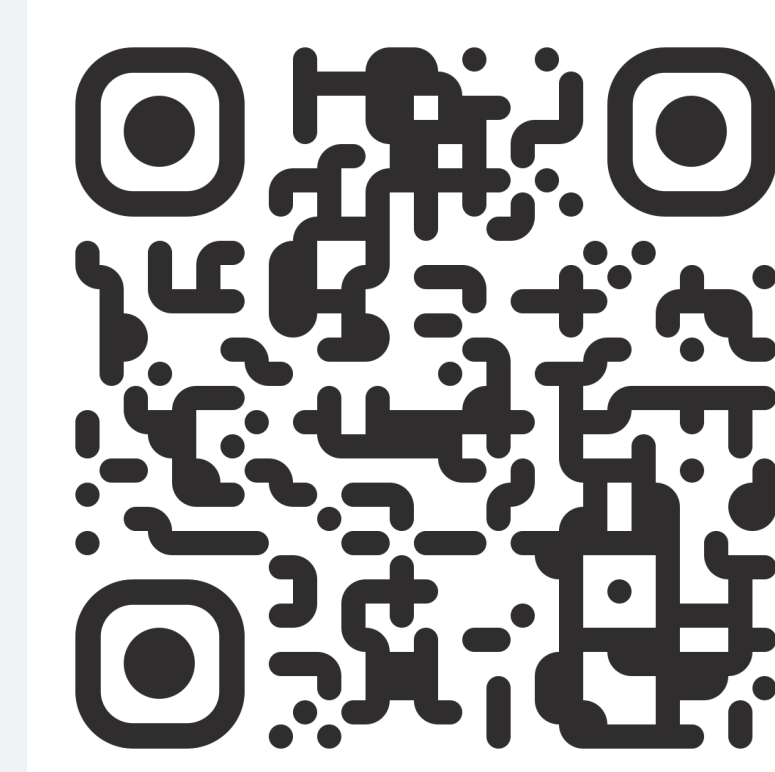


# LAWS: Local Alignment for Water Sites

A method to analyze crystallographic water in simulations



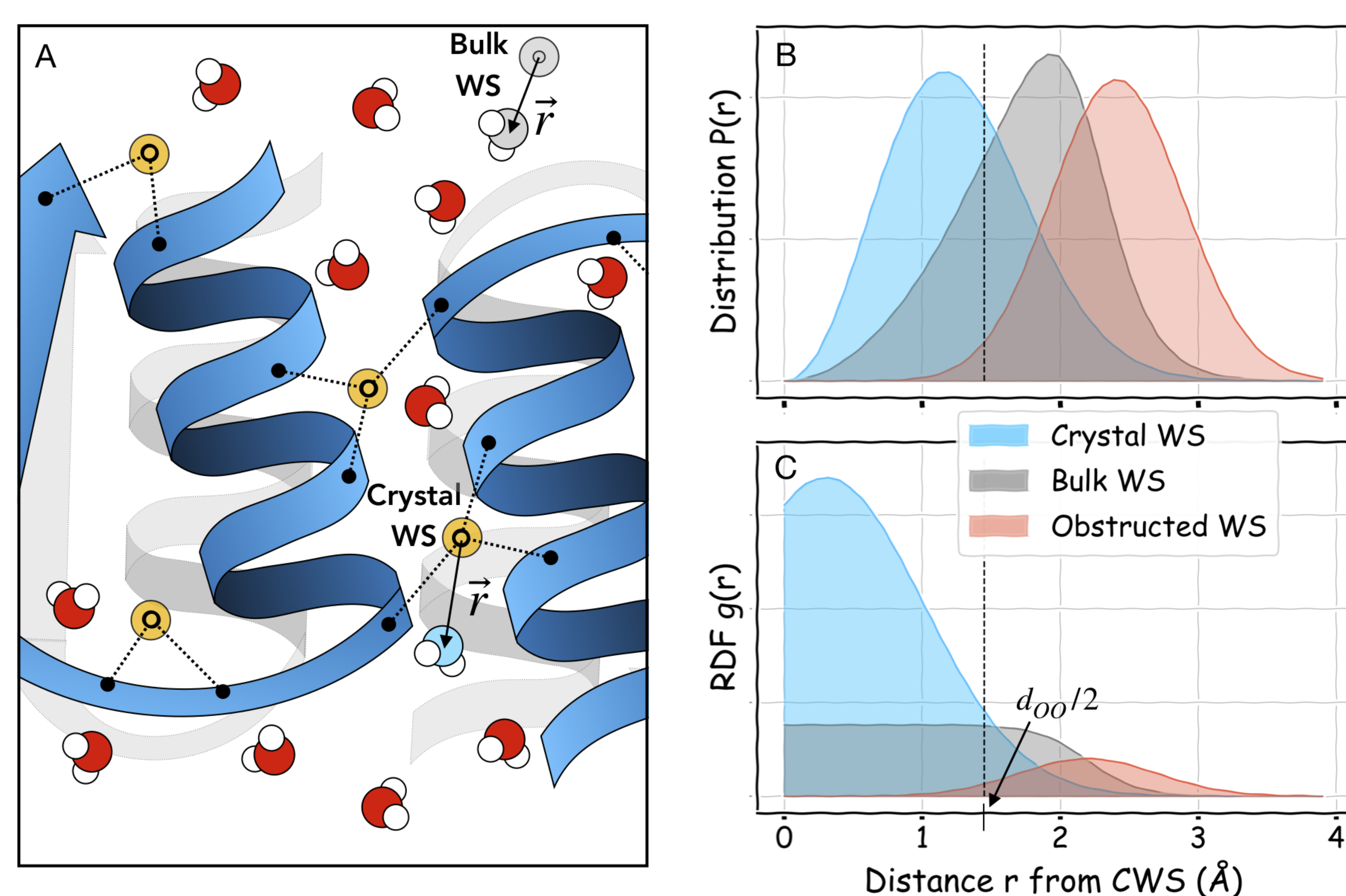
Check out our code

## METHOD

- Track **CWS** (yellow) in simulation based on distances to protein atoms by minimizing **LAWS error** (A):

$$\text{LAWS}(x, y, z) = \sum_{i=1}^n w_i^2 (\sqrt{(x-x_i)^2 + (y-y_i)^2 + (z-z_i)^2} - d_i)^2.$$

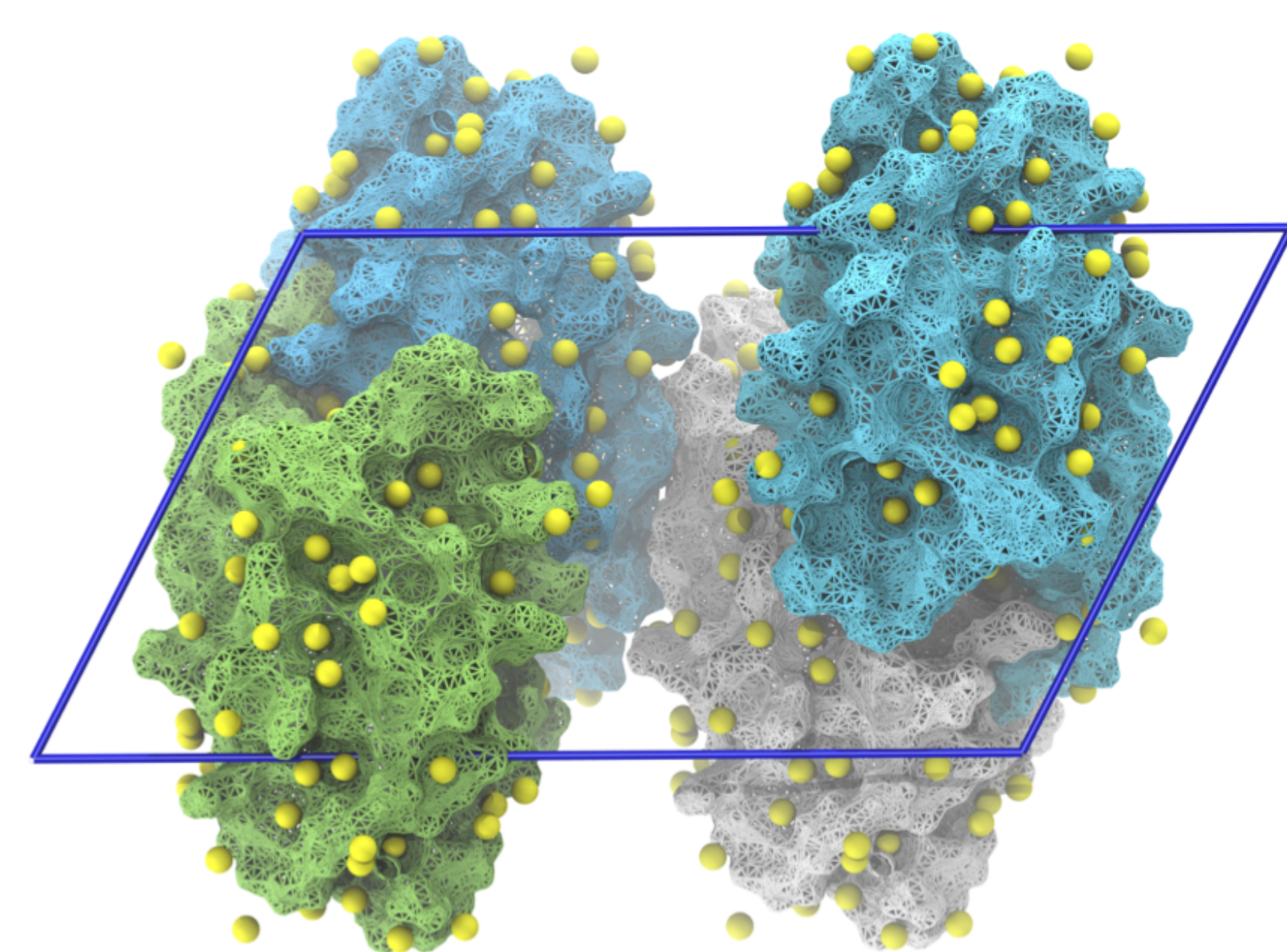
- Randomly sample **Bulk WS** (grey) at least 6 Å from protein (A).
- Compute **P(r)** - distribution of distance **r** to nearest neighbour water (B).
- Compute **g(r)** - radial density profile by **r<sup>2</sup>** normalization (C).
- Classify a CWS into (i) **crystal**, (ii) **bulk-like**, and (iii) **obstructed**.



## APPLICATION

1 μs simulation of protein crystal (single unit cell)

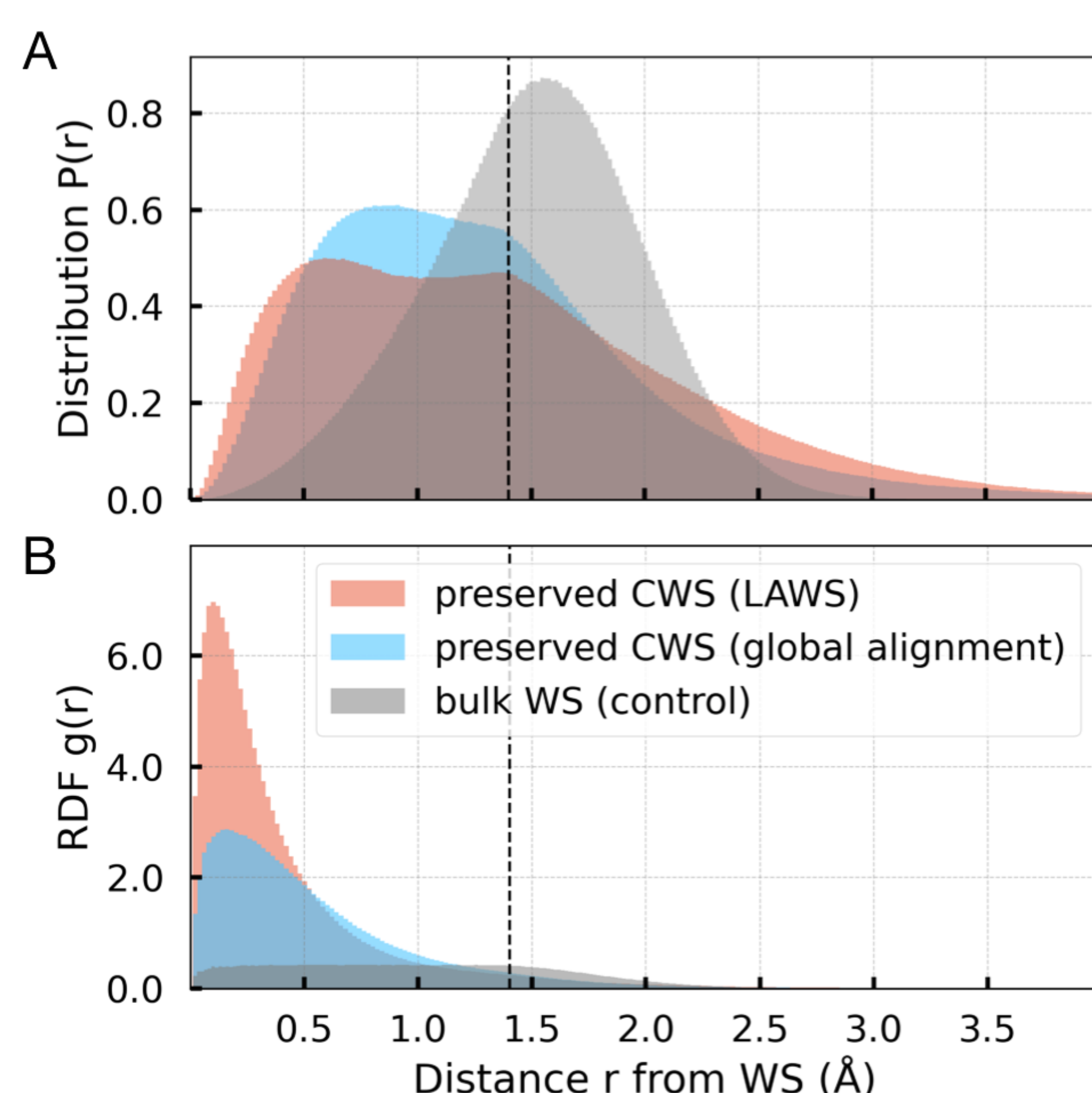
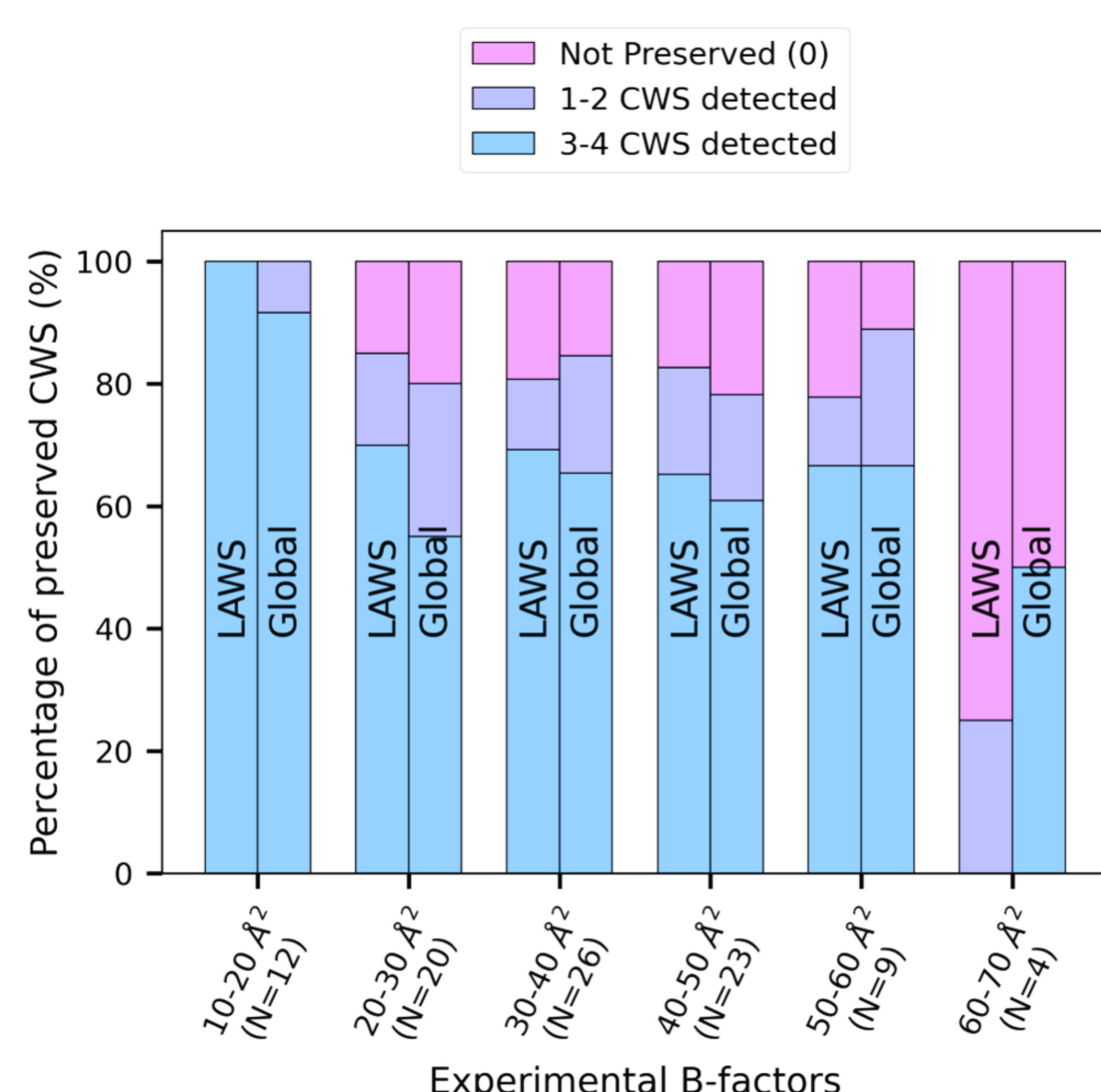
Second PDZ domain of human LNX2 protein



## ADVANTAGES OVER EXISTING METHODS

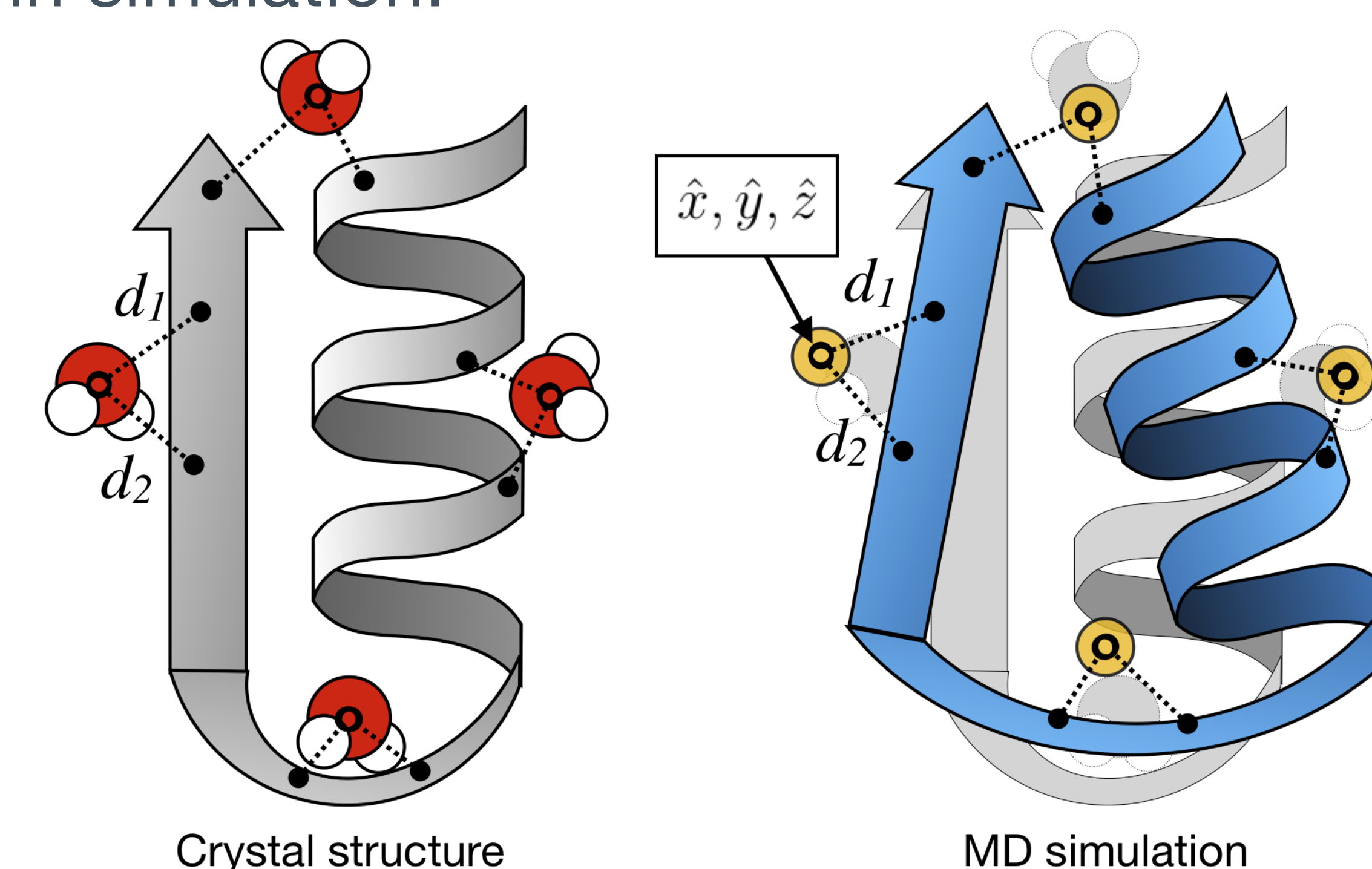
- Higher overall recall of CWS in simulations (table)
- Perfect recall of high confidence (low B-factor) CWS (bar chart)
- Higher water density for detected CWS (distribution)

Methods	Preserved CWS	Bulk-like WS	Obstructed WS
LAWS	76%	11%	14%
Global alignment	68%	9%	23%

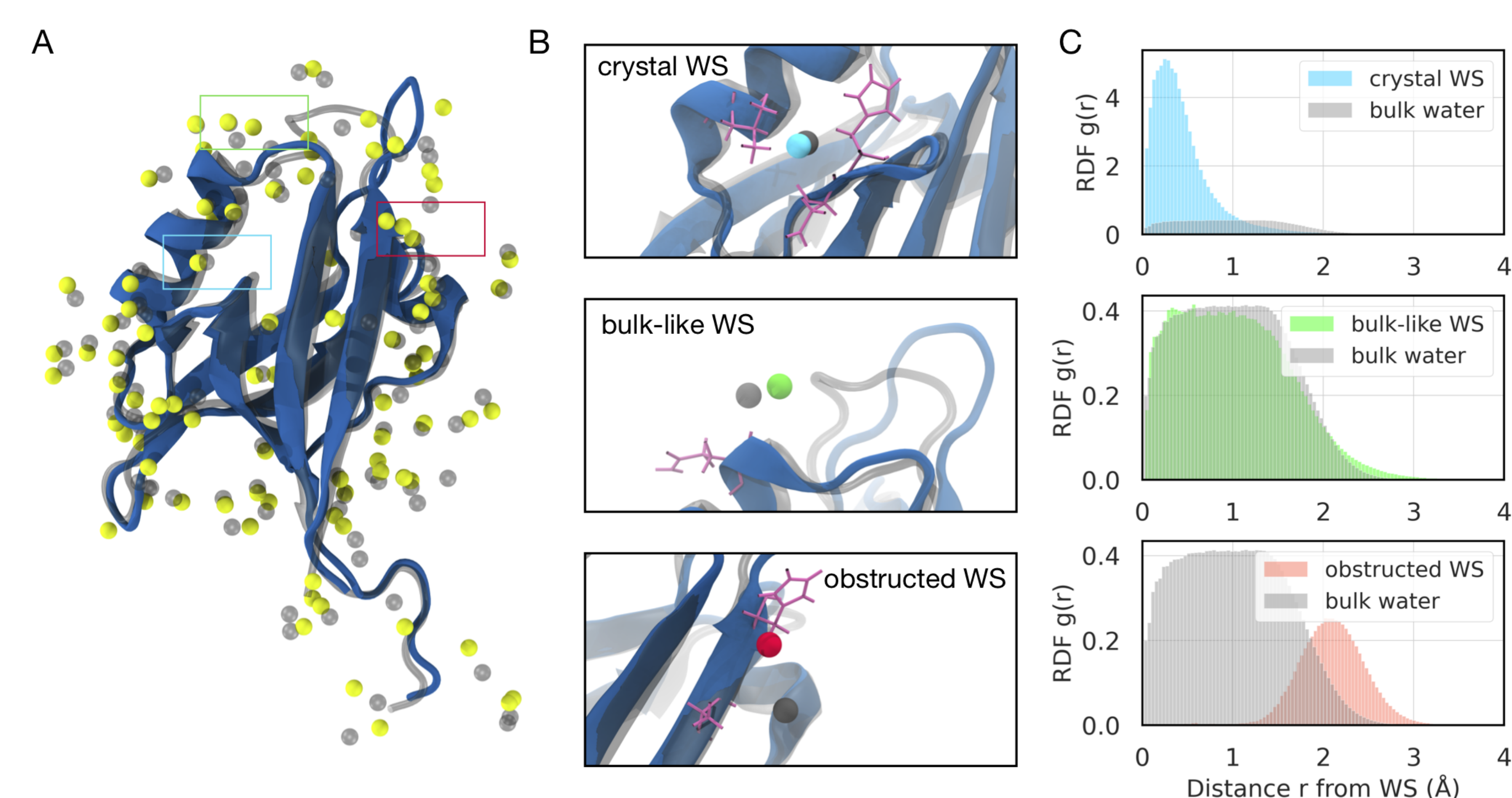


## MOTIVATION

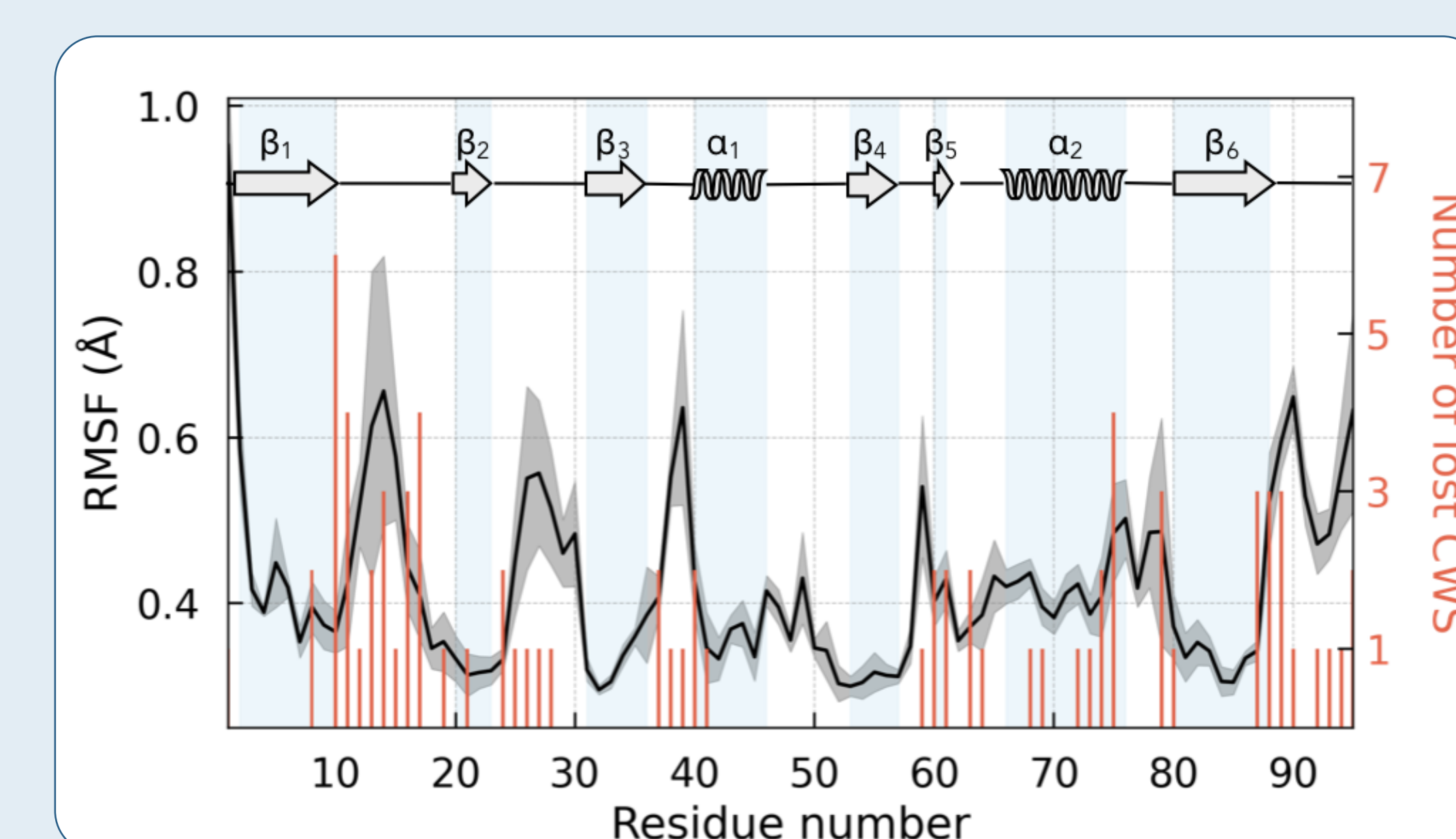
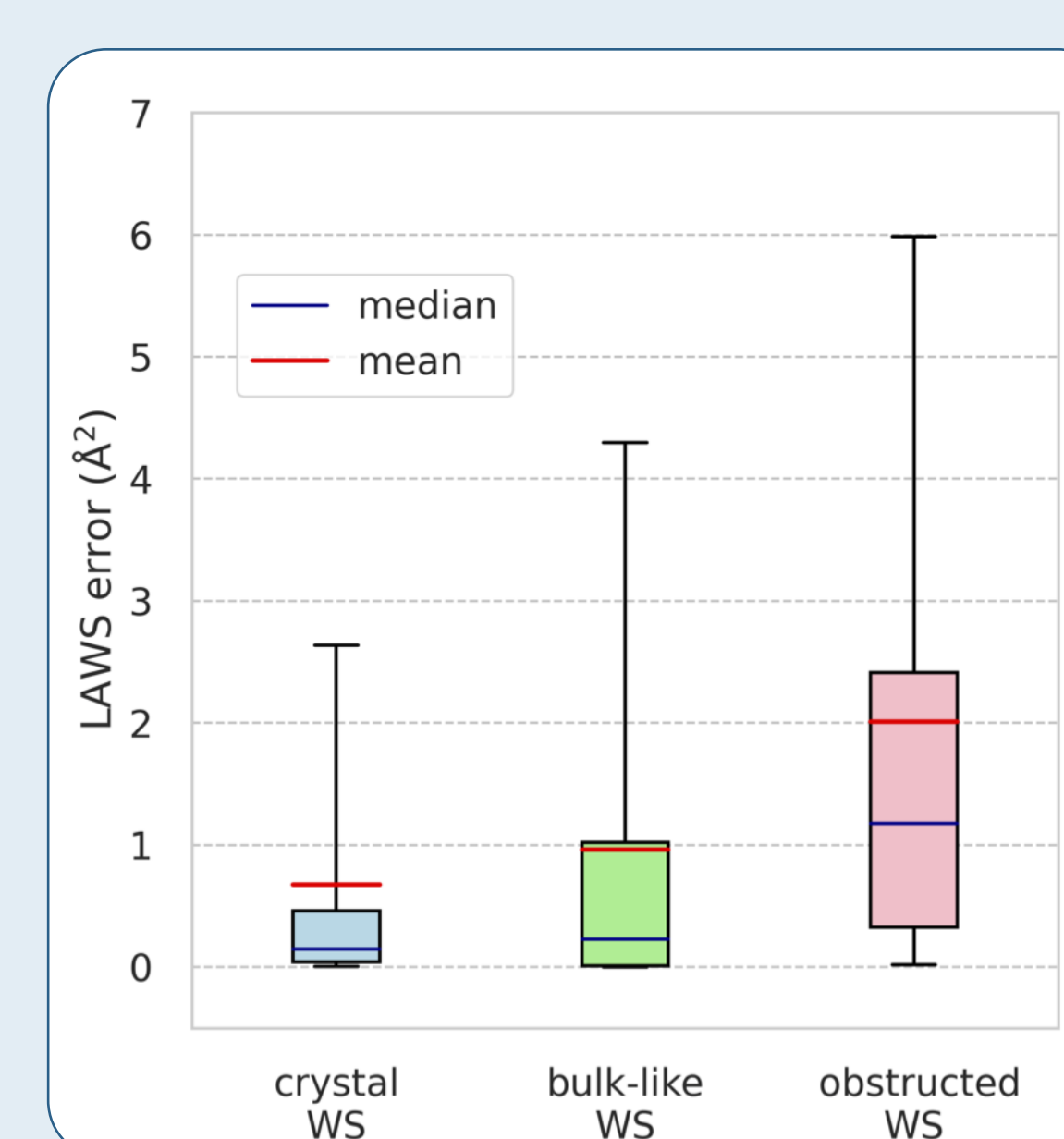
- Accurate **modeling of protein-water** interactions is important for understanding **protein function**.
- X-ray diffraction provides **crystallographic water sites (CWS)** – strong benchmark for modeling accuracy, but methods for **comparison with MD** are required.
- Existing methods rely on **global alignment** of the protein on crystal structure (**introduce errors**), we propose a new method (**LAWS**).
- LAWS considers **contacts formed by CWS and protein atoms** in crystal structure and uses these interaction distances to **track the CWS** in simulation.



## RESULTS



LAWS classifies WS into **crystal** (blue), **bulk-like** (green), and **obstructed** (red). (A) Simulated structure (blue) is overlapped with crystal structure (grey). (B) Representative WS from each group. (C) Corresponding radial density profile  $g(r)$  for each WS.



- Lost CWS have a perturbed protein environment – large LAWS error.
- Lost CWS are located near flexible regions of protein – with high RMSF.

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