

Analysis Report

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

Sample ID: ALZ_Urine_Rack01_RCM_221214_expno810.100000.10r

Measuring Date: 24-Dec-2014 09:00:24

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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:

Benzene and substituted derivatives: Hippuric acid (840 mmol/mol Crea),

Carboxylic acids: Trigonelline (76 mmol/mol Crea).

Further detailed information is provided on the following pages.

Handelsregister Mannheim HRB 10 23 68 Sitz der Gesellschaft: 76287 Rheinstetten



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1 Creatinine

Compound	Conc.	LOD	r	$\mathbf{r} \mid \rho \mid$		95% Range ^(*)
	mmol/L	mmol/L	mmol/L	%	mmol/L	mmol/L
Creatinine	2.7	0.3	2.737	100	0.050	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	_mmol_ mol Crea	_mmol_ mol Crea	mmol/L	%	mmol/L	<u>mmol</u> mol Crea
Dimethylamine	0.09	33	31	0.091	100	0.001	≤ 54 🔲
Trimethylamine	< 0.01	< 2	2	0.001	99	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	mmol mol Crea	mmol mol Crea	mmol/L	%	mmol/L	mmol mol Crea
1-Methylhistidine	< 0.04	< 15	15	0.000	00	0.016	≤ 15 □□□
2-Furoylglycine	< 0.11	< 39	39	0.000	0 🔾	0.028	≤ 40 □
4-Aminobutyric acid	< 0.05	< 20	20	0.013	60	0.061	≤ 20 □ □
Alanine	0.06	20	10	0.056	100	0.003	11 - 72 📗
Arginine	< 2.0	< 750	750	0.181	0 🔾	1.007	≤ 750 □ □
Betaine	0.08	30	7	0.083	100	0.004	9 - 78 🔟
Creatine	< 0.14	< 50	50	0.016	100	0.050	≤ 280 □ □
Glycine	0.28	100	34	0.282	100	0.007	38 - 440
Guanidinoacetic acid	< 0.28	< 100	100	0.039	66 🔾	0.028	≤ 140 🔲
Methionine	< 0.05	< 18	18	0.000	0 🔾	0.099	≤ 18 🔲
N,N-Dimethylglycine	0.04	14	5	0.039	99 🔵	0.004	≤ 15 🔲
Sarcosine	< 0.01	< 2	2	0.004	90	0.004	≤ 7 □ □
Taurine	< 0.39	< 140	140	0.142	95	0.046	≤ 170 🗔
Valine	< 0.01	< 2	2	0.005	74 🔾	0.006	≤ 7 □□□

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



4 Benzene and substituted derivatives

Compound	Conc.	Conc.	LOD	\mathbf{r}	ρ	Δ	95% Range ^(*)
	mmol/L	_mmol_ mol Crea	_mmol_ mol Crea	mmol/L	%	mmol/L	_mmol _ mol Crea
Benzoic acid	< 0.03	< 10	10	0.000	0 🔾	0.019	≤ 10 🗆
D-Mandelic acid	< 0.01	< 2	2	0.000	0 🔾	0.078	2 - 17
Hippuric acid	2.3	840	170	2.303	99	0.247	≤ 660 □ □

^(*) 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 ^(*)
	mmol/L	mmol mol Crea	mmol mol Crea	mmol/L	%	mmol/L	mmol mol Crea
Acetic acid	0.04	15	5	0.042	98	0.006	≤ 51 🔲
Citric acid	1.1	420	40	1.146	100	0.085	≤ 700 🔲
Formic acid	0.11	40	10	0.111	100	0.007	≤ 43 🔲
Fumaric acid	< 0.01	< 2	2	0.001	16 🔾	0.001	≤ 3 □ □
Imidazole	< 0.13	< 48	48	0.000	0 🔾	0.062	≤ 48 🔲
Lactic acid	< 0.13	< 49	49	0.048	97 🔵	0.021	≤ 110 🔲
Proline betaine	< 0.07	< 25	25	0.057	30 🔾	0.073	≤ 280 □ □
Succinic acid	0.02	8	5	0.023	88 🔾	0.006	≤ 39 🔲
Tartaric acid	0.13	47	5	0.128	100	0.003	≤ 110 🔲
Trigonelline	0.21	76	35	0.207	100	0.005	≤ 67 □□□

^(*) 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 ^(*)
	mmol/L	_mmol mol Crea	mmol mol Crea	mmol/L	%	mmol/L	_mmol mol Crea
2-Methylsuccinic acid	< 0.13	< 48	48	0.000	00	0.097	≤ 48 🔲

^(*) 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 ^(*)
	mmol/L	_mmol_ mol Crea	mmol_ mol Crea	mmol/L	%	mmol/L	_mmol_ mol Crea
2-Oxoglutaric acid	< 0.25	< 92	92	0.000	54 🔾	0.165	≤ 92 🔲
3-Hydroxybutyric acid	< 0.28	< 100	100	0.055	32 🔾	0.140	≤ 100 🔲
Acetoacetic acid	< 0.04	< 14	14	0.028	77 🔾	0.020	≤ 30 🔲
Acetone	0.01	3	2	0.009	99	0.001	≤ 7 🔟
Oxaloacetic acid	0.09	31	17	0.086	93 🔾	0.037	≤ 66 🔟
Pyruvic acid	< 0.02	< 9	9	0.010	91 🔵	0.003	≤ 13 🔲

^(*) 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 ^(*)
	mmol/L	_mmol_ mol Crea	mmol_ mol Crea	mmol/L	%	mmol/L	_mmol mol Crea
1-Methyladenosine	< 0.01	< 5	5	0.000	00	0.068	≤ 5 □
1-Methylnicotinamide	< 0.09	< 32	32	0.017	60 🔾	0.010	≤ 32 🔲
Adenosine	< 1.1	< 390	390	0.000	0 🔾	0.517	≤ 390 □ □
Allantoin	< 0.04	< 17	17	0.031	99 🔵	0.003	≤ 47 🔲
Allopurinol	< 0.03	< 10	10	0.015	89 🔵	0.011	≤ 11 □
Caffeine	< 0.12	< 45	45	0.066	93 🔾	0.062	≤ 61 □□□
Inosine	< 0.05	< 19	19	0.009	99 🔵	0.010	≤ 19 🗔

^(*) 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 ^(*)
	mmol/L	mmol mol Crea	mmol mol Crea	mmol/L	%	mmol/L	mmol mol Crea
D-Galactose	< 0.12	< 43	43	0.000	00	0.020	< 44 □ □ □
D-Glucose	0.16	59	34	0.162	65 🔾	0.086	≤ 140 🔲
D-Lactose	< 0.26	< 96	96	0.029	85 🔾	0.021	≤ 96 □ □
D-Mannitol	< 0.50	< 180	180	0.000	0 🔾	0.976	≤ 180 🗔
D-Mannose	< 0.02	< 6	6	0.000	0 🔾	0.039	≤ 8 □ □
Myo-Inositol	< 12	< 4400	4400	0.000	0 🔾	1.671	≤ 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 Δ .

10.1 How to read the result

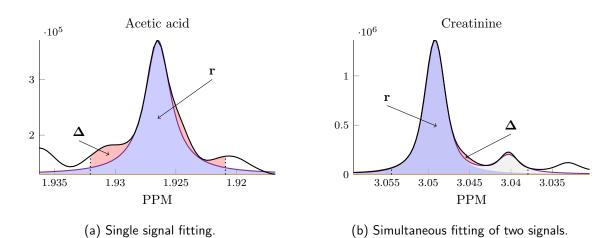


Figure 1: Examples of fitting.

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. 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%,
- O, 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) **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.

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

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

 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.

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