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论文

基于受体结构的药物分子设计系统:维甲类分子与其结合蛋白之间相互作用的研究

迟翰林:郭宗儒:杨光中:褚风鸣:胡文贵:吴文英

中国医学科学院,中国协和医科大学药物研究所

摘要:

大分子解剖程序,配体分子契合适配和DOCK程序,以及计算化学的其它程序等,已集成为基于受体结构和分子间相互作用的进行分子设计的软件系统,定名为BIOS(Biomolecularinteractionsandorientationsimulator)。BIOS软件可在普通的微机上运行。使用BIOS分别剥离了细胞浆维甲结合蛋白(CRBP)和副睾维甲酸结合蛋白(E-RABP)两种蛋白的配体结合腔,剥离是围绕配体以同样的分子距离进行的。从而得到了芳香性残基分布相似的两个结合腔,其结合位点的几何排布却有相当差别。揭示出的结合腔已用于一系列的维甲类化合物的DOCK研究。E-RABP的结合腔可做为设计新维甲类分子的模板。

关键词: 分子图形学 DOCK 维甲类

A MOLECULAR DESIGN SYSTEM BASED ON RECEPTOR STRUCTURES: STUDY ON THE INTERACTIONS BETWEEN RETINOIDS AND THEIR BINDING PROTEINS

HL Chi; ZR Guo; GZ Yang; FM Chu; WG Hu and WY Wu

Abstract:

The macromolecule anatomy ,ligand-fitting ,docking and other computational chemistry programs have been integrated into BIOS(biomolecular interactions and orientation simulator), to be used on IBM compatible microcomputers as a tool for drug design based on receptor structure and molecular interactiOns. Using the BIOS system ,the cellular serum retinol-binding protein(CRBP) and the epididymal retinoic acid binding protein (E-RABP) were scooped around the ligands in the same intermolecular distance to leave two cavities, which show a similarity in distributions of the aromatic residues. However, the geometry of the two binding sites was quite different. The unraveled binding sites were docked by a serics of retinoids, E-RABP binding site may serve as a template for design of new retinoids.

Keywords: Molecular modeling, DOCK, Retinoids

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