



**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	END	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	31	54	
Sub			
Endpoint Limit 2		Linear Check (%)	
<b>Factor</b>		Blank Correction	
Off		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	6
Reagent 1	200
Reagent 2	100
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	40	54	
Sub			
Endpoint Limit 3%		Linear Check (%)	
<b>Factor</b>		Blank Correction	
Off		1.000	
<b>Prozone Check</b>		Start End Limit	
First			
Second			
Third			

**ADA**

**Data Information**

Unit: G/DL  
Decimals: 2

**Analysys**

Type: END  
W.Length 1: 600  
W.Length 2: 700  
Method: BCG

**Corr**

Slope: Inter  
1.000 × +: 0

**Calibration**

Type: LINEAR 1

**Standard**

Blank 0	1 *
2	3
4	5

**Normal Range**

	Low	High
Serum Male	3.5	5
Serum Female	3.5	5
Urine (mg/24h)		

**Data Information**

Unit: U/L  
Decimals: 0

**Analysys**

Type: RATE  
W.Length 1: 405  
W.Length 2: 660  
Method: DGKC

**Corr**

Slope: Inter  
1.000 × +: 0

**Calibration**

Type: LINEAR 1

**Standard**

Blank 0	1 *
2	3
4	5

**Normal Range**

	Low	High
Serum Male	80	306
Serum Female	64	306
Urine (mg/24h)		

**Aspiration**

Kind:  Single  Double  
Volume: \_\_\_\_\_  
Sample: 3  
Reagent 1: 300  
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	21	22
Sub		

Endpoint Limit 3%  
Linear Check (%)

**Factor**

Blank Correction: 1.000

**Prozone Check**

	Start	End	Limit
First			
Second			
Third			

**Aspiration**

Kind:  Single  Double  
Volume: \_\_\_\_\_  
Sample: 5  
Reagent 1: 240  
Reagent 2: 60  
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	36	50
Sub		

Endpoint Limit 3%  
Linear Check (%)

**Factor**

Blank Correction: 1.000

**Prozone Check**

	Start	End	Limit
First			
Second			
Third			

**ALB**

**ALP**

<b>Data Information</b>	
Unit	U/L
Decimals	0
<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>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 checked="" type="checkbox"/> ON
R1 Blank	<input type="checkbox"/> Water <input checked="" 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	
	36	50	
Sub			
Endpoint Limi90			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start	End	Limit
First			
Second			
Third			

**ALT**

<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	6
Reagent 1	300
Reagent 2	
Third Mix	<input type="checkbox"/> Off <input checked="" type="checkbox"/> ON
R1 Blank	<input type="checkbox"/> Water <input checked="" 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	
	15	29	
Sub			
Endpoint Limit3			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start	End	Limit
First			
Second			
Third			

**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 44 End 45
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 36 End 50
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>	
Unit	MG/DL
Decimals	2
<b>Analysys</b>	
Type	END
W.Length 1	546
W.Length 2	700
Method	DMSO
<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	0.3
	Female	0	0.3
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	DMSO
<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	0.1	1.2
	Female	0.1	1.2
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	<input type="radio"/> Single <input checked="" type="radio"/> Double
Volume	
Sample	20
Reagent 1	160
Reagent 2	40
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>	
Read	Low -0.1
	High 3.000
Main	Start 53 End 54
Sub	Start 28 End 29
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="radio"/> Single <input checked="" type="radio"/> Double
Volume	
Sample	4.5
Reagent 1	160
Reagent 2	40
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>	
Read	Low -0.1
	High 3.000
Main	Start 53 End 54
Sub	Start 28 End 29
Endpoint Limit 3	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**BILI.D**

**BILI.T**

<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	90	180
	Female	90	180
Urine (mg/24h)			

<b>Data Information</b>	
Unit	MG/DL
Decimals	1
<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	10	40
	Female	10	40
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	3
Reagent 1	240
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	Start 53 End 54
Sub	Start 28 End 29
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	6
Reagent 1	240
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	Start 53 End 54
Sub	Start 28 End 29
Endpoint Limit 2	
Linear Check (%)	
<b>Factor</b>	
Blank Correction	1.000
<b>Prozone Check</b>	
	Start End Limit
First	
Second	
Third	

**C3**

**C4**

<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 type="radio"/> Single <input type="radio"/> Double
Volume	
Sample	3
Reagent 1	300
Reagent 2	
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>	
Read	Low -0.1
	High 3.000
Main	21 22
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="radio"/> Single <input type="radio"/> Double
Volume	
Sample	3
Reagent 1	300
Reagent 2	
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>	
Read	Low -0.1
	High 3.000
Main	53 54
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	10
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 40 End 54
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	24
Reagent 1	240
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	Start 40 End 54
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 checked="" type="checkbox"/> Single <input type="checkbox"/> Double
Volume	
Sample	15
Reagent 1	300
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 21 End 22
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	25
Reagent 1	150
Reagent 2	150
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 34 End 41
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	30	220
	Female	20	110
Urine (mg/24h)			

<b>Aspiration</b>	
Kind	Single <input type="checkbox"/> <b>Double</b> <input checked="" type="checkbox"/>
Volume	
Sample	3
Reagent 1	240
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	44 45
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	38 52
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>	
Read	Low -0.1
	High 3.000
Main	Start 40 End 54
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	3
Reagent 1	300
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 53 End 54
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	<b>Calibration</b>	
Decimals	1	Type	LINEAR 1
<b>Analysys</b>		<b>Standard</b>	
Type	END	Blank 0	1*
W.Length 1	600	2	3
W.Length 2	700	4	5
Method	DIRECT	<b>Normal Range</b>	
<b>Corr</b>			Low High
Slope	Inter	Serum Male	35 55
1.000 × +	0	Serum Female	45 65
<b>Aspiration</b>		Urine (mg/24h)	
Kind	<input checked="" type="checkbox"/> Single <input type="checkbox"/> Double	<b>Data Process</b>	
Volume	3	Read	Low -0.1
Reagent 1	240	Start End	High 3.000
Reagent 2	80	Main	53 54
Third Mix	<input checked="" type="checkbox"/> Off <input type="checkbox"/> ON	Sub	28 29
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B	Endpoint Limit 3	
<b>Monitor</b>		Linear Check (%)	
0 level Point	1	Factor	
Span	3.000	Blank Correction	1.000
<b>HDL</b>		<b>Prozone Check</b>	
		Start End Limit	
		First	
		Second	
		Third	

Unit	MG/DL	<b>Calibration</b>	
Decimals	0	Type	Logit.Log2
<b>Analysys</b>		<b>Standard</b>	
Type	END	Blank 0	1 cal/16
W.Length 1	600	2 cal/8	3 cal/4
W.Length 2	700	4 cal/2	5 cal
Method	LIA	<b>Normal Range</b>	
<b>Corr</b>			Low High
Slope	Inter	Serum Male	70 400
1.000 × +	0	Serum Female	70 400
<b>Aspiration</b>		Urine (mg/24h)	
Kind	<input checked="" type="checkbox"/> Single <input type="checkbox"/> Double	<b>Data Process</b>	
Volume	3	Read	Low -0.1
Reagent 1	240	Start End	High 3.000
Reagent 2	60	Main	53 54
Third Mix	<input checked="" type="checkbox"/> Off <input type="checkbox"/> ON	Sub	28 29
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B	Endpoint Limit 2	
<b>Monitor</b>		Linear Check (%)	
0 level Point	1	Factor	
Span	3.000	Blank Correction	1.000
<b>IGA</b>		<b>Prozone Check</b>	
		Start End Limit	
		First	
		Second	
		Third	

<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	3
Reagent 1	240
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	53 54
Sub	28 29
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	3
Reagent 1	240
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	53 54
Sub	28 29
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>	
Read	Low -0.1
	High 3.000
Main	Start 53 End 54
Sub	Start 28 End 29
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 type="checkbox"/>
Volume	
Sample	3
Reagent 1	300
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	Start 30 End 31
Sub	
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	6
Reagent 1	240
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>		<b>Abs Limit</b>	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	36	50	
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	3
Reagent 1	240
Reagent 2	80
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>		<b>Abs Limit</b>	
Read	Low	0.000	
	High	3.000	
Main	Start	End	
	53	54	
Sub	28	29	
Endpoint Limit 3			
Linear Check (%)			
<b>Factor</b>			
Blank Correction	1.000		
<b>Prozone Check</b>			
	Start	End	Limit
First			
Second			
Third			

**LDH**

**LDL**

<b>Data Information</b>	
Unit	U/L
Decimals	1
<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>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	36	45
Sub			
		Endpoint Limit 3	
		Linear Check (%)	
<b>Factor</b>			
Blank Correction		1.000	
<b>Prozone Check</b>			
	Start End Limit		
First			
Second			
Third			

**LIPASE**

<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	300
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	21	22
Sub			
		Endpoint Limit 3	
		Linear Check (%)	
<b>Factor</b>			
Blank Correction		1.000	
<b>Prozone Check</b>			
	Start End Limit		
First			
Second			
Third			

**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	6
Reagent 1	240
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>		<b>Abs Limit</b>	
Read		Low	-0.1
		High	3.000
Main	Start End	53	54
Sub	Start End	28	29
		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	3
Reagent 1	300
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>		<b>Abs Limit</b>	
Read		Low	-0.1
		High	3.000
Main	Start End	21	22
Sub	Start End		
		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
Serum 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
Serum Female	150 550
Urine (mg/24h)	

<b>Aspiration</b>	
Kind	Single <b>Double</b>
Volume	
Sample	5
Reagent 1	240
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	53 54
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	25
Reagent 1	250
Reagent 2	75
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	53 54
Sub	28 29
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	6
Reagent 1	240
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	21 22
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	3
Reagent 1	300
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	53 54
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: 3  
Sample: 240  
Reagent 1: 60  
Reagent 2: 60

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	34	41
Sub		

Endpoint Limit 3  
Linear Check (%)

**Factor**

Blank Correction: 1.000

**Prozone Check**

	Start	End	Limit
First			
Second			
Third			

**Aspiration**

Kind:  Single  Double  
Volume: 8  
Sample: 160  
Reagent 1: 160  
Reagent 2: 160

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	44	45
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	150
Serum Female	0	150
Urine (mg/24h)		

**Data Information**

Unit: UG/DL  
Decimals: 0

**Analysys**

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

**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: 20  
Reagent 1: 250  
Reagent 2: 125

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	53	54
Sub	28	29

Endpoint Limit 2  
Linear Check (%)

**Factor**

Blank Correction: 1.000

**Prozone Check**

	Start	End	Limit
First			
Second			
Third			

**Aspiration**

Kind:  Single  Double  
Volume:  
Sample: 15  
Reagent 1: 300  
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	21	22
Sub		

Endpoint Limit 3  
Linear Check (%)

**Factor**

Blank Correction: 1.000

**Prozone Check**

	Start	End	Limit
First			
Second			
Third			

**URINE PROTEIN**

**ZINC**