

Structural Databases II

MIC 405c | Microbial Genomics & Proteomics

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Cn-3D- structure viewers

The screenshot shows the NCBI Structure website interface. At the top, there is a navigation bar with the NCBI logo and the word "Structure" in a large blue font. Below this, there is a search bar with a dropdown menu set to "Structure" and a "Search" button. To the right of the search bar are links for "Limits", "Advanced search", and "Help". Below the search bar, there are three dropdown menus: "Structure Group", "3D Macromolecular Structures", and "Conserved Domains".

Cn3D macromolecular structure viewer

[ABOUT](#) [TUTORIAL](#) [FAQ](#) [INSTALL](#) [PUBLICATIONS](#) [NEWS](#) [RESOURCES](#) [DISCOVER](#)

About Cn3D

Cn3D ("see in 3D") is a helper application for your web browser that allows you to view 3-dimensional structures from NCBI's [Entrez Structure](#) database. Cn3D is provided for [Windows](#) and [Macintosh](#), and can be compiled on [Unix](#). Cn3D simultaneously displays structure, sequence, and alignment, and now has powerful annotation and alignment editing features. *(For those who prefer to view 3D structures on the web, without the need to install a separate application, [iCn3D](#) ("I see in 3D") is available as of April 2016.)*

Below is a relatively simple sample of what **Cn3D** can do. There are many more examples in the [Tutorial](#), along with instructions to help new users get started!

Highlights

Web-based Structure Viewer

- [iCn3D](#) ("I see in 3D"), released in April 2016, provides interactive views of three-dimensional macromolecular structures on the web.
- There is no need to install a separate application in order to use [iCn3D](#); you just need to use a web browser that supports [WebGL](#).
- [iCn3D](#) also allows you to customize the display of a structure and generate a URL that allows you to share the link and to

A comprehensive help document

Cn3D FAQ

Frequently Asked Questions

Cn3D Install

Installation and Configuration

MMDB

NCBI's structure database

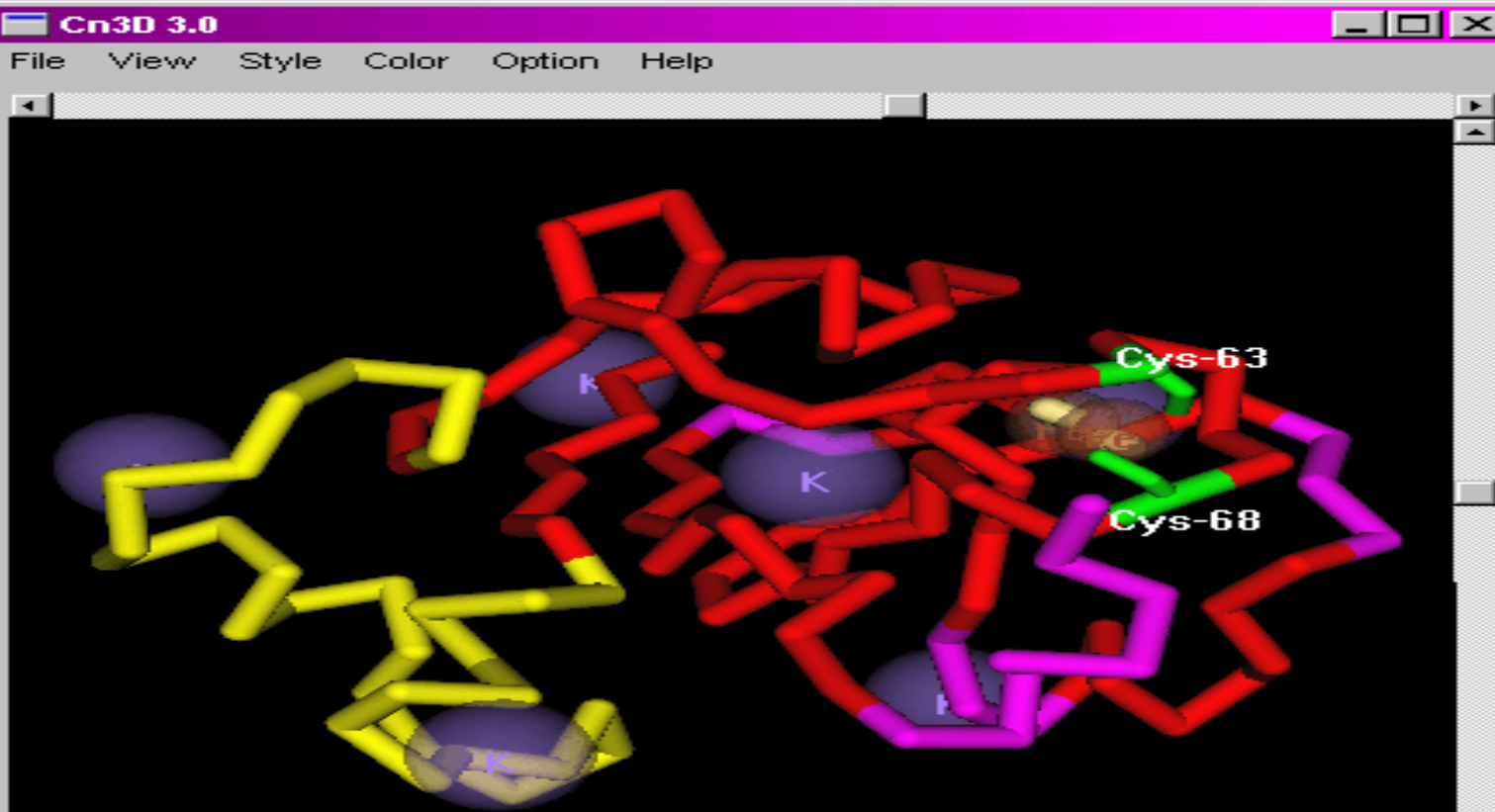
PDBeast

Taxonomy in MMDB

VAST

Structure comparisons

VAST Search



The screenshot shows the Cn3D 3.0 software interface. The main window displays a 3D ribbon representation of a protein structure. Two cysteine residues are highlighted in green and labeled "Cys-63" and "Cys-68". Other residues are shown in red, yellow, and purple. The interface includes a menu bar with "File", "View", "Style", "Color", "Option", and "Help".

Below the main window is the DDV (Distance-Derived Vectors) window. It has a menu bar with "File", "Alignment", "Options", and "Help". It features a "Go to:" field with "row:" and "col:" input boxes, both set to "0". Below this is a sequence alignment view showing two sequences: "1DOI" and "1AWD". The sequence "1DOI" is highlighted in yellow, and "1AWD" is shown in red. The alignment is shown with a scale from 0 to 30. The status bar at the bottom indicates "Ready !".

Rasmol/RasTop

RasMol is a molecular graphics program intended for the visualisation of proteins, nucleic acids and small molecules.

The program reads in a molecule coordinate file and interactively displays the molecule on the screen in a variety of colour schemes and molecule representations.


Currently available representations include depth-cued wireframes, 'Dreiding' sticks, spacefilling (CPK) spheres, ball and stick, solid and strand biomolecular ribbons, atom labels and dot surfaces.

Expert Protein Analysis System (Original): ExPASy-integrated genomics, proteomics resource of SIB



Expasy












Swiss Bioinformatics Resource Portal



e.g. [BLAST](#), [UniProt](#), [MSH6](#), [Albumin](#)...

- Genes & Genomes**
 - Genomics
 - Metagenomics
 - Transcriptomics
- Proteins & Proteomes**
- Evolution & Phylogeny**
 - Evolution biology
 - Population genetics
- Structural Biology**

SIB Resources ⓘ

| | | | |
|--|---|---|---|
|   STRING Protein-protein interaction networks and enrichment analysis |    SWISS-MODEL Protein structure homology-modelling |   UniProtKB/Swiss-Prot Protein knowledgebase |   neXtProt Human protein knowledgebase |
|   SwissLipids Knowledge resource for lipids | | | |

<https://www.expasy.org/resources/nextprot>

Selected WWW database resources for macromolecular structures.

| Databases | URL |
|---|---|
| Structure and sequence/structure databases | |
| SCOP | http://scop.mrc-lmb.cam.ac.uk/scop/ |
| CATH | http://www.biochem.ucl.ac.uk/bsm/cath/ |
| FSSP | http://www2.ebi.ac.uk/dali/fssp/ |
| Molecular Modeling Database | http://www.ncbi.nlm.nih.gov/Structure/ |
| CAMPASS | http://www-cryst.bioc.cam.ac.uk/~compass/ |
| ISSD | http://www.protein.bio.msu.su/issd/ |
| Library of Protein Family Cores (LPFC) | http://WWW-SMI.Stanford.EDU/projects/helix/LPFC/ |
| 3D_ALI (a database of aligned protein structures and related sequences) | http://www.embl-heidelberg.de/argos/ali/ali_info.html |
| IDITIS (relational database and query tool for proteins) | http://www.oxmol.co.uk/prods/iditis/ |
| HSSP | http://www.sander.embl-heidelberg.de/hssp/ |
| Speciality databases | |
| HIV Protease Database | http://www-lbnc.ncifcrf.gov/HIVdb/ |
| Nucleic Acid Database | http://ndbserver.rutgers.edu/ |
| Prolysis (protease and protease inhibitor Web server) | http://delphi.phys.univ-tours.fr/Prolysis/ |
| International Immunogenetics Database (IMGT) | http://imgt.cnusc.fr:8104/ |
| Enzyme Structures Database | http://www.biochem.ucl.ac.uk/bsm/enzymes/ |
| Features databases | |
| Molecular Movements Database | http://bioinfo.mbb.yale.edu/MolMovDB/ |
| OLDERADO | http://neon.chem.le.ac.uk/olderado/ |
| PROCAT | http://www.biochem.ucl.ac.uk/bsm/PROCAT/PROCAT.html |
| Protein Quaternary Structures (PQS) | http://pqs.ebi.ac.uk/ |
| ReLIBase (receptor-ligand complexes database) | http://www2.ebi.ac.uk:8081/home.html |
| PROMISE | http://bioinf.leeds.ac.uk/promise/ |
| PDBSum | http://www.biochem.ucl.ac.uk/bsm/pdbsum/ |
| Biological Macromolecule Crystallization Database (BMCD) | http://h178133.nist.gov:4400/bmcd/bmcd.html |
| Resources | |
| Protein Data Bank | http://www.rcsb.org/pdb/ |

SCOP-Structural Classification of Proteins



[About](#)

[Contact](#)

[Download](#)

The legacy SCOP websites can be accessed at **SCOP 1.75** and **SCOP2 prototype**

SCOP 2

[Learn More](#)

SCOP: Structural Classification of Proteins

Nearly all proteins have structural similarities with other proteins and, in some of these cases, share a common evolutionary origin. The SCOP database, created by manual inspection and abetted by a battery of automated methods, aims to provide a detailed and comprehensive description of the structural and evolutionary relationships between all proteins whose structure is known. As such, it provides a broad survey of all known protein folds, detailed information about the close relatives of any particular protein, and a framework for future research and classification.

Latest update on **2021-05-27** includes **68,816** non-redundant domains representing **772,354** protein structures. Folds, superfamilies and families statistics [here](#).

SCOP

- 1995 (yearly updated) Manual classification of protein structure domains
- Class- general structural architecture of protein (β sheet, α helix, membrane protein, coiled, peptide fragments, multidomain, non natural derived)
- Fold- Similar arrangements of secondary structures
- Superfamily- structural and functional similarity
- Family- sequence similarity shared

classification.

Latest update on **2021-05-27** includes **68,816** non-redundant domains representing **772,354** protein structures. Folds, superfamilies and families statistics [here](#).

Keyword and ID search

Sequence search

Enter free text, SCOP ID, PDB ID or UniProt ID

Go

Browse by structural class

- [All alpha proteins](#)
- [All beta proteins](#)
- [Alpha and beta proteins\(a/b\)](#)
- [Alpha and beta proteins\(a+b\)](#)
- [Small proteins](#)

Browse by protein type

- [Globular proteins](#)
- [Membrane proteins](#)
- [Fibrous proteins](#)
- [Non-globular/Intrinsically unstructured proteins](#)

Please cite: Antonina Andreeva, Dave Howorth, Cyrus Chothia, Eugene Kulesha, Alexey Murzin, SCOP2 prototype: a new approach to protein structure mining. (2014) Nucl. Acid Res., 42 (D1): D310-D314 and Antonina Andreeva, Eugene Kulesha, Julian Gough, Alexey Murzin, The SCOP database in 2020: expanded classification of representative family and superfamily domains of known protein structures. (2020) Nucl. Acid Res., 48 (D1): D376-D382

Show ancestry

Families [1 entry]

- **SARS coronavirus accessory protein X4 (ORF8, ORF7a)** SCOP ID 4007538

Domains [3 entries]

| | ID | Region | Links |
|---|----------------------------------|------------------|---|
| Protein Protein 7a Species <i>Severe acute respiratory syndrome-related coronavirus</i> Representative domain 8055375 Represented structures [1] | P59635 1XAK | 15-82 A:-1-67 | UniProt PDBe RCSB PDB |
| Protein Protein 7a Species <i>Severe acute respiratory syndrome coronavirus 2</i> Representative domain 8092974 | P0DTC7 6W37 | 16-81 A:1-66 | UniProt PDBe RCSB PDB |
| Protein Accessory protein 7a Species <i>Severe acute respiratory syndrome coronavirus 2</i> Representative domain 8102631 | A0A6C0X2S1 7CI3 | 14-82 A:14-82 | UniProt PDBe RCSB PDB |

FOLD

TIM beta/alpha-barrel

SCOP ID: 2000031

(beta-alpha)₈; parallel beta-sheet barrel, closed, n=8, S=8, strand order 12345678 (anticlockwise); the first seven superfamilies have similar phosphate-binding sites

Keywords **beta-barrel** **parallel beta-sheet** **anticlockwise**

Superfamilies [34 entries]

- **(Trans)glycosidases** SCOP ID 3000313 
Families: 25 
- **Metallo-dependent hydrolases** SCOP ID 3000428 
the beta-sheet barrel is similarly distorted and capped by a C-terminal helix has transition metal ions bound inside the barrel
Families: 18 
- **Xylose isomerase-like** SCOP ID 3000560 
different families share similar but non-identical metal-binding sites
Families: 9 
- **Aldolase** SCOP ID 3000445 
Common fold covers whole protein structure
Families: 8 
- **Phosphoenolpyruvate/pyruvate domain** SCOP ID 3000510 

CATH:

-University College of London

-1990 established

- Evolutionary relationships of protein domains

-

The four main levels of the CATH hierarchy:

| # | Level | Description |
|---|-------------------------------|--|
| 1 | Class | the overall secondary-structure content of the domain. (Equivalent to the SCOP Class) |
| 2 | Architecture | high structural similarity but no evidence of homology . (Equivalent to the 'fold' level in SCOP) |
| 3 | Topology/fold | a large-scale grouping of topologies which share particular structural features |
| 4 | Homologous superfamily | indicative of a demonstrable evolutionary relationship. (Equivalent to SCOP superfamily) |

CATH

- Hierarchical semi-automatic
- Classes derived from secondary protein structure and packing (all [alpha](#), all [beta](#), a mixture of alpha and beta, or little secondary structure)
- Architecture: derived from secondary structure arrangement in three-dimensional space
- Topology: information on how the secondary structure elements are connected and arranged is used
- Homology: assignments are made to the [Homologous superfamily](#) (H) level if there is good evidence that the domains are related by evolution

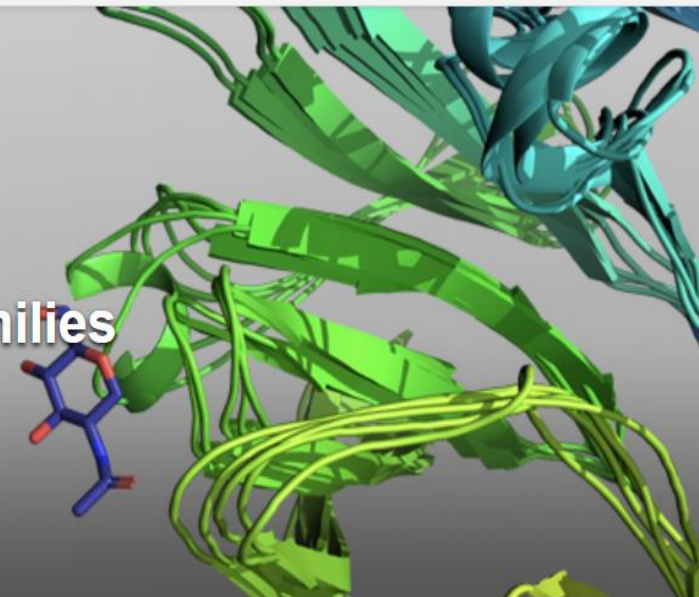


CATH / Gene3D v4.3

151 million protein domains classified into 5,481 superfamilies

Search by keywords, PDB code, GO term, etc

Search



22-23 July 2020 The CATH website experienced some technical issues during this period as a result of a power outage. Everything should now be working as expected now - apologies for the inconvenience.

Core classification files for the latest version of CATH-Plus (v4.3) are [now available to download](#). [Daily updates](#) of our very latest classifications are also available.



3D Structure

Find out what 3D structure your protein adopts

Find out more

Go



Protein Evolution

Learn about a particular protein family and how it evolved

Find out more



Protein Function

Investigate the function of your protein

Find out more

Go



Conserved Sites

Look at protein sites that are highly conserved and implicated in function

Find out more

Go



Download Data

Download data files and query CATH via webservice

Go



Learn more

Find out how CATH is created and maintained, how to link to CATH and more

Go


Specialized Protein Database

← → ↻ prosite.expasy.org

Apps YouTube to Mp3 C... Sci-Hub: removing... eProMIS: Departme... Free Online Course... Microbiology Hom... Giants in genomics...

Expasy PROSITE

[Home](#) | [ScanProsite](#) | [ProRule](#) | [Documents](#) | [Downloads](#) | [Links](#) | [Funding](#)

 **Database of protein domains, families and functional sites**

New [SARS-CoV-2 relevant PROSITE motifs](#)

PROSITE consists of documentation entries describing protein domains, families and functional sites as well as associated patterns and profiles to identify them [[More...](#) / [References](#) / [Commercial users](#)].
PROSITE is complemented by [ProRule](#), a collection of rules based on profiles and patterns, which increases the discriminatory power of profiles and patterns by providing additional information about functionally and/or structurally critical amino acids [[More...](#)].

Release 2021_02 of 07-Apr-2021 contains 1883 documentation entries, 1311 patterns, 1311 profiles and 1342 ProRule.

Search

e.g. PDOC00022, PS50089, SH3, zinc finger

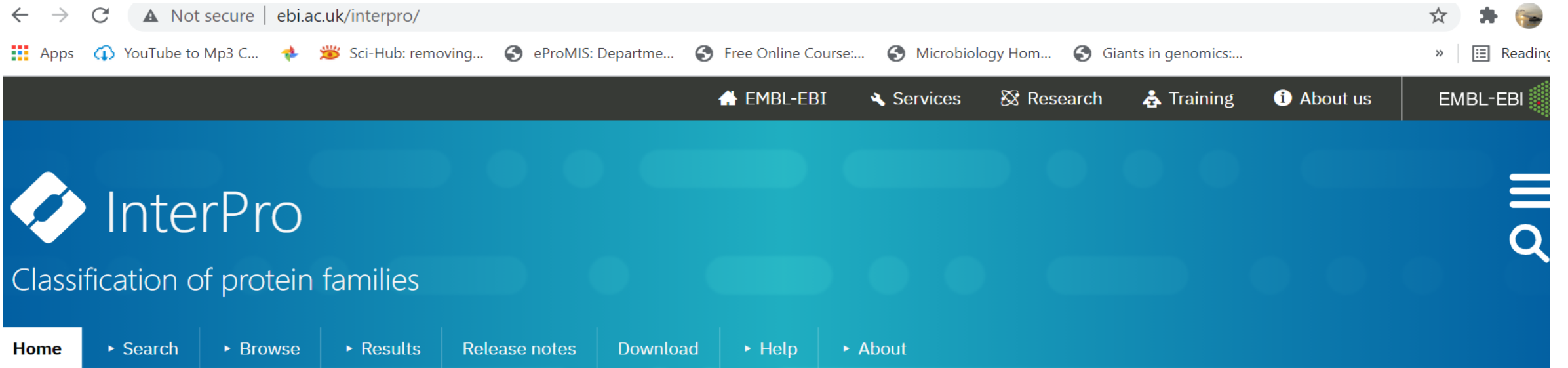
Browse

- [by documentation entry](#)
- [by ProRule description](#)
- [by taxonomic scope](#)
- [by number of positive hits](#)

PROSITE

- 1988 by [Amos Bairoch](#)
 - It is part of the [ExPASy proteomics](#) analysis servers
- Hosted by SIB
- PROSITE offers tools for protein [sequence analysis](#) and motif detection (see [sequence motif](#), [PROSITE patterns](#))

Interpro- functionally analyzes protein sequences and classifies them into [protein families](#) while predicting the presence of [domains](#) and functional sites.



← → ↻ Not secure | ebi.ac.uk/interpro/ ☆ ⚙️ 🌐

Apps YouTube to Mp3 C... Sci-Hub: removing... eProMIS: Departme... Free Online Course:... Microbiology Hom... Giants in genomics... » | Reading

EMBL-EBI Services Research Training About us EMBL-EBI

InterPro

Classification of protein families

Home ▶ Search ▶ Browse ▶ Results Release notes Download ▶ Help ▶ About



85.0

InterPro 85.0
8 April 2021

Classification of protein families

InterPro provides functional analysis of proteins by classifying them into families and predicting domains and important sites. To classify proteins in this way, InterPro uses predictive models, known as signatures, provided by several different databases (referred to as member databases) that make up the InterPro consortium. We combine protein signatures from these member databases into a single searchable resource, capitalising on their individual strengths to produce a powerful integrated database and diagnostic tool.

▶ Citing InterPro

PFAM



Pfam 34.0 (March 2021, 19179 entries)

The Pfam database is a large collection of protein families, each represented by **multiple sequence alignments** and **hidden Markov models (HMMs)**. [Less...](#)

Proteins are generally composed of one or more functional regions, commonly termed **domains**. Different combinations of domains give rise to the diverse range of proteins found in nature. The identification of domains that occur within proteins can therefore provide insights into their function.

Pfam also generates higher-level groupings of related entries, known as **clans**. A clan is a collection of Pfam entries which are related by similarity of sequence, structure or profile-HMM.

The data presented for each entry is based on the [UniProt Reference Proteomes](#) but information on individual UniProtKB sequences can still be found by entering the protein accession. Pfam *full* alignments are available from searching a variety of databases, either to provide different accessions (e.g. all UniProt and NCBI GI) or different levels of redundancy.

QUICK LINKS

[SEQUENCE SEARCH](#)

[VIEW A PFAM ENTRY](#)

[VIEW A CLAN](#)

[VIEW A SEQUENCE](#)

[VIEW A STRUCTURE](#)

[KEYWORD SEARCH](#)

[JUMP TO](#)

YOU CAN FIND DATA IN PFAM IN VARIOUS WAYS...

Analyze your protein sequence for Pfam matches

View Pfam annotation and alignments

See groups of related entries

Look at the domain organisation of a protein sequence

Find the domains on a PDB structure

Query Pfam by keywords

[Go](#)

[Example](#)

Post translational modifications

← → ↻ web.expasy.org/glycomod/ ☆

Apps YouTube to Mp3 C... Sci-Hub: removing... eProMIS: Departme... Free Online Course... Microbiology Hom... Giants in genomics:...

Expasy GlycoMod Home

GlycoMod Tool

GlycoMod is a tool that can predict the possible oligosaccharide structures that occur on proteins from their experimentally determined masses. The program can be used for free or derivatized oligosaccharides and for glycopeptides [[Documentation](#) / [Mass values](#) / [Reference](#) / [Disclaimer](#)].

Note: You can use [GlycanMass](#) to calculate the mass of an oligosaccharide structure from its oligosaccharide composition.

Enter a list of [experimental masses](#):

All mass values are
 average or monoisotopic.

Or upload a file, containing one mass per line, from your computer:
 No file chosen

Mass tolerance: +/- ▾

Ion mode and adducts:

| positive | negative | neutral |
|---|--|---------------------------|
| <input checked="" type="radio"/> [M+H] ⁺ | <input type="radio"/> [M-H] ⁻ | <input type="radio"/> [M] |
| <input type="radio"/> Na ⁺ or <input type="radio"/> K ⁺ | <input type="radio"/> acetate or <input type="radio"/> trifluoroacetic acid | |
| <input type="radio"/> other: <input type="text"/> mass: <input type="text"/> | <input type="radio"/> other: <input type="text"/> mass: <input type="text"/> | |

N-linked oligosaccharides OR **O-linked oligosaccharides**

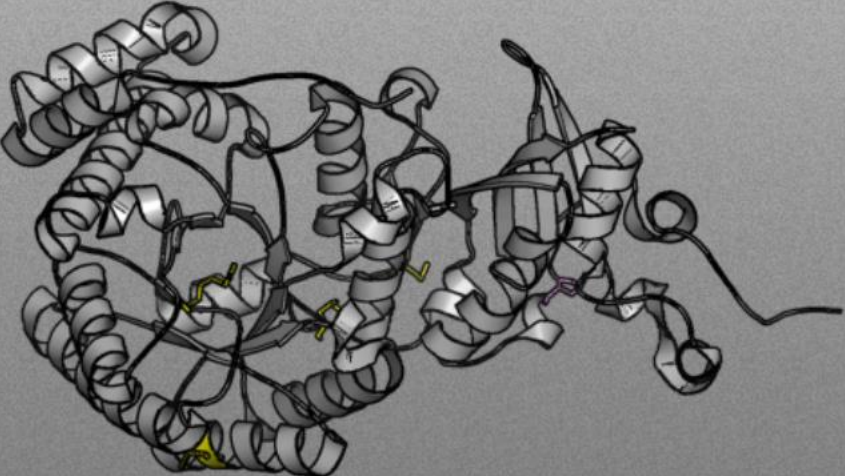
Form of N-linked oligosaccharide: ▾

Form of O-linked oligosaccharide: ▾

PTM STRUCTURAL DATABASE

- HOME
- BROWSE DATABASE
- TOOLS
- CREATE YOUR DATASET
- CONTACT
- LINKS
- ABOUT PTM-SD

- PTM STRUCTURAL DATABASE
- DATA SOURCE
- FLOWCHART
- STATISTICS



Hydroxylation on P-104 in P00877

Welcome to the Post Translational Modification Structural Database (PTM-SD).

Proteins are composed of a succession of amino acid residues. Their 3D structures are the support of major crucial biological functions.

Post translational modifications (PTMs) are covalent chemical modifications of proteins that typically occur after the protein synthesis.

They allow a fine and sometimes obligatory modulation of biological functions; they can determine proteins activity state, localization, turnover, and interactions with other proteins.

PTM-SD provides an access to proteins for which PTMs are both experimentally annotated and structurally resolved.

[Read more...](#)

PTM STRUCTURAL DATABASE

ABOUT PTM-SD

GENERAL REMARKS

BROWSE DATABASE

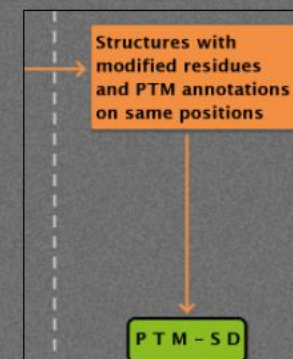
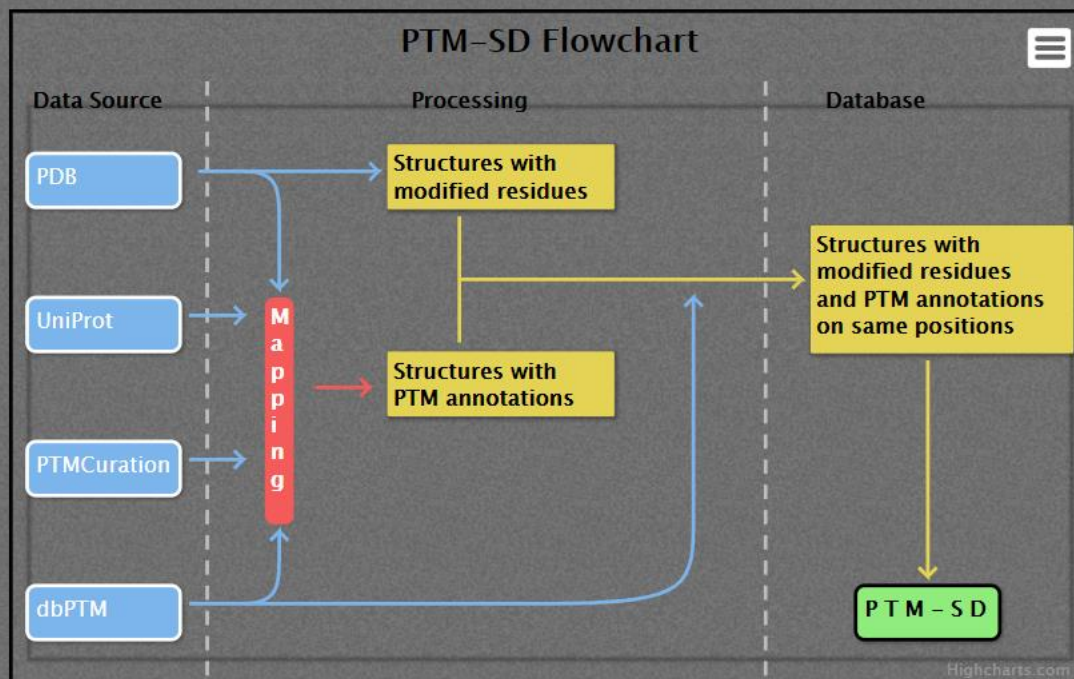
TOOLS

CREATE YOUR DATASET

GALLERY

ALIGNMENT

FLOWCHART



For the last step it was necessary to verify if the PTM annotations correspond to the chemical structure of the modified r

We use automatic and manual verification processes, which are based on the atom info and a [correspondence annotation table](#).

Databases related to Proteomics

- Contain information obtained by 2D-PAGE: master images of the gels and description of identified proteins
- Examples: SWISS-2DPAGE, ECO2DBASE, Maize-2DPAGE, Sub2D, Cyano2DBase, etc.
- Format: composed of image and text files
- Mass Spectrometry (MS) database



SWISS-2DPAGE

Two-dimensional polyacrylamide gel electrophoresis database

SWISS-2DPAGE

Search by

- [\[accession number\]](#)
- [\[description, ID or gene\]](#)
- [\[author names\]](#)
- [\[spot ID / serial number\]](#)
- [\[identification methods\]](#)
- [\[pI / Mw range\]](#)
- [\[combined fields\]](#)

Maps

- [\[experimental info\]](#)
- [\[protein list\]](#)
- [\[graphical interface\]](#)

Select Remote Interfaces

- [All Interfaces]**
- World-2DPAGE Portal**
- World-2DPAGE Repository**

Exclude local DBs
has only effect if a remote interface is selected

SWISS-2DPAGE contains data on proteins identified on various 2-D PAGE and SDS-PAGE reference maps. You can locate these proteins on the 2-D PAGE maps or display the region of a 2-D PAGE map where one might expect to find a protein from UniProtKB/Swiss-Prot [[More details](#) / [References](#) / [Linking to SWISS-2DPAGE](#) / [Commercial users](#)].

Release 19.00, 23rd of May 2011, and updates up to the 9th of November 2011 (containing 1265 entries in 36 reference maps from human, mouse, *Arabidopsis thaliana*, *Dictyostelium discoideum*, *Escherichia coli*, *Saccharomyces cerevisiae*, and *Staphylococcus aureus* (N315)).

Access to SWISS-2DPAGE

- **[How to use this interface]**
 - [by description](#) (any word in the ID, DE, GN and KW lines)
 - [by accession number](#) (AC lines)
 - [by clicking on a spot](#): select one of our 2-D PAGE or SDS-PAGE reference maps, click on a spot and then get the corresponding information from the SWISS-2DPAGE database.
 - [by author](#) (RA lines)
 - [by spot serial number](#) (2D and 1D lines)
 - [by experimental pI/Mw range](#)
 - [by experimental identification methods](#)
 - [by full text search](#)
 - [retrieve all the protein entries identified on a given reference map](#)
 - [user defined / complex queries](#) (SRS like)

SWISS-2DPAGE documents

- **[Facts and statistics]**
 - [User manual](#)
 - [Release notes](#) (September 26, 2006)
 - [FAQ \(Frequently Asked Questions about SWISS-2DPAGE\)](#)
- **Protocols:**
 - [Technical information](#) about 2-D PAGE (IPG's, silver staining, protocols, etc)
- **Figure captions of SWISS-2DPAGE maps available from publications:**
 - Human [CSF](#), [ELC](#), [HEPG2](#), [HEPG2SP](#), [LIVER](#), [LYMPHOMA](#), [PLASMA](#), [PLATELET](#), [RBC](#), [U937](#), [CEC](#), [KIDNEY](#).
 - *Dictyostelium discoideum*, *Escherichia coli*, *Saccharomyces cerevisiae*.

Services

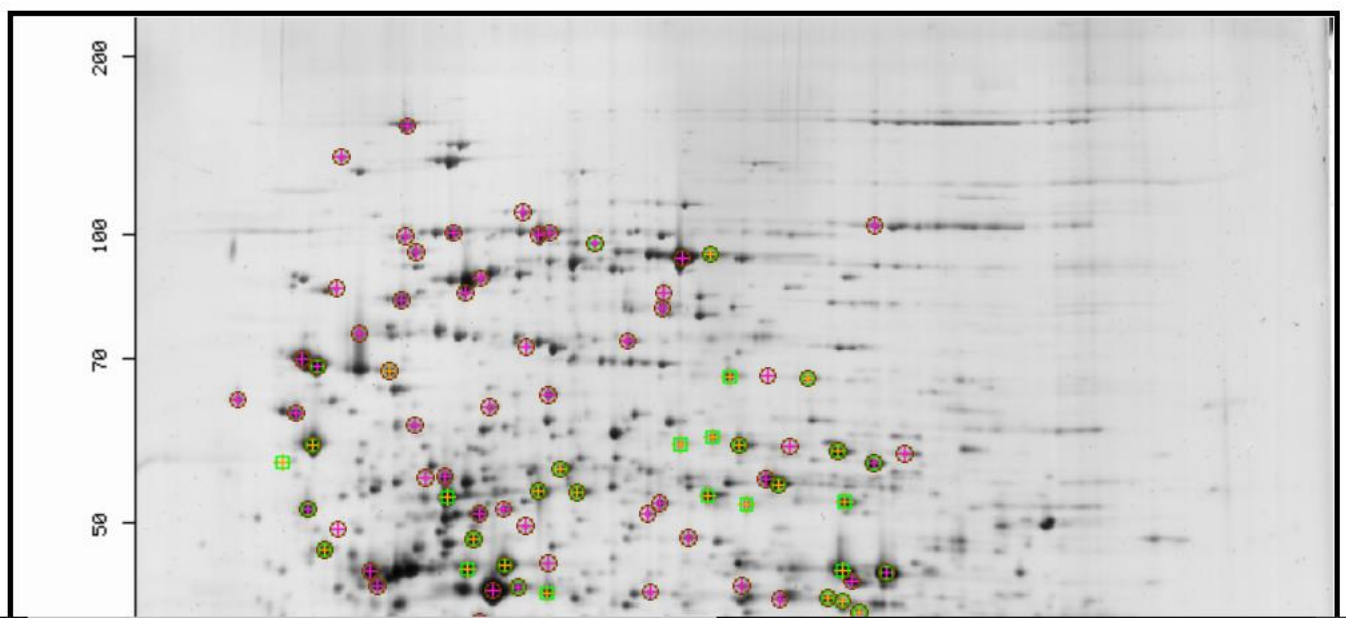
Software

Switch to Gel: Escherichia coli -- ECOLI { Escherichia coli } ▾

Re-scale Gel from 100% to: 100% ▾ View: all identified proteins ▾

Refresh Display: + Identified spots Identification details: show hide
details: X PMF Tandem MS + AA Composition Micro-Sequencing / Tagging Gel Matching Comigration Immunoblotting

-Get more information by dragging your mouse pointer over any highlighted spot -Click on a highlighted spot to access all its associated protein entries

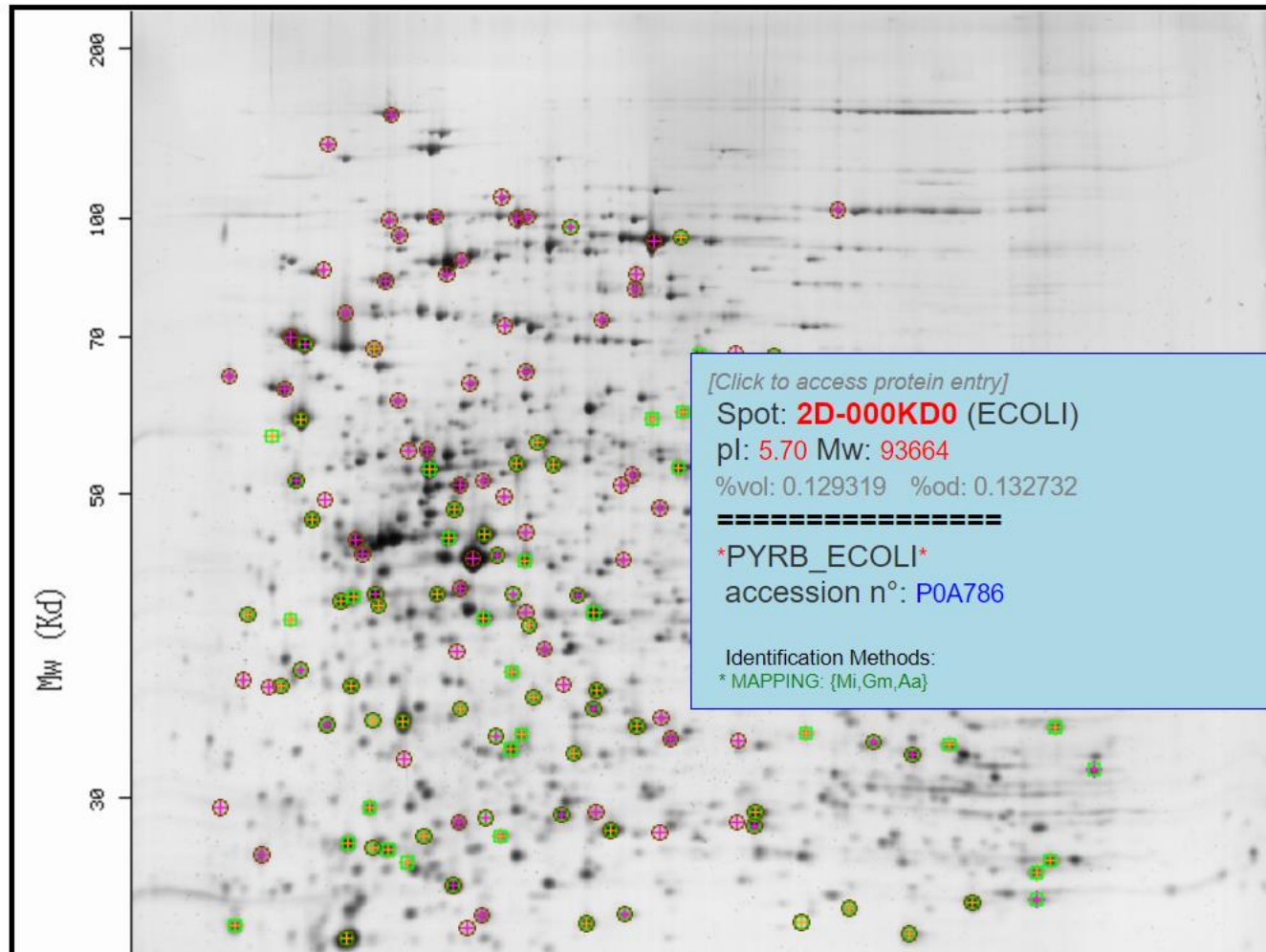


Refresh

Display: + Identified spots Identification details: show hide

details: X PMF Tandem MS + AA Composition Micro-Sequencing / Tagging Gel Matching Comigration Immunobloting

-Get more information by dragging your mouse pointer over any highlighted spot -Click on a highlighted spot to access all its associated protein entries





e.g. [BLAST](#), [UniProt](#), [MSH6](#), [Albumin](#)...

MELANIE



Proteins & Proteomes



Software tool

Melanie combines a unique and flexible interface for the visualization, exploration and analysis of 2D gel and blot images. The software allows differential protein expression analysis of conventional 2-DE and 2D-DIGE gels, to detect protein abundance changes for biomarker discovery. It also features dedicated functionality for Host Cell Protein (HCP) antibody coverage analysis to support development of immunoassays for HCP detection in biopharmaceuticals.

[Browse the resource website](#)

What you can do with this resource

- [Image analysis](#),
- [Protein quantification](#),
- [Protein property calculation](#),
- [Statistical calculation](#),
- [Differential protein expression analysis](#),
- [Expression analysis](#)

Browse these keywords in Expasy

- [2D PAGE image](#),
- [Experimental design and](#)

Melanie

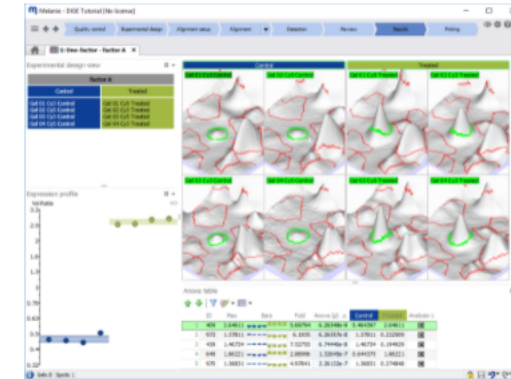
The Proteome Imaging group, affiliated to the [Swiss-Prot Group of SIB Swiss Institute of Bioinformatics](#) has been developing **Melanie** since more than three decades rendering this two-dimensional electrophoresis (2-DE) gel analysis platform one of today's market leaders for analyzing, annotating and querying complex 2-D gel samples.

The latest versions of **Melanie** were developed to replace the **DeCyder™ 2D** and **ImageMaster™ 2D Platinum** applications, with a single goal in mind: help you draw more reliable conclusions from all your 2-D electrophoresis data. With its intuitive workflow and its 100% matching algorithm, analyzing your protein experiment has never been so easy.

The most recent product releases are Melanie 9 enabling our users to seamlessly perform both **differential protein expression analysis** (for single stain and DIGE gels) but also include a dedicated workflow for analysis of **Host Cell Protein (HCP) antibody Coverage analysis**. These versions provide powerful and innovative solutions to shorten the path from data acquisition to protein information. The superior spot detection and matching algorithms facilitate the extraction of statistically valid differences between groups of 2-D gels, while requiring minimal user intervention and therefore speeding up analysis time. The application integrates filtering, querying, reporting, statistical and graphing options so that you can easily view, compare, analyze and present your results.

Melanie is jointly distributed by [SIB Swiss Institute of Bioinformatics](#) and by [Cytiva](#) (formerly **GE Healthcare Life Sciences**), offering to scientists a worldwide network specialists helping them using our software wherever they are and give us a unique way to get user's day-to-day feedback to enhanced our solutions.

For more information, benefits, features, quotes, documentation and a free demo version, we invite you to visit www.2d-gel-analysis.com



Expression analysis



Host cell protein analysis