

Result and Discussion:

The output is visualized for each input sequence one by one which can be retrieved by its sequence name or index number. The predicted PTM's are labelled using their Abbreviations on top of corresponding position. Multiple lobules are shown on top of prediction of that position is predicted to have multiple PTM's. The highlighted colour corresponds to their confidence level.

Protein Accession Identifier (ACCID) BLAST sequence identify and the known PTM annotation on homologous protein are presented for each input sequence.

3D protein Structure is also visualized by integrating E2S a tool to annotate genomic variance on protein structure & NGL viewer a web application for molecular visualization.

Query + Rhodopsin / G-protein coupled receptor /
Trypsin / Actinase.

URL:- <https://www.musite.net>
<https://ncbi.nlm.nih.gov>

Procedure:-

- *> Log on to NCBI website using url <https://ncbi.nlm.nih.gov>.
- *> Copy the query protein in FASTA format.
- *> Now log on to musitedeep website using url <https://www.Musite.net> homepage opens with a text box.
- *> Paste the query protein sequence in FASTA format in the textbox.
- *> Select the preferred selection model from the dropdown menu provided above the query sequence textbox.
- *> Select the start prediction button.
- *> Result will be displayed with label of prediction method. Now click on BLAST based annotation button.
- *> For advanced visualization click on view predicted PTM sites in 3D Structures.
- *> Interpret the results.

Study of post translational modification
using relevant tools.

Aim:- to study post-translational modification
using online tool nussiledeep.

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Results for JobID: 2024-02-29T05:18:36.681Z

00.51

>BBA24442.1 trypsin [Staphylococcus aureus]

SVTWMGAGTGFVVGHTIIITNKHVTYHMKVGDEIAHPNGFYNNGGGLYKVTKIVDYPG

60708090100110

Save the prediction results to a file

Advanced functions

BLAST-BASED ANNOTATION

N-linked glycosylation (N) XUbiquitination (U) XPhosphorylation (S,T) X

(adjust interested PTMs for BLAST)

VIEW PREDICTED PTM SITES IN 3D STRUCTURE

Search results by sequence name:

>BBA24442.1 trypsin [Staphylococcus aureus]

< 1 of 1 >

Phosphorylation: P

Glycosylation: gl

Ubiquitination: ub

SUMOylation: su

Acetylation: ac

Methylation: me

Pyrrolidone carboxylic acid: pc

Palmitoylation: pa

Hydroxylation: Hy

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Results for JobID: 2024-02-29T05:18:36.681Z

00.51

>BBA24442.1 trypsin [Staphylococcus aureus]

Sequence

MNKNIIKSI AAL TILTSVTGVGTTMVEGVQQTAKAENS VKQITNTNVAPYSGVTW MGA

Q7A4V4 (98)

MNKNIIKSI AAL TILTSVTGVGTTMVEGVQQTAKAENS VKQITNTNVAPYSGVTW MGA

A6QH21 (98)

MNKNIIKSI AAL TILTSITGVGTTMVEGVQQTAKAENS VKQITNTNVAPYSGVTW MGA

Q3F9C3 (98)

MNKNIIKSI AAL TILTSITGVGTTMVEGVQQTAKAENS VKQITNTNVAPYSGVTW MGA

Q3HEW5 (98)

MNKNIIKSI AAL TILTSITGVGTTMVEGVQQTAKAENS VKQITNTNVAPYSGVTW MGA

Q9FT61 (98)

MNKNIIKSI AAL TILTSVTGVGTTMVEGVQQTAKAENS VKQITNTNVAPYSGVTW MGA

A7XJQ5 (98)

MNKNIIKSI AAL TILTSVTGVGTTMVEGVQQTAKAENS VKQITNTNVAPYSGVTW MGA

A6Z4V4 (98)

MNKNIIKSI AAL TILTSITGVGTTMVEGVQQTAKAENS VKQITNTNVAPYSGVTW MGA

Q3HFT4 (97)

MNKNIIKSI GAL TILTSITGVGTTMVEGVQQTAKAENS VKQITNTNVAPYSGVTW MGA

Q8NVX3 (97)

MNKNIIKSI AAL TILTSITGVGTTVVDGIQQTAKAENS VKQITNTNVAPYSGVTW MGA

Q6GBC4 (97)

MNKNIIKSI AAL TILTSITGVGTTVVDGIQQTAKAENS VKQITNTNVAPYSGVTW MGA

Save the prediction results to a file

Save the current blast result to a file

Advanced functions

BLAST-BASED ANNOTATION

N-linked glycosylation (N) XUbiquitination (U) XPhosphorylation (S,T) X

(adjust interested PTMs for BLAST)

VIEW PREDICTED PTM SITES IN 3D STRUCTURE

Phosphorylation: P

Glycosylation: gl

Ubiquitination: ub

SUMOylation: su

Acetylation: ac

Methylation: me

Pyrrolidone carboxylic acid: pc

Palmitoylation: pa

Hydroxylation: Hy

trypsin [Staphylococcus aureus]

GenBank: BBA24442.1

[GenPept Identical Proteins Graphics](#)

>BBA24442.1 trypsin [Staphylococcus aureus]

```
MNKNIIIKSIAALTILTSVTGVTMVEGVQQTAKAENSVKQITNTNVAPYSGVTWMGAGTGFVVGNIHTI  
ITNKHVTYHMKVGDEIKAHPNGFYNNGGGLYKVTIKIVDYPGKEDIAVVQVEEKSTQPKGRKFKDFTSKFN  
IASETKENEPISVIGYPNPNGNKLQMYESTGKVLNVNGNIVSSDAIIQPGSSGSPILNSKYEAIGVIYAG  
NKPSGESTRAFAVYFSPEIKKFIADNLDK
```

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MusiteDeep: a deep-learning framework for protein post-translational modification site prediction

5739 unique visitors
1788507 processed proteins
329787762 processed amino acids

Submit your sequence(s)

Please select a prediction model:
☒ N-linked glycosylation (N) ☒ Ubiquitination (U) ☒ Phosphorylation (S/T)

Paste input FASTA sequence(s) (up to 10 sequences or 5000 residues in total) in the area below: [Load example FASTA](#)

>BBA24442.1 trypsin [Staphylococcus aureus]
MNKNIIIKSIAALTILTSVTGVTMVEGVQQTAKAENSVKQITNTNVAPYSGVTWMGAGTGFVVGNIHTI
ITNKHVTYHMKVGDEIKAHPNGFYNNGGGLYKVTIKIVDYPGKEDIAVVQVEEKSTQPKGRKFKDFTSKFN
IASETKENEPISVIGYPNPNGNKLQMYESTGKVLNVNGNIVSSDAIIQPGSSGSPILNSKYEAIGVIYAG
NKPSGESTRAFAVYFSPEIKKFIADNLDK

For larger job, [upload a FASTA file](#)

Start prediction