Analysis Report

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

Sample ID:	Demo_Urine_01
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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	not passed	
Protein Background Test	passed	
Further Indicative Parameter Test	not passed	

Geschäftsführer: Dr. Falko Busse | Patrick Minhorst

Silberstreifen 4
76287 Rheinstetten, Germany
Tel. +49(0)721 5161-0
Fax. +49(0)721 517101
nmr@bruker-biospin.com
www.bruker-biospin.com

Deutsche Bank AG Karlsruhe
Konto 13 15 16 · BLZ 660 700 04
IBAN: DE87 6607 0004 0013 1516 00
SWIFT-BIC: DEUTDESM660

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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	300.002	
P1	8 - 15	10.7	
PRESAT	24 - 26	25	
BF1	599 - 601	600.23	
O1	2700 - 2900	2821.9819	
ERETIC	1000	2159.4824	
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	-0.05	
Residual Water Signal in mmol/L	<30.0	12.5	
BaseLine in mmol/L/Hz	<0.0010	0.0004	

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.

	Creatinine mmol/L	Alanine mmol/L	Fumaric acid mmol/L	Flag
Sample	5.15	0.13	<0.01	
Urine	0.60 - 29.00	<2.20	<0.07	

3.2 Matrix Integrity Parameters

Compound	LOD	Range	Measured Value	Flag
Acetic acid in mmol/L	0.030	<2.90	0.039	
Benzoic acid in mmol/L	0.040	<0.45	<0.040	
Citric acid in mmol/L	0.050	>0.05	1.488	
Formic acid in mmol/L	0.020	<0.71	0.078	
Hippuric acid in mmol/L	0.200	<15.10	1.637	
Lactic acid in mmol/L	0.100	<2.00	<0.100	
Succinic acid in mmol/L	0.020	<0.44	0.045	

3.3 Matrix Contamination Parameters

Contamination	LOD	Measured Value	Flag
Propylene glycol in mmol/L	0.020	0.047	
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	0.399	
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	1.042	
Paracetamol-sulfate in mmol/L	0.060	0.447	
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	0.0005	

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	0.017	
Acetoacetic acid in mmol/L	0.020	<0.22	0.067	
D-Glucose-beta in mmol/L	0.140	<0.14	3.344	

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 aquired 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 overal 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.