

# Secondary Structure Prediction Display User Guide

**Sequence:**

Enter a protein sequence for prediction.  
-Only a single sequence is accepted.  
-Sequence must be between 40 and 4000 characters.  
-Each site has its own maximum sequence length.  
-Only the following characters are allowed:  
A,R,N,D,C,E,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V  
-Spaces will automatically be removed.

**Clear Sequence**

Clears the sequence box of all text.

**Send to:**

☒ JPred ☒ PSIPred ☒ PSSPred  
☒ RaptorX ☒ SABLE ☒ YASPIN  
☒ SSPro

Select which sites the sequence should be sent to for prediction.  
-At least one site should be selected.

**Known Structure:**

Structure Id:   
Chain Id:

Optional. If the entered structure id and chain id are from a valid known structure, then the known elements will be displayed in the output.  
-Both the structure id and chain id must be entered.  
-Chain id's are case sensitive (a is not the same as A).  
-If a valid structure is given, it will be used as the input sequence instead, even if the inputted sequence does not match it.

**Start**

Time Elapsed: 00:00:00

**Prediction Status:**

Prediction progress and any errors will be displayed here.

**Open Results**

Once a prediction is completed, a results page will be created and can be opened.

## Maximum Sequence Lengths

Site	Maximum Sequence Length
JPred	800
PSIPred	1500
PSSPred	4000
RaptorX	4000
SABLE	4000
YASPIN	4000
SSPro	400