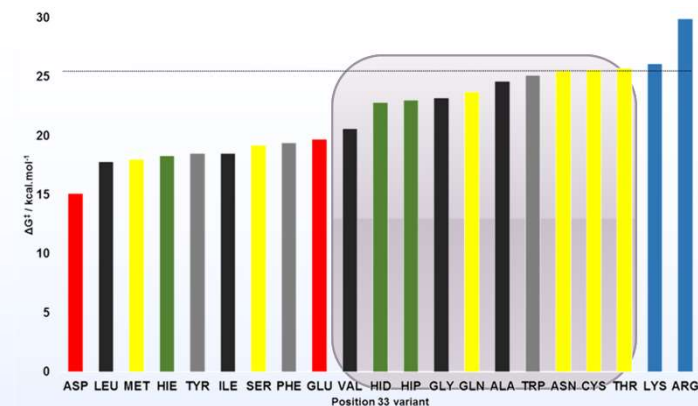
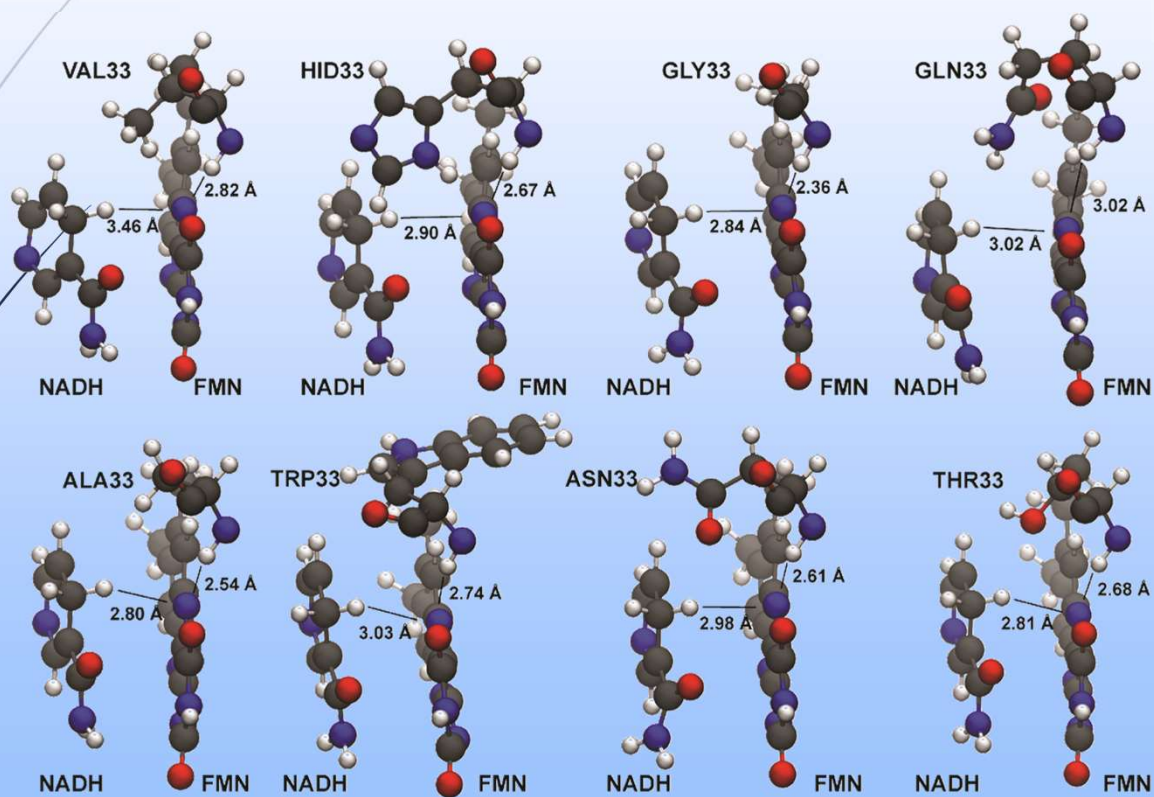


- Side chains stay far from the reaction coordinate
- Conformation of the side chains seem to lock NADH in place.
- Hydrogen bond NH—N5 in the variant with TYR is the weakest of all variants → less stabilization of the reactants structure → reactants and TS energetically closer



# 3. Results

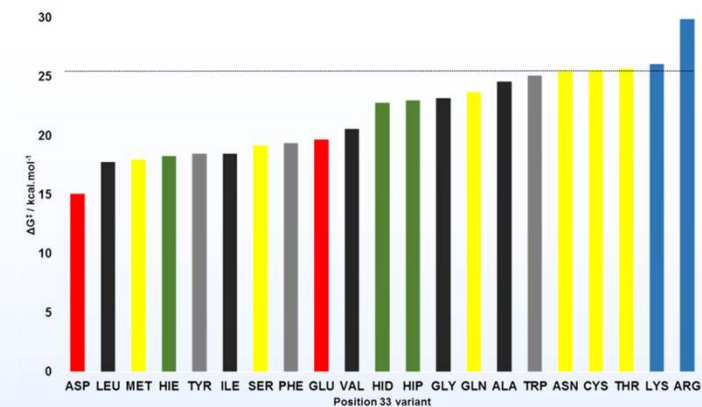
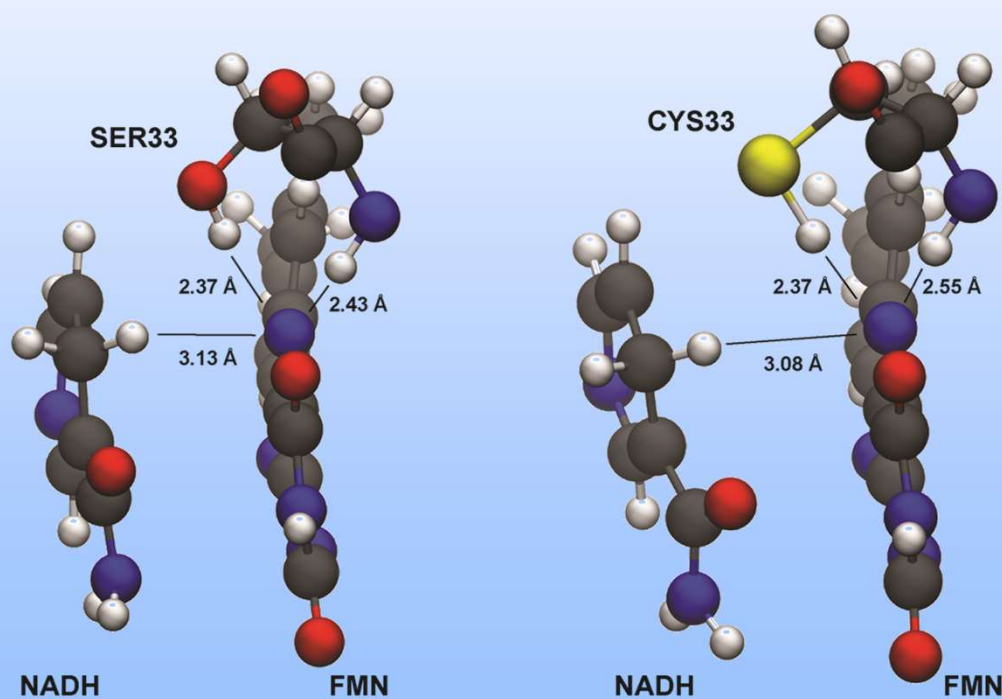
## Structural analysis



- Short or no side chains like those of VAL, ALA and GLY seem to let NADH misalign with respect to FMN
- Polar groups directly pointing to the reaction coordinate, may impair the free flow of the electron to be transferred

### 3. Results

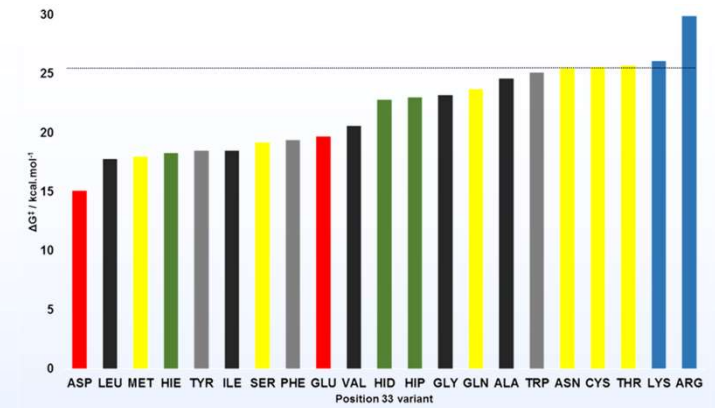
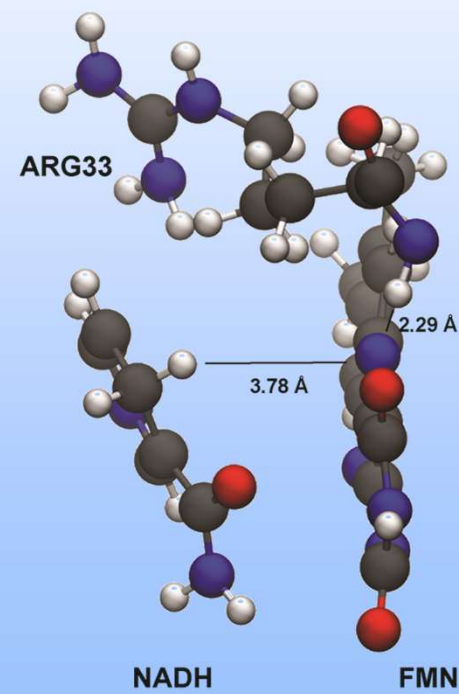
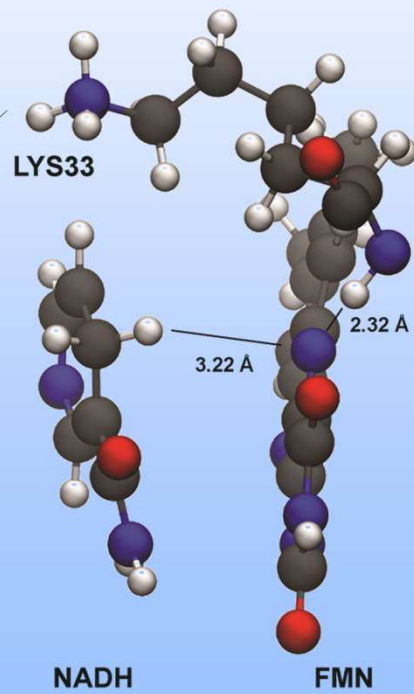
#### Structural analysis



- Misalignment of NADH towards FMN in the variant with CYS
- Hydrogen bond between the  $\text{NH}_{\text{res33}} - \text{N5}_{\text{FMN}}$  weakens more from R  $\rightarrow$  TS with CYS (2.55 Å  $\rightarrow$  2.74 Å) than with SER (2.43 Å  $\rightarrow$  2.54 Å)
- Hydrogen bond  $\text{OH}_{\text{Ser}} - \text{N5}_{\text{FMN}}$  is stronger in the TS than in the reactants

# 3. Results

## Structural analysis

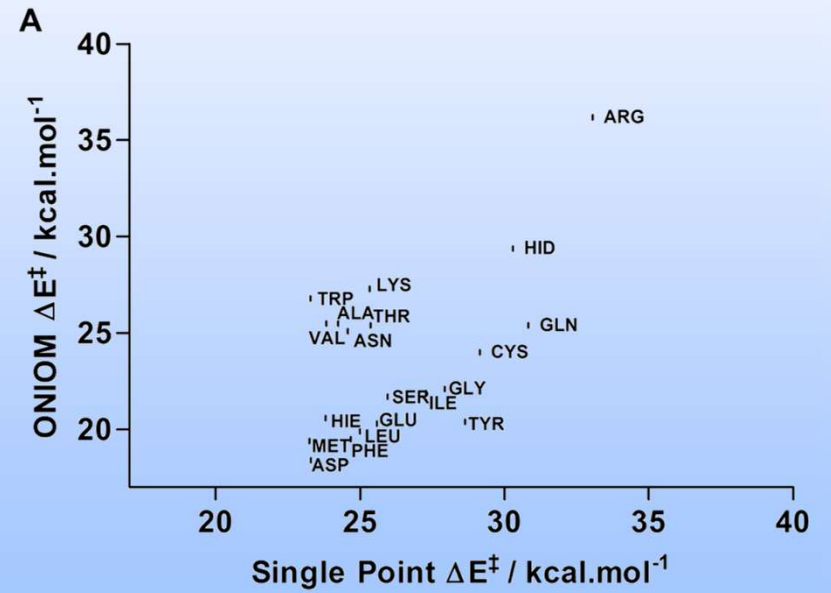
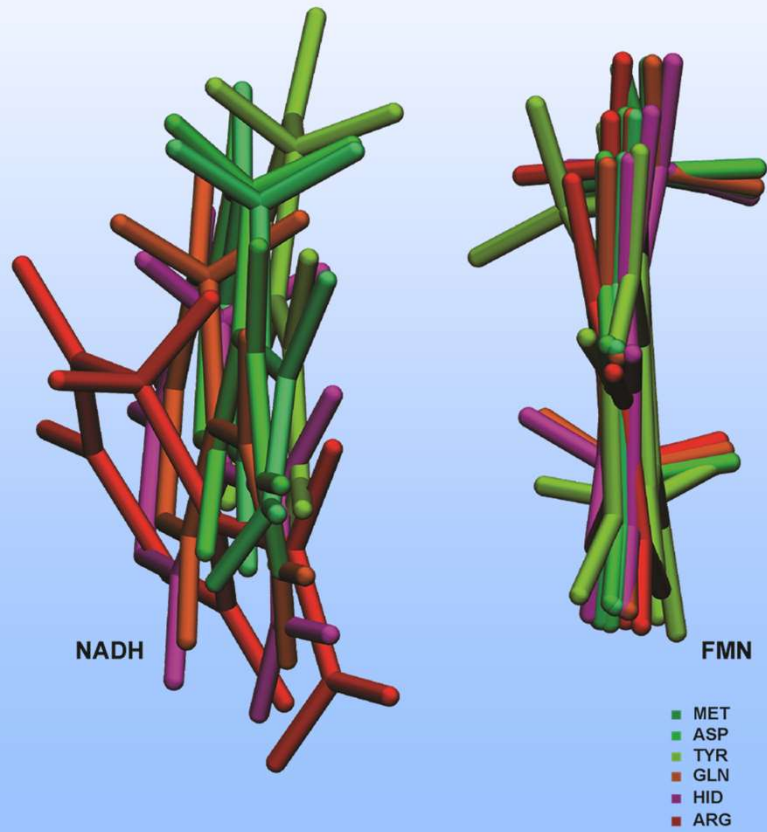


- Positive charge of these residues are pointing to NADH which is oxidized to NAD<sup>+</sup> with the loss of the hydride
- Very bulky residues

# 3. Results

20

## Structural analysis



# 4. Conclusions

## 4. Conclusions

22

- ▶ The spectator residue seems to slow down the reaction
- ▶ The catalytic rate of DszD can be greatly enhanced through point mutations of the spectator residue
- ▶ Enhancement of the other enzymes of the 4S pathway is mandatory to make the 4S pathway industrially attractive comparatively to the chemical processes currently used.



# 5. Acknowledgements

23



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