

Analysis Report

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

Sample ID: ALZ_Urine_Rack01_RCM_221214_expno610.100000.10r

Measuring Date: 24-Dec-2014 04:27:57

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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

All metabolites were found with concentrations inside the 95% range of Bruker Quant-UR B.1.1.0 urine metabolite concentration database.

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



Contents

1	Creatinine	3
2	Amines and derivatives	3
3	Amino acids and derivatives	3
4	Benzene and substituted derivatives	4
5	Carboxylic acids	4
6	Fatty acids and derivatives	4
7	Keto acids and derivatives	5
8	Purine, Pyridine and Pyrimidine derivatives	5
9	Sugars and derivatives	5
10	Explanations	6



1 Creatinine

Compound	Conc.	LOD	r	ρ	Δ	95% Range ^(*)
	mmol/L	mmol/L	mmol/L	%	mmol/L	mmol/L
Creatinine	5.9	0.3	5.930	100	0.111	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	0.28	47	31	0.279	100	0.012	≤ 54 🔲
Trimethylamine	< 0.01	< 2	2	0.004	98	0.001	≤ 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	< 0.09	< 15	15	0.000	00	0.049	≤ 15 □□□
2-Furoylglycine	< 0.23	< 39	39	0.044	88 🔵	0.017	≤ 40 □
4-Aminobutyric acid	< 0.12	< 20	20	0.088	81 🔾	0.075	≤ 20 □ □
Alanine	0.17	29	10	0.174	100	0.016	11 - 72 🔟
Arginine	< 4.4	< 750	750	0.408	0 🔾	1.722	≤ 750 □ □
Betaine	0.17	28	7	0.168	100	0.016	9 - 78
Creatine	< 0.30	< 50	50	0.103	100	0.111	≤ 280 □ □
Glycine	0.47	79	34	0.468	100	0.025	38 - 440
Guanidinoacetic acid	< 0.61	< 100	100	0.395	77 🔾	0.210	≤ 140 🔲
Methionine	< 0.11	< 18	18	0.000	0 🔾	0.187	≤ 18 🔲
N,N-Dimethylglycine	0.06	11	5	0.064	90 🔵	0.019	≤ 15 🔳
Sarcosine	< 0.01	< 2	2	0.006	0 🔾	0.011	≤ 7 □□□
Taurine	< 0.84	< 140	140	0.306	76 🔾	0.149	≤ 170 🗔
Valine	0.02	4	2	0.023	80 🔾	0.009	≤ 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	< 0.06	< 10	10	0.000	0 🔾	0.019	≤ 10 🗆
D-Mandelic acid	< 0.01	< 2	2	0.000	0 🔾	0.102	2 - 17
Hippuric acid	< 1.00	< 170	170	0.978	91 🔵	0.262	≤ 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	0.03	5	5	0.029	89 🔵	0.009	≤ 51
Citric acid	3.0	510	40	3.011	100	0.259	≤ 700 🔲
Formic acid	0.11	19	10	0.111	100	0.006	≤ 43 🔟
Fumaric acid	< 0.01	< 2	2	0.002	94 🔵	0.001	≤ 3 □ □ □
Imidazole	< 0.28	< 48	48	0.036	16 🔾	0.042	≤ 48 🔲
Lactic acid	< 0.29	< 49	49	0.093	85 🔾	0.052	≤ 110 🔲
Proline betaine	0.36	61	25	0.361	100	0.016	≤ 280 🔲
Succinic acid	0.04	7	5	0.041	83 🔾	0.015	≤ 39 🔲
Tartaric acid	< 0.03	< 5	5	0.020	99 🔵	0.002	≤ 110 🗔
Trigonelline	< 0.21	< 35	35	0.127	99	0.008	≤ 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	< 0.28	< 48	48	0.047	00	0.094	≤ 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	< 0.55	< 92	92	0.106	54 🔾	0.164	≤ 92 □ □
3-Hydroxybutyric acid	< 0.61	< 100	100	0.000	0 🔾	0.793	≤ 100 □ □
Acetoacetic acid	< 0.09	< 14	14	0.063	94 🔵	0.037	≤ 30 □ □
Acetone	0.01	2	2	0.013	97 🔵	0.002	≤ 7 🔟
Oxaloacetic acid	0.25	43	17	0.254	95 🔵	0.078	≤ 66 🔳 🗆
Pyruvic acid	< 0.05	< 9	9	0.022	79 🔾	0.008	≤ 13 🔲

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

8 Purine, Pyridine and Pyrimidine 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-Methyladenosine	< 0.03	< 5	5	0.000	00	0.093	≤ 5 □
1-Methylnicotinamide	< 0.19	< 32	32	0.025	78 🔾	0.012	≤ 32 🔲
Adenosine	< 2.3	< 390	390	0.000	0 🔾	1.398	≤ 390 □ □
Allantoin	0.11	19	17	0.113	89 🔵	0.024	≤ 47 🔟
Allopurinol	< 0.06	< 10	10	0.015	94 🔵	0.033	≤ 11 □
Caffeine	< 0.27	< 45	45	0.178	66 🔾	0.207	≤ 61 □□□
Inosine	< 0.11	< 19	19	0.015	97 🔵	0.031	≤ 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	< 0.26	< 43	43	0.043	91 🔾	0.005	< 44 □ □ □
D-Glucose	0.26	43	34	0.257	81 🔾	0.092	≤ 140 🔲
D-Lactose	< 0.57	< 96	96	0.206	93 🔾	0.070	≤ 96 □ □
D-Mannitol	< 1.1	< 180	180	0.000	0 🔾	3.155	≤ 180 🗔
D-Mannose	< 0.04	< 6	6	0.000	0 🔾	0.236	≤ 8 □ □
Myo-Inositol	< 26	< 4400	4400	0.000	0 🔾	4.855	≤ 4400 □

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



3.035

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

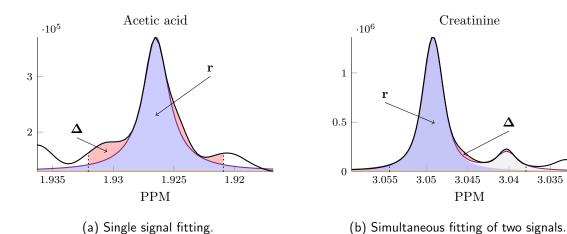


Figure 1: Examples of fitting.

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) 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.

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