

Internal Standard Reference Data for qNMR: 1,4- Bis(trimethylsilyl)b [ISRD-06]^{1st}

edition 2019



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Internal Standard Reference Data for qNMR: 1,4-Bis(trimethylsilyl)benzene [ISRD-06]

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1. Introduction

Nuclear magnetic resonance (NMR) spectroscopy is now well-established as the pre-eminent method for the qualitative structural analysis of organic molecules. The potential for the application of quantitative nuclear magnetic resonance (qNMR) for organic analysis was also recognized soon after the technique became widely commercially available. [1] However it has only been more recently, as instrumental capabilities have achieved a level of accuracy and precision comparable to those attainable by chromatographic techniques, that this potential has begun to be generally realized. Quantitative methods based on NMR spectroscopy, particularly for the assignment of the purity of individual organic compounds, are now actively and extensively implemented. [2], [3], [4] As evidence, an editorial in the *Journal of Medicinal Chemistry* [5] highlighted and recommended the general utility of “absolute quantitative ^1H NMR spectroscopy to determine the purity of biologically tested research compounds”. Purity assignment by qNMR spectroscopy also potentially meets the metrological requirements for a primary ratio measurement procedure. [6] Validated qNMR methods [7] are now being used, often in combination with data obtained by orthogonal chromatographic techniques, to assign the purity of organic materials intended for use as Primary Reference Materials [8] for individual organic analytes. [9], [10], [11] The availability of properly characterized Primary Reference Materials is in turn an essential initial step in establishing the metrological traceability for measurement results for an organic analyte linked through a calibration hierarchy to a specific pure material. [12]

The assignment of the mass fraction purity of an organic analyte A by qNMR in solution using an internal standard S is based on measurement Equation (1) below:

$$w_A = \frac{I_A}{I_S} * \frac{N_S}{N_A} * \frac{M_A}{M_S} * \frac{m_S}{m_A} * w_S \quad (1)$$

w_A is the mass fraction of A in the material subject to assignment, w_S the independently established mass fraction content of the internal standard S , I_A and I_S are the integrals of the quantified signals unique to A and S respectively, N_A and N_S the number of ^1H nuclei contributing to each quantified signal, M_A and M_S the molar masses of the analyte and internal standard and m_A and m_S the masses of the individual aliquots of the analyte and internal standard material used to prepare the solution subject to the qNMR measurement.

In optimal cases and with the data processing carried out by experienced operators the standard uncertainty for purity mass fraction assignments for non-problematic systems has been reported to reach the level of 1 mg g^{-1} on an absolute basis, equivalent to 0.1 % relative. [13] However this level of uncertainty is difficult to achieve on a routine basis and in addition is limited on a case by case basis being contingent on the structural complexity and impurity profile of A . Factors including, *inter alia*, the lineshape and multiplicity of the signals integrated, the extent and nature of potential interferences from impurities present in the analyte, the nature of the internal standard and solvent used, the magnetic field strength, hardware settings and performance characteristics of the spectrometer and the approach taken to transform the time domain free induction decay (FID) signal generated by the NMR experiment and integrate the signals of the resulting frequency domain spectrum can all contribute to the overall uncertainty of the assigned value. Evidently, regardless of the precision of a qNMR measurement, the overall (relative) measurement uncertainty of a qNMR assignment can never be smaller than that associated with the purity of the internal standard used to obtain the result.

The first goal of this document is to furnish general recommendations for the design of a qNMR experiment and for the undertaking of a quantitative ^1H NMR measurement using the internal standard approach to provide a measurement result traceable to the International System of Units (SI). [14] It should be noted that although these principles should be applicable in general to quantitative measurement involving any NMR-active nuclei the specific recommendations in this document are intended only for assignments by ^1H qNMR.

The second goal is to describe a set of internal standard reference materials (ISRM) which the Bureau International des Poids et Mesures (BIPM) in collaboration with the National Metrology Institute of Japan (NMIJ) propose as a “universal” set of higher-order, SI-traceable internal standards for use in routine ^1H qNMR measurements. Different groups have proposed specific compounds or sets of compounds suitable for use as qNMR internal standards. [13], [15], [16], [17] Although there is some commonality between the internal standards recommended in this earlier literature and our proposal the focus of the earlier papers is the application of the materials for general use in purity assignments rather than, as is the case here, of their suitability as higher-order, SI-traceable primary measurement standards for qNMR. At least one ISRM compound should be suitable for use for the assignment of a given organic compound soluble in a specified NMR solvent. The compounds constituting the “universal” ISRM set together with an overview of their solubility and suitability for use in representative deuterated NMR solvents are described in Figure 1 below.

The third goal and the focus of this specific document is to provide guidance regarding the use and limitations of 1,4-bis(trimethylsilyl)benzene (BTMSB) and its tetradeuterated analog (BTMSB- d_4) as an ISRM for qNMR analysis.

Ideally, a qNMR ISRM should consist of a stable crystalline solid which is:

- available as a high purity Certified Reference Material (CRM) whose value has been assigned by a National Metrology Institute (NMI) using methods independent of qNMR or which has been value assigned directly by qNMR using a high purity CRM as the internal standard;
- predominantly a single organic component ($w_s > 995\text{mg} \cdot \text{g}^{-1}$);
- value assigned with small standard uncertainty ($u(w_s) < 1\text{mg} \cdot \text{g}^{-1}$);
- providing unique NMR signals, preferably as singlet or simple multiplet resonances, having Lorentzian lineshape with a narrow signal width;
- free of impurities interfering with the areas to be integrated;
- inert in solution in suitable NMR solvent;
- soluble in the chosen NMR solvent at a level in excess of $2\text{mg} \cdot \text{mL}^{-1}$;
- readily handled for accurate mass determinations:
 - non-hygroscopic
 - non-volatile
 - not subject to electrostatic effects
- having a relative mass content contribution from the hydrogen atoms giving rise to the quantification signal below 5%.⁽¹⁾

⁽¹⁾ When H-content exceeds 5% by mass, the aliquot size for the internal standard used for a typical analysis is constrained to be relatively small and the uncertainty associated with gravimetric operations becomes a limiting factor in the overall uncertainty of a qNMR assignment.

It is recognized that these characteristics constitute a “wishlist” rather than prescriptive requirements that must be met by all materials. However BTMSB and BTMSB- d_4 can meet all except the last of the listed criteria.

The solubility estimates of the ISRMs in the individual solvents listed in Figure 1 are intended as also being indicative of those for solvents having similar capabilities. The four shown were

selected as being the most readily available deuterated solvents. In practice the majority of the reported applications of qNMR for purity assignment in solution have been undertaken using one of these solvents.

At least three ISRM are applicable to each solvent class and provide quantification signals distributed across the standard ^1H chemical shift range.

BTMSB is suitable for use as an internal standard for qNMR purity assignments of non-polar analytes soluble in CD_3OD , $\text{DMSO}-d_6$ and CDCl_3 and solvents with related solubilizing properties. The following section of this reference document and the attached annexes describes specific properties and applications of its use as an ISRM for qNMR.








ISRM	KHP	BTFMBA	DMTP	MA	DMSO ₂	BTMSB- <i>d</i> ₄	DSS- <i>d</i> ₆
Structure							
δ (ppm)	8.3-7.0 (4H)	8.4-8.5 (2H) 8.2-8.4 (1H)	8.1 (4H) 3.9 (6H)	6.3 (2H)	3.0 (6H)	0.2 (18H)	0.1 (9H)
Density (g.cm ⁻³)	1.64 ± 0.17	1.72 ± 0.04	1.2 ± 0.24	1.53 ± 0.03	1.4 ± 0.03	1.0 ± 0.02	1.27 ± 0.03
H content (mg.g ⁻¹)	19.6	11.6	20.6 (4H) 30.9 (6H)	17.2	63.8	79.5	44.5
Solvent ↓	Solubility (mg/mL)						
D ₂ O	> 10	< 1	< 1	> 5	> 10	< 1	> 5
<i>d</i> ₆ -DMSO	> 2	> 10	> 5	> 10	> 5	> 2	> 5
CD ₃ OD	> 2	> 10	> 2 *	*	> 5	> 2	> 5
CDCl ₃	< 1	> 5	> 10	< 1	> 10	> 5	< 1

Figure 1 — qNMR ISRM Suite [18]

* soluble but only for quantifications based on the aromatic proton signal. Exchange of the methyl ester with CD_3OD precludes quantification based on the dimethyl ester.

* soluble but unsuitable for qNMR due to esterification reaction with CD_3OD

KHP Potassium hydrogen phthalate

BTFMBA 3,5-Bis-(trifluoromethyl)benzoic acid

DMTP Dimethyl terephthalate

MA Maleic acid

DMSO₂ Dimethyl sulfone

BTMSB 1,4-bis-Trimethylsilylbenzene (R=H), for BTMSB-*d*₄ R = D;

DSS-*d*₆ Sodium - 1,1,2,2,3,3-hexadeutero-3-(trimethylsilyl)propyl-1-sulfonate [Sodium 4,4-dimethyl-4-silapentane-1-sulfonate -*d*₆]

D₂O Deuterium oxide

DMSO-*d*₆ Dimethyl sulfoxide-*d*₆ / Hexadeuterodimethyl sulfoxide

CD₃OD Methanol-*d*₄ / Tetradeuteromethanol

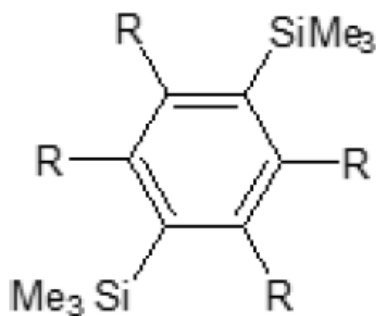
CDCl₃ Chloroform-*d* / Deuteriochloroform

2. Properties of BTMSB and BTMSB- d_4

2.1. Physical Properties

IUPAC Name Trimethyl-(4-trimethylsilylphenyl)silane (R = H)
Trimethyl-(2,3,5,6-Tetradeutero-4-trimethylsilylphenyl)silane (R = D)

Structure +



Synonyms 1,4-Bis(trimethylsilyl)benzene ; *p*-Phenylenebis(trimethylsilane)
(R = H)

CAS Registry Number 13183-70-5 (R = H) ; 1337953-96-4 (R = D)

Molecular Formula $C_{12}H_{22}Si_2$ (R = H) ; $C_{12}H_{18}D_4Si_2$ (R = D)

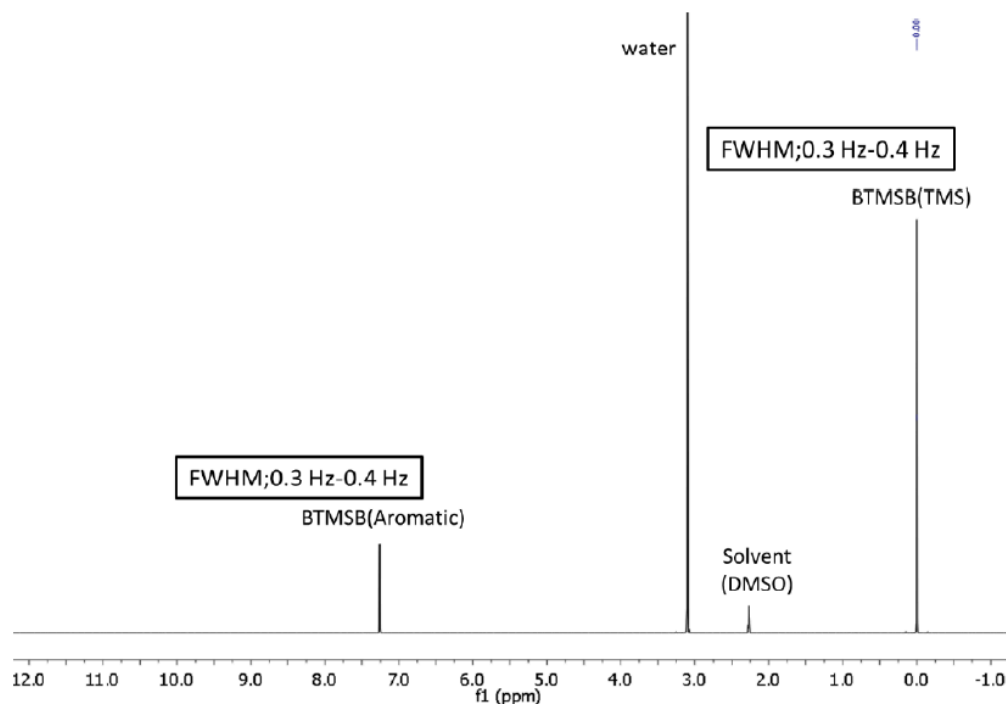
Molar Mass [19] $222.478\text{g} \cdot \text{mol}^{-1}$, $u = 0.015\text{g} \cdot \text{mol}^{-1}$ (R = H)
 $226.502\text{g} \cdot \text{mol}^{-1}$, $u = 0.013\text{g} \cdot \text{mol}^{-1}$ (R = D)

Melting point [20] $91 - 94^\circ\text{C}$

Density $1.0\text{kg} \cdot \text{m}^{-3}$ [21]

Appearance White crystalline powder

^1H NMR [22] $\delta 0.1$ ppm (s, 18H) ; 7.4 ppm (s, 4H – BTMSB only)



4400MHz spectra of BTMSB- d_4 in other solvents are reproduced in Section 5.1.

Figure 2 — ^1H NMR spectrum of BTMSB in $\text{DMSO}-d_6$: JEOL ECS-400 spectrometer with Royal probe.

2.2. NMR Solvent Compatibility

NMR solvents suitable for use with BTMSB are CD_3OD , $\text{DMSO}-d_6$ and CDCl_3 . It is soluble at levels in excess of $2\text{mg} \cdot \text{mL}^{-1}$ in $\text{DMSO}-d_6$ and CD_3OD and in excess of $5\text{mg} \cdot \text{mL}^{-1}$ in CDCl_3 . qNMR studies can also be undertaken in solution in acetone- d_6 and CD_3CN .

2.3. NMR quantification signals

There are four magnetically equivalent aromatic protons and eighteen equivalent methyl protons in BTMSB. The signal due to the aromatic protons is no longer present in the BTMSB- d_4 analog. The chemical shift of these signals depends on the solvent but are in the range 0.1ppm for the TMS protons and 7.4 for the aromatic hydrogens. The exact position of the resonance is a function of factors including but not limited to the solvent, temperature and the concentration of BTMSB and other analytes in the solution. For optimal quantification results the homogeneity of the spectrometer magnetic field should be optimized such that the full width at half maximum (FWHM) of the signal for residual solvent in the solution is less than 1Hz while the base of each resonance retains a suitable Lorentzian peak shape.

2.4. Impurities and artefact signals

In our experience BTMSB and BTMSB- d_4 have typically not contained significant levels ($> 0.1\%$) of related structure impurities. The tetradeuterated analog may contain small amounts of non-deuterated material, but we have not seen evidence of such impurities at levels visible

above the spectrum baseline. In practice the main interferences in a solution containing BTMSB will come from signals due to residual non-deuterated solvent. The chemical shifts of these signals are given in Table 1 below.

2.5. Solvent recommendations & advisories⁽¹⁾

⁽¹⁾ Recommendations for BTMSB apply equally for BTMSB-*d*₄

2.5.1. D₂O and related solvents

BTMSB is not sufficiently soluble in D₂O.

2.5.2. DMSO-*d*₆ and related solvents

DMSO-*d*₆ is a suitable solvent for use with BTMSB.

2.5.3. Methanol-*d*₄ and related solvents

CD₃OD is a suitable solvent for use with BTMSB.

2.5.4. CDCl₃

CDCl₃ is the recommended solvent for initial consideration for use with BTMSB.

Table 1. Solvent and qNMR Signal Parameters for BTMSB & BTMSB-*d*₄

Solvent	qNMR signal 18H (ppm)*	Integration range (ppm)*	<i>T</i> ₁ (s)*	Residual Solvent (ppm)	Comments:
D ₂ O	Not suitable				Insufficient solubility
DMSO- <i>d</i> ₆	0.1 (18H)	-0.3 – 0.3	2.5- 3.5	2.5	
CD ₃ OD	0.1 (18H)	-0.3– 0.3	2.5- 3.5	3.3	
CDCl ₃	0.1 (18H)	-0.3– 0.3	2.5- 3.5	7.25	

3. Good Practice Guidance for SI Traceable qNMR Measurement Results

3.1. Introduction

The first step in any purity assignment by qNMR should be the confirmation by qualitative NMR or other techniques of the identity of the analyte subject to purity assessment. In addition to confirming that the molar mass (M) and the number of nuclei (N) contributing to each signal subject to integration are appropriate, obtaining qualitative NMR spectra also provides a check for the occurrence and extent of any interfering signals in the sections of the NMR spectrum subject to integration.

Once the qualitative identity of the analyte has been appropriately established, the input quantities that influence qNMR measurement results must be evaluated. These are identified from the measurement equation (Equation (1), see p. 6). The mass fraction purity of the internal standard used for the measurement, the source of traceability to the SI for the value to be assigned to the analyte, is established by independent measurements undertaken prior to the qNMR experiment.

The gravimetric procedure used for the preparation of the NMR solution has to be fully validated and fit for its intended purpose, [23], [24] and the spectrometer performance, experimental parameters and the protocol for signal processing and integration must be optimized, [4], [5], [25] in order to produce a result for the ratio of the integral of the analyte and standard signals that accurately reflects the molar ratio of the hydrogen nuclei giving rise to the signals. [26] When these conditions are met the assigned mass fraction purity of the analyte can be regarded as traceable to the SI. [9], [27], [28] Some general guidance for recommended practice for these critical steps is given in the following sections.

3.2. Internal standard

The internal standard used in a qNMR purity assignment should comply as far as possible with the criteria described above regarding composition, physical characteristics, inertness, solubility, impurity profile and relative hydrogen content by mass. In addition in order to establish traceability of the result of the qNMR assignment to the SI, the material should comply with the requirements of a reference measurement standard, and in particular a reference material, as defined in the International Vocabulary of Metrology (VIM). [29]

For SI-traceability the internal standard should consist of one of the following:

1. Certified Reference Material (CRM) characterized for its mass fraction purity and value assigned by a National Measurement Institute;
2. CRM provided as a high purity organic material by a Reference Material Producer accredited to ISO 17034:2016 [30] requirements;
3. high purity material subject to a validated measurement procedure for purity assignment by qNMR using as an internal standard a CRM of type 1) or 2).

3.3. Gravimetry

The realization of accurate and precise qNMR measurements relies on the application of a properly implemented gravimetric procedure for the mass determinations of the internal standard and analyte. Recommended practice in this area in the specific context of qNMR sample preparation has been described in a recent publication. [24] Achieving an overall relative standard measurement uncertainty for a qNMR assignment of 0.1 % requires the relative uncertainty associated with individual gravimetric operations be less than 0.03 %. If the combined standard uncertainty of a mass determination is 3 µg, a level achievable with modern electronic microanalytical balances, this corresponds to a minimum sample size of 10 mg. Care should be exercised to include an appropriate allowance for the uncertainty of each gravimetric operation within the final uncertainty budget for a qNMR purity assay, that adequately takes into account the aliquot sample sizes and the performance characteristics of the balance used.

In addition to suitable control for each mass determination, if the receptacle used for the final solution preparation is not the same as that used for both mass determinations the procedure for transfer of solids into the solution must address the assumption that the ratio of the gravimetric readings from the balance operations is equivalent to the ratio of the masses of each compound in the solution subject to the qNMR analysis.

For the examples reported in the Section 5.2 below, gravimetric operations were undertaken using a balance associated with a measurement uncertainty estimate of 1.3 µg for individual mass determinations. In this case a minimum sample size of 4 mg achieves a relative uncertainty in individual gravimetric operations below 0.03 %. In addition to the measurement uncertainty of the balance reading, for high accuracy measurements correction for sample buoyancy effects and the contribution to the overall measurement uncertainty associated with this correction should also be taken into consideration. [25]

As sample preparation for qNMR involves mass determinations in the milligram range using sensitive balances, the loss of even minute (almost invisible) quantities of powder during the gravimetric procedure will have a measurable influence on the balance reading and hence on the input quantities for the qNMR assignment. Environmental conditions for gravimetry and qNMR sample preparation should be controlled throughout the process, subject to minimum change and kept within the operating range recommended by the manufacturer. [31] It is recommended that mass determinations be performed in an area where the relative humidity is maintained in the range 30 % to 70 %.

The accumulation of surface electrostatic charges is a potential source of bias for mass determinations, particularly for high polarity, hygroscopic compounds. In these cases, pre-treatment of the sample with an electrostatic charge remover or deioniser is advisable prior to the mass determination. Where possible materials subject to qNMR analysis should be evaluated for their hygroscopicity, for example by measurement of the change in observed mass as a function of relative humidity using a dynamic sorption balance. This allows for assessment of the likely impact of variation in the relative humidity in the local environment on the results of gravimetric operations for a given compound.

A minimum of two independent gravimetric sample preparations should be undertaken when assigning the purity of a compound by qNMR.

3.4. NMR spectrometer optimization for quantitative measurements

There is no specification of minimum NMR spectrometer field strength for purity measurements. Increasing field strength results provides enhanced signal separation and increases sensitivity, both of which should increase the accuracy and precision of qNMR measurements. Careful optimization of the lineshape (shimming) is mandatory and critical in order to achieve reliable qNMR results. [32] A general guidance is to choose the simplest signal in the sample, often the residual solvent peak, and to optimize the instrument shimming until this signal is symmetrical with a FWHM below at least 1Hz. Experience has shown that these lineshape requirements are more easily achieved using an inverse probe than a direct type. For lower field magnets (< 300MHz), this recommendation might not be attainable. If the lineshape is broader the level of measurement uncertainty associated with the assigned value will increase. In no case should a signal from a labile, exchangeable hydrogen or one subject to dynamic tautomeric exchange be used for quantitative measurements.

Due to the relatively wide Lorentzian signal shape of NMR resonances the separation of the signals to be quantified from each other and from the remainder of the NMR signals in the spectrum should be considered carefully. Ideally there should be no interfering signals within the range one hundred times the FWHM either side of each signal to be integrated.

3.5. NMR acquisition parameters

The basic experiment to perform quantitative NMR experiments uses a simple 1D pulse sequence designed to minimise differences in the integrated signal intensities due to effects related to incomplete relaxation of the quantification resonances. For highest accuracy assignments use of broadband heteronuclear decoupling should be avoided if possible as it can lead to undesired nuclear Overhauser effects introducing a bias in the intensities of individual measured signals. However in the common case of ^{13}C -decoupling to remove satellite signals, the potential for bias is greatly attenuated because of the low (1.1 %) natural abundance of the ^{13}C isotopomer. In addition although the decoupling efficiency for separate ^{13}C satellite signals is generally not equivalent, the combined potential bias introduced due to both effects from the inclusion of ^{13}C -decoupling is negligibly small in most cases.

The recommended basic sequence for a qNMR measurement consists of a “delay-pulse-acquire” experiment. There are critical parameters associated with each phase of the sequence in order to achieve a reliable, unbiased quantitative signal response. Assuming the experiment starts from an equilibrium magnetization state, the first phase in the experiment is the pulse, which itself is preceded by a delay.

In the pulse phase, the two critical parameters for good qNMR measurement results are the pulse offset and pulse length (also called pulse width or tip angle). When a single “hard” pulse is applied to the bulk magnetization of each compound, off-resonance effects can occur if the frequency offset of the initial pulse is relatively far from that of the signals of interest. Ideally the pulse offset should be positioned as close as possible to the midpoint between the two signals to be quantified. This will not eliminate off-resonance effects but should result in them cancelling out in both signals.

Regarding the pulse length, 90° pulses are recommended for quantitative analyses. A 30° pulse experiment, providing a signal response approximately half that of a 90° pulse, has

the potential advantage of needing a significantly shorter relaxation time to re-establish equilibrium magnetization compared with a 90° pulse while requiring only twice as many transients to achieve an equivalent **signal** response. However this potential practical advantage is offset by the need for four times as many transients as a 90° pulse to achieve the same **signal to noise** ratio. The accuracy (trueness) of the results should not be impacted by the use of different pulse lengths but the acquisition times to achieve equivalent levels of signal precision (repeatability) will.

Additional parameters requiring optimization in the acquisition phase are the spectral window width, the acquisition time, the digital resolution and the relaxation delay time between acquisitions. The spectral window chosen will depend on the design and performance of the instrument used. The theoretical justification for the use of a large spectral window is that oversampling the FID will produce noise filtering. However, the efficiency of digital filters varies by instrument and the appropriate spectral window should be evaluated on a case by case basis.

The acquisition time should be at least 2.5s to avoid truncation of the signals and to allow good digitisation of the spectrum. The ideal acquisition time is the smallest time for which no truncation is observed. Use of longer acquisition times than necessary primarily results in addition of noise to the spectrum. The digital resolution should not exceed $0.4\text{Hz} \cdot \text{pt}^{-1}$ in order to have accurately defined signals that will give meaningful area measurements and suitable repeatability at typical sampling rates.

The relaxation delay between pulses in particular has to be carefully established for each sample mixture. To determine the optimum repetition time for a given qNMR measurement it is critical to determine the longest T_1 time constant of the signals to be quantified. This document presents some observed values measured for BTFMBA in different solvents at the concentration and under the specific instrumental conditions used, but these should be regarded as indicative only, and in any event they are not the determining factor in cases where the T_1 of the analyte quantification signal is longer.

As the T_1 constant arises from a process of spin-lattice relaxation, its values are strongly dependent on the composition of the solution being measured and it should be determined for each signal to be quantified in each mixture on a case by case basis. The most commonly used method to determine the T_1 constant is the inversion-recovery sequence generally available in the factory programmed pulse sequences installed with any NMR. The application of the inversion recovery experiment requires knowledge of the optimized 90° pulses for each quantified signal, which should also be determined for each mixture under investigation. The optimized 90° pulse values can be used for both the T_1 determination and the quantitative measurements.

The repetition time between pulses should correspond to the full loop time in the pulse sequence and not simply the relaxation delay. Since most of the time intervals involved in NMR measurement are negligible relatively to the T_1 values, the repetition time (RT) can be estimated as the sum of acquisition time (AQ) and relaxation delay (RD), where the RT is a multiple T_1 . After a 90° pulse, if the available instrument time permits, 10 times T_1 of the signal with the longest relaxation time will lead to the recovery of $> 99.995\%$ of the magnetization for all quantified signals. In cases where the T_1 of the quantified signals are similar in magnitude, a shorter relaxation delay will be sufficient for equivalent (even if incomplete) magnetization re-equilibration. At least 10 T_1 should be used as a minimum where highest accuracy results are sought.

Thus the pulse RT is given by:

$$RT = RD + AQ = n \cdot T_1 \quad (2)$$

$$(n = 10-15)$$

The number of transients (or scans) should be determined according to the concentration of the samples, the nature of the signals and the available instrument time. To achieve small uncertainty a signal to noise (S/N) ratio of at least 1000 should be achieved for each signal subject to quantification. Smaller S/N values can still lead to acceptable results, but the reported measurement uncertainties increase as the S/N ratio decreases.

Table 2. Recommended NMR Parameters for quantitative measurements.

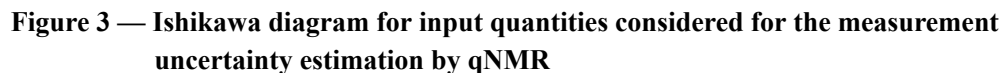
Parameter	Recommended Value	Explanation/Comments
Shimming	FWHM of lineshape signal (eg CHCl ₃ /acetone- <i>d</i> ₆) < 1Hz	Optimization of field homogeneity is critical for uniform response over typical chemical shift range
Pulse Width	90°	Should not change the quality of the results, but the use of a 90° pulse with adequate recovery time leads to a smaller total acquisition time for a target S/N ratio.
Pulse Offset	Midpoint between signals	Theoretically makes off resonance effects equivalent for both signals.
Repetition Time	10–15 × <i>T</i> ₁	After 90° pulse, a delay of 10 <i>T</i> ₁ of the signal with the longest relaxation time necessary for recovery of > 99.995 % of magnetization for all quantified signals.
Number of Transients	As needed for adequate signal to noise ratio	Evaluate on a case by case basis. Minimum requirement is S/N > 1000 for each signal quantified
Spectral Window	> 20ppm	The use of a wide spectral window for data recording (oversampling) has been reported to yield better results in some instruments because of the noise filtering it produces in the quadrature detection scheme. This is instrument dependent and should be evaluated.
Acquisition Time	> 2.5s	The correct acquisition time is essential to give the best digital resolution for good quantitative results. If too short, lower digital resolution and truncated signals result. If too long excessive noise is introduced. A minimum of 2.5s is a useful starting point and 4s has been found to be suitable for many applications.
Digital resolution	< 0.4Hz · pt ⁻¹	The digital resolution is the reciprocal of the acquisition time. Suitable signal shape sensitivity requires not less than 0.4Hz · pt ⁻¹ .

Good practice for performing quantitative experiments is to prepare in addition to the sample mixtures one sample consisting of a solvent blank, one with the analyte only and one with the internal standard only in the same solvent. These additional NMR spectra should be acquired

Each independently weighed analyte/IS mixture (a minimum of two samples) should be measured at least three times in the NMR system. Independent measurements for a particular sample mixture should be non-continuous, where the tube is removed and the measurement process (tuning, locking, shimming) repeated each time for each sample.

The integration range should extend on each side ideally at least seventy six times the FWHM of the signal being measured in order to integrate in excess of 99.9 % of the signal. The estimation of signal width should be done for the outer signals if a multiplet signal is subject to integration. A generally acceptable approximation is to use a range extending 30Hz beyond the furthest ¹³C satellites as the start and end points for the integration range, as this generally exceeds the above described width. In a complex spectrum where other signals are adjacent to one or both of the quantification signals and quantification over the full range is not possible to avoid excessive bias as far as possible apply a consistent approach to the integration of both signals.

Evaluation of the measurement equation previously presented (Equation (1), see p. 6) identifies the factors influencing the input quantities for the measurement uncertainty as shown in the diagram in Figure 3.



The observed repeatability of the integral area ratios, which incorporates contributions from the input factors for excitation, population, detection efficiency and data processing, is amenable to a type A statistical evaluation. [23], [33] Since these measurements come from at least two independent solutions each containing different sample masses, the observed absolute area ratios will vary on a sample by sample basis.

The measurement uncertainty of the value obtained for each preparation can be evaluated separately and the individual purity results for each sample combined statistically. Another approach is to pool the purity values from the replicate results for the separate samples. Analysis of this combined data by ANOVA produces an assigned value and provides an estimate of the intermediate precision of the overall process. It also identifies if additional variance contributions from sample preparation and signal processing exist in addition to that due to the method repeatability.

The final assigned value will be similar regardless of the approach used, although the contribution to the measurement uncertainty of the result may differ.

The standard uncertainties for the other major input quantities are type B estimates and are straightforward to evaluate. Molar masses and their uncertainties are estimated based on the “conventional” values for atomic weights given in Table 3 of the 2016 revision of the IUPAC Technical report of the Atomic weights of the elements, [19] the uncertainties of mass determinations are based on balance performance characteristics and are corrected for buoyancy effects [25] and the uncertainty of the purity of the internal standard is assigned by the material provider.

Other approaches to the evaluation of measurement uncertainty for qNMR and the combination of results from qNMR with orthogonal techniques for purity evaluation have also been reported. [27], [34] Examples of “best case” measurement uncertainty budgets for qNMR analysis are provided in the examples given in Section 5.2.

4. Acknowledgements

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All NMR studies were carried out by the co-authors of this document in the course of secondments at the BIPM. The support of the parent institution of each scientist in making them available for secondment to the BIPM is gratefully acknowledged.

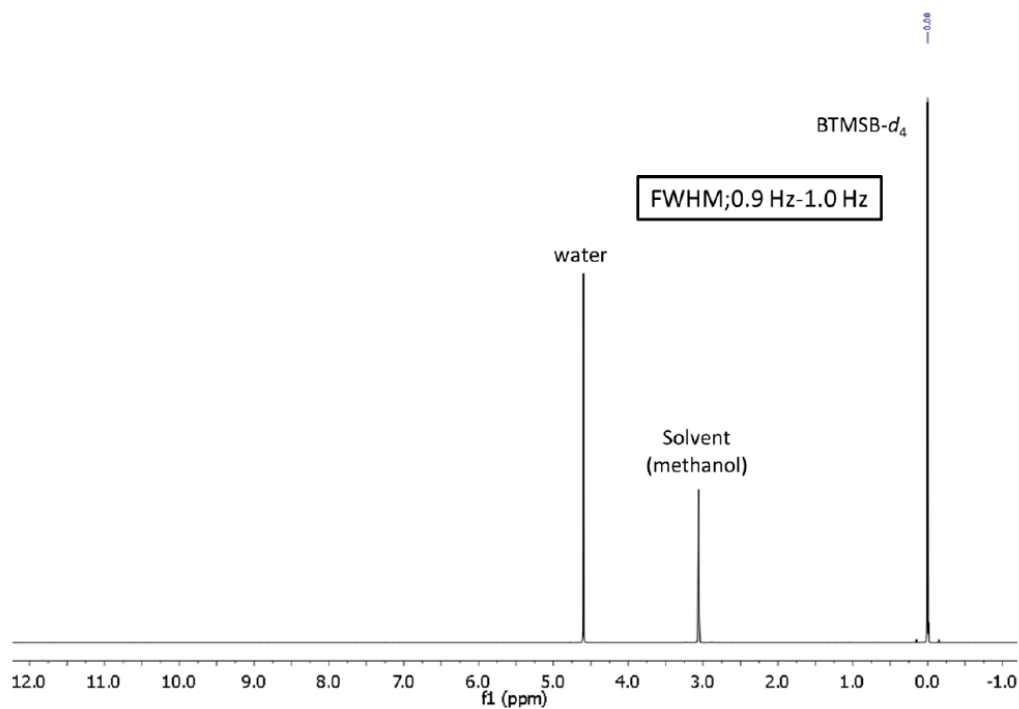
Dr. Bruno Garrido wishes to acknowledge funding for his secondment from the Brazilian Ministry of Education under the Coordination for the Improvement of Higher Education Personnel (CAPES) post-doctoral scholarship programme (process: 99999.007374/2015-01).

DISCLAIMER: Commercial NMR instruments, software and materials are identified in this document in order to describe some procedures. This does not imply a recommendation or endorsement by the BIPM nor does it imply that any of the instruments, equipment and materials identified are necessarily the best available for the purpose.

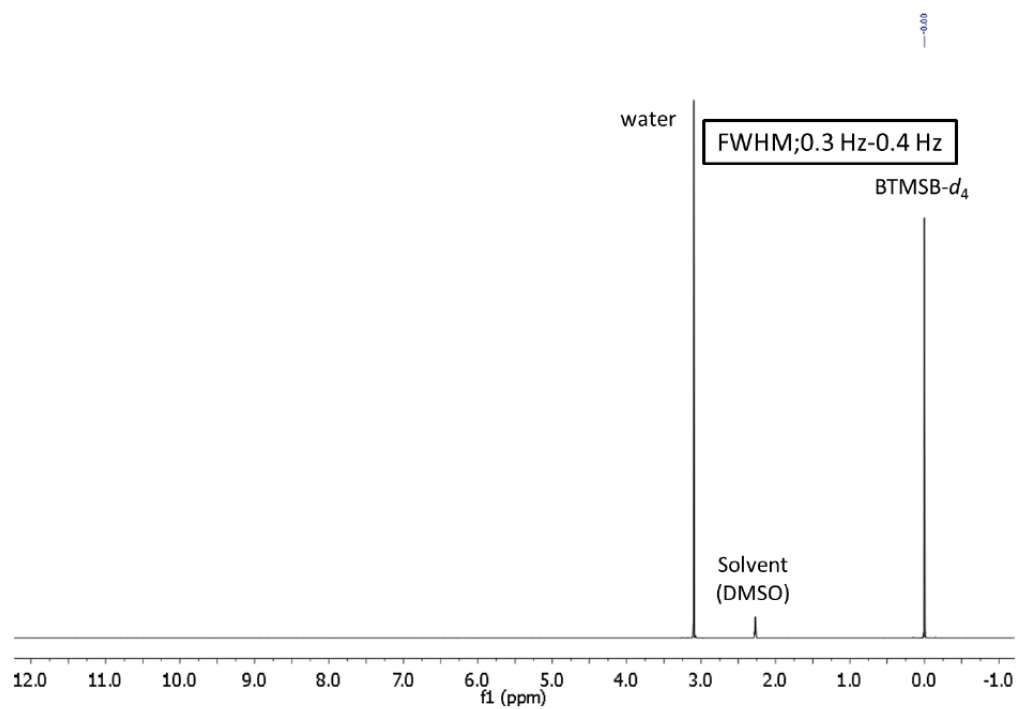
5. Annexes

5.1. Solution NMR Spectra of BTMSB- d_4

5.1.1. BTMSB- d_4 in CD_3OD



5.1.2. BTMSB- d_4 in $DMSO-d_6$



5.2. qNMR using BTMSB- d_4 as internal standard

Two examples are provided of the value assignment by qNMR of the mass fraction content of organic compounds using BTMSB as the ISRM and the associated measurement uncertainty budgets. In the first example BTMSB- d_4 was used in a solution in DMSO- d_6 with as DMSO₂ as analyte. In the second example BTMSB- d_4 was used in a solution in CD₃OD with benzoic acid (BA) as the analyte. [22]

These are intended as “best case” illustrations and should not be regarded as representative of the uncertainty budget achievable when quantifying more structurally complex compounds. The signals for quantification in these examples are clearly separated from each other, have narrow, well-resolved signal shape and there is no significant interference from impurities or solvent signals. As a result the uncertainty contribution due to the reproducibility of the signal integration is smaller (and the relative uncertainty contribution due to gravimetry and the purity of the internal standard correspondingly greater) than should be anticipated for more general applications.

A thorough shimming procedure was used to maximize the homogeneity of the instrument field. Gravimetric determinations were carried out using a microbalance with a readability of 0.1µg and a measurement uncertainty for individual mass determinations of less than 20mg net of 1.3µg.

The BTMSB- d_4 was donated by WAKO Chemicals. The mass fraction content of BTMSB- d_4 in the material was assigned as $999.1 \pm 0.4 \text{ mg} \cdot \text{g}^{-1}$ by qNMR using the NMIJ CRM 4601a for BTFMBA as the internal standard. The DMTP was purchased from a commercial supplier. The benzoic acid (BA) was the NIST SRM 350b. The certified mass fraction content of benzoic acid in this material is $999.978 \pm 0.044 \text{ mg} \cdot \text{g}^{-1}$

Deuterated solvents were purchased from commercial suppliers and were used without further treatment or purification. Borosilicate glass NMR tubes with 5mm internal diameter rated for use in 500MHz spectrometers and purchased from a commercial supplier were used for all measurements.

5.2.1. BTMSB- d_4 (IS) & DMSO₂ (Analyte) in DMSO- d_6

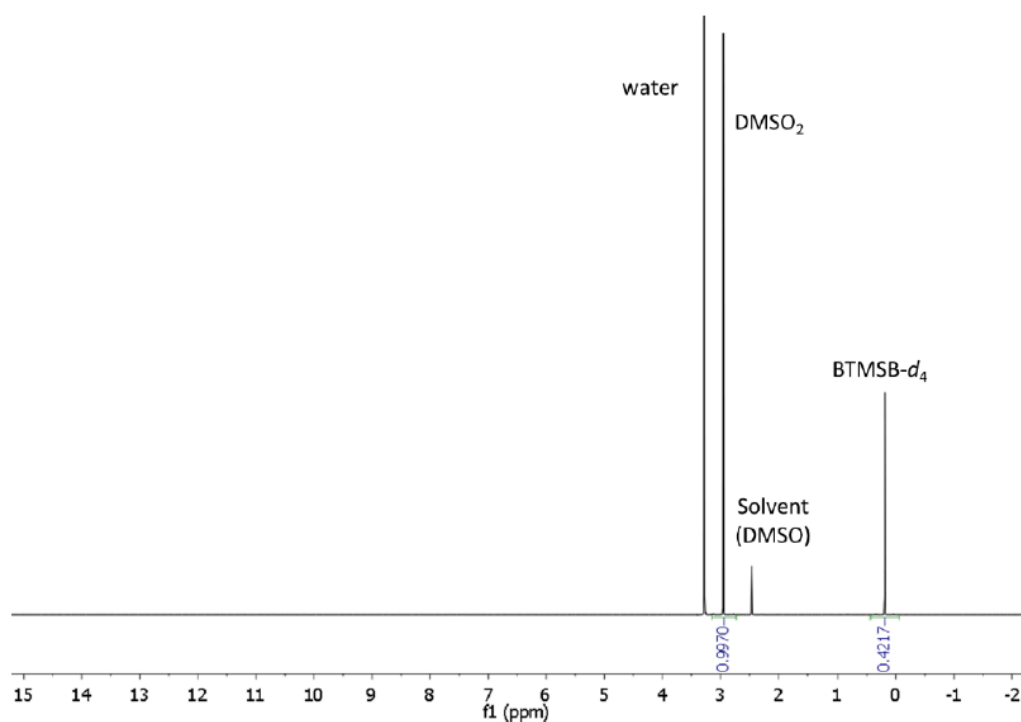


Figure 4 — ^1H NMR spectrum of BTMSB- d_4 and DMSO₂ in DMSO- d_6 .

The parameters for the qNMR assignment using a JEOL ECS-400 spectrometer equipped with a Royal probe are given in Table 3. The sample was made up in solution in approximately 2.5mL of DMSO- d_6 and 800 μL was transferred into the NMR tube for analysis.

Table 3. NMR parameters for purity assignment of DMSO₂ using BTMSB- d_4 in DMSO- d_6 .

Parameter	Value
BTMSB- d_4 Sample size (mg)	1.2 – 2.1
DMSO ₂ Sample size (mg)	3.5 – 3.8
Number of Transients	32
Receiver gain	Automatic
Acquisition time (s)	4
Longest T_1 (s)	< 4.5
Relaxation delay (s)	45
Pulse offset (ppm)	1.6

Spectral width (ppm)	400
Data points	639652
Temperature (K)	298
Spinning	Off
Integral ratio (BTMSB- d_4 :DMSO ₂)	0.4 – 0.8

A baseline correction window of one hundred times the FWHM was applied to each integrated signal. The integration range covered eighty times the FWHM. Four independent sample mixtures were prepared and each sample was measured four times. measurement uncertainty budget is reproduced in Table 4. The integral ratio is the mean of the four replicate values obtained for this sample. The standard uncertainty of the ratio is the standard deviation of the mean. The other uncertainty components are Type B estimations. The relative contribution of each component to the uncertainty of the combined result for this sample is displayed in Figure 5. The mass fraction content of DMSO₂ assigned for this sample was $996.7 \pm 1.6 \text{ mg g}^{-1}$.

Table 4. Uncertainty budget for DMSO₂ purity by qNMR using BTMSB- d_4 in DMSO- d_6 .

Uncertainty sources	Value	Type	Standard Uncertainty	Sensitivity coefficient	Uncertainty Component
I _A /I _S (repeatability)	0.8173	A	0.00011	1.219529875	1.49E-04
Analyte signal ¹ H Nuclei	5.9988	B	0.0003	-0.16615519	4.98E-05
IS signal ¹ H Nuclei	17.9964	B	0.0003	0.055384561	1.66E-05
Analyte Molar Mass	94.128	B	0.007	0.01058911	7.34E-05
IS Molar Mass	226.5024	B	0.0125	-0.004400535	5.52E-05
Analyte mass (mg)	2.6524	B	0.00124	-0.375784857	4.67E-04
IS mass (mg)	2.5969	B	0.00124	0.383815994	4.77E-04
IS purity (mg · g ⁻¹)	0.9991	B	0.0004	0.997629622	3.99E-04
			Combined Uncertainty	0.000797	

996.7 ± 1.6 mg g⁻¹
of
DMSO₂

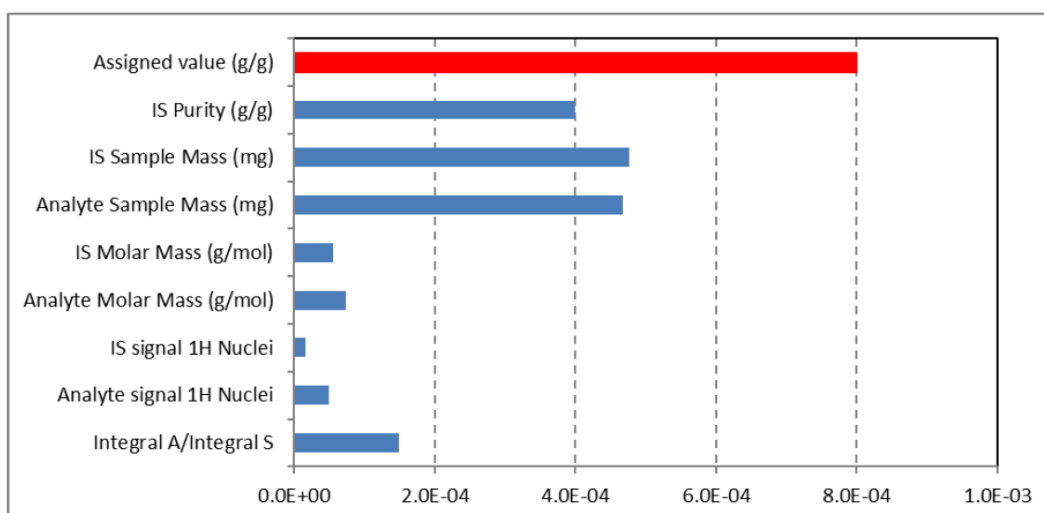


Figure 5 — Relative uncertainty components: DMSO₂ assignment using BTMSB-*d*₄ in DMSO-*d*₆.

5.2.2. BTMSB-*d*₄ (IS) & Benzoic Acid (BA, Analyte) in CD₃OD

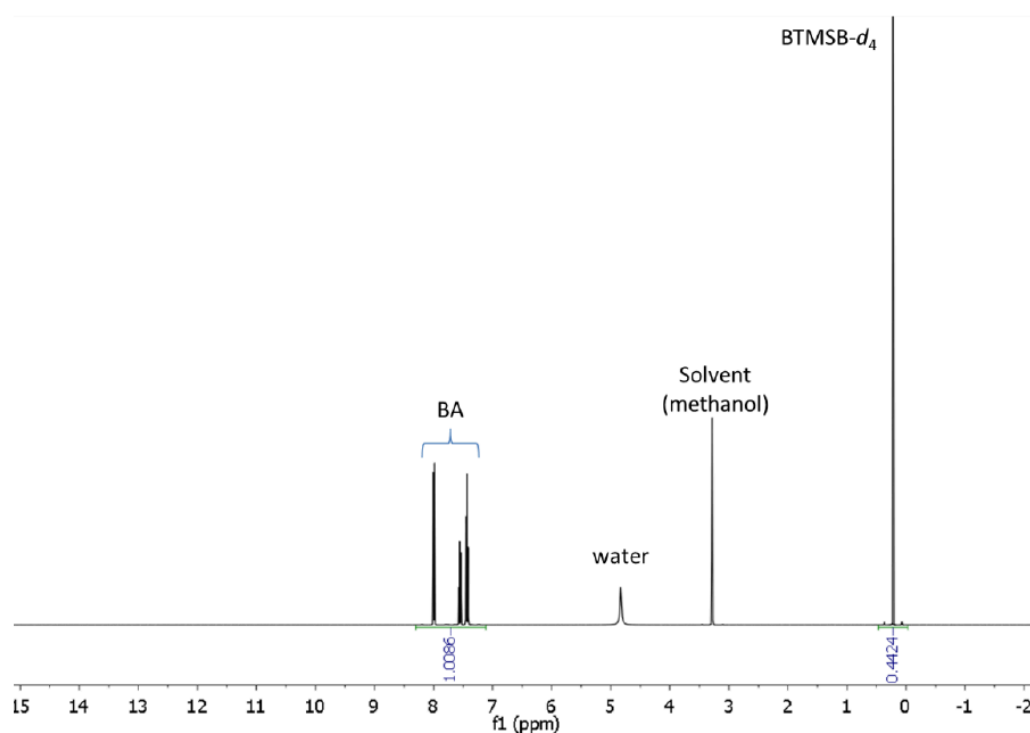


Figure 6 — ¹H NMR of 5.2.2 BTMSB-*d*₄ and benzoic acid in CD₃OD

The parameters for the qNMR assignment using a JEOL ECS-400 spectrometer equipped with a Royal probe are given in Table 3. The sample was made up in solution in approximately 1.2mL of CD₃OD and 800μL was transferred into the NMR tube for analysis.

Table 5. NMR experiment parameters for BA assignment using BTMSB- d_4 in CD_3OD .

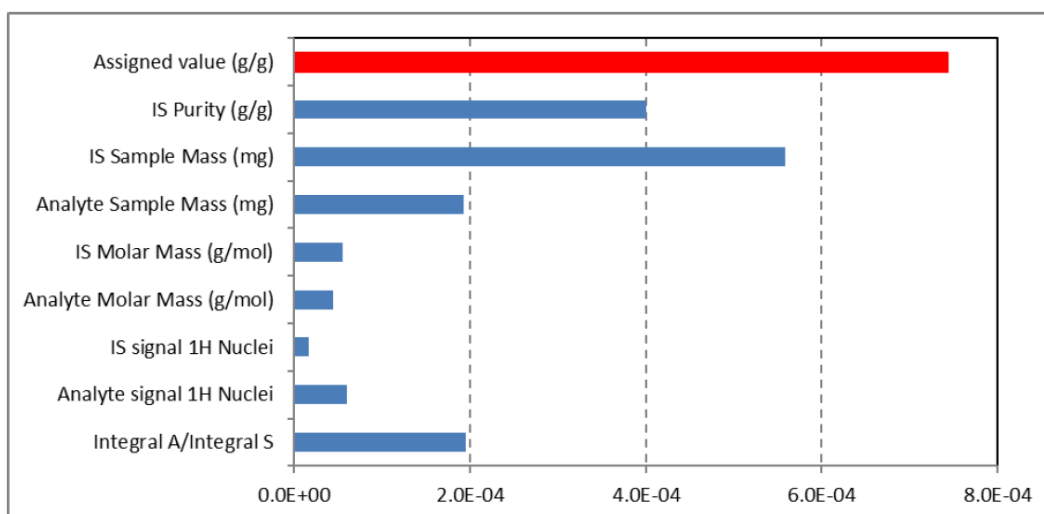
Parameter	Value
BTFMBA Sample size (mg)	6—10
BTMSB- d_4 Sample size (mg)	2.2 – 3.2
Number of Transients	32
Receiver gain	Automatic
Acquisition time (s)	4
T_1 (longest signal except for solvent) (s)	< 4.0
Relaxation delay (s)	50
Pulse offset (ppm)	3.75
Spectral width (ppm)	400
Data points	39979
Temperature (K)	298
Spinning	Off
Integral ratio (BA:BTMSB- d_4)	1.1 – 2.3

The integration range start and end points were placed 30Hz beyond the outermost ^{13}C satellite signals of each quantified peak. Results from four independent sample mixtures each measured four times were obtained. The measurement uncertainty budget from the combined results for the sixteen replicate determinations is reproduced below in Table 6. The integral ratio is the normalized mean of the four replicate values obtained for this sample. The other uncertainty components are Type B estimations. The relative contribution of each component to the uncertainty of the result obtained for this sample is shown in Figure 7. The mass fraction content of BA assigned by qNMR using BTMSB- d_4 as ISRM in this solvent was $999.8 \pm 0.2 / - 1.5 \text{ mg g}^{-1}$. This value was consistent with the certified value for the material obtained by NIST using titrimetry of $999.978 \pm 0.044 \text{ mg} \cdot \text{g}^{-1}$

Table 6. Uncertainty budget for BA purity by qNMR using BTMSB- d_4 in CD_3OD .

Uncertainty sources	Value	Type	Standard Uncertainty	Sensitivity coefficient	Uncertainty Component
I_A/I_S (repeatability)	1.5000	A	0.00026	0.666514833	1.95E-04
Analyte signal 1H Nuclei	4.9990	B	0.0003	-0.199996413	6.00E-05
IS signal 1H Nuclei	17.9964	B	0.0003	0.055553617	1.67E-05
Analyte Molar Mass ($g \cdot mol^{-1}$)	122.123	B	0.0054	0.008186681	4.46E-05
IS Molar Mass ($g \cdot mol^{-1}$)	226.502	B	0.0125	-0.004414002	5.54E-05
Analyte mass (mg)	6.4659	B	0.00124	-0.154623806	1.92E-04
IS mass (mg)	2.2223	B	0.00124	0.449886185	5.59E-04
IS purity ($mg \cdot g^{-1}$)	0.9991	B	0.0004	1.000682682	4.00E-04
Combined Uncertainty				7.44E-04	

999.8 + 0.2/Purity $mg \cdot g^{-1}$
of
Benzoic
acid

**Figure 7 — Relative uncertainty components: BA assignment using BTMSB- d_4 in CD_3OD**

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