Alphabet Soup II: Bruker Parameters and Commands

Common Parameters on the Bruker NMR:

AT	acquisition time (sec)
D1	relaxation delay
D2, ...	other delays in pulse sequences
DS	number of dummy scans
F1	1D: frequency axis of observed nucleus 2D: simulated frequency axis
F2	1D: freq domain of 2nd(decoupled) nucl 2D: frequency axis for observed nucleus
GB	Gaussian broadening factor, for apodization (fraction of FID)
GPZ*x*	strength of gradient pulse *x* along z-axis
LB	line broadening factor, for apodiz'n (Hz): + for noise reduction; − for resolution enhancement (GFP, TRAF)
NS	number of scans
O1P	frequency offset for observed nucl. (ppm)
O1	frequency offset for observed nucl. (Hz)
O2	frequency offset for 2nd(decoupled) nucl.
P1	90° pulse length (μs)
P2	180° pulse length (μs)
PHC0, PHC1	zeroth and first order phase corrections
PL*x*	power level attenuation for pulse *x*, in dB. (120 = "off")
PL2	BB decoupler power-level attenuation
PL24	homonucl decoupler power-level attenuation
RG	receiver gain
SFO*x*	spectrometer frequency on channel *x* (= transmitter freq for nuclus + offset O*x*)
SI	number of data points in processed data. Usually TD/2 .
SWH	spectral width (Hz)
SW	spectral width (ppm)
TD	Total Data points (Time Domain?)
TE	temperature (K)

Common Commands on the Bruker NMR:

apk	autophase
abs n	automatic baseline correction ("n" = "don't create integral regions")
ased	acquisition parameter editor
atmm	tune probe
bsmsdisp	display the BSMS panel (manual shimming)
daisy	multiplet-simulation pkg (2nd order spltg)
dpl	set acquisition window (F1,F2) to region displayed
eda	edit acquisition parameters
edc	edit file-specific params (filename, expno, etc)
edti	edit spectrum title
efp	exponential multiply (LB), FT, recall phasing from previous spectrum
exit	close TopSpin
expl	open an explorer window (file-browser) to current data directory
ej, ij	eject/inject sample
expt	show time run will take
getprosol	get probe- and solvent-dependant parameters (pulse lengths, powers, etc)
gfp	Gaussian multiply (pos. GB, neg. LB), FT, recall phasing from previous spectrum
go	resume acquisition; add to existing data set
gs	acquire w/ interactive setting adjustment
halt	halt acquisition; write data to disk (*cf.* stop)
help *x*	search for *x* in manual
iexpno [*n*]	increment EXPNO by 1 (or change it to *n*)
kill	abort processes (process manager)
lock *x*	lock sample dissolved in solvent *x*
lockdisp	display the lock-signal window
mdisp	display multiple spectra
new	edit file-specific params (same as "edc")
peakw	calculate peak width at half-height
plot	open plottting program
rga	automatically set receiver-gain (RG)
ro on|off	turn spinning on/off
rpar *x*	read parameter file *x*
rsh *x*	read shim file *x*
spdisp	show pulse sequence graphic ("symbolic pulse display")
stop	stop acquisition; discard data (*cf.* halt)
sx *n*	insert sample *n* into magnet (sample exchg)
topshim	perform gradient autoshim on sample
topshim gui	open TopShim control panel
tr	transfer data to disk (in mid-acquisition)
traf	Traficante resolution enhancmt (neg. LB)
wrpa	copy dataset ("write raw + processed data")
xf1,xf2,xfb	FT the 1st | 2nd | both dimensions of a 2D data-set
zg	acquire new data ("zero memory, go")