RasMol v2.6 Quick Reference Card

v2.6 features added May, 1997.

Mouse Buttons

Clicking on an atom identifies that atom in the command window. Moving the mouse whilst holding mouse buttons and/or control keys manipulates the molecule. The default bindings are described below.

Left Button	Rotate X-Y
Right Button	Translate X-Y
Shift Left Button	Zoom
Shift Right Button	Rotate Z
Control Left Button	Z-Clipping (Slab)

General Commands

load [format] <filename> Load a molecule
- **pdb** Brookhaven Protein Databank
- **mdl** Molecular Design Limited's Mol file
- **mol2** Tripos' Sybyl Mol2 file format
- **alchemy** Tripos' Alchemy file format
- **charmm** CHARMm format card file
- **xyz** MSC's XMOL XYZ file format

exit Exit from RasMol Script
quit Terminate pgm execution

help [topic [subtopic]] Display on-line help topic

select <expression> Update part of molecule
restrict <expression> Display only part of mol.

set bondmode [mode] Change bond selection

script <filename> Execute file of commands

zap Delete molecule

Display Commands

wireframe [boolean] Display wireframe
wireframe <value> Display stick bonds

spacefill [boolean] Display spacefill spheres
spacefill <value> Specify atom sphere radius
spacefill temperature
spacefill user

backbone [boolean] Display alpha backbone
backbone <value> Specify backbone radius

ribbons [boolean] Display solid ribbons
ribbons <value> Specify ribbon width

strands [boolean] Draw ribbon as strands
strands <value> Specify ribbon width
set strands <value> Number of ribbon strands

label [boolean] Draw default atom labels
label <string> Label with arbitrary text
set fontsize <value> Set label font height

ssbonds [boolean] Display disulphide bonds
ssbonds <value> Specify ssbond radius

set ssbonds backbone SSBonds between alphas
set ssbonds sidechain SSBonds between sulphurs

hbonds [boolean] Display hydrogen bonds
hbonds <value> Specify hbond radius

set hbonds backbone HBonds between alphas
set hbonds sidechain HBonds donor/acceptor

dots [boolean] Display dot surface
dots <value> Specify dot density

set solvent [boolean] VDW or solvent surface
set radius <value> Specify probe sphere rad.

set axes [boolean] Display co-ordinate axes
set boundbox [boolean] Display bounding box
set unitcell [boolean] Display crystal unit cell

set monitor on (off) Show distance monitor labels
set backfade on (off) Shade to any background color
set display selected Currently selected portion

set picking Series of eight commands:
off | ident | distance
angle | torsion | label
monitor | center

Colour Commands

colour [object] <colour> Colour representation

Objects:
atoms **bonds** **backbone**
ribbons **labels** **hbonds**
ssbonds **dots** **axes**
ribbons1 **ribbons2**

Predefined Colours:
blue **black** **cyan** **green**
greenblue **magenta** **orange** **purple**
red **redorange** **violet** **white**
yellow

Atom Colour Schemes:
cpk **amino** **shapely**
group **chain** **structure**
temperature **charge** **user**

colour hbonds type Colour hbonds by offset
colour dots potential Display potential surface

Manipulation Commands

rotate <axis> [-] <value> Rotate molecule

translate <axis> [-] <value> Translate molecule

zoom [boolean] Scale molecule
zoom <value> Specify magnificatior

slab [boolean] Enable/disable slabbin
slab <value> Move Z-clipping plane
set slabmode <slabmode> Control slabbing meth

centre [expression] Set centre of rotation

reset Initial transformation

set stereo [boolean] Control L & R images

Scripted Commands

pause Suspend script execution
echo Display text on command line
refresh Redraw local image
set write <boolean> Save & write in scripts

Atom Expressions

Predefined Sets:	alpha hydrophobic
Residue Ranges:	3,16,12 9-20
Boolean Operators:	backbone and not alpha ligand or 196-199
Primitive Expressions:	cys, glu, arg, as? ser70a, **p, glu24:1 hem*p.fe, *.sg
Comparison Operators:	atomno=4,atomno=6 temperature>=900
Within Expressions:	within(8.0,ligand)

Predefined Sets

at	**acidic**	**acyclic**	**aliphatic**
alpha	**amino**	**aromatic**	**backbone**
basic	**bonded**	**buried**	**cg**
charged	**cyclic**	**cystine**	**helix**
hetero	**hydrogen**	**hydrophobic**	**ions**
large	**ligand**	**medium**	**neutral**
nucleic	**polar**	**protein**	**purine**
pyrimidine	**selected**	**sheet**	**sidechain**
small	**solvent**	**surface**	**turn**
water (**hoh**)			

define <identifier> <expression> User-defined sets

Rendering Commands

background <colour>	Set background colour
set ambient [value]	Depth-cueing/lighting
set shadows [boolean]	Enable/disable shadows
set specular [boolean]	Enable atom highlights
set specpower [value]	Control atom 'shininess'
set bonds [boolean]	Double and triple bonds
cartoons [boolean]	MolScript-style display
set cartoons [number]	Depth of display
trace [boolean]	Draw a smooth CA spline
trace [value]	Specify trace width

Export Commands

write [format] <filename> Output image file

gif	CompuServe GIF format
ps, epsf	Encapsulated PostScript
monops	Monochrome PostScript
vectps	'Cartoon' PostScript
bmp	Microsoft Bitmap format
pict	Apple 'PICT' file
ppm	Portable Pixmap
sun, sunrle	Sun Rasterfile

set vectps <boolean>	Enable cartoon outlines
write script <filename>	Generate RasMol script
write molscript <filename>	Output MolScript script
write kinemage <filename>	Output Kinemage file
set kinemage <boolean>	Set Mage file detail
clipboard	Copy image to clipboard
print	Image to local printer
save <filename>	Save selected atoms
set transparent <filename>	Output transparent gif

Misc. Commands

structure	DSSP secondry structure
connect [boolean]	Recalculate connectivity
renumber	Sequentially number chains
show information	Display molecule statistics
show sequence	Display molecule sequence
show symmetry	Display crystal space group
set mouse rasmol	Default mouse bindings
set mouse quanta	Polygen's Quanta bindings
set mouse insight	Biosym's Insight II bindings
hetero <boolean>	Excludes HETATMs if false
hydrogen <boolean>	Excludes hydrogens if false
hourglass <boolean>	Enables "hour glass" cursor
set menus <boolean>	Enables menu buttons/bar

Command Line Editing

In addition to the cursor keys, the following 'emacs' control keys may be used to edit the command line.

Ctrl-H / Ctrl-D	Delete previous/next character
Ctrl-B / Ctrl-F	Movebackward/forward a character
Ctrl-A / Ctrl-E	Move to beginning/end of line
Ctrl-P / Ctrl-N	Display previous/next history

Colour Schemes

CPK Atom Colours

Carbon	**light grey**	**[200,200,200]**
Oxygen	**red**	**[240,0,0]**
Nitrogen	**light blue**	**[143,143,255]**
Hydrogen	**white***	**[255,255,255]**
Sulphur	**yellow**	**[255,200,50]**
Phosphorous	**orange***	**[255,165,0]**
Chlorine	**green***	**[0,255,0]**
Sodium	**blue***	**[0,0,255]**
Iron	**orange***	**[255,165,0]**
Calcium, Metals	**dark grey**	**[128,128,144]**
Unknown	**deep pink**	**[255,20,147]**

Amino Acid Colours

ASP, GLU	**bright red**	**[230,10,10]**
CYS, MET	**yellow**	**[230,230,0]**
LYS, ARG	**blue**	**[20,90,255]**
SER, THR	**orange**	**[250,150,0]**
PHE, TYR	**mid blue**	**[50,50,170]**
ASN, GLN	**cyan**	**[0,220,220]**
GLY	**light grey**	**[235,235,235]**
LEU, VAL, ILE	**green**	**[15,130,15]**
ALA	**dark grey**	**[200,200,200]**
TRP	**pink**	**[180,90,180]**
HIS	**pale blue**	**[130,130,210]**
PRO	**flesh**	**[220,150,130]**

Secondary Structure Colours

Alpha Helix	**magenta**	**[240,0,128]**
Beta Sheet	**yellow***	**[255,255,0]**
Turns	**pale blue**	**[96,128,255]**
Other	**white***	**[255,255,255]**

Hydrogen Bond Type Colours

Offset +2	**white***	**[255,255,255]**
Offset +3	**magenta***	**[255,0,255]**
Offset +4	**red***	**[255,0,0]**
Offset +5	**orange***	**[255,165,0]**
Offset -3	**cyan***	**[0,255,255]**
Offset -4	**green***	**[0,255,0]**
default	**yellow***	**[255,255,0]**

***Same as the **Predefined Colours** on the first page.