



**شرکت دلتا درمان پارت**  
سیستم های آزمایشگاهی و مواد مصرفی



دفتر مرکزی: تهران، میدان آرژانتین، خیابان الوند، خیابان سی و پنجم، پلاک ۱۳، طبقه پنجم

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فکس: ۸۸۸۵۶۴۰۳

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<b>Data Information</b>		<b>Calibration</b>	
Unit	U/l	Type	LINEAR 1
Decimals	0	<b>Standard</b>	
<b>Analysys</b>		Blank 0	1 *
Type	RATE	2	3
W.Length 1	340	4	5
W.Length 2	700	<b>Normal Range</b>	
Method	LIA		
<b>Corr</b>			
Slope	Inter	Low	High
1.000 × +	0	Serum Male	13.3 63.9
		Serum Female	13.3 63.9
		Urine (mg/24h)	

<b>Aspiration</b>	
Kind	<u>Single</u> Double
Volume	
Sample	20
Reagent 1	200
Reagent 2	
Third Mix	<u>Off</u> ON
R1 Blank	<u>Water</u> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	High	-0.1
	Start	End	3.000
Main	32	72	
Sub			
Endpoint Limit 2			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start	End	Limit
First			
Second			
Third			

**ACE**

<b>Data Information</b>		<b>Calibration</b>	
Unit	U/L	Type	LINEAR 1
Decimals	1	<b>Standard</b>	
<b>Analysys</b>		Blank 0	1 *
Type	RATE	2	3
W.Length 1	546	4	5
W.Length 2	700	<b>Normal Range</b>	
Method	COLOUR/ENZ		
<b>Corr</b>			
Slope	Inter	Low	High
1.000 × +	0	Serum Male	0 15
		Serum Female	0 15
		Urine (mg/24h)	

<b>Aspiration</b>	
Kind	Single <u>Double</u>
Volume	
Sample	5
Reagent 1	160
Reagent 2	80
Third Mix	<u>Off</u> ON
R1 Blank	<u>Water</u> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	High	-0.1
	Start	End	3.000
Main	52	76	
Sub			
Endpoint Limit 3%			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start	End	Limit
First			
Second			
Third			

**ADA**

<b>Data Information</b>	
Unit	G/DL
Decimals	2
<b>Analysys</b>	
Type	END
W.Length 1	600
W.Length 2	700
Method	BCG
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	3.5	5
	Female	3.5	5
Urine (mg/24h)			

<b>Data Information</b>	
Unit	U/L
Decimals	0
<b>Analysys</b>	
Type	RATE
W.Length 1	405
W.Length 2	660
Method	DGKC
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	80	306
	Female	64	306
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	<input checked="" type="checkbox"/> Single <input type="checkbox"/> Double
Volume	
Sample	2
Reagent 1	200
Reagent 2	
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	Start 32 End 33
Sub	
Endpoint Limit 3%	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

<b>Aspiration</b>	
Kind	<input type="checkbox"/> Single <input checked="" type="checkbox"/> Double
Volume	
Sample	4
Reagent 1	200
Reagent 2	50
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	Start 44 End 68
Sub	
Endpoint Limit 3%	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**ALB**

**ALP**

<b>Data Information</b>	
Unit	U/L
Decimals	1
<b>Analysys</b>	
Type	RATE
W.Length 1	340
W.Length 2	405
Method	IFCC
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0	40
	Female	0	32
Urine (mg/24h)			

<b>Data Information</b>	
Unit	U/L
Decimals	0
<b>Analysys</b>	
Type	RATE
W.Length 1	405
W.Length 2	660
Method	CNPG3
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0	100
	Female	0	100
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <u>Double</u> <input checked="" type="checkbox"/>
Volume	
Sample	20
Reagent 1	160
Reagent 2	40
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	Start 44 End 68
Sub	
Endpoint Limit 90	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

<b>Aspiration</b>	
Kind	<u>Single</u> <input checked="" type="checkbox"/> Double <input type="checkbox"/>
Volume	
Sample	4
Reagent 1	200
Reagent 2	
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	Start 12 End 35
Sub	
Endpoint Limit 3	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**ALT**

**AMY**

<b>Data Information</b>	
Unit	IU/ML
Decimals	0
<b>Analysys</b>	
Type	END
W.Length 1	600
W.Length 2	
Method	LIA
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0	200
	Female	0	200
Urine (mg/24h)			

<b>Data Information</b>	
Unit	U/L
Decimals	1
<b>Analysys</b>	
Type	RATE
W.Length 1	340
W.Length 2	405
Method	IFCC
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0	37
	Female	0	31
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	3
Reagent 1	200
Reagent 2	50
Third Mix	<input type="checkbox"/> Off <input checked="" type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	Start 76 End 77
Sub	
Endpoint Limit 2	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	20
Reagent 1	160
Reagent 2	40
Third Mix	<input type="checkbox"/> Off <input checked="" type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	Start 44 End 68
Sub	
Endpoint Limit	
Linear Check (90%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**ASO**

**AST**

<b>Data Information</b>		<b>Calibration</b>	
Unit	MG/DL	Type	LINEAR 1
Decimals	2	<b>Standard</b>	
<b>Analysys</b>		Blank 0	1 *
Type	END	2	3
W.Length 1	546	4	5
W.Length 2	700	<b>Normal Range</b>	
Method	DMSO		
<b>Corr</b>			
Slope	Inter	Low	High
1.000 × +	0	Serum Male	0 0.3
		Serum Female	0 0.3
		Urine (mg/24h)	

<b>Aspiration</b>	
Kind	<input type="radio"/> Single <input checked="" type="radio"/> Double
Volume	
Sample	25
Reagent 1	200
Reagent 2	50
Third Mix	<input type="radio"/> Off <input type="radio"/> ON
R1 Blank	<input type="radio"/> Water <input type="radio"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read		Low	-0.1
		High	3.000
Main	75 76		
Sub	34 35		
		Endpoint Limit 2	
		Linear Check (%)	
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
		Start	End
First			
Second			
Third			

**BILI.D**

<b>Data Information</b>		<b>Calibration</b>	
Unit	MG/DL	Type	LINEAR 1
Decimals	2	<b>Standard</b>	
<b>Analysys</b>		Blank 0	1 *
Type	END	2	3
W.Length 1	546	4	5
W.Length 2	700	<b>Normal Range</b>	
Method	DMSO		
<b>Corr</b>			
Slope	Inter	Low	High
1.000 × +	0	Serum Male	0.1 1.2
		Serum Female	0.1 1.2
		Urine (mg/24h)	

<b>Aspiration</b>	
Kind	<input type="radio"/> Single <input checked="" type="radio"/> Double
Volume	
Sample	6
Reagent 1	200
Reagent 2	50
Third Mix	<input type="radio"/> Off <input type="radio"/> ON
R1 Blank	<input type="radio"/> Water <input type="radio"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read		Low	-0.1
		High	3.000
Main	75 76		
Sub	34 35		
		Endpoint Limit 3	
		Linear Check (%)	
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
		Start	End
First			
Second			
Third			

**BILI.T**

<b>Data Information</b>		<b>Calibration</b>	
Unit	MG/DL	Type	Logit.Log2
Decimals	0	<b>Standard</b>	
<b>Analysys</b>		Blank 0	1 cal/16
Type	END	2 cal/8	3 cal/4
W.Length 1	340	4 cal/2	5 cal
W.Length 2	700	<b>Normal Range</b>	
Method	LIA	Low	High
<b>Corr</b>		Serum	Male
Slope	Inter		90
1.000 × +	0	Female	180
		Urine (mg/24h)	

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	2
Reagent 1	160
Reagent 2	40
Third Mix	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

**C3**

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	75	76	
Sub	34	35	
Factor		Endpoint Limit 2	
Blank Correction		Linear Check (%)	
		1.000	
<b>Prozone Check</b>			
	Start	End	Limit
First			
Second			
Third			

<b>Data Information</b>		<b>Calibration</b>	
Unit	MG/DL	Type	Logit.Log2
Decimals	1	<b>Standard</b>	
<b>Analysys</b>		Blank 0	1 cal/16
Type	END	2 cal/8	3 cal/4
W.Length 1	340	4 cal/2	5 cal
W.Length 2	700	<b>Normal Range</b>	
Method	LIA	Low	High
<b>Corr</b>		Serum	Male
Slope	Inter		10
1.000 × +	0	Female	40
		Urine (mg/24h)	

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	4
Reagent 1	160
Reagent 2	40
Third Mix	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

**C4**

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	75	76	
Sub	34	35	
Factor		Endpoint Limit 2	
Blank Correction		Linear Check (%)	
		1.000	
<b>Prozone Check</b>			
	Start	End	Limit
First			
Second			
Third			

<b>Data Information</b>	
Unit	MG/DL
Decimals	2
<b>Analysys</b>	
Type	END
W.Length 1	660
W.Length 2	700
Method	ARSENAZO III
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	8.5	10.5
	Female	8.5	10.5
Urine (mg/24h)			

<b>Data Information</b>	
Unit	MG/DL
Decimals	0
<b>Analysys</b>	
Type	END
W.Length 1	505
W.Length 2	660
Method	CHOD-PAP
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0	200
	Female	0	200
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	<input checked="" type="checkbox"/> Single <input type="checkbox"/> Double
Volume	
Sample	2
Reagent 1	200
Reagent 2	
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	32 33
Sub	
Endpoint Limit 3	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

<b>Aspiration</b>	
Kind	<input checked="" type="checkbox"/> Single <input type="checkbox"/> Double
Volume	
Sample	2
Reagent 1	200
Reagent 2	
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	75 76
Sub	
Endpoint Limit 3	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**CA**

**CHOL**

<b>Data Information</b>	
Unit	U/L
Decimals	0
<b>Analysys</b>	
Type	RATE
W.Length 1	340
W.Length 2	405
Method	KINETIC
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	24	195
	Female	24	170
Urine (mg/24h)			

<b>Data Information</b>	
Unit	U/L
Decimals	0
<b>Analysys</b>	
Type	RATE
W.Length 1	340
W.Length 2	405
Method	KINETIC
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0	24
	Female	0	24
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	8
Reagent 1	160
Reagent 2	40
Third Mix	<input type="checkbox"/> Off <input checked="" type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	Start 52 End 76
Sub	
Endpoint Limit 3	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	16
Reagent 1	160
Reagent 2	40
Third Mix	<input type="checkbox"/> Off <input checked="" type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	Start 52 End 76
Sub	
Endpoint Limit 3	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**CK NAC**

**CK-MB**

<b>Data Information</b>	
Unit	UG/DL
Decimals	0
<b>Analysys</b>	
Type	END
W.Length 1	570
W.Length 2	700
Method	LIA
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1*		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	70	140
	Female	80	155
Urine (mg/24h)			

<b>Data Information</b>	
Unit	MG/DL
Decimals	2
<b>Analysys</b>	
Type	RATE
W.Length 1	505
W.Length 2	660
Method	JAFFE
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1*		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0.7	1.4
	Female	0.6	1.3
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	<input type="checkbox"/> Single <input checked="" type="checkbox"/> Double
Volume	
Sample	10
Reagent 1	200
Reagent 2	
Third Mix	<input type="checkbox"/> Off <input checked="" type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	Start 32 End 33
Sub	
Endpoint Limit 2	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

<b>Aspiration</b>	
Kind	<input type="checkbox"/> Single <input checked="" type="checkbox"/> Double
Volume	
Sample	20
Reagent 1	100
Reagent 2	100
Third Mix	<input type="checkbox"/> Off <input checked="" type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	Start 41 End 53
Sub	
Endpoint Limit 3	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**COPPER**

**CREATININE JAFFE**

<b>Data Information</b>	
Unit	MG/L
Decimals	1
<b>Analysys</b>	
Type	END
W.Length 1	600
W.Length 2	
Method	LIA
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	SPLINE		
<b>Standard</b>			
Blank 0	1 cal/8		
2 cal/4	3 cal/2		
4 cal	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0	6
	Female	0	6
Urine (mg/24h)			

<b>Data Information</b>	
Unit	UG/L
Decimals	0
<b>Analysys</b>	
Type	RATE
W.Length 1	570
W.Length 2	800
Method	LIA
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	Logit.Log2		
<b>Standard</b>			
Blank 0	1 cal/16		
2 cal/8	3 cal/4		
4 cal/2	5 cal		
<b>Normal Range</b>			
	Low High		
Serum	Male	20	250
	Female	20	110
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	2
Reagent 1	160
Reagent 2	40
Third Mix	<input type="checkbox"/> Off <input checked="" type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	76 77
Sub	
Endpoint Limit 2	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	15
Reagent 1	180
Reagent 2	60
Third Mix	<input type="checkbox"/> Off <input checked="" type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	41 76
Sub	
Endpoint Limit 2	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**CRP**

**FERRITIN**

<b>Data Information</b>	
Unit	U/L
Decimals	0
<b>Analysys</b>	
Type	RATE
W.Length 1	405
W.Length 2	660
Method	CARBOXY
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1*		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	11	50
	Female	7	32
Urine (mg/24h)			

<b>Data Information</b>	
Unit	MG/DL
Decimals	0
<b>Analysys</b>	
Type	END
W.Length 1	505
W.Length 2	660
Method	GOD-PAP
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1*		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	70	115
	Female	70	115
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	<input checked="" type="checkbox"/> Single <input type="checkbox"/> Double
Volume	
Sample	20
Reagent 1	160
Reagent 2	40
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	52	76	
Sub			
Endpoint Limit 3			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start	End	Limit
First			
Second			
Third			

<b>Aspiration</b>	
Kind	<input checked="" type="checkbox"/> Single <input type="checkbox"/> Double
Volume	
Sample	2
Reagent 1	200
Reagent 2	
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	75	76	
Sub			
Endpoint Limit 3			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start	End	Limit
First			
Second			
Third			

**GGT**

**GLU**

Unit	MG/DL	Calibration Type	LINEAR 1		
Decimals	1		Standard	Blank 0	1*
Analysys		2		3	
Type	END	4		5	
W.Length 1	600	Normal Range			
W.Length 2	700		Low	High	
Method	DIRECT	Serum	Male	35	55
Corr			Female	45	65
Slope	Inter	Urine (mg/24h)			
1.000 × +	0				

Aspiration	Kind	<input type="checkbox"/> Single	<input type="checkbox"/> Double
	Volume	2	
Reagent 1	180		
Reagent 2	60		
Third Mix	<input type="checkbox"/> Off	<input type="checkbox"/> ON	
R1 Blank	<input type="checkbox"/> Water	<input type="checkbox"/> R1 - B	
Monitor			
0 level Point	1		
Span	3.000		

Data Process	Read	Low	-0.1
		High	3.000
Main	75	76	
Sub	34	35	
Factor		Endpoint Limit 3	
Blank Correction		Linear Check (%)	
Prozone Check			
First	Start	End	Limit
Second			
Third			

**HDL**

Unit	MG/DL	Calibration Type	Logit.Log2		
Decimals	0		Standard	Blank 0	1 cal/16
Analysys		2 cal/8		3 cal/4	
Type	END	4 cal/2		5 cal	
W.Length 1	600	Normal Range			
W.Length 2	700		Low	High	
Method	LIA	Serum	Male	70	400
Corr			Female	70	400
Slope	Inter	Urine (mg/24h)			
1.000 × +	0				

Aspiration	Kind	<input type="checkbox"/> Single	<input type="checkbox"/> Double
	Volume	2	
Sample	160		
Reagent 1	160		
Reagent 2	40		
Third Mix	<input type="checkbox"/> Off	<input type="checkbox"/> ON	
R1 Blank	<input type="checkbox"/> Water	<input type="checkbox"/> R1 - B	
Monitor			
0 level Point	1		
Span	3.000		

Data Process	Read	Low	-0.1
		High	3.000
Main	75	76	
Sub	34	35	
Factor		Endpoint Limit 2	
Blank Correction		Linear Check (%)	
Prozone Check			
First	Start	End	Limit
Second			
Third			

**IGA**

<b>Data Information</b>	
Unit	MG/DL
Decimals	0
<b>Analysys</b>	
Type	END
W.Length 1	600
W.Length 2	700
Method	LIA
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	Logit.Log2		
<b>Standard</b>			
Blank 0	1 cal/16		
2 cal/8	3 cal/4		
4 cal/2	5 cal		
<b>Normal Range</b>			
	Low High		
Serum	Male	700	1600
	Female	700	1600
Urine (mg/24h)			

<b>Data Information</b>	
Unit	MG/DL
Decimals	0
<b>Analysys</b>	
Type	END
W.Length 1	340
W.Length 2	700
Method	LIA
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	Logit.Log2		
<b>Standard</b>			
Blank 0	1 cal/16		
2 cal/8	3 cal/4		
4 cal/2	5 cal		
<b>Normal Range</b>			
	Low High		
Serum	Male	40	230
	Female	40	230
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	2
Reagent 1	240
Reagent 2	60
Third Mix	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	75 76
Sub	34 35
Endpoint Limit 2	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	2
Reagent 1	160
Reagent 2	40
Third Mix	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	75 76
Sub	34 35
Endpoint Limit 2	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**IGG**

**IGM**

<b>Data Information</b>	
Unit	UG/DL
Decimals	0
<b>Analysys</b>	
Type	END
W.Length 1	570
W.Length 2	
Method	FERROZINE
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	35	168
	Female	39	149
Urine (mg/24h)			

<b>Data Information</b>	
Unit	MG/L
Decimals	0
<b>Analysys</b>	
Type	END
W.Length 1	505
W.Length 2	660
Method	LIA
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1 *		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	4.5	19.8
	Female	4.5	19.8
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> Double <input checked="" type="checkbox"/>
Volume	
Sample	20
Reagent 1	160
Reagent 2	40
Third Mix	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start End	75	76
Sub	Start End	34	35
Endpoint Limit 3			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start End Limit		
First			
Second			
Third			

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> Double <input checked="" type="checkbox"/>
Volume	
Sample	2
Reagent 1	200
Reagent 2	
Third Mix	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start End	46	47
Sub	Start End		
Endpoint Limit 2			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start End Limit		
First			
Second			
Third			

**IRON**

**LAC**

<b>Data Information</b>	
Unit	U/L
Decimals	0
<b>Analysys</b>	
Type	RATE
W.Length 1	340
W.Length 2	405
Method	DGKC
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1*		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0	530
	Female	0	530
Urine (mg/24h)			

<b>Data Information</b>	
Unit	MG/DL
Decimals	1
<b>Analysys</b>	
Type	END
W.Length 1	600
W.Length 2	700
Method	DIRECT
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1*		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0	130
	Female	0	130
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	5
Reagent 1	200
Reagent 2	50
Third Mix	
	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input checked="" type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start End	44	68
Sub	Start End		
Endpoint Limit 2			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start End Limit		
First	Start End Limit		
Second	Start End Limit		
Third	Start End Limit		

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	2
Reagent 1	180
Reagent 2	60
Third Mix	
	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input checked="" type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	0.000	
	High	3.000	
Main	Start End	75	76
Sub	Start End	34	35
Endpoint Limit 3			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start End Limit		
First	Start End Limit		
Second	Start End Limit		
Third	Start End Limit		

**LDH**

**LDL**

<b>Data Information</b>	
Unit	U/L
Decimals	0
<b>Analysys</b>	
Type	RATE
W.Length 1	570
W.Length 2	700
Method	KINETIC
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1*		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0	60
	Female	0	60
Urine (mg/24h)			

<b>Data Information</b>	
Unit	MG/DL
Decimals	2
<b>Analysys</b>	
Type	END
W.Length 1	546
W.Length 2	700
Method	XYLIDYL BLUE
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1*		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	1.8	2.6
	Female	1.9	2.5
Urine (mg/24h)		24	244

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	3
Reagent 1	250
Reagent 2	50
Third Mix	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start End	44	60
Sub	Start End		
Endpoint Limit 3			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start End Limit		
First	Start End Limit		
Second	Start End Limit		
Third	Start End Limit		

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	2
Reagent 1	200
Reagent 2	
Third Mix	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start End	32	33
Sub	Start End		
Endpoint Limit 3			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start End Limit		
First	Start End Limit		
Second	Start End Limit		
Third	Start End Limit		

**LIPASE**

**MG**

<b>Data Information</b>	
Unit	MG/L
Decimals	1
<b>Analysys</b>	
Type	END
W.Length 1	340
W.Length 2	700
Method	
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>		
Type	Logit.Log2	
<b>Standard</b>		
Blank 0	1 cal/16	
2 cal/8	3 cal/4	
4 cal/2	5 cal	
<b>Normal Range</b>		
	Low High	
Serum	Male	0 30
	Female	0 30
Urine (mg/24h)		

<b>Data Information</b>	
Unit	MG/DL
Decimals	2
<b>Analysys</b>	
Type	END
W.Length 1	340
W.Length 2	700
Method	UV
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>		
Type	LINEAR 1	
<b>Standard</b>		
Blank 0	1*	
2	3	
4	5	
<b>Normal Range</b>		
	Low High	
Serum	Male	2.6 4.5
	Female	2.6 4.5
Urine (mg/24h)		300 1000

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	5
Reagent 1	200
Reagent 2	50
Third Mix	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	75 76
Sub	34 35
Endpoint Limit 2	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	2
Reagent 1	200
Reagent 2	
Third Mix	Off <input type="checkbox"/> ON <input type="checkbox"/>
R1 Blank	Water <input type="checkbox"/> R1 - B <input type="checkbox"/>
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	32 33
Sub	
Endpoint Limit 3	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**MICRO ALBUMIN**

**PHOS**

<b>Data Information</b>	
Unit	IU/ML
Decimals	1
<b>Analysys</b>	
Type	END
W.Length 1	600
W.Length 2	
Method	UA
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>		
Type	SPLINE	
<b>Standard</b>		
Blank 0	1 Cal/16	
2 Cal/8	3 Cal/4	
4 Cal/2	5 CAL	
<b>Normal Range</b>		
	Low High	
Serum	Male	0 20
	Female	0 20
Urine (mg/24h)		

<b>Data Information</b>	
Unit	UG/DL
Decimals	0
<b>Analysys</b>	
Type	END
W.Length 1	660
W.Length 2	800
Method	DIRECT
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>		
Type	LINEAR 1	
<b>Standard</b>		
Blank 0	1*	
2	3	
4	5	
<b>Normal Range</b>		
	Low High	
Serum	Male	150 550
	Female	150 550
Urine (mg/24h)		

<b>Aspiration</b>	
Kind	Single <b>Double</b>
Volume	
Sample	4
Reagent 1	160
Reagent 2	40
Third Mix	Off ON
R1 Blank	Water R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	76 77
Sub	
Endpoint Limit 2	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

<b>Aspiration</b>	
Kind	Single <b>Double</b>
Volume	
Sample	20
Reagent 1	200
Reagent 2	60
Third Mix	Off ON
R1 Blank	Water R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	75 76
Sub	34 35
Endpoint Limit 3	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**RF**

**TIBC**

<b>Data Information</b>	
Unit	G/DL
Decimals	2
<b>Analysys</b>	
Type	END
W.Length 1	546
W.Length 2	700
Method	BIURET
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1*		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	6.6	8.8
	Female	6.6	8.8
Urine (mg/24h)			

<b>Data Information</b>	
Unit	MG/DL
Decimals	0
<b>Analysys</b>	
Type	END
W.Length 1	505
W.Length 2	660
Method	
<b>Corr</b>	
Slope	Inter
1.000 × +	0

<b>Calibration</b>			
Type	LINEAR 1		
<b>Standard</b>			
Blank 0	1*		
2	3		
4	5		
<b>Normal Range</b>			
	Low High		
Serum	Male	0	200
	Female	0	200
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	<input checked="" type="checkbox"/> Single <input type="checkbox"/> Double
Volume	
Sample	5
Reagent 1	200
Reagent 2	
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	32 33
Sub	
Endpoint Limit 3	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

<b>Aspiration</b>	
Kind	<input checked="" type="checkbox"/> Single <input type="checkbox"/> Double
Volume	
Sample	2
Reagent 1	200
Reagent 2	
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

<b>Data Process</b>	
Read	Low -0.1
	High 3.000
Main	75 76
Sub	
Endpoint Limit 3	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

TOTAL.PRO

TG

**Data Information**

Unit: MG/DL  
Decimals: 1

**Analysys**

Type: RATE  
W.Length 1: 340  
W.Length 2: 405  
Method: UV

**Corr**

Slope: Inter  
1.000 × +: 0

**Calibration**

Type: LINEAR 1

**Standard**

Blank 0	1 *
2	3
4	5

**Normal Range**

	Low	High
Serum Male	19	44
Serum Female	15	40
Urine (mg/24h)	26	43

**Data Information**

Unit: MG/DL  
Decimals: 2

**Analysys**

Type: END  
W.Length 1: 546  
W.Length 2: 700  
Method: PAP

**Corr**

Slope: Inter  
1.000 × +: 0

**Calibration**

Type: LINEAR 1

**Standard**

Blank 0	1 *
2	3
4	5

**Normal Range**

	Low	High
Serum Male	3.6	8.2
Serum Female	2.3	6.1
Urine (mg/24h)		

**Aspiration**

Kind:  Single  Double  
Volume: 2  
Sample: 2  
Reagent 1: 160  
Reagent 2: 40

Third Mix:  Off  ON  
R1 Blank:  Water  R1 - B

**Monitor**

0 level Point: 1  
Span: 3.000

**Data Process**

Read: Low -0.1, High 3.000

Main	41	53
Sub		

Endpoint Limit 3  
Linear Check (%)

**Factor**

Blank Correction: 1.000

**Prozone Check**

	Start	End	Limit
First			
Second			
Third			

**Aspiration**

Kind:  Single  Double  
Volume: 5  
Sample: 5  
Reagent 1: 100  
Reagent 2: 100

Third Mix:  Off  ON  
R1 Blank:  Water  R1 - B

**Monitor**

0 level Point: 1  
Span: 3.000

**Data Process**

Read: Low -0.1, High 3.000

Main	60	61
Sub		

Endpoint Limit 3  
Linear Check (%)

**Factor**

Blank Correction: 1.000

**Prozone Check**

	Start	End	Limit
First			
Second			
Third			

**UREA**

**URIC ACID**

**Data Information**

Unit: MG/L  
Decimals: 1

**Analysys**

Type: END  
W.Length 1: 505  
W.Length 2: 700  
Method: BENZYL CHLORIDE

**Corr**

Slope: Inter  
1.000 × +: 0

**Calibration**

Type: SPLINE

**Standard**

Blank 0	1	cal/16
2	cal/8	3 cal/4
4	cal/2	5 cal

**Normal Range**

	Low	High
Serum Male	0	15
Serum Female	0	15
Urine (mg/24h)		

**Data Information**

Unit: UG/DL  
Decimals: 0

**Analysys**

Type: END  
W.Length 1: 570  
W.Length 2: 700  
Method: LIA

**Corr**

Slope: Inter  
1.000 × +: 0

**Calibration**

Type: LINEAR 1

**Standard**

Blank 0	1*
2	3
4	5

**Normal Range**

	Low	High
Serum Male	76.2	127
Serum Female	77	114
Urine (mg/24h)		

**Aspiration**

Kind:  Single  Double  
Volume: \_\_\_\_\_  
Sample: 16  
Reagent 1: 160  
Reagent 2: 80

Third Mix:  Off  ON  
R1 Blank:  Water  R1 - B

**Monitor**

0 level Point: 1  
Span: 3.000

**Data Process**

Read: Low -0.1, High 3.000

Main	75	76
Sub	34	35

Endpoint Limit 2  
Linear Check (%)

**Factor**

Blank Correction: 1.000

**Prozone Check**

	Start	End	Limit
First			
Second			
Third			

**Aspiration**

Kind:  Single  Double  
Volume: \_\_\_\_\_  
Sample: 10  
Reagent 1: 200  
Reagent 2: \_\_\_\_\_

Third Mix:  Off  ON  
R1 Blank:  Water  R1 - B

**Monitor**

0 level Point: 1  
Span: 3.000

**Data Process**

Read: Low -0.1, High 3.000

Main	32	33
Sub		

Endpoint Limit 3  
Linear Check (%)

**Factor**

Blank Correction: 1.000

**Prozone Check**

	Start	End	Limit
First			
Second			
Third			

**URINE PROTEIN**

**ZINC**

<b>Data Information</b>		<b>Calibration</b>	
Unit	umol/l	Type	LINEAR 1
Decimals	1	<b>Standard</b>	
<b>Analysys</b>		Blank	* 1 *
Type	END	2	3
W.Length 1	505	4	5
W.Length 2	800	<b>Normal Range</b>	
Method	Enzymatic	Low	High
<b>Corr</b>		Serum	Male
Slope	Inter		
1.000 × +	0	Female	
		Urine (mg/24h)	

<b>Aspiration</b>	
Kind	<u>Single</u> Double
Volume	
Sample	12
Reagent 1	180
Reagent 2	
Third Mix	<u>Off</u> ON
R1 Blank	<u>Water</u> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

**HB**

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	34		
Sub			
Endpoint Limit 2		Linear Check (%)	
<b>Factor</b>		Blank Correction	
		1.000	
<b>Prozone Check</b>		Start	End
First			
Second			
Third			

<b>Data Information</b>		<b>Calibration</b>	
Unit	umol/l	Type	LINEAR 1
Decimals	1	<b>Standard</b>	
<b>Analysys</b>		Blank	* 1 *
Type	END	2	3
W.Length 1	660	4	5
W.Length 2	800	<b>Normal Range</b>	
Method	Enzymatic	Low	High
<b>Corr</b>		Serum	Male
Slope	Inter		
1.000 × +	0	Female	
		Urine (mg/24h)	

<b>Aspiration</b>	
Kind	Single <u>Double</u>
Volume	
Sample	12
Reagent 1	180
Reagent 2	60
Third Mix	<u>Off</u> ON
R1 Blank	<u>Water</u> R1 - B
<b>Monitor</b>	
0 level Point	1
Span	3.000

**A1C**

<b>Data Process</b>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	75	76	
Sub	34	35	
Endpoint Limit 3%		Linear Check (%)	
<b>Factor</b>		Blank Correction	
		1.000	
<b>Prozone Check</b>		Start	End
First			
Second			
Third			

Data Information		Calibration	
Unit	mg/L	Type	Logit.Log2
Decimals	0	<b>Standard</b>	
<b>Analysys</b>		Blank 0	1 cal/16
Type	RATE	2 cal/8	3 cal/4
W.Length 1	600	4 cal/2	5 cal
W.Length 2	-	<b>Normal Range</b>	
Method	LIA		
<b>Corr</b>			
Slope	Inter	Serum	Male
1.000 × +	0		Female
			Low
			High
		Urine (mg/24h)	
<b>Aspiration</b>		<b>Data Process</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>	Read	Low
Volume			-0.1
Sample	2	Start	End
Reagent 1	160	41	76
Reagent 2	40		
			High
			3.000
Third Mix	Off <input checked="" type="checkbox"/> ON <input type="checkbox"/>	Endpoint Limit 2	
R1 Blank	Water <input checked="" type="checkbox"/> R1 - B <input type="checkbox"/>	Linear Check (%)	
<b>Monitor</b>		<b>Abs Limit</b>	
0 level Point	1		
Span	3.000		
<b>CRP HL</b>		<b>Factor</b>	
		Blank Correction	1.000
		<b>Prozone Check</b>	
		Start	End
		Limit	
		First	
		Second	
		Third	