

蛋白质结构预测

COMPARATIVE MODELING

1. SwissModel – In the following assignment, you will predict a relatively easy structure – the structure of **mouse lysozyme C**. This structure is already in the PDB, but you will try to predict it without having this information, i.e. using a template of the human lysozyme. Later, you will compare the 2 structures.

Note: SwissModel is not necessarily the best modeling tool. However, the excellent tutorials by Gale Rhodes and the excellent interface with Swiss-PDBViewer make it an ideal tool for understanding the advantages and pitfalls of modeling. For a recent, good comparative study of comparative modeling tools (as studied in class), see: Wallner B. & Elofsson A. (2005) All are not equal: a benchmark of different homology modeling programs Protein Sci.14(5):1315-27. <http://www.ncbi.nlm.nih.gov/pubmed/15840834?dopt=Abstract>

Assignment

2. Use the sequence of mouse lysozyme C and search the PDB via the RCSB site or NCBI site (in advanced search, change the preferences of the form to allow fasta-format sequence search). What is the best NMR and crystal-structure alignment to this sequence?
Provide the e-value and the alignment from the RCSB search results site.

