



**FACULTY OF ENGINEERING AND
TECHNOLOGY**

Department of Biotechnology

Protein identification and characterization is one of the important parts of [recombinant protein expression](#).



AACompldent

1. **Constellation 0: ALL amino acids:** Ala, Ile, Pro, Val, Arg, Leu, Ser, Thr, Gly, Met, His, Phe, Tyr, Lys, Asp, Asn, Gln, Glu, Cys and Trp.
2. **Constellation 1:** Ala, Ile, Pro, Val, Arg, Leu, Ser, Asx, Thr, Glx, Gly, Met, His, Phe and Tyr.
(Asp+Asn=Asx; Gln+Glu=Glx; Lys, Cys and Trp are not considered).
3. **Constellation 2:** Ala, Ile, Pro, Val, Arg, Leu, Ser, Asx, Lys, Thr, Glx, Gly, Met, His, Phe and Tyr.
(Asp+Asn=Asx; Gln+Glu=Glx; Cys and Trp are not considered).
4. **Constellation 3:** Ala, Ile, Pro, Val, Arg, Leu, Ser, Asx, Lys, Thr, Glx, Gly, Met, His and Phe.
(Asp+Asn=Asx; Gln+Glu=Glx; Tyr, Cys and Trp are not considered).
5. **Constellation 4:** Ala, Ile, Pro, Val, Arg, Leu, Ser, Asx, Lys, Thr, Glx, Met, His, Phe and Tyr.
(Asp+Asn=Asx; Gln+Glu=Glx; Gly, Cys and Trp are not considered).
6. **Constellation 5:** Ala, Ile, Pro, Val, Arg, Leu, Ser, Asx, Lys, Thr, Glx, Gly, Met, His, Phe, Tyr and Cys.
(Asp+Asn=Asx; Gln+Glu=Glx; Trp is not considered).

TagIdent

Name of your query (optional):

pI range: min max

Mw (in Daltons, not kD):

Mw range (in percent): %

Check for protein sequences with cysteines in reduced form (-SH) with cysteines oxidized (-S-S-)

Organism [name](#) or [classification](#) or [NCBI TaxID](#) (e.g. homo sapiens, eukaryota, 9606):

Keyword from KW lines (for search in Swiss-Prot only):

Tagging

With this option, the first 40 amino acids (or the last 40 aa or the matching internal subsequence) of each protein are printed in the result, in addition to the protein name. You may optionally also enter a tag which will be matched with the sequences. If the tag is found in the displayed sequence, it will be shown in lower case, and the numerical position of the tag in the protein will be given. '*' can be used to mean 'any amino acid'.

Tag (up to 6 amino acids):

Search for all possible tag permutations.

Display only the sequences matching the tag.

Include scan of your tag against all fragments in UniProtKB matching your organism criteria (and KW terms for Swiss-Prot only). **Note: pI and Mw are not computed for fragments.**

Display the predicted N-terminal sequence or the C-terminal sequence or the (internal) area of the protein that matches your tag.

Send the result by e-mail

With this option, you will receive the result by e-mail.

Your e-mail:

Database(s) on which the scan should be performed:

UniProtKB/Swiss-Prot

UniProtKE/Swiss-Prot and UniProtKB/TrEMBL

UniProtKE/TrEMBL

PROPSEARCH

To find the putative protein family if querying a new sequence has failed using alignment methods

By neglecting the order of amino acid residues in a sequence, it uses the amino acid composition

144 properties like mol.wt, hydrophobicity, average charge etc., are weighted individually and are used as query vector

PROPSEARCH-DISTANCE

TABLE 1: RELIABILITY OF FAMILY IDENTIFICATION AS FUNCTION OF PROPSEARCH-DISTANCE

DIST		RELIABILITY [percent]
between	and	
0.0	1.3	99.9
1.3	7.5	99.6
7.5	8.7	94
8.7	10.0	87
10.0	11.2	80
11.2	12.5	68
12.5	13.7	53
13.7	14.9	41
14.9	16.2	36
16.2	17.5	32
17.5	18.7	25
18.7	19.9	19

PepSea

Tool for identification by peptide mapping or peptide Sequencing



Protein mass range [kDa]: < Mr <

Cleavage agent:

Cysteine is:

Oxidized Methionine

Peptide mass (neutral):

Mass accuracy:

Peptide sequence tag: [Syntax: (start mass)XYZ(end mass)]

Match regions:

Pattern Match: Search by:

Only for Edman type searches:

Allowed number of errors:

Nominal mass:

I = L

Q = K

Cleavage specificities:

N-terminal specificity (needs to be off for Match Regions = "2 and 3")

C-terminal specificity (needs to be off for Match Regions = "1 and 2")

On each result page show this number of matches:

Do not search, only compute probability of false-positive match

Peptide mass fingerprinting tools

PepMAPPER: Takes peptide mass as the input

Mascot: Can take the following as input,

- 1) Peptide mass fingerprint
- 2) Sequence query
- 3) MS/MS ion search



PepMAPPER

*Pep*MAPPER ⁽¹⁾

Organism: yeast Enzyme: Trypsin

peptide parameters

Peptide Masses(m/z) Masses are average monoisotopic

Charge Fixed state
 Unknown

Missed Cleavages (max possible)

N-terminal amino acid

Error +/-

fixed peptide modifications **protein parameters**

Acetylation (N-term,K)
Biotinylated (N-term,K)
Carbamidomethyl (C)
Carbonyl (N-term)

Mass Range -

Isoelectric point to +/-

Report top matches

[\[mapper1\]](#)[\[mapper2\]](#)[\[mapper3\]](#)[\[mapper4\]](#)[\[mapper5\]](#)[\[linkspage\]](#)[\[Help Pages\]](#)

MASCOT

MASCOT Peptide Mass Fingerprint

Your name	<input type="text"/>	Email	<input type="text"/>
Search title	<input type="text"/>		
Database	MSDB <input type="button" value="v"/>		
Taxonomy	All entries <input type="button" value="v"/>		
Enzyme	Trypsin <input type="button" value="v"/>	Allow up to	1 <input type="button" value="v"/> missed cleavages
Fixed modifications	<input type="button" value="v"/> Acetyl (K) Acetyl (N-term) Acetyl (Protein N-term) Amidated (C-term) Amidated (Protein C-term) <input type="button" value="v"/>	Variable modifications	<input type="button" value="v"/> Acetyl (K) Acetyl (N-term) Acetyl (Protein N-term) Amidated (C-term) Amidated (Protein C-term) <input type="button" value="v"/>
Protein mass	<input type="text"/> kDa	Peptide tol. ±	1.2 <input type="text"/> Da <input type="button" value="v"/>
Mass values	<input checked="" type="radio"/> MH ⁺ <input type="radio"/> M _r <input type="radio"/> M-H ⁻	Monoisotopic	<input checked="" type="radio"/> Average <input type="radio"/>
Data file	<input type="text"/>	<input type="button" value="Browse..."/>	
Query NB Contents of this field are ignored if a data file is specified.	<input type="text"/>		
Decoy	<input type="checkbox"/>	Report top	AUTO <input type="button" value="v"/> hits
<input type="button" value="Start Search ..."/>		<input type="button" value="Reset Form"/>	

Transmembrane helices prediction

TMAP

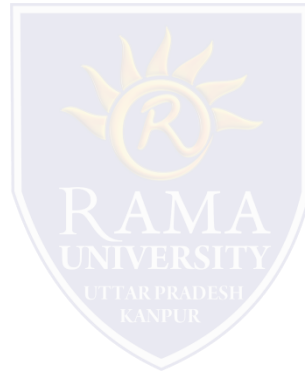
TMHMM

TMPRED

TopPred2

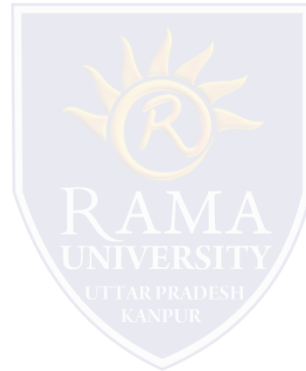
PHDhtm

DAS



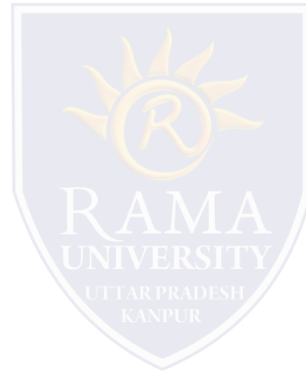
XYZ

abc



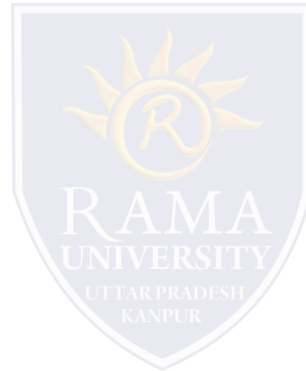
XYZ

abc



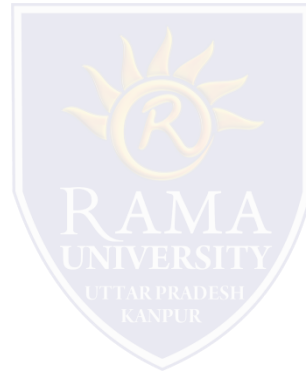
XYZ

abc



XYZ

abc



MCQs

1. A
2. A
3. A
4. A
5. A
6. A
7. A
8. A
9. A
10. A

