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## T.M.I. (too much information)

### Keep your information in check

With the sheer volume of information that has to be processed in laboratories today, the determination of researchers to continue exploring and discovering is remarkable. To help manage all of the information you uncover, take a look at the software applications below. You might find just what you are looking for.

**NIS-Elements**, from **Nikon**, is an integrated platform of imaging software developed by Nikon to achieve a comprehensive control of microscope image capture and document data management. NIS-Elements handles multidimensional imaging tasks flawlessly with support for capture, display, peripheral device control, and data management & analysis of images (up to six-dimensional images). The system also handles archiving, searching, and analysis of large numbers of multidimensional image files. Unified control of the entire imaging system offers significant benefits to users for cutting-edge research, such as live cell imaging. The NIS-Elements suite is available in three distinct packages scaled to meet user needs and applications: "Ar" (NIS-Elements Advanced Research software) for fully automated acquisition and device control through full 6D (X, Y, Z,  $\lambda$ , T, multi-point) acquisition and analysis; "Br" (NIS-Elements Basic Research software) for standard research applications such as analysis and photo documentation of fluorescent imaging, supporting 4D (X, Y, Z, T), (X, Y, Z,  $\lambda$ ) acquisition; and "D" (NIS-Elements Documentation software) for superior workflow management and archiving capabilities.

**Ariadne** announces the release of **Pathway Studio 5.0** software for pathway and molecular interaction analysis. Pathway Studio 5.0 powered by MedScan Technology adds functionality for transcriptomics, metabolomics, and proteomics data interpretation. The new Pathway Studio 5.0 integrates Desktop, Workgroup, and

Enterprise editions, allowing customers to easily upgrade from one to the other. Pathway Studio helps to interpret experimental data in the context of pathways, gene regulation networks and protein interaction maps. The software uses the IDs from all popular microarray platforms and public databases to recognize biological entities in an experiment. Pathway Studio takes into account up-, down-, and non-changers in an expression experiment and, through interaction network and GO group analyses, helps identify the processes in which genes of interest are involved, revealing the biological meaning underlying the expression change.

**ACD/Labs** unveils the **ACD/Method Development Suite for Mass Spectrometry**, the first software package that supports LC/MS data for HPLC method optimization and project management. ACD/Method Development Suite for MS allows chromatographers to manage their projects, not just their samples. Users see a dashboard-view of their method development project. A concise overview of the project is presented, including the experiments performed, component retention times, chromatograms, and spectra, along with the rationale behind each experiment. From the summary table, links to the raw data are retained, giving users the ability to dig down into the original files, and even reprocess them when necessary.

**Active Motif** introduces **bioalma's** new **Knowledge Application Programming Interface (KAPI)** for the latest text mining system, AKS2. This programming library, based on Java, enables software developers

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ExpressPro software from Guava



Lara Controlled Lab Reactor and software from Radleys

**“The ability to rapidly evaluate resequencing data could significantly advance research...”**

Dr. Nicholas Marini, Ph. D.,  
Research Scientist,  
University of California at Berkeley

to have high-level access to the AKS2 information in a structured and direct way. The interface is able to present and analyze the AKS2 information in a very versatile and flexible way, facilitates the integration with other biomedical software, and is able to utilize the AKS2 information for different types of bioinformatics processes.

**Applied Biosystems** announces the new **Variant Reporter Software** designed to accelerate the analysis of genetic variation data. The software can reduce up to half the time currently required to evaluate genetic variation data generated during medical sequencing projects, also known as resequencing. To streamline the analysis process, Variant Reporter Software uses proprietary algorithms to identify genetic variations based on standardised or user-defined parameters. Results are then presented for validation in a visual format that allows researchers to simultaneously compare multiple quality control metrics. “The ability to rapidly evaluate resequencing data could significantly advance research focused on the molecular basis of disease or an individual’s potential drug response,” said Dr. Nicholas Marini, Ph. D., a researcher at the University of California at Berkeley who is studying the positive effects of using folate during pregnancy. “The Variant Reporter software addresses a major log jam that currently exists in this process by providing a better way to rapidly evaluate variation data and identify targets of interest,” he adds.

**SimGlycan**, from **Sigma Aldrich**, predicts the structure of a glycan from the MS/MS data acquired by mass spectrometry, facilitating the study of glycosylation and post translational modification studies. SimGlycan accepts the experimental MS profiles generated by a mass spectrometer, matches them with its

own database of theoretical fragmentation of over 7,000 glycans and generates a list of probable glycan structures. Each structure is scored to reflect how closely it matches your experimental data. Other biological information for the probable glycan structures such as the glycan class, reaction, pathway and enzyme are also made available for easy reference.e.

**Guava** introduces the **ExpressPro** software, designed to simplify the traditional complexity of multi-color detection. Designed for both data acquisition and analysis, the intuitive software interface allows you to visualize up to 8 plots simultaneously, while still accessing operation or data analysis functions on a single screen. Features including the plot type, marker selection, statistics, gates, and other functions, are easily selected and customized to your experimental design. Color coded dots allow you to simply follow your gating strategies across multiple plots and histograms. Special batch file printing of 96-well data and downloading of screenshots to a clipboard provide easy incorporation into presentation or report writing formats.

**Radleys** announces an improved version of its Lara reactor control software for medicinal and process scale-up, scale-down or optimisation experiments. The versatile software provides reactor users with a wide range of functionality; including third party equipment control, automated data logging, graphing functions and post experimental analysis. Designed for intuitive control, the version **2.0 Lara control software** offers enhanced flexibility, expanded safety features and simple operation. To enable 'on-the-fly' control, the new software provides users with direct access to editing parameters including temperature, stirring speed and pump/additions rate while an experiment/recipe is running. New feedback

loops allow users to set limits enabling precise automated control of reactions using data from external sensors attached to the system, such as temperature, pH, turbidity, etc.

**Thermo Fisher Scientific** introduces the **Thermo Scientific LTQ Orbitrap** software. Based on the fast and highly sensitive Thermo Scientific LTQ XL linear ion trap, the LTQ Orbitrap hybrid mass spectrometer identifies more proteins with greater confidence than any other mass spectrometry (MS) system. The high-quality data generated by the LTQ Orbitrap reduces false-positive rates (FPRs) compared with results obtained from other hybrids. To make the most of this high-quality data, Thermo Scientific software leverages the accurate mass capabilities of the LTQ Orbitrap to achieve differential expression analysis, de novo sequence analysis, and metabolite identification for proteomics and pharmaceutical users.

#### Companies mentioned in this Product Focus:

Ariadne – [www.ariadnegenomics.com](http://www.ariadnegenomics.com)  
ACD/Labs – [www.acdlabs.com](http://www.acdlabs.com)  
Active Motif – [www.activemotif.com](http://www.activemotif.com)  
Applied Biosystems – [www.appliedbiosystems.com](http://www.appliedbiosystems.com)  
Guava – [www.guavatechnologies.com](http://www.guavatechnologies.com)  
Nikon – [www.nikon.com](http://www.nikon.com)  
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