

Analysis Report

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

ALZ_Urine_Rack01_RCM_221214_expno60.100000.10r Sample ID:

Measuring Date: 23-Dec-2014 14:46:48

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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:

Purine, Pyridine and Pyrimidine derivatives: Allopurinol (19 mmol/mol Crea).

Further detailed information is provided on the following pages.

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 ^(*)
	mmol/L	mmol/L	mmol/L	%	mmol/L	mmol/L
Creatinine	14	0.3	13.73	100	0.281	1 - 19

^(*) 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 ^(*)
	mmol/L	_mmol_ mol Crea	_mmol_ mol Crea	mmol/L	%	mmol/L	_mmol mol Crea
Dimethylamine	< 0.42	< 31	31	0.317	100	0.012	≤ 54 🔲
Trimethylamine	< 0.03	< 2	2	0.003	00	0.006	≤ 3 □ □

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

3 Amino 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
1-Methylhistidine	< 0.20	< 15	15	0.012	50 🔾	0.029	≤ 15 🔲
2-Furoylglycine	< 0.53	< 39	39	0.231	79 🔾	0.093	≤ 40 □
4-Aminobutyric acid	< 0.27	< 20	20	0.057	11 🔾	0.265	≤ 20 □ □
Alanine	0.33	24	10	0.333	100	0.028	11 - 72
Arginine	< 10.0	< 750	750	1.128	66 🔾	1.329	≤ 750 □ □
Betaine	0.12	9	7	0.120	100	0.070	9 - 78
Creatine	< 0.69	< 50	50	0.000	100	0.281	≤ 280 🗔
Glycine	1.1	81	34	1.108	100	0.033	38 - 440
Guanidinoacetic acid	< 1.4	< 100	100	1.219	30 🔾	0.949	≤ 140 🔲
Methionine	< 0.25	< 18	18	0.000	0 🔾	0.447	≤ 18 🔲
N,N-Dimethylglycine	< 0.07	< 5	5	0.049	72 🔾	0.018	≤ 15 🔲
Sarcosine	< 0.03	< 2	2	0.021	78 🔾	0.011	≤ 7 □□□
Taurine	< 2.0	< 140	140	0.664	63 🔾	0.301	≤ 170
Valine	0.04	3	2	0.038	91 🔾	0.024	≤ 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	< 0.13	< 10	10	0.000	00	0.058	≤ 10 🗔
D-Mandelic acid	< 0.03	< 2	2	0.000	0 🔾	0.324	2 - 17
Hippuric acid	7.6	560	170	7.637	100	0.585	≤ 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	0.07	5	5	0.070	82 🔾	0.043	≤ 51
Citric acid	2.6	190	40	2.563	100	0.287	≤ 700 🔟
Formic acid	< 0.13	< 10	10	0.112	100	0.005	≤ 43 🗔
Fumaric acid	< 0.03	< 2	2	0.018	75 🔾	0.007	≤ 3 □
Imidazole	< 0.66	< 48	48	0.104	59 🔾	0.091	≤ 48 🔲
Lactic acid	< 0.67	< 49	49	0.135	90 🔾	0.192	≤ 110 🗔
Proline betaine	< 0.35	< 25	25	0.086	0 🔾	0.131	≤ 280 □ □
Succinic acid	< 0.07	< 5	5	0.065	98	0.006	≤ 39 🔲
Tartaric acid	0.23	17	5	0.230	99 🔵	0.019	≤ 110 🔃
Trigonelline	0.82	60	35	0.822	100	0.015	≤ 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	< 0.66	< 48	48	0.000	00	0.347	≤ 48 🔲

^(*) 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 ^(*)
	mmol/L	_mmol_ mol Crea	mmol_ mol Crea	mmol/L	%	mmol/L	_mmol_ mol Crea
2-Oxoglutaric acid	< 1.3	< 92	92	0.112	55 🔾	0.349	≤ 92 □ □
3-Hydroxybutyric acid	< 1.4	< 100	100	0.000	0 🔾	1.153	≤ 100 □
Acetoacetic acid	< 0.20	< 14	14	0.174	86 🔵	0.065	≤ 30 □ □
Acetone	< 0.03	< 2	2	0.020	93 🔵	0.005	≤ 7 □□□
Oxaloacetic acid	0.31	23	17	0.310	88 🔾	0.180	≤ 66 🔟
Pyruvic acid	< 0.12	< 9	9	0.063	71 🔾	0.029	≤ 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	< 0.07	< 5	5	0.000	00	0.182	≤ 5 □
1-Methylnicotinamide	< 0.43	< 32	32	0.071	99 🔵	0.007	≤ 32 🔲
Adenosine	< 5.3	< 390	390	0.000	0 🔾	2.441	≤ 390 □ □
Allantoin	0.26	19	17	0.257	99 🔵	0.018	≤ 47 🔟
Allopurinol	0.27	19	10	0.266	80 🔾	0.291	≤ 11 □ □ □
Caffeine	< 0.62	< 45	45	0.238	98	0.241	≤ 61 □□□
Inosine	< 0.26	< 19	19	0.036	84 🔾	0.301	≤ 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	< 0.59	< 43	43	0.031	93 🔾	0.006	< 44 □ □ □
D-Glucose	< 0.47	< 34	34	0.376	83 🔾	0.150	≤ 140 🗔
D-Lactose	< 1.3	< 96	96	0.179	0 🔾	0.315	≤ 96 □
D-Mannitol	< 2.5	< 180	180	2.030	90 🔵	0.969	≤ 180 🗔
D-Mannose	< 0.08	< 6	6	0.000	0 🔾	0.149	≤ 8 □ □
Myo-Inositol	< 61	< 4400	4400	0.000	0 🔾	11.18	≤ 4400 □

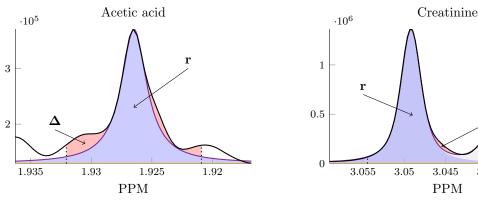
^(*) Gray horizontal boxes represent 95% concentration range, black vertical lines represent sample value.



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



(a) Single signal fitting.

(b) Simultaneous fitting of two signals.

3.04

3.035

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.

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