

quantex C3



### Kit Configuration

P/N 3000-2308 1 x 60 mL C3 R1  
4 x 12 mL C3 R2

### Reagent Preparation

P/N 3000-2308 C3 R1: Ready to use  
C3 R2: Ready to use.  
Place the bottles into reagent tray.

### In Use Stability

For optimal stability remove reagents from the system and store them at 2-8°C in the original vial securely closed.

### Specimen

Serum.

### Calibration

Use quantex Proteins standard multipoint Cat. No 300-2121. See calibrator chart for lot specific concentrations. Recalibrate every 90 days or when a new lot of reagent is used.

### Quality Control

Use quantex Proteins Control I/II Cat. No. 3000-2122.

### Calculation of Analytical Results

The results concentration is automatically calculated by the instrument against the Calibration curve. For detailed description, refer to the Instrument settings and to the ILab 350 Operator Manual.

### Reference Interval

Concentrations of C3 between 90 and 180 mg/dL (0.9 - 1.8 g/L) are considered normal.

### References / Literatur / Bibliografia / Bibliographie / Bibliografía /

See package insert enclosed in the kit

## Performance Characteristics

### Limitation/Interfering Substances

No significant interference from lipemia up to sample absorbance of 4.9/cm at 660 nm, triglycerides up to concentrations of 640 mg/dL, bilirubin up to concentrations of 38 mg/dL (646 µmol/L) and hemoglobin up to concentrations of 500 mg/dL (0.3 mmol/L). For a comprehensive review of interfering substances, refer to the publication by Young *et al.*<sup>1</sup>

### Precision

	Samples/Runs	Mean (mg/dL)	CV(%)	Mean (mg/dL)	CV(%)
Within run	4/10	84.5	4.7	222.5	2.0
Total	4/10	84.5	4.9	222.5	3.0

### Method Comparison

Comparison Method (x)	same reagent
Comparison Instrument (x)	Nephelometer (Behring, BN II)
Slope	0.965
y intercept	0.109
Mean X (mg/dL)	1.307
Mean Y (mg/dL)	1.371
r	0.94
n	100

### Linearity

no rerun 62 - 490 mg/dL ; with rerun 62 - 3920 mg/dL

### Minimum Detection Limit

4.6 mg/dL

### Quantification Limit

62 mg/dL



### Instrument Settings

<b>Chemistry Parameters</b>				<b>R1</b>			
Method	<input type="text"/>	Reagent Name	<input type="text" value="C3/C4"/>	Volume	<input type="text" value="190 μL"/>		
Name	<input type="text" value="C3"/>	R2	<input type="text" value="enable"/>	Volume	<input type="text" value="190 μL"/>		
Unit	<input type="text" value="mg/dL"/>	Reagent Name	<input type="text" value="C3"/>	Volume	<input type="text" value="190 μL"/>		
Assay Type	<input type="text" value="End"/>	Wash	<input type="text" value="disable"/>	Reagent Name	<input type="text"/>		
		Diluent	<input type="text" value="enable"/>	Reagent Type	<input type="text"/>		
		Reagent Name	<input type="text" value="Saline"/>				
Measuring Points	1 enable	start	<input type="text" value="12"/>	Decimal Points	<input type="text" value="0"/>		
		end	<input type="text" value="13"/>	Normal Range	<input type="text" value="90"/>	<input type="text" value="180"/>	
	2 enable	start	<input type="text" value="25"/>				
		end	<input type="text" value="26"/>				
Wave Length				Technical Range (Conc)	<input type="text" value="0.0"/>	<input type="text" value="490"/>	
Prim	<input type="text" value="340"/>	Sec	<input type="text"/>	mAbs/10	<input type="text" value="-30000 / 30000"/>		
Sampling Volume	<input type="text" value="3 μL"/>			RPT Wash (R1)	<input type="text" value="Sys Water"/>		
Dilution	<input type="text" value="disable"/>			(R2)	<input type="text" value="Sys Water"/>		
Rerun ( High)	<input type="text" value="3 μL"/>			Instrument Factor a	<input type="text" value="1"/>	b	<input type="text" value="0"/>
Dilution	<input type="text" value="enable"/>			Stirring Speed	R1 <input type="text" value="high"/>	R2	<input type="text" value="high"/>
Rerun ( Low)	<input type="text" value="20 μL"/>		<input type="text" value="140 μL"/>				
	<input type="text" value="9 μL"/>						

### Calibration Checks

** Duplicate Limit	<input type="text"/>	** mAbs/10	<b>Sampling Method for Standards</b>	
** Sensitivity Limit	<input type="text"/>	** mAbs/10	<input checked="" type="checkbox"/> Duplicate	
			<input type="checkbox"/> Triplicate	
** Linearity Limit	<input type="text"/>	** %	<b>Blank measurement</b>	
** Prozone Limit	<input type="text"/>	** upper	<input checked="" type="checkbox"/> Enable Reagent blank	
SL1-S	<input type="text"/>	** SL1-F **	<input type="text" value="None"/>	
SL2-S	<input type="text"/>	** SL2-F **	<b>Reagent blank measurement at calibration</b>	
Sens	<input type="text"/>	** mAbs/10	<input checked="" type="checkbox"/> Reagent blank (system water)	
<input checked="" type="checkbox"/> Absorbance Limit			<b>Multiplex measurement is the same as standards</b>	
Reaction	<input type="text" value="Increase"/>		<b>Reagent Blank Limit Checks</b>	
Limit	<input type="text" value="25000"/>	mAbs/10	** Duplicate limit	<input type="text" value="50"/> mAbs/10

### Calibration

Method	<input type="text"/>	Name	<input type="text" value="C3"/>	Interval	<input type="text" value="90"/> days
Calculation	<input type="text" value="Point to Point"/>				
	Conc	WORK	MASTER	Lot No	
S1	<input type="text" value="0"/>	<input type="text" value="-10"/>			K <input type="text" value="N/A"/>
S2	<input type="text" value="49"/>	<input type="text" value="1200"/>			
S3	<input type="text" value="122"/>	<input type="text" value="3511"/>			
S4	<input type="text" value="245"/>	<input type="text" value="6351"/>			
S5	<input type="text" value="367"/>	<input type="text" value="8676"/>			
S6	<input type="text" value="489"/>	<input type="text" value="10782"/>			

### Reagent Registration

Reagent Code	<input type="text" value="7778"/>	<input type="text" value="0177"/>			
Reagent Name	<input type="text" value="C3/C4"/>	<input type="text" value="C3"/>			
	Volume (L)		Volume (S)	Stability Check	Term
R1	<input checked="" type="checkbox"/> enable	<input type="text"/>	mL	<input checked="" type="checkbox"/> enable	<input type="text"/>
R2	<input checked="" type="checkbox"/> enable	<input type="text"/>	mL	<input checked="" type="checkbox"/> enable	<input type="text"/>
**	Operator definable	N/A	not applicable to this test	Calibration curve is only as example	