

46 data points from 205 to 250 nm

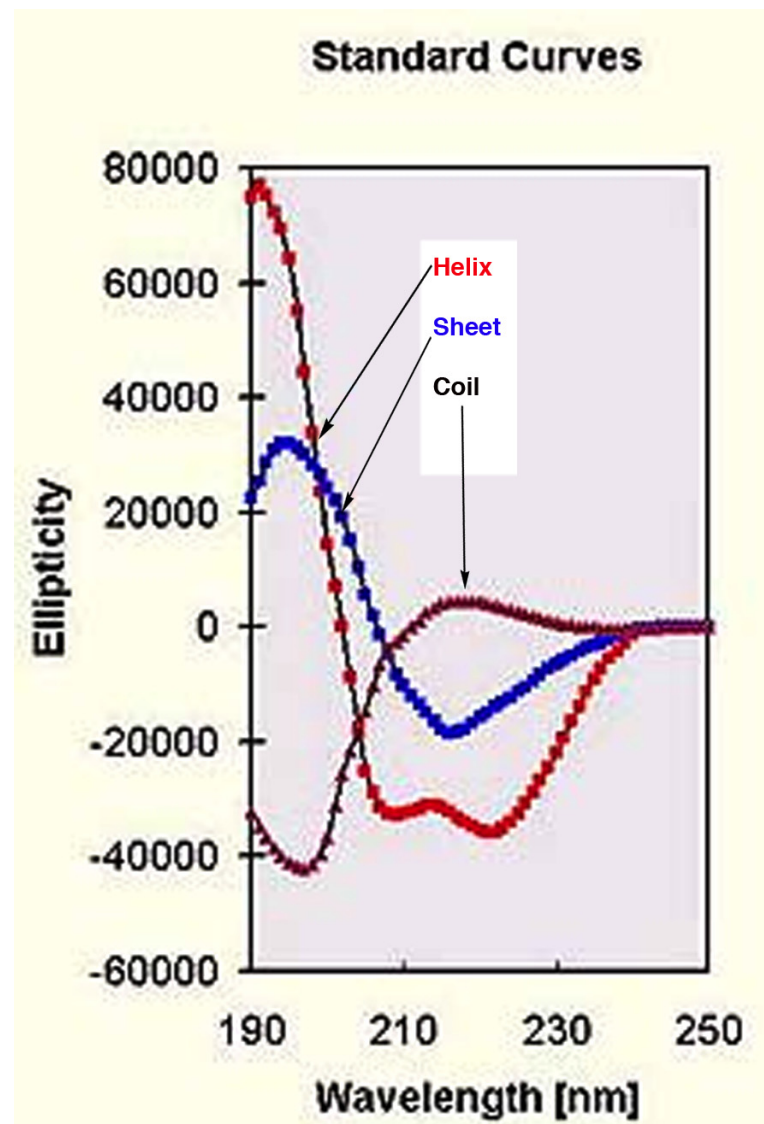
-----  
Molecular weight g/mol : 26698.00  
Sample concentration mg/cm3 : .500000  
Sample concentration g/cm3 : .00050000  
Sample concentration mol/cm3 : .00000002  
Cell path mm : .500000  
Cell path cm : .050000  
Number of residues : 269.000000  
Conversion factor [cm2/dmole] :106792000.00  
-----

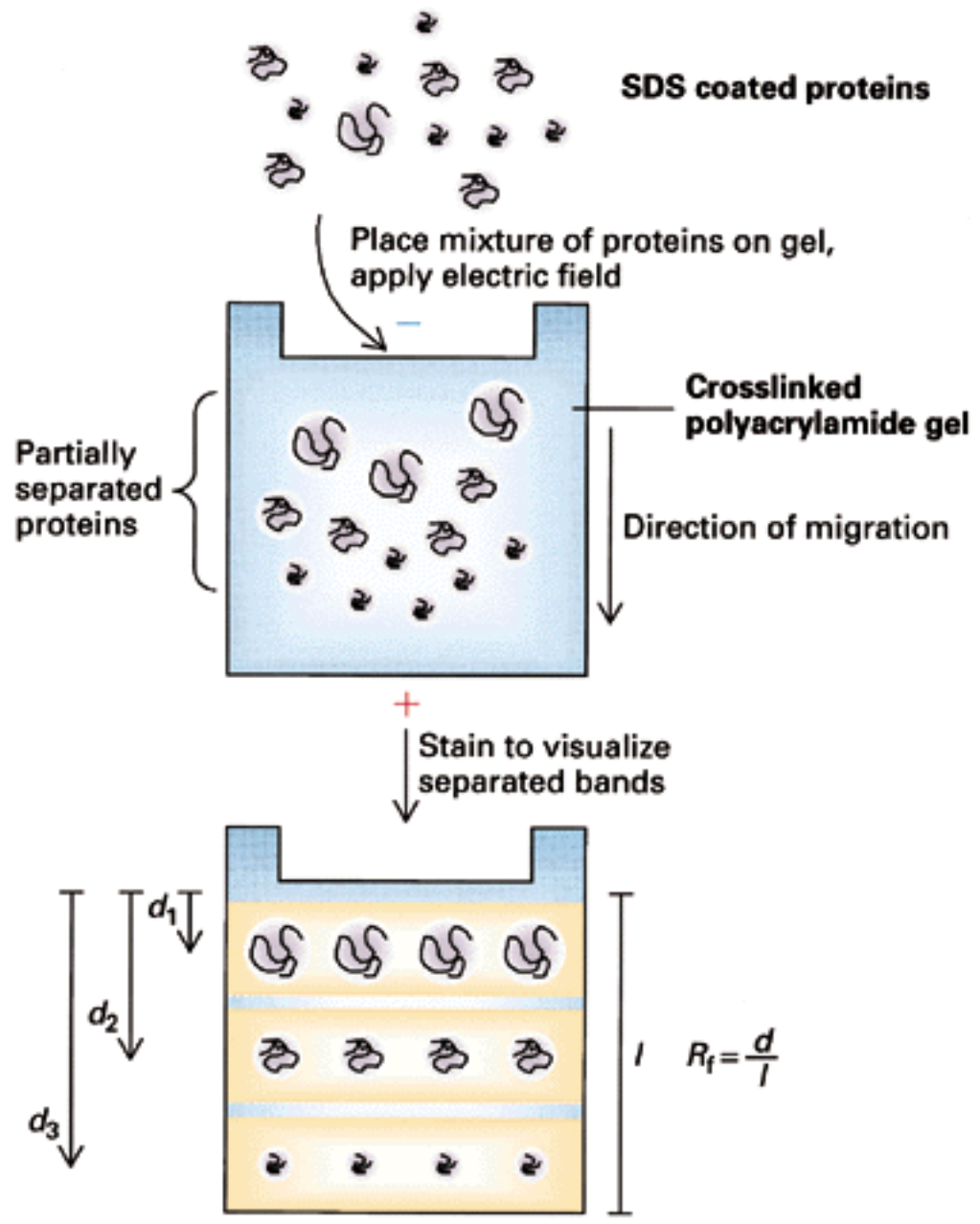
Zero shift applied : 2.

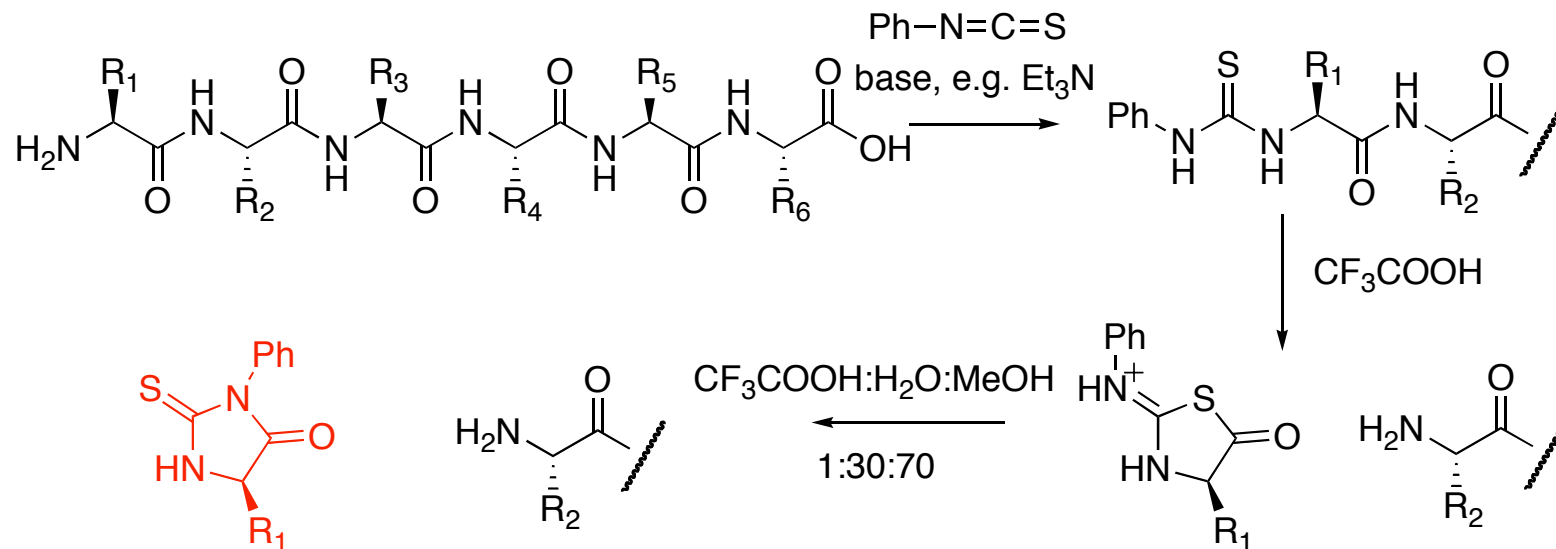
Least squares percentage(s) and scale factor  
57.92 26.22 15.85 .77

rmsd	helix	sheet	coil	scale
68.08	44.58	20.18	12.20	.77
Rfac %	helix	sheet	coil	
3.15	57.92	26.22	15.85	

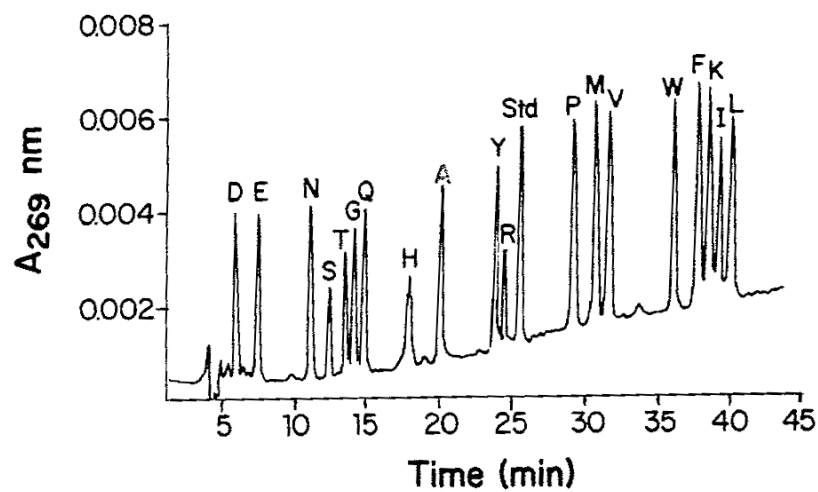
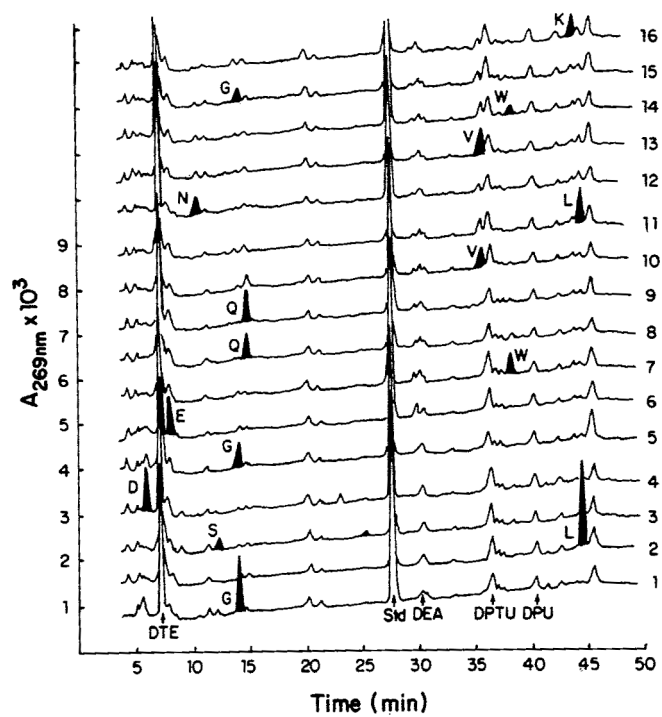
-----

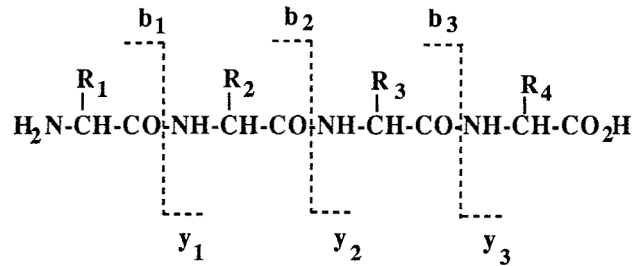
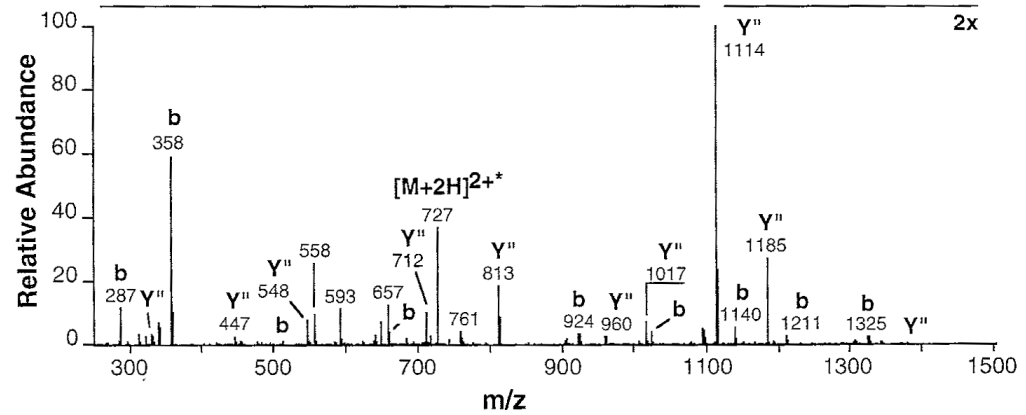






UV detection ~269nm  
by HPLC

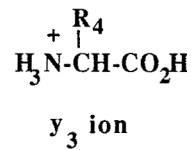
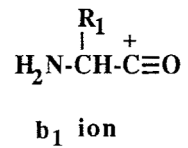




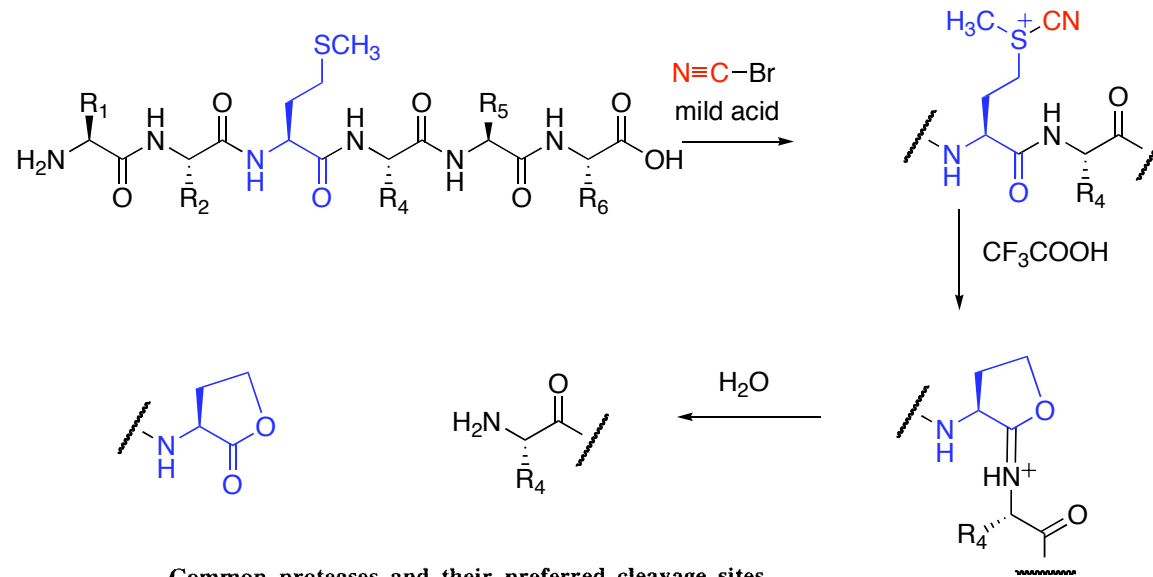
T G Q A P G F T Y D A N K

n	b	Y''	n
0	1.0	1470.7	14
1	102.1	1369.6	13
2	159.1	1312.6	12
3	287.1	1184.6	11
4	358.2	1113.5	10
5	455.2	1016.5	9
6	512.2	959.4	8
7	659.3	812.4	7
8	760.4	711.3	6
9	923.5	548.3	5
10	1024.5	447.2	4
11	1139.5	333.2	3
12	1210.5	261.2	2
13	1324.6	147.1	1
14	1452.7	19.0	0

Examples

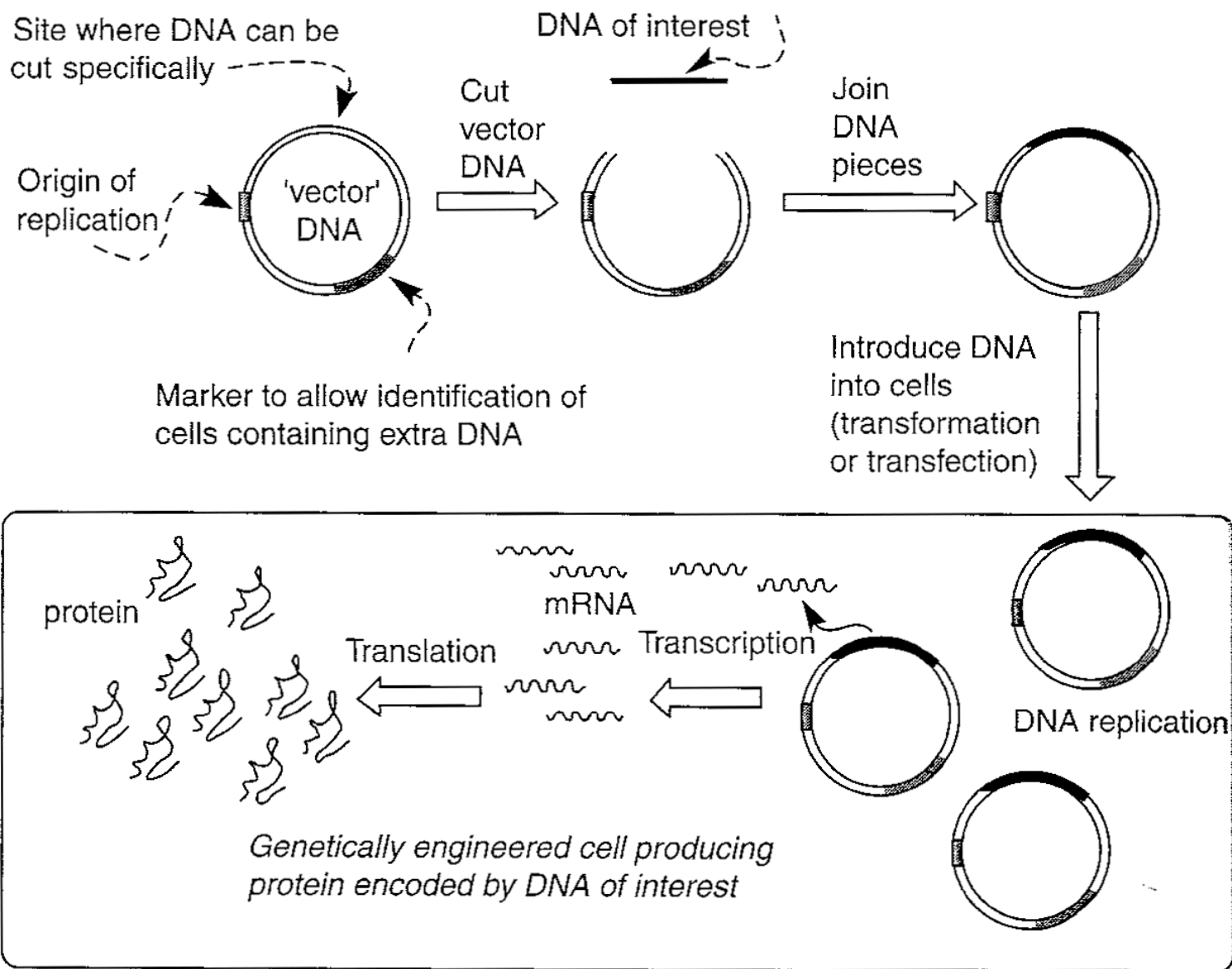


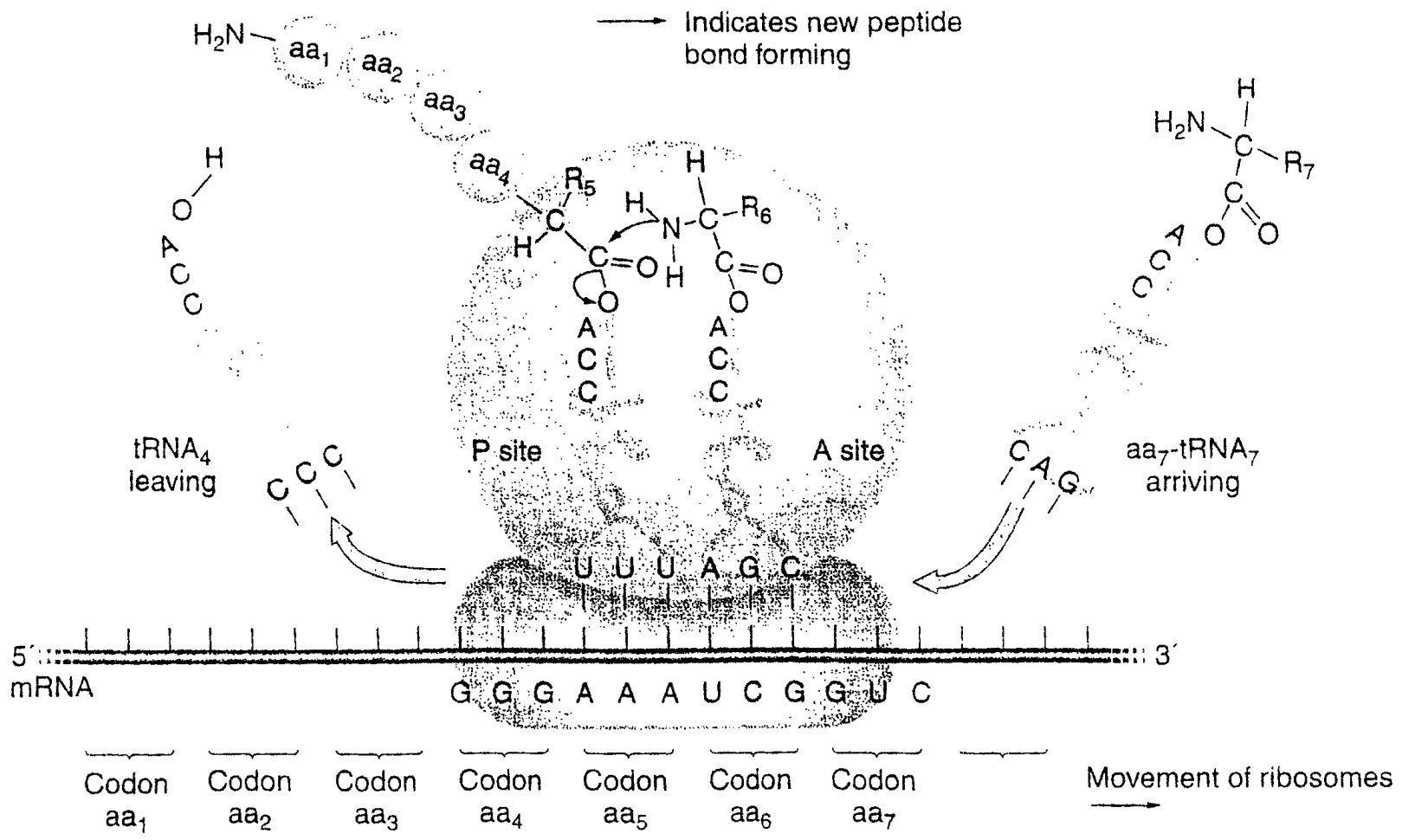
This fragment came from an EndoLys cleavage.  
The  $\text{MH}_2^{2+}$  peak (m/z 727) was 'mass selected'



Common proteases and their preferred cleavage sites.

Protease	Type	Preferred Cleavage Sites
$\alpha$ -chymotrypsin and subtilisins	Ser	-Trp(Tyr,Phe,Leu,Met) $\downarrow$ Xaa-
elastase	Ser	-Ala(Ser,Met,Phe) $\downarrow$ Xaa-
pepsin	Asp	-Phe(Tyr,Leu) $\downarrow$ Leu(Phe)-
thermolysin	metallo	-Phe(Gly,Asp,Leu) $\downarrow$ Leu(Phe)-
papain	Cys	-Phe(Leu,Val)-Xaa $\downarrow$ Xaa-
trypsin	Ser	-Arg(Lys) $\downarrow$ Xaa-
clostripain	Cys	-Arg $\downarrow$ Xaa-
endoprotease Lys-C ( <i>Achromobacter</i> )	Ser	-Lys $\downarrow$ Xaa-
endoprotease Glu-C (V8 protease)	Ser	-Glu (Asp) $\downarrow$ Xaa-
carboxypeptidase Y	Ser	-Xaa $\downarrow$ Xaa-OH
carboxypeptidase B	metallo	-Xaa $\downarrow$ [Arg,Lys]-OH
carboxypeptidase A	metallo	-Xaa $\downarrow$ [Asp,Glu,Phe,Leu]-OH
aminopeptidase M	metallo	$H_2N$ -Xaa $\downarrow$ Xaa-
pyroglutamate-aminopeptidase	Cys	pGlu $\downarrow$ Xaa-
cathepsin C	Cys	$H_2N$ -Xaa-Xaa $\downarrow$ Xaa-
proline iminopeptidase	Ser	Pro $\downarrow$ Xaa-

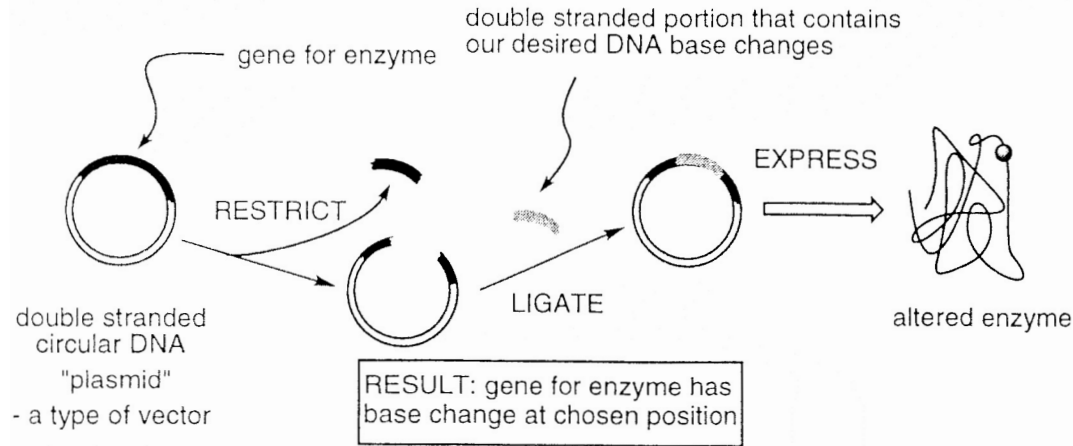




.....|UUU|UUA|GGG|AAA|UUC|GGU|C| ..... → .....|UUU|UUA|GGG|AAA|UGC|GUC| .....  
 ..... Phe Leu Gly Lys Ser Val ..... → ..... Phe Leu Gly Lys Cys Val

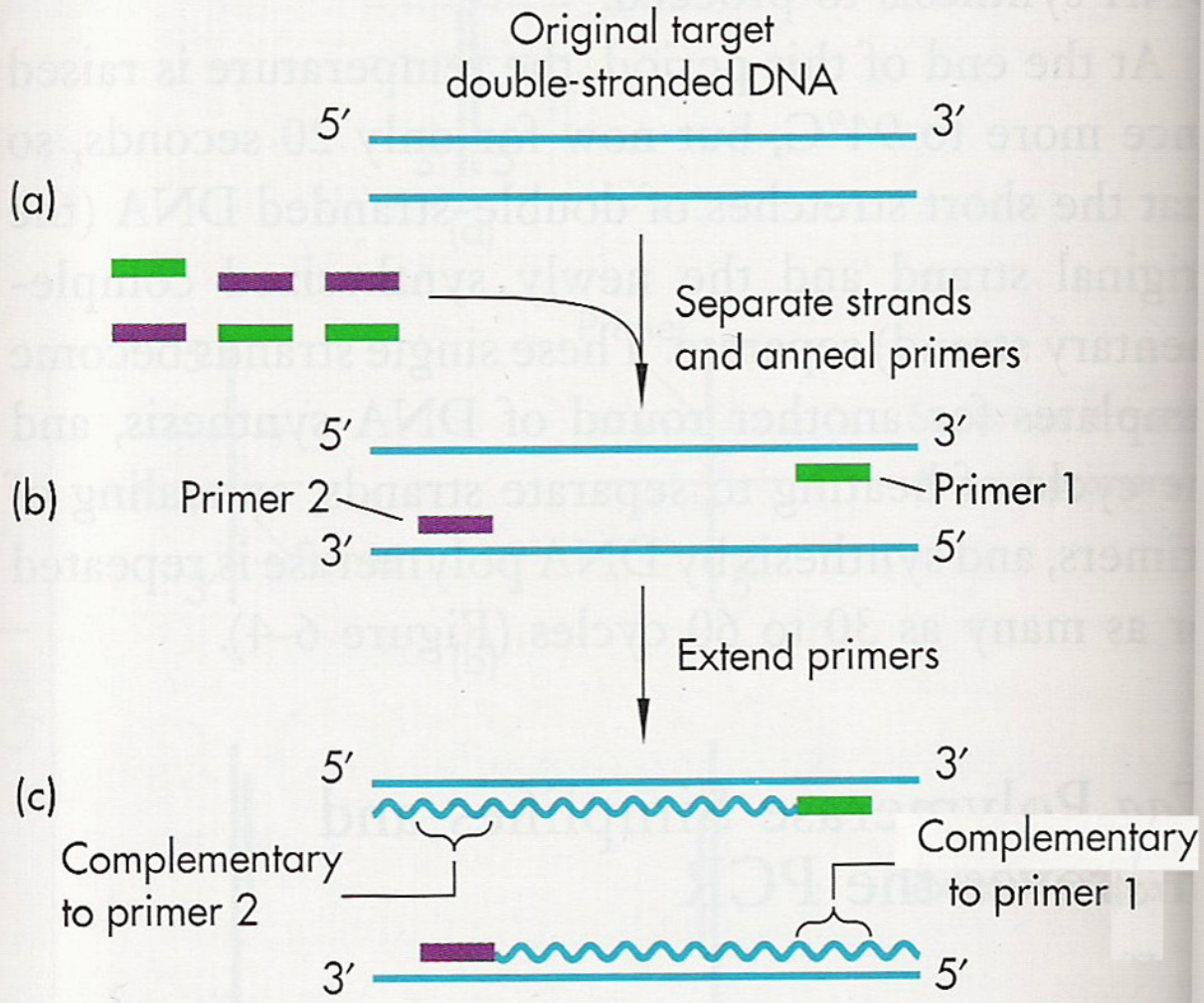


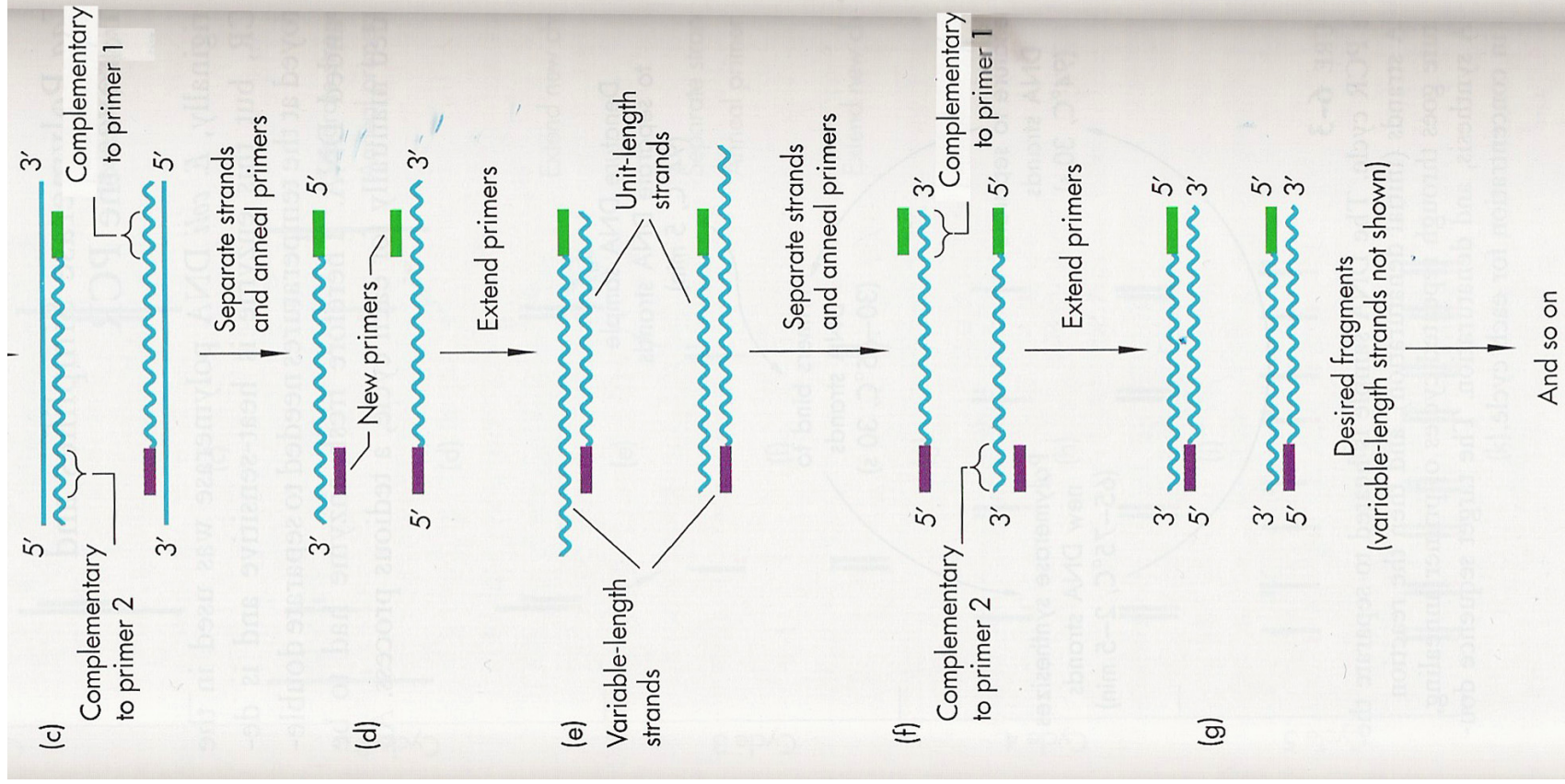
# Site-Directed Mutagenesis



		Second letter							
		U	C	A	G				
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC		UCC		UAC		UGC		C
	UUA	Leu	UCA	Stop	UAA	Stop	UGA	Stop	A
	UUG		UCG		UAG		UGG		Trp
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U
	CUC		CCC		CAC		CGC		C
	CUA	Leu	CCA	Gin	CAA	Gin	CGA	Arg	A
	CUG		CCG		CAG		CGG		G
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	U
	AUC		ACC		AAC		AGC		C
	AUA	Met	ACA	Lys	AAA	Lys	AGA	Arg	A
	AUG		ACG		AAG		AGG		G
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	U
	GUC		GCC		GAC		GGC		C
	GUA	Val	GCA	Glu	GAA	Glu	GGA	Gly	A
	GUG		GCG		GAG		GGG		G

# Amplification of target sequence

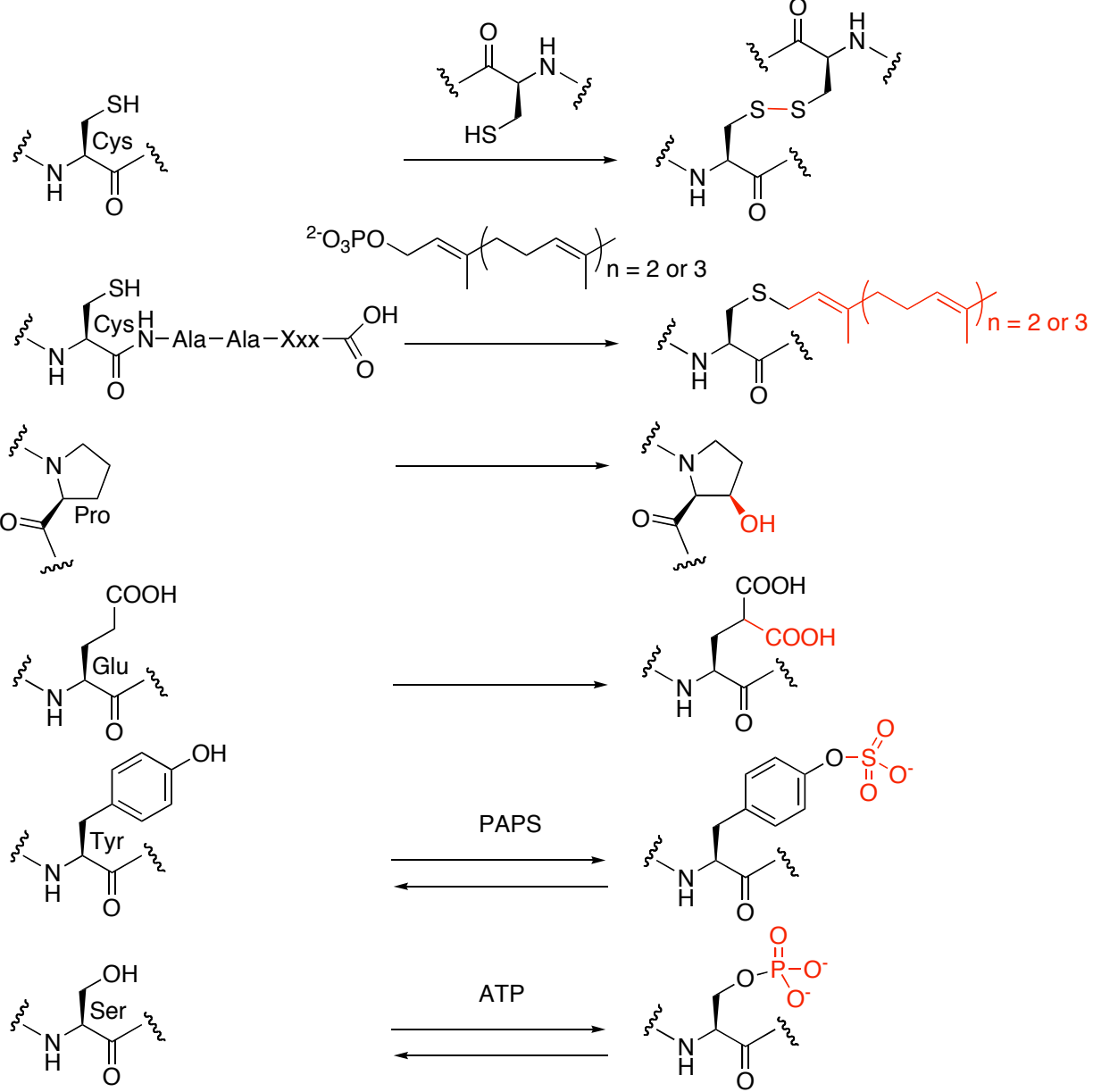






**PROTEIN**

**PROTEIN with PTM**



PROTEIN

PROTEIN with **PTM**

