The PROSITE database, its status in 1995

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Received October 3, 1995; Revised and Accepted October 13, 1995

ABSTRACT

The PROSITE database consists of biologically significant patterns and profiles formulated in such a way that with appropriate computational tools it can help to determine to which known family of proteins (if any) a new sequence belongs or which known domain(s) it contains.

INTRODUCTION

PROSITE (1,2) is a method of determining the function of uncharacterized proteins translated from genomic or cDNA sequences. It consists of a database of biologically significant patterns and profiles formulated in such a way that with appropriate computational tools it can rapidly and reliably determine to which known family of proteins (if any) the new sequence belongs or which known domain(s) it contains.

In some cases the sequence of an unknown protein is too distantly related to any protein of known structure to detect its resemblance by overall sequence alignment, but relationships can be revealed by the occurrence in its sequence of a particular cluster of residue types, which is variously known as a pattern, motif, signature or fingerprint. These motifs arise because specific region(s) of a protein which may be important, for example for their binding properties or for their enzymatic activity, are conserved in both structure and sequence. These structural requirements impose very tight constraints on the evolution of these small but important portions of a protein sequence. The use of protein sequence patterns or profiles to determine the function of proteins is becoming very rapidly one of the essential tools of sequence analysis. This reality has been recognized by many authors (3,4). Based on these observations, we decided in 1988 to actively pursue the development of a database of regular expression-like patterns which could be used to search against sequences of unknown function.

However, while sequence patterns are very useful, there are a number of protein families, as well as functional or structural domains, that cannot be detected using patterns, due to their extreme sequence divergence. Typical examples of important functional domains which are weakly conserved are the globin, the immunoglobulin, the SH2 and the SH3 domains. In such domains there are only a few sequence positions which are well conserved. Any attempt to build a consensus pattern for such regions will either fail to pick up a significant proportion of the protein sequences that contain such a region (false negatives) or will pick up too many proteins that do not contain the region (false positives).

The use of techniques based on profiles or weight matrices (the two terms are used synonymously here) allows detection of such proteins or domains. A profile is a table of position-specific amino acid weights and gap costs. These numbers (also referred to as scores) are used to calculate a similarity score for any alignment between a profile and a sequence or parts of a profile and a sequence. An alignment with a similarity score higher than or equal to a given cut-off value constitutes a motif occurrence. As with patterns, there may be several matches to a profile in one sequence, but multiple occurrences in the same sequences must be disjoint (non-overlapping) according to a specific definition included in the profile. Another feature that distinguishes patterns from profiles is that the latter are usually not confined to small regions with high sequence similarity. Rather, they attempt to characterize a protein family or domain over its entire length.

We therefore started in 1994 to complement the approach based on patterns by gradually adding to PROSITE profile entries. The profile structure (5,6) used in PROSITE is similar to, but slightly more general than, that introduced by Gribskov and co-workers (7); additional parameters allow representation of other motif descriptors, including the currently popular hidden Markov models. Profiles can be constructed by a large variety of different techniques. The classical method developed by Gribskov and co-workers (8) requires a multiple sequence alignment as input and uses a symbol comparison table to convert residue frequency distributions into weights. The profiles included in PROSITE are generated by this procedure, applying recently described modifications (9,10). In the future we intend to apply additional profile construction tools, including structure-based approaches and methods involving hidden Markov modelling.

LEADING CONCEPTS

The design of PROSITE follows four leading concepts.

Completeness

For such a compilation to be helpful in the determination of protein function it is important that it contains as many biologically meaningful patterns and profiles as possible.

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Table 1. List of patterns documentation entries which have been added to PROSITE since the last publication of the NAR database issue

C1q domain signature
Death domain profile
Forkhead-associated (FHA) domain profile
Src homology 2 (SH2) domains profile
Src homology 3 (SH3) domains profile
S-layer homology domain signature
TPR repeat profile
WW domain signature and profile
Prokaryotic dksA/traR C4-type zinc finger
PHD finger profile
Copper-fist domain
Bacterial regulatory proteins, iclR family signature
Bacterial regulatory proteins, marR family signature
Sigma-70 factors ECF subfamily signature
Ribosomal protein L10 signature
Ribosomal protein L24 signature
Ribosomal protein L31 signature
Ribosomal protein L7Ae signature
Ribosomal protein L13e signature
Ribosomal protein L18e signature
Ribosomal protein L24e signature
Ribosomal protein L27e signature
Ribosomal protein L31e signature
Ribosomal protein L34e signatures
Ribosomal protein L35Ae signature
Ribosomal protein L37e signature
Ribosomal protein S6 signature
Homoserine dehydrogenase signature
Aspartate-semialdehyde dehydrogenase signature
Pyridoxamine 5′-phosphate oxidase signature
Respiratory chain NADH dehydrogenase 20 kDa subunit signature
Respiratory chain NADH dehydrogenase 24 kDa subunit signature
NNMT/PNMT/TEMT family of methyltransferases signature
Ribosomal RNA adenine dimethylases signature
Squalene and phytoene synthases signatures
ROK family signature
Casein kinase II regulatory subunit signature
Shikimate kinase signature
Prokaryotic diacylglycerol kinase signature
Acetate and butyrate kinases family signatures
RNA polymerases H 23 kDa subunits signature
RNA polymerases N 8 kDa subunits signature
RNA polymerases L 13–16 kDa subunits signature
RNA polymerases RPB6 6 kDa subunits signature
Lipolytic enzymes ‘G-D-S-L’ family, serine active site
DNA/RNA non-specific endonucleases active site
Thermonuclease family signature
Chitinases family 18 signature
Glycosyl hydrolases family 45 active site
ATP-dependent serine proteases, lon family, serine active site
Interleukin-1β converting enzyme family active sites
Hydroxymethylglutaryl-coenzyme A lyase active site
DNA photolyases class 2 signatures
Adenylate cyclases class-I signatures
Ribulose-phosphate 3-epimerase family signatures
PpiC-type peptidyl-prolyl *cis-trans* isomerase signature
Terpene synthases signature
SAICAR synthetase signatures
NAD-dependent DNA ligase signatures
Transposases, IS30 family, signature
Molybdenum cofactor biosynthesis proteins signatures
Radical activating enzymes signature
Electron transfer flavoprotein beta-subunit signature
Heavy metal-associated domain
Sulfate transporters signature
Xanthine/uracil permeases family signature
OmpA-like domain
GPR1/FUN34/yaaH family signature
FtsZ protein signatures
Bacterial microcompartiments proteins signature
Flagella transport protein fliP family signatures
Scorpion short toxins signature
grpE protein signature
Bacterial type II secretion system protein C signature
Bacterial type II secretion system protein N signature
Protein secE/sec61-gamma signature
Fimbrial biogenesis outer membrane usher protein signature
Apoptosis regulator proteins, Bcl-2 family signature
GTP-binding nuclear protein ran signature
Elongation factor Ts signatures
Translation initiation factor SUI1 signature
Calponin family repeat
CAP protein signatures
Hydrogenases expression/synthesis hupF/hypC family signature
NOL1/NOP2/fmu family signature
Hypothetical SUA5/yciO/yrdC family signature
Hypothetical YBL055c/yjjV family signatures
Hypothetical YBR002c family signature
Hypothetical YBR177c/yheT family signature
Hypothetical YER057c/yjgF family signature
Hypothetical YKL151c/yjeF family signatures
Hypothetical hesB/yadR/yfhF family signature
Hypothetical yabO/yceC/yfiI family signature
Hypothetical yciL/yejD/yjbC family signature
Hypothetical yedF/yeeD/yhhP family signature
Hypothetical yhdG/yjbN/yohI family signature

High specificity

In the majority of cases we have chosen patterns or profiles that are specific enough that they do not detect too many unrelated sequences, yet they will detect most, if not all, sequences that clearly belong to the set in consideration.

Documentation

Each of the entries in PROSITE is fully documented. The documentation includes a concise description of the protein family that it is designed to detect, as well as a summary of the reasons leading to the development of the pattern or profile.

Periodic reviewing

It is important that each entry be periodically reviewed to ensure that it is still valid.

FORMAT AND DOCUMENT FILES

The core of the PROSITE database is composed of two ASCII (text) files. The first file (prosite.dat) is a computer readable file that contains all the information necessary for programs that make use of PROSITE to scan sequences for the occurrence of the patterns and/or profiles. This file also includes, for each of the entries described, statistics on the number of hits obtained while scanning for that pattern or profile in the SWISS-PROT protein sequence database (9). Cross-references to the corresponding SWISS-PROT entries are also present in the file. The second file (prosite.doc), which we call the textbook, contains textual information that documents each pattern.

A sample textbook entry is shown in Figure 1a (see following pages). This particular entry is linked to two entries in the prosite.dat file, a pattern and a profile (Fig. 1b).

Several document files are also distributed with the database:
prosuser.txt, the database user's manual;
profile.txt, a detailed description of the syntax for the profiles;
prosite.lis, a list of PROSITE documentation entries;
prosite.get, a document on how to obtain a local copy of PROSITE;
prosite.prg, a description of programs and electronic mail servers that make use of PROSITE;
pautindx.txt, an index of authors cited in the prosite.doc file.

CONTENT OF THE CURRENT RELEASE

Release 13 of PROSITE (October 1995) contains 883 documentation entries describing 1156 different patterns, rules and profiles. The list of entries which have been added since publication of the previous article (2) describing PROSITE is provided in Table 1. The database requires ~5 Mb disk storage space. The present distribution frequency is two releases per year. No restrictions are placed on use or redistribution of the data.

HOW TO OBTAIN A LOCAL COPY OF PROSITE

By CD-ROM

PROSITE is distributed on CD-ROM by the EMBL Outstation–the European Bioinformatics Institute (EBI) (12). For all enquiries regarding subscription to and distribution of PROSITE one should contact The EMBL Outstation–The European Bioinformatics Institute, Hinxton Hall, Hinxton, Cambridge CB10 1RQ, UK (tel. +44 1223 494 400; fax +44 1223 494 468; email datalib@ebi.ac.uk).

By anonymous ftp

If you have access to a computer system linked to the Internet you can obtain PROSITE using ftp (File Transfer Protocol) from the following file servers:

EBI anonymous ftp server (ftp.ebi.ac.uk or 192.54.41.33);

NCBI Repository, National Library of Medicine, NIH, Washington, DC (ncbi.nlm.nih.gov or 130.14.20.1);

ExPASy (Expert Protein Analysis System) server, University of Geneva, Switzerland, (expasy.hcuge.ch or 129.195.254.61);

National Institute of Genetics (Japan) ftp server (ftp.nig.ac.jp or 133.39.16.66).

By email through the EBI file server

PROSITE can be obtained from the EBI file server (13). Detailed instructions on how to make the best use of this service and, in particular, on how to obtain PROSITE can be obtained by query to the network address netserv@ebi.ac.uk

HELP
HELP PROSITE

HOW TO MAKE USE OF PROSITE

Computer programs

Many academic groups and commercial companies have developed computer programs that make use of the pattern entries in PROSITE. The prosite.prg file contains a full list of these programs, their operating system specificity and characteristics, as well as information on how to obtain them.

To make use of profile entries we are distributing, with the PROSITE release the source code (in FORTRAN77) of two programs that should help software developers implement profile-specific routines in their application(s): pfscan loads a sequence from a file and scans it with all (or one) of the PROSITE profiles; pfsearch loads a profile from a file and scans for it in a SWISS-PROT database file.

Email servers

There are many email servers that are available to molecular biologists (14). At least three of these servers can be used in conjunction with PROSITE.

Name: EBI Mail-PROSITE Server.
Organization: European Bioinformatics Institute, Hinxton, UK.
Description: Allows rapid comparison of a new protein sequence against all patterns stored in PROSITE.
Server email address: prosite@ebi.ac.uk.
Address to report problems: nethelp@ebi.ac.uk.

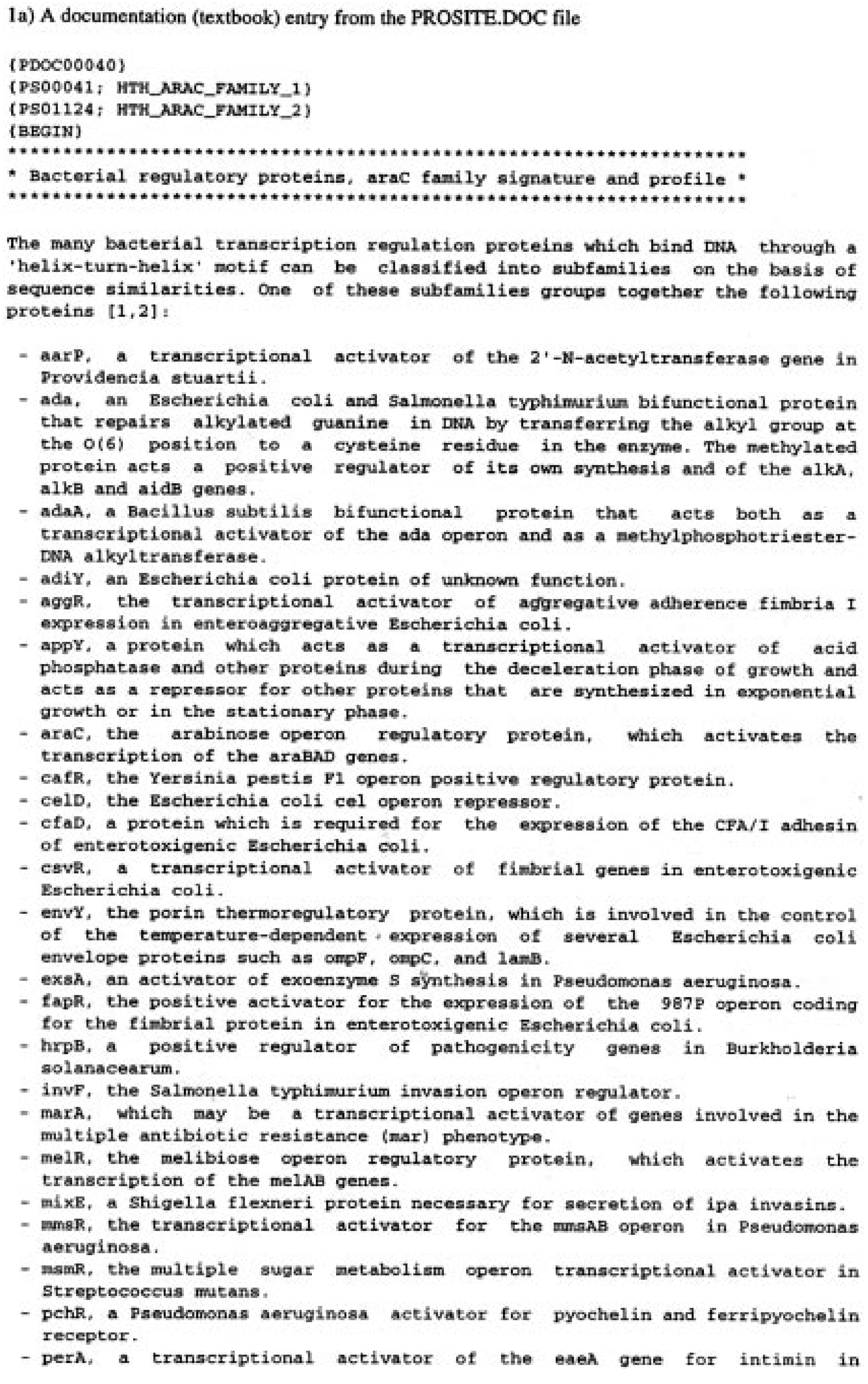
Name: BLOCKS e-mail searcher.
Organization: Fred Hutchinson Center, Seattle, WA, USA.
Description: Compares a protein or DNA sequence to the database of protein blocks. Blocks are short multiply aligned ungapped segments corresponding to the most highly conserved regions of proteins. The BLOCKS database (15) has been derived from PROSITE. This server can also be used to retrieve specifics blocks and PROSITE entries.
Server email address: blocks@howard.fhcrc.org.
Address to report problems: henikoff@howard.fhcrc.org.

Name: MOTIF E-Mail Server on GenomeNet.
Organization: Supercomputer Laboratory, Kyoto Institute for Chemical Research, Japan.
Description: Allows rapid comparison of a new protein sequence against all patterns stored in PROSITE, as well as in the MotifDic library (16).
Server email address: motif@genome.ad.jp.
Address to report problems: motif-manager@genome.ad.jp.

INTERACTIVE ACCESS TO PROSITE USING THE WORLD WIDE WEB

The most efficient and user friendly way to browse interactively in PROSITE, as well as to analyse a sequence for the occurrence of a pattern or a profile, is to use the World Wide Web (WWW) molecular biology server ExPASy (17). WWW is a global information retrieval system merging the power of worldwide networks, hypertext and multimedia. Through hypertext links it gives access to documents and information available on thousands of servers around the world. To access a WWW server one needs a WWW browser. Popular browsers available for most computer platforms include Mosaic™, developed at the National Center for Supercomputing Applications (NCSA) of the University of Illinois at Champaign (obtainable by anonymous ftp from

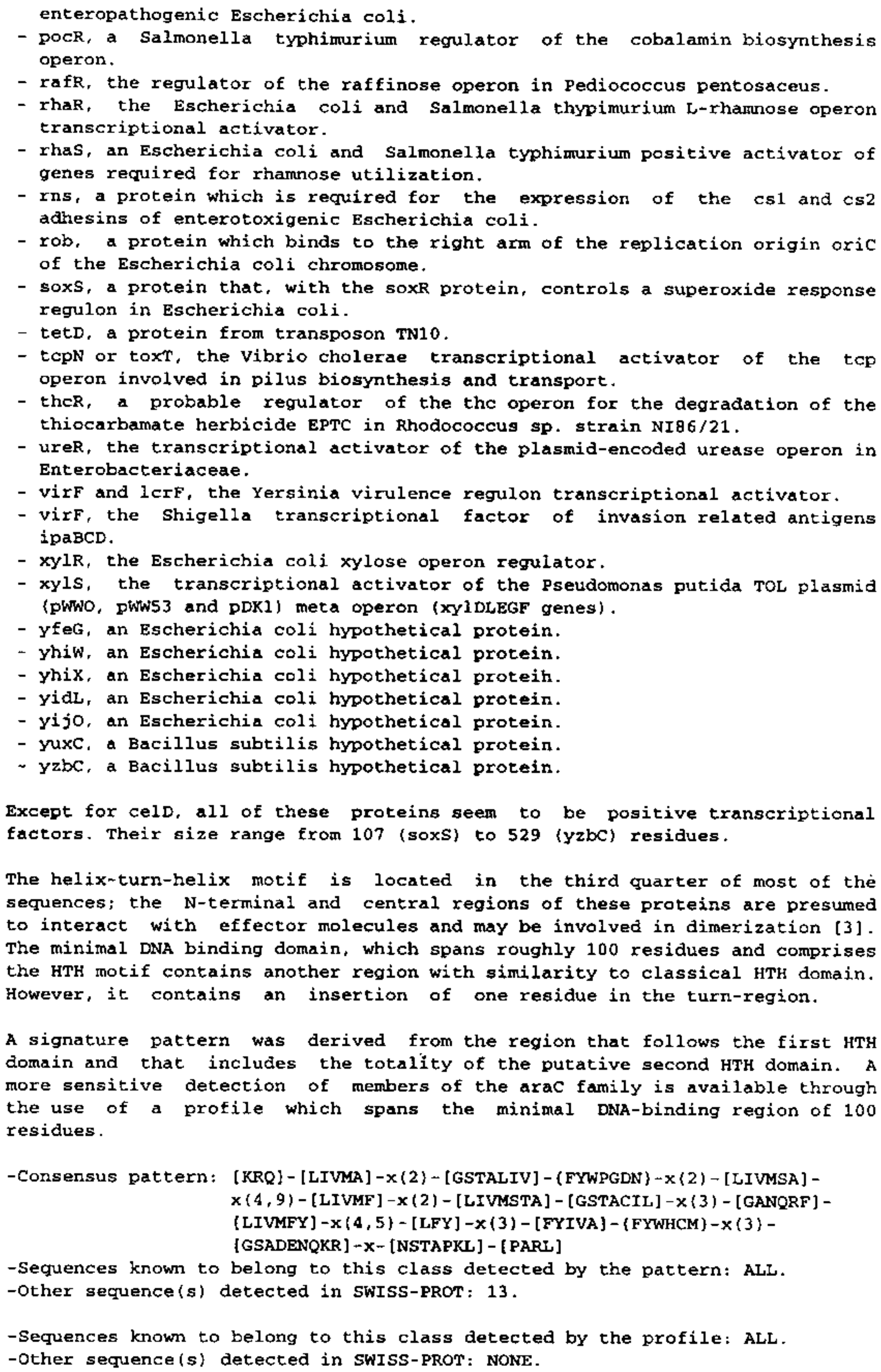
Figure 1. Sample data from PROSITE.



1a) A documentation (textbook) entry from the PROSITE.DOC file

```
{PDOC00040}
{PS00041; HTH_ARAC_FAMILY_1}
{PS01124; HTH_ARAC_FAMILY_2}
{BEGIN}
*****************************************************************
* Bacterial regulatory proteins, araC family signature and profile *
*****************************************************************

The many bacterial transcription regulation proteins which bind DNA  through a
'helix-turn-helix' motif can  be  classified into subfamilies  on the basis of
sequence similarities. One  of these subfamilies groups together the following
proteins [1,2]:

 - aarP,  a  transcriptional  activator  of the 2'-N-acetyltransferase gene in
   Providencia stuartii.
 - ada,  an  Escherichia  coli and Salmonella typhimurium bifunctional protein
   that repairs  alkylated  guanine  in DNA by transferring the alkyl group at
   the O(6)  position  to  a  cysteine  residue  in the enzyme. The methylated
   protein acts  a  positive  regulator  of its own synthesis and of the alkA,
   alkB and aidB genes.
 - adaA, a Bacillus subtilis  bifunctional  protein  that  acts  both  as  a
   transcriptional activator of the ada operon and as a methylphosphotriester-
   DNA alkyltransferase.
 - adiY, an Escherichia coli protein of unknown function.
 - aggR,  the  transcriptional  activator  of  aggregative adherence fimbria I
   expression in enteroaggregative Escherichia coli.
 - appY, a protein  which  acts  as  a  transcriptional  activator  of  acid
   phosphatase and other proteins during  the deceleration phase of growth and
   acts as a repressor for other proteins that  are synthesized in exponential
   growth or in the stationary phase.
 - araC, the  arabinose operon  regulatory  protein,  which  activates  the
   transcription of the araBAD genes.
 - cafR, the Yersinia pestis F1 operon positive regulatory protein.
 - celD, the Escherichia coli cel operon repressor.
 - cfaD, a protein which is required for  the  expression of the CFA/I adhesin
   of enterotoxigenic Escherichia coli.
 - csvR,  a  transcriptional  activator  of  fimbrial genes in enterotoxigenic
   Escherichia coli.
 - envY, the porin thermoregulatory  protein, which is involved in the control
   of  the  temperature-dependent  expression  of  several  Escherichia  coli
   envelope proteins such as ompF, ompC, and lamB.
 - exsA, an activator of exoenzyme S synthesis in Pseudomonas aeruginosa.
 - fapR, the positive activator for the expression of  the  987P operon coding
   for the fimbrial protein in enterotoxigenic Escherichia coli.
 - hrpB, a  positive  regulator  of pathogenicity  genes  in  Burkholderia
   solanacearum.
 - invF, the Salmonella typhimurium invasion operon regulator.
 - marA,  which  may  be  a transcriptional activator of genes involved in the
   multiple antibiotic resistance (mar) phenotype.
 - melR, the  melibiose  operon  regulatory  protein,  which  activates  the
   transcription of the melAB genes.
 - mixE, a Shigella flexneri protein necessary for secretion of ipa invasins.
 - mmsR, the transcriptional  activator  for  the mmsAB operon  in Pseudomonas
   aeruginosa.
 - msmR, the multiple  sugar  metabolism  operon  transcriptional activator in
   Streptococcus mutans.
 - pchR, a Pseudomonas aeruginosa  activator for  pyochelin and ferripyochelin
   receptor.
 - perA,  a  transcriptional  activator  of  the  eaeA  gene  for  intimin  in
```

Figure 1. *continued*



enteropathogenic Escherichia coli.

- pocR, a Salmonella typhimurium regulator of the cobalamin biosynthesis operon.
- rafR, the regulator of the raffinose operon in Pediococcus pentosaceus.
- rhaR, the Escherichia coli and Salmonella thypimurium L-rhamnose operon transcriptional activator.
- rhaS, an Escherichia coli and Salmonella typhimurium positive activator of genes required for rhamnose utilization.
- rns, a protein which is required for the expression of the cs1 and cs2 adhesins of enterotoxigenic Escherichia coli.
- rob, a protein which binds to the right arm of the replication origin oriC of the Escherichia coli chromosome.
- soxS, a protein that, with the soxR protein, controls a superoxide response regulon in Escherichia coli.
- tetD, a protein from transposon TN10.
- tcpN or toxT, the Vibrio cholerae transcriptional activator of the tcp operon involved in pilus biosynthesis and transport.
- thcR, a probable regulator of the thc operon for the degradation of the thiocarbamate herbicide EPTC in Rhodococcus sp. strain NI86/21.
- ureR, the transcriptional activator of the plasmid-encoded urease operon in Enterobacteriaceae.
- virF and lcrF, the Yersinia virulence regulon transcriptional activator.
- virF, the Shigella transcriptional factor of invasion related antigens ipaBCD.
- xylR, the Escherichia coli xylose operon regulator.
- xylS, the transcriptional activator of the Pseudomonas putida TOL plasmid (pWWO, pWW53 and pDK1) meta operon (xylDLEGF genes).
- yfeG, an Escherichia coli hypothetical protein.
- yhiW, an Escherichia coli hypothetical protein.
- yhiX, an Escherichia coli hypothetical proteih.
- yidL, an Escherichia coli hypothetical protein.
- yijO, an Escherichia coli hypothetical protein.
- yuxC, a Bacillus subtilis hypothetical protein.
- yzbC, a Bacillus subtilis hypothetical protein.

Except for celD, all of these proteins seem to be positive transcriptional factors. Their size range from 107 (soxS) to 529 (yzbC) residues.

The helix-turn-helix motif is located in the third quarter of most of the sequences; the N-terminal and central regions of these proteins are presumed to interact with effector molecules and may be involved in dimerization [3]. The minimal DNA binding domain, which spans roughly 100 residues and comprises the HTH motif contains another region with similarity to classical HTH domain. However, it contains an insertion of one residue in the turn-region.

A signature pattern was derived from the region that follows the first HTH domain and that includes the totality of the putative second HTH domain. A more sensitive detection of members of the araC family is available through the use of a profile which spans the minimal DNA-binding region of 100 residues.

```
-Consensus pattern: [KRQ]-[LIVMA]-x(2)-[GSTALIV]-{FYWPGDN}-x(2)-[LIVMSA]-
                    x(4,9)-[LIVMF]-x(2)-[LIVMSTA]-[GSTACIL]-x(3)-[GANQRF]-
                    [LIVMFY]-x(4,5)-[LFY]-x(3)-[FYIVA]-{FYWHCM}-x(3)-
                    [GSADENQKR]-x-[NSTAPKL]-[PARL]
-Sequences known to belong to this class detected by the pattern: ALL.
-Other sequence(s) detected in SWISS-PROT: 13.

-Sequences known to belong to this class detected by the profile: ALL.
-Other sequence(s) detected in SWISS-PROT: NONE.
```

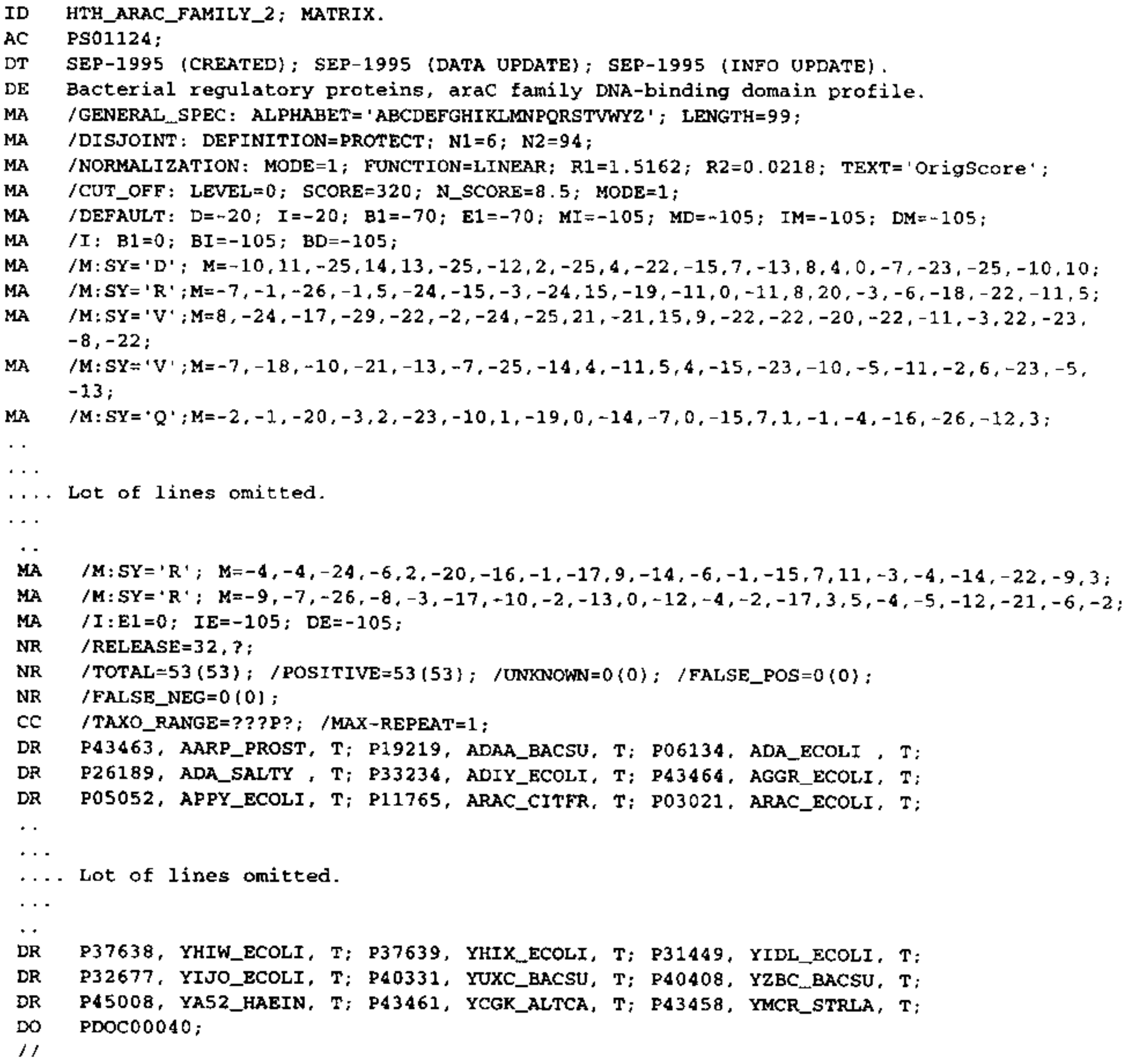
Figure 1. *continued*

```
-Expert(s) to contact by email: Ramos J.L.
                                jlramos@samba.cnb.uam.es
                                Gallegos M.-T.
                                mtrini@samba.cnb.uam.es

-Note: this  documentation  entry  is linked to both a signature pattern and a
 profile. As  the  profile is much more sensitive than the pattern, you should
 use it if you have access to the necessary software tools to do so.

-Last update: September 1995 / Pattern and text revised; profile added.

[ 1] Gallegos M.-T., Michan C., Ramos J.L.
     Nucleic Acids Res. 21:807-810(1993).
[ 2] Henikoff S., Wallace J.C., Brown J.P.
     Meth. Enzymol. 183:111-132(1990).
[ 3] Bustos S.A., Schleif R.F.
     Proc. Natl. Acad. Sci. USA 90:5638-5642(1993).
(END)
```

1b) The corresponding pattern and profile entries in the PROSITE.DAT file

```
ID   HTH_ARAC_FAMILY_1; PATTERN.
AC   PS00041;
DT   APR-1990 (CREATED); SEP-1995 (DATA UPDATE); SEP-1995 (INFO UPDATE).
DE   Bacterial regulatory proteins, araC family signature.
PA   [KRQ]-[LIVMA]-x(2)-[GSTALIV]-{FYWPGDN}-x(2)-[LIVMSA]-x(4,9)-[LIVMF]-
PA   x(2)-[LIVMSTA]-[GSTACIL]-x(3)-[GANQRF]-[LIVMFY]-x(4,5)-[LFY]-x(3)-
PA   [FYIVA]-{FYWHCM}-x(3)-[GSADENQKR]-x-[NSTAPKL]-[PARL].
NR   /RELEASE=29,38303;
NR   /TOTAL=76(76); /POSITIVE=63(63); /UNKNOWN=0(0); /FALSE_POS=13(13);
NR   /FALSE_NEG=0(0);
CC   /TAXO-RANGE=???P?; /MAX-REPEAT=1;
DR   P43463, AARP_PROST, T; P19219, ADAA_BACSU, T; P06134, ADA_ECOLI , T;
DR   P26189, ADA_SALTY , T; P33234, ADIY_ECOLI, T; P43464, AGGR_ECOLI, T;
DR   P05052, APPY_ECOLI, T; P11765, ARAC_CITFR, T; P03021, ARAC_ECOLI, T;
DR   P07642, ARAC_ERWCH, T; P03022, ARAC_SALTY, T; Q03320, ARAL_STRAT, T;
DR   P35319, ARAL_STRLI, T; P26950, CAFR_YERPE, T; P17410, CELD_ECOLI, T;
DR   P43460, CSVR_ECOLI, T; P25393, CFAD_ECOLI, T; P10805, ENVY_ECOLI, T;
DR   P26993, EXSA_PSEAE, T; P23774, FAPR_ECOLI, T; P31778, HRPB_BURSO, T;
DR   P39437, INVF_SALTY, T; P28808, LCRF_YERPE, T; P27246, MARA_ECOLI, T;
DR   P10411, MELR_ECOLI, T; P28809, MMSR_PSEAE, T; Q00753, MSMR_STRMU, T;
DR   Q04642, MXIE_SHIFL, T; P40883, PCHR_PSEAE, T; P43459, PERA_ECOLI, T;
DR   Q05587, POCR_SALTY, T; P43465, RAFR_PEDPE, T; P09378, RHAR_ECOLI, T;
DR   P40865, RHAR_SALTY, T; P09377, RHAS_ECOLI, T; P27029, RHAS_SALTY, T;
DR   P16114, RNS_ECOLI , T; P27292, ROB_ECOLI , T; P22539, SOXS_ECOLI, T;
DR   P29492, TCPN_VIBCH, T; P28816, TETD_ECOLI, T; P43462, THCR_RHOSO, T;
DR   P32326, URER_ECOLI, T; Q02458, URER_PROMI, T; Q04248, VIRF_SHIDY, T;
DR   P13225, VIRF_YEREN, T; P37390, XYLR_ECOLI, T; P45043, XYLR_HAEIN, T;
DR   P07859, XYLS_PSEPU, T; Q04710, XYS1_PSEPU, T; Q05092, XYS2_PSEPU, T;
DR   Q05335, XYS3_PSEPU, T; Q04713, XYS4_PSEPU, T; P36547, YFEG_ECOLI, T;
DR   P37638, YHIW_ECOLI, T; P37639, YHIX_ECOLI, T; P31449, YIDL_ECOLI, T;
DR   P32677, YIJO_ECOLI, T; P40331, YUXC_BACSU, T; P40408, YZBC_BACSU, T;
DR   P45008, YA52_HAEIN, T; P43461, YCGK_ALTCA, T; P43458, YMCR_STRLA, T;
DR   P28647, AA3R_RAT  , F; P23577, CYF_CHLRE , F; P23969, MEND_BACSU, F;
DR   P35349, MGR6_RAT  , F; P40931, MPL_MPLV  , F; P29801, NU2C_SYNP7, F;
DR   P40238, TPOR_HUMAN, F; Q08351, TPOR_MOUSE, F; P28531, RL5_CHLTR , F;
DR   P33983, RP54_ACICA, F; P23626, V3A_TAV   , F; P15911, VFP3_FOWPV, F;
DR   P29940, YCB7_PSEDE, F;
DO   PDOC00040;
//
```

Figure 1. *continued*



```
ID   HTH_ARAC_FAMILY_2; MATRIX.
AC   PS01124;
DT   SEP-1995 (CREATED); SEP-1995 (DATA UPDATE); SEP-1995 (INFO UPDATE).
DE   Bacterial regulatory proteins, araC family DNA-binding domain profile.
MA   /GENERAL_SPEC: ALPHABET='ABCDEFGHIKLMNPQRSTVWYZ'; LENGTH=99;
MA   /DISJOINT: DEFINITION=PROTECT; N1=6; N2=94;
MA   /NORMALIZATION: MODE=1; FUNCTION=LINEAR; R1=1.5162; R2=0.0218; TEXT='OrigScore';
MA   /CUT_OFF: LEVEL=0; SCORE=320; N_SCORE=8.5; MODE=1;
MA   /DEFAULT: D=-20; I=-20; B1=-70; E1=-70; MI=-105; MD=-105; IM=-105; DM=-105;
MA   /I: B1=0; BI=-105; BD=-105;
MA   /M:SY='D'; M=-10,11,-25,14,13,-25,-12,2,-25,4,-22,-15,7,-13,8,4,0,-7,-23,-25,-10,10;
MA   /M:SY='R';M=-7,-1,-26,-1,5,-24,-15,-3,-24,15,-19,-11,0,-11,8,20,-3,-6,-18,-22,-11,5;
MA   /M:SY='V';M=8,-24,-17,-29,-22,-2,-24,-25,21,-21,15,9,-22,-22,-20,-22,-11,-3,22,-23,
     -8,-22;
MA   /M:SY='V';M=-7,-18,-10,-21,-13,-7,-25,-14,4,-11,5,4,-15,-23,-10,-5,-11,-2,6,-23,-5,
     -13;
MA   /M:SY='Q';M=-2,-1,-20,-3,2,-23,-10,1,-19,0,-14,-7,0,-15,7,1,-1,-4,-16,-26,-12,3;
..
...
.... Lot of lines omitted.
...
 ..
 MA   /M:SY='R'; M=-4,-4,-24,-6,2,-20,-16,-1,-17,9,-14,-6,-1,-15,7,11,-3,-4,-14,-22,-9,3;
 MA   /M:SY='R'; M=-9,-7,-26,-8,-3,-17,-10,-2,-13,0,-12,-4,-2,-17,3,5,-4,-5,-12,-21,-6,-2;
 MA   /I:E1=0; IE=-105; DE=-105;
 NR   /RELEASE=32,?;
 NR   /TOTAL=53(53); /POSITIVE=53(53); /UNKNOWN=0(0); /FALSE_POS=0(0);
 NR   /FALSE_NEG=0(0);
 CC   /TAXO_RANGE=???P?; /MAX-REPEAT=1;
 DR   P43463, AARP_PROST, T; P19219, ADAA_BACSU, T; P06134, ADA_ECOLI , T;
 DR   P26189, ADA_SALTY , T; P33234, ADIY_ECOLI, T; P43464, AGGR_ECOLI, T;
 DR   P05052, APPY_ECOLI, T; P11765, ARAC_CITFR, T; P03021, ARAC_ECOLI, T;
 ..
 ...
 .... Lot of lines omitted.
 ...
 ..
 DR   P37638, YHIW_ECOLI, T; P37639, YHIX_ECOLI, T; P31449, YIDL_ECOLI, T;
 DR   P32677, YIJO_ECOLI, T; P40331, YUXC_BACSU, T; P40408, YZBC_BACSU, T;
 DR   P45008, YA52_HAEIN, T; P43461, YCGK_ALTCA, T; P43458, YMCR_STRLA, T;
 DO   PDOC00040;
 //
```

ftp.ncsa.uiuc.edu), and 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 many other WWW servers, and also can make use of many sequence analysis software tools.

The ExPASy server may be accessed through its Uniform Resource Locator (URL, the addressing system defined in WWW), which is http://expasy.hcuge.ch/. You can directly access the 'top page' of the section of ExPASy that allows you to browse through the PROSITE documentation and data entries by opening the URL http://expasy.hcuge.ch/sprot/prosite.html.

To use the PROSITE patterns and profiles you can make use of the following software tools. ScanProsite allows either scanning of a protein sequence, from SWISS-PROT or provided by the user, for the occurrence of patterns stored in PROSITE or scanning of the SWISS-PROT database, including weekly releases, for the occurrence of a pattern that can originate from PROSITE or be provided by the user. The URL for scanprosite is http://expasy.hcuge.ch/sprot/scnpsite.html. ProfileScan allows scanning of a protein sequence, from SWISS-PROT or provided by the user, for the occurrence of profiles stored in PROSITE. The URL for profilescan is
http://ulrec3.unil.ch/software/profilescan.html

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