

3diag - C5 - TIA

REF TD-42571 - C5 Complement - for Turbidimetry

ANNEX to IFU: ADVIA® 1800 System

Proposal of Application - using 3diag - C5 - CAL SET (REF TD-42562)

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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	70	R2 volume	30
R1 diluent vol	0.0	R2 diluent vol	0.0
Serum reac.s.vol	10 (Dil. Factor = 1:5)	Serum dil.method	Standard
Serum dil.s.vol	30	Serum dil.volume	120
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	2 (Recommended)
SI/Common	Common	Unit	mg/dl
M-wave.L.	340 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)	10 (Dil. Factor = 1:20 = 1:5 + 1:4)	Serum dilut.method (u)	Special
Serum dil.smp.vol (u)	30	Serum diluent vol (u)	90
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 proceed to an automatic 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		
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)		
FV - BLK	0		
FV - 1 to 5	Enter the concentrations of the Levels #2 to #6 of the Calibrator Set (discard Level #1)		
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.l	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
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For **IMA setting** calculation method setting leave default settings.