The SWISS-2DPAGE database of two-dimensional polyacrylamide gel electrophoresis, its status in 1995

Ron D. Appel, Jean-Charles Sanchez[1], Amos Bairoch[2,*], Olivier Golaz[1], Florence Ravier[1], Christian Pasquali[1], Graham J. Hughes[2] and Denis F. Hochstrasser[1]

Hospital Informatics Centre, Geneva University Hospital, 24 rue Micheli-du-Crest, 1211 Geneva 14, Switzerland, [1]Central Laboratory for Clinical Chemistry, Geneva University Hospital, Geneva, Switzerland and [2]Department of Medical Biochemistry, University of Geneva, 1 rue Michel Servet, 1211 Geneva 4, Switzerland

ABSTRACT

SWISS-2DPAGE is a database of proteins identified on two-dimensional polyacrylamide gel electrophoresis (2-D PAGE). The current release contains 343 entries of human, yeast (*Saccharomyces cerevisiae*) and *Escherichia coli* origin, as well as virtual entries for each of the protein sequences in the SWISS-PROT database.

INTRODUCTION

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 (1,2). 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 (3). The identification (ID) and the accession (AC) number are the same as the corresponding sequence entry in SWISS-PROT. The description (DE) line contains general descriptive information about the protein. The reference lines (RN, RP, RC, RX, RA and RL) contain bibliographical references. Each entry also holds a database cross-reference (DR) line pointing to the related SWISS-PROT entry, as well as to related entries in other 2-D PAGE databases, such as YEPD for *Saccharomyces cerevisiae* (4) and ECO2DBASE for *Escherichia coli* (5). Three line types are specific to SWISS-2DPAGE: (i) the master (MT) line lists what types of maps the protein has been identified on (examples are LIVER and PLASMA); (ii) the images (IM) line lists the 2D PAGE images which are associated with the entry (for example TUMOR LIVER or NORMAL LIVER); (iii) the 2-dimensional gel (2D) line gives specific information such as mapping procedure (matching with another gel, microsequencing, etc.), the number, molecular weight and pI of spots and their amino acid composition or describes normal and pathological variants (6,7).

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ID   METE_YEAST;    STANDARD; 2DG.
AC   P05694;
DT   01-AUG-1995 (REL. 02, CREATED)
DT   01-AUG-1995 (REL. 02, LAST UPDATE)
DE   5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE S-
DE   METHYLTRANSFERASE (EC 2.1.1.14) (METHIONINE SYNTHASE, VITAMIN-B12
DE   INDEPENDENT ISOZYME) (DELTA-P8 PROTEIN).
MT   YEAST.
IM   YEAST.
RN   [1]
RP   MAPPING ON GEL.
RA   SANCHEZ J.-C., GOLAZ O., SCHALLER D., MORCH F.,
RA   FRUTIGER S., HUGHES G., APPEL R.D., DESHUSSES J.,
RA   HOCHSTRASSER D.F.;
RL   SUBMITTED (JAN-1995) TO THE SWISS-2DPAGE DATABASE.
RN   [2]
RP   MAPPING ON GEL.
RX   MEDLINE; 95203288.
RA   GARRELS J.I., FUTCHER B., KOBAYASHI R., LATTER G.I.,
RA   SCHWENDER B., VOLPE T., WARNER J.R., MCLAUGHLIN C.S.;
RL   ELECTROPHORESIS 15:1466-1486(1994).
CC   -!- SUBUNIT: MONOMER;
2D   -!- MASTER: YEAST;
2D   -!-   PI/MW: SPOT 2D-000IRM=6.27/86893;
2D   -!-   PI/MW: SPOT 2D-000IRQ=6.36/86406;
2D   -!-   PI/MW: SPOT 2D-000IRS=6.47/86163;
2D   -!-   MAPPING: GEL MATCHING [1] AND IDENTIFIED BY
2D           J. GARRELS [2].
DR   SWISS-PROT; P05694; METE_YEAST.
DR   YEPD; 5770; -.
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Figure 1. A sample entry from SWISS-2DPAGE (textual part).

The image data associated with a SWISS-2DPAGE entry is made up 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: (i) the spots, highlighted in colour, corresponding to the protein; (ii) 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 (8). 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 the Macintosh operating system. Popular browsers available for all three platforms include Mosaic™, developed at the National Center for Supercomputing Applications (NCSA) of the University of Illinois at Champaign (obtainable by anonymous ftp from ftp.ncsa.uiuc.edu), and

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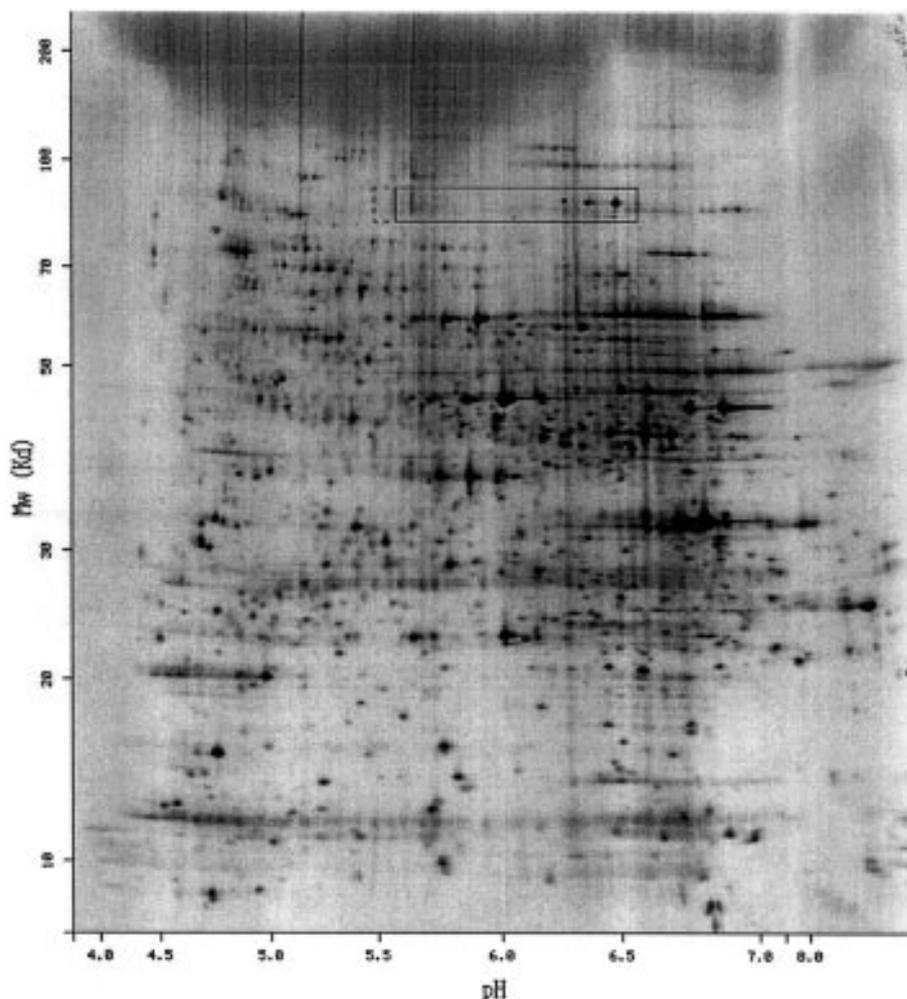
Figure 2. The protein from Figure 1 shown on the YEAST reference map.

Netscape Navigator™, from Netscape Communications Corp. (available from ftp.netscape.com). 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. (i) By keyword search on the protein name, accession number or referenced author. (ii) 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. (iii) By selecting a spot on one of the 2-D PAGE reference maps.

CONTENT OF THE CURRENT RELEASE

The current release contains 343 entries of human, yeast and *E.coli* origin, as well as virtual entries for each of the protein sequences in the SWISS-PROT database. SWISS-2DPAGE entries are linked to reference 2-D PAGE maps. Maps for the following biological samples are available: human liver, plasma, HepG2, HepG2 secreted proteins, red blood cell, lymphoma, cerebrospinal fluid, macrophage-like cell line, erythroleukaemia cell and platelet, as well as yeast (*S.cerevisiae*) and *E.coli*.

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