

● Analysis Report

Bruker IVDr Quantification in URine B.I.Quant-UR bTM

Sample ID: ALZ_Urine_Rack01_RCM_221214_expno80.100000.10r

Measuring Date: 23-Dec-2014 14:31:22

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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.

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
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1 Creatinine

Compound	Conc. mmol/L	LOD mmol/L	r mmol/L	ρ %	Δ mmol/L	95% Range ^(*) mmol/L
Creatinine	12	0.3	12.09	100 ●	0.248	1 - 19 















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

2 Amines and derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range ^(*) $\frac{\text{mmol}}{\text{mol Crea}}$
Dimethylamine	< 0.37	< 31	31	0.314	100 ●	0.010	≤ 54 
Trimethylamine	< 0.02	< 2	2	0.014	97 ●	0.003	≤ 3 




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

3 Amino acids and derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range ^(*) $\frac{\text{mmol}}{\text{mol Crea}}$
1-Methylhistidine	< 0.18	< 15	15	0.000	0 ○	0.227	≤ 15 
2-Furoylglycine	< 0.47	< 39	39	0.139	46 ○	0.060	≤ 40 
4-Aminobutyric acid	< 0.24	< 20	20	0.000	0 ○	0.764	≤ 20 
Alanine	0.41	34	10	0.411	99 ●	0.065	11 - 72 
Arginine	< 9.0	< 750	750	0.566	8 ○	1.569	≤ 750 
Betaine	0.10	9	7	0.105	100 ●	0.042	9 - 78 
Creatine	< 0.60	< 50	50	0.371	100 ●	0.248	≤ 280 
Glycine	0.85	71	34	0.853	100 ●	0.033	38 - 440 
Guanidinoacetic acid	< 1.2	< 100	100	0.272	86 ●	0.101	≤ 140 
Methionine	< 0.22	< 18	18	0.000	0 ○	0.361	≤ 18 
N,N-Dimethylglycine	0.07	6	5	0.075	81 ○	0.025	≤ 15 
Sarcosine	< 0.02	< 2	2	0.004	0 ○	0.013	≤ 7 
Taurine	< 1.7	< 140	140	0.412	53 ○	0.400	≤ 170 
Valine	0.03	3	2	0.034	52 ○	0.056	≤ 7 











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4 Benzene and substituted derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
Benzoic acid	< 0.12	< 10	10	0.000	0 ○	0.043	≤ 10 
D-Mandelic acid	< 0.03	< 2	2	0.000	0 ○	0.203	2 - 17 
Hippuric acid	5.1	420	170	5.058	100 ●	0.383	≤ 660 


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

5 Carboxylic acids

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
Acetic acid	0.09	8	5	0.094	94 ●	0.033	≤ 51 
Citric acid	2.1	180	40	2.119	99 ●	0.318	≤ 700 
Formic acid	0.31	25	10	0.307	100 ●	0.018	≤ 43 
Fumaric acid	< 0.02	< 2	2	0.006	99 ●	0.001	≤ 3 
Imidazole	< 0.58	< 48	48	0.000	0 ○	0.210	≤ 48 
Lactic acid	< 0.59	< 49	49	0.143	98 ●	0.218	≤ 110 
Proline betaine	< 0.30	< 25	25	0.196	0 ○	0.401	≤ 280 
Succinic acid	< 0.06	< 5	5	0.030	96 ●	0.005	≤ 39 
Tartaric acid	0.60	50	5	0.603	100 ●	0.023	≤ 110 
Trigonelline	0.74	62	35	0.744	100 ●	0.021	≤ 67 







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6 Fatty acids and derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
2-Methylsuccinic acid	< 0.58	< 48	48	0.000	0 ○	1.076	≤ 48 








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

7 Keto acids and derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
2-Oxoglutaric acid	< 1.1	< 92	92	0.141	0 ○	0.260	≤ 92 
3-Hydroxybutyric acid	< 1.2	< 100	100	0.000	0 ○	1.455	≤ 100 
Acetoacetic acid	< 0.17	< 14	14	0.117	85 ●	0.075	≤ 30 
Acetone	0.03	3	2	0.031	96 ●	0.008	≤ 7 
Oxaloacetic acid	0.50	41	17	0.498	84 ○	0.268	≤ 66 
Pyruvic acid	< 0.11	< 9	9	0.057	86 ●	0.017	≤ 13 







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8 Purine, Pyridine and Pyrimidine derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
1-Methyladenosine	< 0.06	< 5	5	0.000	0 ○	0.146	≤ 5 
1-Methylnicotinamide	< 0.38	< 32	32	0.055	98 ●	0.008	≤ 32 
Adenosine	< 4.7	< 390	390	0.000	0 ○	2.088	≤ 390 
Allantoin	0.23	19	17	0.234	93 ●	0.047	≤ 47 
Allopurinol	< 0.12	< 10	10	0.082	94 ●	0.087	≤ 11 
Caffeine	< 0.55	< 45	45	0.271	74 ○	0.341	≤ 61 
Inosine	< 0.23	< 19	19	0.029	34 ○	0.129	≤ 19 

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

9 Sugars and derivatives

Compound	Conc. mmol/L	Conc. $\frac{\text{mmol}}{\text{mol Crea}}$	LOD $\frac{\text{mmol}}{\text{mol Crea}}$	r mmol/L	ρ %	Δ mmol/L	95% Range(*) $\frac{\text{mmol}}{\text{mol Crea}}$
D-Galactose	< 0.52	< 43	43	0.189	87 ●	0.017	≤ 44 
D-Glucose	0.87	72	34	0.868	96 ●	0.155	≤ 140 
D-Lactose	< 1.2	< 96	96	0.106	88 ●	0.056	≤ 96 
D-Mannitol	< 2.2	< 180	180	1.169	62 ○	1.214	≤ 180 
D-Mannose	< 0.07	< 6	6	0.000	0 ○	0.138	≤ 8 
Myo-Inositol	< 54	< 4400	4400	0.000	0 ○	10.65	≤ 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 r , ρ and Δ .

10.1 How to read the result

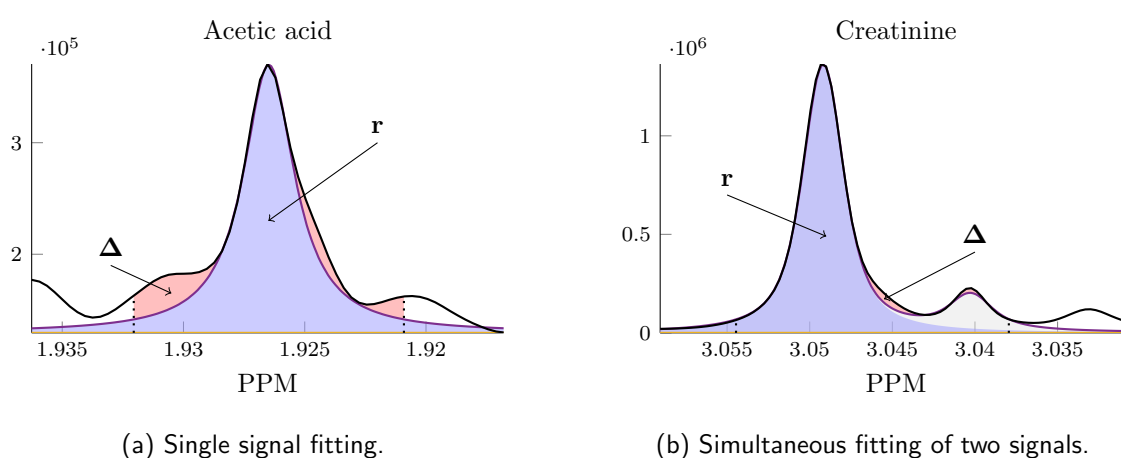


Figure 1: Examples of fitting.

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

- Conc.** is the final result concentration of the metabolite,
- LOD** is the *limit of detection* of the given metabolite,
- 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),
- 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%,
 - ●, 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

$$r = \frac{1}{P_N} \int_{\mathbb{R}} f(\xi) d\xi.$$

β) ρ is the *correlation* of the functions s and $f + b$, i.e.

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

where \bar{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.

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