Why upgrade from PDQuest to SameSpots?

If you've purchased PDQuest™ in the past or you're considering purchasing it, you've already invested in 2D gel analysis, so why should you upgrade to SameSpots? PDQuest users we speak to say analysis can be very cumbersome so it's difficult and time consuming to get reliable and accurate results.

- **SPEED**
- **EASE-OF-USE**
- **PERFORMANCE/ACCURACY**

Additional reasons given for upgrading from to SameSpots from PDQuest have been:

- **100% matching, no missing values and advanced statistical analysis functionality**
- **High throughput compared to PDQuest**
- **Rapid and responsive development**
- **Works with Bio-Rad spot-pickers**

SameSpots	PDQuest
Active development. Works on Windows 7, 8, 10 and 11 (32-bit and 64-bit) operating systems and is still being actively developed and improved (as of May 2023). There have been 5 major releases since the product was launched in 2006, and we remain committed to supporting the software. Users with an active support contract have direct access to the software developers themselves, we never use call centres or online ticketing.	Was **discontinued in 2018**, presumably now a completely unsupported and no longer developed product. Unknown if supported on modern operating systems.
Reproducibility. Proven to provide reproducible results between different labs, proving the objectivity you can achieve with our workflow.	No published evidence that results are reproducible across labs.
100% Matching, automatically. 100% matching and no missing values in your data. **SameSpots outperformed DeCyder** in matching accuracy in a recent independent study[1].	Laborious and subjective editing is required to achieve good matching across all images. Missing values may still be present in your data, which can compromise statistical analysis.
Spot detection. Automatic detection occurs during analysis. We don't generate spot models; we quantify the actual spot shape as it appears on the image.	Requires considerable manual guidance and user judgment. Gaussian distribution spot models are used for detection, reports and calculations, which can misinterpret spots.
Publications. 9.5 fold increase in publications citing SameSpots 2009-2011[2].	1.2 fold increase in publications citing DeCyder 2009 - 2011[2].
Functionality. Single stain, DIGE, Stats, and secondary staining comparisons, e.g., Western blots and phosphor staining, are all combined in one package.	Does not include proper alignment, only old-style "warping", with limited editing of image warping.
Statistics. In v5.0 you can import statistical test results from third party software that are specific for your research needs. You can label any results you import with a user defined tag and link it back to the original spot data.	Missing values may still be present in your data, which can compromise statistical analysis.
Ease-of-Use. One package to easily install on your desktop. A single step-wise guided workflow end to end. No interface issues or tricky installations.	Latest version includes wizards but based on a menu driven "tool box" workflow, like PG240.

1. Kang Y, Techanukul T, Mantalaris A, Nagy JM (2009) Comparison of three commercially available DIGE analysis software packages: minimal user intervention in gel-based proteomics. J Proteome Res 8: 1077-1084.

2. Comparison of within-data variation for a same-sample vs. same-sample DIGE experiment using DeCyder v6.0 (GE Healthcare) analysis filter volume of 50,000 and estimated spot number of 2,500) vs. SameSpots. * "Maximising sensitivity for detecting changes in protein expression: experimental design using Minimal CyDyes" Karp, N.A. , and Lilley, K.S. Proteomics (2005) 5 (12):3105*

People who have already upgraded from PDQuest and why:

"Unbiased differential quantitative analysis of clinical material can be performed by 2D-PAGE. However the high inter-individual variation usually found in clinical material demands for a method that allows for the analysis of large number of samples in combination with a small gel-to-gel variation. 2D-DIGE is a method that full fills the requirement for low gel-to-gel variation and a reasonable throughput. However, this approach only become useful if all protein spots from a large number of samples can be correctly matched in a efficient way. SameSpots meet these criteria because it takes full advantage of the DIGE concept, not only for generating the quantitative data but also by its unique matching technology which generates a 100% match rate, regardless how many samples that are analyzed."

Jorgen Ostling, AstraZeneca R&D Molndal, Sweden

“SameSpots and its statistic tools have become indispensable in our gel based proteomics workflows."

Dr Friedrich Lottspeich, Max Planck Institute of Biochemistry, Martinsried, Germany

“SameSpots delivers an alternative starting point for 2D image analysis - offering significant improvements in image matching. The benefit of reliably matching spots across all gel images from the start means you can quickly focus your research efforts on investigating the few spots showing statistically valid changes, which are indicative of potentially interesting expression profiling changes"

Professor Mark S. Baker, CEO, Australian Proteome Analysis Facility Ltd (APAF)

North America	Europe	Asia/Pacific Region
Dr. Susan Weintraub, University of Texas Health Science Center at San Antonio. Texas	**Prof. Friedrich Lottspeich,** Max Planck Institute MPI for Biochemistry, Martinsried, Germany	**Dr. Mark Baker,** Australian Proteome Analysis Facility (APAF),
Dr. John Arthur, Medical University of South Carolina , S. Carolina	**Dr. Jorgen Ostling,** AstraZeneca, Sweden	**Chinese Academy of Inspection and Quarantine (CIAQ),** China
Prof. Frank Witzmann, Indiana University, Indianapolis	**Dr. Reto Portmann,** Friedrich Miescher Institut for Biomedical Research, Switzerland	**Dr. Ing-Feng Chang,** National Taiwan University, Taiwan
Ms. Nataliya Lenchik, University of Tennessee Health Science Center, Memphis	**Dr. Francis Mulholland,** Institute of Food Research, UK	