

## Three Dimension Structure Modeling of The Superoxide Dismutase (SOD) of Rice (*Oryza sativa*) Using Fold Recognition Method Using Phyre<sup>2</sup> Web Server

### Pemodelan Struktur Tiga Dimensi Enzim Superoxide Dismutase (SOD) Padi (*Oryza Sativa*) dengan Metode Fold Recognition Menggunakan Web Server Phyre<sup>2</sup>

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#### ABSTRACT

*Determining the 3D structure of proteins using laboratory instrumentation is time-consuming and expensive. The in silico method can be used as an alternative to predict the 3D structure of proteins, such as the fold recognition method. This study aims to create a 3D structural model of rice's (*Oryza sativa*) protein superoxide dismutase (SOD). The 3D structure modeling of the protein was carried out with the Phyre2 web server. The protein sequence was obtained from the UniProt KB database with the code A0A6F8FUX1. The results showed that the suitable template used to build the model was the template with the code c1unfX. The c1unfX template has a coverage value of 80%, 100% confidence, and i.d. of 51%. Validation of the model with the PROCHECK program showed that the most favored area on the Ramachandran Plot was 87.8%, and the disallowed area was 1.1%. The disallowed area, which is still below 15%, indicates that the three-dimensional structure model of the SOD protein built from the c1unfX template has good a value.*

**Keywords:** fold recognition, Phyre<sup>2</sup>, 3D protein structure, superoxide dismutase

#### ABSTRAK

*Penentuan struktur 3D protein dilakukan menggunakan instrumentasi laboratorium yang memakan waktu dan biaya yang mahal. Metode in silico dapat digunakan sebagai alternatif untuk memprediksi struktur 3D protein, misalnya metode fold recognition. Penelitian ini bertujuan membuat model struktur 3D protein superoxide dismutase (SOD) padi (*Oryza sativa*). Pemodelan struktur 3D protein dilakukan dengan web server Phyre<sup>2</sup>. Sekuen protein didapat dari database UniProt KB dengan kode A0A6F8FUX1. Hasil penelitian menunjukkan bahwa template yang digunakan untuk membangun model adalah template dengan kode c1unfX. Template c1unfX memiliki nilai coverage 80%, confidence 100% dan i.d. 51%. Hasil validasi model menggunakan program PROCHECK menunjukkan daerah most favored pada Ramachandran Plot sebesar 87,8% dan daerah yang disallowed sebesar 1,1%. Daerah disallowed yang masih dibawah 15% menunjukkan model struktur tiga dimensi protein superoxide dismutase yang dibangun dari template c1unfX bernilai baik.*

**Kata Kunci:** fold recognition, Phyre<sup>2</sup>, struktur 3D protein, superoksida dismutase

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