

# Protein conformation in amorphous solids by hydrogen-deuterium exchange

*International Symposium on the Higher Order Structure of Protein Therapeutics  
Biological Consequences of HOS Session  
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# Acknowledgements

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## ***Purdue University (current)***

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- Dr. Ben Walters
- Dr. Lokesh Kumar
- Dr. Kathleen Abadie

## ***AbbVie***

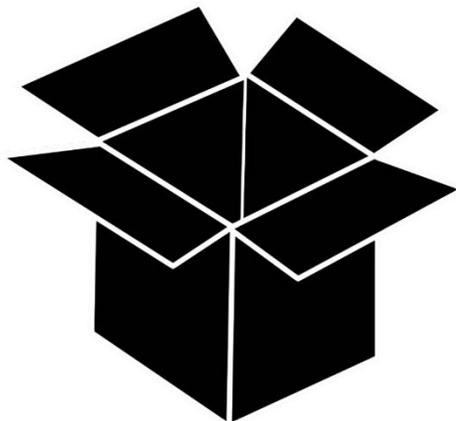
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# Proteins in the solid state

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- Protein drugs are an important part of the biopharmaceutical industry.
- Over the past decade, ~40% of newly approved protein drugs have been marketed as solids.
- Maintaining HOS in the solid state is important for storage stability.
- But methods to measure HOS in solids are few and low-resolution.

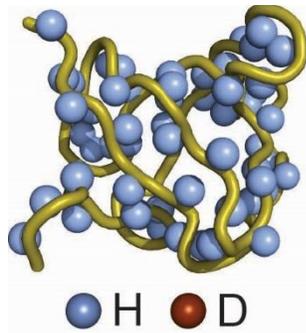


**Stability  
Studies**  
3 -24  
months

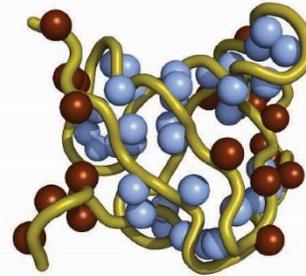
# Hydrogen-deuterium exchange (HDX)

MS analysis

## H/D Exchange

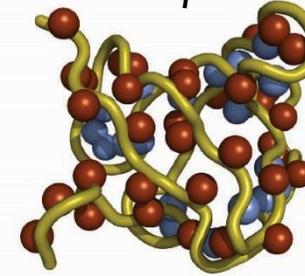


$D_2O$   
Time



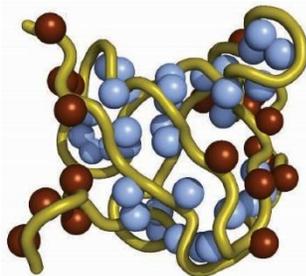
Dynamic regions  
exchange rapidly

$D_2O$   
Time

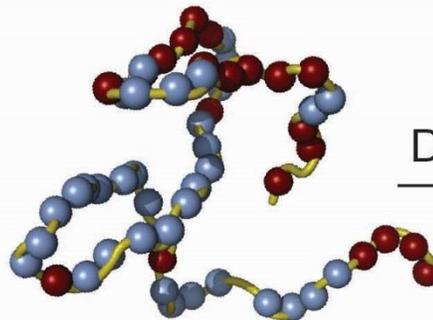


Structured regions  
exchange slowly

## Quench and Digest

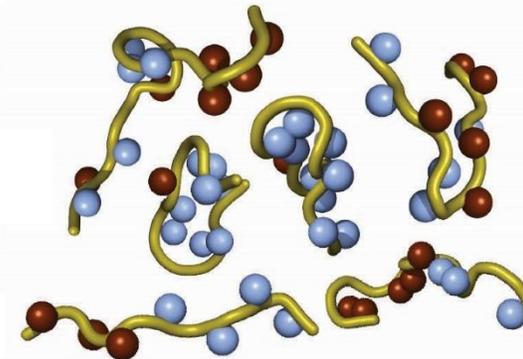


Quench  
pH 2.5  
0 °C



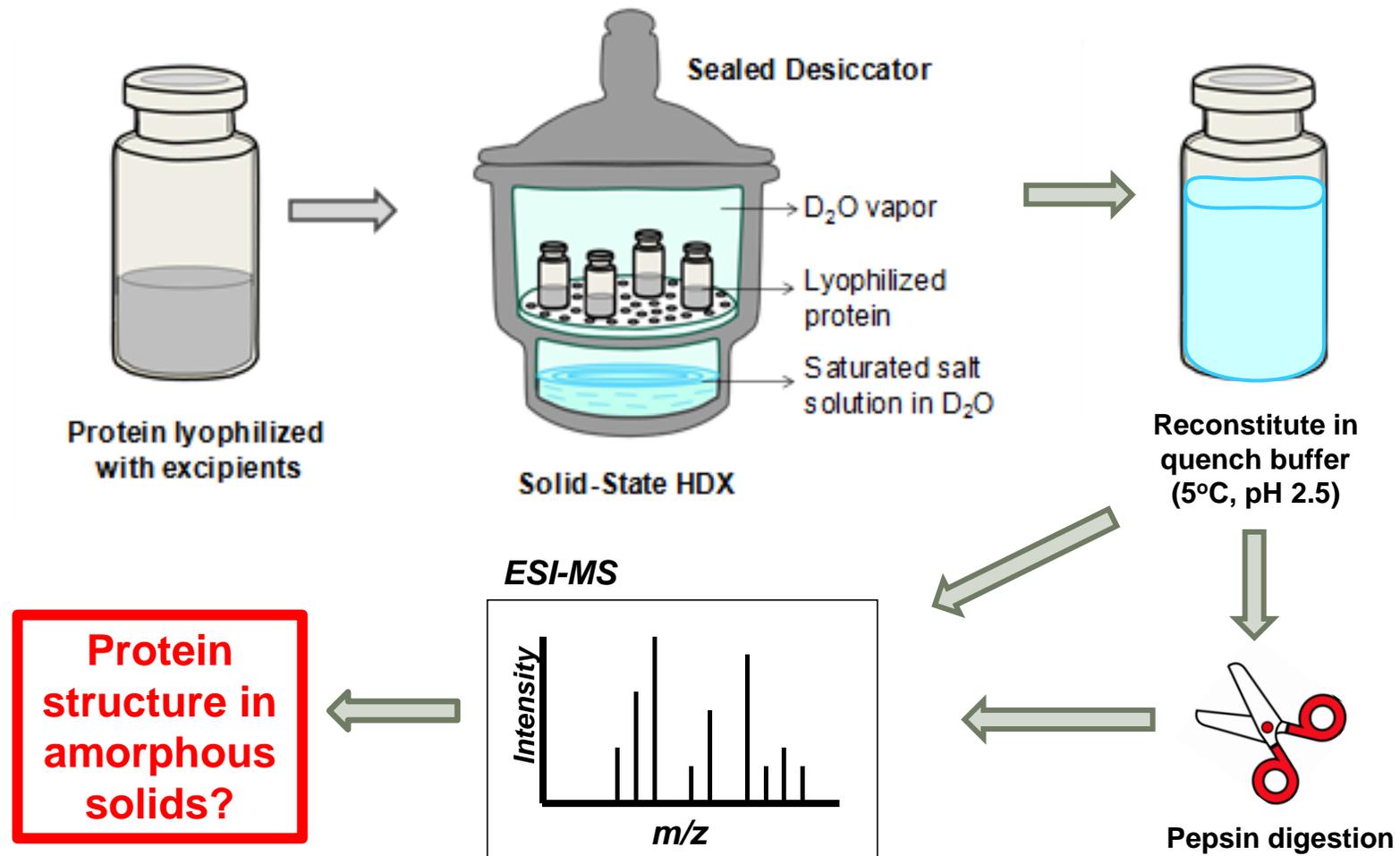
Quenching locks in deuterium  
and unfolds the protein

Digest



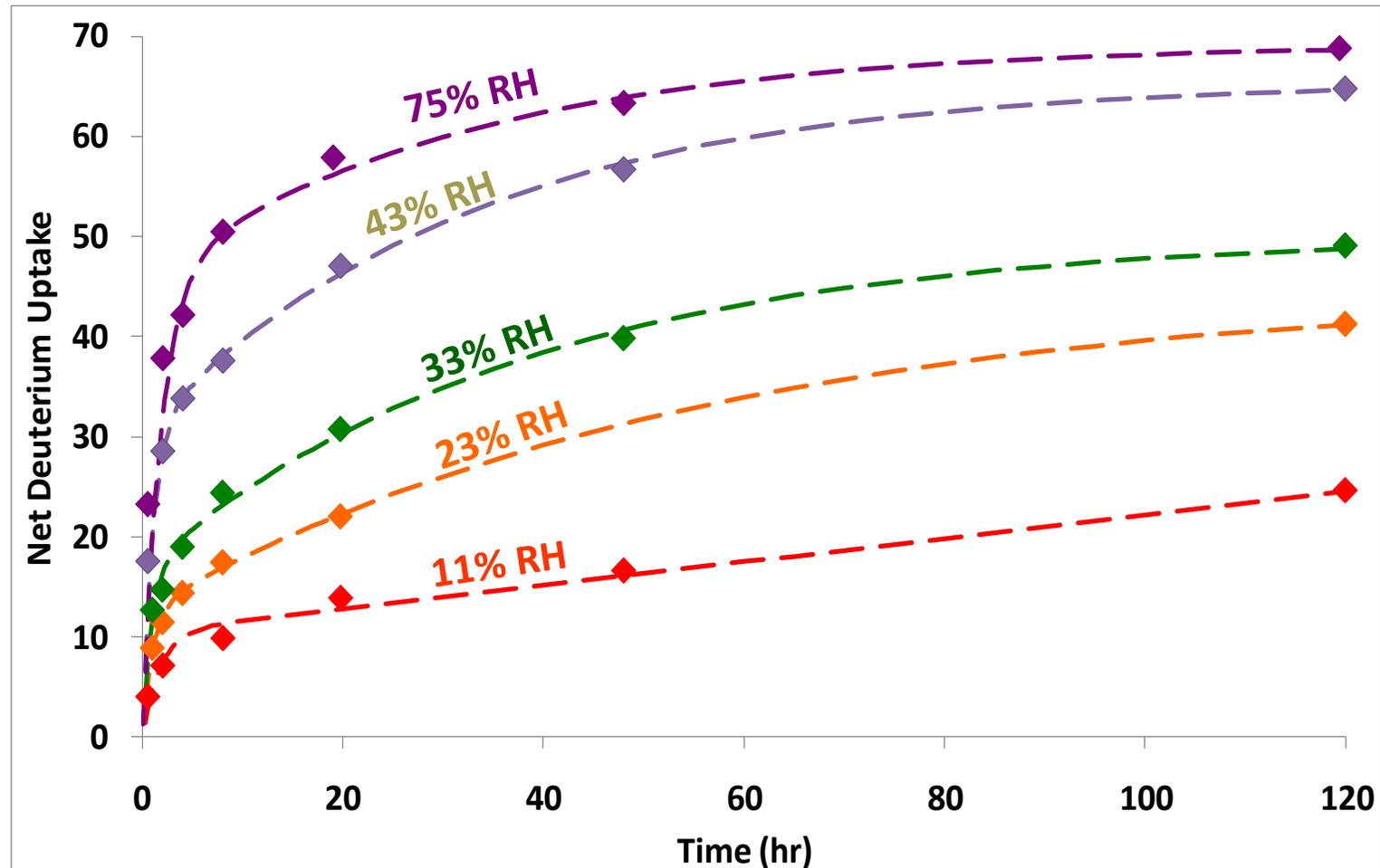
Digestion localizes the  
information

# Solid-state HDX (ssHDX-MS)



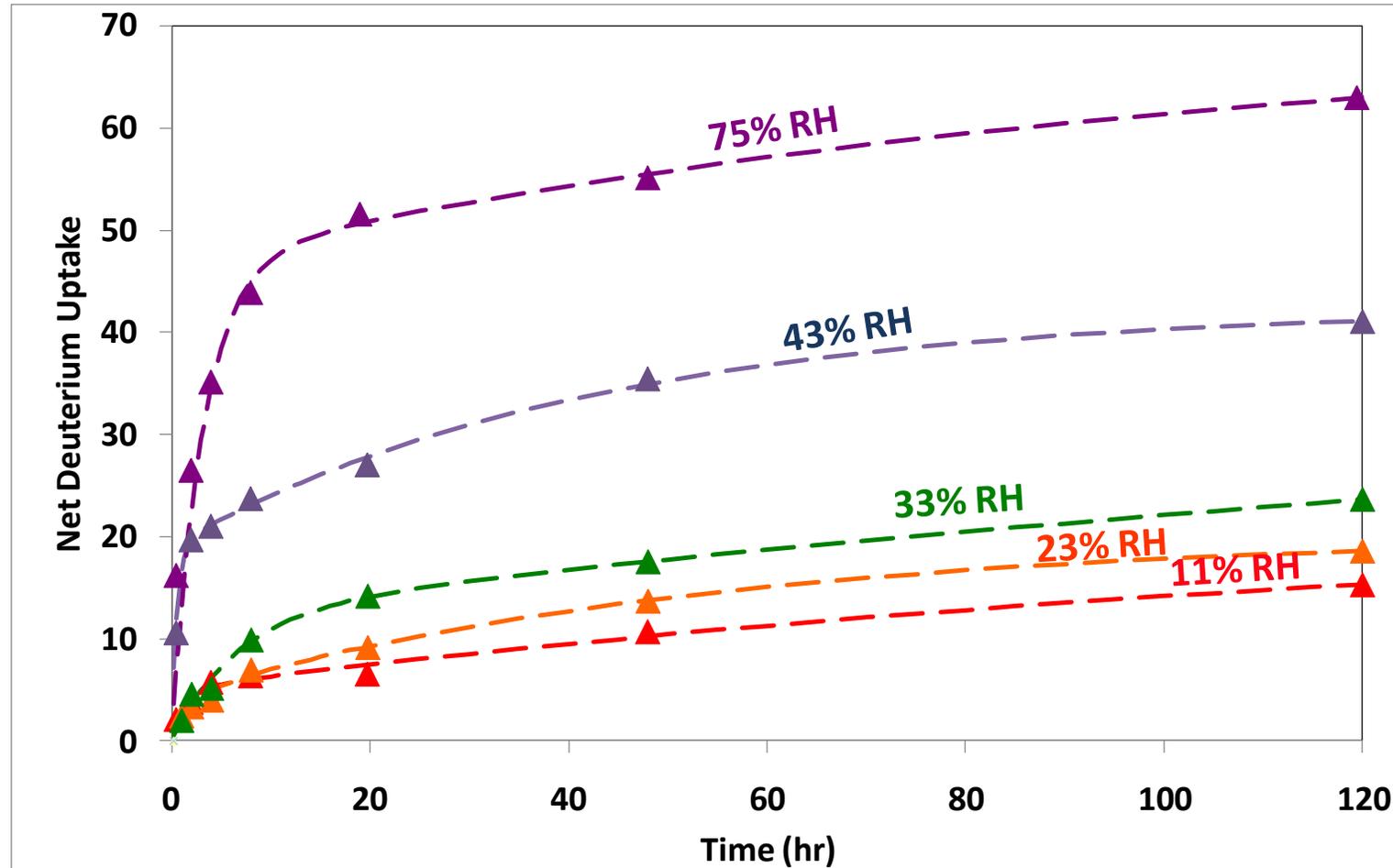
# Effect of RH on deuterium uptake

Intact protein: *Myoglobin* / mannitol 1:1, 5 °C



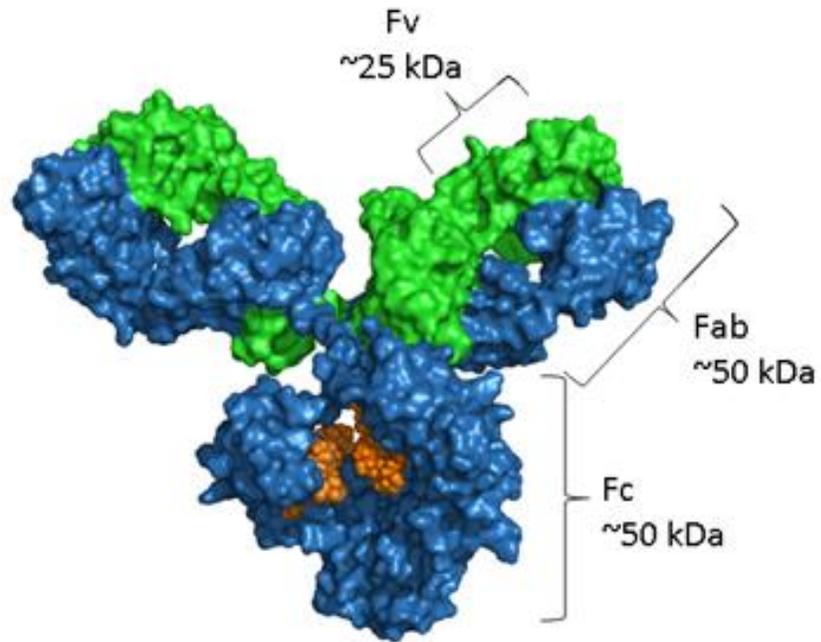
# Effect of RH on deuterium uptake

Intact protein: *Myoglobin* / sucrose 1:1, 5 °C



# mAb formulations

Can ssHDX be applied to mAbs?

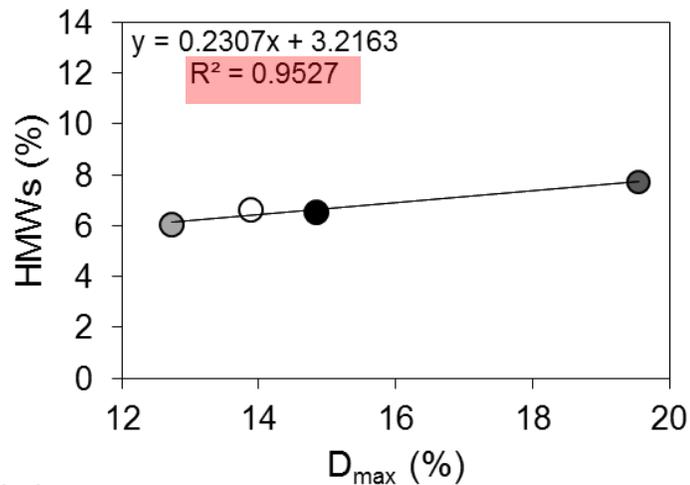


Formulation	Composition		
	Basic composition	Mannitol (mg/mL)	Sucrose (mg/mL)
F1	50 mg/mL mAb1 in buffer at pH 6.0	-	40
F2		-	80
F3		32	8
F4		53	27

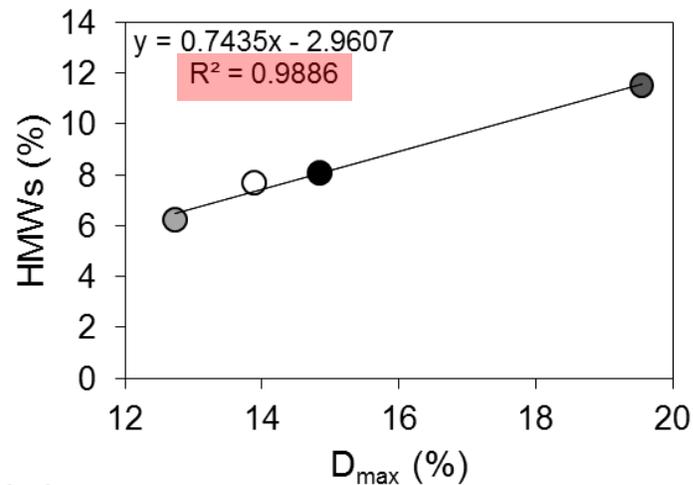
Knowing only this, rank order the storage stability of the four formulations using ssHDX-MS.

# mAb stability and ssHDX-MS

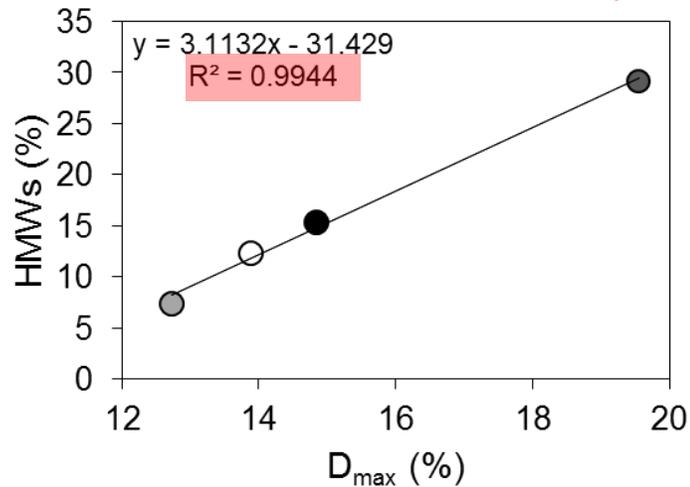
(A) Stored @ 5°C, 960 days



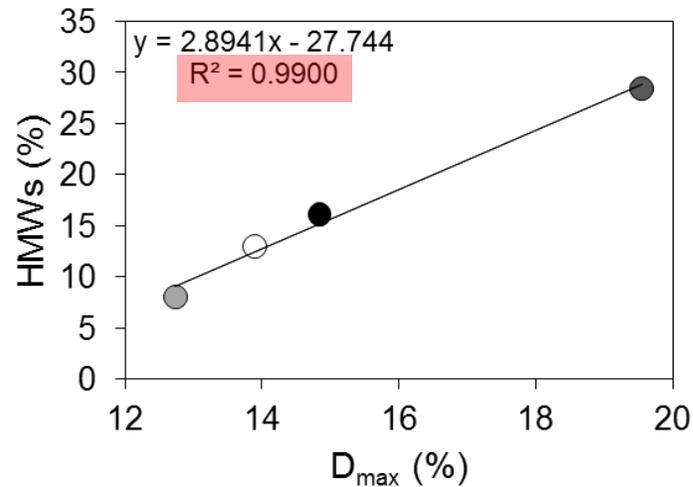
(B) Stored @ 25°C, 960 days



(C) Stored @ 40°C, 960 days

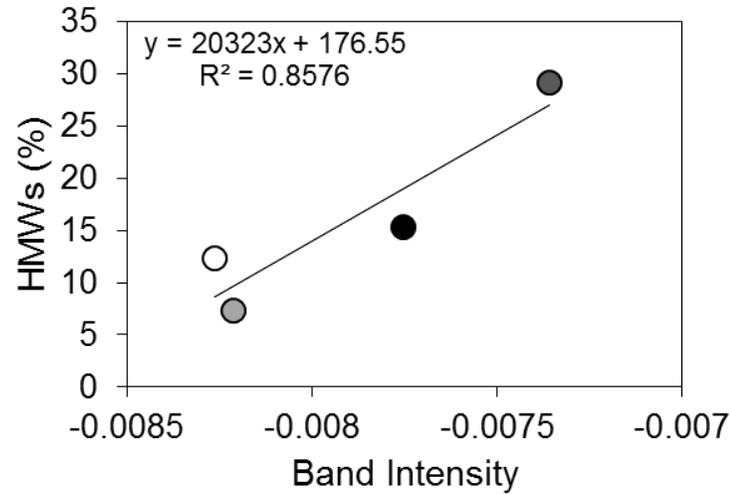


(D) Stored @ 50°C, 180 days

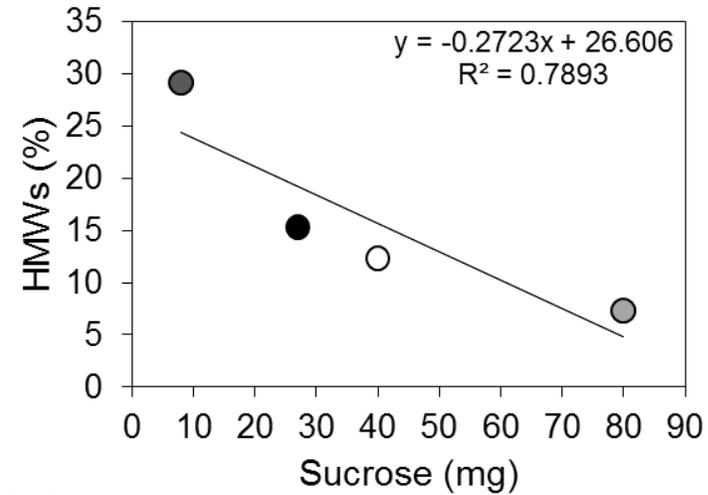


# mAb stability and solid properties

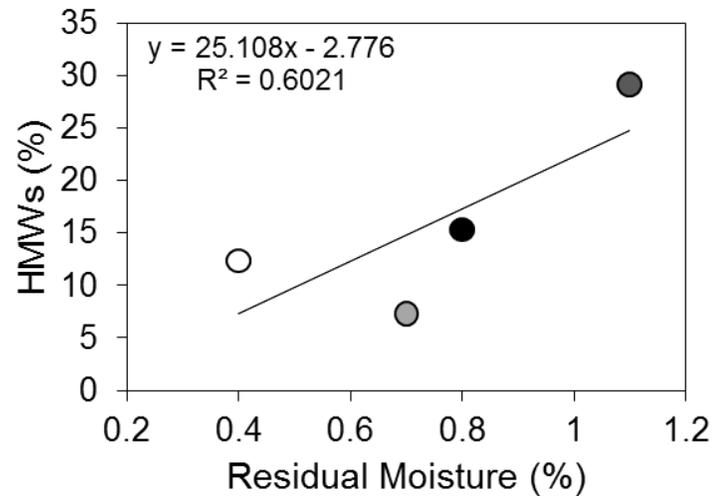
(A) FTIR band intensity



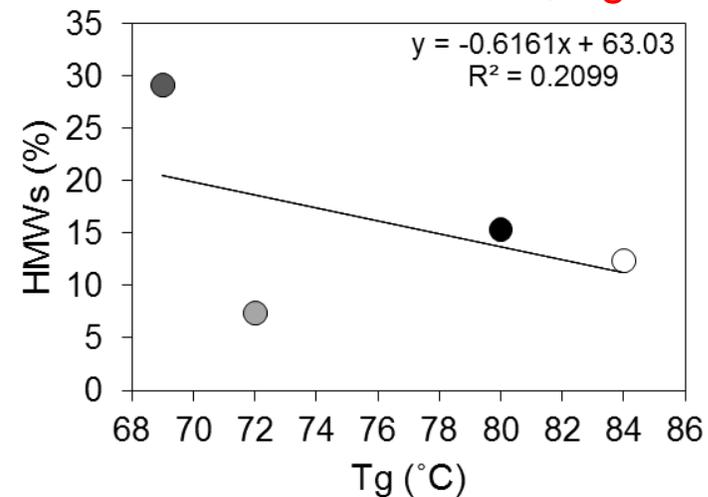
(B) Sucrose content



(C) Moisture content

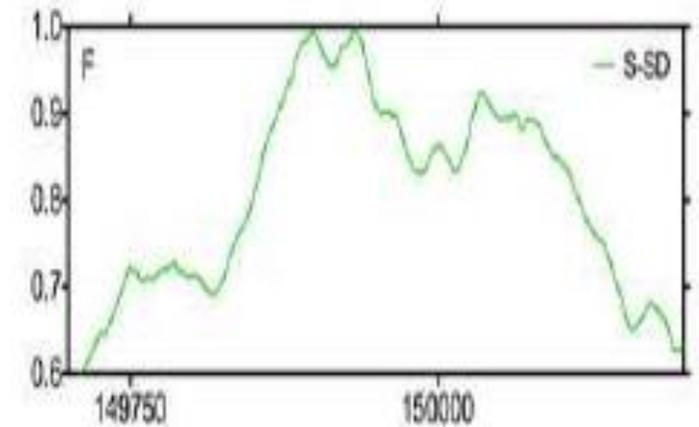
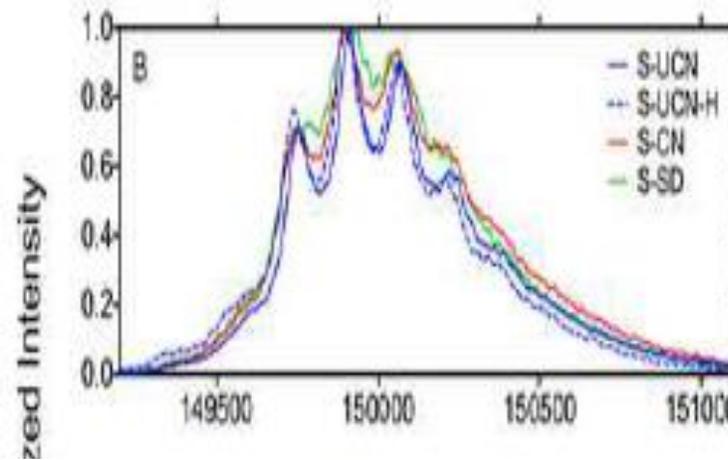
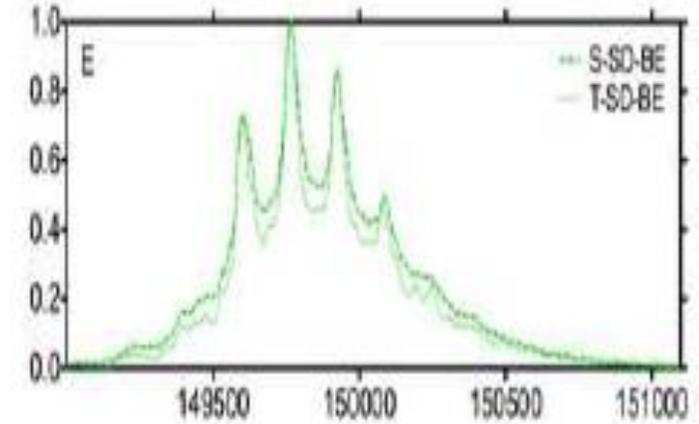
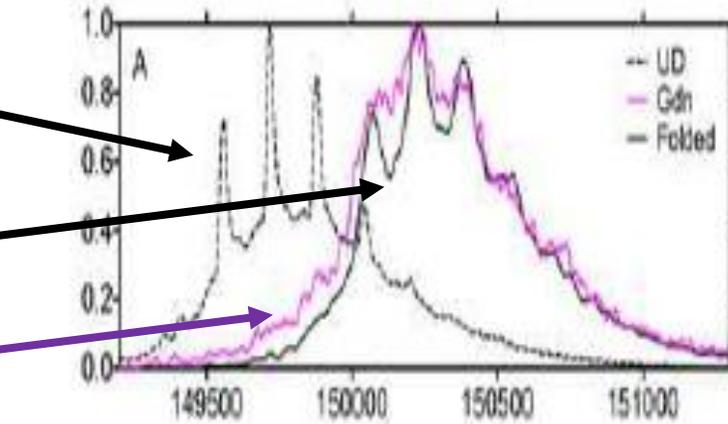


(D) Glass transition, Tg

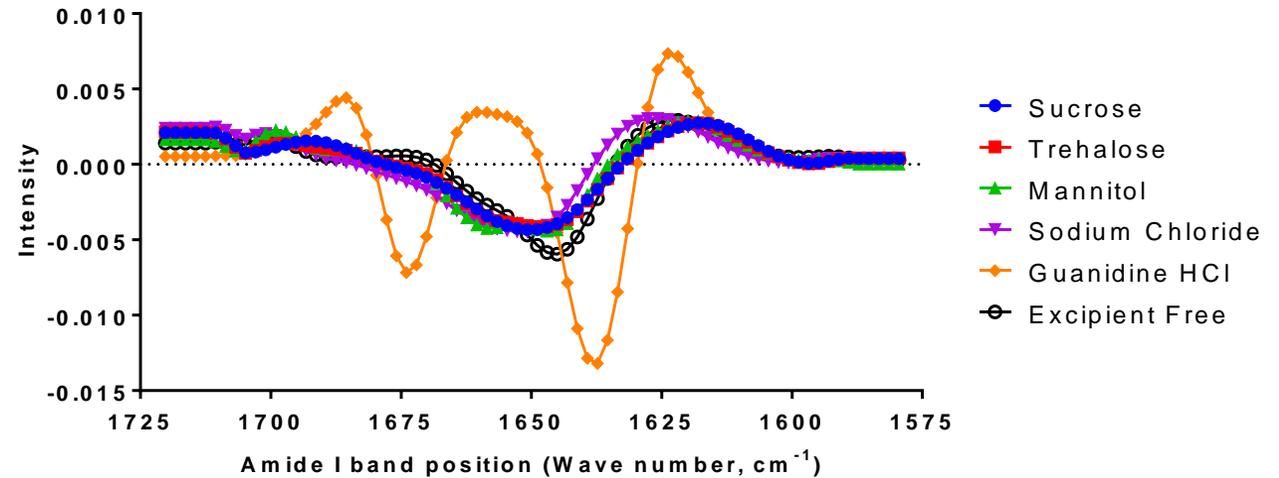
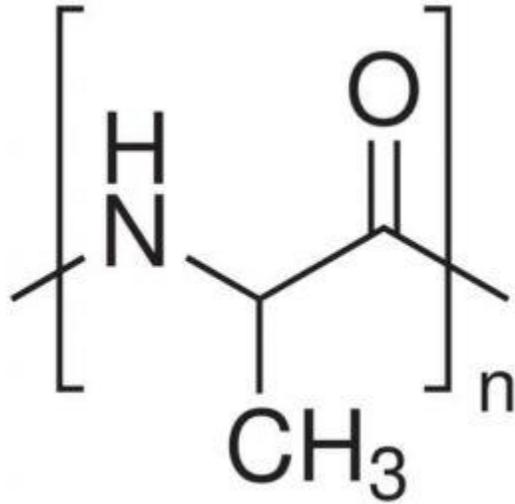


# Process effects

- Native
- Native, deuterated
- Unfolded, deuterated
- Lyophilized, uncontrolled nucleation
- Lyophilized, controlled nucleation
- Lyophilized, uncontrolled nucleation with hydration
- Spray dried

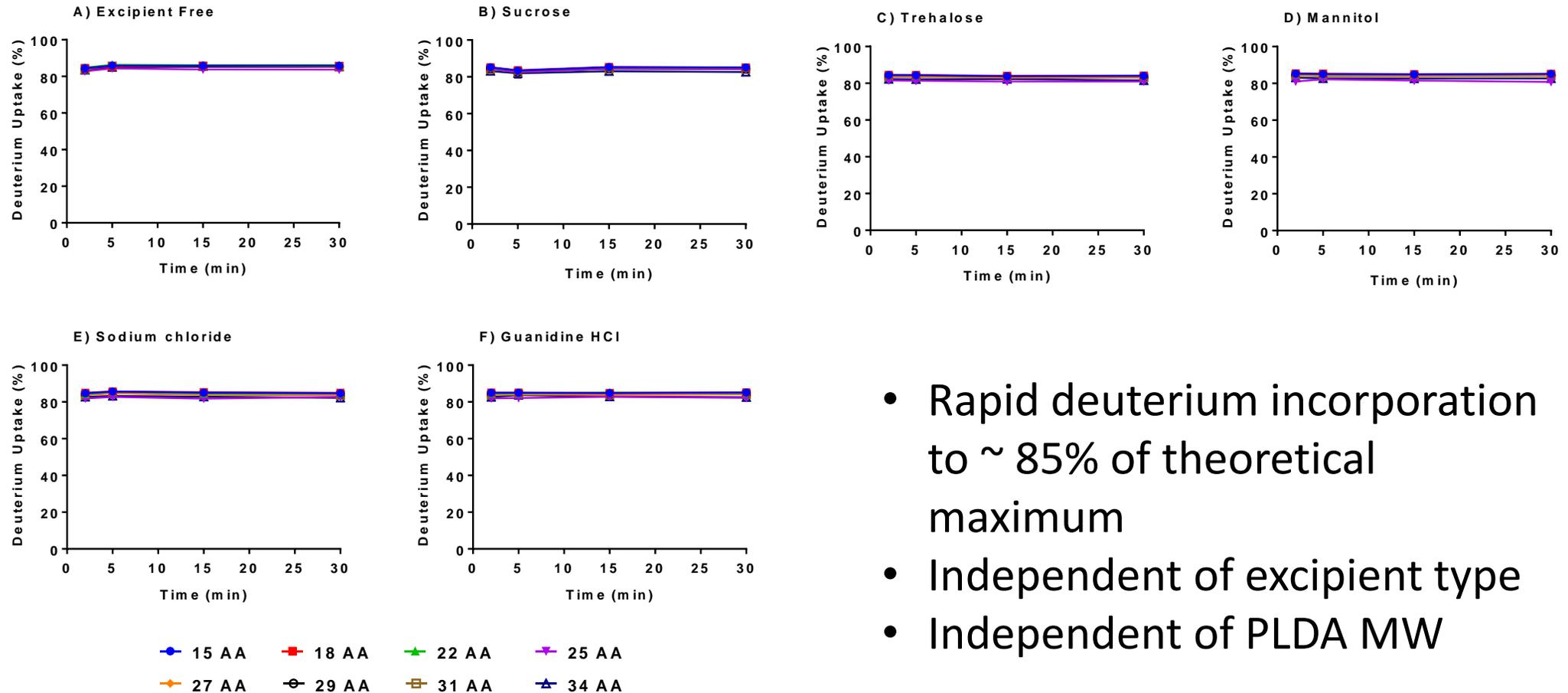


# Poly-D,L-alanine (PDLA)



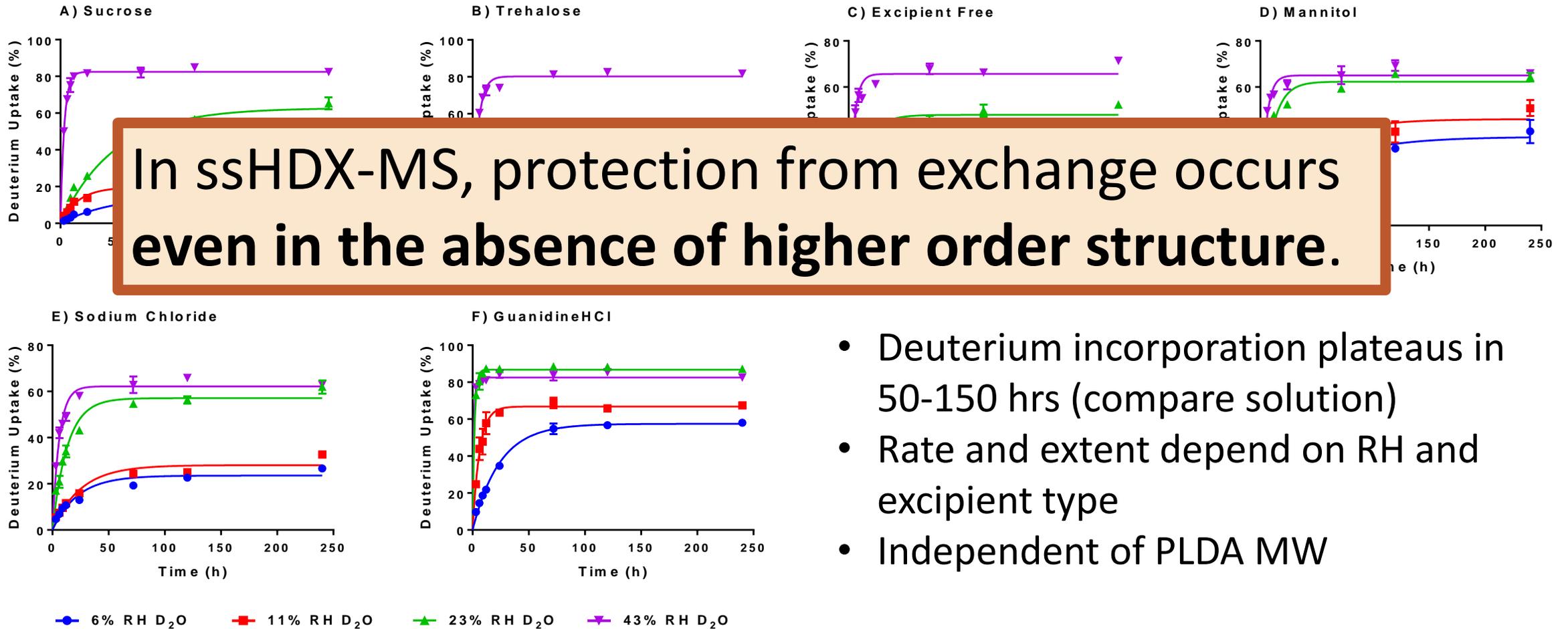
- Unstructured poly-amino acid
- Polydisperse mixture – oligomers with 15-34 aa selected
- Formulated with sucrose, trehalose, no excipient, mannitol, NaCl, Gdn HCl
- Lyophilized solids and solution controls

# Solution HDX-MS of PLDA

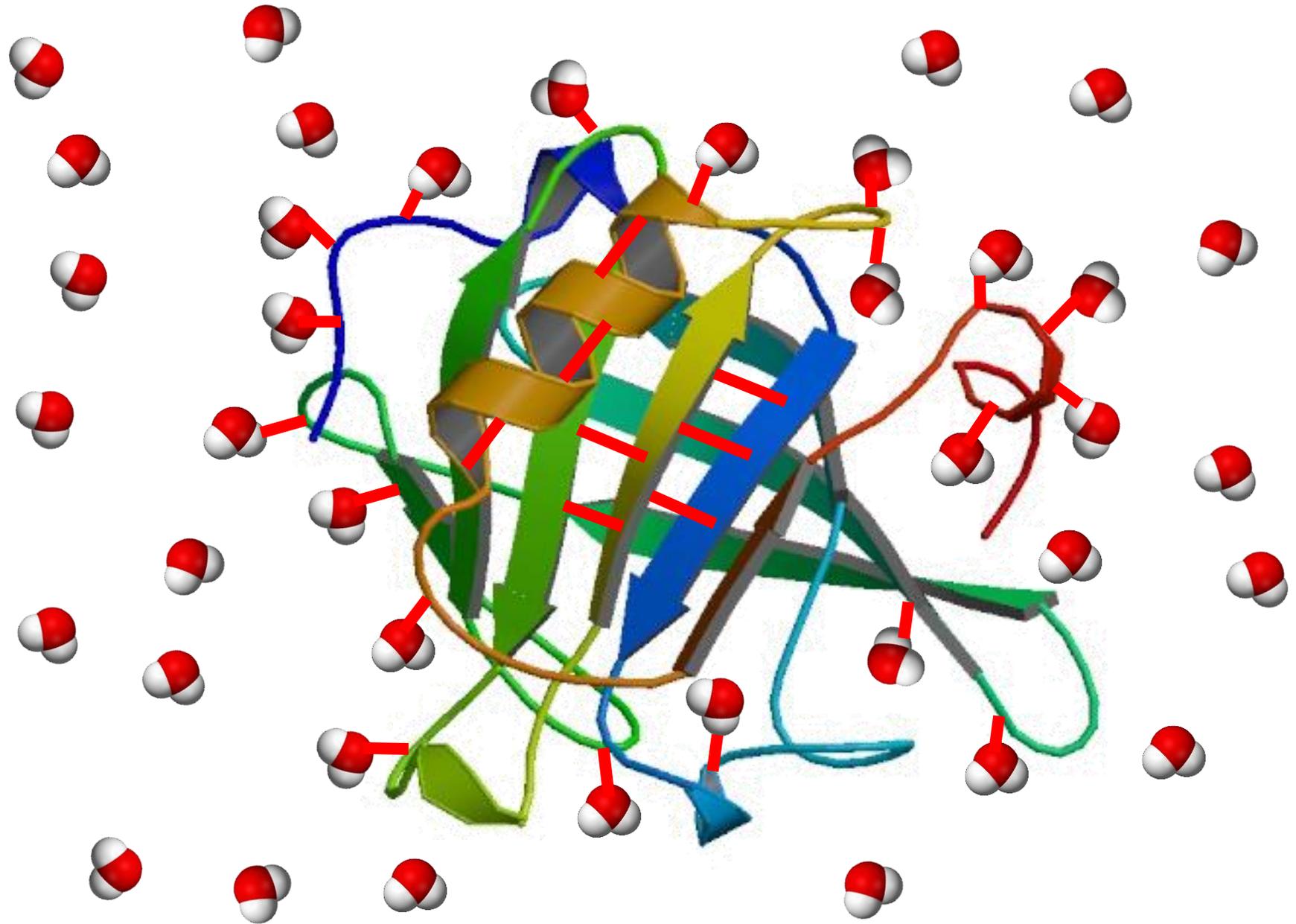


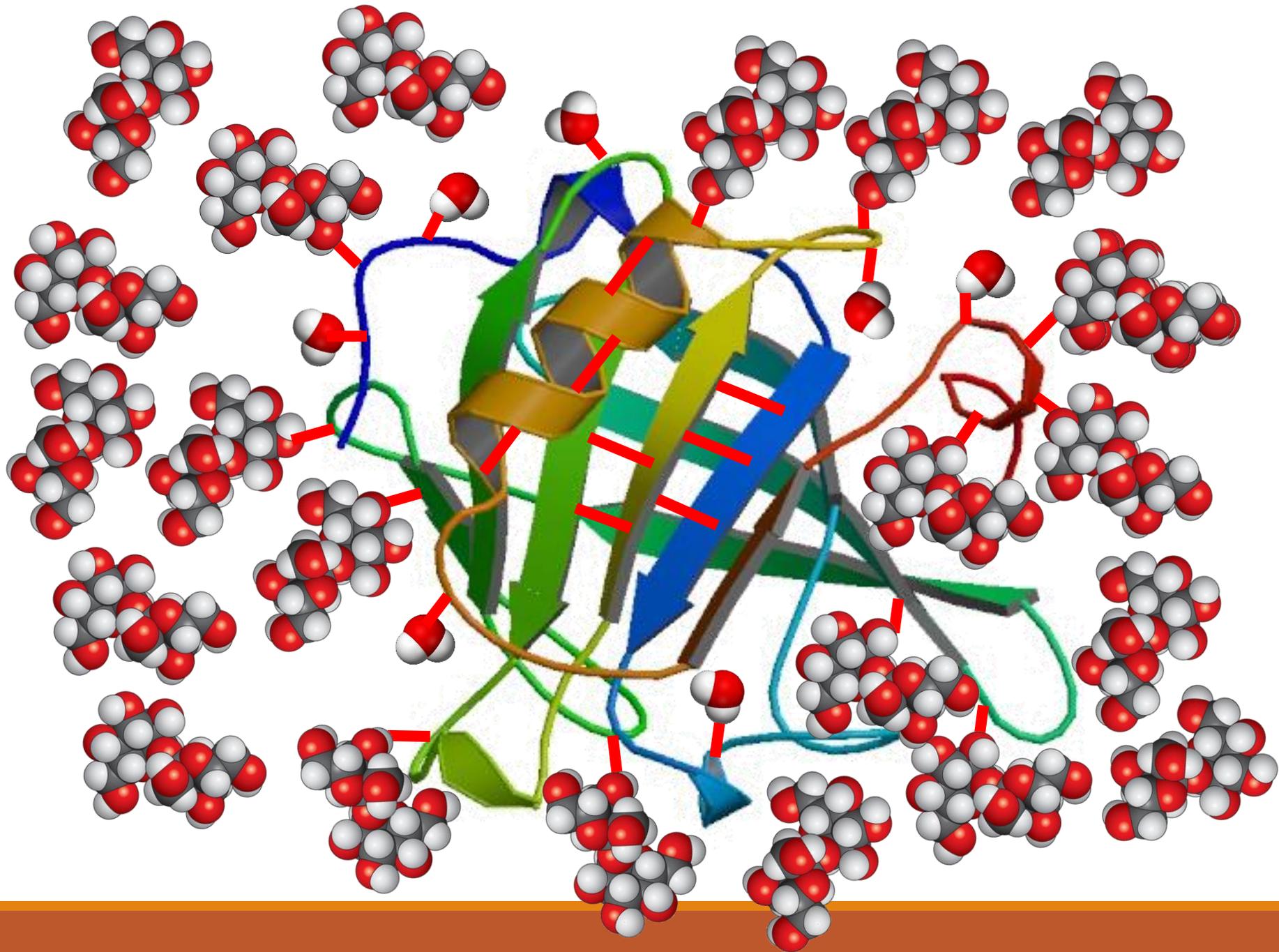
- Rapid deuterium incorporation to ~ 85% of theoretical maximum
- Independent of excipient type
- Independent of PLDA MW

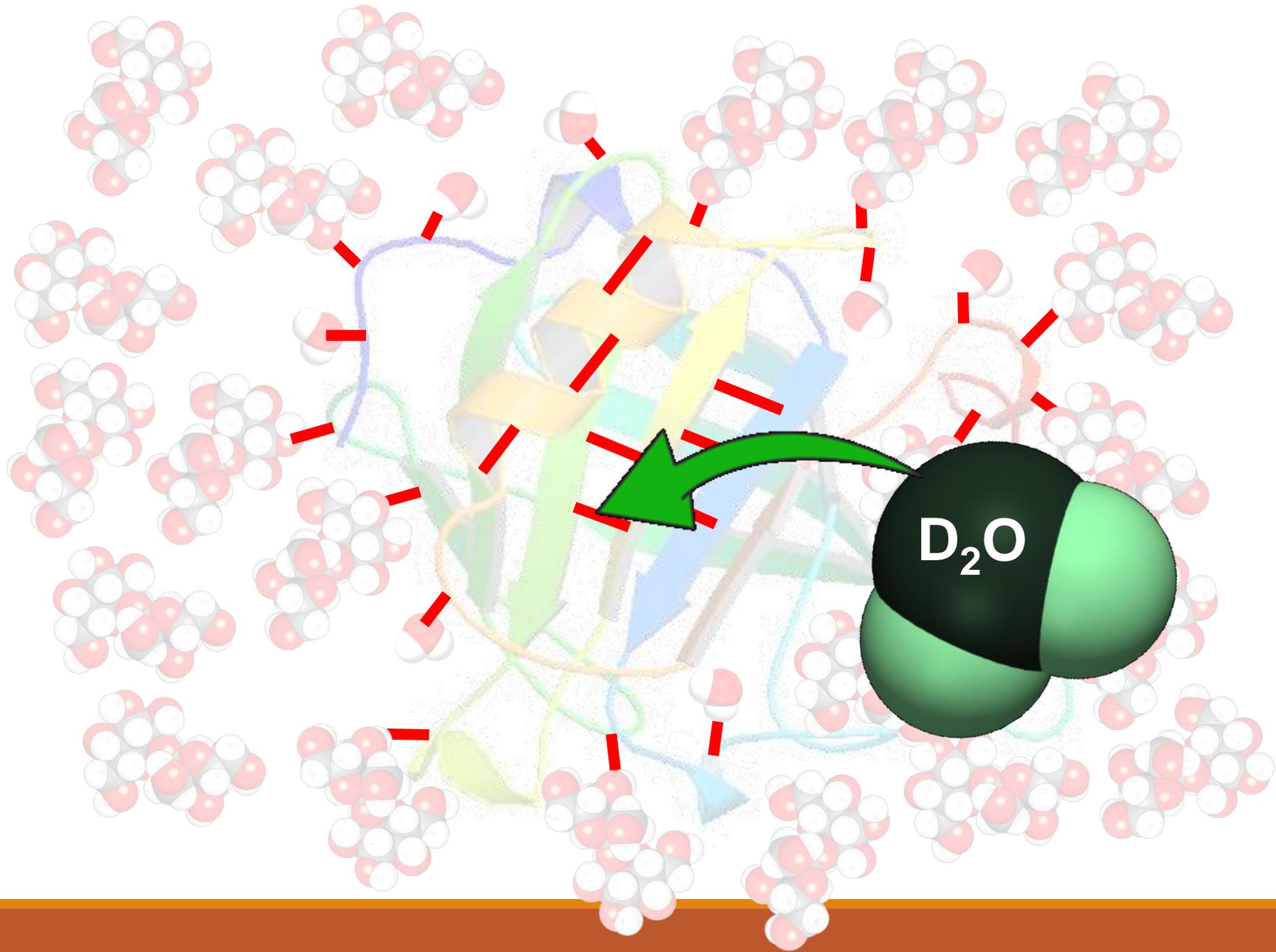
# ssHDX-MS of PDLA



- Deuterium incorporation plateaus in 50-150 hrs (compare solution)
- Rate and extent depend on RH and excipient type
- Independent of PLDA MW







# Summary

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- ssHDX-MS **interrogates the H-bond network** of proteins in solid powders, providing information on HOS and matrix interactions with peptide-level resolution.
- For a given protein, ssHDX-MS kinetics are affected by excipient type and amount, RH in D<sub>2</sub>O, temperature and processing method.
- The extent of deuterium incorporation ( $D_{\max}$ ) is **correlated with aggregation** on storage.
- Studies with unstructured peptides (PDLA) show protection from exchange in ssHDX-MS, in the absence of structure.