

Protein Folding and Design for Making Mechanically-Robust Protein-Based Materials

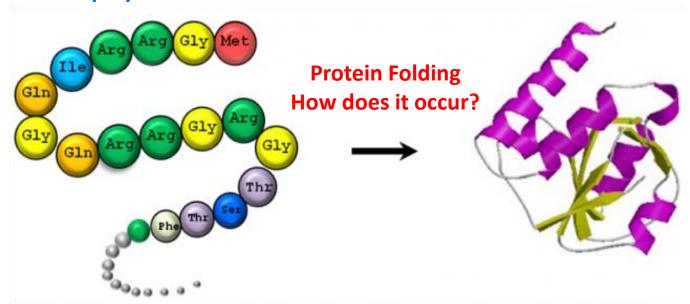
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Proteins – Natural molecular (nano)machines

Proteins are biopolymers



String of amino acids (Unstructured)

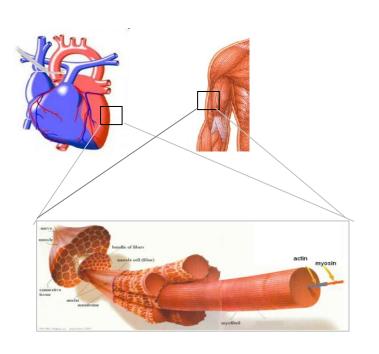
Native (Functional) state
(Folded structure)
(AlphaFold 2 can predict the 3D structure)

Sidechains:

Ionic (+ve, -ve), Polar, Hydrophobic, H-bonding, etc.

Natural World: Proteins have the ultimate molecular strength

Muscle Proteins



Spider silk (web)

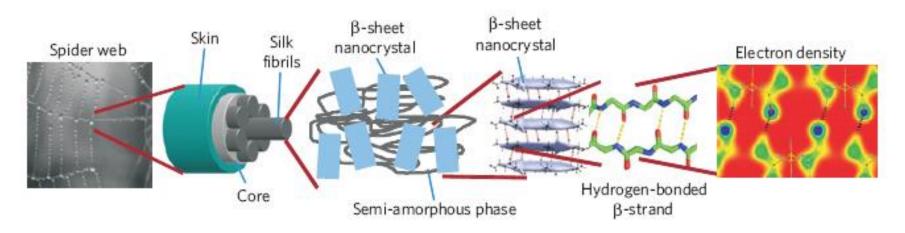


- ~ 1000 times thinner than a human hair
- ~ 5 times stronger than steel!

Proteins are molecular springs!

Muscle and Spider silk:
Both contain **organized protein networks**which impart mechanical properties

Spider silk (complex) protein network

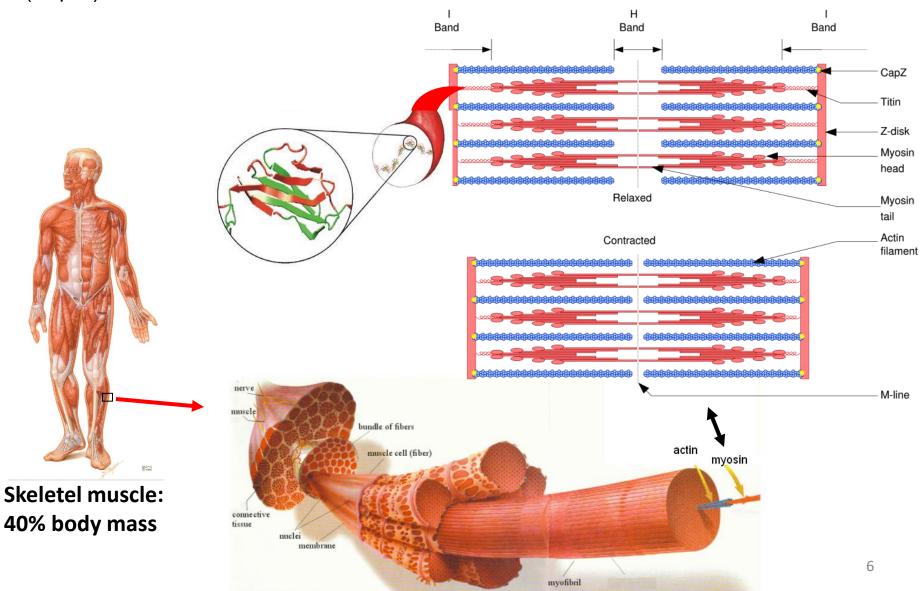




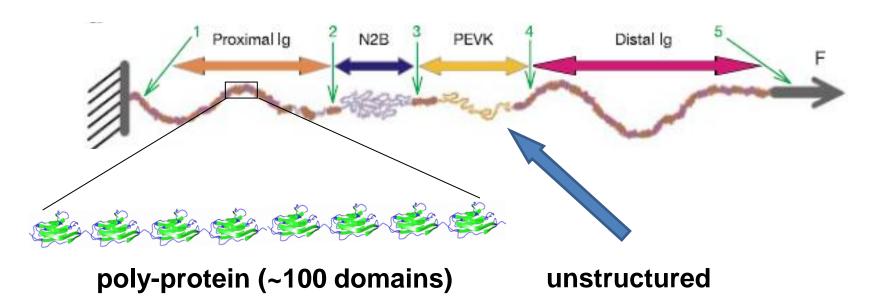
Titin and tension: molecular spring in skeletal muscle

Titin:

 Giant elastomeric protein (~1μm)



Mulscle protein (complex) architecture Molecular Force sensor



Titin:

•Giant elastomeric protein (~1µm)

What We do? And How do we do?

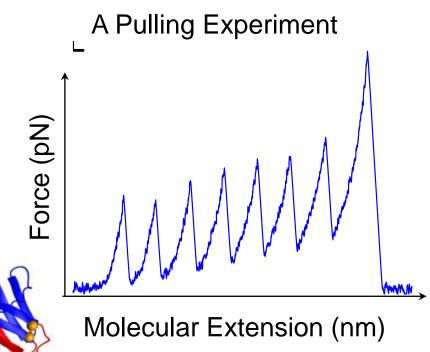
Stretching protein (**single**) molecules one at a time using AFM and MagTweezers

Importance:

- Fundamental understanding on the origin of mechanical stability
- Sequence-structure-(mechanical stability)
- Correlation between Mutations diseases
- Multiple scales: Nanoscale to whole organism
- Etc.

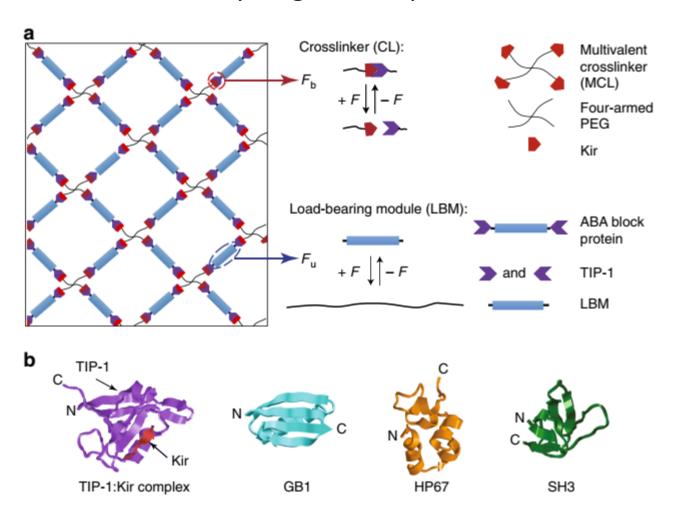
Limitations:

- Low-throughput (single-molecules)
- Difficult problem (mechanical anisotropy)

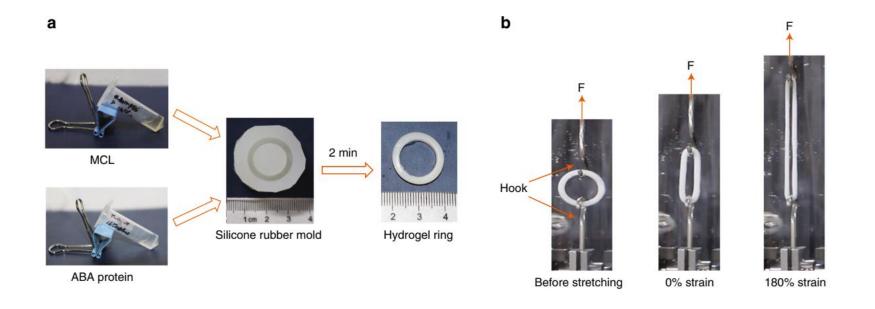


Rational design

Protein-based hydrogels with predictable mechanical properties



Protein-based bulk-material with tailor-made mechanical properties



Applications in: (1) Protein-based, self-repair materials

(2) Protein-based hydrogels for biomedical applications

How Machine Learning (ML)/ Deep Learning (DL) Will Benefit This Field?

- Use the existing dataset of mechanical stability information from many different proteins (they vary in size, structure, topology, function, organisms, etc.)
- Protein descriptors (?) (use the strategies from 'directed evolution of protein design' known in enzyme catalysis)
- Identify the substructures of proteins in complex large proteins
- Sequence comparison across similar topology (homologous proteins)
- Combine (elastic) Network Model
- Design new proteins (à la Alpha-fold) and test them for mechanical stability
- Etc.
- 55

Acknowledgements



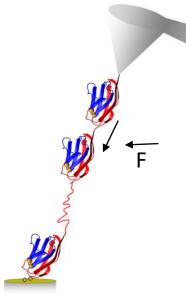
Thank You!

Department of Chemical Sciences

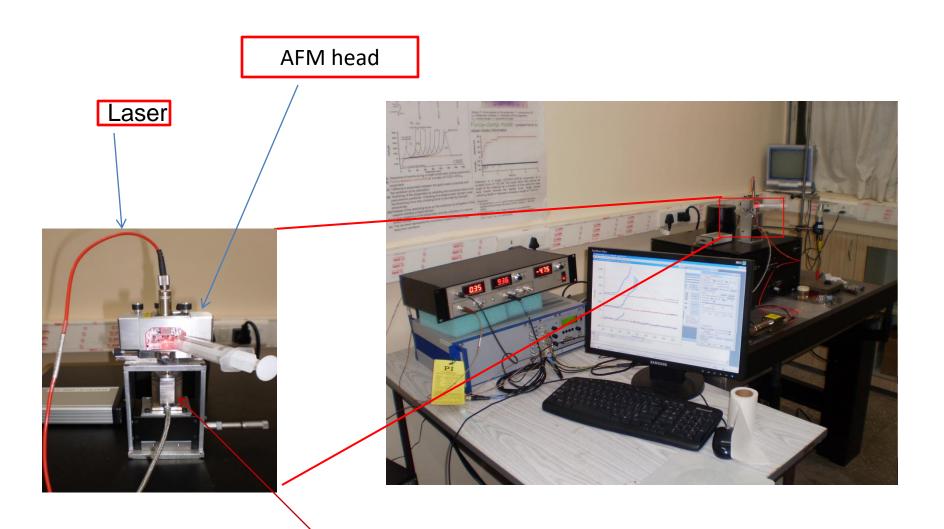
Lab members, Collaborators, and Funding Agencies







Custom-built AFM for single-molecule pulling



Piezo positioner

Current Research Theme in Our Laboratory:

Probing (Mechano)chemical and (Mechano)biological processes

Chemical bonds to biological cells

