## **Bruker Avance 300 NMR Instructions for 1D Experiments**

Dissolve solid (20 - 40 mg) or liquid (20 - 40 uL) into 600 uL deuterated solvent for  $^1H$  and up to 80 mg or uL for  $^{13}C$ . Double click on TOPSPIN 1.3 icon

Action	Description	
"new file" or new file icon	NAME: begin with initials EXPONO: 1, PROCNO: 1, DIR: /disk2 USER: CHM411 Experiment: see options in table on right	
"lockdisp"	opens lock level display	
"bsmsdisp"	opens bsms control panel	
in BSMS window, select [Lock]	turn lock off	
select [LIFT]	eject standard - replace with your sample	
select [LIFT]	inject sample	
if deuterium signal shows in the center of the lock display, select [Lock] - otherwise, "lock solvent"	lock on deuterium signal or begin autolock procedure using solvent parameters you chose when creating the file	
wait for [SPIN] to turn green, then adjust lock power/gain as needed	see table to right	
shim z & z <sup>2</sup>	adjust to maximize signal strength z is sensitive and should be adjusted with step-size < 10, whereas z² is less sensitive and can be adjusted with step-size = 10.	
close BSMS window		
adjust "ns" if needed	if 20 mg for <sup>1</sup> H, then ns=16 (multiple of 4) if 80 mg for <sup>13</sup> C, then ns=16 (multiple of 16)	
"rga"	set receiver gain	
"zg"	begin acquisition	
"ft" (proton) or "ef" (carbon)	process data	
select interactive phasing icon	optimize 0 & 1 - save changes	
if needed: select calibration icon	calibrate TMS or other known signal	
if needed: "pp" to peak pick	peak pick entire spectrum	
select interactive integration icon (¹H only)	select pick range icon, then drag with left mouse button through each signal	
"plot"	enter plot editor	
<file>, <open></open></file>	select: turk1H, turk13C or turkDEPT	
for DEPT, add full <sup>13</sup> C spectra beneath DEPT spectra	select spectral region, then [data]. Choose <sup>13</sup> C experiment, then [append] and [apply]	
adjust spectral height if needed	select spectral region, then 1D/2D edit	
<file>, <print> or ctrl-P</print></file>	print	

Command	Description
"re" name expno procno	open file
"ns"	# scans
"expt"	experiment time
"mi" - can also be edited in "pp" window	adjusts threshold for peak picking

Adjustment	CDCI <sub>3</sub>	DMSO
Lock Power	-25	-30
Lock Gain	120-125	150
Values are approximate		

Experiment Files		
protonC	<sup>1</sup> H NMR: CDCl <sub>3</sub> , MeOD-d <sub>4</sub>	
protonD	<sup>1</sup> H NMR, DMSO-d <sub>6</sub>	
carbonC	<sup>13</sup> C NMR, CDCl <sub>3</sub>	
carbonD	<sup>13</sup> C NMR, DMSO-d <sub>6</sub>	
DEPT135	All solvents	



