The SWISS-2DPAGE database of two-dimensional polyacrylamide gel electrophoresis

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Abstract

SWISS-2DPAGE is a database of proteins identified on two-dimensional polyacrylamide gel electrophoresis (2-D PAGE), created and maintained at the University Hospital of Geneva in collaboration with the Department of Medical Biochemistry of Geneva University. The proteins have been identified on various 2-D PAGE reference maps by microsequencing, immunoblotting, gel comparison and amino acid composition.


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The SWISS-2DPAGE database of two-dimensional polyacrylamide gel electrophoresis

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ABSTRACT

SWISS-2DPAGE is a database of proteins identified on two-dimensional polyacrylamide gel electrophoresis (2-D PAGE), created and maintained at the University Hospital of Geneva in collaboration with the Department of Medical Biochemistry of Geneva University [1]. The proteins have been identified on various 2-D PAGE reference maps by microsequencing, immunoblotting, gel comparison and amino acid composition.

FORMAT

Each entry in the SWISS-2DPAGE database corresponds to one protein and contains textual as well as image data. A sample entry is shown in Figure 1. The textual part of the database follows the conventions used in the SWISS-PROT protein sequence database [2]. The ID (identification) and the AC (accession number) are the same than the corresponding sequence entry in SWISS-PROT. The DE (Descripition) line contains general descriptive information about the protein. The reference lines (RN, RP, RC, RM, RA and RL) contain bibliographical references. Each entry holds also a DR (Database cross-Reference) line pointing to the related SWISS-PROT entry. Three line types are specific to SWISS-2DPAGE:

- The MT (MasTer) lines list what types of maps the protein has been identified on. Examples are LIVER and PLASMA.
- The IM (IMages) lines list the 2D PAGE images which are associated to the entry. These may be, for example, TUMOR LIVER or NORMAL LIVER.
- The 2D (2 Dimensional gel) lines gives specific information such as mapping procedure (matching with another gel, microsequencing, etc.), the number, molecular weight and pl of spots, or describes normal and pathological variants [3,4].

The image data associated to a SWISS-2DPAGE entry is made of one 2D PAGE image for each map described in the IM line. The image (currently in Compuserve GIF format) shows two pieces of information on the protein map: 1. the spots, highlighted in color, corresponding to the protein; 2. the region of the gel in which the spots should theoretically appear, computed from the protein sequence using data from SWISS-PROT (Fig. 2).

DATABASE ACCESS

SWISS-2DPAGE is currently available on the ExPASy World-Wide Web (WWW) molecular biology server [5]. To access this server (or any other WWW server), one needs a WWW browser. Public domain browsers exist for a variety of computer systems, including Unix, MS-Windows and Macintoshes. One popular browser available for all three platforms is Mosaic, developed at the National Center for Supercomputing Applications (NCSA) of the University of Illinois at Champaign. It may be obtained by anonymous ftp from ftp.ncsa.uiuc.edu, in the directories /Mosaic, respectively /PC and /Mac. Using a WWW browser, one has access to all the hypertext documents stored on the ExPASy server (as well as other WWW servers).

The ExPASy WWW server may be accessed through its Uniform Resource Locator (URL - the addressing system defined in WWW), which is:

http://expasy.hcuge.ch/

A SWISS-2DPAGE entry may be obtained from the server in one of three ways:

1. direct access, by selecting an entry by its name;
2. from a SWISS-PROT entry, by selecting the hypertext link in the cross-reference (DR) line to SWISS-2DPAGE; if no corresponding entry exists in SWISS-2DPAGE, a virtual entry is created, from which one may view any of the 2-D PAGE reference maps. The theoretical pI and molecular weight for the protein are computed and its position is shown on the map;
3. by selecting a spot on one of the 2-D PAGE reference maps.

CONTENT OF THE CURRENT RELEASE

The current release contains 137 human protein entries, as well as virtual entries for each of the entries in the SWISS-PROT database, with links to reference 2-D PAGE maps of the following biological samples: human liver, plasma, HepG2, HepG2 secreted proteins, red blood cell, lymphoma, cerebrospinal fluid, macrophage like cell line, erythroleukemia cell and platelet.

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REFERENCES


ID APE_HUMAN PRELIMINARY; 2DG.
AC P02649;
DT 01-AUG-1993 (REL. 01, CREATED)
DT 01-AUG-1993 (REL. 01, LAST UPDATE)
DE APOLIPOPROTEIN E (APO-E).
MT PLASMA, CSF.
IM PLASMA, CSF.
RN [1]
RP MAPPING ON GEL.
RA ANDERSON N.L., ANDERSON N.G.;
CC -/- SUBUNIT: MONOMER.
2D -/- MASTER: PLASMA;
2D -/- PI/MW: SPOT 2D-000573=5.23/35391;
2D -/- PI/MW: SPOT 2D-000578=5.35/35037;
2D -/- PI/MW: SPOT 2D-00057M=5.49/34269;
2D -/- MAPPING: IMMUNOBLOTTING [1];
2D -/- NORMAL LEVEL: 30 – 50 MG/L;
2D -/- PATHOLOGICAL LEVEL: APOE ABNORMALITIES IN TYPE III AND IV HYPERLIPAEMIA;
2D -/- POSITIONAL VARIANTS: APOE 2–2, 2–3, 2–4, 3–3, 3–4 AND 4–4;
2D -/- MASTER: CSF;
2D -/- PI/MW: SPOT 2D-00057W=5.08/34370;
2D -/- PI/MW: SPOT 2D-00057F=5.24/33209;
2D -/- PI/MW: SPOT 2D-00057Q=5.35/32804;
2D -/- PI/MW: SPOT 2D-000579=5.46/31852;
2D -/- MAPPING: MATCHING WITH THE PLASMA MASTER GEL.
DR SWISS-PROT; P02649; APE_HUMAN.