

Homology model-inspired engineering of marine epoxide hydrolase to enhance the catalytic efficiency for the biosynthesis of chiral epoxides

이은열*, 최성희¹, 김희숙¹

경희대학교 화학공학과; ¹경성대학교 식품생명공학과

(eunylee@khu.ac.kr*)

Homology modeling is an efficient method for predicting a structure model from its amino acid sequence based on known protein structures as the template. We applied homology modeling to predict suitable target amino acid residue for molecular engineering of the epoxide hydrolase from marine fish. The epoxide hydrolase from *Aspergillus niger* was used as the template. The catalytic efficiency of the engineered epoxide hydrolase of marine fish could be enhanced by site-directed mutagenesis of the target residues that identified on the basis of homology modeling with *A. niger* epoxide hydrolase. Acknowledgement: This work was supported by the Marine and Extreme Genome Research Center Program, Ministry of Land, Transportation and Maritime Affairs, Republic of Korea.