

## **Ultra-clean pure shift NMR with optimal water suppression for analysis of aqueous pharmaceutical samples**

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### *Electronic Supporting Information*

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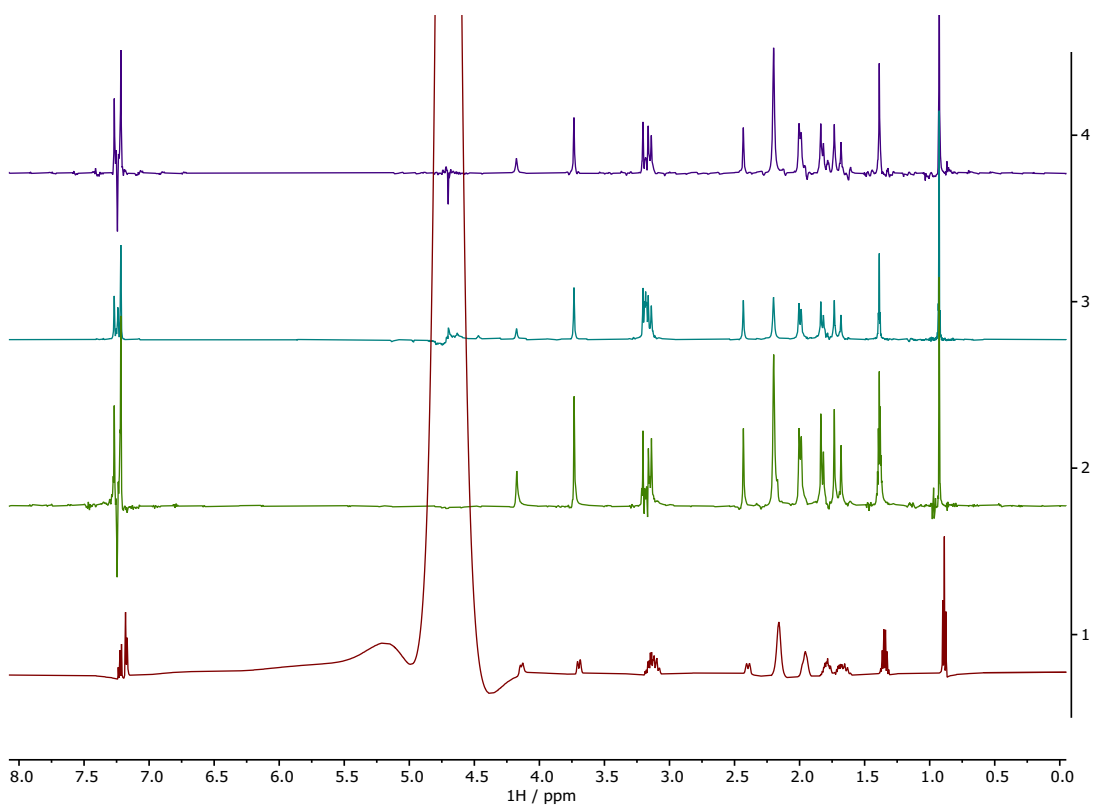
#### Sample information:

- 1) Bupivacaine HCl: 10.9 mg of bupivacaine hydrochloride from Sigma-Aldrich (lot P500128, catalog # PHR1128-1G) was diluted in 0.55 mL of a mixture of 90% H<sub>2</sub>O/10% D<sub>2</sub>O (v/v), and this solution was transferred to a 5 mm NMR tube.
- 2) Aurobasidin A (AbA): Approximately 2 mg of purified AbA from Merck & Co. Inc., Kenilworth, NJ, USA was dissolved in 150  $\mu$ L of a mixture of CD<sub>3</sub>CN:H<sub>2</sub>O (*vide* manuscript) and transferred to a 3 mm NMR tube.

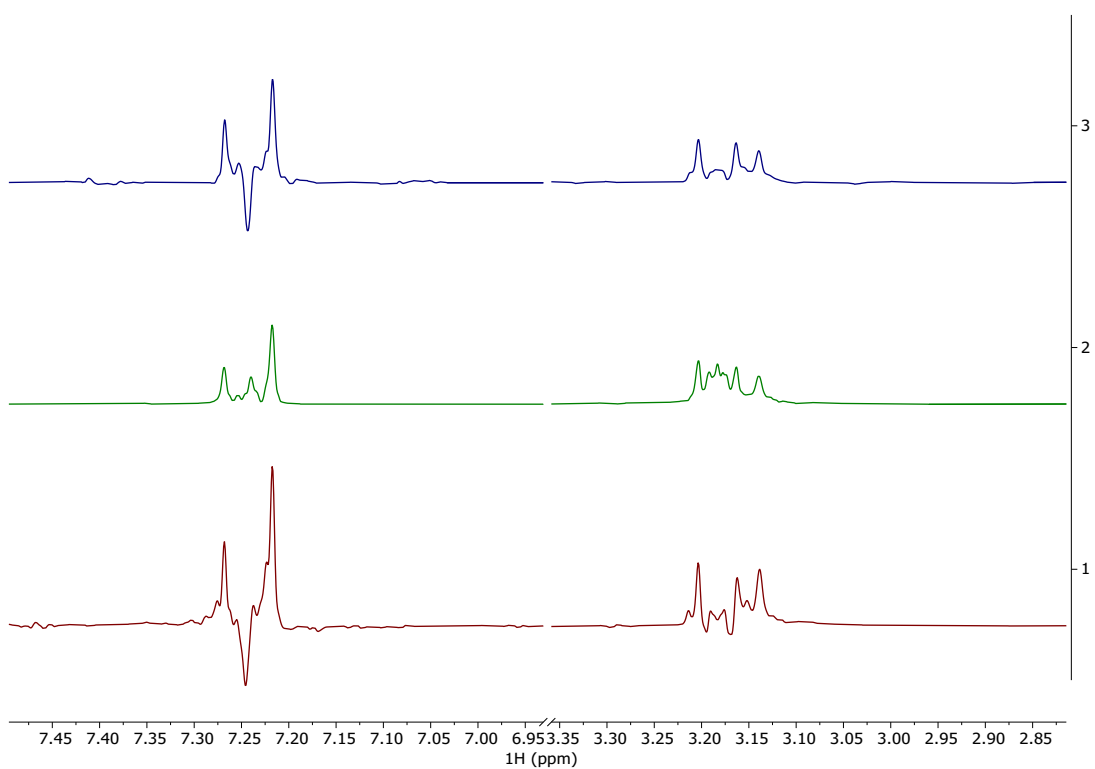
#### NMR parameters and instrumentation:

All data was acquired in a Avance III 600 MHz Bruker instrument equipped with a 5mm TCI cryoprobe at 308 K. 8.0  $\mu$ s was used for the duration of hard 90° <sup>1</sup>H pulses for all experiments. The duration of the SAPPHIRE NOESY pre-saturation, iES and iW5 were approximately 1h 12 min, 44min, and 42 min, respectively, for the AbA sample. The duration of the double Saltire was set to 30ms, with a bandwidth of 10 kHz and flip angle of 15°, for all pure shift experiments. RSNOB pulses of 37 ms duration (50 Hz bandwidth) were used for all ES experiments. SINE.100 was used for gradient shape in all pure shift experiments, except in the double Saltire element, where RECT.1 was used. 8 scans and 4096 complex points were used in the acquisition of all SAPPHIRE experiments, with 4 increments in the SAPPHIRE dimension (TD2) and 50 chunks (TD1) of 10 ms each. The delay to keep T2 weighting constant between SAPPHIRE increments (d2) was set to 6 ms for all SAPPHIRE experiments. 4 drop points (cnst4) was used for all pure shift experiments.

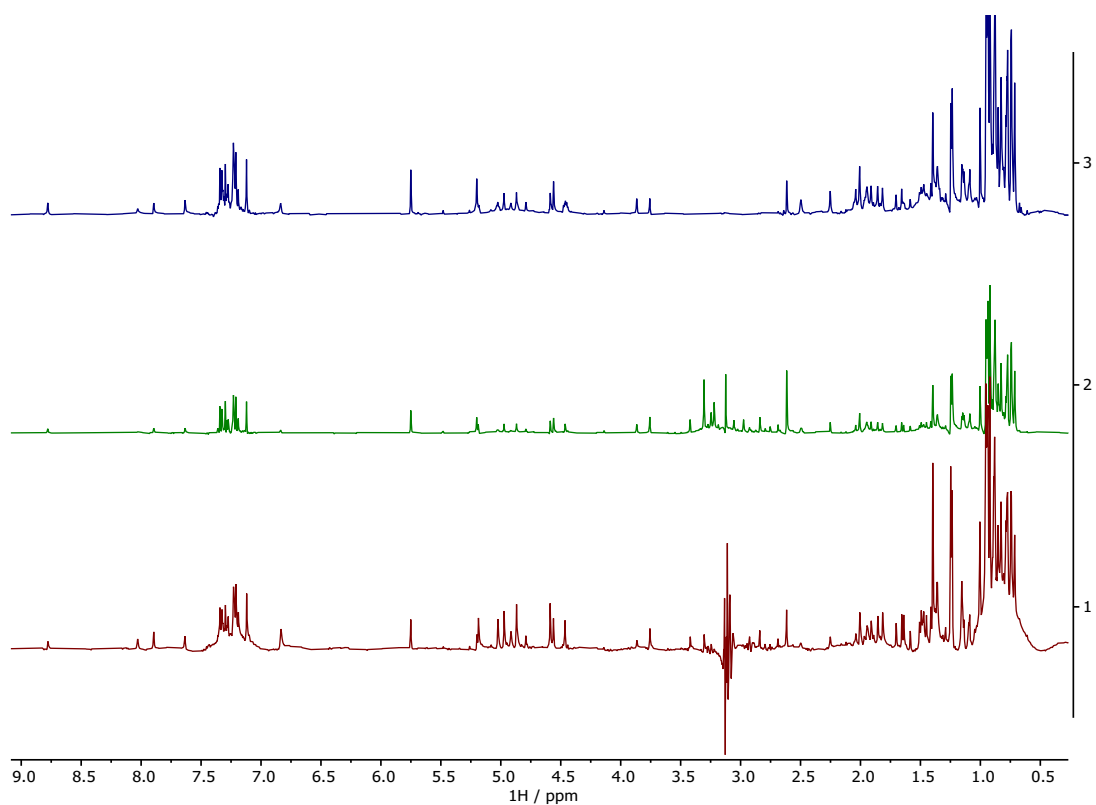
Data acquisition and processing of SAPPHIRE data follow the same steps as described by Moutzouri *et. al.* [1] The interferogram FIDs were reconstructed with TopSpin 3.x macros available at <https://www.nmr.chemistry.manchester.ac.uk/>. The reconstruction for SAPPHIRE data is a two-step process: (i) the FID chunks are arrayed to form new FID interferograms, one per SAPPHIRE increment; (ii) each SAPPHIRE increment is added for the final averaged pure shift FID. For TopSpin 4.x the macro "sertoint.ptg" should be used before step (i) to convert the FID file into integer.



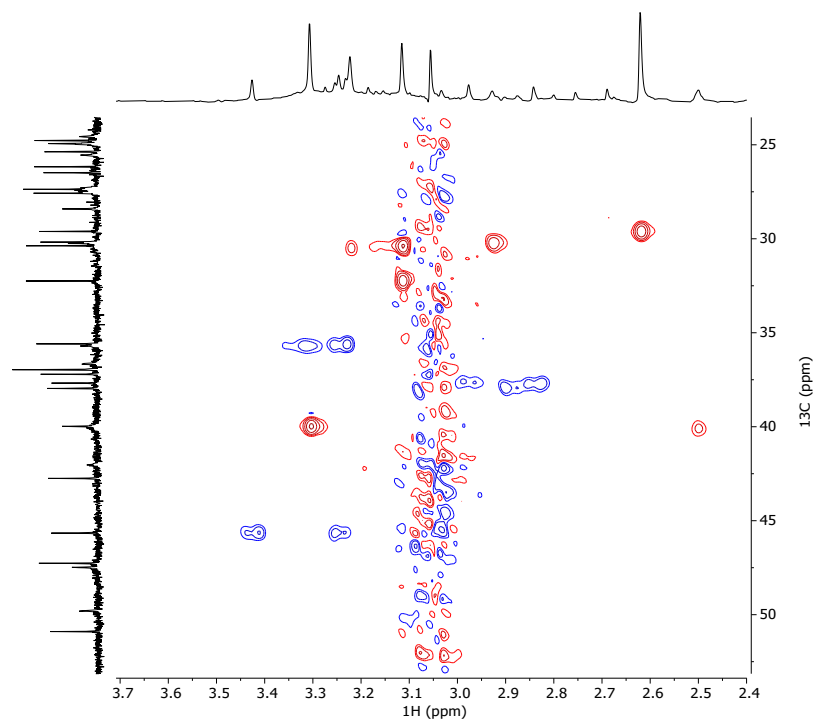
**Fig. ESI 1.**  $^1\text{H}$  NMR pure shift spectra of bupivacaine hydrochloride in 90%  $\text{H}_2\text{O}/10\%$   $\text{D}_2\text{O}$  (v/v) (1) conventional  $^1\text{H}$ , (2) SAPHIRE-iW5, (3) SAPHIRE-iES, and (4) PSYCHE-NOESY-pre-saturation.



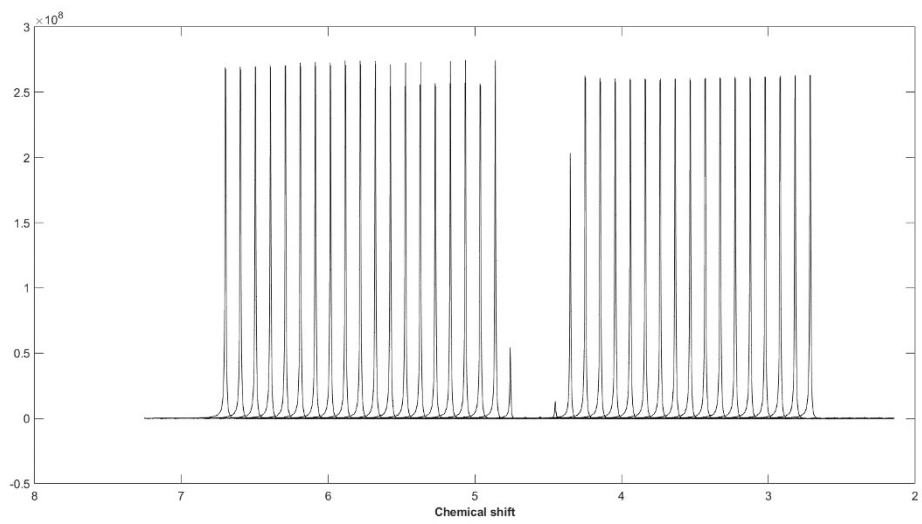
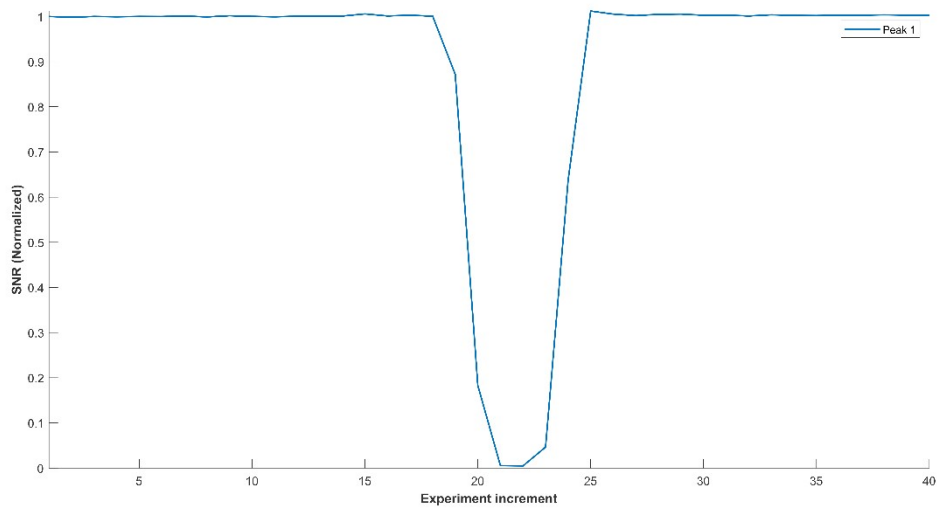
**Fig. ESI 2.** Zoom of Fig. ESI 1 for strongly coupled signals. (1) SAPHIRE-iW5, (2) SAPHIRE-iES, and (3) PSYCHE-NOESY-pre-saturation.



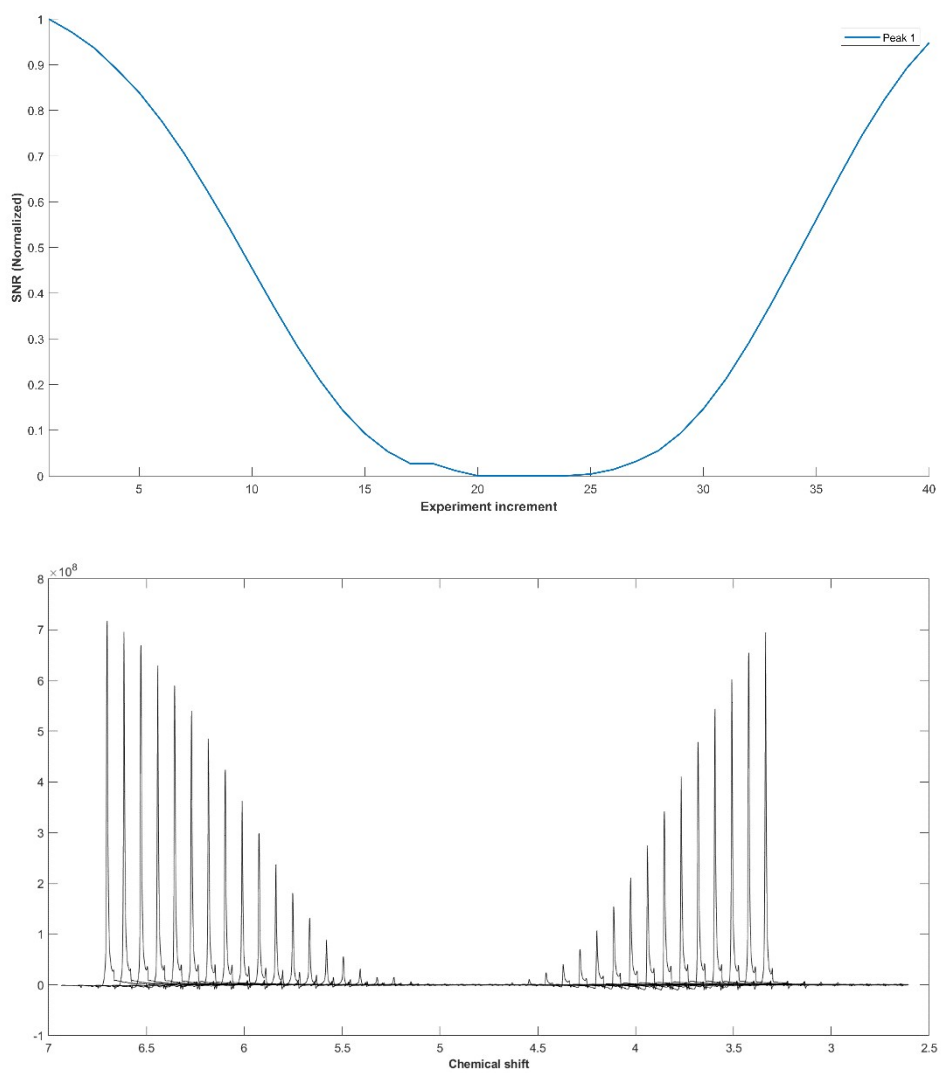
**Fig. ESI 3.** Full  $^1\text{H}$  NMR pure shift spectra of Aureobasidin A 10%  $\text{H}_2\text{O}/90\%$   $\text{CD}_3\text{CN}$  for: (1) SAPHIRE-NOESY-pre-saturation, (2) SAPHIRE-iES, and (3) SAPHIRE-iW5.



**Fig ESI 4.** HSQC real-time pure shift with multiplicity editing of Aureobasidin A in 90%  $\text{H}_2\text{O}/10\%$   $\text{D}_2\text{O}$  (v/v). Vertical projection was replaced by  $^{13}\text{C}\{^1\text{H}\}$  spectrum and top projection was replaced by SAPHIRE-iES



**Fig ESI 5.** Suppression profiles for the PSYCHE-SAPPHIRE-iES experiment



**Fig ESI 6.** Suppression profiles for the PSYCHE-SAPPHIRE-iW5 experiment

```

;sapphire_es
; updated 21/06/2022 RAHWAY
;
;   Guilherme Dal Poggetto, PhD
;   email: guilherme.dal.poggetto@merck.com
;   Analytical Enabling Capabilities - Rahway, NJ
;
;       Sideband Averaging with Periodic PHase
;       Incrementation of Residual J Evolution
;       for the acquisition of clean PSYCHE pure shift spectra
; with excitation sculpting
;
;       The pulse sequence involves a 3D acquisition scheme.
;       F3 is the direct dimension. F1 is the incremented dimension
for the reconstruction of the pure shift interferogram.
;       F2 is the incremented dimension for the J-evolution.
;
;       The data can be reconstructed using the two following AU
programs (downloaded from: http://nmr.chemistry.manchester.ac.uk)
;           1) pm_pshift (produces pure shift spectra for each
different J-evolution time, adjusting the length of the first chunk
appropriately)
;           2) pm_fidadd (averages the pure shift spectra acquired
with different J-evolution times)
;
;$CLASS=HighRes
;$DIM=3D
;$TYPE=
;$SUBTYPE=
;$COMMENT=

#include <Avance.incl>
#include <Grad.incl>
#include <Delay.incl>

define delay tauA
define delay tauAA
define delay tauB
define delay tauBB
define delay tauBBB
define delay tauBBBB
define delay tauC
define delay tauD

"p2=p1*2"

"l0=0"
"l8=0"

"in0=inf1/2"
"in10=inf2"

"d0=inf1/2"
"d10=inf2"

```

```

"d30=in0/2"
"d40=in0/2-in10"

"cnst5=(td2/2)+1"

"tauA=0"
"tauAA=inf1/4"
"tauB=d2-p17-2*d16-20u"
"tauBB=d2-p17-2*d16-20u-inf2"
"tauBBB=d2-p17-2*d16-20u"
"tauBBBB=d2-p17-2*d16-20u+inf2"
"tauC=inf2"
"tauD=(dw*2*cnst4)"

"cnst50=(cnst20/360)*sqrt((2*cnst21)/(p40/2000000))"
"p30=1000000.0/(cnst50*4)"

"cnst31= (p30/p1) * (p30/p1)"
"spw40=plw1/cnst31"

"p10=p40"

;%%%%%%%% WaveMaker Parameters %%%%%%%%%
"d11=30m+1s/(cnst12)-1s/(cnst12)"
"d11=30m+1s/(cnst13)-1s/(cnst13)"
;sp12:wvm:gdp_rsnob:f1 rsnob(cnst12 Hz, cnst13 ppm; PA=0.5,
NPOINTS=5000);

"d11=30m"

"acqt0=0"
baseopt_echo
aqseq 312

1 ze
2 50m          d1 p11:f1
3 50u UNBLKGRAD

if "l8 < cnst5"
{
    "tauA=(l8*in10)"
    "tauB=d2-p17-2*d16-20u-(l8*in10)"
    "d30=(in0/2+(l8*in10))+((l0-1)*in0)"
    "tauBBB=(d2-p17-2*d16-20u)-(l8*in10)"

    p1 ph1

    if "l0==0"
    {
        tauA
    }
else

```



```

        {
            tauAA
        }
        p16:gp1
        d16
        8u
        p2 ph2
        4u p10:f1
        (p12:sp12 ph5):f1
        4u p11:f1
        p16:gp1
        d16

if "l0==0"
{
    tauA
}
else
{
    tauAA
}

if "l0==0"
{
}
else
{
    d30
}

if "l0==0"
{
    tauB
}
else
{
    tauBBB
}

        d16
        p17:gp2
        d16
        20u p10:f1
        ;
        ( center (p40:sp40 ph3):f1 (p10:gp10) )
        ;
        20u p11:f1
        d16
        p17:gp2
        d16

if "l0==0"

```

```

        {
            tauB
        }
else
    {
        tauBBB

        tauD
        p18:gp3
        d16 p10:f1
        4u
        (p12:sp12 ph6):f1
        4u p11:f1
        p2 ph4
        8u
        p18:gp3
        d16 BLKGRAD
    if "l0==0"
        {
        }
    else
        {
            d30
        }

lab1, goto lab7
    }

else
    {
        "tauC=(in10)+((18-cnst5)*in10)"
        "tauBB=(d2-p17-2*d16-20u-in10)-((18-cnst5)*in10)"
        "d40=((in0/2-in10)-((18-cnst5)*in10))+((10-1)*in0)"
        "tauBBBB=(d2-p17-2*d16-20u+in10)+((18-cnst5)*in10)"

        p1 ph1
        if "l0==0"
            {
            }
        else
            {
                tauAA

                p16:gp1
                d16
                8u
                p2 ph2
                4u p10:f1
            }
    }

```

```

                (p12:sp12 ph5):f1
                4u p11:f1
                p16:gp1
                d16
            if "l0==0"
            {
            }
else
            {
                tauAA
            }

            if "l0==0"
            {
            }
            else
            {
                d40
            }

            if "l0==0"
            {
                tauBB
            }
else
            {
                tauBBBB
            }

                d16
                p17:gp2
                d16
            20u p10:f1
            ;
            ( center (p40:sp40 ph3):f1 (p10:gp10) )
            ;
            20u p11:f1
                d16
                p17:gp2
                d16
            if "l0==0"
            {
                tauBB
            }
else
            {
                tauBBBB
            }

            tauD

            if "l0==0"

```

```

        {
            tauC
        }
    else
        {
            p18:gp3
            d16 p10:f1
            4u
            (p12:sp12 ph6):f1
            4u p11:f1
            p2 ph4
            8u
            p18:gp3
            d16 BLKGRAD

            if "l0==0"
                {
                    tauC
                }
            else
                {
                }

            if "l0==0"
                {
                }
            else
                {
                    d40
                }
        }

```

```

lab2, goto lab7
    }

```

```

lab7, go=2 ph31
50m mc #0 to 2
    F1QF(calclc(l0,1))
    F2QF(calclc(l8,1))
exit

```

```

ph1 =0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1
ph2 =0 0 0 0 1 1 1 1 0 0 0 0 1 1 1 1
ph3 =0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1
ph4 =0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1
ph5 =2 2 2 2 3 3 3 3 2 2 2 2 3 3 3 3
ph6 =2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3
ph31=0 2 3 1 2 0 1 3 2 0 1 3 0 2 3 1

```

```

;POWER LEVEL
;p10 : zero power (0W)
;p11 : power level for pulse (default)
;spw40 : power level of PSYCHE selective pulse

;PULSE DURATION
;p1: high power 90 pulse width
;p2: high power 180 pulse width
;p10 : duration of weak gradient during PSYCHE pulse element
;p12 : duration of water excitation sculpting
;p40 : duration of double-chirp PSYCHE pulse element

;PULSE SHAPE
;spnam12 : file name for the 180 water excitation sculpting
;spnam40: file name for PSYCHE pulse element

;GRADIENT DURATION
;p16: CTP gradient pulse width
;p17: CTP gradient pulse width
;p18: CTP gradient pulse width

;GRADIENT SHAPE
;gpnam1: SINE.100
;gpnam2: SINE.100
;gpnam3: SINE.100
;gpnam10: RECT.1

;GRADIENT STRENGTH
;gpz1 : CTP gradient [77%]
;gpz2 : CTP gradient [49%]
;gpz3 : CTP gradient [63%]
;gpz10 : weak gradient during PSYCHE element (1-4%)
;gpz10 : weak gradient during PSYCHE element (1-4%)

;DELAYS
;d1: relaxation delay; 1-5 * T1
;d16: gradient stabilisation delay
;d2: delay to keep the T2 weighting constant between the pure shift
experiments acquired with different evolution time [greater than
1/4SW1+p16+2*d16]

;CONSTANTS
;cnst4: number of points to drop when collecting FID
;cnst5:(td2/2)+1
;cnst12: bandwidth for selective inversion pulse (in Hz)
;cnst13: chemical shift for selective inversion pulse (in ppm)
;cnst20: desired flip angle for PSYCHE pulse element (degree)
(normally 10-25)
;cnst21: bandwidth of each chirp in PSYCHE pulse element (Hz)
(normally 10000)

```

```
;OTHERS
;td1: number of chunks to be acquired
;td2: number of different J evolution times to be averaged (N)
;ns: 8 * n, total number of scans
;ds: 8, number of dummy scans
;sw1: sw3/n (n must be an integer number)
;sw2: 2*N*sw1 where N is the steps in the SAPPHIRE suppression (this
pulse sequence works when N is an even number)
;2sw3/sw2 should be integer
;in10: 1/sw2
;l8: loop counter for F2 dimension
;l0: loop counter for F1 dimension
;FnMODE1: QF
;FnMODE2: QF
```

```
;sapphire_w5
```

```

; updated 07/06/2022 RAHWAY
;
;   Guilherme Dal Poggetto, PhD
;   email: guilherme.dal.poggetto@merck.com
;   Analytical Enabling Capabilities - Rahway, NJ
;
;   Sideband Averaging with Periodic PHase
;   Incrementation of Residual J Evolution
;   for the acquisition of clean PSYCHE pure shift spectra
;   Hard 180o pulses were replaced by W5 water-saturation
;
;   The pulse sequence involves a 3D acquisition scheme.
;   F3 is the direct dimension. F1 is the incremented dimension
for the reconstruction of the pure shift interferogram.
;   F2 is the incremented dimension for the J-evolution.
;
;   The data can be reconstructed using the two following AU
programs (downloaded from: http://nmr.chemistry.manchester.ac.uk)
;       1) pm_pshift (produces pure shift spectra for each
different J-evolution time, adjusting the length of the first chunk
appropriately)
;       2) pm_fidadd (averages the pure shift spectra acquired
with different J-evolution times)
;
; $CLASS=HighRes
; $DIM=3D
; $TYPE=
; $SUBTYPE=
; $COMMENT=

#include <Avance.incl>
#include <Grad.incl>
#include <Delay.incl>

define delay tauA
define delay tauAA
define delay tauB
define delay tauBB
define delay tauBBB
define delay tauBBBB
define delay tauC
define delay tauD

"p2=p1*2"

"l0=0"
"l8=0"

"in0=inf1/2"
"in10=inf2"

"d0=inf1/2"
"d10=inf2"
"d30=in0/2"

```

```

"d40=in0/2-in10"

"cnst5=(td2/2)+1"

"tauA=0"
"tauAA=inf1/4"
"tauB=d2-p17-2*d16-20u"
"tauBB=d2-p17-2*d16-20u-inf2"
"tauBBB=d2-p17-2*d16-20u"
"tauBBBB=d2-p17-2*d16-20u+inf2"
"tauC=inf2"
"tauD=(dw*2*cnst4)"

"cnst50=(cnst20/360)*sqrt((2*cnst21)/(p40/2000000))"
"p30=1000000.0/(cnst50*4)"

"cnst31= (p30/p1) * (p30/p1)"
"spw40=plw1/cnst31"

"p10=p40"

"d11=d11+cnst7*d11-cnst7*d11"
"d11=d11+cnst29*d11-cnst29*d11"
"cnst28=01"
"cnst30=(cnst29*bf1)-cnst28"
"cnst27=0"

"p27=1000000.0/(cnst6*4)"
"cnst46= (p27/p1) * (p27/p1)"
"plw18=plw1/cnst46"
"cnst7=18*d19+5.95*p27+4*d12"

"d11=30m"
"d12=20u"
"acqt0=0"
baseopt_echo

aqseq 312

1 ze
2 50m
    d1 p11:f1
3 50u UNBLKGRAD

if "l8 < cnst5"
{
    "tauA=(18*in10)"
    "tauB=d2-p17-2*d16-20u-(18*in10)"
    "d30=(in0/2+(18*in10))+((l0-1)*in0)"
    "tauBBB=(d2-p17-2*d16-20u)-(18*in10)"

    p1 ph1

```



```

if "l0==0"
{
    tauA
}
else
{
    tauAA

    p16:gp1
    d16 p18:f1
    d12 fq=cnst30:f1
    d12
    p27*0.087 ph2
    d19*2
    p27*0.206 ph2
    d19*2
    p27*0.413 ph2
    d19*2
    p27*0.778 ph2
    d19*2
    p27*1.491 ph2
    d19*2
    p27*1.491 ph3
    d19*2
    p27*0.778 ph3
    d19*2
    p27*0.413 ph3
    d19*2
    p27*0.206 ph3
    d19*2
    p27*0.087 ph3
    d12 fq=cnst27:f1
    d12 p11:f1
    p16:gp1
    d16

```

```

if "l0==0"
{
    tauA
}
else
{
    tauAA
}

```

```

if "l0==0"
{
}
else
{
    d30
}

```

```

if "l0==0"
{
    tauB
}
else
{
    tauBBB

    d16
    p17:gp2
    d16
    20u p10:f1
    ;
    ( center (p40:sp40 ph4):f1 (p10:gp10) )
    ;
    20u p11:f1
    d16
    p17:gp2
    d16

if "l0==0"
{
    tauB
}
else
{
    tauBBB

    tauD
    p18:gp3
    d16 p118:f1
    d12 fq=cnst30:f1
    d12
    p27*0.087 ph5
    d19*2
    p27*0.206 ph5
    d19*2
    p27*0.413 ph5
    d19*2
    p27*0.778 ph5
    d19*2
    p27*1.491 ph5
    d19*2
    p27*1.491 ph6
    d19*2
    p27*0.778 ph6
    d19*2
    p27*0.413 ph6
    d19*2
    p27*0.206 ph6
    d19*2

```

```

p27*0.087 ph6
d12 fq=cnst27:f1
d12 p11:f1
p18:gp3
d16 BLKGRAD
if "l0==0"
{
}
else
{
d30
}

lab1, goto lab7
}

else
{
"tauC=(in10)+((18-cnst5)*in10)"
"tauBB=(d2-p17-2*d16-20u-in10)-((18-cnst5)*in10)"
"d40=((in0/2-in10)-((18-cnst5)*in10))+((l0-1)*in0)"
"tauBBBB=(d2-p17-2*d16-20u+in10)+((18-cnst5)*in10)"

p1 ph1
if "l0==0"
{
}
else
{
tauAA

p16:gp1
d16 p118:f1
d12 fq=cnst30:f1
d12
p27*0.087 ph2
d19*2
p27*0.206 ph2
d19*2
p27*0.413 ph2
d19*2
p27*0.778 ph2
d19*2
p27*1.491 ph2
d19*2
p27*1.491 ph3
d19*2
p27*0.778 ph3
d19*2

```

```

p27*0.413 ph3
d19*2
p27*0.206 ph3
d19*2
p27*0.087 ph3
d12 fq=cnst27:f1
d12 p11:f1
p16:gp1
d16
    if "l0==0"
    {
    }
else
    {
        tauAA
    }
    if "l0==0"
    {
    }
    else
    {
        d40
    }
    if "l0==0"
    {
        tauBB
    }
else
    {
        tauBBBB
    }

    d16
    p17:gp2
    d16
    20u p10:f1
    ;
    ( center (p40:sp40 ph4):f1 (p10:gp10) )
    ;
    20u p11:f1
    d16
    p17:gp2
    d16
    if "l0==0"
    {
        tauBB
    }
else
    {
        tauBBBB
    }

```

```

    }
    tauD
    if "l0==0"
    {
        tauC
    }
else
    {
    }

    p18:gp3
    d16 p18:f1
    d12 fq=cnst30:f1
    d12
    p27*0.087 ph5
    d19*2
    p27*0.206 ph5
    d19*2
    p27*0.413 ph5
    d19*2
    p27*0.778 ph5
    d19*2
    p27*1.491 ph5
    d19*2
    p27*1.491 ph6
    d19*2
    p27*0.778 ph6
    d19*2
    p27*0.413 ph6
    d19*2
    p27*0.206 ph6
    d19*2
    p27*0.087 ph6
    d12 fq=cnst27:f1
    d12 p11:f1
    p18:gp3
    d16 BLKGRAD

    if "l0==0"
    {
        tauC
    }
else
    {
    }

    if "l0==0"
    {
    }
else

```

```
{
                                d40
}
```

```
lab2, goto lab7
      }
```

```
lab7, go=2 ph31
50m mc #0 to 2
      F1QF(calclc(10,1))
      F2QF(calclc(18,1))
exit
```

```
ph1 =0 0 0 0 0 0 0 0 2 2 2 2 2 2 2 2 0 0 0 0 0 0 0 0 2 2 2 2 2 2 2 2
ph2 =0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1 0 0 1 1
ph3 =2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3 2 2 3 3
ph4 =0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 2 3 2 3 2 3 2 3 2 3 2 3 2 3 2 3
ph5 =0 0 0 0 1 1 1 1 0 0 0 0 1 1 1 1 0 0 0 0 1 1 1 1 0 0 0 0 1 1 1 1
ph6 =2 2 2 2 3 3 3 3 2 2 2 2 3 3 3 3 2 2 2 2 3 3 3 3 2 2 2 2 3 3 3 3

ph31=0 2 2 0 2 0 0 2 2 0 0 2 0 2 2 0 0 2 2 0 2 0 0 2 2 0 0 2 2 0 2 2 0
```

```
;POWER LEVEL
;p10 : zero power (0W)
;p11 : power level for pulse (default)
;p118 : power level for 3-9-19-pulse (watergate)
;spw40 : power level of PSYCHE selective pulse
```

```
;PULSE DURATION
;p1: high power 90 pulse width
;p2: high power 180 pulse width
;p10 : duration of weak gradient during PSYCHE pulse element
;p27 : 90 degree pulse at p118
;p40 : duration of double-chirp PSYCHE pulse element
```

```
;PULSE SHAPE
;spnam40: file name for PSYCHE pulse element
```

```
;GRADIENT DURATION
;p16: CTP gradient pulse width
;p17: CTP gradient pulse width
;p18: CTP gradient pulse width
```

```
;GRADIENT SHAPE
;gpnam1: SINE.100
;gpnam2: SINE.100
;gpnam3: SINE.100
;gpnam10: RECT.1
```

```
;GRADIENT STRENGTH
```

```

;gpz1 : CTP gradient [77%]
;gpz2 : CTP gradient [49%]
;gpz3 : CTP gradient [63%]
;gpz10 : weak gradient during PSYCHE element (1-4%)

;DELAYS
;d1: relaxation delay; 1-5 * T1
;d16: gradient stabilisation delay
;d2: delay to keep the T2 weighting constant between the pure shift
experiments acquired with different evolution time [greater than
1/4SW1+p16+2*d16]
;d19: delay for binomial water suppression
;    d19 = (1/(2*cnst10)), d = distance of next null (in Hz)

;CONSTANTS
;cnst4: number of points to drop when collecting FID
;cnst5:(td2/2)+1
;cnst6: bandwidth of WATERGATE transfer [10k - 20k Hz]
;cnst10: distance of next null (in Hz) [2500-5000 Hz]
;cnst17: duration of W5 pulse (in sec)
;cnst20: desired flip angle for PSYCHE pulse element (degree)
(normally 10-25)
;cnst21: bandwidth of each chirp in PSYCHE pulse element (Hz)
(normally 10000)
;cnst29: solvent frequency (in ppm)

;OTHERS
;td1: number of chunks to be acquired
;td2: number of different J evolution times to be averaged (N)
;ns: 8 * n, total number of scans
;ds: 8, number of dummy scans
;sw1: sw3/n (n must be an integer number)
;sw2: 2*N*sw1 where N is the steps in the SAPPHIRE suppression (this
pulse sequence works when N is an even number)
;2sw3/sw2 should be integer
;in10: 1/sw2
;l8: loop counter for F2 dimension
;l0: loop counter for F1 dimension
;FnMODE1: QF
;FnMODE2: QF

```

REFERENCES

- (1) P. Moutzouri, Y. Chen, M. Foroozandeh, P. Kiraly, A. R. Phillips, S. R. Coombes, M. Nilsson and G. A. Morris, *Chem Commun* **2017**, 53, 10188-10191.