J(^{1}H,^{1}H)-resolved spectrum

****Capitalized words are icons in the menu. The italic text you have to type****

Get a good 1D NMR
Set the cursor at ±1ppm to the outside peaks. Type *movesw*
hom2dj
set *ni=64*
nt=8 or *16*
sw1=xx
Take a look at your 1D NMR. Wide peaks, vinyl, etc may have a width of more than 50Hz. This is the standard value in J-resolve (sw1). Be sure you increase it to 100 or 150Hz otherwise you get folded peaks.
go
Standard acquisition time 16-45 min depending on ni

!!!! The splitting in 2nd dimension is due to 1H only. If you have F or any other atom that may split the signal you'll see in the first dimension. For instance, if you have one proton and one F splitting the signal you'll see a doublet in the 2nd dimension (1H splitting) and a doublet in 1st dimension (19F splitting) !!!
!!! The spectrum must be tilted!!!

Plot/save:
1) Define your window:
wc=xx
wc2=xx (the xx value should be between 100 and 250 (Define the size of the window. If wc=wc2 you'll get a square plot. I would recommend the value of wc around 100)

2) Plot: PROJ / HPROJ MAX / PLOT / CANCEL / MAIN /
MENU / DISPLAY / PLOT / ALL CONTOURS / PAGE
After HPROJ MAX you'll get the projection. Adjust the height with the mouse.
In J Resolve you do not need both projections.

3) Save file as **.eps
PROJ / HPROJ MAX / PLOT / VPROJ MAX / PLOT / CANCEL / MAIN MENU / DISPLAY / PLOT / ALL CONTOURS / *page('file name.eps')* /