


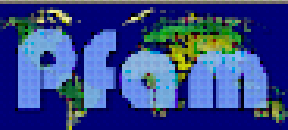
網址: <http://tw.expasy.org/prosite/>

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Search for

 **PROSITE**
Database of protein families and domains

網址: <http://www.sanger.ac.uk/Software/Pfam/>

 Protein families database of alignments and HMMs

Pfam: Pfam Home Page

網址: <http://pfam.wustl.edu/index.html>

 **Washington University in St. Louis**

Pfam :: Home
The Pfam database of protein families and HMMs

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ExPASy - PROSITE - Microsoft Internet Explorer

檔案(F) 編輯(E) 檢視(V) 我的最愛(A) 工具(T) 說明(H)

← 上一頁 → 搜尋 ★ 我的最愛 媒體

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Search for

PROSITE

Database of protein families and domains

PROSITE is a database of protein families and domains. It consists of biologically significant sites, patterns and profiles that help to reliably identify to which known protein family (if any) a new sequence belongs [[More details](#) / [References](#) / [Disclaimer](#)].

Release 18.34, of 19-Aug-2004 (contains 1277 documentation entries that describe 1736 different patterns, rules and profiles/matrices).

Access to PROSITE

in PROSITE by AC, ID or documentation text
☐ Prefix and append wildcard '*' to words.

- [Browse PROSITE documentation entries](#)
- [Search by author](#)
- [Search by citation](#)
- [Search by description](#)
- [Search by full text search](#)
- [SRS - Sequence Retrieval System](#)
- [Download by FTP](#)

Tools for PROSITE

Scan PROSITE patterns, profiles and rules with a Swiss-Prot/TrEMBL AC, ID or paste your own sequence in the box below (for more options, use the [ScanProsite](#) form):

- [ScanProsite](#) - Scan a sequence against PROSITE or a pattern against Swiss-Prot or PDB and visualize matches on structures
new with graphical view and feature detection

網際網路 下午 01:52

Windows taskbar: Bioinfo_B89 - ... ExPASy - PRO... Pfam - Protein ... MEME - Introd... Microsoft Powe...

ScanProsite - Microsoft Internet Explorer

檔案(F) 編輯(E) 檢視(V) 我的最愛(A) 工具(T) 說明(H)

← 上一頁 → 搜尋 我的最愛 媒體

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Search PROSITE for

proSite ScanProsite

The ScanProsite tool [\[Help\]](#) allows to scan protein sequence(s) (either from [Swiss-Prot](#) or [TrEMBL](#) or provided by the user) for the occurrence of patterns, profiles and rules (motifs) stored in the [PROSITE](#) database, or to search protein database(s) for hits by specific motif(s) [[Reference](#) / [Download ps_scan, the standalone version](#)]. The program [PRATT](#) can be used to generate your own patterns. You may either:

- Enter one or more PROSITE accession numbers and/or patterns [1 by line] to search the Swiss-Prot/TrEMBL and/or PDB databases, **OR**
- Enter one or more sequences [raw, Swiss_Prot or fasta format] and/or Swiss-Prot/TrEMBL accession numbers [1 by line] to be scanned with all patterns, profiles, rules in PROSITE, **OR**
- Fill in both fields to find all occurrences of a motif in a sequence.

Protein(s) to be scanned:

Enter one or more Swiss-Prot/TrEMBL accession number(s) [AC] (e.g. **P00747**) and/or sequence identifier(s) [ID] (e.g. **ENTK_HUMAN**), and/or PDB identifier, and/or paste **your own protein sequence(s)** in the box below:
(leave this box blank to scan PROSITE entrie(s) against selected protein databases)

PROSITE pattern(s)/profile(s) to scan for:

Enter one or more PROSITE accession number(s) (e.g. **PS50240**), and/or identifier(s) (e.g. **CHEB**), and/or type **your pattern(s)** in [PROSITE format](#) in the box below:
(leave this box blank to scan sequence(s) against the entire PROSITE database)

完成 網際網路

開始 Bioinfo_B... ScanProsit... Pfam : Pro... MEME - I... 簡報2 week6_motif 下午 01:54

Pfam: Pfam Home Page - Microsoft Internet Explorer

檔案(F) 編輯(E) 檢視(V) 我的最愛(A) 工具(T) 說明(H)

← 上一頁

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網址(D) <http://www.sanger.ac.uk/Software/Pfam/> 移至

 **Protein families database of alignments and HMMs** 

Pfam: Pfam Home Page


Home Search by Browse by ftp iPfam Help

Pfam is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains and families. For each family in Pfam you can:

- Look at multiple alignments
- View protein domain architectures
- Examine species distribution
- Follow links to other databases
- View known protein structures

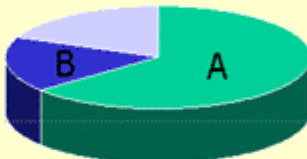
For more information on Pfam, on using this site, or on the changes between Pfam releases 14 and 15, click [here](#).

Pfam can be used to view the domain organisation of proteins. A typical example is shown below. Notice that a single protein can belong to several Pfam families.



Version 15.0

August 2004, **7503** families




| | |
|---|--------------------------------|
| ■ | Sequence coverage Pfam-A : 74% |
| ■ | Sequence coverage Pfam-B : 24% |
| ■ | Other |

Enter your keyword(s) here

Go

Example

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bioinf...

2 Mic...

Pfam: P...

Adobe ...

Micros...



上午 10:44

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Protein families database of alignments and HMMs

Wellcome Trust
Sanger
Institute

Pfam: Pfam Home Page

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Protein name or sequence

Keyword

Domain query

DNA sequence


Taxonomy query

Pfam is a database of protein families, alignments and hidden Markov models covering many protein families. For each family in Pfam you can:

- Look up a protein
- View a protein's domain architecture
- Examine species distribution
- Follow links to other databases
- View known protein structures

For more information on Pfam, on using this site, or on the changes between Pfam releases 14 and 15, click [here](#).

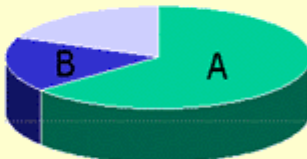
Pfam can be used to view the domain organisation of proteins. A typical example is shown below. Notice that a single protein can belong to several Pfam families.



voltage_CLC CBS CBS [687 residues]

Version 15.0

August 2004, 7503 families



■ Sequence coverage Pfam-A : 74%

■ Sequence coverage Pfam-B : 24%

■ Other

Enter your keyword(s) here

Go Example

開始

bioinf...

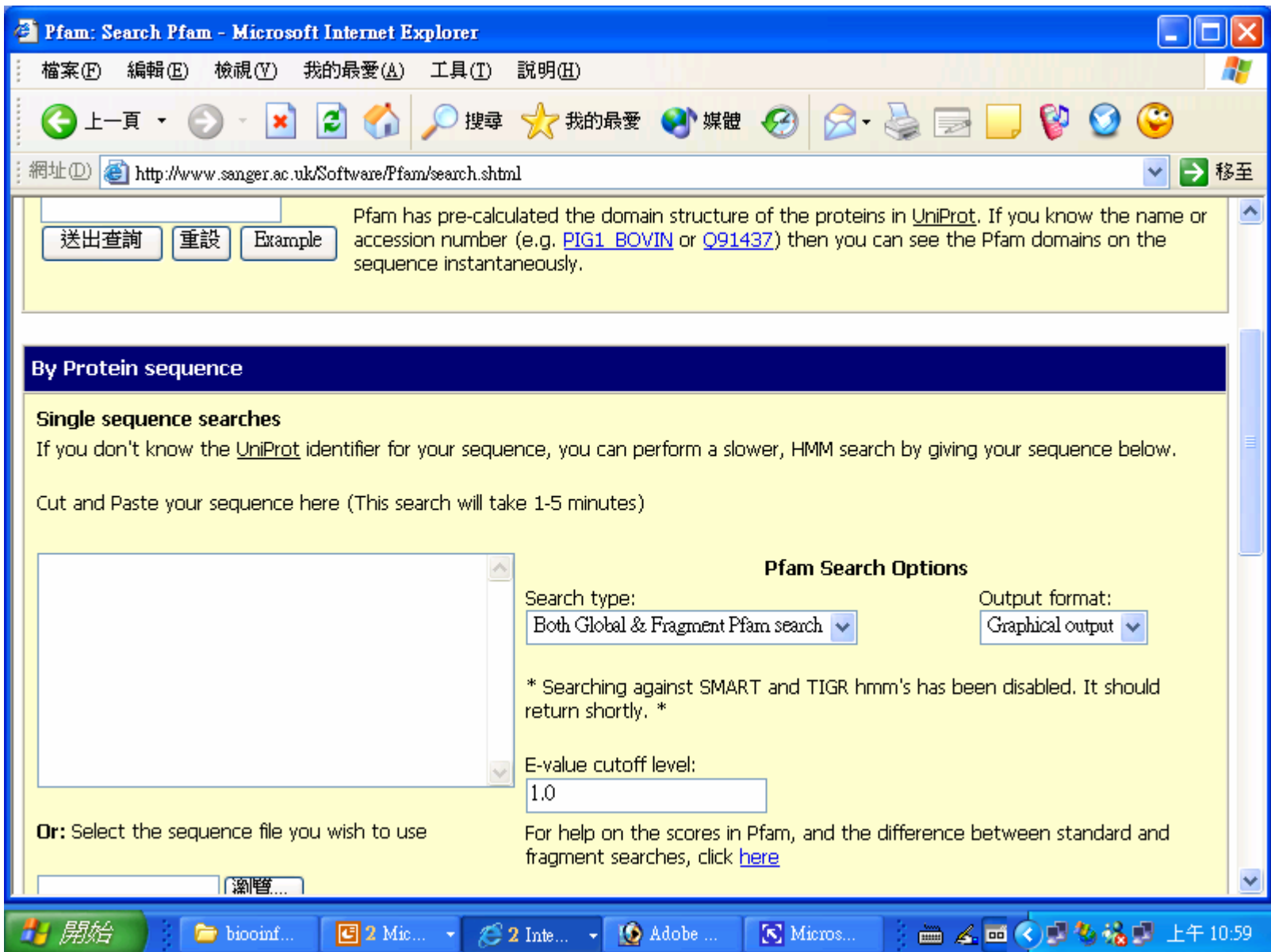
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2 Inte...

Adobe ...

Micros...

上午 10:58



Pfam : Home (Saint Louis) - Microsoft Internet Explorer

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The Pfam database of protein families and HMMs

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Pfam 14.0 (June 2004, 7459 families)

Pfam is a large collection of **multiple sequence alignments** and **hidden Markov models** covering many common protein families. Pfam version **14.0** (June 2004) contains alignments and models for **7459** protein families, based on the **Swissprot 43.2** and **SP-TrEMBL 26.2** protein sequence databases.

- [HELP](#) More information on Pfam, using this site, and the changes between Pfam releases.
- [PROTEIN SEARCH](#) Analyze a protein query sequence to find Pfam family matches.
- [DNA SEARCH](#) Analyze a DNA query sequence to find Pfam family matches. (Uses the GeneWise server at the Sanger Centre.)
- [BROWSE PFAM](#) View Pfam annotation and alignments.
- [KEYWORD SEARCH](#) Query Pfam by keywords.
- [TAXONOMY SEARCH](#) Find Pfam families by taxonomy.
- [BROWSE SWISSPFAM](#) View the domain organization of a SWISSPROT/TrEMBL sequence according to Pfam.

開始 Pfam : Ho... MEME - I... 簡報2 The RCSB... NCBI Seq... Yahoo!奇... 下午 03:05



Washington University in St. Louis

Pfam :: Protein Search

Analyze a query sequence using the Pfam HMM database

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[Home](#) | [Protein search](#) | [DNA search](#) | [Browse Pfam](#) | [Keyword search](#) | [Taxonomy search](#) | [SwissPfam](#) | [Help](#)

Analyze a query sequence by searching Pfam HMMs

Cut and paste your sequence here.
FASTA format or raw sequence are acceptable:

Or

Select the query sequence file you wish to use:

More advanced options



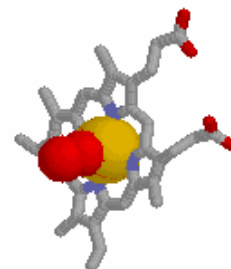
Molecular Visualization Freeware

[Protein Explorer](#), [Chime](#) & [RasMol](#)

This is the *RasMol Home Page*
visited by over 500,000 people
from over 115 countries!

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[Oxy-hemoglobin](#) zooming in to [oxy-heme](#) (from [1hho.pdb](#) by B. Shaanan). This is an [animated picture](#); unlike with [Protein Explorer](#), you cannot move it with your mouse.

[Protein Explorer](#), a RasMol-derivative, is the [easiest-to-use and most powerful](#) software for looking at macromolecular structure and its relation to function. And it's free! It runs on Windows or Macintosh/PPC computers. ([linux users see below](#).) RasMol users will find its menus very familiar, and it understands RasMol commands. It is very fast: rotating a protein or DNA molecule shows its 3D structure. If you have never seen this, watch the image at the upper right of this page. (Click here to [see another molecule rotate](#).) Look at our [gallery](#) to see still snapshots of other molecules. Also available here are Chime-based tutorials on

- [DNA](#),
- [Hemoglobin](#),
- [Antibody](#),
- [The Protein Morpher](#),
- [Infrared spectra with animated molecular vibrations](#),
- Tutorials on [many other popular molecules](#).

The above resources employ the Netscape plug-in [Chime](#), freeware from MDL, and derived from RasMol. Here are reference materials and templates about [how to create your own Chime websites](#).



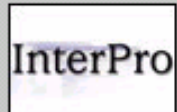
<http://www.ebi.ac.uk/interpro/>

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- Documentation
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InterPro

InterPro is a useful resource for whole genome analysis and has already been used for the proteome analysis of a number of completely sequenced organisms including *preliminary* analyses of the mouse and human genomes.



Further information on InterPro can be found in the Documentation page, which includes links to the release notes, the user manual, a list of deleted InterPro entries, the dataflow scheme of the database, a fully annotated sample entry and references for the member databases.

InterPro is headed by **Rolf Apweiler**.

[Updated Documents and New Links](#)

Proteome Analysis



Statistical and comparative analysis of the predicted proteomes of fully sequenced organisms.

QuickGO

