



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

ایمیل info@delta dp.ir
وب سایت: www.delta dp.ir

Data Information		Calibration	
Unit	U/l	Type	LINEAR 1
Decimals	0	Standard	
Analysys		Blank 0	1 *
Type	END	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	<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
Monitor	
0 level Point	1
Span	3.000

ACE

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	31	54
Sub			
Factor		Endpoint Limit 2	
Blank Correction		Linear Check (%)	
		1.000	
Prozone Check			
	Start End Limit		
First			
Second			
Third			

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	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
Monitor	
0 level Point	1
Span	3.000

ADA

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	40	54
Sub			
Factor		Endpoint Limit 3%	
Blank Correction		Linear Check (%)	
		1.000	
Prozone Check			
	Start End Limit		
First			
Second			
Third			

Data Information		Calibration	
Unit	G/DL	Type	LINEAR 1
Decimals	2	Standard	
Analysys		Blank 0	1 *
Type	END	2	3
W.Length 1	600	4	5
W.Length 2	700	Normal Range	
Method	BCG		
Corr			
Slope	Inter		
1.000 × +	0		

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

ALB

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
Sub	21	22	
Factor		Endpoint Limit 3%	
Blank Correction		Linear Check (%)	
		1.000	
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

Data Information		Calibration	
Unit	U/L	Type	LINEAR 1
Decimals	0	Standard	
Analysys		Blank 0	1 *
Type	RATE	2	3
W.Length 1	405	4	5
W.Length 2	660	Normal Range	
Method	DGKC		
Corr			
Slope	Inter		
1.000 × +	0		

Aspiration		Data Process		Abs Limit	
Kind	<input type="checkbox"/> Single <input checked="" type="checkbox"/> Double	Read	Low	-0.1	
Volume			High	3.000	
Sample	5	Main	Start	End	
Reagent 1	240	Sub	36	50	
Reagent 2	60	Factor		Endpoint Limit 3%	
Third Mix	<input type="checkbox"/> Off <input type="checkbox"/> ON	Blank Correction		Linear Check (%)	
R1 Blank	<input checked="" type="checkbox"/> Water <input type="checkbox"/> R1 - B			1.000	
Monitor		Prozone Check			
0 level Point	1		Start	End	Limit
Span	3.000	First			
		Second			
		Third			

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)			

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	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
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	36	50	
Sub			
Endpoint Limi90			
Linear Check (%)			
Factor			
Blank Correction	1.000		
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

Aspiration	
Kind	<u>Single</u> <input checked="" type="checkbox"/> Double <input 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	
	15	29	
Sub			
Endpoint Limit3			
Linear Check (%)			
Factor			
Blank Correction	1.000		
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

ALT

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)			

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		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	44	45
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		

ASO

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	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
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start End	36	50
Sub	Start End		
Endpoint Limit			
Linear Check (90%)			
Factor			
Blank Correction		1.000	
Prozone Check			
	Start End Limit		
First	Start End Limit		
Second	Start End Limit		
Third	Start End Limit		

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	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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 53 End 54
Sub	Start 28 End 29
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	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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start 53 End 54
Sub	Start 28 End 29
Endpoint Limit 3	
Linear Check (%)	
Factor	
Blank Correction	1.000
Prozone Check	
	Start End Limit
First	
Second	
Third	

BILI.D

BILI.T

Data Information		Calibration	
Unit	MG/DL	Type	Logit.Log2
Decimals	0	Standard	
Analysys		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	Normal Range	
Method	LIA	Low	High
Corr		Serum	Male
Slope	Inter		90 180
1.000 × +	0		Female
			90 180
		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	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

C3

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	53	54	
Sub	28	29	
Factor		Endpoint Limit 2	
Blank Correction		Linear Check (%)	
1.000			
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

Data Information		Calibration	
Unit	MG/DL	Type	Logit.Log2
Decimals	1	Standard	
Analysys		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	Normal Range	
Method	LIA	Low	High
Corr		Serum	Male
Slope	Inter		10 40
1.000 × +	0		Female
			10 40
		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	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

C4

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	53	54	
Sub	28	29	
Factor		Endpoint Limit 2	
Blank Correction		Linear Check (%)	
1.000			
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

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 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
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	<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
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	53 54
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 54
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 54
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)			

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	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	
Read	Low -0.1
	High 3.000
Main	21 22
Sub	
Endpoint Limit 2	
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	25
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	
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	

COPPER

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	20 250
	Female	20 110
Urine (mg/24h)		

Aspiration	
Kind	Single Double
Volume	
Sample	3
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	44 45
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	15
Reagent 1	180
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	38 52
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	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
Monitor	
0 level Point	1
Span	3.000

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
	Start	End	
Main	40	54	
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		Abs Limit	
Read	Low	-0.1	
	High	3.000	
	Start	End	
Main	53	54	
Sub			
Endpoint Limit 3			
Linear Check (%)			
Factor			
Blank Correction	1.000		
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

GGT

GLU

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

Aspiration	
Kind	<input type="checkbox"/> Single <input type="checkbox"/> Double
Volume	3
Reagent 1	240
Reagent 2	80
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		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	53	54	
Sub	28	29	
Factor		Endpoint Limit 3	
Blank Correction		Linear Check (%)	
1.000			
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

HDL

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

Aspiration	
Kind	<input type="checkbox"/> Single <input type="checkbox"/> Double
Volume	3
Sample	240
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		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	53	54	
Sub	28	29	
Factor		Endpoint Limit 2	
Blank Correction		Linear Check (%)	
1.000			
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

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	2
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	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 <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	53 54
Sub	28 29
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	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"/>
Monitor	
0 level Point	1
Span	3.000

Data Process	
Read	Low -0.1
	High 3.000
Main	Start End 53 54
Sub	28 29
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 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 End 30 31
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	
Read	Low -0.1
	High 3.000
Main	Start 36 End 50
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	
Read	Low 0.000
	High 3.000
Main	Start 53 End 54
Sub	28 29
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)			

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	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	45	
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	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	
	21	22	
Sub			
Endpoint Limit 3			
Linear Check (%)			
Factor			
Blank Correction	1.000		
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

LIPASE

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
Serum 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
Serum 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	Start 53 End 54
Sub	Start 28 End 29
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	Start 21 End 22
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	6
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	Start End 53 54
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	Start End 53 54
Sub	28 29
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	21 22
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	53 54
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	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/DL**

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:

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

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

Aspiration	
Kind	<u>Single</u> Double
Volume	
Sample	14
Reagent 1	210
Reagent 2	
Third Mix	<u>Off</u> ON
R1 Blank	<u>Water</u> R1 - B
Monitor	
0 level Point	1
Span	3.000

HB

Data Process		Abs Limit	
Read	Low	-0.1	
	High	3.000	
Main	Start	End	
	28	29	
Sub			
Endpoint Limit 2			
Linear Check (%)			
Factor			
Blank Correction	1.000		
Prozone Check			
	Start	End	Limit
First			
Second			
Third			

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

Aspiration		Data Process		Abs Limit	
Kind	Single <u>Double</u>	Read	Low	-0.1	
Volume			High	3.000	
Sample	14	Main	Start	End	
Reagent 1	210		53	54	
Reagent 2	70	Sub	28	29	
Third Mix	<u>Off</u> ON	Endpoint Limit 3%			
R1 Blank	<u>Water</u> R1 - B	Linear Check (%)			
Monitor		Factor			
0 level Point	1	Blank Correction	1.000		
Span	3.000	Prozone Check			
			Start	End	Limit
		First			
		Second			
		Third			

A1C

Data Information		Calibration												
Unit	mg/L	Type	Spline											
Decimals	0	Standard												
Analysys		<table border="1"> <tr> <td>Blank 0</td> <td>1 cal 1</td> </tr> <tr> <td>2 cal 2</td> <td>3 cal 3</td> </tr> <tr> <td>4 cal 4</td> <td>5 cal 5</td> </tr> </table>		Blank 0	1 cal 1	2 cal 2	3 cal 3	4 cal 4	5 cal 5					
Blank 0	1 cal 1													
2 cal 2	3 cal 3													
4 cal 4	5 cal 5													
Type	RATE	Normal Range												
W.Length 1	600	<table border="1"> <tr> <td></td> <td>Low</td> <td>High</td> </tr> <tr> <td rowspan="2">Serum</td> <td>Male</td> <td>0 6</td> </tr> <tr> <td>Female</td> <td>0 6</td> </tr> <tr> <td>Urine (mg/24h)</td> <td></td> <td></td> </tr> </table>			Low	High	Serum	Male	0 6	Female	0 6	Urine (mg/24h)		
	Low	High												
Serum	Male	0 6												
	Female	0 6												
Urine (mg/24h)														
W.Length 2														
Method														
Corr														
Slope	Inter													
1.000 × +	0													
Aspiration		Data Process												
Kind	Single <input type="checkbox"/> Double <input checked="" type="checkbox"/>	Read	Low -0.1											
Volume		Start End High	3.000											
Sample	3	Main	38 52											
Reagent 1	240	Sub												
Reagent 2	60	Endpoint Limit 2												
Third Mix	Off <input type="checkbox"/> ON <input type="checkbox"/>	Linear Check (%)												
R1 Blank	Water <input checked="" type="checkbox"/> R1 - B <input type="checkbox"/>	Factor												
Monitor		Blank Correction												
0 level Point	1	1.000												
Span	3.000	Prozone Check												
CRP HL		First	Start End Limit											
		Second												
		Third												