

# Coot Crib Sheet

October 7, 2015

## 1 Keyboard

### 1.1 Dialog Shortcuts

F6 Post Go To Atom window  
F7 Post Display Control Window

### 1.2 Previous/Next Residue

"Space" Next Residue  
"Shift" "Space" Previous Residue

### 1.3 Closest Residue

"p" go to an atom of the closest residue (the "CA" atom if the residue has one)

### 1.4 Go To Residue

Ctrl-g <Residue-number><Enter>  
Jump to the give residue (you can provide a chain-id too<sup>1</sup>)

### 1.5 Next NCS Chain

"o" - other NCS chain.

### 1.6 "Undo" Move

"u" to undo the move recent screen recentering (e.g. move back after recentering after reading a new PDB file)

---

<sup>1</sup>The chain-id goes directly before the residue number, i.e.  
Ctrl-g <Chain-id><Residue-number><Enter>

### 1.7 Previous/Next Rotamer

When in "Rotamer" mode, these keyboard shortcuts are available<sup>2</sup>:

"." Next Rotamer  
"," Previous Rotamer

### 1.8 Keyboard Chi Angles

Instead of pressing the buttons in the Chi Angles button box, you can use keyboard "1" for Chi1, "2" for Chi2 *etc.*

### 1.9 Keyboard Contouring

Use "+" or "-" to change the contour level

### 1.10 Keyboard Labelling

"l" to label closest atom

### 1.11 Quick Save As

Ctrl-s to save the state and any unsaved molecules (to default file names).

### 1.12 Keyboard Residue Info

Ctrl-i then click on residue to open Residue Info dialog

---

<sup>2</sup>note: focus must be in the graphics window, not the Rotamer dialog

### 1.13 Keyboard Translation

Keypad 3 Push View (+Z translation)

Keypad . Pull View (-Z translation)

### 1.14 Keyboard Undo/Redo

Ctrl-z Undo last modification

Ctrl-y Redo last modification

u Undo last move/navigation

### 1.15 Editing

Ctrl-c Copy active molecule

Ctrl-y Delete active residue

### 1.16 Keyboard Zoom and Clip

n Zoom out

m Zoom in

d Slim clip

f Fatten clip

### 1.17 Crosshairs

c: cross-hairs

### 1.18 Skeleton

s: Generate skeleton around current point<sup>3</sup>

### 1.19 Continuous Rotate

i: Toggle continuous spin

### 1.20 Baton Mode

b: toggle into baton rotate mode<sup>4</sup>

<sup>3</sup>if a skeleton is being displayed

<sup>4</sup>rather than view rotate mode

## 2 Mouse

Mouse actions are occasionally augmented with keyboard modifiers:

Left-mouse Drag

Ctrl Left-Mouse Drag

Shift Left-Mouse Click

Right-Mouse Drag

Shift Right-Mouse Drag

Rotate view

Translates view

Label Atom

Zoom in and out

Change clipping and Transl. Screen Z

The movement is along or axes:

up+right/down+left shifts

up+left/down+right change slab

Ctrl Shift Right-Mouse Drag

Middle-mouse Click

Scroll-wheel Forward

Scroll-wheel Backward

Rotate View about Screen Z

Centre on atom

Increase map contour level

Decrease map contour level

Intermediate (white) atoms can be dragged around by clicking on them:

Left-mouse Drag: Move all intermediate atoms by linear shear

Left-mouse Drag with "A" key: as above with non-linear shear

Left-mouse Drag with "Ctrl": Move a single atom

## 3 Refinement Extras

Use "A" to define a residue range<sup>5</sup> with a single-click. Useful in Refinement and Regularization.

- Click "Real Space Refine Zone"
- Click on an atom
- Press the "A" key

<sup>5</sup>+/- n residues from the current residue

## 4 Template Key-bindings

E	Flip Ligand
G	Go To Blob (under cursor)
H	Neighbour refine
J	Jiggle Fit This Residue
K	Fill Partial Side-chain
R	Refine Active Residue
T	Triple Residue Refine
X	Refine Active Residue and Auto-accept
W	Add Water
Y	Add Terminal Residue
Shift-Q	Rotamer Dialog for Residue
Shift-R	Sphere Refine
Shift A	Accept Baton Position
Shift-B	Sphere Regularize
Shift P	Delete Residue Hydrogens
Shift V	Undo Symmetry View
Shift-X	Edit Chi Angles
Shift-W	Add Water to Blob
Shift 4	Ball and Stick for Ligand