

MAXline[™] Microplate Readers

Application Note 26

PathCheck applied to measurement of protein solutions in the SPECTRAmax[®] PLUS microplate spectrophotometer

INTRODUCTION Protein concentration is commonly estimated by measuring the absorbance at 280 nm and calculating the concentration using the extinction coefficient of the protein. The procedure is feasible because extinction coefficients are typically obtained using standard cuvettes with a fixed 1 cm pathlength. Extinction-based protein assays can also be done in microplates, but they have not been widelyused because of the inconvenience of compensating for variable pathlengths of samples in microplate wells. The introduction of the Molecular Devices' SPEC-TRAmax PLUS microplate spectrophotometer marks the first time that photometric measurements made in a microplate format can be automatically normalized such that the resultant values are identical to those obtained with the corresponding solutions in a standard 1 cm pathlength cuvette. The following application note outlines the use of the pathlength correction feature "Pathcheck", compares absorbance results obtained in cuvettes and microplate, and gives an example where Pathcheck is applied to column chromatographic fractions and the elution profile displayed.

MATERIALS

For details of the principles of pathlength correction, refer to MAXline application note #25, "Optical density measurements automatically normalized to a 1 cm pathlength in the SPECTRAmax PLUS microplate spectrophotometer".

- 1 SPECTRAmax PLUS microplate spectrophotometer
- 2 UV-transparent microplates; e.g.:
 - SPECTRAplate[®] Quartz, Molecular Devices Corp. (catalog # R8024)
 - SPECTRAplate Quartz half-area microplate, Molecular Devices Corp., (catalog # R8028)
 - Quartz microtest 8-well strip, Hellma (catalog # 730.010QS); use with a frame for 8-well strips, E & K Scientific Products (catalog # 564101). *Note: the 8-well strip frame sold by Evergreen Scientific does not fit properly.*
 - Disposable UV Plate, Corning Costar Corp. (catalog # 3635)
 - UV-MAX, (Polyfiltronics, Inc., catalog # VO32SCXP8)

- 3 Pipettor and tips or transfer pipets suitable for use with microplates.
- 4 Samples (100-300 µL each)
- 5 Quartz cuvette

Set up to make pre-read measurements

- **Step 1** Launch SOFTmax PRO[®], then open a Plate section or, if necessary, create a new Plate section.
- **Step 2** Set up the Instrument Settings dialog box as shown in Figure 1. In the Instrument Settings dialog box, select to perform an endpoint read at 280 nm. Select PathCheck, (Pre-read plate will automatically be checked) and select Cuvette Reference. (Alternatively, you can use the factory-installed Water Constant as a shortcut, though it is potentially less accurate.)

Instrumen	t Settings
Endpoint 🕢	Khetis 🚺 Spectrum
-Wavelengthe: 1 -	- I Politikeek
L1:200 Trm	Weter Constant Bead Cavetta Reference
Automix Before Pirat Read 5 38ca	Read entire plats Blacking Read entire plats Image: Proc Read Plats Strips
(Hide Detail	Cancel OK

Figure 1: The Instrument Settings dialog box, set up to measure absorbance at 280 nm with PathCheck

- **Step 3** Use the Template Editor to create a template showing where standards, blanks, and unknowns will be located on the microplate.
- **Step 4** Set up the Reduction dialog box as shown in Figure 2. Set the wavelength combination to L1 and the data mode to Absorbance. Make sure that 'Use pre-read plate' and 'Apply Pathcheck' are selected.

	Reduction
Vavelength Cambination	
Absorbance Wirzasznittace	 ☑ Use premiest plate ☐ Switch somed and premiesd ☑ Apply PubClock
	Cancel OK

Figure 2: The Reduction dialog box set up to apply PathCheck

METHOD

Making pre-read measurements

The purpose of the pre-read is to subtract the background absorbance of the plate. In contrast, blanks (plate, sample or group) are designated in the template and are subtracted after pathlength correction. In some cases, you may choose to use stored pre-read values (See below).

- **Step 1** Select a clean microplate and pipet distilled water into the wells in approximately the same volumes as the intended samples. Accurate pipetting is not necessary.
- **Step 2** Put the plate into the drawer of the SPECTRAmax PLUS, then click the Read button in SOFTmax PRO's toolbar to make the pre-read measurements.
- **Step 3** Remove the plate, pour out the water and blot the plate dry.

Making pathlength-corrected absorbance measurements

Note: If you have elected to use the pre-programmed Water Constant, you may skip Step 1.

- **Step 1** Place a clean quartz cuvette containing your sample buffer or distilled water into the SPECTRAmax PLUS cuvette port.
- Step 2 Transfer aliquots of your samples and blanks into their designated wells in the microplate. Accurate pipetting is not necessary, though the volumes should between 100 μ L and 300 μ L for best pathlength-corrected results.
- **Step 3** Put the plate into the SPECTRAmax PLUS drawer, then click the Read button in SOFTmax PRO's toolbar to make the absorbance measurements. (The cuvette will be read in the near-infrared at the same time the plate is read, and its absorbance values used in the PathCheck calculations.)

To avoid evaporation error, make the readings within a few minutes of putting the samples in the microplate. If the readings must be delayed, cover the plate with an adhesive seal. Remove the seal immediately prior to reading the plate.

Storing and re-using pre-read data

Quartz plates are so uniform that it is not necessary to subtract the plate background on a well-by-well basis. Instead, you can pre-read one plate, then store the pre-read data in a SOFTmax PRO file for subsequent re-use, being careful to save the data under a different file name each time, to avoid over-writing the pre-read data.

If you use Costar UV plates, you may or may not want to use stored pre-read values, depending on the precision you require. At 280 nm, the average absorbance of Costar wells containing water is approximately $.050 \pm .002$ OD. Thus, samples having raw absorbance values of 1 OD would be subject to less than 1% potential error due plate background variation. However, the lower the absorbance in the wells, the greater the maximum potential error due to plate variability.

Example 1: Demonstration of the utility of PathCheck using a protein standard curve

To illustrate the performance of the instrument, a protein "standard curve" was prepared. Bovine serum albumin (BSA) was dissolved in phosphate-buffered saline (PBS), pH 7.4, filter-sterilized and diluted to 6, 5, 4, 3, 2, 1, 0.5 and 0.25 mg/mL. Absorbance measurements made in a microplate were compared with measurements made on the same solutions in a 1 cm cuvette.

SOFTmax PRO was launched and a Group entitled "Plate Standard" was created and given a 'Standards' format in the Template Editor of a Plate section. The standards were assigned to wells as illustrated in Figure 3. "Standard 01" was PBS with no added protein (0 mg/mL). An identical template was set up in the Template Editor of a Cuvette Set, except the group was named "Cuvette Standard".



Figure 3: The Template Editor for the Plate section

The instrument settings and data reduction for the Plate section were set up as shown in Figures 1 and 2 above. The CuvetteSet section was set up for an endpoint read at 280 nm.

A cuvette containing PBS was placed in the cuvette port to serve as the cuvette reference for PathCheck. Pre-read measurements were made with 200 µL water in each well of a Costar UV plate, after which the plate was emptied and blotted dry. Aliquots of the protein 'standard' solutions were transferred into their designated wells using disposable transfer pipets. The volumes in each well were deliberately varied in order to demonstrate the utility of the PathCheck feature. The plate was placed into the drawer of the microplate reader and read.

In the Cuvette Set, a reference read was taken on the PBS-containing cuvette in the cuvette port. Then, one by one, each of the protein 'standard' solutions was read in the cuvette.

Sample	Concentration	Wells	Veloxy	Plear/Value	Rev Values
01	0.000	41	0.008	T00.0	0.004
		81	0.005		
02	0.125	42	0.079	030.0	0.037
		82	0.081		
05	0.290	48	0.184	0.158	0.077
		85	0.182		
04	0.900	#4	0.800	0.501	0.170
		84	0.802		
05	1.000	48	0.7790	0.566	0.857
		83	0.7555		
06	1.900	AB-	0.897	0.899	0.605
		86	0.901		
07	2.000	AT	1.185	1.195	0.707
		87	1.211		
08	2.900	48	1.477	1.469	0.841
		88	1.901		
09	8.000	43	1.755	1.795	1.255
		87	1.755		
10	5.900	A10	2.082	2.095	1.248
		810	2,107		
11	4.000	A11	2,887	2.599	1.097
		811	2,412		
12	5.000	A12	2.945	2.948	1.671
		812	2,755		
18	6.000	C1	5.455	8,440	1.968
		D1	8.421		

The Group Table associated with the Plate section is shown in Figure 4.

Figure 4: The Group Table for the Plate section

All columns except the far right column in the Group Table were created automatically by SOFTmax PRO when the "Plate Standard" group was created in the template. The numbers in the "Values" column are absorbance values corrected to a 1.0 cm pathlength. The numbers in the far right column titled "Raw Values" are raw absorbance values (pre-read subtracted) before pathlength correction. These values were obtained by back-calculation using the custom formula shown in the Calculation dialog box for that column (Figure 5). Basically, the Raw Values were calculated by multiplying the corrected values by their corresponding pathlengths and taking the average of the replicates.

	Calculation
Name:	Raw Values
Formula:	Average(Values*!WellPathLength)
	Decimal Places: 3
	(Accept) Cancel OK

Figure 5: The Calculation dialog box for the "Raw Values" column

The Group Table ("Cuvette Standard") displays the data from the absorbance readings in the cuvette (Figure 6). The column 'Values' contains the absorbance values at 280 nm.

Curvette Standard (mg/ml)				
Sample	Concentration	Wellb	Veloce	HearWalter
01	0.000	41	0.004	0.004
		81	0.004	
02	0.125	42	0.075	0.075
		82	0.075	
05	0.290	48	0.151	0.151
		85	0.151	
04	0.900	#4	0.800	0.299
		84	0.277	
05	1.000	48	0.7770	0.565
		83	0.337	
06	1.900	AB-	0.8%	0.895
		86	0.875	
07	2.000	AT	1.198	1.198
		87	1.198	
08	2.900	A8	1.468	1.410
		88	1.471	
09	8.000	43	1.768	1.768
		87	1.768	
10	5.900	A10	2.007	2.006
		810	2,005	
11	4.000	411	2.289	2.258
		811	2.257	
12	5.000	A12	2.842	2.555
		812	2,355	
18	6.000	C1	2.655	2.678
		01	2.678	

Figure 6: The Group Table for the Cuvette Set

Next, the standard curves from the plate and cuvette were plotted in a single graph. A Graph section was created, then the Plots dialog box was used to create three plots by selecting the corresponding Group tables from the Groups pop-up menu, then specifying the x and y variables for each plot (Figure 7). In the example shown in the figure, the highlighted plot is "Plate with PathCheck". The data came from the group "Plate Standard", the x variable is concentration, and the y variable is "MeanValue" (i.e. the mean pathlength-corrected absorbance value).



Figure 7: The Plots dialog box associated with the Graph Section

The resulting graph (Figure 8) shows the three plots (plate values with and without PathCheck and the cuvette values). The plot of raw plate absorbance values without PathCheck (bottom line) is irregular because the volumes in the wells (and therefore the pathlengths in the wells) were not uniform. The plot of plate values with PathCheck is linear through the highest concentration (6 mg/mL). The corrected plate values are superimposable on the cuvette values up through approximately 3 mg/ml, above which the cuvette plot begins to deviate

from linearity. The corrected plate plot extends above the cuvette plot because the values are calculated values and their raw absorbance values (bottom plot) are still well within the linear range of the curve.



Figure 8: BSA standard curves obtained in a microplate and in a cuvette. The standards were read at 280 nm in a 1 cm pathlength cuvette (\bigcirc) and in microplate wells with (\square) and without (\triangle) pathlength correction

Example 2: Using PathCheck to evaluate column fractions during purification of antibody-enzyme conjugate on a gel filtration column

Fractions were collected during purification of an antibody-enzyme conjugate on a Pharmacia S-100 gel filtration column. The fractions in the void volume were discarded and fractions 21 through 61 were each read at 280 nm in a Costar UV plate and also in a standard quartz cuvette for comparison. Fractions 24 through 29 were too concentrated and therefore were diluted 1 to 5 to bring them into the linear range of absorbency.

Initial setup of the Group Table

There are two ways in SOFTmax PRO to set up a Group Table for samples (e.g. column fractions) that have dilution factors, but are not going to be quantitated against a standard curve:

- 1 Assign the 'Unknowns(dilution)' format to the group. SOFTmax PRO will automatically activate the Dilution Factor field and include columns for Dilution (Factor) and Adj.Result in the Group Table. The software also will assume a standard curve is being created, and will create 5 columns that are unnecessary for the present example (calculations of concentrations based on a standard curve and statistical information). Because these columns will not be needed in any calculations, you can delete them from the Group Table.
- 2 Assign the 'Basic' format to the group, then modify the group to include the dilution factor information, either via the Group Settings dialog box, or via the Series dialog box. Two columns must then be added to the Group Table: one that contains the dilution factors, and a second that multiplies the absorbance values by the dilution factors.

In this example, the second method was used to create the Group Table and assign sample names to the wells. A new group named "Plate" was created in the Plate section Template Editor and assigned the Basic format. Rows A though D were highlighted and the Series button clicked to access the Series dialog box (Figure 9).

	Series
Start From: Dop Bottom SSE © Left SSE © Right	First Sample: 21
Replicates 01	Cancel OK

Figure 9: The Series Settings dialog box, set up for column fractions

The starting sample was set at 21 (to correspond to its fraction number) and the series was set to proceed from left to right with one replicate. The Sample Descriptor box was checked to activate it, then 'dilution factor' typed into the field. The Units field was cleared and left blank. After clicking the OK button to create the series, the template displayed the sample names (fraction numbers) assigned to the wells (Figure 10). Samples with dilution factors other than 1 had the dilution factor added by clicking the well in the template to select it, then typing in the appropriate factor into the Dilution Factor field. In the figure, well A5 (fraction #25) is highlighted and its sample name (25) and its dilution factor (5) are displayed in their respective fields. The buffer blanks were assigned to wells D6 and D7.

Note: the series feature initially filled all of Row D because SOFTmax PRO by default fills complete rows or columns. Wells D6 through D12 were cleared so that the series would stop at sample #61.



Figure 10: The Plate section Template Editor, showing the series set up

In an analogous manner, the same sample names were assigned to a CuvetteSet section.

Experimental details and customization of the group table

The instrument settings were identical to those used in Example 1 above. Plate pre-read measurements were made in a Costar UV plate. Aliquots of each column fraction and the buffer blank were transferred into their designated wells using disposable transfer pipets, then read in the SPECTRAmax PLUS. As in the example above, the volumes in each well were deliberately varied in order to demonstrate the utility of the PathCheck feature. The column fractions were also read in a quartz cuvette as described above.

The Group Table for the Plate section (after customizing) is shown in Figure 11. Of the seven columns, only three (Sample, Wells and Correct.Values) were created automatically by SOFTmax PRO. (The "Correct.Values" column was originally entitled "Values", but was renamed in this example to distinguish pathlength-corrected values from raw absorbance values. The other four columns were given custom formulas. The "Fraction#" column was created so that the samples could be given numeric values corresponding to their fraction numbers, then graphed. (In the Sample column, the sample numbers are treated as names and therefore cannot be graphed.)

Plate						
Sample	Vella	Fraction [®]	Raw Values	Derrest Walkes	Dribution	Final Values
21	61	21	0.062	0.097	1.000	0.097
22	62	22	0.063	0.092	1.000	0.092
23	AT.	23	0.079	D.102	1.000	D.102
24	64	24	0.067	0.099	5.000	D.496
25	45	25	0.402	0.595	5.000	2.973
26	46	26	0.919	0.960	5.000	4.900
27	67	27	0.449	0.701	5.000	3.503
28	AR	29	0.369	0.514	5.000	2,569
29	69	29	0.152	0.196	5.000	0.991
30	A10	20	0.061	0.0%	1.000	0.096
31	611	31	0.072	0.099	1.000	0.099
32	612	32	0.177	0.249	1.000	0.249
33	Q1	11	0.141	0.199	1.000	D.199
34	92	34	0.092	0.099	1.000	0.099
35	93	15	0.068	0.099	1.000	0.099
36	94	36	0.057	0.099	1.000	0.099
37	85	37	0.074	0.097	1.000	0.097
38	04	29	0.127	0.205	1.000	0.205
39	97	39	0.290	0.412	1.000	0.412
40	23	-40	0.302	0.451	1.000	0.451
41	22	-41	0.359	0.434	1.000	0.434
42	010	-42	0.270	0.369	1.000	0.269
43	911	-41	0.294	0.799	1.000	0.799
44	912	- 44	0.311	0.365	1.000	0.765

Figure 11: The Group Table for the gel filtration column fractions read in the microplate

The custom formula for the Fraction # column (Figure 12) is "Index+20" so that the first entry is 21.

		Calculation
Name:	Fraction#	
Formula:	Index+20	
1		Decimal Places:
		(incrept) (cancel) (uk

Figure 12: The Calculation dialog box for the "Fraction#" column

The "Raw Values" column contains the absorbance values before pathlength correction and were obtained by back-calculation from the corrected values using the

custom formula: "Correct.Values «!WellPathLength" (Figure 13).

	Calculation
Name:	Raw Values
Formula:	Correct.Values*!WellPathLength
	Decimal Places: 3
	Accept Cancel OK

Figure 13: The Calculation dialog box for the "Raw Values" column

The custom formula for the "Dilution" column is shown in Figure 14. The term "!factor" refers to the sample descriptor defined in the template.

Name	Dilution	
Formula:	Factor	
	2	Decimal Places:
		(Recept) (Cancel) OK

Figure 14: The Calculation dialog box for the "Dilution" column

The column "Final Values" contains the corrected absorbance values multiplied by the dilution factor. The custom formula is Correct.Values*Dilution (Figure 15). In the Cuvette Group Table, an analogous column was created to multiply the absorbance values by the dilution factors.

	Calculation
Name:	Final Values
Formula:	Correct.Values*Bilution
	Decimal Places: 3
	_
	Recept Cancel OK

Figure 15: The Calculation dialog box for the "Final Values#" column

Figure 16 shows the elution profiles from the gel column obtained in the plate and the cuvette. The lower plot (plate values not pathlength corrected), not surprisingly, does not strictly mirror the upper profiles because the volumes in the wells were not uniform. However, when PathCheck was applied to the plate values, the





Figure 16: Elution profile of column fractions obtained during purification of antibody-enzyme complex. The fractions were read at 280 nm in a 1 cm pathlength cuvette (\bigcirc), and in microplate wells with (\square) and without (\triangle) pathlength correction

The above examples illustrate the utility of the PathCheck feature of the SPECTRA max PLUS. Protein solutions can be read in a microplate and the absorbance values are identical to those obtained by reading the same solutions in a standard 1 cm cuvette. A ccurate pipetting is not necessary. An additional benefit of PathCheck is that the linear range is extended above the cuvette linear range (as long as the raw absorbance values in the wells are within the linear range of the instrument).

SALES OFFICE

United States & Canada Molecular Devices Tel. +1-800-635-5577 Fax +1-408-747-3601

Brazil Molecular Devices Brazil Tel. +55-11-3616-6607 Fax +55-11-3616-6607 *China* Molecular Devices Shanghai Tel. +86-21-6887-8820 Fax +86-21-6887-8890

Germany Molecular Devices GmbH Tel. +49-89/96-05-88-0 Fax +49-89/9-62-02-34-5 Japan Molecular Devices Japan, Osaka Tel. +81-6-6399-8211 Fax +81-6-6399-8212

Molecular Devices Japan, Tokyo Tel. +81-3-5282-5261 Fax +81-3-5282-5262 *South Korea* Molecular Devices Korea, LLC Tel. +82-2-3471-9531 Fax +82-2-3471-9532

United Kingdom Molecular Devices Ltd. Tel. +44-118-944-8000 Fax +44-118-944-8001

www.moleculardevices.com

FOR RESEARCH USE ONLY. NOT FOR USE IN DIAGNOSTIC PROCEDURES.

The trademarks used herein are the property of Molecular Devices, Inc. or their respective owners.

©2010 Molecular Devices, Inc. Printed in U.S.A. 6/10 #0120-1127B