Analysis Report

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

Sample ID: ALZ_Urine_Rack01_RCM_221214_expno710.100000.10r

Measuring Date: 24-Dec-2014 06:32:09
Reporting Date: 12-Dec-2020 15:51:43, 7 page(s), Version 1.1.0
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:

Amino acids and derivatives: 4-Aminobutyric acid (22 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

USt-Ident.-Nr DE 143 239 759
WEEE-Reg.-Nr. DE 43 181 702
Steuer-Nr. 31190/39205
Handelsregister Mannheim HRB 10 23 68
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	4.8	0.3	4.834	100 ●	0.087	1 - 19

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

2 Amines and derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
Dimethylamine	< 0.15	< 31	31	0.121	100 ●	0.006	≤ 54
Trimethylamine	< 0.01	< 2	2	0.003	76 ○	0.002	≤ 3

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

3 Amino acids and derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
1-Methylhistidine	< 0.07	< 15	15	0.000	0 ○	0.092	≤ 15
2-Furoylglycine	< 0.19	< 39	39	0.000	0 ○	0.036	≤ 40
4-Aminobutyric acid	0.11	22	20	0.109	59 ○	0.116	≤ 20
Alanine	0.18	38	10	0.185	100 ●	0.007	11 - 72
Arginine	< 3.6	< 750	750	0.416	0 ○	1.841	≤ 750
Betaine	0.06	13	7	0.062	100 ●	0.013	9 - 78
Creatine	< 0.24	< 50	50	0.044	100 ●	0.087	≤ 280
Glycine	0.61	130	34	0.609	100 ●	0.051	38 - 440
Guanidinoacetic acid	< 0.50	< 100	100	0.370	99 ●	0.068	≤ 140
Methionine	< 0.09	< 18	18	0.000	0 ○	0.418	≤ 18
N,N-Dimethylglycine	0.07	14	5	0.066	91 ●	0.014	≤ 15
Sarcosine	< 0.01	< 2	2	0.005	31 ○	0.004	≤ 7
Taurine	< 0.69	< 140	140	0.213	84 ○	0.187	≤ 170
Valine	0.02	4	2	0.021	69 ○	0.011	≤ 7

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

4 Benzene and substituted derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
Benzoic acid	< 0.05	< 10	10	0.000	0 ○	0.021	≤ 10
D-Mandelic acid	< 0.01	< 2	2	0.000	0 ○	0.100	2 - 17
Hippuric acid	0.92	190	170	0.922	99 ●	0.081	≤ 660

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

5 Carboxylic acids

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
Acetic acid	0.05	11	5	0.054	96 ●	0.013	≤ 51
Citric acid	1.6	320	40	1.558	100 ●	0.226	≤ 700
Formic acid	0.15	30	10	0.146	98 ●	0.015	≤ 43
Fumaric acid	< 0.01	< 2	2	0.003	92 ●	0.001	≤ 3
Imidazole	< 0.23	< 48	48	0.000	0 ○	0.077	≤ 48
Lactic acid	< 0.23	< 49	49	0.032	0 ○	0.128	≤ 110
Proline betaine	1.1	220	25	1.078	100 ●	0.078	≤ 280
Succinic acid	0.10	20	5	0.099	99 ●	0.008	≤ 39
Tartaric acid	< 0.02	< 5	5	0.012	96 ●	0.003	≤ 110
Trigonelline	< 0.17	< 35	35	0.055	100 ●	0.002	≤ 67

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

6 Fatty acids and derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
2-Methylsuccinic acid	< 0.23	< 48	48	0.000	0 ○	0.146	≤ 48

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

7 Keto acids and derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
2-Oxoglutaric acid	< 0.45	< 92	92	0.031	2 ○	0.170	≤ 92
3-Hydroxybutyric acid	< 0.50	< 100	100	0.083	21 ○	0.382	≤ 100
Acetoacetic acid	0.08	17	14	0.082	92 ●	0.043	≤ 30
Acetone	< 0.01	< 2	2	0.009	79 ○	0.004	≤ 7
Oxaloacetic acid	0.09	18	17	0.085	90 ●	0.055	≤ 66
Pyruvic acid	< 0.04	< 9	9	0.025	88 ●	0.007	≤ 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. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
1-Methyladenosine	< 0.02	< 5	5	0.000	0 ○	0.084	≤ 5
1-Methylnicotinamide	< 0.15	< 32	32	0.022	82 ○	0.013	≤ 32
Adenosine	< 1.9	< 390	390	0.000	0 ○	0.960	≤ 390
Allantoin	< 0.08	< 17	17	0.048	97 ●	0.008	≤ 47
Allopurinol	< 0.05	< 10	10	0.019	87 ●	0.016	≤ 11
Caffeine	< 0.22	< 45	45	0.141	64 ○	0.173	≤ 61
Inosine	< 0.09	< 19	19	0.011	97 ●	0.015	≤ 19

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

9 Sugars and derivatives

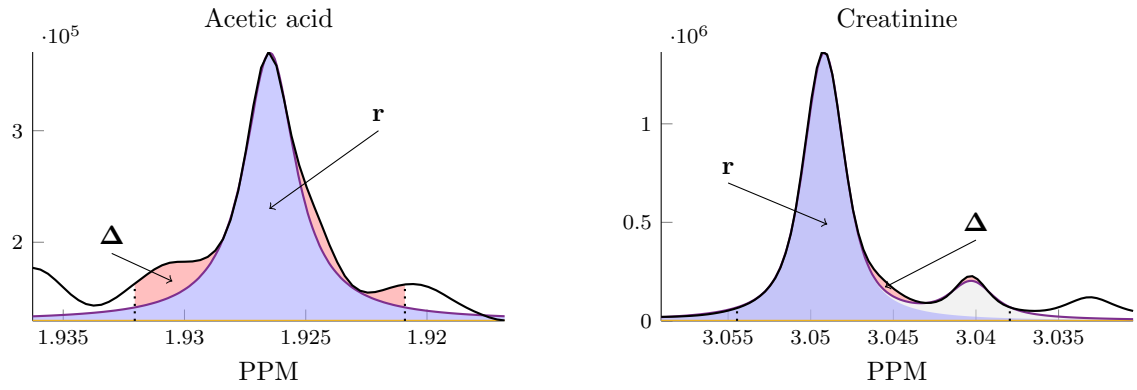
Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
D-Galactose	< 0.21	< 43	43	0.000	0 ○	0.068	≤ 44
D-Glucose	0.21	43	34	0.208	70 ○	0.146	≤ 140
D-Lactose	< 0.46	< 96	96	0.131	92 ●	0.040	≤ 96
D-Mannitol	< 0.89	< 180	180	0.000	0 ○	1.799	≤ 180
D-Mannose	< 0.03	< 6	6	0.000	0 ○	0.055	≤ 8
Myo-Inositol	< 21	< 4400	4400	0.000	0 ○	6.697	≤ 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 $\mathbf{\Delta}$.

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 $\mathrm{CH_3}$ 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) **Δ** 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) **Δ** 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.

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