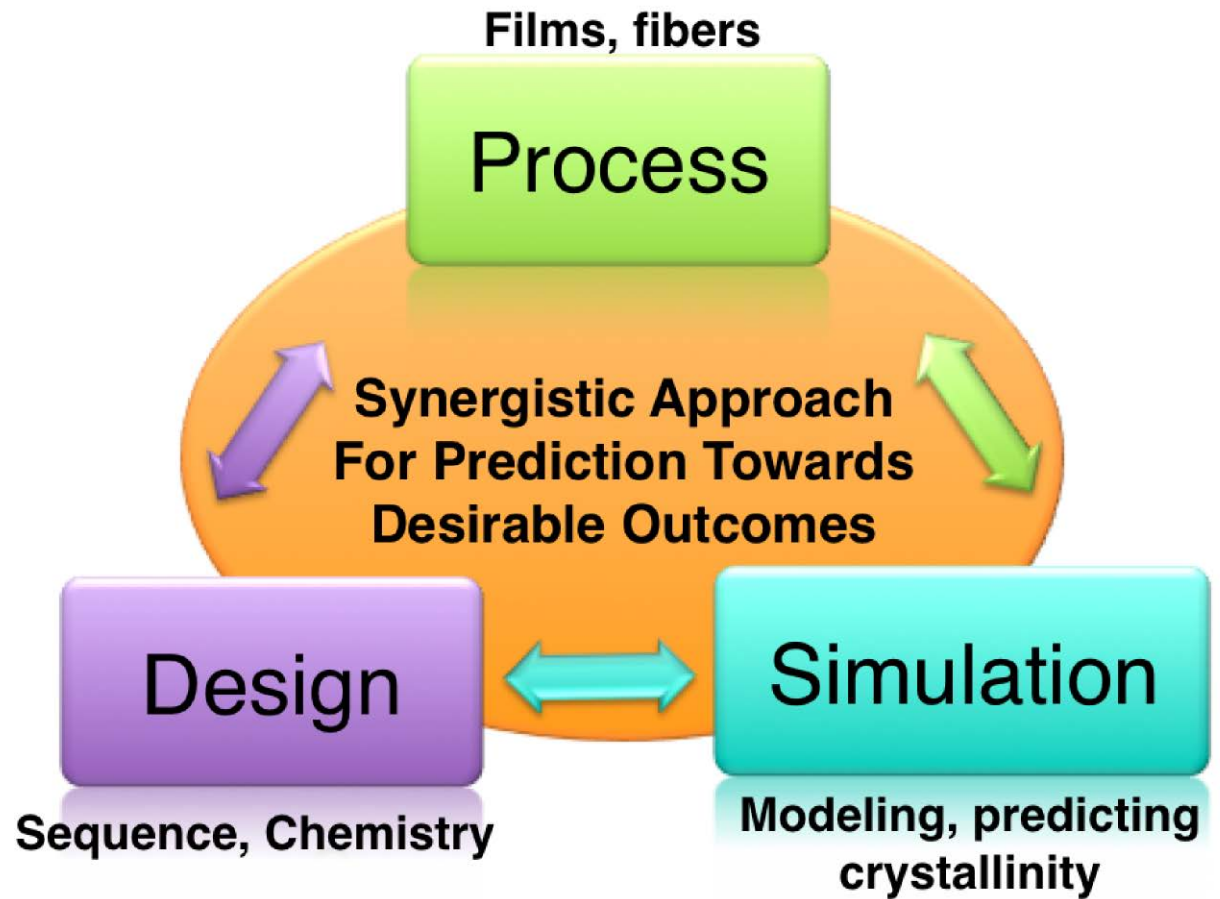


***Models to
Predict Protein
Biomaterial
Performance***

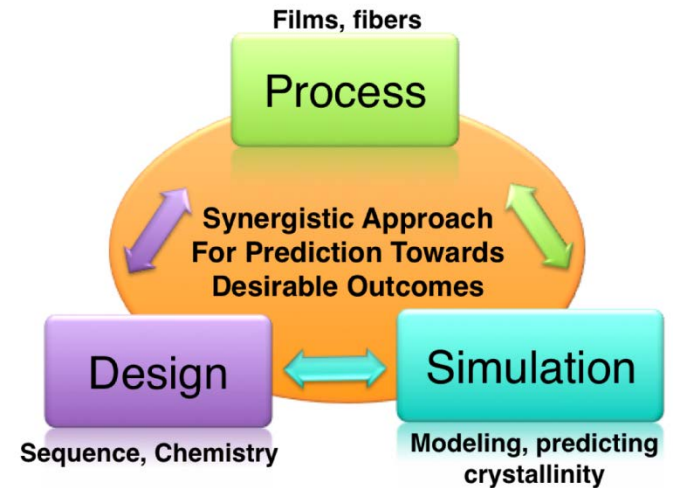


Markus Buehler (MIT)

David L. Kaplan (Tufts University)

Joyce Wong (Boston University)

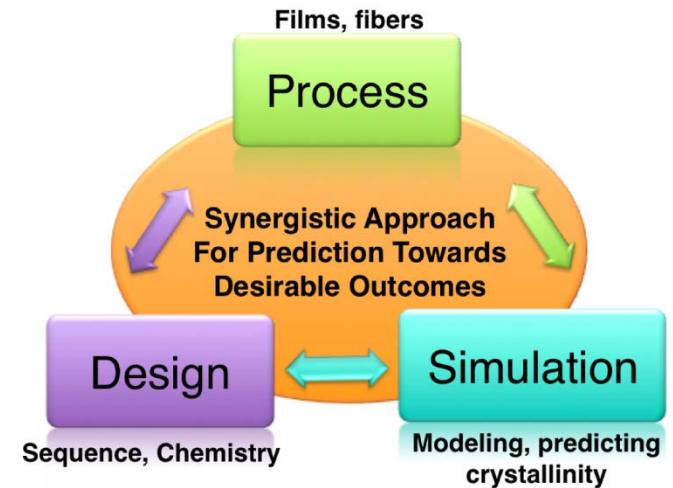
Objective



Develop **predictive assessments** of the in vivo performance of protein biomaterials

Reduce the current trial-and-error approach utilized in the field with a **more rational approach** based on **bottom-up multiscale modeling** to guide the preparation of the required materials

Hypothesis



Predictions of biomaterials performance can be attained by the **combined use of suitable experimental models** to cover **polymer features** (chemistry, molecular weight), **processing** (fiber morphology, hierarchical structure) and **modeling** at different length scales of a **material's structural hierarchy** (from chemical to macroscopic scales)

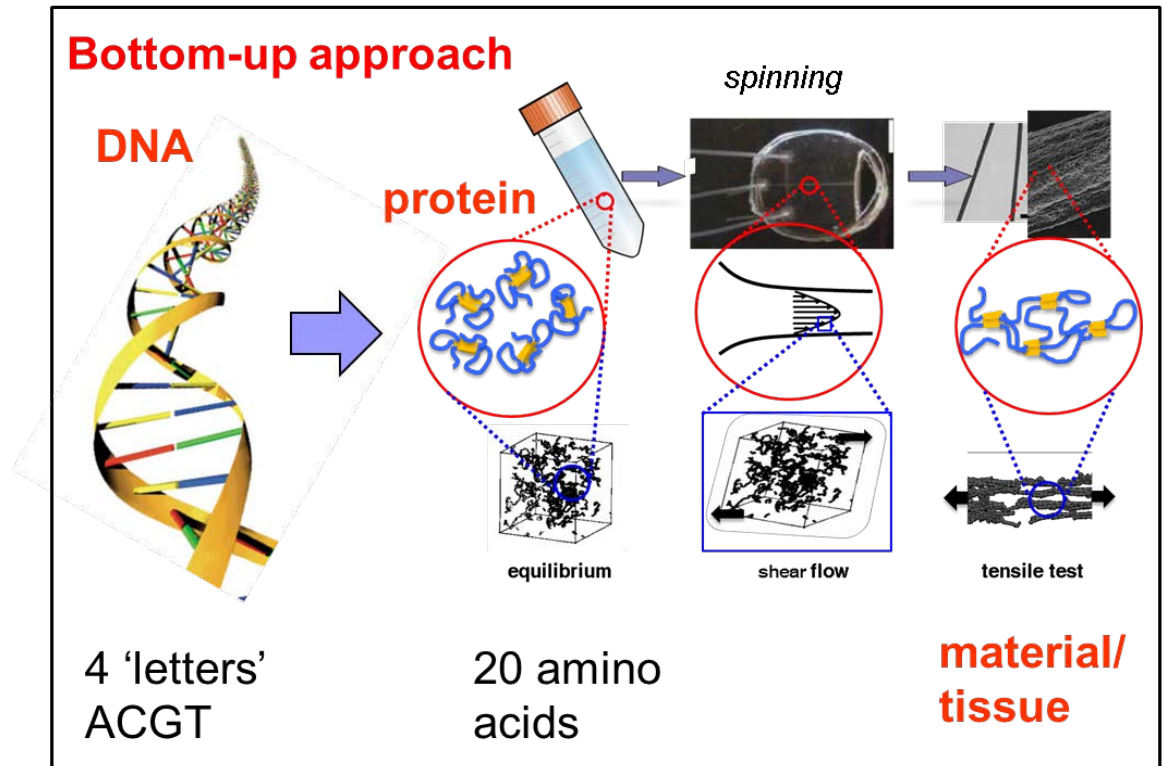
Conventional vs. new material design and manufacturing approaches

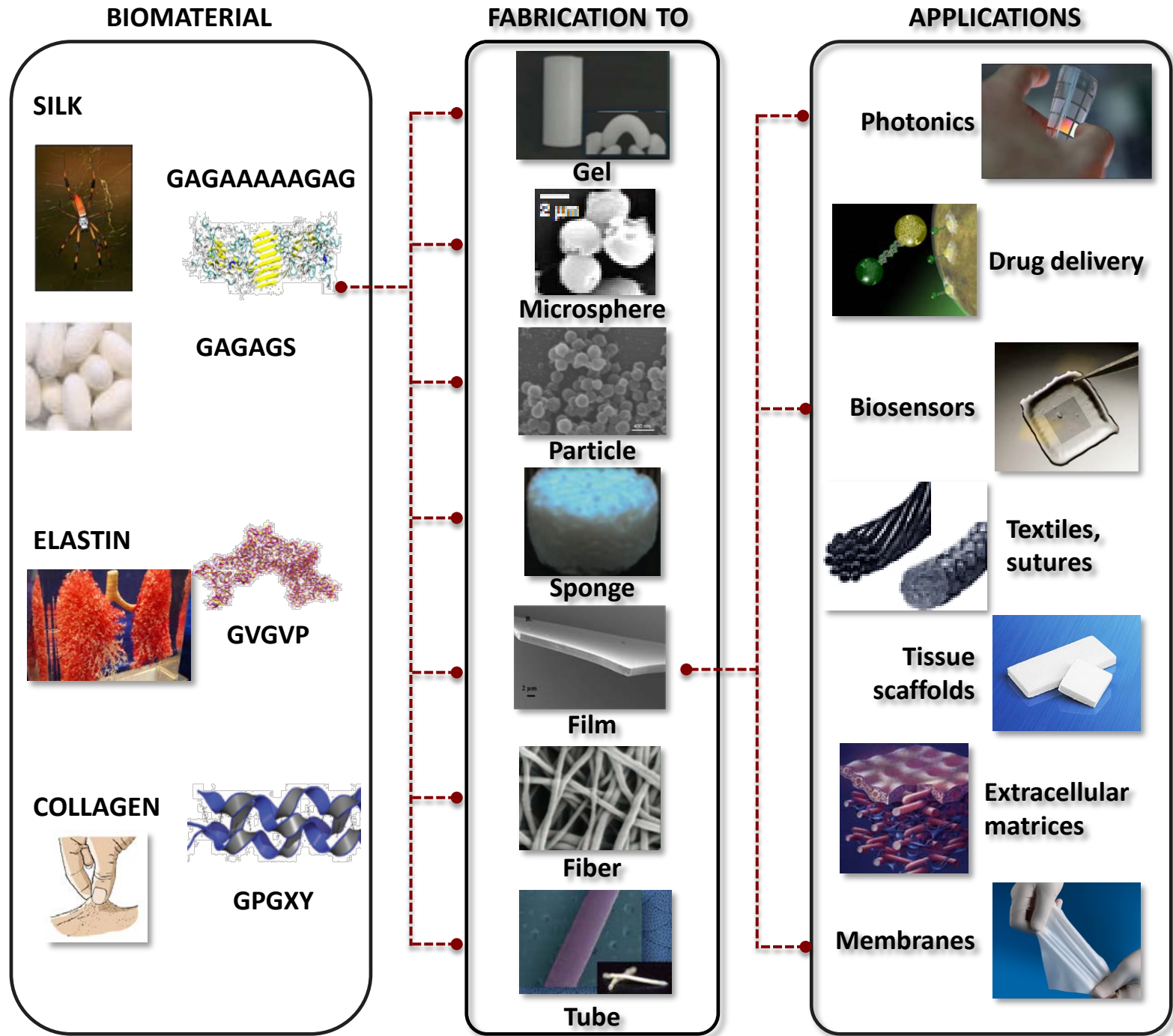
Top-down approach



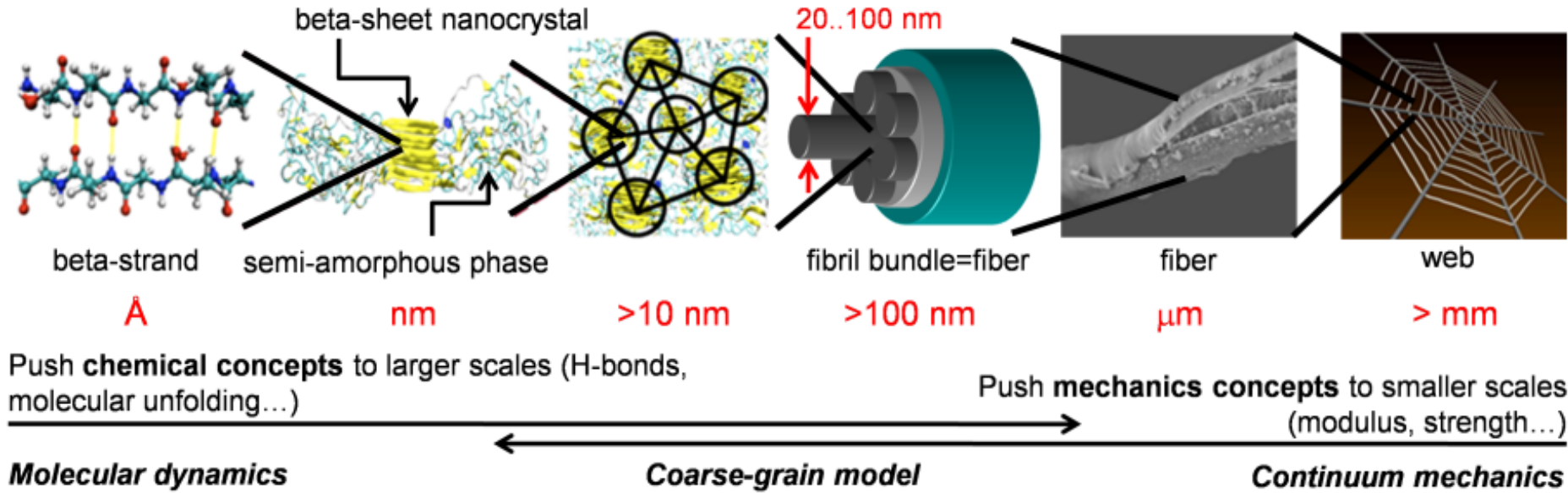
Protein-based biomaterials as the example

Bottom-up approach

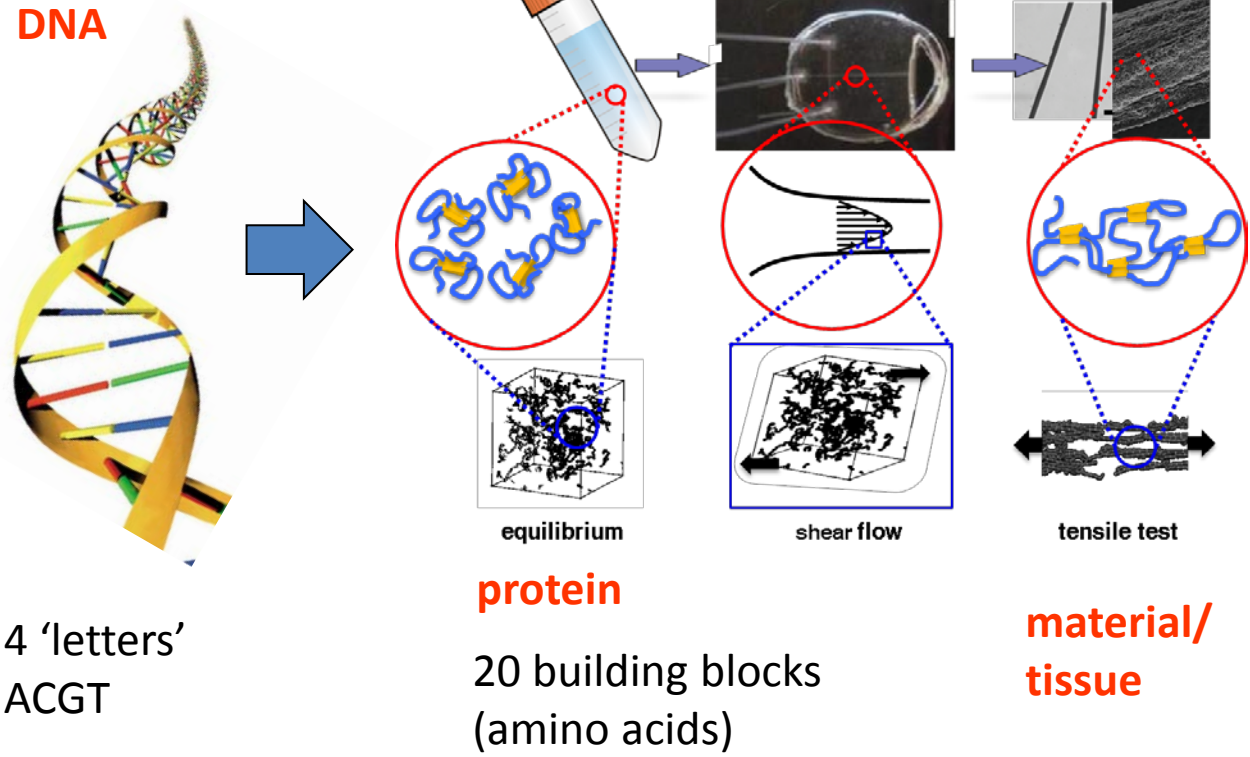




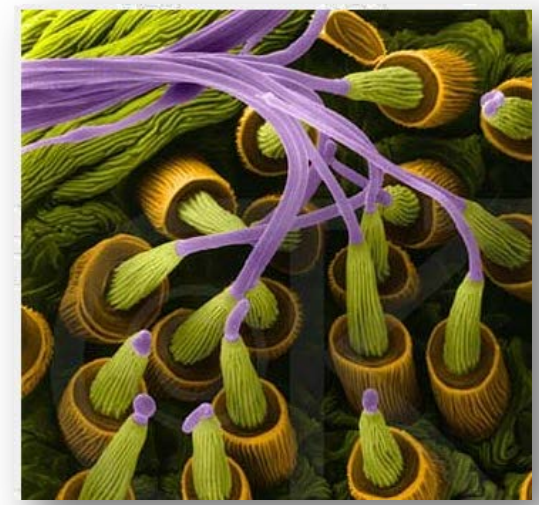
Multiscale hierarchical structure illustrated for silk



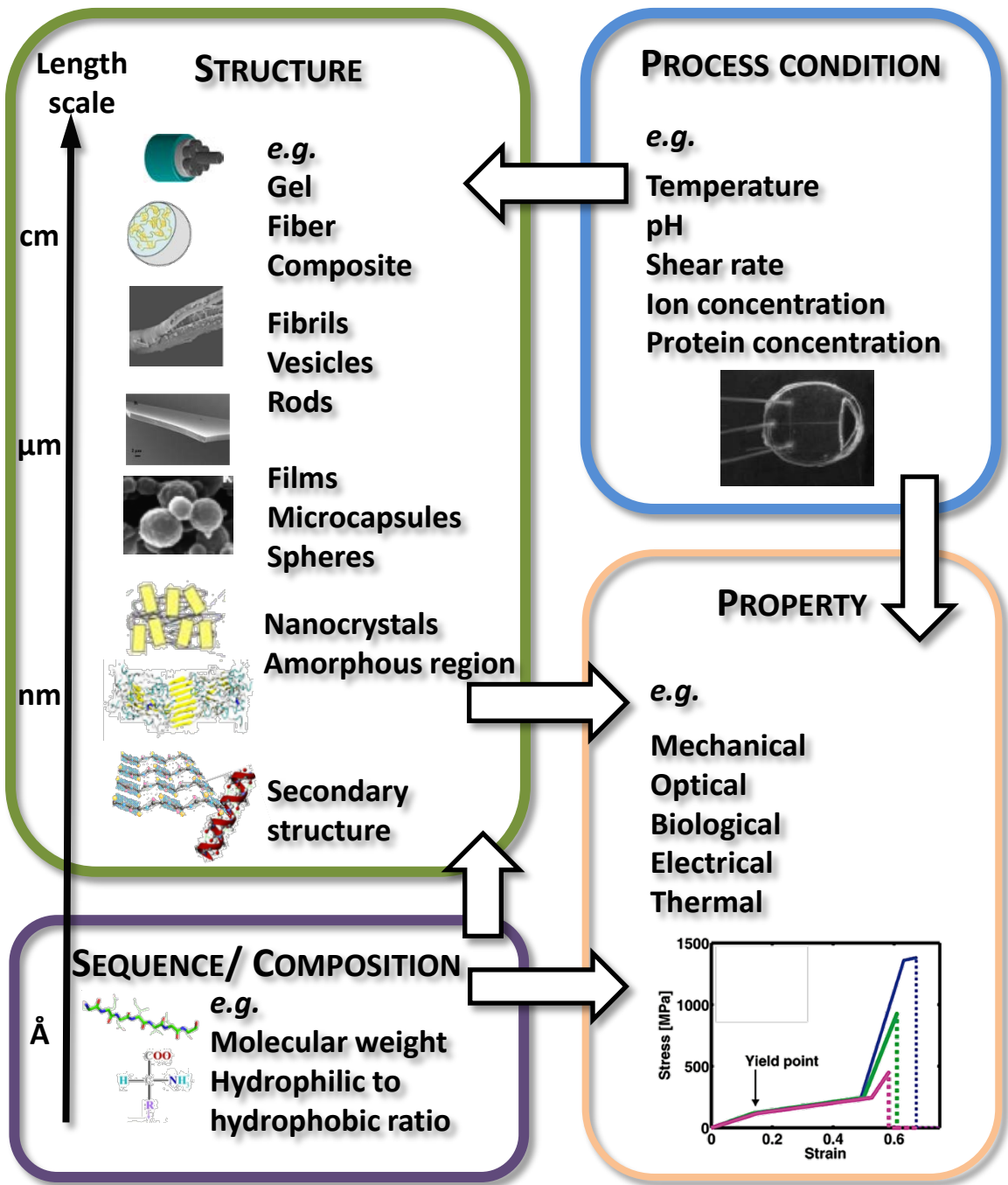
Design, processing, and material properties are closely linked



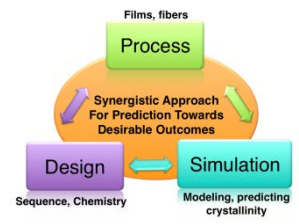
Copyright Dennis Kunel
Microscopy



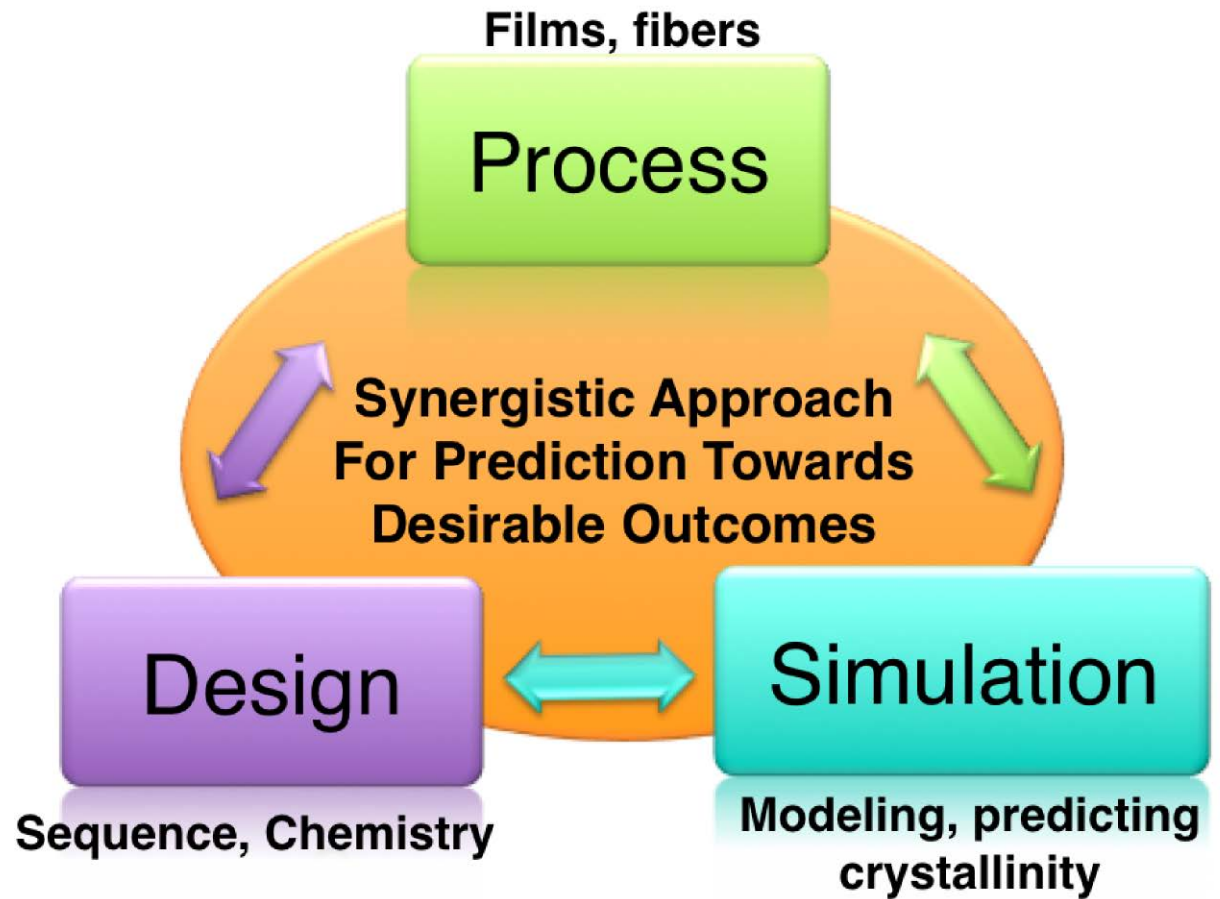
(spider) silk spinning
liquid to solid



Biopolymer design: sequence, structure, process condition and properties



***Models to
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Markus Buehler (MIT)

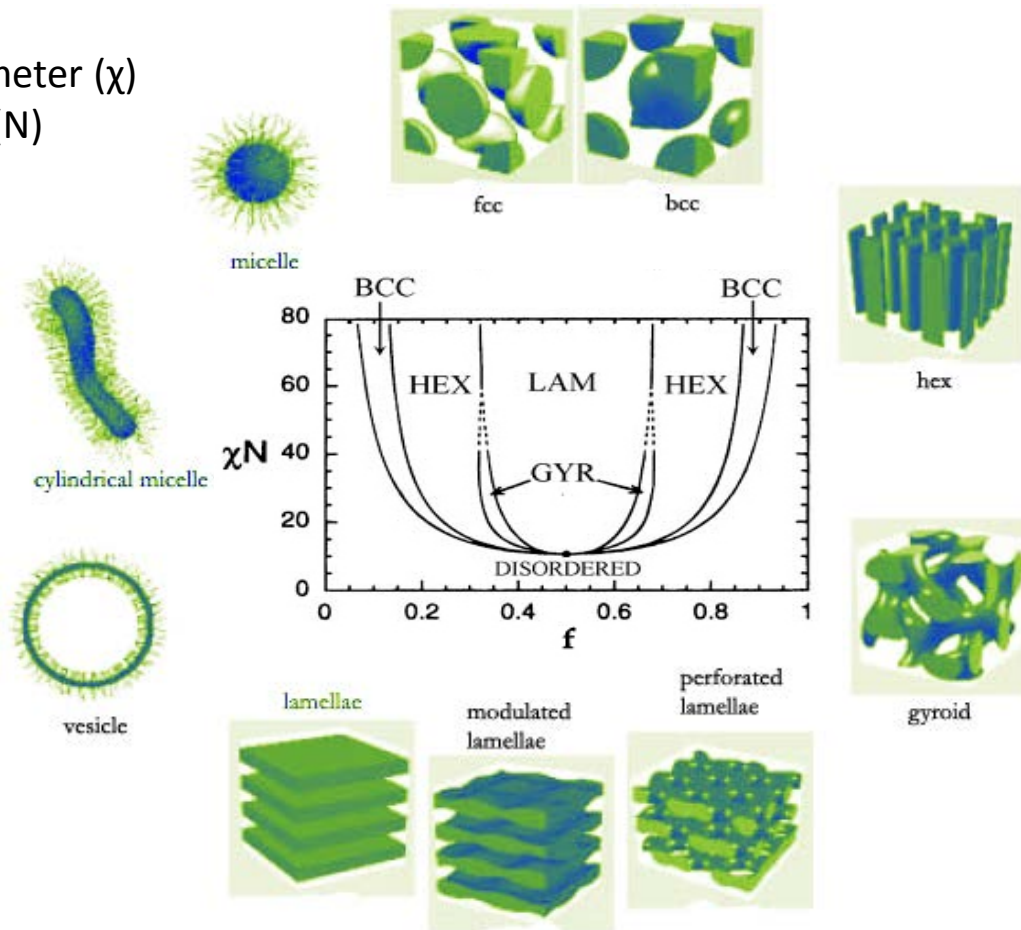
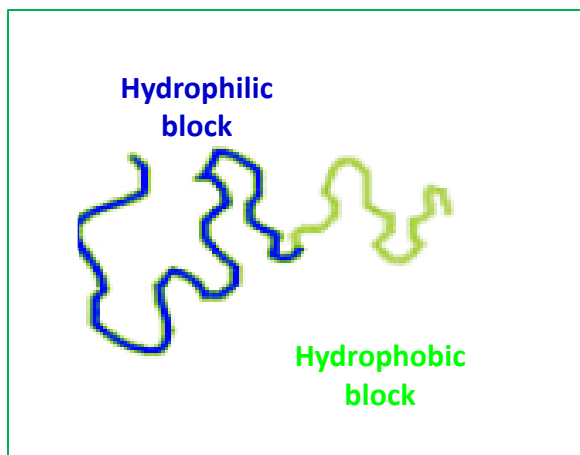
David L. Kaplan (Tufts University)

Joyce Wong (Boston University)

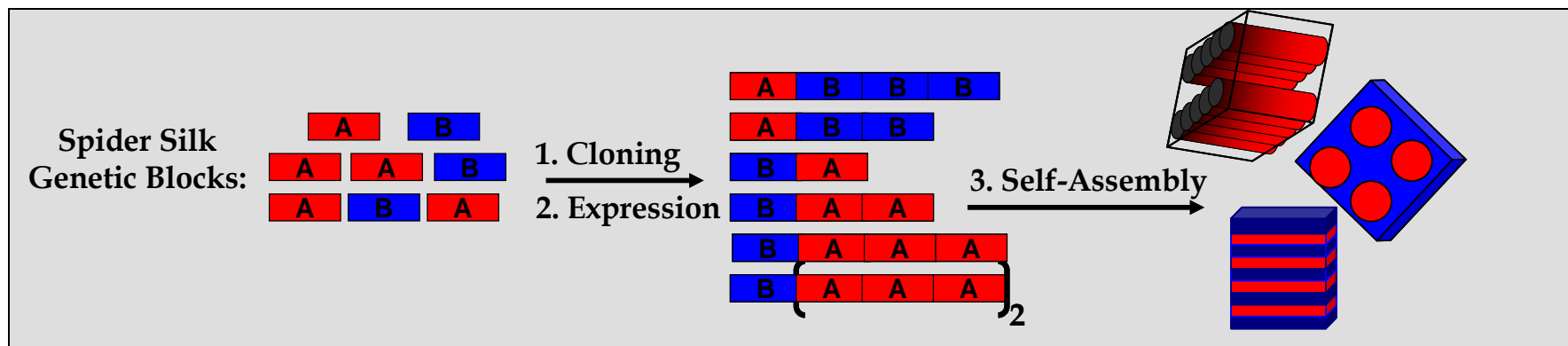
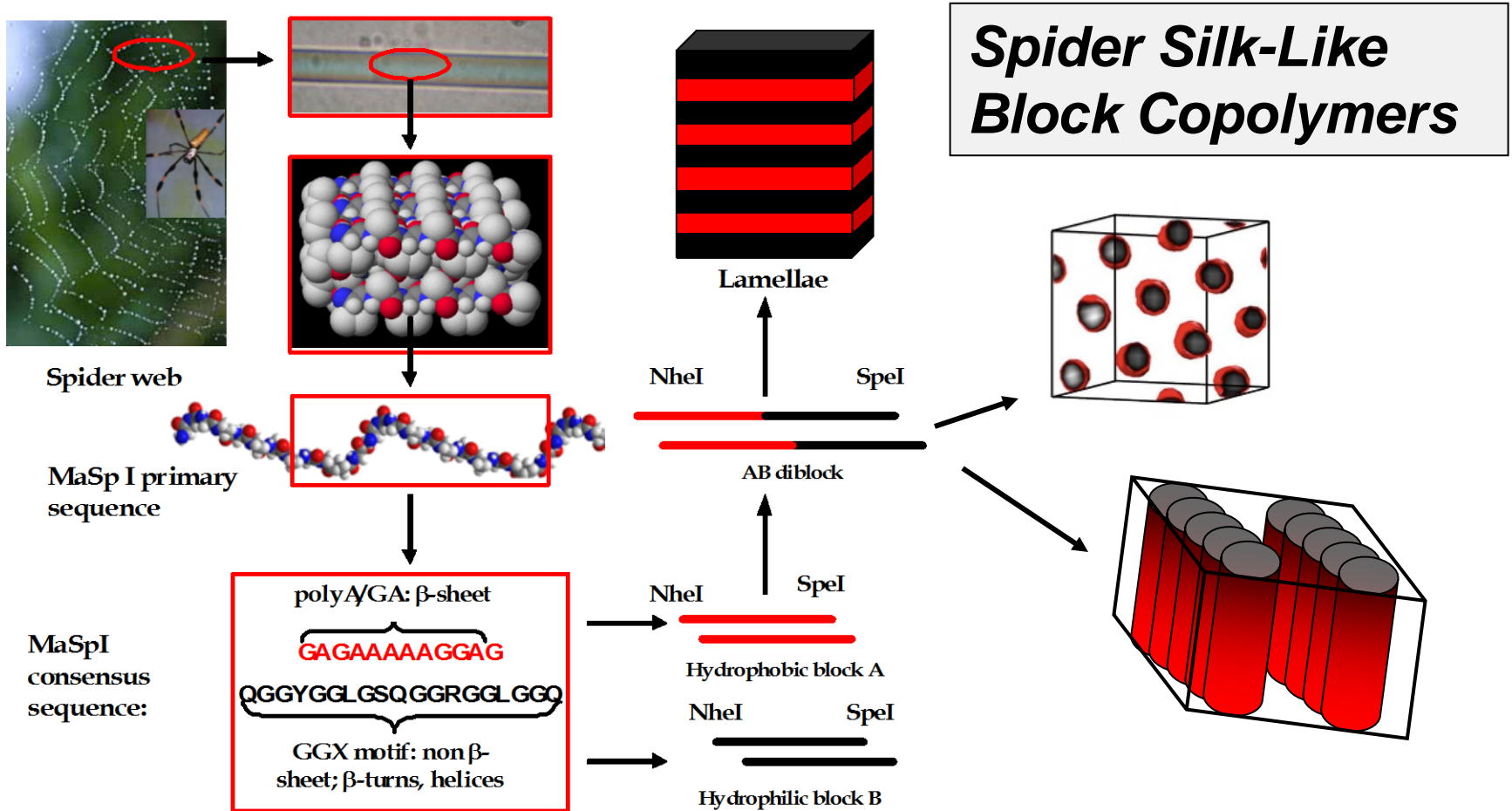
Silk Block Copolymers – Design & Self-Assembly

Phase separation controlled by:

- Block length ratio (f_A)
- Segregation (Flory-Huggins) parameter (χ)
- Overall degree of polymerization (N)



Self-assembled structures of polymeric materials

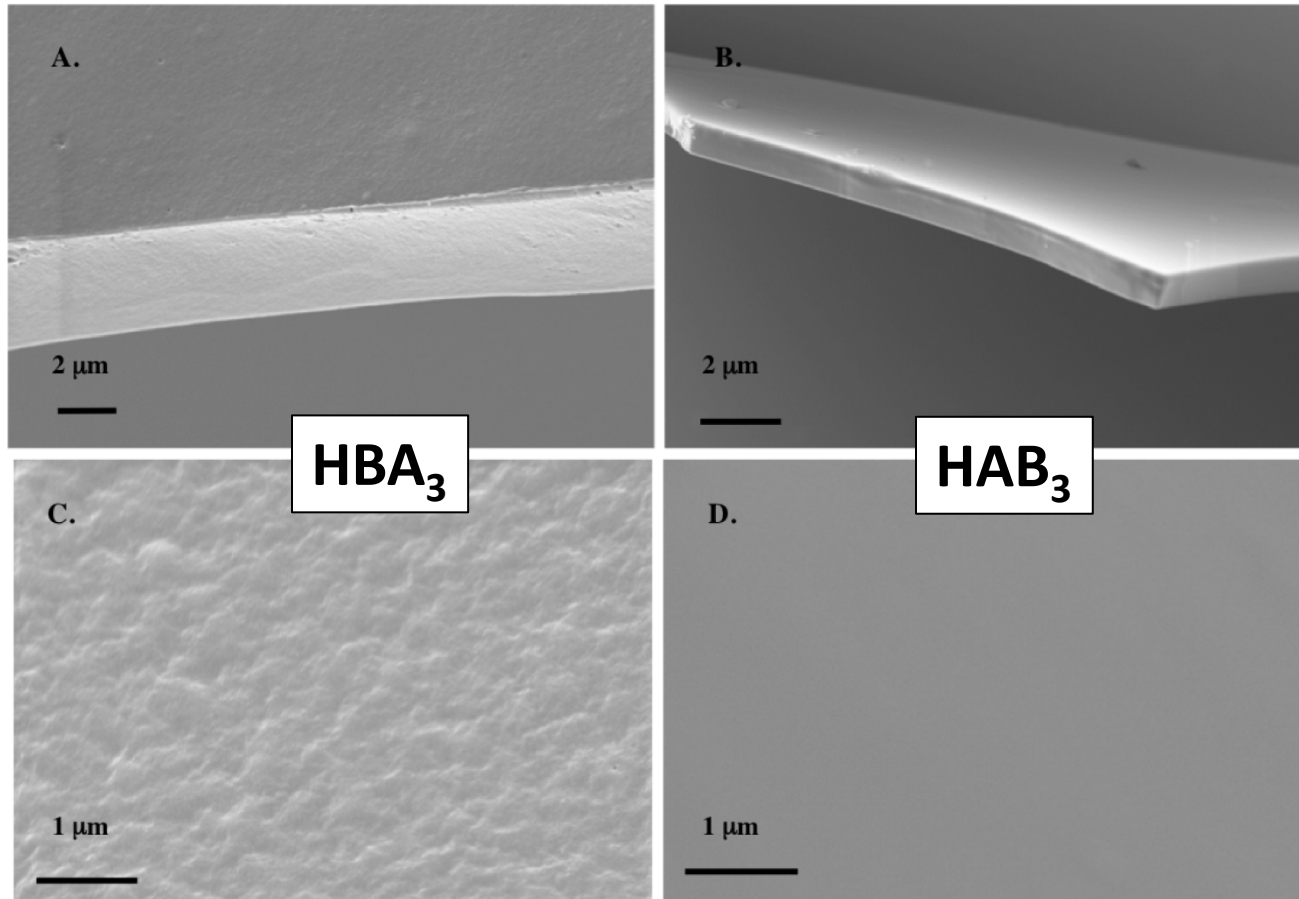


Example – Biosynthesis of protein variants based on spider silk

Code	Spider silk-like block copolymers	Mw [Da]
HBA ₃	<i>MHHHHHSSGLVPRGSGMKETAALKF</i> <i>ERQHMDSPDLGTDDDDKAMAAS<u>QGGY</u></i> <u><i>GGLGSQGSGRGGLGGQTS</i></u> <i>GAGAAAA</i> <i>GGAGTSGAGAAAAAGGAGTSGAGAAA</i> <i>AAGGAGTS</i>	10,068
HAB ₃	<i>MHHHHHSSGLVPRGSGMKETAALKF</i> <i>ERQHMDSPDLGTDDDDKAMAASGAGA</i> <i>AAAAGGAGTS</i> <u><i>QGGYGGLGSQGSGRGG</i></u> <u><i>LGGQTSQGGYGGLGSQGSGRGGLGGQ</i></u> <u><i>TSQGGYGGLGSQGSGRGGLGGQTS</i></u>	11,967

hydrophilic block B is underlined
hydrophobic Block A bold
hexahistidine tag italicized.

Films – materials formation from spider silk block copolymers



Scanning Electron Microscopy

Characterization of Spider Silk Block Copolymers

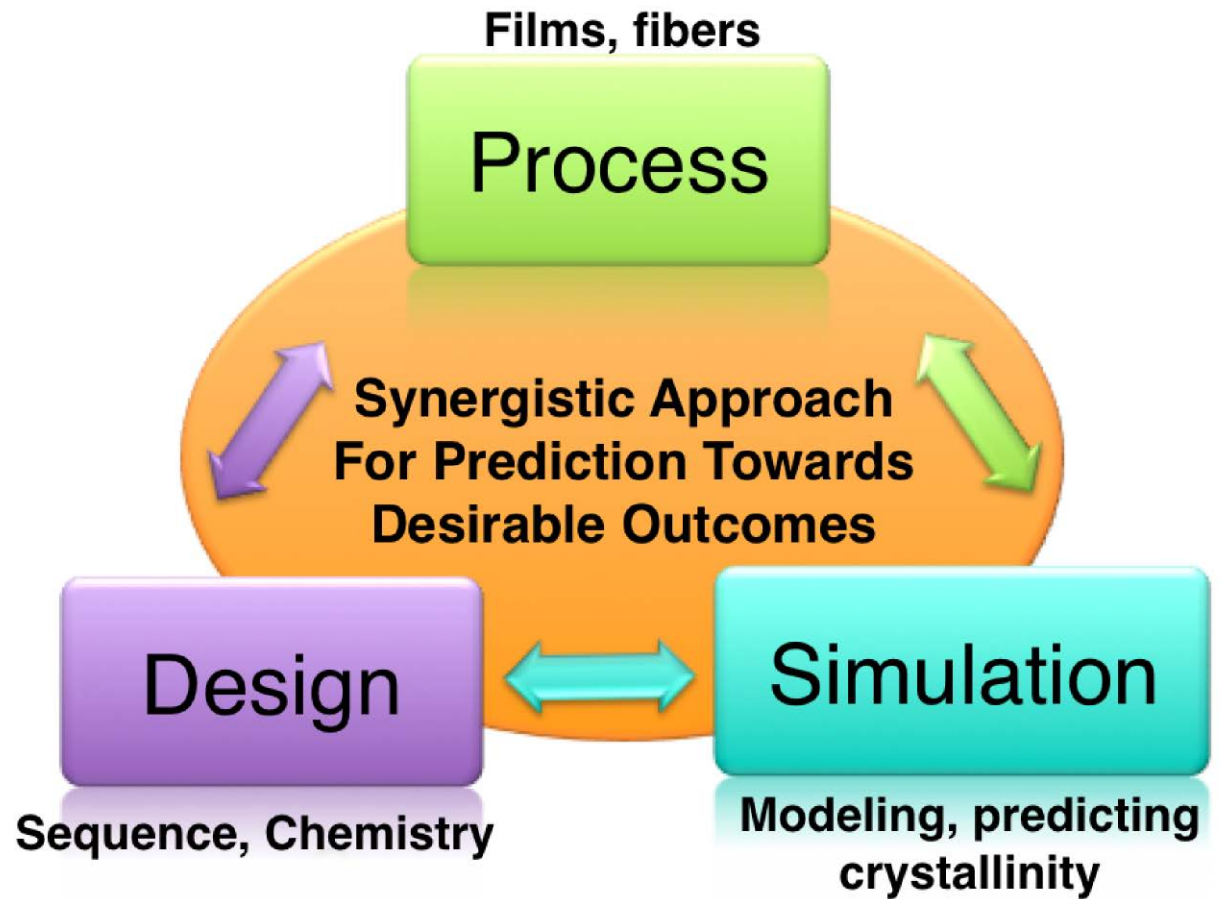
Percentage of structures after FTIR and Deconvolution

Code	Beta sheet	Turn	Alpha helix	Random coil
HBA ₃	21.1±5	24.8±3	13.2±5	12.6±5
HAB ₃	10.8±3	27.4±5	8.7±4	11.8±5

Mechanical properties - water annealed films

Code	Linear Elastic Modulus @ 2-3% strain [MPa]	Ultimate Tensile Strength [MPa]	Failure strength [%]
HBA ₃	161.9±27.5	13±0.7	43.8±16.9
HAB ₃	553±31.3	20.9±7	6.1±3.4

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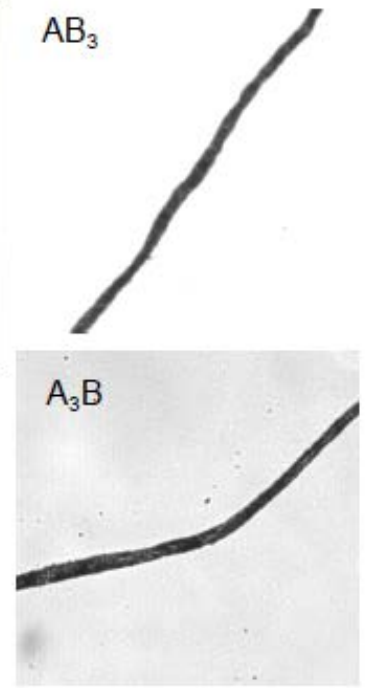
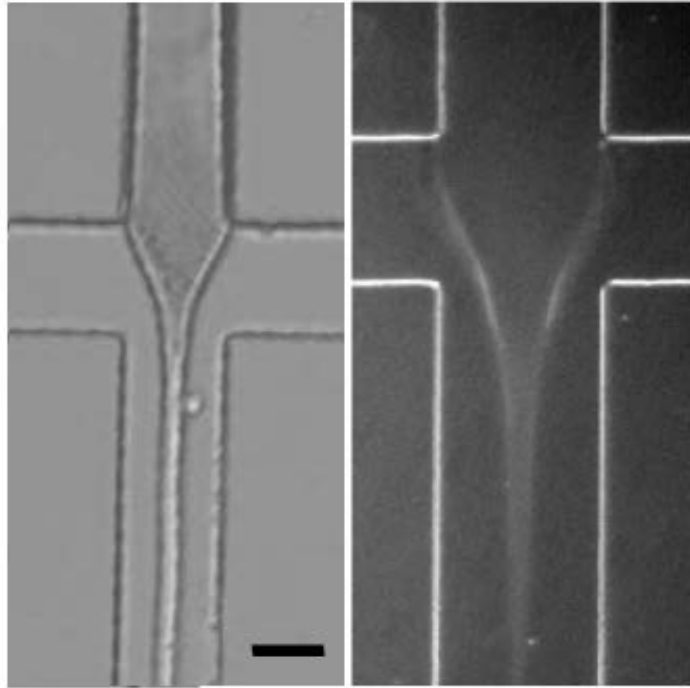


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Joyce Wong (Boston University)

Regenerated silk fibers + block copolymers



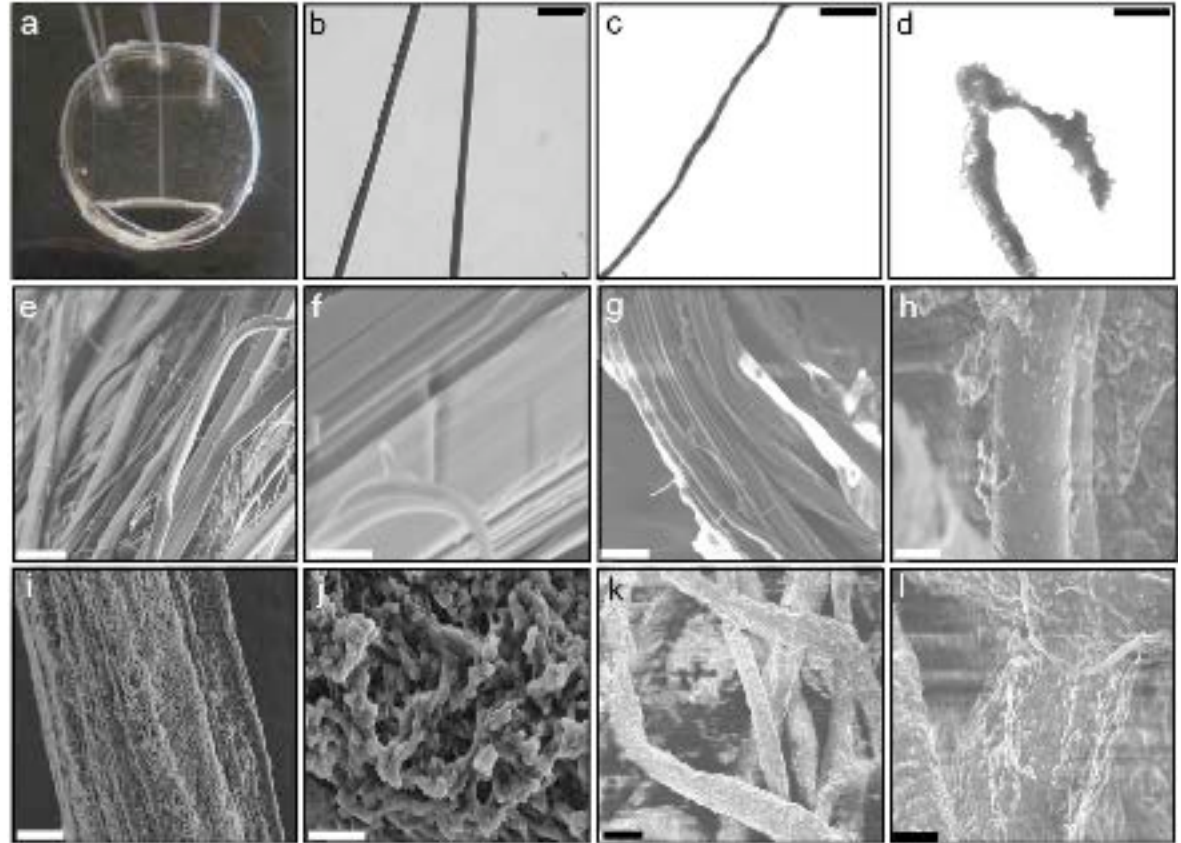
gland

microfluidic device
(fluid focusing)

spun fibers
(AB₃ & BA₃)

Fiber Morphology

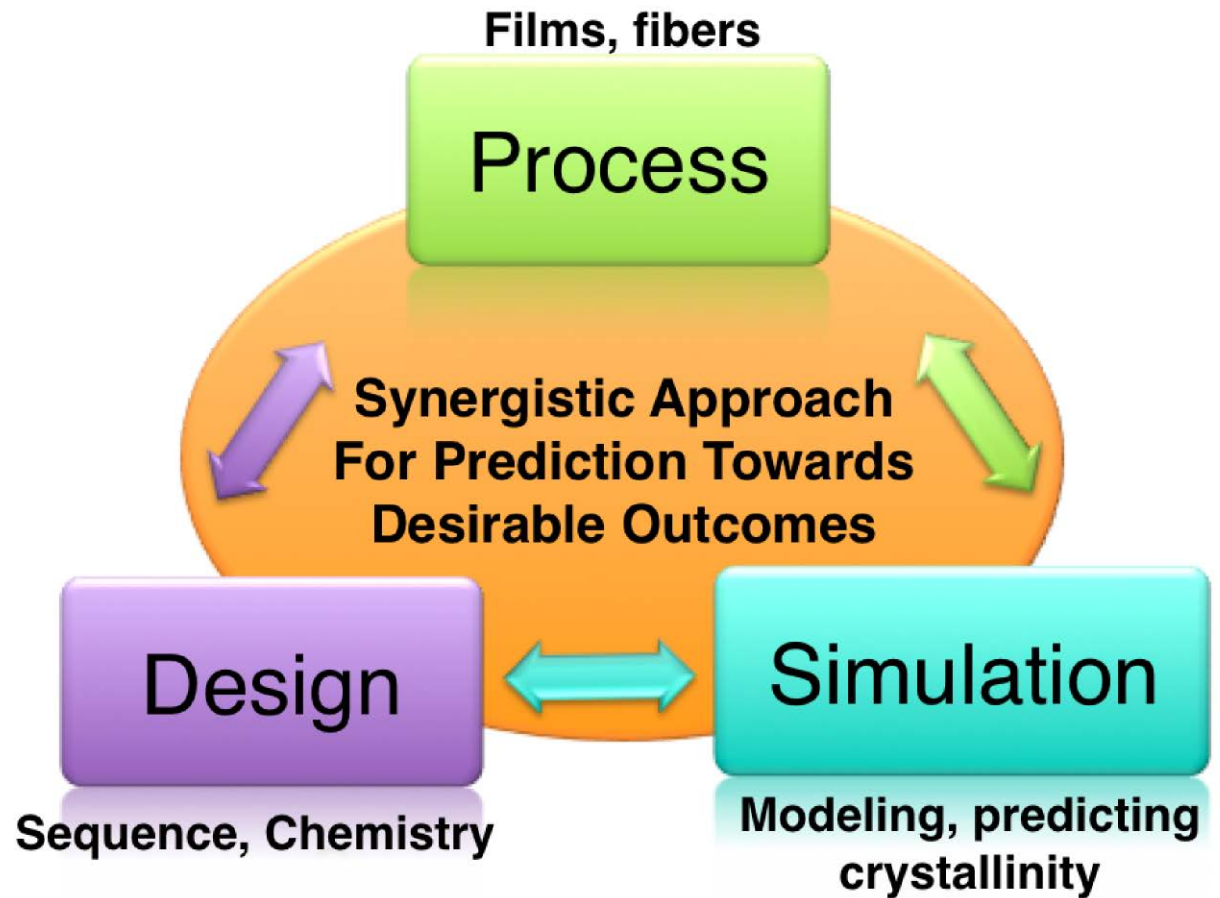
spun from regenerated silk fibroin (RSF) and mixtures with HAB₃ and HBA₃ (30% RSF/70% copolymer)



Brightfield images [RSF (B, scale bar 150 mm) RSF/HAB₃ blend (C, scale bar 150 mm) and RSF/HBA₃ blend (D, scale bar 150 mm) fibers]

E-L - SEM images of fibers [(E) Native silk, scale bar 30 mm, (F) Native silk, scale bar 2 mm, (g) RSF fibers, scale bar 8 mm, (H) RSF fibers, scale bar 4 mm, (I) RSF/HAB₃ blend, scale bar 30 mm, (J) RSF/HAB₃ blend, scale bar 2 mm, (K) RSF/HBA₃ blend, scale bar 20 mm, (L) RSF/HBA₃ blend, scale bar 5 mm]

***Models to
Predict Protein
Biomaterial
Performance***



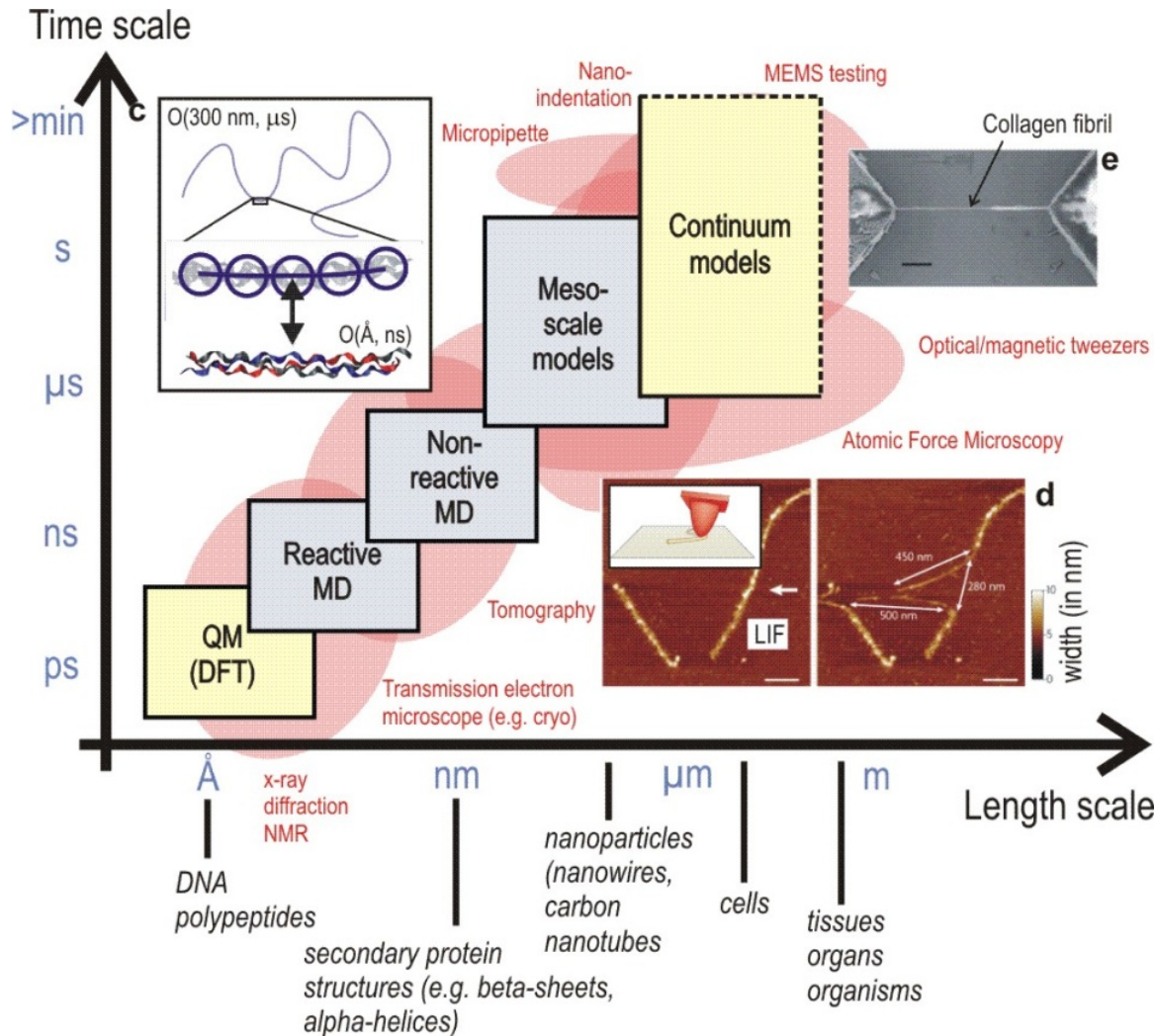
Markus Buehler (MIT)

David L. Kaplan (Tufts University)

Joyce Wong (Boston University)

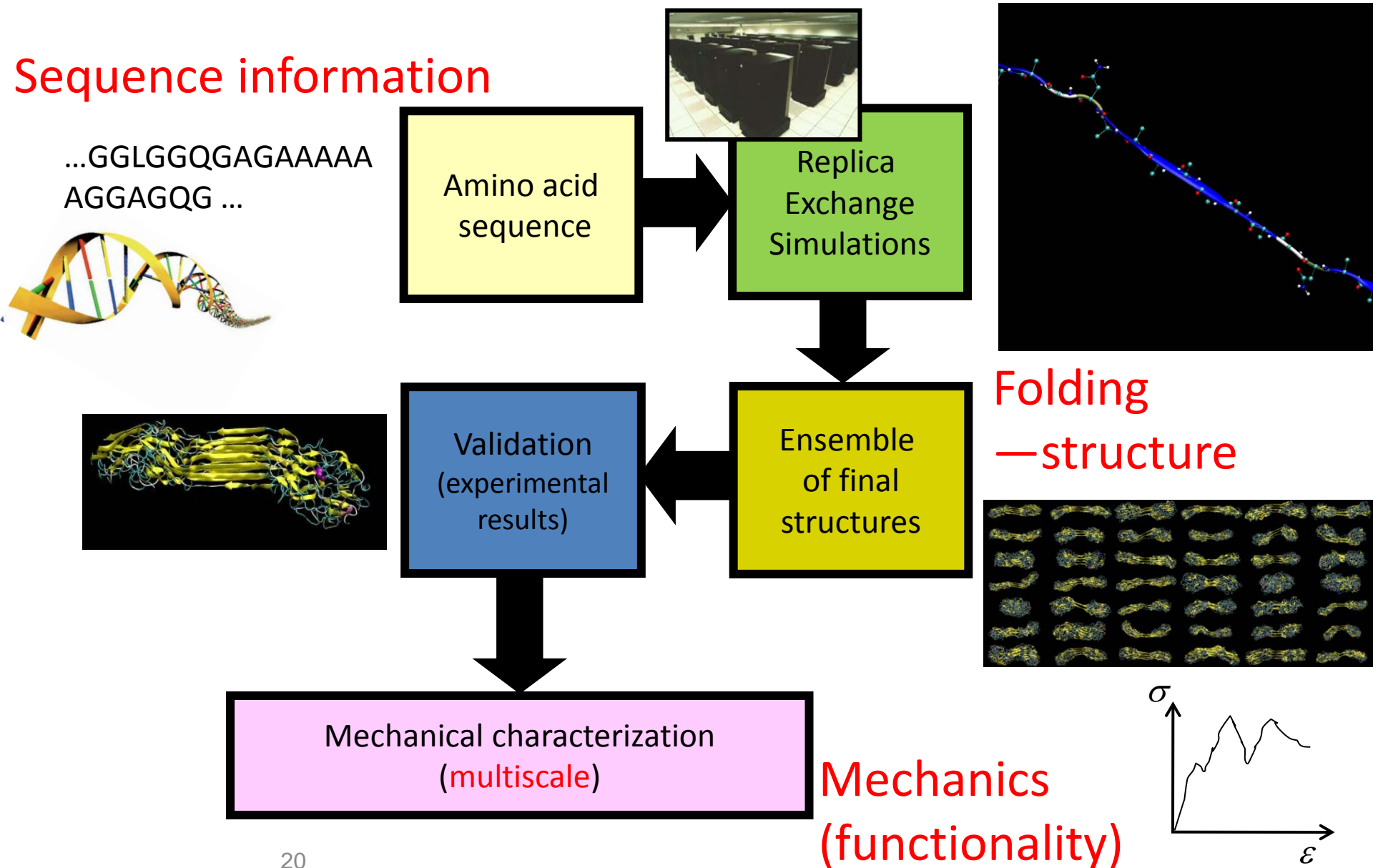
Multi-scale integration of computational and experimental tools

→ structure-property-process relationships in protein materials

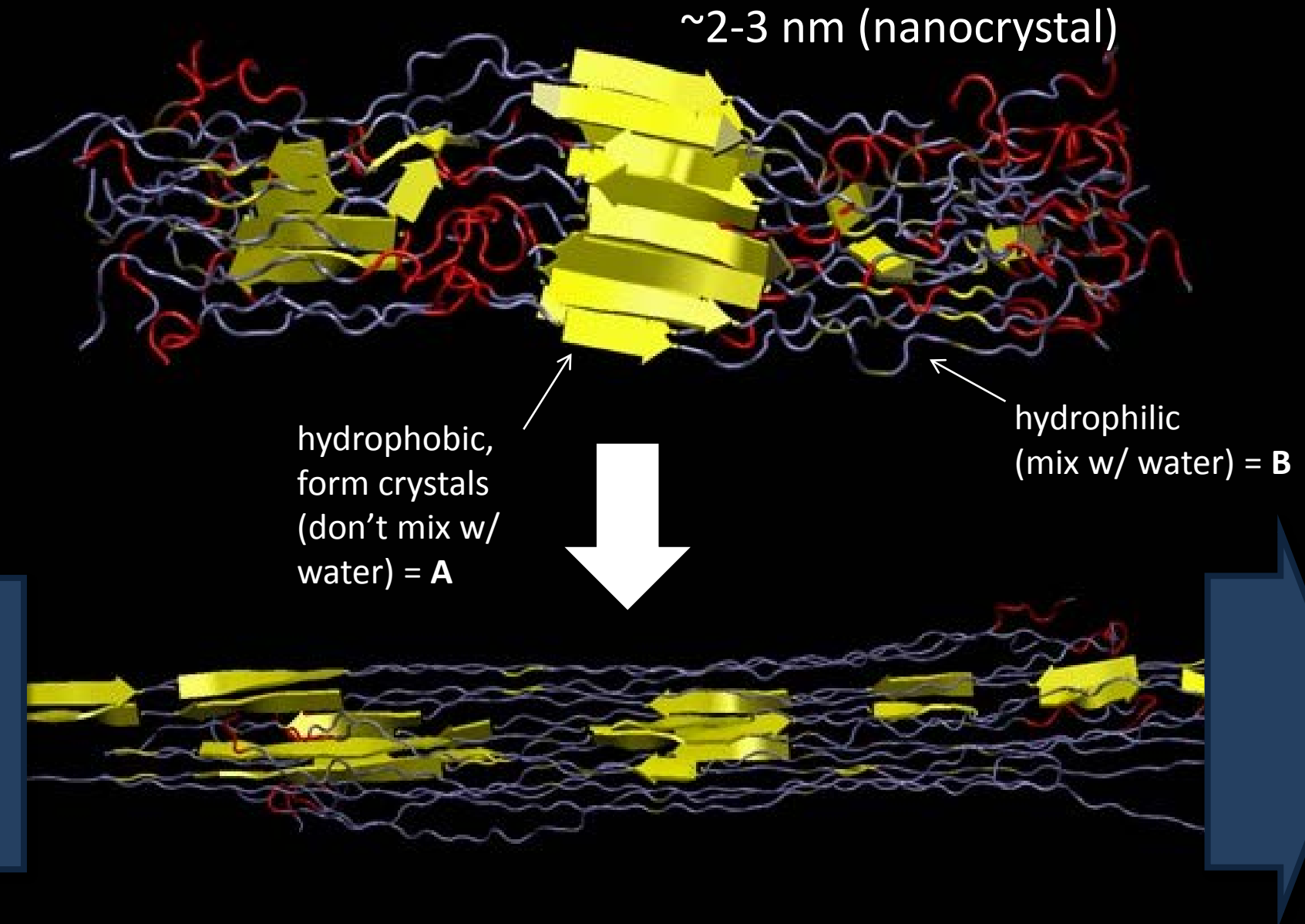


Reactive, nonreactive molecular dynamics (MD), mesoscale (coarse-grained) and continuum models to span Angstrom to micrometers and meters and time-scales from femtoseconds to seconds

Structure prediction and functional properties



Example: molecular mechanics of silk

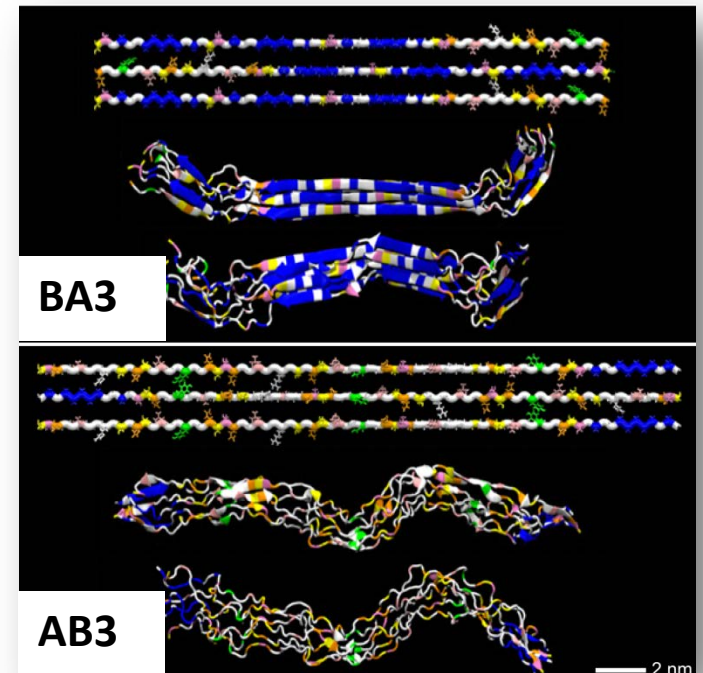
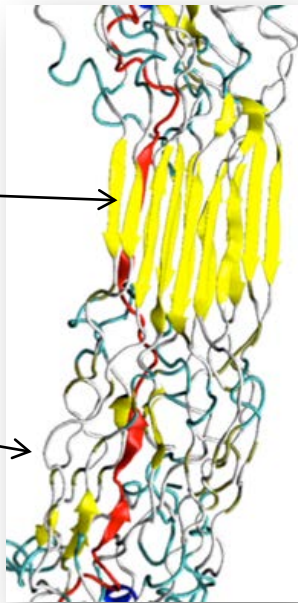


De novo sequences: in silico model

AB3 vs. BA3

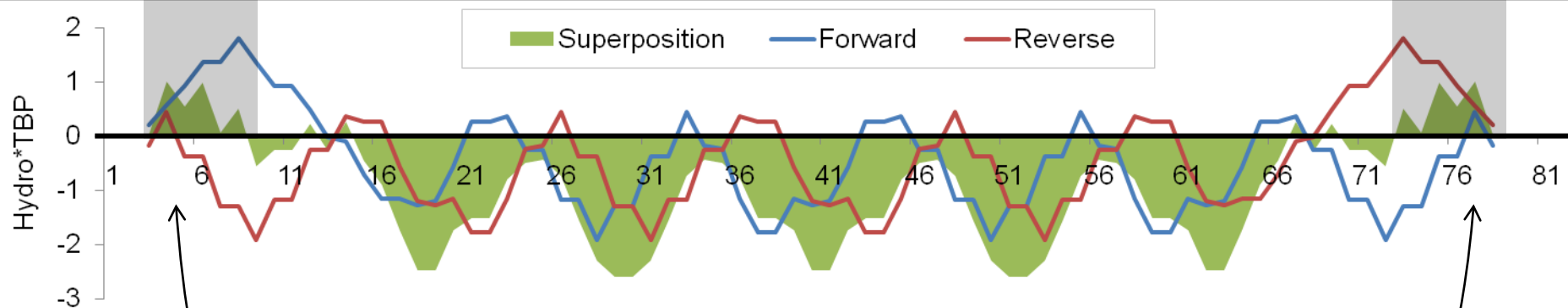
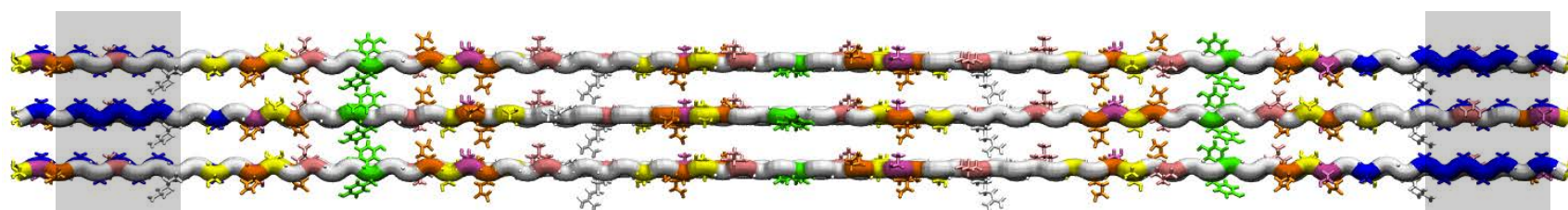
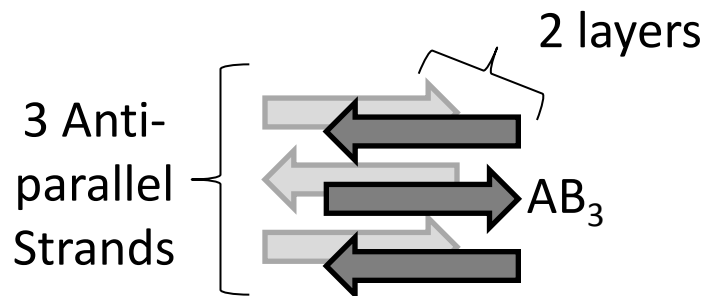
● A = hydrophobic domain

● B = hydrophilic domain



AB₃ Lattice 3x2

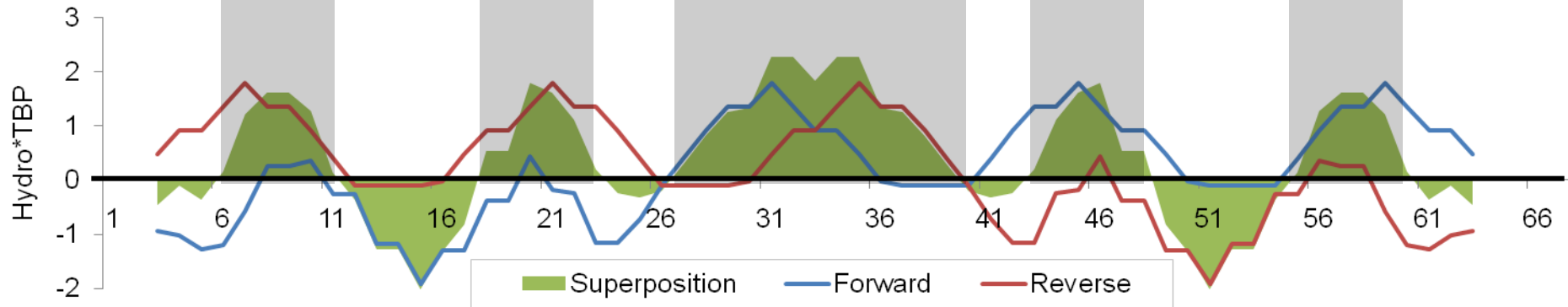
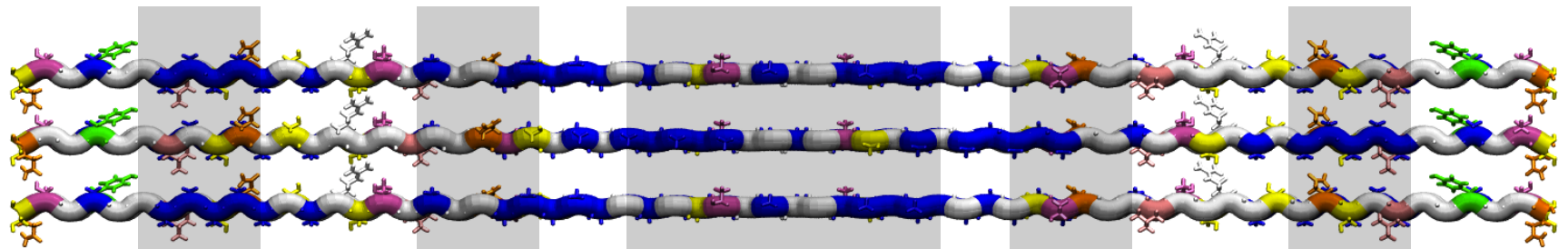
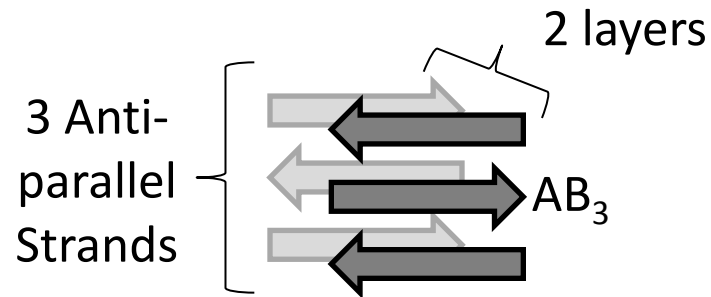
AB₃
Length: 80 res, 27 nm



Slight change of β -sheet at A (poly-Ala)

BA₃ Lattice 3x2

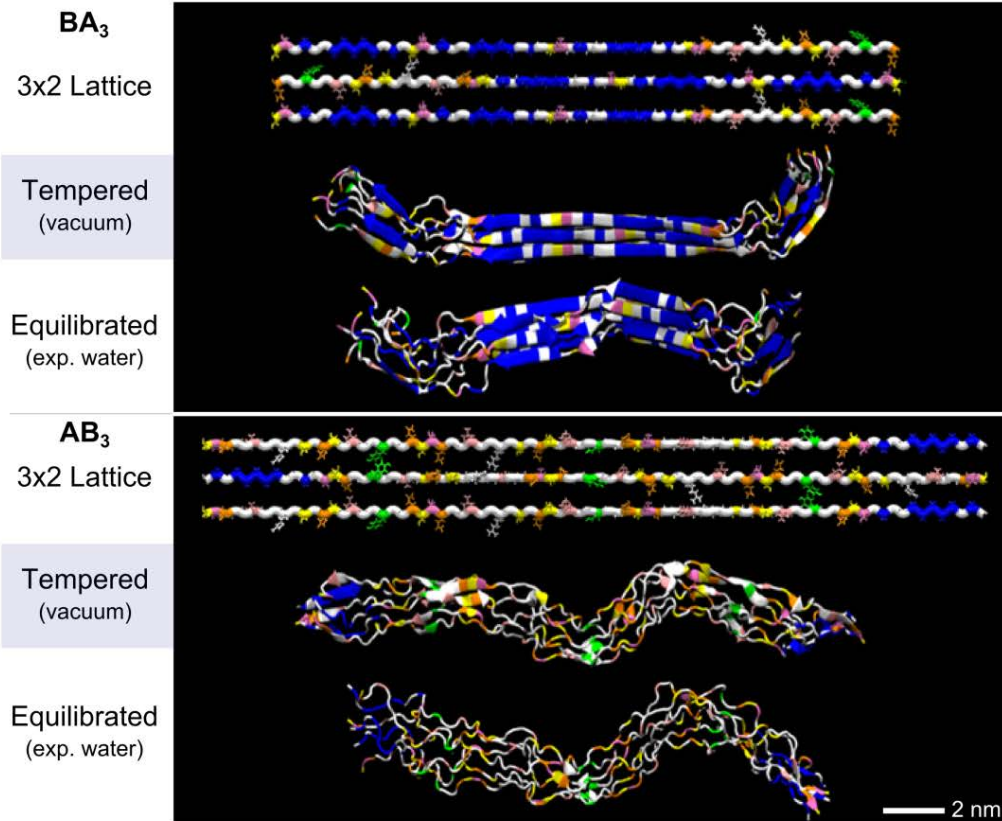
BA₃
Length: 64 res, 22 nm



Strong chance of many β -sheets because of overlapping A

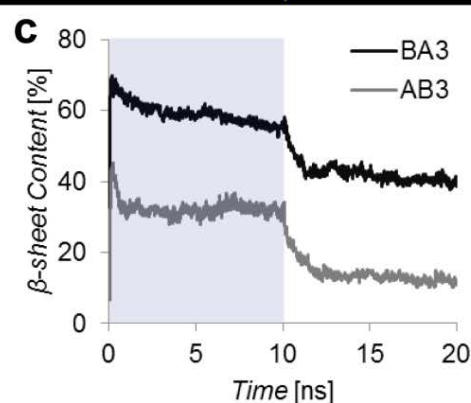
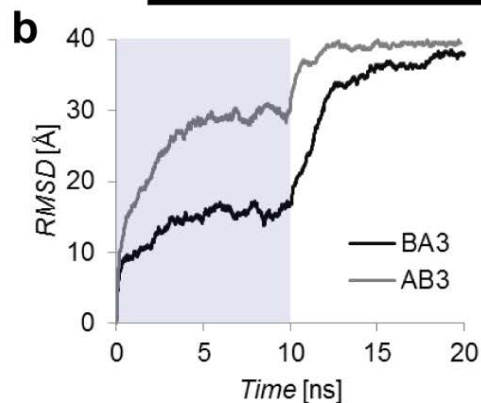
Equilibration & structure convergence - computation

a



Length and secondary structure change visible during tempering in implicit water and equilibration in explicit water (water molecules hidden for clarity)

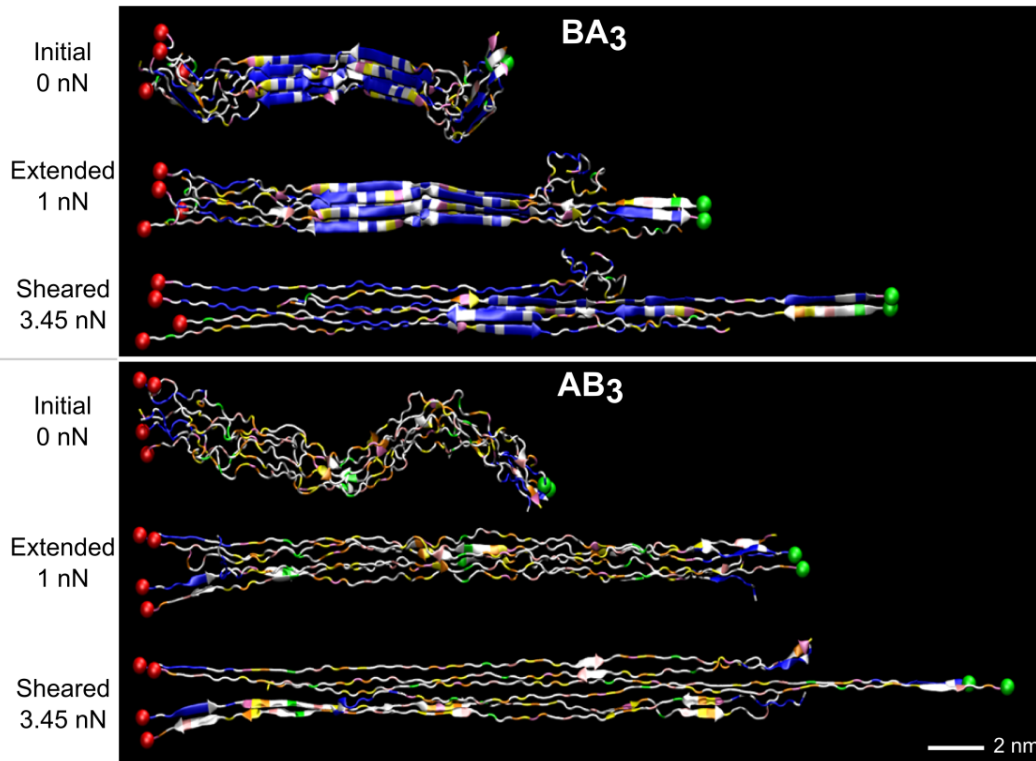
Residues are colored by secondary structure: **β -sheet is in blue.**



Convergence for each stage is determined by:
(b) RMSD and
(c) changes in total β -sheet content.

Pull out testing - computation

a

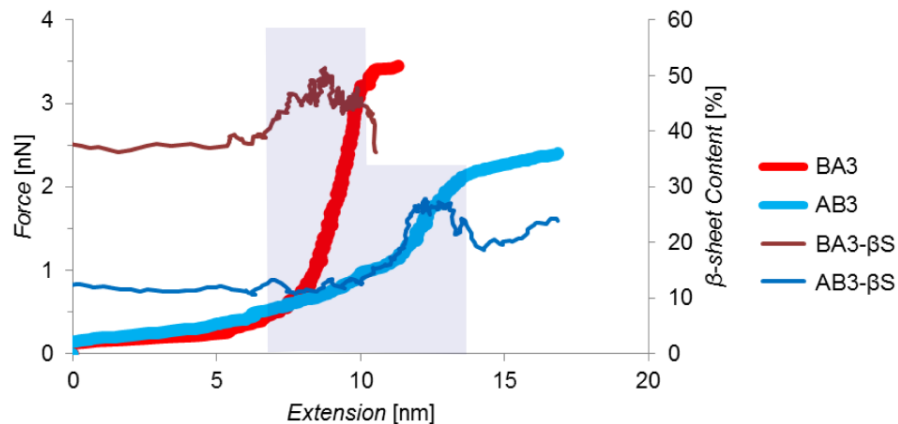


Force-control pullout testing of the equilibrated structures in explicit water

Length and secondary structure change visible during deformation

Residues are colored by secondary structure: **β-sheet is in blue.**

b



Total instantaneous β-sheet content (thin line) correlated with the force-extension curves (thick line) for each structure: **AB₃ stiffer than AB₃**

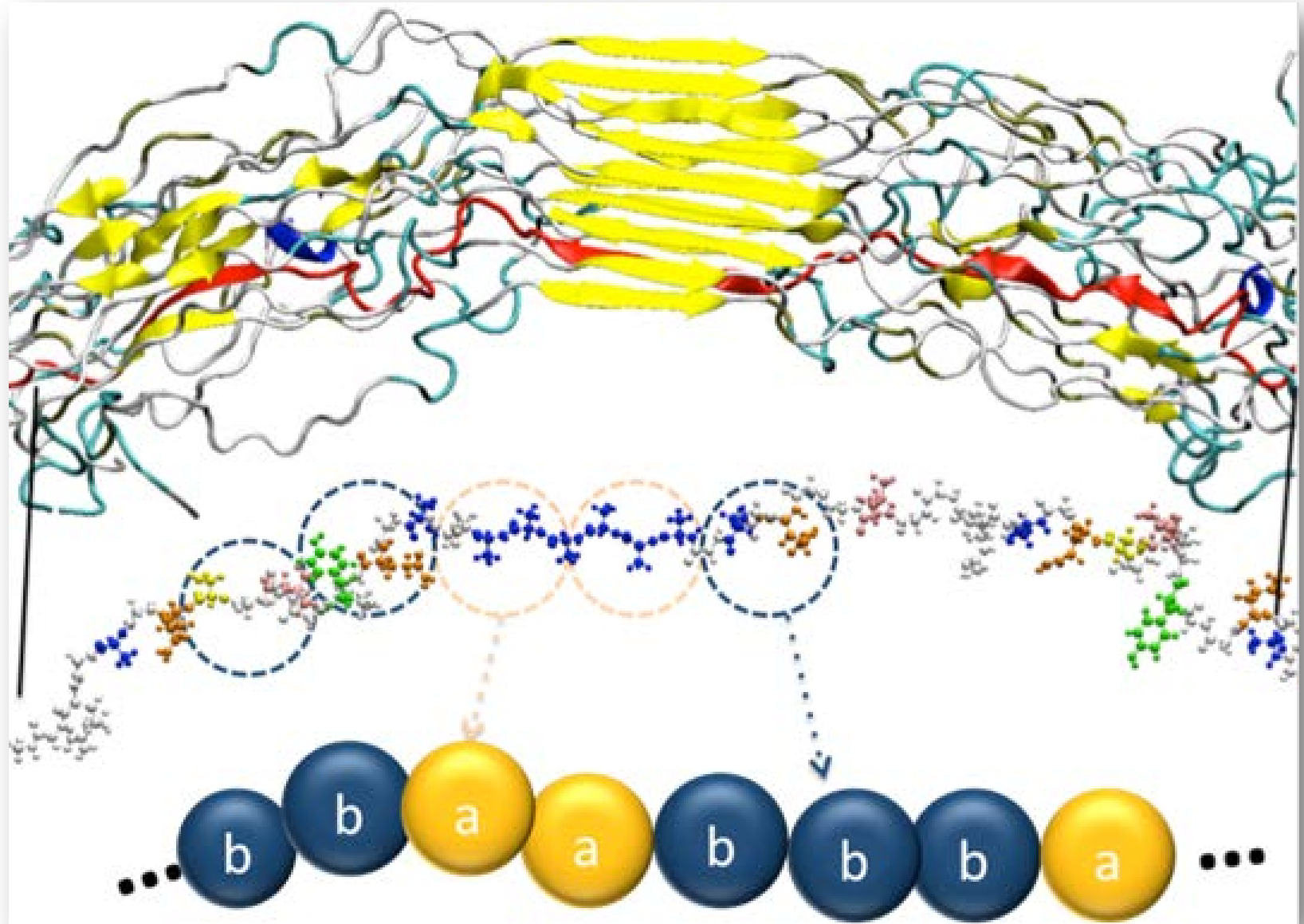
Comparison: Experimental modulus

$$E_{AB_3} = 0.16 \pm 0.03 \text{ GPa}$$

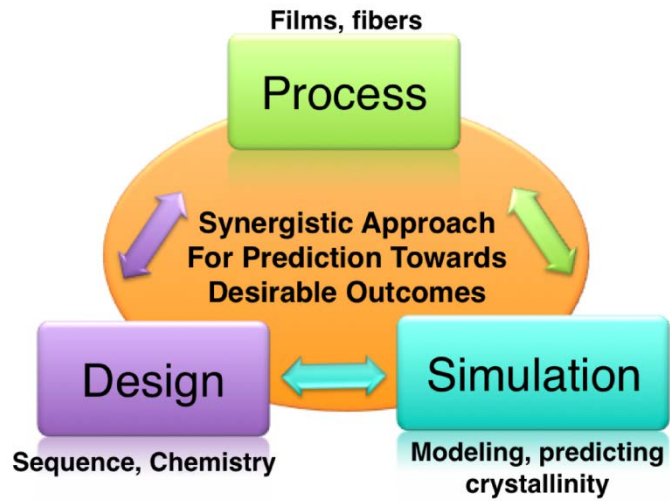
$$E_{BA_3} = 0.44 \pm 0.1 \text{ GPa}$$

Scaling up: Dissipative Particle Dynamics (DPD) model

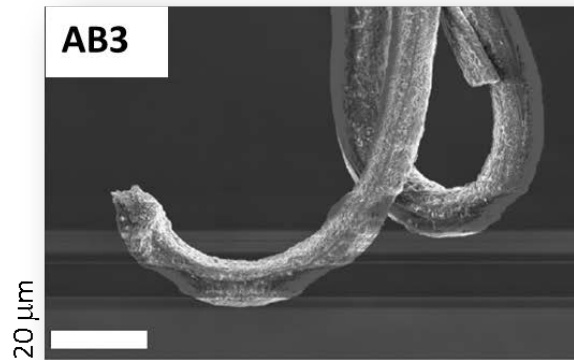
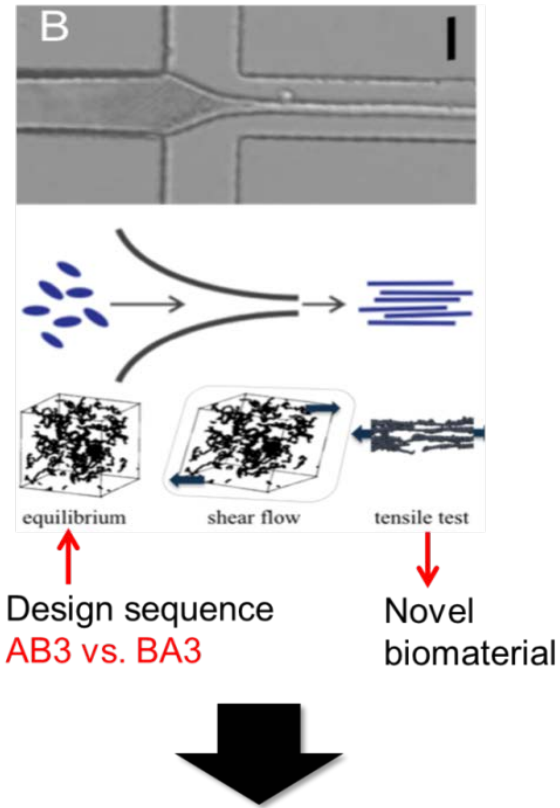
Gronau, Kaplan, Wong, Buehler et al., *Biomaterials*, 2012



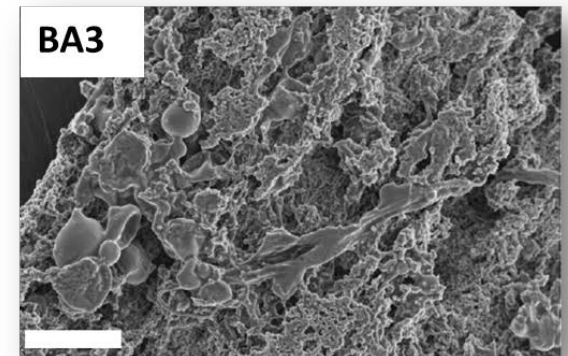
Summary



Microfluidic model of the spider's spinning duct

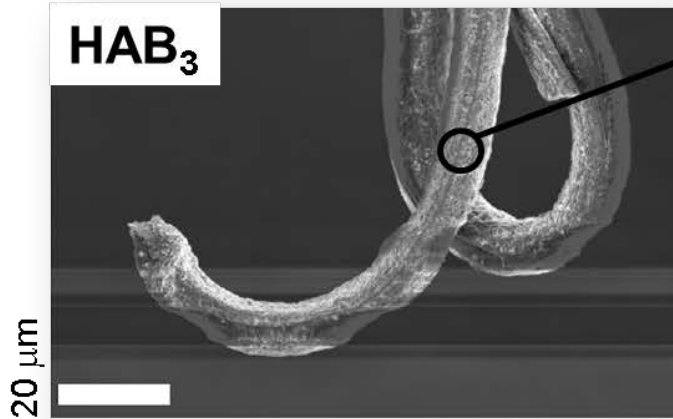


Forms fibers from microfluidic spinning device

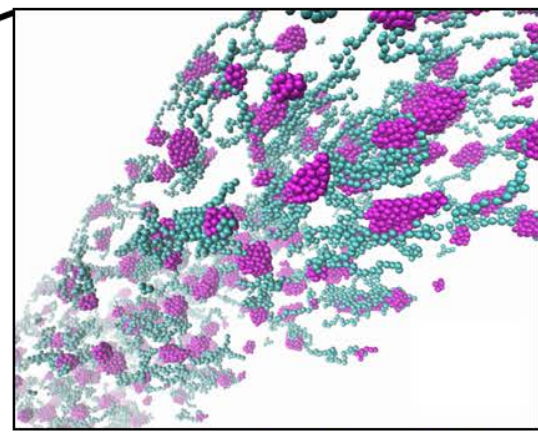


Clogging and no fiber formation

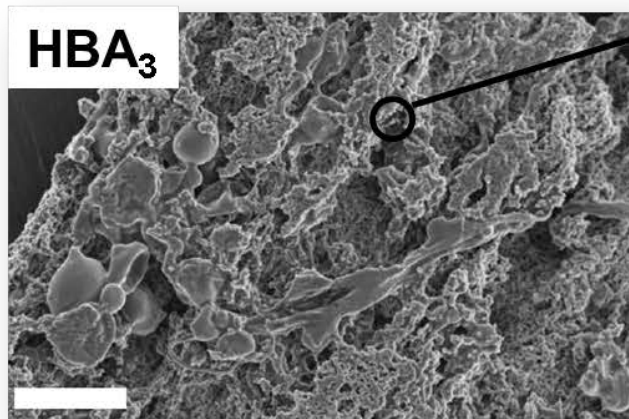
Microscopic insight from molecular simulation



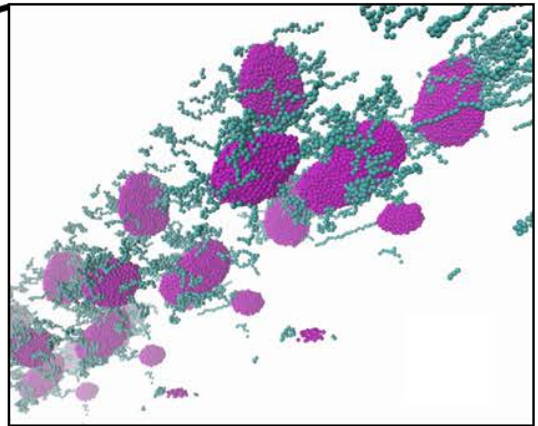
Forms fibers



Increased hydrophilic residues has positive effect on assembly process



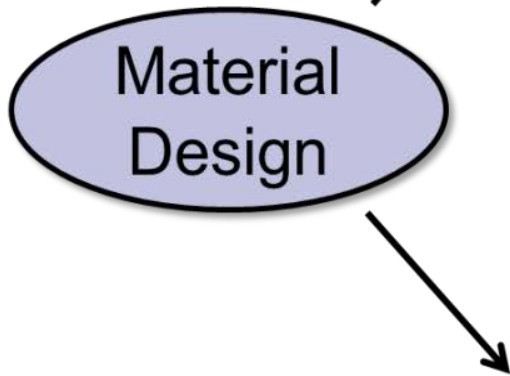
Clogging, no fiber formation



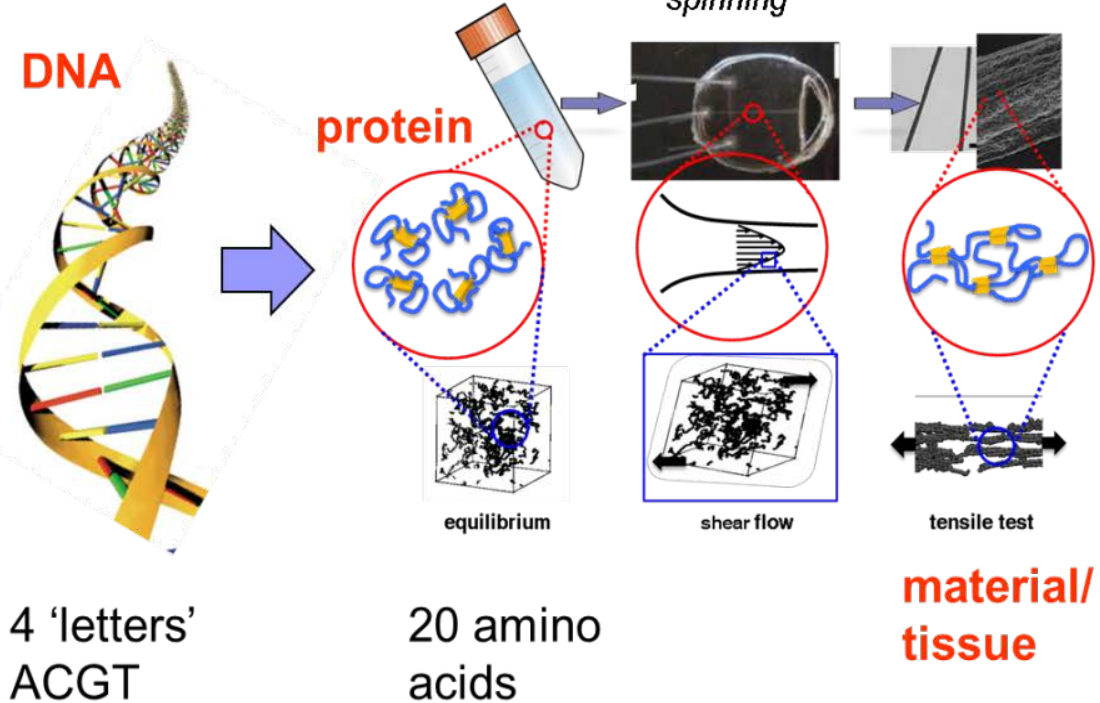
Proteins form 'globular structures', hence few/no cross-links = no fiber

Conclusion – A New Approach to Materials Design

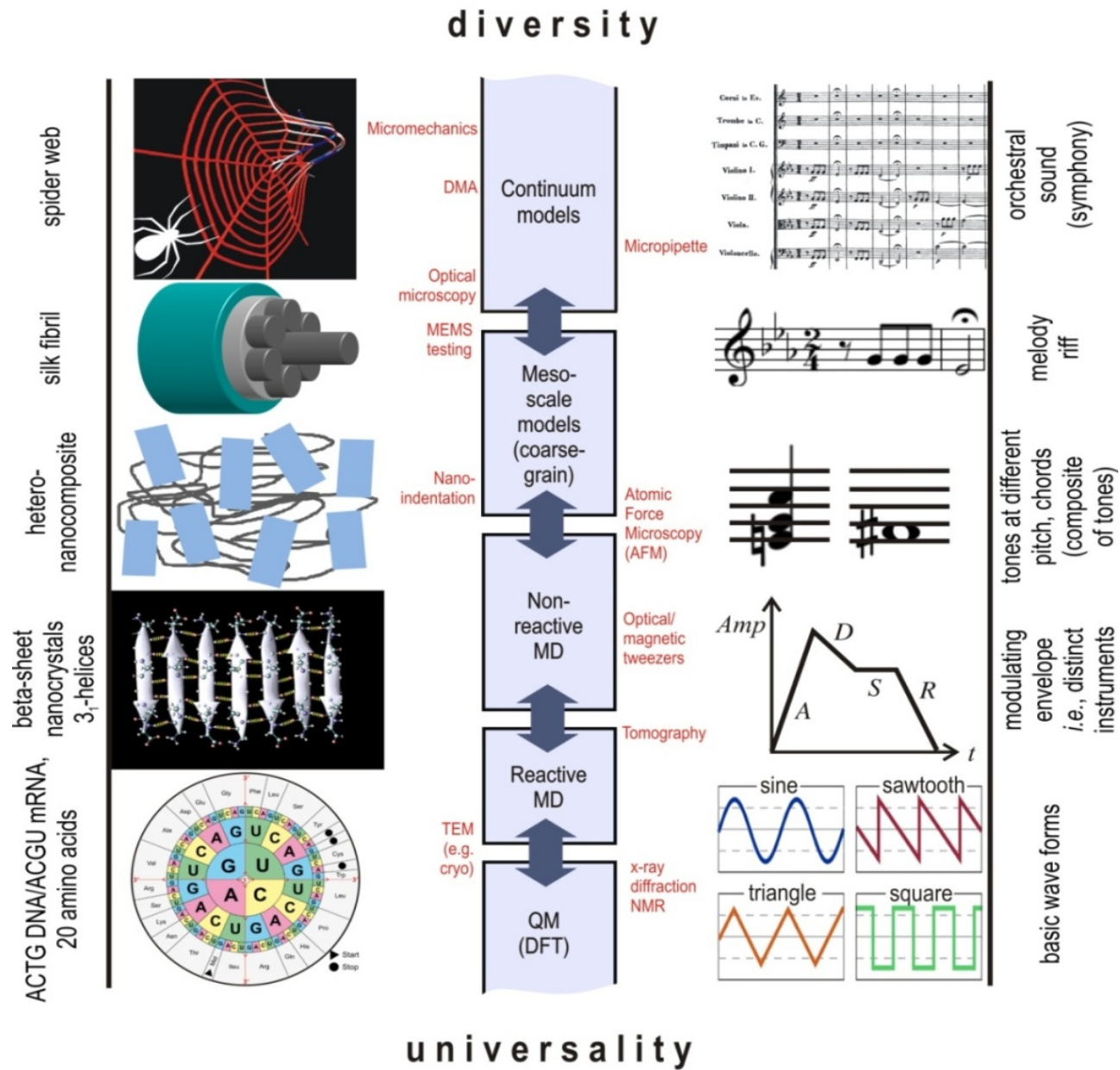
Conventional: “Top-down approach”



New: “Bottom-up approach”



Conclusions & Broader implications



Multifunctionality (**diversity**) created by changing structural arrangements of few (**universal**) constituents

No need to invent new building blocks

Powerful biocompatible paradigm for materials innovation

- Fewer resources
- More flexibility
- Wider design space