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研究论文

酵母AHAS酶与磺酰脲类抑制剂作用模型的分子对接研究

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摘要 基于酵母乙酰羟酸合成酶(AHAS)与磺酰脲类抑制剂复合物的晶体结构, 用分子对接方法对AHAS与5个磺酰脲类抑制剂相互作用的方式进行了系统的分子对接研究. 晶体复合物对接和假复合物对接两种模式对接的结果基本相同, 并与实验结果吻合. 在进一步的对接中逐级考虑了辅酶FAD和TPP的影响, 结果表明, 辅酶FAD和TPP的加入, 对AHAS酶与磺酰脲类抑制剂的结合顺序基本没有影响. 其中FAD的加入使AHAS与抑制剂的结合更加稳定, 这主要是由于抑制剂的R2取代基与FAD中的平面基团Flavin环间存在的范德华相互作用所致; 抑制剂与TPP间存在的静电相互作用可能是加速TPP降解的原因.

关键词 酵母乙酰羟酸合成酶(AHAS) 对接 磺酰脲 作用模型

分类号 0641

Molecular Docking Study on Interaction Mode Between Yeast AHAS and Sulfonylureas Inhibitors

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Abstract On the basis of the complex structures of AHAS and sulfonylureas inhibitors, systematic molecule docking study of five sulfonylureas inhibitors to AHAS were performed with autodock 3.0 package. The systematic docking results indicate that two kinds of docking modes are consistent basically each other, and closely correlated with experimental results as well. The further research reveals that the sequence of docking results were not affected via the appearance of FAD and TPP. Due to the VDW interaction between R_2 substituent and flavin ring of FAD, the docking complex of inhibitors to AHAS became more stable. It was assumed that the unfavorable electrostatic interaction between the inhibitors and TPP may be the factor which accelerates the degradation of TPP.

Key words Yeast AHAS Docking Sulfonylureas Interaction mode

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