Analysis Report

Bruker IVDr Quantification in URine B.I.Quant-UR b™

Sample ID: ALZ_Urine_Rack01_RCM_221214_expno270.100000.10r

Measuring Date:	23-Dec-2014 20:05:39
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Quantification Method Version:	Quant-UR B.1.1.0

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.

Application of B.I.Quant-UR B 1.1.0 requires use of Bruker's B.I.Methods SOP for urine.

Summary

The following metabolites were found with concentrations outside the 95% range of Bruker Quant-UR B.1.1.0 urine metabolite concentration database:

Amines and derivatives: *Dimethylamine (56 mmol/mol Crea).*

Further detailed information is provided on the following pages.

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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Sitz der Gesellschaft: 76287 Rheinstetten

Contents

1 Creatinine

Compound	Conc. mmol/L	LOD mmol/L	r mmol/L	ρ %	Δ mmol/L	95% Range(*) mmol/L
Creatinine	3.1	0.3	3.098	100	0.053	1 - 19

(*) Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

2 Amines and derivatives

Compound	Conc. mmol/L	Conc. mmol/mol Crea	LOD mmol/mol Crea	r mmol/L	ρ %	Δ mmol/L	95% Range(*) mmol/mol Crea
Dimethylamine	0.17	56	31	0.172	100	0.004	≤ 54
Trimethylamine	< 0.01	< 2	2	0.002	91	0.001	≤ 3

(*) Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

3 Amino acids and derivatives

Compound	Conc. mmol/L	Conc. mmol/mol Crea	LOD mmol/mol Crea	r mmol/L	ρ %	Δ mmol/L	95% Range(*) mmol/mol Crea
1-Methylhistidine	< 0.05	< 15	15	0.023	90	0.010	≤ 15
2-Furoylglycine	< 0.12	< 39	39	0.024	90	0.008	≤ 40
4-Aminobutyric acid	< 0.06	< 20	20	0.000	0	0.116	≤ 20
Alanine	0.05	17	10	0.053	100	0.006	11 - 72
Arginine	< 2.3	< 750	750	0.251	19	8.682	≤ 750
Betaine	0.06	19	7	0.059	100	0.047	9 - 78
Creatine	< 0.15	< 50	50	0.020	100	0.053	≤ 280
Glycine	0.22	72	34	0.223	100	0.006	38 - 440
Guanidinoacetic acid	< 0.32	< 100	100	0.099	47	0.075	≤ 140
Methionine	< 0.06	< 18	18	0.000	0	0.112	≤ 18
N,N-Dimethylglycine	0.02	8	5	0.023	94	0.005	≤ 15
Sarcosine	< 0.01	< 2	2	0.000	0	0.002	≤ 7
Taurine	< 0.44	< 140	140	0.290	88	0.153	≤ 170
Valine	0.01	2	2	0.006	66	0.009	≤ 7

(*) Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

4 Benzene and substituted derivatives

Compound	Conc. mmol/L	Conc. mmol/mol Crea	LOD mmol/mol Crea	r mmol/L	ρ %	Δ mmol/L	95% Range(*) mmol/mol Crea
Benzoic acid	< 0.03	< 10	10	0.000	0 ○	0.019	≤ 10
D-Mandelic acid	< 0.01	< 2	2	0.000	0 ○	0.036	2 - 17
Hippuric acid	1.7	560	170	1.728	99 ●	0.165	≤ 660

(*) Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

5 Carboxylic acids

Compound	Conc. mmol/L	Conc. mmol/mol Crea	LOD mmol/mol Crea	r mmol/L	ρ %	Δ mmol/L	95% Range(*) mmol/mol Crea
Acetic acid	0.03	10	5	0.032	93 ●	0.008	≤ 51
Citric acid	0.56	180	40	0.563	100 ●	0.046	≤ 700
Formic acid	0.13	42	10	0.130	99 ●	0.011	≤ 43
Fumaric acid	< 0.01	< 2	2	0.001	59 ○	0.001	≤ 3
Imidazole	< 0.15	< 48	48	0.000	0 ○	0.063	≤ 48
Lactic acid	< 0.15	< 49	49	0.046	91 ●	0.021	≤ 110
Proline betaine	< 0.08	< 25	25	0.060	0 ○	0.111	≤ 280
Succinic acid	0.03	10	5	0.032	86 ●	0.007	≤ 39
Tartaric acid	< 0.01	< 5	5	0.005	99 ●	0.001	≤ 110
Trigonelline	< 0.11	< 35	35	0.101	100 ●	0.003	≤ 67

(*) Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

6 Fatty acids and derivatives

Compound	Conc. mmol/L	Conc. mmol/mol Crea	LOD mmol/mol Crea	r mmol/L	ρ %	Δ mmol/L	95% Range(*) mmol/mol Crea
2-Methylsuccinic acid	< 0.15	< 48	48	0.000	0 ○	0.144	≤ 48

(*) Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

7 Keto acids and derivatives

Compound	Conc. mmol/L	Conc. mmol/mol Crea	LOD mmol/mol Crea	r mmol/L	ρ %	Δ mmol/L	95% Range(*) mmol/mol Crea
2-Oxoglutaric acid	$<$ 0.29	$<$ 92	92	0.013	32	0.103	$\leq$ 92
3-Hydroxybutyric acid	$<$ 0.32	$<$ 100	100	0.045	39	0.082	$\leq$ 100
Acetoacetic acid	$<$ 0.04	$<$ 14	14	0.024	87	0.025	$\leq$ 30
Acetone	0.01	5	2	0.015	99	0.002	$\leq$ 7
Oxaloacetic acid	0.08	27	17	0.084	89	0.045	$\leq$ 66
Pyruvic acid	$<$ 0.03	$<$ 9	9	0.021	97	0.002	$\leq$ 13

(*) Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

8 Purine, Pyridine and Pyrimidine derivatives

Compound	Conc. mmol/L	Conc. mmol/mol Crea	LOD mmol/mol Crea	r mmol/L	ρ %	Δ mmol/L	95% Range(*) mmol/mol Crea
1-Methyladenosine	$<$ 0.01	$<$ 5	5	0.000	0	0.072	$\leq$ 5
1-Methylnicotinamide	$<$ 0.10	$<$ 32	32	0.017	60	0.014	$\leq$ 32
Adenosine	$<$ 1.2	$<$ 390	390	0.000	0	0.578	$\leq$ 390
Allantoin	0.06	20	17	0.061	97	0.008	$\leq$ 47
Allopurinol	$<$ 0.03	$<$ 10	10	0.011	98	0.013	$\leq$ 11
Caffeine	$<$ 0.14	$<$ 45	45	0.097	98	0.044	$\leq$ 61
Inosine	$<$ 0.06	$<$ 19	19	0.011	98	0.012	$\leq$ 19

(*) Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

9 Sugars and derivatives

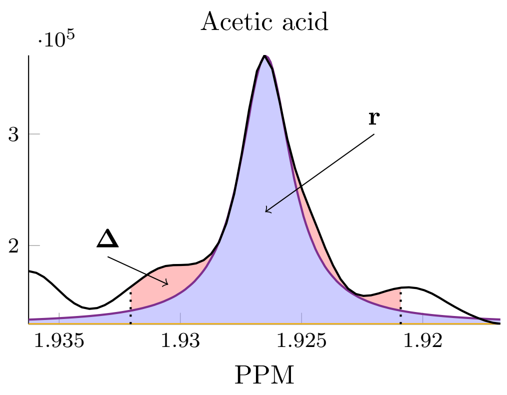
Compound	Conc. mmol/L	Conc. mmol/mol Crea	LOD mmol/mol Crea	r mmol/L	ρ %	Δ mmol/L	95% Range(*) mmol/mol Crea
D-Galactose	$<$ 0.13	$<$ 43	43	0.000	0	0.040	$\leq$ 44
D-Glucose	$<$ 0.11	$<$ 34	34	0.053	64	0.028	$\leq$ 140
D-Lactose	$<$ 0.30	$<$ 96	96	0.045	79	0.029	$\leq$ 96
D-Mannitol	$<$ 0.57	$<$ 180	180	0.000	0	1.079	$\leq$ 180
D-Mannose	$<$ 0.02	$<$ 6	6	0.000	0	0.041	$\leq$ 8
Myo-Inositol	$<$ 14	$<$ 4400	4400	0.000	0	15.20	$\leq$ 4400

(*) Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

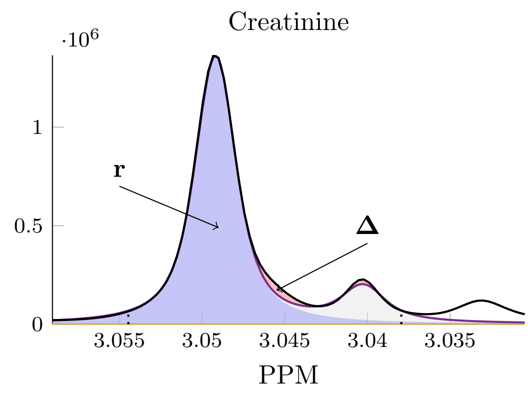
10 Explanations

This section contains the definition of the parameters used above. In the section 10.1 a short manual, how to interpret the results, is presented. The section 10.3 contains the exact definitions of the parameters $\mathbf{r}$, ρ and $\boldsymbol{\Delta}$.

10.1 How to read the result



(a) Single signal fitting.



(b) Simultaneous fitting of two signals.

Figure 1: Examples of fitting.

In the figure 1(a), the black line, the blue line and the yellow line represent the original spectrum, the calculated signal fit and its baseline, respectively.

The blue area relates to the metabolite concentration to be determined and the red area represents a residue.

In case of the signal overlap a different approach is used: two or more overlapping signals are being fitted simultaneously. The most iconic example of such signals are the ones generated by CH_3 groups of Creatinine and Creatine. In such a case, the blue line and the grey area relate the sum of all fitted signals. The blue area corresponds to the concentration of the metabolite of interest (cf. figure 1(b)).

10.2 Result parameters

a) **Conc.** is the final result concentration of the metabolite,

b) **LOD** is the *limit of detection* of the given metabolite,

c) $\mathbf{r}$ is the *raw concentration* i.e. the concentration equivalent of the resulting signal fit prior to comparing to **LOD** (relates to the blue area, cf. α)),

d) ρ is the correlation of lineshape metabolite signal with calculated fit characterizing the match between metabolite signal and fit (cf. β)). Depending on the value of ρ, the following *flag* is displayed:

- 🟢, if the correlation is 95%,
- 🟡, if the correlation is in between 85% and 95%,
- ◯, if the correlation is less than 85%,

e) $\boldsymbol{\Delta}$ is the concentration equivalent of the difference between metabolite signal and calculated fit (residue corresponding to the the red area, cf. γ)).

10.3 Detailed definitions

Let s, f and b denote the functions describing the *raw spectra*, *fitted curve* and *(fitted) baseline* respectively. These functions are chosen such that $s \approx f + b$. Moreover, let I be a relevant PPM interval and P_N be the proton number for given metabolite/signal.

α) $\mathbf{r}$ (*raw concentration*) is defined as

$$\mathbf{r} = \frac{1}{P_N} \int_{\mathbb{R}} f(\xi)\, \mathrm{d}\xi.$$

β) ρ is the *correlation* of the functions s and $f + b$, i.e.

$$\rho = \max\left(0, \operatorname{corr}\left(\overline{s}, \overline{f + b}\right)\right),$$

where $\overline{s}$, $\overline{f+b}$ are numerical representations of the functions s and $f+b$ on sufficiently fine mesh of the interval I.

γ) $\boldsymbol{\Delta}$ is the the area between the raw signal s and the fitted data $f + b$ on the interval I expressed in the terms of the concentration, i.e.

$$\boldsymbol{\Delta} = \frac{1}{P_N} \int_I |s(\xi) - f(\xi) - b(\xi)|\, \mathrm{d}\xi.$$