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Presentation Notes

* Research Question:
  + We investigated adhesins in *C. auris* that contribute to its stickiness, which is a major contributor to the pathogenicity in clinical environments.
  + Our question is, why does *C. auris* display such strong adhesive properties compared to closely related fungi, and what proteins are the cause of this adhesiveness.
* Approach:
  + Search literature and databases for “adhesin(s)” or adhesion-related proteins in Candida species
  + Use BLAST and other programs to find a related protein in C. auris
  + Analyze the functional domains of the C. auris protein for adhesive properties
  + Found out that all three of our proteins contain the GPI-anchored superfamily as a domain.
* My protein (CJI97\_000055) is structurally uncharacterized.
* There we no significant results returned from protein database search on NCBI BLAST.
* SWISS-MODEL template searches did not return any templates with over 40% identity.
  + Low % identity even after restricting my search to the 1-150bp segment with the highest coverage in similar sequences.
* Therefore, I used the I-TASSER threading program to build a protein model.
* Rachel and Lindsay both submitted their proteins to TASSER, but have not received results yet, presumably because their proteins are much longer.
* Threading Algorithms determine the fold family a protein likely belongs to:
  + Step 1. Use an average structure representing all the structures in a family.
  + Step 2. Evaluate quality of resulting structure if the protein were to assume this conformation.
  + Step 3. Repeat for each fold family.
  + Step 4. The conformation with the most favorable score is selected as the likely fold family for the target sequence.
* Used I-TASSER threading to build models for my protein.
* \*\*\*\*\*\* (go to slides) \*\*\*\*\*\*
* Results from I-TASSER match expectations for the protein CJI97\_000055 since it is thought to contain a GPI-anchored domain involved in adhesion
* Confidence-related scores (Z-score, C-score) were all relatively poor, so the results should be referenced with caution
  + Threading was the only option for modeling the structurally uncharacterized CJI97\_000055
* Demonstrates the need for actual modeling of the protein for further analysis.
  + Structural characterization of this or closely related proteins would be useful.