基于PC/Linux的核酸序列电子延伸系统的构建及其应用

Construction and Application of an in Silico Elongation System of Nucleic Acid Sequence

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新基因全长cDNA序列的获得常常是分子生物学工作者面临的难题。人类基因组计划及其相关计划的实施导 致了大量表达序列标签(EST)的产生。利用一定的生物信息学算法,这些EST序列往往可用来对新基因片段进行延 伸。采用Linux操作系统,利用Blast软件和Phrap软件以及EST数据库在微机上构建了EST序列的电子延伸系统,并 对来自于人胎肝的11386条EST序列和511条插入片段全长cDNA序列进行了电子延伸,结果显示8373条EST序列和389 ▶浏览反馈信息 条插入片段全长cDNA序列得到了程度不等的延伸,部分结果通过RACE实验得到证实。该套系统可高效地、规模化 进行EST序列的延伸,可为通过实验获得新基因全长cDNA序列提供重要线索。

Abstract: Normally it is difficult to obtain full-length cDNA sequence of novel genes. More and more expressed sequence tags(ESTs) have been obtained since the start-up of human genome project. Powerful system is badly needed for data mining on these EST sequences. Based on a personal computer coupled with Linux operating system and EST database, the Blast software and Phrap software were used to construct a platform for in silico elongation of ESTs in our lab. The performance was tested using 11386 EST sequences and 511 partial-length cDNA sequences. Results demonstrated that 8373 EST and 389 cDNA sequence were elongated using this system. Thus the platform seems to be a fast way for full-length cDNA sequence cloning of new genes.

生物信息学 表达序列标签 cDNA 电子序列延伸 微机 Linux操作系统 Key words bioinformatics expressed sequence tag cDNA in Silico sequence elongation personal computer Linux operation system 分类号

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