File commands

fo	open UCSF NMR data, a Felix matrix, or a Sparky spectrum file
fs	save a Sparky spectrum annotation file
fa	save spectrum with a new name
jo	open several spectra at once
js	save all spectra
ja	save project with a new name

View commands

ci	change background color
xh	display view scale axes in Hz
xp	display view scale axes in parts per million
vc	center a view on the selected peak
vs	show scales (ppm, hz, or index units) along view axes
vp	show peak position / height / linewidth in status bar
vR	show resonances along edge of spectrum
vd	make another view window
zf	show entire spectrum
zi	zoom in by a factor of 2
zo	zoom out by a factor of 2

Peak commands

at	make assignments
dr	delete resonances not used in any peak assignments
pc	center selected peaks at local maxima or minima.
pg	create a peak group from selected peaks
lu	move labels so they don't overlap each other
pa	select all peaks in a spectrum

Dialogs

tb	table of chemical shifts
ct	set contour levels and colors
ot	change ornament colors and sizes
lt	show a list of peaks for a spectrum
rr	rename atoms and groups
rl	list group/atom chemical shifts, standard deviations
yt	make views scroll in parallel

Pointer Modes

F1	click or drag to select or move peaks, labels, lines, ...
F2	clicking centers view on point
F3	place vertical and horizontal grid lines
F4	add a line extending across whole spectrum
F5	add a line extending across whole spectrum
F6	add a text label to a peak
F7	add a horizontal or vertical line between end points
F8	click to place a peak or drag to find peaks
F10	click or drag to integrate peaks
F11	drag to select a new region to show
F12	drag to zoom and duplicate a view

Pressing the shift key and clicking on a selected **peak** will **deselect** it without deselecting other selected **peaks**.