This is a big title

Sometimes I like a subtitle too

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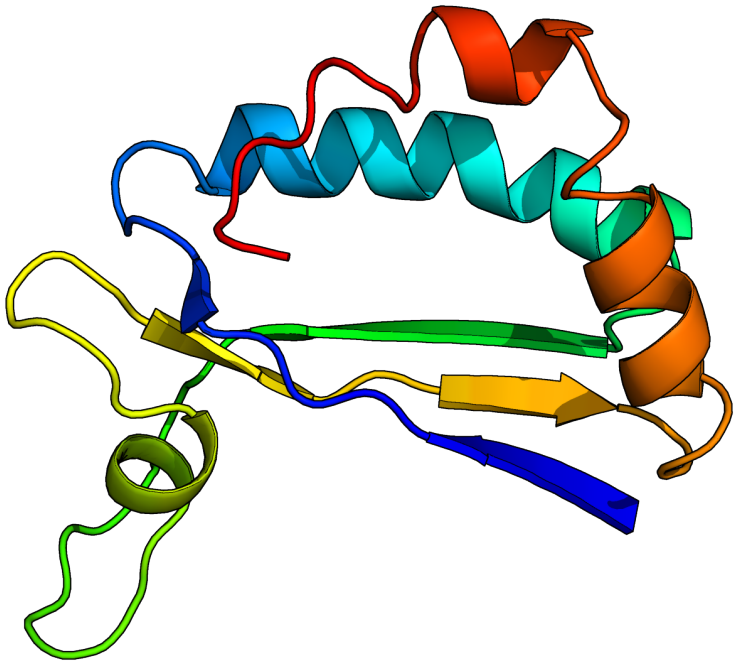
A secret non-numbered slide

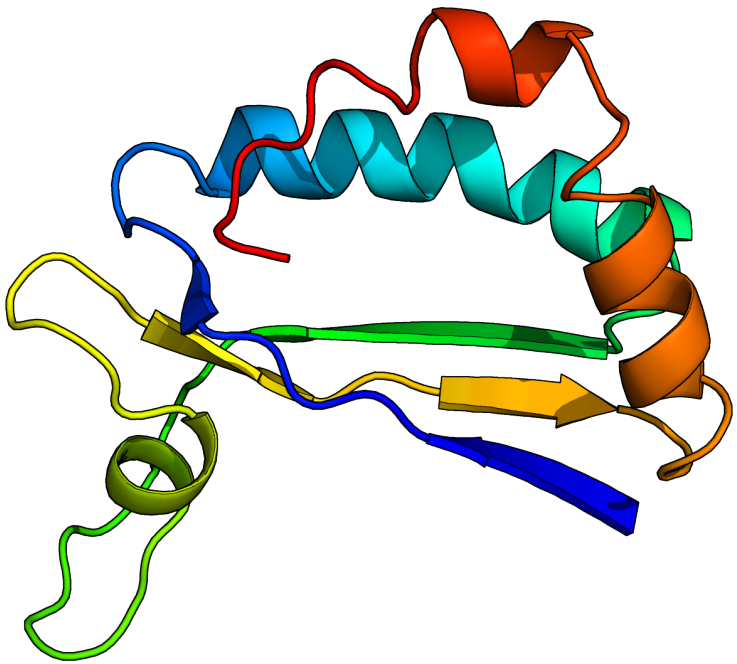
- This slide is ignored by the slide numbering bottom right - a secret extra slide
- Current structure prediction heuristics are limited by the enormous conformational search space
- Proteins adopt their native structures *in vivo* by searching conformational space very efficiently
- Biologically-inspired sequential prediction has improved protein structure prediction

Figure-on-top slide example, with "new" label



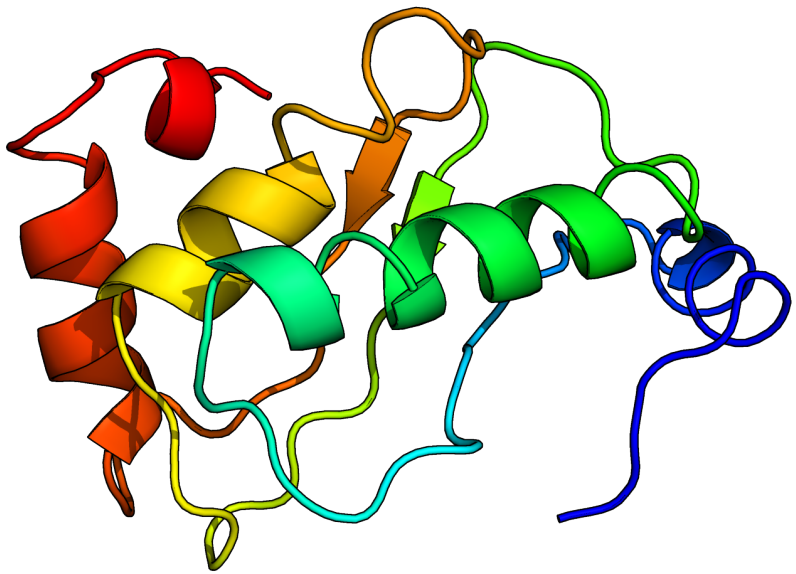
- On this slide, the figure is on top and the text is underneath
- This is also an example of the new label for exciting new things

Figure-on-one-side slide example, with changing figure



- This text is to the right of the figure
  - Wow look at that structure
  - Over there on the left
  - I like it
  - Very nice
- This figure will change on the next slide, but the slide number will be the same

Figure-on-one-side slide example, with changing figure

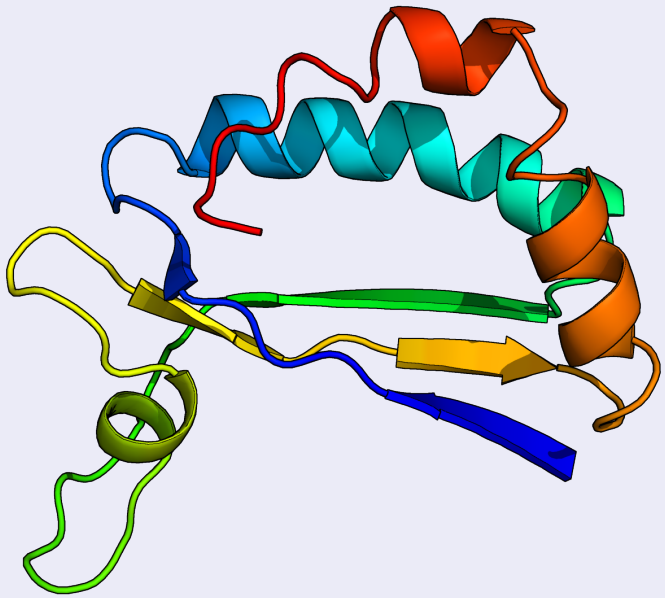


- This text is to the right of the figure
  - Wow look at that structure
  - Over there on the left
  - I like it
  - Very nice
- Great! Now I don't have to duplicate slides or scare the audience with the slide count

Block slide example

Block title

- I'm partial to a block slide:
  - To be honest
  - I don't know why
  - I just like it
  - sometimes
- Models are ranked and grouped into confidence categories

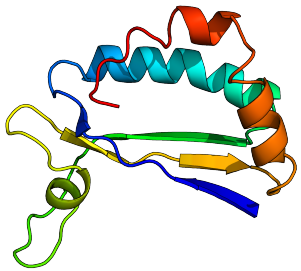


Include citations like this, if I need them. For example this structure is 2OKQA

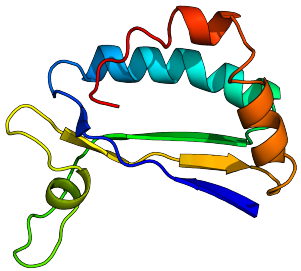
Protocol and set of example cases

NEW

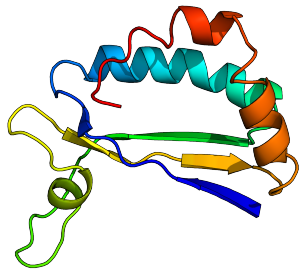
- Slide for presenting examples of targets or models
  - Some details in case I need them
- Some more details about the structures
- Validation: aligned RMSD ($\leq$5Å) and minimised RMSD ($\leq$2.5Å) of sampled region



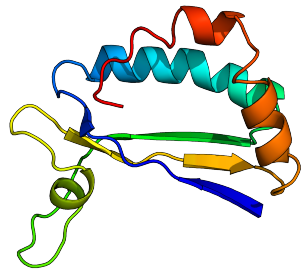
2.32, 1.99
Good



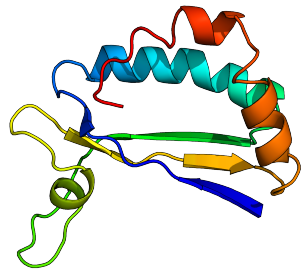
9.56, 8.58
Bad



11.20, 8,16
Bad



2.67, 1.75
Good



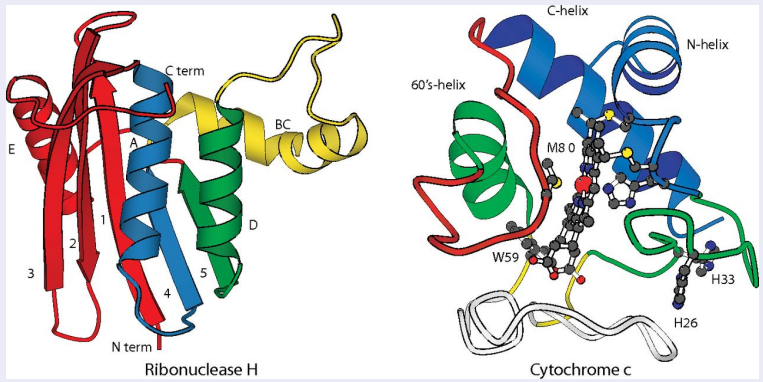
6.05, 3.48
Okay

Foldons and Protein Folding

The Foldon Hypothesis

- **Foldons: small, separately cooperative units**
- Folding occurs via an ordered process of foldon-determined steps, in which formed foldons guide and stabilise the next foldons

- Foldons are...
  - small enough to overcome the Levinthal time scale problem
  - large enough to provide the energy bias to drive folding



Jeng, M.F., Englander, S.W., 1991. Stable submolecular folding units in a non-compact form of cytochrome c. J. Mol. Biol. 221, 104561.
Maity, H., Maity, M., Walter Englander, S., 2004. How cytochrome c folds, and why: Submolecular foldon units and their stepwise sequential stabilization. J. Mol. Biol. 343, 223233.
Hu, W., Kan, Z.-Y., Mayne, L., Englander, S.W., 2016. Cytochrome c folds through foldon-dependent native-like intermediates in an ordered pathway. Proc. Natl. Acad. Sci. U. S. A. 113, 380914.

To do list

- Big difficult task
  - ☑ A task I've completed already
  - ☑ Another task I've completed already
  - ☐ A task I haven't completed
  - ☐ A task I haven't completed
- Another related big difficult task on the same topic
  - ☑ Something that I've already done
  - ☑ Something that I haven't yet done
  - ☆ Something that I would do in my dreams

Acknowledgements

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