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The Protein Folding Problem: The Role of Theory

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Abstract

The *protein folding problem* was first articulated as question of how order arose from disorder in proteins: How did the various native structures of proteins arise from interatomic driving forces encoded within their amino acid sequences, and how did they fold so fast? These matters have now been largely resolved by theory and statistical mechanics combined with experiments. There are general principles. Chain randomness is overcome by solvation-based codes. And in the needle-in-a-haystack metaphor, native states are found efficiently because protein haystacks (conformational ensembles) are funnel-shaped. Order-disorder theory has now grown to encompass a large swath of protein physical science across biology.

Keywords

protein folding theory; statistical mechanics; disordered proteins; protein aggregation; coarse-grained modeling

The History of the Folding Problem

What is (or was) the protein folding problem^{1–4}? And, why does it matter? First of all, among classes of molecules, proteins occupy a niche of special importance. Not only are they components of all living things, and not only do they matter for health and disease, but also their material powers are extraordinary: they are the *working* components of beings that walk, talk and think. The folding problem was viewed as a grand challenge of high order, natural catnip for scientists. It was a basic science problem that attracted great interest.

A central question in the folding problem arose from the first experimental determinations of globular protein structures around 1957 by Perutz, Kendrew, Levinthal, Anfinsen,

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¹Exact doesn't mean exactly true or exactly right; it just refers to a model that leaves no discretion for the modeler – no free parameters, no choices about sampling, no approximations. It is perfectly faithful to some underlying prescription.

DECLARATION OF COMPETING INTEREST

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Kauzmann, Baldwin, Tanford, Zimm, Creighton, Englander and others. The chain trace was not random. The native structure was unique, yet without apparent symmetry⁵⁻¹⁰ (Fig. 1). Proteins were neither disordered like polymers nor ordered like sodium chloride salts. What explained the shape of the chain trace in a protein structure? What forces, encoded within the sequence, drove these structures? What was the sequence-to-structure folding code? As knowledge grew, proteins increasingly appeared to be unlike ordinary materials. Unlike other polymers, proteins fold into unique structures. They have a sequence-to-structure code: different folds are encoded within different sequences. And different folds perform different actions.

Second, what could explain how proteins fold so quickly^{2,4,11,3}? Despite their large conformational spaces, proteins often fold in the microsecond or millisecond time range. What are the rates and routes (pathways) by which the astronomically large conformational spaces of a protein are searched so efficiently, by random processes, to find these uniquely structured native states? How could order arise from disorder so fast?

Third, it was clear there was not just one story to be told here, but a whole library-full. In addition to the most stable native structure of huge numbers of sequences,¹² the many non-native structures would be crucial for understanding human health and disease. Proteins differ in a universe of shapes, of jobs that they do, how they do them, and their roles in organisms. There are huge numbers of stories to tell: for about 20,000 human proteins, 9 million different organisms, many different mutations, and shapes that depend on conditions, environments and binding partners.

The community sought a framework of logic for physical reasoning that would be applicable across all proteins. We needed to find universal principles, to progress from descriptions applicable to individual proteins or sets of conditions. We confronted questions about proteins as a general state of matter, so very different from other materials, including other polymeric materials. These fundamental aspects of the protein folding problem boiled down to questions about how order arises from disorder, often cooperatively, in sequence-patterned chain molecules.

How could theory and computation address these issues? In the early days, modeling aimed to test whether the inter-atomic potentials of the day could explain native structures.¹³⁻¹⁶ Over time, three roles emerged: **(1) Database models.** Using the growing database of protein structures (Protein DataBank, PDB), could we determine unknown structures using sequence homologies to known structures? **(2) Computational molecular physics.** As Molecular Dynamics (MD) with semi-empirical force fields improved, they joined with experiments to tell protein *microstories*, i.e. the details of motions, binding and other actions, roughly one protein at a time, one condition at a time. **(3) Theory & coarse-grained simulations.** Statistical mechanics and polymer theories were developed to tell *macrostories*, i.e. to address more global questions of principle, of commonalities and differences among proteins.

Think about these three steps in solving a crime mystery: First, you get static snapshots of the suspects. Second, you trace his/her steps and actions. Third, you aim to

learn their motives. (1) Database modeling gives snapshots of native structure culprits. Database inference approaches have dominated the 14 Critical Assessment of protein Structure Prediction (CASP) events over 27 years of community-wide structure prediction competitions. These underwent a major advance this year with Google's AlphaFold deep learning algorithm.¹⁷ (2) MD gives the step-by-step physical actions that we call the microstories. MD-based protein storytelling is reviewed elsewhere.¹² (3) Theory seeks to learn the macrostories, the universal drives and principles. While all three approaches give insights into proteins, a grounding in physical truths is important for modern protein storytelling. In the present work, we summarize the role of theory that, in conjunction with experiments, has explained disorder-to-order processes in proteins.

Seeking Principles from Polymer Theories

Starting in the 1980's, we and others looked to polymer statistical mechanics for insights into protein folding.^{18–23} The polymer perspective went against the grain at the time because protein science was generally seen by protein experimentalists to be about atomistic detail and structural specifics. In contrast, synthetic polymer properties were understood through their disorder – their chain length and conformational distributions, often modeled in random-flight and lattice solution theories, and by Flory length distributions.²⁴

What questions could polymer physics address about how proteins found native states (*needles in haystacks*) among all possible conformations (*the haystacks*)? Could polymer physics describe the forces that drive stabilities of certain states (native) relative to others, and the speed of the search? The questions were about the nature of the seemingly astronomically large conformational spaces of non-native states of proteins, the equilibrium structures they attained, and the kinetics of searching those spaces and finding native states.

In the 19th century, research on proteins and polymers had tracked together. JJ Berzelius coined both terms, *polymer* in 1832 and *protein* in 1839. The idea that small molecules could form chains through covalent linkages was controversial until Hermann Staudinger's macromolecule hypothesis of the late 1920's (Nobel Prize in Chemistry in 1953) was proven true by parallel work on proteins – from both Theo Svedberg's centrifugation experiments on hemoglobin in the 1920's (Nobel Prize in Chemistry 1926) and Wallace Carothers' syntheses in the 1930s of polymers such as neoprene and nylon. The protein and polymer fields then diverged for years as Flory and others showed that the properties of synthetic macromolecules were explainable by disorder – distributions of chain lengths and conformations, while Perutz and Kendrew and structural biologists in the 1950s and '60s showed that proteins had atomistically detailed structures, different for different proteins, and that those differences matter for function.

On the one hand, polymer theories at that time were mostly focused on the simplest polymers – homopolymers and random or block co-polymers. Modeling had not previously explored sequence-structure relationships because it had not been possible to make specific sequences of non-biological synthetic polymers. Nor was there work on polymers that had unique folded structures like the native states of proteins. On the other hand, polymer theory was a good starting point for several reasons.

First, astronomical conformational spaces are the daily business of polymer statistical mechanics. Once you take the logarithm of a count of conformations and turn it into an entropy, the numbers are all quite measurable and ordinary. Unlike thinking about small molecules, which is often more about energies than entropies, thinking about polymers means confronting large conformational spaces, disorder-to-order transitions (like protein folding), and how various simple interactions can direct fast searches of conformational spaces to reach ordered states.

Second, traditional polymer theory had provided many good simplifications that clearly added value to models. For example, chains were often approximated as a string of beads, each representing roughly a monomer unit. Bonds were approximated as fixed-length vectors. Bond pairs were represented with simple orientational freedom. On the one hand, that *random-flight model* and its variants was sufficient to model some size properties of denatured states. On the other hand, Flory-Huggins theory had successfully modeled more compact states in polymer liquids with averaged solvent-mediated contact interactions among non-neighboring beads.^{24,25} In these ways, polymers in complex situations could be reduced to smaller sub-problems, either of rotational freedom in short segments, or of contact interactions of the isolated beads, measurable in simple solvation transfer experiments. Combined with small-molecule model-compound experiments, you could get coarse-grained insights into conformational shapes, chain entropies and enthalpies.

In the early days of harnessing such ideas from polymer science, there was push-back from some quarters, where it was felt that the details should matter. However, important lessons from polymer science were (i) that entropies are often large, sometimes dominant (as in elastic solids, viscoelastic liquids, and in polymer blends, mixtures and melts); and (ii) that getting right the entropies and disorder is more about the general nature of whole conformational spaces, through the largescale sampling and lack of bias in coarse-grained models, even at the sacrifice of atomic detail.

What is the nature of disorder in denatured proteins?

Characterizing a disordered protein is less straightforward than describing a folded protein.^{26–28} A useful, comprehensible, and general description of conformational ensembles of large numbers of microscopic states is needed. Polymer theory has provided crucial concepts and tools for this. First, it defines certain ensemble averages, such as the radius of gyration (R_g) or end-to-end distance (R_e), that are good descriptors of the sizes of conformational ensembles.

Second, polymer theories explain the huge importance the solvent plays in polymer conformations. A key organizing principle here is of the *Flory theta solvent* or Θ *point*. Imagine a fictitious *dial* with which you could control an energetic property of solvent molecules, ranging from preferentially interacting with other solvent molecules to preferentially interacting with monomers of a polymer chain. When monomer-solvent interactions are strongly favorable (a “good solvent”), a polymer chain will expand extensively. When monomer-solvent interactions are very unfavorable (“poor solvent”), the chain will collapse to avoid the solvent. When the dial is in the middle, that balance point is a theta solvent. At the theta solvent point, a polymer chain will obey ideal

random-flight statistics. It will be neither more collapsed nor more expanded than a random-flight chain. Proteins generally fold in poor solvents (like pure water) and unfold in good solvents (denaturants). But unlike homopolymers, proteins can have more complex sequence-dependent behaviors in solvents. Water may act as good or poor solvent for unfolded states of proteins.^{29,30}

Third, these ideas about solvation give ways to learn key features of protein conformational ensembles. The radius of gyration R_g of a chain will depend on its number of chain monomers N , as $R_g \approx N^\nu$,^{33–38,29,39} where ν , called the “Flory exponent” depends on the solvent. In a random-flight chain, $\nu = 1/2$, and for denatured proteins in good solvents, $\nu \approx 0.6$ (Fig. 2). Unfolded proteins in high denaturant are in Flory good solvents. Unfolded proteins in low denaturant have varying compactness, and depend on hydrophobicity and charge. These simple homopolymer theory concepts have been much more powerful than we had any right to expect for protein conformational distributions.^{31,32,40–42,39,43,44}

Fourth, ensembles can sometimes seem *chameleon-like*, where different experiments give different weightings to ensemble sub-components. This is where theory and modeling can be useful, in calculating these different facets properly, resolving apparent differences from different experiments.^{41,45–47,44}

How Does a Protein Reach its Ordered Folded State from its Unfolded Ensemble?

What is the nature of the ordering in a folded native protein, and how does that ordering arise from its highly disordered denatured state? The basic ideas are expressed through statistical mechanics. The relative stabilities of states depend on their free energies. At equilibrium, the probability of occupying a state depends on its Boltzmann’s weight, $\exp(-G/k_B T)$, where G is the difference in free energies of the states, native and unfolded in this case, k_B is Boltzmann’s constant and T is temperature.^{48,49} Small proteins typically fold cooperatively, i.e. through relatively sharp transitions between the disordered and ordered states.^{50,51}

Disorder can be overcome by energetic preferences for certain states over others. For proteins, there was early focus on hydrogen bonding. In 1951, Linus Pauling deduced that hydrogen bonding would favor α -helical structures in peptides.^{56,57} The early evidence for α -helices in proteins raised the possibility that short model peptide chains might undergo helix-coil transitions in solution, in the absence of the other parts of the protein, and that such model systems might give insights into the bigger questions of protein folding. Consistent with that speculation, Perutz and Kendrew observed considerable amounts of α -helix in the first protein structures that were learned at atomic resolution, myoglobin in 1957 and hemoglobin in 1959 (Fig. 1 shows an early low-resolution structure).^{58,6} For this discovery, they were awarded the Nobel Prize in 1962.⁵⁹

Helix-coil transition: order from disorder in peptides.

Among the first successes in modeling protein conformational changes were the helix-coil theories of Schellman,⁶⁰ Zimm and Bragg,⁶¹ and Lifson and Roig⁶² (reviewed in Ref.⁵¹).

How is a helical chain conformation stable inside a protein, in light of the large entropic favorability of the much larger number of the chain's disordered conformational states ("coil")? The answer, in the language of the Zimm-Bragg theory, was that the entropic challenge of so many open configurations could be balanced against factors for (i) the difficulty of forming the first turn of a helix (expressed as an equilibrium constant σ), and (ii) the energetic gain of hydrogen bonding of additional turns (expressed as an equilibrium constant s). These theories, in conjunction with an associated experimental enterprise,^{63,64} showed that although nucleation is entropically disfavored [$10^{-4} < \sigma < 10^{-2}$], a small energetic preference for propagation [s slightly greater than 1] favors cooperative formation of helices, provided the chains are long enough, and σ is sufficiently small (Fig. 3). It was later shown by Baldwin and coworkers^{63,65} that short peptides (<20 amino acids) comprising certain amino acid sequences can display substantial helical character. Helix-coil propensities of peptides are summarized in database models.⁶⁴

Thus, simple theories that elucidated the organizing principle of helical ordering shone light on hydrogen bonding as an important driver, and showed how to ground our understanding in experimental physical chemistry.

Protein folding: collapse, the folding code & cooperativity.

Like helix-coil processes, much of protein folding is also highly cooperative.⁵⁰ However, protein folding was more challenging to understand than the coil-to-helix transition. Proteins are much longer chains, and their native structures are very well packed with various internal organizations of helices and coils, β -sheets and loops. There was found to be a folding code where different native structures are encoded by different sequences, but the physical basis of that code was not clear. Partly based on successes of helix-coil theory, a prominent view at the time was that the folding code that determined how one protein differed from another was predominantly due to hydrogen bonding interactions. Hydrophobic interactions were seen as a sort of nonspecific glue that just made proteins compact in some oily glob-like way.

Our group took an alternative view. We supposed that the folding code must reside within the sequence of side chains, not the backbone, because each protein has a different side-chain ordering, but all proteins have the same backbone. We assumed that hydrophobicity was the dominant interaction. We supposed that the folding code was mostly a solvation code in the hydrophobic interactions, and was not from hydrogen bonding. To explore the folding transition, polymer theory was recruited and included in an approximate analytical theory¹⁸ and in a so-called "exact" lattice model.²¹ We explored the ideas that the hydrophobic interactions embedded in the protein sequence determined why each protein folded to a different structure, and that the hydrogen bonding was just a generic "glue" that stabilized compact states. And, we supposed that the atomistic details of the tight van der Waals packing was more of a consequence than a driver.^{66,67}

Proteins fold on funnel-shaped energy landscapes.

Lattice polymer models indicated how a binary code with two types of monomers, hydrophobic (H) and polar (P), could lead many different HP sequences to have different

native folds. Even with only HH interactions, which are weak, nondiscriminatory and combinatoric – any one H can interact with any other H (except its nearest neighbors in the sequence) – the models predicted sharp cooperative transitions from the large unfolded ensemble to a single native state that maximizes the number of HH *contacts* (i.e., spatial neighbors on the lattice that are not neighbors in the sequence), depending on the HP sequence.^{68–70,21,71} These models demonstrated that the folding code was predominantly a solvation-based binary code of relatively nonspecific interactions, driving a chain to a native state encoded in its sequence of hydrophobic and polar monomers. Thus, a protein in a poor solvent (see above for definition), like water, collapses to a particular native fold due to its particular HP sequence. HP models also showed a *funnel-like* shape in the folding energy landscape, describing the transition from many states at the top having few HH contacts to very few conformations at the bottom having many HH contacts.^{72,73}

The seeds of the folding-funnel concept came from insights of polymer theory about how chain conformational space reduces as chain density increases, as when proteins fold from random configurations to a compact folded state.^{18,74} In modeling polymer liquids, PJ Flory predicted a factor of $(1/e)^N$ as the reduction in numbers of conformations available to each chain having N beads, in bulk liquid polymer relative to its random flight state.⁷⁵ The effect was called *excluded volume*. Put into folding conditions, we inferred that a protein chain forms increasing numbers of hydrophobic contacts, some native and some not. As the chain becomes increasingly compact, the space of remaining viable conformations diminishes sharply.

Further analytical modeling based on defining protein free energy as the summation of pairwise contact energies quantified the number of sequences expected to fold to a given native structure.^{76–79} Rather than studying how protein sequences fold into a given structure, this inverse computation provided insight into how certain protein structures can be more amenable to encoding by several different sequences.^{80,81}

Experimental validation of the binary HP code hypothesis.

Proofs of principle followed. First, experiments tested the binary HP code hypothesis. Sauer et al. demonstrated that protein structures are highly tolerant to extensive mutations, provided that the core hydrophobic residues are preserved.^{82,83} And, Kamtekar et al. randomized the amino acid sequences of a 4-helix bundle protein, keeping only the hydrophobic and polar code intact and fixing given loops. They found that the large preponderance of these non-biological sequences still fold to the correct native structure.⁸⁴ Similar results were recently observed by Koga et al. for designed proteins.⁸⁵ Moreover, the thermodynamics of hydrophobic and polar interactions were found to give enthalpies, entropies and heat capacities of folding consistent with experiments.^{86–88} A key prediction was that a large excluded-volume entropy opposed folding. Subsequently, a useful minimal alphabet for folding for a broader range of native folds was found to be IKEAG – a hydrophobe, one positive and one negative amino acid, alanine and glycine.^{89,90} Recent refined models also incorporate helix-coil cooperativity into the folding collapse cooperativity.^{51,64}

From the folding code to non-biological foldamers.

These notions about folding codes were useful in developing new polymeric materials called foldamers.^{91–93} The implication from modeling that the backbone was not critical in creating sequence-dependent foldable polymers led to explorations in non-biological types of materials, such as peptoids.^{94,95}

How is protein folding so fast and so directed?

The protein folding problem has also been regarded as two questions of folding speeds and paths: (a) How is folding so fast, from unfolded to folded states? (b) Is there a folding mechanism, a particular route or pathway that is both specific enough to explain how a given amino-acid sequence reaches its native state, and general enough to say why most proteins have such routes?

(a) The Levinthal paradox of folding speeds.—At a meeting in 1969,⁹⁶ Cyrus Levinthal noted that the number of atomistic level conformations of a protein would be huge, of the order of 10^{300} , and that a random search of them would require essentially forever for the protein to find its native state; see also DB Wetlaufer⁹⁷ and TE Creighton.⁹⁸ The implications were that even though folding is stochastic, nevertheless it must also involve some physical basis for not exploring the vastness of entire conformational spaces. Folding funnels gave an explanation, both from equilibrium modeling of densities of states^{18,72,73} and kinetic models.^{74,99} When jumped to folding conditions, the chain randomly forms increasingly many HH contacts, lowering the free energy, at the same time reducing the remaining space of searchable conformations. Folding is not a random search; it is strongly pruned by the exponentially diminishing numbers of conformations available to search as the protein becomes increasingly compact. Even so, it raised the question of how to compute folding rates across proteins.

The Thirumalai glassy kinetics model presciently predicted folding rates. In 1995, Dave Thirumalai formulated the relationship $k_f \sim \exp(-\sqrt{N})$ between protein folding rates k_f and protein chain length, N .¹⁰⁰ His insight originated from the resemblance of protein ensemble behavior at low energies and entropies to those of glassy dynamics, where the transitions from the many compact near-native ensembles to the presumably unique native state are separated by a free energy barrier G^\ddagger having a Gaussian distribution, where the relevant property is the size of the average fluctuation (standard deviation) $\sim \sqrt{N}$. Consequently, the Arrhenius folding rates are given by $k_f \sim \exp(-\Delta G^\ddagger) \sim \exp(-\sqrt{N})$ at a given temperature. This prediction long preceded its experimental validation (Fig. 4). Thirumalai and coworkers also predicted that folding occurs most efficiently when the chain is put into a temperature T_Θ , close to the folding midpoint temperature T_f at which the polypeptide chain behaves as an ideal polymer chain.^{100–103} This prediction was confirmed by Hofmann et al.,³² and later others,^{42,40} using single-molecule spectroscopy. Those groups measured the Flory scaling exponent ν of unfolded proteins under varying conditions of denaturant. Under native conditions (low-denaturant), they found that denatured chains are near the theta state ($\nu = 0.5$), i.e. more compact than highly denatured chains are.^{104,105} The next puzzle,

described below, was to understand how different folding pathways were physically encoded in different protein amino-acid sequences.

(b) The folding mechanism: the conformational routes.—What is the mechanism of protein folding? The term “mechanism” has meant *a narrative of a protein’s pathways of folding at a level that is sufficiently general and coarse-grained to apply to all proteins, and yet sufficiently granular to account for the differences across proteins*. This would not be an atom-by-atom nanosecond-by-nanosecond sequence of events, for that would surely apply only to one protein. Nor is the funnel concept alone a sufficient descriptor of mechanism because it is too generic to tell us differences in folding routes of different proteins.

Early on, experimental kineticists had observed that a protein’s secondary structures would often form early in its folding pathway. These kinetic building block units were termed “foldons”.^{107–111} But, the physics was not clear. Secondary structures were not stable by themselves. How did the protein know where to start? How were the folding pathways encoded in the amino-acid sequence? How did the protein avoid searching the vast majority of its conformational space to follow its pathway? What was sought was a general theory that would be grounded, like helix-coil theory is, in known physical chemistry experimental model systems. Among the first efforts to embody the secondary-structure-first idea was *diffusion-collision theory*, where secondary structures formed early then diffused and collided ultimately into a native structure.^{52,53} A more microscopic physical treatment was the Ising-like model of Eaton and coworkers.^{54,55} Each residue could adopt one of two states, native or non-native, and the model formulated a partition sum over them, successfully describing generic folding kinetics with foldons for the simplest proteins. But, it remained to understand how residues knew native from non-native.

In the Foldon Funnel Model,^{112,51} the first kinetic steps of folding are those based on local conformational preferences in the chain, such as helices and turns, that populate fractionally and transiently, but not at sufficiently high levels to be stable by themselves. Consider a helix bundle protein. Next along the folding route, two local helical pieces then assemble together to persist as a pair over longer time scales. Those pair units then accrete additional helices to persist even longer, and so on. Each step is more persistent than the last, even though none is yet fully stable. The barrier to folding here comes from the substantial conformational entropy loss of forming the ordered helices, with the gain of native contacts not yet sufficient to offset it. Full stability is only achieved at the end when all of the helices are in their native structure. Such landscapes look like volcanoes: uphill at first, then the downhill funnel only for the last steps; see Fig. 5.

This model explains how “local-first, global later” results simply from the nature of the time scales of polymer molecules sampling their conformations.¹¹³ Two residues i and j close to each other in sequence have fewer degrees of freedom between them than two residues that are further apart. And sampling speed of smaller spaces is faster than of larger spaces. Of course, if wrong local structures, or competing native contacts, are formed early, then some backtracking is required later.^{114,115} However, exact lattice model studies show that there are almost always routes where local-first, global-later can achieve native structures without backtracking.¹¹⁶ Hue Sun Chan and coworkers used lattice models of a

small protein with varying levels of cooperativity within and between the helices (i.e. local and nonlocal interactions) to reason about the ordering of folding events and shed light on observations from hydrogen exchange experiments.^{117,118}

Key points of such modeling are: to give quantitative relationships between macro observables, such as folding rates over many different proteins, the general two-state thermodynamics across simple proteins, and the observation of folding by foldons; and to give micro properties that can be measured in physical chemical model experiments, such as helix-coil properties σ and s , and a hydrophobic interaction equilibrium constant among amino acids. A principal prediction from folding kinetics theories was that individual chains would fold stochastically – each following a different microscopic process, but with averaged behavior as described by this mechanism. This predicted folding route heterogeneity came to be called the “new view”,¹¹⁹ and has been confirmed by experiments^{120,121} and simulations.^{122,123}

Chaperones help other proteins to fold by unfolding them.

Some proteins are able to fold into their native structure in isolation, while many proteins could use a little help to overcome the thermodynamic and kinetic barriers to folding.^{124–127} Proteins called chaperones can generically help other proteins reach their unique folded state.^{128–130} Although originally thought to function by a lock and key mechanism, chaperones are now known to help perform the complicated act of folding by instead performing the uncomplicated act of randomly unfolding proteins through iterative annealing.^{131–135} Many proteins, especially large ones, can get stuck in kinetic traps, i.e. misfolded states that are not able to proceed to the folded state. By ‘iteratively’ unfolding misfolded proteins powered by ATP hydrolysis, chaperones allow proteins with complex funnel landscapes to successfully traverse the landscape and ‘anneal’ to the native state.¹³²

This mechanism of action elucidates how one chaperone is capable of assisting hundreds of different proteins in folding.^{124,136,129} Chaperone activity is important in the context of protein homeostasis in the cell. If chaperones do not properly operate, the number of copies of functional proteins can be too low for the cell to remain healthy.¹³⁷ In addition, the number of misfolded proteins can overwhelm the proteostasis machinery, causing cell collapse.¹³⁸

Intrinsic Disorder: leveraging disorder for function.

There has been growing interest in protein conformations that are unfolded or disordered.^{139,140} Some proteins are entirely or partially disordered. These *intrinsically disordered proteins* (IDPs) and *intrinsically disordered regions* (IDRs) themselves often have biological functions.^{141,142} Conformational heterogeneity is often found to play a critical role in biological processes such as regulation by post-translational modification, transient binding interactions, autoinhibition, and assembly into non-stoichiometric cellular assemblies.^{143–145,28,146} These proteins may function while fully disordered, or may sample ordered conformations that encode function.^{147,148}

Averages, such as R_g and R_e , over polymer conformational ensembles often usefully describe how IDP properties depend on concentrations of denaturants^{32,40,149,45} or

temperature.^{150–152} Protein conformations are often well modeled by simple classical homopolymer theories.³³ But sometimes more subtle insights are sought. To fill that need, more granular metrics can help differentiate the properties of different IDPs, their conformational ensembles, interactions, and functions. For instance, one can use the full ensemble-averaged distance matrix of all residue pairs, $\langle R_{ij} \rangle$.^{153–155} This level of modeling gives deeper insights about distinct IDP conformations,^{43,156,157} and can give insight into functional relationships between IDPs where sequence conservation cannot be used as with folded proteins.¹⁵⁷ Experimental validation of these metrics remains a forefront challenge.

Why do the sizes of IDPs matter? Intrinsic disorder can have biological relevance; it can be modulated through covalent modifications to amino acid side chains, or through post-translational modifications (PTMs).^{143,158} PTMs can shift conformational ensembles by altering their electrostatic *charge compositions*¹⁵⁹ or their specific *charge sequence patterns*.¹⁶⁰ The consequence is that ensemble radii or shape distributions can depend differently on external stimuli, such as salt concentration.^{159,161,162}

For explaining sequence effects on IDP conformational properties, statistical mechanical modeling and coarse-grained simulations have been critical. Sequence patterning effects occur through the local clustering of like and unlike charges, expressed through Pappu's κ parameter¹⁶¹ or on the pairwise distances between like and unlike charges in Ghosh's sequence charge decoration (SCD) parameter.¹⁶⁶ These parameters stem from earlier polymer physics theories.^{167–169} Both of these quantities correlate well with the average properties (i.e. R_g , R_c , ν) of IDPs.¹⁷⁰ Theory involved in development of SCD has successfully predicted the size of an IDP and its phosphorylated variants (Fig. 6B,C). The variants were designed to minimize or maximize SCD and to observe the greatest degree of collapse or expansion in the IDP, demonstrating the role of theory in determining PTM hotspots that would be difficult to identify otherwise (Fig. 6). In addition to charge patterning in amino-acid sequences, hydrophobic and polar (HP) patterning can also shift ensembles of disordered protein chains.^{171,172} More advanced recent theory treats more granular patterns in which certain amino acids distribute as *blocks* or *clusters* within the sequences (Fig. 6A).¹⁶⁵ Together with charge patterning metrics, one can predict experimentally-determined IDP dimensions with good accuracy (Fig. 6D,E). In short, improved theory and modeling of disordered protein states, which should help to understand biological control and regulation, is ever more accurate in capturing their compactness, exposure, and interactions with other biomolecules.^{173–175}

Order-disorder Processes Also Contribute to Multi-protein Associations

While folding is a single-chain disorder-to-order transition, agglomeration and complex formation are multi-chain disorder-to-order transitions. Agglomeration can occur in the formation of amyloid assemblies and fibrils in neurodegenerative diseases^{176,177} or in functional cellular processes^{178,179}; in unwanted states of biotech formulations of proteins and antibody biologics¹⁸⁰; in the assembly of membraneless organelles, which may be highly organized or completely disordered^{181,182}; and in protein crystallization, a major step in determining native structures.¹⁸³ These order-disorder transitions, which are predominantly along a protein concentration coordinate rather than an intramolecular

folding coordinate, are appropriately treated using the statistical physics of solutions and polymers.

Modeling liquid phase equilibria dates back more than a century for simple liquids, and to Flory-Huggins theory for polymers in the 1940's.³⁴ But proteins posed new challenges in their heterogeneity of intra- and inter-molecular structures and in their sequence-structure relationships. How do different proteins associate into different morphologies with different properties? And, how can we explain the rates of association, including those that are extremely slow, such as the growth of amyloid in neurodegeneration that takes place over individual lifetimes? The cooperativity of protein aggregation is best studied by statistical mechanical theory. Atomistic molecular simulations are challenged to treat multiple proteins, or the big state changes with density from dilute to dense, or the need to compute free energies and populations in addition to the structures.

Proteins can assemble into native-like aggregates.

Proteins at sufficiently high concentrations in solution can agglomerate. Examples include formulations of antibodies as biological drugs, which can form reversible or irreversible aggregates^{184,185}; liquid-like droplets formed through a liquid-liquid phase separation^{186,187}; and small reversible clusters that give rise to very high solution viscosities in the absence of macroscopic aggregates.^{188,189} Collagens are another well-known example of proteins that self-associate and aggregate.^{190,191} They are the most abundant proteins in mammals, having major structural roles in bone, skin and muscle tissue. Crystallins are proteins kept at high concentrations in the lens of the eye, whose aggregation results in cataract disease.^{192–194} Such assemblies have translational ordering as a function of protein concentration – a sharp change to high local density, like the freezing of solids or the crystallization of salts in solution. The process is generic; many different proteins do it.

Simplifications are needed to model large systems of many associating proteins. Early modeling of native-state association treated proteins as spheres with radial like-charge repulsions and sticky van der Waals interactions distributed uniformly across their surfaces.^{195–201} In the past decade, more microscopically realistic structures and energetics have become possible due to advances in theory and computing power. Successful coarse-grained models have been developed based on population balance equations that quantitatively reproduce experimental measurements of aggregate concentrations increasing with time.^{202–206} A recent development is the adaptation of the Wertheim statistical mechanics theory of strongly associating liquids to describe liquid solutions of proteins such as antibodies, which have complex shapes.^{207–212} Here, the antibodies are represented as 7-bead molecular structures held together by strong sticking forces, which associate with each other in aqueous solution by weaker forces (Fig. 7).^{209,213} These models show how protein shapes and protein-protein interactions predict the formation of dimers, clusters and higher associations, reflected in solution properties of phase equilibria and viscosities.

Proteins can assemble into amyloid oligomers and fibrils.

Remarkably, many different proteins are capable of forming fibrils. At high concentrations, peptides and proteins can form organized multi-molecular β -sheet fibril structures.^{176,177,214}

They often have a second stable, less ordered oligomeric state. Theory describes the equilibrium states of the oligomers as micelle-like: relatively disordered assemblies of a few protein molecules, driven to form hydrophobic cores. The fibril state is more ordered, with a further loss of entropy of the aligned chains, but a further gain of stability from the hydrogen bonding and tight packing of the multiple aligned chains in the fibrils, bunched together like dry spaghetti in a box.^{215–218} Indeed, combined experimental and computational studies have explained the remarkable nanomechanical stabilities of amyloid fibrils in terms of hydrogen bonding densities and side chain packing efficiencies.^{219–223} Intriguingly, studies have shown that fibrils are more thermodynamically stable than the isolated native states, but kinetically separated from them on the energy landscape.²²⁴

Prions are misfolded aggregated states of proteins that can further promote the misfolding and recruitment of normal variants of the protein into the aggregate, hence, showing a protein-based infectious character, often leading to incurable pathologies such as the Creutzfeldt-Jacob disease in humans and mad cow disease in cattle.²²⁵ HP lattice modeling shows the existence of stable non-native states in small model prion proteins.^{226,227} Two or more proteins can achieve greater stability by non-native assembly in dimers or trimers. Often the assemblies have β sheet-like character, and the potential to incorporate more monomers into the assembly, resembling amyloid forms.

Theory has also been developed for the kinetics of fibril formation.^{228,229} Fibrils form on very slow time scales – tens of years in human amyloid diseases, much too slowly for modeling by molecular dynamics simulations. Schmit et al. modeled fibril formation as the zippering of a landing chain onto an existing partial fibril. This is a 1-dimensional random walk with sticking and unsticking steps representing hydrogen bonds (Fig. 8). Each added bond holds the landing chain in place longer than the last one did, as each bond adds stability to the zippered chain. Overall, fibril growth is slow because it is so rare that a landing chain will randomly align in the proper register. But, when it does, zipping is fast. Fig. 8 shows that the model captures well the growth rates of insulin fibers depending on temperature and denaturant.

Rates of fibril formation have been modeled with mass-action kinetics by Knowles and Dobson. They capture the temperature effects by assuming the Arrhenius rate equation $k = A \exp(-G^\ddagger/RT)$, with standard thermodynamic relations, $G^\ddagger = H^\ddagger - T S^\ddagger$ and $H^\ddagger/R = -(\log k)/(1/T)$. Cohen and coworkers^{231,232} recently used integrated kinetic rate laws to quantitatively determine the size of activation energy barriers (G^\ddagger) and the corresponding enthalpy (H^\ddagger) and entropy (S^\ddagger) contributions for describing experimental fibril growth curves for A β 42, a peptide whose aggregation is implicated in Alzheimer's disease.

The model of Knowles and Dobson^{233,234,230,232} that best agrees with experiments describes amyloid oligomer (nuclei) formation via three competing pathways: fibril fragmentation (breakage), *primary* nucleation through direct monomer associations, and *secondary* nucleation through fibril surface auto-catalysis (Fig. 9). These microscopic pathways have distinct kinetic and thermodynamic hallmarks, and quantitatively characterizing them revealed that the dominant pathway for A β 42 oligomer formation is through the secondary nucleation mechanism.²³¹ Saric et al.²³⁵ developed theory for this self-replication behavior

of amyloid fibrils. They varied the monomer-monomer and monomer-fibril interaction energies, showing that fibril self-replication occurs only under very specific combinations of the interaction strengths, as observed in experiments. Nucleation can also be accelerated by adsorption to surfaces, such as lipid membranes.²³⁶ A fuller review is given in Ref. 237

Proteins undergo phase separations inside the cell.

Inside the cell, proteins (and other biomolecules) can become concentrated, driving a phase transition,^{238,181} like the crystallization of folded proteins¹⁸³ or the phase equilibria in disordered protein polymers.²³⁹ These intracellular phase transitions have been linked to decision-making in cell division, signalling, stress responses, and other biological actions.^{238,181,240–242} They've also been linked to disease pathologies,²⁴³ including the formation of amyloids.^{244–246} Through phase separation, proteins and other biomolecules create compartments in the absence of lipid membranes, and are thus called *membraneless organelles* (MLOs) or more generally, biomolecular condensates.²⁴⁷ The first MLO to be observed was likely the nucleolus, first described in the 1830s by Wagner and by Valentin.^{248–250} Although the phase separation of proteins *in vitro* has long been known, it was only recognized in the formation of cellular inclusion bodies in 1995²⁵¹ and demonstrated experimentally in 2009.²³⁸

The basic process of general nonspecific protein-protein association arises from a balance of attractions and repulsions. The attractions come from interchain “sticky” interactions. The repulsions come from steric interactions, from like charges in the sequences, and from the entropy losses of translational and rotational freedom when free chains join together. Polymer theories, such as the Flory-Huggins theory of homopolymer liquids and mixing,^{24,25} have proven useful for describing the phase separations that occur in biology.^{146,252,253,174,254,153} A key prediction of Flory-Huggins theory is that longer polymers will phase separate at lower concentrations. Similar length effects are also observed for proteins.^{181,252,255,256}

A second key result from classical theories of homopolymers is a relationship between a single-chain property of collapse and a multi-chain property of dense liquid solutions. A classic polymer theory result is that a solvent that is dialed to be at the Θ point for the collapse of a single polymer chain will also cause multi-chain systems to be at their liquid-liquid phase equilibrium *critical point*.^{35,257,170} Remarkably, this basic principle of uncharged homopolymers is also true for many proteins, even though they are sequence-specific heteropolymers.²⁵⁸ This is found in computer simulations of HP-like chains^{255,259} (Fig. 10) and evidenced by experiments.^{260,241,152,261}

Even more remarkably, this single-chain/multiple-chain correspondence principle often holds even for proteins having sequence-dependent charges,^{262,170} and multicomponent phase separation.²⁵⁴ Major advances in theory and modeling relating liquid protein phase equilibria to sequence dependent collapse and folding of individual chains derive from: the HPS theory of Jeetain Mittal's lab;^{153,175} the stickers-and-spacers framework from Rohit Pappu's lab^{263,264,152} originating from Rubinstein's associative polymer models;²⁶⁵ the analytical random phase approximation (RPA) theory of Hue Sun Chan's lab;²⁶⁶ and others^{267–269} (reviewed in Refs. 270–272).

Protein self-assembly into virus capsids.

The self-assembled capsids of virus particles are beautiful examples of protein ordering and organization. A capsid, which is a protective shell around a virus, is a symmetrical construct of hundreds of protein subunits. Theory has made two major contributions to understanding how viral capsids form: (i) a general formalism for explaining the various capsid architectures of different viruses and (ii) thermodynamic and kinetic models that describe the process of capsid assembly.

Early geometrical analysis by Caspar and Klug led to mathematical principles of symmetry for the common icosahedral capsids. They showed how capsid symmetries arise from the symmetries of their pentameric and hexameric protein subunits.²⁷³ They described capsids as icosahedra whose size varies based on the number of hexamers that are placed in between the 12 pentamers occupying the vertices of the icosahedron (Fig. 11). The number of hexamers in the capsid is $10(T-1)$, where T is the triangulation number given by discrete integers $T = 1, 3, 4, 7$, etc. The pioneering work of Caspar and Klug has since led to insights into design laws, protein subunit mosaics and layout deviations in capsid structures of various viruses.²⁷⁴⁻²⁷⁶ Only two types of protein-protein interaction – a rigid-body repulsion and an effective hydrophobic interaction – are needed to explain the stable states for these diverse icosahedral symmetries, and to give the design rules noted above. Such minimal statistical mechanical models also allow prediction of pH and salt effects on capsid formation.²⁷⁷

What is the assembly process? The Zlotnick and Rudnick groups developed kinetic models for an assembly pathway from free monomers to partially formed intermediates to full capsids. They consider the growth of objects having n subunits through rates of addition and removal.^{278,279} They express the ratio of on and off rates through the intermediate state free energy G as $(k_+/k_-) \sim \exp(-\beta G)$. They find that early stage oligomers are unstable and transient due to the small number of favorable contacts any protein subunit can make, and that full stability is achieved only at the last step of assembling the entire capsid. Substantial additional insights are described elsewhere.^{280,281} This *unstable till the end* strategy resembles that of the foldon assembly model of protein folding described above.

What are tomorrow's protein order-disorder grand challenges? Here are just a few. (1) *Proteome actions in cell behaviors.* How do cells maintain *proteostasis* (homeostasis of proteome folding)?^{282,283} How is that balance lost in cells that are sick or old?^{138,284} (2) *Understanding cotranslational folding.* How do folding rates and mechanisms differ for proteins that emerge from ribosomes?²⁸⁵⁻²⁸⁸ (3) *Rates of evolution.* What protein properties determine rates of cell evolution?^{289,290} For some enzymes at certain timescales, evolution depends on the rates of product formation,²⁹¹⁻²⁹⁵ which are relevant to the efficacies of antibiotics, for example.^{296,297} In other cases, cell evolution rates depend on folding stabilities, misfolding, aggregation and chaperoning.²⁹⁸⁻³⁰⁹ Insofar as living systems are seemingly endless hierarchies of organization and complexity, there is no shortage of protein disorder-to-order challenges to explicate.

Conclusions

Proteins constitute an extraordinary state of matter. Unlike other polymers, their power arises from their many physical and chemical actions encoded within their monomer sequences. The protein folding problem was a set of questions about disorder-to-order equilibria, rates, forces and the folding code that specify these unique compact non-symmetrical native structures. In the needle-in-a-haystack metaphor, these were questions not just about needles, but also importantly about their haystacks, the conformational ensembles in which they were embedded and how they were searched.

These problems have now largely been solved by statistical mechanics, polymer theory and coarse-grained computer simulations, in conjunction with experiments. In short, polymer chains having irregular sequences and a solvation code have funnel-shaped haystacks. While proteins have polymeric conformational disorder, as well as steric and charge repulsions, they also have attractions from hydrophobic interactions, solvation and unlike-charge attractions that can overcome the disorder. Across scales of size and time, these forces drive coils into helices, disordered chains into compact unique native states, peptides into amyloid and prion assemblies, proteins into solid and liquid agglomerates, chaperones to fold proteins by unfolding them, and viral capsids to self-assemble. Those few early questions of basic science have now mushroomed into an important component of protein physical chemistry.

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Fig. 1. The first view of a protein structure. Myoglobin at 6 Å resolution, published in 1958 by Kendrew and coworkers.⁶ Its basic chain trace (white) did not have the simple symmetries or regularities previously seen in crystals of smaller molecules. [With permission from the Medical Research Council Laboratory of Molecular Biology].

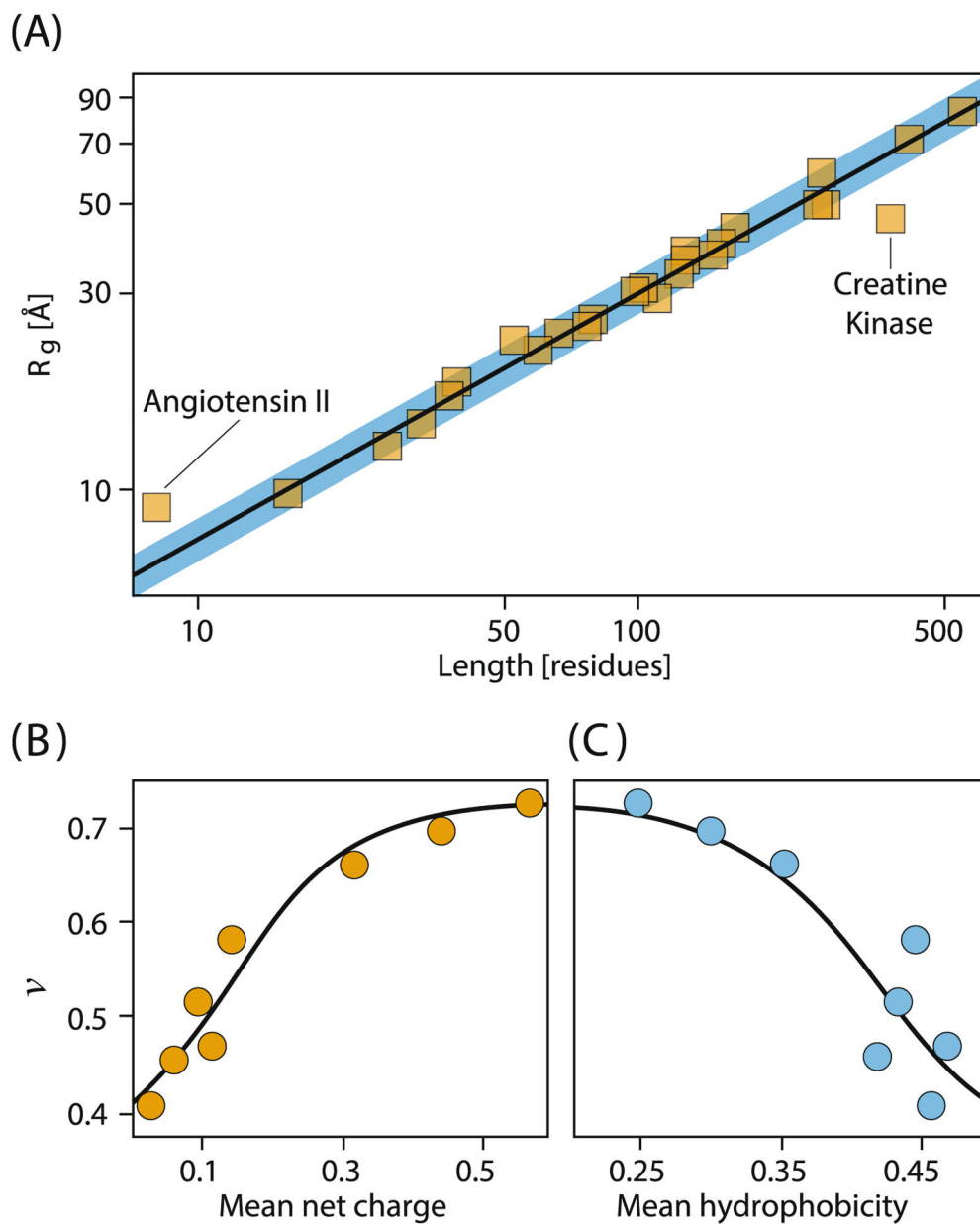


Fig. 2. Unfolded-state radii depend on chain length, charge and hydrophobicity. (A) Unfolded proteins in concentrated denaturant are highly expanded like polymers in Flory good solvents ($R_g \sim N^\nu$, where N is number of monomers and $\nu \approx 0.6$). (B,C) In low denaturant, the compactnesses of unfolded proteins depend on hydrophobicity and charge. Data from Refs. 31,32

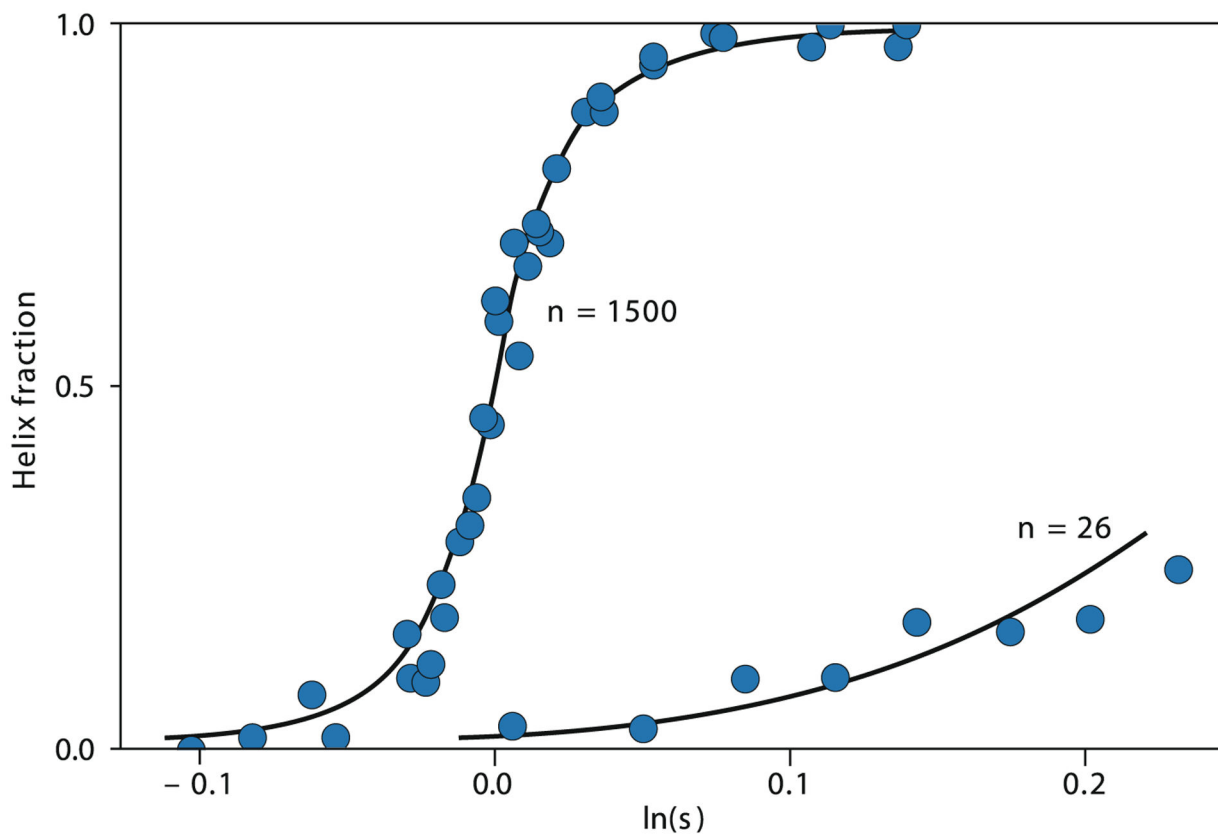


Fig. 3. The helix-coil transition (Zimm and Bragg, 1959).⁶¹ The model was among the first explanations of disorder-order in helices, which are a key component of folded proteins. It's not a full explanation for general folding, however, because β -sheets also fold cooperatively, and because these helix forces are weak (here, 1500-mer helices are required to show the same level of folding cooperativity as typical 100-mer proteins).

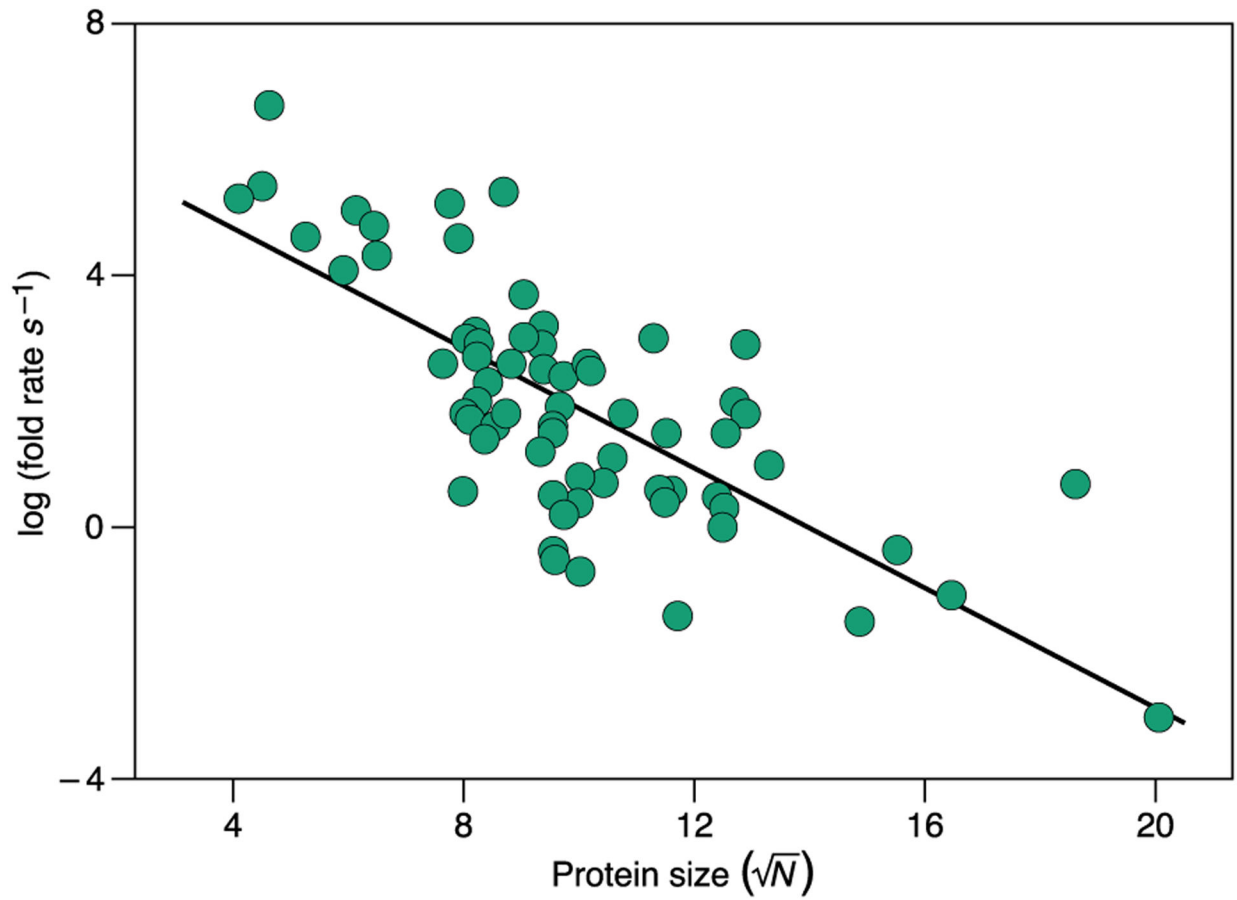


Fig. 4.

Experimental validation of the Thirumalai glassy folding kinetics model. Protein folding rates as a function of size. The folding rates were computed as the inverse of folding times from the data in Ref. 106 confirming the theoretically derived relation $\log k_f \sim N^{1/2}$ over 10 orders of magnitude. The black line is a linear fit to the data.

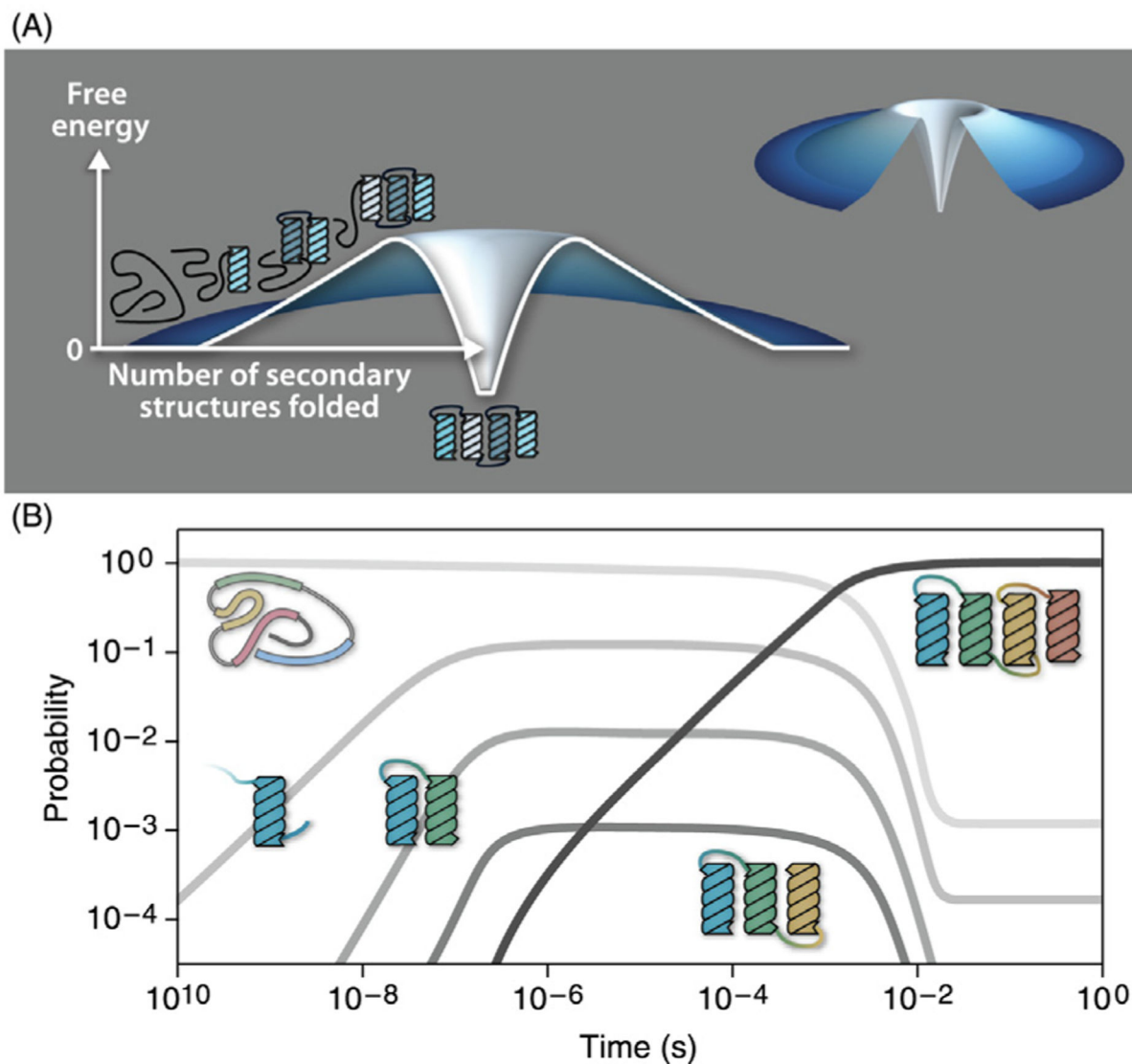


Fig. 5. The Foldon Funnel Model describes the thermodynamics and kinetics of folding. (A) The energy landscape of folding is volcano-shaped for a 4-helix-bundle. As the protein progresses along the folding pathway it accumulates local secondary structures that are not stable by themselves (uphill landscape). Tertiary folds result from the cooperative associations of secondary structural elements that ultimately confer the protein its stable native fold at the last step (downhill landscape). (B) The Foldon Funnel Model describes state populations versus time. A single helix is meta-stable long enough to form helix dimers, then trimers, and so on. The black line shows the native state rising late and becoming fully populated with time as dimers and trimers progress on the folding landscape. Reproduced from Ref. 112

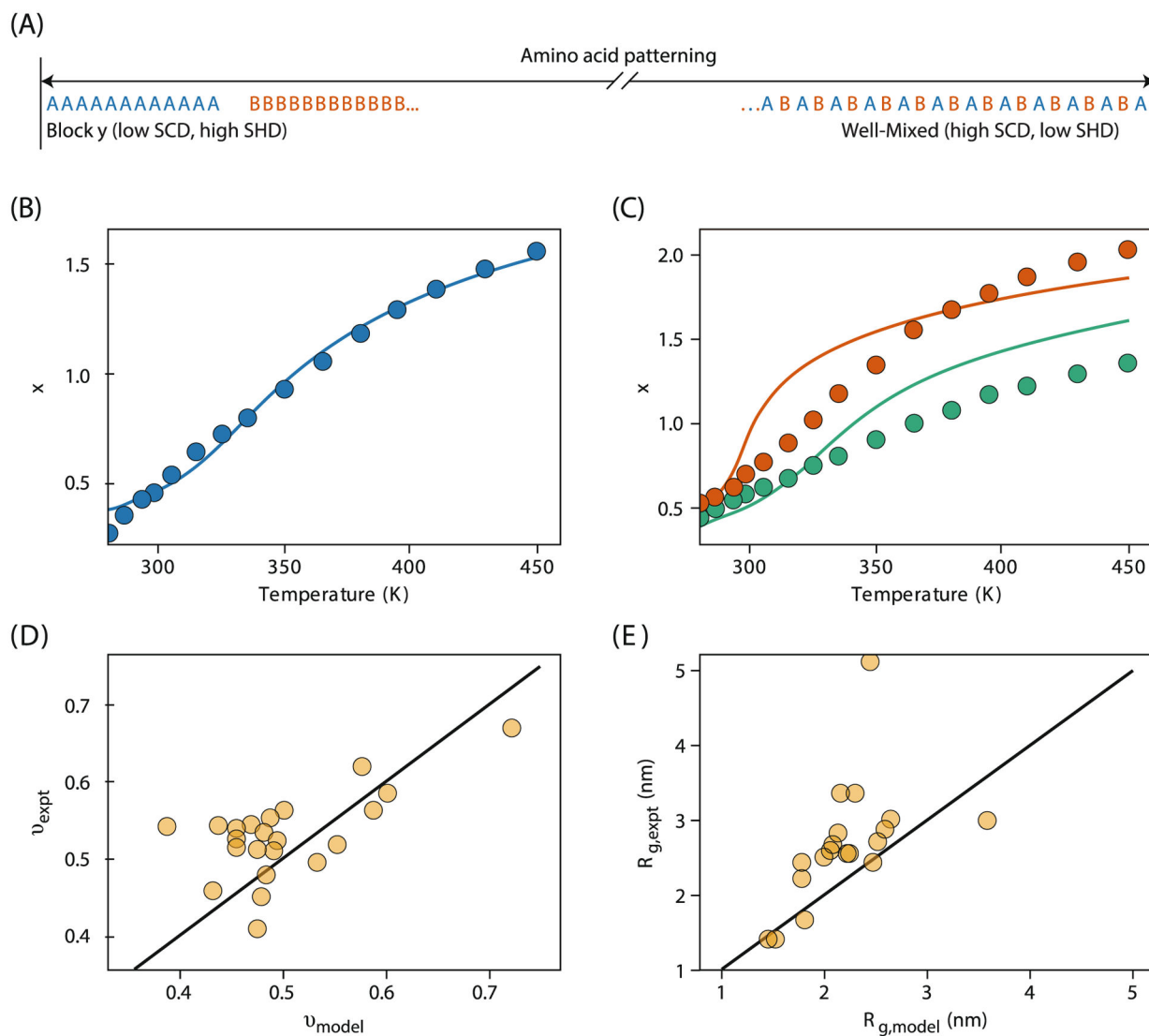


Fig. 6. IDP conformations depend on sequence patterns, as explained by models and simulations. (A) Two sequence patterns: blocky (left) and strictly alternating (right). SCD measures the blockiness of anionic and cationic residues, while SHD measures the blockiness of amino acids of differing hydrophathy values. (B,C) Analytical theory of SCD predicts IDP conformations (x) (where $x = \langle R_e^2 \rangle / \langle R_{e,\text{randomcoil}}^2 \rangle$) for (B) wild type and (C) its two phosphorylated variants. Theory (lines) agrees well with all-atom simulations (points) (Ref. 159). (D,E) Modeling predicts the effects of charge and hydrophathy patterning on the scaling exponent and R_g from experiments^{32,40,45,41,152,163,164} (Ref. 165).

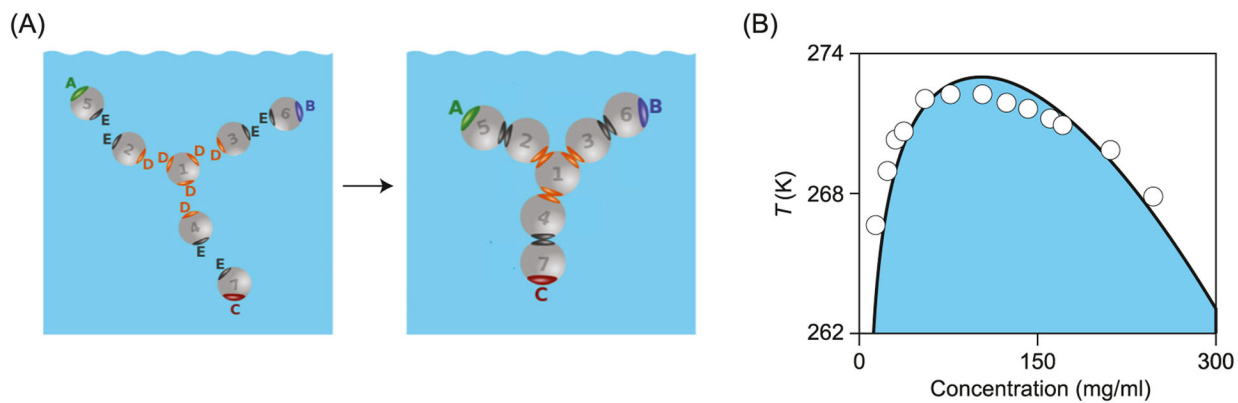
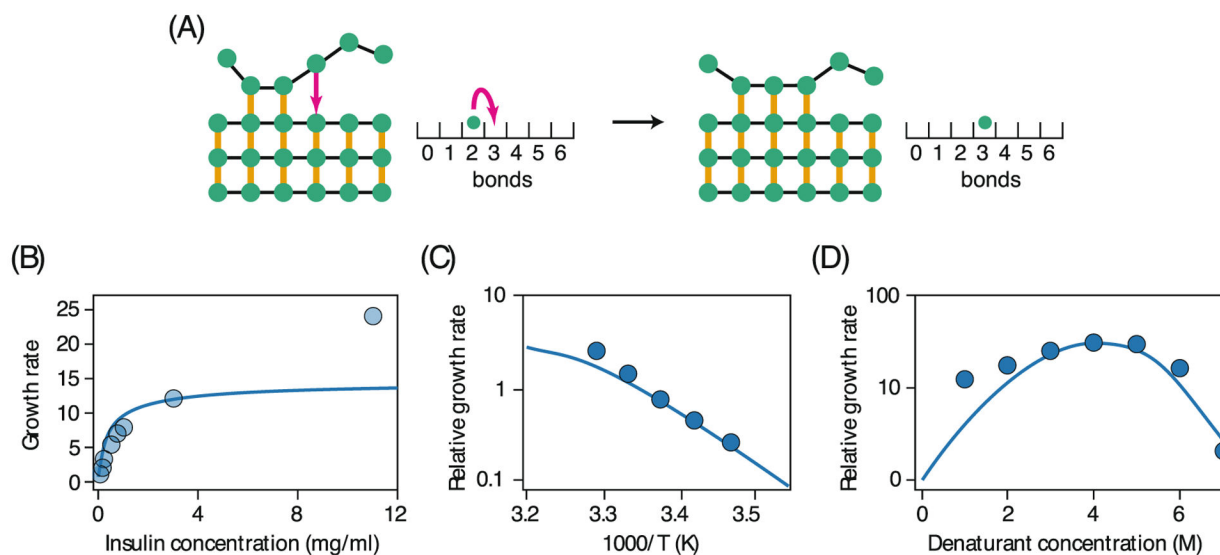


Fig. 7. Antibody liquid phase equilibria computed from Wertheim liquid theory. (A) Isolated beads first stick together as 7-bead Y-shaped (covalent) molecules. These can then come together into (noncovalent) assemblies in solution. (B) Phase diagram of temperature T versus antibody concentration from experiments (points) and theory (line). Adapted from Ref. 213

**Fig. 8.**

Kinetic theory for amyloid fibril formation. (A) The number of hydrogen bonds made at the templating fibril is a quantity that undergoes a random walk in the range $[0, N]$ where $N = 6$ is number of monomers in the incoming peptide. The time for a chain to fully attach (or release) from the fibril is computed from the rates of forming (or breaking) all hydrogen bonds in this simplified scheme. The growth rate for insulin fibrils computed by this theory qualitatively matches that measured by experiments as a function of (B) peptide concentration, (C) temperature and (D) denaturant concentration (Ref. 228).

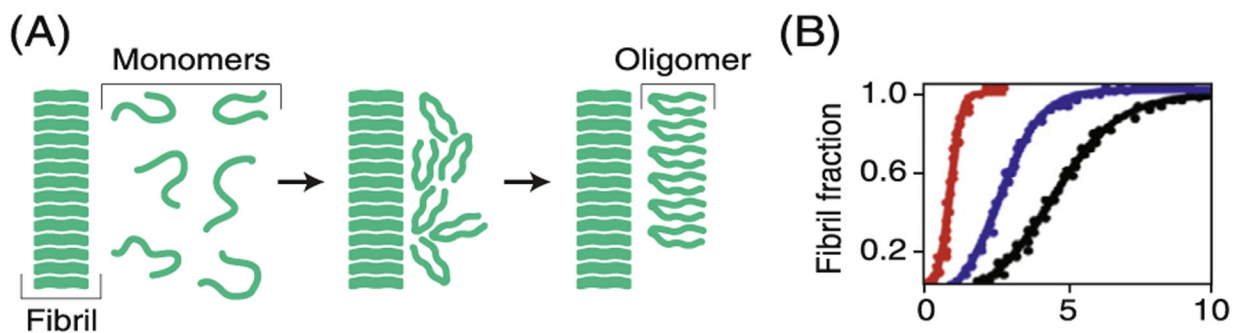
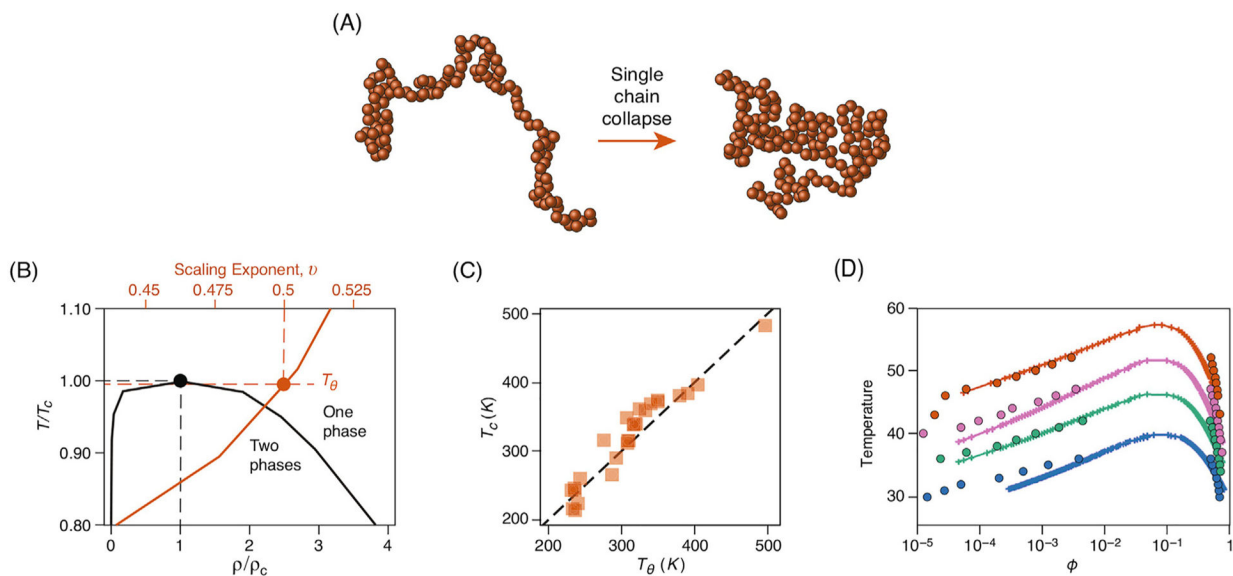
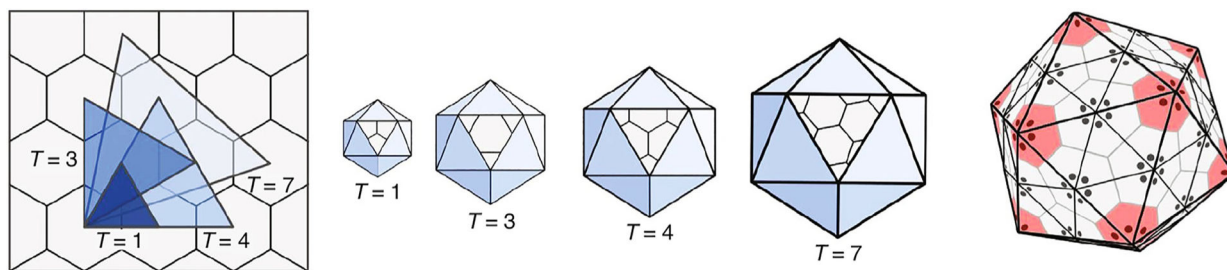


Fig. 9.

The dominant mechanism of forming amyloid oligomers. (A) Free monomers attach to an existing fibril surface and rearrange into new oligomers with rate k_2 . This is known as secondary nucleation. (B) By solving the population balance equations under different scenarios, the likely mechanism dominating fibril nucleation, the secondary pathway shown here, can be inferred by fitting to experimental data at different monomer concentrations (colored lines). The kinetic data were obtained from Ref. 230.

**Fig. 10.**

A single-chain collapse property predicts a multi-chain phase equilibrium property of IDPs. (A) Collapse transition of an IDP (B) The critical temperature and Θ temperature of an IDP were determined in coarse-grained simulations, and show good agreement. (C) The agreement is consistent over a wide range of IDPs. Reproduced from Ref. 255 (D) Information from single chain simulations can be used to predict coexistence concentrations (+ symbols) and show agreement with concentrations obtained with coarse-grained phase-separation simulations (o symbols). Temperatures are in reduced units. Reproduced from Ref. 259.

**Fig. 11.**

Viral capsids result from simple geometry rules. (Left) Different capsid sizes come from different geometric triangulations T , between the centers of polyhedra on a hexagonal lattice. (Middle) Stable capsids result by placing pentamers on the 12 icosahedral vertices and hexamers in between. (Right) The individual pentameric and hexameric protein complexes of the capsid are formed from the individual proteins shown as dot bundles at the center of each pentamer/hexamer. Reproduced from Ref. 276