



# Gencarta™

THE ULTIMATE GENOME, TRANSCRIPTOME AND PROTEOME DATABASE RIGHT IN YOUR OWN LAB

Ile Leu Lys Met Phe Gly Pro Ser Thr Trp Tyr Val  
 AAA ACA GAC GAGGGA AAC ACA GTT TAGAAT GTA ACA  
 ACA GTT TAGAAT AAA ACA GAC GAGGGA  
 Leu Arg Asn Asp Cys Gln Glu  
 GAC AGGGAA AAC ACAGTT AGA ATAAAG ACA  
 GTT TAGAAT AAA ACA GAC GAGGGA AAC ACA GTT TAGAAT AAA ACA  
 Gln Glu Gly His Ile Leu Lys Met Phe Gly His Ser Thr Trp Tyr Val

We invite you to order a trial evaluation of our GeneGuide™ reports, illustrating the depth and breadth of the Gencarta database, its quality, and its novel information. Each GeneGuide report represents a single Gencarta entry. For more information, please visit [www.labonweb.com/GeneGuide](http://www.labonweb.com/GeneGuide), or contact us at [info@cgen.com](mailto:info@cgen.com).

## ABOUT COMPUGEN

Compugen (Nasdaq: CGEN) develops and markets platforms, tools and products to accelerate post-genomic research, advance the study of proteins and protein pathways, and support drug target discovery. These products include: LEADS, Gencarta, DNA Chip design, C-gen OligoLibrary, Z3, LabOnWeb.com and Bioccelerators. The Company's products and methodologies are developed through its leadership position in the convergence of the life sciences and computational technologies. Utilizing its in-house molecular biology laboratories, Compugen both validates its methodologies and is engaged in original genomic and proteomic research. Genes, proteins and other intellectual property discovered by the Company in its original research activities are patented by the Company and will be commercialized, primarily by licensing to third parties, through its Novel Genomics Division.

For additional information, please visit Compugen's corporate website at [www.cgen.com](http://www.cgen.com) and the Company's Internet research engine for molecular biologists, [www.labonweb.com](http://www.labonweb.com)

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NOW THAT SCIENCE HAS VALIDATED PROOF OF THE INHERENT COMPLEXITY OF THE HUMAN GENOME, THE REAL CHALLENGE LIES IN ACCESSING RELIABLE EXPRESSED TRANSCRIPTOME DATA—THE MISSING LINK BETWEEN THE GENOME AND THE PROTEOME. WHETHER YOU ARE DESIGNING A NEW EXPERIMENT, IDENTIFYING AND PRIORITIZING RESULTS OR VALIDATING FINDINGS, YOU NEED FAST AND SIMPLE ACCESS TO ALL-INCLUSIVE, UP-TO-DATE EXPRESSED AND GENOMIC DATA, INCLUDING AN AUTHORITATIVE SOURCE FOR mRNAs, SPLICE VARIANTS, AND MODELING OF BIOLOGICAL PHENOMENA. GENCARTA, AN ANNOTATED COLLECTION OF THE GENOME, TRANSCRIPTOME AND PROTEOME, IS WHAT YOU NEED.

## GENCARTA

Gencarta is the most authoritative database accessed via flexible query tools for advanced post-genomic research. Gencarta includes more than 150,000 fully annotated transcripts and their derived proteins. By applying Compugen's LEADS™ technology to vast amounts of scientific data, Gencarta accurately accesses and extracts the most comprehensive data available. With Gencarta, researchers can now uncover the wealth of the transcriptome, turning it into relevant knowledge to accelerate research processes and facilitate new biological discoveries.

## HARNESSING THE POWER OF LEADS™ TECHNOLOGY AND THE TRANSCRIPTOME

The rich pool of splice variants, antisense and other modeled biological phenomena available through Gencarta is the result of years of experience with LEADS technology and of rigorous molecular biology laboratory validation. LEADS is Compugen's core technology, employing proprietary and public advanced algorithms and thorough mining of EST (Expressed Sequence Tag) to analyze expressed and genomic data. This is the essence of the transcriptome, the bridge between genes and their coded proteins, and the foundation of Gencarta. Gencarta reflects this multi-layered map of the human genome, enabling in-depth, accurate understanding of underlying biological processes that are being applied in drug target discovery and therapeutic research.



## THE GENCARTA ADVANTAGE

- Enables unique biological discoveries
- Accelerates target discovery processes
- Enhances the probability of success in experimental design and implementation
- Facilitates access to combined analyses of expressed and genomic data
- Extracts and deploys the intrinsic value of the transcriptome

## GENCARTA IS MADE UP OF THREE COMPONENTS:

### DATABASE

The Gencarta database addresses underlying biological phenomena, novel information, predicted transcripts and proteins. Samples of LEADS results were tested and verified with a success rate of over 90% in Compugen's molecular biology laboratory. The Gencarta database comprises predicted genes, splice variants, SNPs, genomic alignments, chromosomal information, and alignment of ESTs to known mRNAs and transcripts. Each splice variant is further annotated with expression profiles, functional analysis, detailed domain summaries, known and predicted proteins, and detailed homology reports.

### GRAPHICAL USER INTERFACE

Gencarta's cross browser interface provides an intuitive graphic presentation of database elements and their inter-relationships, such as alignment with the genome, splice variant structure, and supporting ESTs. The viewer enables users to efficiently browse the genome.

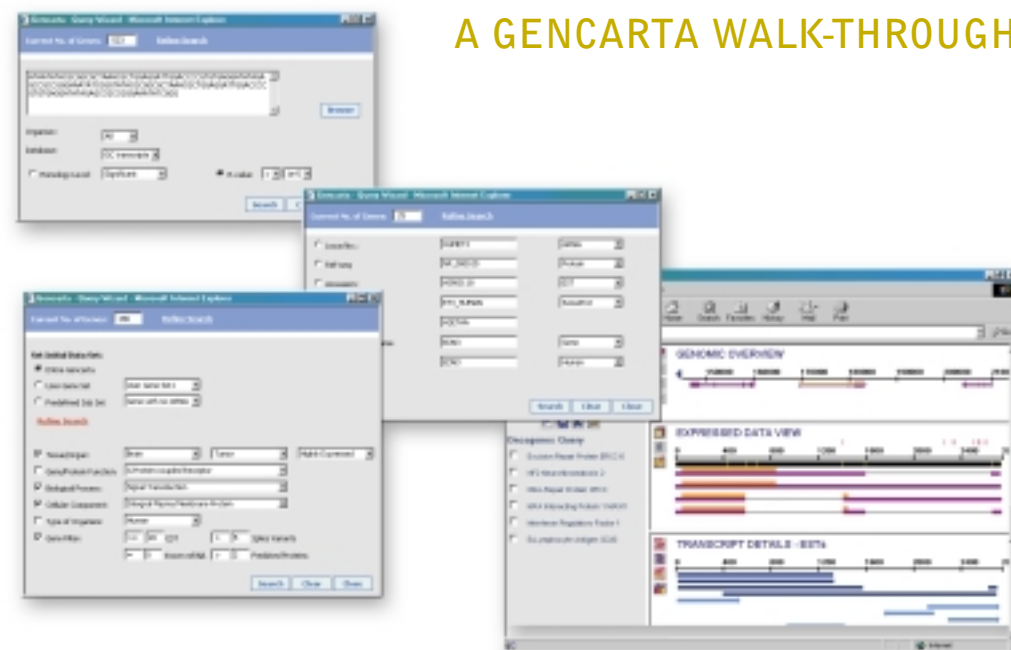
### QUERY TOOLS

The Gencarta database is mined using the built-in Gencarta Query Wizard, a set of dedicated query tools that are suitable for various types of experiment results, and support flexible point of entry. Searches are carried out by user's entered sequence, accession number, SAGE™ tags, tissue distribution, chromosomal location, sub-cellular localization, and more.

## GENCARTA FEATURES\*

- The genome, transcriptome and proteome combined in one authoritative data source
- Annotated genomic information including tens of thousands of putative genes, introns, exons and de-novo exon prediction.
- Most accurate representation of the genes and their respective splice variants and derived proteins
- Correct modeling of underlying biological processes, such as alternative splicing, SNPs, repeats, chimeric events and other new biological phenomena
- More than 150,000 putative transcripts and derived proteins
- Annotation of known and predicted transcripts and proteins including relative alignment, homology report, functional data sub-cellular localization, and more
- Expression patterns provided via SAGE™ technology, EST annotation, and more
- Multi entry-point query options: accession number, transcript sequence, peptide sequence, EST, chromosomal location (and optional customized attributes on special demand)
- Advanced query options: multiple criteria such as function, sub-cellular localization, chromosomal location and domains, filtered by organ, tissue, length of ORF, number of variants, and more
- User-friendly, informative interface, with easy-to-read printable report
- On-site installation ensuring unlimited, easy, fast, and secure access
- Frequent, regular database updates
- Cost-effective and adaptable for any size company or research facility

## A GENCARTA WALK-THROUGH



## TECHNICAL SPECIFICATIONS

Servers:	- Standard Unix server, running Oracle® 8i Release 2 version 8.1.6 (or higher).
Users workstations:	- Microsoft® Internet Explorer, version 4.5 and above, or Netscape® Communicator, version 4.7 and above. - Recommended screen resolution - 1024x768, or higher.

## SUBSCRIPTION OPTIONS

Gencarta is a complete self-contained package installed at customer sites and updated regularly. Gencarta is available in a range of customized installation and delivery packages. Partial or fully customized solutions uniquely suited to meet our clients' specific needs are available upon special request.

\*Gencarta database is updated regularly. The features listed in this document will be available during 2001.