

## **Protein Structural Bioinformatics, National Cancer Institute, Bethesda MD**

Most proteins work as multimeric complexes, which are often symmetric even when the monomer units are not. However, there are also a large number of proteins that are symmetric in the monomeric state. Examples of such internally symmetric proteins are the TIM barrels, beta-propellers, beta-trefoils, ferredoxins, alpha-alpha superhelices, leucine-rich repeats, etc. Such internally symmetric proteins are interesting objects from the point of view of their folding, subunit interaction, function, and evolution. They are also a unique model system for studying the protein-protein and protein subunit interactions and sequence-structure relations in general.

We have developed a program, called SymD, which detects such internally symmetric proteins in the protein structure database (Kim, Basner, Lee (2010) BMC Bioinfo. 11:303). We are currently working to improve this program. The new person's research program will be mainly on analyzing the collection of symmetric proteins that we have using this program.

### **Requirements:**

The successful candidate will have excellent mathematical skills, particularly in analytical geometry, and computer programming skills. Familiarity with, and a love for, three-dimensional protein structures are a must.

### **To Apply:**

Send inquiries and applications to [bk@nih.gov](mailto:bk@nih.gov) <<mailto:bk@nih.gov>> .

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This position is subject to a background investigation.