Challenge
Determination of the elements Al, Cd, Cr, Cu, Fe, Pb, Se and Zn in body fluids

Solution
Quantification of elements using the ZEEnit 650P

Intended audience
Laboratories in medical diagnostics

Quantification of Elements in Body Fluids Using GF-AAS

Introduction

The analysis of trace elements such as aluminium, lead, cadmium, chromium, iron, copper, selenium and zinc in body fluids is critical to understanding the metabolism, toxicology and health status of an individual. These elements perform both essential and harmful functions in the body. While iron, copper, selenium and zinc play important roles in enzymes and metabolic processes, elevated levels of lead and cadmium can cause toxic effects. Accurate determination of these elements provides valuable information for diagnosing deficiencies, toxicity or monitoring therapeutic interventions.

Atomic absorption spectrometry (AAS) is an important part of elemental analysis due to its robustness, precision and flexibility. In particular, graphite furnace AAS (GF-AAS) is a powerful technique that can reliably determine even the lowest element concentrations with minimal sample requirements. The aim of this application note is to demonstrate the applicability of GF-AAS for the analysis of elements in body fluids.

The determination of aluminium, iron, copper, selenium, and zinc in serum is described below. The application procedure for the serum matrix and the method parameters mentioned can also be used for the plasma matrix. This application note includes whole blood as an additional sample type. Chromium, lead and cadmium were determined in this body fluid. Cadmium and copper were determined in urine. Commercial control standards of the matrix types were measured to validate the results. Calibration was performed with acid-stabilised elemental standards or with matrix-matched calibrators. Selenium in particular shows matrix interferences, so the use of matrix calibrators or the addition method (calibration) is mandatory for the correct determination of this element concentration in body fluids.

The ZEEnit 650P atomic absorption spectrometer is equipped with an eight position lamp turret for hollow cathode lamps (HCL). The graphite furnace with 3rd generation Zeeman background correction and variable

magnetic field up to 1 tesla magnetic flux density is the ideal instrument for the quantification of elements in the low µg L^{-1} concentration range and below. The powerful Zeeman background correction allows even low atomic absorption signals to be reliably separated from the background absorption without the need for mathematical models. This feature makes it easy to routinely analyze even difficult matrices. With the variable magnetic field and 3-field mode, the measurement sensitivity can be attenuated to a level that allows the determination of sensitively detectable elements such as zinc under normal laboratory conditions.

The AS-GF autosampler can perform fully automatic dilutions before the actual measurement and when the highest calibration standard is exceeded. This autosampler can also be used to automatically prepare the solutions required for the calibration function from a stock standard. Another function of the AS-GF is the fully automatic performance of the method of addition (calibration) procedure, the automatic dosing of the modifier solution and the spiking of the sample with a known standard concentration.

Materials and Methods

Control standards

- Control standard, whole blood, lyophilized (RECIPE, ClinChek® Level I, II, III)
- Control standard, serum (RECIPE, ClinChek® Level I, II)
- Control standard, urine (RECIPE, ClinChek® Level I, II)

Reagents

- Concentrated HNO_3 (approx. 60%, purified via sub-boiling distillation)
- Tergitol™ 15-S-9, alternatively TritonX-100™
- Mg matrix modifier (10 g L^{-1})
- Pd matrix modifier (10 g L^{-1}), alternatively Pd standard solution (1 g L^{-1}) if contamination problems occurs
- Ascorbic acid (p.a.)
- Acetic acid (≥ 95,9%)
- Certified individual element standards for Al, Cd, Cr, Cu, Fe, Pb, Se and Zn (analyte concentration 1000 mg L^{-1} each)
- Calibrators for whole blood, serum and urine (RECIPE, ClinCal®)

Sample preparation

A solution containing 0.2% (v/v) HNO_3 and 0.1% (w/w) Tergitol 15-S-9 (alternatively 0.1% (w/w) TritonX 100) based on ultrapure water was used as a diluent for body fluids. The dilution factors used are listed in table 7. Whole blood samples were diluted by a factor of 10, serum samples 3-fold and urine by a factor of 2 to 4.

Calibration

The measurement can be calibrated using either commercially available matrix-matched calibrators or acid-stabilized elemental standard solutions, with the exception of selenium. For this analyte either the use of a matrix calibrator or the method of addition (calibration) is required. If the method of addition calibration is used, a calibration line from one standard addition provides the reference for subsequent samples. With this method setting the spiking steps of the standard addition can be omitted for the subsequent samples. Recommended analyte concentrations for calibration are given in tables 1 to 3.

In this application note, a selenium concentration of 100 µg L^{-1} was used as a stock standard for the method of addition calibration. The injected sample volume of a 3-fold diluted sample was 20 µL and the added volume of the stock standard was 5 to15 µL. The preparation of calibration standards and the performance of the method of addition or method of addition calibration can be conducted entirely automatically with the AS-GF autosampler.

The diluent for the calibration using matrix-matched calibrators consists of 0.2% (v/v) HNO_3 and 0.1% (w/w) Tergitol 15-S-9 or TritonX 100. The dilution solution serves as the zero value. For calibration with acid-stabilized solutions, a diluent of 0.5% (v/v) HNO_3 was used for the standards. 0.5% (w/w) HNO_3 is also the solution for the calibration zero for this variant. If the calibration is performed using acid-stabilized standards, a blank value correction for the diluent of the samples (0.2% (v/v) HNO_3 and 0.1% (w/w) Tergitol 15-S-9 or TritonX 100) needs to be tested.

Table 1: Recommended concentrations for the calibration to quantify analytes in serum

Standard	Concentration [µg L^{-1}]						
	Al*	Se*	Se**	Cu	Fe	Zn	Zn*
Cal. 0	0	0	-	0	0	0	0
Std. 1	26.1	44.0	25	12.5	12.5	6.25	8.5
Std. 2			50	25.0	25.0	12.5	17
Std. 3			75	37.5	37.5	18.75	25.5
Std. 4				50.0	50.0	25	34

* Use of a matrix calibrator (RECIPE ClinCal®)
** Concentration of the standard addition (stock solution Stock: 100 µg L^{-1} Se)

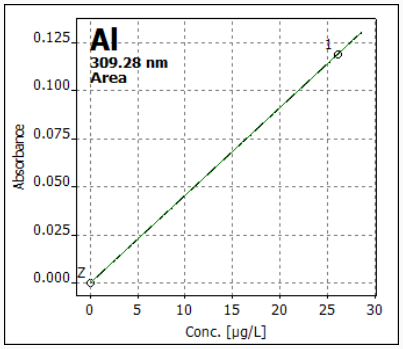
Table 2: Recommended concentrations for the calibration to quantify analytes in whole blood

Standard	Concentration [µg L^{-1}]						
	Cd	Cd*	Cr	Cr*	Pb	Pb*	Se*
Cal. 0	0	0	0	0	0	0	0
Std. 1	1.25	0.897	0.5	1.29	6	33.1	28.7
Std. 2	2.5		1.0		12		
Std. 3	3.75		1.5		18		
Std. 4	5		2.0		24		
Std. 5			2.5		30		

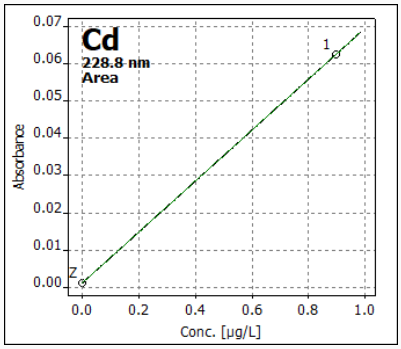
* Use of a matrix calibrator (RECIPE ClinCal®)

Table 3: Recommended concentrations for the calibration to quantify analytes in urine

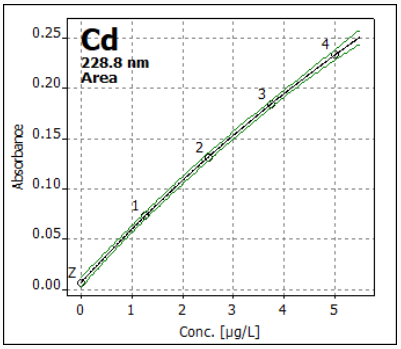
Standard	Concentration [µg L^{-1}]	
	Cd	Cu
Cal. 0	0	0
Std. 1	1.25	12.5
Std. 2	2.5	25.0
Std. 3	3.75	37.5
Std. 4	5	50



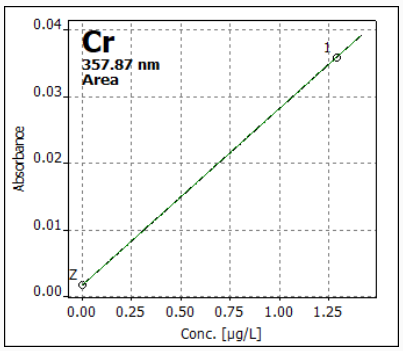
No modifier, calibration: serum calibrator



Modifier Pd/Mg, calibration: whole blood calibrator



$R^2_{(adj.)}$ 0.9996 (non-linear), modifier Pd/Mg, calibration: acid stabilized standards



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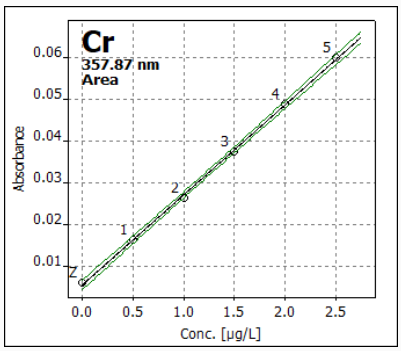
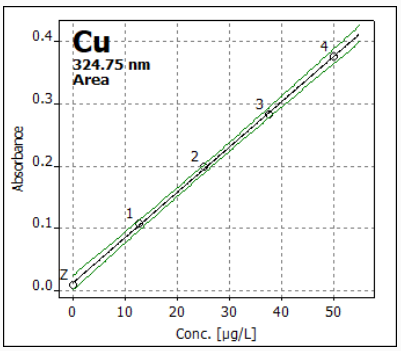
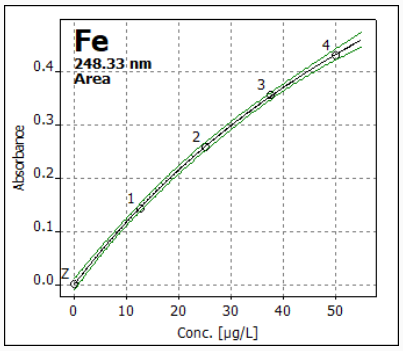


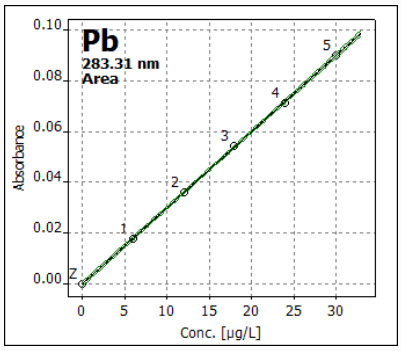
$R^2_{(adj.)}$ 0.9990 (linear), modifier Mg, calibration: acid stabilized standards



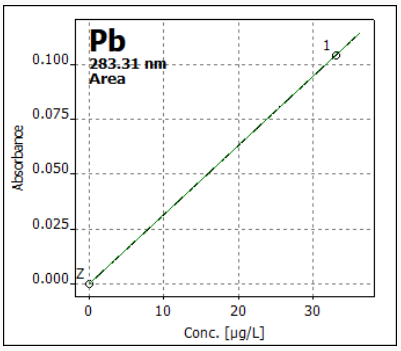
$R^2_{(adj.)}$ 0.9990 (linear), modifier Pd/Mg, calibration: acid stabilized standards



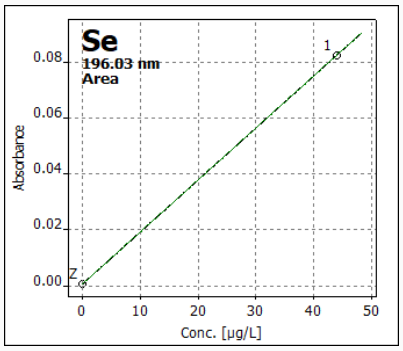
$R^2_{(adj.)}$ 0.9992 (non-linear), modifier Mg, calibration: acid stabilized standards



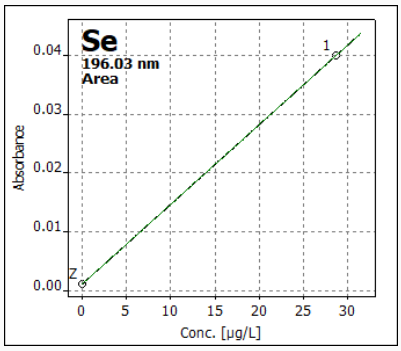
$R^2_{(adj.)}$ 0.9992 (linear), modifier Pd/Mg, calibration: acid stabilized standards



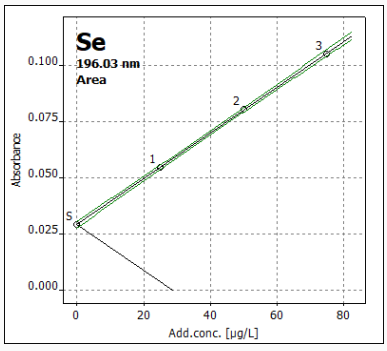
Modifier $NH_4H_2PO_4$, calibration: whole blood calibrator



Modifier Pd/Mg, calibration: serum calibrator

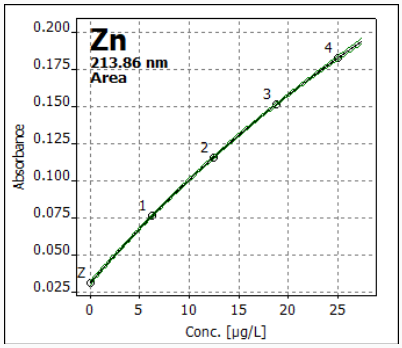


Modifier Pd/Mg, calibration: whole blood calibrator

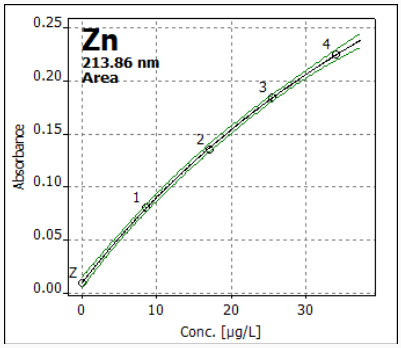


$R^2_{(adj.)}$ 0,9997 (linear), modifier Pd/Mg, calibration: method of addition calibration serum

Figure 1: Illustrations of typical calibration functions



$R^2_{(adj.)}$ 0.99993 (non-linear), modifier Pd/Mg, calibration: acid stabilized standards



$R^2_{(adj.)}$ 0,9996 (non-linear), modifier Pd/Mg, calibration: serum calibrator

Figure 1 continued: Illustrations of typical calibration functions

Instrument settings

The ZEEnit 650P atomic absorption spectrometer was used to determine the content of the analytes in the tested samples of body fluids (serum, whole blood, and urine). The AS-GF autosampler can automatically perform variable sample dilutions or the preparation of calibration solutions, the standard addition method, and the spiking of samples.

The device specifications and measurement parameters used are listed in table 4 to 6.

Magnesium nitrate with a concentration of 0.5 g L^{-1} and a mixture of palladium and magnesium nitrate were used as matrix modifiers (concentration: 1 g L^{-1} Pd and 0.5 g L^{-1} $Mg(NO_3)_2$). Another possibility of matrix modifier for the analyte Pb is ammonium dihydrogen phosphate. A concentration of 10 g L^{-1} $NH_4H_2PO_4$ was used in this series of measurements. The used modifier solutions for each individual analyte are listed in figure 1 and table 4.

In electrothermal AAS, volatile chlorine compounds of the analytes can lead to lower signal intensities. For the quantification of some elements, it is possible that systematic differences may occur between calibration and samples. By reducing the palladium modifier with ascorbic acid (concentration of the ascorbic acid solution: 1 g L^{-1}) this interference can be minimized or even eliminated. To prevent the palladium(II) nitrate from precipitating in the pipetting tube, it is recommended to separate the modifier solution from the reducing solution. This option can be set in the software.

Table 4: General instrument and method settings

Parameter	Specification	
Device	ZEEnit 650P	
Tube type	PIN plattform	
Injection volume	Al: 25 µL Cd: 20 µL Cr: 25 µL Cu: 20 µL Fe: 20 µL Pb: 20 µL	Se: *calibrator* 30 µL *method of addition* 20 µL (sample) 15 µL (standard) Zn: 20 µL
Modifier	5 µL injection volume Al: none Cd: Pd/Mg Cr: Mg Cu: Pd/Mg	 Fe: Mg Pb: $NH_4H_2PO_4$ or Pd/Mg Se: Pd/Mg Zn: Pd/Mg
Settings of the magnectic field	2-Field Mode: Al: 0.8T Cd: 0.8T Cr: 0.8T Cu: 1.0T Fe: 0.8T Pb: 0.8T Se: 0.8T	3-Field Mode: Zn: 1.00/0.65T
Rinsing solution	2% (v/v) acetic acid, 0.05% (w/w) Tergitol™ 9-S-15 (alternatively TritonX™-100)	

Table 5: Applied lamp and spectrometer parameters

Element	Wavelength [nm]	Slit width [nm]	HCL current [mA]
Al	309.3	0.8	4
Cd	228.8	0.8	2
Cr	357.9	0.2	4
Cu	324.7	0.8	2
Fe	248.3	0.2	5
Pb	283.3	0.8	3
Se	196.0	1.2	5
Zn	213.8	0.8	2

Table 6: Recommended temperature-time programs for the analytes

Element: Al

Temperature-time program

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	30	39.2	Min	Stop
2		Drying	95	3	42	45.3	Min	Stop
3		Drying	110	4	10	13.8	Min	Stop
4		Ash	575	50	50	59.3	Min	Max
5		Pyrolysis	575	0	18	18.0	Max	Stop
6		Pyrolysis	1000	250	7	8.7	Max	Stop
7		AZ*	1000	0	6	6.0	Stop	Stop
8		Atomize	2450	1450	2	3.0	Stop	Stop
9		Clean	2550	500	4	4.2	Max	Stop

Serum

Element: Cd

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	30	39.2	Min	Stop
2		Drying	90	3	45	46.7	Min	Stop
3		Drying	110	4	10	15.0	Min	Stop
4		Ash	580	75	72	78.3	Min	Max
5		Pyrolysis	580	0	17	17.0	Max	Stop
6		Pyrolysis	650	250	7	7.3	Max	Stop
7		AZ*	650	0	6	6.0	Stop	Stop
8		Atomize	1700	1450	3	3.7	Stop	Stop
9		Clean	2450	500	4	5.5	Max	Stop

Whole blood

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	30	39.2	Max	Stop
2		Drying	90	3	40	41.7	Max	Stop
3		Drying	110	2	10	20.0	Max	Stop
4		Ash	570	75	30	36.1	Min	Max
5		Pyrolysis	570	0	17	17.0	Max	Stop
6		Pyrolysis	600	250	15	15.1	Max	Stop
7		AZ*	600	0	6	6.0	Stop	Stop
8		Atomize	1500	1450	3	3.6	Stop	Stop
9		Clean	2450	500	4	5.9	Max	Stop

Urine

Table 6 continued: recommended temperature-time programs for the analytes

Element | **Temperature-time program**

Cr

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	30	39.2	Min	Stop
2		Drying	90	3	45	46.7	Min	Stop
3		Drying	110	4	10	15.0	Min	Stop
4		Ash	580	75	72	78.3	Min	Max
5		Pyrolysis	580	0	17	17.0	Max	Stop
6		Pyrolysis	1100	250	7	9.1	Max	Stop
7		AZ*	1100	0	6	6.0	Stop	Stop
8		Atomize	2400	1450	4	4.9	Stop	Stop
9		Clean	2550	500	5	5.3	Max	Stop

Whole blood

Cu

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	15	24.2	Max	Stop
2		Drying	95	3	15	18.3	Max	Stop
3		Drying	110	2	5	12.5	Max	Stop
4		Pyrolysis	550	75	10	15.9	Min	Max
5		Pyrolysis	550	0	15	15.0	Max	Stop
6		Pyrolysis	850	300	10	11.0	Max	Stop
7		AZ*	850	0	6	6.0	Stop	Stop
8		Atomize	2250	1450	4	5.0	Stop	Stop
9		Clean	2500	500	4	4.5	Max	Stop

Serum

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	20	29.2	Max	Stop
2		Drying	95	3	20	23.3	Max	Stop
3		Drying	110	2	5	12.5	Max	Stop
4		Pyrolysis	550	75	30	35.9	Min	Max
5		Pyrolysis	550	0	15	15.0	Max	Stop
6		Pyrolysis	850	300	15	16.0	Max	Stop
7		AZ*	850	0	6	6.0	Stop	Stop
8		Atomize	2250	1450	4	5.0	Stop	Stop
9		Clean	2500	500	4	4.5	Max	Stop

Urine

Fe

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	15	24.2	Max	Stop
2		Drying	95	3	15	18.3	Max	Stop
3		Drying	110	2	5	12.5	Max	Stop
4		Pyrolysis	550	75	10	15.9	Min	Max
5		Pyrolysis	550	0	15	15.0	Max	Stop
6		Pyrolysis	850	300	10	11.0	Max	Stop
7		AZ*	850	0	6	6.0	Stop	Stop
8		Atomize	2450	1450	3	4.1	Stop	Stop
9		Clean	2500	500	4	4.1	Max	Stop

Serum

Pb

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	30	39.2	Min	Stop
2		Drying	90	3	45	46.7	Min	Stop
3		Drying	110	2	10	20.0	Min	Stop
4		Ash	570	75	65	71.1	Min	Max
5		Pyrolysis	570	0	17	17.0	Max	Stop
6		Pyrolysis	700	250	7	7.5	Max	Stop
7		AZ*	700	0	6	6.0	Stop	Stop
8		Atomize	1700	1450	2	2.7	Stop	Stop
9		Clean	2450	500	4	5.5	Max	Stop

Whole blood, modifier: $NH_4H_2PO_4$

Table 6 continued: Recommended temperature-time programs for the analytes

Element	Temperature-time program

Pb

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	30	39.2	Min	Stop
2		Drying	90	3	45	46.7	Min	Stop
3		Drying	110	4	10	15.0	Min	Stop
4		Ash	570	75	65	71.1	Min	Max
5		Pyrolysis	570	0	17	17.0	Max	Stop
6		Pyrolysis	800	250	7	7.9	Max	Stop
7		AZ*	800	0	6	6.0	Stop	Stop
8		Atomize	1950	1450	3	3.8	Stop	Stop
9		Clean	2450	500	4	5.0	Max	Stop

Whole blood, modifier: Pd/Mg

Se

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	30	39.2	Min	Stop
2		Drying	95	3	41	44.3	Min	Stop
3		Drying	110	4	10	13.8	Min	Stop
4		Ash	575	75	50	56.2	Min	Max
5		Pyrolysis	575	0	17	17.0	Max	Stop
6		Pyrolysis	850	250	7	8.1	Max	Stop
7		AZ*	850	0	6	6.0	Stop	Stop
8		Atomize	2300	1450	2	3.0	Stop	Stop
9		Clean	2450	500	4	4.3	Max	Stop

Serum calibrator

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	25	34.2	Min	Stop
2		Drying	95	3	62	65.3	Min	Stop
3		Drying	110	3	19	24.0	Min	Stop
4		Ash	575	75	62	68.2	Min	Med
5		Pyrolysis	575	0	17	17.0	Max	Stop
6		Pyrolysis	850	250	7	8.1	Max	Stop
7		AZ*	850	0	6	6.0	Stop	Stop
8		Atomize	2300	1450	2	3.0	Stop	Stop
9		Clean	2450	500	4	4.3	Max	Stop

Serum method of addition

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	30	39.2	Min	Stop
2		Drying	95	3	41	44.3	Min	Stop
3		Drying	110	4	10	13.8	Min	Stop
4		Ash	575	75	65	71.2	Min	Max
5		Pyrolysis	575	0	17	17.0	Max	Stop
6		Pyrolysis	850	250	7	8.1	Max	Stop
7		AZ*	850	0	6	6.0	Stop	Stop
8		Atomize	2300	1450	2	3.0	Stop	Stop
9		Clean	2450	500	4	4.3	Max	Stop

Whole blood calibrator

Zn

Step	*	Name	Temp. [°C]	Ramp [°C/s]	Hold s	Time s	Gas int.	Gas Add.
1		Drying	85	6	15	24.2	Max	Stop
2		Drying	95	3	15	18.3	Max	Stop
3		Drying	110	2	5	12.5	Max	Stop
4		Pyrolysis	550	75	10	15.9	Min	Max
5		Pyrolysis	550	0	15	15.0	Max	Stop
6		Pyrolysis	750	300	5	5.7	Max	Stop
7		AZ*	750	0	6	6.0	Stop	Stop
8		Atomize	1850	1300	3	3.8	Stop	Stop
9		Clean	2450	500	4	5.2	Max	Stop

Serum

Results and Discussion

The elements aluminum, lead, cadmium, chromium, iron, copper, selenium, and zinc were determined in body fluids. Table 7 shows the results of the series of measurements for the ClinCheck® Control (RECIPE) samples and the manufacturer's specifications for the mean value and control range. The measurement uncertainty of the AAS determination is based on the standard deviation of the three repetitions of the measurements.

Table 7: Measurement results of the determination of analytes in serum, whole blood and urine control standards

Sample	Element	Dilution factor	Unit	Measurement value (±SD*)		Mean value and control range	
Serum Level I	Al	3	µg L^{-1}	16.8	±0.65	16.9	11.8 - 21.9
	Cu	50	mg L^{-1}	0.784	±0.007	0.841	0.715 - 0.967
	Fe	50	mg L^{-1}	0.768	±0.002	0.777	0.666 - 0.893
	Se	3	µg L^{-1}	55.0	±2.6	54.8	43.9 - 65.8
	Zn	100	mg L^{-1}	1.55	±0.02	1.55	1.32 - 1.78
Serum Level II	Al	3	µg L^{-1}	58.2	±0.26	58.6	43.9 - 73.2
	Cu	50	mg L^{-1}	1.28	±0.02	1.39	1.18 - 1.60
	Fe	50	mg L^{-1}	1.13	±0.01	1.13	0.959 - 1.30
	Se	3	µg L^{-1}	112	±3.4	110	88.0 - 132
	Zn	100	mg L^{-1}	2.03	±0.01	1.92	1.63 - 2.21
Whole blood Level I	Cd	10	µg L^{-1}	1.54	±0.11	1.46	1.09 - 1.82
	Cr	10	µg L^{-1}	2.73	±0.02	2.40	1.68 - 3.11
	Pb	10	µg L^{-1}	31.7	±0.02	34.0	27.2 - 40.7
	Se	10	µg L^{-1}	83.2	±3.7	85.6	68.5 - 103
Whole blood Level II	Cd	10	µg L^{-1}	3.51	±0.18	3.44	2.75 - 4.12
	Cr	10	µg L^{-1}	5.69	±0.07	5.57	4.18 - 6.96
	Pb	10	µg L^{-1}	87.3	±1.3	91.1	72.9 - 109
	Se	10	µg L^{-1}	167.4	±16	162	130 - 195
Whole blood Level III	Cd	10	µg L^{-1}	6.73	±0.05	6.68	5.35 - 8.02
	Cr	10	µg L^{-1}	10.1	±0.05	10.6	8.47 - 12.7
	Pb	10	µg L^{-1}	234	±5.0	251	201 - 302
	Se	10	µg L^{-1}	204	±8.9	204	164 - 254
Urine Level I	Cd	2	µg L^{-1}	2.65	±0.03	2.46	1.97 - 2.95
	Cu	2	µg L^{-1}	37.2	±0.12	36.7	29.0 - 44.1
Urine Level II	Cd	4	µg L^{-1}	15.4	±0.08	14.4	11.5 - 17.2
	Cu	2	µg L^{-1}	88.7	±0.038	91.9	73.5 - 110

* SD: standard deviation of three measurement replicates

Summary

Cost-effective analysis of the elements aluminum, lead, cadmium, chromium, iron, copper, selenium and zinc in medical samples using the atomic absorption spectrometer with electrothermal atomization in the ZEEnit 650P graphite furnace is simple and user-friendly. The 3rd generation Zeeman furnace combines the precise measurement of analytes, even with a high background signal, with the ability to attenuate very sensitive analyte measurements to a level that allows sample handling under conventional laboratory conditions. Convenient and automatic sample handling is guaranteed by the AS-GF autosampler.

Figure 2: ZEEnit 650P

Recommended device configuration

Table 8: Overview of devices, accessories, and consumables

Item	Part number	Description
ZEEnit 650P	813-0650P-2-K	ZEEnit 650P – Graphite Furnace AAS with Zeeman background correction
Chiller, 50 Hz	810-60053-0	Software-controlled cooling system, (50 Hz power supply)
Chiller, 60 Hz	810-60052-0	Software-controlled cooling system, (60 Hz power supply)
Graphite tube platform	407-152.314	Z-graphite tube PIN-platform-pyrolytically coated (10 pcs.)
Sample vials 5 mL	407-230.073	PP-sample vials, 5 mL (10 pcs)
Sample vials 1,5 mL	407-218.852	Polystyrene-sample vials 1.5mL (1000 pcs)
Cd-HCL	480-450.008C	Coded Hollow Cathode Lamp Cadmium (Cd)
Cr-HCL	480-450.012C	Coded Hollow Cathode Lamp Chromium (Cr)
Cu-HCL	480-450.014C	Coded Hollow Cathode Lamp Cupper (Co)
Fe-HCL	480-450.026C	Coded Hollow Cathode Lamp Iron (Fe)
Pb-HCL	480-450.028C	Coded Hollow Cathode Lamp Lead (Pb)
Se-HCL	480-450.049C	Coded Hollow Cathode Lamp Selenium (Se)
Zn-HCL	480-450.067C	Coded Hollow Cathode Lamp Zinc (Zn)

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