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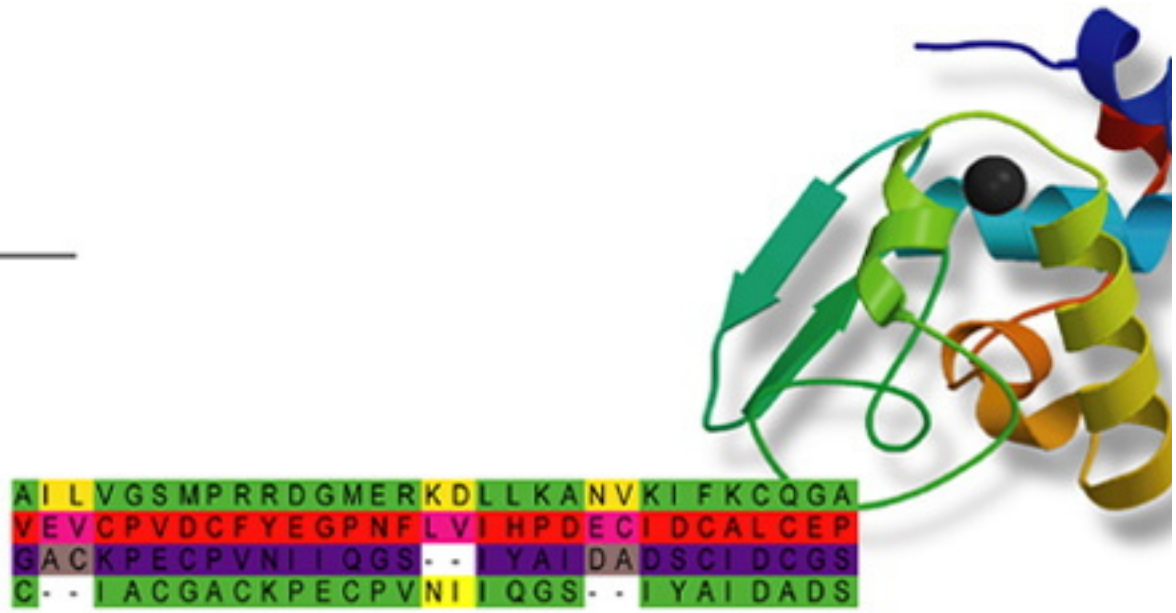

Modeling with cryo-EM

This tutorial covers the use of MODELLER to build complete 3D models of an 'unknown' protein structure (i.e. not solved by X-ray crystallography) given three sources of experimental information:

- The amino acid sequence of the **unknown** protein structure.
- The PDB database of other, **known** protein structures.
- A cryo-EM map of the **unknown** protein structure.

In order to follow through this tutorial, the input files must first be downloaded. These files are available as a compressed archive in both .tar.gz (for Mac or Linux) and zip (for Windows) format (the same files are contained in each format archive). The archive contains a subdirectory for each step in the tutorial, and each step in turn contains a `results` subdirectory containing sample results from running the scripts.

The protein used in this example is a novel gene for lactate dehydrogenase that was identified from the genomic sequence of *Trichomonas vaginalis* (TvLDH). For some other sample studies with this system, please refer to the regular MODELLER tutorial.