

# Analysis Report

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

Sample ID: ALZ\_Urine\_Rack01\_RCM\_221214\_expno800.100000.10r

Measuring Date: 24-Dec-2014 08:45:48

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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:

<u>Carboxylic acids:</u> Formic acid (54 mmol/mol Crea), Trigonelline (110 mmol/mol Crea), <u>Keto acids and derivatives:</u> Acetoacetic acid (35 mmol/mol Crea), Oxaloacetic acid (72 mmol/mol Crea).

Further detailed information is provided on the following pages.

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	3.1	0.3	3.086	100	0.074	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	0.14	46	31	0.141	100	0.006	≤ 54 🔳
Trimethylamine	< 0.01	< 2	2	0.003	96	0.001	≤ 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	< 0.05	< 15	15	0.017	00	0.031	≤ 15 🗔
2-Furoylglycine	< 0.12	< 39	39	0.109	99 🔵	0.010	≤ 40 □
4-Aminobutyric acid	< 0.06	< 20	20	0.000	0 🔾	0.450	≤ 20 □
Alanine	0.14	45	10	0.140	100	0.012	11 - 72 🔲
Arginine	< 2.3	< 750	750	0.270	0 🔾	1.728	≤ 750 □ □
Betaine	0.23	74	7	0.227	100	0.016	9 - 78
Creatine	< 0.15	< 50	50	0.088	100	0.074	≤ 280 🔲
Glycine	1.2	390	34	1.190	100	0.032	38 - 440
Guanidinoacetic acid	< 0.32	< 100	100	0.281	98 🔵	0.050	≤ 140 🔲
Methionine	< 0.06	< 18	18	0.000	0 🔾	0.284	≤ 18 🔲
N,N-Dimethylglycine	0.04	14	5	0.045	98 🔵	0.008	≤ 15 🔲
Sarcosine	0.01	3	2	0.009	41 🔾	0.006	≤ 7 □
Taurine	< 0.44	< 140	140	0.204	37 🔾	0.288	≤ 170 🗔
Valine	0.01	4	2	0.012	85 🔾	0.015	≤ 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	< 0.03	< 10	10	0.000	00	0.017	≤ 10 🗆
D-Mandelic acid	< 0.01	< 2	2	0.000	0 🔾	0.006	2 - 17
Hippuric acid	1.2	370	170	1.152	100	0.062	≤ 660 🔟

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

### 5 Carboxylic acids

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
Acetic acid	0.05	16	5	0.049	78 🔾	0.036	≤ 51 🔲
Citric acid	1.8	580	40	1.777	100	0.171	≤ 700 □
Formic acid	0.17	54	10	0.166	100	0.008	≤ 43 □ □
Fumaric acid	< 0.01	< 2	2	0.004	99 🔵	0.000	≤ 3 □ □
Imidazole	< 0.15	< 48	48	0.000	0 🔾	0.110	≤ 48 🔲
Lactic acid	< 0.15	< 49	49	0.059	93 🔾	0.094	≤ 110 🔲
Proline betaine	< 0.08	< 25	25	0.072	71 🔾	0.068	≤ 280 □ □
Succinic acid	0.04	12	5	0.036	69 🔾	0.019	≤ 39 🔲
Tartaric acid	< 0.01	< 5	5	0.007	41 🔾	0.010	≤ 110 🔲
Trigonelline	0.34	110	35	0.337	100	0.007	≤ 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	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	< 0.15	< 48	48	0.000	0 🔾	0.207	≤ 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	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	< 0.28	< 92	92	0.086	57 🔾	0.190	≤ 92 □ □
3-Hydroxybutyric acid	< 0.32	< 100	100	0.000	0 🔾	0.883	≤ 100 □ □
Acetoacetic acid	0.11	35	14	0.108	98	0.028	≤ 30 □ □
Acetone	0.02	5	2	0.016	97 🔵	0.002	≤ 7 □
Oxaloacetic acid	0.22	72	17	0.223	94 🔵	0.082	≤ 66 □
Pyruvic acid	< 0.03	< 9	9	0.016	89 🔵	0.005	≤ 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	< 0.01	< 5	5	0.000	00	0.087	≤ 5 □
1-Methylnicotinamide	< 0.10	< 32	32	0.026	90 🔵	0.011	≤ 32 🔲
Adenosine	< 1.2	< 390	390	0.000	0 🔾	0.879	≤ 390 □ □
Allantoin	< 0.05	< 17	17	0.023	80 🔾	0.011	≤ 47 🔲
Allopurinol	< 0.03	< 10	10	0.016	74 🔾	0.023	≤ 11 □□□
Caffeine	< 0.14	< 45	45	0.102	66 🔾	0.134	≤ 61 □
Inosine	< 0.06	< 19	19	0.021	72 🔾	0.027	≤ 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	< 0.13	< 43	43	0.000	00	0.012	< 44 □ □ □
D-Glucose	0.24	77	34	0.238	87 🔵	0.053	≤ 140 🔟
D-Lactose	< 0.30	< 96	96	0.090	89 🔵	0.027	≤ 96 □ □
D-Mannitol	< 0.57	< 180	180	0.000	0 🔾	1.596	≤ 180 🗔
D-Mannose	< 0.02	< 6	6	0.000	0 🔾	0.054	≤ 8 □ □
Myo-Inositol	< 14	< 4400	4400	0.000	0 🔾	3.359	≤ 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

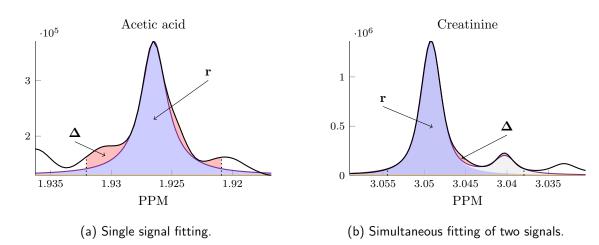


Figure 1: Examples of fitting.

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  $\mathrm{CH}_3$  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.  $\alpha$ )),
- 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.

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