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研究论文

人顶体酶三维结构的同源模建及其与**KF950**的分子对接研究

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摘要 采用同源模建方法首次构建了人顶体酶的三维结构模型,
模型的可靠性经Ramachandran图和Profile_3D图验证. 采用InsightII/Binding
site方法准确定位了人顶体酶的活性位点, 并研究了顶体酶重要功能残基在活性位点的立体分布. 在此基础上,
通过柔性分子对接方法首次阐明了顶体酶高效抑制剂KF950与靶酶活性位点的相互作用模式,
发现特异性的氢键相互作用是KF950产生高抑制活性的重要分子基础.
其研究结果将为合理设计新型顶体酶抑制剂, 寻找男性口服避孕药奠定坚实基础.

关键词 人顶体酶 同源模建 活性位点 4-胍基苯甲酸(4-甲氧甲酰基)苯酯甲烷磺酸盐 分子对接

分类号

Homology Modeling of Human Acrosin and Its Molecular Docking Study with KF950

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Abstract Homologous 3D model of human acrosin was built on the basis of the crystal coordinates of ram and boar acrosin, while the reliability of the model was assessed by Ramachandran plot and Profile-3D analysis. The active site of human acrosin was searched by Insight II/binding site analysis and important functional residues were located at the active site. To explore the binding mode of the 4-guanidinobenzoates with the active site of human acrosin, KF950 was docked into the active site and specific hydrogen-bonding interaction was found to play an important role in inhibitor recognition and orientation. These results provided a basis for the rational design of specific inhibitors to the target enzyme and the discovery of novel contraceptive agents with high potency.

Key words human acrosin homology modeling active site 4-guanidinozoic acid (4-methoxycarbonyl)- phenyl ester monomesylate molecular docking

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