Guide to the Graphical Interfaces of CCP4

Kyle Stevenson, STFC

Science & Technology Facilities Council

The Graphical Interfaces of CCP4

There are currently two standard graphical interfaces available in the CCP4 suite of programs. We also have a cloud based gui system, jsCofe, which is currently in development.

CCP4i
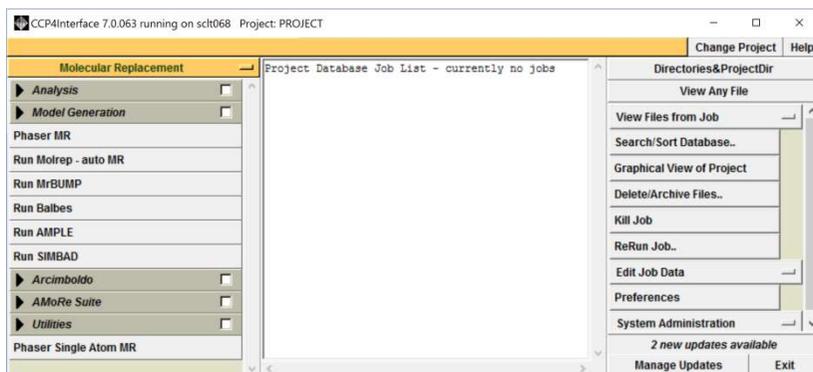
CCP4i2

CCP4i is the original graphical interface for CCP4, which was introduced in '99. Before that, the command line.
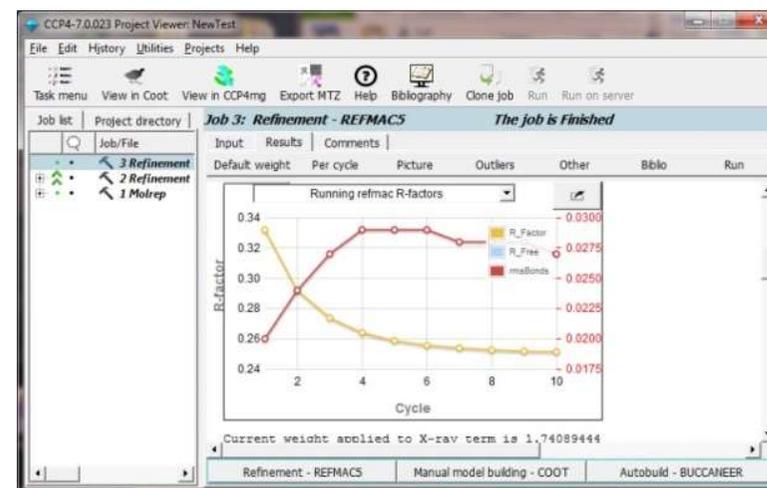
CCP4i2 is a later development, and in large part, is a replacement for CCP4i and incorporates a modernised interface and improved internal data handling.

What is Gui-2 ?

Gui-2 is the new(er) graphical interface for CCP4, which allows you to run the various programs of CCP4 without having to revert to the command line. This should simplify the process of determining the structure of a protein, especially in more straightforward cases.
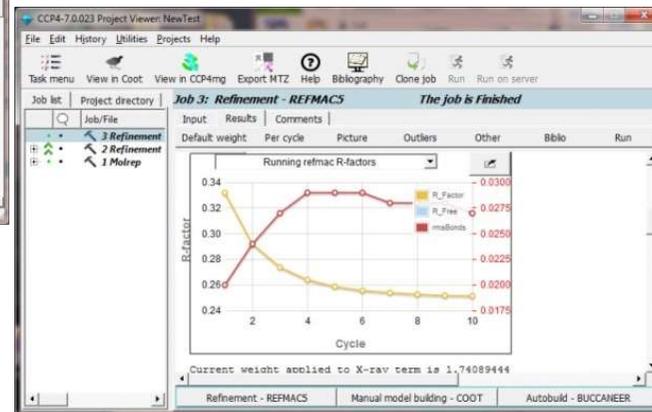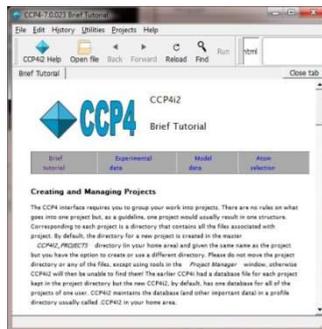
Today in this session we will cover the basics of how to install and use Gui-2.

We will then cover the use Gui-2 to find the correct phasing for example protein structures (we will cover both MR & Experimental Phasing if we have time).

Users can run a series of jobs in order to determine protein structures, with job details shown linearly on the left panel; the right hand side panel allows the user to input run conditions and to also view reports & run follow-up runs.

Installing Gui-2 (& CCP4) on Ubuntu/Mac

First download a copy of the Package Manager from www.ccp4.ac.uk (downloads tab). Unzip this file & then run it (double click) & follow the instructions on-screen.
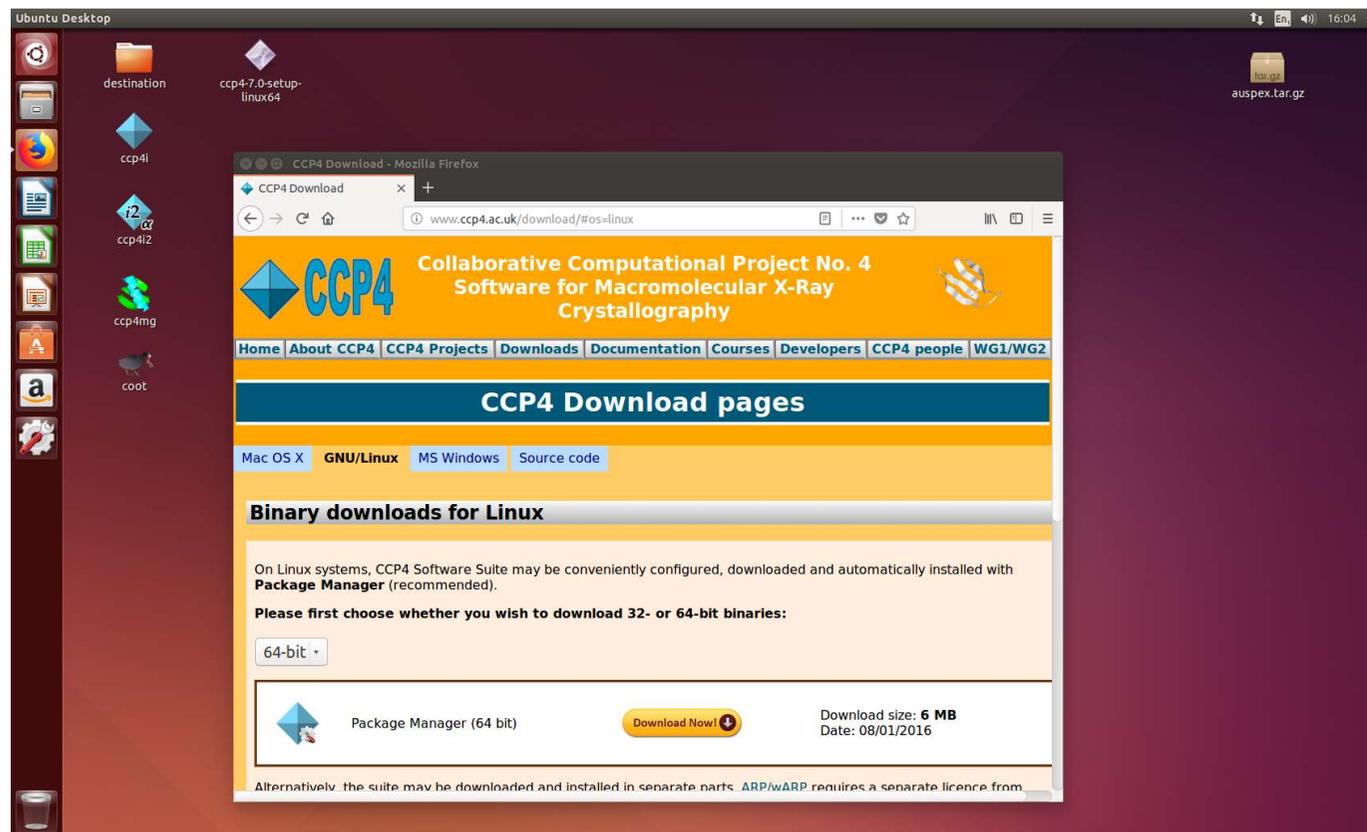
You may need to run (Ubuntu): sudo apt-get install tcsh   (use ctrl+T to get terminal up)

Starting up Gui-2 : Initial Stages

There are two ways of doing this, either with the console/terminal or by just double clicking on the Gui-2 icon (much easier for new users & recommended).

To then start Gui-2 from the terminal:

Hold down "Ctrl + Alt + T"

Right click on the screen & "Open Terminal"

```
cd <where it is installed>
source bin/ccp4.setup-sh
ccp4i2
```

Browser

Project Viewer
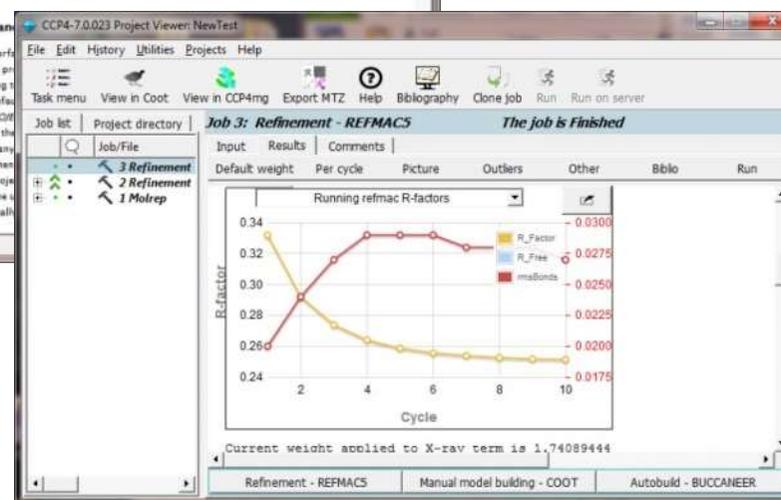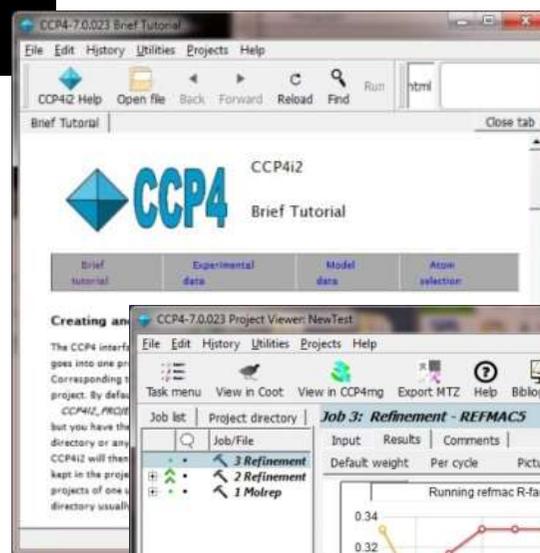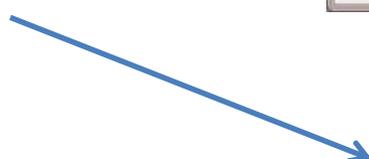
Basic Use of Gui-2 for New Projects
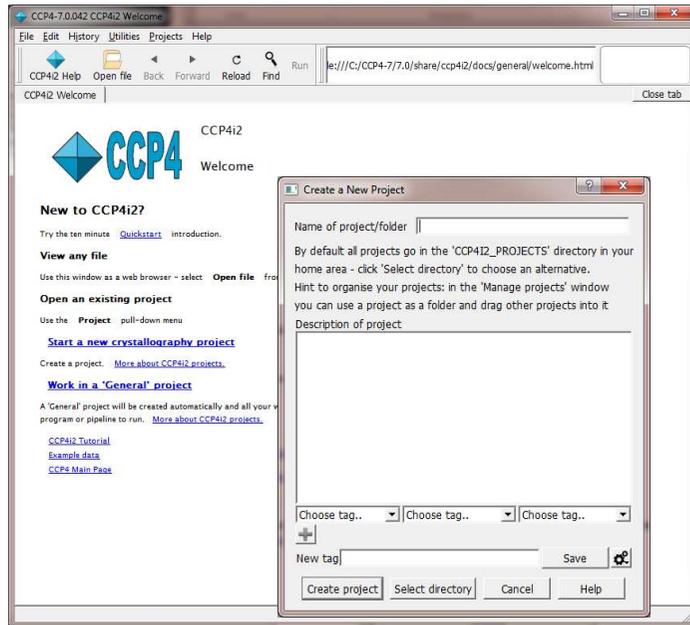
To start a new project, say for the study of a new crystal, go to **'Projects'** on the drop down menu & select **'New Project'**.

A box will appear; simply type in a name for your project at the top of the box, 'BAG-Gamma' for example, & then left click on the **Create Project** Button.

At this point a project viewer will appear with a list of tasks. Go to utilities & select **'Copy demo data'** – for starters try **'Gamma'**.

Also try the **'more info'** tab underneath the list of demo data. This will list info about the tutorials including a pdf file.
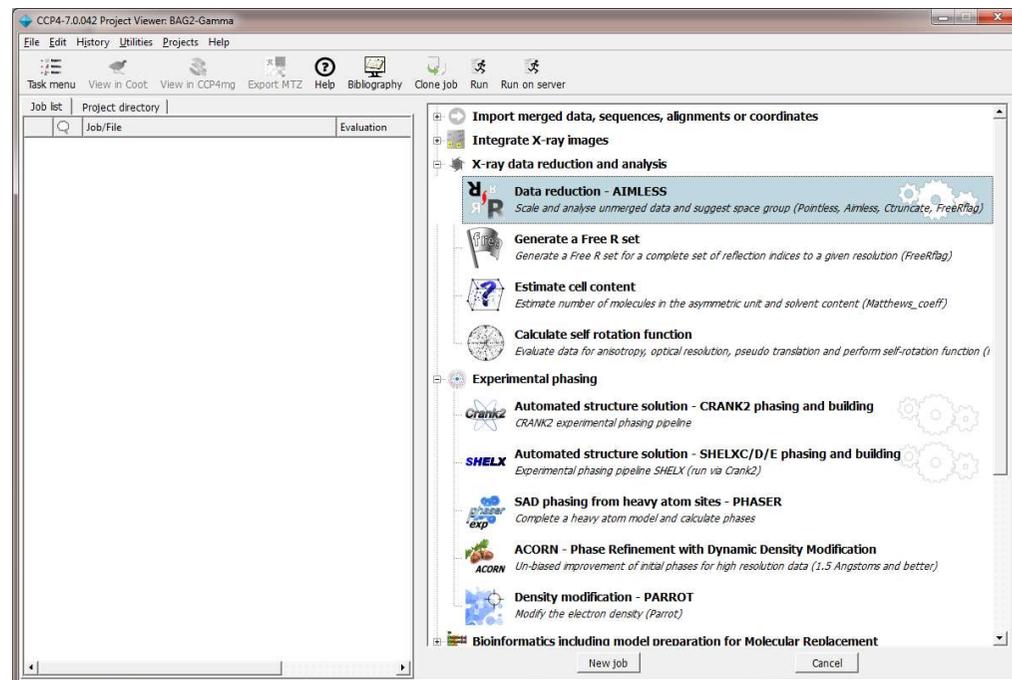
Gui-2 : What's Available in the Interface

Integrate X-ray images

Automated integration of images with DIALS using xia2
Select a directory containing images and integrate them

Automated integration of images with XDS using xia2
Select a directory containing images and integrate them

Integrate images with Mosflm
Launch iMosflm and capture output

X-ray data reduction and analysis

Data reduction - AIMLESS
Scale and analyse unmerged data and suggest space group (Pointless, Aimless, Ctruncate, FreeRflag)

Generate a Free R set
Generate a Free R set for a complete set of reflection indices to a given resolution (FreeRflag)

Estimate cell content
Estimate number of molecules in the asymmetric unit and solvent content (Matthews_coeff)

Calculate self rotation function
Evaluate data for anisotropy, optical resolution, pseudo translation and perform self-rotation function (Molrep)

Experimental phasing

Automated structure solution - CRANK2 phasing and building
CRANK2 experimental phasing pipeline

Automated structure solution - SHELXC/D/E phasing and building
Experimental phasing pipeline SHELX (run via Crank2)

SAD phasing from heavy atom sites - PHASER
Complete a heavy atom model and calculate phases

Density modification - PARROT
Modify the electron density (Parrot)

ACORN - Phase Refinement with Dynamic Density Modification
Un-biased improvement of initial phases for high resolution data (1.5 Angstoms and better)

Molecular Replacement

Automated structure solution - MrBUMP
Run a quick MrBUMP job with streamlined settings

Basic Molecular Replacement - PHASER
Simple MR with optional refinement and rebuilding (Phaser)

Expert Mode Molecular Replacement - PHASER
Advanced MR options followed by refinement and rebuilding (Phaser, Refmac5, Coot)

Molecular Replacement and refinement - MOLREP
Molecular replacement (Molrep)

Molecular replacement with electron density - MOLREP
Use electron density as the search model (Molrep)

Match model to reference structure
Match symmetry and origin of output model to reference structure (Csymmatch)

Density modification - PARROT
Modify the electron density (Parrot)

Automated molecular replacement - MORDA
Molecular Replacement with Domains and Assemblies

Gui-2 : What's Available in the Interface

Model building and Graphics

Autobuild protein - BUCCANEER
Iterations of model building (Buccaneer) and refinement (Refmac5, Prosmart and Coot)

Manual model building - COOT
Interactive building (Coot)

Scripted model building - COOT
Use scripts to fit sidechains, perform stepped refinement, fill and fit... (non-interactive Coot)

Find waters - COOT
Find and filter waters based on electron density and contacts (non-interactive Coot)

Model building from Molecular Replacement solution using Shelxe
Use Shelxe to attempt to improve (or verify) a solution from Molecular Replacement

Density modification - PARROT
Modify the electron density (Parrot)

ARP/wARP
Build model (ARP/wARP classic)

Molecular graphics visualization and figure creation - CCP4MG
Interactive molecular graphics: visualization, figure preparation, analysis.

Refinement

Refinement - REFMAC5
Refine (Refmac5) with optional restraints (Prosmart)

Low Resolution Refinement Pipeline (LORESTR)
Automated Low Resolution Structure Refinement Pipeline (LORESTR)

Import and/or edit TLS set definitions
Enter TLS information to be used later in the project

Rigid body refinement - PHASER
Define rigid bodies for refinement (Phaser), fill partial residues (Coot) and refine (Refmac)

Ligands

Automated solution of isomorphous ligand complex
A ligand workflow, starting from merged or unmerged reflections, SMILES, and an isomorphous parent structure

Make Ligand - Acedrg
Generate a PDB file and dictionary (acedrg) from MOL file, SMILES string/file, or sketch (lidia). Optionally match atom names to known structures.

Using Gui-2 to Determine Protein Structures

We are going to cover the solution of two (rather straightforward) protein structures. These examples cover both Molecular Replacement and Experimental Phasing techniques in order to give you some familiarisation with using CCP4 Gui-2.
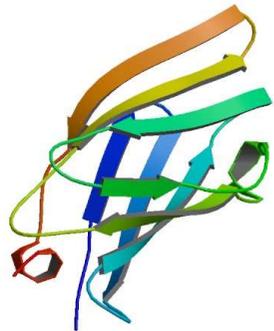
Gamma-adaptin (1GYU) - This structure will be solved using experimental methods (SAD) to get the phasing.

House Mouse
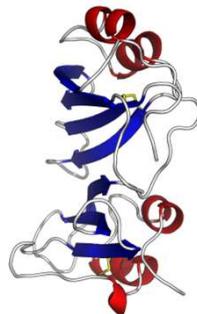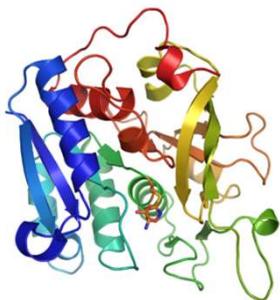
Beta Lactamase + Inhibitor (Beta/BLIP) - This protein complex will be solved using the molecular replacement technique (MR).
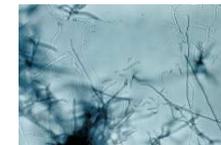
Bacteria

Quick Run-through of a Project

We now have the data, this will be in the CCP4I2 folder, under the project name (gamma in this case).

1. Load the data file (this will be the unmerged data from the derivative protein soaked with Xe) 'gamma_Xe_mosfilm.mtz'.
2. Enter a crystal and data-set name.
3. Hit the run button
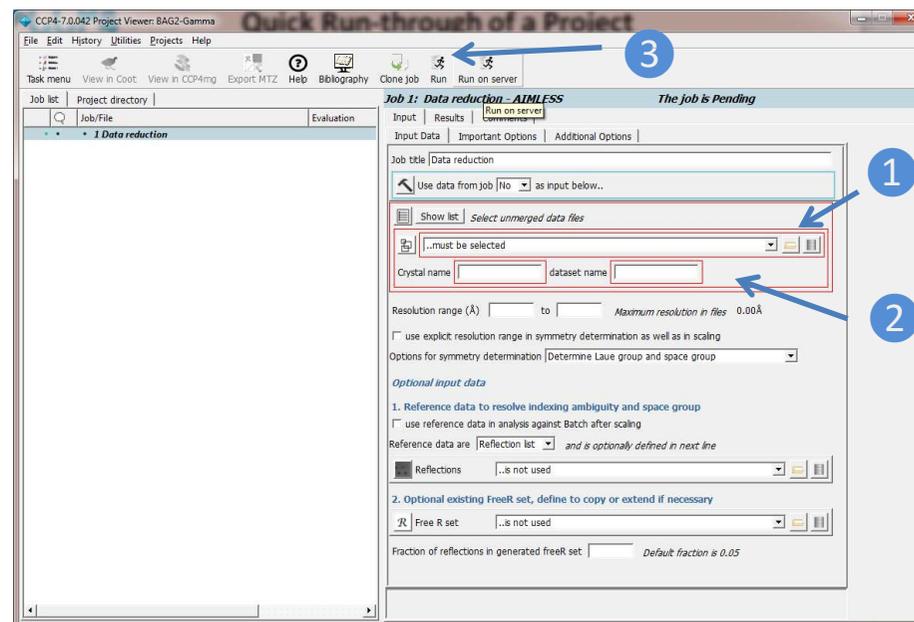
Next you can try **Crank2** to solve this structure; you can either hit the **Crank2** button at the bottom of the results page for the above job, or use the menu (ps. it's best to select data from, what will hopefully be, job 1).

Run the crank 2 job, run it from substructure to density modification; then you can follow this up with either manual model building in **coot** or auto-building with **buccaneer**.

New for 2018

There should be noticeable improvements in the response times of the various interface functions and the startup. More robust and improvements made to database handling.

Various new crystallography programs were added to Gui-2 during the early part of this year (Morda & Lorestr already added in late '17).

- Morda – MR pipeline
- Simbad – Sequence independent MR
- Lorestr – Low resolution refinement
- DUI – The Dials Graphical Interface
- Ab-initio phasing with Arcimboldo
- Auspex – Ice Ring Diagnostics
- Ample – Auto ab-init search model gen for MR
- Fragon – Molecular Replacement with Fragments
- Nautilus – RNA/DNA building from Electron density
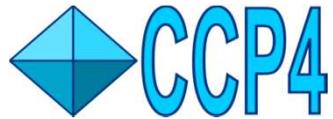
A (Very) Short FAQ

One scenario you might face is wanting to transfer a project from one computer to another. You can do this by going to Manage Projects under the Projects menu item and using the Import/Export features.

ps. Transferring between Linux & Mac ⇄ Windows is not supported, Linux ⇄ Mac is fine though.

Often people want to look directly at files; first these can be found in your home directory in CCP4I2_PROJECTS. This is for info purposes, it is STRONGLY recommended that you do not move or rename or change data files. It will very likely break everything.

You can export the various files from Gui-2 though using either as right click on the file or by using the export MTZ feature for a job.

Currently the Gui-2 interface does not officially support 4k monitors. It is possible to up the font size & it should be workable if not perfect.
This will be improved & rectified in the early part of this year.

Additional Tutorials You Can Try
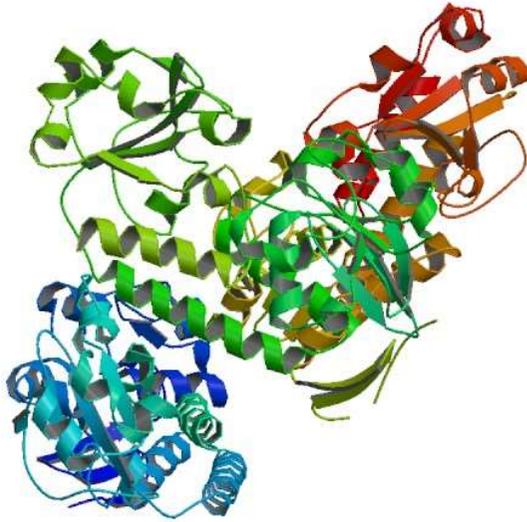
CeuE (3ZKW) – This crystallized protein structure is a combination of three different monomers. Typically found in bird guts & can be a cause of food poisoning. This is typically solved using molecular replacement.

MDM2/Nutilin-3A (4HG7) – This is an example of protein that crystalizes while bound to a ligand structure. MDM2 plays a part in the P53 tumour suppression system.