ScanProsite (/scanprosite/) allows to scan proteins for matches against the PROSITE collection of motifs (/cgi-bin/prosite/prosite_browse.cgi?order=hits%2

At the beginning the user has to choose between three options:

Option 1 - Submit PROTEIN sequences (#mo_prot_seq) to scan them against the PROSITE collection of motifs (/cgi-bin/prosite/prosite_browse.cgi?order=
Option 2 - Submit MOTIFS (#mo_motifs) to scan them against a PROTEIN sequence database (#mo_prot_db) .
Option 3 - Submit PROTEIN sequences (#mo_prot_seq) and MOTIFS (#mo_motifs) to scan them against each other.

Quick Scan

The Quick Scan mode of ScanProsite corresponds to a simplified version of 'Option 1 - Submit PROTEIN sequences (#mo_prot_seq) to scan them against
Enter or paste up to 10 protein sequences in the textarea.
The accepted input is:

- UniProtKB accessions e.g. P98073 or identifiers e.g. ENTK_HUMAN*
- PDB identifiers e.g. 4DGJ
- Sequences in FASTA format

**All UniProtKB/Swiss-Prot accessions/identifiers and all UniProtKB/TrEMBL accessions/identifiers of entries belonging to reference proteomes are accepte*

Your input sequences will be scanned against all PROSITE motifs including or excluding the ones with a high probability of occurrence (see the Exclude mo
Once the scan carried out, the results will be displayed in the ' Graphical view (#of_graphical) ' output format.

Main operations

Submit PROTEIN sequences

You can either enter or paste protein sequences in the textarea or submit a protein database.
If you choose to enter sequences in the textarea, the accepted input is:

- UniProtKB accessions e.g. P98073 or identifiers e.g. ENTK_HUMAN*
- PDB identifiers e.g. 4DGJ
- Sequences in FASTA format

**All UniProtKB/Swiss-Prot accessions/identifiers and all UniProtKB/TrEMBL accessions/identifiers of entries belonging to reference proteomes are accepte*

If your in 'Option 1' (scan against all PROSITE motifs), the maximum number of sequences that you can submit is 10; while if your in 'Option 3' (scan agains

If you want the scan to be carried out against your own sequence database either enter a database code or submit a file in FASTA (max. 16MB). Once your

Submit MOTIFS (Enter a MOTIF or a combination of MOTIFS)

Enter a motif or a combination of motifs in the textarea, the supported input is:

- A PROSITE accession e.g. PS50240 or identifier e.g. TRYPSIN_DOM
- Your own pattern e.g. P-x(2)-G-E-S-G(2)-[AS]
- A combination of PROSITE accessions/identifiers e.g. PS50240 and PS50068, e.g. PS50240 and not (PS00134 or PS00135)
- A combination of PROSITE accessions/identifiers and your own pattern e.g. PS50240 and P-x(2)-G-E-S-G(2)-[AS]

Then you have the possibility to modify a couple of default scanning parameters (scanning options (#scanning_options))

- Mimimal number of hits per matched sequences (#so_min_nbhit) (only in 'Option 2')
- Run the scan at high sensitivity (show weak matches for profiles) (#so_low_level)
- Number of X characters in a scanned sequence that can be matched by a conserved position in a pattern
- Match mode (#so_matchmode)

Pattern syntax

- The standard IUPAC one letter code for the amino acids (http://www.bioinformatics.org/sms/iupac.html) is used in PROSITE.
- The symbol 'x' is used for a position where any amino acid is accepted.
- Ambiguities are indicated by listing the acceptable amino acids for a given position, between square brackets '[ ]'. For example: [ALT] stands for Ala o
- Ambiguities are also indicated by listing between a pair of curly brackets '{ }' the amino acids that are not accepted at a given position. For example: {A
- Each element in a pattern is separated from its neighbor by a '-'.
- Repetition of an element of the pattern can be indicated by following that element with a numerical value or, if it is a gap ('x'), by a numerical range be
  Examples:
  - x(3) corresponds to x-x-x
  - x(2,4) corresponds to x-x or x-x-x or x-x-x-x
  - A(3) corresponds to A-A-A
- When a pattern is restricted to either the N- or C-terminal of a sequence, that pattern respectively starts with a '<' symbol or ends with a '>' symbol.
  In some rare cases (e.g. PS00267 (/PS00267) or PS00539 (/PS00539)), '>' can also occur inside square brackets for the C-terminal element. 'F-[GS

Note:

- Ranges can only be used with with 'x', for instance 'A(2,4)' is not a valid pattern element.
- Ranges of 'x' are not accepted at the beginning or at the end of a pattern unless resticted/**anchored** to respectively the N- or C-terminal of a sequenc

Extended syntax for ScanProsite:

- If your pattern does not contain any ambiguous residues, you don't need to specify separation with '-'.
  Example: **M-A-S-K-E** can be written as **MASKE**.
  It means that in such a case you can directly copy/paste peptide sequences into the textfield.
- To search all sequences which do not contain a certain amino acid, e.g. Cys, you can use **<{C}*>**.

You can use the program PRATT (https://web.expasy.org/pratt/) to generate your own pattern.

Pattern	Explanation
[AC]-x-V-x(4)-{ED}	[Ala or Cys]-any-Val-any-any-any-any-{any but Glu or Asp}
<A-x-[ST](2)-x(0,1)-V	Ala-any-[Ser or Thr]-[Ser or Thr]-(any or none)-Val at the N-terminal of the sequence
<{C}*>	No Cys from the N-terminal to the C-terminal i.e. All sequences that do not contain any Cys.
IIRIFHLRNI	Ile-Ile-Arg-Ils-Phe-His-Leu-Arg-Asn-Ile

Combination of MOTIFS

You can submit multiple motifs at the same time. The upper limit is 8 motifs for a scan against a protein database (Option 2 - Step 1) and 16 for a scan agai
You can use logical operators: 'and', 'or' and 'not' with parentheses if needed.

Examples of logical expressions
PS50240 PS50068
PS50240 and PS50068
PS50240 and P-x(2)-G-E-S-G(2)-[AS]
PS50240 and not PS50068
PS50240 and (PS00134 or PS00135)
PS50240 and not (PS00134 or PS00135)

- The 'or' is implicit which means that for instance 'PS50240 PS50068' is equivalent to 'PS50240 or PS50068' if you want to look for sequences matche
- (Innermost) parentheses are handled first.
- The 'not' is right associative, which means that what's on ther right of the 'not' is evaluated before the 'not'.
- The 'and' and 'or' are left associative, which means that what's on the left of an 'and' or an 'or' is evaluated before the 'and' or 'or'.
- A root 'not' like in 'not PS50240' is not allowed because it would give too many matches.
- If you use parentheses, put a space before and after each of them. For instance 'PS50240 and not (PS00134 or PS00135)' is correct while 'PS5024(
- If you use logical operators, all your expressions must be explicit, i.e. you cannot use white spaces standing for 'or'. For instance 'PS50240 and not (F

Select a PROTEIN sequence database

Select between these PROTEIN sequences databases

- UniProtKB (https://www.uniprot.org/) Swiss-Prot and/or TrEMBL*
- PDB (http://www.rcsb.org/pdb/home/home.do)
- Your own sequence database
- Randomized UniProtKB/Swiss-Prot (#mo_prot_db_random) : reversed or window20

**For UniProtKB/TrEMBL, only entries belonging to reference proteomes are included in the set.*

If you want the scan to be carried out against your own sequence database either enter a database code or submit a file in FASTA (max. 16MB). Once your

Randomized UniProtKB/Swiss-Prot

It is often useful to be able to search a pattern against a random database in order to evaluate its specificity. It is desirable for that database not to be comp

- reverse: reverse sequences - created by taking the reverse sequence of each individual entry.
- window20: shuffled sequences - created by local shuffling of each individual sequence entry using a window width of 20 residues

The reverse sequences method is generally recommendable, but it is not adapted for patterns which are strongly enriched in one amino acid e.g. C-C-C-[LI

Note: Scanning a randomized sequence database only makes sense against patterns.

Filters

Filter	
length >= than	Specifies a minimal length Must be a positive integer or zero, e.g. 150
length <= than	Specifies a maximal length Must be a positive integer, e.g. 500
Taxonomy	Enter a taxonomical term e.g. 'Homo sapiens', e.g. 'Fungi; Arthropoda' or corresponding NCBI TaxID e.g. 9606, e.g. '4751; 6656' that you c Multiple terms must be separated by a semicolon.

Scanning options

	Description

Exclude motifs with a high probability of occurrence (#so_no_highprob)	Does not scan against motifs with a high probability of occurrence.
Exclude profiles (#so_no_profile)	Does not scan against profiles. => Scans only against patterns.
Run the scan at high sensitivity (#so_low_level)	Runs the scan at a low level (shows weak matches). Concerns profiles only.
Minimal number of hits per matched sequence (#so_min_nbhit)	Defines how many hits there must be in a sequence for the matched sequence to
Match mode (#so_matchmode)	Defines the match mode for pattern matching. Concerns patterns only.

Exclude motifs with a high probability of occurrence

Description	Default value
Does not scan against patterns with a high probability of occurrence. Concerns patterns only.	On

Motifs with a high probability of occurrence are in most cases patterns that are found in many protein sequences. Some of them describe for example comn
While it is generally useful to note their presence, some programs may want, in some cases, to ignore those entries. For this purpose these entries are indi

```
ID   ASN_GLYCOSYLATION; PATTERN.
AC   PS00001;
DT   APR-1990 (CREATED); APR-1990 (DATA UPDATE); APR-1990 (INFO UPDATE).
DE   N-glycosylation site.
PA   N-{P}-[ST]-{P}.
CC   /SITE=1,carbohydrate;
CC   /SKIP-FLAG=TRUE;
CC   /VERSION=1;
PR   PRU00498;
DO   PDOC00001;
//
```

Matches by frequently occuring motifs are displayed under 'hits by patterns/profiles with a high probability of occurrence' if the output format is 'Graphical vi

Exclude profiles

Description	Default value
Does not scan against profiles. => Scans only against patterns.	Off

Run the scan at high sensitivity

Description	Default value
Runs the scan at a low level (shows weak matches). Concerns profiles only.	Off

PROSITE profiles normally use two cut-off levels, a reliable cut-off (LEVEL=0) and a low confidence cut-off (LEVEL=-1) [more (/prosuser.html#conv_pp)].

Runs the scan at a low confidence cut-off (LEVEL=-1) and hence shows matches that are below the the reliable cut-off (LEVEL=0).
Weak hits are tagged with '[warning: hit with a low confidence level (-1)]' if the output format is 'Graphical view' and '[low confidence]' if the output format is '

Minimal number of hits per matched sequence

Description	Default value
Defines how many hits there must be in a sequence for the matched sequence to be displayed.	1

Match mode

Three parameters allow to finely tune the behaviour of the pattern-matching engine:

parameter	action
greed	extends at most variable-length pattern elements
overlap	allows partially overlapping matches
include	allows matches included within one another (implies overlap)

The default behavior is greedy, allows overlaps but not included matches. This means that two overlapping matches are rejected if one is entirely contained
For example, consider the sequence "ABACADAEAFA" and the simple pattern "A-x(1,3)-A". The six possible combinations of the switches produce the follo

- greed=1, overlap=1, include=0 (default) : 4 matches

```
ABACADAEAFA
ooooo......
..ooooo....
....ooooo..
......ooooo
```

- greed=1, overlap=1, include=1 : 5 matches

```
ABACADAEAFA
ooooo......
..ooooo....
....ooooo..
......ooooo
........ooo
```

- greed=1, overlap=0 : 2 matches

```
ABACADAEAFA
ooooo......
......ooooo
```

- greed=0, overlap=1, include=0 or 1 : 5 matches

```
ABACADAEAFA
ooo........
..ooo......
....ooo....
......ooo..
........ooo
```

- greed=0, overlap=0 : 3 matches

```
ABACADAEAFA
ooo........
....ooo....
........ooo
```

Output formats

Graphical view

HTML view with a graphical representation of hits on proteins (as downloadable images) and prediction (for certain profiles) of features inside matches.

This Web tool displays for each hit within a protein sequence: the hit sequence, the score (for hits against a profile), the PROSITE description and link. In a
Results are separated into different kinds of hits: hits by 'profiles', 'profiles with a high probability of occurrence', 'patterns', 'patterns with a high probability o
In addition for each matched protein, a graphical view in form of a downloadable png (Portable Network Graphics) image represents all its matches (of the a
If a match overlaps with the previous one, it will be shown on a different line or if the overlap size is smaller than 10% of the match size, the match will be sł

Biological features:
For certain profiles, additional biologically meaningful information about residues inside matches is defined. This additional information comes from the map
If certain conditions expected for the functional and/or structural properties associated with the domain are fulfilled the properties are shown as 'Predicted fe
Conditions can be specific amino acid inside hit, group of sub-conditions in which all conditions must be true in order for the group condition to be true, case
Features associated with conditions that were not fulfilled are shown as 'Absent features' in the same way as for predicted ones except that condition here s
On the graphical view, features are shown on top of hits; depending on their type as bridges, horizontal bars, vertical pins.

Individual view:
For a scan of more than one sequence against all PROSITE motifs (Option 1), you can click on 'individual view' next to the graphical display so as to see or

View all PROSITE motifs hits on sequence:
For a scan of specific sequences against specific motifs (Option 3), you can click on 'View all PROSITE motifs hits on sequence' in order to sea all PROSIT

Match/sequence highlighting:

When hits for only one protein are shown, and if you have a Mozilla based web browser (Mozilla, FireBird/Fox, Netscape 7) you'll be able to see feature res
Highlights are persistent as long as you don't move your cursor over another match/feature (note that left/right margins are immune to cursor moves).

Simple view

Simple HTML view of results without graphical representation of hits and feature prediction.

Text

Text-only view (without any html link).

FASTA

Text only view, in FASTA format, each hit is shown as a FASTA (http://en.wikipedia.org/wiki/FASTA_format) sequence where the sequence header/name is:
[the matched protein]/[hit start]-[hit stop]/[the matching PROSITE motif]/the score (only for profiles)/the confidence level (if any).
Note: If 'Retrieve complete sequence' is selected, the complete protein sequence replaces the matched sequence and only one hit per matched sequence

Table

Text view containing for each hit on a sequence:
[the matched protein] [hit start] [hit stop] [the matching PROSITE motif] [the score (only for profiles)] [the confidence level (if any)] [the matched region]
Note: If 'Retrieve complete sequence' is selected, the complete protein sequence replaces the matched sequence and only one hit per matched sequence

Match list

List of matches (UniProtKB accessions if you submitted UniProtKB accessions or identifiers, PDB identifiers if you submitted PDB identifiers, first space del

Miniprofiles

PROSITE pattern hits are validated by automatically generated 'miniprofiles' that assign a status to pattern matches.

Most PROSITE patterns have an associated miniprofile. Miniprofiles are stored in evaluator.dat (https://ftp.expasy.org/databases/prosite/evaluator.dat) and
When there's a hit by a given pattern, the sequence is scanned against the pattern's associated miniprofile: if the miniprofile also matches the region match

The table below shows, for each output format, what is displayed when the pattern's hit is also matched or respectively not matched by the pattern's associ

Output format	matched by miniprofile	not matched by miniprofile
Graphical view	confidence level: (0)	confidence level: (-1)
Simple view	confidence level: (0)	confidence level: (-1)
Text view	confidence level: (0)	confidence level: (-1)
FASTA	(0)	(-1)
Table	(0)	(-1)
Matchlist	/	/

For more information on miniprofiles, please consult " The 20 years of PROSITE (http://nar.oxfordjournals.org/content/36/suppl_1/D245.full) ".

Output options

Maximum number of displayed matches

The maximum number of distinct matched proteins that can be shown in the output.
This number is by default set to 10'000. If you choose 100'000 the results won't be shown in your web browser as a security measure to prevent too much c

Retrieve complete sequences

Adds the complete protein sequence to the information displayed for each matched protein.
This option limits the choices of output formats to 'Simple view', 'Text', 'FASTA' and 'Table'; it also limits the 'Maximum number of displayed matches' to 1'00
Note: For the output formats 'FASTA' and 'Table', the complete protein sequence replaces the matched sequence and only one hit per matched sequence is

Email and job title

Results returned by email limits the choice of output format to 'Text', 'FASTA', 'Table' and 'Matchlist'.
If the chosen 'Maximum number of displayed matches' is 1'000, results have to be send by email and a valid email address is then required. In other situatic

Job title: If you've entered a valid email address and you fill in this field, the 'Job title' will appear in the subject of the email you receive for that job.

Programmatic acces: REST web service

REST introduction

REST: REpresentational State Transfer

REST originally referred to a collection of architectural principles, but now the acronym is often coined to describe any simple web-based interface for progr
The 'naked' data, without any envelope is retrieved as the content of the HTTP query response.
The options for the operation to be performed are part of the HTTP query parameters, the target URL representing the resource being accessed.
The REST *philosophy* also implies using HTTP 'verbs' (PUT, GET, POST, DELETE) to perform distinct operations (respectively: Create, Read, Update, Dele
For more information on REST, consult the the Wikipedia REST article (http://en.wikipedia.org/wiki/Representational_State_Transfer) .

For ScanProsite, as it is a scanning tool, some of the resources are provided by the users (sequences or/and patterns); to minimize the number of required
Note: in the ScanProsite service, POST is not used to update data, but like GET, just to (pass input data and parameters and) read scan result data.

REST usage for ScanProsite

Make an HTTP GET or POST query to the service; retrieve scan output data (in XML or JSON) in the HTTP response content.

e.g. (GET) just query for: https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=ENTK_HUMAN&output=xml

Service url: https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi

Parameters:

GET or POST parameters (name, description):

Name	Correspondence in ScanProsite form)	
seq	*Submit PROTEIN sequences*	Sequence(s) to be scanned: UniProtKB accessions e.g. P98073 or identifiers e.g. ENTK_HUMAN* or PDB identifiers e.g. 4DG Do not repeat parameter; multiple sequences can be specified by separating them with new lines (%0A in url). 'seq' takes precedence over 'db', i.e. that if they're both specified, 'db' will be ignored. **For UniProtKB/TrEMBL accessions and identifiers, only the ones of entries belonging to references proteomes are accepted.* **Default:** seq="" (empty) Examples: • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=P98073 (https://prosite.expasy.org/cgi-bin/prosite/s • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=ENTK_HUMAN (https://prosite.expasy.org/cgi-bin/ (https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=ENTK_HUMAN) • (https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=ENTK_HUMAN) https://prosite.expasy.org/cgi-bin (https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=>ENTK_HUMAN_in_FASTA_%0AMGSKRGISSR • (https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=>ENTK_HUMAN_in_FASTA_%0AMGSKRGISSR (https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=4DGJ)

		• (https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=4DGJ) https://prosite.expasy.org/cgi-bin/prosite/sc (https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=P98073%0AQ3SYW2%0AQ867B7%0AP23604% • (https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=P98073%0AQ3SYW2%0AQ867B7%0AP23604% seq=>ENTK_HUMAN_in_FASTA_%0AMGSKRGISSRHHSLSSYEIMFAALFAILVVLCAGLIAVSCLTIKESQRGAALGQSHE (https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi? seq=>ENTK_HUMAN_in_FASTA_%0AMGSKRGISSRHHSLSSYEIMFAALFAILVVLCAGLIAVSCLTIKESQRGAALGQSHE (https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi? seq=>ENTK_HUMAN_in_FASTA_%0AMGSKRGISSRHHSLSSYEIMFAALFAILVVLCAGLIAVSCLTIKESQRGAALGQSHEARA
db	*Select a PROTEIN sequence database*	Target protein database for scans of motifs against whole protein databases: 'sp' (UniProtKB/Swiss-Prot) or 'tr' (UniProtKB/TrE 'seq' takes precedence over 'db', i.e. that if they're both specified, 'db' will be ignored. **Default:** db=sp (if no "seq" and no "db" are specified, the scan is carried out agains UniProKB/Swiss-Prot) Examples: • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS00134&output=txt (https://prosite.expasy.org/cgi • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS00134&output=txt&db=sp (https://prosite.expasy • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS00134&output=txt&db=pdb (https://prosite.expas
varsplic	*Include isoforms*	If on (varsplic=1): includes UniProtKB/Swiss-Prot splice variants. Only relevant on scans against UniProtKB/Swiss-Prot. **Default:** varsplic=0 (off, UniProtKB/Swiss-Prot splice variants are not scanned) Examples: • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50068&output=list (https://prosite.expasy.org/cgi • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50068&output=list&varsplic=0 (https://prosite.ex • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50068&output=list&varsplic=1 (https://prosite.ex
sig	*Enter a MOTIF or a combination of MOTIFS*	Motif(s) to scan against: PROSITE accession e.g. PS50240 or identifier e.g. TRYPSIN_DOM or your own pattern e.g. P-x(2)-G If not specified, all PROSITE motifs are used. Do not repeat parameter; multiple motifs can be specified by separating them with new lines (%0A in url). **Default:** sig="" (empty) Examples: • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?output=html&varsplic=1&sig=PS50240 (https://prosite.e • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?output=html&varsplic=1&sig=TRYPSIN_DOM (https://p • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?output=html&varsplic=1&sig=P-x(2)-G-E-S-G(2)-[AS] (h • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?output=html&varsplic=1&sig=PS50240%20and%20PS • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?output=html&varsplic=1&sig=PS50240%20and%20not • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?output=html&varsplic=1&varsplic=1&sig=PS50240%20
lineage	*Filters* *On taxonomy*	Any taxonomical term e.g. 'Homo sapiens', e.g. 'Fungi%3BArthropoda' or corresponding NCBI TaxID (http://www.ncbi.nlm.nih.g Separate multiple terms with a '%3B'. Only works on scans against UniProtKB/Swiss-Prot and UniProtKB/TrEMBL. **Default:** lineage="" (empty) Examples: • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50240&output=fasta (https://prosite.expasy.org/c • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50240&output=fasta&lineage=Homo%20sapien • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50240&output=fasta&lineage=9606 (https://pros • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50240&output=fasta&lineage=Fungi%3BArthrop • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50240&output=fasta&lineage=4751%3B6656 (h

max_x	*Number of X characters in a scanned sequence that can be matched by a conserved position in a pattern*	Number of X characters in a scanned sequence that can be matched by a conserved position in a pattern. Only relevant if 'sig' is defined and is a pattern. **Default:** max_x=0 (no X character in a scanned sequence that can be matched by a conserved position in a pattern)
output	*Output format*	txt, xml, json, nice, html, plain, fasta, tabular, list **Default:** output=plain Examples: • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=H2QKV6_PANTR (https://prosite.expasy.org/cgi-bi • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=H2QKV6_PANTR&output=plain (https://prosite.exp • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=H2QKV6_PANTR&output=txt (https://prosite.expas • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=H2QKV6_PANTR&output=xml (https://prosite.expa • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=H2QKV6_PANTR&output=json (https://prosite.exp • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=H2QKV6_PANTR&output=list (https://prosite.expa • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=H2QKV6_PANTR&output=tabular (https://prosite.e • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=H2QKV6_PANTR&output=fasta (https://prosite.exp • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=H2QKV6_PANTR&output=html (https://prosite.exp • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=H2QKV6_PANTR&output=nice (https://prosite.exp
skip	*Exclude motifs with a high probability of occurrence from the scan*	If on (defined, non empty, non zero): excludes motifs with a high probability of occurrence. Only relevant if 'seq' is defined and 'sig' is not defined, i.e. on scans of specific sequence(s) against all PROSITE motifs. **Default:** skip=1 (on, PROSITE motifs with are high probability of occurrences are excluded from the scan) Examples: • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=3BP1_RAT&output=json (https://prosite.expasy.org • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=3BP1_RAT&output=json&skip=1 (https://prosite.ex • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=3BP1_RAT&output=json&skip=0 (https://prosite.ex
lowscore	*Run the scan at a high sensitivity (show weak matches for profiles)*	If on (lowscore=1): shows matches with low level scores. Only relevant for PROSITE profiles. **Default:** lowscore=0 (off, PROSITE profiles are scanned with cut-off of level 0) Examples: • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=CO2_BOVIN&output=tabular (https://prosite.expas • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=CO2_BOVIN&output=tabular&lowscore=0 (https:// • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=CO2_BOVIN&output=tabular&lowscore=1 (https://
noprofile	*Exclude profiles from the scan*	If on (noprofile=1): does not scan against profiles. Only works if 'seq' is defined and 'sig' is not defined, i.e. on scans of specific sequence(s) against all PROSITE motifs. **Default:** noprofile=0 (off, PROSITE profiles are included in the scan) Examples: • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=ENTK_HUMAN&output=xml (https://prosite.expasy • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=ENTK_HUMAN&output=xml&noprofile=0 (https://p • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?seq=ENTK_HUMAN&output=xml&noprofile=1 (https://p
minhits	*Mimimal number of hits*	Mimimal number of hits per matched sequences. Only works if 'sig' and 'db' are defined, i.e. on scans of protein database(s) against specific motif(s).

per matched sequences	**Default:** minhits=1 (Scanned sequences with one match or more are reported in the results) Examples: • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50070&output=nice (https://prosite.expasy.org/c • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50070&output=nice&minhits=1 (https://prosite.e • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50070&output=nice&minhits=2 (https://prosite.e • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50070&output=nice&minhits=3 (https://prosite.e • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50070&output=nice&minhits=4 (https://prosite.e • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50070&output=nice&minhits=5 (https://prosite.e • https://prosite.expasy.org/cgi-bin/prosite/scanprosite/PSScan.cgi?sig=PS50070&output=nice&minhits=10 (https://prosite.