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3diag - IgD - TIA

REF TD-42561 - IgD Immunoglobulins - for Turbidimetry

ANNEX to IFU: *ADVIA® 1800 System*

Proposal of Application - using 3diag - IgD - CAL SET (REF TD-42642)

NOTE: Grey text indicates default values.
If you are entering the parameters in an empty or restarted method (thus with default values), then you can enter only the values highlighted in red and bold, and leave the others at their default value.

Analytical conditions

Analy.Cond.no.	**User Defined**		
R1 volume	**100**	R2 volume	**40**
R1 diluent vol	0.0	R2 diluent vol	0.0
Serum reac.s.vol	**3** (Dil. Factor = 1:10)	Serum dil.method	**Special**
Serum dil.s.vol	**12**	Serum dil.volume	**108**
Serum dil.posit.	**0**	Reaction Time	**10 min.**
Reagent 1 stir	**Weak**	Reagent 2 stir	**Weak**

For **Urine set** analytical conditions leave default settings.

Sub-analyt.conditions #1 (#2 and #3 not defined)

Name	**User Defined**	Digits	**1** (Recommended)
SI/Common	**Common**	Unit	**mg/dl**
M-wave.L.	**694 nm**	S-wave.L.	*******
Analy.mthd	**EPA**	Calc.mthd	**MSTD**
Qualit.judge	Not do		

For **Qualit.set** sub-analytical conditions leave default settings.

For **Real-time correct.form.** sub-analytical conditions leave default settings.

Reanalysis conditions

Serum reac.smp.vol (u)	**3** (Dil. Factor = 1:80 = 1:10 + 1:8)	Serum dilut.method (u)	**Special**
Serum dil.smp.vol (u)	**15**	Serum diluent vol (u)	**105**
Serum diluent posi (u)	**0**	Serum reac.smp.vol (d)	3 (Not Used)
Serum dilut.method (d)	None	Serum dil.smp.vol (d)	0
Serum diluent vol (d)	0	Serum diluent posi (d)	0

For **Urine set** reanalysis conditions leave default settings.

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Rerun.cond. - Reanalysis Conditions Set screen

In order to procede to an authomatic reanalysIs of samples with a concentration higher than the upper limit of the assay range, it is proposed to define the following condition:

Abnormal v.limit (H)	**A mark exist. To be rerun. (U condition)**

In order to not activate the rest of conditions, they can be defined as:

other conditions	**A mark exist. No rerun**

NOTE: These reanalysis conditions have value only as a proposal, the user should define their own conditions.

Standards setting

FV	1		
Abnml (serum) H	**enter the value of the highest calibrator, multiplied by 2**		
Abnml (serum) L	-999999		
Abnml (urine) H	999999	Abnml (urine) L	-999999

For **One-Point Cal Setting** standards setting leave default settings.

For **RBL Setting** standards setting leave default settings.

For **Normal value set** standards setting, the user can leave default settings or define their own ones.

Multipoint Cal Setting - Multi-Standards Set screen

Formula	**Logit Log 3**	Axis conv.	No convert.
Points	**6**	Curve Type	Increasing
Blank	**Blank is zero (use Saline as Blank calibrator, discard Level #1 of the Calibrator Set)**		
FV - BLK	0		
FV - 1 to 5	**Enter the concentrations of the Levels #2 to #6 of the Calibrator Set, multiplied by 2 (Level #1 has to be discarded)**		
Dilution Method - BLK	**Standard**	Dilution Method - 1 to 5	**Standard**
Dil.smp.volume - BLK	30	Dil.smp.volume - 1 to 5	30
Diluent Volume - BLK	120	Diluent Volume - 1 to 5	120
Diluent position - BLK	0	Diluent position - 1 to 5	0
Max Fit Deviation - BLK	99999.99	Max Fit Dev. - 1 to 5	99999.99
Max. Rep Deviat - BLK	9.9999	Max. Rep Deviat - 1 to 5	9.9999
Min. No Rep	**1**		
Min. Abs Delta Lhi-Llow	0.0000	Max. RMS of Fit	99999999.00

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Calculation Method Setting

M-DET.P.l	0		
M-DET.P.m	**97**	M-DET.P.n	**98**
S-DET.P.p	**50**	S-DET.P.r	**51**
Reac.type	Inc.	Max. Limit	2.5000
Check D.P.I	0	Limit value	0.003
Variance	10.0		

Prozone

Prozone form	None	Prozone limit	9.999
Prozone judge	Upper limit	Judge limit	9.999
P-DET.P.m	0	DET.E.P.p	0
P-DET.P.n	0	DET.E.P.r	0

Reaction Rate method

Cycle	3	Factor	3.0
E2 corre	Not do	Blank (u)	9.9999
Blank (d)	-9.999	Sample (u)	9.9999
Sample (d)	-9.999		

Endpoint method

Re.absorb (u)	9.9999	Re.absorb (d)	-9.999

For **IMA setting** calculation method setting leave default settings.