Analysis Report

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

Sample ID: ALZ_Urine_Rack01_RCM_221214_expno290.100000.10r

Measuring Date: 23-Dec-2014 20:36:10
Reporting Date: 12-Dec-2020 15:21:58, 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:

Amines and derivatives: Trimethylamine (13 mmol/mol Crea),
Carboxylic acids: Acetic acid (190 mmol/mol Crea),
Purine, Pyridine and Pyrimidine derivatives: Allantoin (52 mmol/mol Crea).

Further detailed information is provided on the following pages.

Contents

1 Creatinine

Compound	Conc. mmol/L	LOD mmol/L	r mmol/L	ρ %	Δ mmol/L	95% Range(*) mmol/L
Creatinine	5.1	0.3	5.148	100 ●	0.151	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	< 0.16	< 31	31	0.148	100 ●	0.009	≤ 54
Trimethylamine	0.07	13	2	0.069	99 ●	0.005	≤ 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	< 0.08	< 15	15	0.000	0 ○	0.059	≤ 15
2-Furoylglycine	< 0.20	< 39	39	0.000	0 ○	0.029	≤ 40
4-Aminobutyric acid	< 0.10	< 20	20	0.000	0 ○	0.124	≤ 20
Alanine	0.14	26	10	0.136	89 ●	0.064	11 - 72
Arginine	< 3.9	< 750	750	0.000	0 ○	1.474	≤ 750
Betaine	0.18	36	7	0.184	100 ●	0.014	9 - 78
Creatine	< 0.26	< 50	50	0.073	100 ●	0.151	≤ 280
Glycine	0.92	180	34	0.924	100 ●	0.049	38 - 440
Guanidinoacetic acid	< 0.53	< 100	100	0.137	75 ○	0.104	≤ 140
Methionine	< 0.09	< 18	18	0.000	0 ○	0.170	≤ 18
N,N-Dimethylglycine	0.04	7	5	0.035	91 ●	0.013	≤ 15
Sarcosine	< 0.01	< 2	2	0.004	33 ○	0.003	≤ 7
Taurine	< 0.73	< 140	140	0.203	44 ○	0.159	≤ 170
Valine	< 0.01	< 2	2	0.004	0 ○	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. $\frac{\text{mmol}}{\text{mol Crea}}$	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 ○	0.037	≤ 10
D-Mandelic acid	< 0.01	< 2	2	0.000	0 ○	9.614	2 - 17
Hippuric acid	< 0.88	< 170	170	0.111	97 ●	0.712	≤ 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	0.97	190	5	0.974	99 ●	0.089	≤ 51
Citric acid	0.76	150	40	0.762	100 ●	0.118	≤ 700
Formic acid	< 0.05	< 10	10	0.016	92 ●	0.003	≤ 43
Fumaric acid	0.01	2	2	0.010	96 ●	0.002	≤ 3
Imidazole	< 0.25	< 48	48	-0.03	100 ●	0.000	≤ 48
Lactic acid	0.26	50	49	0.259	98 ●	0.052	≤ 110
Proline betaine	< 0.13	< 25	25	0.036	15 ○	0.036	≤ 280
Succinic acid	0.06	12	5	0.060	91 ●	0.018	≤ 39
Tartaric acid	0.07	13	5	0.068	98 ●	0.011	≤ 110
Trigonelline	< 0.18	< 35	35	0.106	100 ●	0.004	≤ 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	< 0.25	< 48	48	0.000	0 ○	0.094	≤ 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	< 0.48	< 92	92	0.009	76 ○	0.173	≤ 92
3-Hydroxybutyric acid	< 0.53	< 100	100	0.000	0 ○	0.347	≤ 100
Acetoacetic acid	< 0.07	< 14	14	0.052	85 ●	0.027	≤ 30
Acetone	< 0.01	< 2	2	0.006	63 ○	0.004	≤ 7
Oxaloacetic acid	< 0.09	< 17	17	0.082	91 ●	0.046	≤ 66
Pyruvic acid	< 0.05	< 9	9	0.031	98 ●	0.004	≤ 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	< 0.03	< 5	5	-0.00	100 ●	0.000	≤ 5
1-Methylnicotinamide	< 0.16	< 32	32	0.045	89 ●	0.017	≤ 32
Adenosine	< 2.0	< 390	390	0.000	0 ○	0.443	≤ 390
Allantoin	0.27	52	17	0.267	57 ○	0.254	≤ 47
Allopurinol	< 0.05	< 10	10	-0.00	100 ●	0.000	≤ 11
Caffeine	< 0.23	< 45	45	0.057	79 ○	0.075	≤ 61
Inosine	< 0.10	< 19	19	-0.01	100 ●	0.000	≤ 19

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

9 Sugars and derivatives

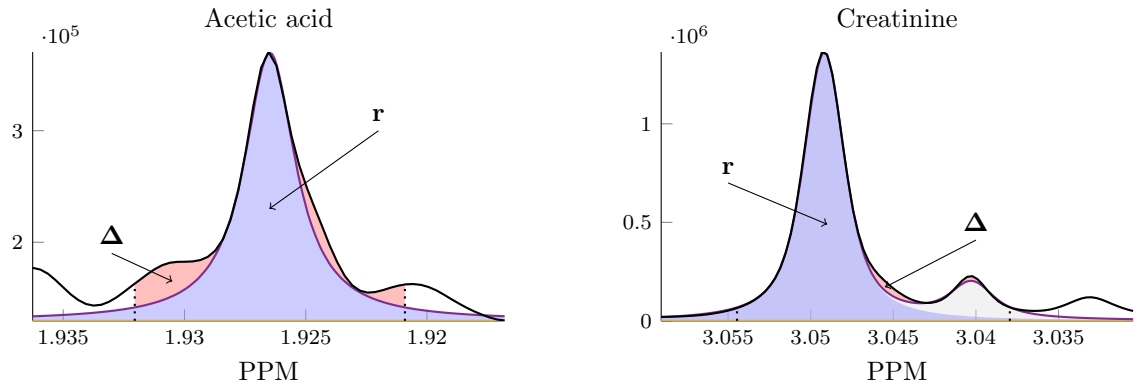
Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
D-Galactose	< 0.22	< 43	43	0.000	0 ○	2.582	≤ 44
D-Glucose	0.52	100	34	0.518	0 ○	3.232	≤ 140
D-Lactose	< 0.49	< 96	96	0.063	34 ○	0.331	≤ 96
D-Mannitol	< 0.94	< 180	180	0.000	0 ○	1.296	≤ 180
D-Mannose	< 0.03	< 6	6	0.000	0 ○	8.221	≤ 8
Myo-Inositol	< 23	< 4400	4400	0.000	0 ○	4.944	≤ 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 $\mathrm{CH_3}$ 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.

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