

Algorithms in Bioinformatics I, WS2002/3

Assignment sheet # 15

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The main objective of this assignment sheet is to motivate you to run the Rosetta de novo protein folding webserver at <http://www.bioinfo.rpi.edu/~bystrc/hmmstr/server.php>.

1 Running de novo protein folding (7 points)

- Obtain an interesting protein domain sequence of approximately 100 amino acids that has no known homologs. (If it has a strong homolog, then the website may refuse to run Rosetta).
- Submit your sequence to the Rosetta server.
- Save and print the generated log web-page.
- For each computation reported in the log page, give a brief description of what is being done and why.
- Produce a three-dimensional picture of your sequence using secondary structure cartoons (or using your own PDB viewer).
- By inspection-by-eye, which of the seven fold-space-attractor-regions of the Dali dictionary would you place your protein domain in?

2 SCOP classification (3 points)

Please report and explain the SCOP classification obtained for the following protein: *p53 tumor suppressor, DNA-binding domain from Human (Homo sapiens)*.

Additional useful activities:

Try designing a protein sequence from scratch whose structure is predicted by Rosetta to be a coiled coil.

Due by 10am, Monday, Feb 10, 2003.