

δ257-MSTAI SVLLAQAVFLLLTSQRLPET
δ206-FPNGTNYQDVTFYLI IRRKPLFYVI

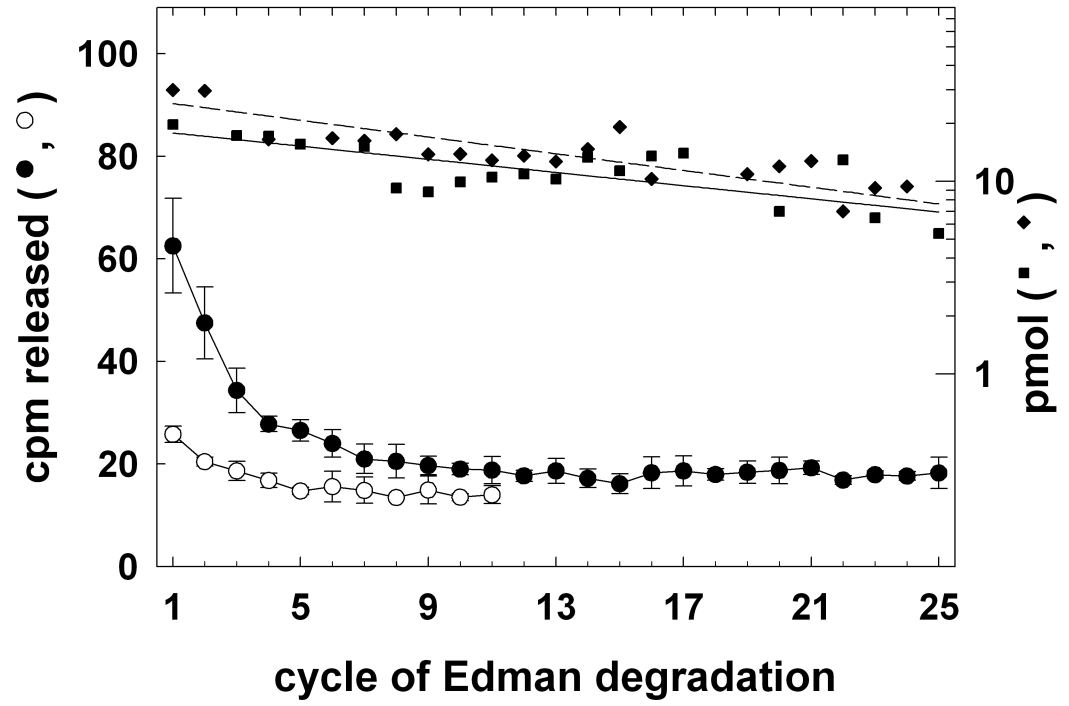


Figure 2-11 Sequence Analysis of δ V8-20 EndoLysC digest fragments.

Sequence analysis of fraction 31 from HPLC purification of Figure 2-10. For each sample, 67% of each cycle of Edman degradation was analyzed for released ^3H (\bullet , \circ), and 33% for released PTH-amino acids (\blacksquare , \blacklozenge). For both labeling conditions, two sequences were detected, one beginning at δ Met-257, the N-terminus of the M2 segment, and one beginning at δ Phe-206. +/- (\bullet): δ Met-257 (\blacksquare): $I_0=19$ pmol, $R=96\%$; δ Phe-206 (\blacklozenge): $I_0=27$ pmol, $R=95\%$, 3800 cpm loaded, 1100 cpm remaining after 25 cycles. +/- (\circ): δ Met-257: $I_0=5$ pmol, $R=99\%$; δ Phe-206: $I_0=12$ pmol, $R=92\%$, 860 cpm loaded, 170 cpm remaining after 11 cycles. The sequences of the identified peptides are shown above.