

quantex B-2-MICROGLOBULIN (B2M)



Kit Configuration

P/N 3000-2307	1 x 40 mL β_2 m R1
	4 x 3 mL β_2 m R2

Reagent Preparation

P/N 3000-2307	β_2 m R1: Ready to use
	β_2 m 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 β_2 -microglobulin standard Cat. No 300-2192. See vial label for lot specific concentration. A reagent blank should be run daily before sample analysis. Recalibrate every 37 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

Serum β_2 m concentrations have been reported to be independent of body mass and sex but to be slightly increased in elderly persons. In the serum or plasma of apparently healthy persons the normal range is approximately 0.97 to 2.64 mg/L by a RIA technique. Concentrations of β_2 m in urine from healthy subjects averaged 0.098 mg/L with an upper normal limit of 0.32 mg/L.

References / Literatur / Bibliografia / Bibliographie / Bibliografía /

See package insert enclosed in the kit

Performance Characteristics

Limitation/Interfering Substances

No significant interference from lipemia up to a sample absorbance of 4.3/cm at 660 nm, bilirubin up to concentrations of 25 mg/dL (425 μ mol/L), hemoglobin up to concentrations of 400 mg/dL (0.24 mmol/L) and rheumatoid factor up to 750 IU/mL. For a comprehensive review of interfering substances, refer to the publication by Young *et al.*¹

Precision

Serum	Samples/Runs	Mean (mg/L)	CV(%)
Within run	4/10	2.6	1.4
Total	4/10	2.6	3.3

Method Comparison

Comparison Method (x)	same reagent
Comparison Instrument (x)	ILab 900
Slope	1.04
y intercept	-0.35
Mean X (mg/L)	7.8
Mean Y (mg/L)	8.1
r	0.99
n	40

Linearity

no rerun 0.2 - 16 mg/L ; with rerun 0.2 - 96 mg/L

Minimun Detection Limit

0.12 mg/L

Quantification Limit

0.2 mg/L



Instrument Settings

Chemistry Parameters				R1			
Method	<input type="text"/>			Reagent Name	<input type="text" value="B2M"/>	Volume	<input type="text" value="150 μL"/>
Name	<input type="text" value="B2M"/>			R2	<input type="text" value="enable"/>		
Unit	<input type="text" value="mg/L"/>			Reagent Name	<input type="text" value="B2M"/>	Volume	<input type="text" value="120 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="14"/>	Decimal Points	<input type="text" value="2"/>		
		end	<input type="text" value="15"/>				
	2 enable	start	<input type="text" value="25"/>	Normal Range	<input type="text" value="1"/>	<input type="text" value="2.64"/>	
		end	<input type="text" value="26"/>				
Wave Length							
Prim	<input type="text" value="570"/>	Sec	<input type="text"/>	Technical Range (Conc)	<input type="text" value="0.0"/>	<input type="text" value="16"/>	
					mAbs/10	<input type="text" value="-30000 / 30000"/>	
Sampling Volume	<input type="text" value="3 μL"/>						
Dilution	<input type="text" value="disable"/>				RPT Wash (R1)	<input type="text" value="Sys Water"/>	
	<input type="text" value="μL"/>	<input type="text" value="μL"/>			(R2)	<input type="text" value="Sys Water"/>	
Rerun (High)	<input type="text" value="3 μL"/>						
Dilution	<input type="text" value="enable"/>				Instrument Factor a	<input type="text" value="1"/>	b <input type="text" value="0"/>
	<input type="text" value="25 μL"/>	<input type="text" value="125 μL"/>			Stirring Speed	R1 <input type="text" value="high"/>	R2 <input type="text" value="high"/>
Rerun (Low)	<input type="text" value="6 μL"/>						

Calibration Checks

** Duplicate Limit	<input type="text"/>	** mAbs/10	Sampling Method for Standards			
** Sensitivity Limit	<input type="text"/>	** mAbs/10	<input checked="" type="checkbox"/> Duplicate			
			<input type="checkbox"/> Triplicate			
** Linearity Limit	<input type="text"/>	** %				
** Prozone Limit	<input type="text" value="upper"/>			Blank measurement		
SL1-S	** <input type="text" value="SL1-F"/>	**	<input checked="" type="checkbox"/> Enable Reagent blank			
SL2-S	** <input type="text" value="SL2-F"/>	**	<input type="text" value="None"/>			
Sens	<input type="text" value="mAbs/10"/>		Reagent blank measurement at calibration			
			<input checked="" type="checkbox"/> Reagent blank (system water)			
<input checked="" type="checkbox"/> Absorbance Limit			Multiplex measurement is the same as standards			
Reaction	<input type="text" value="Increase"/>			Reagent Blank Limit Checks		
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="B2M"/>	Interval	<input type="text" value="37"/>	days
Calculation	<input type="text" value="Linear"/>					
	Conc	WORK	MASTER	Lot No		
S1	<input type="text" value="0"/>	<input type="text" value="30"/>			K	<input type="text" value="N/A"/>
S2	<input type="text" value="4"/>	<input type="text" value="1626"/>				
S3						
S4						
S5						
S6						

Reagent Registration

Reagent Code	<input type="text" value="0182"/>					
Reagent Name	<input type="text" value="B2M"/>					
			Volume (L)	Volume (S)	Stability Check	Term
R1	<input checked="" type="checkbox"/> enable	<input type="text" value="**"/>	mL	<input type="text" value="**"/>	<input checked="" type="checkbox"/> enable	<input type="text" value="**"/> days
R2	<input checked="" type="checkbox"/> enable	<input type="text" value="**"/>	mL	<input type="text" value="**"/>	<input checked="" type="checkbox"/> enable	<input type="text" value="**"/> days

** Operator definable N/A not applicable to this test Calibration curve is only as example