

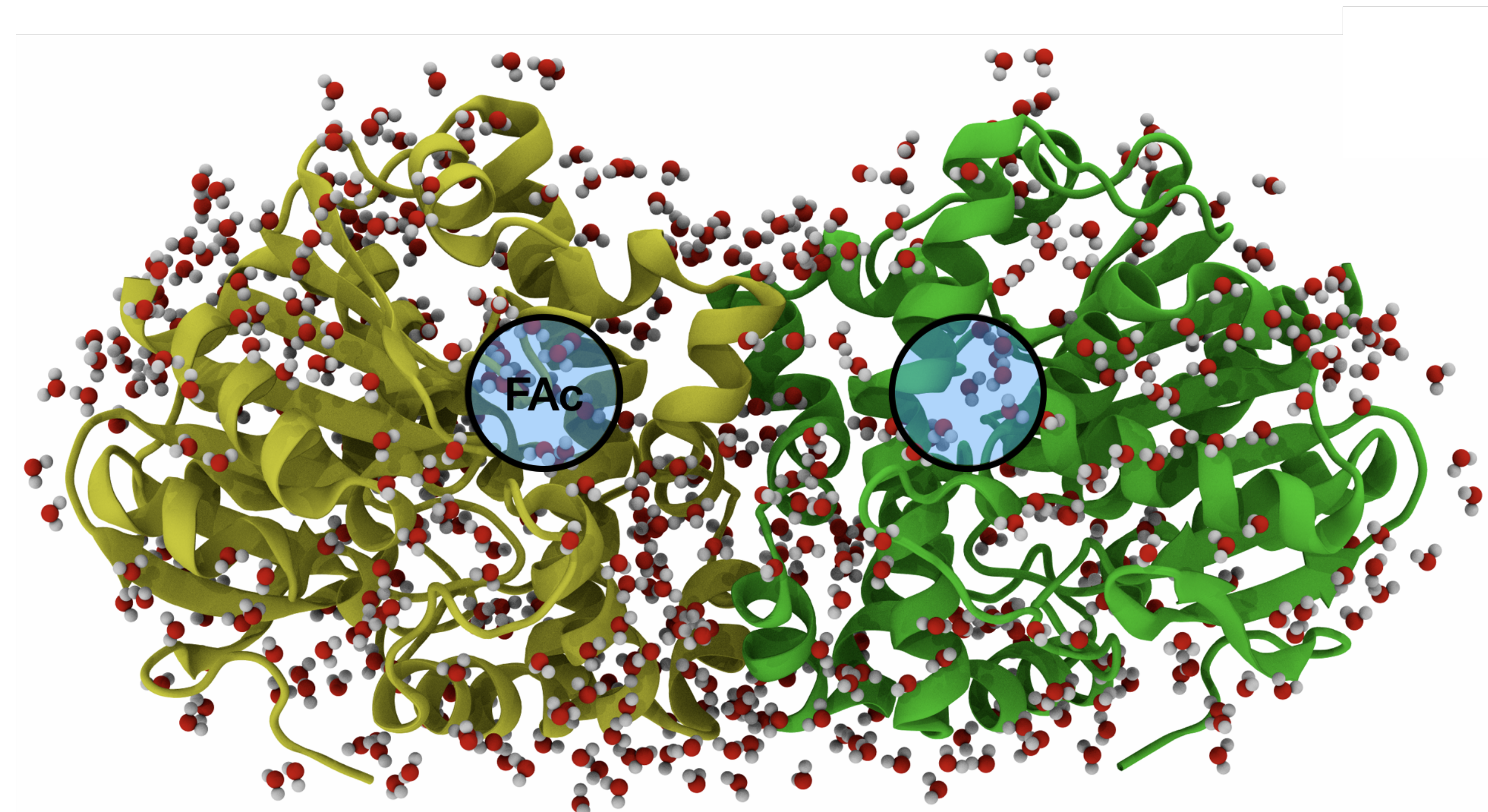
# Describing Allosteric Water Networks In Enzymes



See Method

## MOTIVATION

- Fluoracetate dehalogenase (FACD) hydrolyses FAc via a cleavage of C-F bond.
- Half-of-site reactivity: catalysis happens only when one protomer is occupied by substrate. Requires strong coupling between protomers, i.e. allosteric network.



Experiments highlight the importance of water in the function of FACD

Experiments are conducted in  $D_2O$  and  $H_2O$ : hydrogen bonds are stronger in  $D_2O$ .

- The rate of catalysis increases in  $D_2O$  ( $^{19}F$  NMR).
- Inter-protomer dynamics is enhanced in  $D_2O$  ( $^{19}F$  NMR).
- Crystal structure (protein + water) and fold-stability does not change (NMR, X-ray).

**Hypothesis:** an allosteric water network contributes to the signal propagation between binding sites.

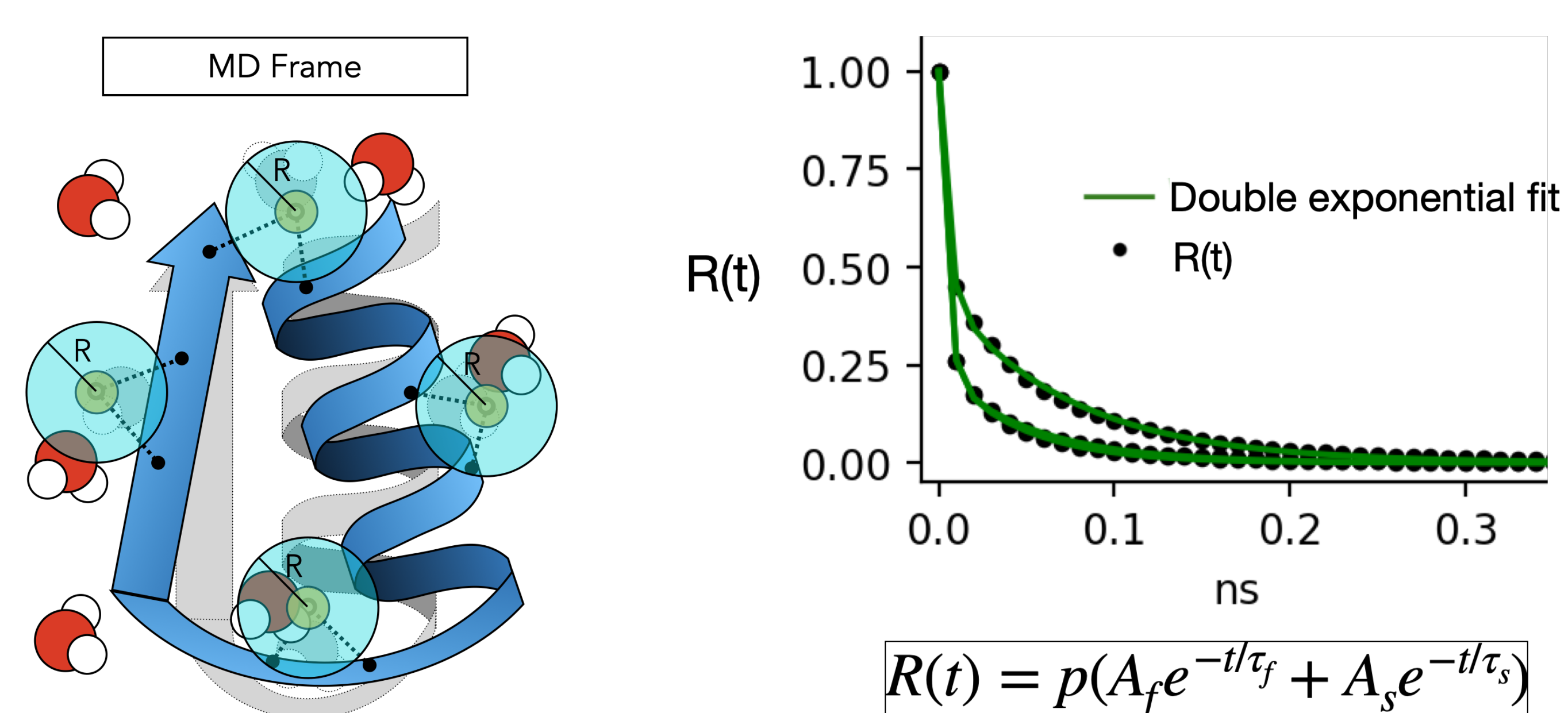
**Objective:** to identify water molecules that might be involved in the allosteric regulation of enzymatic activity

## METHODS

Protein conformational ensembles are similar between  $H_2O$  and  $D_2O$   
- consistent with experiments

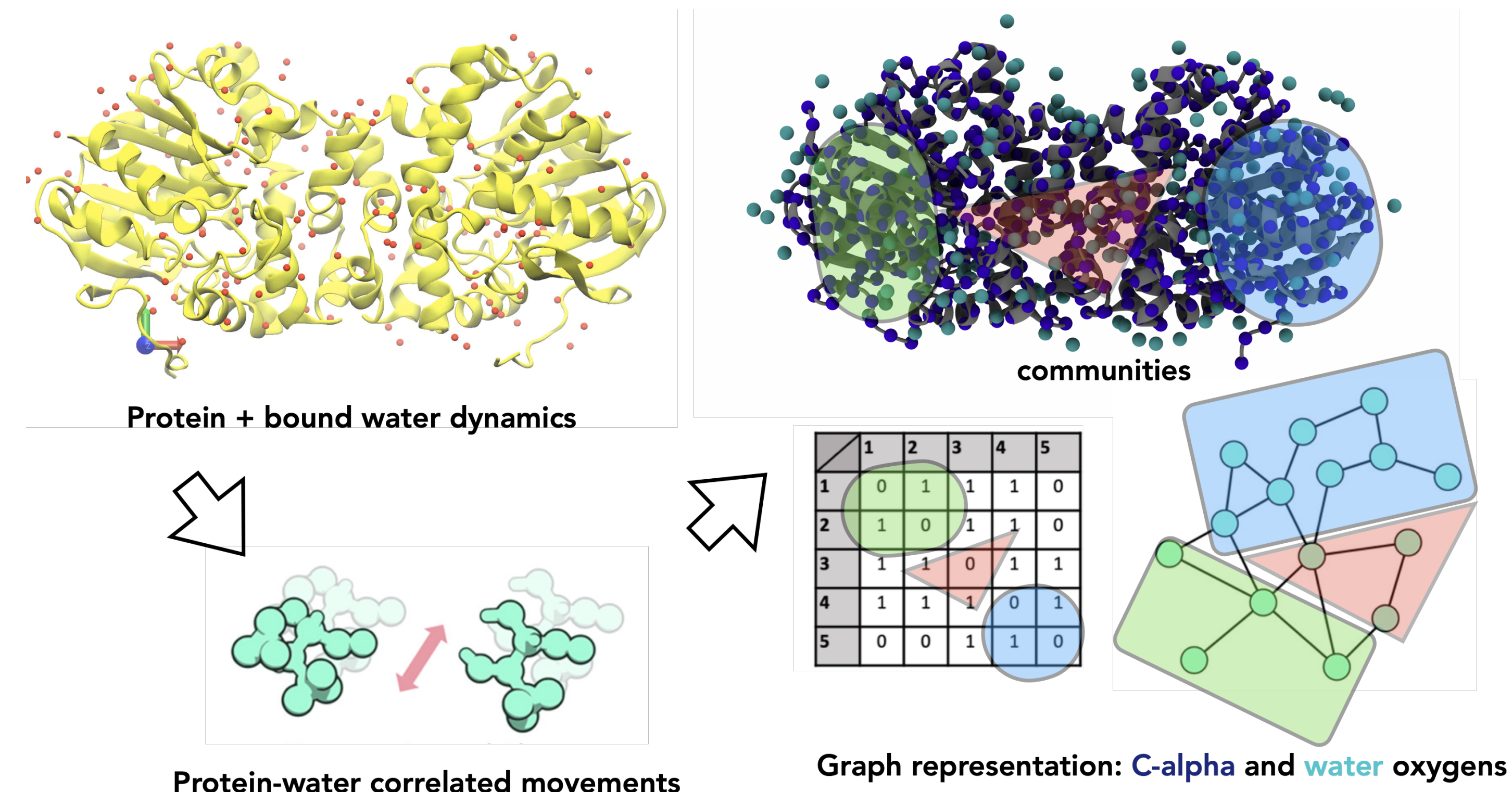
MD Simulations	$H_2O$	$D_2O$
Water model	TIP3P	TIP3P-HW*
Force field	Amber ff14SB	
Simulation length	3 × 600 ns @ T=300K of <b>substrate-bound</b> structure 3 × 1500 ns @ T=300K of <b>apo</b> structure	

Determining occupancy and residence times of water molecules



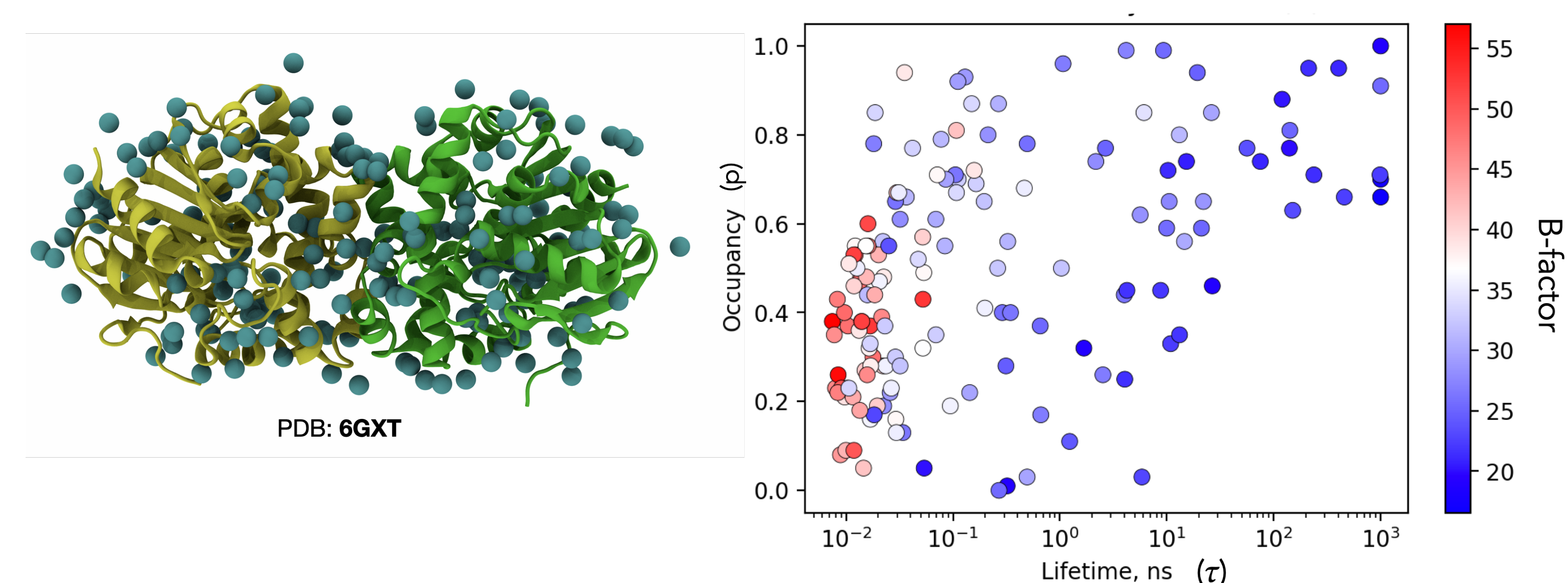
- Check how often water occupies a sphere of  $R=1.4 \text{ \AA}$  around a water site to determine occupancy ( $p$ ).
- Compute autocorrelation function  $R(t)$  for each WS to determine the average residence time via a double exponential fit.

Analysis of correlated dynamics of protein and water using graph theory

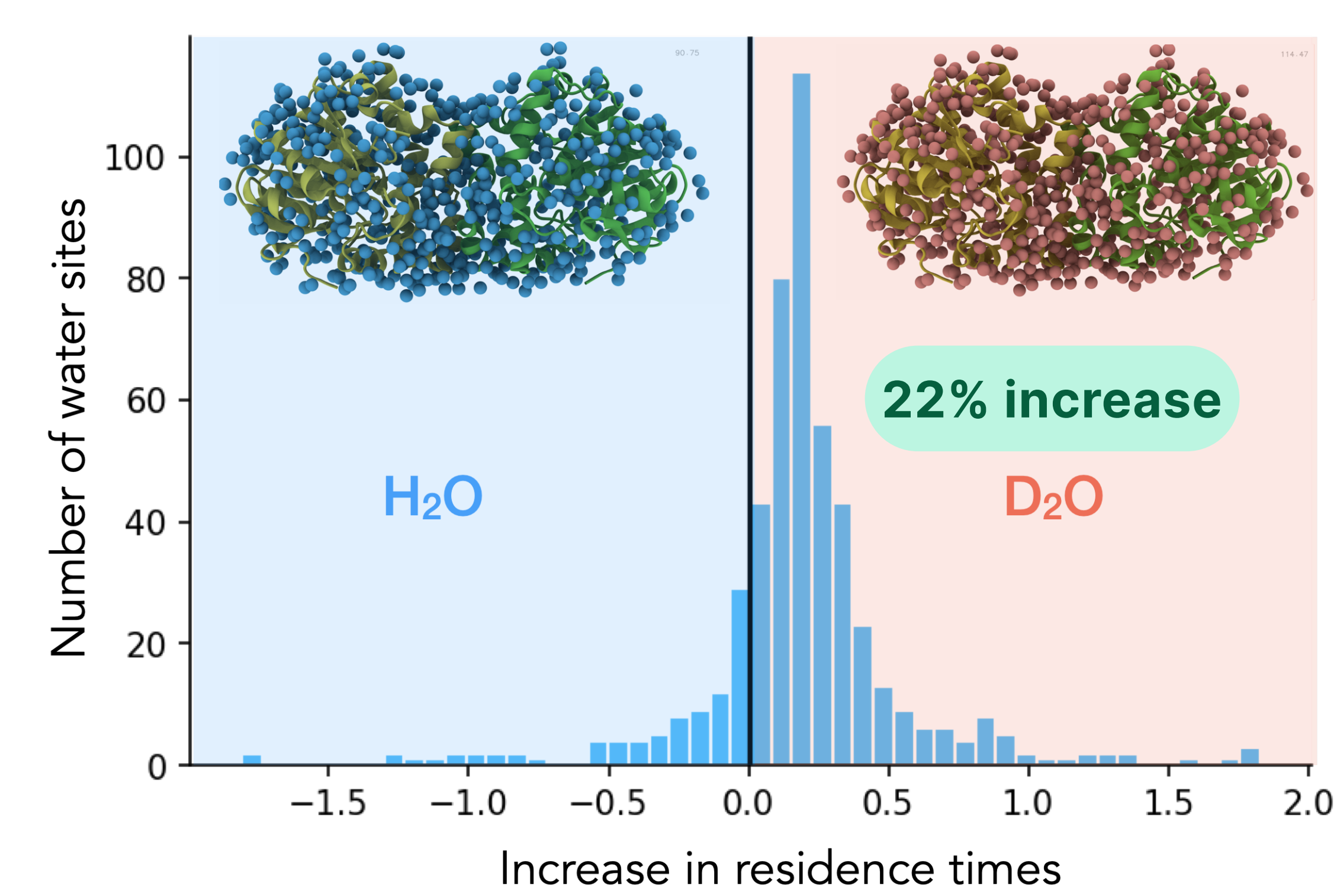


## VALIDATION

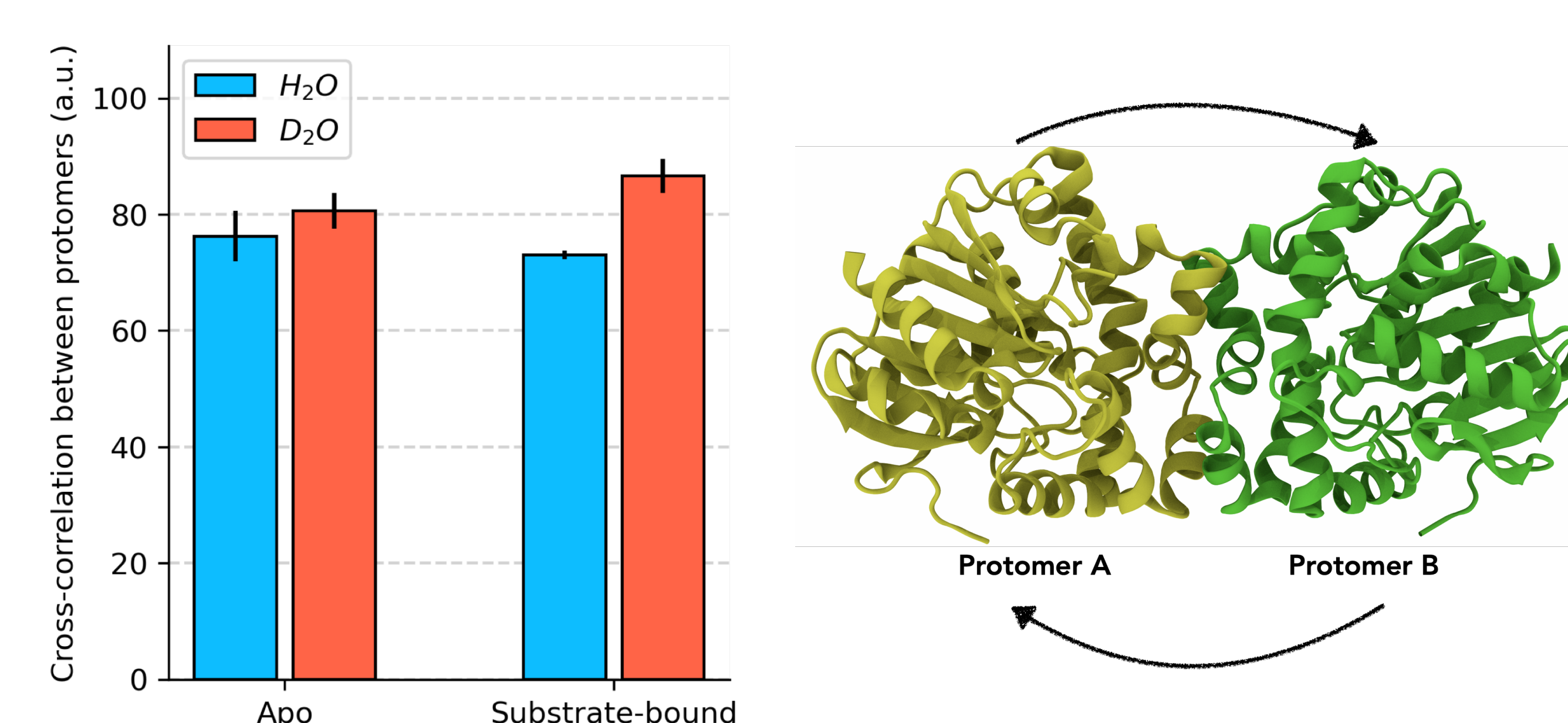
Higher occupancy and residence times of water molecules correspond to lower experimental B-factors



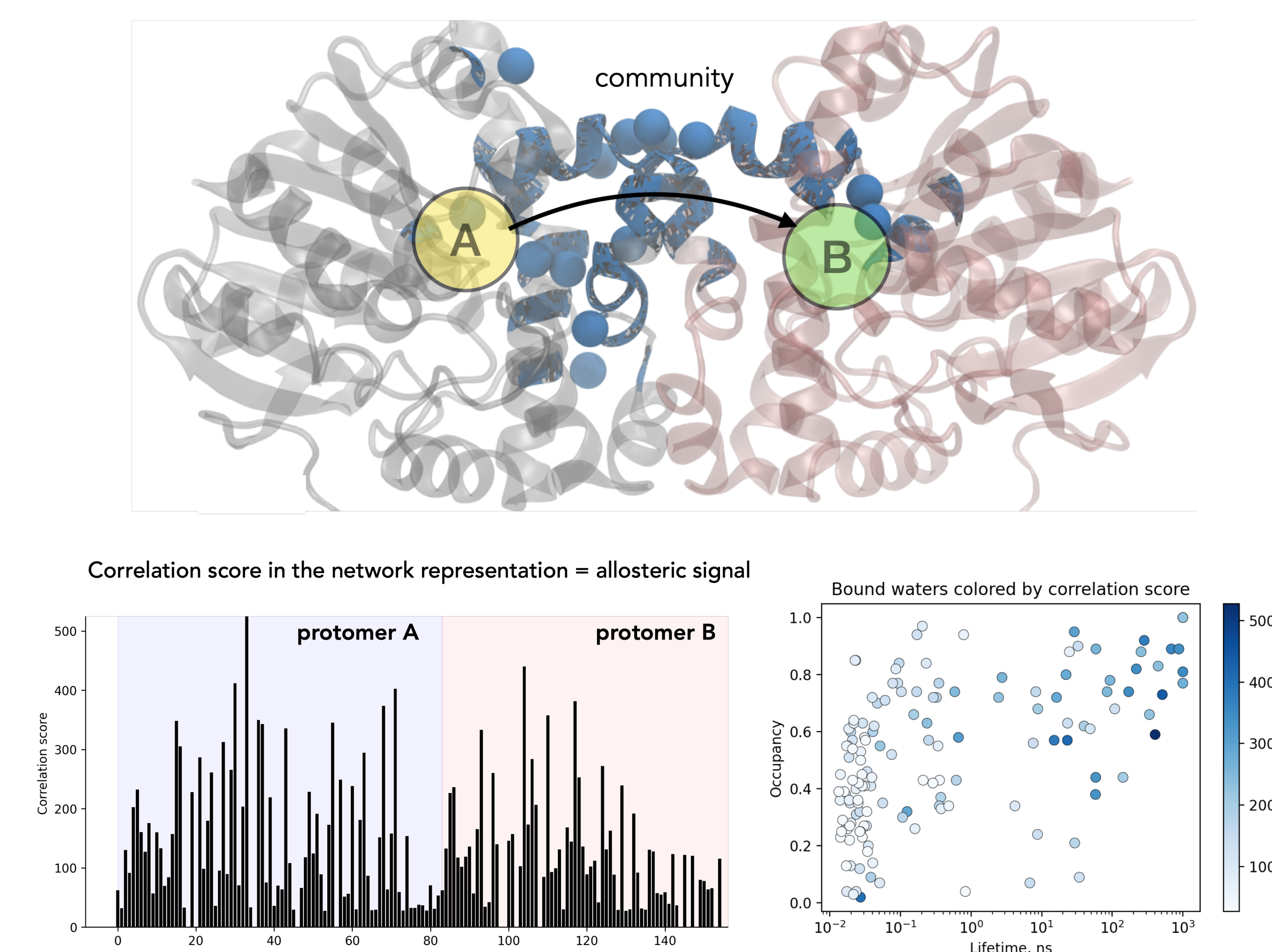
## STIFFENING OF THE WATER NETWORK IN $D_2O$



## HIGHER CORRELATION BETWEEN PROTOMERS IN $D_2O$



## ALLOSTERIC PATHWAY CONNECTING BINDING SITES



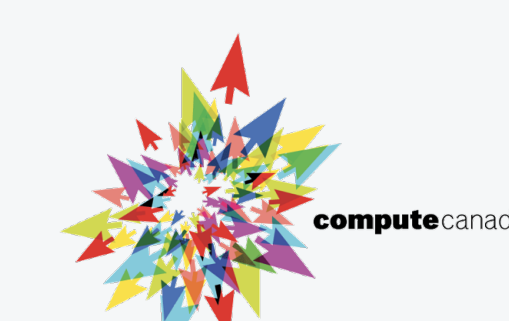
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Acknowledgments



CONNAUGHT FUND