



RasMol v2.7.2 Quick Reference Card

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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.

Mac	Windows	Action
---	Left	Rotate X-Y
Command	Right	Translate X-Y
Shift	Shift Left	Zoom
Shift-Cmnd	Shift Right	Rotate Z
Control	Control Left	Z-Clipping (Slab)

General Commands

load [format] <filename> Load a molecule (up to 5)

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
mopac	J.P. Stewart's MOPAC file format
cif	IUCr CIF or mmCIF 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

Bond Commands

bond <src> <dst> + Add a bond

bond <src> <dst> pick

Pick bond for rotation

unbond <src> <dst> Remove a bond

Display Commands

wireframe [boolean] Display wireframe
wireframe<rad> [-<rad>] Display stick bonds
set bondmode all Mark all atoms
set bondmode none Mark no atoms
set bondmode not bonded Mark non-bonded atoms

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

spacefill temperature
spacefill user
star ... Display stars for spheres

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> [FS|PS] Set label font height
set fontstroke<value> Set label stroke width

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
Display crystal unit cell

set monitor [boolean] Show distance monitor labels
set backfade [boolean]

Shade to any background color
Currently selected portion

set display selected

set picking Series of ten commands:
off | ident | distance
angle | torsion | label
monitor | center | coord | bond

Colour Commands

colour [object] <colour> Colour representation

Objects:

atoms	bonds	backbone
ribbons	labels	hbonds
ssbonds	dots	axes
ribbons1	ribbons2	

Predefined Colours:

Black	Blue	BlueTint	Brown
Cyan	Gold	Grey	Green
GreenBlue	GreenTint	HotPink	Magenta
Orange	Pink	PinkTint	Purple
Red	RedOrange	SeaGreen	SkyBlue
Violet	White	Yellow	YellowTont

Atom Colour Schemes:

cpk	amino	shapely
group	chain	structure
temperature	charge	user
alt	model	

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

Manipulation Commands

rotate <axis> [-] <value> Rotate molecule
rotate bond Rotate bond
rotate molecule Rotate selected molecule
rotate all Rotate all molecules

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

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

slab [boolean] Enable/disable slabbing
slab <value> Move Z-clipping plane

centre [expression] Set centre of rotation

reset Initial transformation

set stereo [boolean] Control L&R images

Scripted Commands

load [format] inline Load molecule from script
pause Suspend script execution
echo Display text on command line
refresh Redraw 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			

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'

Export Commands

write [format] <filename>	Output image file
gif	CompuServe GIF format
iris	IRIS RGB
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 povray <filename>	Generate POVray data
write vrml <filename>	Generate VRMLdata
write molscript <filename>	Output MolScript script
write kinemage <filename>	Output Kinemage file
save <filename>	Save selected atoms
set kinemage <boolean>	Set Mage file detail
set transparent<boolean>	Allow transparent GIFs
write phipsi<filename>	Generate phi-psi data
write RDF<filename>	Ramachandran plot data
write RPP<filename>	Ramachandran printer plot

Misc. Commands

structure	DSSP secondry structure
connect [boolean]	Recalculate connectivity
renumber	Sequentially number chains
show information	Display molecule statistics
show phipsi	Display trosion angles
show RPP	Ramachandran printer plot
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

set cisangle CIS angle cutoff

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	Move backward /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	sky blue	[143,143,255]
Hydrogen	white	[255,255,255]
Sulphur	yellow	[255,200,50]
Phosphorous	orange	[255,165,0]
Chlorine	green	[0,255,0]
Bromine, Zinc	brown	[165,42,42]
Calcium	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]
others	tan	[190,160,110]

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]