

# Secondary Structure Prediction Display User Guide

**Sequence:**  
MHGLQDDPDLQALLKGSQLLKVKSSSWRRE  
RFYKLEDEDCTIWQESRKVMRSPESQLFSI  
EDIQEVRMGHRTEGLEKFARDIPEDRCFSI  
VFKDQRNTLDLIAPSPADAQHWVQGLRKII  
HSGSMDQRQK

**Clear Sequence**  
Clears the sequence box of all text.

**Send to:**  
☒ JPred ☒ PSIPred ☒ PSSPred  
☒ RaptorX ☒ SABLE ☒ YASPIN  
☒ SSPro

**Known Sequence:**  
Structure Id: 1MAI  
Chain Id: A

**Start**  
Time Elapsed: 00:13:06

**Prediction Status:**  
-JPred finished  
-PSI finished  
-Yaspin finished  
-Sable finished  
-RaptorX finished  
-PSS finished  
-SSPro finished (does not provide conf)  
-All predictions completed.

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

**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.

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

**Optional. If the entered sequence is a known structure, parts of it will be colored in the results.**  
-Both the structure id and chain id must be entered.  
-Chain id's are case sensitive (a is not the same as A).

**Prediction progress and any errors will be displayed here.**

## Maximum Sequence Lengths

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