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# All about proteins

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Chang-Su Lim

## Abstract

The Protein Information Database (PIR) is a non-redundant, comprehensive, highly and expertly annotated, fully classified and extensively cross-referenced protein sequence database in the public domain

# Content

The Protein Information Database (PIR) is a non-redundant, comprehensive, highly and expertly annotated, fully classified and extensively cross-referenced protein sequence database in the public domain. It is composed of the PIR auxiliary databases, including:

PIR-International Protein Sequence Database (PIR-PSD)

PIR-Archive Protein Sequence Database

FAMBASE

ProClass

PIR Integrated Environment for Sequence Analysis

Sequence-Structure Database (PIR-NRL3D)

Residues Database (PIR-RESID)

PIR-Alignment Database

PIR Non-Redundant Reference Sequence Database (PIR-ALN)

Annotation and Similarity Database (PIR-NREF)

[Link11]

Altogether, these provide integration of sequence and biological (structure and function) information to support genomics and proteomics research. The database includes all sequences that are in PIR-PSD, Swiss-Prot, TrEMBL, RefSeq, GenPept, and Protein Data Bank (PDB).

# Navigation

The PIR and its auxiliary databases are freely available to the public. Once you get onto the site, available databases are shown and are usefully classified into two large categories: database retrieval, and sequence search and analysis. Conducting a search is a bit of a challenge, which means that you have to know quite precisely what you want in order to retrieve the desired information. It is helpful to look through 'Demo Search' and/or 'How to use the PIR search request'. The website supports direct retrieval of PIR-NREF reports on the basis of sequence-unique identifiers obtained from the site, as well as full-scale BLAST search and peptide/pattern matching for functional identification of query proteins or peptides. The results are linked to the underlying databases for retrieval of up-to-date source entries.

# Reporter's comments

## Timeliness

Bi-weekly updates are made.

## Best feature

Comprehensiveness, non-redundancy, timeliness, quality annotation and full classification are the aims of this site, and their continuous development and improvement is its best feature.

## Worst feature

The database is not as user-friendly as it could be. The site would be improved by including obvious links to help files with definitions of the database terminology and explanations of all the parameters and abbreviations used. Another innovation that would make the database more user-friendly would be to have pop-up windows that offer help when the search text parameters are entered incorrectly.

## Related websites

Information on protein sequence and structure is also available through the websites of the [Link12], the [Link13], the [Link14], and the [Link15].

# Table of links

Protein Information Resource (PIR)

PIR-International Protein Sequence Database (PIR-PSD)

PIR-Archive Protein Sequence Database

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# References

1.  Protein Information Resource (PIR).

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