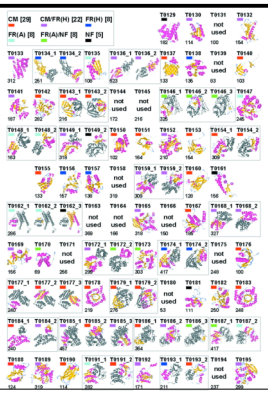
The Five Categories of CASP Targets

1. CM/E (Comparative Modeling / Easy) ← Structural homolog found by BLAST.
2. CM/H (Comparative Modeling / Hard) ← structural homolog found by 5 rounds of PSI-BLAST.
3. FR/H (Fold Recognition / Homology) ← Structural comparison to PDB finds a structure found by PSI-BLAST.
4. FR/A (Fold Recognition / Analogy) ← Finds a similar structure, no evidence of sequence homology.
5. NF (New Fold) ← nothing “similar” in the PDB

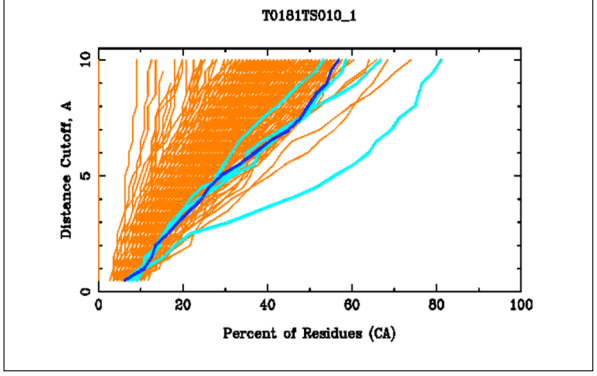
CASP



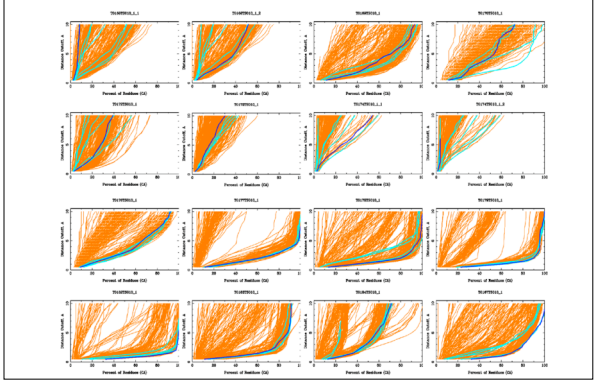
CASP Questions

1. Are the models produced similar to the corresponding experimental structure?
2. Is the mapping of the target sequence onto the proposed structure (i.e. the alignment) correct?
3. Have similar structures that a model can be based on been identified?
4. Are the details of the models correct?
5. Has there been progress from the earlier CASPs?
6. What methods are most effective?
7. Where can future effort be most productively focused?

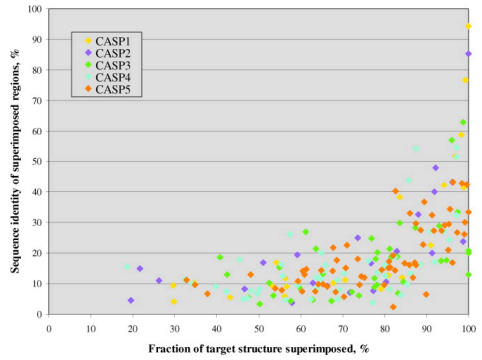
Hubbard Plot



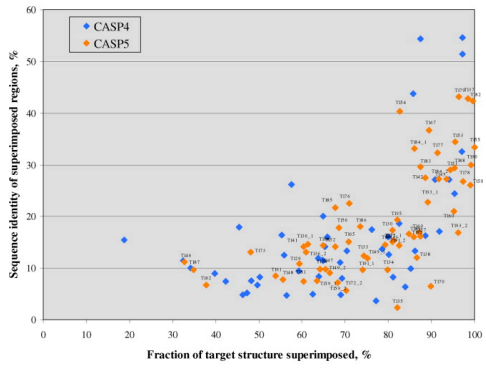
Hubbard Plots



Distribution of Target Difficulty



Distribution of Target Difficulty

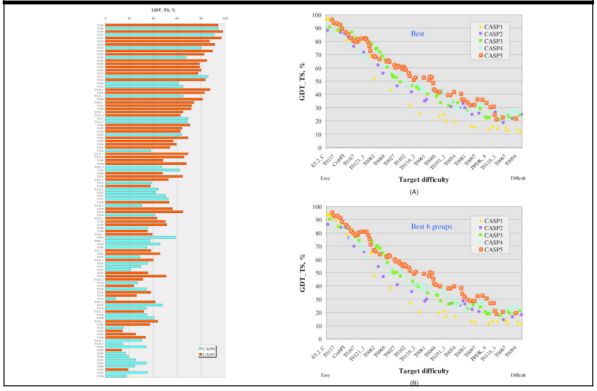


Overall Model Quality Assessment

Venclovas et al (2003): ”A large sample of possible structure superpositions of the model on the corresponding experimental structure is generated by superposing all sets of three, five, and seven consecutive Ca along the backbone (each peptide segment provides one superposition). Each of these initial superpositions is iteratively extended, including all residue pairs under a specified threshold in the next iteration, and continuing until there is no change in included residues. The procedure is conducted by using thresholds of 1, 2, 4, and 8 Å, and the superposition that includes the maximum number of residues, is selected for each threshold ... GDT_TS is then obtained by averaging over the four superposition scores for the different thresholds:

$$GDT\_TS = (N1+N2+N4+N8) / 4$$

CASP5 Progress

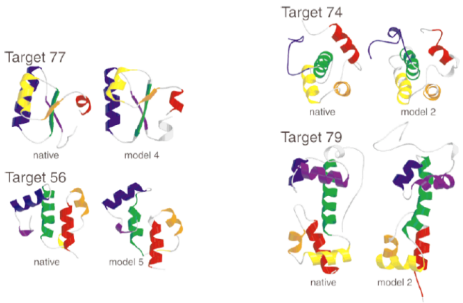


CASP Problem Areas and Bottlenecks

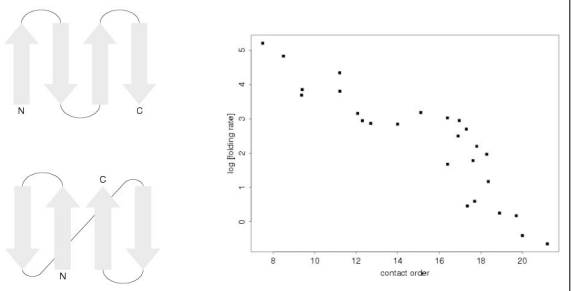
1. Alignment of a sequence onto a template fold.
2. Model refinement - improving accuracy of initial models.
3. Accurately modeling regions of insertion and deletion relative to a template structure.
4. Improved fold recognition, particularly for analogous, analogous/new fold targets.
5. Improved New Fold methods (for recognizing new folds).

Always the same …

CASP3 Predictions



Contact Order



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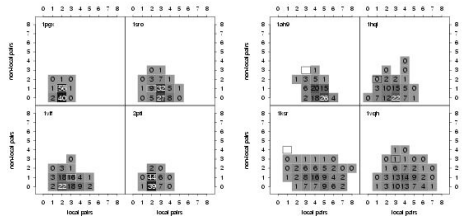
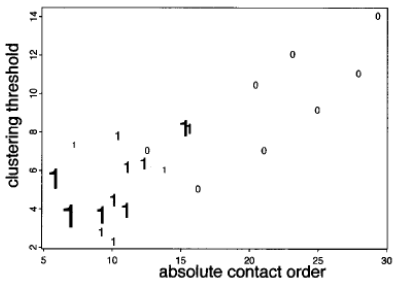
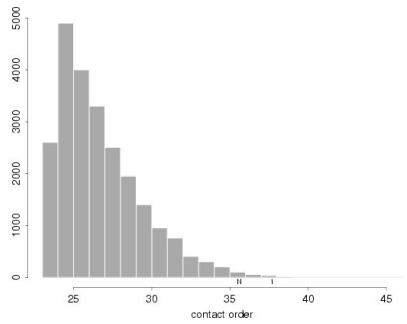


Clustering and Contact Order



Decoy Enrichment in CASP4

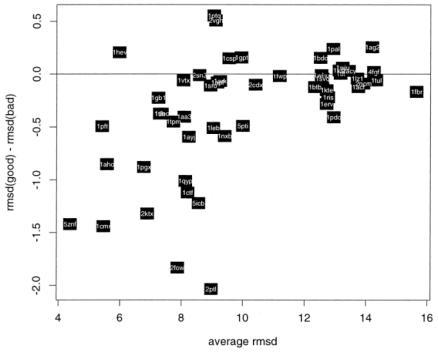


A Filter for Bad β-Sheets

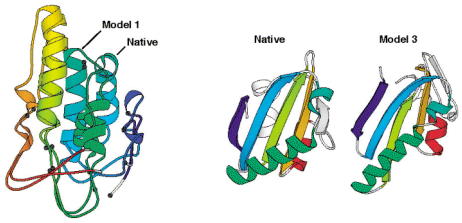
Many decoys do not have proper sheets. Filtering those out seems to enhance the rmsd distribution in the decoy set. Bad features we see in decoys include:

- No strands,
- Single strands,
- Too many neighbours,
- Single strand in sheets,
- Bad dot-product,
- False handedness,
- False sheet type (barrel),
- …

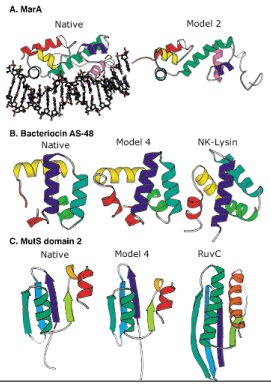
A Filter for Bad β-Sheets

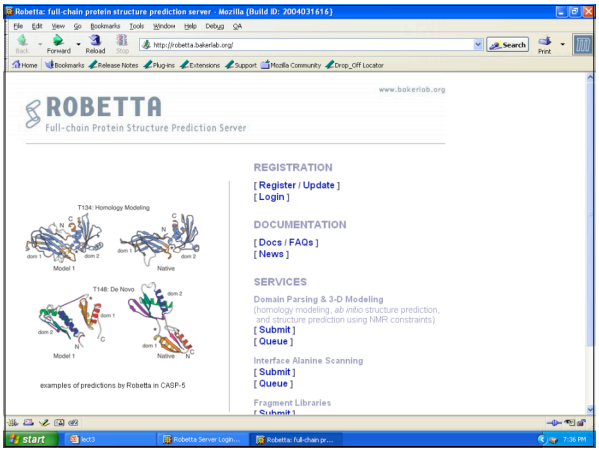


Rosetta in CASP4



CASP 4

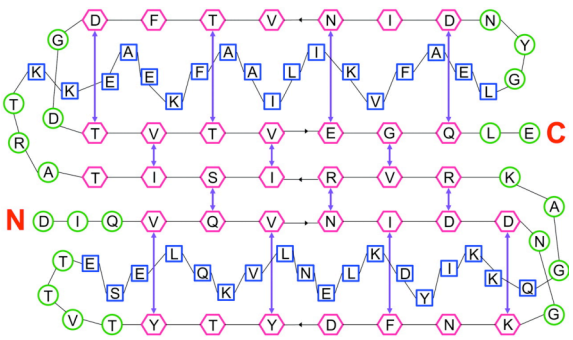




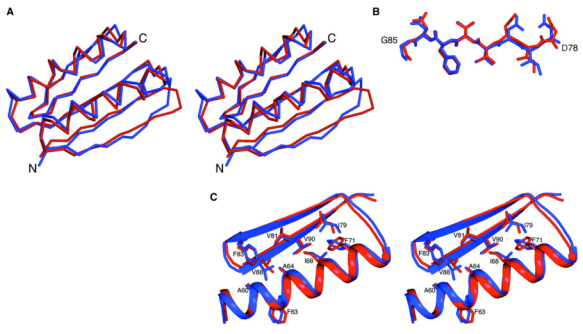
Applications and Other Uses of Rosetta

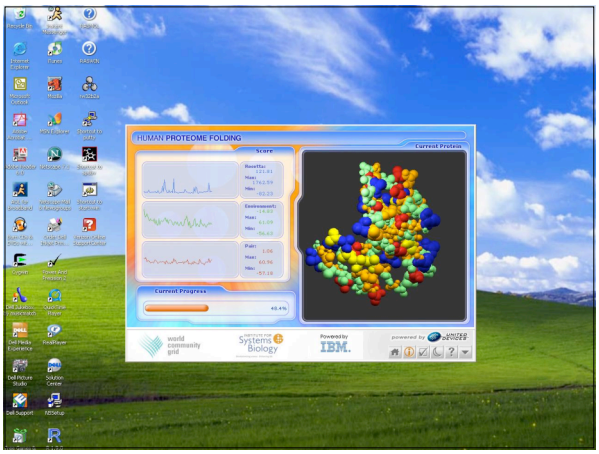
- Other uses of Rosetta:
  - Homology modeling.
  - Rosetta NMR.
  - Protein interactions (docking).
- Applications of Rosetta:
  - Functional annotation of genes.
  - Novel protein design.

Protein Design



Protein Design




HUMAN PROTEOME FOLDING
Current Protein
Current Progress
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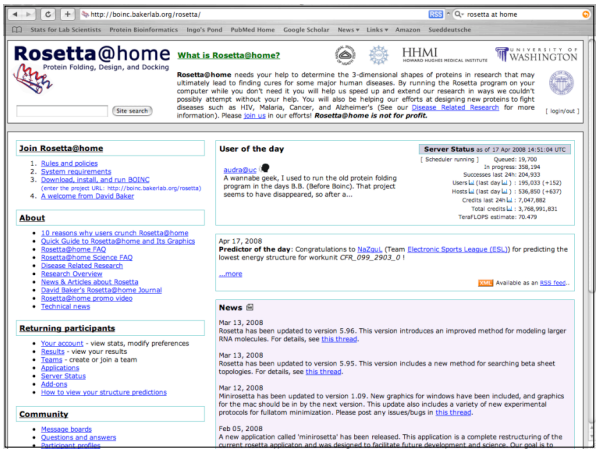
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3. Download, install, and run BOINC
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4. A welcome from David Baker
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Rosetta@home FAQ
Rosetta@home Science FAQ
Disease Related Research
Research Overview
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Results - view your results
Teams - create or join a team
Applications
Server Status
Add-ons
How to view your structure predictions
Community
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Questions and answers
User of the day
Server Status
News
Mar 13, 2008
Rosetta has been updated to version 5.96. This version introduces an improved method for modeling larger RNA molecules. For details, see this thread.
Mar 13, 2008
Rosetta has been updated to version 5.95. This version includes a new method for searching beta sheet topologies. For details, see this thread.
Mar 12, 2008
Minirosetta has been updated to version 1.09. New graphics for windows have been included, and graphics for the mac should be in by the next version. This update also includes a variety of new experimental protocols for fullatom minimization. Please post any issues/bugs in this thread.
Feb 05, 2008
A new application called 'minirosetta' has been released. This application is a complete restructuring of the