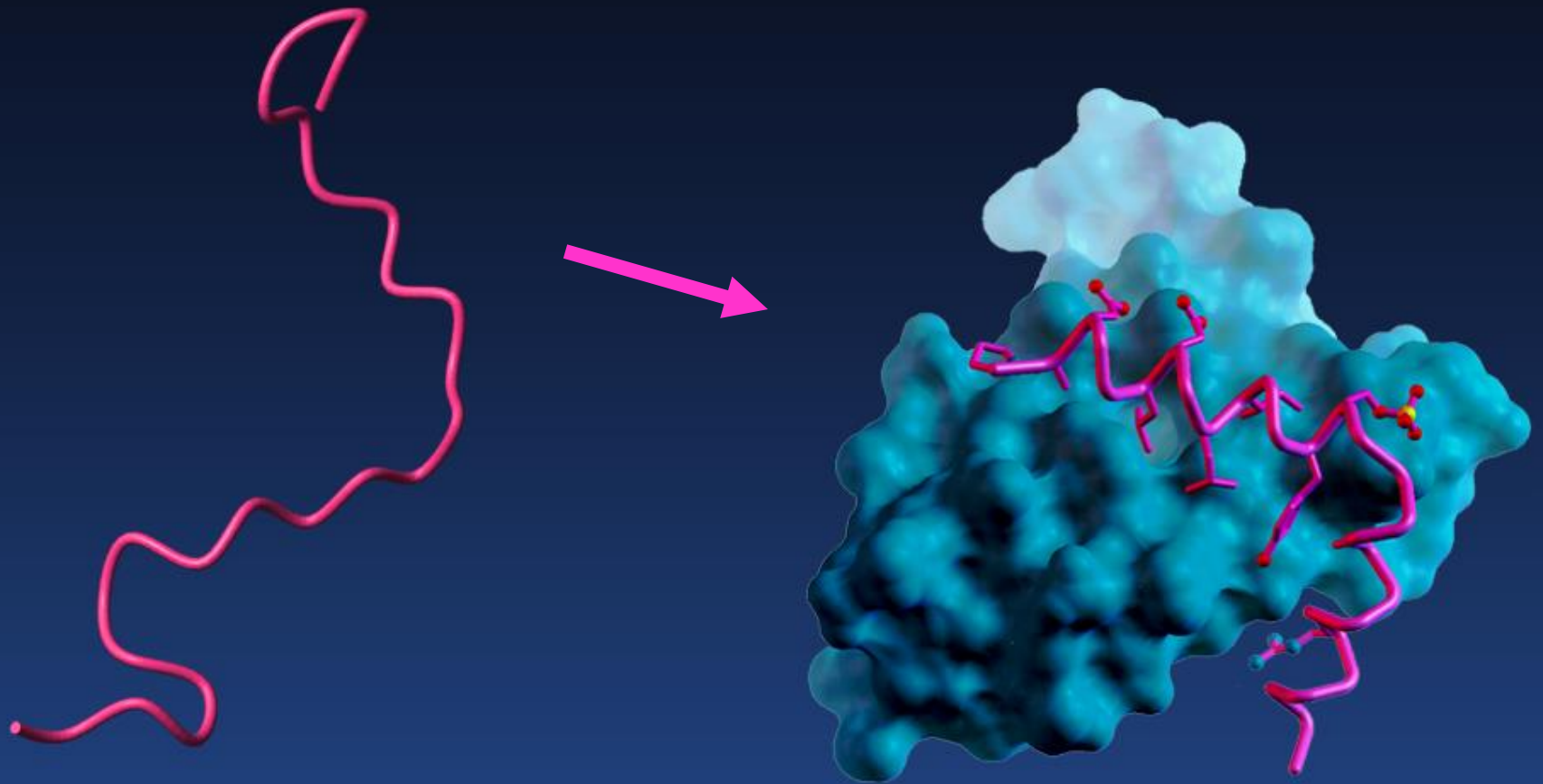


Solution NMR of intrinsically disordered proteins at ultrahigh fields



Intrinsically disordered proteins (IDPs) and intrinsically disordered regions (IDRs)

- unable to fold spontaneously into well-defined, stable globular 3D structures
- 30-50% of eukaryotic proteins are predicted to be partially or entirely disordered
- many eukaryotic proteins contain structured domains and long disordered regions

The abundance and importance of IDPs was not recognized until the mid-1990s

The protein conformational continuum

Dynamic disorder



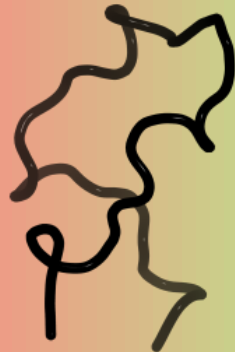
Order



extended



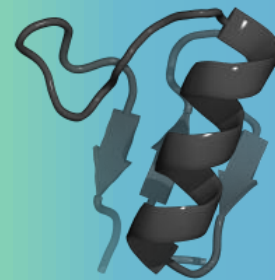
transient secondary structure



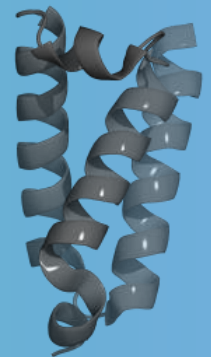
compact globule



molten globule



disordered loop



folded protein

Compaction, foldedness



IDPs play a central role in dynamic regulatory and assembly processes in the cell

- central component of the control circuitry of the cell (transcription, translation, cell cycle control, signaling, etc.)
- associated with debilitating diseases (cancer, leukemia, cardiovascular disease, diabetes, infectious disease, neurodegenerative diseases, traumatic brain injury)
- disordered regions impart flexibility in assembly of macromolecular complexes
- cellular organization (form membrane-less compartments)
- ramifications for basic molecular and cell biology, bioenergy, and design of bio-inspired materials

IDPs play a central role in the dynamic regulation of key cellular processes

- unique characteristics of IDPs impart flexibility and complexity to dynamic cellular signaling networks
- IDP signaling modulated by posttranslational modifications (phosphorylation, acetylation, methylation, ubiquitination, SUMOylation, O-GlcNAc addition)
- PTMs modulate interactions with target proteins and determine signaling outcome (switches, rheostats, threshold responses)
- understanding of IDPs is central to understanding regulatory and signaling networks in the cell

The Human Dark Proteome Initiative

Executive committee

Peter Wright (chair)

Jean Baum

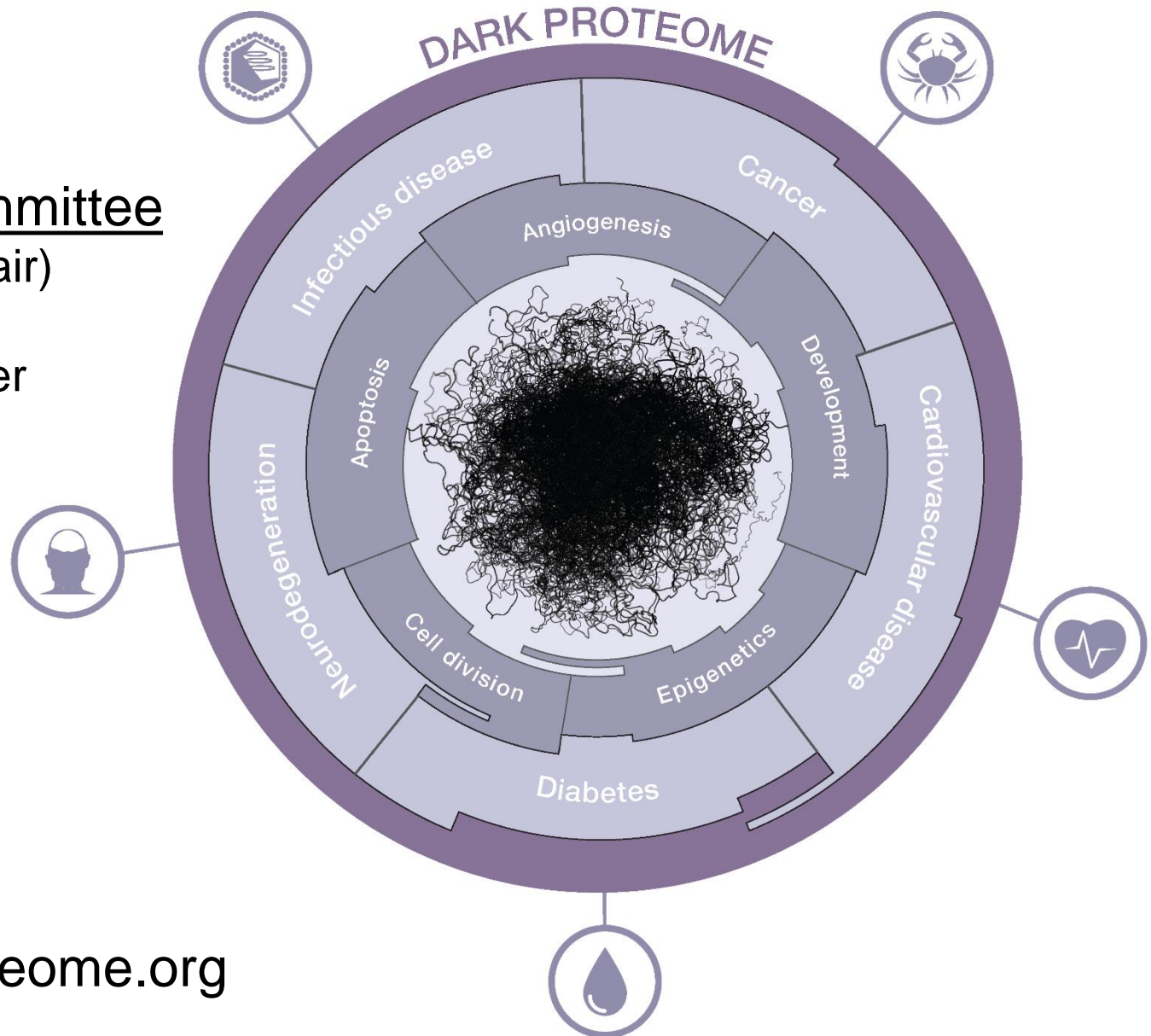
Steven Finkbeiner

Jeffrey Hoch

Richard Kriwacki

Arthur Palmer

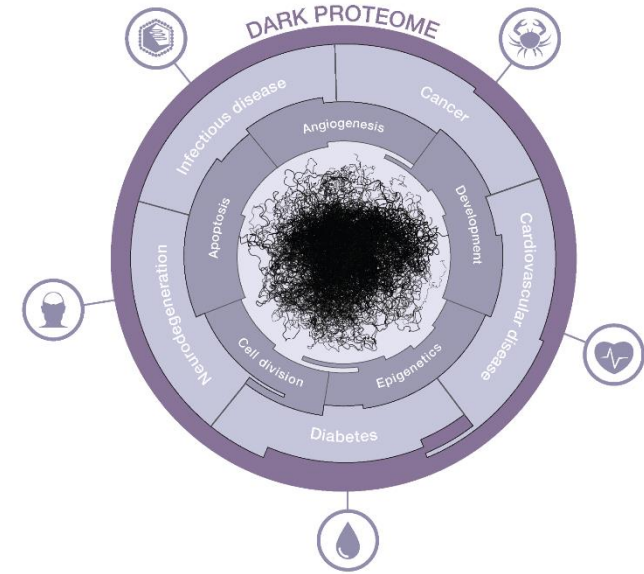
Rohit Pappu



<http://darkproteome.org>

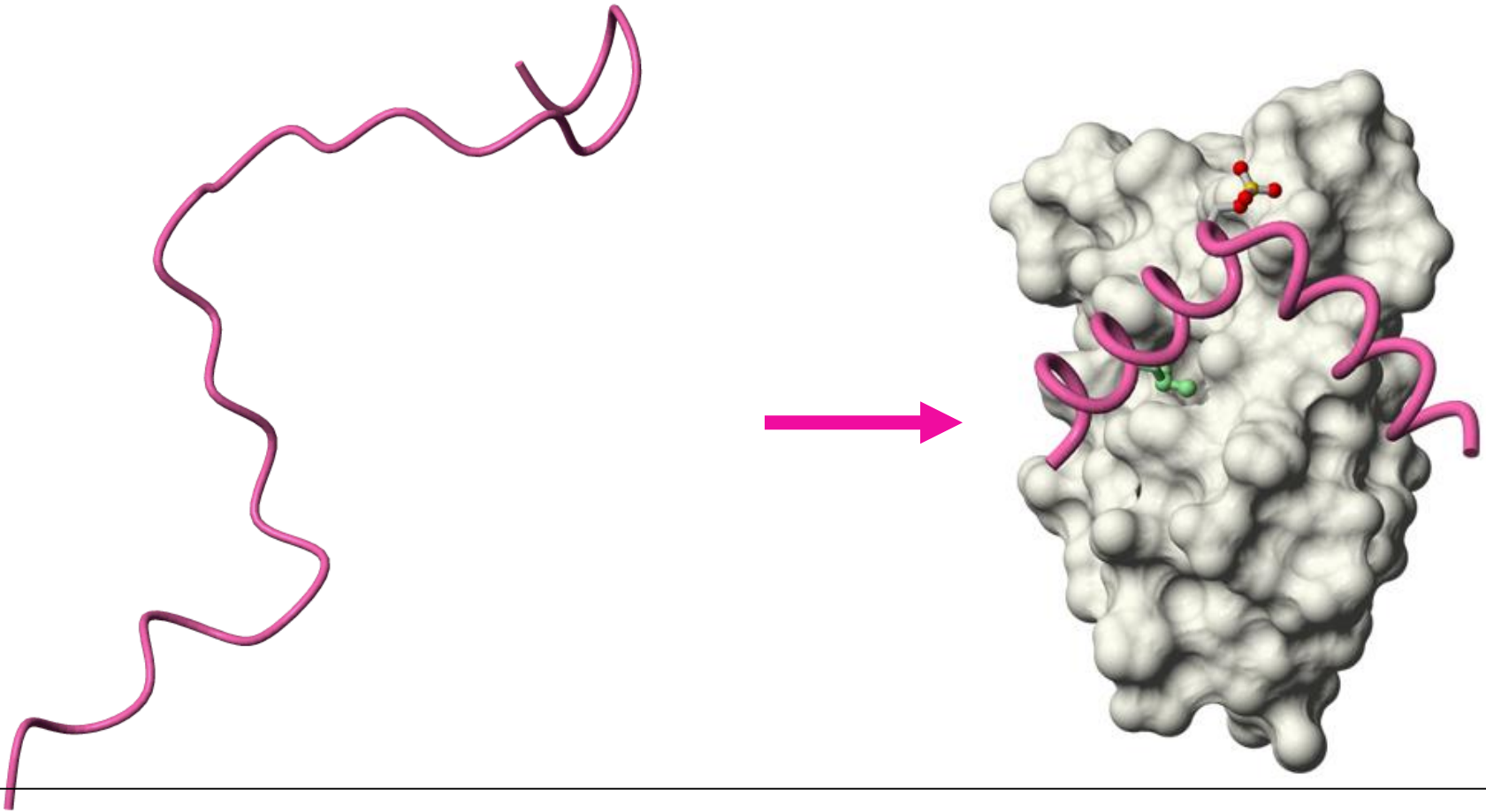
Goals of the dark proteome initiative

- Draw attention to the human dark proteome and its myriad roles in human biology and disease.
- Promote research on intrinsically disordered proteins and “invisible” excited states.
- Advocate for cutting edge infrastructure and creation of centers of excellence to research the human dark proteome and translate discoveries into cures for devastating diseases.



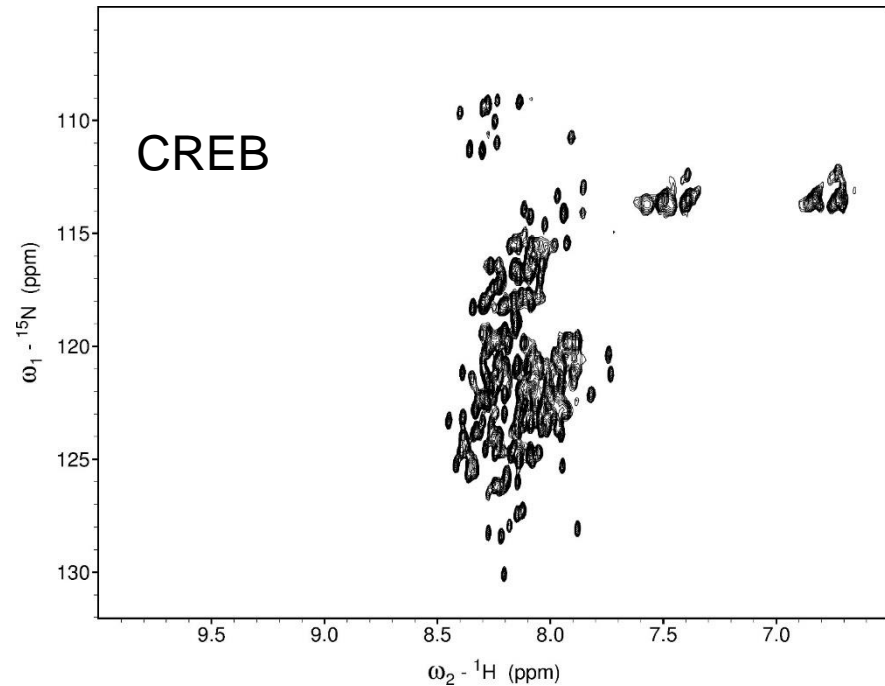
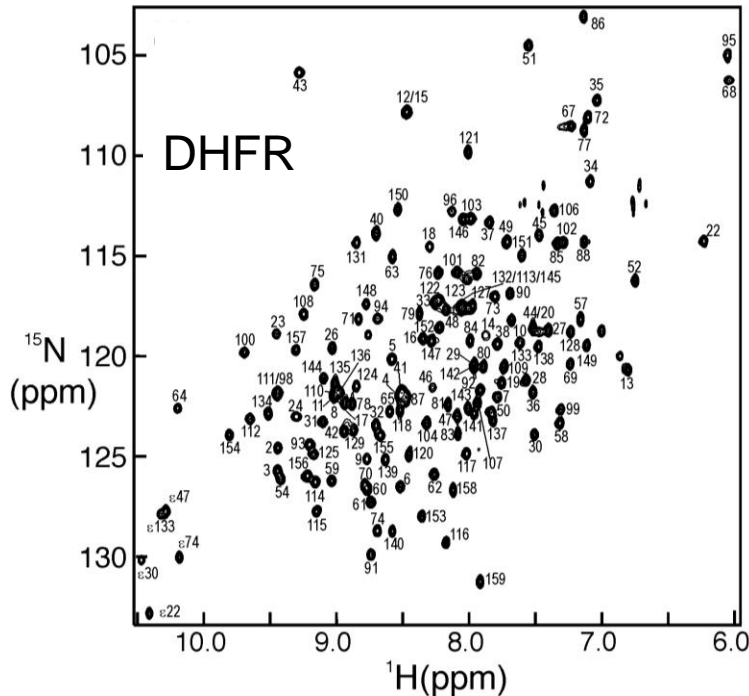
<http://darkproteome.org>

NMR is a unique tool for characterization of IDPs



Insights into structural ensemble, dynamics, interactions, and posttranslational modifications of IDPs - both free and bound to their targets

NMR spectra of IDPs



- limited dispersion and pathological signal overlap
- highly variable line widths
- frequently require $< 10\mu\text{M}$ concentration
- exchange broadening in complexes

NMR spectra of IDPs

- limited dispersion and pathological signal overlap
- exchange broadening in complexes

Solutions:

- apply reductionist, divide-and-conquer strategy
- generate fusion constructs to minimize exchange broadening
- acquire high dimensional (5D, 6D) NMR spectra

Partial solutions only: need for UHF NMR

Divide-and-conquer approach

Pros:

- relatively straightforward, can provide valuable insights

Cons:

- protein domains do not function in isolation but act synergistically in the cell
- divide-and-conquer approach unable to reveal how complex proteins function
- results can be highly misleading

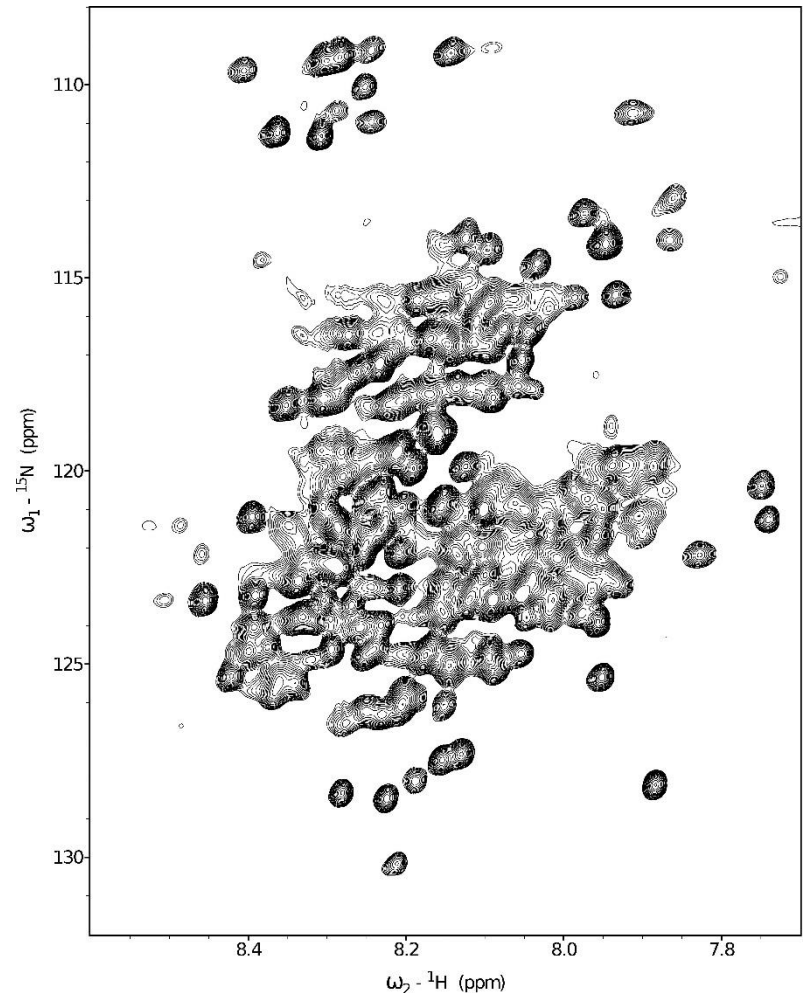
We need holistic approaches to characterize full-length IDPs and their interactions

TROSY spectrum of ^{15}N , ^2H CREB(1-341)

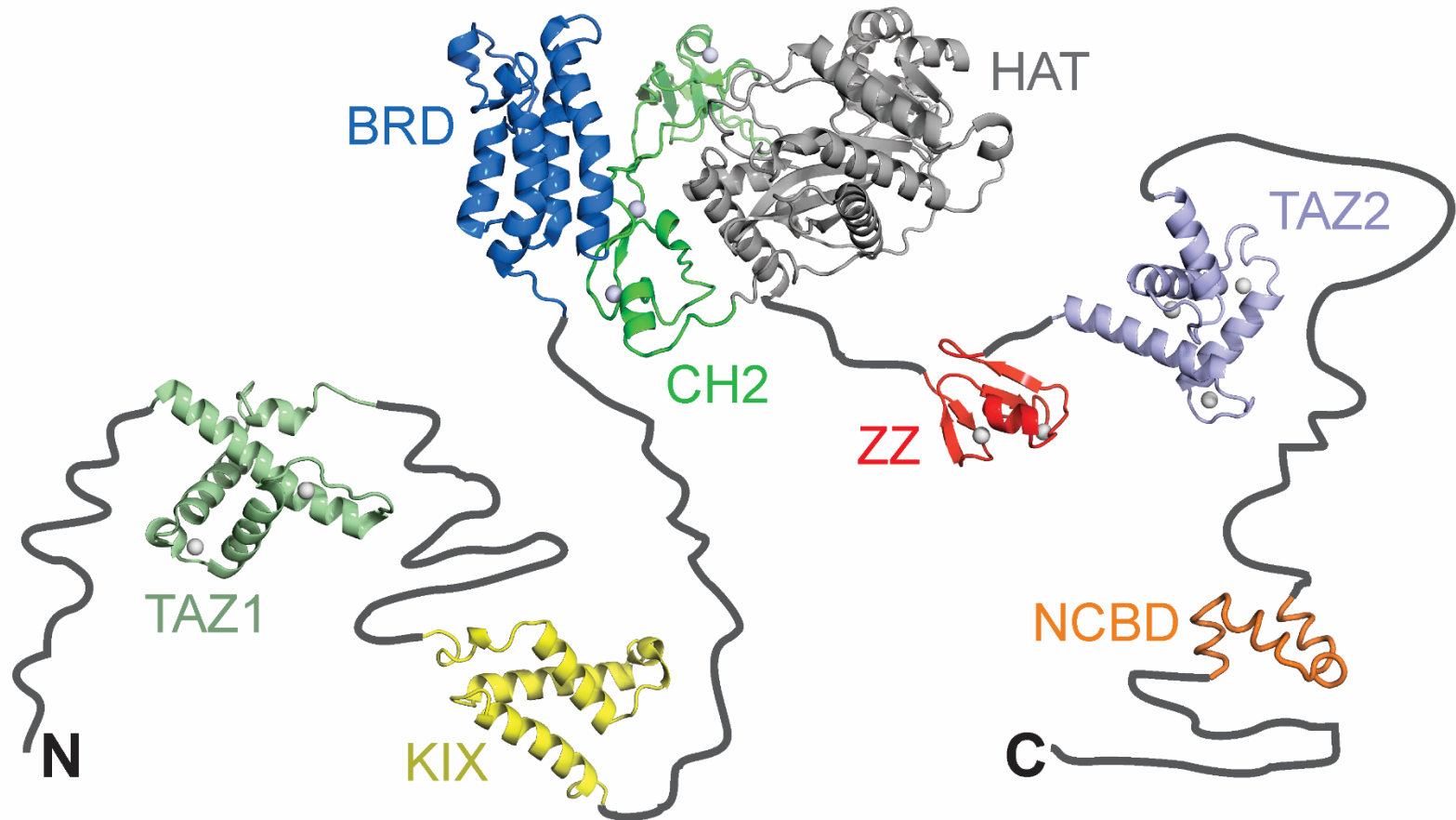
- pathologically overlapped, highly variable linewidth

- many cross peaks broadened
- fast relaxation makes higher dimensional (4D, 5D) experiments impossible
- such systems need UHF NMR

Full-length CREB dimer, 900 MHz



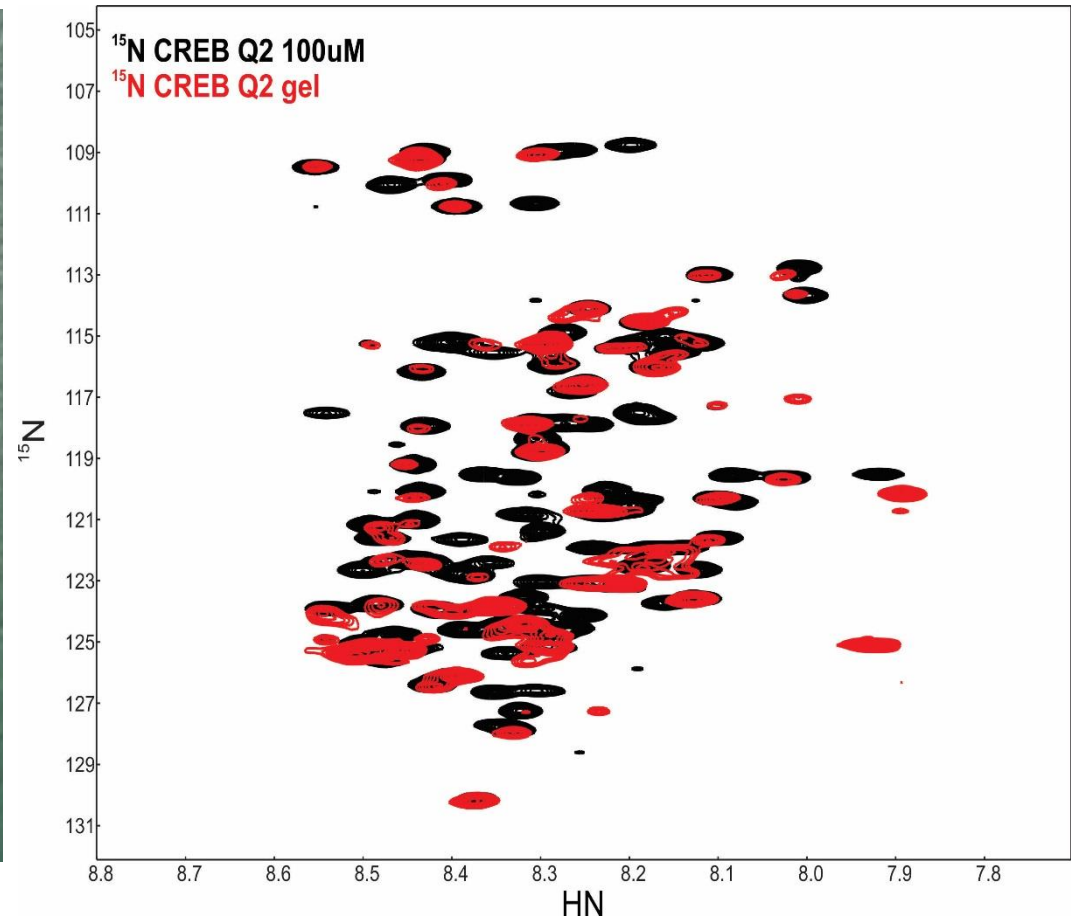
The challenge of “real” eukaryotic proteins with both structured and disordered regions



Transcriptional coactivator CBP/p300

IDP phase separation: membrane-less organelles

- hydrogel formation by Q2 domain of CREB
- insights into molecular interactions in phase-separated state



UHF NMR will be a central, enabling technology for characterization of IDPs and their interactions

- increased dispersion (increased resolution)
- increased sensitivity (low μM concentrations)
- enhanced capability to perform ^{13}C and ^{15}N direct detect experiments
- different exchange regime (may move from exchange broadening to slow exchange)
- extended frequency range for relaxation measurements, analysis of dynamics
- access faster timescales, lower excited state population in CPMG dispersion experiments