# The 1999 SWISS-2DPAGE database update

# Christine Hoogland<sup>1,\*</sup>, Jean-Charles Sanchez<sup>2</sup>, Luisa Tonella<sup>2</sup>, Pierre-Alain Binz<sup>1,2,3</sup>, Amos Bairoch<sup>3</sup>, Denis F. Hochstrasser<sup>2</sup> and Ron D. Appel<sup>1</sup>

<sup>1</sup>Swiss Institute of Bioinformatics, 1 rue Michel-Servet, CH-1211 Genève 4, Switzerland, <sup>2</sup>Central Clinical Chemistry Laboratory, Geneva University Hospital, Geneva, Switzerland and <sup>3</sup>Department of Medical Biochemistry, University of Geneva, Geneva, Switzerland

Received October 5, 1999; Accepted October 7, 1999

# ABSTRACT

SWISS-2DPAGE (http://www.expasy.ch/ch2d/) is an annotated two-dimensional polyacrylamide gel electrophoresis (2-DE) database established in 1993. The current release contains 24 reference maps from human and mouse biological samples, as well as from Saccharomyces cerevisiae, Escherichia coli and Dictyostelium discoideum origin. These reference maps have now 2824 identified spots, corresponding to 614 separate protein entries in the database, in addition to virtual entries for each SWISS-PROT sequence or any user-entered amino acids sequence. Last year improvements in the SWISS-2DPAGE database are as follows: three new maps have been created and several others have been updated; crossreferences to newly built federated 2-DE databases have been added; new functions to access the data have been provided through the ExPASy proteomics server.

# INTRODUCTION

The SWISS-2DPAGE database collects data on proteins identified on various two-dimensional polyacrylamide gel electrophoresis (2-DE) maps (1). The identification of proteins on 2-DE maps was obtained by various techniques (2), including gel comparison, microsequencing, immunoblotting, amino acid composition analysis, peptide mass fingerprinting using mass spectrometry, or a combination of some of these. The core of the SWISS-2DPAGE database consists thus in the description of the proteins identified, including mapping procedures, physiological and pathological information, experimental data (isoelectric point, molecular weight, amino acid composition, peptide masses) and bibliographical references, in addition to the 2-DE images showing the protein locations. Cross-references are provided to MEDLINE, to other 2-DE databases [ECO2DBASE (3), HSC-2DPAGE (4), YEPD (5), and the two newly built SIENA-2DPAGE (6-8) and PHCI-2DPAGE (9,10)], and to SWISS-PROT (11), which itself provides many links to other molecular databases [EMBL (12), GenBank (13), PROSITE (14), MIM (15), etc.]. The SWISS-2DPAGE database is maintained by the Swiss Institute of Bioinformatics, in collaboration with the Central Clinical Chemistry Laboratory of Geneva University Hospital.

TD F6A2 ECOLI; STANDARD; 2DG. AC P53509; DT 01-OCT-1999 (Rel. 11, Created) 01-0CT-1999 (Rel. 11, Last update) DT CS6 FIMBRIAL SUBUNIT A (CS6 PILIN). DE os Escherichia coli. or Bacteria; Proteobacteria; gamma subdivision; OC Enterobacteriaceae; Escherichia. MT ECOLI5-6. IM ECOL15-6. RN [1] MAPPING ON GEL. RP TONELLA L., SANCHEZ J.-C., APPEL R.D., BAIROCH A., RA HOOGLAND C., BINZ P.-A., HOCHSTRASSER D.F.; Submitted (OCT-1999) to the SWISS-2DPAGE database. ΒV RL 2D -!- MASTER: ECOLI5-6; PI/MW: SPOT 2D-001L5W=5.36/14345; 2D - 1 -PEPTIDE MASSES: SPOT 2D-001L5W: 950.45; 982.426; 1093.523; 1175.545; TRYPSIN. 2D -1-2D 2D-1-MAPPING: MASS FINGERPRINTING [1]. СС CC This SWISS-2DPAGE entry is copyright the Swiss Institute of CC Bioinformatics. There are no restrictions on its use by CC non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for CC commercial entities requires a license agreement (See CC http://www.isb-sib.ch/announce/ or send an email to CC license@isb-sib.ch). CC SWISS-PROT; P53509; F6A2\_ECOLI. DR 11

Figure 1. Example of a SWISS-2DPAGE entry.

#### FORMAT

The protein entries in SWISS-2DPAGE are text files structured to be readable by human as well as by computer programs. Each entry is composed of defined lines, used to record various kinds of data (Fig. 1). For standardization purposes, the format of SWISS-2DPAGE entries is similar to the SWISS-PROT database (11) and contains specific lines dedicated to 2-DE data: (i) the master line (MT) lists the reference maps where the entry has been identified; (ii) the images line (IM) lists the 2-DE images available for the entry; (iii) the 2D lines integrate different topics including mapping procedure, spot coordinates, protein amino acid composition, peptide masses from mass spectrometry, protein expression levels and modifications. On the ExPASy Web server (see availability section) the data image associated with a protein entry displays the experimental location of the protein on the chosen map, together with a theoretical region computed from the protein sequence (Fig. 2).

# **CURRENT CONTENT**

Release 11 of SWISS-2DPAGE (October 1999) contains twenty-four reference maps. Fourteen are from human cells or tissues (kidney, liver, lymphoma, platelet cells, red blood cells,

\*To whom correspondence should be addressed. Tel: +41 22 372 6281; Fax: +41 22 372 6198; Email: christine.hoogland@isb-sib.ch

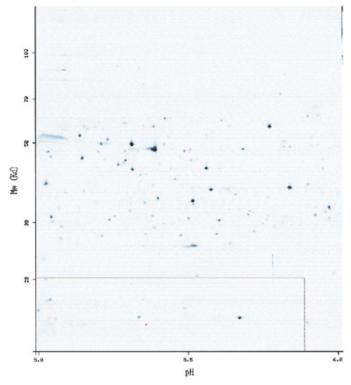


Figure 2. The protein from Figure 1 shown on the SWISS-2DPAGE *E.coli* reference map for pI range from 5 to 6 (ECOLI5–6). The protein spot itself is highlighted in red, and the red rectangle around shows the theoretical region where one would expect to see the protein, computed from the SWISS-PROT protein sequence.

colorectal epithelia cells), body fluids (cerebrospinal fluid, plasma), culture cells (colorectal adenocarcinoma cells, erythroleukemia cell line, hepatoblastoma carcinoma derived cells, hepatoblastoma carcinoma derived cell line secreted proteins, macrophage like cell line, promyelocytic leukemia derived cells); four are from mouse cells or tissues (liver, gastrocnemius muscle, pancreatic islet cells, epididymal fat pad); the other maps are from Saccharomyces cerevisiae, Escherichia coli (obtained for four pI ranges: 3.5-10, 4-5, 4.5-5.5, 5-6) and Dictyostelium discoideum origin. Table 1 gives detailed descriptions for each of these maps, including creation and release dates, number of detected spots, number of identified spots, and number of distinct protein entries. On these maps a total of 2824 spots have been identified by gel matching (51%), immunoblotting (24%), co-migration (3%), microsequencing (17%), amino acids composition (6%) and mass spectrometry (15%). Total exceeds 100% as some of the spots have been identified by several methods. These identifications correspond currently to 614 different protein entries from human, mouse, yeast, E.coli and D.discoideum origin (Fig. 3). In addition, there are as many virtual entries as protein sequences in the SWISS-PROT database or as any user-entered amino acids sequence.

# AVAILABILITY

The SWISS-2DPAGE database is freely available for nonprofit organizations. It is submitted to an annual subscription fee for commercial entities (for details, see URL http://www. expasy.ch/announce/). In both cases, users can get a local copy

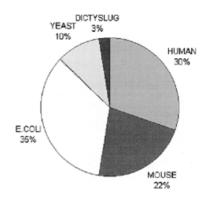


Figure 3. Species distribution of the SWISS-2DPAGE entries. Abbreviations as follows: E.COLI, *E.coli*; YEAST, *S.cerevisiae*; DICTYSLUG, *D.discoideum*.

of SWISS-2DPAGE using anonymous ftp from the ExPASy FTP server (ftp://ftp.expasy.ch/databases/swiss-2dpage/). In addition, SWISS-2DPAGE entries can be reached through a 2-D gel analysis software such as Melanie 3 (http://www.expasy. ch/melanie/) (16).

However, the most efficient and user-friendly way to interactively browse in SWISS-2DPAGE is through the ExPASy proteomics server (http://www.expasy.ch/). The SWISS-2DPAGE top page provides several textual and graphical queries and displays results with active links to other databases. A SWISS-2DPAGE entry may be reached by keyword search (protein name, accession number, description, authors or full text) or by selecting a spot on one of the 2-DE maps. New features have been added to improve interactions in accessing the SWISS-2DPAGE data. First, all searching functions in the database are now accessible from the top page and results page of each keyword search function. This feature (http://www.expasy.ch/ cgi-bin/ch2d-search-de ) has been designed to facilitate the navigation between the different ways to query the database. Second, for both textual and graphical queries, the result now displays SWISS-2DPAGE entries using a 'nice view' tool. This tool provides users with an easily readable alternative to the original text file representation, by collecting in blocks related information such as general information, origin of the protein, references, etc. Moreover the 2D part combines all 2-DE data in a cooperating view (eg., http://www.expasy.ch/cgi-bin/ nice2dpage.pl?P00938 ). For each reference maps where the protein shown has been identified, this integrated view includes a map icon in front of the detailed 2-DE information. Direct links have also been added from amino acid composition and peptide masse data to the concerned section in the user manual (http://www.expasy.ch/ch2d/manch2d.html ) describing data format and protocols. Finally, an additional tool allows users to retrieve in a table all the protein entries identified on a given reference map, with all the 2-DE attributes and references (http://www.expasy.ch/cgi-bin/get-ch2d-table.pl).

#### ACKNOWLEDGEMENTS

The authors thank M. Cawthorne for providing mouse sample, R. Joubert-Carron for HL60 sample, M. Raymond for colorectal sample, C. Sarto for kidney sample, J. Yan for *Dictyostelium* sample; and W. Bienvenut, I. Demalte, S. Frutiger, G. Hughes, S. Jaccoud, S. Paesano, C. Pasquali, F. Ravier, G. Rosselat, V. Rouge for their technical assistance.

Map	Creation	Last modification	Detected spots	Identified spots	No. of entries
HUMAN					
CEC	Jan-98	Jan-98	3077	56	40
CSF	Aug-93	Nov-98	1664	309	30
DLD1	Jan-99	Jan-99	3440	108	67
ELC	Aug-93	Jun-97	2144	35	19
HEPG2	Aug-93	Sep-97	2862	98	45
HEPG2SP	Aug-93	Jan-96	1734	155	25
HL60	Sep-97	Sep-97	3164	26	17
KIDNEY	Sep-97	Sep-97	2896	42	27
LIVER	Aug-93	Sep-97	2413	138	68
LYMPHOMA	Aug-93	Jun-97	1890	60	33
PLASMA	Aug-93	Sep-97	1966	626	70
PLATELET	Aug-93	Jun-99	2193	41	18
RBC	Aug-93	Sep-97	1800	190	33
U937	Aug-93	Jun-97	895	42	32
DICTYSLUG	Sep-97	Sep-97	3164	25	16
ECOLI					
3.5-10	Aug-95	Jan-98	2364	206	180
4–5	Jun-99	Oct-99	449	18	12
4.5-5.5	Oct-98	Jun-99	1025	86	59
5-6	Oct-99	Oct-99	542	24	21
YEAST	Feb-95	Jun-97	1940	101	62
MOUSE					
EFP	Sep-98	Sep-98	3540	87	52
ISLETS	Sep-98	Jun-99	2528	7	2
LIVER	Sep-98	Oct-99	2836	201	107
MUSCLE	Sep-98	Oct-99	2650	143	72

Abbreviations are as follows: CEC, colorectal epithelia cells; CSF, cerebrospinal fluid; DLD1, colorectal adenocarcinoma cells; ELC, erythroleukemia cell line; HEPG2, hepatoblastoma carcinoma derived cells; HEPG2SP, hepatoblastoma carcinoma derived cell line secreted proteins; HL60, promyelocytic leukemia derived cells; RBC, red blood cells; U937, macrophage like cell line; DICTYSLUG, *D.discoideum*; ECOLI, *E.coli*, with pI range from 3.5 to 10 (3.5–10), from 4 to 5 (4–5), from 4.5 to 5.5 (4.5–5.5) and from 5 to 6 (5–6); YEAST, *S.cerevisiae*; EFP, epididymal fat pad; ISLETS, pancreatic islet cells; MUSCLE, gastrocnemius muscle.

#### REFERENCES

- Appel,R.D, Sanchez,J.-C., Bairoch,A., Golaz,O., Miu,M., Vargas,R. and Hochstrasser,D.F. (1993) *Electrophoresis*, 14, 1232–1238.
- Wilkins, M.R. and Gooley, A.A. (1997) In Wilkins, M.R., Williams, K.L., Appel, R.D. and Hochstrasser, D.F. (eds.), *Proteome Research: New Frontiers in Functional Genomics*. Springer Verlag, pp. 35–64.
- VanBogelen,R.A., Abshire,K.Z., Moldover,B., Olson,E.R. and Neidhardt,F.C. (1997) *Electrophoresis*, 18, 1243–1251.
- 4. Dunn,M.J., Corbett,J.M. and Wheeler,C.H. (1997) *Electrophoresis*, **18**, 2795–2802.
- 5. Payne, W.E. and Garrels, J.I. (1997) Nucleic Acids Res., 25, 57-62.
- Bini,L., Sanchez-Campillo,M., Santucci,A., Magi,B., Marzocchi,B., Comanducci,M., Christiansen,G., Birkelund,S., Cevenini,R., Vretou,E., Ratti,G. and Pallini V. (1996) *Electrophoresis*, **17**, 185–190.
- Bini,L., Heid,H., Liberatori,S., Geier,G., Pallini,V. and Zwilling,R. (1997) *Electrophoresis*, 18, 557–562.
- Bini,L., Magi,B., Marzocchi,B., Arcuri,F., Tripodi,S., Cintorino,M., Sanchez,J.-C., Frutiger,S., Hughes,G.J., Pallini,V., Hochstrasser,D.F. and Tosi,P. (1997) *Electrophoresis*, 18, 2832–2841.

- Shaw,A.C., Larsen,M.R., Roepstorff,P., Holm,A., Christiansen,G. and Birkelund,S. (1999) *Electrophoresis*, 20, 977–983.
- Shaw,A.C, Larsen,M.R., Roepstorff,P., Justesen,J., Christiansen,G. and Birkelund,S. (1999) *Electrophoresis*, 20, 984–993.
- Bairoch, A. and Apweiler, R. (1999) Nucleic Acids Res., 27, 49–54. Updated article in this issue: Nucleic Acids Res. (2000), 28, 45–48.
- Stoesser,G., Tuli,M.A., Lopez,R. and Sterk,P. (1999) Nucleic Acids Res., 27, 18–24. Updated article in this issue: Nucleic Acids Res. (2000), 28, 19–23.
- Benson, D.A., Boguski, M.S., Lipman, D.J., Ostell, J., Ouellette B.F.F., Rapp, B.A. and Wheeler, D.L. (1999) *Nucleic Acids Res.*, 27, 12–17. Updated article in this issue: *Nucleic Acids Res.* (2000), 28, 15–18.
- 14. Hofmann,K., Bucher,P., Falquet,L. and Bairoch,A. (1999) Nucleic Acids Res., 27, 215–219.
- Pearson, P., Francomano, C., Foster, P., Bocchini, C., Li, P. and McKusick, V.A. (1994) *Nucleic Acids Res.*, 22, 3470–3473.
- Appel,R.D., Palagi,P.M., Walther,D., Vargas,J.R., Sanchez,J.-C., Ravier,F., Pasquali,C. and Hochstrasser,D.F. (1997) *Electrophoresis*, 18, 2724–2734.