生物化学与生物物理进展
Progress in Biochemistry and Biophysics

生物信息学辅助定位及延伸辐射诱导未知表达序列标签

Chromosome Location and Elongation of Radiation-induced Expressed Sequence Tag by the Aid of Bioinformatics

投稿时间：2000-2-28　　最后修改时间：2000-3-31

稿件编号：20010215

中文关键词：辐射诱导基因　RIG1　外显子预测

英文关键词：radiation induced gene　RIG1　exon prediction

基金项目：国家自然科学基金资助项目(39870214).

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中文摘要：

研究辐射诱导的基因表达调控对于认识细胞对辐射损伤的应激反应有重要意义.在低剂量辐射诱导新基因RIG1表达序列标签(expression sequence tag,EST)片段的基础上，通过非克隆cDNA文库和RACE(rapid amplification of cDNA end)技术获得了其3′末端.依据实验得到的这两段EST序列所提供的信息，通过生物信息学分析将RIG1基因初步定位在20号染色体.对20号染色体RIG1区基因组序列进行外显子扫描，发现预测的外显子正好与实验得到的EST相吻合.利用预测的外显子设计特异引物，成功地克隆了RIG1基因全长序列.同时，对20号染色体RIG1区的生物信息学分析表明，在RIG1基因的上游存在启动子区，从而确定了RIG1基因的基因组序列.因此，通过生物信息学辅助设计实验，快捷地定位及延伸了未知EST片段RIG1，基本完成了RIG1的全基因、基因组序列及染色体定位研究.

英文摘要：

Regulation of gene expression is one of the most important responses of cells to DNA damage induced by radiation. A novel expressed sequence tag (EST) fragment had been cloned from human embryo lung cells induced by 50cGy radiation and named RIG1. To clone the full-length cDNA of RIG1, a non-cloned cDNA library of human embryo lung cells induced by low dose irradiation had been established. This library was used as template in enchanced nest RACE PCR and biotin-labeled probe was used for further purification. The 3′ flanking sequence of this EST was cloned and sequenced with this set of technology. It was illuminated by homology analysis that this 3′ flanking sequence and the original EST are well aligned with a BAC clone of 20th chromosome and the predicted exons' sequence of this chromosome is well consistence with the real EST. Thus the RIG1 can be roughly located in 20th chromosome. By use of the exons' sequence predicted from chromosome sequence by GENSCAN, full-length of RIG1 gene has been cloned. Chromosome location of RIG1 gene is further determined by this successful verification of Bioinformatics prediction by experiment. By the same step, genome sequence of RIG1 has been determined. Therefore,by the combined use of Bioinformatics analysis, the full-length cDNA sequence and genome sequence of RIG1 gene are obtained and the predicted protein sequence is determined.

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