

# PSpro 1.1

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pspro: a suite of programs to predict protein 1D and 2D structure features (secondary structure, solvent accessibility, contact map).

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Reference:

1. J. Cheng, A. Randall, M. Sweredoski, and P. Baldi, SCRATCH: a Protein Structure and Structural Feature Prediction Server. Nucleic Acids Research, vol. 33 (web server issue), w72-76, 2005.

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Installation:

open `configure.pl`

set `$install_dir` to the directory of `prosys`

save the file.

run `configure.pl` to configure it.

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## 1. predict\_ss\_sa\_cm.pl fasta\_file output\_dir

predict the secondary structure, solvent accessibility, and contact map for one single sequence in fasta\_file  
output files are stored in output\_dir.

This script uses only ab initio methods.

Test:

```
cd ./test  
../bin/predict_ss_sa_cm.pl 1aqta.fasta ./out
```

The results in out should be the same as in ./1aqta.

## 2. predict\_homo\_cm.pl fasta.file output\_dir

predict the secondary structure, solvent accessibility, and contact map for one single sequence in fasta\_file  
output files are stored in output\_dir.

This script uses only both ab initio and homology methods.

Test:

```
cd ./test  
../bin/predict_ss_sa_cm.pl 1aqta.fasta ./out
```

The results in out should be the same as in ./1aqta\_homo.