Analysis Report

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

Sample ID: ALZ_Urine_Rack01_RCM_221214_expno520.100000.10r

Measuring Date:	24-Dec-2014 02:15:38
Reporting Date:	12-Dec-2020 15:32:57, 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

All metabolites were found with concentrations inside the 95% range of Bruker Quant-UR B.1.1.0 urine metabolite concentration database.

Contents

1 Creatinine

Compound	Conc.	LOD	r	ρ	Δ	95% Range[*]
	mmol/L	mmol/L	mmol/L	%	mmol/L	mmol/L
Creatinine	2.8	0.3	2.805	100 🟢	0.071	1 - 19

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

2 Amines and derivatives

Compound	Conc.	Conc.	LOD	r	ρ	Δ	95% Range[*]
	mmol/L	$\frac{mmol}{mol\ Crea}$	$\frac{mmol}{mol\ Crea}$	mmol/L	%	mmol/L	$\frac{mmol}{mol\ Crea}$
Dimethylamine	< 0.09	< 31	31	0.075	100 🟢	0.002	≤ 54
Trimethylamine	< 0.01	< 2	2	0.001	97 🟢	0.000	≤ 3

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

3 Amino acids and derivatives

Compound	Conc.	Conc.	LOD	r	ρ	Δ	95% Range[*]
	mmol/L	$\frac{mmol}{mol\ Crea}$	$\frac{mmol}{mol\ Crea}$	mmol/L	%	mmol/L	$\frac{mmol}{mol\ Crea}$
1-Methylhistidine	< 0.04	< 15	15	0.000	0 ⚪	0.042	≤ 15
2-Furoylglycine	< 0.11	< 39	39	0.000	0 ⚪	0.029	≤ 40
4-Aminobutyric acid	< 0.06	< 20	20	0.000	0 ⚪	0.207	≤ 20
Alanine	0.09	31	10	0.087	100 🟢	0.004	11 - 72
Arginine	< 2.1	< 750	750	0.180	0 ⚪	1.215	≤ 750
Betaine	0.08	29	7	0.082	100 🟢	0.007	9 - 78
Creatine	< 0.14	< 50	50	0.076	100 🟢	0.071	≤ 280
Glycine	0.22	79	34	0.221	100 🟢	0.005	38 - 440
Guanidinoacetic acid	< 0.29	< 100	100	0.162	99 🟢	0.025	≤ 140
Methionine	< 0.05	< 18	18	0.000	0 ⚪	0.894	≤ 18
N,N-Dimethylglycine	0.04	14	5	0.040	81 ⚪	0.013	≤ 15
Sarcosine	< 0.01	< 2	2	0.004	27 ⚪	0.004	≤ 7
Taurine	< 0.40	< 140	140	0.000	0 ⚪	0.538	≤ 170
Valine	0.01	3	2	0.008	84 ⚪	0.003	≤ 7

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

4   Benzene and substituted derivatives

Compound	Conc. mmol/L	Conc. $\frac{mmol}{mol\ Crea}$	LOD $\frac{mmol}{mol\ Crea}$	r mmol/L	ρ %	Δ mmol/L	95% Range[*] $\frac{mmol}{mol\ Crea}$
Benzoic acid	< 0.03	< 10	10	0.000	0 ○	0.040	≤ 10
D-Mandelic acid	0.01	2	2	0.006	0 ○	0.010	2 - 17
Hippuric acid	0.81	290	170	0.810	100 ●	0.039	≤ 660

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

5   Carboxylic acids

Compound	Conc. mmol/L	Conc. $\frac{mmol}{mol\ Crea}$	LOD $\frac{mmol}{mol\ Crea}$	r mmol/L	ρ %	Δ mmol/L	95% Range[*] $\frac{mmol}{mol\ Crea}$
Acetic acid	0.04	14	5	0.038	78 ○	0.018	≤ 51
Citric acid	1.1	380	40	1.053	100 ●	0.076	≤ 700
Formic acid	0.07	24	10	0.068	100 ●	0.003	≤ 43
Fumaric acid	< 0.01	< 2	2	0.002	24 ○	0.001	≤ 3
Imidazole	< 0.13	< 48	48	0.000	0 ○	0.057	≤ 48
Lactic acid	< 0.14	< 49	49	0.048	95 ●	0.013	≤ 110
Proline betaine	0.12	42	25	0.119	57 ○	0.052	≤ 280
Succinic acid	0.03	11	5	0.032	95 ●	0.006	≤ 39
Tartaric acid	0.01	5	5	0.014	92 ●	0.005	≤ 110
Trigonelline	< 0.10	< 35	35	0.058	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. $\frac{mmol}{mol\ Crea}$	LOD $\frac{mmol}{mol\ Crea}$	r mmol/L	ρ %	Δ mmol/L	95% Range[*] $\frac{mmol}{mol\ Crea}$
2-Methylsuccinic acid	< 0.13	< 48	48	0.000	0 ○	0.101	≤ 48

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

7 Keto acids and derivatives

Compound	Conc. mmol/L	Conc. $\frac{mmol}{mol\ Crea}$	LOD $\frac{mmol}{mol\ Crea}$	r mmol/L	ρ %	Δ mmol/L	95% Range[*] $\frac{mmol}{mol\ Crea}$
2-Oxoglutaric acid	< 0.26	< 92	92	0.020	51○	0.042	≤ 92
3-Hydroxybutyric acid	< 0.29	< 100	100	0.000	0○	0.413	≤ 100
Acetoacetic acid	0.07	25	14	0.071	74○	0.047	≤ 30
Acetone	0.01	3	2	0.009	99●	0.001	≤ 7
Oxaloacetic acid	0.14	49	17	0.137	91●	0.064	≤ 66
Pyruvic acid	< 0.03	< 9	9	0.008	72○	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. $\frac{mmol}{mol\ Crea}$	LOD $\frac{mmol}{mol\ Crea}$	r mmol/L	ρ %	Δ mmol/L	95% Range[*] $\frac{mmol}{mol\ Crea}$
1-Methyladenosine	< 0.01	< 5	5	0.000	0○	0.067	≤ 5
1-Methylnicotinamide	< 0.09	< 32	32	0.022	94●	0.007	≤ 32
Adenosine	< 1.1	< 390	390	0.000	0○	0.689	≤ 390
Allantoin	< 0.05	< 17	17	0.040	99●	0.002	≤ 47
Allopurinol	< 0.03	< 10	10	0.011	93●	0.023	≤ 11
Caffeine	< 0.13	< 45	45	0.122	84○	0.087	≤ 61
Inosine	< 0.05	< 19	19	0.000	0○	0.097	≤ 19

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

9 Sugars and derivatives

Compound	Conc. mmol/L	Conc. $\frac{mmol}{mol\ Crea}$	LOD $\frac{mmol}{mol\ Crea}$	r mmol/L	ρ %	Δ mmol/L	95% Range[*] $\frac{mmol}{mol\ Crea}$
D-Galactose	< 0.12	< 43	43	0.000	0○	0.019	≤ 44
D-Glucose	0.13	48	34	0.135	72○	0.059	≤ 140
D-Lactose	< 0.27	< 96	96	0.014	51○	0.040	≤ 96
D-Mannitol	< 0.51	< 180	180	0.000	0○	1.706	≤ 180
D-Mannose	< 0.02	< 6	6	0.000	0○	0.092	≤ 8
Myo-Inositol	< 12	< 4400	4400	0.000	0○	1.865	≤ 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 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.

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

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.

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