



Investigating the microbial biodegradation of polyfluoroalkyl substances (PFAS) by molecular docking and molecular dynamic simulations

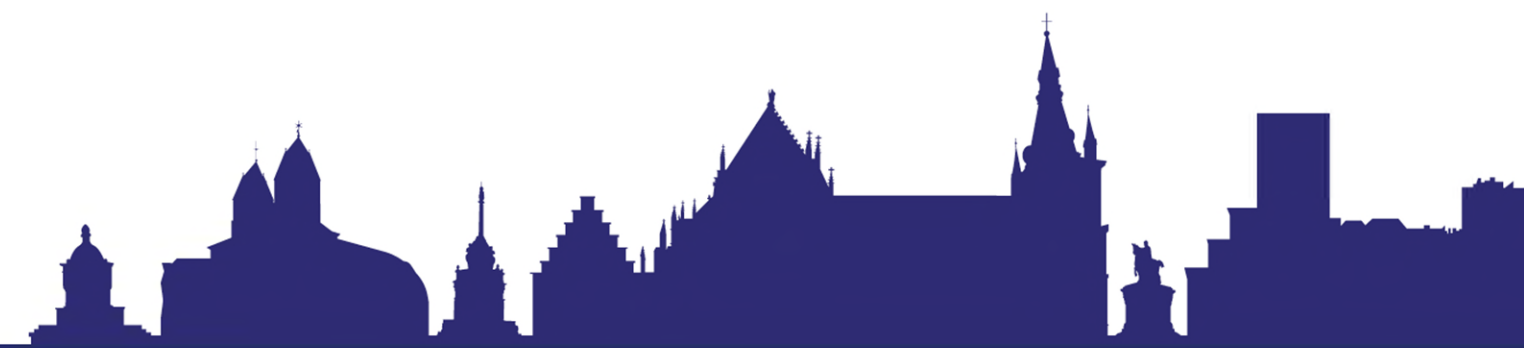
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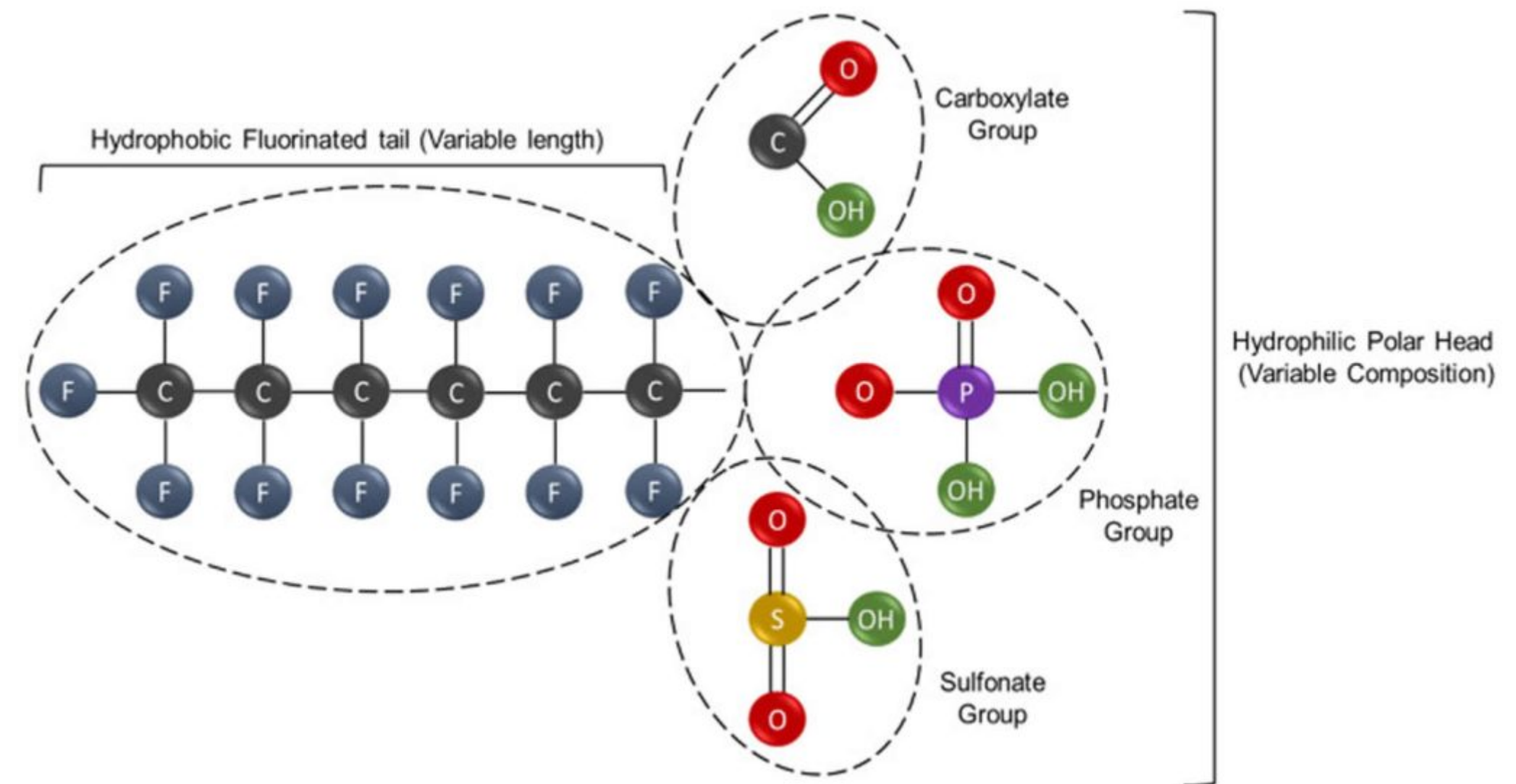


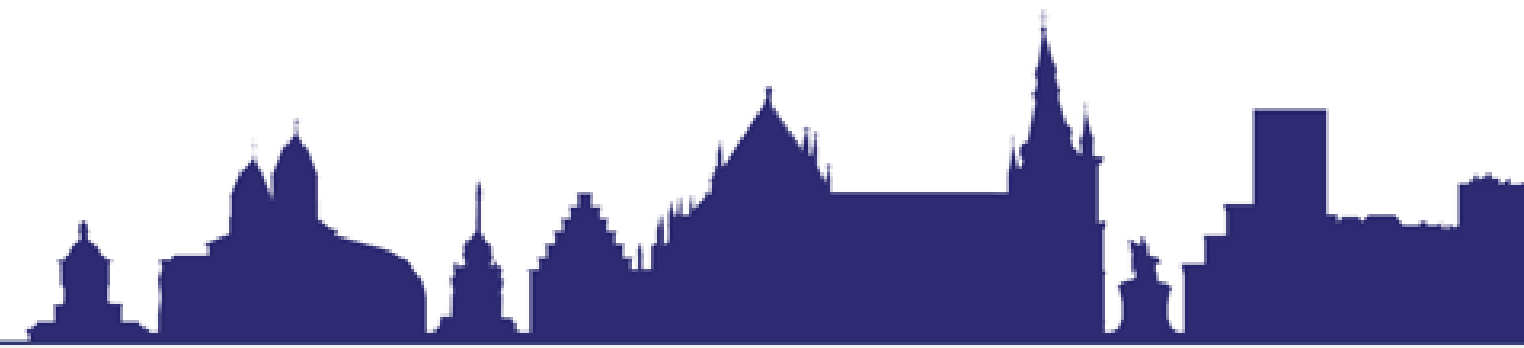
EBIC Environmental
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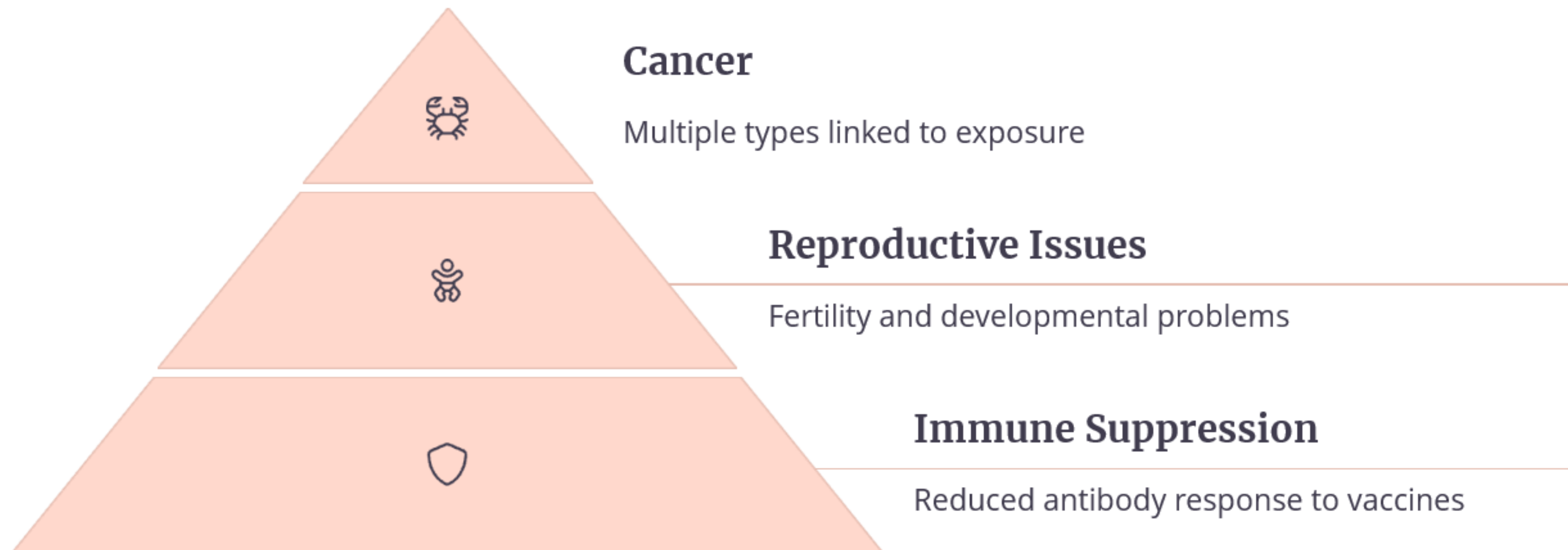
What is PFAS?

- Over 170 PFAS substances
- “Forever chemicals” due to strong C-F bond
- Found in everyday products from cookware to cosmetics
- Bioaccumulate in the environment and living organisms
- Significant technical challenges for PFAS removal





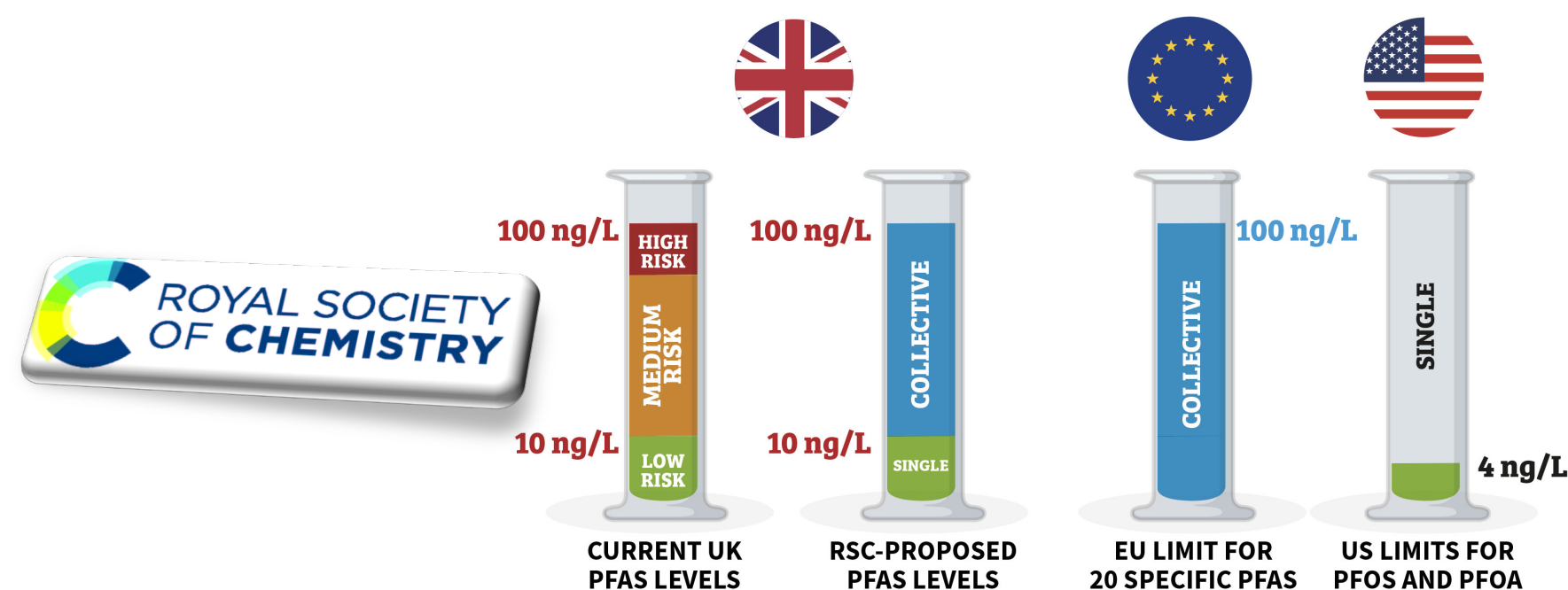
Health & Environmental Risks of PFAS

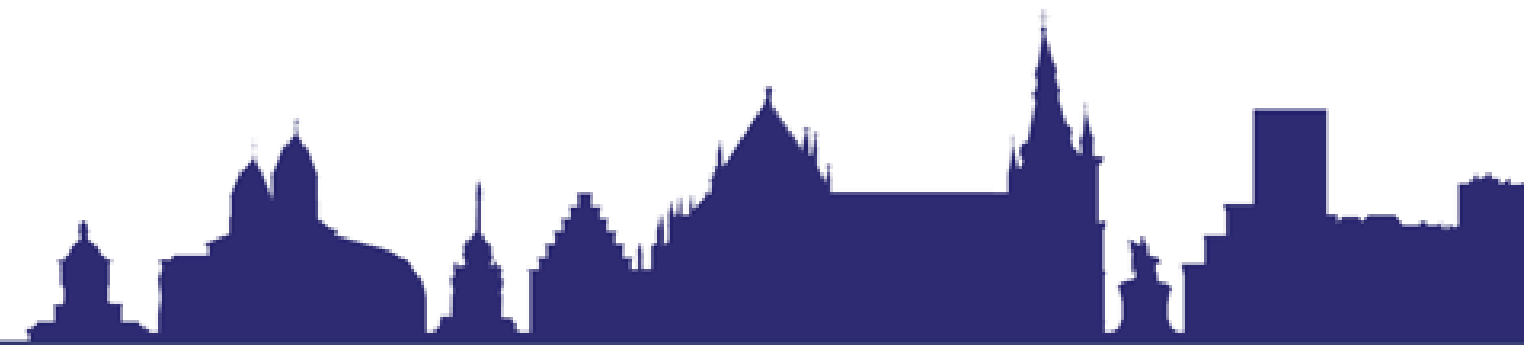




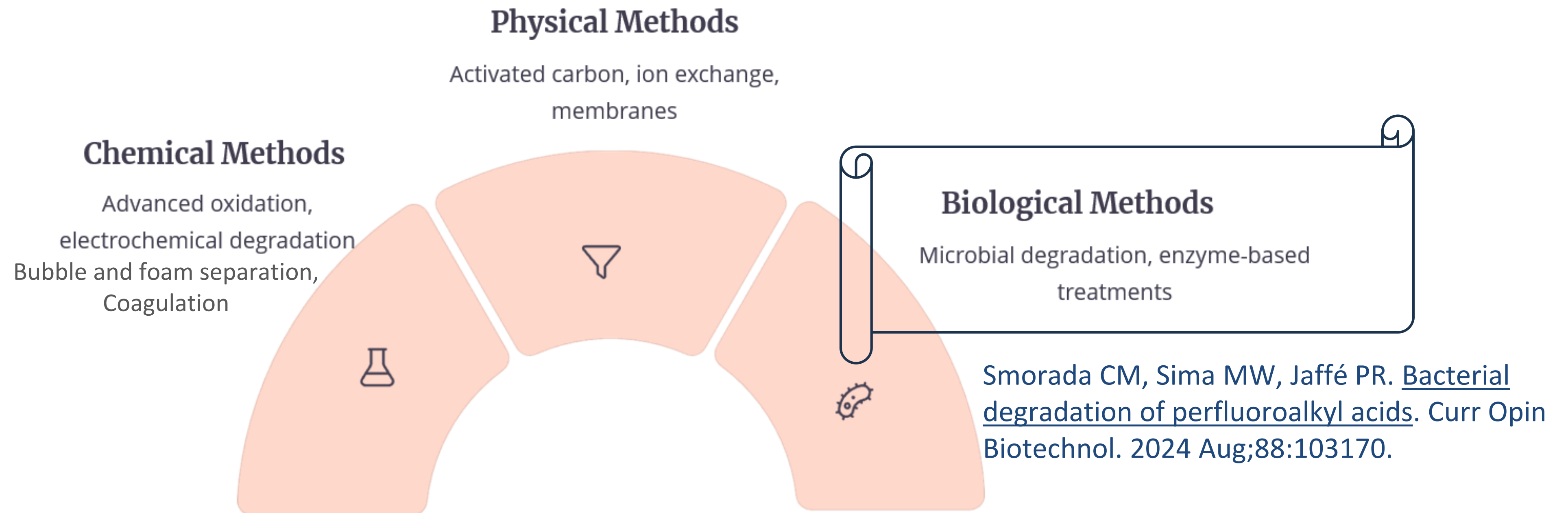
Regulations for controlling PFAS

- In England and Wales 35 and 37 percent of water courses contain medium or high-risk levels of PFOS and PFOA respectively.
- UK water companies are not required by law to reduce them until they are deemed 'high risk'.
- Concentrations of each individual PFAS is allowed at up to ten times the level considered 'low risk'
- Currently no overarching limit on the total concentration when they are combined.





Overview of PFAS Removal Methods

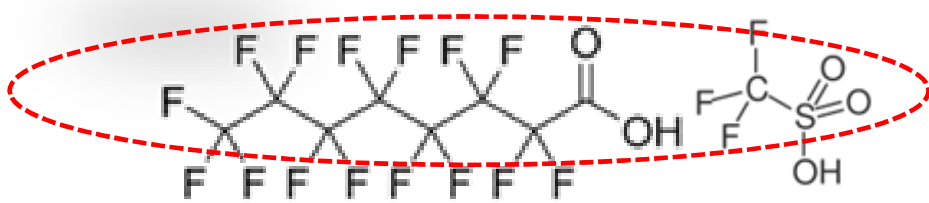


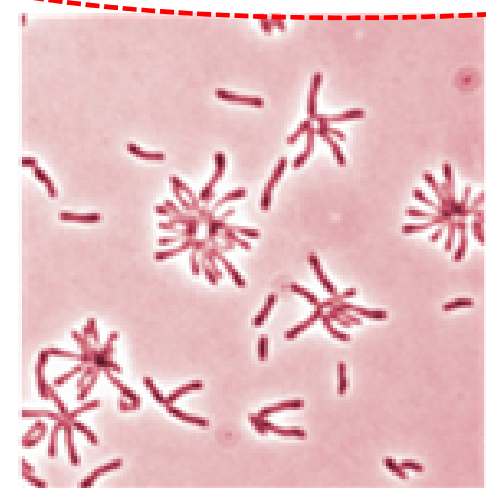


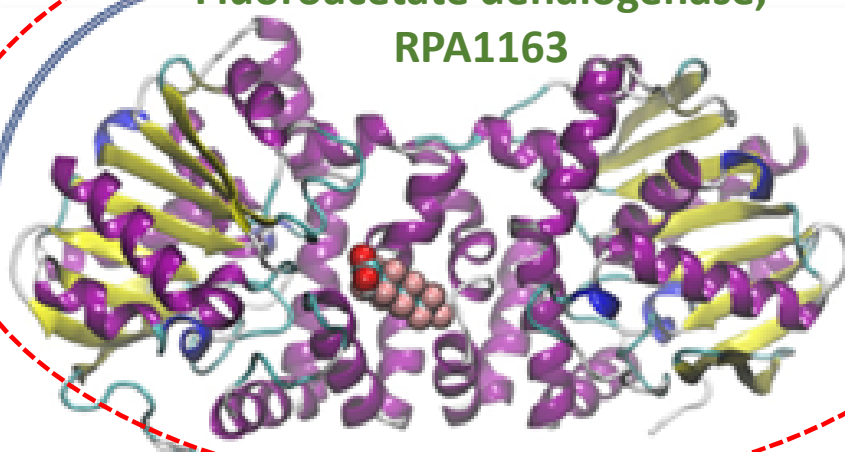
Project overview

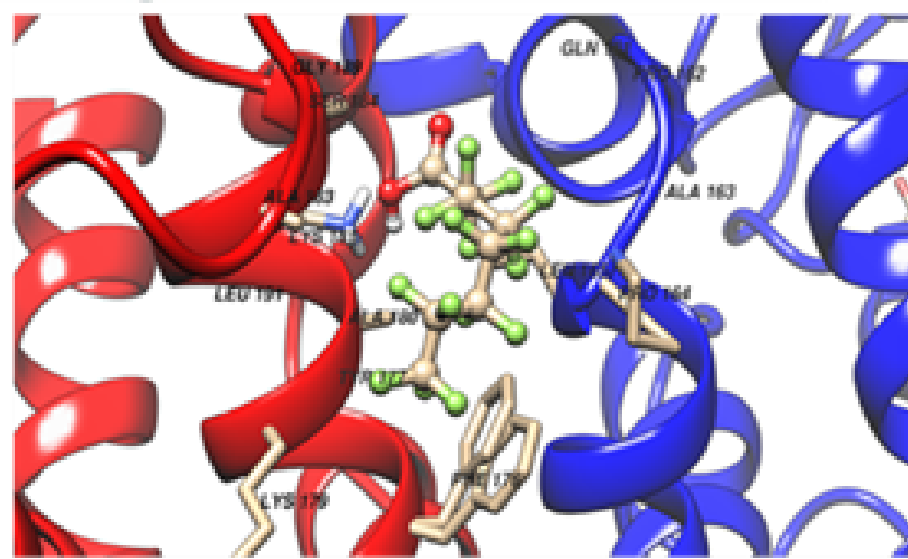


Bioremediation

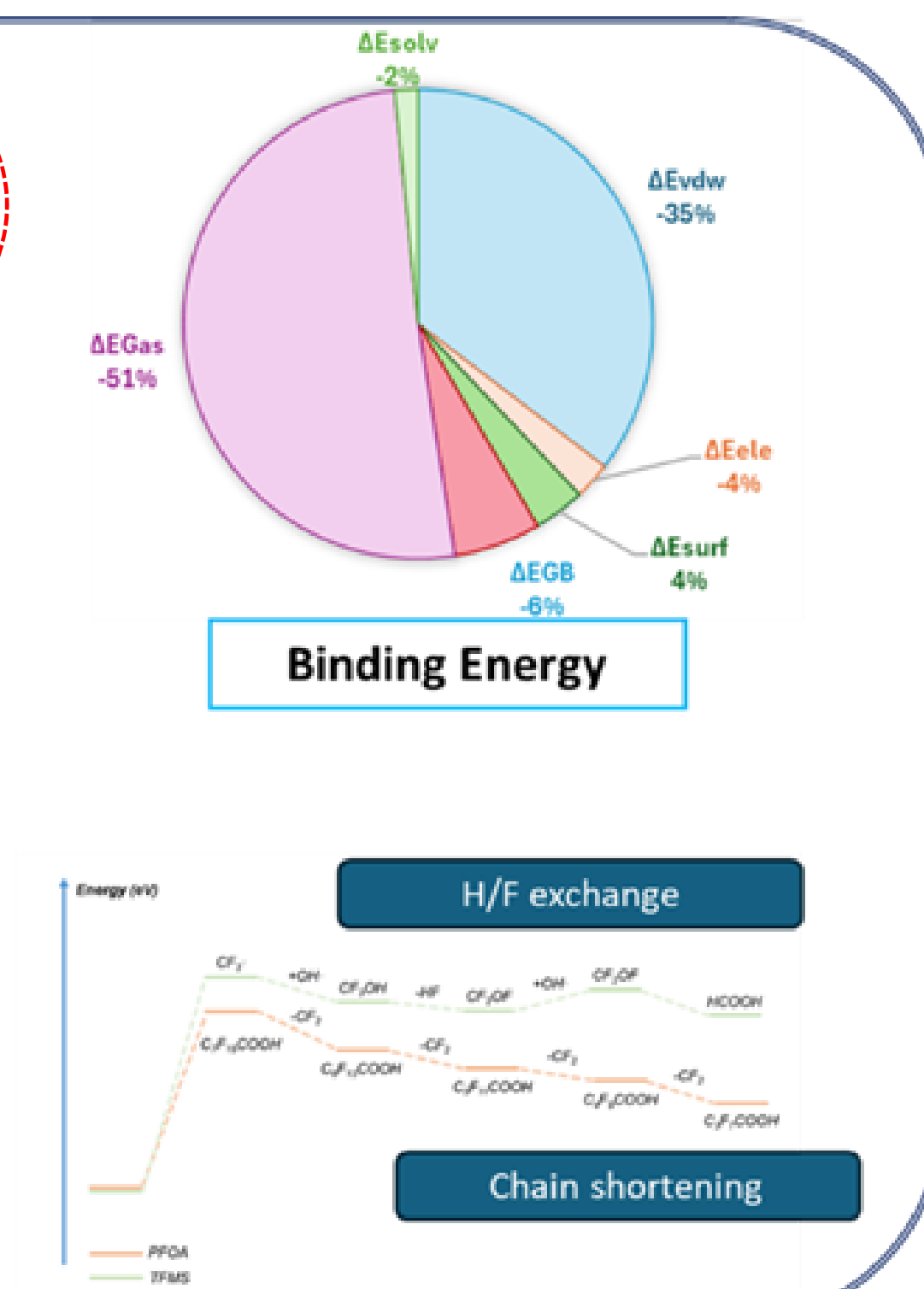


Rhodopseudomonas palustris


Fluoroacetate dehalogenase,
RPA1163
 



Molecular docking
Molecular dynamic
simulation





Methodology

In silico investigation of biodegradation of long chain and short chain PFAS with different functional group

-Enzyme Selection:

Nominated a model enzyme based on relevance to PFAS degradation pathways.

-Structure Acquisition:

Built the 3D structure of the enzyme (from PDB).

-Molecular Docking:

Docked PFAS molecules to the enzyme active site to predict binding poses and affinities (using AutoDock Vina).

Molecular Dynamics Simulation:

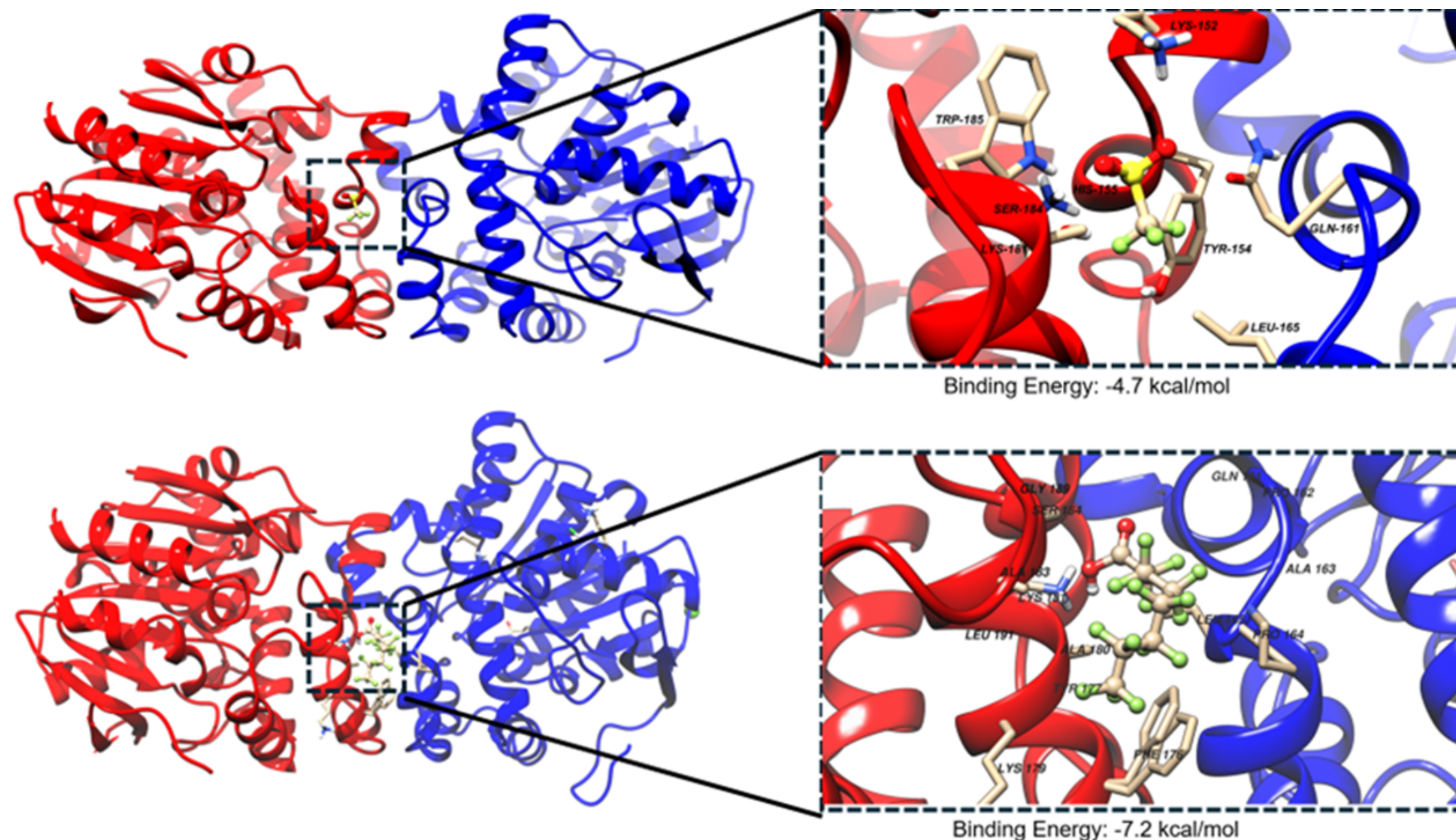
Performed MD simulations to assess stability and dynamics of the PFAS-enzyme complex in solvated conditions (using GROMACS with AMBER 99SB force field)

-QM/MM Calculations:

Applied quantum mechanics/molecular mechanics (QM/MM) hybrid methods to model electronic-level interactions at the active site.



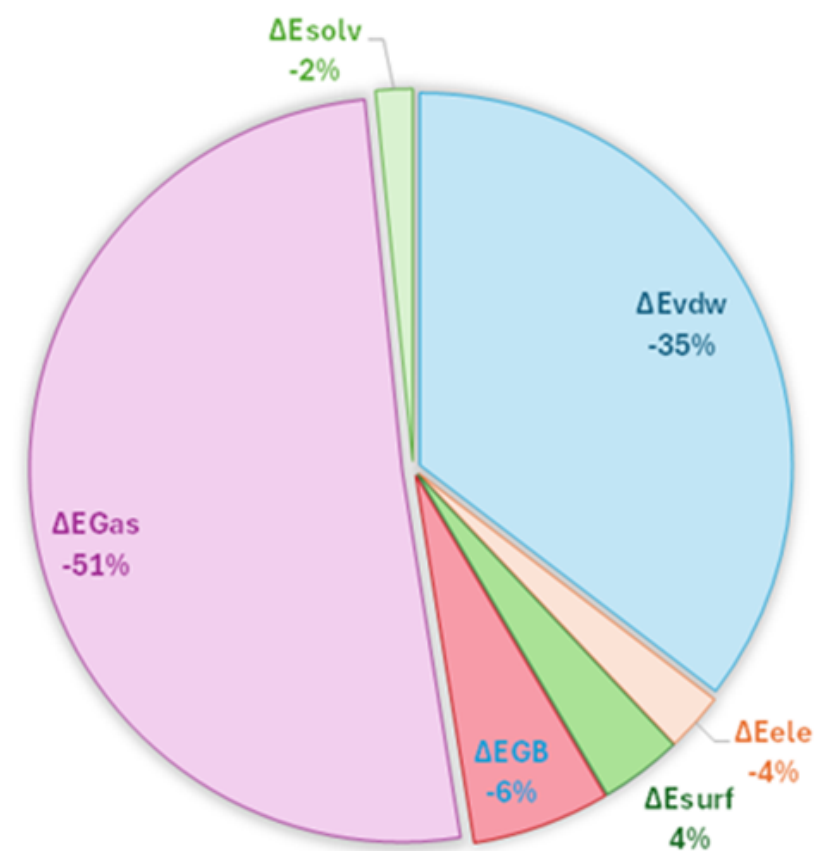
Molecular Docking



- AutoDock Tool, AutoDock Vina v1.2.x, CHIMARA software
- Scores of different ligand-protein poses are based on binding affinity and conformation of molecules at active sites of enzyme
- TFMS near TYR and HIS amino acid residue in enzyme
- PFOA in regions with Leu and Tyr
- Higher number of hydrogen-bond receptor in PFOA, higher binding affinity



Molecular Dynamic Simulation

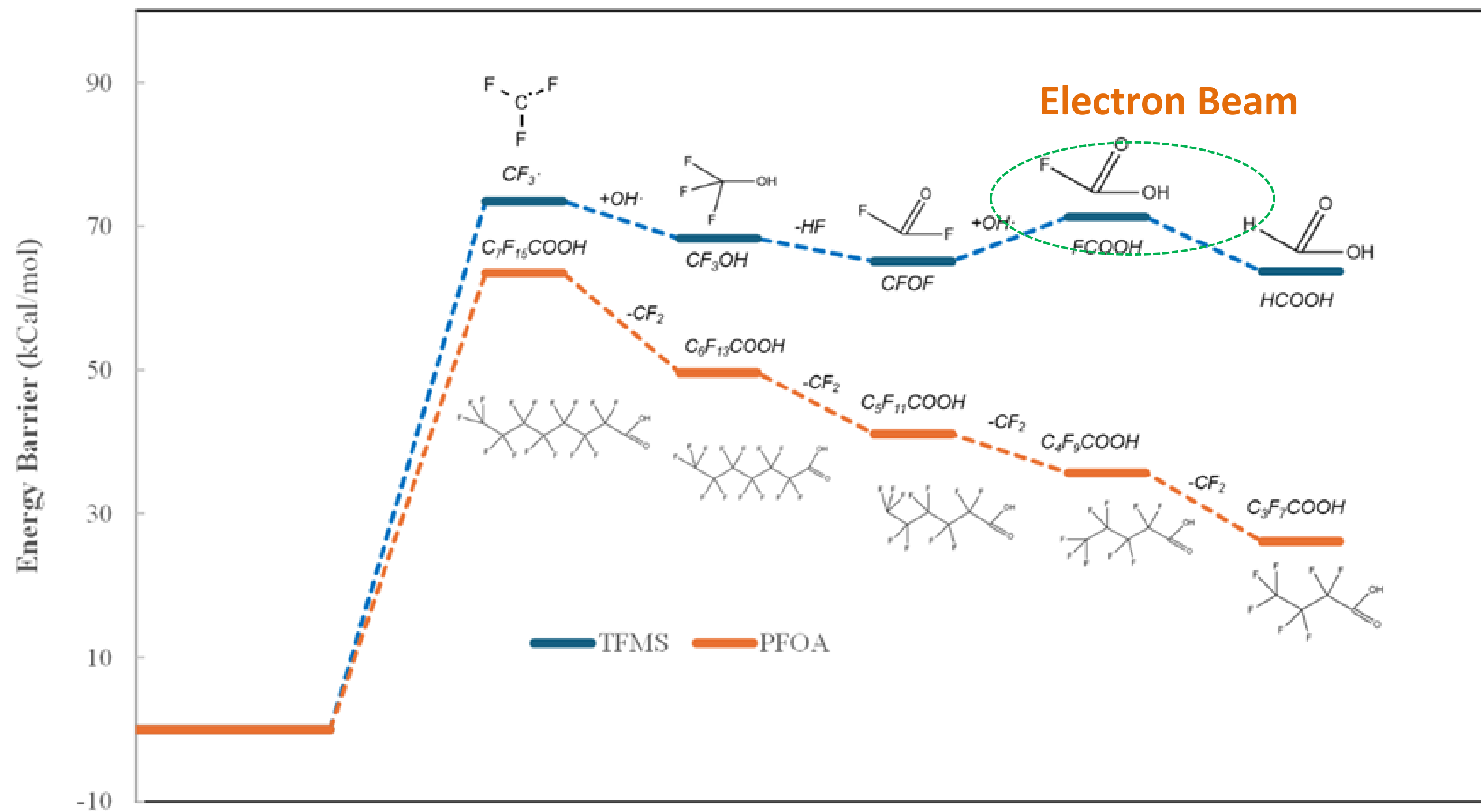


- Calculating binding energy using Gromacs
- Dominance of van der Waals due to the hydrophobic interactions
- Gas-phase energy an indication of intrinsic molecular mechanic and complementary shape of enzyme and ligand than solvent-mediated effect.

Enzyme should focus on hydrophobic residue to strengthen van der Waals interactions and geometry of binding pocket for better shape complementary.

Degradation Pathway and Energy Barrier

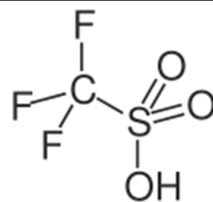
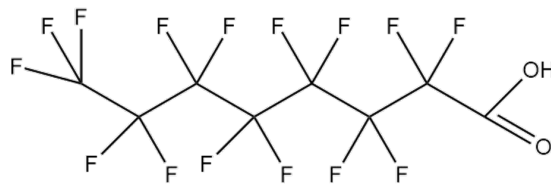
Construct a reaction energy profile using QM/MM and DFT calculations





Conclusion

- ✓ Enzyme and PFAS interactions are investigated using simulation techniques
- ✓ Degradation of long chain and short chain PFAS were compared
- ✓ Fluoroacetate dehalogenase, RPA1163 could degrade only the PFAS containing acetate functional group

<u>PFAS Compound</u>	<u>Molecular structure</u>	<u>Functional group</u>	<u>Binding energy</u>	<u>Activation energy</u>	<u>Pathway</u>
TFMS		Triflate	-27.02	63.49	H/F exchange
PFOA		Acetate	-77.85	73.525	Chain shortening



Future Research Direction

- ✓ Integration of simulation and experimental evaluation to understanding biodegradation potential of different PFAS
- ✓ Using insight from MD simulation for enzyme engineering
- ✓ Looking through engineering biology solution for enhancing bacterial potential for PFAS biodegradation and biosensing for PFAS detection, through multidisciplinary collaboration





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