Ex 10 p 65 :

**Commonly Used RasMol Commands**

*Last modified on 14 December 2001.*

1. Commands which can be performed using the menu of the RasMol window:

| **File** | **Display** | **Colours** | **Options** | **Export** |
| --- | --- | --- | --- | --- |
| Open... Save as... Close Exit | Wireframe Backbone Sticks Spacefill Ball and Stick Ribbons Strands Cartoons | Monochrome CPK Shapely Group Chain Temperature Structure User Model Alt | Slab Mode Hydrogens Heteroatoms Specular Shadows Stereo Labels | GIF... PostScript... PPM... IRIS RGB... Sun Raster... BMP... PICT... |

1. **Example) To save a postscript file:** go to "Export" - select "PostScript" - type "filename.ps"
2. Mouse operation (using 3-button mouse):
   * **To rotate:** use the left mouse button
   * **To translate:** use the middle mouse button
   * **To zoom in or out:** use the Shift key + the left mouse button
3. Commands which can be run on the command line:
   * **To measure distance/angle/torsion angle:**
     + type "set picking distance", then pick two atoms
     + type "set picking angle", then pick three atoms
     + type "set picking torsion", then pick four atoms
   * **To trace the chain:**
     + select \*
     + trace
     + trace off [turn off trace]
   * **To select nucleic acids/proteins only:** select [nucleic|protein]
   * **To select residues and label, change colors, and highlight them:**
     + select mmm,nnn,ooo,ppp,..., then go to the menu and select "Options - Labels"
     + color yellow/green/blue/orange/...
     + wireframe/backbone/ribbons 60/80/200/400/...

**Example 1)**

* + - select 500
    - spacefill 400
    - color green

**Example 2)**

* + - select 500
    - wireframe 80
    - color blue
  + **To select atoms within a specific distance from a specific residue(s):**
    - select within(4.5, nnn)  
      **Example)** select within(8.5, 500)
    - select within(4.5, mmm-nnn)  
      **Example)** select within(30.0, 500-600)
  + **To select all atoms in the currently loaded structure:**
    - select \*
    - select all
  + **To select all atoms in a specific chain (A or B or C or ...):**
    - select \*:a
    - select \*:b
    - select \*:c
  + **To label a specific atom using the *E. coli*, *T. thermophilus*, or *H. marismortui* numbers** (this requires you to select positions manually by going through the PDB file and manually interconvert to type in the numbers)"
    - select atomno=xxx, then
    - label "nnn"

**Example)**

* + - select atomno=1400
    - label "756"

x-1 \ -1

2-2x //

x-1/2-2x +1/1>/

x-1/2-2x+2-2x/2-2x>/0

x-1+~~2~~-~~2x~~/~~2~~-~~2x~~>/0

x-1>/0

x>/-1