

# Resource Summary Report

Generated by T1D on Aug 3, 2026

## SecStr

RRID:SCR\_006220

Type: Tool

---

### Proper Citation

SecStr (RRID:SCR\_006220)

---

### Resource Information

**URL:** <http://athina.biol.uoa.gr/SecStr/>

**Proper Citation:** SecStr (RRID:SCR\_006220)

**Description:** A tool to Predict the Secondary Structure of a protein from its amino acid sequence alone. The SecStr package uses six different secondary structure prediction methods (Nagano, Garnier et al., Burges et al., Chou and Fasman, Lim and Dufton and Hider). The results of those methods are combined into a Joint Prediction Histogram (JPH) as described by Hamodrakas, 1988 and Hamodrakas et al., 1982. As previously mentioned, the SecStr package contains computer programs making use of the secondary structure prediction methods of Nagano, Garnier et al., Burges et al., Chou and Fasman, Lim and Dufton and Hider. These programs were written in Fortran. The results of individual prediction methods are combined as described by Hamodrakas (1988), using a Perl program, to produce joint prediction histograms (JPH), for three types of secondary structure, which may be presented separately on a Java Applet. The output may be given either in text or graphics mode. For the latter a Java capable browser is required.

**Abbreviations:** SecStr

**Synonyms:** SecStr - Secondary Structure Prediction, Secondary Structure Prediction, Secondary Structure Prediction of Proteins

**Resource Type:** production service resource, data analysis service, service resource, analysis service resource

**Keywords:** secondary structure, prediction, protein, algorithm, text, graphics

**Availability:** All rights are reserved for the whole or part of the program. Permission to use, Copy, And modify this software and its documentation is granted for academic use provided that:1. this copyright notice appears in all copies of the software and related documentation; 2. bugs will be reported to the authors.

**Resource Name:** SecStr

**Resource ID:** SCR\_006220

**Alternate IDs:** nlx\_151767

**Record Creation Time:** 20220129T080235+0000

**Record Last Update:** 20260803T040432+0000

---

## Ratings and Alerts

No rating or validation information has been found for SecStr.

No alerts have been found for SecStr.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 7 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Träger TK, et al. (2024) Disorder-to-order active site capping regulates the rate-limiting step of the inositol pathway. Proceedings of the National Academy of Sciences of the United States of America, 121(34), e2400912121.

Spatharas PM, et al. (2022) Clusterin in Alzheimer's disease: An amyloidogenic inhibitor of amyloid formation? Biochimica et biophysica acta. Molecular basis of disease, 1868(7), 166384.

Orze? U, et al. (2021) The Role of Cholesterol in Amyloidogenic Substrate Binding to the ?-Secretase Complex. Biomolecules, 11(7).

Pal D, et al. (2021) Spike protein fusion loop controls SARS-CoV-2 fusogenicity and infectivity. Journal of structural biology, 213(2), 107713.

Dobrovolska O, et al. (2021) Investigating the Disordered and Membrane-Active Peptide A-Cage-C Using Conformational Ensembles. Molecules (Basel, Switzerland), 26(12).

Hasanbaşı? S, et al. (2019) Prolines Affect the Nucleation Phase of Amyloid Fibrillation Reaction; Mutational Analysis of Human Stefin B. ACS chemical neuroscience, 10(6), 2730.

Ahmed AB, et al. (2013) Breaking the amyloidogenicity code: methods to predict amyloids from amino acid sequence. FEBS letters, 587(8), 1089.