Discovery Studio® (DS) Gene brings the legendary ease of use of MacVector, our award-winning Macintosh sequence analysis application, to the Windows platform. DS Gene provides a native Windows look and feel while retaining the intuitive functionality of its Macintosh counterpart. Initiate sequence editing, PCR primer analysis, Internet database searches, protein analysis, and a wide variety of other functions with a single mouse click. View the results of any analysis function in interactive graphical or text format. A unique interactive Workbench window simplifies the organization and analysis of sequences on your computer’s hard drive.

In addition to the stand alone functionality, DS Gene provides a client interface hub that meets the bioinformatics needs of your entire organization, allowing users to seamlessly access DS GCG® programs to run proven searching and sequence analysis algorithms.

**Multiple Sequence Analysis.** Create alignments using ClustalW. Choose from integrated options, including a full-featured, color-coded alignment editor and a control panel to create customizable, publication-quality images from the alignment.

**Mapping.** Perform restriction digests and proteolytic analyses. You can add your own restriction enzymes and proteolytic agents.

**Primer Analysis.** Predict PCR and sequencing primers and hybridization probes. Save time by testing your personal primers against a template sequence in DS Gene before performing the experiment in the lab.

**Motif Searching.** Find sequence motifs for nucleic acids and peptides. You can also customize DS Gene by adding your own motifs for searches.

**Nucleic Acid Property Profiles.** View interactive graphs of base composition, coding preference plots, structural features and other properties to aid in the identification of open reading frames, promoters and other gene functions.

**Protein Analysis.** Predict protein secondary structure, hydropathy, antigenicity, and flexibility using the integrated Protein Analysis Toolbox.

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File Import and Export. Import and export sequence (and features) data in a variety of file formats, including BSML, GenBank, GenPept, EMBL, SWISS-PROT, FastA, FastP, Staden, GCG, and IG-Suite. Import and export multiple sequence alignments in PHYLIP, NEXUS, NBRF, and GCG-MSF formats.

Chromatogram Files. View, edit, align and analyze trace files from automated sequencing machines. DS Gene supports the formats used by most major manufacturers including ABI, SCF, ALF, CTF and ZTR formats.

DS Gene Advantages

Interactive Workbench. Use DS Gene’s Workbench view to navigate around your file system, preview the contents of sequence files and edit them without opening up a second window. Launch analysis functions directly from the Workbench or select multiple files to initiate sequence comparison or multiple alignment algorithms.

Integrated Internet BLAST and Entrez Searches. Perform gapped or ungapped BLAST searches against the databases at the NCBI. Or search the most current sequence data available including the High Throughput Genome Sequences (HTGS) division of Entrez. Retrieve sequences directly to your desktop without having to reformat them.

Interactive Gene Prediction. Designate the 5’ and 3’ ends of your inserted sequence as start or stop codons, or detect open reading frames with the coding preference plot analysis function. Select from a variety of algorithms, including Staden’s algorithms, Fickett’s statistical method, and Gribskov’s codon preference method. Click on an open reading frame in the plot and the corresponding region is highlighted in the sequence editor, ready for further analysis.

Multiple Sequence Comparison. Perform sequence comparisons in several ways on your desktop: create a multiple sequence alignment using ClustalW; compare a query sequence to a set of your own sequences; and produce a graphical dot plot using the Dot Plot function.

Customizable Sequence Graphics. Modify features and results maps of your sequence. You can choose which features and results to display, and change their appearance and labels. Easily import the resulting graphics into desktop publishing software for publication or into slide show software for presentations.

Accessing Powerful Searching Capabilities

DS Gene provides easy access to select DS GCG algorithms. You can run DS GCG sequence analysis programs directly from the Windows desktop with full integration into the DS Gene workflow environment. DS Gene supports a select number of database searching and sequence retrieval algorithms.
Like DS Gene, Discovery Studio desktop tools are built upon the popular, well-established Windows operating system, making it easier for scientists who are new or occasional users of computational tools to learn and use them to their potential. Being Windows-based also facilitates the quick transfer of analysis results to desktop productivity tools for further study or for communicating findings with colleagues.

System Requirements
- Windows® 2000 or XP
- 64 MB RAM
- CD-ROM drive
- 800 x 600 or larger color monitor
- Internet connection for BLAST/Entrez searches

Discovery Studio: An Integrated Platform for Drug Research

DS Gene is a component of Discovery Studio, Accelrys’ software architecture specially designed for the unique requirements of the pharmaceutical and biotechnology industries. This emerging suite of informatics, modeling, and simulation tools provides great science from easy-to-use desktop software that interacts with the databases throughout the corporate IT infrastructure. As a result, chemists and biologists realize better collaboration and R&D workflow because they can seamlessly transfer information between modules, applications, users, and workgroups.

LookUp. Identifies sequence database entries by name, accession number, author, organism, keyword, title, reference, feature, definition, length, or date.

BLAST. Searches for sequences similar to a query sequence. The query and the database searched can be either peptide or nucleic acid in any combination. Sites can create custom BLAST databases to use in addition to standard public databases.

FastA. Performs a Pearson and Lipman search for similarity between a query sequence and a group of sequences of the same type (nucleic acid or protein). For nucleotide searches, FastA is often more sensitive than BLAST.

Run powerful, secure database searches behind firewalls using the built-in DS GCG interface. BLAST results can be viewed as standard hit lists and alignments or in the interactive graphical map view like the one shown above.

Selections in analysis result windows are linked to the original sequence. You can easily create annotations from analysis result with a few simple mouse clicks.

Like DS Gene, Discovery Studio desktop tools are built upon the popular, well-established Windows operating system, making it easier for scientists who are new or occasional users of computational tools to learn and use them to their potential. Being Windows-based also facilitates the quick transfer of analysis results to desktop productivity tools for further study or for communicating findings with colleagues.