



شرکت دلتا درمان پارت
سیستم های آزمایشگاهی و مواد مصرفی

Prestige **24i**



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

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

Aspiration	
Kind	<input type="checkbox"/> Single <input checked="" type="checkbox"/> Double
Volume	
Sample	30
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
Monitor	
0 level Point	1
Span	3.000

ACE

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	32 52	
Sub	Start End		
Endpoint Limit 2			
Linear Check (%)			
Factor			
Blank Correction	1.000		
Prozone Check			
	Start End Limit		
First	Start End Limit		
Second	Start End Limit		
Third	Start End Limit		

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

Aspiration	
Kind	<input type="checkbox"/> Single <input checked="" type="checkbox"/> Double
Volume	
Sample	6
Reagent 1	200
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
Monitor	
0 level Point	1
Span	3.000

ADA

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	41 51	
Sub	Start End		
Endpoint Limit 3%			
Linear Check (%)			
Factor			
Blank Correction	1.000		
Prozone Check			
	Start End Limit		
First	Start End Limit		
Second	Start End Limit		
Third	Start End Limit		

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
	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
	Female	64	306
Urine (mg/24h)			

Aspiration	
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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 24 End 25
Sub	
Endpoint Limit 3%	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
Kind	<input type="checkbox"/> Single <input checked="" type="checkbox"/> Double
Volume	
Sample	5
Reagent 1	240
Reagent 2	60
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input checked="" 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	Start 36 End 48
Sub	
Endpoint Limit 3%	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

ALB

ALP

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

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

Aspiration	
Kind	Single <input type="checkbox"/> <u>Double</u> <input checked="" type="checkbox"/>
Volume	
Sample	30
Reagent 1	240
Reagent 2	60
Third Mix	<input type="checkbox"/> Off <input checked="" type="checkbox"/> ON
R1 Blank	<input type="checkbox"/> Water <input checked="" type="checkbox"/> R1 - B
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	36 48	
Sub	Start End		
Endpoint Limi90			
Linear Check (%)			
Factor			
Blank Correction		1.000	
Prozone Check			
	Start End Limit		
First	Start End Limit		
Second	Start End Limit		
Third	Start End Limit		

ALT

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

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

Aspiration	
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
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	18 30	
Sub	Start End		
Endpoint Limit3			
Linear Check (%)			
Factor			
Blank Correction		1.000	
Prozone Check			
	Start End Limit		
First	Start End Limit		
Second	Start End Limit		
Third	Start End Limit		

AMY

Data Information	
Unit	IU/ML
Decimals	0
Analysys	
Type	END
W.Length 1	600
W.Length 2	
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	0	200
	Female	0	200
Urine (mg/24h)			

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

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

Aspiration	
Kind	Single <input type="checkbox"/> Double <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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 43 End 44
Sub	
Endpoint Limit 2	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
Kind	Single <input type="checkbox"/> Double <input checked="" type="checkbox"/>
Volume	
Sample	30
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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 36 End 48
Sub	
Endpoint Limit	
Linear Check (90%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

ASO

AST

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

Calibration			
Type	LINEAR 1		
Standard			
Blank 0	1*		
2	3		
4	5		
Normal Range			
	Low High		
Serum	Male	0	0.3
	Female	0	0.3
Urine (mg/24h)			

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

Calibration			
Type	LINEAR 1		
Standard			
Blank 0	1*		
2	3		
4	5		
Normal Range			
	Low High		
Serum	Male	0.1	1.2
	Female	0.1	1.2
Urine (mg/24h)			

Aspiration	
Kind	<input type="radio"/> Single <input checked="" type="radio"/> Double
Volume	
Sample	30
Reagent 1	240
Reagent 2	60
Third Mix	<input type="radio"/> Off <input type="radio"/> ON
R1 Blank	<input type="radio"/> Water <input type="radio"/> R1 - B
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	51	52
Sub	Start End	29	30
		Endpoint Limit 2	
		Linear Check (%)	
Factor			
Blank Correction	1.000		
Prozone Check			
	Start End Limit		
First			
Second			
Third			

Aspiration	
Kind	<input type="radio"/> Single <input checked="" type="radio"/> Double
Volume	
Sample	7
Reagent 1	240
Reagent 2	60
Third Mix	<input type="radio"/> Off <input type="radio"/> ON
R1 Blank	<input type="radio"/> Water <input type="radio"/> R1 - B
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	51	52
Sub	Start End	29	30
		Endpoint Limit 3	
		Linear Check (%)	
Factor			
Blank Correction	1.000		
Prozone Check			
	Start End Limit		
First			
Second			
Third			

BILI.D

BILI.T

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

Calibration			
Type	Logit.Log2		
Standard			
Blank 0	1 cal/16		
2 cal/8	3 cal/4		
4 cal/2	5 cal		
Normal Range			
	Low High		
Serum	Male	90	180
	Female	90	180
Urine (mg/24h)			

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

Calibration			
Type	Logit.Log2		
Standard			
Blank 0	1 cal/16		
2 cal/8	3 cal/4		
4 cal/2	5 cal		
Normal Range			
	Low High		
Serum	Male	10	40
	Female	10	40
Urine (mg/24h)			

Aspiration	
Kind	Single <input type="checkbox"/> Double <input checked="" type="checkbox"/>
Volume	
Sample	3
Reagent 1	240
Reagent 2	60
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input checked="" 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	Start 51 End 52
Sub	Start 29 End 30
Endpoint Limit 2	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
Kind	Single <input type="checkbox"/> Double <input checked="" type="checkbox"/>
Volume	
Sample	6
Reagent 1	240
Reagent 2	60
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON
R1 Blank	<input checked="" 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	Start 51 End 52
Sub	Start 29 End 30
Endpoint Limit 2	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

C3

C4

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

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

Data Information	
Unit	MG/DL
Decimals	0
Analysys	
Type	END
W.Length 1	505
W.Length 2	660
Method	CHOD-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	0	200
	Female	0	200
Urine (mg/24h)			

Aspiration	
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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 24 End 25
Sub	
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 51 End 52
Sub	
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

CA

CHOL

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

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

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

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

Aspiration	
Kind	Single <input type="checkbox"/> Double <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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 40 End 52
Sub	
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
Kind	Single <input type="checkbox"/> Double <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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 40 End 52
Sub	
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

CK NAC

CK-MB

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	70	140
	Female	80	155
Urine (mg/24h)			

Aspiration	
Kind	<input type="checkbox"/> Single <input checked="" type="checkbox"/> Double
Volume	
Sample	15
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
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	24	25
Sub			
Endpoint Limit 2			
Linear Check (%)			
Factor			
Blank Correction		1.000	
Prozone Check			
	Start End Limit		
First			
Second			
Third			

COPPER

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

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

Aspiration	
Kind	<input type="checkbox"/> Single <input checked="" type="checkbox"/> Double
Volume	
Sample	30
Reagent 1	150
Reagent 2	150
Third Mix	<input type="checkbox"/> Off <input checked="" type="checkbox"/> ON
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	34	40
Sub			
Endpoint Limit 3			
Linear Check (%)			
Factor			
Blank Correction		1.000	
Prozone Check			
	Start End Limit		
First			
Second			
Third			

CREATININE JAFFE

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

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

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

Calibration			
Type	Logit.Log2		
Standard			
Blank 0	1 cal/16		
2 cal/8	3 cal/4		
4 cal/2	5 cal		
Normal Range			
	Low High		
Serum	Male	30	220
	Female	20	110
Urine (mg/24h)			

Aspiration	
Kind	Single <input type="checkbox"/> Double <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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	43 44
Sub	
Endpoint Limit 2	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
Kind	Single <input type="checkbox"/> Double <input checked="" type="checkbox"/>
Volume	
Sample	8
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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	38 54
Sub	
Endpoint Limit 2	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

CRP

FERRITIN

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

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

Data Information	
Unit	MG/DL
Decimals	0
Analysys	
Type	END
W.Length 1	505
W.Length 2	660
Method	GOD-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	70	115
	Female	70	115
Urine (mg/24h)			

Aspiration	
Kind	<input checked="" type="checkbox"/> Single <input type="checkbox"/> Double
Volume	
Sample	30
Reagent 1	240
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	Start 40 End 52
Sub	
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 51 End 52
Sub	
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

GGT

GLU

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

Calibration			
Type	LINEAR 1		
Standard			
Blank 0	1*		
2	3		
4	5		
Normal Range			
	Low High		
Serum	Male	35	55
	Female	45	65
Urine (mg/24h)			

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

Calibration			
Type	Logit.Log2		
Standard			
Blank 0	1 cal/16		
2 cal/8	3 cal/4		
4 cal/2	5 cal		
Normal Range			
	Low High		
Serum	Male	70	400
	Female	70	400
Urine (mg/24h)			

Aspiration	
Kind	<input type="radio"/> Single <input type="radio"/> Double
Volume	3
Reagent 1	240
Reagent 2	80
Third Mix	<input type="radio"/> Off <input type="radio"/> ON
R1 Blank	<input type="radio"/> Water <input type="radio"/> R1 - B
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start End
	51 52
Sub	29 30
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
Kind	<input type="radio"/> Single <input type="radio"/> Double
Volume	3
Sample	3
Reagent 1	240
Reagent 2	60
Third Mix	<input type="radio"/> Off <input type="radio"/> ON
R1 Blank	<input type="radio"/> Water <input type="radio"/> R1 - B
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start End
	51 52
Sub	29 30
Endpoint Limit 2	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

HDL

IGA

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

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

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

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

Aspiration	
Kind	Single <input type="checkbox"/> Double <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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	51 52
Sub	29 30
Endpoint Limit 2	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
Kind	Single <input type="checkbox"/> Double <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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	51 52
Sub	29 30
Endpoint Limit 2	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

IGG

IGM

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

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

Data Information	
Unit	MG/L
Decimals	0
Analysys	
Type	END
W.Length 1	505
W.Length 2	660
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	4.5	19.8
	Female	4.5	19.8
Urine (mg/24h)			

Aspiration	
Kind	Single <input type="checkbox"/> Double <input checked="" type="checkbox"/>
Volume	
Sample	30
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"/>
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 51 End 52
Sub	Start 29 End 30
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
Kind	Single <input type="checkbox"/> Double <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"/>
Monitor	
0 level Point	1
Span	3.000

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

IRON

LAC

Data Information	
Unit	U/L
Decimals	0
Analysys	
Type	RATE
W.Length 1	340
W.Length 2	405
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	0	530
	Female	0	530
Urine (mg/24h)			

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

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

Aspiration	
Kind	Single <input type="checkbox"/> Double <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
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	36	48	
Sub			
Endpoint Limit 2			
Linear Check (%)			
Factor			
Blank Correction	1.000		
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

Aspiration	
Kind	Single <input type="checkbox"/> Double <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
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read	Low	0.000	
	High	3.000	
Main	Start	End	
	51	52	
Sub	29	30	
Endpoint Limit 3			
Linear Check (%)			
Factor			
Blank Correction	1.000		
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

LDH

LDL

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

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

Aspiration	
Kind	Single <input type="checkbox"/> Double <input checked="" type="checkbox"/>
Volume	
Sample	3
Reagent 1	250
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
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read		Low	-0.1
		High	3.000
Main	Start End	36	44
Sub			
		Endpoint Limit 3	
		Linear Check (%)	
Factor			
Blank Correction		1.000	
Prozone Check			
	Start End Limit		
First			
Second			
Third			

LIPASE

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

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

Aspiration	
Kind	Single <input type="checkbox"/> Double <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
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read		Low	-0.1
		High	3.000
Main	Start End	24	25
Sub			
		Endpoint Limit 3	
		Linear Check (%)	
Factor			
Blank Correction		1.000	
Prozone Check			
	Start End Limit		
First			
Second			
Third			

MG

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

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

Data Information	
Unit	MG/DL
Decimals	2
Analysys	
Type	END
W.Length 1	340
W.Length 2	700
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	2.6 4.5
	Female	2.6 4.5
Urine (mg/24h)		300 1000

Aspiration	
Kind	Single <input type="checkbox"/> Double <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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	51 52
Sub	29 30
Endpoint Limit 2	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
Kind	Single <input type="checkbox"/> Double <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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	24 25
Sub	
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

MICRO ALBUMIN

PHOS

Data Information	
Unit	IU/ML
Decimals	1
Analysys	
Type	END
W.Length 1	600
W.Length 2	
Method	UA
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 20
Serum Female	0 20
Urine (mg/24h)	

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

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

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	51 52
Sub	
Endpoint Limit 2	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
Kind	Single Double
Volume	
Sample	25
Reagent 1	250
Reagent 2	75
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	51 52
Sub	29 30
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

RF

TIBC

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

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

Data Information	
Unit	MG/DL
Decimals	0
Analysys	
Type	END
W.Length 1	505
W.Length 2	660
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	0	200
	Female	0	200
Urine (mg/24h)			

Aspiration	
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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 24 End 25
Sub	
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

Aspiration	
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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 51 End 52
Sub	
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	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	40
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	43	44
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	51	52
Sub	29	30

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	24	25
Sub		

Endpoint Limit 3
Linear Check (%)

Factor

Blank Correction: 1.000

Prozone Check

	Start	End	Limit
First			
Second			
Third			

URINE PROTEIN

ZINC