JNet Secondary Structure Prediction

JNet Secondary Structure Prediction - complete

New Window

Cuff J. A and Barton G.J (2000) Application of multiple sequence alignment profiles to improve protein secondary structure prediction, Proteins 40:502-511

--format = msf
--Running pre-Jnet processing
--Running Jnet
15 sequence homologues found
Found HMM profile data
Running final predictions!

WARNING!: Only using the sequence alignment, and HMM profile
Accuracy will average 74.4%

--Running ncoils and multicoil
        1 sequences   97 aas   0 in coil
        1 sequences   97 aas   0 in coil
        1 sequences   97 aas   0 in coil
--creating output
"JNETPSSM" data not present
"JNETFREQ" data not present

ALSCRIPT (ALignment to PostScript)
ALSCRIPT Version 2.07a - 21 March 2000

See ALSCRIPT.DOC for details