

Analysis Report

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

Sample ID: ALZ_Urine_Rack01_RCM_221214_expno660.100000.10r

Measuring Date: 24-Dec-2014 05:42:37

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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:

Amino acids and derivatives: Betaine (8 mmol/mol Crea),

Keto acids and derivatives: Oxaloacetic acid (140 mmol/mol Crea),

Sugars and derivatives: D-Mannitol (520 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	ρ	Δ	95% Range ^(*)
	mmol/L	mmol/L	mmol/L	%	mmol/L	mmol/L
Creatinine	4.9	0.3	4.861	100	0.083	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	0.20	41	31	0.200	100	0.002	≤ 54 🔳
Trimethylamine	< 0.01	< 2	2	0.007	100	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	< 0.07	< 15	15	0.022	93 🔾	0.230	≤ 15 🔲
2-Furoylglycine	< 0.19	< 39	39	0.000	0 🔾	0.457	≤ 40 □ □
4-Aminobutyric acid	< 0.10	< 20	20	0.000	0 🔾	0.418	≤ 20 □ □
Alanine	0.15	31	10	0.148	100	0.010	11 - 72
Arginine	< 3.6	< 750	750	0.388	0 🔾	1.521	≤ 750 □□□
Betaine	0.04	8	7	0.039	100	0.018	9 - 78
Creatine	< 0.24	< 50	50	0.030	100	0.083	≤ 280 □ □
Glycine	0.32	66	34	0.320	100	0.009	38 - 440
Guanidinoacetic acid	0.55	110	100	0.548	16 🔾	0.827	≤ 140 🔳
Methionine	< 0.09	< 18	18	0.000	0 🔾	0.197	≤ 18 🔲
N,N-Dimethylglycine	0.04	8	5	0.038	88 🔵	0.015	≤ 15 🔟 🗆
Sarcosine	< 0.01	< 2	2	0.004	0 🔾	0.012	≤ 7 □ □
Taurine	< 0.69	< 140	140	0.380	96	0.083	≤ 170 🗔
Valine	0.02	4	2	0.020	00	0.043	≤ 7 🔟

^(*) 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 ^(*)
	mmol/L	_mmol_ mol Crea	_mmol_ mol Crea	mmol/L	%	mmol/L	_mmol_ mol Crea
Benzoic acid	< 0.05	< 10	10	0.000	00	0.027	≤ 10 □
D-Mandelic acid	< 0.01	< 2	2	0.000	0 🔾	0.009	2 - 17
Hippuric acid	1.3	260	170	1.254	100	0.093	≤ 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	0.06	12	5	0.058	71 🔾	0.035	≤ 51
Citric acid	2.2	440	40	2.158	100	0.192	≤ 700 🔲
Formic acid	< 0.05	< 10	10	0.028	99 🔵	0.003	≤ 43 🔲
Fumaric acid	< 0.01	< 2	2	0.006	79 🔾	0.003	≤ 3 □
Imidazole	< 0.23	< 48	48	0.000	0 🔾	0.101	≤ 48 🔲
Lactic acid	< 0.24	< 49	49	0.063	98 🔵	0.114	≤ 110 🗔
Proline betaine	< 0.12	< 25	25	0.036	0 🔾	0.057	≤ 280 □ □
Succinic acid	0.03	7	5	0.032	76 🔾	0.013	≤ 39 🔃
Tartaric acid	< 0.02	< 5	5	0.013	92 🔾	0.009	≤ 110 🗔
Trigonelline	< 0.17	< 35	35	0.060	100	0.003	≤ 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	< 0.23	< 48	48	0.000	00	0.159	≤ 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	< 0.45	< 92	92	0.000	00	0.531	≤ 92 🔲
3-Hydroxybutyric acid	< 0.50	< 100	100	0.159	35 🔾	0.238	≤ 100 🔲
Acetoacetic acid	0.13	27	14	0.134	97 🔵	0.042	≤ 30 🔲
Acetone	0.01	3	2	0.014	97 🔵	0.004	≤ 7 □
Oxaloacetic acid	0.69	140	17	0.688	98 🔵	0.112	≤ 66 □ □
Pyruvic acid	< 0.04	< 9	9	0.028	82 🔾	0.014	≤ 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	< 0.02	< 5	5	0.000	00	0.101	≤ 5 □
1-Methylnicotinamide	< 0.15	< 32	32	0.024	77 🔾	0.013	≤ 32 🔲
Adenosine	< 1.9	< 390	390	0.000	0 🔾	1.212	≤ 390 □ □
Allantoin	0.20	41	17	0.198	100	0.012	≤ 47 🔟
Allopurinol	< 0.05	< 10	10	0.022	93 🔵	0.020	≤ 11 □
Caffeine	< 0.22	< 45	45	0.104	76 🔾	0.130	≤ 61 □□□
Inosine	< 0.09	< 19	19	0.010	99 🔵	0.018	≤ 19 🗔

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

9 Sugars 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
D-Galactose	< 0.21	< 43	43	0.000	00	0.016	< 44 □ □ □
D-Glucose	0.39	79	34	0.386	90 🔵	0.067	≤ 140 🔳
D-Lactose	< 0.47	< 96	96	0.045	71 🔾	0.043	≤ 96 □ □
D-Mannitol	2.5	520	180	2.508	92 🔵	0.955	≤ 180 🔲 📗
D-Mannose	< 0.03	< 6	6	0.000	0 🔾	0.110	≤ 8 □ □
Myo-Inositol	< 22	< 4400	4400	0.000	0 🔾	3.934	≤ 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

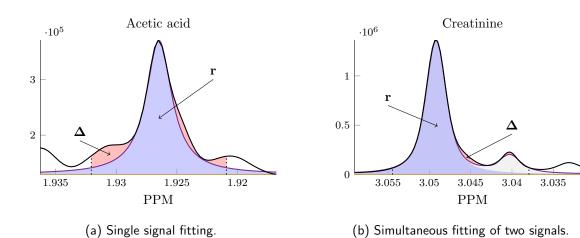


Figure 1: Examples of fitting.

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) ${\bf r}$ 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.

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