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FOR IMMEDIATE RELEASE

VizX Labs Releases First GeneSifter.Net™ Update
Seattle bioinformatics company breaks new ground
with regular upgrades to its Web-based system

Seattle, WA – February 25, 2003 – VizX Labs, LLC today announced the release of its first upgrade to GeneSifter.Net. Available online now, the upgrade includes new microarray data analysis tools, data management options, and the most current gene summary information. Current GeneSifter.Net users can access the upgrades immediately by simply logging onto their existing accounts.

Today's announcement kicks off VizX Labs' unique program of regular upgrades of its Web-based GeneSifter.Net system to keep researchers ahead of the curve on new developments in statistical analysis, data management, and ever-changing genomic data.

The automatic upgrades, made possible by GeneSifter.Net's unique Web-based architecture, frees researchers from the time-consuming tasks of data management and allows them to spend more time concentrating on their research and discoveries.

"We are listening to researchers and responding to what they're asking of us," said VizX Labs CEO Tom Ranken. "GeneSifter.Net's Web-based architecture provides the most efficient, affordable, and easiest interface available for researchers. They don't need to mess with the cost or inconvenience of purchasing the latest software. Our upgrades ensure we're providing researchers with the most current microarray analysis tools available without disrupting their work."

The new Statistical Analysis Features include the Wilcoxon rank sum test, an adjustable p-value cutoff, and clustering compatibility. New Data Management Features include directories for managing large datasets. One-Click Gene Summary™ additions include Gene Ontology™ designations and an export option, a link to the NCBI Reference Sequence (RefSeq) collection, accessibility from scatter plots, and fruit fly and rat updates.

The Company also announced that the second upgrade to GeneSifter.Net, scheduled for April 1, will include additional gene ontology and analytic enhancements such as access to LOWESS normalization techniques.

About VizX Labs

VizX Labs (www.vizxlabs.com) combines expertise in biology and computing to develop products based on new insights in life science. The company has developed knowledge discovery systems that enhance the ability of researchers to understand the genetic mechanisms of disease. The company's first product, GeneSifter.Net, is a Web-based system providing microarray data analysis and knowledge management for life scientists. VizX Labs was recognized as a "Venture All Star Company" in September 2002, one of the top 25 promising new companies in Washington State.

Downloadable graphics, including screenshots of GeneSifter.Net, may be viewed online at: http://www.vizxlabs.com/downloadable_images.html.

To view the VizX Labs newsroom, visit: <http://www.vizxlabs.com/newsroom.html>.

About GeneSifter.Net

GeneSifter.Net (www.genesifter.net) helps researchers manipulate, analyze, and make sense of the mountains of genomic data now being made available. Combining power and convenience, GeneSifter.Net is the first completely Web-based solution for microarray data analysis. This approach means GeneSifter.Net users always have the latest version along with instant access to the latest gene data on the Internet. GeneSifter.Net is compatible with virtually any hardware, running the same on Windows, Linux, or Macintosh browsers and works with data from multiple platforms, i.e. spotted cDNA and oligo arrays as well as Affymetrix® GeneChip® brand arrays. Scientists spend less time with IT tech support and more time on their research.

A full list of the new features can be found at http://www.genesifter.net/product-info_releases.php#history.

Free GeneSifter.Net trial accounts are available by logging onto <http://www.genesifter.net/>.

About One-Click Gene Summaries

Researchers can find out what is known about any gene, anywhere on the Internet, with automatic One-Click Gene Summaries created by GeneSifter.Net from UniGene and LocusLink, plus click-throughs to other databases such as HomoloGene, GenBank®, GeneCards™, and OMIM™. Researchers can retrieve sequences, BLAST® or store them as part of their annotation for genes on arrays.

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