解效果差，以及裂解后引起C端封闭，虽然成熟的C端测序技术至今尚未问世，但是人们还是在不断发现成功的趋势，尤其在化学降解方面．因为尽管质谱有其极大的吸引力，没有经验丰富的质谱专家或功能复杂齐全的计算机很难分析数据，因此许多从事蛋白质结构分析的生化学家仍倾向于化学法能如N端序列分析一样自动、微量分析C端20—40个左右氨基酸残基的序列．但是以上两种方法，将来何者会占据上风，作者认为现在还难以预料．

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