



Metallo protein quantification by LC-ICP-MSMS

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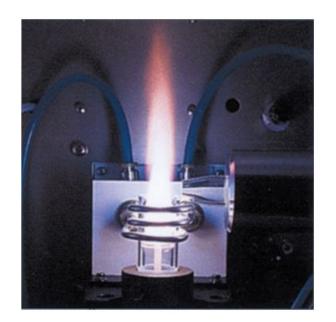


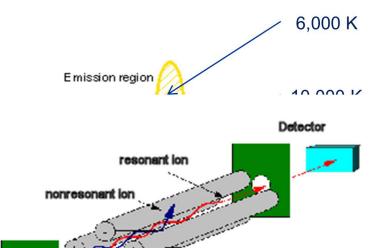
- // ICP-MS and Metalloproteins
- // Wilson disease and anaemia

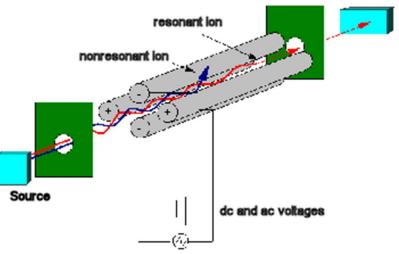
// Challenges and solutions in quantitation



Plasma: Gas stream passes through plasma maintained by a strong RF field (1-2 kWatt, 27 - 41 MHz) and Argon

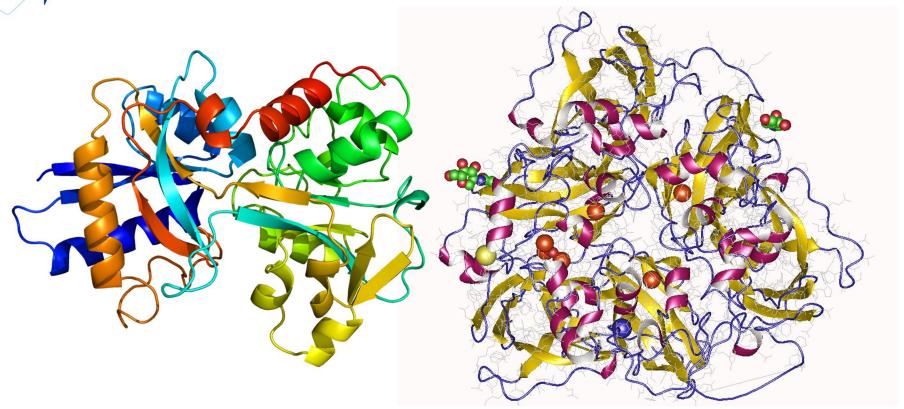








Metallo proteins

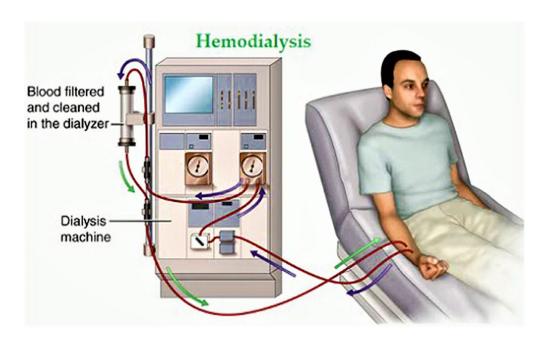


Transferrin (76kDa)

Ceruloplasmin (151 kDa)
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Anaemia due to hemodialysis in Chronic Kidney Disease



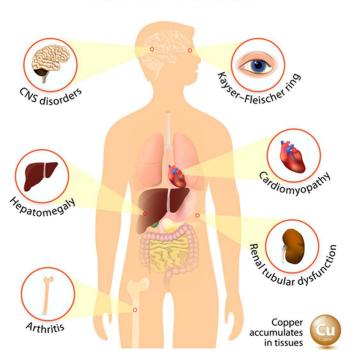
Key analytical parameters

- ► Total Iron (CI on ICP-MS)
- ► Transferrin bound iron (LC-ICP-MS)
- ► Total Iron binding capacity (LC-ICP-MS)



Wilson disease (copper metabolism disorder)

WILSON'S DISEASE



Key analytical parameters

- ► Total copper (FIA on ICP-MS)
- Ceruloplasmin bound copper (LC-ICP-MS)
- ► Free / echangeable copper (LC-ICP-MS)





Total Iron / Copper by Continuous Infusion or Flow Injection Analysis

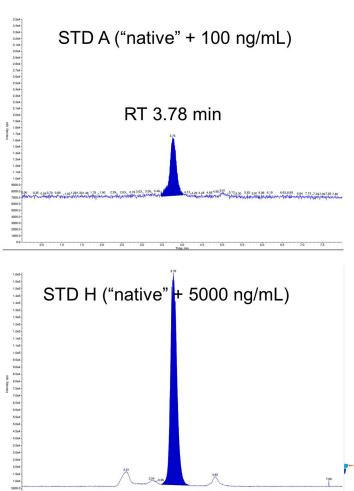
- "Dilute and shoot", no sample preparation, no chromatography
- Proxy matrices for the calibration curve for absolute quantitation
- Low level plasma/serum and standard addition for QC-levels (LLOQ often in proxy matrix)
- Fast
- Fe suffers from interference from Argon (ArO⁺ is m/z 56, same as Fe) → remedy is addition of H₂





Transferrin bound iron in heparin plasma

- Separation on a Waters BEH200Å SEC 7.8
 x 150 mm column, isocratic elution
- Due to addition: study samples within normal reference ranges
- Proxy matrix for calibration samples in a PBS HSA / transferrin solution (Fe spiked)
 - Not homogenious at this scale -> native concentration based on standard addition of the calibration curve
- Low QC: low concentration matrix, higher QC's: standard addition of Fe solution





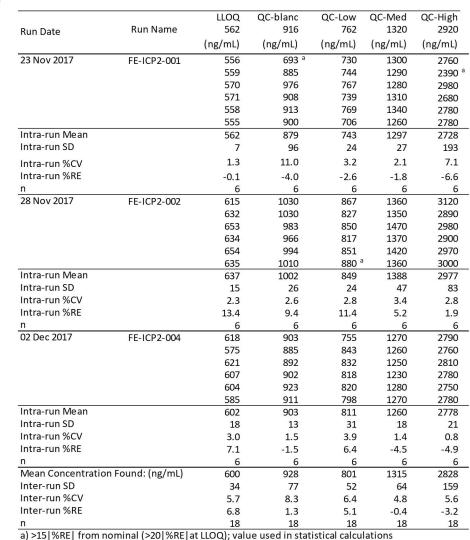
Challenges for transferrin bound iron detection

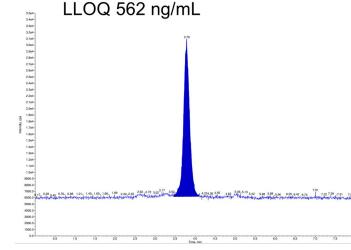
- In general concentrations within (or above) normal reference ranges
- Lyophilyzed transferrin behaves simmilar to native transferrin
- ► Added Iron (Fe²⁺) readily binds to transferrin, no equilibrium or volume effect
- Human serum albumin and lyophilyzed transferrin pose a small challenge
 - Material is not homogeneous in the scale (low mg) used
 - Different batches have different iron contents (same as different matrices)
- Solution: determine native concentration per calibration curve and for each batch of prepared QC's

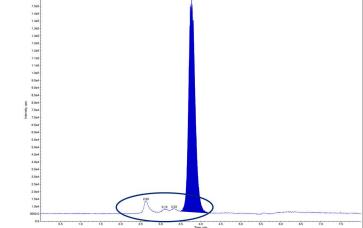
Linearity demonstrated up to +5000 ng/mL

	Nominal					Native	Corr nom.
Sample description	conc	Ratio	(Y2-Y1)	(X2-X1)	d(x/y)	conc	conc
	(ng/mL)					(ng/mL)	(ng/ml)
Blank_artificial_matrix_+_IS	0.00	0.171	N.Ap.	0.00	N.Ap.	522	N.Ap
Blank_artificial_matrix_+_IS	0.00	0.171	N.Ap.	0.00	N.Ap.	022	N.Ap
STD_A_(Y+_100_ng/mL_07_Mar_2019)	100	0.212	0.0405	100	800000000000000000000000000000000000000		622
STD_B_(Y+_200_ng/mL_07_Mar_2019)	200	0.242	0.0703	200	0.000352	488	722
STD_C_(Y+_500_ng/mL_07_Mar_2019)	500	0.341	0.170	500	0.000339	505	1022
STD_D_(Y+_1000_ng/mL_07_Mar_2019)	1000	0.499	0.327	1000	0.000327	524	152
STD_E_(Y+_2000_ng/mL_07_Mar_2019)	2000	0.797	0.625	2000	0.000313	548	252
STD_F_(Y+_3000_ng/mL_07_Mar_2019)	3000	1.06	0.892	3000	0.000297	577	352
STD_G_(Y+_4000_ng/mL_07_Mar_2019)	4000	1.35	1.18	4000	0.000296	580	452
STD_H_(Y+_5000_ng/mL_07_Mar_2019)	5000	1.65	1.48	5000	0.000295	580	552
STD_A_(Y+_100_ng/mL_07_Mar_2019)	100	0.206	0.0344	100	0.0000044		62:
STD_B_(Y+_200_ng/mL_07_Mar_2019)	200	0.250	0.0786	200	0.000393	436	72:
STD_C_(Y+_500_ng/mL_07_Mar_2019)	500	0.339	0.168	500	0.000335	511	102
STD_D_(Y+_1000_ng/mL_07_Mar_2019)	1000	0.524	0.352	1000	0.000352	486	152
STD_E_(Y+_2000_ng/mL_07_Mar_2019)	2000	0.867	0.696	2000	0.000348	493	2522
STD_F_(Y+_3000_ng/mL_07_Mar_2019)	3000	1.14	0.974	3000	0.000325	528	3522
STD_G_(Y+_4000_ng/mL_07_Mar_2019)	4000	1.45	1.28	4000	0.000320	535	4522
STD_H_(Y+_5000_ng/mL_07_Mar_2019)	5000	1.81	1.64	5000	0.000328	523	5522

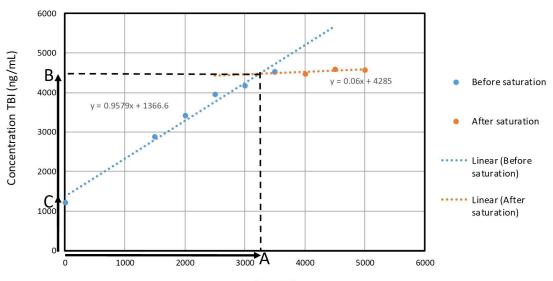


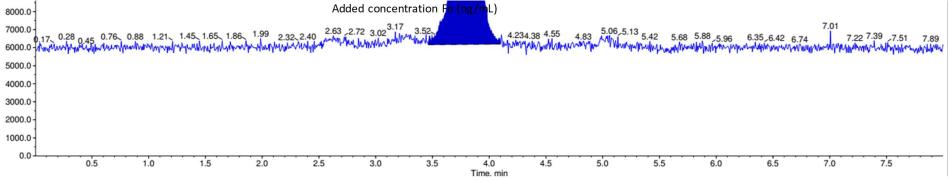






Iron binding capacity (linearity truncated due to saturation)





Precision and accuracy

Run Date	Run Name	Serum 1	Serum 2	Serum 3	Serum 4
		(ng/mL)	(ng/mL)	(ng/mL)	(ng/mL)
		2898	3277	4286	3641
		3060	3497	4552	3368
		3346	3627	4378	3635
Intra-run Mean		3101	3467	4405	3548
Intra-run SD		227	177	135	156
Intra-run %CV		7.3	5.1	3.1	4.4

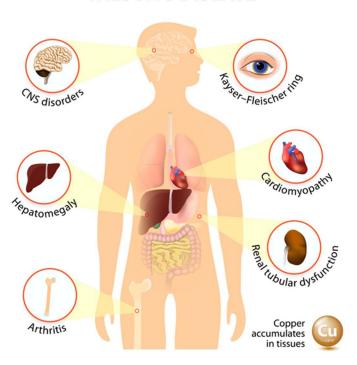
- "Normal" precision and accuracy met
 - Method validation for Transferrin bound iron was validated already
- "Subjective" method, but differences between technicians are acceptable
- Normal stability program completed successfully

TIBC MIN	TIBC MAX	MAX/MIN*100%
2898	2898	100.0%
3277	3235	98.7%
4286	4286	100.0%
3641	3641	100.0%
3060	3201	104.6%
3497	3938	112.6%
4552	4586	100.8%
3368	3481	103.3%
3346	3281	98.1%
3627	3047	84.0%
4378	4833	110.4%
3635	3765	103.6%
4033	3933	97.5%
5117	5425	106.0%
3891	4340	111.5%
4467	4174	93.4%
3195	3302	103.3%
3311	3344	101.0%
4318	4305	99.7%
4144	4427	106.8%
3789	4274	112.8%
4442	4257	95.8%
4457	4387	98.4%
4546	4243	93.3%
3570	3570	100.0%
4358	4492	103.1%
4017	4205	104.7%
4051	3860	95.3%
4290	3966	92.5%
3214	3361	104.6%
2955	2874	97.2%
3329	3153	94.7%
4166	4089	98.1%
3195	3344	104.7%
4202	4173	99.3%
3133	3345	106.8%



Ceruloplasmin bound copper

WILSON'S DISEASE



Important to realize

- All known patients are under treatment
- Typical treatment is administration of a chelating agent
- Resulting in low, to very low, copper concentrations (both total and ceruloplasmin bound)
- Control of NCC is key in the treatment



Three approaches to determine NCC

- Total copper and available kits for ceruloplasmin content
 - The golden standard
- Ultra centrifugation after EDTA addition and total copper`measurement
- ► EDTA addition and ion exchange chromatography











"Golden" standard: Substraction of Cu-Ceruloplasmin of total Copper

Cons

- ▶ Subtraction of two relatively large numbers with match uncertainties can lead to negative values for NCC
- Cumbersome: 2 analysis required
- ► Approximation on the number of Cu bound to each ceruloplasmin peptide
- ► Stability data between ceruloplasmin and other techniques does not match

Pro

- Esthablished method
- Characteristics are well known
- Technically least critical

To convert the ceruloplasmin activity in **mU/mL** to a concentration in **mg/L**:

[Ceruloplasmin] in mg/L = (Response in mU/mL / 3.33) * 10

To convert the copper concentration from ng/mL to μ g/L:

[Copper] in μ g/L = concentration in ng/mL x 1000 ml/L / 1000 ng / μ g/L

To calculate the NCC concentration in μ g/L:

[NCC] in μ g/L = [Copper] in μ g/L - 3 in μ g / mg X [Ceruloplasmin] in mg/





- ► Samples are treated with EDTA (3 g/L) and incubated for 60 minutes
- ► Centrifuged over a 10kDa MWCO filter (4000g, 60 minutes) with WIS in collection tube (Yttrium)
- ▶ Take an aliquot of the eluate and dilute in 1 ml nitric acid solution
- ► Analyse by continuous infusion in ICP-MS
- Calculate the actual NCC concentration
 - Internal standard response compared to standards: to caculate the filtrate volume
 - Response ratio internal standard and analyte: to calculate the concentration
 - Both: to calculate the amount of "exchangeagble" copper in the filtration sample
 - Correct for the diluton by EDTA to come to the actual Cuex concentration







▶ Total measurements, so proxy matrices can be used for copper response.

- Accuracy and precision very good (not in PBS, due
- to the instability in PBS)
- Fresh plasma/serum stored directly after collection at

- -80°C yields lowest NCC results

Intra-run Mean Intra-run SD Intra-run %CV Intra-run %RE

Run Date

06 Apr 2017

10 Apr 2017

Intra-run Mean

Intra-run SD

Intra-run %CV

Intra-run %RE

Intra-run Mean

Intra-run SD

Intra-run %CV

Intra-run %RE

Inter-run SD

Inter-run %CV

Inter-run %RE

Mean Concentration Found: (ng/mL)

11 Apr 2017

(ng/mL) CU-ICP3-001

Run Name

CU-ICP3-002

CU-ICP3-003

28.0 28.4 28.9 29.2 29.8 29.6 29.0 0.7

2.4

15.9

30.0

30.5 a

30.6 a

29.7

29.8

30.2

0.4

1.4

20.8

6

32.7 a

32.2 a

32.4 a

32.3 a

31.3 a

34.4 a

32.6

1.0

3.1

30.2

30.6

1.7

5.5

22.3

a) >15|%RE| from nominal (>20|%RE|at LLOQ); value used in statistical calculations

18

6

30.6 a

6

LLOQ

25.0

27.4 28.9 28.0 27.6 27.6 29.0 28.1 0.7 2.5

-0.1

26.8

26.5

28.0

28.9

28.3

30.5

28.2

1.5

5.2

0.2

30.0

29.6

29.7

28.3

30.7

30.1

29.7

0.8

2.7

5.8

28.7

1.3

4.4

2.0

18

QC-blanc

(ng/mL)

28.1

QC-Low

(ng/mL)

75.0

78.2

79.3

79.2

79.3

78.2

78.4

78.8

0.6

0.7

5.0

80.9

78.3

80.6

80.6

77.9

82.0

80.1

1.6

2.0

6.7

80.7

80.1

68.7

82.7

79.8

82.2

10.6

12.9

9.6

80.4

6.0

7.5

7.1

18

101 a

QC-Med

(ng/mL)

178

195

190

200

192

193

195

194

1.8

9.1

192

195

197

190

191

194

193

1.4

8.5

193

192

195

188

191

247 a

201

11.3

12.9

196

13

6.6

18

10.2

23

6

QC-High

(ng/mL)

628

639

671

657

683

662

646

660

16

2.4

5.0

606

595

603

601

606

605

603

0.7

-4.0

510

620

632

611

612

607

599

44

7.4

-4.7

620

38

6.2

-1.2

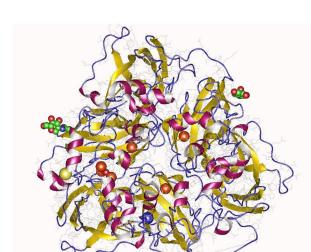
18

6

6

Very low stability (Days)

- Very low stability in plasma and serum at -20°C (ultrafiltrates are OK) in freeze/thaw and storage
- More exchangeable copper: released from proteins (albumin, ceruloplasmin etc...)



Run Date	Mail Name	04.1	150	505	050
		(ng/mL)	(ng/mL)	(ng/mL)	(ng/mL)
10 Apr 2017	CU-ICP3-002 (FT1)	69.3	123	480 a	723
		65.6	120	524	774
		66.9	123	560	774
		64.1	121	512	788
		64.2	133	548	794
		9.7	47	17	-
Intra-run Mean		66.0	124	525	771
Intra-run SD		2.2	5	31	28
Intra-run %CV		3.3	4.2	6.0	3.6
Intra-run %RE		3.0	-4.6	-10.0	-10.0
n		5	5	5	5
20 Apr 2017	CU-ICP3-006 (FT2)	79.6 ^a	148	546	837
		87.1 ^a	150 a	550	789
		88.7 a	141	537	848
		86.1 ^a	155 a	558	792
		81.4 ^a	126	538	848
		£1	12	- 1	
Intra-run Mean		84.6	144	546	823
Intra-run SD		3.9	11	9	30
Intra-run %CV		4.6	7.8	1.6	3.6
Intra-run %RE		32.0	10.8	-6.4	-3.9
n		5	5	5	5
20 Apr 2017	CU-ICP3-006 (FT3)	88.1 ^a	139	518	872
		82.4 ^a	150 a	539	851
		88.9 a	159 a	576	880
		89.8 a	137	562	853
		95.5 ^a	151 ^a	520	858
Intra-run Mean		88.9	147	543	863
Intra-run SD		4.7	9	26	13
Intra-run %CV		5.3	6.2	4.7	1.5
Intra-run %RE		38.8	13.2	-6.9	0.8
n		5	5	5	5
	nominal (>20 %RE at L	LOQ); value u	sed in statis		
a) >15 %RE from nominal (>20 %RE at LLOQ); value used in statistical calculations					

QC-blanc

Run Name

Run Date

64.1

QC-Low

130

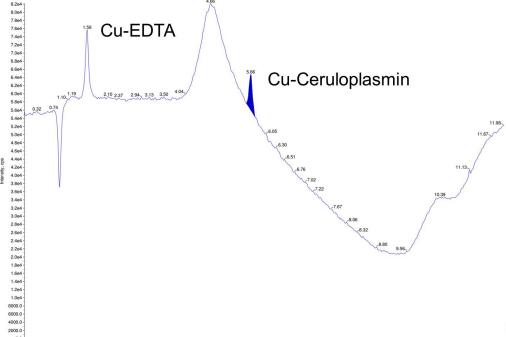
QC-Med

QC-High

856

Direct NCC (both Cu-Ceruloplasmin and Cu-EDTA in 1 assay)

- ▶ Plasma samples are treated with EDTA (3 g/L) incubate for three hours
- ► Analyze over a TSK-GEL Q-STAT 7 µm 4.6 mm x 10 cm Column (ammonium acetate gradient)





Direct NCC (both Cu-Ceruloplasmin and Cu-EDTA in 1 assay)

Challenges

- Low concentrations in study samples due to medication, far outside of the range of healthy volunteers
- ▶ Ethical obstacle to obtain matrix from patients (+ medication) *or* expensive
- Lyopholized Cu-Ceruloplasmin shows different stability profile than "native" Cu-Ceruloplasmin
- ▶ "Depletion" of the matrix using selective Ceruloplasmin antibodies leads to a non-representative matrix
 - Efficiency was limited





- ▶ Use "low" and "High" native concentration plasma samples for the calibration curve and QC's
- ▶ Prepare Cu-EDTA concentration bij addition of Cu to (diluted) plasma samples
- ▶ Prepare Cu-Ceruloplasmin concentrations by dilution of a high concentration plasma pool
- ▶ Things to consider with this approach:
 - Matrix effect
 - Effect of dilution on equilibrium values
 - No direct information on Cu-ceruloplasmin concentration
 - Lyopholized Ceruloplasmin insufficiently homogeneous, stated concentration too wide to be of use
- ▶ 1) Determine total copper
- ▶ 2) Calibration curve in proxy matrix to determine Cu-EDTA concentration (in the chromatography assay)
- ▶ 3) the substractions yields the starting Cu-Ceruloplasmin concentration



Performance

		Concentration (ng/mL)					
Run ID:	Analysis date:	LLOQ		LQC	MQC	HQC	
		17.1		42.7	427	854	
QCB2111-00447	23 Nov 2021	18.9		44.6	465	868	
		18.1		44.2	478	880	
		17.4		43.1	441	846	
		17.8		42.6	448	893	
		18.0		43.6	442	862	
		18.9		44.1	443	811	
Intra-run Mean		18.2		43.7	453	860	
Intra-run SD		0.6		0.7	15	29	
Intra-run %RE		6.3		2.3	6.0	0.7	
Intra-run %CV		3.3		1.7	3.4	3.4	
n		6		6	6	6	
QCB2111-00566	30 Nov 2021	17.7		46.7	461	883	
		18.9		44.6	440	817	
		17.5		44.3	422	795	
		17.3		44.6	419	845	
		19.3		44.0	417	747	
		19.2		44.1	423	765	
Intra-run Mean		18.3		44.7	430	809	
Intra-run SD		0.9		1.0	17	51	
Intra-run %RE		7.1		4.7	0.8	-5.3	
Intra-run %CV		5.0		2.2	4.0	6.3	
n		6		6	6	6	
QCB2201-00447	26 Jan 2022	20.5		46.6	469	835	
		20.9	a)	46.5	448	827	
		20.9	a)	48.8	465	845	
		21.2	a)	46.8	456	844	
		20.5		47.0	443	809	
		20.3		46.9	437	815	
Intra-run Mean		20.7		47.1	453	829	
Intra-run SD		0.3		0.9	13	15	
Intra-run %RE		21.2		10.3	6.1	-2.9	
Intra-run %CV		1.6		1.8	2.8	1.8	
n		6		6	6	6	
Inter-run Mean		19.1		45.2	445	833	
Inter-run SD		1.4		1.7	18	39	
Inter-run %RE		11.5		5.8	4.3	-2.5	
Inter-run %CV		7.1		3.7	4.0	4.7	
n		18		18	18	18	

		Concentration (ng/mL)			
Run ID:	Analysis date:	LLOQ	LQC		
		21.0	52.4		
QCB2111-00447	24 Nov 2021	23.1	51.1		
		20.3	54.6		
		22.5	53.0		
		22.1	53.3		
		21.6	55.3		
		23.1	54.9		
Intra-run Mean		22.1	53.7		
Intra-run SD		1.1	1.6		
Intra-run %RE		5.3	2.5		
Intra-run %CV		4.8	2.9		
n		6	6		
QCB2201-00447	26 Jan 2022	21.3	50.8		
		23.0	56.4		
		21.7	53.9		
		21.7	52.6		
		22.1	55.5		
		23.0	50.2		
Intra-run Mean		22.1	53.2		
Intra-run SD		0.7	2.5		
Intra-run %RE		5.4	1.6		
Intra-run %CV		3.2	4.7		
n		6	6		
QCB2204-00244	19 Apr 2022	22.6	49.8		
		21.6	50.0		
		23.6	51.6		
		23.9	55.4		
		24.2	56.7		
		24.1	53.5		
Intra-run Mean		23.3	52.8		
Intra-run SD		1.0	2.9		
Intra-run %RE		11.1	0.8		
Intra-run %CV		4.4	5.4		
n		6	6		
Inter-run Mean		22.5	53.3		
Inter-run SD		1.1	2.3		
Inter-run %RE		7.3	1.6		
Inter-run %CV		4.7	4.2		
n		18	18		



Take home messages

- ▶ ICP-MS can be a valuable tool to measure metallo-proteins
- ▶ Proxy matrices can be usefull, depending on the relative stability of the protein of interest in
- ► Working at or above normal references ranges is easier than below
- ▶ Be prepared to work outside of the guidelines: what is the goal, rather than trying to follow them

With creativity most problems can be solved

