

## ABSTRACT

The Support Vector Machine method and the covariant discrimination algorithm, which is an elegant component-coupled method, are expected to combine their computational capabilities in predicting protein structural classes.

## INTRODUCTION

Introduction The goal of this work is to provide an introduction for a medical research titled: 'Support Vector Machines for predicting protein structural class'. The proposed approach is based on the principle that the class structure of a protein is determined by its sequence number and its sequence number position in the sequence tree. The class structure is then determined by the number of protein subunits (or protein-like units) in the protein. The proposed approach is based on the principle that the class structure of a protein is determined by its sequence number and its sequence number position in the sequence tree. The proposed approach is based on the principle that the class structure of a protein is determined by its sequence number and its sequence number position in the sequence tree. The proposed approach is based on the principle that the class structure of a protein is determined by its sequence number and its sequence number position in the sequence tree.

## CONCLUSION

The approach of SVMs in the current study has reinforced the conclusion drawn by Chou and his colleagues, as well as Zhou, that if the coupling effect among various amino acid components is properly considered, the prediction quality of protein structural classes can be significantly improved.