

# ● Analysis Report

## Bruker IVDr BioBank QC B.I.BioBankQC™ in Urine

Sample ID: test\_urine\_005

Measuring Date: 14-Jun-2018 07:18:24

Reporting Date: 18-Jun-2018 17:56:31, 7 page(s), Version 1.0.0

Quantification Method Version: BioBankQC UR 1.0.0

### Disclaimer

RESEARCH USE ONLY: This is no clinical diagnostic analysis report. Must not be used for clinical (medical or IVD) diagnosis or for patient management! Additional concentration range information (95% range) provided numerically or graphically in this report must not be used for clinical diagnostic interpretation.

### Summary

Test	Result	Flag
NMR Experiment Parameter Test	passed	●
NMR Experiment Quality Test	passed	●
NMR Preparation Quality Test	passed	●
Matrix Identity Test	Urine	●
Matrix Integrity Test	passed	●
Matrix Contamination Test	passed	●
Medication Test	passed	●
Protein Background Test	passed	●
Further Indicative Parameter Test	passed	●

## 1 NMR Experiment Parameters

Parameter	Target Value	Applied Value	Flag
EXP	PROF_URINE_NOESY	PROF_URINE_NOESY	●
PULPROG	noesygppr1d	noesygppr1d	●
AUNM	au_ivdr_noesy	au_ivdr_noesy	●
AUNMP	proc_ivdr_noesy	proc_ivdr_noesy	●
SOLVENT	Urine	Urine	●
TE	299.9 - 300.1	299.9997	●
P1	8 - 15	10.48	●
PRESAT	24 - 26	25	●
BF1	599 - 601	600.23	●
O1	2700 - 2900	2821.65	●
ERETIC	1000	2226.6466	●
D1	4	4	●
SWH	12019.23	12019.2308	●
OVERFLOW	0	0	●
TD	65536	65536	●
NS	32	32	●
DS	4	4	●
LB	0.3	0.3	●
SI	131072	131072	●
PHC1	0	0	●

## 2 NMR and Preparation Performance Evaluation

### 2.1 NMR Spectral Quality Parameters

Parameter	Target Value	Measured Value	Flag
LineWidth in Hz	<1.30	1.0	●
Line Asymmetry in Hz	-0.20 - 0.20	-0.02	●
Residual Water Signal in mmol/L	<30.0	27.8	●
BaseLine in mmol/L/Hz	<0.0010	0.0003	●

### 2.2 NMR Sample Preparation Quality Parameters

Parameter	Target Value	Measured Value	Flag
NMR visible TSP in mmol/L	0.50 - 0.58	0.53	●

### 3 Matrix Validation

#### 3.1 Matrix Identity Test

The spectral fingerprint of the sample is consistent with Urine.

	<b>Creatinine</b> mmol/L	<b>Alanine</b> mmol/L	<b>Fumaric acid</b> mmol/L	<b>Flag</b>
Sample	2.90	<0.05	<0.01	
Urine	0.60 - 29.00	<2.20	<0.07	●

#### 3.2 Matrix Integrity Parameters

<b>Compound</b>	<b>LOD</b>	<b>Range</b>	<b>Measured Value</b>	<b>Flag</b>
Acetic acid in mmol/L	0.030	<2.90	<0.030	●
Benzoic acid in mmol/L	0.040	<0.45	<0.040	●
Citric acid in mmol/L	0.050	>0.05	0.222	●
Formic acid in mmol/L	0.020	<0.71	<0.020	●
Hippuric acid in mmol/L	0.200	<15.10	<0.200	●
Lactic acid in mmol/L	0.100	<2.00	<0.100	●
Succinic acid in mmol/L	0.020	<0.44	0.025	●

#### 3.3 Matrix Contamination Parameters

<b>Contamination</b>	<b>LOD</b>	<b>Measured Value</b>	<b>Flag</b>
Propylene glycol in mmol/L	0.020	<0.020	●
Isopropanol in mmol/L	0.020	<0.020	●

## 4 Test for Medication, Protein Background and further indicative Parameters

### 4.1 Medication and related Metabolites

Compound	LOD	Measured Value	Flag
D-Mannitol in mmol/L	0.150	<0.150	●
D-Mannose-alpha in mmol/L	0.060	<0.060	●
Paracetamol in mmol/L	0.060	<0.060	●
Paracetamol-glucuronide in mmol/L	0.060	<0.060	●
Paracetamol-sulfate in mmol/L	0.060	<0.060	●
Cefuroxim in mmol/L	0.500	<0.500	●

### 4.2 Protein Background Assessment

Parameter	Target Value	Measured Value	Flag
Hump (-0.5ppm - 0.5ppm) in mmol/L/Hz	<0.0010	0.0003	●

### 4.3 Further Indicative Parameters

Compound	LOD	Range	Measured Value	Flag
3-Hydroxybutyric acid in mmol/L	0.240	<0.24	<0.240	●
Acetone in mmol/L	0.010	<0.04	<0.010	●
Acetoacetic acid in mmol/L	0.020	<0.22	0.020	●
D-Glucose-beta in mmol/L	0.140	<0.14	<0.140	●

## 5 Explanations

### NMR Experiment Parameters

Related tests need to be passed successfully in order to document that NMR parameters applied to the sample are consistent with the parameters specified in the B.I.Methods™.

### NMR Spectral Quality Parameters

Shim performance is crucial, both, for water suppression quality and resolution. The linewidth of the TSP signal and its asymmetry as well as the residual water signal absolute value intensity are used as respective indicators. Bad shim can have multiple reasons, from just non-optimum shim values, over concentration gradients in the sample, contrast agents from prior MRI investigations, sedimentation or particles in the sample, to tube imperfections. If NMR spectral quality parameter tests are not successfully passed, one may try one or more of the following steps in subsequent order:

- (1) Check standard shim file loaded prior to shimming.
- (2) Take out sample from magnet, shake it and re-run sample afterwards.
- (3) Do TopShim 3d. Re-run sample afterwards.
- (4) Fill sample in other NMR tube.
- (5) Re-prepare sample and then re-run sample.
- (6) Ask for a new sample from the same subject if study design allows for that.

### NMR Sample Preparation Quality Parameters

Urine sample preparation is straight forward. It is mixing of urine and Bruker's IVDr urine buffer at a ratio of 9:1. The TSP concentration is an important indicator for application of the correct buffer at correct concentration. If this parameter is outside specification, it would indicate either application of a wrong buffer or a wrong urine-to-buffer ratio. Either of the scenarios could result in deviations in peak intensities and peak positions or in the worst case even changes of chemical equilibria in the mixture. As a consequence, subsequent application of NMR based urine quantification methods optimized for spectra acquired under B.I.Methods SOPs could provide wrong results.

### Matrix Identity Test

This test checks the concentrations of a minimum set of metabolites which should be present in a urine. If it fails there is strong indication that the sample is not a urine sample.

### Matrix Integrity Parameters

The integrity of a urine sample may be impaired due to inappropriate pre-analytics and inappropriate temperature exposure which may result in e.g. bacterial growth. Bacterial growth may strongly affect concentrations of the metabolites included in the test.

### **Matrix Contamination Parameters**

Propylene glycol and Isopropanol may often be used in one or more steps of pre-analytics procedures. Introduction of these compounds into the urine sample should be avoided in order not to impair the overall spectral fingerprint of the sample.

### **Medication and related Metabolites**

Depending on study design, application of medication may be an exclusion criterion from a study. While it is impossible to test for all possible medications, the compounds tested for (especially the unspecific ones like D-Mannitol and D-Mannose) may give some first indication if compliance is an issue in a study.

### **Protein Background Assessment**

In this test, deviation of the baseline from zero characteristic for the presence of proteins in urine is tested for in the region between -0.5ppm to 0.5ppm. This deviation is measured in terms of a concentration equivalent mmol/L per Hz baseline. This parameter is proportional but not identical to the protein concentration.

### **Further Indicative Parameters**

Some studies require fasting or non-fasting. Parameters checked for in this test may be indicative in this context.