Peningkatan stabilitas Riboflavin Synthase Eremothecium gossypii untuk produksi Riboflavin melalui pendekatan simulasi dinamika molekul = Increasing stability of Riboflavin Synthase Eremothecium gossypii to produce of Riboflavin through molecular dynamics simulation

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Abstrak

Riboflavin synthase merupakan enzim yang mengkatalisis pembentukan riboflavin dengan mengkonversi dua molekul 6,7-dimethyl-8-ribityllumazine secara dismutasi. Interaksi riboflavin synthase Eremothecium gossypii dipelajari dengan pendekatan secara komputasional, untuk melihat keterlibatan residu asam amino sisi aktif enzim yang berperan dalam proses produksi riboflavin. Struktur riboflavin synthase Saccharomyces pombe dengan kode PDB 1KZL digunakan sebagai template untuk memodelkan riboflafin synthase Eremothecium gossypii.

Stabilitas termal enzim diperoleh dengan melakukan simulasi dinamika molekul pada 300K, 315K, 325K, 350K dan 400K. Hasil yang diperoleh menunjukkan bahwa pembentukan riboflavin terjadi pada sisi aktif N-terminal dan residu asam amino yang berinteraksi meliputi Thr56, Gly68, Ala70, Val109, dan His108. Residu His108 pada N-terminal domain merupakan subunit enzim yang berperan sebagai tahap awal reaksi katalisis biosintesis riboflavin.

Hasil simulasi dinamika molekul memperlihatkan kestabilan enzim pada 300K sampai 315K yang ditunjukkan dengan nilai RMSD (root mean square deviation) yang tidak jauh berbeda. Pada 325K dan 350 nilai RMSD makin tinggi menunjukkan ketidakstabilan enzim. Hasil RMSF (root mean square fluctuation) menunjukkan bahwa pada 315K terjadi fleksibilitas tertinggi, dengan memperlihatkan bahwa residu Ala13, Asp19, Ser21, Arg98, Gly162, dan Ala175 merupakan residu yang labil. Prediksi mutasi menyarankan beberapa substitusi residu meliputi Ala13Leu, Asp19Met, Ser21Leu, Arg98Ala, dan Ala175Glu yang mengarah pada peningkatan stabilitas enzim.

.....Riboflavin synthase is an enzyme that catalyzes the formation of riboflavin by converting two molecules of 6, 7-dimethyl-8-ribityllumazine through dismutation reaction. To study the interaction of riboflavin synthase Eremothecium gossypii, we performed a computational approach, to find out the involvement of amino acid residues in the active site of enzymes that play a role in the production of riboflavin. In this research, the structure of riboflavin synthase Saccharomyces pombe with PDB code 1KZL was used as a template.

To determine the thermal stability of the enzyme, we performed molecular dynamics simulation approach at 300K, 315K, 325K, 350K and 400K, respectively. The results showed that the formation of riboflavin occurred in the active site of N-terminal and the amino acid residues that interact include Thr56, Gly68, Ala70, Val109, and His108. His108 is residue a subunit of an enzyme that acts as an early stage of riboflavin formation on the active site of N-terminal.

The results of molecular dynamics simulations showed that stability of the enzyme at 300K to 315K which were indicated by RMSD values were not much different. At 325K and 350K, the RMSD values were higher, it showed instability of the enzyme. The results of RMSF were showed that at 315K occurred highest

flexibility, by showing that residues of Ala13, Asp19, Ser21, Arg98, Gly162, and Ala175 were labile residues. Prediction of mutation were suggest some replacement of residues included Ala13Leu, Asp19Met, Ser21Leu, Arg98Ala, and Ala175Glu that lead to increase the stability of the enzyme.