

Quality-Assurance for the NMR Data Consumer

Integrating NMR into Modern Laboratory Workflow

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EAS
2008

NMR's Assimilation into Analytical Chemistry

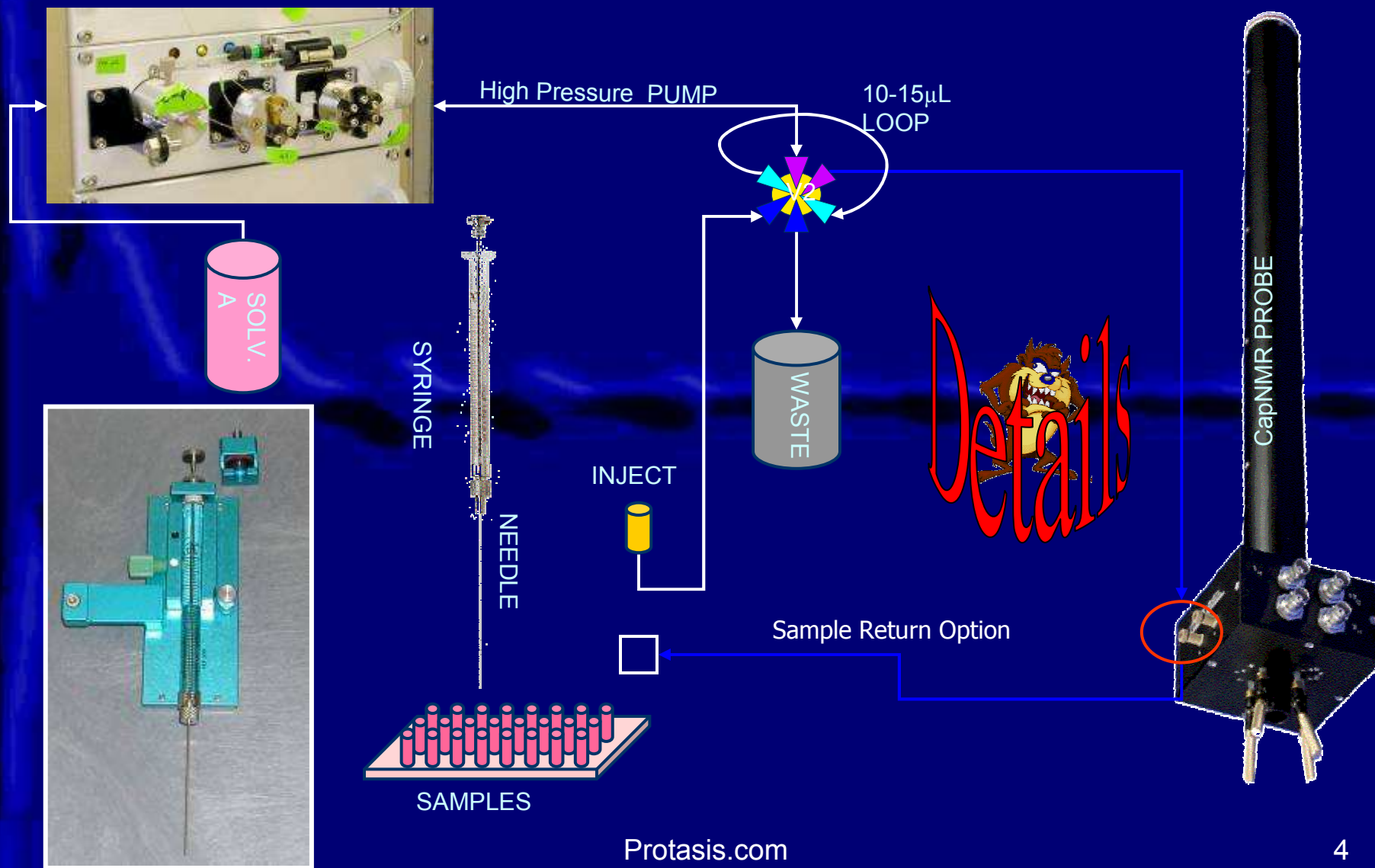
- Samples in plates and vials
- Robotic injection
- Walkup instruments
- Quantitative analysis
- Data interpretation software interface
- **Quality Assurance** with system suitability samples



One-Minute NMR™ and CapNMR™

Background Information

Automated Capillary Flow NMR



Tubeless

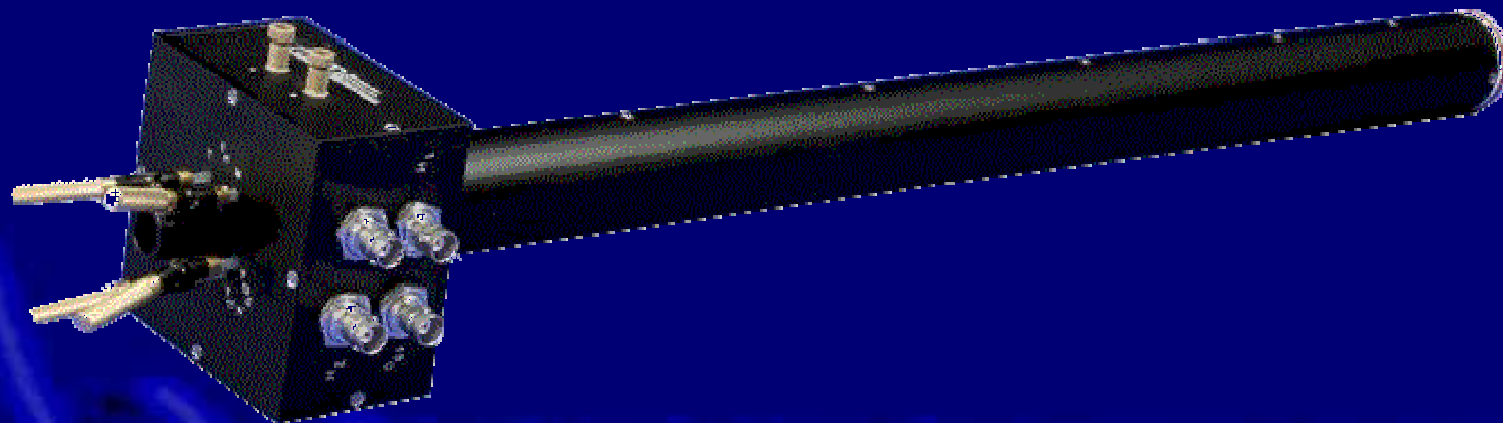


For incredible Time Savings

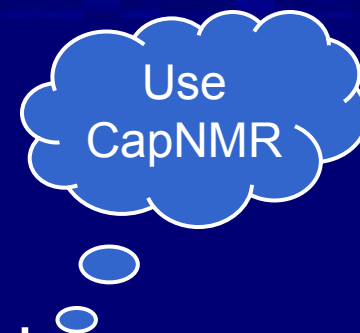
- **Directly Use LC or MS samples**
- **No shimming** between samples
- No washing tubes
- No buying tubes (\$2 - \$25)
- Efficient storage
- Disposable



CapNMR™ Flow Probe



- 10 - 200 μ g Samples
- Best mass sensitivity
- 5 or 10 μ L flow cell
- Proton, Carbon, Nitrogen, Deuterium Lock
- Dual flow cell available



CapNMR™

A Great Scale-Match or HPLC Purified Fractions

- **UPLC™ Scale** (2.1x150mm 1.7μ)
 - < ~2 mg sample, plenty for MS (.1μg) + CapNMR (50μg)
 - Amazing chromatographic resolution
 - highest purity fractions
 - CapNMR on 2.5% of total fraction mass
- **Analytical Scale** – (4.6x150mm 3-5μ)
 - < ~7mg sample
 - Good chromatographic resolution
 - CapNMR on 0.7% of total fraction mass
- **Semi-Prep Scale**
 - 50mg to grams of sample
 - Longer runs
 - Less resolution, more impure fractions
 - Typical for compound libraries
 - CapNMR on < 0.1% of total fraction mass

Leap / CTC Liquid Handler

- Fast
- Low Volume Pickup
- Low Dead Volume
- Syringe-Only Technology
- Flexible Sample Storage
- Dilute / Reconstitute
- Sample Return





One-Minute NMR Software

- Customizable multi-user open-access
- Web based with e-mail reporting
- Sample and user list importing

- Accepts any plate or vial in multiple solvents
- Interface to processing software (ACD/Labs, DataChord)
- Closed-loop NMR Instrument control enables **system suitability samples**

1.

Account: Protasis

Username: Bob Albrecht

Password:

Pressure: 134 PSI

> Initialization Error

System Status Refresh

Attached to NMR: 600 MHz

Priority Samples in queue: 0

Run samples in queue: 0

Night samples in queue: 0

Number of your samples to go: 0

Number of your samples completed: 59

Instrument status: IDLE

Reset Sample counter: 762

2.

Name: NameofNMRFile Vial

Notebook: Custom Field

Page: Custom Field

Collection Date: 123456789

Test2: a

Title: Any free-form title

Number of injections: 1

Solvent: D2O

Molecule:

Import Molecule...

NMR Experiments To Run: H11D, H15QC, Proton, OMNMR_gCOSY

Run Parameters For: H11D

Number Of Scans: 1

Spectral Width: 10 ppm

3.

MT1-Rear

	1	2	3	4	5	6	7	8	9	10	11	12
A	●	●	●	●	●	●	●	●	●	●	●	●
B	●	●	●	●	●	●	●	●	●	●	●	●
C	●	●	●	●	●	●	●	●	●	●	●	●
D	●	●	●	●	●	●	●	●	●	●	●	●
E	●	●	●	●	●	●	●	●	●	●	●	●
F	●	●	●	●	●	●	●	●	●	●	●	●
G	●	●	●	●	●	●	●	●	●	●	●	●
H	●	●	●	●	●	●	●	●	●	●	●	●

Import... Select All Remove Cancel

4. Queue/Run Priority Night OC

Pause Automation

One-Click System Suitability Samples

Interface to NMR Processing Software

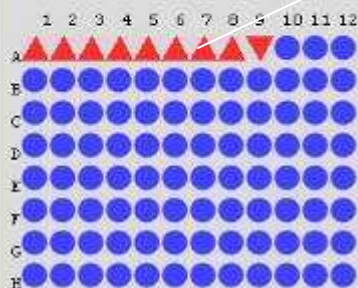
- Full control of basic NMR System Processing
- ACD/Labs automated structure confirmation with HTML reporting and Web Librarian
- ADC/Labs Enterprise Database archival
- One-Moon Scientifics' DataChord connection

In your Inbox

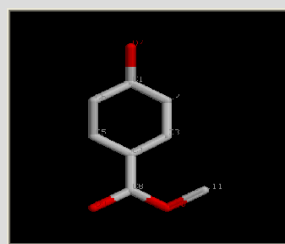
Integrated ACD/Labs Web Librarian



Tray02



Click...



td_1 : Tray02 1 (1)
[H11D_Score=0.65](#)
[HSQC_Score=0.66](#)
Average Score=0.66 (>=0.65)

Structure Confirmation Results

Sample ID	Code	H11D	HSQC
td_1	CONF	0.65	0.66
td_2	CONF	0.65	0.66
td_3	CONF	0.65	0.66
td_4	CONF	0.65	0.66
td_5	CONF	0.65	0.66
td_6	CONF	0.65	0.66
td_7	CONF	0.65	0.66
td_8	CONF	0.65	0.66
td_9	REJ	0.06	0.66

Microsoft Internet Explorer window showing the ACD/Labs Web Librarian interface. The browser address bar displays: http://100:8100/WebLibrarian/index.html?wreq=true&connect_to=C:\AS_MRM\DATA\MRM.nd8&rec_id=96

The interface shows the following information:

- Search Records:** A: 96/112 B: 112
- Spectrum Parameters:** Acquisition Time (sec): 0.9998, Comment: 5% methyl iodide in DMSO-d6, Date: Nov 25 2005, Date Stamp: Nov 25 2005, File: c:\ACD\VerificationTestData\td_1 Name: \H11D fid\phasefid, Frequency (MHz): 399.78, Nucleus: 1H, Number of Transients: 1, Original Points Count: 4223, Points Count: 32789, Pulse Sequence: s2pul, Receiver Gain: 30.00, Solvent: DMSO-d6, Spectrum Offset (Hz): 1950.3170, Sweep Width (Hz): 4000.00
- Record User Data:** HNMR Structure Purity: 81.57, HNMR RMS of Assignment: 0.10, HNMR Reliability: 87.00, HNMR Match Factor: 0.80
- Document User Data:** Verification Product: 0.65256, Original File: C:\AS_MRM\DATA\td_1_1H_MF.esp, Name: C:\AS_MRM\DATA\td_1_1H_MF.esp, Number of DR added from HSQC: 2***, 0.24***3.33

The 1H NMR spectrum shows peaks at 7.82, 7.80, 6.86, 6.83, 3.46, and 3.78 ppm. The solvent peak is labeled DMSO-d6. The x-axis is Chemical Shift (ppm) from 10 to 0, and the y-axis is Normalized Intensity from 0 to 1.00.

Chemical structure of Methyl 4-hydroxybenzoate is shown: CC(=O)Oc1ccc(O)cc1

Hot-linked E-mail report

Protasis.com

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NMR Quantitation

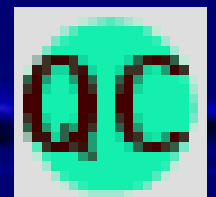
- Perfect for novel compounds
- Linear proton counter
- **Flow NMR works best:** No re-tuning with fixed flow-cell for constant signal response
- Use ERETIC for artificial internal standard
- Good results with external standards
- Reproducible robotic injection

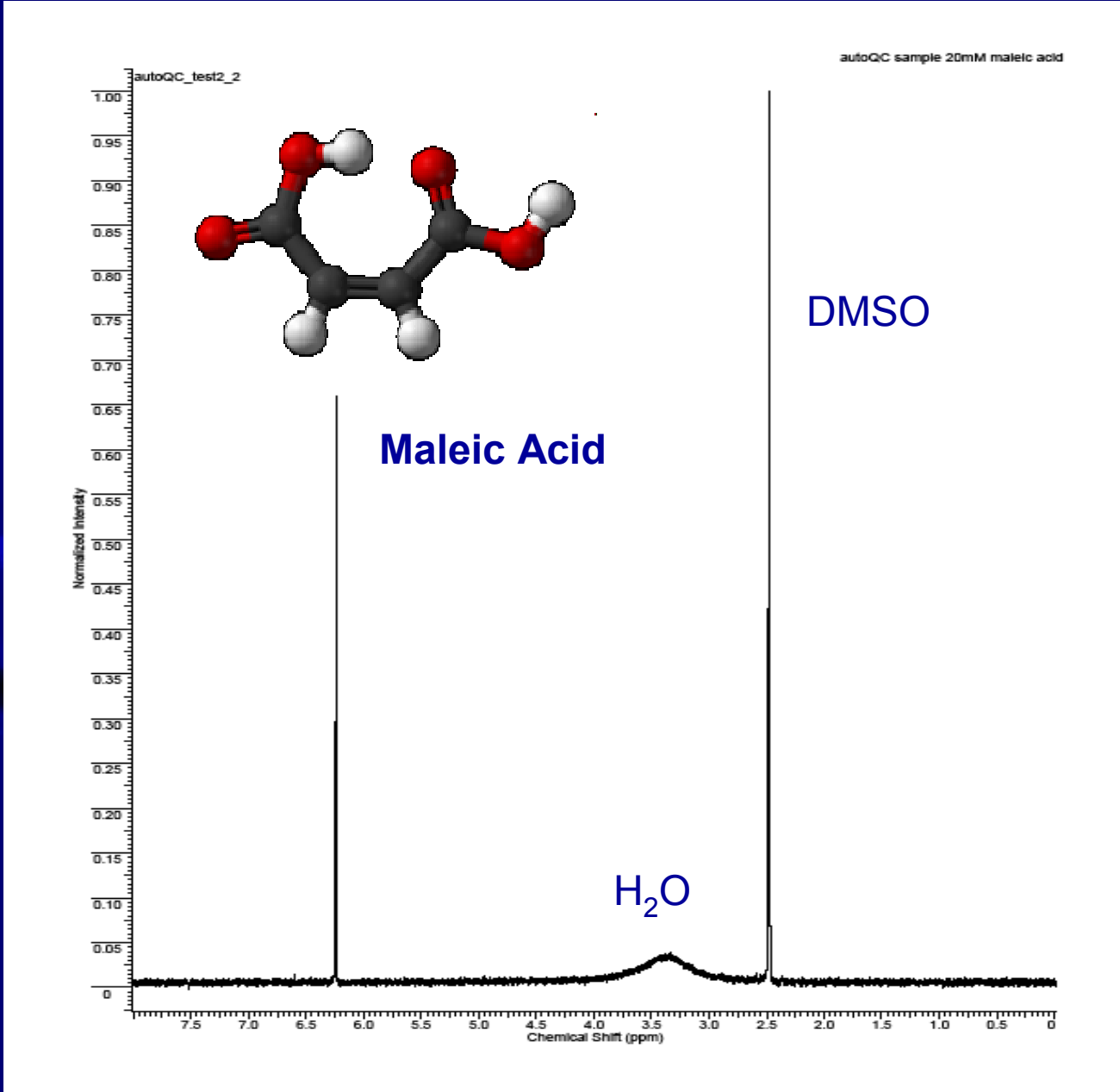
Why System Suitability?

- Does the average walkup chemist know good system performance?
- Trust is important with precious samples, especially with flow NMR
- Optimized automated structure verification, elucidation, and quantitation
- Automation makes system suitability painless

Automated System Suitability

- The only way to test the entire system:
Run a Sample, Analyze Results
- Flow has many benefits, but more complexity
- Tests all sub-systems: auto-sampler, fluidics, probe, magnet, shims, tuning, spectrometer, and software
- Confidence for precious samples





Maleic Acid

- Boring NMR Spectrum (1 peak)
- Great for system suitability standard
- Easy signal/noise calculation
- Clean spectrum for residual peak detection
- Sharp line for asymmetry and width calculation
- Dissolves in aqueous and organic solvents
- Non-toxic

We Sell Certified QC Standards or Make Your Own

- Pre-tested known concentration (20mM)
- Sealed vials
- Dry solvents of known purity

- High-purity maleic acid
- Inexpensive
- Convenient
- Use to verify make-your-own standards

Loading QC Samples

Main Web Page

Place Vials



MT2-Front

Reserve Space

	1	2	3	4	5	6	7	8	9
01	QC	QC	QC	QC	QC	QC	QC	QC	QC
10	QC	QC	QC	QC	QC	QC	QC	QC	QC
19	QC	QC	QC	QC	QC	QC	QC	QC	QC
28	QC	QC	QC	QC	QC	QC	QC	QC	QC
37	QC	QC	QC	QC	QC	QC	QC	QC	QC
46	QC	QC	QC	QC	QC	QC	QC	QC	QC

3.

Import...

Select All

Remove

Cancel

4.



Queue/Run



Priority



Night



Click QC

Software Configuration

- Solvent specific S/N limit
- Solvent specific line-shape limit
- Maximum number of bands
- Checking frequency (every Nth sample, startup)

Settings Category: Settings Filter:

	Setting	Value	Description
Edit	QC.BrukerWindows.omnmr_qc	c:\protasis\omnmr_qc.bat	Program to run for Bruker.Windows to get QC results.
Edit	QC.Countdown	1	Counter for QC samples.
Edit	QC.Enabled	true	True enables QC samples.
Edit	QC.ExperimentName	autoqc	The name of the experiment to run for QC samples.
Edit	QC.Frequency	4	How often to run a check sample.
Edit	QC.LineShapeLimit	1.5	The maximum line shape deformation.
Edit	QC.LineShapeLimit.D2O	1.5	The maximum line shape deformation.
Edit	QC.LineShapeLimit.DMSO	1.5	The maximum line shape deformation.
Edit	QC.MaximumNumberOfSignals	3	The maximum number of signals in the region tested for S/N.
Edit	QC.SignalToNoiseLimit	10	The minimum signal to noise value.
Edit	QC.SignalToNoiseLimit.D2O	10	The minimum signal to noise value.
Edit	QC.SignalToNoiseLimit.DMSO	10	The minimum signal to noise value.
Edit	QC.SignalToNoiseLowerPPM	2	Lower ppm limit for signal to noise calculation.
Edit	QC.SignalToNoiseUpperPPM	12	Upper ppm limit for signal to noise calculation.

QC Sample Automation Details



- QC Samples can be run *at will*, or..
- Run after every Nth sample
- A QC Sample is loaded and positioned in the CapNMR probe
- The 1D proton experiment *autoQC_setup* is automatically started by One-Minute NMR

QC Sample Automation Details

- Post processing experiment *autoQC_proc* calculates signal / noise, asymmetry, and the number of peaks in a ppm window
- Results are stored in *qc.log* and retrieved by One-Minute NMR using the *omnmr_qc* macro
- Results are compared to acceptable limits,
- Out of range, automation is stopped and an e-mail alert explaining why is sent

QC Documentation

- QC Sample results are stored as NMR FIDs and can be reviewed later
- Path to most recent QC FID, and the calculated results for *S/N*, *Asymmetry*, and *Peak Count* are stored in a tabular file
- NMR data file parameters can be created and stored with QC information

Future NMR QC Directions

- Injection volume detector
- Automated system pressure profile monitor
- Sample identity verification with barcodes
- Automated sample scan count measurements
- Automated sample return efficiency measurements

Conclusions

- NMR data consumers need quality data
- Chemists sometimes don't recognize poor instrument performance
- Automation makes QC easy and routine
- One-Minute NMR provides a comprehensive and flexible solution

Thank You

Craig Milling, PhD for developing Varian macros and system testing

Dean Olson, PhD for developing chemistry and selecting / testing containers for certified samples

Contacting Protasis

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- 508-481-4163

On the web:

- <http://protasis.com>

By e-mail:

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Download these slides

- <http://protasis.com/Slides/eas2008.pdf>