Saturation Transfer Difference (STD) NMR
ref: Mayer and Meyer, JACS (2001) 123:6108

(1) Start with a regular 1H spectrum
lock, shim, tuning, sample check, reference phase, reference intensity,
record any optimized parameters:
D1= o1p= SW=. TD =

(2) create a new experiment number (“edc” OR “ix” OR “wra” OR . . .)
rpar satxfr-bbo
Update your parameters: D1, o1p, SW, TD

(3) set the frequency of irradiation of gaussian pulse train:
eda --> sp07 --> offset of sp2 (NEED TO ALREADY KNOW THE OFFSET, can be determined from the "zg" reference spectrum of step 1)

rga
zg

(NOTE saturation transfer of on vs. off resonance irradiation - either separately or alternatively vis phase cycling)

STD
protein only:
1. selective saturation leads to efficient/rapid total saturation (in the spin-diffusion limit, i.e. high field and high MW, saturation times of 250ms were sufficient)
2. Tip filter (~30ms) removes broad protein peaks and leaves sharpt lines due to small molecules (important for clarity where proteins and ligand signals overlap in 1D 1H spectra)
3. 1nmole protein (MW>10kDa)

protein-ligands:
1. on/off rates (Kd ~ exp-03(=mM) to exp-08(=nM)
2. optimal excess (>20-fold)
3. strongest signals = closest contact with the protein

STD Gaussian calibrations
86Hz (mayer+meyer) power = 4.3 nutations
if using a 50ms gaussian pulse - how much power do we need?

1. reference phase = zg (pulprog)
2. pulprog selzg (single gaussian and acquire)
gaussian = sp1 & p11
3. start with approx amplitude (sp1) equivalent to a 5.8ms 180
4. paropt on pulse duration (constant amplitude) to estimate the number of nutations at 50ms (86Hz = 4.3 nutations)(paropt: 2.5m, 2.5m, 21)(number 20 is 50ms)
5. to fine-tune sp1, paropt of sp1 holding 50m constant