

Welcome!

**4th DLS-CCP4 Data Collection and
Structure Solution Workshop**

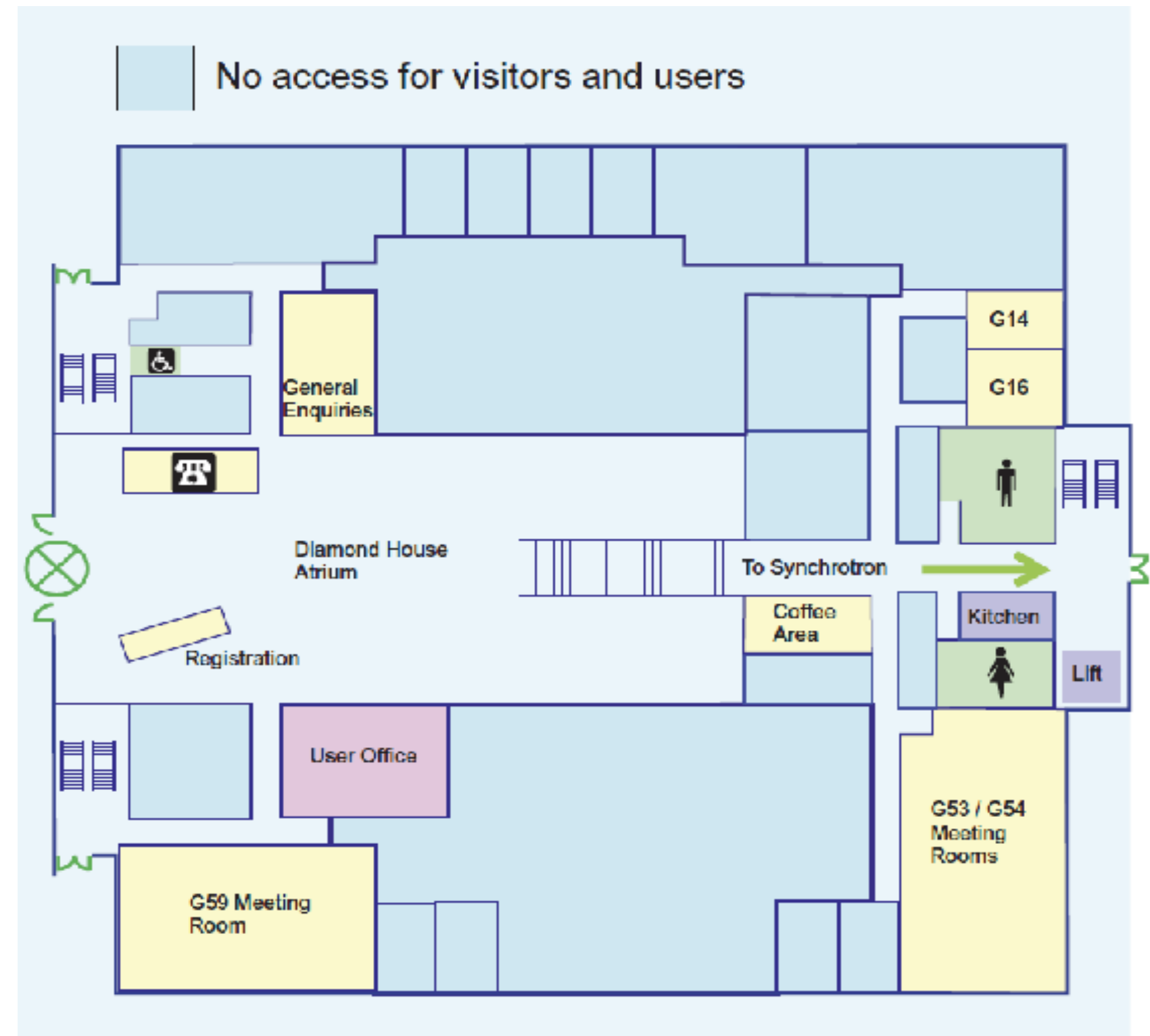
Fire Alarm

If the fire alarm sounds, there will be an alarm which alternates with a voice message stating that "there is an emergency in the building".

You should leave the building by the closest fire exit and congregate in the carpark in front of Diamond House.

Emergency Contacts

In case of emergency within Diamond House, please call the RAL emergency line on **2222** from any internal phone or **01235 778888** from a mobile.



How to get the most out of the workshop

- **Ask questions!** The tutors are experts and developers of the software you will use. They are not all available for the full week, please approach them if you need help.
- **Talk to your neighbours.** The attendees at the course have various levels of expertise and scientific backgrounds. You may learn from each other and not just the tutors.
- **Take your time.** You will get the most out of the tutorials if you work through each step carefully and think about what you are doing
- **Course materials** will be uploaded to the website <http://www.ccp4.ac.uk/schools/DLS-2017>, so don't feel you have to copy every slide. You will have them available at the end of the workshop.

If progress you make during the workshop leads to published results we ask that you please acknowledge this in your papers. We will link to them on our website. This helps us to keep delivering similar workshops in the future.

We wish you every success with your projects!



Collaborative Computational Project No. 4
Software for Macromolecular X-Ray Crystallography



[2017 Home](#)

[2016 Home](#)

[2015 Home](#)

[2014 Home](#)

DLS-CCP4 Data Collection and Structure Solution Workshop



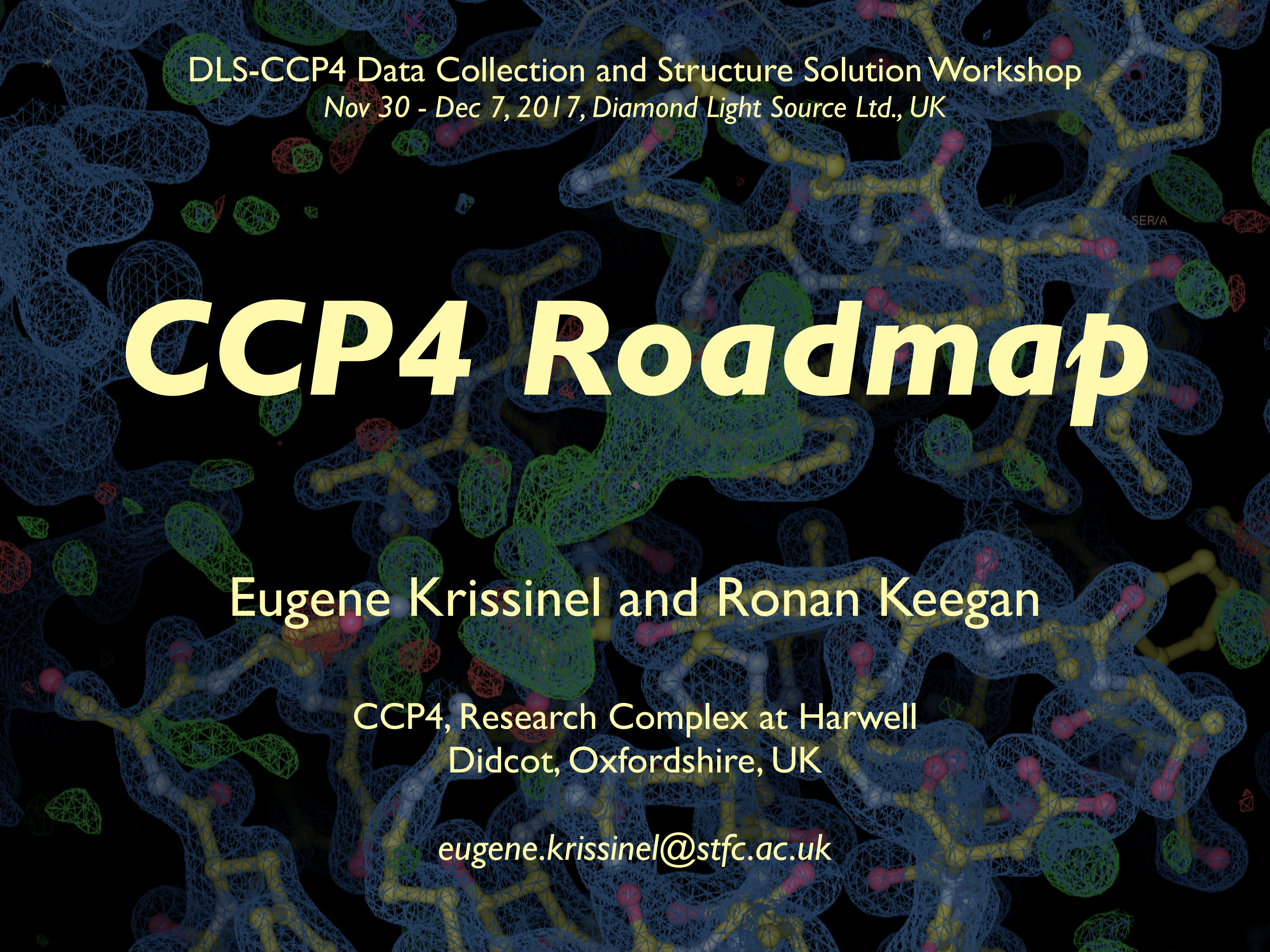
This page lists some of the publications where the research involved benefited from the assistance given at the DLS-CCP4 workshop. We are grateful to each of the authors for acknowledging the help they received at the workshop.

- [2015 Publications](#)
- [2014 Publications](#)

2015 Publications

The authors of the following publications have expressed their gratitude for the help they received in solving their structures at the DLS-CCP4 school in 2015.

- **"Super-complexes of adhesion GPCRs and neural guidance receptors"** - Verity A. Jackson, Shahid Mehmood, Matthieu Chavent, Pietro Roversi, Maria Carrasquero, Daniel del Toro, Goenue Seyit-Bremer, Fanomezana M. Ranaivoson, Davide Comoletti, Mark S. P. Sansom, Carol V. Robinson, Rüdiger Klein and Elena Seiradake **Nature Communications** 7 (2016).
- **"Structural snapshots of Xer recombination reveal activation by synaptic complex remodeling and DNA bending"** - Aleksandra Bebel, Ezgi Karaca, Banushree Kumar, W Marshall Stark and Orsolya Barabas. **eLIFE** 5 (2016).



DLS-CCP4 Data Collection and Structure Solution Workshop
Nov 30 - Dec 7, 2017, Diamond Light Source Ltd., UK

CCP4 Roadmap

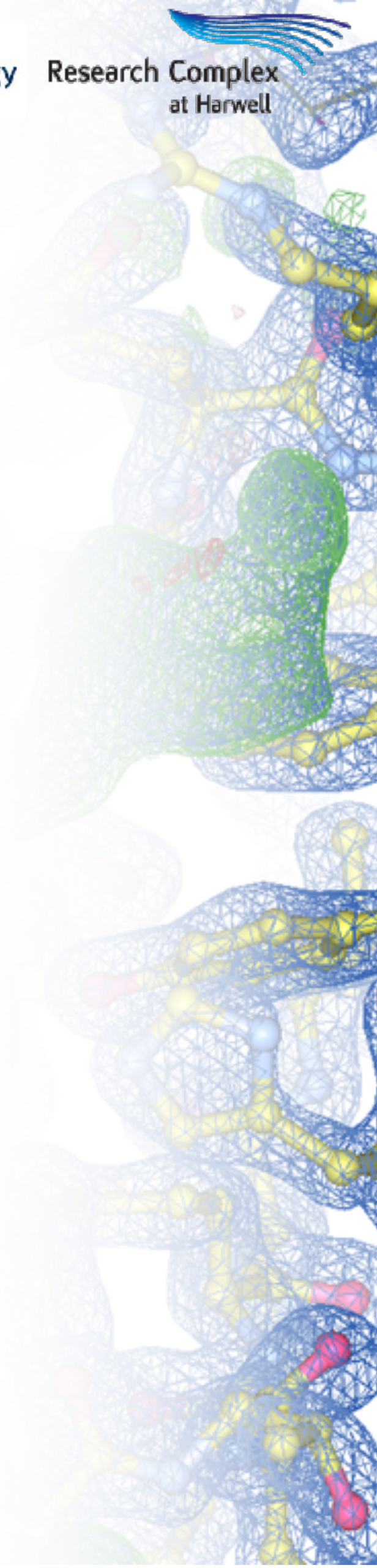
Eugene Krissinel and Ronan Keegan

CCP4, Research Complex at Harwell
Didcot, Oxfordshire, UK

eugene.krissinel@stfc.ac.uk

Outline

- What is CCP4
- The CCP4 Software Suite
 - ~ ccp4i2: graphical user interface
 - ~ what the Suite is used for
 - ~ each step in the process
- Other useful information



What is CCP4?

- CCP4 stands for “*Collaborative Computational Project No. 4 in Protein Crystallography*”
- One of several CCPs set up in the UK to advance and support scientific software developments
- CCP4 is not a single group in RCaH-Rutherford but a world-wide collaboration of developers and users
- CCP4 was formally set up in **1979** to support collaboration between researchers working on MX software in the UK, and to assemble a comprehensive collection of software to satisfy the computational requirements of the relevant UK groups
- CCP4 was originally supported by the UK Science and Engineering Research Council (SERC), and is now supported by the Biotechnology and Biological Sciences Research Council (BBSRC).
- The project is coordinated at the Scientific Computing Department of STFC UK

Main CCP4 Groups

- Core Group (Oxford)
 - ~ maintain and support software suite
 - ~ application and infrastructural software developments
 - ~ collaborate with Diamond on beam line deployment of CCP4 software and joint developments
 - ~ educational outreach
 - ~ maintain CCP4 resources such as the CCP4 bulletin board
- MRC/LMB (Cambridge)
 - ~ data processing software (Mosflm, Aimless)
 - ~ refinement software (Refmac)
 - ~ model building (Coot)
- Phaser group (University of Cambridge)
- University of York
 - ~ Software developments (CCP4mg, Buccaneer, Privateer)
 - ~ CCP4 GUI-2 developments
- Others
 - ~ Experimental Phasing from Leiden (Crank-2)
 - ~ Ab-initio MR, University of Liverpool (AMPLE)
- Associated projects
 - ~ Arp/wArp (EMBL-Hamburg)
 - ~ PDB redo (NKI, the Netherlands)



CCP4 Users Geography



CCP4 Study Weekend

- Annual CCP4 users meeting taking place in January in the UK
- Each year tackles a different topic:
 - ~ Data processing
 - ~ Experimental phasing
 - ~ Molecular replacement
 - ~ Model building and refinement
 - ~ Related topics: Complementary methods (EM, NMR, SAX etc.), Structure analysis, Complexes, Ligands, Databases
- Proceedings published in special edition of Acta Cryst. D
- 2016: “*Ligands*”
- 2017: “*From crystals to structure with CCP4*”
- 2018: “*Micro/nano crystals — data collection*” (*provisional*)

CCP4 Schools and Workshops

- Main aim is to give education and expert help to researchers working with collected crystal data
- Some schools also provide expert help with collecting crystal data (APS, Hamburg, Diamond)
- Applicants with challenging crystals and/or data are given strong consideration but this is not mandatory
- Software developers from CCP4, Phenix (APS Workshop), SHELX, Arp/wArp, XDS and HKL as well as others give lectures, tutorials and are also available to help with data processing and data solution throughout the meetings

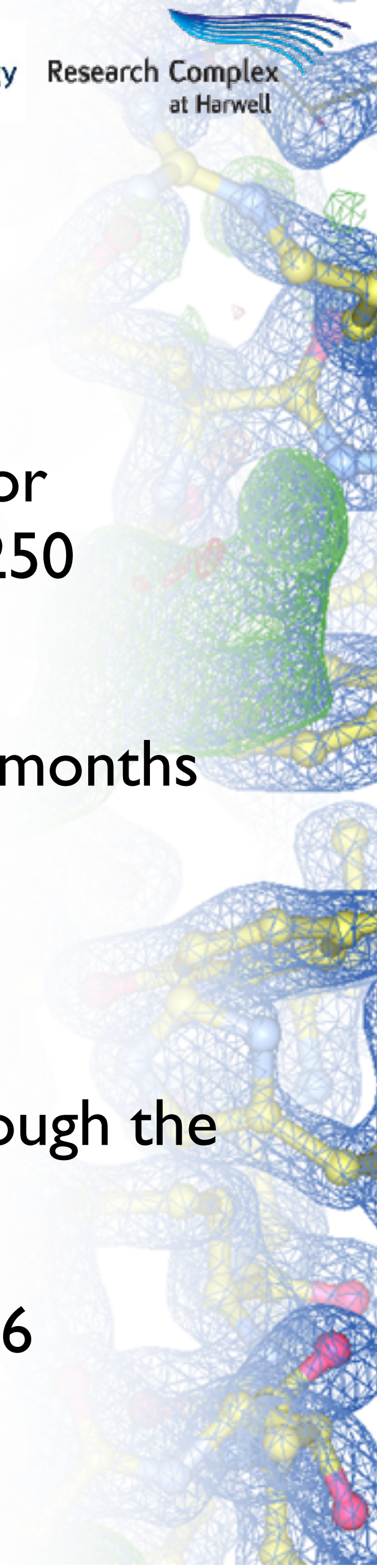
<http://www.ccp4.ac.uk> – Courses & Events

Other CCP4 Resources

- CCP4BB mailing list — bulletin board, news, expert help and advice
- CCP4 help desk — ccp4@ccp4.ac.uk — bug reports, problems with software
- CCP4 wiki — <http://ccp4wiki.org> — program documentation and tutorials
- CCP4 wiki @ Konstanz — <http://strucbio.biologie.uni-konstanz.de/ccp4wiki/index.php/Crystallography> — owing to Kay Diederichs
- CCP4 web site — <http://www.ccp4.ac.uk>

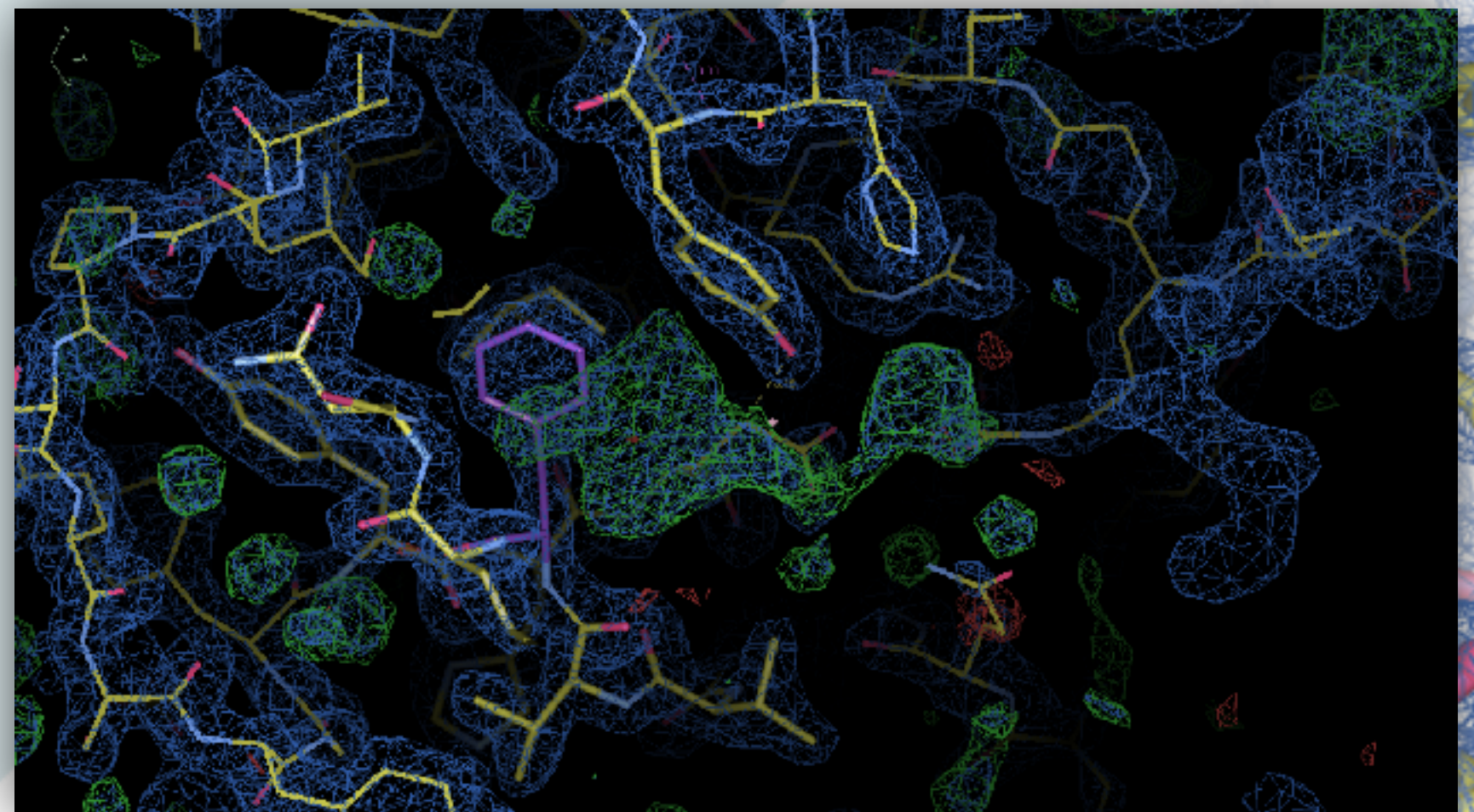
The CCP4 Software Suite

- The CCP4 Suite is a comprehensive suite of software for macromolecular crystallography and it contains about 250 program components
- New versions of the suite are released about every 12 months
 - ~ New programs
 - ~ Major updates to existing programs
 - ~ Other new features such as changes to CCP4i interface
- Revisions to the current release are made available through the CCP4 updates manager
- Current release version — CCP4 7.0 from January 2016



Structure Solution in Essence

- As an ultimate goal, one would like to generate an atomic model for their target
- This could be achieved by applying the inverse Fourier transform to experimental structure factors (which are Fourier transform of the structure's atomic coordinates) if they were known or could be indeed obtained in an experiment
- In reality, the X-ray diffraction experiment gives only moduli, **but not phases**, of structure factors
- Therefore, phases need to be elicited by other means



Structure Solution Pathway

- As a first step, one need to derive structure factor amplitudes from the intensities of spots in X-ray images
- Next, phases need to be approximated by using methods such as
 - ~ Experimental Phasing: SAD, MAD, SIRAS etc.
 - ~ Molecular Replacement
 - ~ Combination of the above
- Then, structure factors can be converted into electron density via *inverse Fourier transform*
- The obtained electron density map needs to be interpreted via model building and refinement to produce a model for target structure
- The model need to be analysed to answer biochemical questions and deposited in the PDB

sounds like we know what to do ...

CCP4 Scope

PiMS

Crystallisation

Data Collection

Data Processing
and Reduction

DIALS
Collection Integration for Advanced Light Sources

Experimental
Phasing

Molecular
Replacement

Density
Modification

Model Building

Refinement

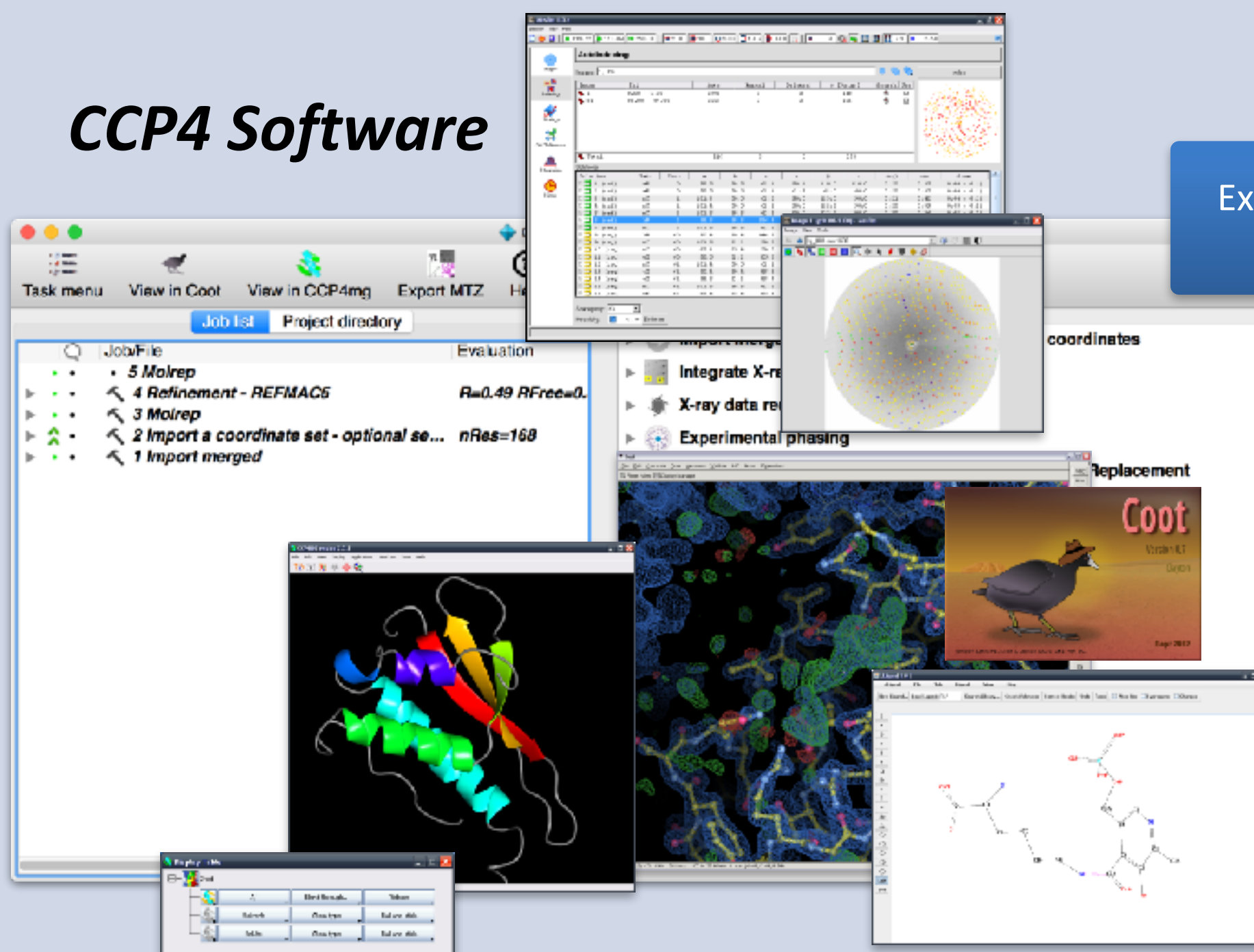
Structure Analysis

Deposition

SHELX

7.3
ARP
wARP

CCP4 Software



PDB_REDO

External components

*SHARP/
autoSHARP*

PiMS

*XDS &
autoPROC*

Crystallisation

Data Collection

Data Processing
and Reduction

DIALS
Collection Integration for Advanced Light Sources

Experimental
Phasing

Molecular
Replacement

Density
Modification

Model Building

Refinement

Structure Analysis

Deposition

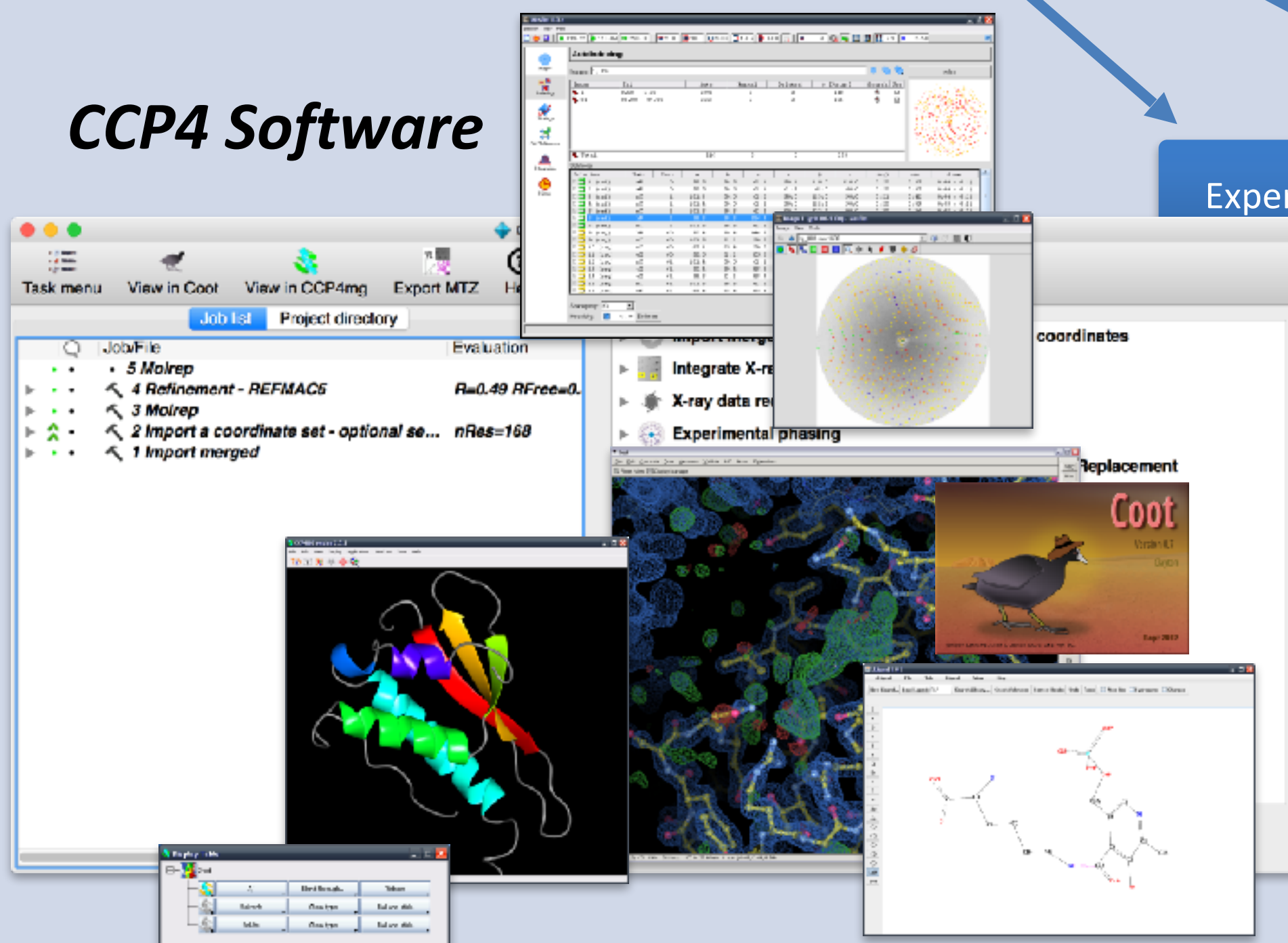
SHELX

7.3
ARP
wARP

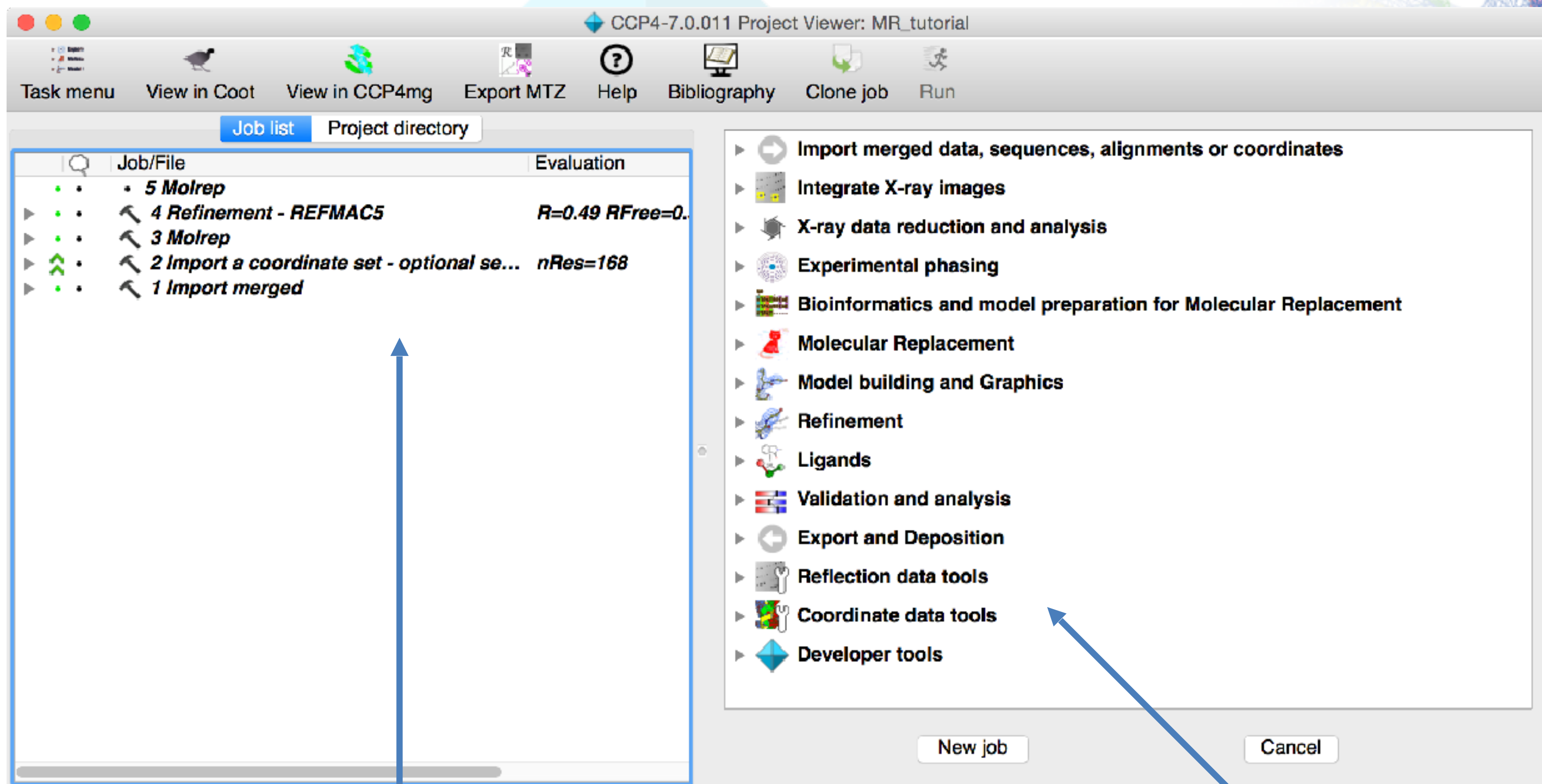
BUSTER

PDB_REDO

CCP4 Software



The CCP4i2 Interface



The screenshot displays the CCP4-7.0.011 Project Viewer: MR_tutorial window. The interface includes a top toolbar with icons for Task menu, View in Coot, View in CCP4mg, Export MTZ, Help, Bibliography, Clone job, and Run. Below the toolbar are two tabs: Job list (selected) and Project directory. The Job list tab shows a table with columns Job/File and Evaluation. The Project directory tab shows a list of tasks with icons and descriptions. At the bottom are buttons for New job and Cancel.

Job/File	Evaluation
5 Molrep	
4 Refinement - REFMAC5	R=0.49 RFree=0.
3 Molrep	
2 Import a coordinate set - optional se...	nRes=168
1 Import merged	

- Import merged data, sequences, alignments or coordinates
- Integrate X-ray images
- X-ray data reduction and analysis
- Experimental phasing
- Bioinformatics and model preparation for Molecular Replacement
- Molecular Replacement
- Model building and Graphics
- Refinement
- Ligands
- Validation and analysis
- Export and Deposition
- Reflection data tools
- Coordinate data tools
- Developer tools

Job list

Task menu

The CCP4i2 Interface

CCP4-7.0.011 Project Viewer: MR_tutorial

Task menu View in Coot View in CCP4mg Export MTZ Help Bibliography Clone job Run

Job list Project directory

Job/File Evaluation

- 6 Autobuild - BUCCANEER
- 5 Molrep
- 4 Refinement - REFMAC5 *R=0.49 RFree*
- 3 Molrep
- 2 Import a cool
- 1 Import merge

Job actions (right-click)

- Delete
- Clone
- Edit label
- Open
- View
- Export
- Next task..

Input Output Comments

Job 4: Refinement - REFMAC5 The job is Finished

Input Results Comments

Default weight Per cycle Picture Outliers Other Biblio Run

No. reflections all/free	21135 / 106
R-factor/R-free	0.492 / 0.53
RMS Deviations	
Bonds	0.0135
Angles	1.782
Chain mean B (No. atoms)	
AA	17.7914 (1)
Aa	42.3363 (6)

Download

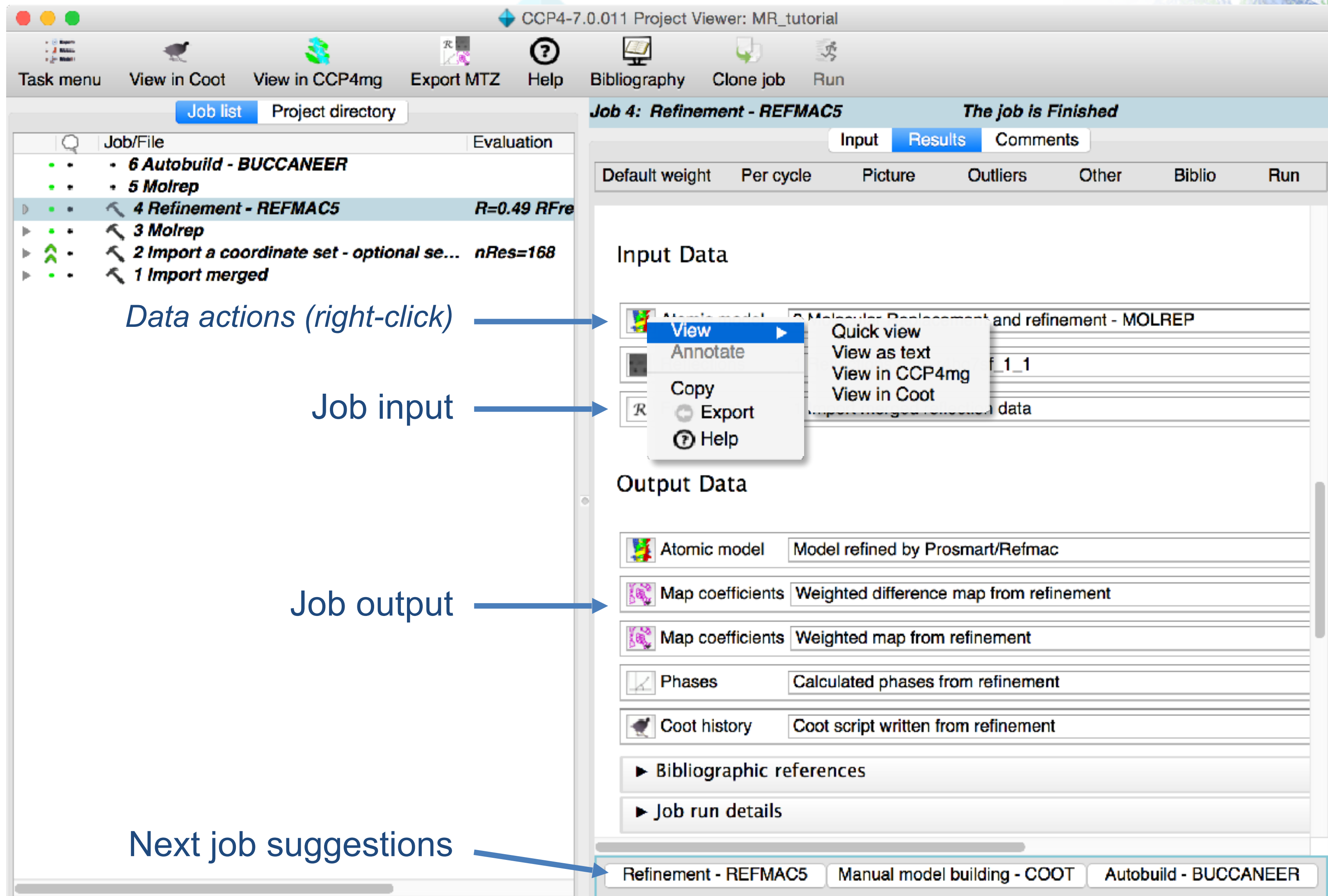
Running refmac R-factors

R-factor

Cycle

Refinement - REFMAC5 Manual model building - COOT Autobuild - BUCCANEER

The CCP4i2 Interface



CCP4-7.0.011 Project Viewer: MR_tutorial

Task menu View in Coot View in CCP4mg Export MTZ Help Bibliography Clone job Run

Job list Project directory

Job/File Evaluation

- • 6 Autobuild - BUCCANEER
- • 5 Molrep
- ▶ • 4 Refinement - REFMAC5 $R=0.49$ RFre
- ▶ • 3 Molrep
- ▶ • 2 Import a coordinate set - optional se... nRes=168
- ▶ • 1 Import merged

Data actions (right-click) →

Job input →

Job output →

Next job suggestions →

Job 4: Refinement - REFMAC5 *The job is Finished*

Input Results Comments

Default weight Per cycle Picture Outliers Other Biblio Run

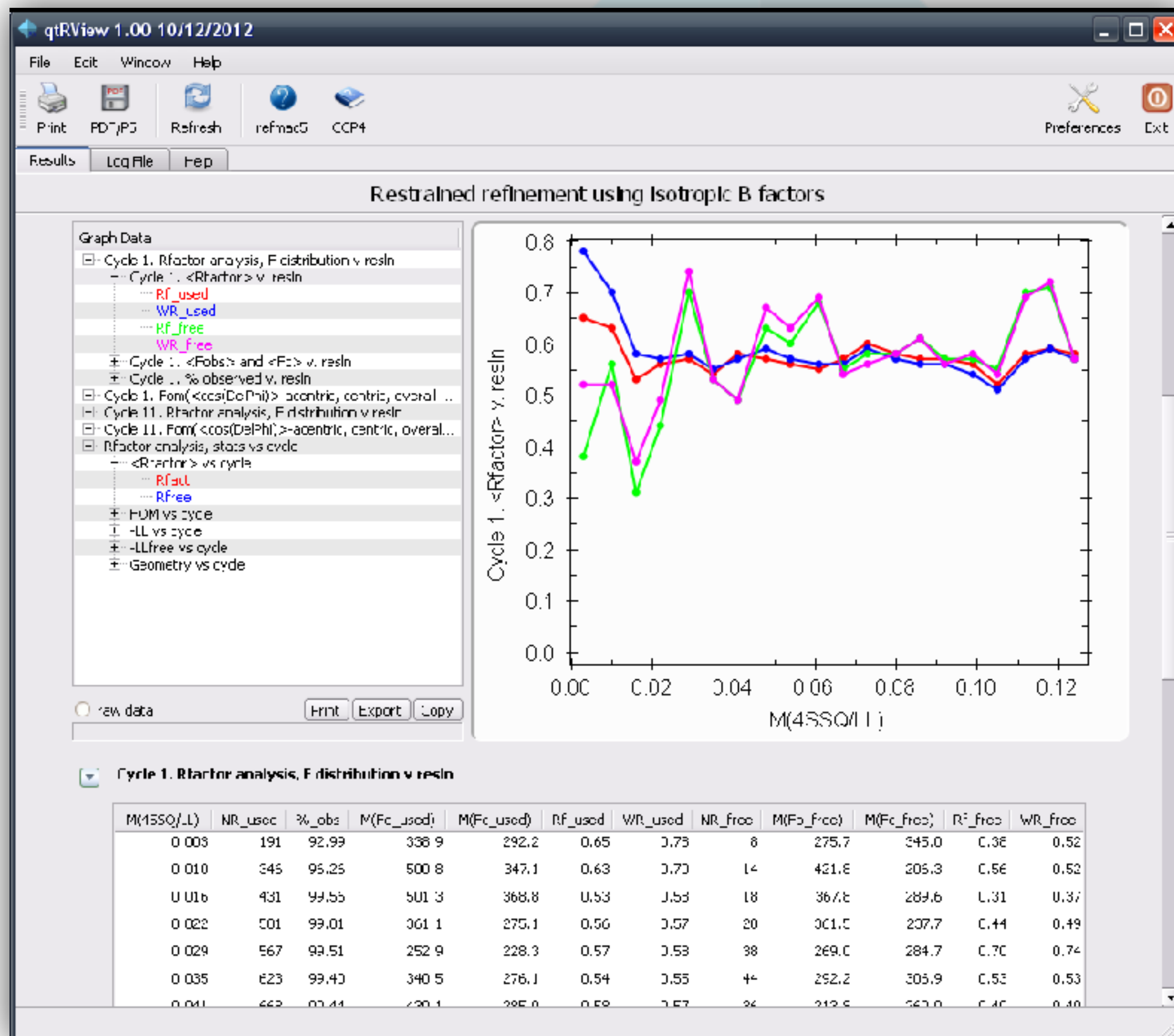
Input Data

- Atomic model 2 Molecular Replacement and refinement - MOLREP
- Map coefficients Weighted difference map from refinement
- Map coefficients Weighted map from refinement
- Phases Calculated phases from refinement
- Coot history Coot script written from refinement
- Bibliographic references
- Job run details

Output Data

Refinement - REFMAC5 Manual model building - COOT Autobuild - BUCCANEER

Report Viewer QtRView



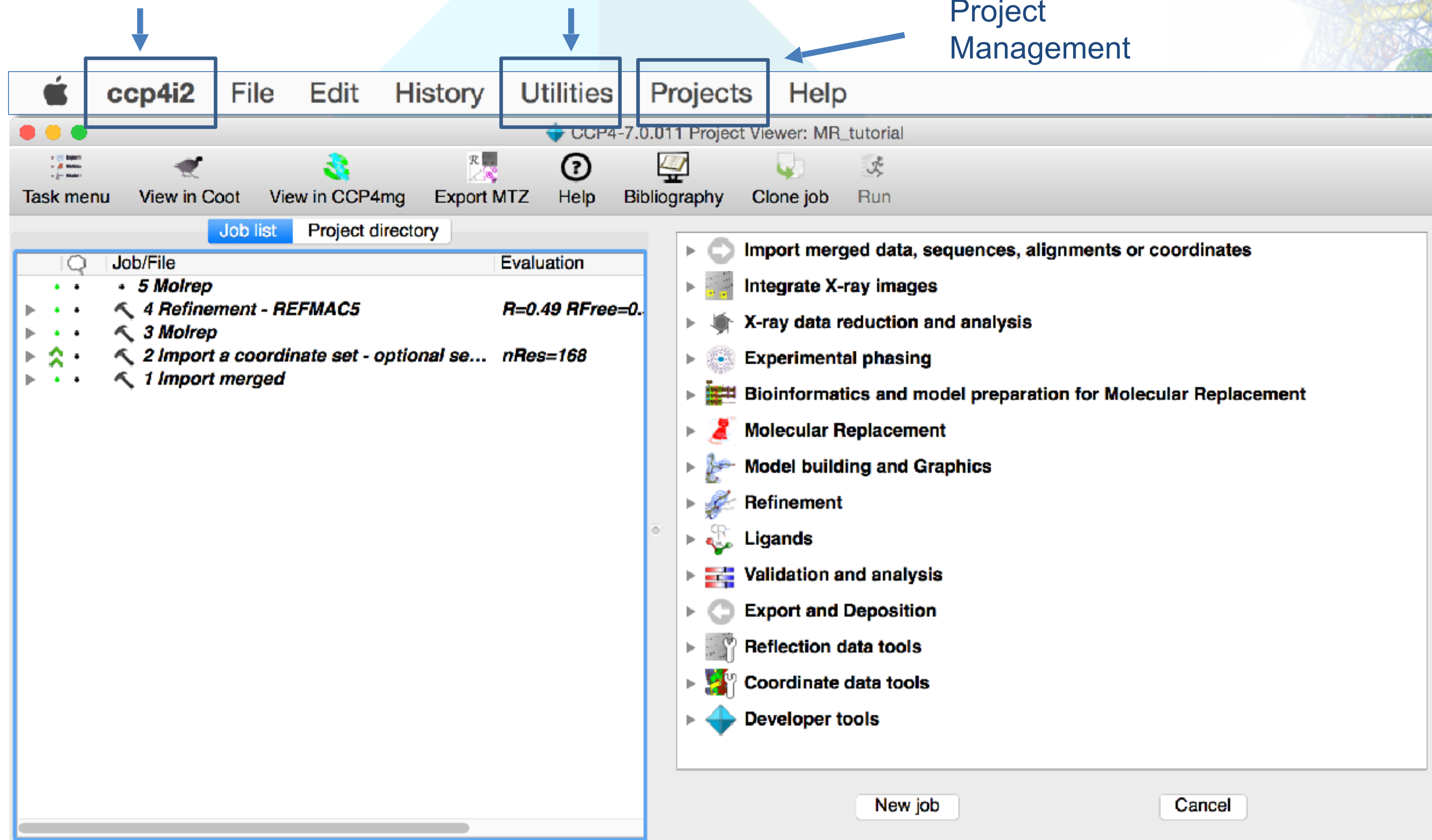
- Graphical log file viewer
- View graphs, tables and job summary information
- Launch Coot, CCP4mg and ViewHKL to work with the content of data files
- Export result files
- Can still view the original (plain text) log file

The CCP4i2 Interface

Preferences
and Settings

Managing Software Updates

Project
Management



The screenshot displays the CCP4i2 application window. The menu bar includes Apple, ccp4i2, File, Edit, History, Utilities, Projects, and Help. The task menu below the menu bar contains icons for Task menu, View in Coot, View in CCP4mg, Export MTZ, Help, Bibliography, Clone job, and Run. The main window is divided into two panes. The left pane, titled 'Job list', shows a table of jobs with columns for Job/File and Evaluation. The right pane, titled 'Project directory', shows a list of project tasks. At the bottom right, there are 'New job' and 'Cancel' buttons.

Job/File	Evaluation
5 Molrep	
4 Refinement - REFMAC5	$R=0.49$ $R_{Free}=0.5$
3 Molrep	
2 Import a coordinate set - optional se...	$nRes=168$
1 Import merged	

- Import merged data, sequences, alignments or coordinates
- Integrate X-ray images
- X-ray data reduction and analysis
- Experimental phasing
- Bioinformatics and model preparation for Molecular Replacement
- Molecular Replacement
- Model building and Graphics
- Refinement
- Ligands
- Validation and analysis
- Export and Deposition
- Reflection data tools
- Coordinate data tools
- Developer tools

The CCP4i(1) Interface

Project
Management

CCP4Interface 6.5.004 running on rmxps Project: pierreHD

List of jobs for project. Double-click on a job displays the log file, shift-double-click reruns the job.

Molecular Replacement

- Automatic structure solution
- Data Reduction and Analysis
- Experimental Phasing
- Molecular Replacement
- Density Improvement
- Model Building
- Refinement
- Structure Analysis
- Validation & Deposition

Map & Mask Utilities

- Reflection Data Utilities
- Coordinate Utilities
- Graphics and Viewing Utilities

Program List

Job ID	Date	Status	Program	Notes
25	18 Dec 14	KILLED	buccaneer_pipeline	yray
22	18 Dec 14	FINISHED	molrep	tesy
21	18 Dec 14	FINISHED	refmac5	test
20	18 Dec 14	FAILED	xia2	test
19	18 Dec 14	FAILED	xia2	test
18	18 Dec 14	FINISHED	mr bump	test
17	18 Dec 14	FINISHED	aimless	test
16	18 Dec 14	FINISHED	pointless	test
15	18 Dec 14	FAILED	dimple	test
14	17 Dec 14	KILLED	mr bump	test
13	12 Dec 14	FAILED	mr bump	test
12	12 Aug 14	KILLED	mr bump	[No title given]
11	12 Aug 14	FINISHED	mr bump	[No title given]
10	12 Aug 14	FINISHED	mr bump	[No title given]
9	12 Aug 14	FAILED	mr bump	[No title given]
8	12 Aug 14	KILLED	mr bump	[No title given]
7	12 Aug 14	FINISHED	mr bump	[No title given]
6	12 Aug 14	FAILED	mr bump	[No title given]
5	13 May 13	FINISHED	phaser_MR	[No title given]
4	13 May 13	FINISHED	phaser_MR	[No title given]
3	13 May 13	FINISHED	phaser_MR	[No title given]
2	13 May 13	FINISHED	phaser_MR	[No title given]
1	13 May 13	FINISHED	phaser_MR	[No title given]

Directories&ProjectDir

- View Any File
- View Files from Job
- Search/Sort Database..
- Graphical View of Project
- Delete/Archive Files..
- Kill Job
- ReRun Job..
- Edit Job Data

Preferences

- System Administration

3 new updates available

- Manage Updates
- Exit

Task/program
menu

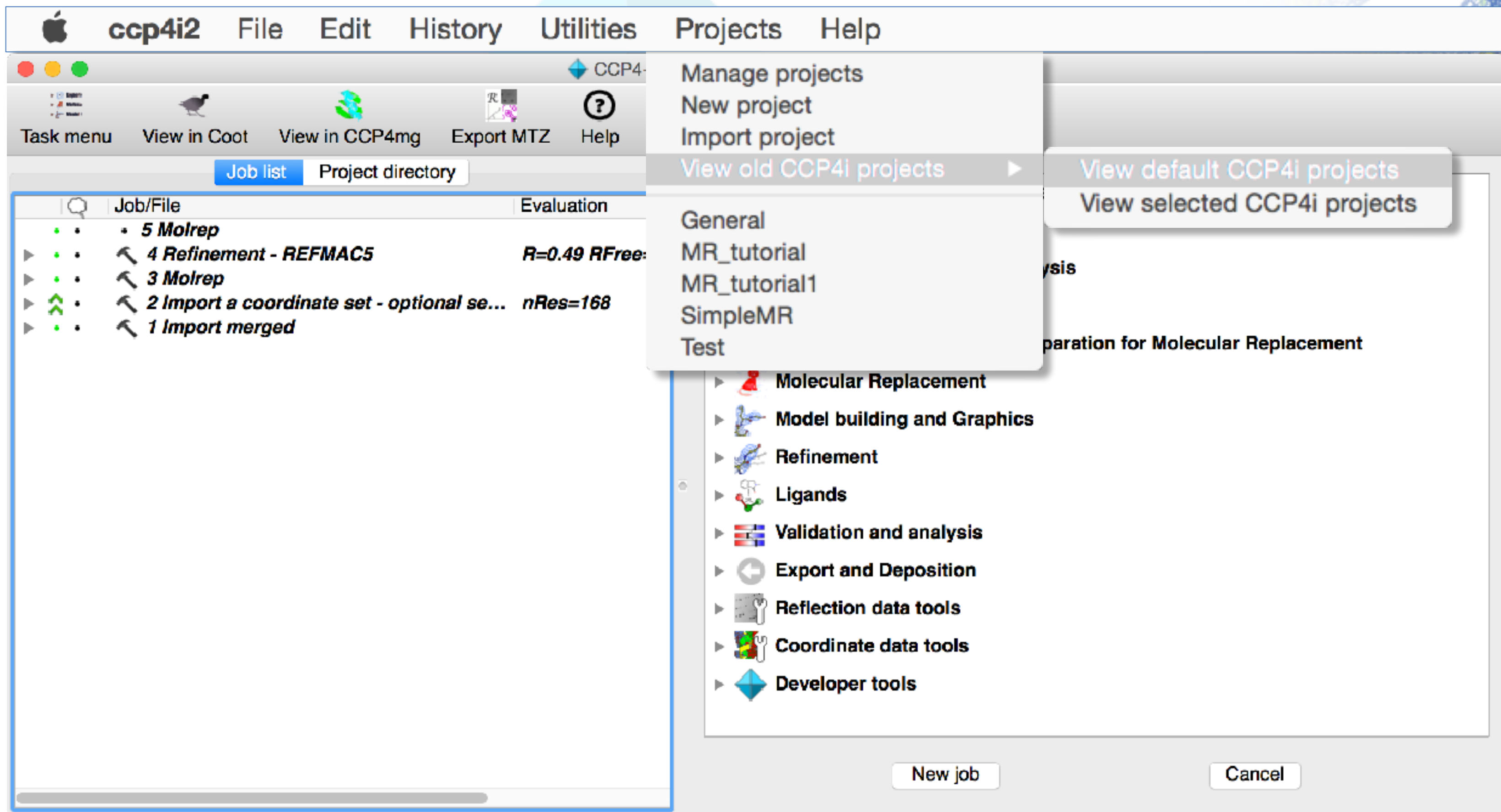
Job list

Job actions:
clone, kill, delete,
view files, etc.

Preferences
and Settings

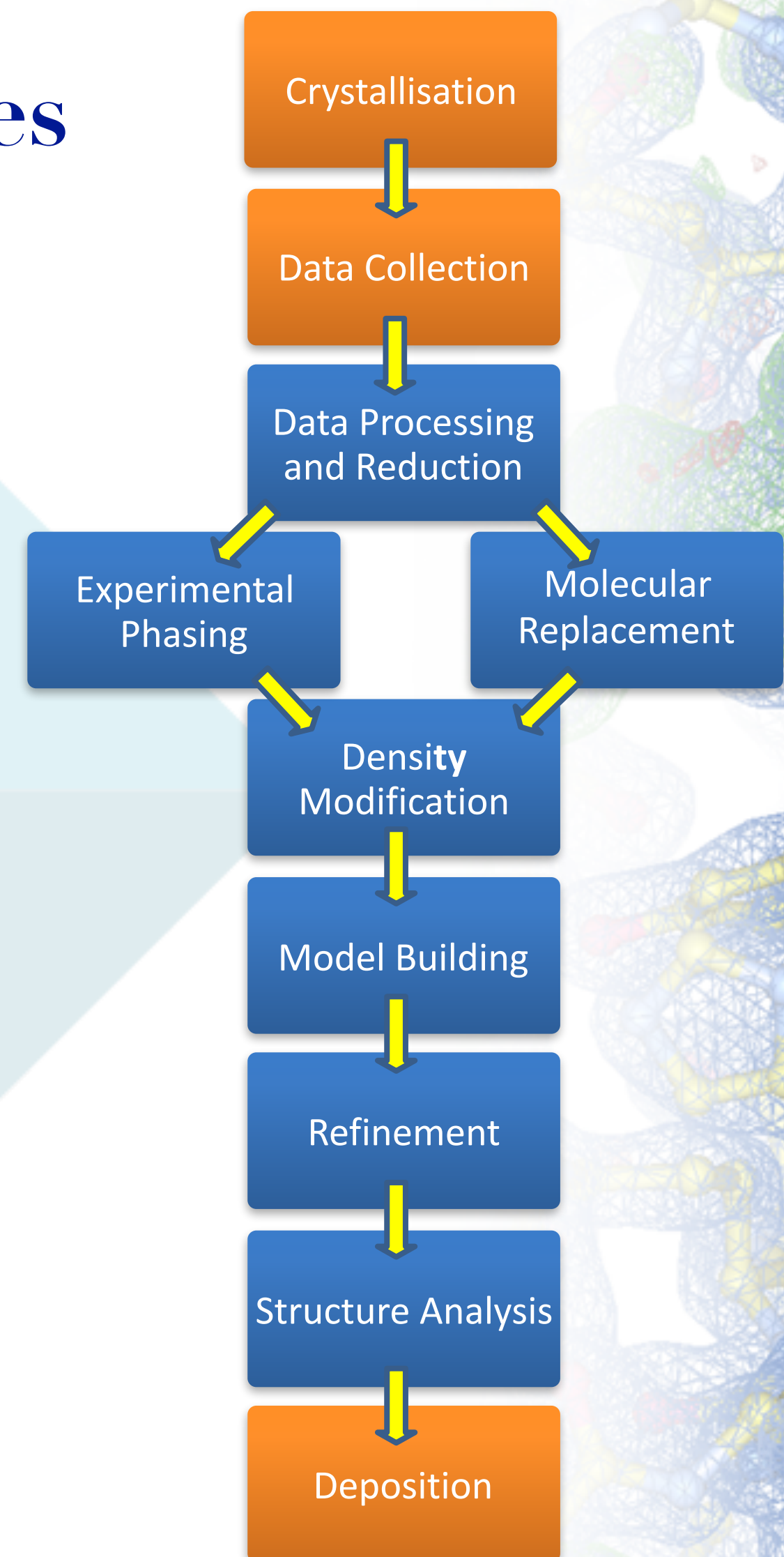
CCP4
Updates

From CCP4i(1) to CCP4i2



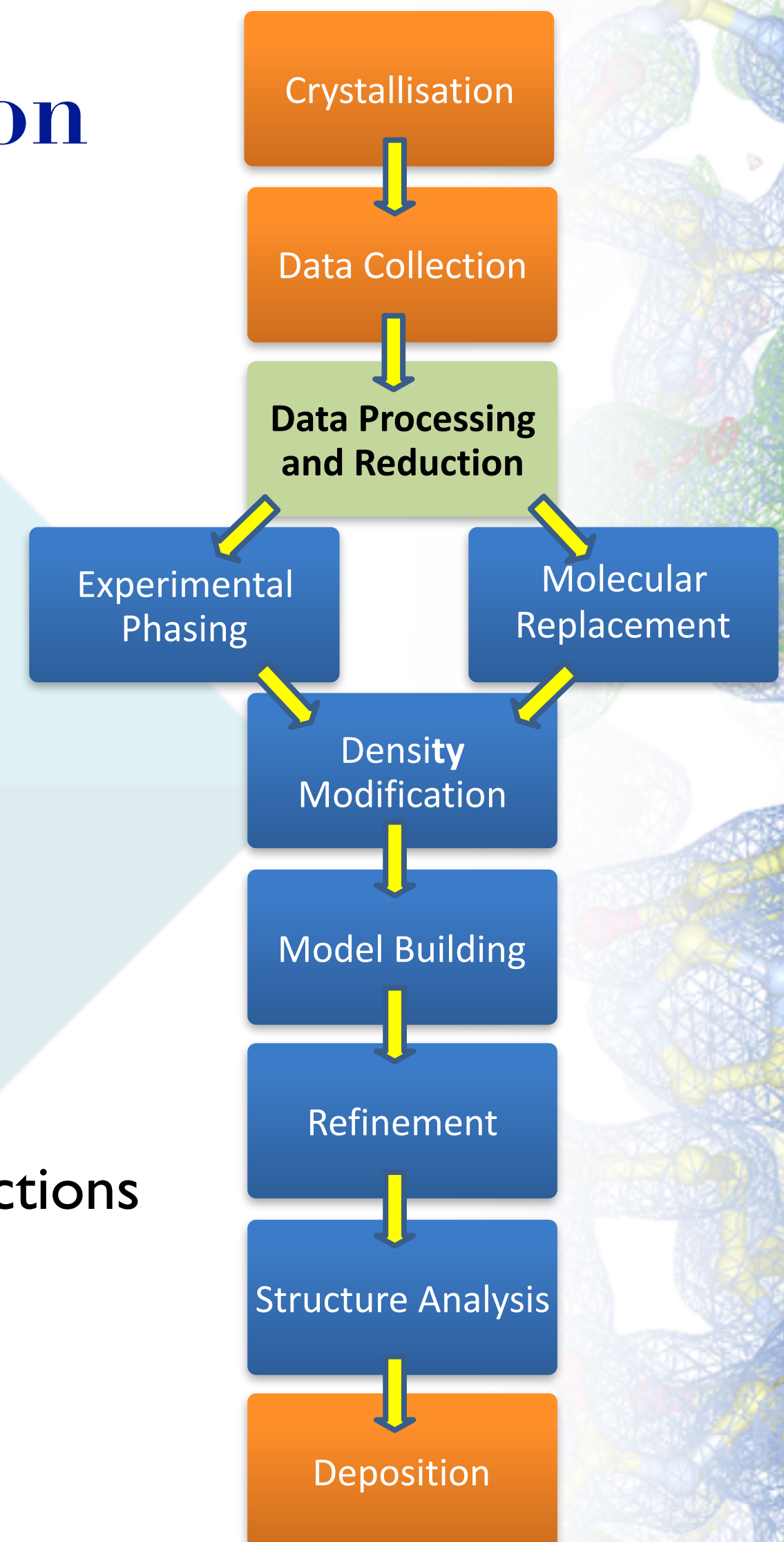
... one-way road

The Structure Solution Stages

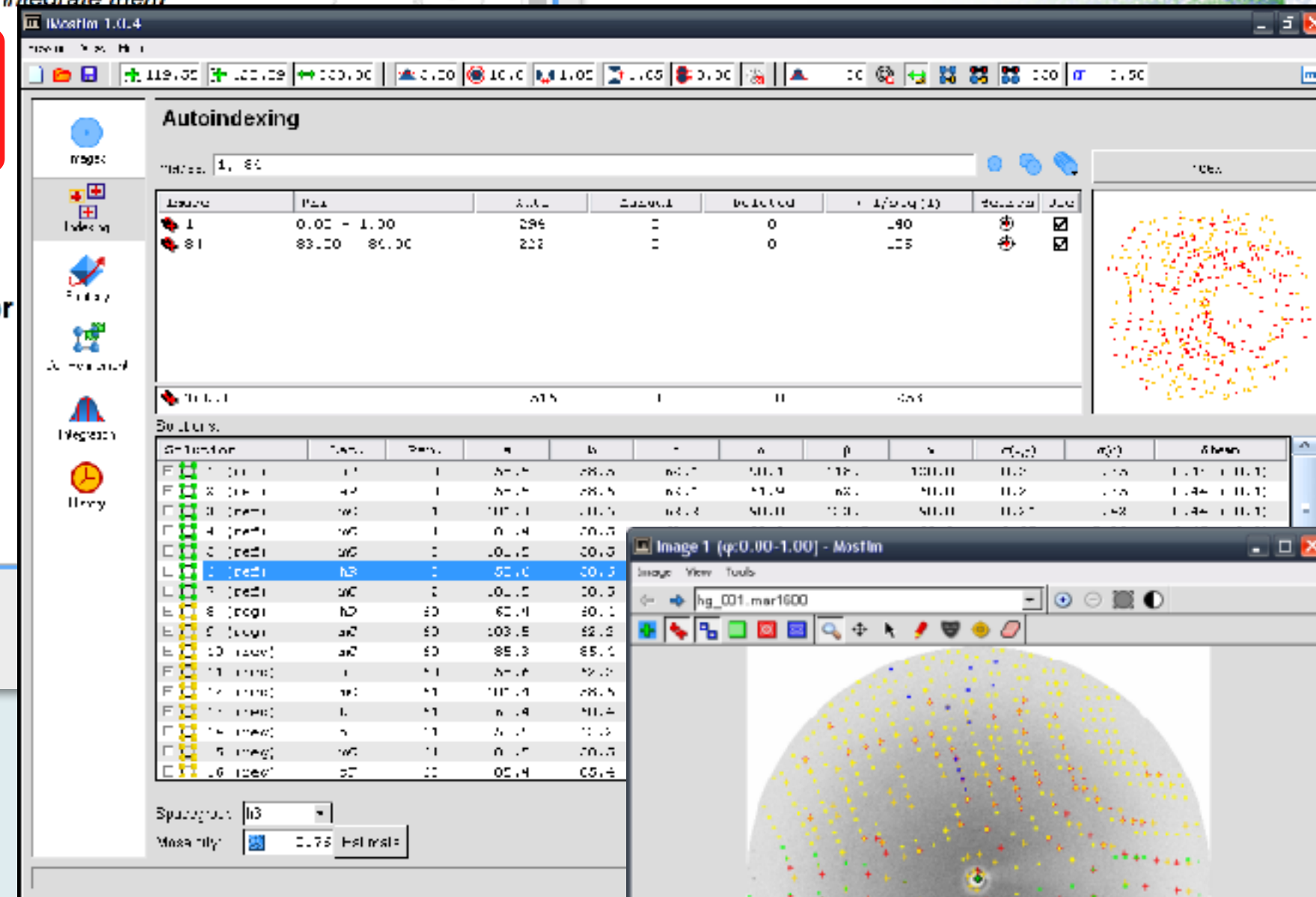
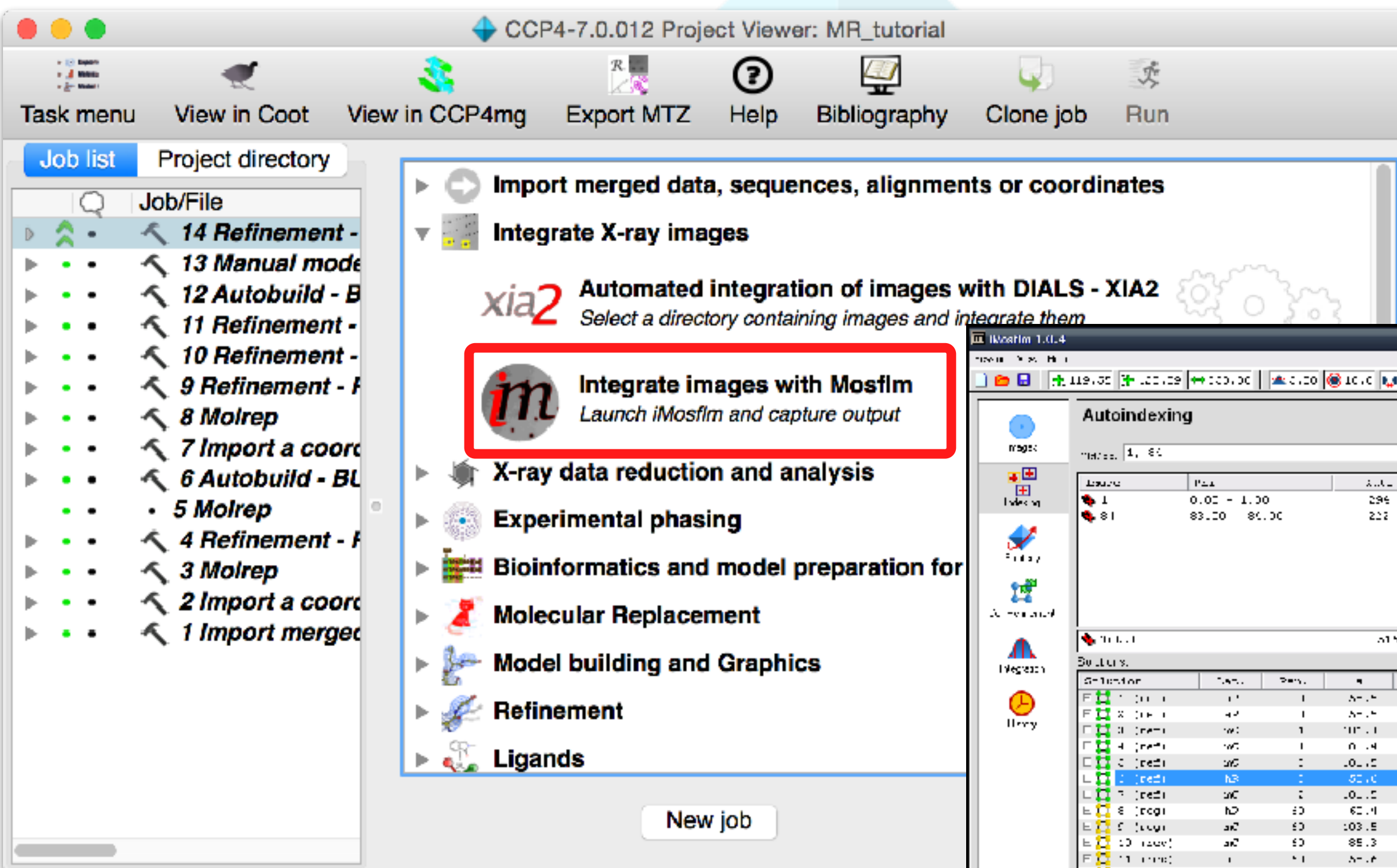


Data Processing and Reduction

- Data Processing:
 - ~ Calculate intensities from images
 - ~ Initial estimation of space group and cell parameters (indexing)
 - ~ Look for problems in images
 - ◆ multiple lattices,
 - ◆ weak reflections
 - ◆ mosaicity
 - ◆ anisotropy
- Data Reduction: Scaling and merging
 - ~ Scale and merge multiple observations of reflections
 - ~ Assignment of point group/space group
 - ~ Look for problems in images
 - ~ Calculate structure factor amplitudes



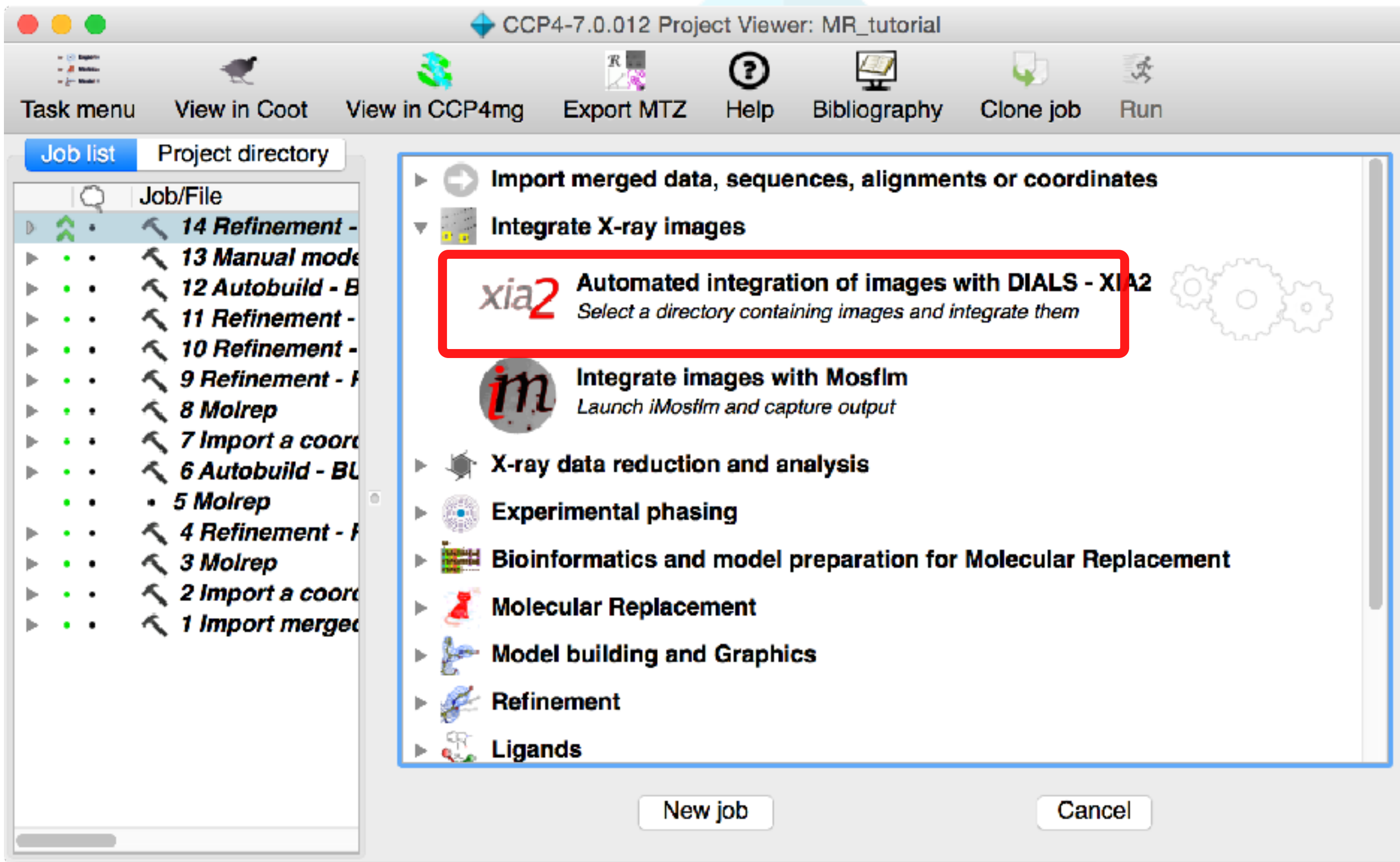
Data Processing



iMosflm

Integration of diffraction spots
including indexing

Data Processing



xia2

DIALS: Integration of diffraction spots and indexing; also available through Xia-2 pipeline

Xia-2: Expert knowledge-based, decision-making system for automated data processing from images to merged MTZ file. Uses DIALS and XDS.

Data Reduction

Pointless

- Determines point-group (and space group)

Aimless

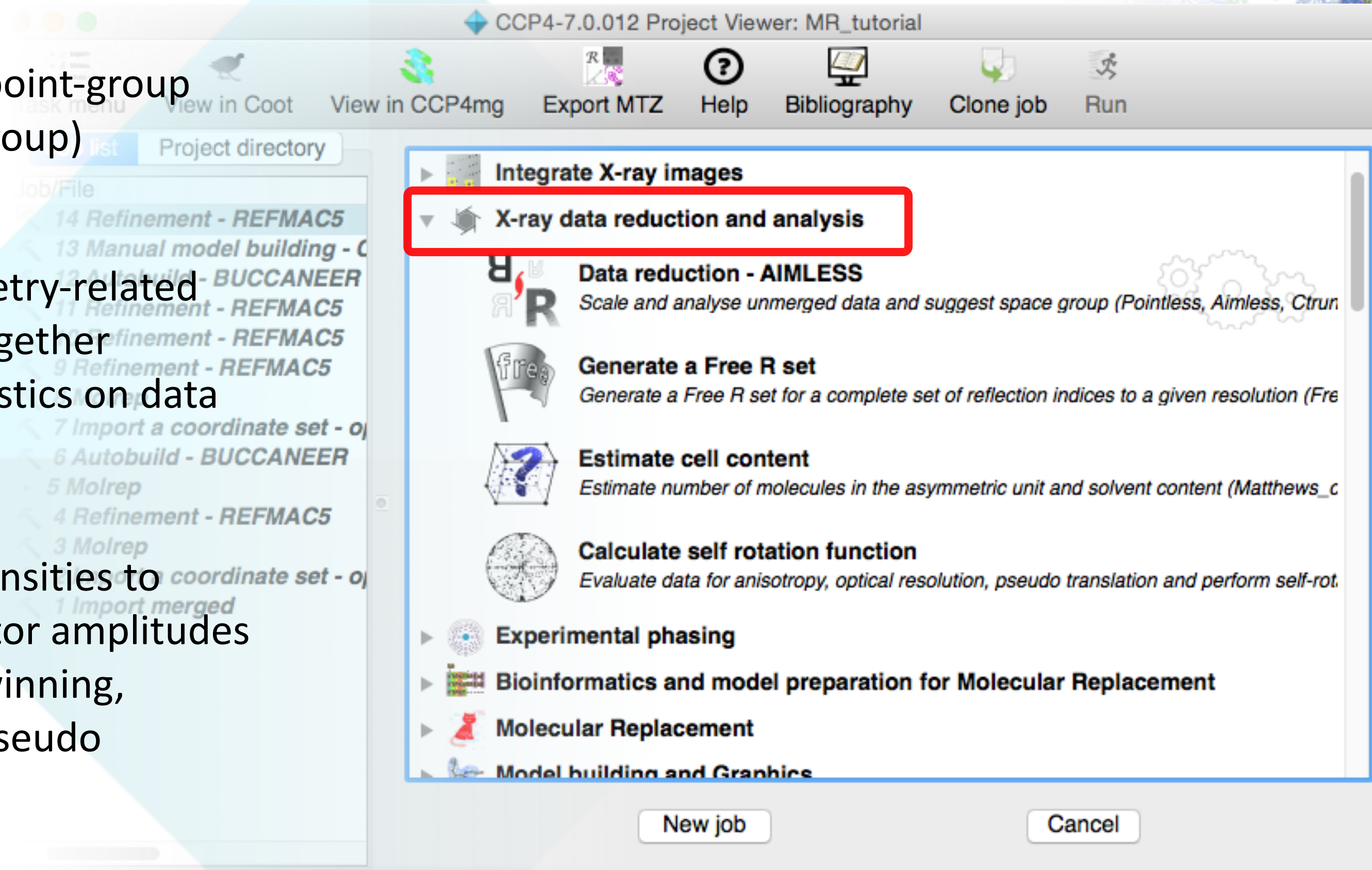
- Scales symmetry-related intensities together
- Produce statistics on data quality

Ctruncate

- Converts intensities to structure factor amplitudes
- Checks for twinning, anisotropy, pseudo symmetry

SFcheck

- Analyses data and check for problems – postscript report



Phasing

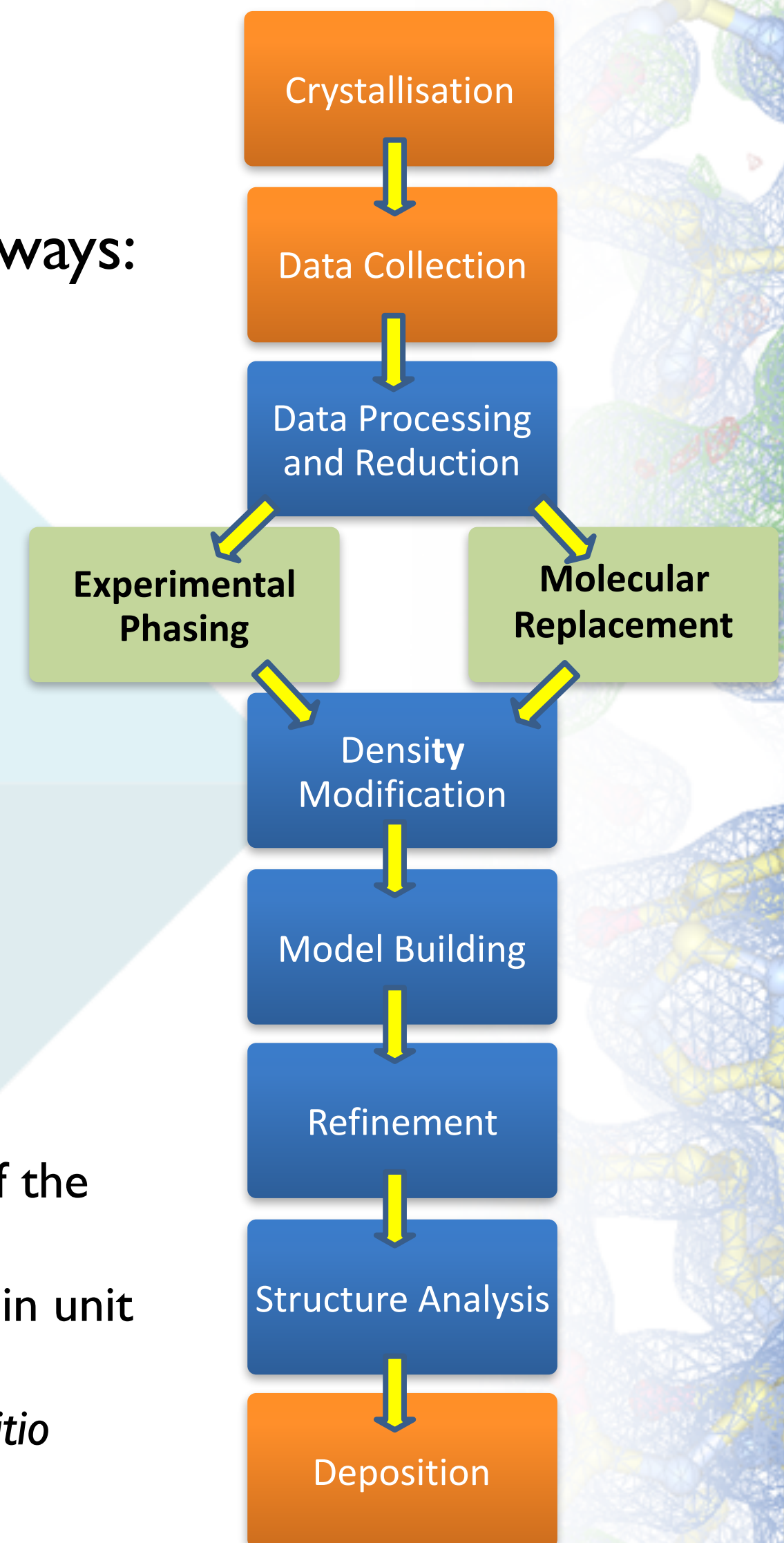
- Phase information may be derived in two main ways:

- *Experimental phasing:*

- ~ collect multiple data sets with anomalous or isomorphous differences or differences produced by radiation damage
- ~ Determine the differences in atomic structure which lead to the differences in observations — usually a heavy atom substructure
- ~ Refine the parameters of the substructure and use the observations and the substructure to estimate phases

- *Molecular Replacement:*

- ~ Use the structure of an already solved, homologous macromolecule as a first approximation for the phases of the target
- ~ Requires correct repositioning of homologous structure in unit cell of target
- ~ Can also generate homologue from sequence using *ab initio* modelling



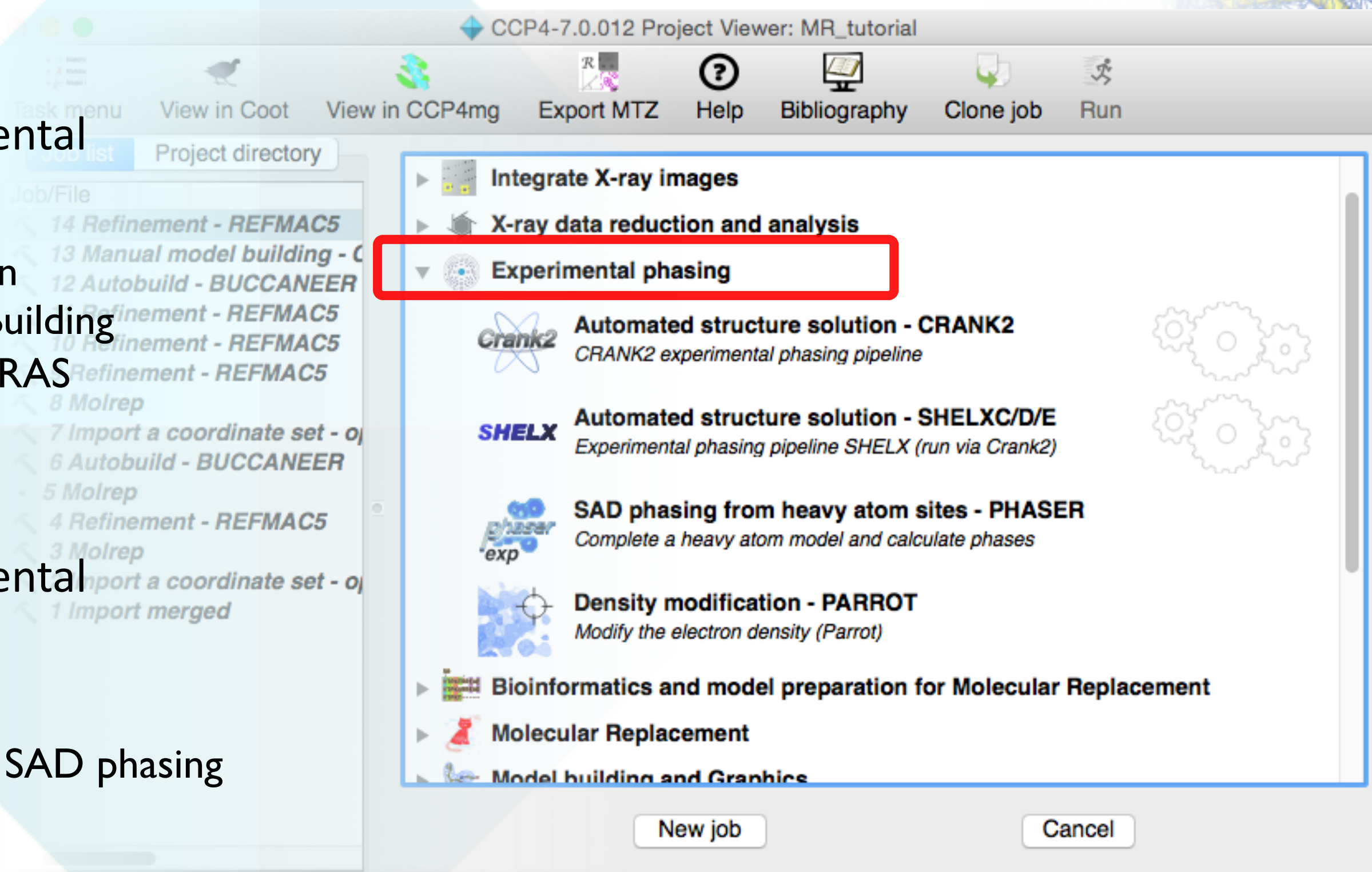
Experimental Phasing

Crank2 & SHELX

- Automated experimental phasing pipelines
 - ~ Heavy atom location through to Model Building
 - ~ SAD(-MR), MAD, SIRAS

Phaser EP

- Automated experimental phasing
 - ~ SAD phasing
 - ~ Combined MR and SAD phasing



Molecular Replacement

Phaser MR

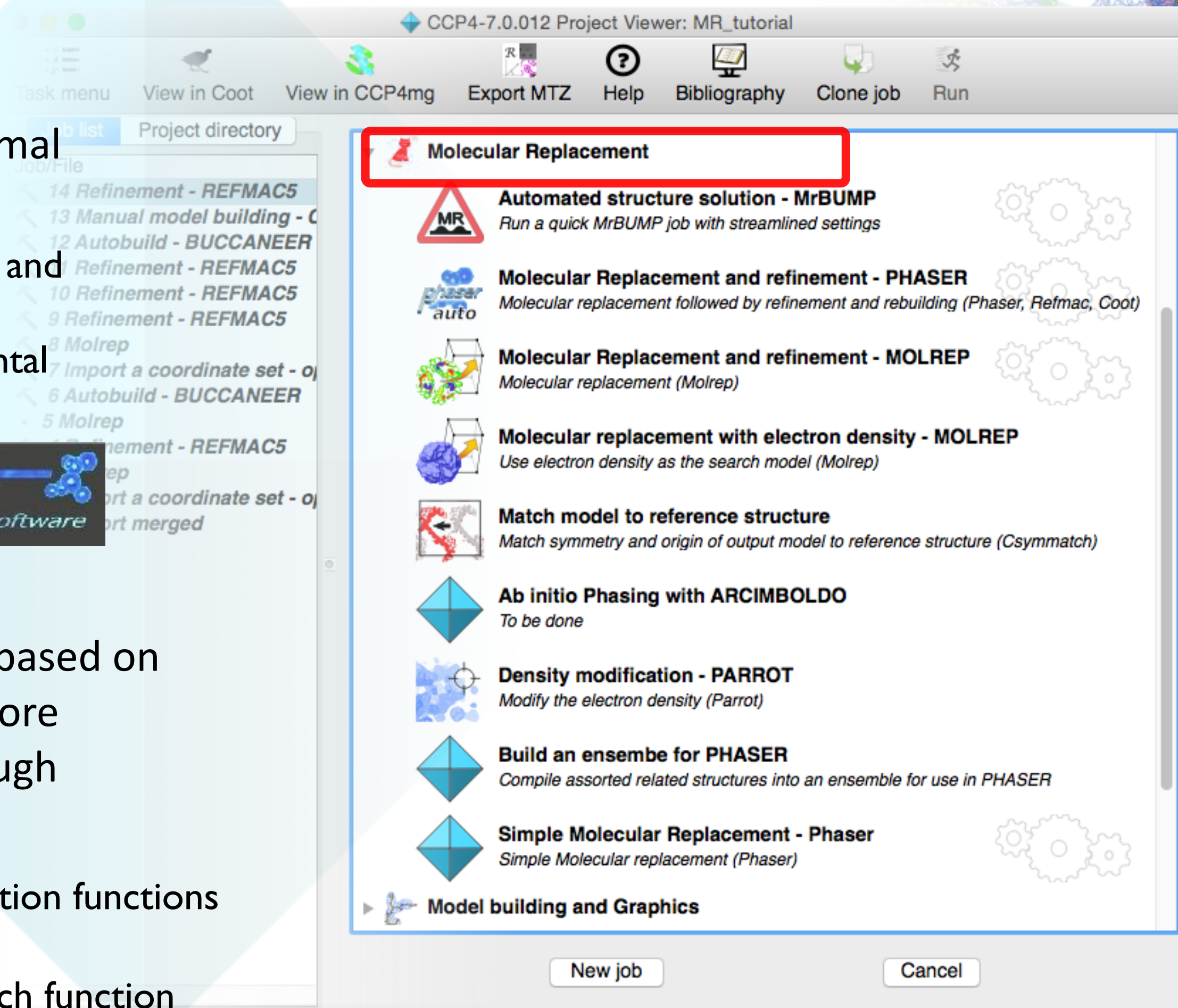
- Automated molecular replacement using Maximal Likelihood method

- ~ Sophisticated workflow and decision making
- ~ Accounts for experimental and model errors



Molrep

- Molecular replacement based on Patterson search with more manual interaction through specialised functions
- ~ Phased Translation/Rotation functions
- ~ Multi-copy search
- ~ Spherical averaging search function



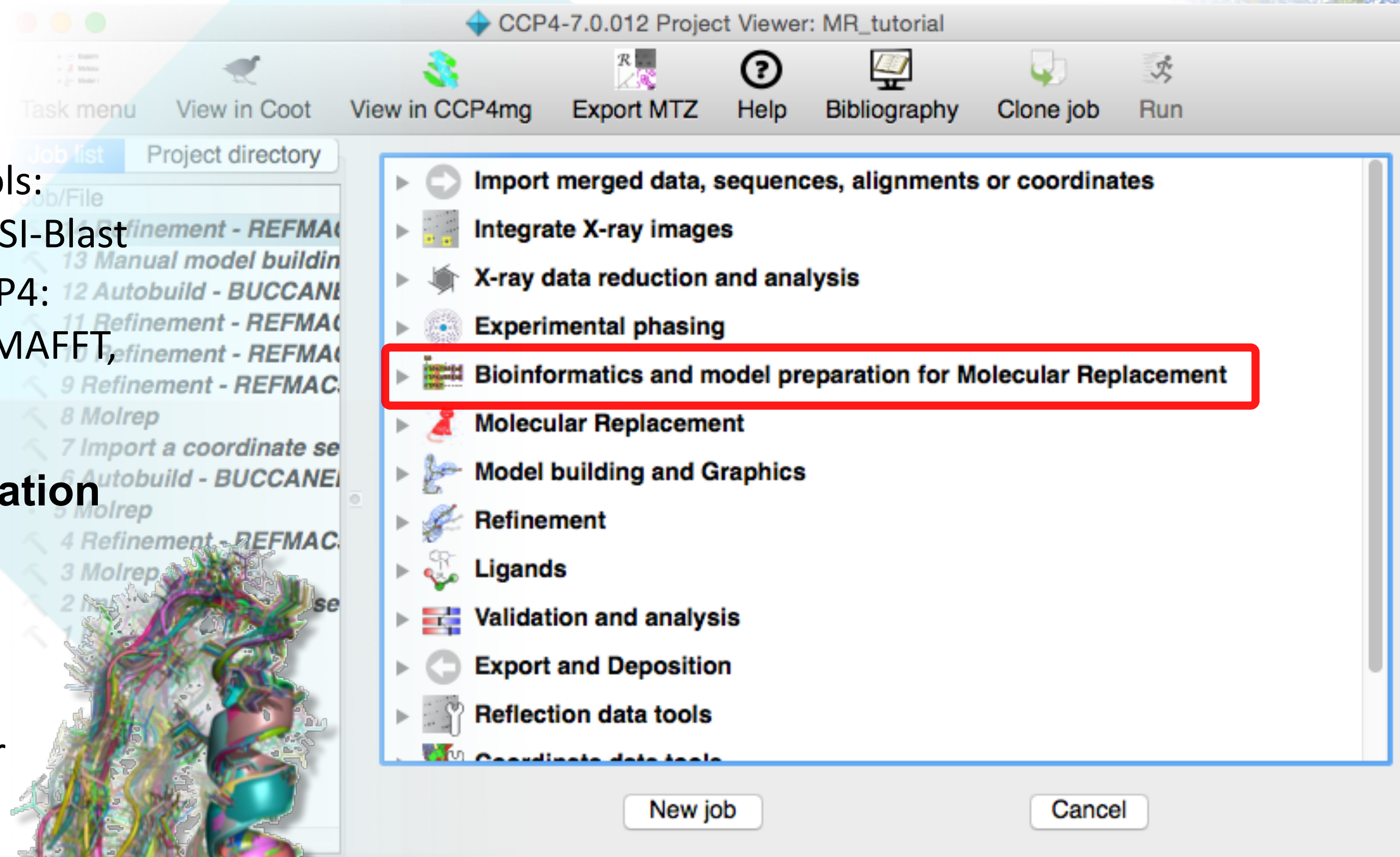
Searching for MR Models and Model Preparation

Model search

- Online tools:
HHpred, PSI-Blast
- Within CCP4:
Phmmer, MAFFT,
Clustalw

Model preparation

- Molrep
- Chainsaw
- Sculptor
- Ensembler



Automatic Molecular Replacement

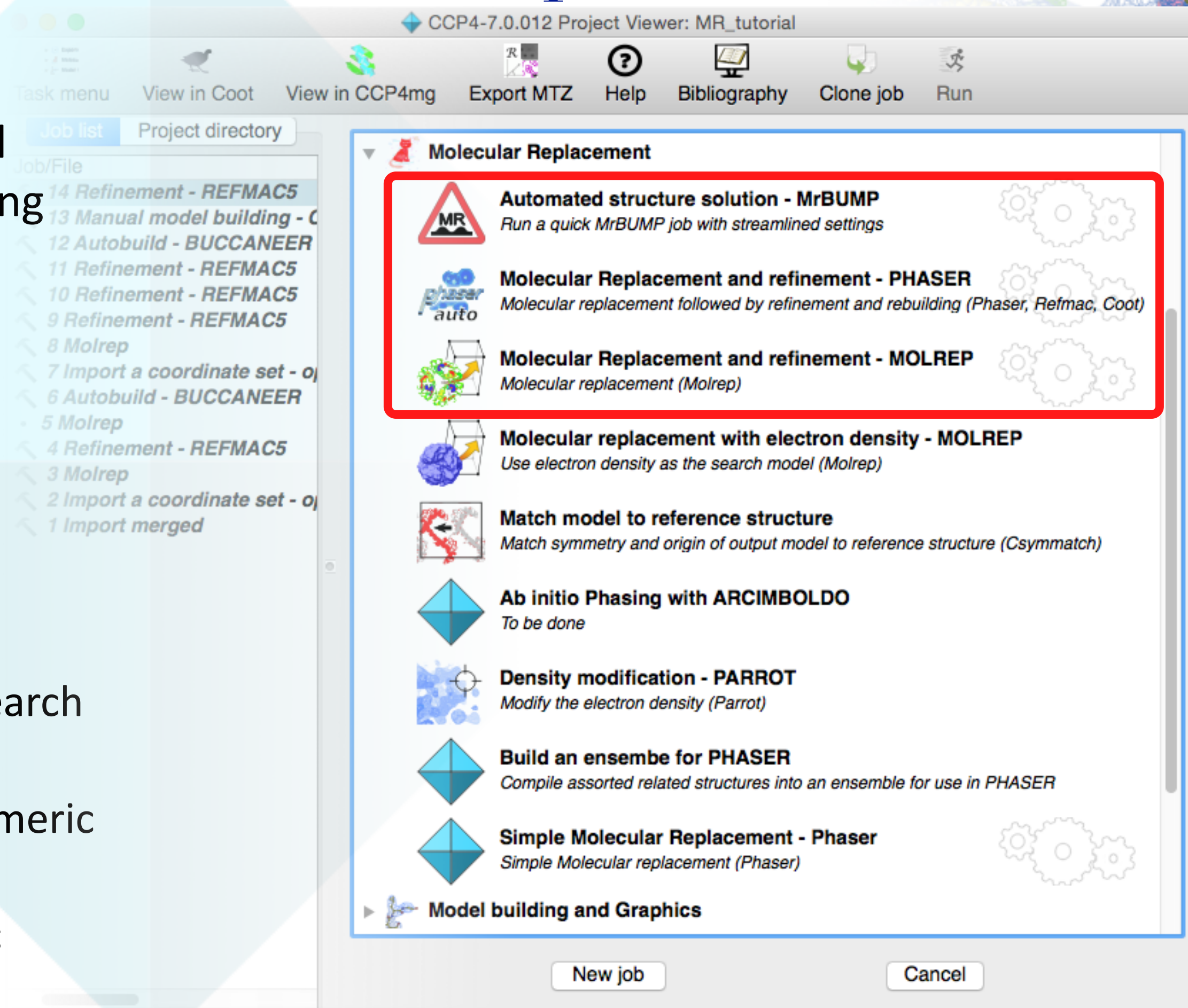
From model search and preparation through to initial refinement and model building

MrBUMP

- Online model search
- Uses Phaser and Molrep

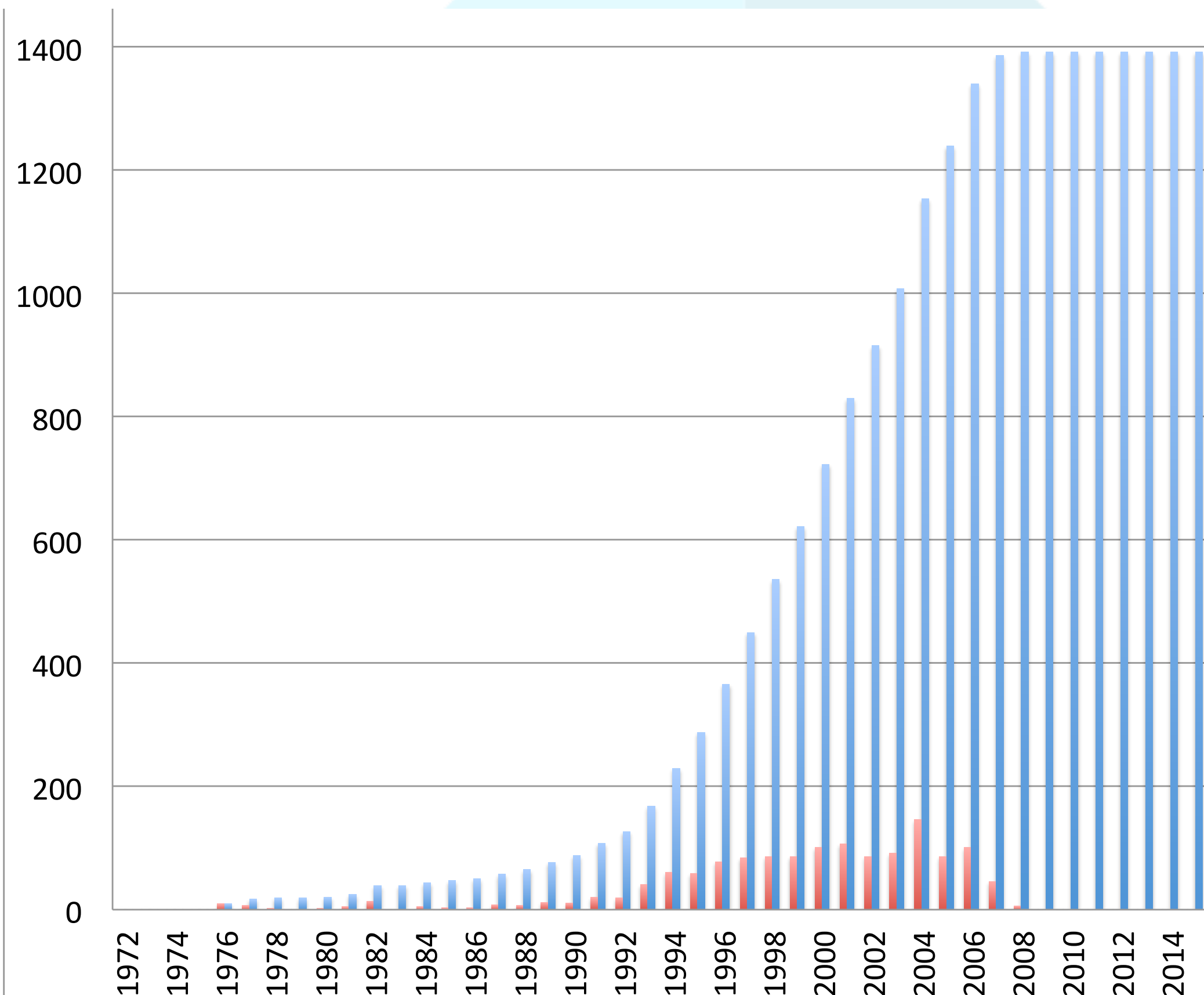
BALBES

- Custom database with search models
- Capable of making multimeric models (uses PISA)
- Uses Molrep and Refmac



The Protein Data Bank (PDB)

- Currently over 110,000 structures (90,000 X-ray structures)
- For an X-ray crystallographer, a treasury of models for MR



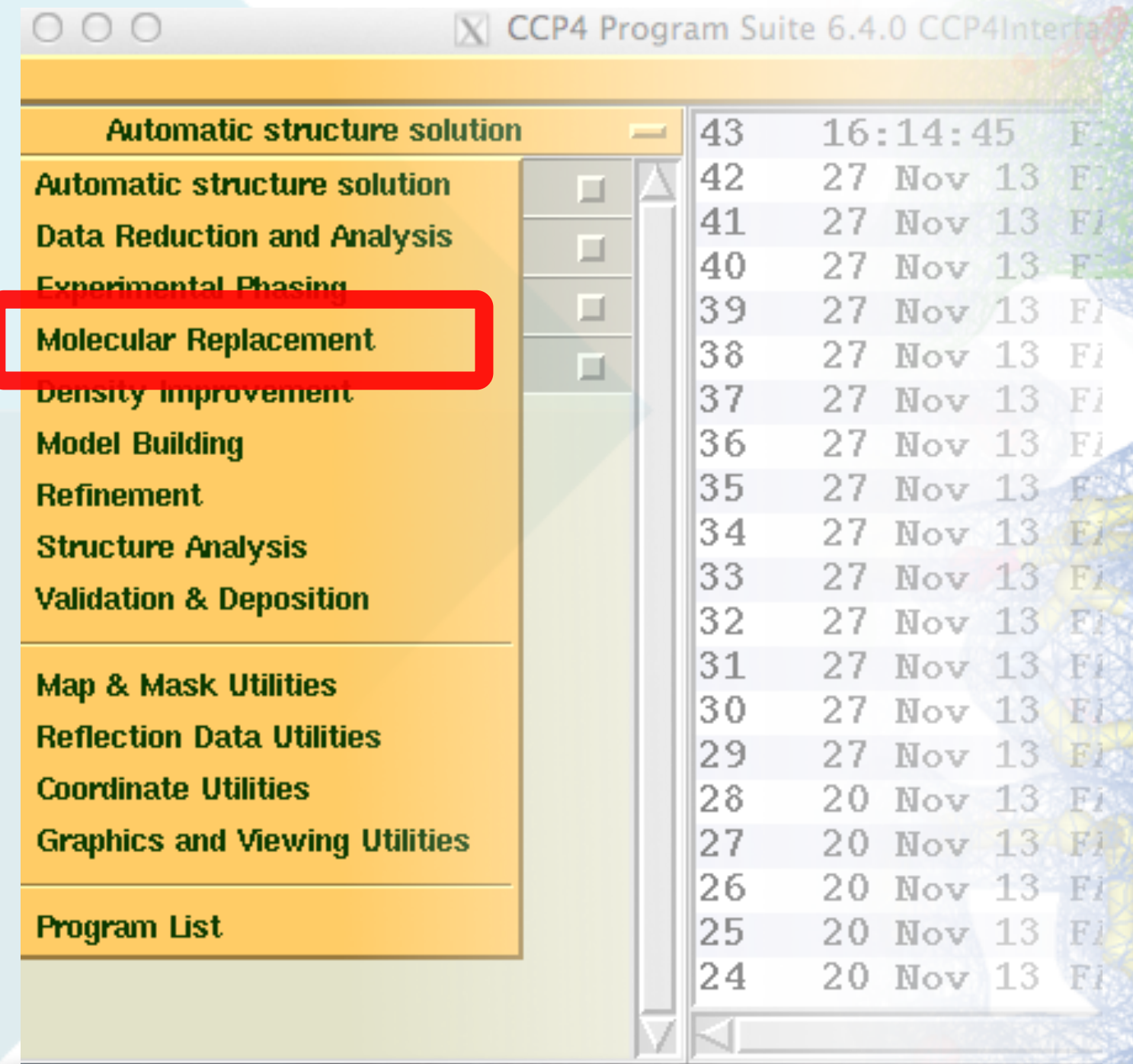
Chothia C: *One thousand families for the molecular biologist. Nature* 1992, **357**: 543-544.

MR is the dominating phasing method in today's protein crystallography

Ab initio Modelling for Molecular Replacement

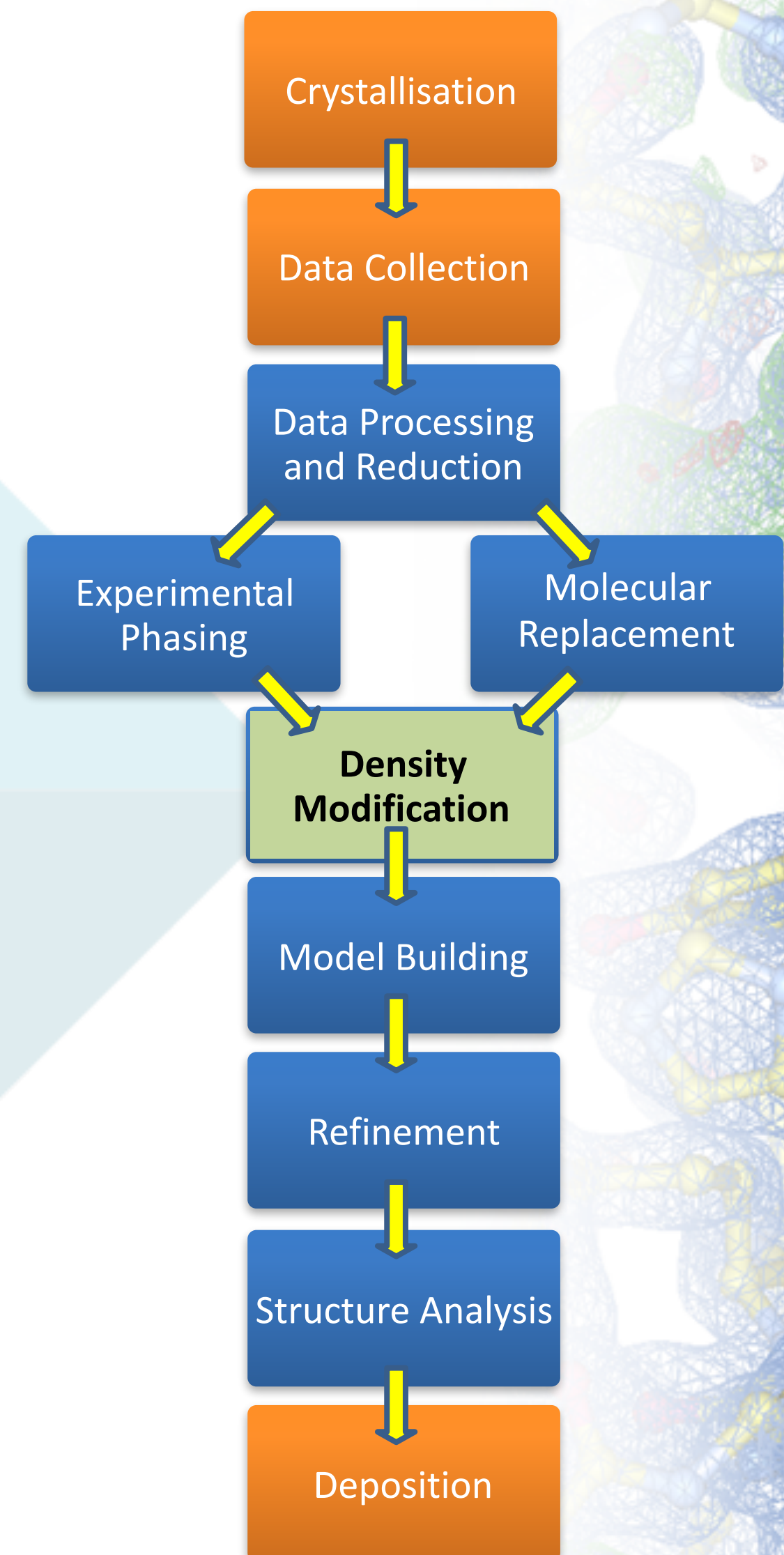
AMPLE

- Generate and prepare *ab initio* or *de novo* models using Rosetta or Quark software for use as search models in molecular replacement
- Works well for smaller, α -helical proteins (<120 residues), but has been known to work for larger targets

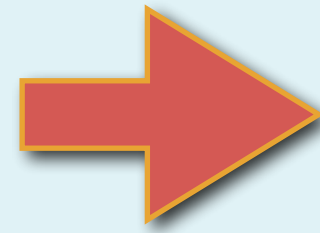


Density Modification

- A tool for phases improvement
- *Traditional approaches:*
 - ~ NCS averaging
 - ~ Histogram matching
 - ~ Solvent flattening
 - ~ Phase combination
 - ◆ Experimental phases
 - ◆ Phases from modified map
 - ~ Iterative procedure
- *Statistical approaches:*
 - ~ Improved phase probability distributions
 - ~ Removes bias
 - ~ Slower than traditional approaches



Density Modification



- DM can be perfect if noise is genuinely statistical (never the case)
- Otherwise, DM is equivalent to bringing in additional data
- Imperfectness can potentially lead to artefacts
- Existing programs are robust and DM is known to work

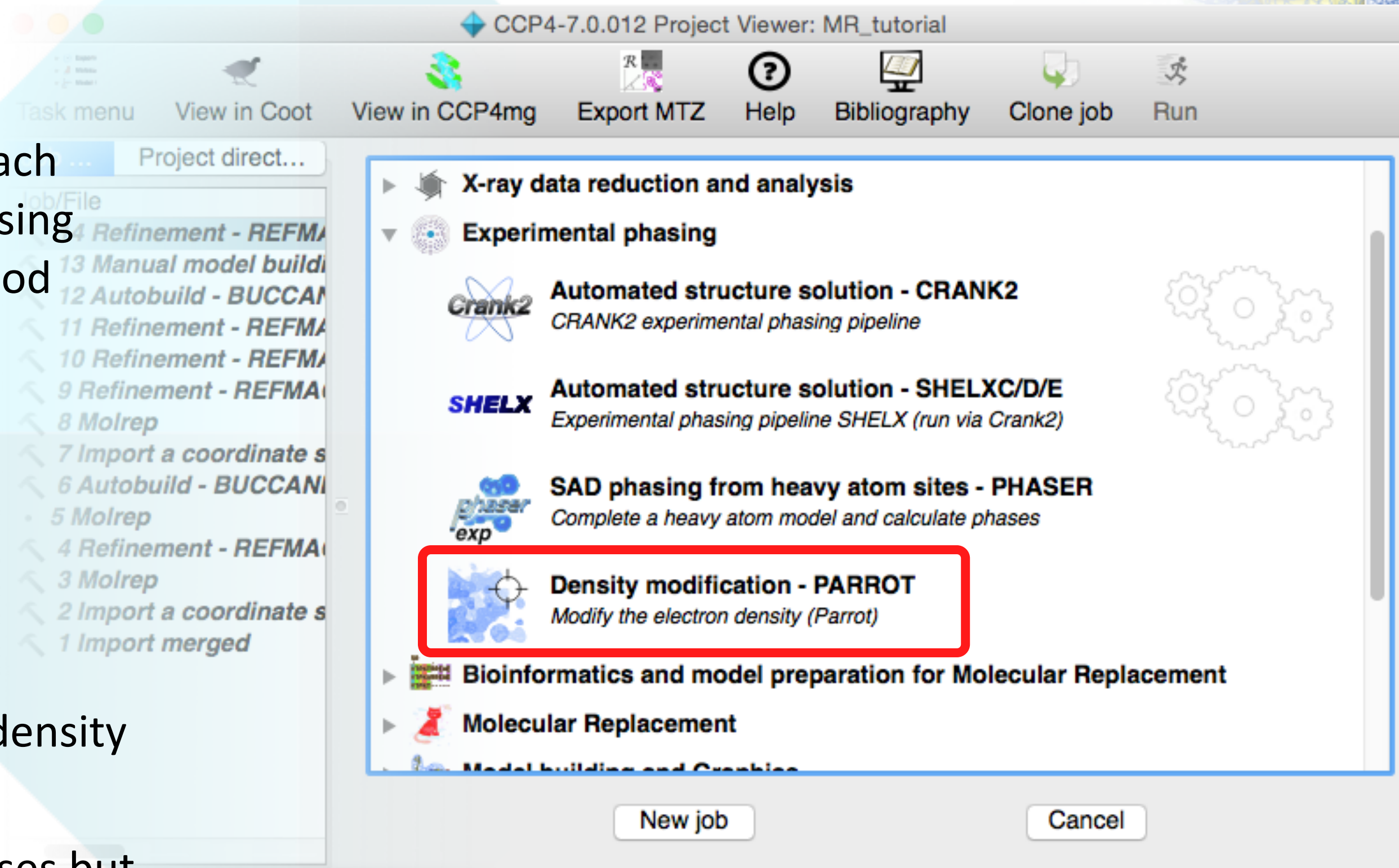
Density Modification Tools

Parrot

- Traditional approach benefiting from using maximum likelihood methods
- Fast and fully automated

Pirate

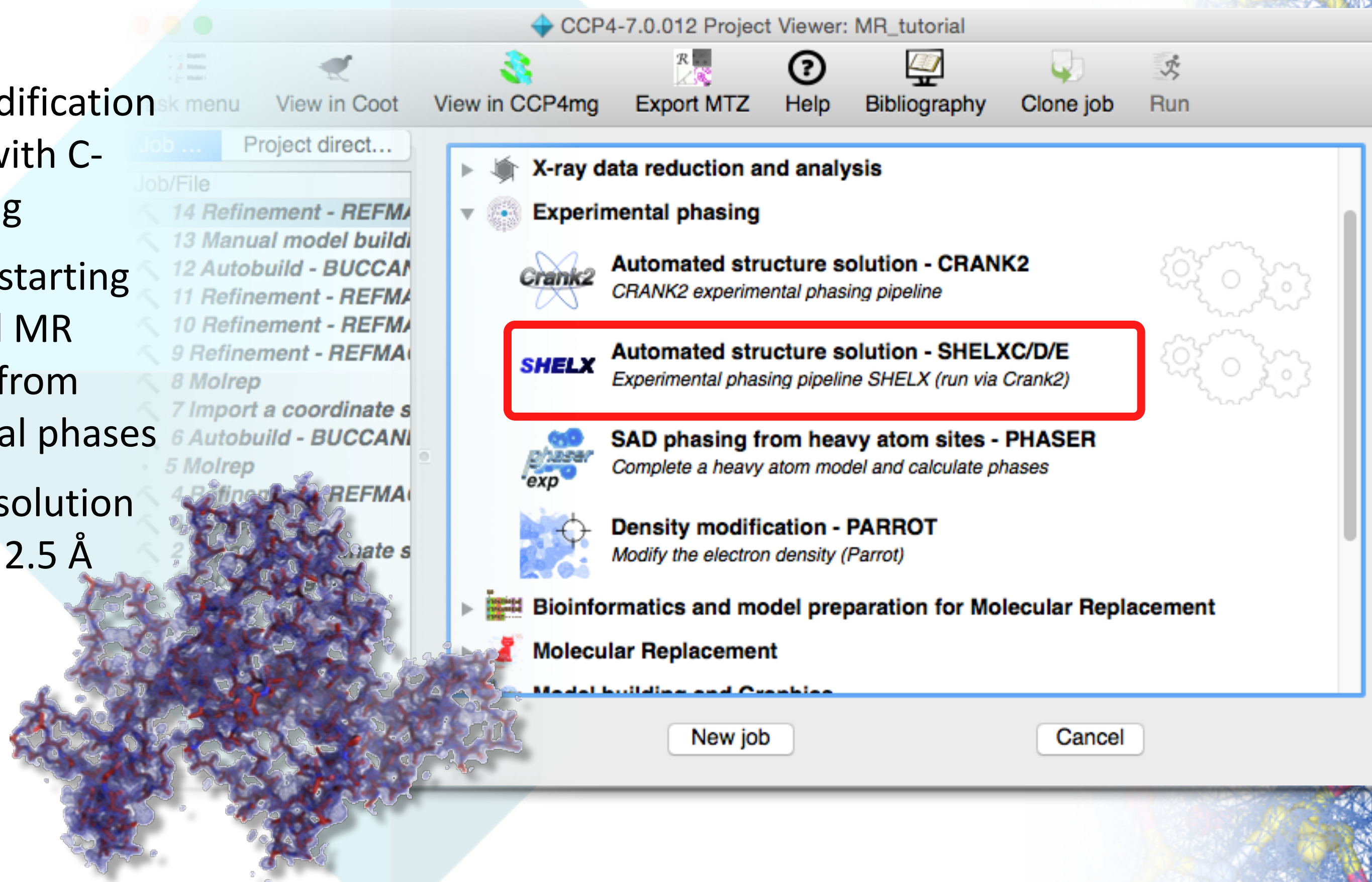
- Statistical-based density modification
- Better in some cases but slower than Parrot



Density Modification Tools

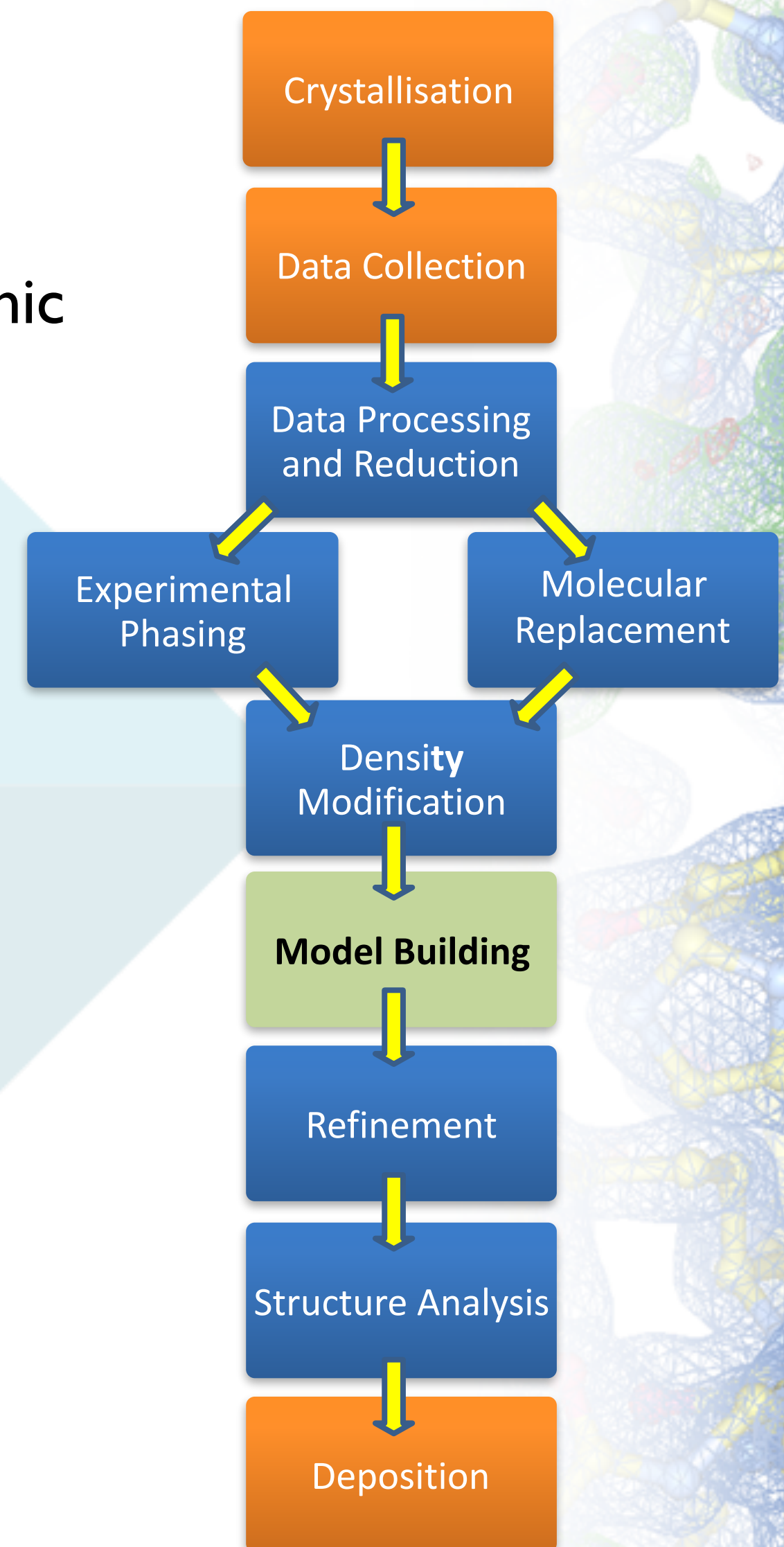
SHELXE

- Density modification combined with C-alpha tracing
- Works well starting from partial MR solution or from Experimental phases
- Requires resolution better than 2.5 Å



Model Building

- Interpret electron density map in terms of atomic coordinates
 - ~ X-ray experiment and phasing yield the electron density map
 - ~ Model's atom need to be put in the correct locations of the map
 - ~ The process is aided by the chemical knowledge of residue structure, as well as secondary structure assignments
 - ~ Validation tools are essential for choosing the right electron density interpretation:
 - ◆ Quality of density fit
 - ◆ Ramachandran restraints
 - ◆ Geometry analysis
- Try to account for as much of the density as possible including solvent molecules



Model Building Tools

Buccaneer

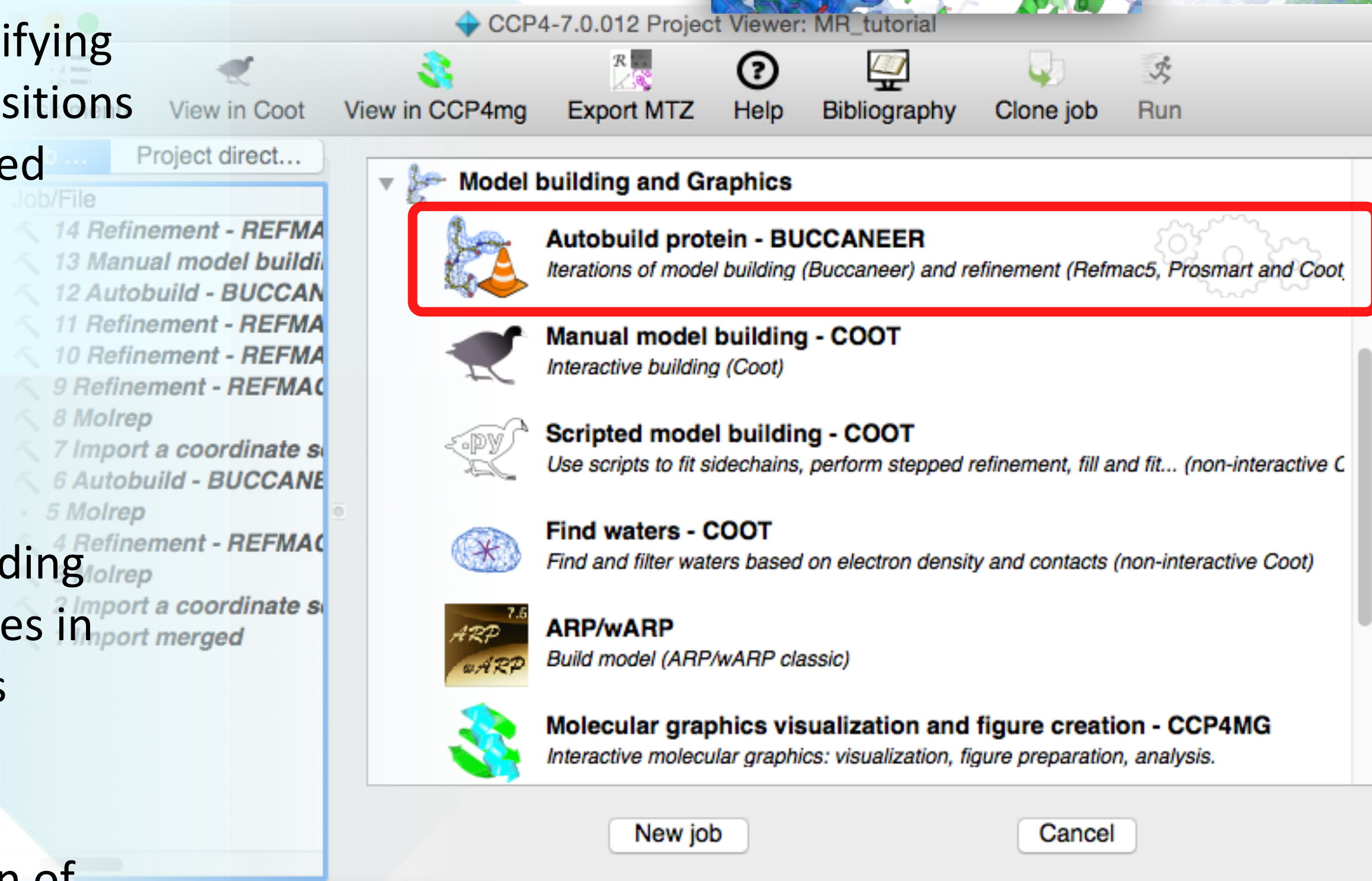
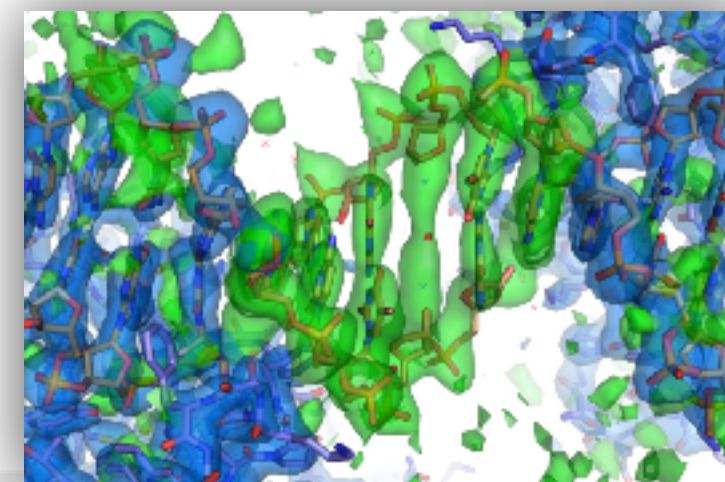
- Chain tracing by identifying connected C-alpha positions using a likelihood-based density target
- Low-resolution model building

Nautilus

- Automatic model building of nucleotide structures in electron density maps

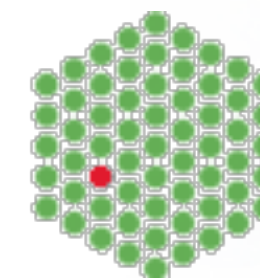
Privateer

- Building and validation of carbohydrates



Model Building Tools

EMBL

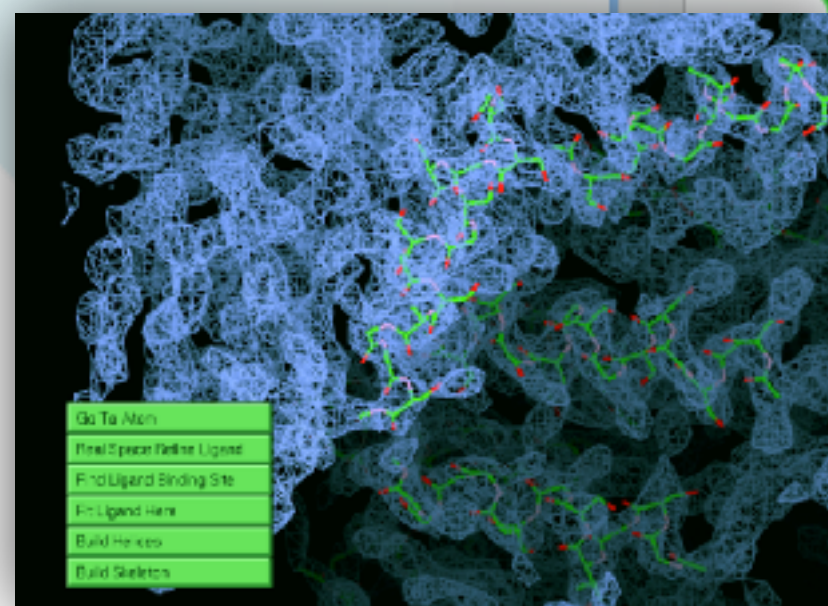
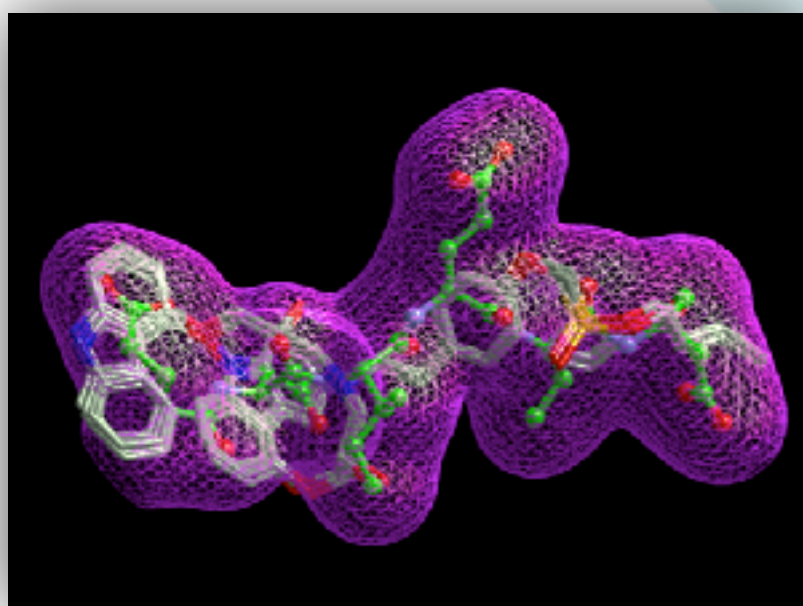
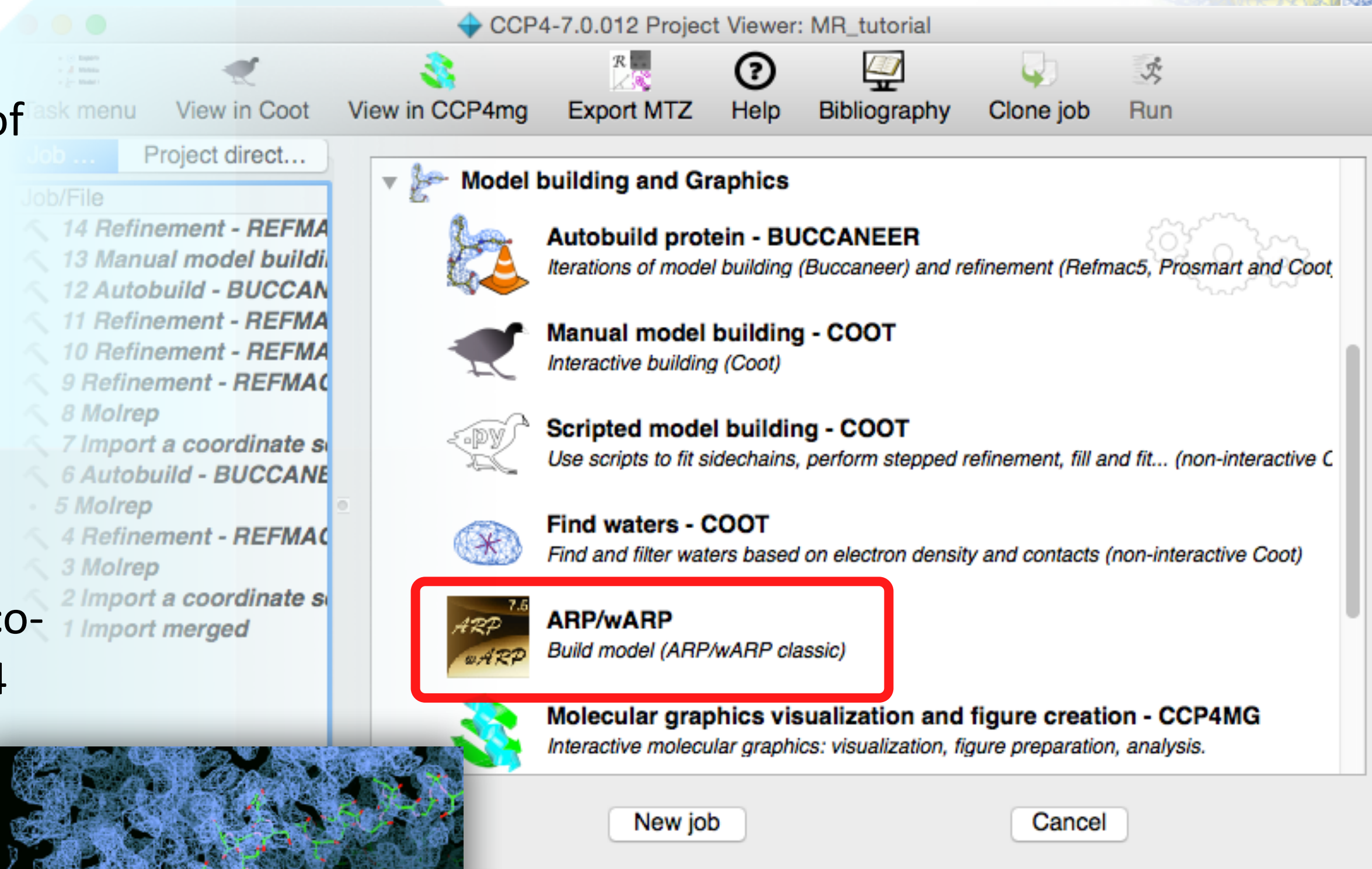


Arp/wArp 7.6

- Automated building of

- ~ proteins
- ~ RNA/DNA
- ~ secondary structure
- ~ side chains
- ~ loops
- ~ solvent
- ~ ligands

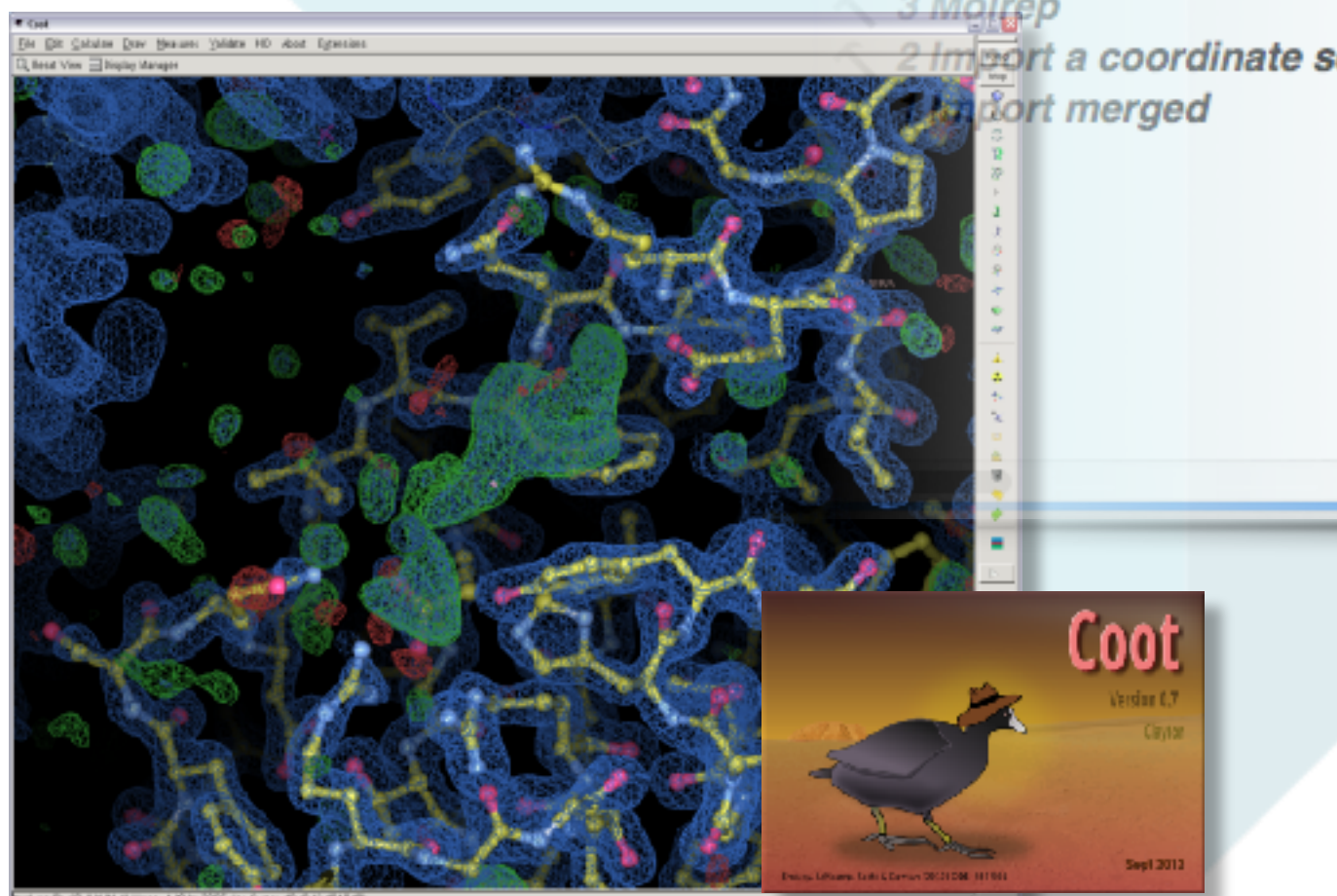
- Now integrated and co-distributed with CCP4



Model Building Tools

Coot 0.8.8

- Manual and semiautomatic model building
- Interactive graphics
- Ligand building and fitting
- Real-space refinement
- Paired with Refmac and jLigand
- Wealth of validation tools
- Integrated with CCP4



CCP4-7.0.012 Project Viewer: MR_tutorial

Task menu View in Coot View in CCP4mg Export MTZ Help Bibliography Clone job Run

Job ... Project direct...

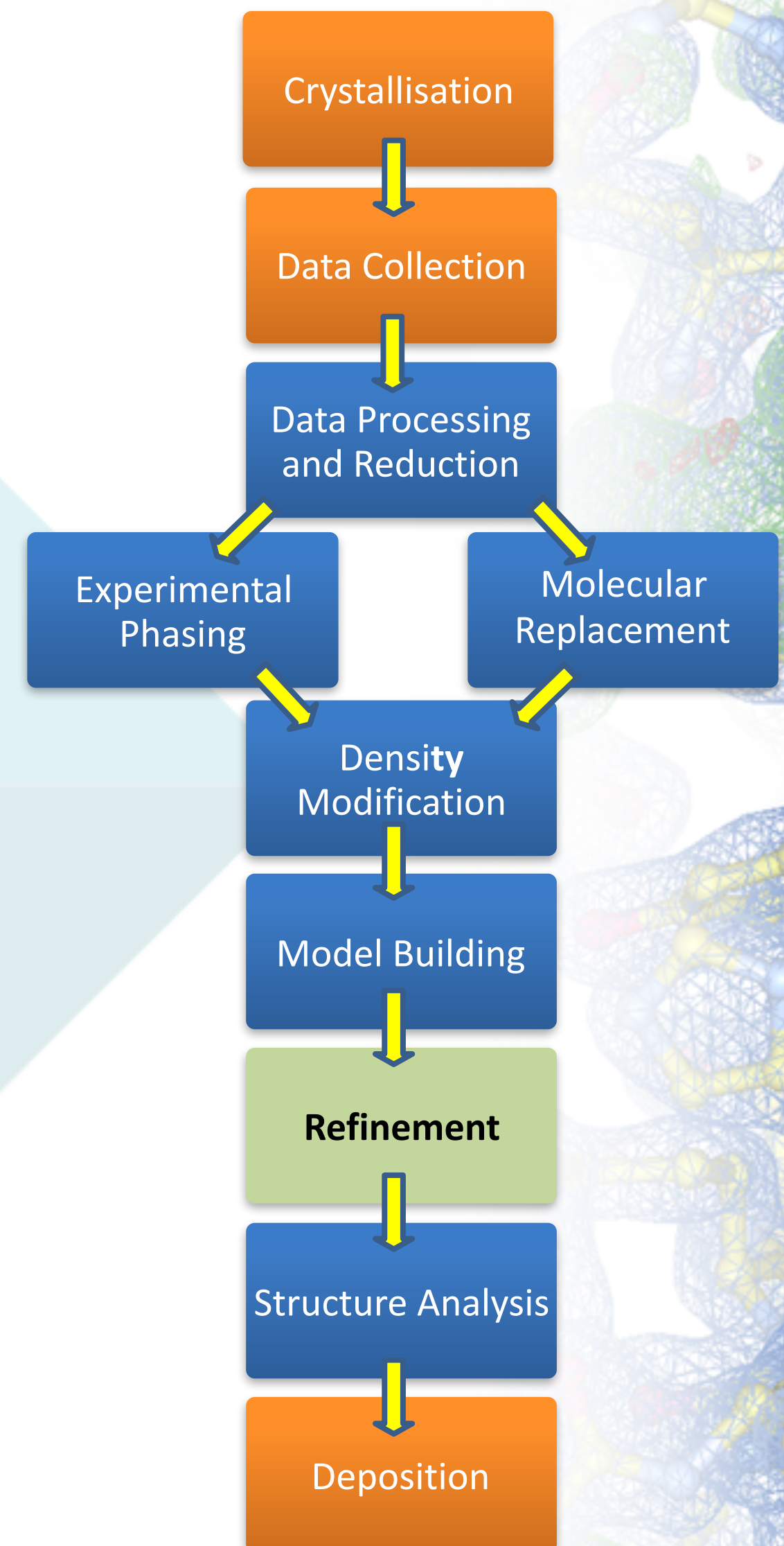
Model building and Graphics

- 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)
- ARP/wARP**
Build model (ARP/wARP classic)
- Molecular graphics visualization and figure creation - CCP4MG**
Interactive molecular graphics: visualization, figure preparation, analysis.

New job Cancel

Refinement

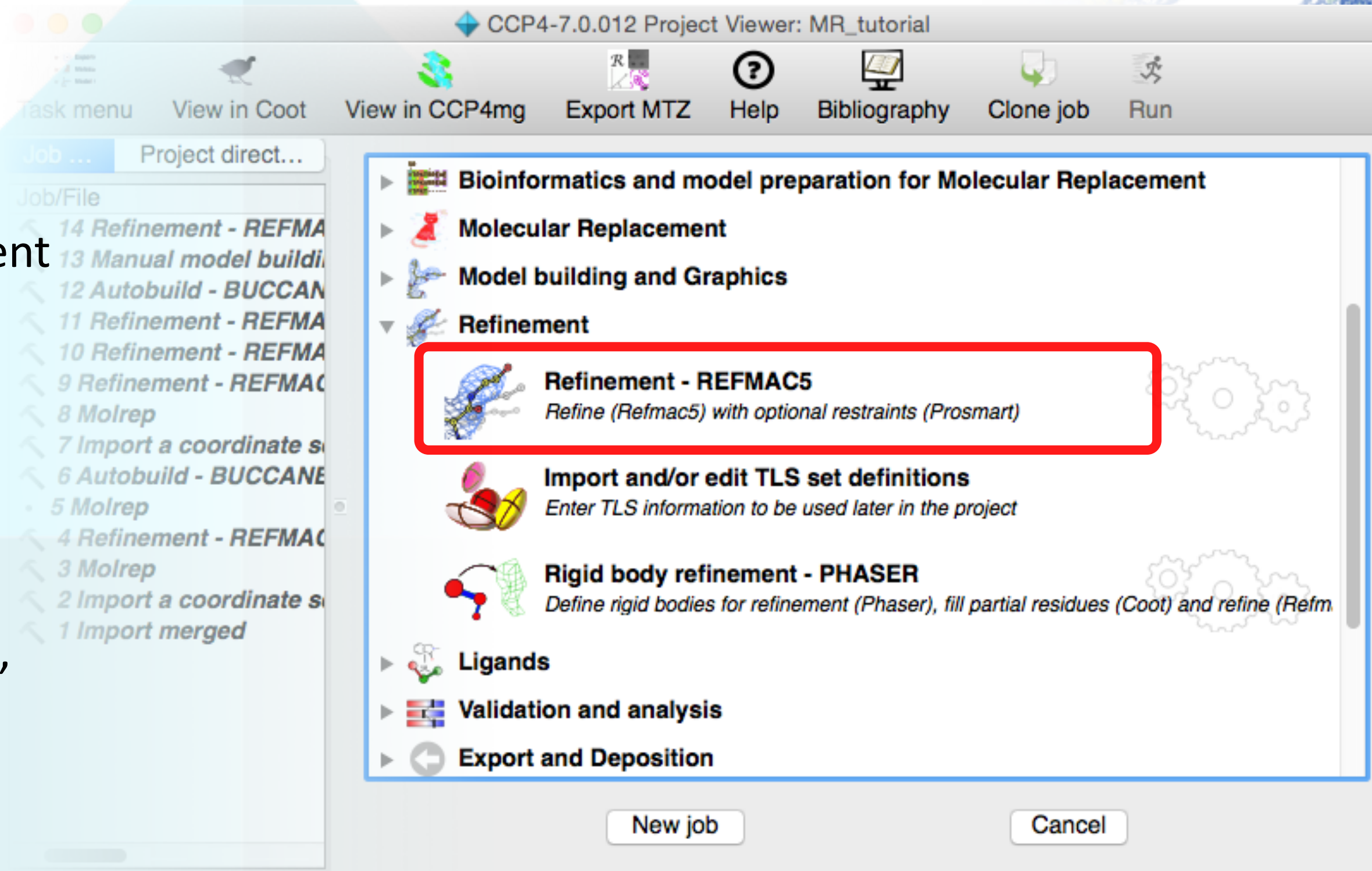
- Refinement is one of most important procedures in structure solution process
- Refinement is used mainly to
 - ~ produce a structure which is properly balanced between chemistry restraints and experimental observations
 - ~ improve density maps for further cycle of model building
- Refinement often uses additional information from various sources
 - ~ Phases
 - ~ Twinning (if detected)
 - ~ External restraints
 - ~ NCS restraints
 - ~ TLS groups



Refinement

Refmac 5.8

- CCP4's main refinement program
- Implements several likelihood target functions for experimental data (amplitudes, twinned data, external phases, Lattman coefficients)
- Restraints
 - ~ CCP4 monomer library
 - ~ Custom library
 - ~ External restraints

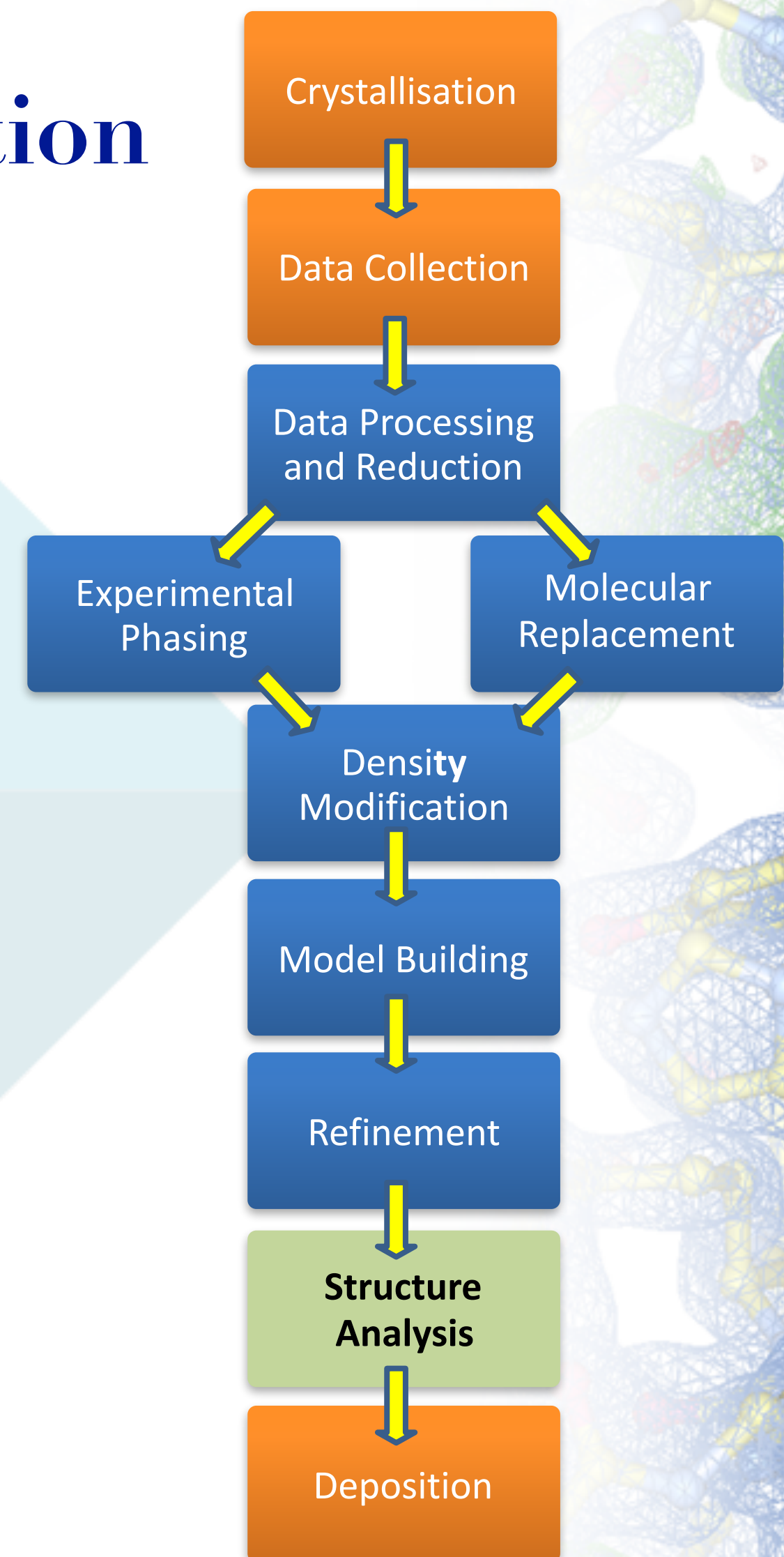


- Several refinement protocols
 - ~ Rigid body
 - ~ Restrained
 - ~ Jelly-body

- NCS refinement
 - ~ local
 - ~ global

Structure Analysis & Visualisation

- To find out structural features which may shed light on chemical activity or structure function
- Identification of complexes (quaternary structures)
- Finding and comparing structure homologues
- Visualise and inspect the target structure
- Can also be used earlier on in structure solution process
- ~ Provide information on complexes, domains, mobility of structure for use in molecular replacement or for construct design



PISA

- Automatic inference on multimeric states from crystal packing
- Analysis of macromolecular interfaces and macromolecular interactions
- Analysis of protein oligomerisation versus concentration

Structure Analysis

CCP4-7.0.012 Project Viewer: MR_tutorial

Job ... Project direct...

Job/File

- 14 Refinement - REFMA
- 13 Manual model buildi
- 12 Autobuild - BUCCAN
- 11 Refinement - REFMA
- 10 Refinement - REFMA
- 9 Refinement - REFMA
- 8 Molrep
- 7 Import a coordinate s
- 6 Autobuild - BUCCANE
- 5 Molrep
- 4 Refinement - REFMA

Ligands

Validation and analysis

- Analyse agreement between model and density - EDSTATS**
Calculates real-space metrics for evaluating the agreement between model and density
- Validation of carbohydrate structures - PRIVATEER**
Checks stereochemistry, conformation and fit to positive omit density, and describes gl
- Interface and quaternary structure analysis - PISA**
Interface and assembly analysis (qtpisa)
- Analyse model geometry**
Calculate mean B-factors, Ramachandran plots and other metrics to aid in validation (C

Export and Deposition

- Reflection data tools
- Coordinate data tools

New job Cancel

QtPISA 1.12 25/06/2012 [PDB => 1nio]

Assembly summary

Multimeric state	2	Surface area, sq. Å	6561404.6	Free energy of dissociation, kcal/mol	0910.2
Copies in Unit Cell	2	Buried area, sq. Å	561296.4	Entropy of dissociation, kcal/mol	71.5
Symmetry number	2				

Formula A(2)
Composition A(2)
Dissociation pattern 2{A}

Engaged interfaces

Monomer 1	Monomer 2	Spec.	Sym. op-n	Sym. ID	Area	Delta G	P-value	Nhb	Nsb	Nds
4	A	A	1*	X1,Y,7+1	2 456 280648.2	8080.7	0.339	2	0	0

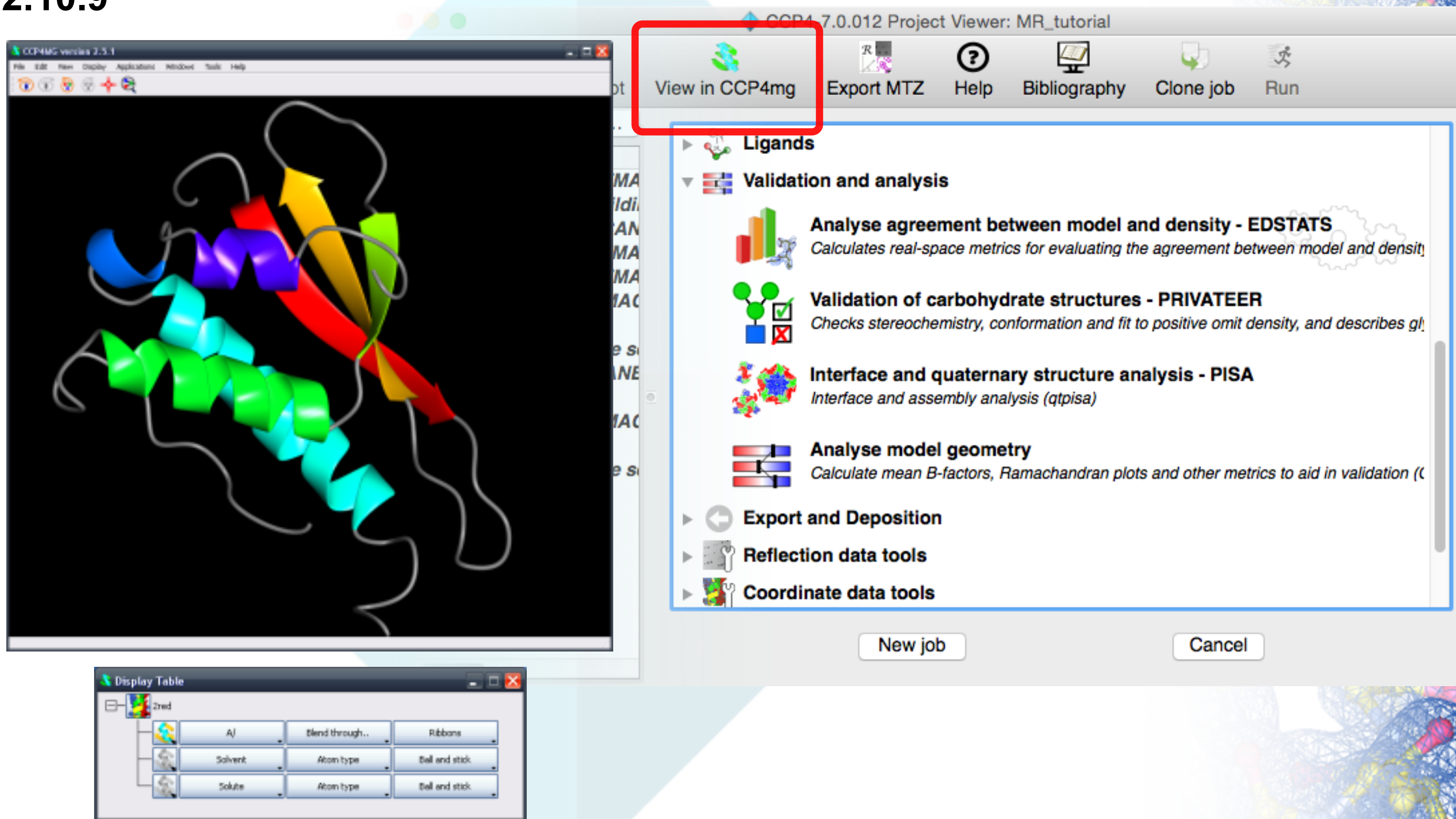
Assembled monomers

Monomer	Class	Type	Sym. op-n	Sym. ID	Area	BSA	Delta G	Nhb	Nsb	Nds
1	A	Protein	1	X,Y,7	1 555 3561350.5	280648.2	4490.4	2	0	0
2	A	Protein	1	-X-1,Y,-7+1	2 456 3561350.5	280648.2	-4490.4	2	0	0

- QtPisa – QT based interface

CCP4MG
2.10.9

Structure Analysis



The screenshot displays the CCP4MG 2.10.9 interface. The main window shows a 3D ribbon model of a protein structure. A sidebar on the right, titled 'CCP4 7.0.012 Project Viewer: MR_tutorial', contains a list of tools. The 'Validation and analysis' section is expanded, showing several options:

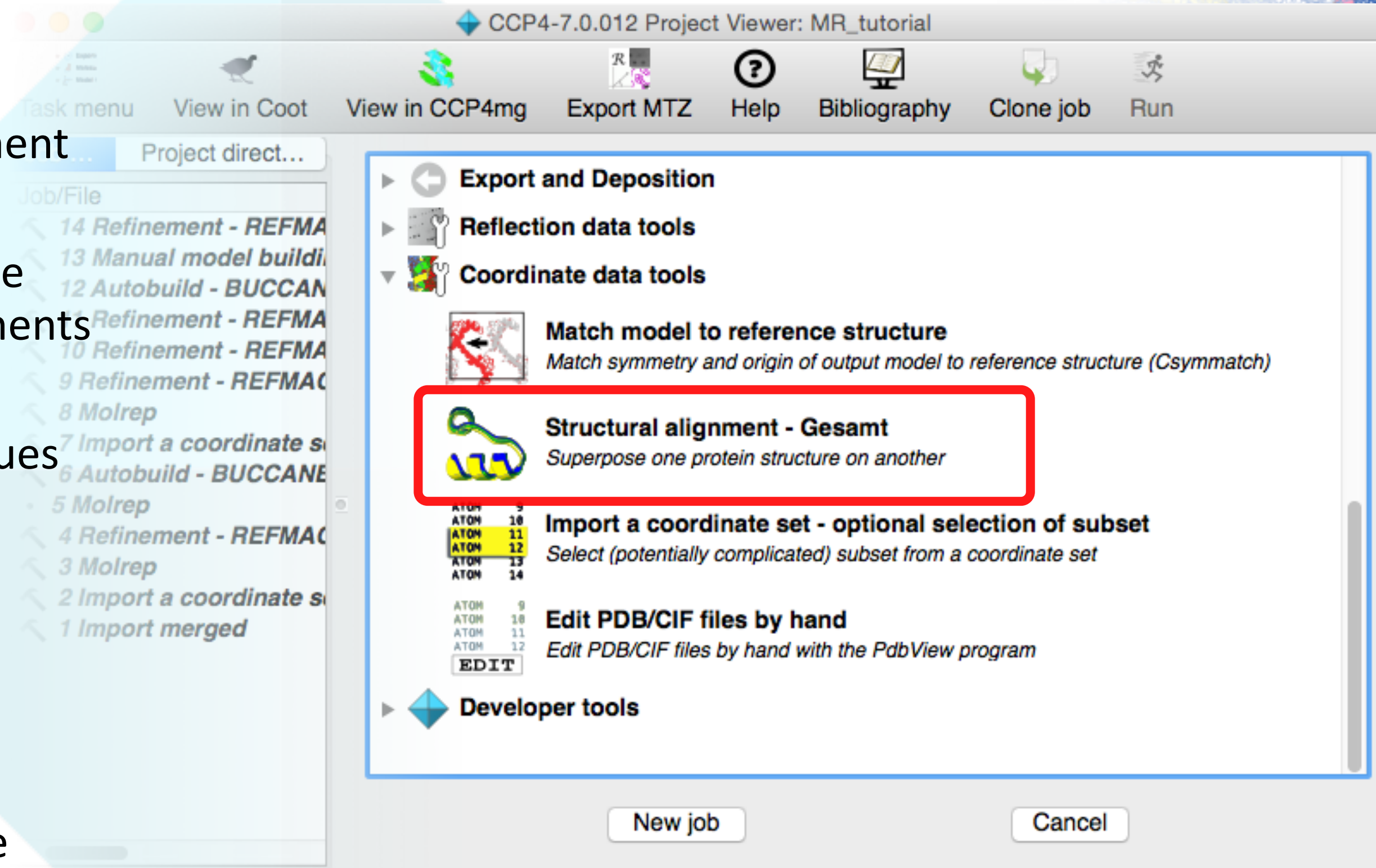
- Analyse agreement between model and density - EDSTATS**: Calculates real-space metrics for evaluating the agreement between model and density.
- Validation of carbohydrate structures - PRIVATEER**: Checks stereochemistry, conformation and fit to positive omit density, and describes glycosylation.
- Interface and quaternary structure analysis - PISA**: Interface and assembly analysis (qtpisa).
- Analyse model geometry**: Calculate mean B-factors, Ramachandran plots and other metrics to aid in validation (Coot).

Below these are sections for 'Export and Deposition', 'Reflection data tools', and 'Coordinate data tools'. At the bottom of the sidebar are 'New job' and 'Cancel' buttons. A 'Display Table' window is also visible in the bottom left corner, showing a table with columns for 'Atom type' and 'Ball and stick'.

Structure Analysis

Gesamt

- 3D structure alignment and superposition
- Makes both pairwise and multiple alignments
- Fast PDB scans for structural homologues
- Identification of structural domains
- Replacement for Superpose (SSM)
- Doesn't rely on secondary structure



Validation and Deposition

Coot

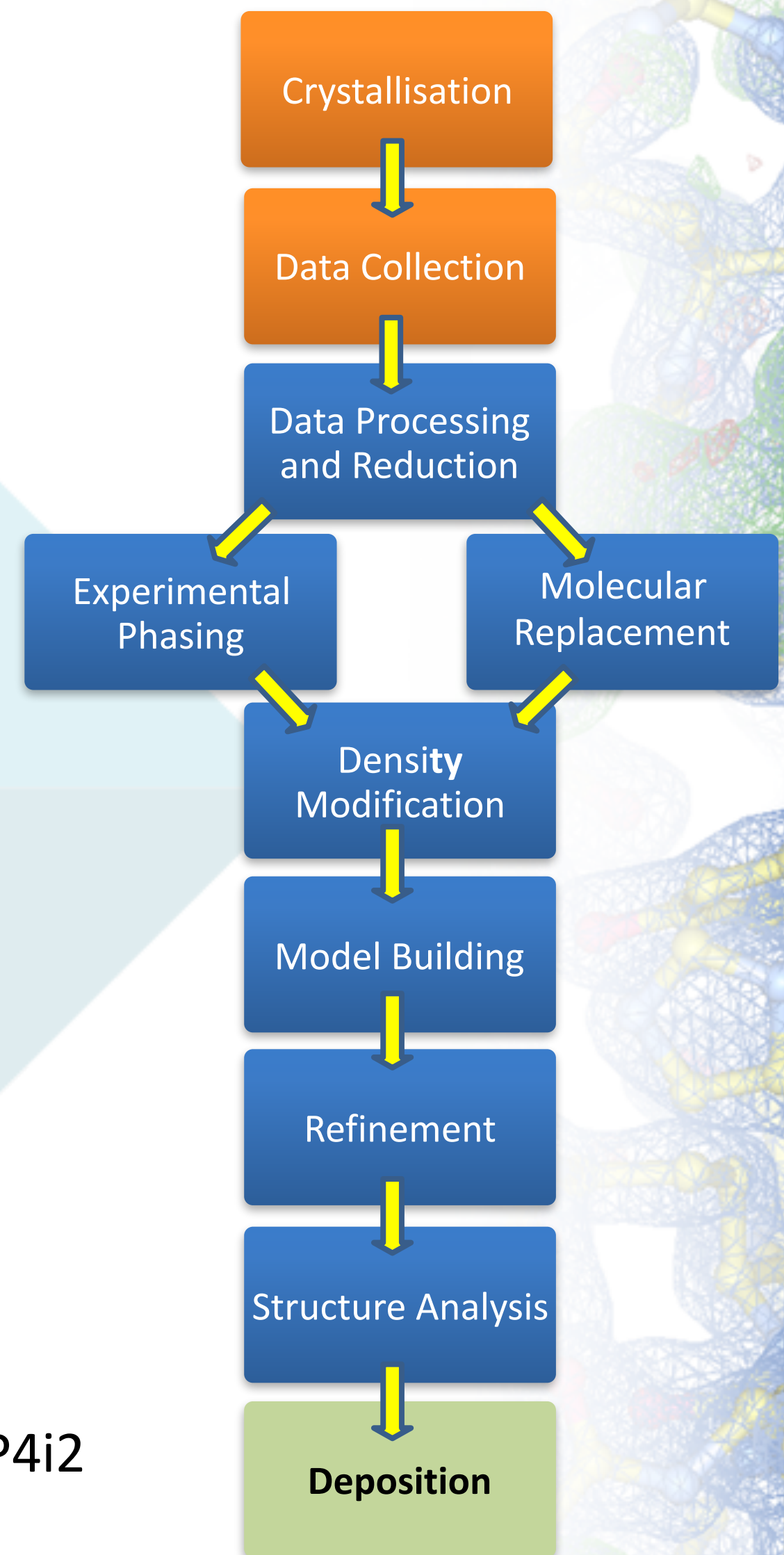
- Comprehensive set of validation tools: Ramachandran plots, density fit analysis, geometry analysis, unmodelled blobs etc.

PDB_REDO

- Optimisation of refinement parameters: weighting of X-ray terms, B-factors
- Checking rotomers
- Comparison of refinement with rest of PDB statistics

Deposition

- Dedicated deposition preparation module in CCP4i2



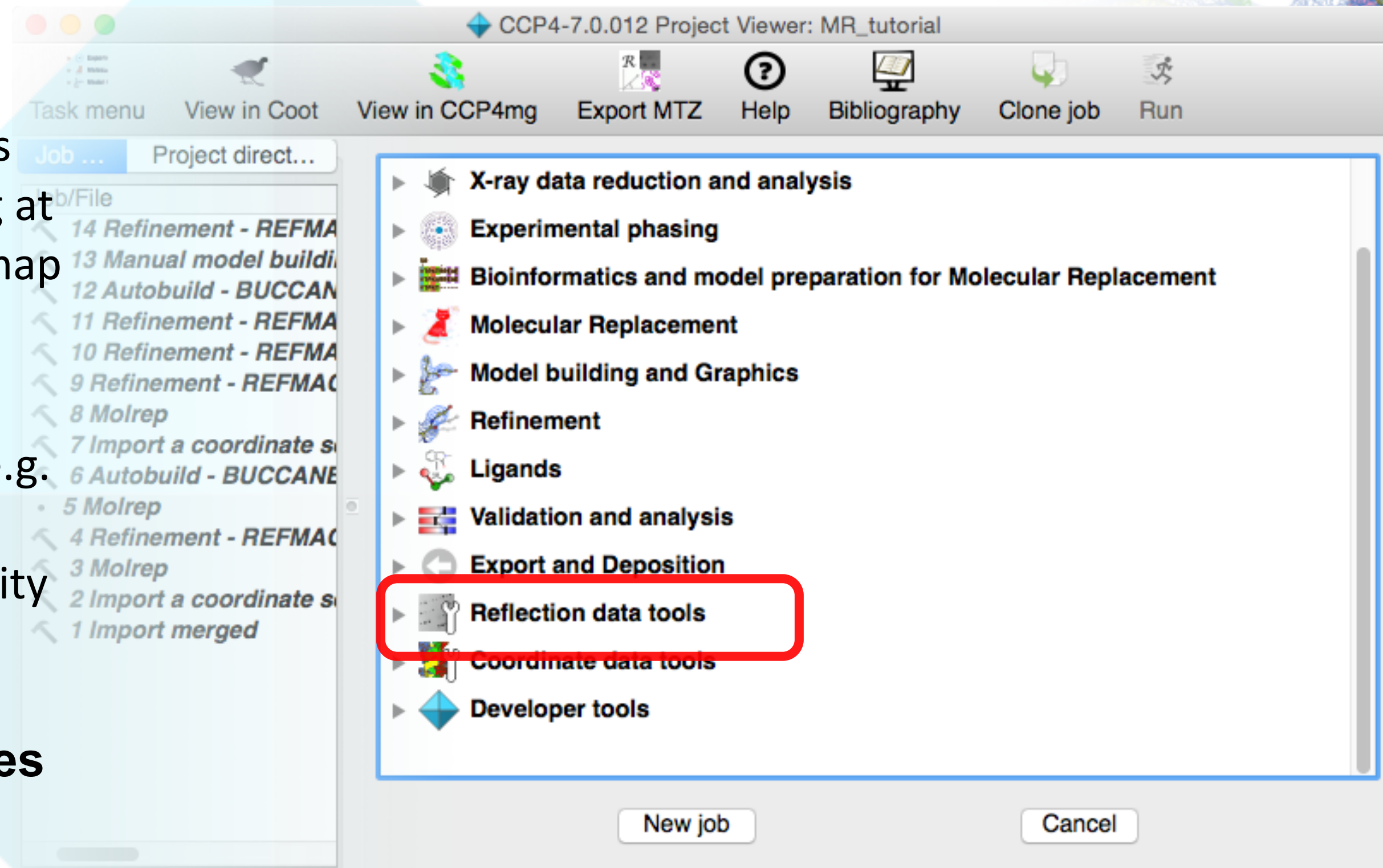
Utility Programs

Map & Mask Utilities

- Generating map files for density – looking at peaks in Patterson map or generation of difference maps
- Creating masks for e.g. use in multi-crystal averaging or in density modification

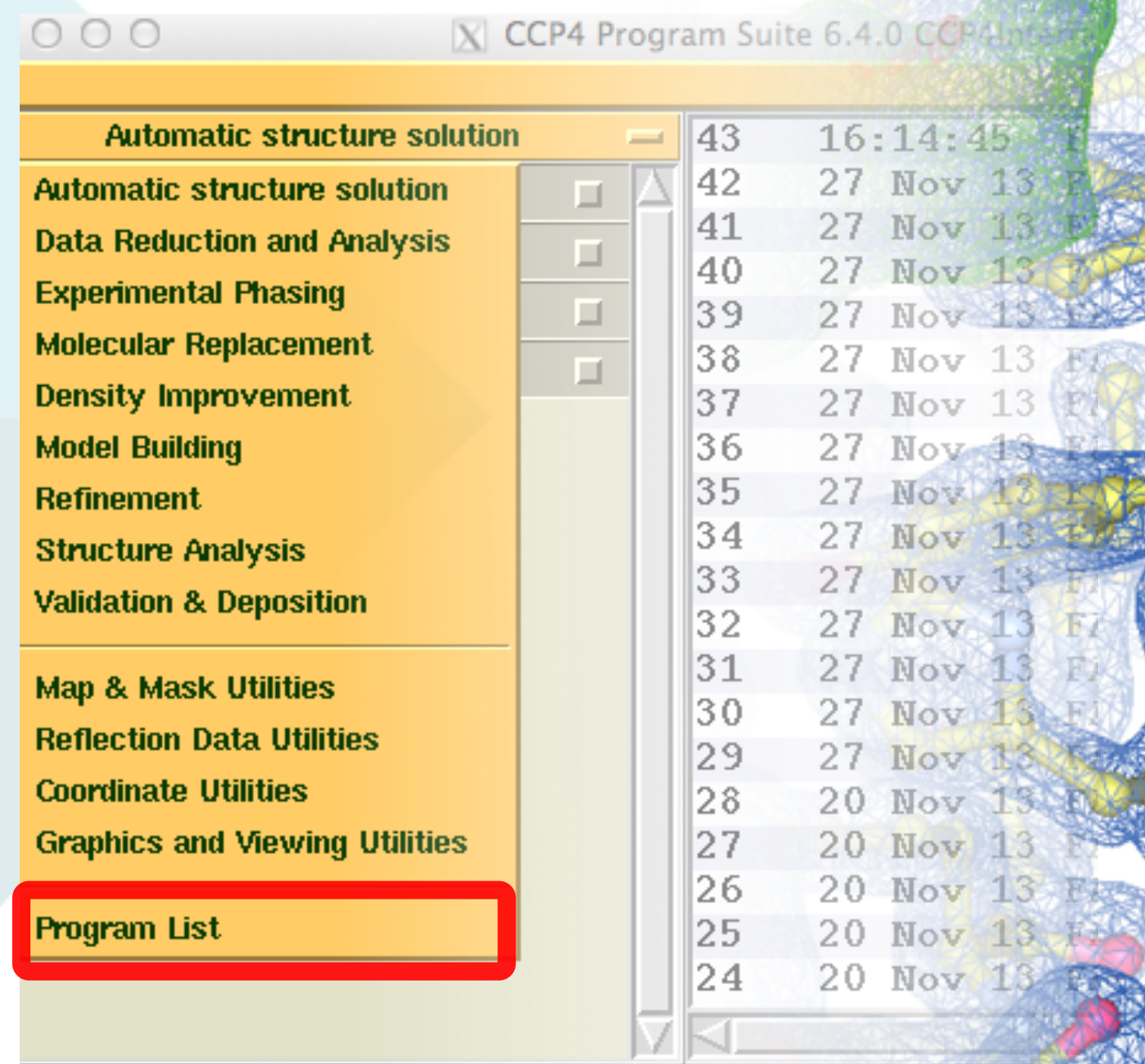
Reflection Data Utilities

- Merging MTZ files
- Manipulating columns in MTZ files
- Format conversion
- Reindexing



Program List

- Direct access to all programs in the suite
- Allows for more fine-grained control of process



CCP4 Program Suite 6.4.0 CCP4 Interface

Automatic structure solution					
Automatic structure solution	☐	43	16:14:45	F1	
Data Reduction and Analysis	☐	42	27 Nov 13	F1	
Experimental Phasing	☐	41	27 Nov 13	F1	
Molecular Replacement	☐	40	27 Nov 13	F1	
Density Improvement	☐	39	27 Nov 13	F1	
Model Building		38	27 Nov 13	F1	
Refinement		37	27 Nov 13	F1	
Structure Analysis		36	27 Nov 13	F1	
Validation & Deposition		35	27 Nov 13	F1	
Map & Mask Utilities		34	27 Nov 13	F1	
Reflection Data Utilities		33	27 Nov 13	F1	
Coordinate Utilities		32	27 Nov 13	F1	
Graphics and Viewing Utilities		31	27 Nov 13	F1	
Program List		30	27 Nov 13	F1	
		29	27 Nov 13	F1	
		28	20 Nov 13	F1	
		27	20 Nov 13	F1	
		26	20 Nov 13	F1	
		25	20 Nov 13	F1	
		24	20 Nov 13	F1	

Command Line Operation

Example:

refmac5 HKLIN my.mtz HKLOUT output.mtz XYZIN my.pdb XYZOUT output.pdb

Keywords:

- Most CCP4 programs take “keywords” as command options through standard input to the program
- Gives access to all options of the program and the most fine-grained control
- Can be provided through ccp4i using “**Run & view com file**”

Scripting:

- Repetitive tasks can be scripted
- Pipelines of programs can be created in a script

*Command
line*

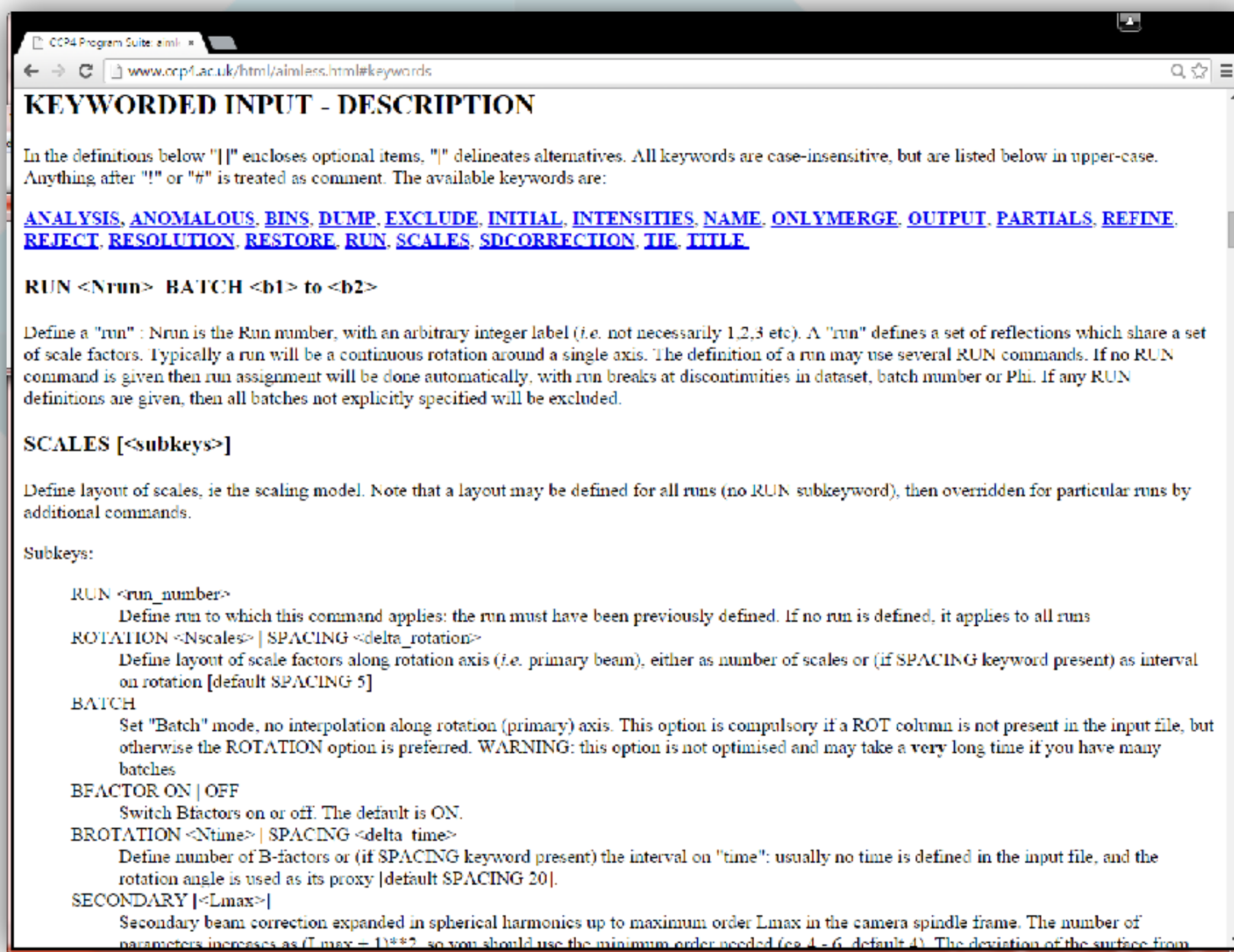
```
f2mtz hklin ${1} hklout shelxe-output.mtz << eof
```

```
TITLE ample  
cell      ${cell}  
symm      ${symm}  
labout    H K L F FOM PHI SIGF  
CTYPOUT   H H H F W P Q  
pname     ample  
dname     ample  
END
```

Keywords

Command Line Operation

- Documentation for CCP4 program keywords provided by documentation pages online or in the suite (`$CCP4/html/INDEX.html`):



CCP4 Program Suite: aimless

← → ↻ www.ccp4.ac.uk/html/aimless.html#keywords 🔍 ☆ ☰

KEYWORDED INPUT - DESCRIPTION

In the definitions below "[" encloses optional items, "|" delineates alternatives. All keywords are case-insensitive, but are listed below in upper-case. Anything after "!" or "#" is treated as comment. The available keywords are:

[ANALYSIS](#), [ANOMALOUS](#), [BINS](#), [DUMP](#), [EXCLUDE](#), [INITIAL](#), [INTENSITIES](#), [NAME](#), [ONLYMERGE](#), [OUTPUT](#), [PARTIALS](#), [REFINE](#), [REJECT](#), [RESOLUTION](#), [RESTORE](#), [RUN](#), [SCALES](#), [SDCORRECTION](#), [TIE](#), [TITLE](#)

RUN <Nrun> BATCH <b1> to <b2>

Define a "run": Nrun is the Run number, with an arbitrary integer label (*i.e.* not necessarily 1,2,3 etc). A "run" defines a set of reflections which share a set of scale factors. Typically a run will be a continuous rotation around a single axis. The definition of a run may use several RUN commands. If no RUN command is given then run assignment will be done automatically, with run breaks at discontinuities in dataset, batch number or Phi. If any RUN definitions are given, then all batches not explicitly specified will be excluded.

SCALES [<subkeys>]

Define layout of scales, *i.e.* the scaling model. Note that a layout may be defined for all runs (no RUN subkeyword), then overridden for particular runs by additional commands.

Subkeys:

RUN <run_number>
Define run to which this command applies: the run must have been previously defined. If no run is defined, it applies to all runs

ROTATION <Nscale> | SPACING <delta_rotation>
Define layout of scale factors along rotation axis (*i.e.* primary beam), either as number of scales or (if SPACING keyword present) as interval on rotation [default SPACING 5]

BATCH
Set "Batch" mode, no interpolation along rotation (primary) axis. This option is compulsory if a ROT column is not present in the input file, but otherwise the ROTATION option is preferred. WARNING: this option is not optimised and may take a very long time if you have many batches

BFACTOR ON | OFF
Switch Bfactors on or off. The default is ON.

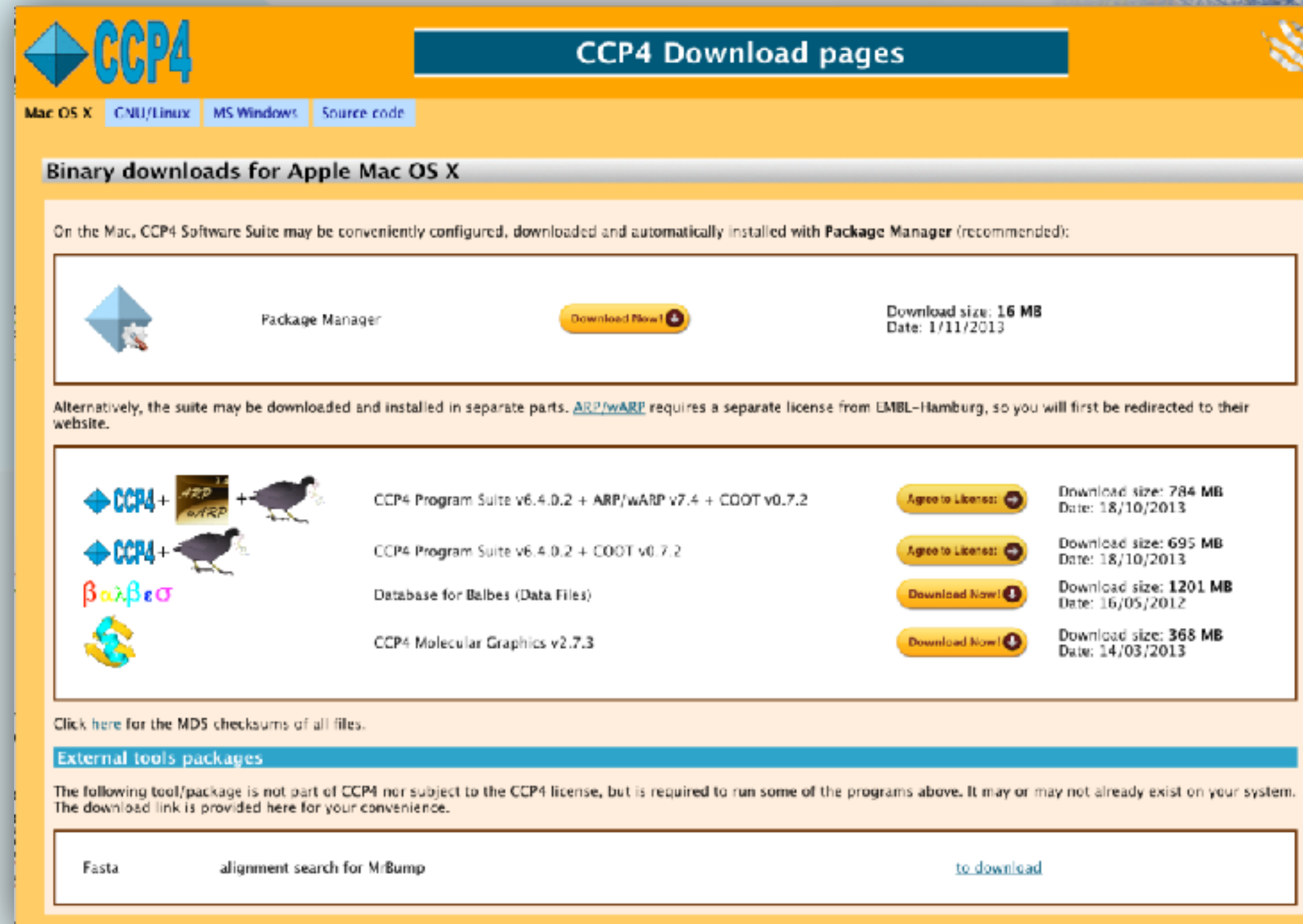
BROTATION <Ntime> | SPACING <delta_time>
Define number of B-factors or (if SPACING keyword present) the interval on "time": usually no time is defined in the input file, and the rotation angle is used as its proxy [default SPACING 20].

SECONDARY [<Lmax>]
Secondary beam correction expanded in spherical harmonics up to maximum order Lmax in the camera spindle frame. The number of parameters increases as $(L_{max} + 1)^2$, so you should use the minimum order needed (e.g. 4 - 6, default 4). The deviation of the surface from

Downloading the Suite

- Download CCP4 for Windows, Mac or Linux
- Co-distribution of ARP/wARP
- Package Manager – easy installation
- Only 64-bit version for Mac OSX, both 32-bit and 64-bit versions for other systems
- Additional software dependencies also available
- Download page accessible at

<http://www.ccp4.ac.uk/download>



The screenshot shows the CCP4 Download pages website. The header includes the CCP4 logo and navigation tabs for Mac OS X, GNU/Linux, MS Windows, and Source code. The main content area is titled "Binary downloads for Apple Mac OS X" and provides instructions on how to install the software using Package Manager. It lists several download options with their respective sizes and dates, including the CCP4 Program Suite v6.4.0.2 + ARP/wARP v7.4 + COOT v0.7.2 (784 MB), CCP4 Program Suite v6.4.0.2 + COOT v0.7.2 (695 MB), Database for Balbes (Data Files) (1201 MB), and CCP4 Molecular Graphics v2.7.3 (365 MB). A section for "External tools packages" mentions the Fasta alignment search for MrBump.

CCP4 Download pages

Mac OS X GNU/Linux MS Windows Source code

Binary downloads for Apple Mac OS X

On the Mac, CCP4 Software Suite may be conveniently configured, downloaded and automatically installed with Package Manager (recommended):

Package Manager Download Now! Download size: 16 MB Date: 1/11/2013

Alternatively, the suite may be downloaded and installed in separate parts. ARP/wARP requires a separate license from EMBL-Hamburg, so you will first be redirected to their website.

Download Link	Download size	Date
CCP4 Program Suite v6.4.0.2 + ARP/wARP v7.4 + COOT v0.7.2	784 MB	18/10/2013
CCP4 Program Suite v6.4.0.2 + COOT v0.7.2	695 MB	18/10/2013
Database for Balbes (Data Files)	1201 MB	16/05/2012
CCP4 Molecular Graphics v2.7.3	365 MB	14/03/2013

Click here for the MD5 checksums of all files.

External tools packages

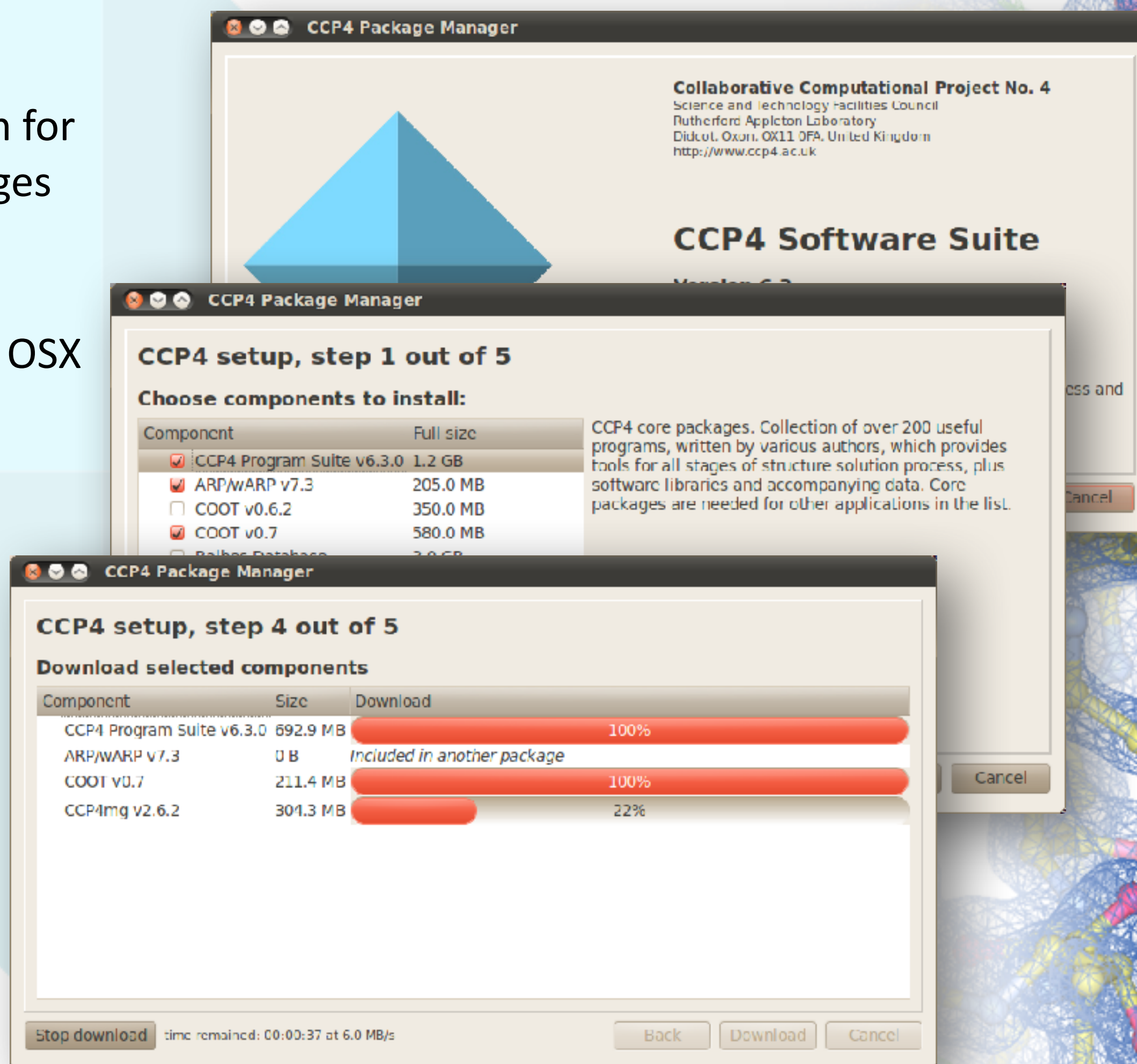
The following tool/package is not part of CCP4 nor subject to the CCP4 license, but is required to run some of the programs above. It may or may not already exist on your system. The download link is provided here for your convenience.

Fasta alignment search for MrBump to download



CCP4 Setup Manager

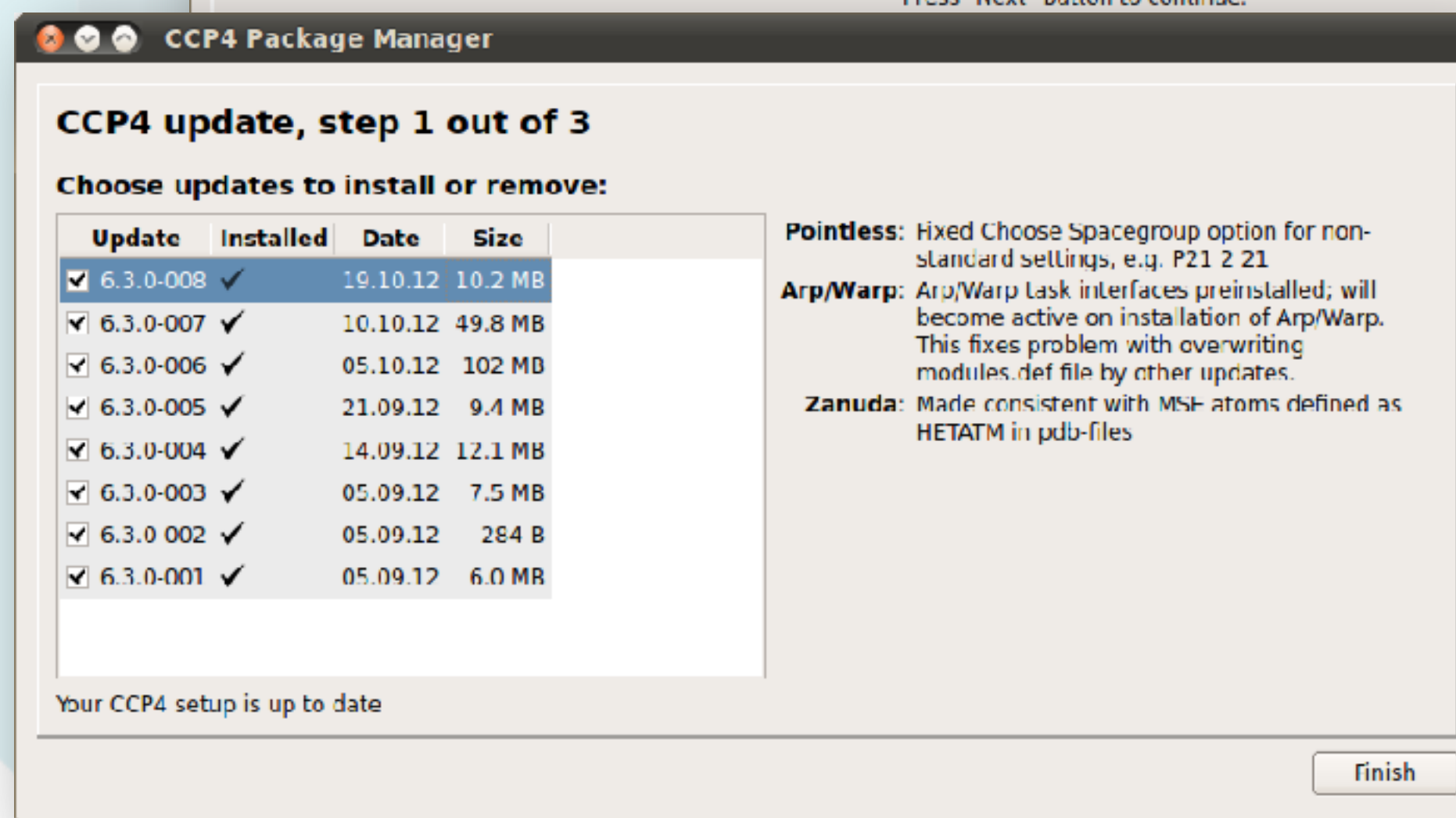
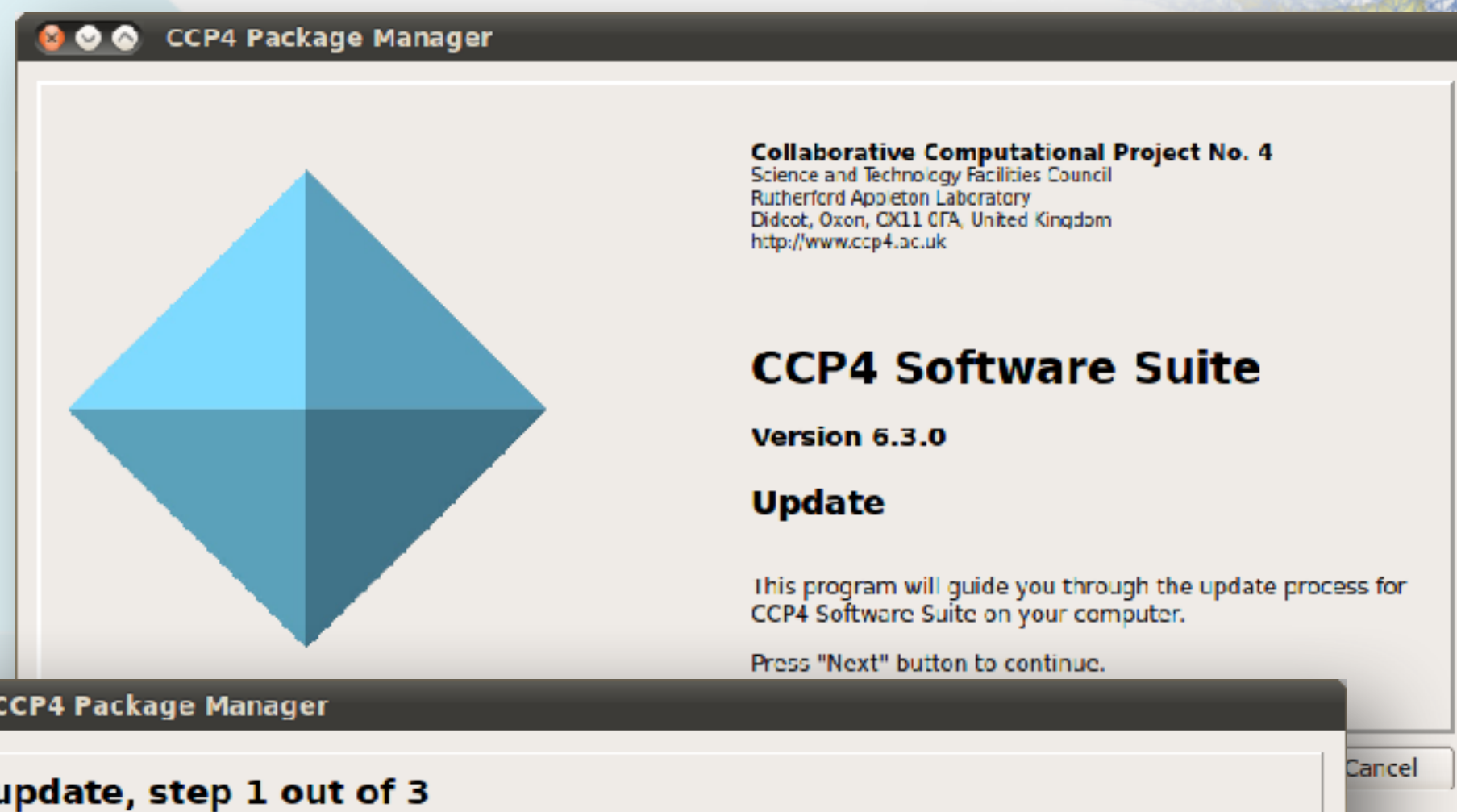
- Easy installation mechanism for CCP4 and associated packages (Coot, ARP/wARP, CCP4mg)
- Available on Linux and Mac OSX platforms
- Sets up system variables automatically if you wish





Update Manager

- Automatically install latest fixes and new features
- Allows for rolling back to previous versions
- Updates made available once every two weeks or as and when they are needed
- Available on Linux, Mac OSX and Windows



CCP4 on-line services

<http://www.ccp4.ac.uk/ccp4online>

Welcome to CCP4 online

Login

Other Options - [Register](#), [Forgot](#)

Runnable programs

The following programs and pipelines are available:

Balbes

An automated Molecular Replacement pipeline that searches for the correct orientation and position of the components necessary for the structure.

MrBUMP

An automated Molecular Replacement pipeline that searches for the correct orientation and position of the components necessary for the structure. It will search from the template structure and restrained refinement.

Zanuda

Space group and crystallographic data.

jsPISA

Calculation and analysis of interfaces.

AMPLE

Automated ab initio search.

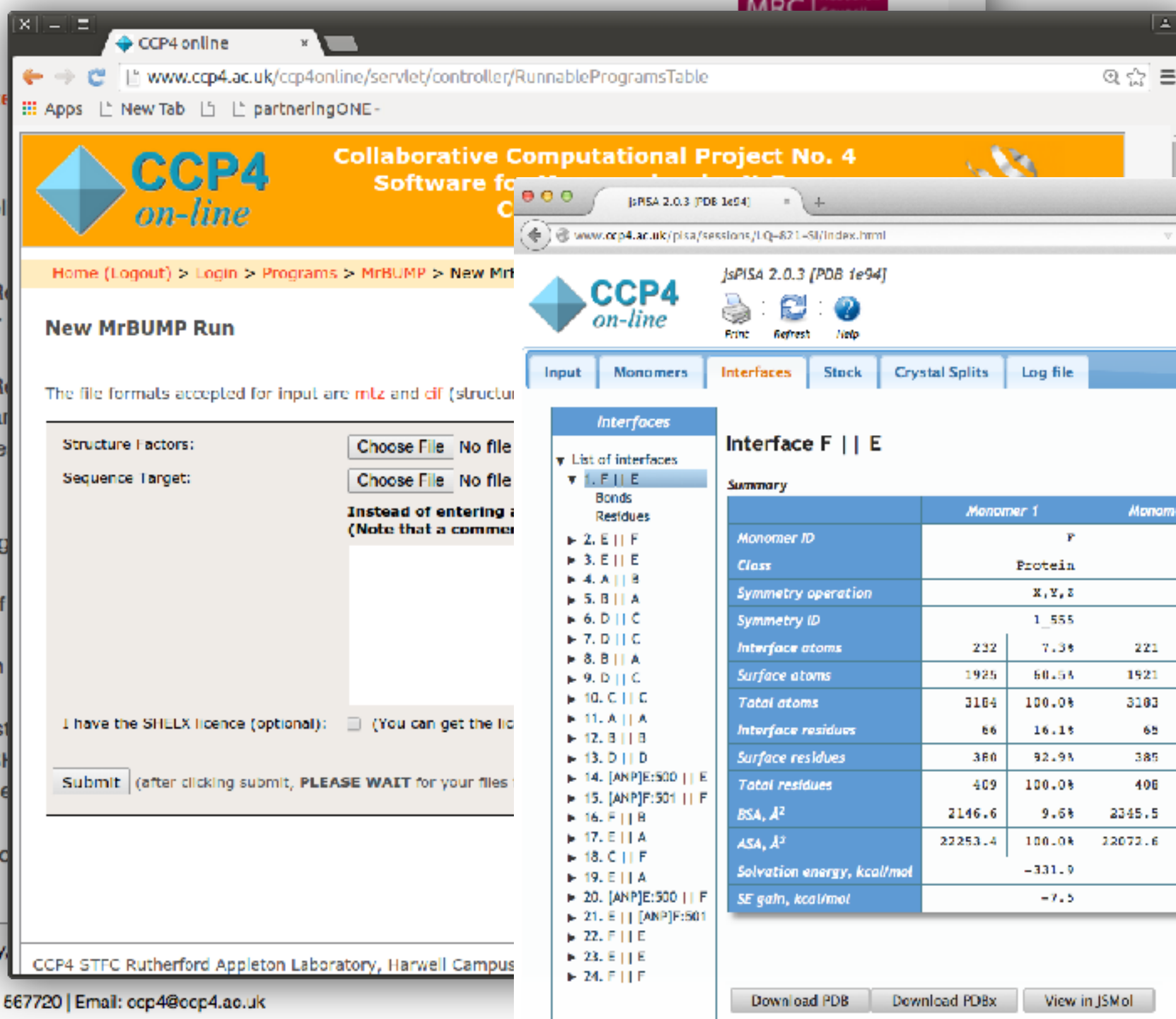
SHELX

Automated SHELXC/D/E suite for processing X-ray diffraction data in XDS, Scalepack, SHARP. A protein sequence is provided.

CRANK2

Automated structure solution.

BETA



Home (Logout) > Login > Programs > MrBUMP > New MrBUMP Run

New MrBUMP Run

The file formats accepted for input are **mtz** and **cif** (structure factors).

Structure factors: No file

Sequence target: No file

Instead of entering a file name, you can enter a PDB ID (Note that a comma is not allowed).

I have the SHELX licence (optional): ☐ (You can get the licence from the CCP4 website)

(after clicking submit, PLEASE WAIT for your files)

Interfaces

List of interfaces

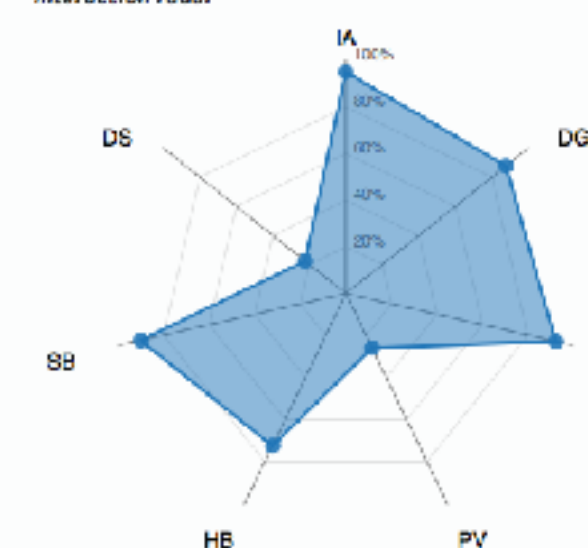
Interface	Bonds	Residues
1. F E		
2. E F		
3. E E		
4. A B		
5. B A		
6. D C		
7. D C		
8. B A		
9. D C		
10. C C		
11. A A		
12. B B		
13. D D		
14. [ANP]E:500 E		
15. [ANP]F:501 F		
16. F B		
17. E A		
18. C F		
19. E A		
20. [ANP]E:500 F		
21. E [ANP]F:501		
22. F E		
23. E E		
24. F F		

Interface F || E

Summary

	Monomer 1		Monomer 2	
	F	E	F	E
Monomer ID	Protein		Protein	
Class	X,Y,Z		X,Y,Z	
Symmetry operation	1_555		1_555	
Symmetry ID	232		221	
Interface atoms	7.3%	6.9%	7.3%	6.9%
Surface atoms	1925	1921	60.5%	60.4%
Total atoms	3164	3163	100.0%	100.0%
Interface residues	66	65	16.1%	15.9%
Surface residues	360	385	92.9%	94.4%
Total residues	409	406	100.0%	100.0%
BSA, Å ²	2146.6	2345.5	9.6%	10.6%
ASA, Å ²	22253.4	22072.6	100.0%	100.0%
Solvation energy, kcal/mol	-331.9	-334.3		
SE gain, kcal/mol	-7.5	-5.0		

Interaction radar



Interface parameters

IA : Interface area, Å ²	2246
DG : Solvation Energy, kcal/mol	-12.46
BE : Total Binding Energy, kcal/mol	-26.65
PV : Hydrophobic P-value	0.3542
HB : Number of Hydrogen Bonds	11
SB : Number of Salt Bridges	25
DS : Number of Disulphide Bonds	0



[2] Morda Automated Molecular Replacement



0002-01_morda Download

Nothing here. Press H for help.

Close

21

[illegible]

14.12.2017]

Acknowledgements

CCP4 Core group: Andrey Lebedev, Ronan Keegan, Charles Ballard, David Waterman, Marcin Wojdyr, Ville Uski, Karen McIntyre, Carol Malpass, Martyn Winn

LMB/MRC: Andrew Leslie, Phil Evans, Garib Murshudov, Rob Nicholls, Harry Powell, Owen Johnson, Fei Long, Paul Emsley, Andrea Thorn

Phaser Group: Airlie McCoy, Randy Read, Rob Oeffner, Gabor Bunkoczi

YSBL York: Keith Wilson, Kevin Cowtan, Liz Potterton, Stuart McNicholas, Eleanor Dodson

Diamond: Gwyndaf Evans, Graeme Winter

Leiden: Raj Pannu, Pavol Skubak

Others: Bernhard Lohkamp, Clemens Vornrhein, Ruslan Sanishvili, Frank Von Delft, Martin Noble, Jaclyn Bibby, Daniel Rigden, Jens Thomas, Alun Ashton, David Brown, Arwen Pearson, Tim Gruene, George Sheldrick and many more..

CCP4 People (core and associated developers)



Martyn
Winn



Charles
Ballard



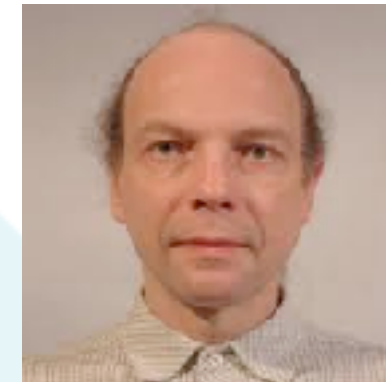
Eugene
Krissinel



Ronan
Keegan



David
Waterman



Andrey
Lebedev



Keith
Wilson



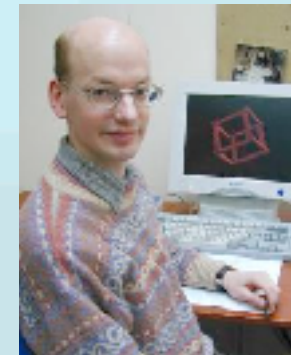
Eleanor
Dodson



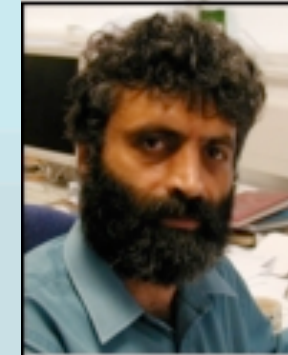
Liz
Potterton



Stuart
McNicholas



Kevin
Cowtan



Garib
Murshudov



Alexei
Vagin



Fei
Long



Phil
Evans



Andrew
Leslie



Harry
Powell



Owen
Johnson



Randy
Reed



Martin
Noble



Paul
Emsley



Raj
Pannu



Chris
Morris



Graeme
Winter