

# Analysis Report

# **B**ruker IVDr **Quant**ification in **UR**ine B.I.Quant-UR $b^{TM}$

Sample ID: ALZ\_Urine\_Rack01\_RCM\_221214\_expno480.100000.10r

Measuring Date: 24-Dec-2014 01:16:59

Reporting Date: 12-Dec-2020 15:33:07, 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.

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



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#### 1 Creatinine

Compound	Conc.	LOD	r	ρ	Δ	95% Range <sup>(*)</sup>
	mmol/L	mmol/L	mmol/L	%	mmol/L	mmol/L
Creatinine	7.1	0.3	7.083	100	0.142	1 - 19

<sup>(\*)</sup> Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

#### 2 Amines and derivatives

Compound	Conc.	Conc.	LOD	$\mathbf{r}$	ρ	Δ	95% Range <sup>(*)</sup>
	mmol/L	_mmol_ mol Crea	_mmol_ mol Crea	mmol/L	%	mmol/L	_mmol mol Crea
Dimethylamine	0.22	31	31	0.222	100	0.008	≤ 54 🔲
Trimethylamine	< 0.01	< 2	2	0.006	93 🔾	0.002	≤ 3 □ □

<sup>(\*)</sup> 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 <sup>(*)</sup>
	mmol/L	mmol mol Crea	mmol mol Crea	mmol/L	%	mmol/L	mmol mol Crea
1-Methylhistidine	< 0.11	< 15	15	0.000	00	0.062	≤ 15 🗔
2-Furoylglycine	< 0.27	< 39	39	0.035	91 🔾	0.010	≤ 40 □
4-Aminobutyric acid	< 0.14	< 20	20	0.003	0 🔾	0.229	≤ 20 □
Alanine	0.15	21	10	0.148	100	0.013	11 - 72 🔟
Arginine	< 5.3	< 750	750	0.496	0 🔾	1.369	≤ 750 🗔
Betaine	0.10	14	7	0.097	100	0.027	9 - 78
Creatine	< 0.35	< 50	50	0.083	100	0.142	≤ 280 □ □
Glycine	0.32	45	34	0.320	100	0.017	38 - 440
Guanidinoacetic acid	< 0.73	< 100	100	0.386	96 🔵	0.101	≤ 140 🔲
Methionine	< 0.13	< 18	18	0.007	74 🔾	0.041	≤ 18 🔲
N,N-Dimethylglycine	0.05	7	5	0.046	94 🔵	0.013	≤ 15 🔲
Sarcosine	< 0.01	< 2	2	0.003	0 🔾	0.012	≤ 7 □□□
Taurine	< 1.00	< 140	140	0.331	65 🔾	0.230	≤ 170 🗔
Valine	0.02	3	2	0.023	76 🔾	0.011	≤ 7 □□□

<sup>(\*)</sup> Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.



#### 4 Benzene and substituted derivatives

Compound	Conc.	Conc.	LOD	r	ρ	Δ	95% Range <sup>(*)</sup>
	mmol/L	_mmol_ mol Crea	_mmol_ mol Crea	mmol/L	%	mmol/L	_mmol_ mol Crea
Benzoic acid	< 0.07	< 10	10	0.000	00	0.028	≤ 10 □
D-Mandelic acid	< 0.01	< 2	2	0.000	0 🔾	0.043	2 - 17
Hippuric acid	2.6	360	170	2.554	100	0.168	≤ 660 🔟

<sup>(\*)</sup> Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

### 5 Carboxylic acids

Compound	Conc.	Conc.	LOD	$\mathbf{r}$	ρ	Δ	95% Range <sup>(*)</sup>
	mmol/L	mmol mol Crea	mmol mol Crea	mmol/L	%	mmol/L	mmol mol Crea
Acetic acid	0.04	5	5	0.035	73 🔾	0.018	≤ 51
Citric acid	2.2	300	40	2.155	100	0.184	≤ 700 🔟
Formic acid	0.09	13	10	0.091	99 🔵	0.009	≤ 43 🔃
Fumaric acid	< 0.01	< 2	2	0.003	98 🔵	0.000	≤ 3 □ □
Imidazole	< 0.34	< 48	48	0.042	90 🔾	0.031	≤ 48 🔲
Lactic acid	< 0.34	< 49	49	0.127	88 🔾	0.043	≤ 110 🗔
Proline betaine	< 0.18	< 25	25	0.146	97 🔵	0.034	≤ 280 □ □
Succinic acid	< 0.03	< 5	5	0.029	88 🔾	0.008	≤ 39 🔲
Tartaric acid	< 0.04	< 5	5	0.006	0 🔾	0.017	≤ 110 🗔
Trigonelline	< 0.25	< 35	35	0.073	100	0.003	≤ 67 □□□

<sup>(\*)</sup> Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

## 6 Fatty acids and derivatives

Compound	Conc.	Conc.	LOD	$\mathbf{r}$	ρ	Δ	95% Range <sup>(*)</sup>
	mmol/L	_mmol mol Crea	mmol mol Crea	mmol/L	%	mmol/L	_mmol mol Crea
2-Methylsuccinic acid	< 0.34	< 48	48	0.036	66 🔾	0.076	≤ 48 🔲

<sup>(\*)</sup> Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.



#### 7 Keto acids and derivatives

Compound	Conc.	Conc.	LOD	$\mathbf{r}$	ρ	Δ	95% Range <sup>(*)</sup>
	mmol/L	_mmol_ mol Crea	_mmol_ mol Crea	mmol/L	%	mmol/L	_mmol_ mol Crea
2-Oxoglutaric acid	< 0.65	< 92	92	0.010	48 🔾	0.258	≤ 92 □
3-Hydroxybutyric acid	< 0.73	< 100	100	0.000	0 🔾	0.681	≤ 100 🔲
Acetoacetic acid	< 0.10	< 14	14	0.092	77 🔾	0.061	≤ 30 □ □
Acetone	< 0.01	< 2	2	0.010	98	0.002	≤ 7 □□□
Oxaloacetic acid	0.14	20	17	0.140	87 🔵	0.098	≤ 66 🔟
Pyruvic acid	< 0.06	< 9	9	0.033	92 🔵	0.007	≤ 13 🔲

<sup>(\*)</sup> Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

### 8 Purine, Pyridine and Pyrimidine derivatives

Compound	Conc.	Conc.	LOD	r	ρ	Δ	95% Range <sup>(*)</sup>
	mmol/L	_mmol_ mol Crea	mmol_ mol Crea	mmol/L	%	mmol/L	_mmol _ mol Crea
1-Methyladenosine	< 0.04	< 5	5	0.000	00	0.108	≤ 5 □
1-Methylnicotinamide	< 0.22	< 32	32	0.112	100	0.007	≤ 32 🔲
Adenosine	< 2.7	< 390	390	0.000	0 🔾	1.343	≤ 390 □ □
Allantoin	< 0.12	< 17	17	0.084	95 🔵	0.015	≤ 47 🔲
Allopurinol	< 0.07	< 10	10	0.043	75 🔾	0.067	≤ 11 □
Caffeine	< 0.32	< 45	45	0.157	69 🔾	0.123	≤ 61 □□□
Inosine	< 0.13	< 19	19	0.017	89 🔵	0.058	≤ 19 🔲

<sup>(\*)</sup> Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.

## 9 Sugars and derivatives

Compound	Conc.	Conc.	LOD	r	ρ	Δ	95% Range <sup>(*)</sup>
	mmol/L	mmol mol Crea	mmol mol Crea	mmol/L	%	mmol/L	mmol mol Crea
D-Galactose	< 0.31	< 43	43	0.030	92 🔵	0.003	≤ 44 □ □ □
D-Glucose	0.25	35	34	0.248	86 🔾	0.063	≤ 140 🔲
D-Lactose	< 0.68	< 96	96	0.033	70 🔾	0.044	≤ 96 □ □
D-Mannitol	< 1.3	< 180	180	0.000	00	2.229	≤ 180 🗔
D-Mannose	< 0.04	< 6	6	0.000	00	0.045	≤ 8 □ □
Myo-Inositol	< 31	< 4400	4400	0.000	0 🔾	5.190	≤ 4400 □

<sup>(\*)</sup> 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  $\mathbf{r}$ ,  $\rho$  and  $\Delta$ .

#### 10.1 How to read the result

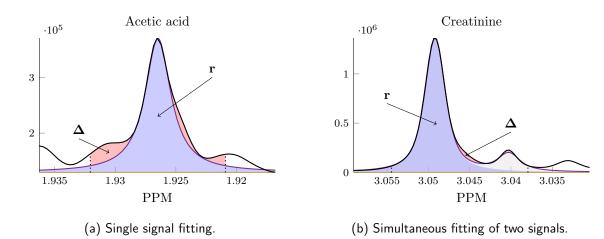


Figure 1: Examples of fitting.

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.  $\alpha$ )),
- d)  $\rho$  is the correlation of lineshape metabolite signal with calculated fit characterizing the match between metabolite signal and fit (cf.  $\beta$ )). Depending on the value of  $\rho$ , the following flag is displayed:



- , if the correlation is 95%,
- O, if the correlation is in between 85% and 95%,
- (), if the correlation is less than 85%,
- e)  $\Delta$  is the concentration equivalent of the difference between metabolite signal and calculated fit (residue corresponding to the the red area, cf.  $\gamma$ )).

#### 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.

 $\alpha$ ) **r** (raw concentration) is defined as

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

 $\beta$ )  $\rho$  is the *correlation* of the functions s and f+b, i.e.

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

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

 $\gamma$ )  $\Delta$  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.

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