

Product: BioRS Integration and Retrieval System

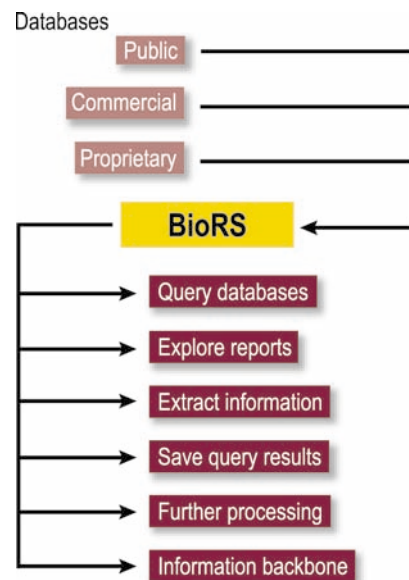
Applications: search and retrieval of public and proprietary databases, information backbone based on relational and flat-file formats in a distributed environment

Contact: info@biomax.com



TBX3_HUMAN						
T-box transcription factor TBX3 (T-box protein 3).						
▲	Overview	Features	Comments	Cross-references	References	Sequence
Accession number	O15119 Q8TB20					
Gene name(s)	TBX3					
Keywords	3D-structure, Alternative splicing, Developmental protein, Disease mutation, DNA-binding, Nuclear protein, Repressor, Transcription, Transcription regulation					
Organism source	Homo sapiens					
Taxonomy	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo,					
NCBI TaxID	9606					
Created	07/15/1999					
Sequence update	02/15/1999					
Annotation update	05/01/2005					
▲	Overview	Features	Comments	Cross-references	References	Sequence
DESCRIPTION : T-box, second part. COORDINATES : 241 - 304						

Excerpt from a BioRS view of a UniProt entry



Information integration and retrieval

As the amount and complexity of data continues to grow, quick and efficient information retrieval is a critical goal for research and development. Extracting information from multiple heterogeneous sources — including your own data as well as data from public and commercial databases — is an essential part of nearly every biological research project in the areas of biotechnology, medicine, pharmacology and agriculture.

Proprietary data — even when stored at different locations — can be combined with public and commercial databases and integrated into a unified environment. Scientists can locate related information from multiple sources using the extensive cross-linking between databases and combined reports.

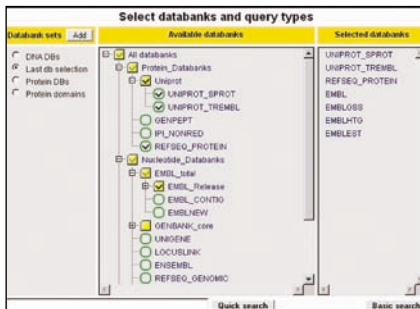
The BioRS™ system provides a convenient database search environment for users of various levels — whether occasional user, every-day user or expert. Multiple databases of different flat-file or relational formats can be searched simultaneously with a single query. Convenient tools are available for viewing and exporting retrieved information, and additional tools, such as BLAST or pattern search, can be integrated as necessary.

The BioRS system can be run as a stand-alone data integration and retrieval system or, alternatively, can be used as an information backbone supporting other software, such as the Pedant-Pro™ and BioXM™ systems.

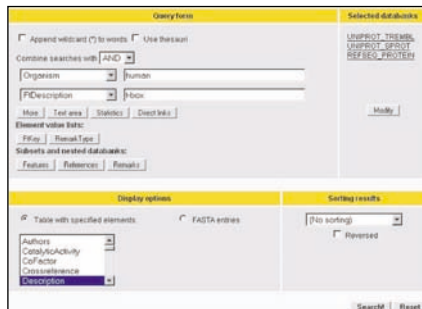
Get the most from your data

- Show protein information from UniProt together with the information from EMBL
- Select genes from BioRS query results and retrieve similar sequences from your proprietary database
- Find all human kinases with transmembrane domains which are associated with liver cancer
- Save genes from a specific plant pathway in a spreadsheet
- Retrieve specific bacterial genes for antibiotic resistance and export to plan cloning experiments
- Download a list of all plant storage proteins for input into pattern searches to find protease cleavage sites





Database selection page



BioRS query page

Accession	Description	Length	Score	Hit	Hit	Hit	Hit	Hit	Hit
U00000	Genome of Escherichia coli O157:H7	4,850,267	100.00	100.00	100.00	100.00	100.00	100.00	100.00
U00000	Genome of Escherichia coli O157:H7	4,850,267	100.00	100.00	100.00	100.00	100.00	100.00	100.00
U00000	Genome of Escherichia coli O157:H7	4,850,267	100.00	100.00	100.00	100.00	100.00	100.00	100.00

BioRS query result list

Find the information you want

Whether you want to perform a quick search on several databases simultaneously or a detailed search that takes advantage of database-specific features, the BioRS system provides easy-to-use tools for building queries and viewing search results.

Comfortable work environment

Both queries and search results can be saved in an individual archive for subsequent reuse or modification. Researchers can define their individual work environment with pre-selected sets of databases and user-specific views. Queries and environment customization can be made available to all users.

Efficient use of retrieved data

Query results can be downloaded in various formats (e.g., Excel) for use with other applications. External applications (e.g., perform a BLAST search with retrieved sequences) can be started from within the BioRS system.

Create an information backbone for your company

BioRS provides a search environment that is perfectly tailored to your company, combining public and proprietary databases from local and remote instances. Both flat-file and relational databases of different formats can be integrated into a unified environment. New databases can be easily added and indexed — parser-development support is available for making new database formats available. The Biomax™ Update Tool guarantees that all data are always up-to-date.

Integrate the BioRS system into your IT infrastructure

The BioRS system can be easily integrated into different computing environments. Parallel processing on multiprocessor computers or computer clusters provides optimal scalability for the growing amount of data and large user groups. Different interfaces are available for integration into the software environment: a command-line interface, HTTP and Web services.

Technical description

Using client-server architecture, the BioRS system provides individual modules for searching and indexing as services within a distributed computing environment. While the server runs on a UNIX® system, users can access the BioRS system with commonly used Web browsers. As the BioRS system does not require Internet access, maximal confidentiality is ensured. Individual users and user groups can be assigned privileges for controlling access to sensitive information.

External applications can be seamlessly integrated. The modular structure of the system together with the distributed programming approach allows parallel processing.

Extensible Markup Language (XML) is used for internal representation of heterogeneous biological, medical or literature databases, allowing semantic inter-operability and normalization regardless of differences between source data formats.

