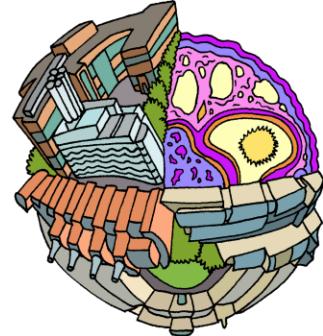




University of  
**BRISTOL**



**BrisSynBio**  
biomolecules to biosystems  
from understanding to design

# Rational & computational design of self-assembling peptide barrels

Woolfson Group from the past decade

**Rokas Petrenas, Katherine Albanese,**

Elise Naudin, Bram Myelmans,

Fabio Pirro, & Will Dawson

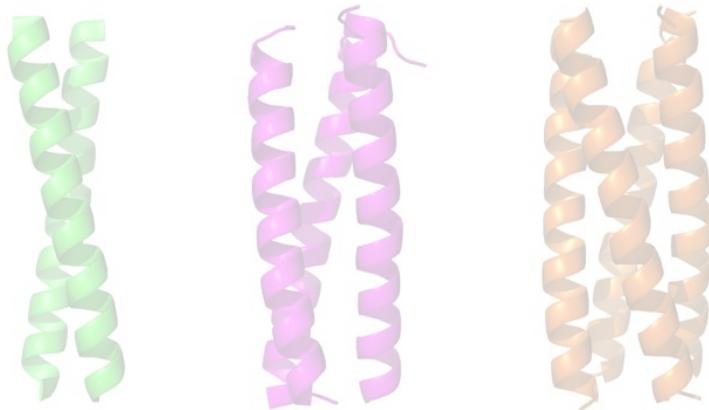
**Graham Leggett, Tom Oliver, Nigel Savery, Arne Scott**

Dek Woolfson

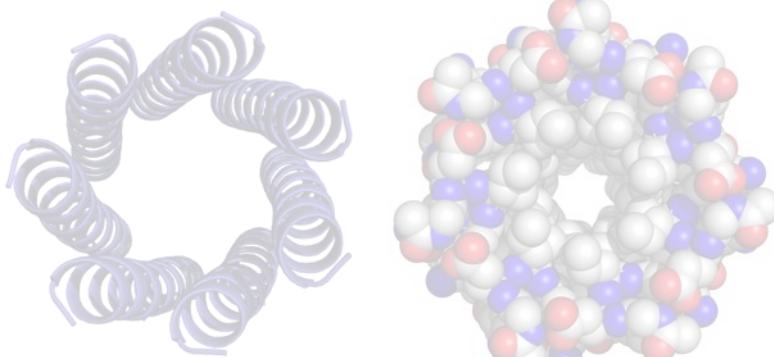
Chemistry, Biochemistry, & Bristol BioDesign

# About today's talk

## 1. How we design peptide assemblies

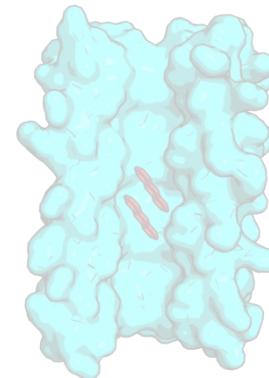


*ACS Synth Biol* 1, 240-250 (2012)  
*J Am Chem Soc* 135, 5161-5166 (2013)



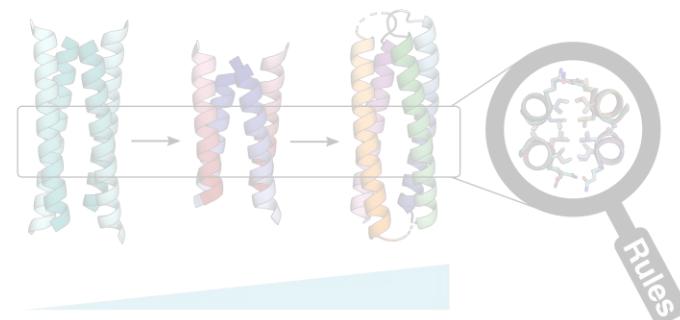
*Science* 346, 485-488 (2014)

## 2. Peptidic molecular flasks



Rokas Petrenas  
unpublished work

## 3. From peptides to proteins...



Potential for sequence diversity and utility

*Chem Sci* 13, 11330-40 (2022)  
& some unpublished work

# Why design peptides and proteins?

- It's still a challenge

- Fundamental science

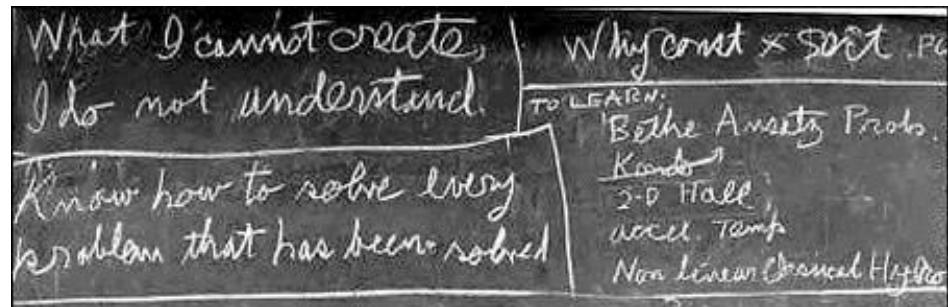
- *It's the acid test of our **understanding** of the protein-folding problem; i.e., how does the amino-acid sequence of a protein determine and maintain its 3D structure?*

- Frontier science

- *To design proteins that do not exist in nature; i.e., to explore the dark matter of protein space.*

- Applied science

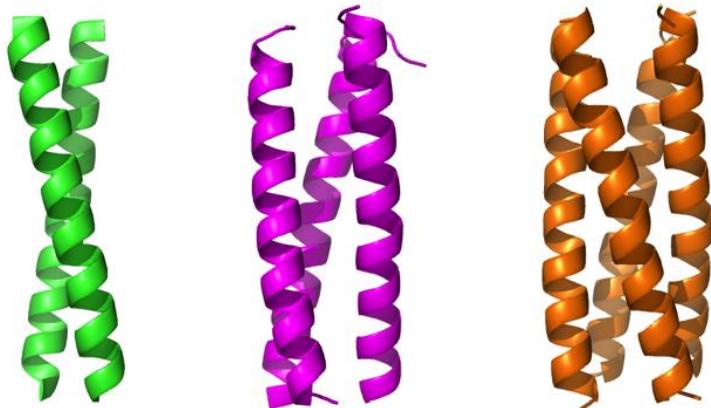
- *Where possible, translate this to design proteins that address real-world problems & applications.*



- It's fun

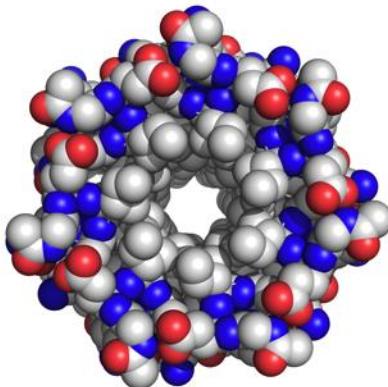
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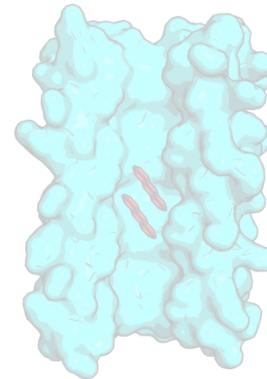
*ACS Synth Biol* 1, 240-250 (2012)

*J Am Chem Soc* 135, 5161-5166 (2013)



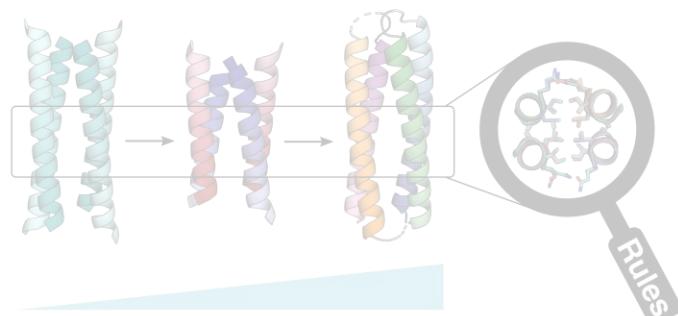
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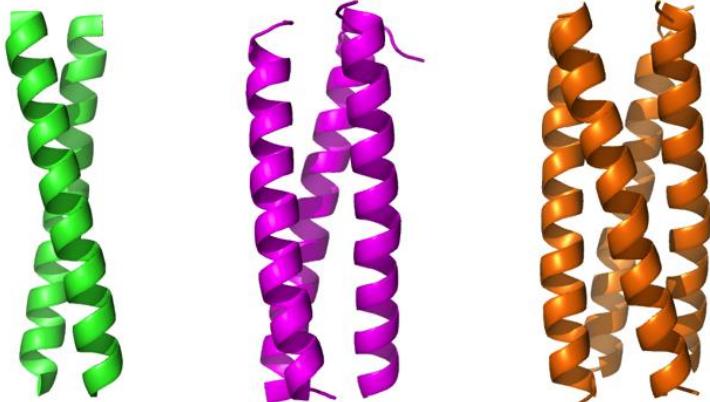
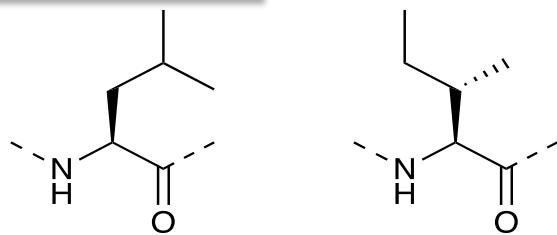
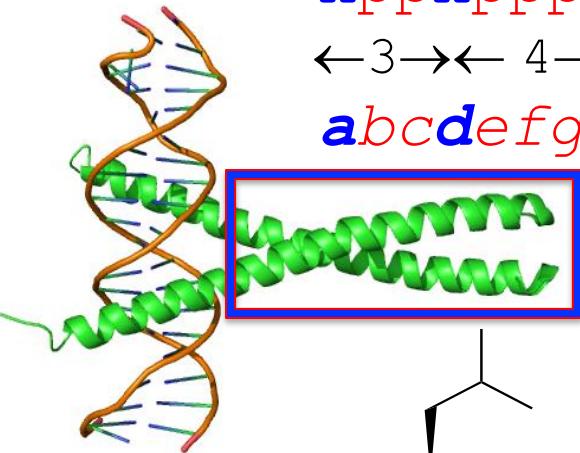
*Chem Sci* 13, 11330-40 (2022)  
& some unpublished work

# How we design peptide assemblies

## 1. Rationally

hpphppphpphpph  
↔ 3 → ↔ 4 → ↔ 3 → ↔ 4 →

a b c d e f g a b c d e f g a



ACS Synth Biol 1, 240-250 (2012)  
J Am Chem Soc 135, 5161-5166 (2013)

## 2. Computationally

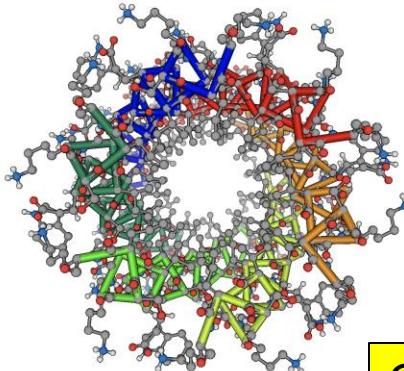
CCBuilder 2.0

Build

Alpha ▾ Basic ▾  
Oligomeric State  
6 ▾  
Parameters  
Radius  
0.5  
Pitch  
162  
Interface Angle  
18.2  
Sequence (Register: c ▾)  
EIAKSLKEIAKSLKEIAKSLKEIAKSLK  
Submit Clear

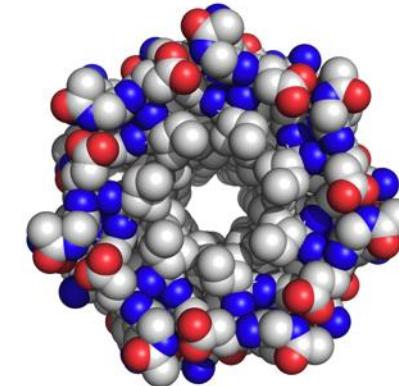
Model Information

BUDE Energy  
-812.1  
Residues per Turn  
3.62  
Highlight Knobs  
Download PDB

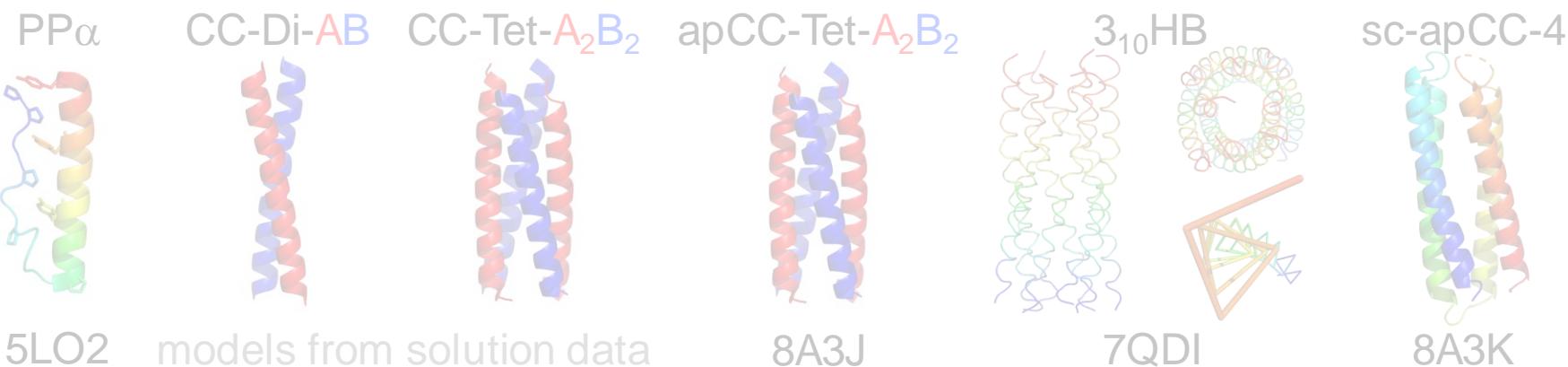
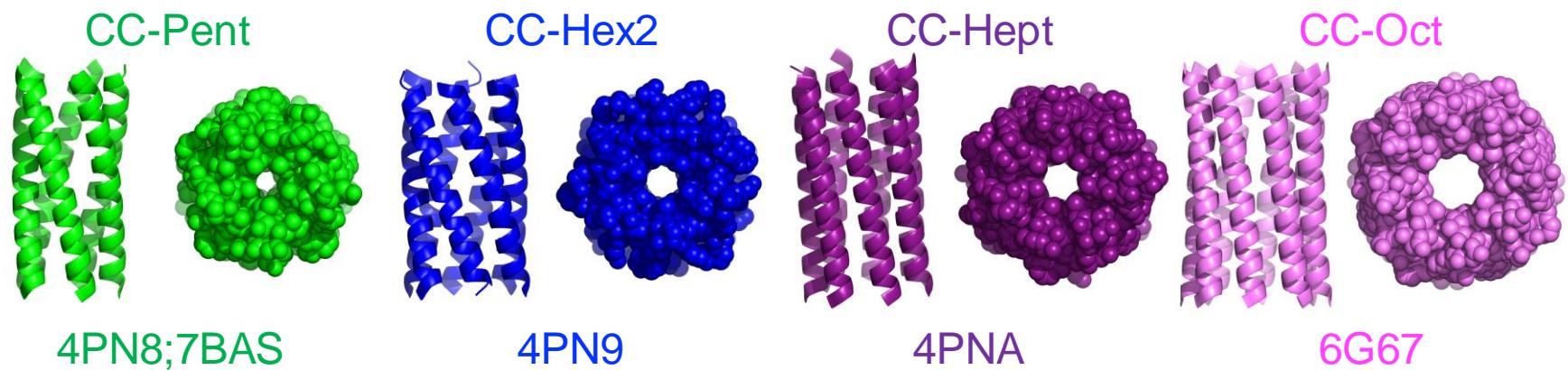
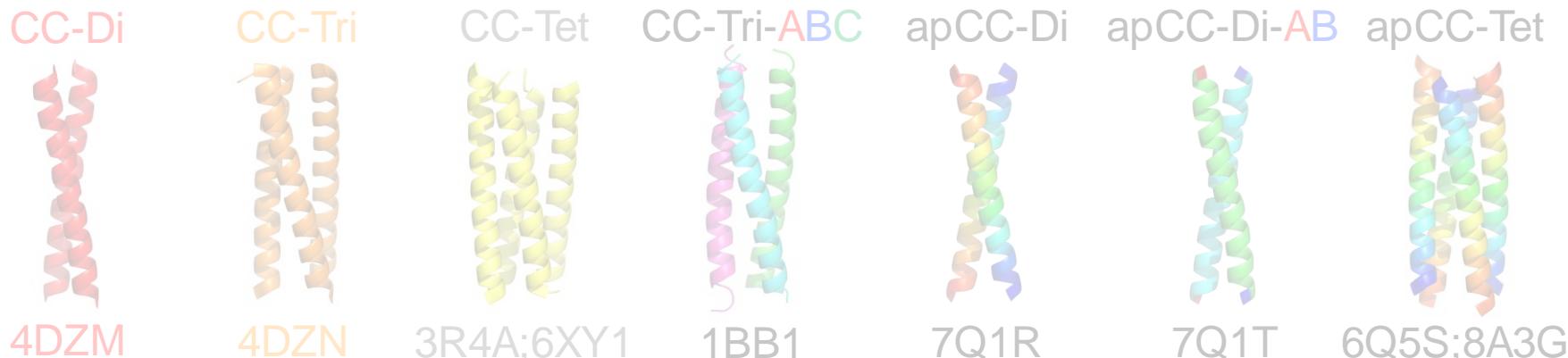


Chris Wood

[coiledcoils.chm.bris.ac.uk/ccbuilder2/builder](http://coiledcoils.chm.bris.ac.uk/ccbuilder2/builder)

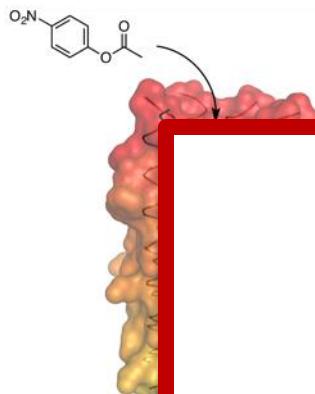


Science 346, 485-488 (2014)



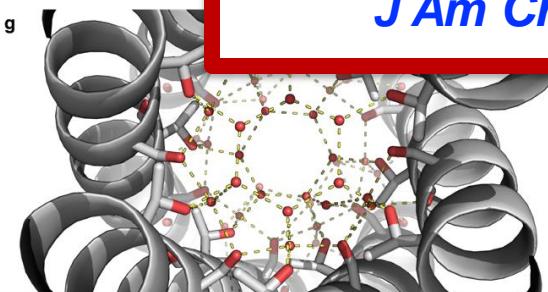
# Functions we've added to $\alpha$ HBs ...

... catalysis



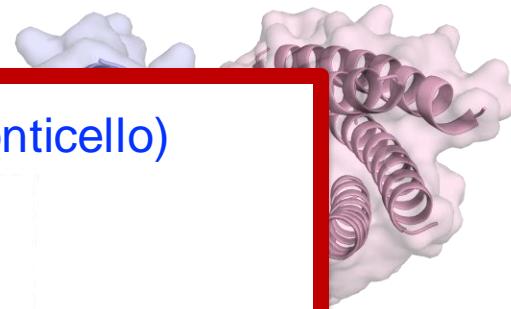
*Nature Chemistry*

... membrane-s



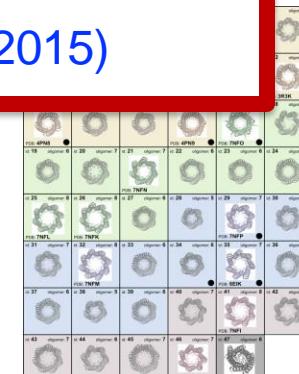
*Nature Chemistry* 13, 643-50 (2021)

... inducible structural switches



TN 1530 (2021)

based biosensor

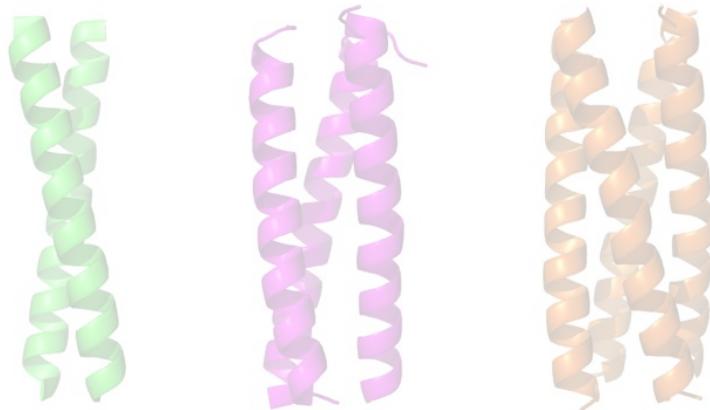


*Nature Commun* 14, ARTN 383 (2023)

*J Am Chem Soc* 137, 10554-62 (2015)

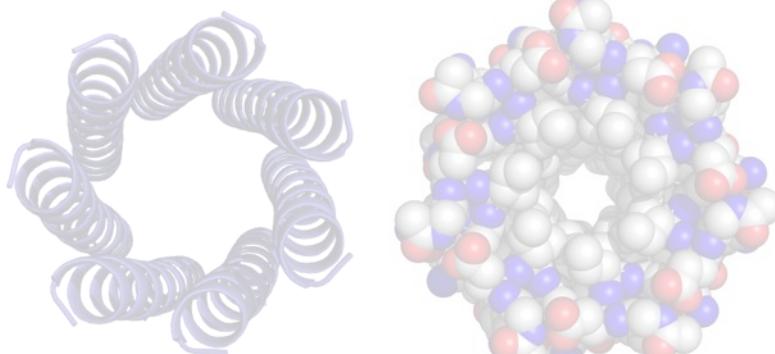
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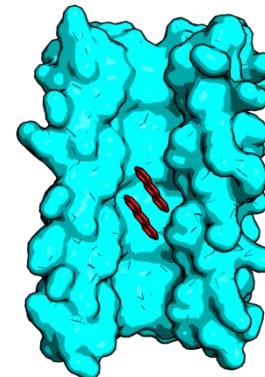
*ACS Synth Biol* 1, 240-250 (2012)

*J Am Chem Soc* 135, 5161-5166 (2013)



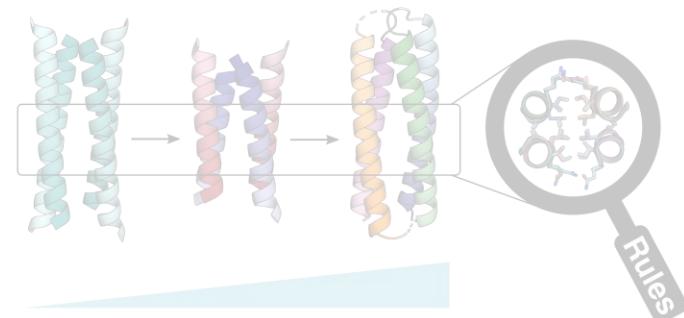
*Science* 346, 485-488 (2014)

## 2. Peptidic molecular flasks



**Rokas Petrenas**  
unpublished work

## 3. From peptides to proteins...

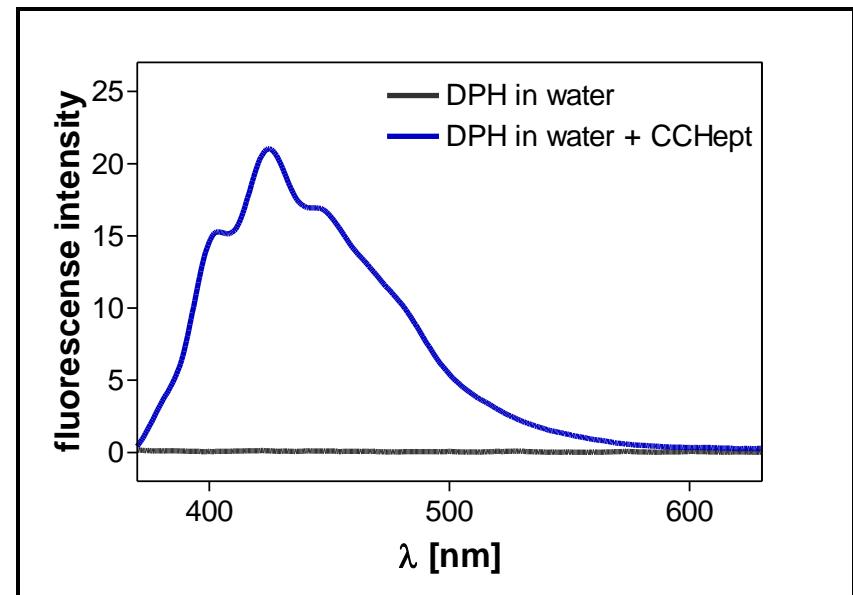
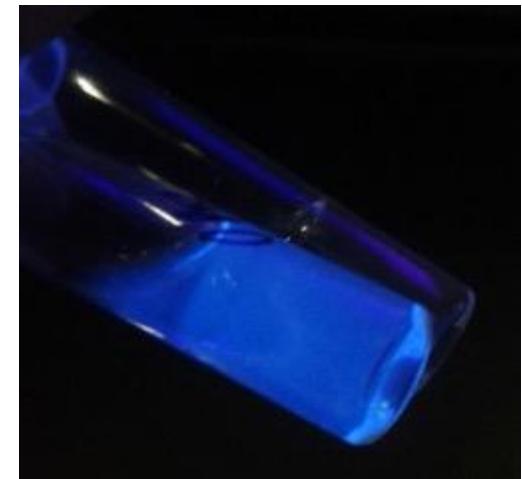
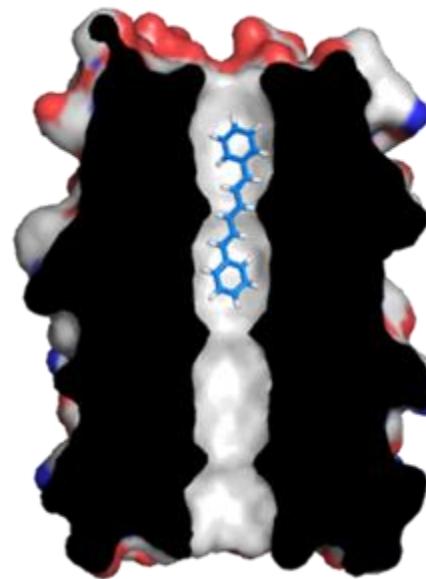
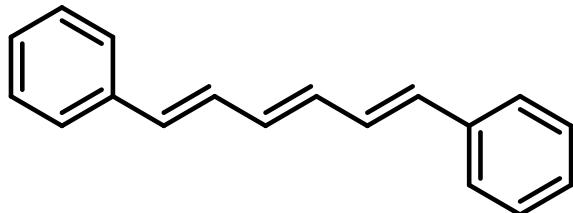


Potential for sequence diversity and utility

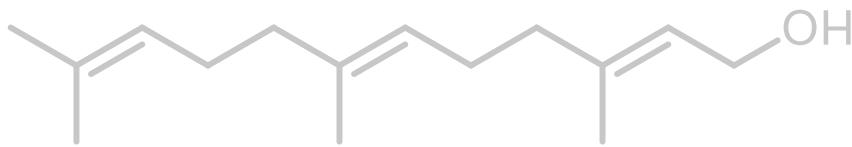
*Chem Sci* 13, 11330-40 (2022)  
& some unpublished work

# Organic dyes bind peptide barrels

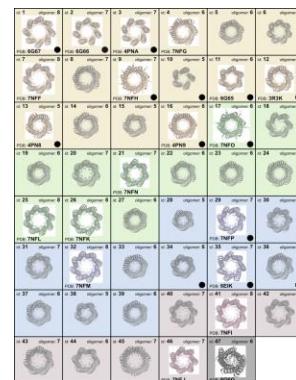
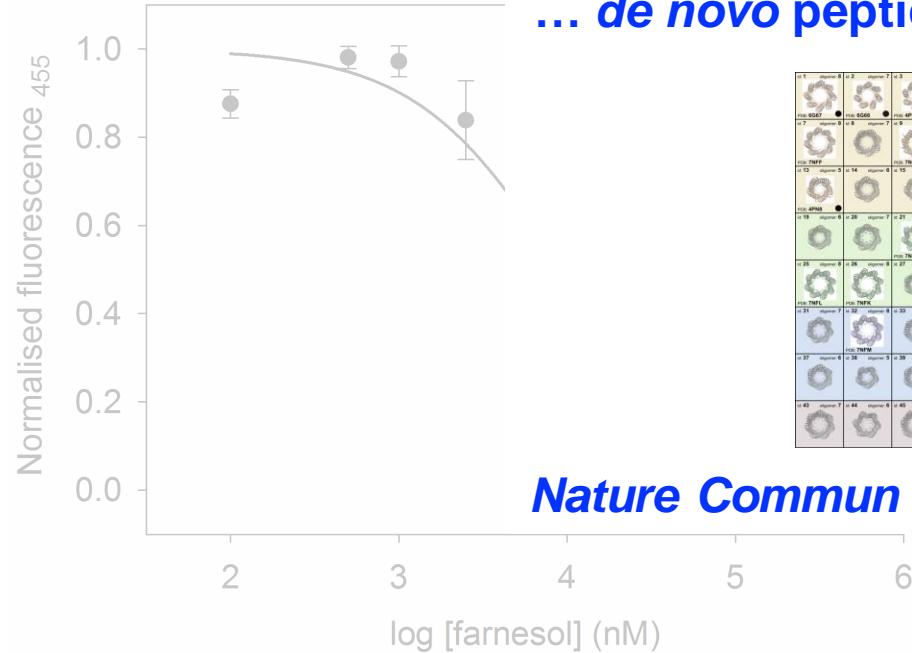
1,6-Diphenylhexatriene (DPH)



... & displaced by *interesting* moles.



... *de novo* peptide-based biosensor



Nature Commun 14, ARTN 383 (2023)

$$K_I = 0.6 \pm 0.2 \mu\text{M}$$

1.8 Å X-ray crystal structure  
R<sub>work</sub> = 0.2120; R<sub>free</sub> = 0.2635

Franziska Thomas *et al.* ACS Synth Biol 7 1808-1816 (2018)

- Redacted slides from here as this was all unpublished work. Sorry.

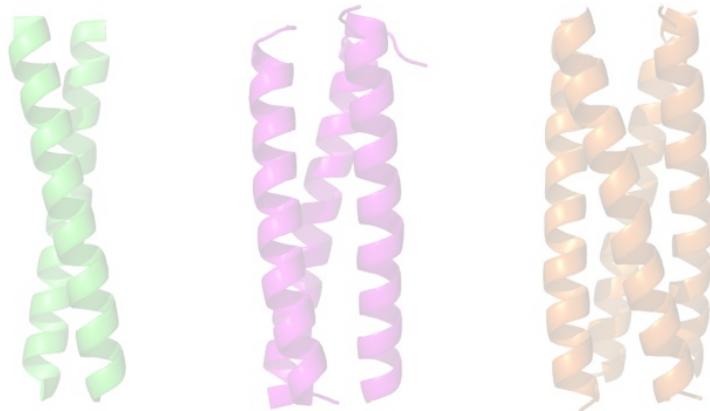


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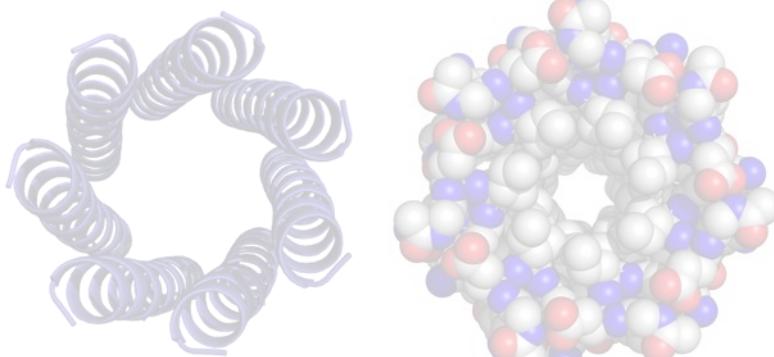


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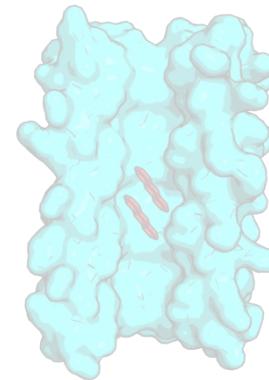


*ACS Synth Biol* 1, 240-250 (2012)  
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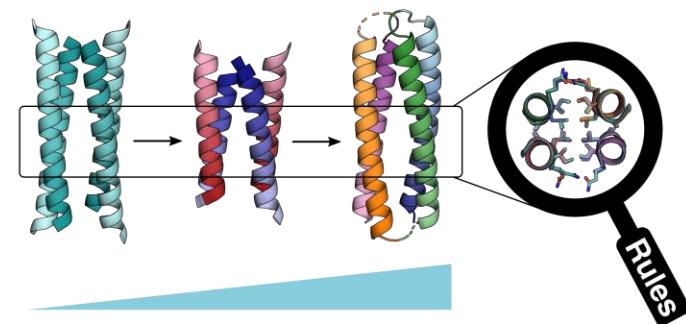
*Science* 346, 485-488 (2014)

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Rokas Petrenas  
unpublished work

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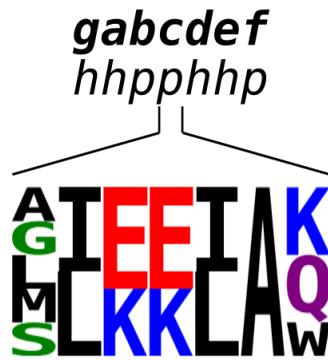


Potential for sequence diversity and utility

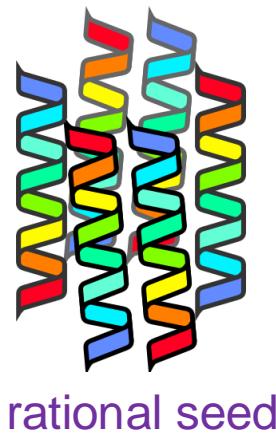
*Chem Sci* 13, 11330-40 (2022)  
& some unpublished work

# Rationally seeded computational design

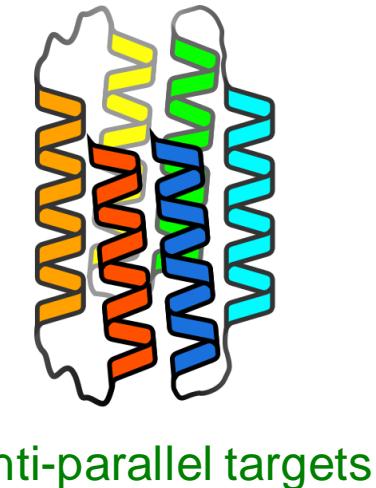
*gabcdef*  
*hhppphhp*



  
*de novo*  
peptide design  
coiled-coil  
rules



  
loop search  
MASTER

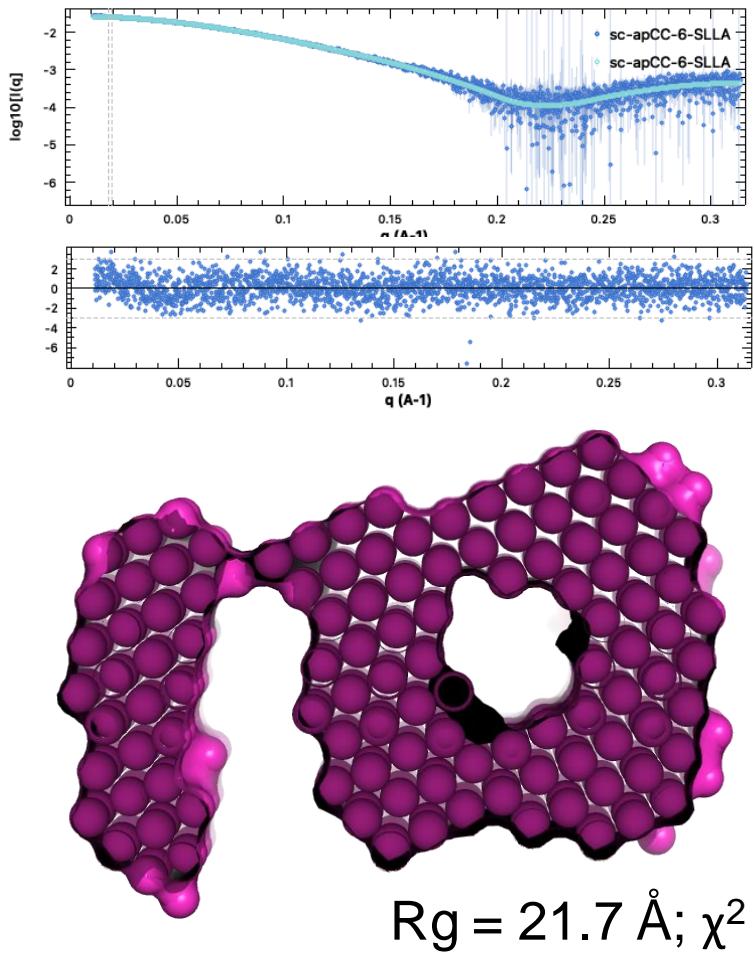


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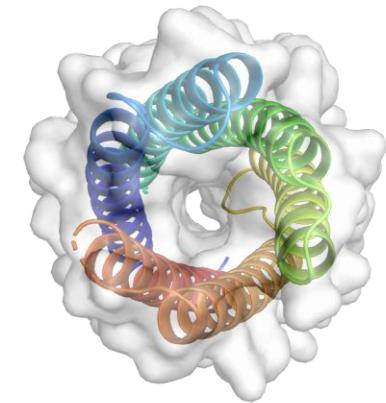
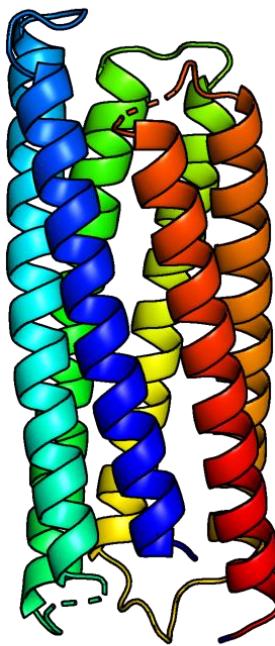
Katherine Albanese & Rokas Petrenas

# → single-chain anti-parallel 6HB

SAXS model



X-ray crystal structure



crystal structure  
for sc-apCC-6  
 $1.7 \text{ \AA}$

$R_{\text{work}} = 0.24$ ,  $R_{\text{free}} = 0.30$

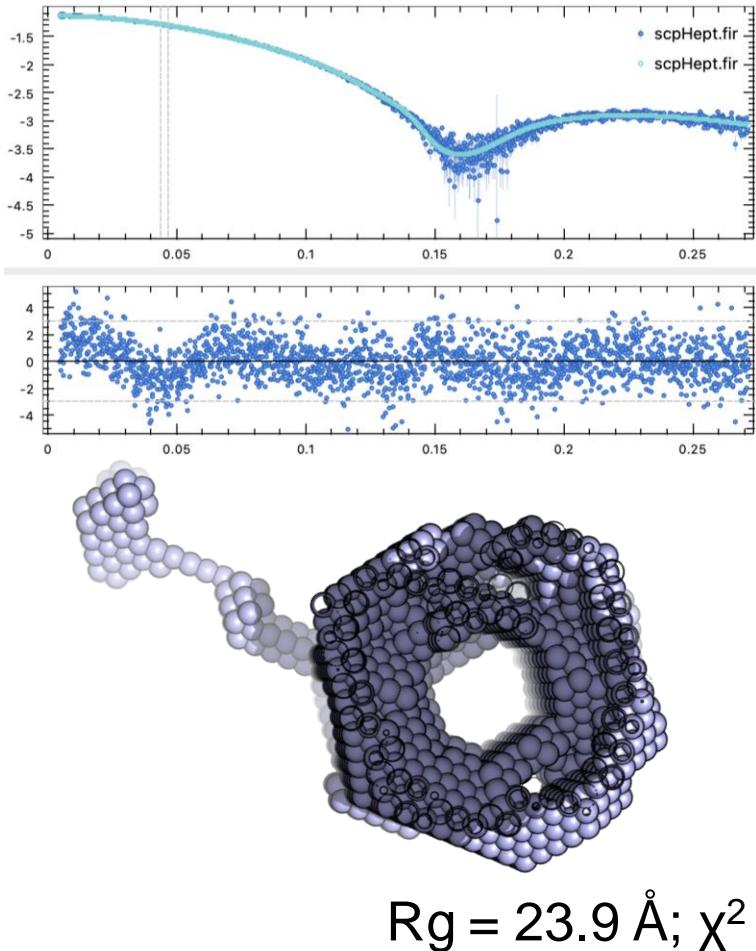


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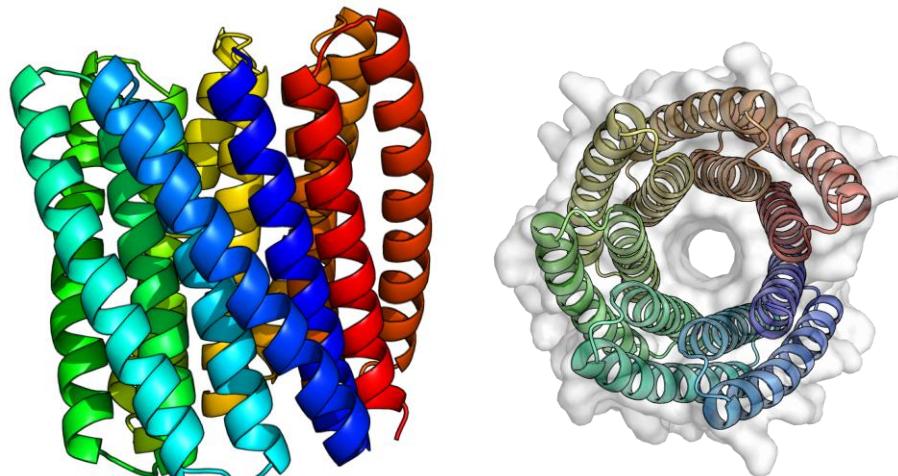
Katherine Albanese  
5 constructs – 4 expressed – 2 diffracted

# → single-chain parallel 7+6HB

SAXS model



X-ray crystal structure



crystal structure  
for sc-pCC-7  
 $2.3 \text{ \AA}$

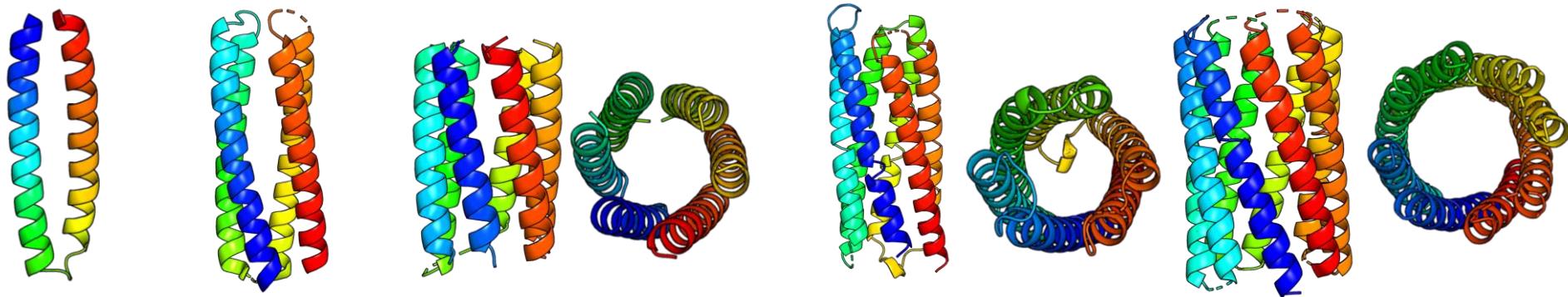
$R_{\text{work}} = 0.19$ ,  $R_{\text{free}} = 0.24$



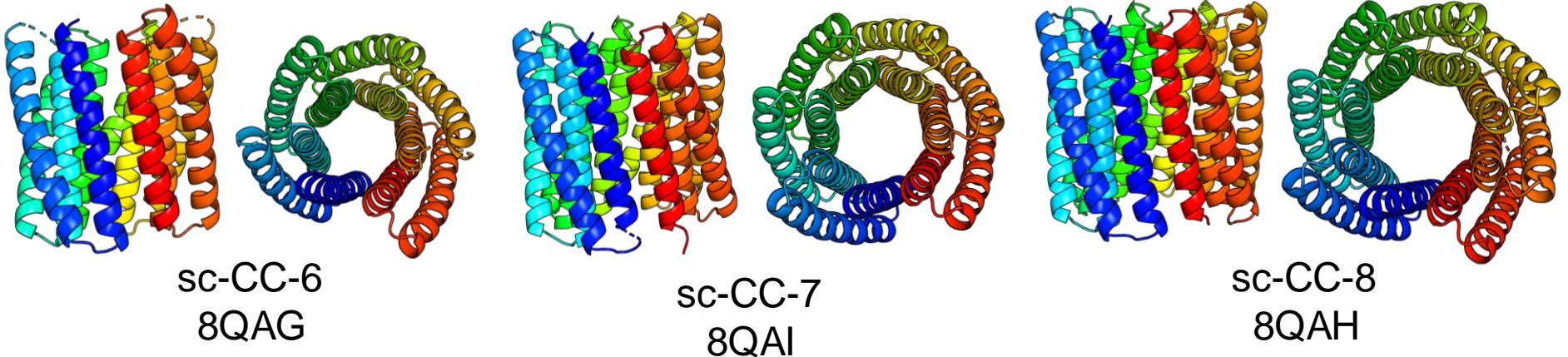
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Rokas Petrenas  
100 models – 4 constructs – 1 structure

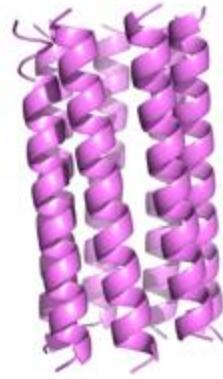
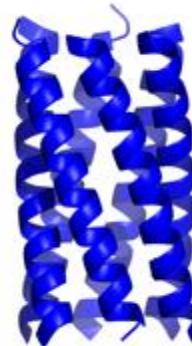
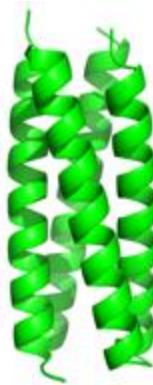
# Single-chain *de novo* proteins so far...



<5 constructs each; 80% success

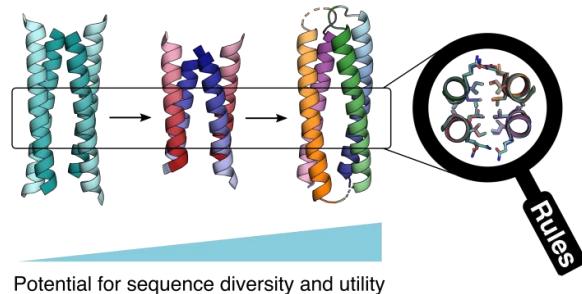
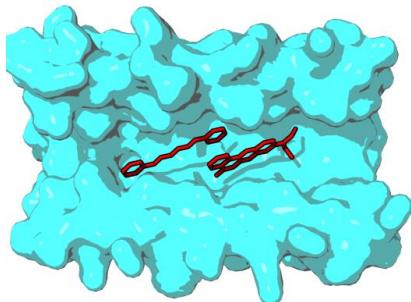


# Summary



*ACS Synth Biol 2012*

*Nature Chem Biol 2011;  
Science 2014; Nature Commun 2018*



*Unpublished*

*Chem Sci 2022 & Unpublished*



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# Katherine



Elise Naudin, Fabio Pirro, &  
Will Dawson  
Arne Scott (Rosa Biotech)

# Joel



**rosa**  
biotech



Alexander von Humboldt  
Stiftung / Foundation