

论文

针对H1N1病毒的多特征siRNA设计

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摘要:

针对甲型流感病毒H1N1基因,从RNAi的角度出发,采用多特征融合的方法,进行siRNA预测。对2009年的46株病毒序列的PA片段进行分析,从经过序列分析所获得的众多靶系列中,采用结构分析手段对靶序列进行筛选,获得较易干扰的靶序列及设计出相应的siRNA。研究发现,2009年爆发的H1N1病毒,序列保守性高,靶序列一致性高,结构保守性高。该方法可以有效选择可能的靶序列,并在此基础上进一步筛选,以获得少量较易干扰的靶序列,该方法为复杂序列siRNA的设计提供了新思路,对siRNA的优化设计有指导意义,有助于利用RNAi进行H1N1治疗的后续研究。

关键词: 生物信息学 RNAi siRNA 二级结构

siRNA design for H1N1 based on multi characters

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Abstract:

Aiming at H1N1 gene and starting from the point of RNAi, siRNA prediction is conducted by means of multi characters analyses, such as sequence and structure. First 46 viral sequence's PA fragments in year 2009 are analyzed. Then the siRNA target genes with strong ability of interference are selected on the basis of the secondary structure of siRNA target sequence. Our research reveals that the outbreaking H1N1 virus in 2009 is characterized by steady heredity, high sequence conservativeness, uniform siRNA target gene sequence, and high conservative structure. This method can be employed to choose the possible siRNA and obtain less but more valuable siRNA target genes by further sifting. It provides a new idea for the design of complex sequence siRNA, and it is of instructional significance for optimal design of siRNA. The research is helpful to the study of H1N1 treatment by RNAi.

Keywords: bioinformatics RNA interfering small interfering RNA secondary structure

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