



Quick Guide

Submitting Sequences to PredictProtein

- PredictProtein supports only single sequence submission
 - If you want to predict multiple sequences, you can contact us via email
- Sequence format
 - Optional: Sequences can have a FASTA header
 - Sequences must not contain non-standard amino acids
 - Sequences must be at least 17 amino acids long

Submitting Sequences to PredictProtein

 PredictProtein is free to use and open to all users with no login requirements. 

If you're looking for PredictProtein with account access, please visit login.predictprotein.org

Optional: FASTA header



```
>sp|O15105|SMAD7_HUMAN Mothers against decapentaplegic homolog 7 OS=Homo sapiens GN=SMAD7 PE=1 SV=1
MFRTKRSALVRRLWRSRAPGGEDDEEGAGGGGGGGELRGEGATDSRAHGAGGGGPGRAGCCLGKAVRGAKGHHHPHPPAAGAGAAGGAEADLKALTHSVLKKLKERQLELLLQAVESRGGTR
TACLLLPGRLDCRLGPGAPAGAQAQPPSSYSPLLLLCKVFRWPDLRHSSEVKRLCCCESYGKINPELVCCNPHLSRLCELESPPPPYSRYPMDFLKPTADCPDAVPSSAETGGTNYLAPGGLSDS
QLLLEPGDRSHWCWAYWEEKTRVGRLYCVQEPSLDIFYDLPQGNFCLGQLNSDNKSQLVQKVRKIGCGIQLTREVDGWWVYRSSYPFIKSATLDNPDSRTLLVHKVFPGFSSIKAFDYEKAYSLQ
RPNDHEFMQQPWTGFTVQISFVKGWGQCYTRQFISSCPCWLEVIFNSR
```

Press to submit your protein sequence



Clear

PredictProtein

[Example Input 1 Example Input 2]

Submitting Sequences to PredictProtein

- If the results are already in our PredictProtein cache, you will be automatically directed to the results page. If not, you will get a notification box with the associated job ID and link.
- Optional: You can provide an email address which will be notified once the job has been completed.

Submission Success ×

Job submitted to the queue

Current status: Waiting

Use the following link to check on the job's status.
[https://open.predictprotein.org/get_results?req_id=\\$1\\$aEyJ3tp\\$wqZfhSZJn/WkvBgmtarY8](https://open.predictprotein.org/get_results?req_id=1aEyJ3tp$wqZfhSZJn/WkvBgmtarY8).

OPTIONAL: enter your email address and we will notify you when the results are ready

update notification email

OPTIONAL: enter a job name

update job name

This window can safely be closed without affecting processing.

Close

PredictProtein Result: Dashboard

- The main results page (dashboard) contains an overview of all results
 - Sequence alignments
 - Predicted sequence features
 - Length and amino acid composition
- Navigation menu to more specialized tabs on the left
- Export button to quickly download all result files

PredictProtein Result: Dashboard

IEWS

Dashboard >

STRUCTURE ANNOTATION

- Secondary Structure and Solvent Accessibility >
- Transmembrane Helices >
- Protein Disorder and Flexibility >
- Disulphide Bridges >

FUNCTION ANNOTATION

- Effect of Point Mutations >
- Gene Ontology Terms >
- Subcellular Localization >
- Binding Sites >

ADDITIONAL SERVICES

- Literature Search >

HELP

- Site Tutorial >

feedback

Navigation menu

Export **Download result files**

Dashboard Overview for SMAD7_HUMAN [\(display my sequence\)](#)

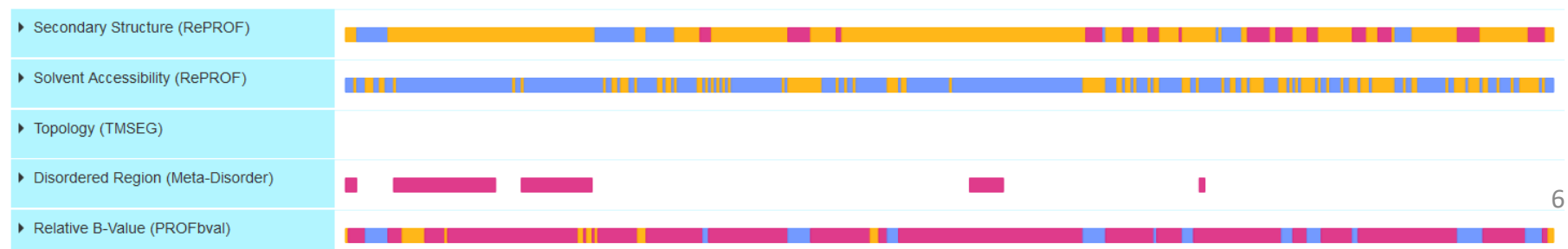
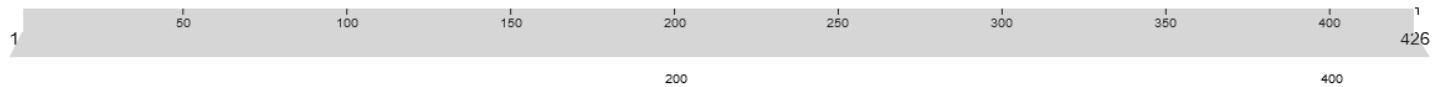
Would you like to see the TEXT output return?

About your sequence

- [Click here to visualize your input sequence.](#)
- [Click here to visualize a table of aligned sequences with UniProt and PDB identifiers.](#)
- [Click here to visualize an alignment of your sequence with UniClust30.](#)
- [Click here to visualize an alignment of your sequence with PDB.](#)

Predicted features

What am I seeing Here? This viewer lays out predicted features that correspond to regions within the queried sequence. Mouse over the different colored boxes to learn more about the annotations



PredictProtein Result: Old Results

The results for this sequence were pre-calculated on **Wed Dec 23 2020** and are older than 3 months. We recommend that you resubmit this job to get a more up-to-date (and possibly more accurate) result. You can resubmit the job by pressing the "Resubmit Job" or "Force Resubmit Job" button.

Note: *Resubmit Job* will resubmit the sequence to our cluster for processing, allowing continued access to outdated results until finished. *Force Resubmit Job*, alternatively, will delete all cached results for this sequence before resubmitting the sequence to our cluster, immediately eliminating access to outdated results until processing has completed.

Resubmit Job

Force Resubmit Job

- Results older than 3 months are marked, as they may be outdated.
- You can resubmit them by pressing the “**(Force) Resubmit Job**” button on the dashboard

Resubmit Job

X

Are you sure you would like to resubmit this job? Resubmitting will compute up-to-date results, including those of new methods, in the background and replace the cached result once completed. In the meantime you can still access the current (outdated) cached results. The re-computation might take a bit, so please resubmit only once.

Yes

No

Force Resubmit Job

X

Are you sure you would like to *force* resubmit this job? Forcefully resubmitting will compute up-to-date results in the background, including those of new methods, completely creating a new result set. Outdated cached results will first be erased, thereby making current results inaccessible. The re-computation might take a bit, so please resubmit only once.

Yes

No

PredictProtein Result: No or Weak Alignments

WARNING

The submitted sequence could not be aligned to any other sequence. Prediction ability for this sequence is thus SEVERELY affected, as most results rely on evolutionary information obtained by multiple sequence alignments.

If you have any doubts, please contact us at help@predictprotein.org

WARNING

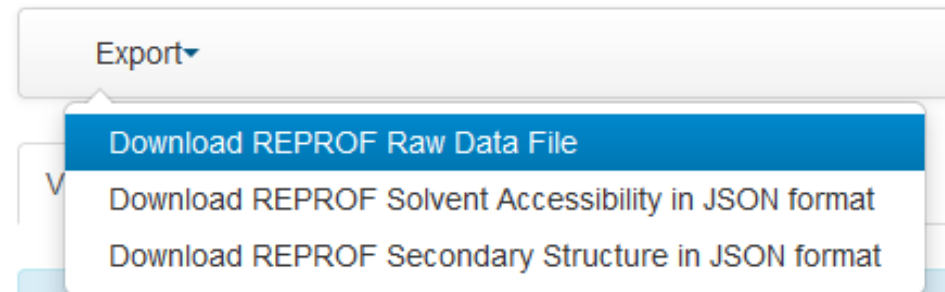
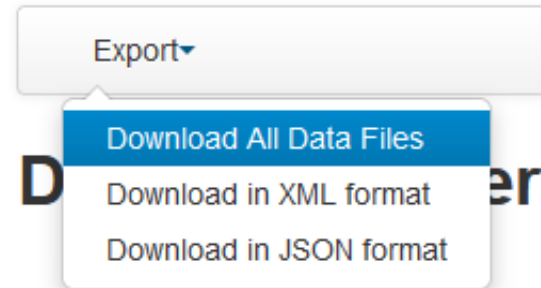
The submitted sequence has a very shallow alignment. Prediction ability for this sequence is thus affected, as most results rely on evolutionary information obtained by multiple sequence alignments.

If you have any doubts, please contact us at help@predictprotein.org

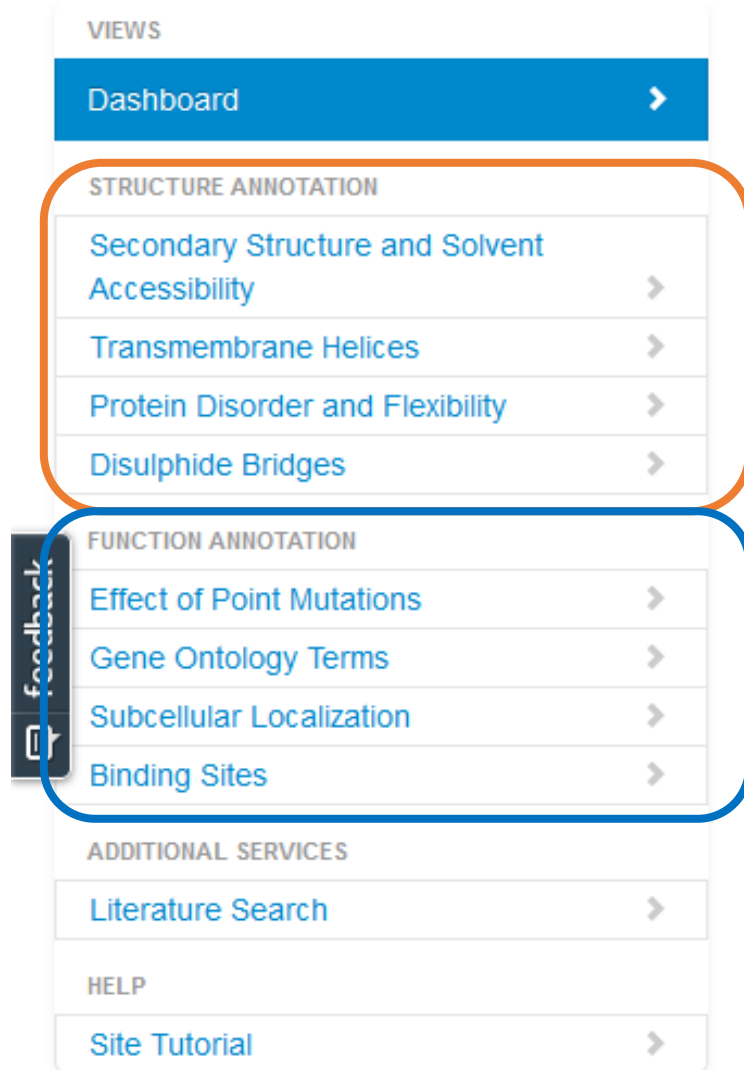
- Many of the methods run by PredictProtein use sequence alignments as part of their input (either PSSMs or MSAs).
- The web server will display a warning if no or only a few sequences have been aligned with the query, as this can affect the reliability of the predictions.

PredictProtein Result: Download Files

- You can download results via the export button on the dashboard
- The specialized tabs provide downloads for individual results



PredictProtein Result: Specialized Tabs



Specialized tabs on the left provide predictions for **structural** and **functional** aspects of the submitted protein sequence

PredictProtein Result: Specialized Tabs

Specialized tabs contain a quick **summary of the visualized results** and a *help* tab with more details about the prediction methods

Subcellular Localization Prediction for SMAD7_HUMAN [\(display my sequence\)](#)

Export ▾

Visual **Help**

What am I seeing Here? This viewer shows a cell schematic with the predicted subcellular localization compartment highlighted in green. The predicted compartment is also referenced by a GO ID for better clarity.

Domains: Archaea Bacteria **Eukarya**


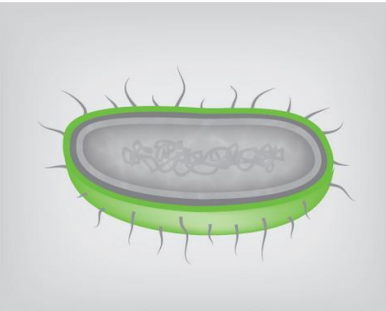



Predicted localization for the Eukarya domain: Nucleus (GO term ID: [GO:0005634](#)) Prediction confidence 44

Visual **Help**

Prediction visualization

Dependent on the identified source organism (listed in the Dashboard Summary) we provide the sub-cellular localization prediction in one of the three domains of life (Archaea, Bacteria and Eukaryota) and highlight the results in green. For example:

Nucleus in Eukaryota	Plasma membrane in Bacteria	Extra-cellular in Archaea
		

How we predict the sub-cellular localization?

LocTree3 predicts the sub-cellular localization by combining *de-novo* and homology-based predictions. LocTree3 classifies proteins in the so far largest number of cellular compartments:

- 18 classes for Eukaryota: chloroplast, chloroplast membrane, cytosol, ER, Golgi, ER membrane, Golgi membrane, extra-cellular, mitochondria, mitochondria membrane, nucleus, nucleus membrane, peroxisome, peroxisome membrane, plasma membrane, plastid, vacuole and vacuole membrane
- 6 classes for Bacteria: cytosol, extra-cellular, fimbrium, outer membrane, periplasmic space and plasma membrane
- 3 classes for Archaea: cytosol, extra-cellular and plasma membrane