

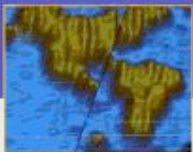
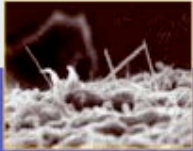
Protein Engineering

Challenges and applications for composite nanosystems

Eric Drexler

RosettaCon 2008

nanorex



Productive Nanosystems

A Technology Roadmap

December 2007

Leadership:

**Battelle
Memorial Institute**

Hosting National Labs:

Oak Ridge

Brookhaven

Pacific Northwest

Organized by:



Sponsors:



Hosting National Labs:



Roadmap partners:





Modular molecular systems

Useful parts that don't fit

Putting it together: composite systems

Protein–DNA complementarity

Applications and challenges

Modular Molecular Composite Nanosystems:

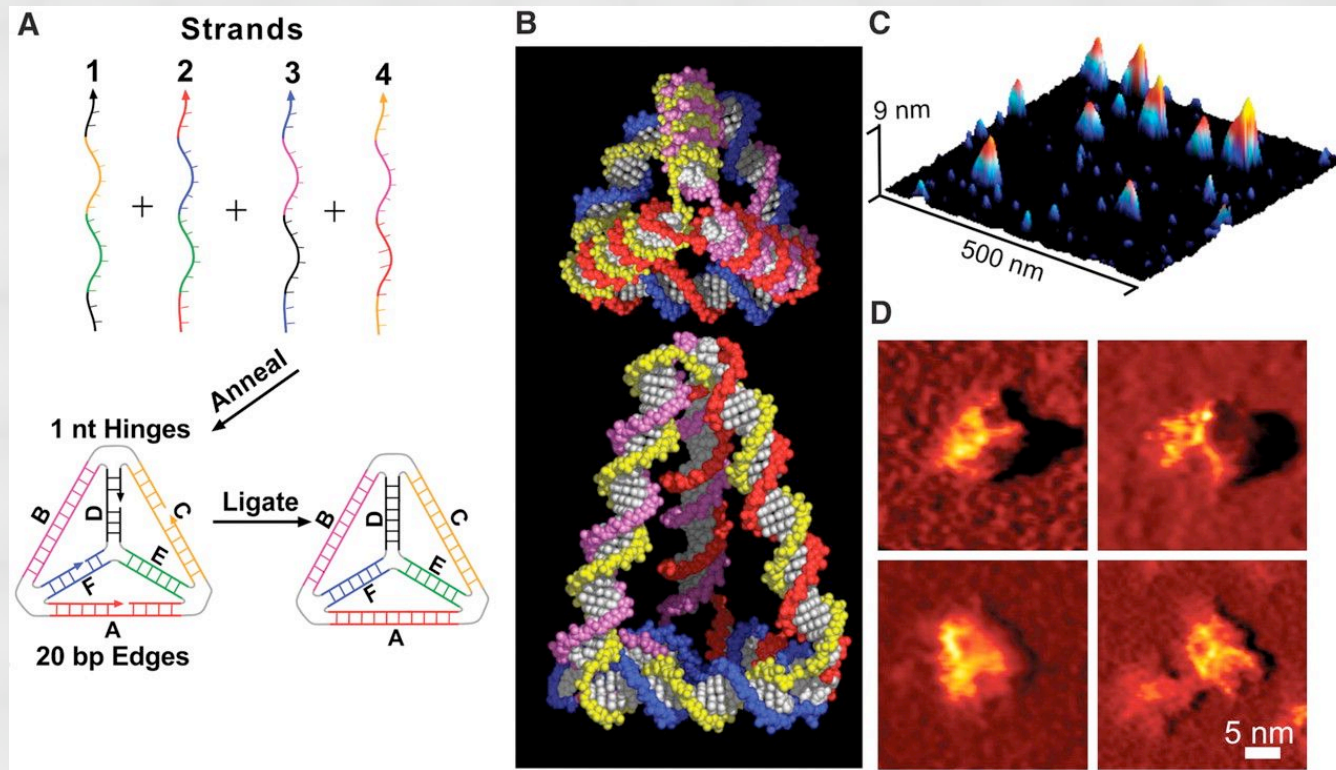
	DNA	Protein	Specialized
Limitations	narrow range of functions, limited binding	small structures, difficult design, slow production	non-modular, seldom much design freedom
Strengths	large structures, easy design, fast production	broad range of functions, versatile binding	unlimited range of materials and functions
Natural roles	structural frames, large-scale pattern organization	assembly interfaces, precise alignment, diverse functions	catalytic, optical, mechanical, electronic...

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Integrate components to build systems:

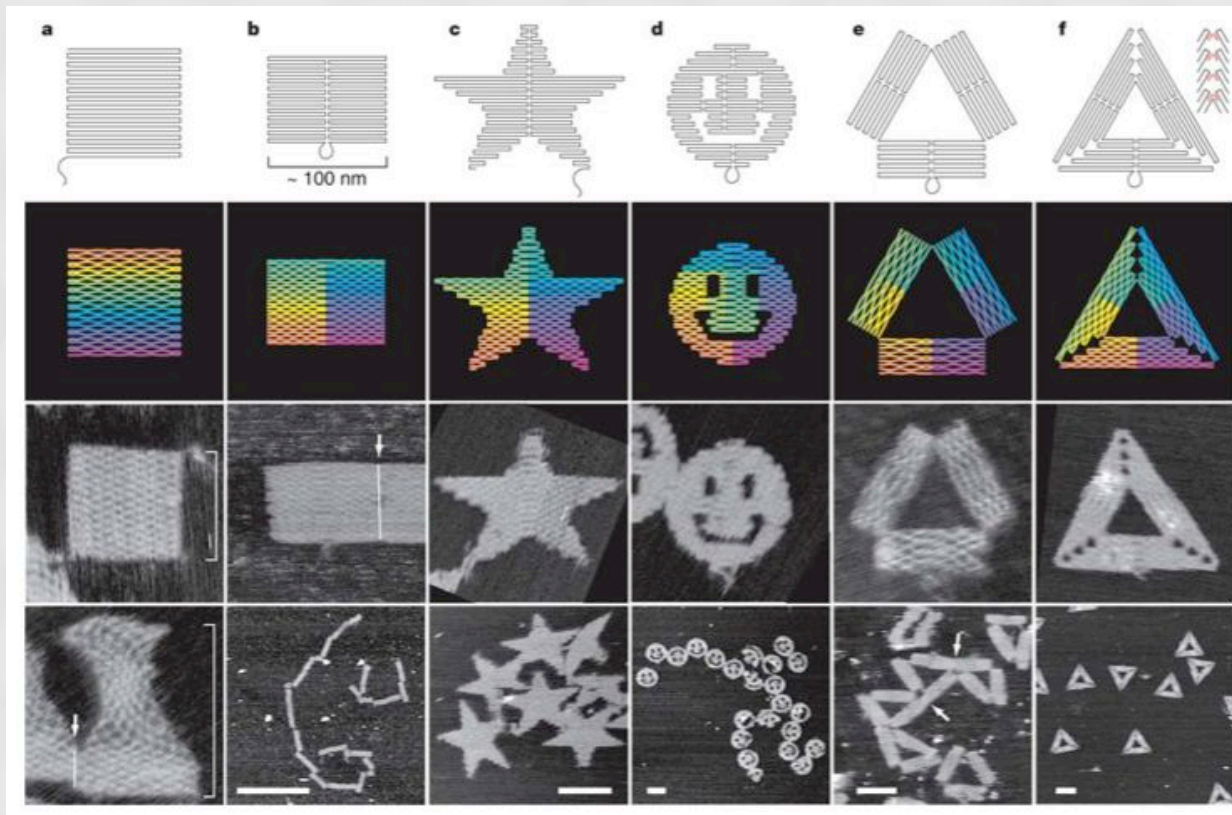
- 3D, atomically precise scaffold, easily re-configured
- 100s to 1000s of parts in addressable locations

“Rapid chiral assembly of rigid DNA building blocks for molecular nanofabrication”



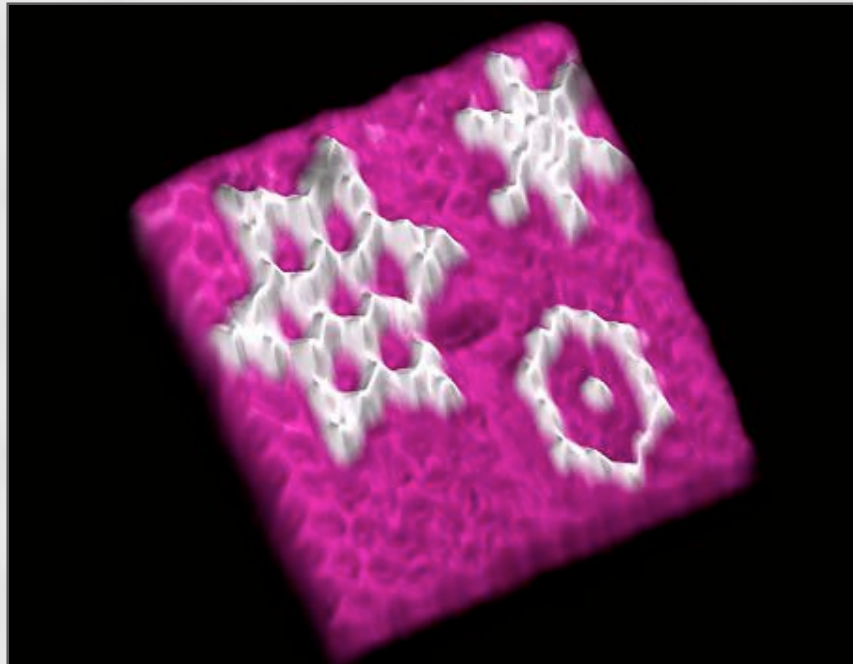
R. P. Goodman *et al.*, *Science* **310**, 1661 -1665 (2005)

~ 1/2 million atoms per structure

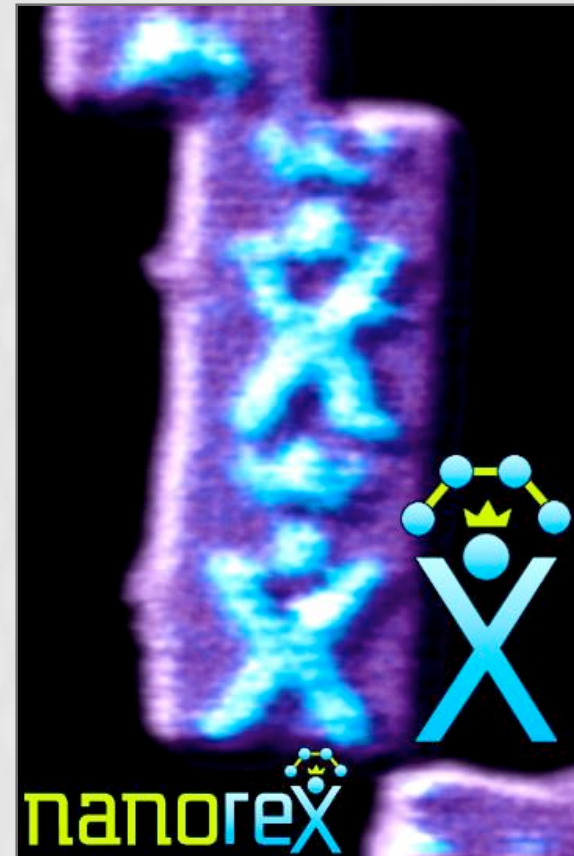


Rothemund P.W.K., "Folding DNA to create nanoscale shapes and patterns." *Nature*, 440:297–302 (2006).

Fast, routine, reliable

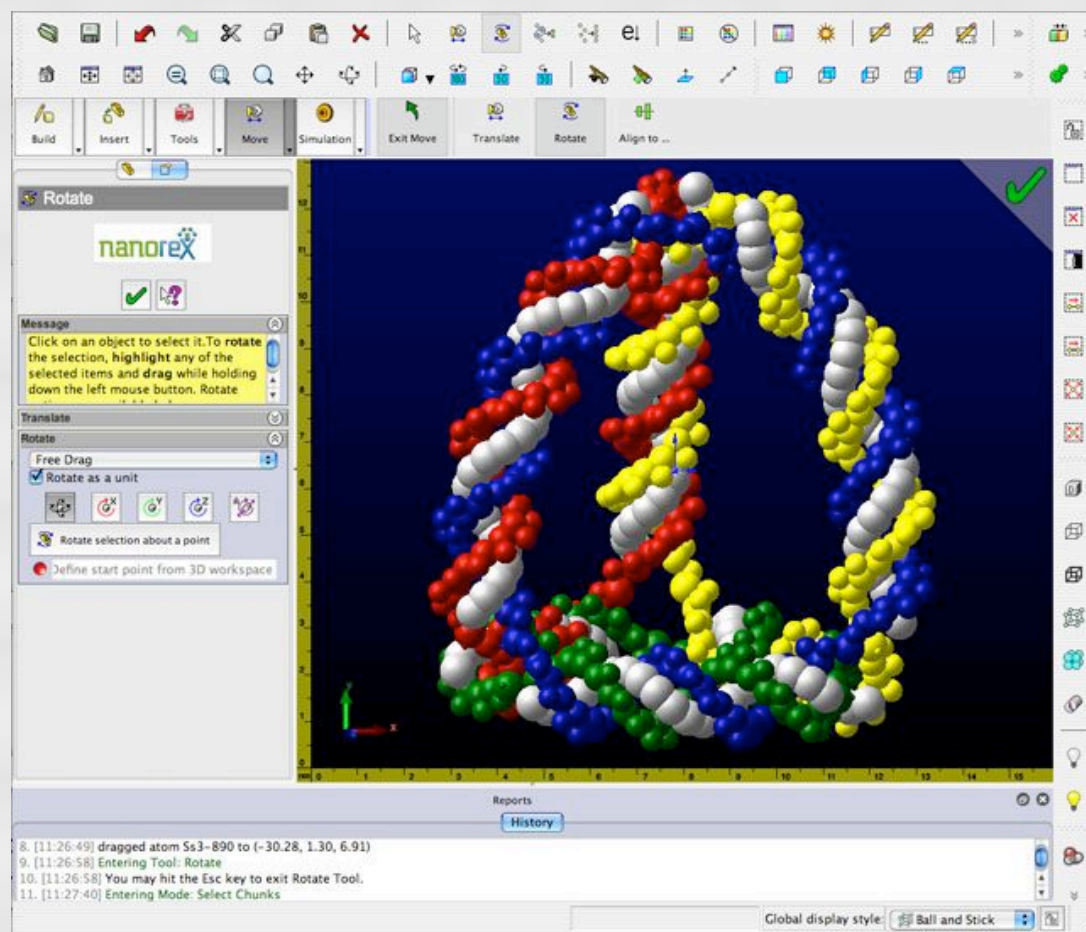


Paul Rothemund (2005).



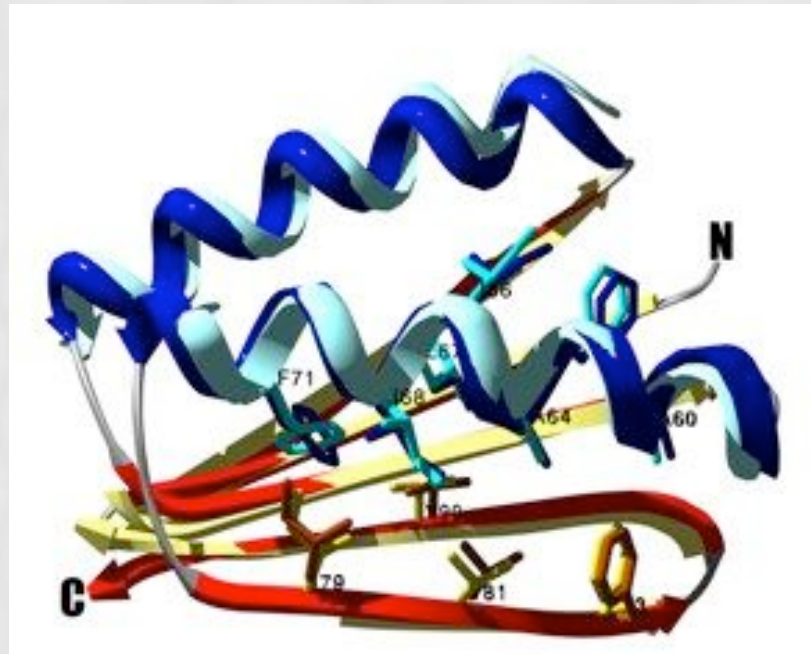
Mark and Erika Sims,
21–25 August (2006)

NanoEngineer-1 (July 2008, v.1.1.1)



**Computer-aided design for molecular systems,
open-source software from Nanorex**

“Design of a Novel Globular Protein Fold with Atomic-Level Accuracy”



Kuhlman *et al.*, *Science* **302**:1364–68 (2003)

“RosettaDesign server for protein design”

www.rosettadesign.med.unc.edu

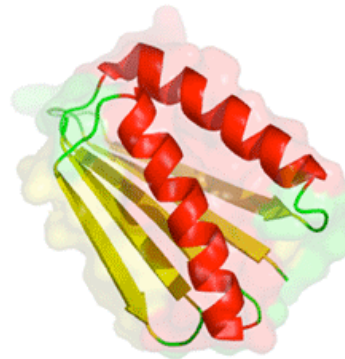
<http://rosettadesign.med.unc.edu/index.html>

RosettaDesign

Welcome to the RosettaDesign web server.

RosettaDesign identifies low energy sequences for specified protein backbones, and has been used previously to stabilize proteins and create new protein structures.

Please login to begin using RosettaDesign.



Liu and Kuhlman, *Nucleic Acids Res*
34:W235–W238 (2006)



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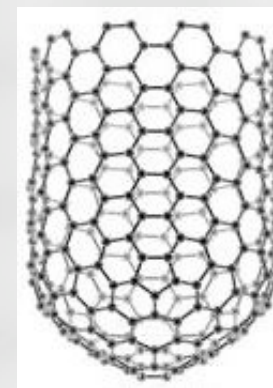
Specialized functional structures:

(atomically precise parts)

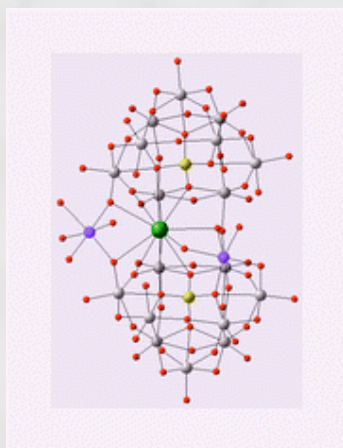
electronic, chemical,
biological, structural,
electronic, optical,
optoelectronic,
electromechanical,
electrochemical...



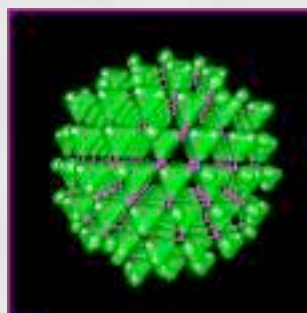
Porphyrins



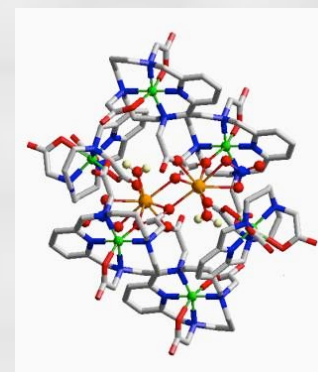
Nanotube segments



Metal-oxide clusters



Quantum dots



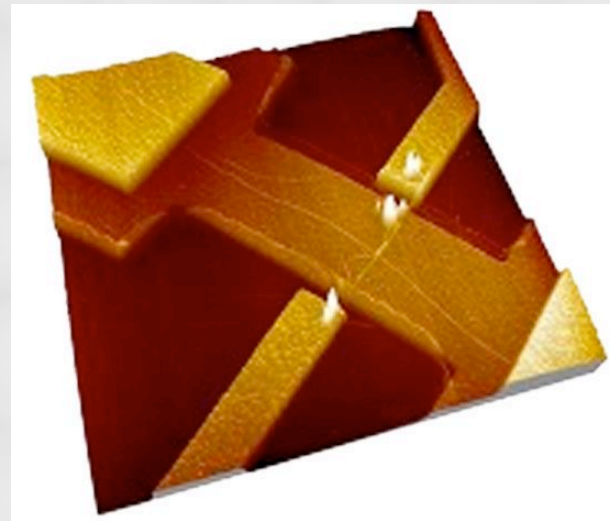
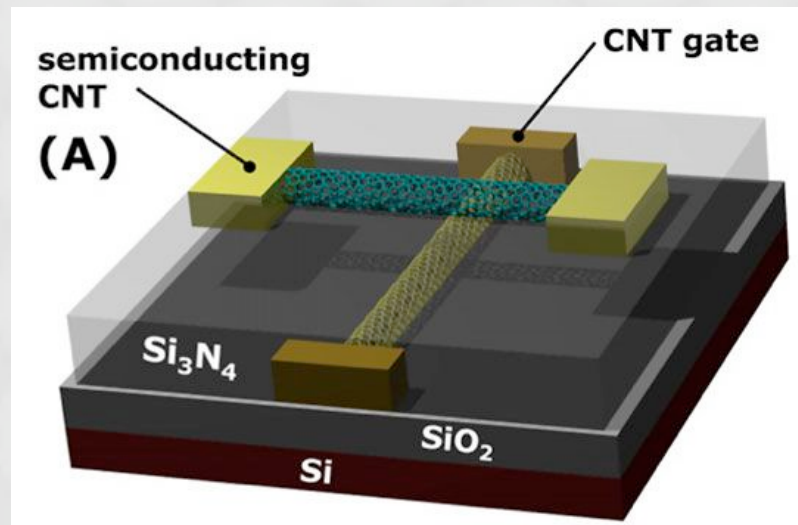
Metal complexes

Have components for:

- **molecular sensing**
- **photovoltaic energy conversion**
- **photochemistry**
- **efficient light emission**
- **plasmonic devices**
- **molecular electronics**
- **carbon nanotubes (lots of functions)**

**Abundant parts, but no way to assemble
them to build complex systems
— Need circuit boards and sockets! —**

“A carbon nanotube gated carbon nanotube transistor
with 5 ps gate delay”



J Svensson *et al.* Nanotechnology **19**:1–6 (2008)



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Applications and challenges

Modular Molecular Composite Nanosystems:

	DNA	Protein	Specialized
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Integrate components to build systems:

- 3D, atomically precise scaffold, easily re-configured
- 100s to 1000s of parts in addressable locations

Modular Molecular Composite Nanosystems:

	DNA	Protein	Specialized
Limitations	narrow range of functions, limited binding	small structures, difficult design, slow production	non modular, seldom much design freedom
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RosettaDNA

RosettaDesign

RosettaSurface

Rosetta



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**DNA origami strand, at 7.5 kilobases,
could encode ~ 10 medium-size proteins,
but...**

Information densities:

DNA \approx 2 bits/nm³

Protein \approx 40 bits/nm³

Pentium $< 10^{-4}$ (*in the structure, data is less dense!*)

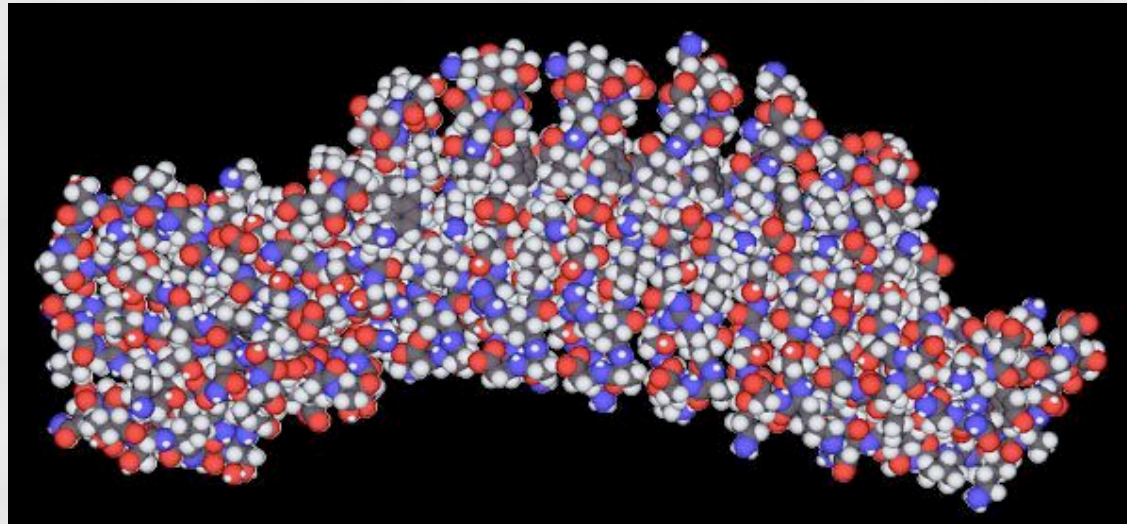
***Information density* is part of the reason why proteins
are designed to bind DNA, and not *vice versa*.
Functional diversity is not enough.**

Values of Young's modulus for several biomolecular and inorganic materials



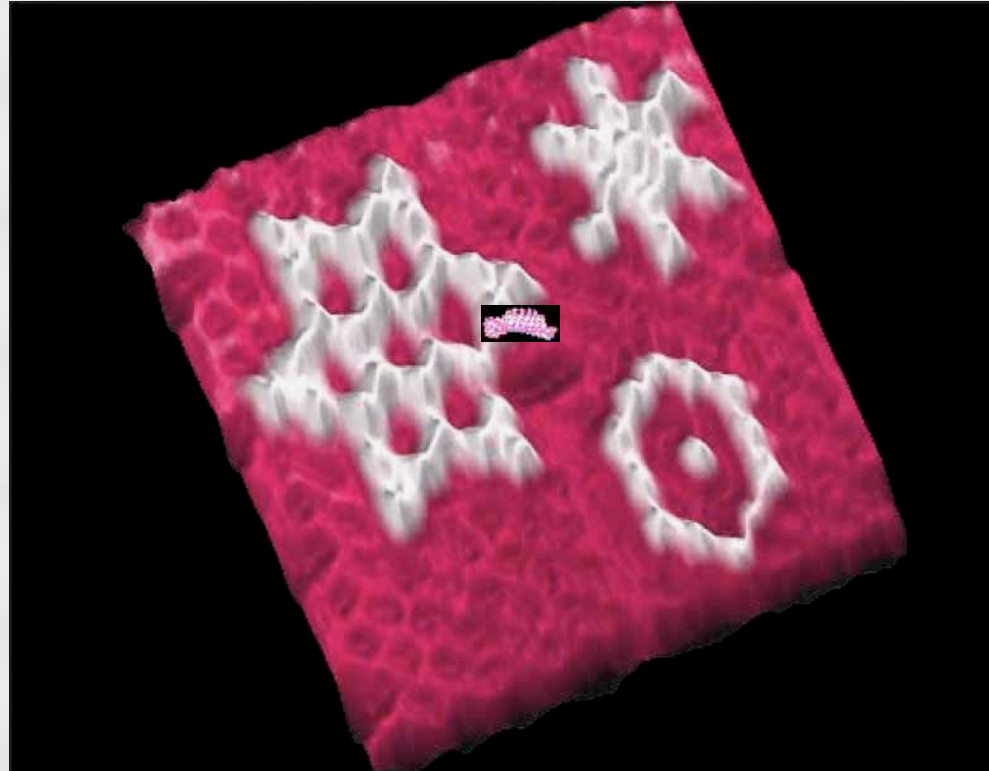
**Protein advantage: 10 to 100 x modulus of DNA
=> 1/10 to 1/100 as much area within
the r.m.s thermal fluctuation radius**

**De novo protein, 329 residues (almost all beta-sheet)
length = 11 nm**



**“Crystal structure of OspA mutant” (PDB 2oy7)
Makabe, K., Biancalana, M., Yan, S., Gawlak, G.,
Koide, A., Koide, S. (2008, *to be published*)**

**DNA origami, 7.5 kilobases,
length, width = 100 nm**



Paul Rothemund, *Nature* 440:297 (2006)



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Composite-system applications:

- **Biomedical sensing & targeting using boolean logic and counting**
- **“Nanochips in microsockets” for general purpose digital systems**
(a major yield/reliability challenge)
- **Epitaxial macromolecular crystals on nanolithographic patterns: stacked RAM cells for petabit chips**
(a lesser yield/reliability challenge)
- **Workbenches for nanoscience**
*(must work **sometimes...**)*

High-payoff directions:

- Improving methodologies for interface design, for proteins, DNA, crystals, nanostructures...
 - Rules defining combinatorial design domains: “protein origami” (or “protein Legos”)
 - Improved physical *and chemical* stability:
 - design rules, restricted set of amino acids, non-aqueous environments (eg, ionic liquids)
 - Creative cheating: unnatural amino acids, organic crosslinkers, template components...
 - Integrated, multi-material, multi-scale modeling, design, and data analysis
- Additional promise + a broader community
+ a unified message = Vast Funding

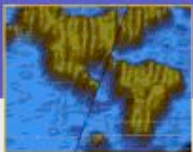
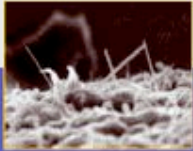
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PDFs posted at www.e-drexler.com