RasMol Hints

To get started with any model:
select protein
wireframe off
backbone 300
color chain (or: color group or: color red)
set hbond backbone
hbond 225
color hbond blue (or whatever color you want)
select ligand
spacefill (or: wireframe 225, or a combination of wireframe and cpk)
color cpk (or whatever color you want)

Important commands:
select trp187A.CA
residue number chain . atomname
select *:A
select all atoms in chain A
select 187 and (sidechain or alpha)
selecting atoms in “clean” sidechains
select protein
very useful!
select ligand
select not protein and not water
set hbond backbone
backbone-style hbonds
select protein
hbond on
select 101 or 103
removing a “triangle” hbond
hbond off

color cpk
coloring by atom type

color hbond blue
coloring hbonds

save script NAME.script
saving a script
script NAME.script
using a script

for monitor lines, in the “Settings” menu, choose “Pick monitor”
to get back to the normal picking, choose “Pick ident”
or:
monitor 784 1733
use atom numbers for monitor lines
**Values for Models**

backbone 300
hbond 225
spacefill 275
wireframe 225
ssbond 225

*important atom names:*

“CA“ or alpha alpha carbon (the central carbon atom of each amino acid)
“N“ peptide nitrogen (makes hbonds)
“O“ peptide oxygen (makes hbond)

*for amino acids, use the three letter names:*

ala alanine (A)
asn asparagine (N)
asp aspartate (D)
arg arginine (R)
cys cysteine (C)
gly glycine (G)
glu glutamate (E)
gln glutamine (Q)
his histidine (H)
il ile isoleucine (I)
leu leucine (L)
lys lysine (K)
met methionine (M)
phe phenylalanine (F)
pro proline (P)
ser serine (S)
trp tryptophan (W)
tyro tyrosine (Y)
thr threonine (T)
val valine (V)