

Intro

Protein Quantitation with BCA (bicinchoninic acid)

- PROTOCOL CUSTOMIZATION:
- 1. Delete unwanted Sections.
 - 2. Modify the Instrument Settings according to your specific reader (if applicable).
 - 3. Click the [Template] button and assign wells to existing groups or newly-created groups. You can print the assigned template to help prepare your microplate.
 - 4. Select your desired Reduction and Display options.
 - 5. If you wish, you can save your customized protocol with a different name elsewhere on the file system. For easy access to the modified protocol, you can put its location in the Protocol Manager (through the Folder Locations button).

READER SUITABILITY:
All SpectraMax readers with Absorbance Read Mode

PROTOCOL REVISION HISTORY:
v 1.1; Imported from SMP 5.4.2 April 2011 (ELM)

Plate1

	1	2	3	4	5	6	7	8	9	10	11	12
A						0.093	1.860	1.880				
B						0.160	1.685	1.646				
C						0.221	1.569	1.487				
D						0.386	1.483	1.519				
E						0.592	1.829	1.804				
F												
G												
H												

Reduction Settings
Optical Density
Wavelength Combination : !Lm1

Settings Information
Endpoint
▲ Absorbance
Lm1 562
▲ More Settings
Shake Off
Calibrate On
Carriage Speed Normal
Column Priority

Read Information
SpectraMax M5
ROM v3.0.22 16Feb11
Start Read : 5:56 AM
3/17/2020
Mean Temperature : 23.6 °C

Standards

Sample	Standard Value µg/ul	BackCalcConc	Wells	OD_Values	MeanODValue	SD	CV
01	0.000	-0.030	A6	0.093	0.093	0.000	0.0
02	0.250	0.233	B6	0.160	0.160	0.000	0.0
03	0.500	0.475	C6	0.221	0.221	0.000	0.0
04	1.000	1.127	D6	0.386	0.386	0.000	0.0
05	2.000	1.945	E6	0.592	0.592	0.000	0.0

MinStd = 0.093

MaxStd = 0.592

Unk_Dilution

Sample	Wells	OD_Values	R	Concentration	MeanConc	SD	CV	Dilution	AdjConc
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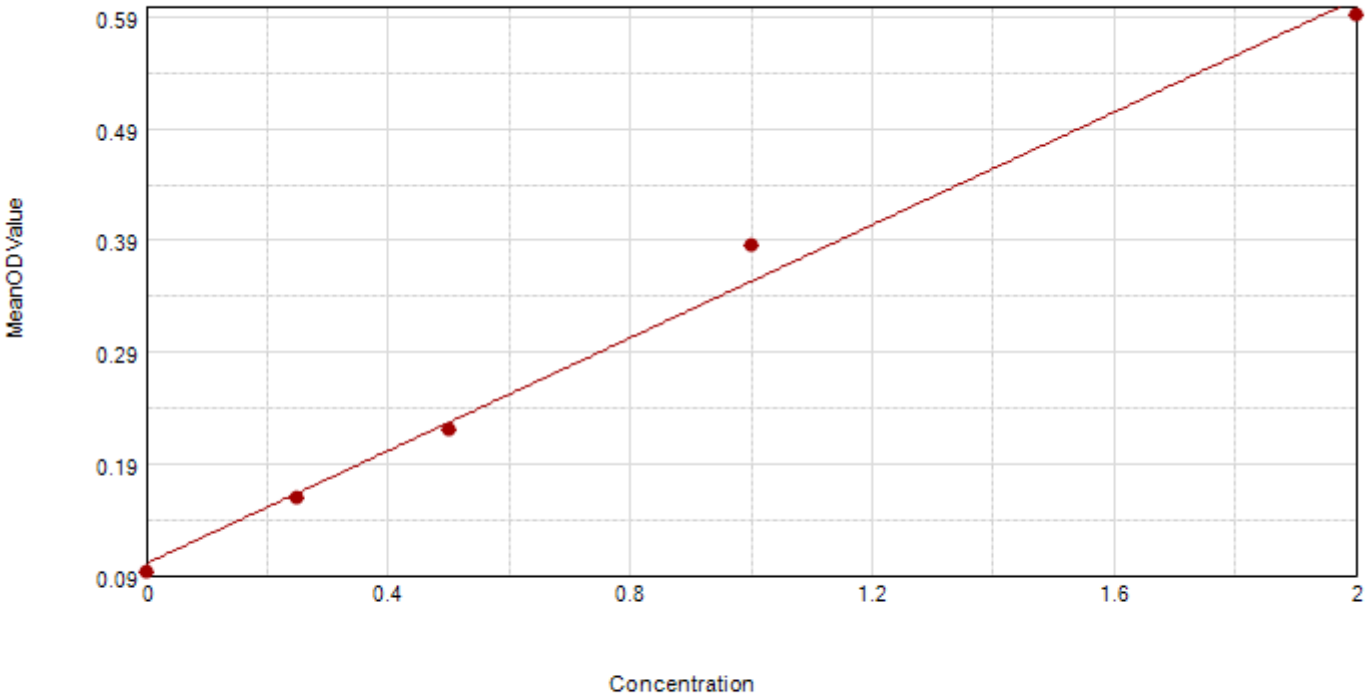
R = Outside standard range

Unknowns

Sample	Wells	OD_Values	R	Concentration	MeanConc	SD	CV
01	A7	1.860	R	6.959	7.000	0....	0.8
	A8	1.880	R	7.040			
02	B7	1.685	R	6.267	6.189	0....	1.8
	B8	1.646	R	6.112			
03	C7	1.569	R	5.810	5.648	0....	4.1
	C8	1.487	R	5.486			
04	D7	1.483	R	5.467	5.539	0....	1.9
	D8	1.519	R	5.612			

R = Outside standard range

StandardCurve



STD01 (Standards@ProteinQuant_BCA: MeanOD... vs Standard...)

Curve Fit Results ▼