

ScanProsite: Scanning consensus protein motifs.

Prosite URL: <https://prosite.expasy.org/scanprosite/>



ScanProsite tool

This form allows you to enter protein sequences and motifs and scan them against the PROSITE collection of motifs as well as user-defined motifs and patterns.

Step 1: Select option 2 for user motifs.

- Option 1 - Submit PROTEIN sequences to scan them against the PROSITE collection of motifs.
- Option 2 - Submit MOTIFS to scan them against a PROTEIN sequence database.**
- Option 3 - Submit PROTEIN sequences and MOTIFS to scan them against each other.

Reset

STEP 1 - Enter a MOTIF or a combination of MOTIFS [Examples](#) [\[help\]](#)

C-x-[LIVMFQ]-x-[LIVMF]-x(2)-[FY]-P-x-D-x(3)-C

Step 2: Type or Paste in consensus motif.

Supported input:

- 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]

STEP 3 - Select output options and submit your job

Output format:

Graphical view

Maximum number of displayed matches:

10'000

If you select 100'000, results are available.

Retrieve complete sequences:

If you choose this option, a maximum of 1'000 output formats are available.

Receive your results by email

Step 3: Click "START THE SCAN" at bottom of page.

START THE SCAN

Reset

Prosite: Interpretation of motif search results.

hits by patterns: [304 hits (bv 1 pattern) on 304 sequences]

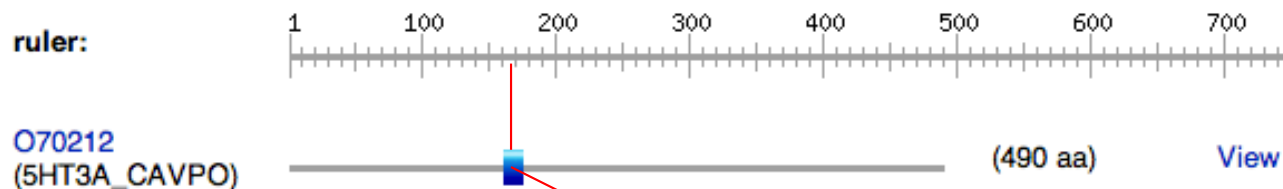
The motif found matches in 304 sequences.

Hits by **USERPAT1** :

Pattern: **C-x-[LIVMFQ]-x-[LIVMF]-x(2)-[FY]-P-x-D-x(3)-C**

Approximate number of expected random matches [Ref: PMID 11535175] in ~ 100'000 sequences

Guinea pig sequence match.



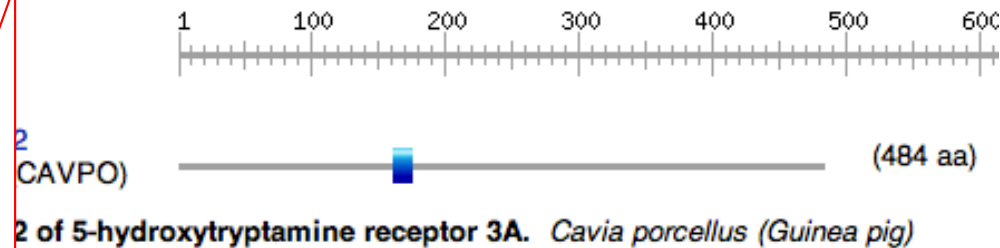
5-hydroxytryptamine receptor 3A. *Cavia porcellus* (Guinea pig)

162 - 176: CsLdIynFPfDvqnC

Relative position of match on primary sequence (aa 162to aa 176).

The name of the protein.

The sequence that matched the motif.



162 - 176: CsLdIynFPfDvqnC

The **O70212** link connects to the Uniprot database entry of the Guinea pig sequence.