

Analysis Report

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

Sample ID: ALZ_Urine_Rack04_RCM_191214_expno320.100000.10r

Measuring Date: 19-Dec-2014 23:45:25

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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



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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	8.6	0.3	8.606	100	0.113	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	0.30	34	31	0.296	100	0.009	≤ 54 🔲
Trimethylamine	< 0.02	< 2	2	0.005	86 🔾	0.002	≤ 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	< 0.13	< 15	15	0.000	00	0.175	≤ 15 🗔
2-Furoylglycine	< 0.33	< 39	39	0.104	47 🔾	0.039	≤ 40 □
4-Aminobutyric acid	< 0.17	< 20	20	0.096	18 🔾	0.197	≤ 20 □
Alanine	0.28	33	10	0.280	100	0.019	11 - 72 🔟
Arginine	< 6.4	< 750	750	0.700	0 🔾	3.190	≤ 750 🗔
Betaine	0.20	24	7	0.203	100	0.037	9 - 78 📗
Creatine	< 0.43	< 50	50	0.229	100	0.113	≤ 280 □ □
Glycine	0.94	110	34	0.939	100	0.036	38 - 440
Guanidinoacetic acid	< 0.89	< 100	100	0.356	89 🔵	0.108	≤ 140 🔲
Methionine	< 0.15	< 18	18	0.000	0 🔾	0.451	≤ 18 🔲
N,N-Dimethylglycine	0.05	5	5	0.046	93 🔾	0.009	≤ 15 🔲
Sarcosine	< 0.02	< 2	2	0.002	0 🔾	0.012	≤ 7 □□□
Taurine	< 1.2	< 140	140	0.757	91 🔾	0.262	≤ 170 🗔
Valine	0.03	4	2	0.033	90 🔵	0.010	≤ 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	< 0.08	< 10	10	0.020	76 🔾	0.015	≤ 10 🗔
D-Mandelic acid	< 0.02	< 2	2	0.000	0 🔾	0.095	2 - 17
Hippuric acid	3.5	410	170	3.505	99	0.326	≤ 660 🔲

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

5 Carboxylic acids

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
Acetic acid	0.20	23	5	0.200	99 🔵	0.020	≤ 51 🔲
Citric acid	2.4	280	40	2.409	100	0.269	≤ 700 🔟
Formic acid	0.26	31	10	0.265	99 🔵	0.019	≤ 43 🔲
Fumaric acid	< 0.02	< 2	2	0.007	96 🔵	0.001	≤ 3 □ □
Imidazole	< 0.41	< 48	48	0.000	0 🔾	0.167	≤ 48 🔲
Lactic acid	< 0.42	< 49	49	0.228	99 🔵	0.033	≤ 110 🔲
Proline betaine	0.30	35	25	0.301	98	0.057	≤ 280 🔲
Succinic acid	0.10	11	5	0.098	98	0.013	≤ 39 🔲
Tartaric acid	0.13	15	5	0.130	100	0.008	≤ 110 🔃
Trigonelline	0.34	39	35	0.337	100	0.007	≤ 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	< 0.41	< 48	48	0.051	00	0.111	≤ 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	< 0.79	< 92	92	0.142	65 🔾	0.212	≤ 92 □ □
3-Hydroxybutyric acid	< 0.89	< 100	100	0.086	24 🔾	0.350	≤ 100 □ □
Acetoacetic acid	< 0.12	< 14	14	0.115	92 🔵	0.060	≤ 30 □ □
Acetone	0.02	3	2	0.023	100	0.004	≤ 7 □□□
Oxaloacetic acid	0.21	24	17	0.207	89 🔵	0.117	≤ 66 🔟
Pyruvic acid	< 0.08	< 9	9	0.045	80 🔾	0.015	≤ 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	< 0.04	< 5	5	0.000	00	0.152	≤ 5 □
1-Methylnicotinamide	< 0.27	< 32	32	0.059	99 🔵	0.006	≤ 32 🔲
Adenosine	< 3.3	< 390	390	0.000	0 🔾	1.701	≤ 390 □ □
Allantoin	< 0.14	< 17	17	0.105	96	0.016	≤ 47 🔲
Allopurinol	< 0.09	< 10	10	0.050	81 🔾	0.048	≤ 11 □
Caffeine	< 0.39	< 45	45	0.183	91 🔾	0.204	≤ 61 □□□
Inosine	< 0.16	< 19	19	0.031	93 🔾	0.052	≤ 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	< 0.37	< 43	43	0.025	87 🔵	0.003	< 44 □ □ □
D-Glucose	0.79	91	34	0.786	86 🔵	0.279	≤ 140 🔲
D-Lactose	< 0.82	< 96	96	0.029	77 🔾	0.050	≤ 96 □ □
D-Mannitol	< 1.6	< 180	180	0.000	0 🔾	3.929	≤ 180 🗔
D-Mannose	< 0.05	< 6	6	0.046	70	0.037	≤ 8 □ □
Myo-Inositol	< 38	< 4400	4400	0.000	0 🔾	10.27	≤ 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

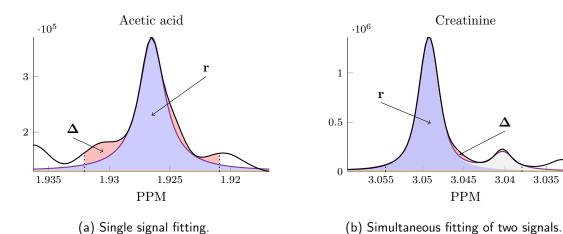


Figure 1: Examples of fitting.

3.045

PPM

3.04

3.035

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.

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