Why upgrade from DeCyder to SameSpots?

If you've purchased DeCyder™ in the past or you're considering purchasing it, you've already invested in 2D gel analysis, so why should you upgrade to SameSpots?

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

Most people we speak to say SameSpots has equal or better accuracy than DeCyder but they decided to upgrade to SameSpots for its other benefits - it's much faster, (we've heard "we got results in 2 days instead of 2 weeks" or "analysis took weeks instead of months") and easier to use. Other reasons we've had from customers for upgrading are:

- **Quality of the spot matching and no missing values in your data set**
- **Rapid, responsive and continual product development**
- **It's compatible with existing GE hardware so no need to change your existing experimental setup**

SameSpots	DeCyder
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 December 2015**, 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.
Lower technical variation. Matches more spots across all the images with lower variance vs. DeCyder[2]. This increases your ability to detect small fold changes in protein expression accurately and reliably.	Matching can break down and variation increases for the smaller/fainter spots across the series. This is exactly where you want low variation in analysis to pick out the biologically significant results.
Publications. 9.5 fold increase in publications citing SameSpots 2009-2011[3].	1.3 fold increase in publications citing DeCyder 2009 - 2011[3].
Functionality. Single stain, DIGE, Stats, and secondary staining comparisons, e.g., Western blots and phosphor staining, are all combined in one package.	DIGE-only product. v7.0 has a form of alignment up front but this is two generations behind the technology used in SameSpots.
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.	DIA, BVA and EDA modules that you need to move between. Need to buy and maintain Oracle as well as DeCyder, which can be complex to install and maintain.

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*

3. Comprehensive search of publications referencing 2D image analysis software over 3 years 2007 -2009

People who have already upgraded from DeCyder and why:

“We moved to SameSpots as it gives much more robust analysis of DIGE experiments - no "missing data" issues and lots of statistical tools. The other major factor is that Nonlinear are continually improving the software and work closely with customers to respond to their needs and suggestions. In contrast GE has made few "improvements" to the DeCyder software over the last few years.” **Mike Dunn, Professor of Biomedical Proteomics, UCD Conway Institute, Ireland and Vice-President of the British Society for Proteome Research, Dublin, Ireland**

"The alignment procedure in SameSpots allows truly near complete matching of all spots across all the images of the experiment. And this is done in a fast, nearly automatic way. This makes not only image analysis much easier and operator independent, but it makes statistics much more robust... No worries about differences not detected as significant because of poor matching, without spending hours and hours reviewing the results. The built-in statistics provide also nice tools to check the consistency of the data through PCA analysis, find patterns of expression, and evaluate the significance of observed differences." **Francesc Canals, Institut de Recerca Hospital Univ. Vall d'Hebron, Barcelona**

"SameSpots has greatly reduced the time needed for 2D-DIGE analysis. I can now complete an analysis in less than one-quarter of the time that it would have taken when using the previous supplier's software, while at the same time obtaining more consistent and reliable results due to the excellent gel alignment and spot matching features. SameSpots is also very easy to use and makes spot editing across gels as simple as just one click, rather than having to visit each gel individually to make all of the changes. I have no doubt that SameSpots will very quickly pay for itself in the terms of salary time alone." **Todd M. Umstead, Pennsylvania State University College of Medicine, US**

"In clinical proteome research, many samples must be analyzed because of individual differences. We are currently running more than 1500 2D-DIGE gels per year. SameSpots accurately analyses such large gel numbers in a very short period. We also need to use data-mining tools effectively, which makes matching very important. SameSpots generates good data for data-mining study." **Prof. Tadashi Kondo, National Cancer Center Research Institute, Japan**

North America	Europe	Asia/Pacific Region
Prof. Mark Duncan, University of Colorado in Denver Health Science Center, Colorado	**Prof. Michael Dunn,** University College Dublin, Ireland	**Prof. Tadashi Kondo,** National Cancer Center Research Institute, Japan
Dr. Angel Aponte, National Institutes of Health (NIH), Maryland	**Dr. Francesc Canals,** University Hospital Vall d'Hebron,, Spain	**Chinese Academy of Inspection and Quarantine (CIAQ)** China
Dr. John Baatz & Dr. Daniel Knapp, Medical University of South Carolina, S. Carolina	**Prof. Angelika Gorg,** Technical University of Munich, Germany	
Dr. Peter Yau, University of Illinois at Urbana-Champaign, Illinois	**National Institute for Agricultural Research (INRA),** 8 sites in France	
Dr. Kari Green-Church, The Ohio State University, Ohio,	**Dr. Florence Pinet[1] & Mr. Abdelkader Namane[2]** Institut Pasteur (1. Lille, 2. Paris) France	