Bio-Rad
Laboratories

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RE: Alternative software for PDQuest Software

Dear Customer,

Thank you for contacting Bio-Rad Laboratories about our PDQuest Software for 2D analysis (catalog numbers 1709620 and 1709630). Although this has been a great product for many years we are in the process of transitioning to a new software package due to a range of business factors

Catalog #	**Product Description**
1709620	PDQuest Basic 2-D Analysis Software
1709630	PDQuest Advanced 2-D Analysis Software

The software packages we are recommending are SameSpots and SpotMap from TotalLab Limited, our preferred alternative vendor for 2D analysis software. We have evaluated the software and found it to be comparable to our software and will suit your needs for 2D analysis and beyond.

SameSpots v5.1
- For differential expression analysis to detect proteomic changes between conditions
- Supports single stain and DIGE gels and 2-way Anova experiments

SpotMap v3.0
- For the comparison of 2D gels and Western blots which is particularly useful for HCP coverage analysis
- Version 4.0 is due for release mid-2018

Please find below the discount code that customers should refer to for purchasing, pricing for each product, and the contact information for TotalLab Limited. Also included are their product information sheets for both SameSpots and SpotMap.

Discount code:	BIORADTL201801	
Product codes:	L-4020-SS-1	SameSpots Single User Licence
	L-4040-SM-1	SpotMap Single User Licence
2018 Pricing:		
SameSpots	$6,240	
SpotMap	$15,600	

Contact Details:
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Best Regards,

Mona Chin
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FAQ Sheet for SameSpots

1. **Is there a performance difference between PDQuest and SameSpots software?**

The biggest difference between the two software is the fact that PDQuest is not supported on OS Windows 7 and newer while SameSpots is. Another advantage is the SameSpots is very powerful for the analysis of DIGE experiments and is an advantage over PDQuest.
The analysis features of SameSpots are very similar to PDQuest. SameSpots allows you to quickly and reliably analyze single stain, multiple stained and DIGE 2D gel electrophoresis images for differential expression analysis. Comparable to PDQuest SameSpots provides a simple and intuitive workflow for differential expression analysis:

A. Experimental set-up and image editing
The first step is to import your gel images. All common image formats are supported including .tiff, .img, .png, .gel and .mel. If needed the images can be edited (crop, flip, invert, rotate) without compromising the data integrity of the original file.

B. Image alignment
Automated alignment removes any positional variation between the spot patterns of the gels, mainly introduced during the electrophoresis processes. During alignment vectors are automatically created and manual vectors can be added to aid the alignment.

C. Spot detection
Spots are automatically co-detected on all images in the analysis, creating a single spot pattern of the analysis. Normalized spot volumes are automatically calculated following detection. The filtering stage allows removal of spots based upon position, area, normalized volume or a combination of these.

D. Automatic gel analysis
Images are grouped into conditions to be analyzed and multiple experimental designs can be set up. P-values and fold change between each of the conditions are automatically calculated. Each spot can be visualized in a number of ways with expression profiles and spot details available. Spots can be sorted by p-value or fold change, spots of interest can be tagged and the list can be filtered to include only the spots of interest. Additional details can be added to the spots including MS data, pI and MW information or notes.

E. Statistics
Statistical analyses which can be completed within SameSpots include: Principle component analysis (PCA), correlation analysis – dendrogram, ANOVA p-value calculation, power analysis and q-value calculation.

F. Reporting, spot picking and import of mass spec data
At the end of an experiment you can create a powerful HTML report of the results, export the spot measurements to a CSV file that can be opened in Excel or other spreadsheet applications, create spot picking files and choose which spots to include. Results from Mass Spec, including MASCOT searches, can be imported into the program so you can look at and review this information in the program.

2. What major functionalities are different?

- The spot detection and gel matching processes in both software packages are based on different gel evaluation strategies. PDQuest uses *Gaussian modelling* to generate spots and all gel images are *individually spot detected and matched*. In contrast SameSpots creates a series of *spot shapes* after gel alignment which are used to produce a *single spot pattern* (the spot map) that is used for all the images in the experiment. The latter approach is very powerful for the analysis of DIGE experiments and is a major advantage over PDQuest.

- SameSpots software offers extended data evaluation possibilities compared to PDQuest. Statistical tests in SameSpots include p-values (standard ANOVA, repeated measures ANOVA and two-way ANOVA), q-values, principle component analysis, correlation analysis and power analysis.

3. How long will this offer be available?
4. What's the price difference?
5. Who should I contact if I have questions about the software?
6. Is there a multiuser license?
7. What if I need a security version?