3D protein structure prediction of Rhodococcus UKMP-5M phenol hydroxylase using homology modelling

ABSTRACT

The Swiss-prot data-base was used for the protein sequence of Rhodococcus UKMP-5M. BlastP was used to determine the suitable template for homology modelling. Swiss Model is the homology modelling software was used to determine the 3D structure which passed the ProQ quality test for further analysis. Validation result for the predicted structure of Rhodococcus UKMP-5M, in which the prediction structure has passed the validation test with 5.951 Lgscore. This is lies in the range of extremely good model and 0.514 MaxSub which is lies in the range of very good model.

Keyword: Rhodococcus UKMP-5M; Phenol hydroxylase; BlastP; 3D structure; ProQ