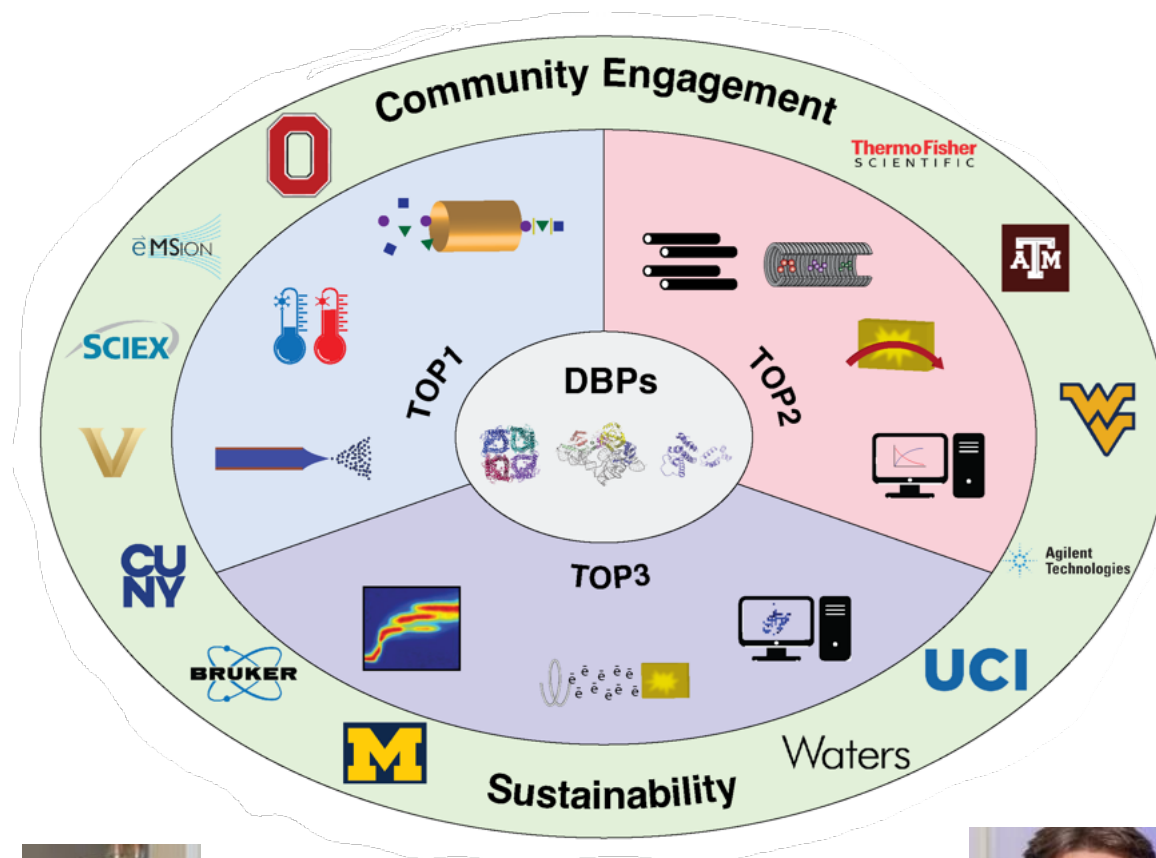


# NIH Biomedical Technology Optimization and Dissemination Center

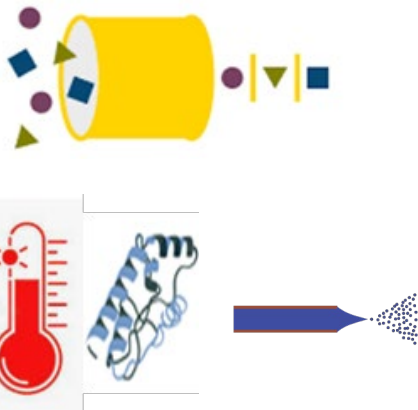
## *Native Mass Spectrometry Guided Structural Biology*



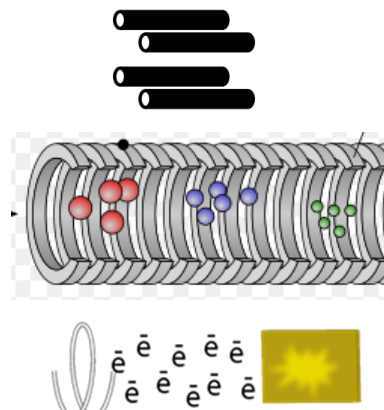
# Native MS Guided Structural Biology

user-compatible native MS technology to characterize the assembly and disassembly of macromolecular protein complexes

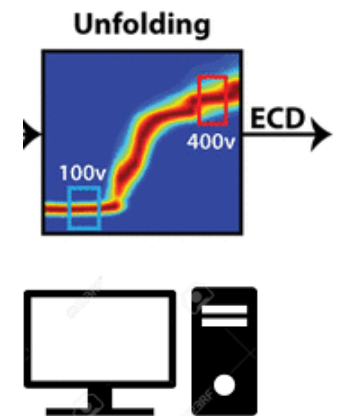
## TOP1 Front End/ Solution Phase



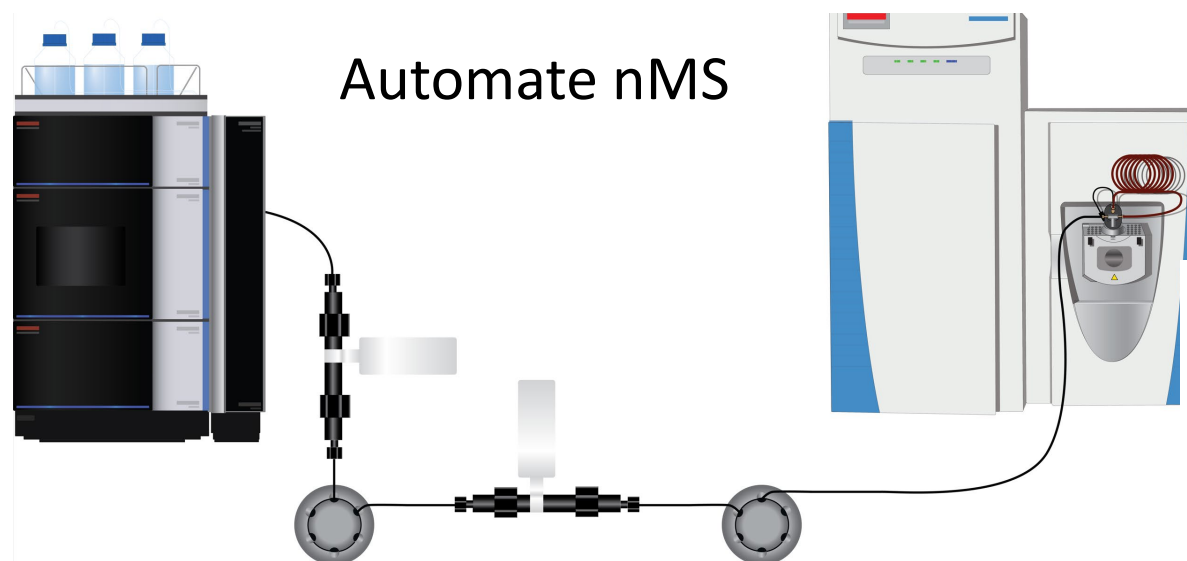
## TOP2 Ion Selection/ Separation/Manipulation



## TOP3 Ion Stability/ Computations



# 1D and 2D Online buffer exchange and CZE

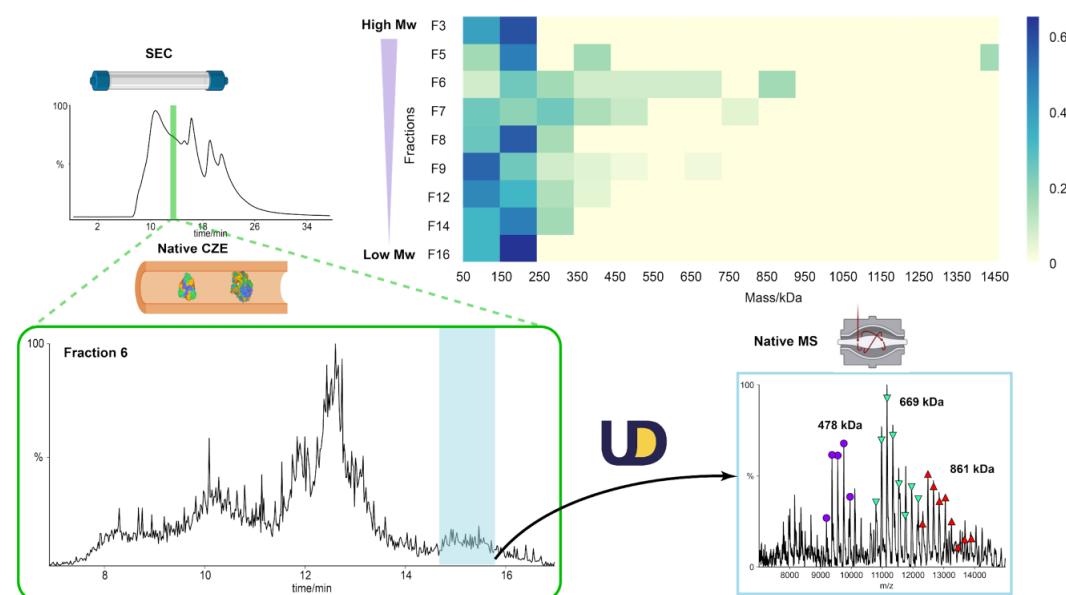


Automate nMS

column now commercial  
adoption in multiple labs

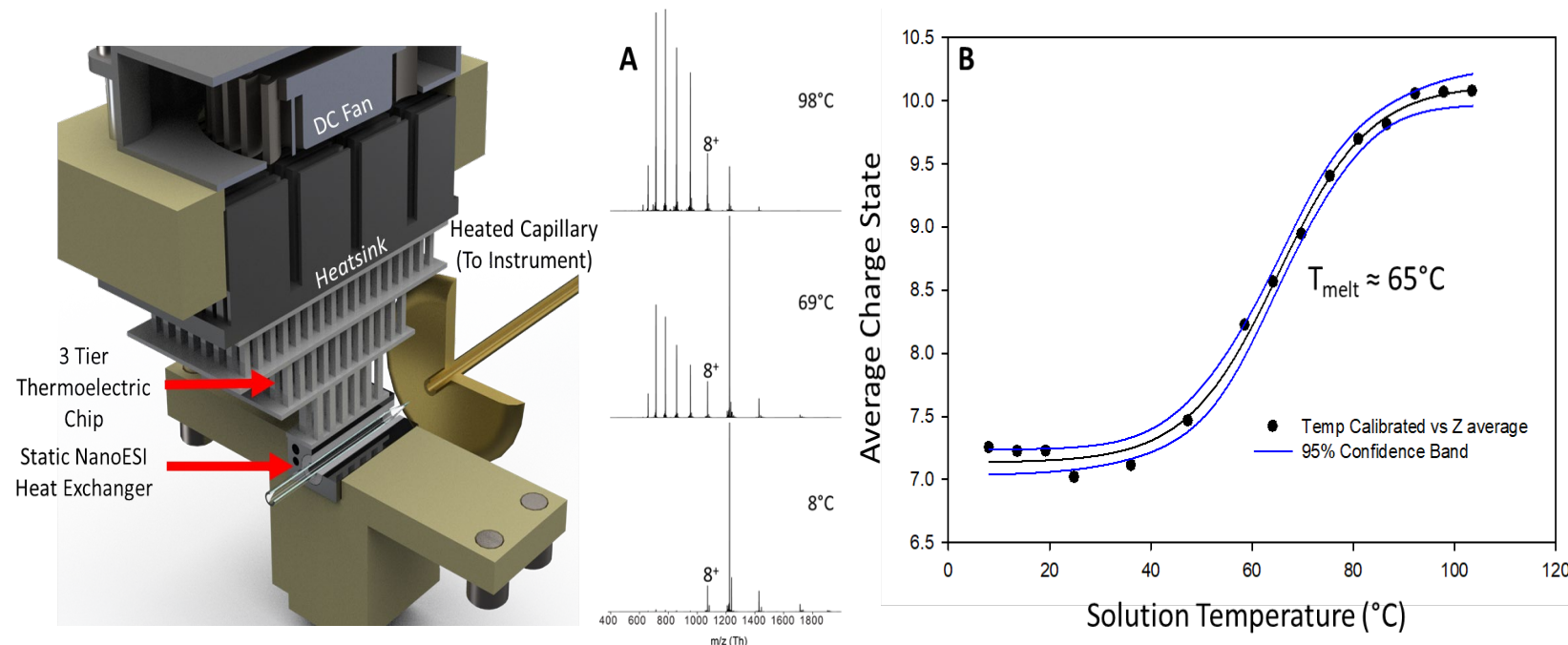
SEC CZE nMS SID

Mass distribution by SEC-nCZE-MS



[https://connect.acspubs.org/CENWebinar\\_Thermo\\_3\\_23\\_22](https://connect.acspubs.org/CENWebinar_Thermo_3_23_22)

# Variable temperature ESI (vT-ESI)

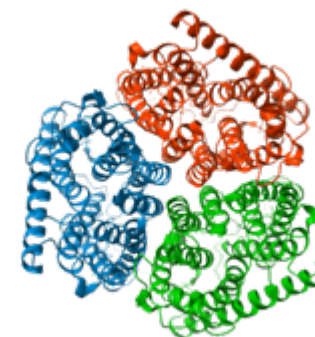


## Driving Biomedical Projects

Amyloid disease



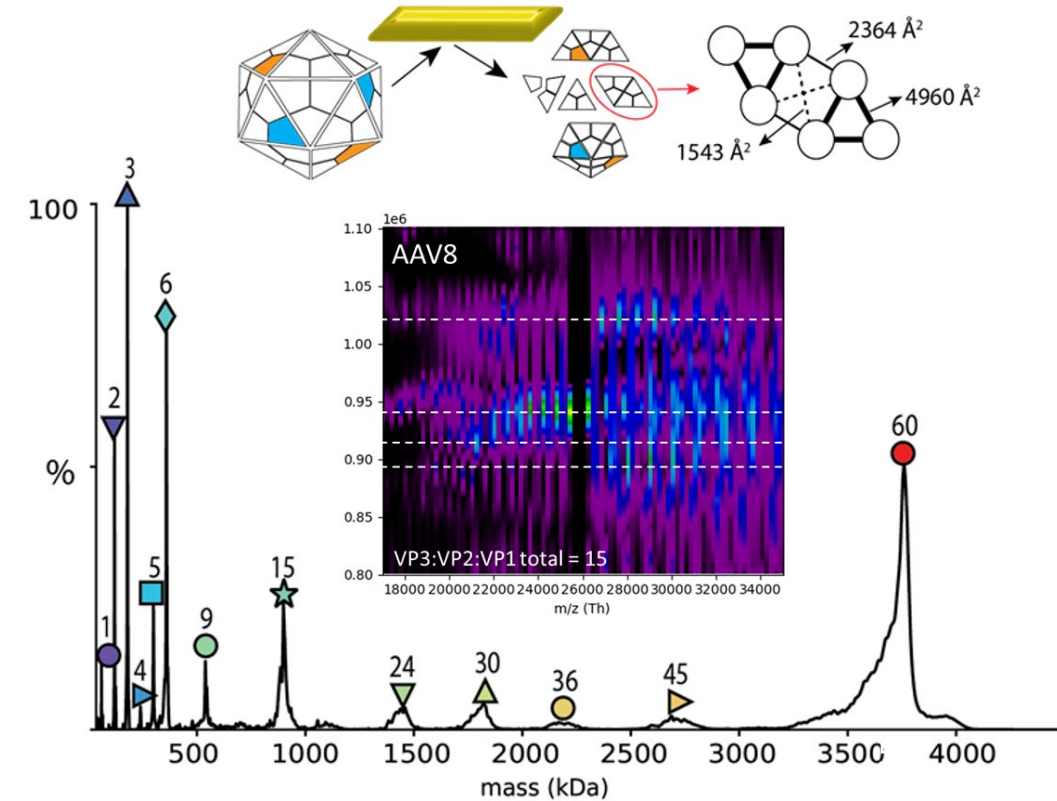
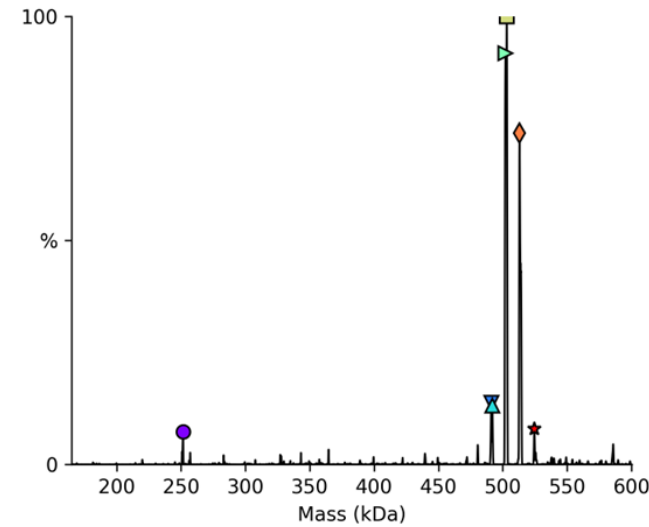
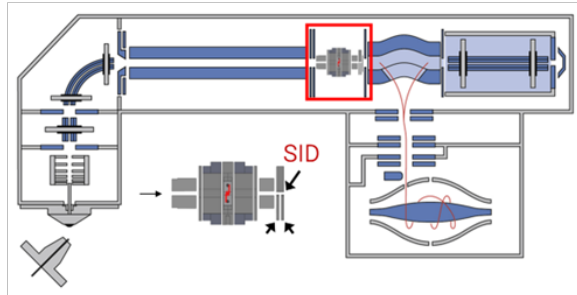
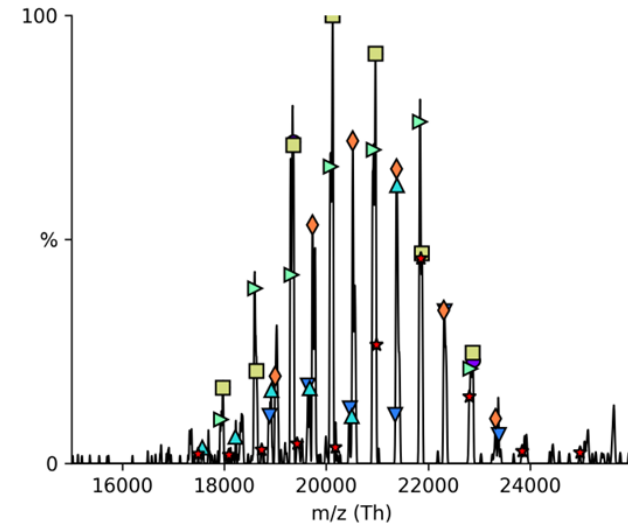
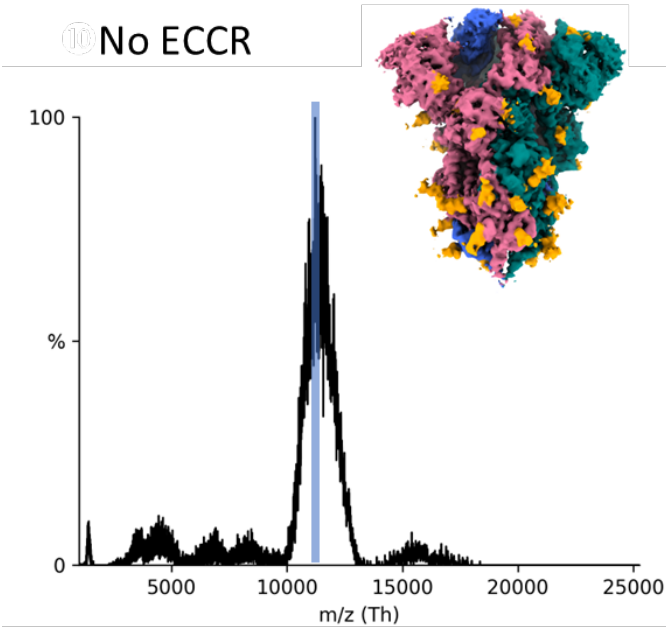
Membrane protein lipid interactions



adoption in multiple labs  
pharma collaborations  
multi-vendor adoption possible

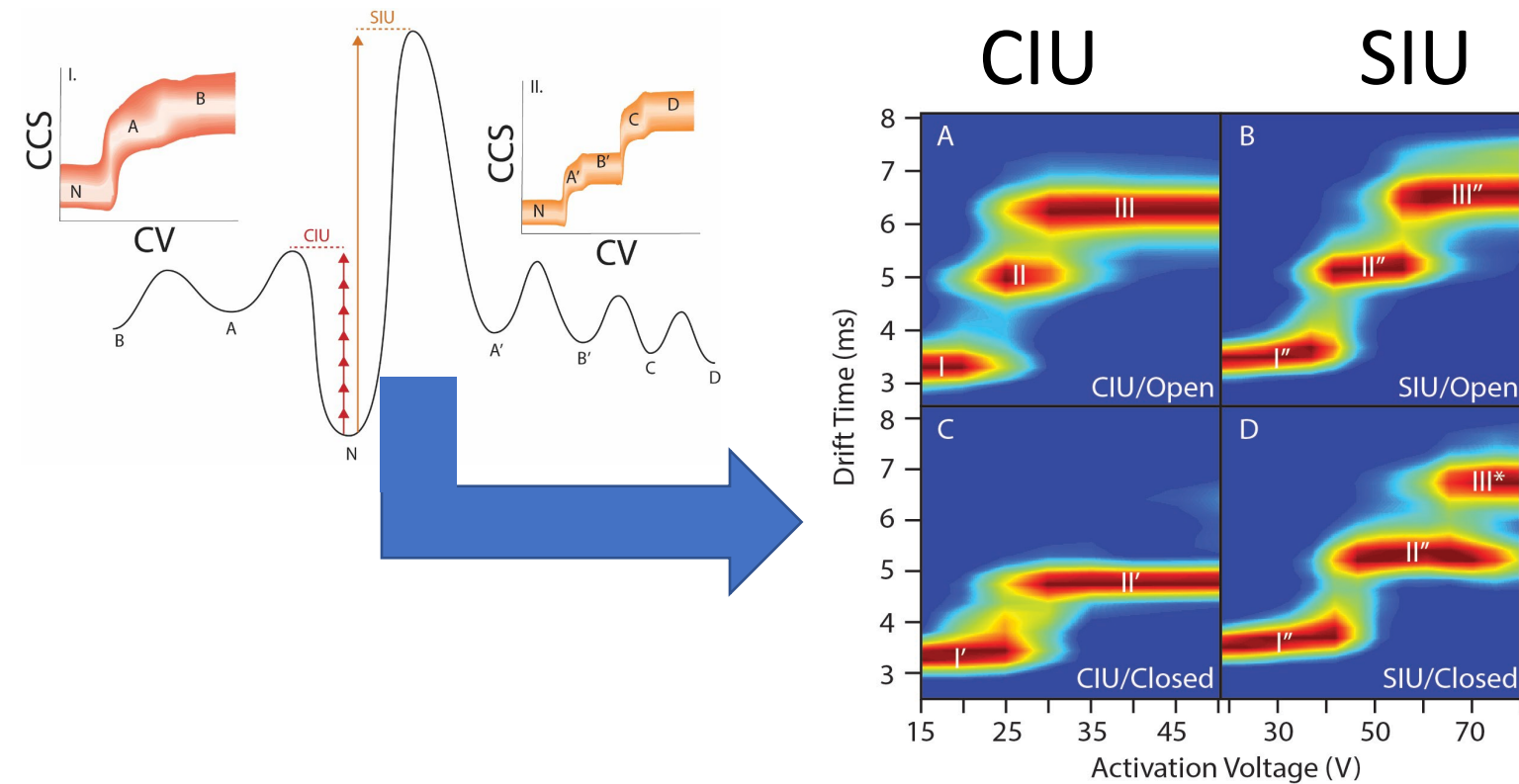
Dissecting the Thermodynamics of ATP Binding to GroEL One Nucleotide at a Time  
T. E. Walker et al. ACS Cent Sci 2023, 9, 466-475.

# Electron Capture Charge Reduction, Surface Induced Dissociation



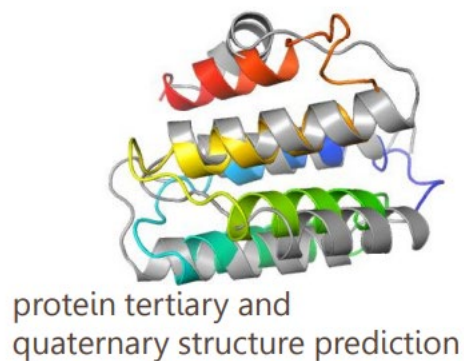
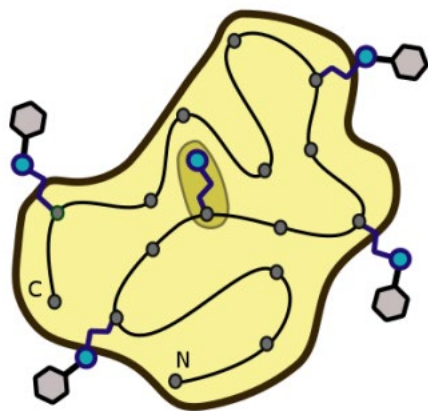


# TOP3, Protein Stability: Collision induced unfolding

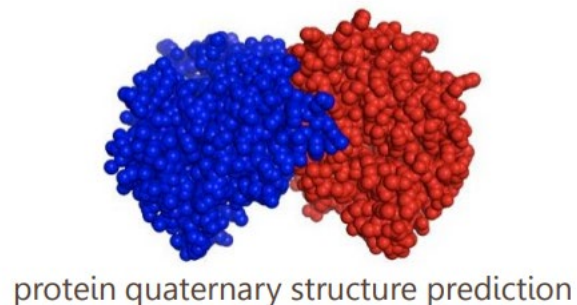
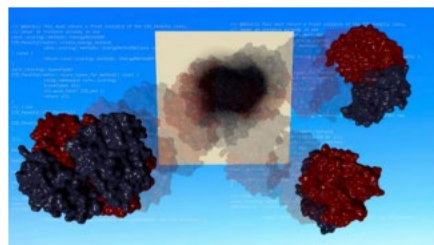


CIU option across dozens of labs worldwide  
many pharma collaborations  
multi-vendor adoption in progress

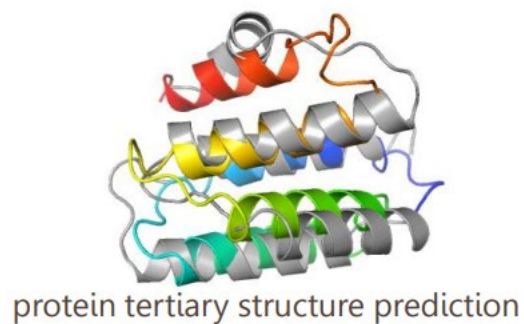
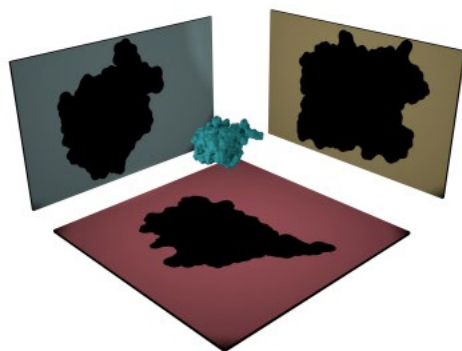
# Computations: Integrative Modeling for Quaternary Structure



protein tertiary and  
quaternary structure prediction



protein quaternary structure prediction



protein tertiary structure prediction

Combine MS and/or ion mobility data with complementary low resolution structural data for integrative modeling

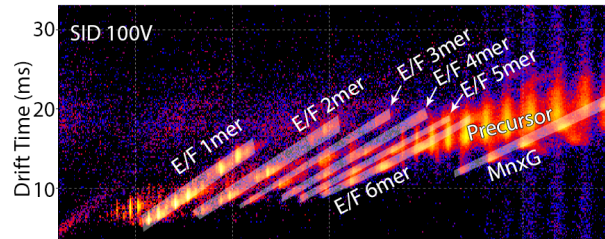
tools are beta tested and provided as developed, extended, and improved (Rosetta or OpenFold)

# Complementarity between native MS and cryoEM

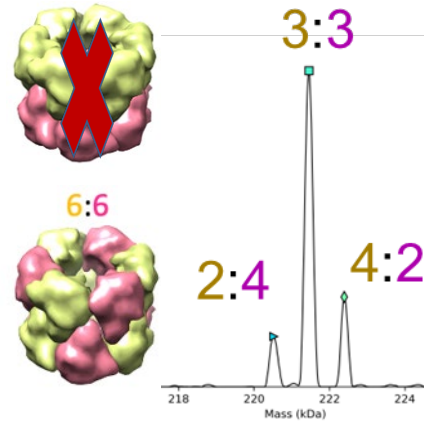
TNH



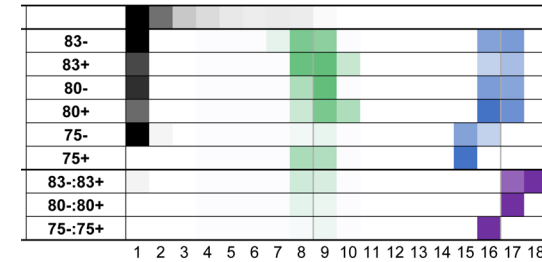
Mnx



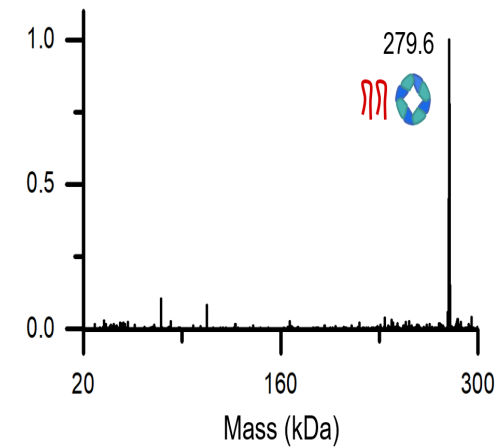
PDX



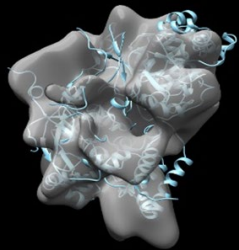
Red beta



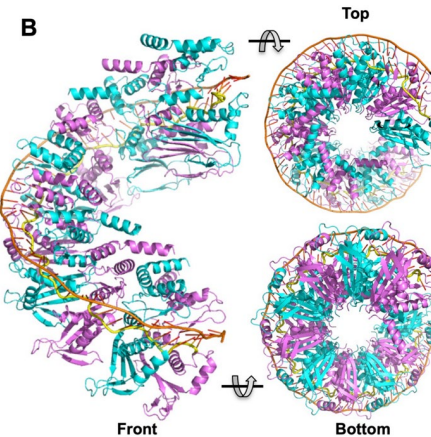
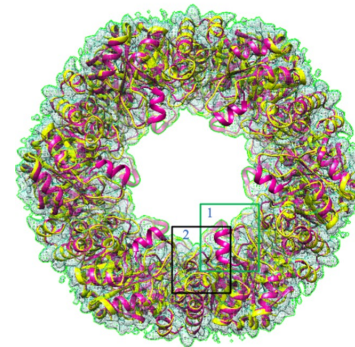
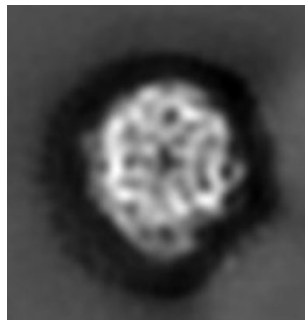
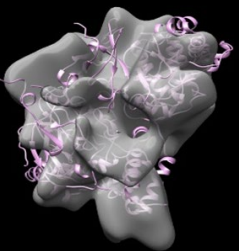
VP40



Complex 1



Complex 2



RNA-generated ring

