DOSY for Topspin 3.2

Create a new dataset by typing **new** and naming your experiment as needed.

Lock, tune (atma), shim (topshim) and run a normal ^{1}H NMR experiment manually.

Stop the spin.

Create a new experiment by typing **new** and changing the EXPNO to 2 and selecting a new experiment DOSY1D (check getprosol).

Type **ased** and note: **gpz6** – Z-gradient power, **d20** – diffusion time, and **p30** – gradient pulse length.

Set **gpz6** to 2%.

Type **rga**;**zg** to obtain a reference 1D DOSY spectrum in EXPNO 2.

Create a new experiment by typing **new** and changing the EXPNO to 3. Select "use current parameters" and clicking save.

Type **ased** and set **gpz6** to 95%. Type **zg** (not **rga**) and acquire another 1D spectrum. Note: **rg** and **ns** must match spectrum in EXPNO 2.

To optimize the experiment so that the diffusion coefficients are accurate - compare the two spectra on the same screen using the multiple display icon. Select the 2nd spectrum (EXPNO 3) and decrease the intensity until the peaks intensity matches the 1st spectrum (EXPNO 2). Read the scaling factor.

If the factor number is less than 0.02, the current spectrum does not have enough signal intensity. To correct this decrease the **p30** (in **ased**). Rerun the spectrum (in EXPNO 3) until the factor is between 0.02-0.05 (2%-5% intensity of spectrum in EXPNO 2). Adjust **p30** as necessary never increasing it more than 4000µs. Note the **p30** and **d20** which results in the correct attenuation.

Create a new experiment by typing **new** and changing the EXPNO to 4 selecting a new experiment DOSY1D (check getprosol).

Input **p30** and **d20** from EXPNO 3. Adjust **sw** and **o1p** and **ns** if necessary.
Input the value of **rg** from EXPNO 3 (same as EXPNO 2).

Type **dosy** to begin the experiment. Answer the questions: The first gradient amplitude should be 2-5%, the final gradient amplitude should be 90-95%, the number of points (number of spectra acquired for the gradient decay) can be 32 (the larger the more accurate – and longer experiment), ramp type is l (linear) and click on OK to start.

When the acquisition is finished, type **xf2** to begin the data processing. Phase this spectrum manually.

Type **abs2** and then load the diffusion parameters by typing **setdiffparm**.

To view the diffusion coefficients, type **dosy2d**. Plot the data using the Plot Editor.

Reference the spectrum using the **sr** value from your referenced 1D proton.