



KJM 9250
1D-SELECTIVE NMR Experiments on the
AVIIIHD-800

Version 1.0

Topspin 3.5
Windows 7



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1.1 Introduction

aw coded 1D-SELECTIVE xperiments use soft 180° refocusing pulses with a default prosol Table linked pulse time of 80000 usec. Pulse powers are read in using the **getprosol** command.

The effective excitation window of an 80000 usec 180° soft pulse experiment is ca 25 Hz. For a wider or narrower excitation window use one of the power and time combinations below. The greater the pulse power attenuation (larger the db value) the narrower the excitation window. Adding 6 db halves the pulse power.

Selective pulse power + time combinations

Default: 80000 usec at the PLW level read in by the **getprosol** command .

Other: 40000 usec, subtract 6 db to the PLW level read in by the **getprosol** command
120000 usec, add 3 db to the PLW level read in by the **getprosol** command
160000 usec, add 6 db to the PLW level read in by the **getprosol** command
240000 usec, add 9 db to the PLW level read in by the **getprosol** command

1.2 NS x TD0 option

1D-SELECTIVE experiments can be run using the **NS x TD0** option where **NS** is a multiple of 8, 16, 32, 64 (etc) and **TD0** is any number >1.

Do NOT use the **TR** command as a **NS x TD0** experiment proceeds. Multiples of **NS** scans will be automatically saved and can be processed using the **FT** or **EFP** commands the experiment proceeds. A run can be terminated at any time using the **STOP** (*NB not the HALT*) command. This will ensure a multiple of 4 or 8 scans is saved as is required by some of the selective excitation experiments.

1.3 1D-SELECTIVE NMR Experiments

The following 1D-Selective experiments have been set up on the AVI and AVII 600 MHz spectrometers

2.1 SELCOSY spectra

2.2 SELTOCSY spectra

2.3 SELDIPSI2 spectra

2.4 Phasing SELNOESY and SELROESY spectra

2.5 SELNOESY spectra

2.6 SELROESY spectra

2.7 SELROESY.2 spectra

2.8 SELHSQC and SELHSQCND spectra

2.9 SELHSQC-DIPSI2 and SELHSQCND-DIPSI2 spectra

2.1 SELCOSY Spectra

Parameter set: **awselcosy** (+ **getprosol**)

Pulse programme: **selco**

TD = 64 K, **SI** = 64 K, **SW** = 20 ppm.

O1 = Frequency in Hz of signal to be selectively correlated. **O1** Excitation is applied *on resonance* at the middle of SW. Check SW is wide enough.

NS = multiple of 8 or 16, **DS** = 4 or 8.

or **NS x TDO** scans where **TDO** = any positive number.

D1 = 1 sec or other time of your choice.

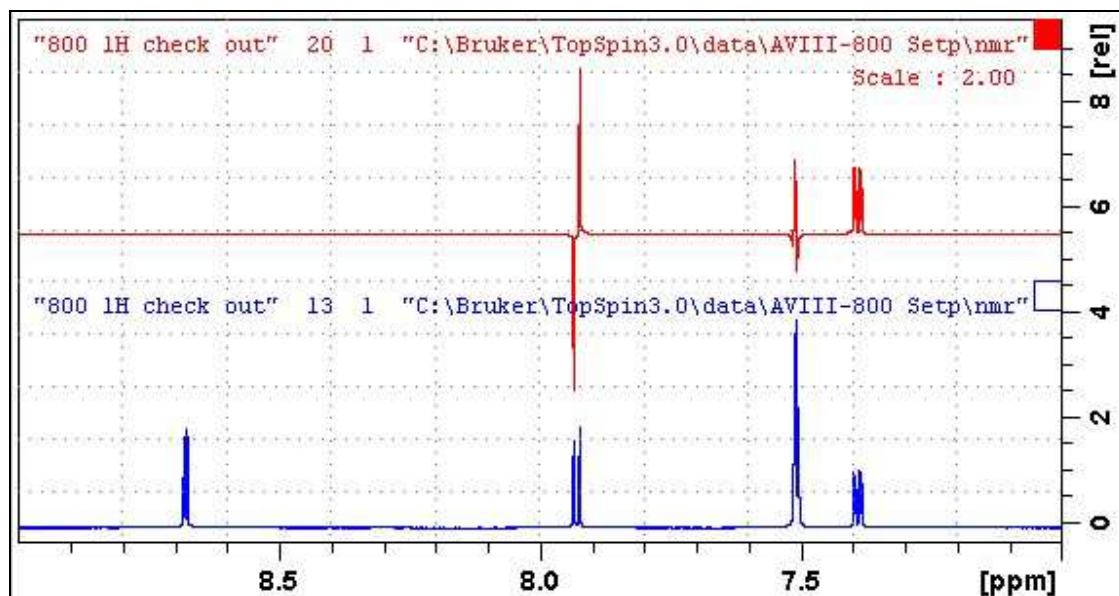
D14 = $1/4J_{H-H}$ where **D14** (the interval between the hard 90° and soft 180° pulse is corrected by half the width of the soft 180 degree pulse. In practice a **D14** value in the range 30-40 msec (default 35 msec) generally works well irrespective of J_{H-H} .

P12 = 80000 usec, **SPW2** = shaped pulse power read in using the getprosol command.

Process with **EFP** (applies **LB**, typically use 0.1 - 0.3 Hz),

Phase the spectrum to afford *antiphase positive and negative signal intensities*.

Alternatively process the spectrum in **PS (Power)** mode to afford *positive correlation peaks* (see the next page).



Lower: 7-9 ppm region of the 800 MHz ^1H NMR spectra of quinine in D_6 -DMSO.

Upper: SELCOSY spectrum ex the signal at 7.39 ppm

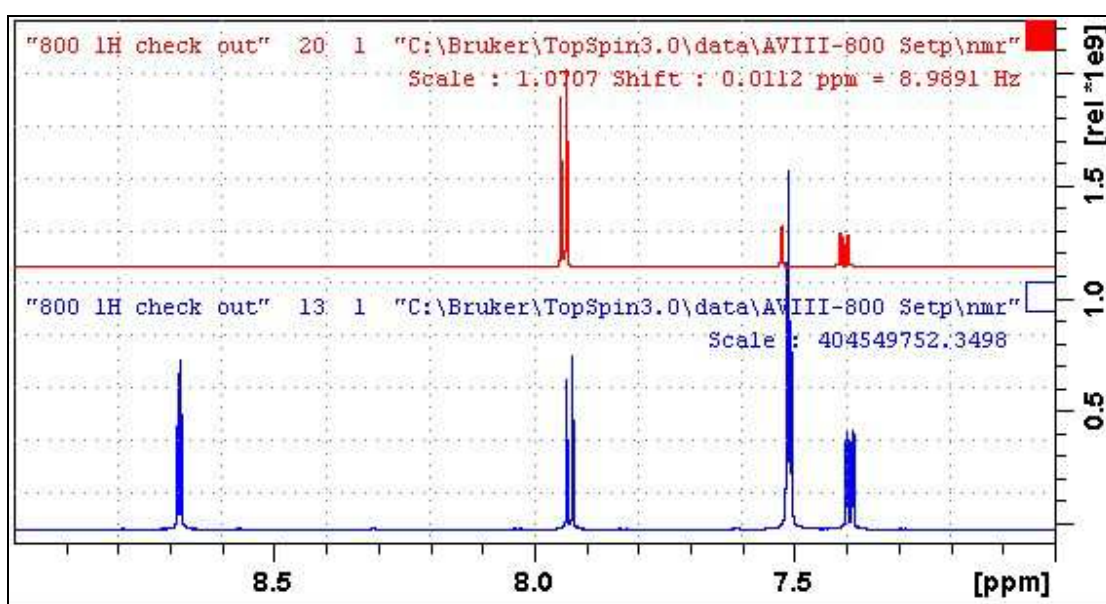
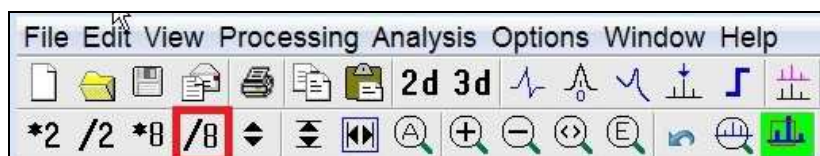
Power mode (PS) processing of a SELCOSY spectrum

To convert an antiphase SELCOSY spectrum generated by normal **FT** or **EF** processing to a **Power Spectrum** (intensity squared spectrum), type:

PS (return),

abs (return) to center the spectrum of on its baseline

click the **/8** button several times until the spectrum is appropriately scaled.



Lower: 7-9 ppm region of the 800 MHz ^1H NMR spectra of quinine in D_6 -DMSO.

Upper: Power mode processed SELCOSY spectrum ex the signal at 7.39 ppm.

2.2 SELTOCSY Spectra

Parameter set: **awseltocsy** (+ **getprosol**)

Pulse programme: **selmlgp**

TD = 128 K, **SI** = 128 K, **SW** = 20 ppm.

O1 = Frequency in Hz of signal to be selectively correlated. **O1** Excitation is applied *on resonance* at the middle of SW. Check SW is wide enough.

NS = multiple of 8 or 16, **DS** = 4 or 8.
or **NS** x **TD0** scans where **TD0** = any positive number.

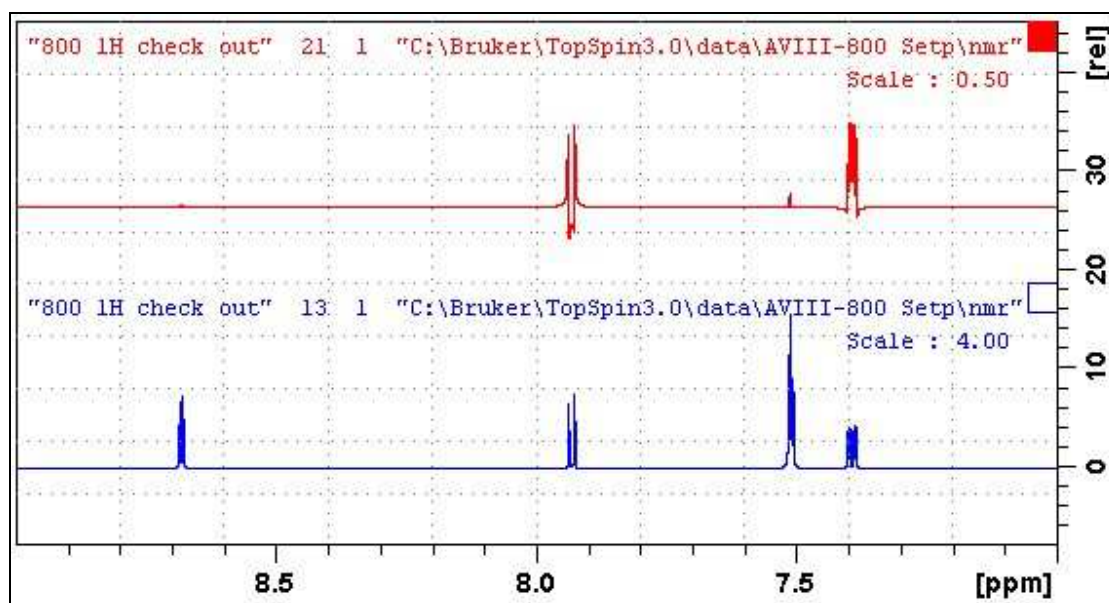
D1 = 1 sec or other time of your choice.

D9 = 80 msec for medium range correlations or other time of your choice.
160 msec for long range correlations, 6-15 msec for short range correlations.

P12 = 80000 usec, **SPW2** = shaped pulse power read in using the **getprosol** command.

PLW10 = TOCSY spin lock power level read in using the **getprosol** command.

Process with **EFP** (applies **LB**, typically use 0.1 - 0.3 Hz); all peaks should be positive. Strongly coupled peaks may exhibit some negative artifact lines which tend to decrease as **D9** is increased.



Lower: 7-9 ppm region of the 800 MHz ¹H NMR spectra of quinine in D₆-DMSO.

Upper: D₉ = 80 msec SELTOCSY spectrum ex the signal at 7.39 ppm.

2.3 SELDIPS12 Spectra

Parameter set: **awseldipsi2** (+ **getprosol**)

Pulse programme: **seldigp**

TD = 64 K, **SI** = 64 K, **SW** = 20 ppm.

O1 = Frequency in Hz of signal to be selectively correlated. **O1** Excitation is applied *on resonance* at the middle of SW. Check SW is wide enough.

NS = multiple of 8 or 16, **DS** = 4 or 8.

or **NS x TD0** scans where **TD0** = any positive number.

D1 = 1 sec or other time of your choice.

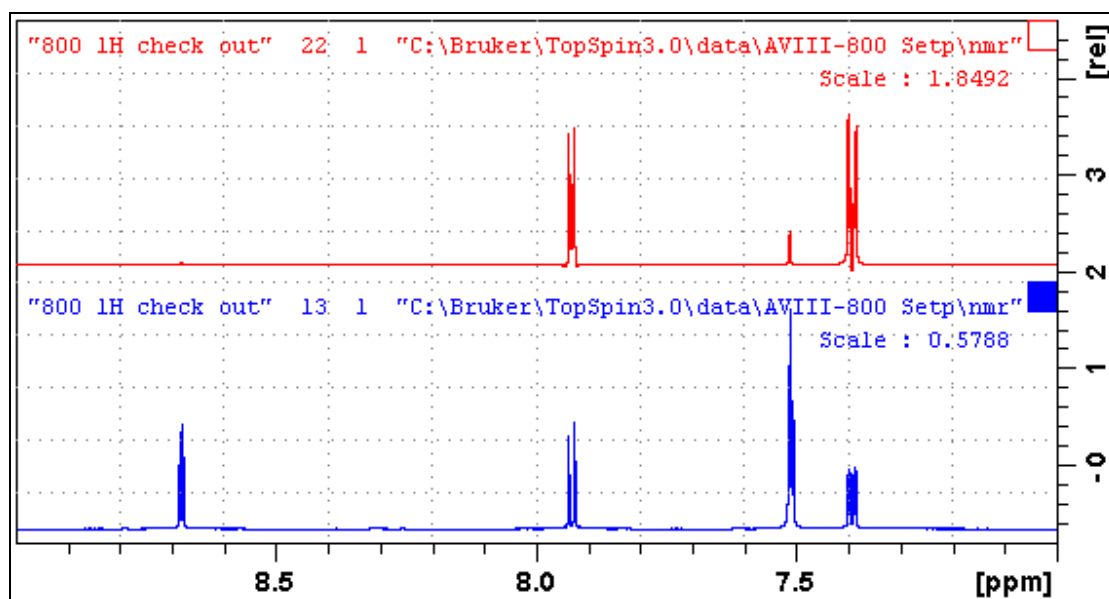
D9 = 80 msec for medium range correlations or other time of your choice.

160 msec for long range correlations, 6-15 msec for short range correlations.

P12 = 80000 usec, **SPW2** = shaped pulse power read in using the **getprosol** command.

PLW10 = TOCSY spin lock power level read in using the **getprosol** command.

Process with (applies **LB**, typically use 0.1 - 0.3 Hz); all peaks should be positive.



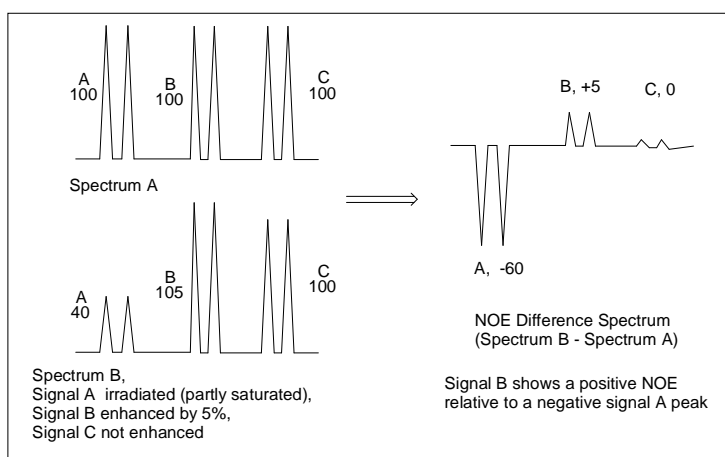
Lower: 7-9 ppm region of the 800 MHz ^1H NMR spectra of quinine in D_6 -DMSO.

Upper: $\text{D9} = 80$ msec SELDIPS12 spectrum ex the signal at 7.39 ppm

2.4 Phasing of 1D-SELNOESY and SELROESY spectra

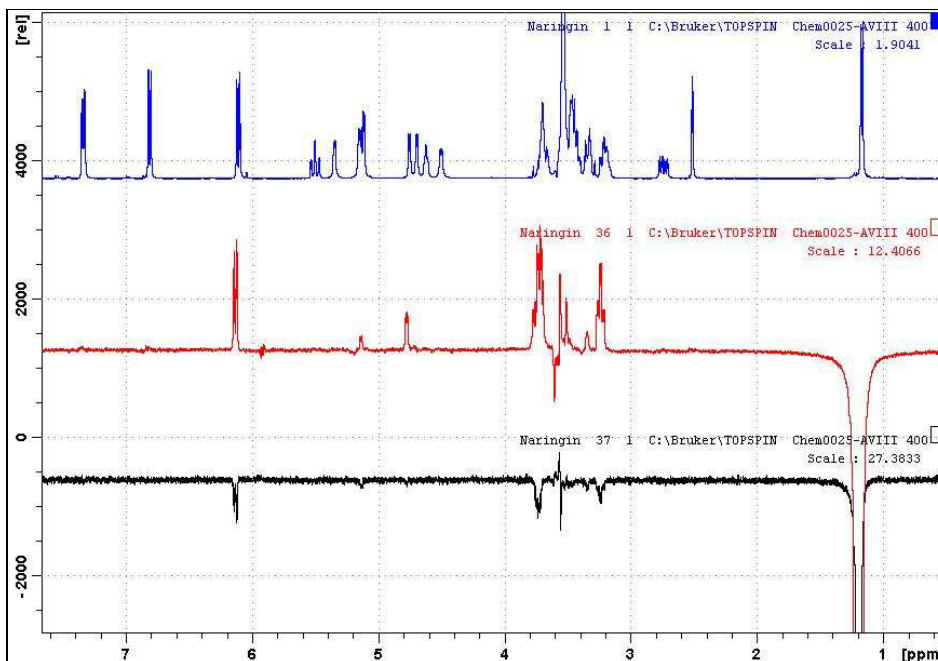
NOESY and SELNOESY peaks may be positive, zero or negative depending on correlation times whereas ROESY and SELROESY peaks are always positive.

In a **classic NOE-difference experiment** a positive NOE is one which affords a positive enhanced signal relative to the residual negative irradiated signal observed when a reference spectrum is subtracted from the irradiated spectrum.



A positive NOE is one in which a positive enhanced peak is observed relative to a negative irradiated peak in a 1D-SELNOESY experiment, or a negative diagonal peak in a 2D-NOESY experiment.

An example of a signal showing a positive ROESY response and a negative NOESY response is shown below.



Upper: ^1H NMR spectrum of naringin (0.5-8 ppm region plotted)

Center: SELROESY spectrum ex the methyl signal at 1.2 ppm

Lower: SELNOESY spectrum ex the methyl signal at 1.2 ppm

2.5 SELNOESY Spectra

Parameter set: **awselnoesy** (+ **getprosol**)

Pulse programme: **selnogp4**

TD = 64 K, **SI** = 64 K, **SW** = 20 ppm.

O1 = Frequency in Hz of signal to be selectively correlated. **O1** Excitation is applied *on resonance* at the middle of SW. Check SW is wide enough.

NS = multiple of 4, 8 or 16, **DS** = 4 or 8.

or **NS x TD0** scans where **TD0** = any positive number.

D1 = 1 sec or other time of your choice.

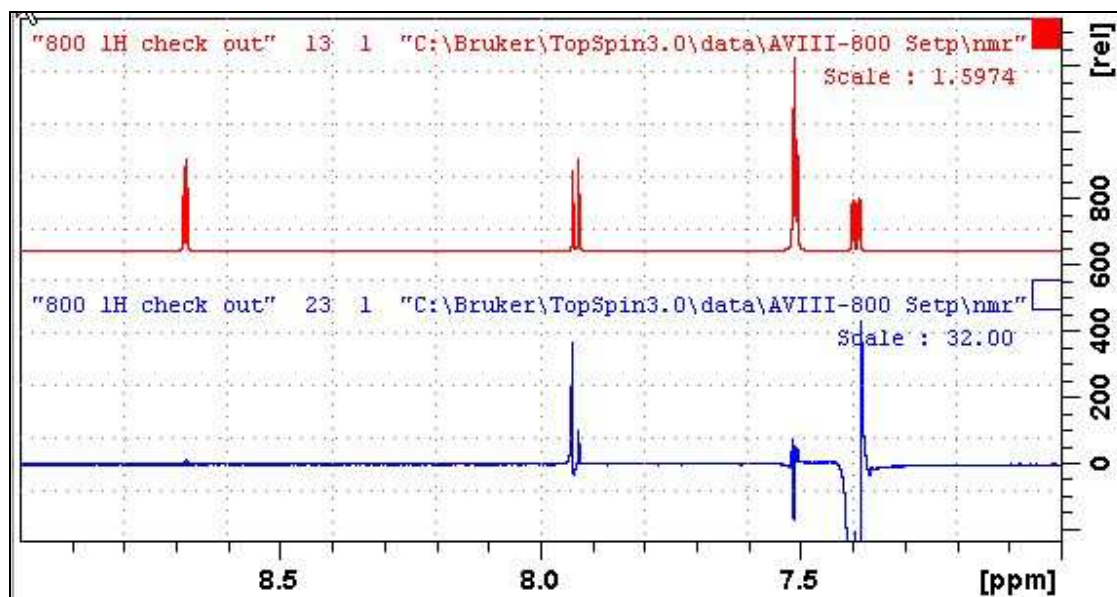
D6 = 0.5 to 0.8 sec (NOESY correlation time).

P12 = 80000 usec, **SPW2** = shaped pulse power read in using the **getprosol** command

PLW10 = TOCSY spin lock power level read in using the **getprosol** command

Process with **EFP** (applies **LB**, typically use 0.1 - 0.3 Hz).

Phase the spectrum to afford a **negative** excited signal. NOESY peaks may be *positive*, *zero* or *negative* depending on correlation times. COSY artifact peaks ex strongly coupled signals may occasionally be present in NOESY spectra.



Upper: 7-9 ppm region of the 800 MHz ^1H NMR spectra of quinine in $\text{D}_6\text{-DMSO}$.

Lower: SELNOSY spectrum ex the signal at 7.39 ppm.

2.6 SELROESY (CW spin locked) Spectra

Parameter set: **awselroesy (+ getprosol)**

Pulse programme: **selrogp**

TD = 64 K, **SI** = 64 K, **SW** = 20 ppm.

O1 = Frequency in Hz of signal to be selectively correlated. **O1** Excitation is applied *on resonance* at the middle of SW. Check SW is wide enough.

NS = multiple of 4, 8 or 16, **DS** = 4 or 8.

or **NS x TD0** scans where **TD0** = any positive number.

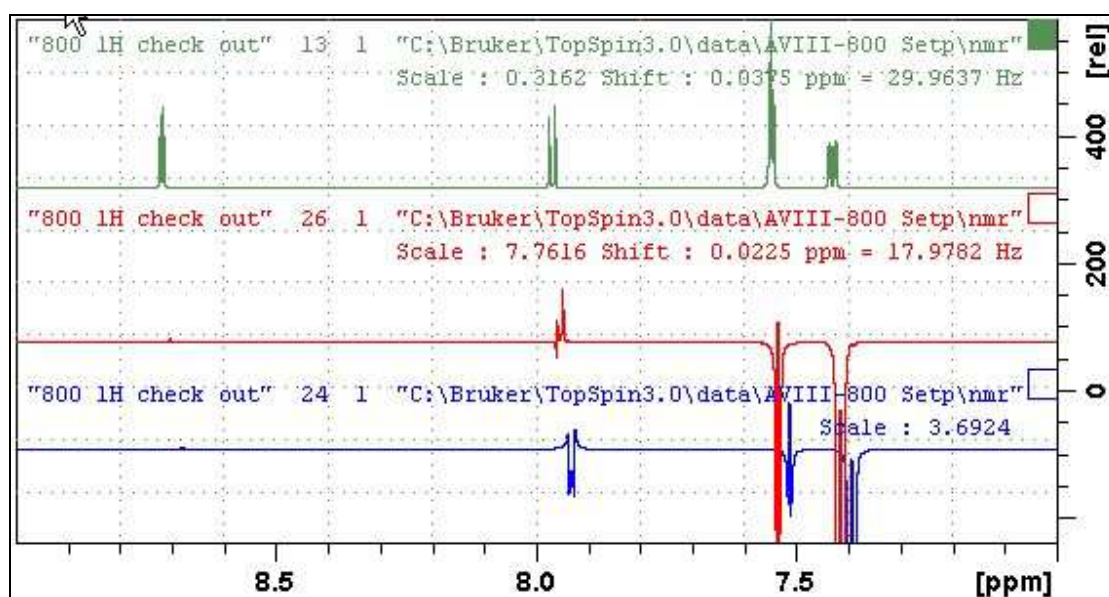
D1 = 2 sec or other time of your choice

P15 = 250000 usec (ROESY spinlock time)

SPW2 = Shaped pulse power level (read in by the getprosol command)

PL11 = ROESY CW spin lock power (read in by the getprosol command)

Process with **EFP** (applies **LB**, typically use 0.1 - 0.3 Hz). *Phase the spectrum to afford a **negative** excited signal and positive ROESY peaks. Negative or antiphase TOCSY artifact peaks may be present in ROESY spectra.*



Upper: 7-9 ppm region of the 800 MHz ^1H NMR spectra of quinine in D_6 -DMSO.

Center: SELROESY spectrum ex the signal at 7.39 ppm with PLW11 = 20.48 db

Lower: SELROESY spectrum ex the signal at 7.39 ppm with PLW11 = 8.48 db

In this example strong negative TOCSY artifact peaks are seen at 7.52 ppm, even when the CW SELROESY spin lock power is attenuated by 12 db (ie: reduced from 8.48 db = the prosol Table value to 20.48 db). TOCSY artifacts are generally much less significant in pulsed spin locked SELROESY.2 spectra (see Section 3.7).

3.7 SELROESY2 (pulsed spin locked) Spectra

Parameter set: **awselroesy2 (+ getprosol)**

Pulse programme: **selrogp.2**

TD = 64 K, **SI** = 64 K, **SW** = 20 ppm.

O1 = Frequency in Hz of signal to be selectively correlated. **O1** Excitation is applied *on resonance* at the middle of SW. Check SW is wide enough.

NS = multiple of 4, 8 or 16, **DS** = 4 or 8.

or **NS x TD0** scans where **TD0** = any positive number.

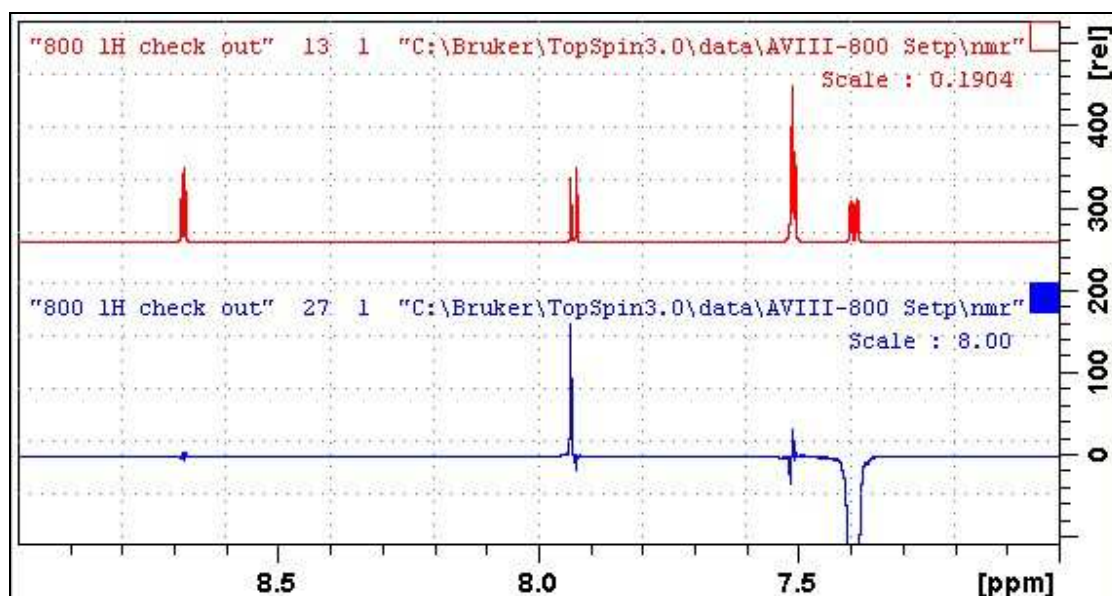
D1 = 2 sec or other time of your choice.

P15 = 250000 usec (ROESY spinlock time)

SPW2 = Shaped pulse power level (read in by the getprosol command).

PLW27 = ROESY pulsed ROESY spinlock power (read in by the getprosol command).

Process with **EFP** (applies **LB**, typically use 0.1 - 0.3 Hz). *Phase the spectrum to afford a **negative** excited signal and positive ROESY peaks.*



Upper: 7-9 ppm region of the 800 MHz ¹H NMR spectra of quinine in D₆-DMSO.

Lower: SELROESY2 spectrum ex the signal at 7.39 ppm with PLW11 = 8.48 db

Antiphase (mixed positive/negative) TOCSY artifact peaks may occasionally be present in SELROESY.2 spectra. TOCSY artifact peaks are generally much less significant in pulsed spin locked SELROESY.2 spectra than is the case for CW spin locked SELROESY spectra..

2.8 SELHSQC and SELHSQCND Spectra

Parameter set: **awselhsqc** or **awselhsqcnd** (+ **getprosol**)

Pulse programme: **awselhsqcgpsisp** or **awselhsqcndgpsisp**

Prior to running a **SELHSQC** experiment run a standard ^{13}C or **DEPT** experiment and determine the **O1** frequency of the ^{13}C signal in **Hz** to be selectively excited. Enter this value as **O2 (Hz)**.

TD = 64 K, **SI** = 64 K.

SW = 20 ppm, **O1P** = 8 ppm. Adjust **SW** and **O1P** as required.

O2 = frequency of the ^{13}C signal in **Hz** to be selectively excited.

NS = multiple of 8 or 16, **DS** = 4 or 8.

or **NS x TD0** scans where **TD0** = any positive number.

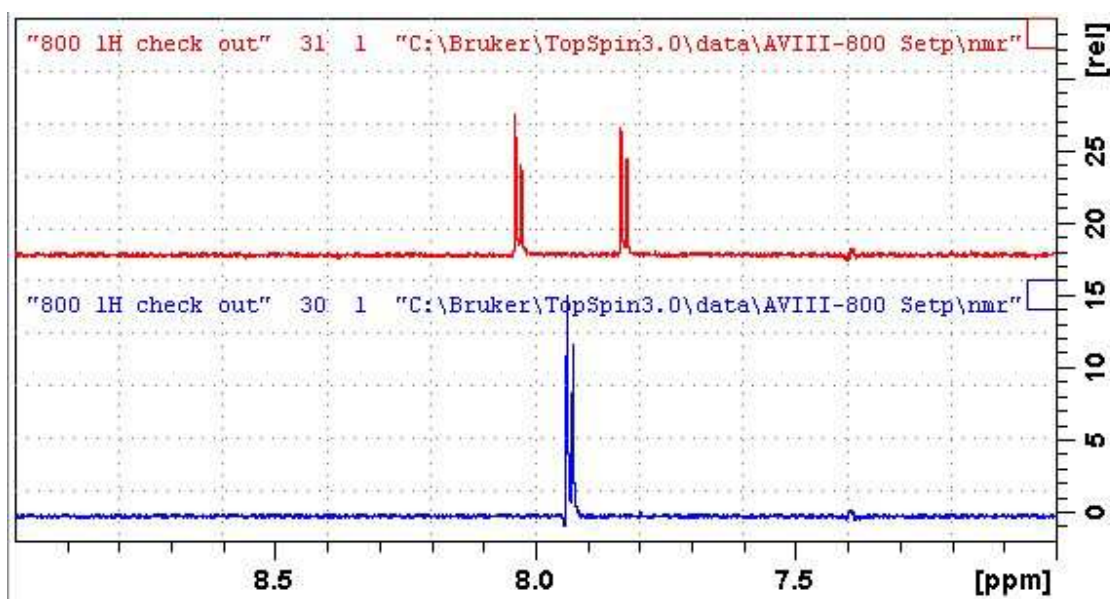
D1 = 1 sec or other value of your choice.

D24 is automatically calculated from **CNST2** ($^1J_{\text{C-H}}$).

CNST2 = $^1J_{\text{C-H}}$; typically 125 to 160 Hz for $\text{sp}^3\text{-sp}^2$ carbons. Furan or pyrrole ring carbons adjacent to hetero atoms will have $^1J = 200\text{-}220$ Hz.

Shaped pulse types and powers are read in by the **getprosol** command.

Process with **EFP** (applies **LB**, typically use 0.1 - 0.3 Hz).



7-9 ppm region of 800 MHz **SELHSQC** (*lower*) and **SELHSQCND** (*upper*) spectra determined for quinine in $\text{D}_6\text{-DMSO}$ with selective excitation of the ^{13}C signal at 131.6 ppm (**O2** = 26475 Hz). The 1J correlated proton signal occurs at 7.95 ppm.

2.9 SELHSQC-DIPSI2 and SELHSQCND-DIPSI2 Spectra

Parameter set: **awselhsqc-dipsi2** or **awselhsqcnd-dipsi2** (+ **getprosol**)

Pulse programme: **awselhsqcgpdigpsisp** or **awselhsqcgpdigpndsisp**

Prior to running a **SELHSQC-DIPSI2** experiment run a standard ^{13}C or **DEPT** experiment and determine the **O1** frequency of the ^{13}C signal in **Hz** to be selectively excited. Enter this value as **O2 (Hz)**.

TD = 64 K, **SI** = 64 K.

SW = 20 ppm, **O1P** = 8 ppm. Adjust **SW** and **O1P** as required.

O2 = frequency of the ^{13}C signal in **Hz** to be selectively excited.

NS = multiple of 8 or 16, **DS** = 4 or 8.

or **NS x TD0** scans where **TD0** = any positive number.

D1 = 1 sec or other value of your choice.

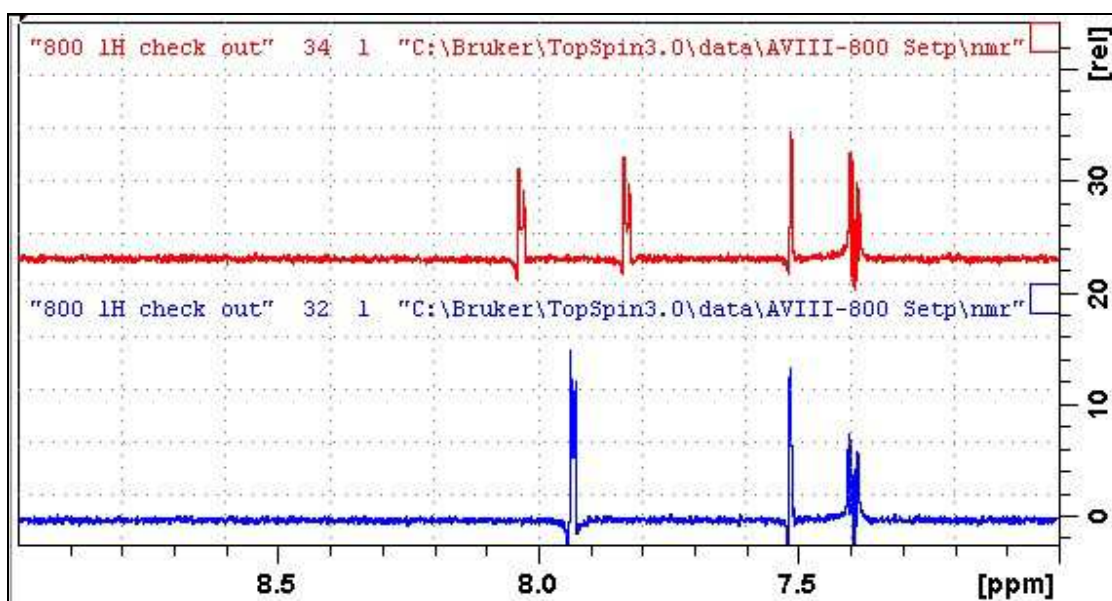
D9 = 80 msec or other time of your choice (6-160 msec).

D24 is automatically calculated from **CNST2** ($^1J_{\text{C-H}}$).

CNST2 = $^1J_{\text{C-H}}$; typically 125 to 160 Hz for $\text{sp}^3\text{-sp}^2$ carbons. Furan or pyrrole ring carbons adjacent to hetero atoms will have $^1J = 200\text{-}220$ Hz.

Shaped pulse types and powers read in by the **getprosol** command

Process with **EFP** (applies **LB**, typically use 0.1 - 0.3 Hz).



7-9 ppm regions of the **SELHSQC-DIPSI2** (*lower*) and **SELHSQCND-DIPSI2** (*upper*) spectra determined for quinine in $\text{D}_6\text{-DMSO}$ with selective excitation of the ^{13}C signal at 131.6 ppm (**O2** = 26475 Hz). The 1J correlated proton signal occurs at 7.95 ppm.

Correlated ^1H NMR signals observed in coupled SELHSQCND-DIPSI2 spectra show 1J , 2J , or nJ $^{13}\text{C}\text{-}^1\text{H}$ couplings depending on the number of bonds between the selectively excited ^{13}C signal and correlated proton signals.